



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:22 PM GMT

PDB ID : 4V4K  
Title : Bacteriophage P22 Portal Protein bound to middle Tail Factor GP4. This file contain the second biological assembly  
Authors : Olia, A.S.; Cingolani, G.  
Deposited on : 2010-04-19  
Resolution : 3.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

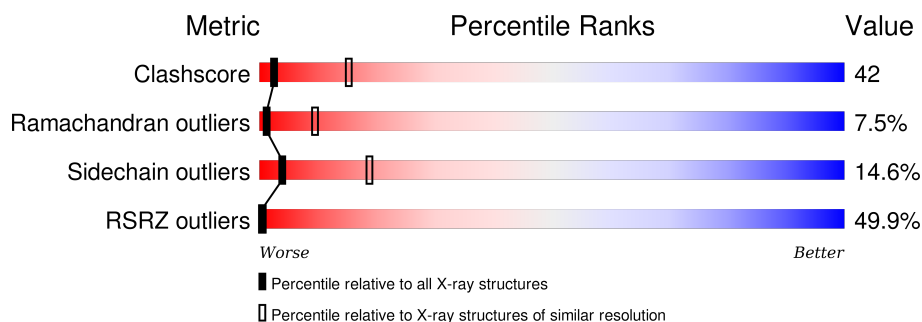
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1806 (3.32-3.20)
Ramachandran outliers	100387	1773 (3.32-3.20)
Sidechain outliers	100360	1771 (3.32-3.20)
RSRZ outliers	91569	1632 (3.32-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	602	<div> <div>48%</div> <div>38% 44% 12% • 5%</div> </div>
1	B	602	<div> <div>52%</div> <div>38% 44% 12% • 5%</div> </div>
1	C	602	<div> <div>50%</div> <div>37% 45% 12% • 5%</div> </div>
1	D	602	<div> <div>44%</div> <div>38% 44% 12% • 5%</div> </div>
1	E	602	<div> <div>47%</div> <div>38% 45% 12% • 5%</div> </div>
1	F	602	<div> <div>44%</div> <div>38% 43% 12% • 5%</div> </div>
1	G	602	<div> <div>46%</div> <div>38% 44% 12% • 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	H	602	
1	I	602	
1	J	602	
1	K	602	
1	L	602	
1	M	602	
1	N	602	
1	O	602	
1	P	602	
1	Q	602	
1	R	602	
1	S	602	
1	T	602	
1	U	602	
1	V	602	
1	W	602	
1	X	602	
2	Y	166	
2	Z	166	
2	a	166	
2	b	166	
2	c	166	
2	d	166	
2	e	166	
2	f	166	

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Mol	Chain	Length	Quality of chain
2	g	166	
2	h	166	
2	i	166	
2	j	166	
2	k	166	
2	l	166	
2	m	166	
2	n	166	
2	o	166	
2	p	166	
2	q	166	
2	r	166	
2	s	166	
2	t	166	
2	u	166	
2	v	166	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 135120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PORTAL PROTEIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	M	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	N	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	O	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	P	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	Q	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	R	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	S	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	T	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	U	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	V	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	W	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	X	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	A	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	B	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	C	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	D	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	F	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	G	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	H	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	I	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	J	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	K	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	L	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

- Molecule 2 is a protein called PACKAGED DNA STABILIZATION PROTEIN GP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	k	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	l	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	m	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	n	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	o	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	p	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	q	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	r	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	s	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	t	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	u	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	v	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	Y	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	Z	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	a	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	b	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	c	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	d	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	e	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	f	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	g	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	h	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	i	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	j	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
l	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
m	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
n	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
o	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
p	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
q	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
r	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
s	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
t	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
u	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
v	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
Y	150	PRO	ALA	ENGINEERED	UNP P26746

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	150	PRO	ALA	ENGINEERED	UNP P26746
a	150	PRO	ALA	ENGINEERED	UNP P26746
b	150	PRO	ALA	ENGINEERED	UNP P26746
c	150	PRO	ALA	ENGINEERED	UNP P26746
d	150	PRO	ALA	ENGINEERED	UNP P26746
e	150	PRO	ALA	ENGINEERED	UNP P26746
f	150	PRO	ALA	ENGINEERED	UNP P26746
g	150	PRO	ALA	ENGINEERED	UNP P26746
h	150	PRO	ALA	ENGINEERED	UNP P26746
i	150	PRO	ALA	ENGINEERED	UNP P26746
j	150	PRO	ALA	ENGINEERED	UNP P26746

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	M	21	Total O 21 21	0	0
3	N	21	Total O 21 21	0	0
3	O	21	Total O 21 21	0	0
3	P	21	Total O 21 21	0	0
3	Q	21	Total O 21 21	0	0
3	R	21	Total O 21 21	0	0
3	S	21	Total O 21 21	0	0
3	T	21	Total O 21 21	0	0
3	U	21	Total O 21 21	0	0
3	V	21	Total O 21 21	0	0
3	W	21	Total O 21 21	0	0
3	X	21	Total O 21 21	0	0
3	A	22	Total O 22 22	0	0
3	B	22	Total O 22 22	0	0

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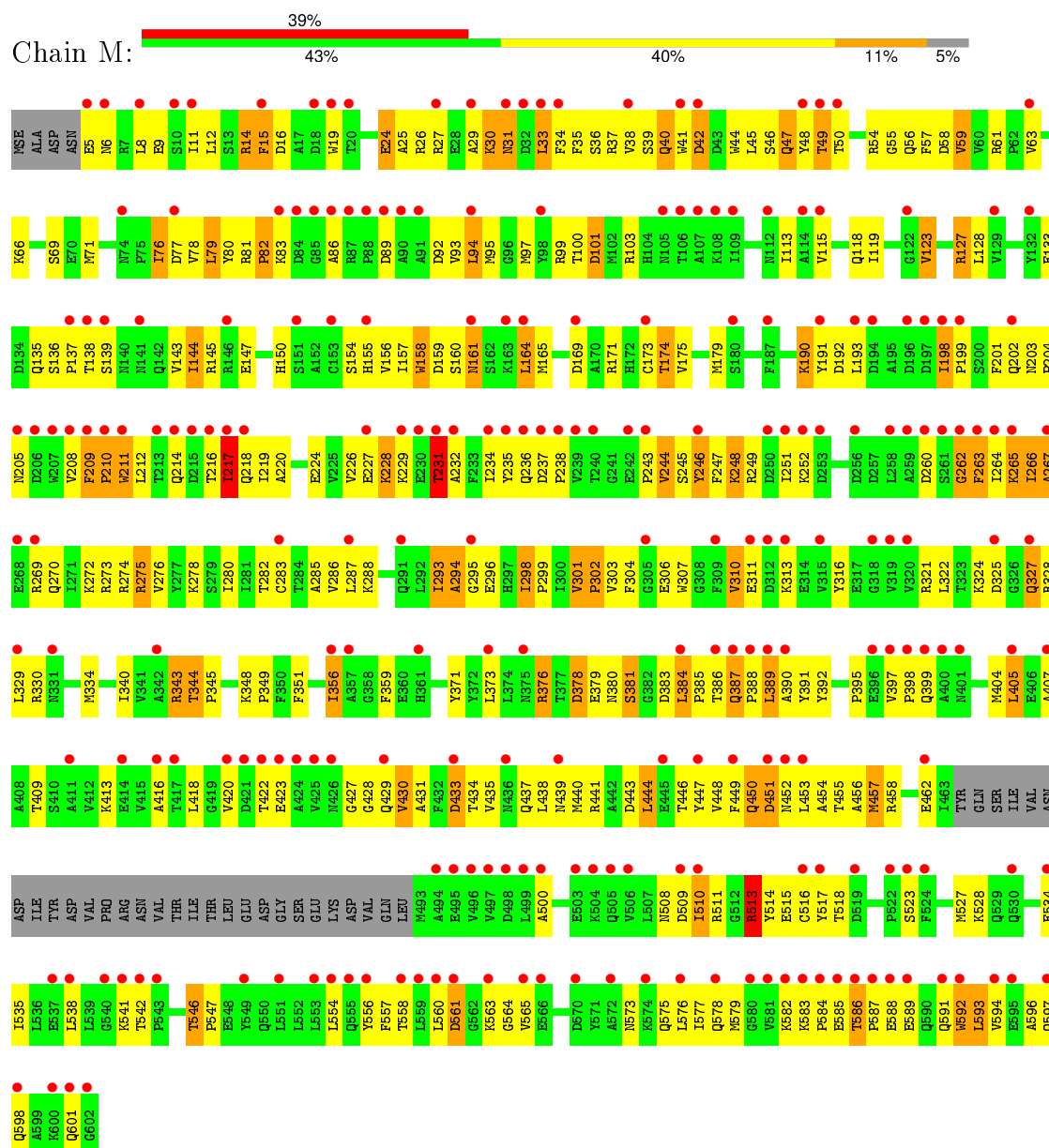
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	22	Total 22	O 22	0	0
3	D	22	Total 22	O 22	0	0
3	E	22	Total 22	O 22	0	0
3	F	22	Total 22	O 22	0	0
3	G	22	Total 22	O 22	0	0
3	H	22	Total 22	O 22	0	0
3	I	22	Total 22	O 22	0	0
3	J	22	Total 22	O 22	0	0
3	K	22	Total 22	O 22	0	0
3	L	22	Total 22	O 22	0	0

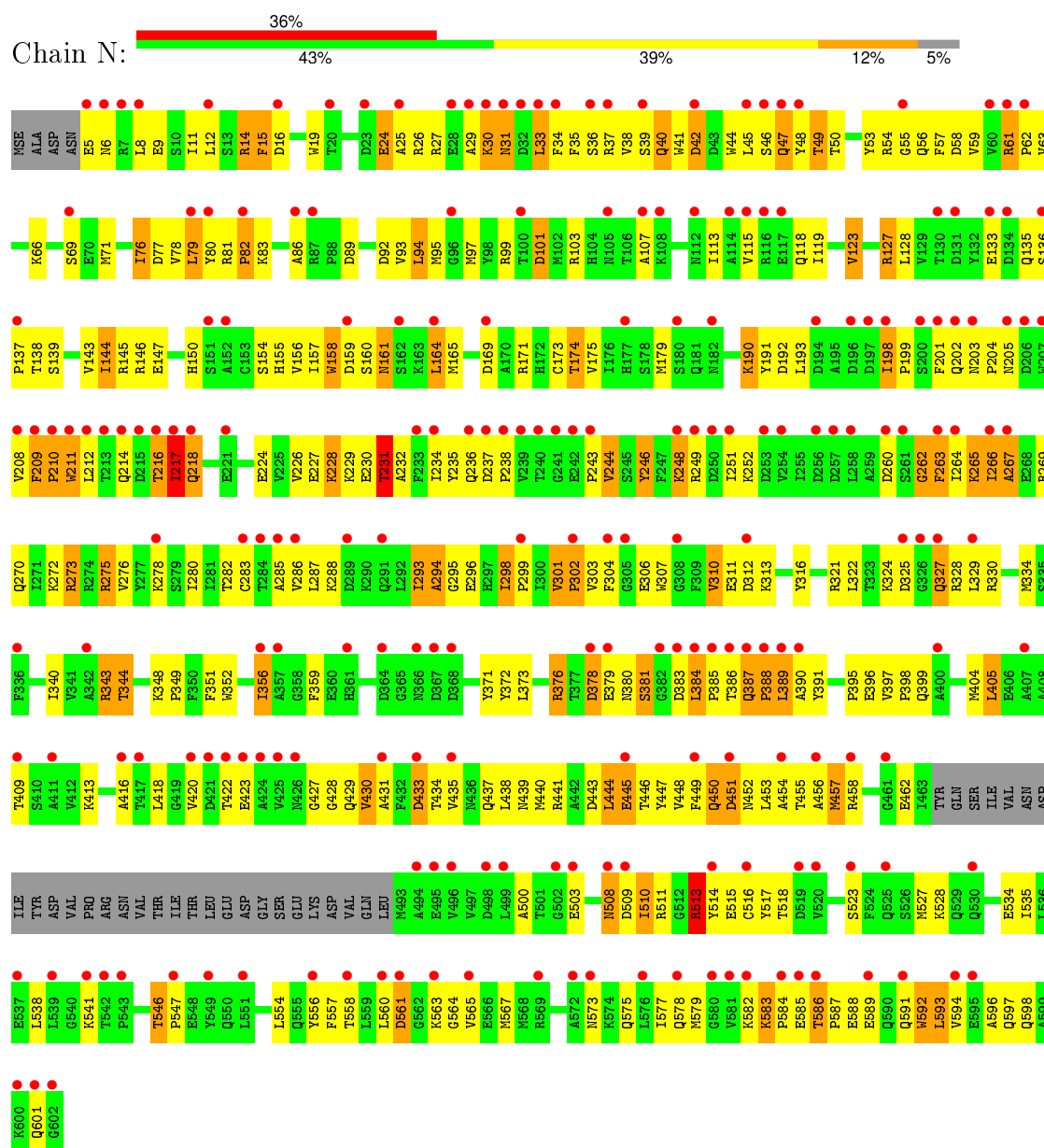
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

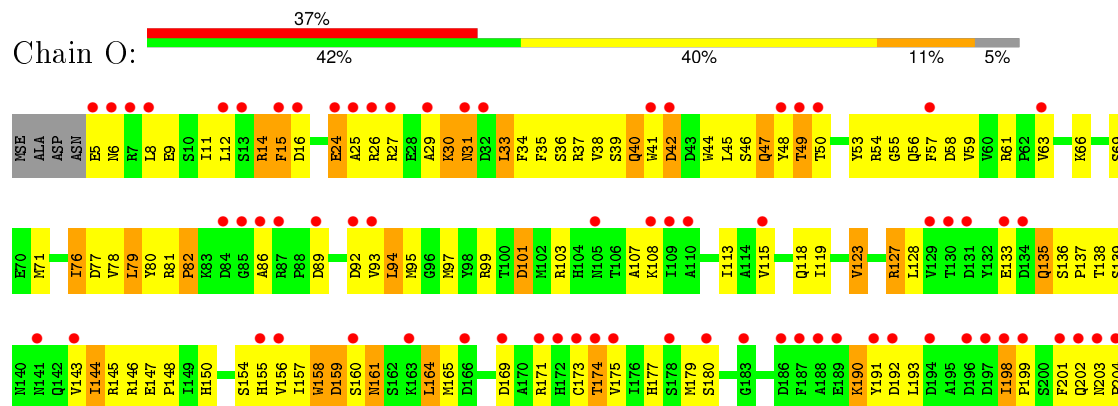
#### • Molecule 1: PORTAL PROTEIN



#### • Molecule 1: PORTAL PROTEIN



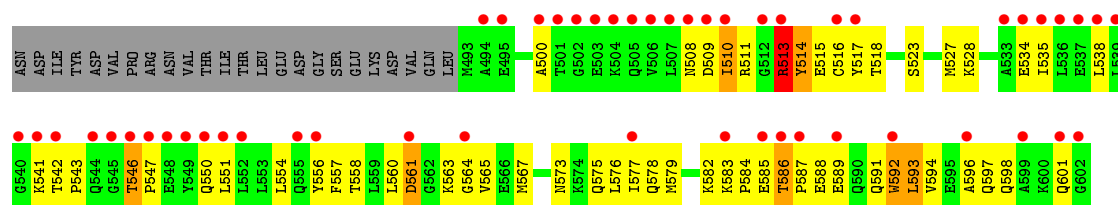
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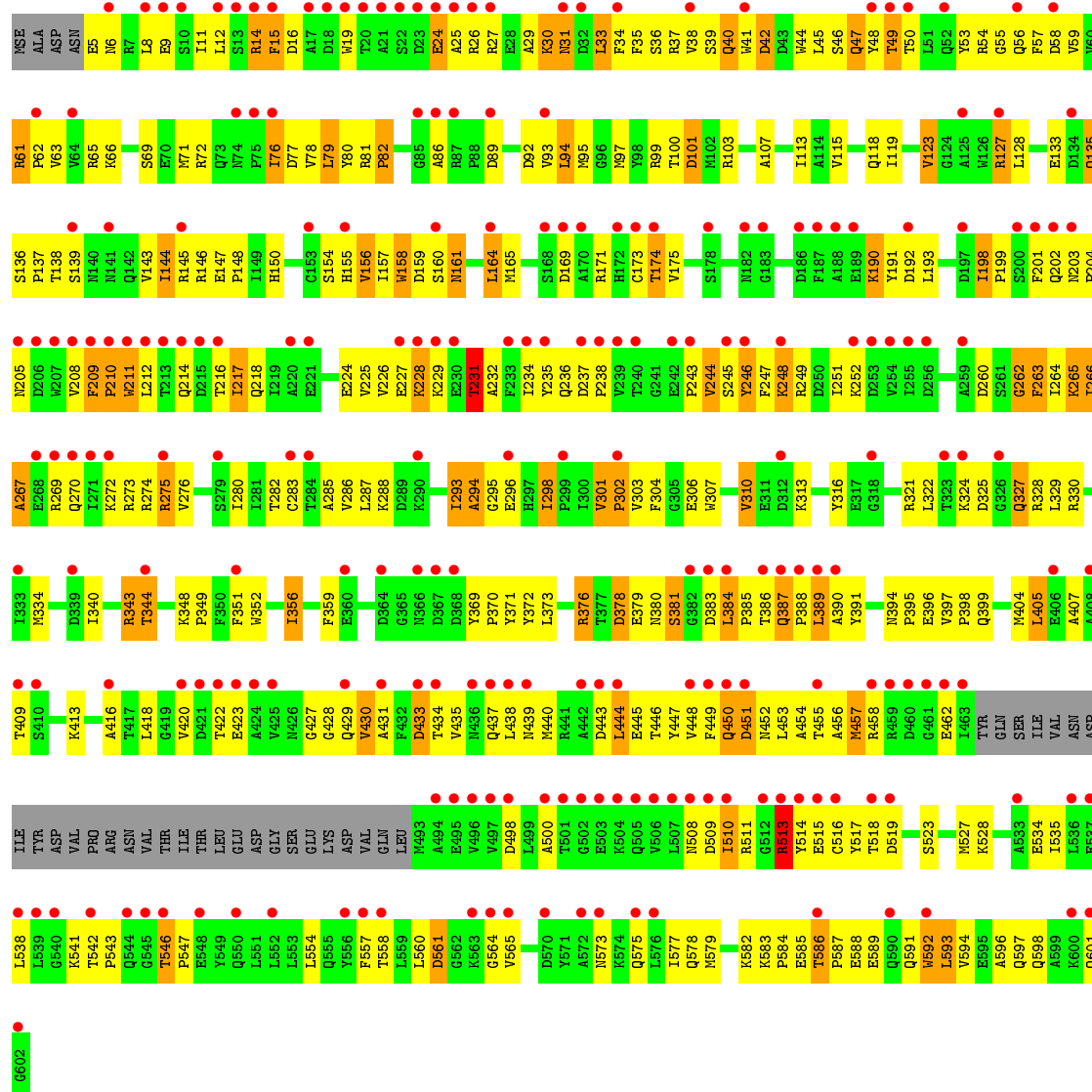
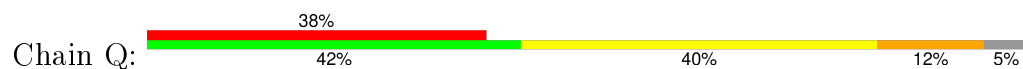


Entity	Percentage
U.S.	39%
U.S. and its allies	42%

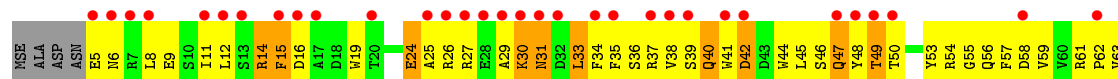


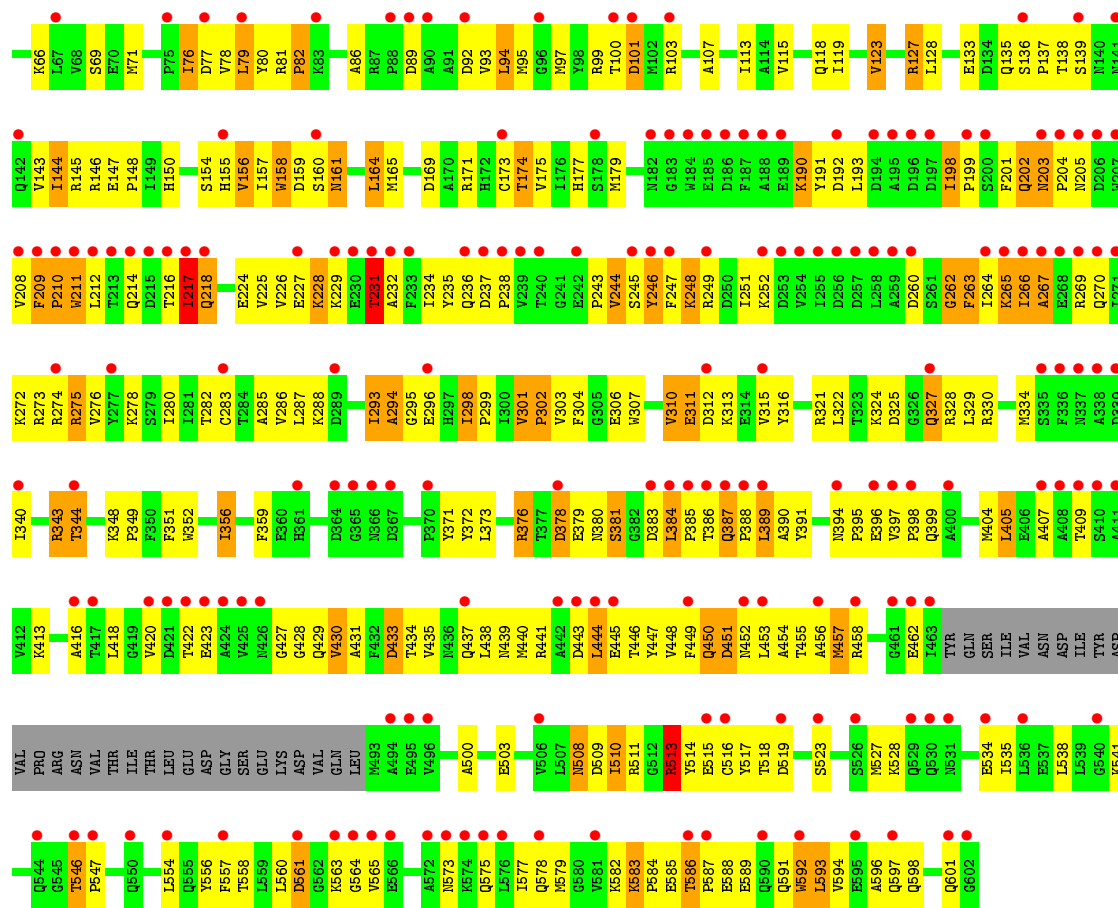


### • Molecule 1: PORTAL PROTEIN

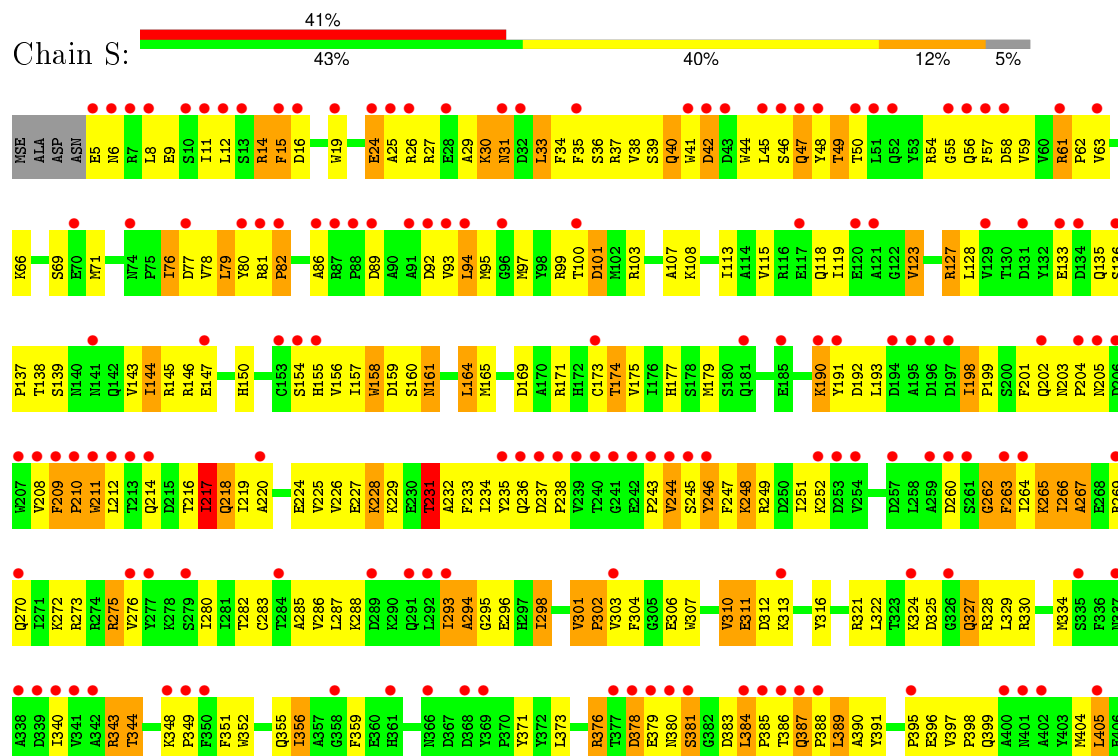


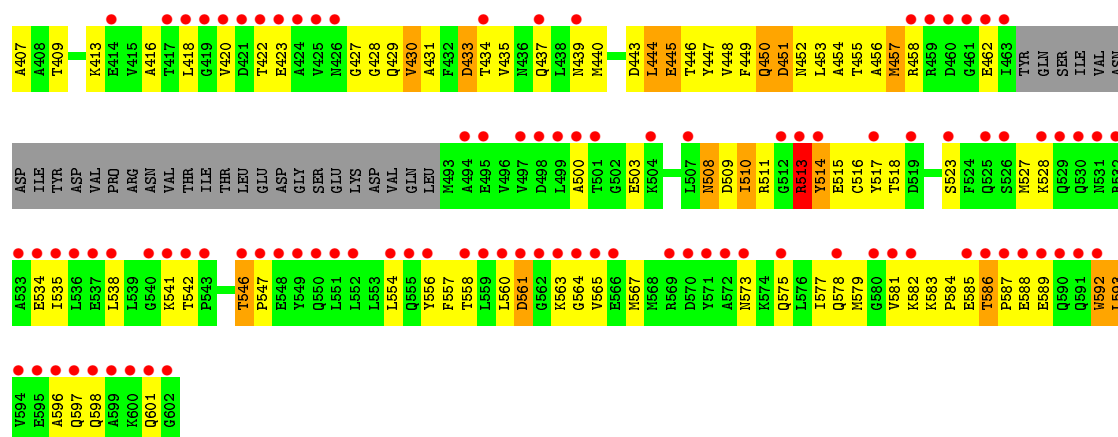
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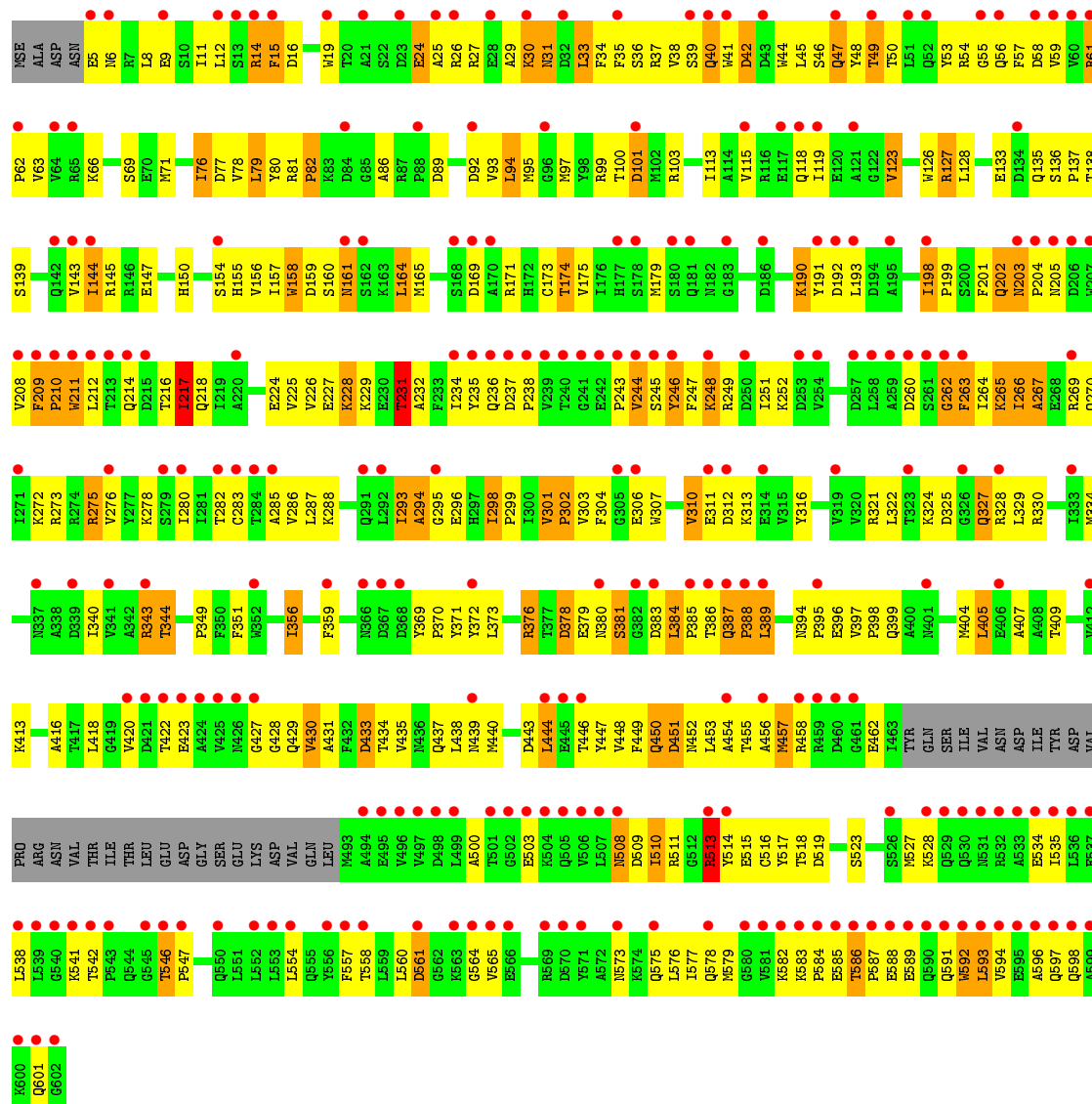
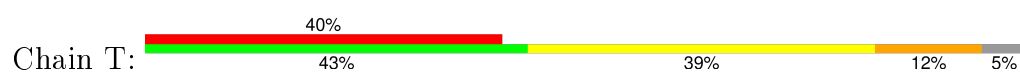


- Molecule 1: PORTAL PROTEIN

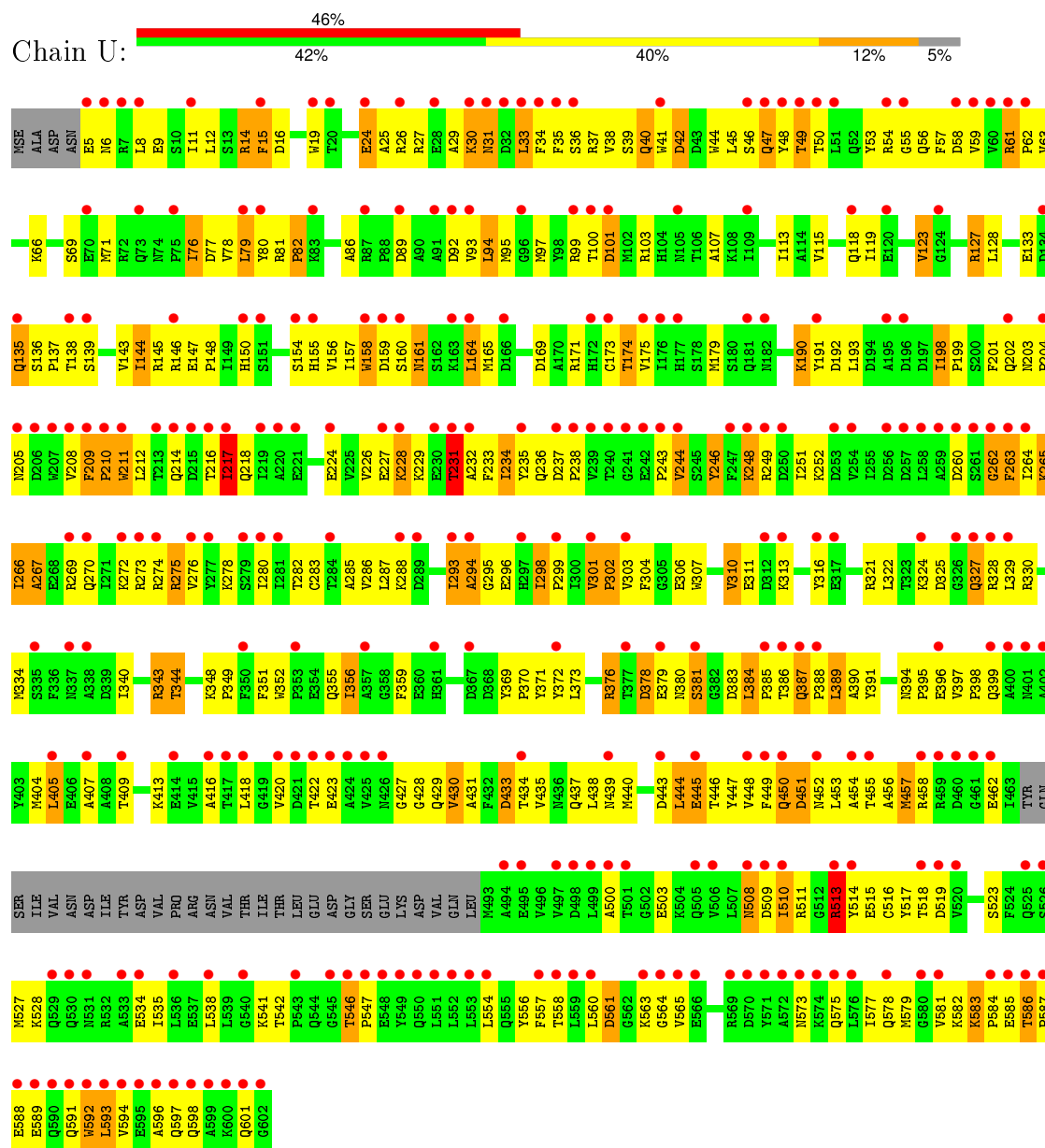




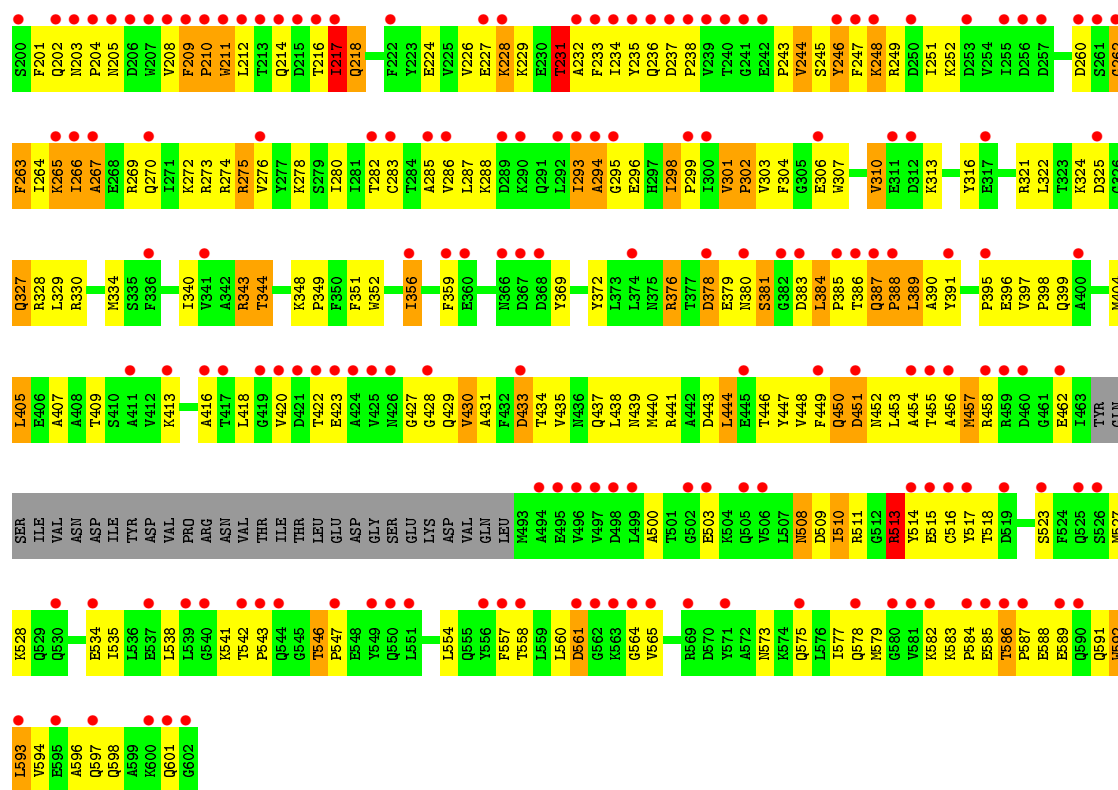
### • Molecule 1: PORTAL PROTEIN



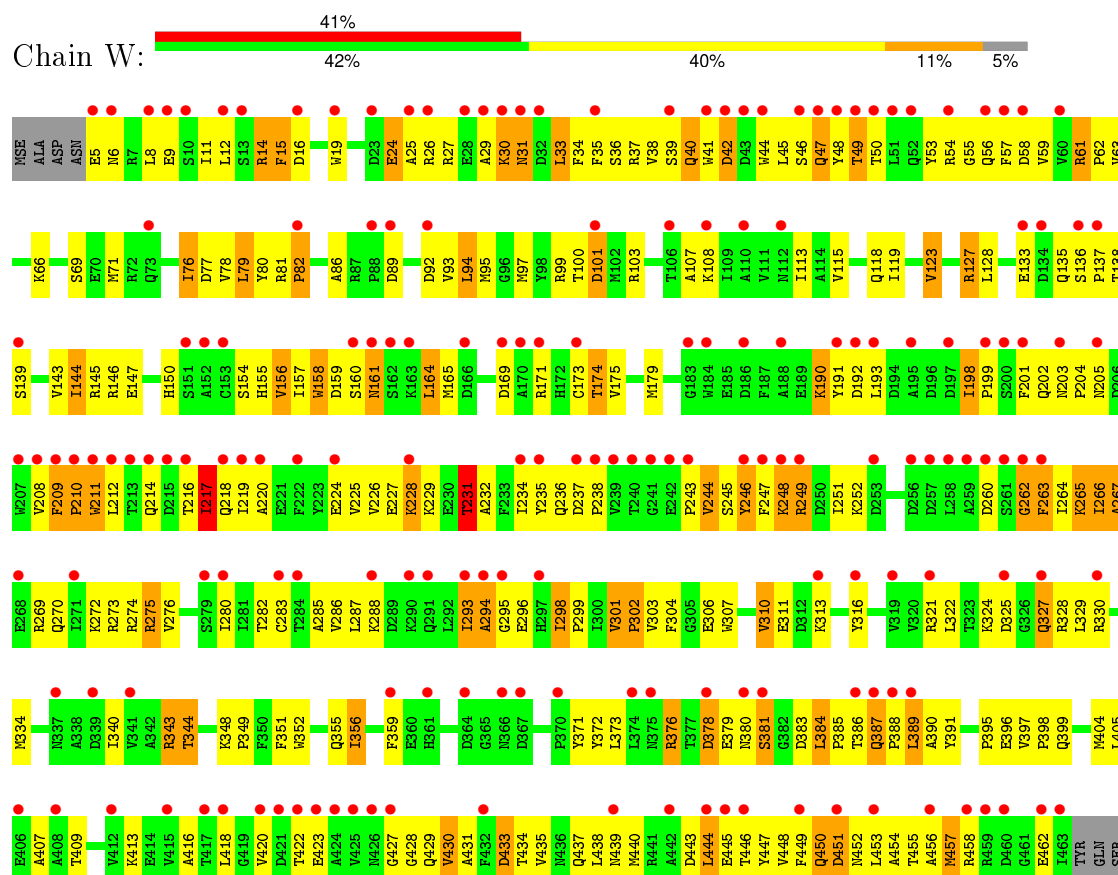
• Molecule 1: PORTAL PROTEIN

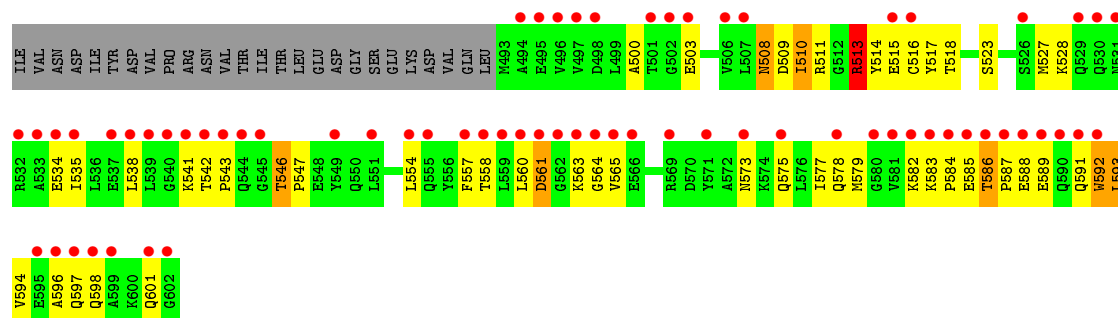




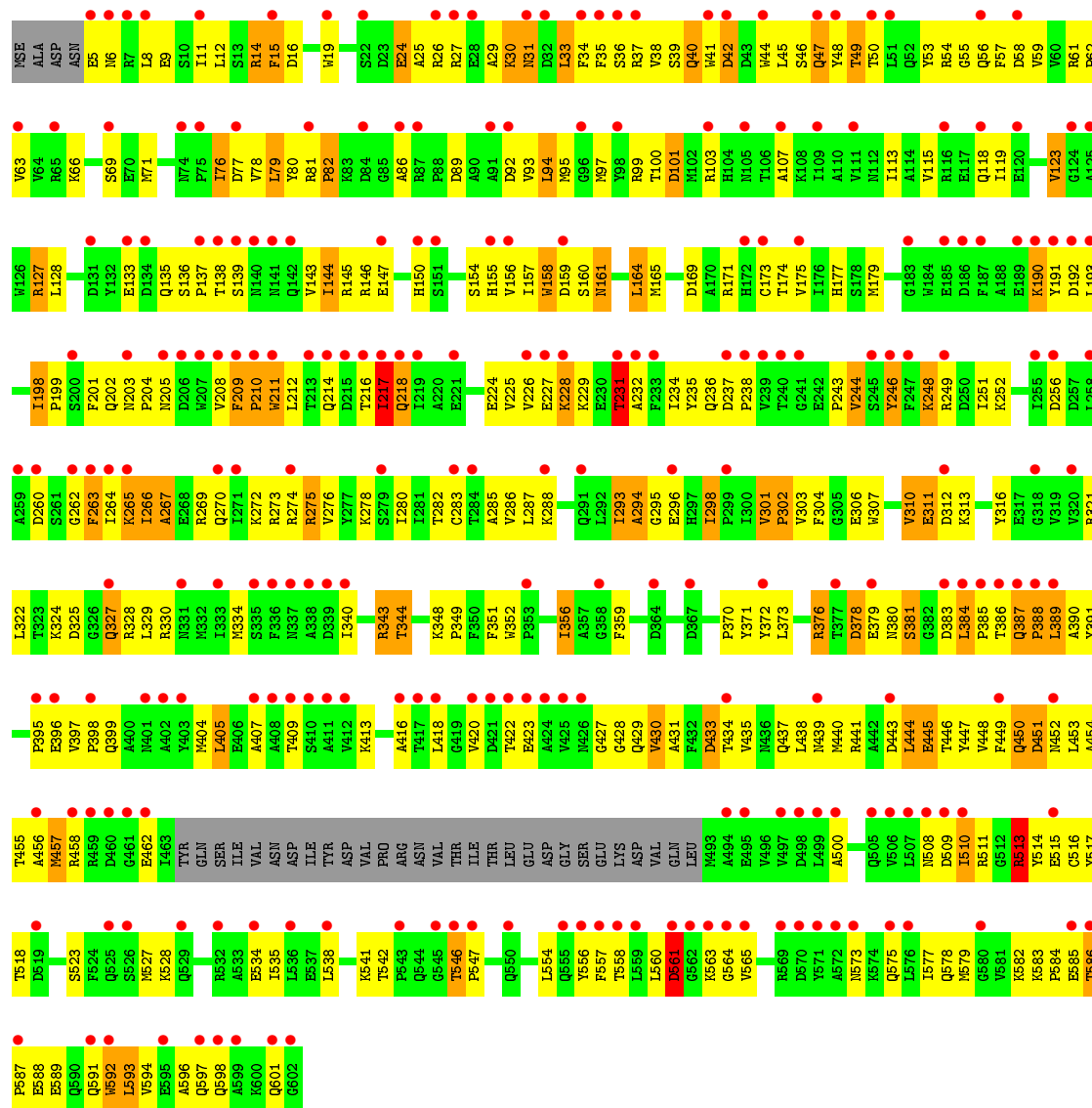
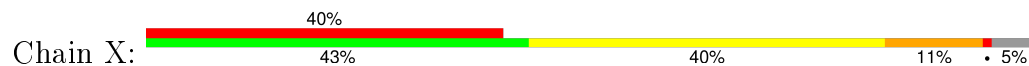


### • Molecule 1: PORTAL PROTEIN

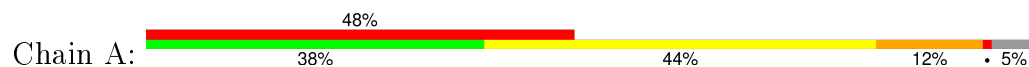


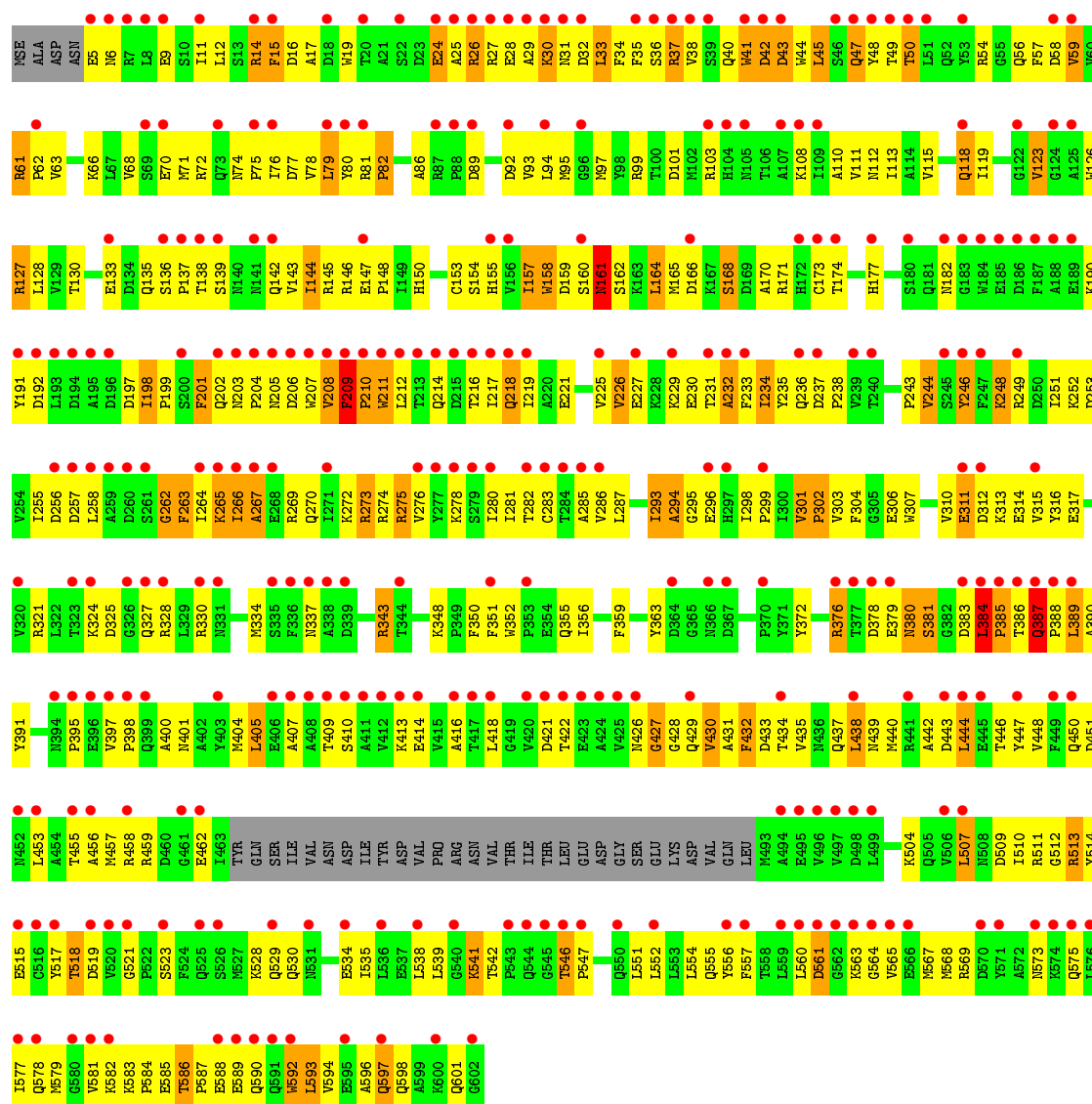


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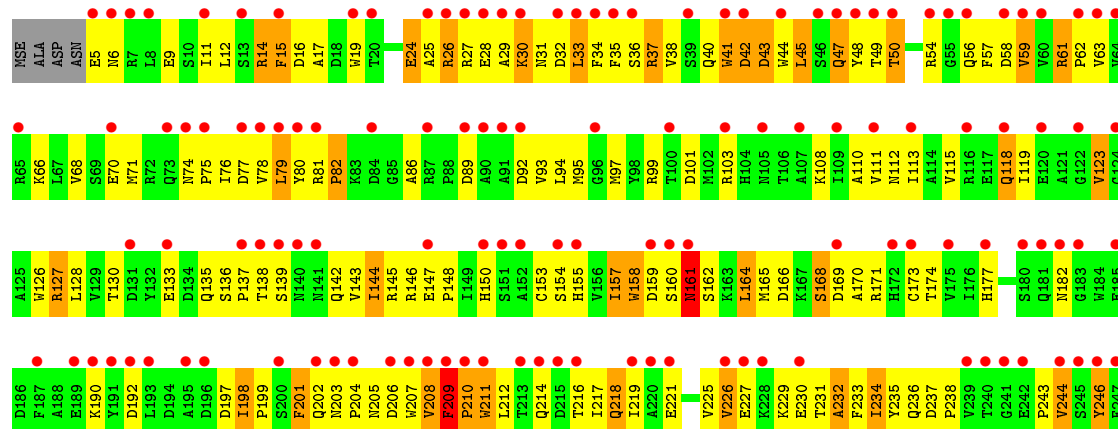
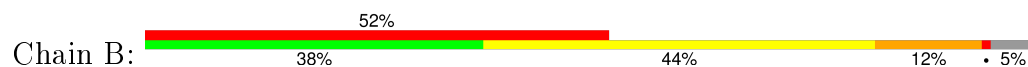


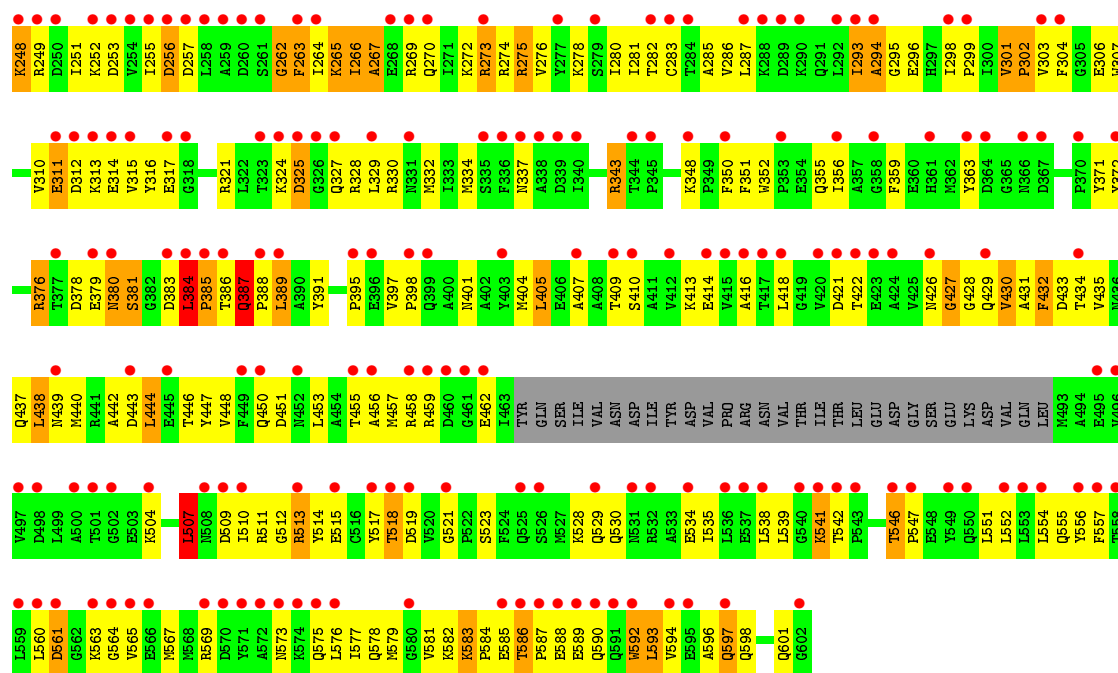
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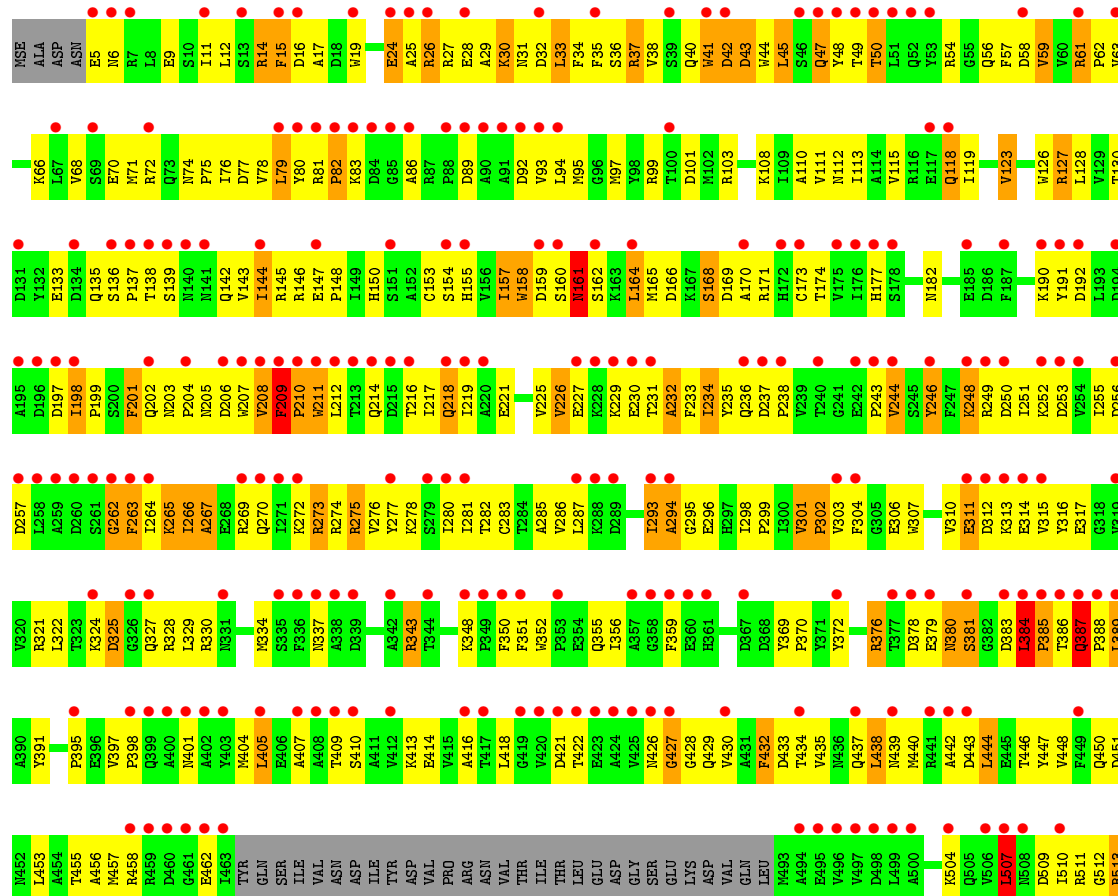


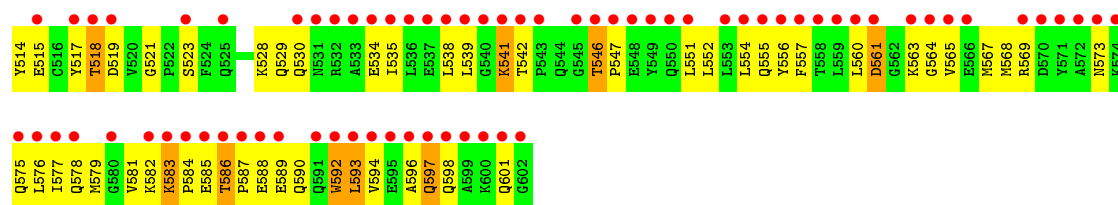
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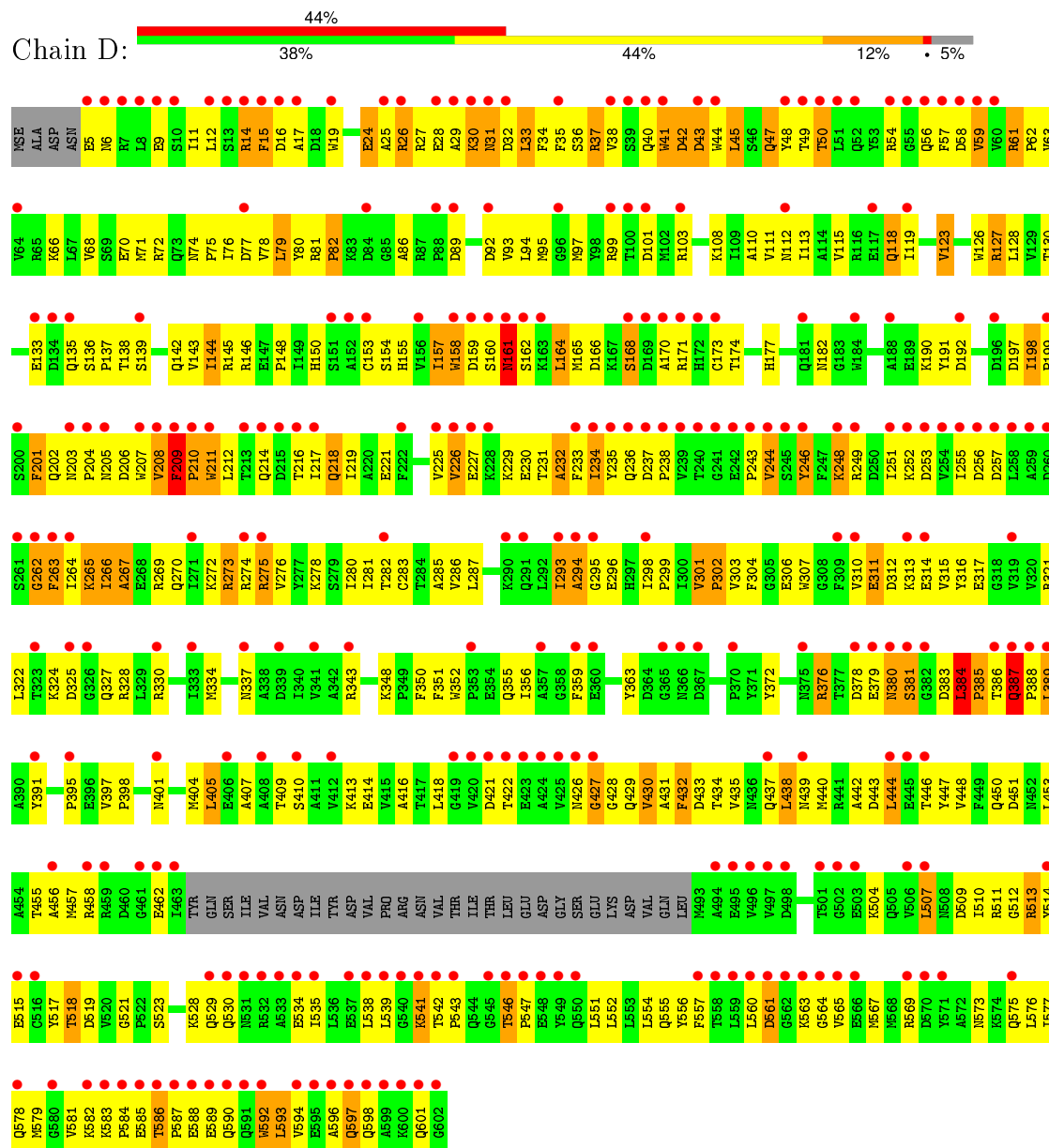


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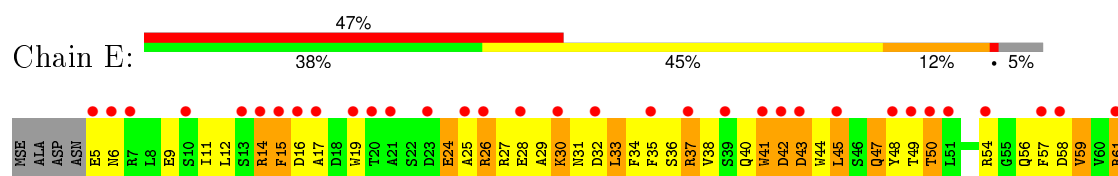


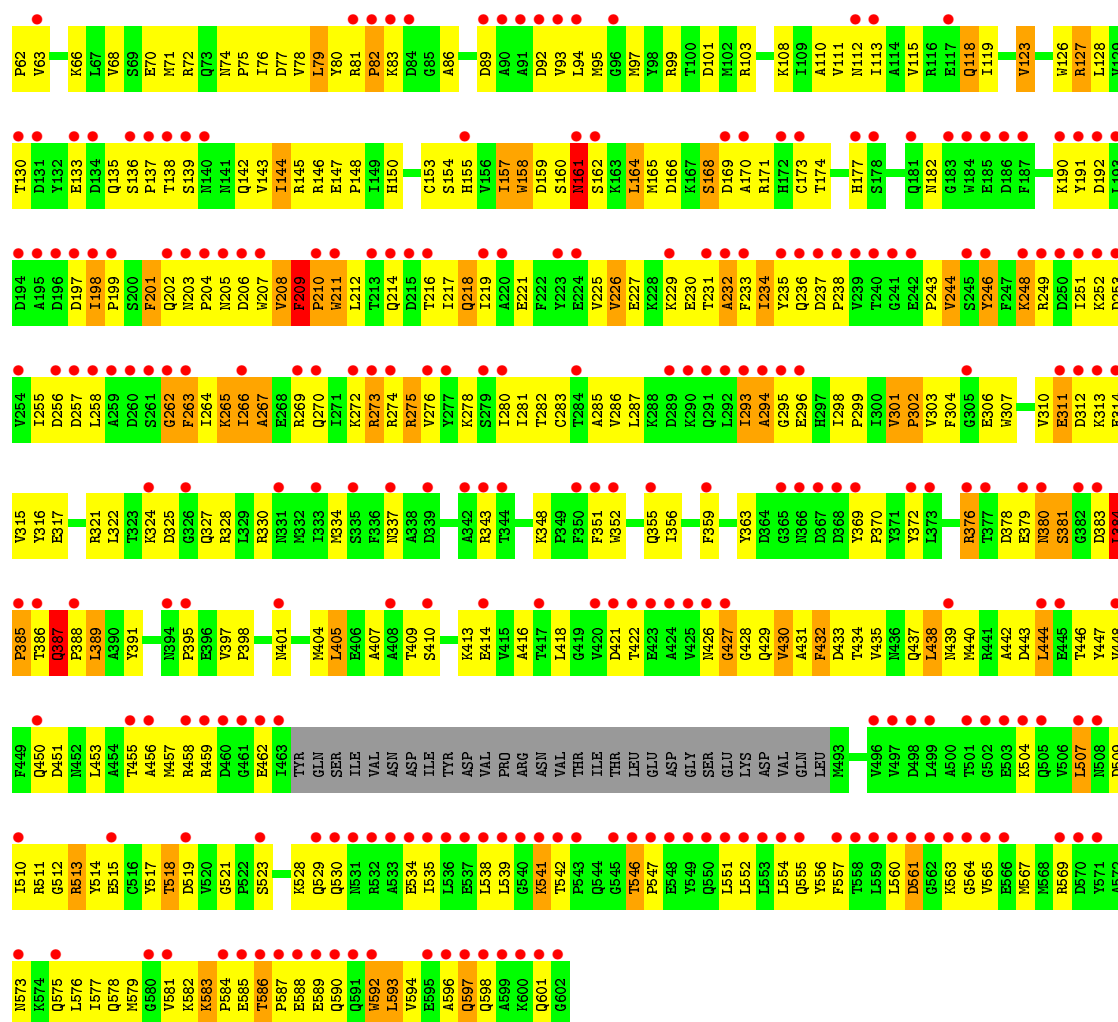


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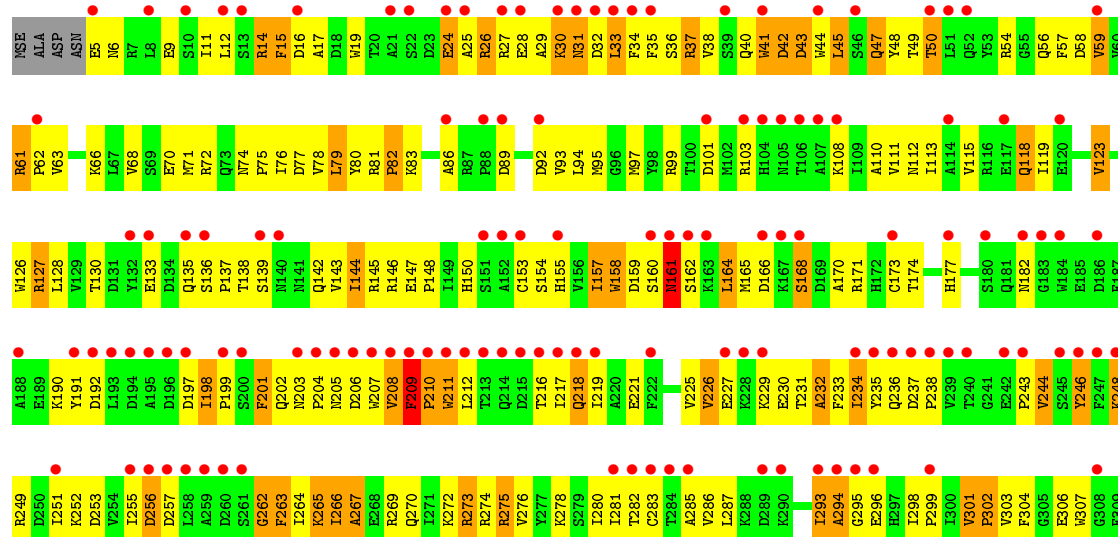
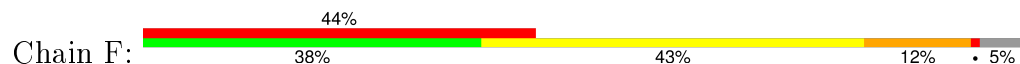


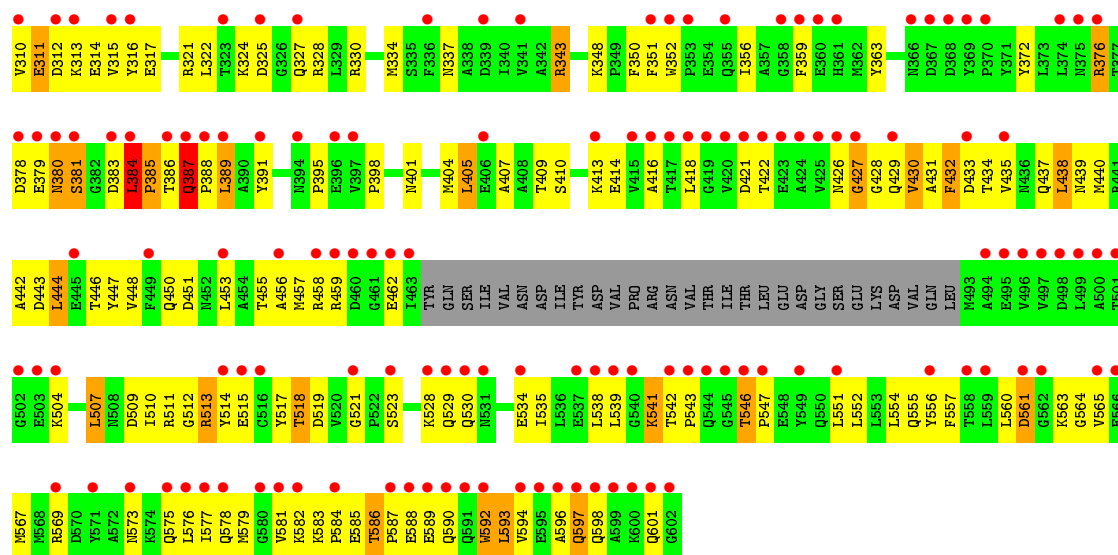
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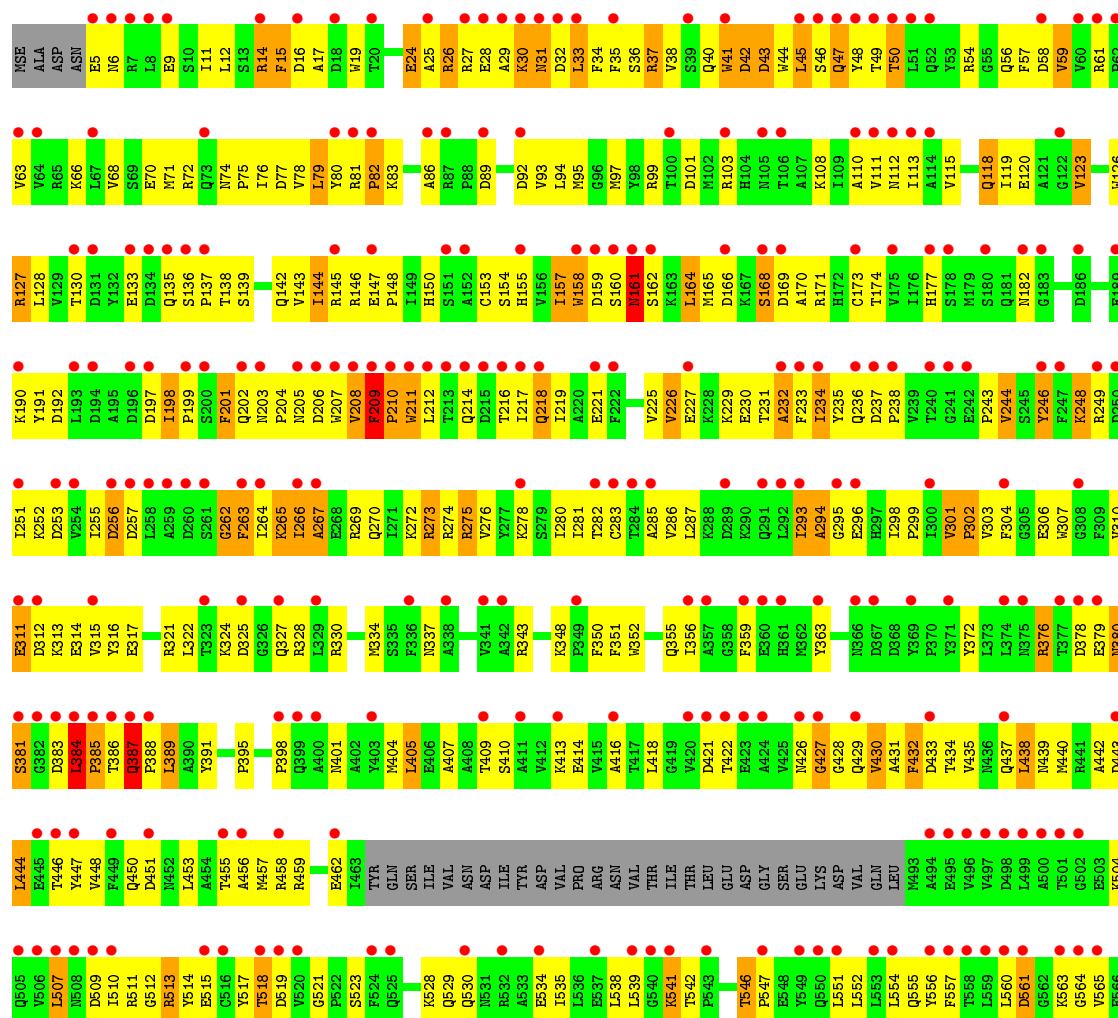


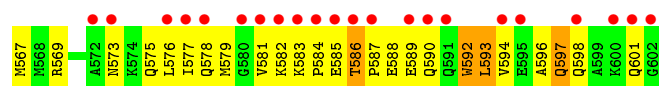
- Molecule 1: PORTAL PROTEIN



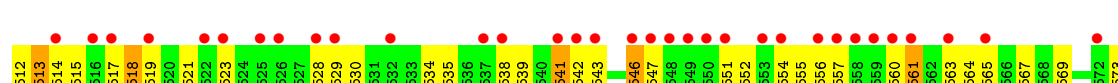
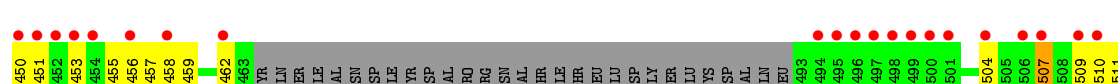
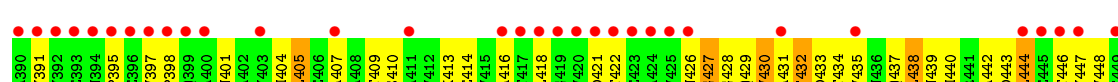
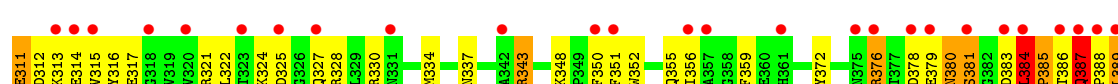
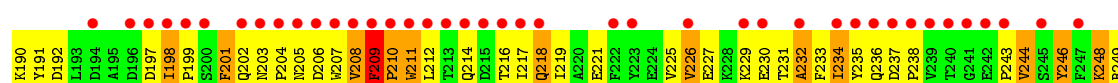
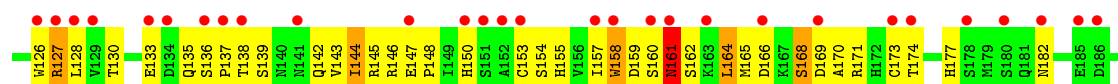
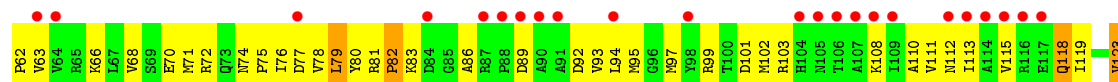
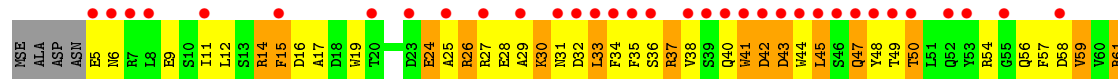


### • Molecule 1: PORTAL PROTEIN

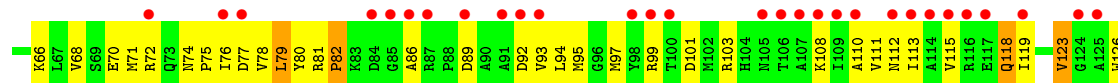
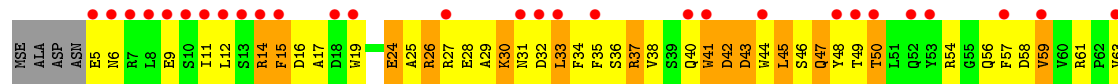




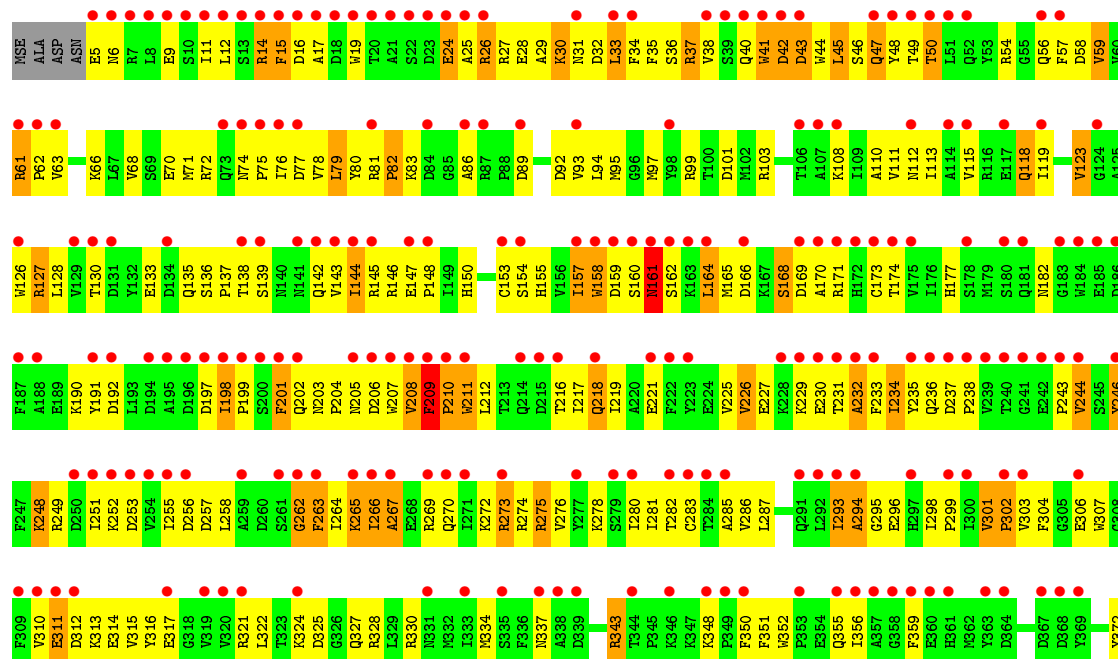
### • Molecule 1: PORTAL PROTEIN

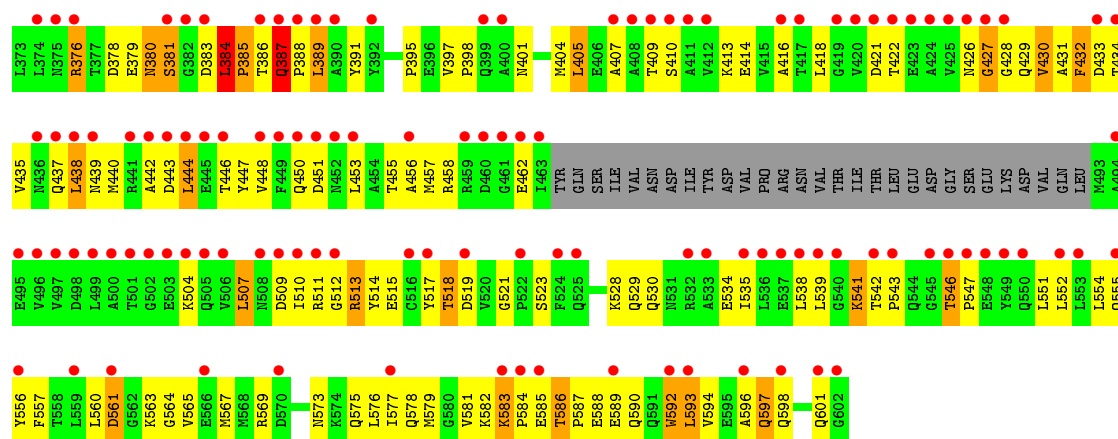


### • Molecule 1: PORTAL PROTEIN

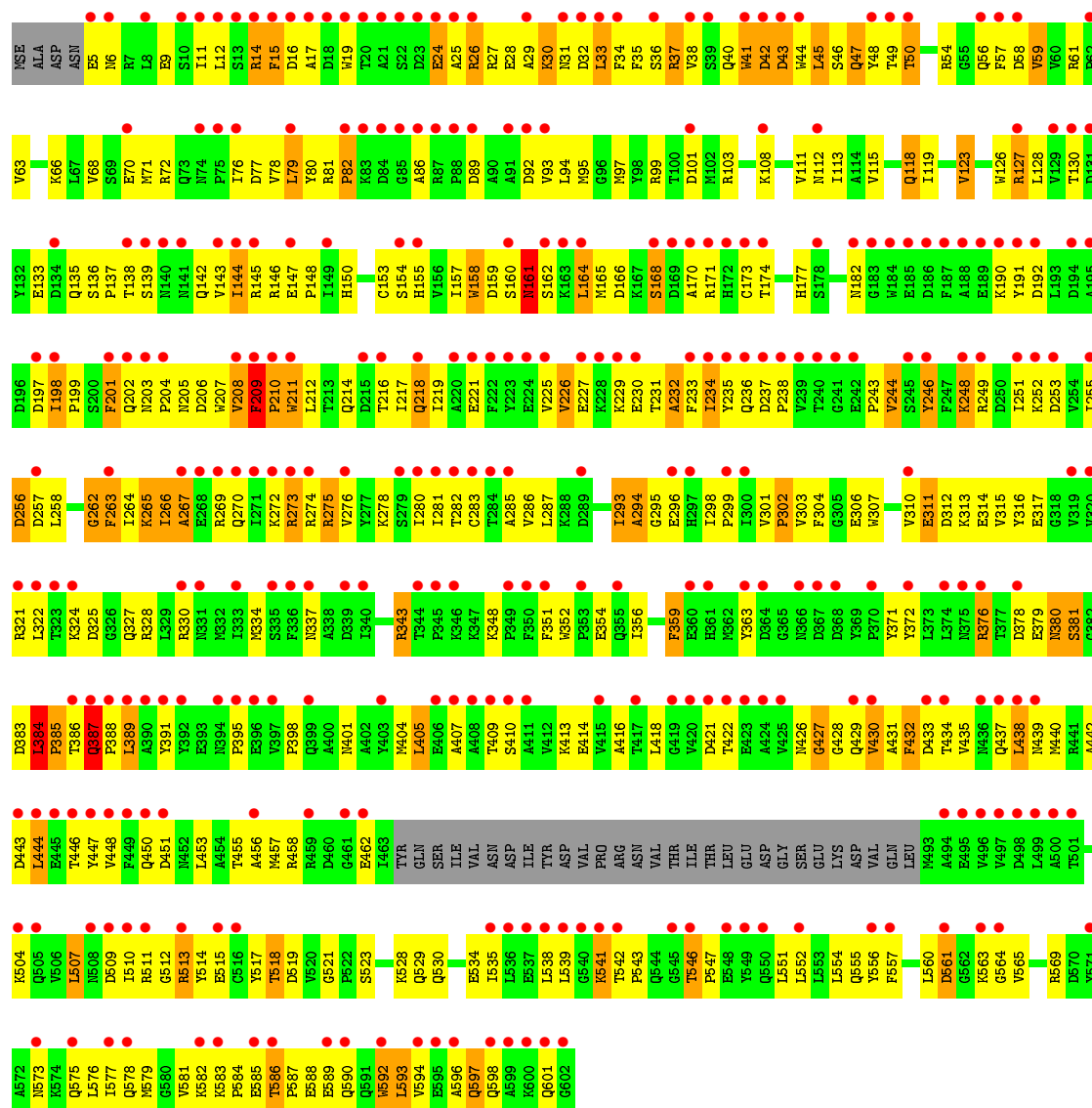




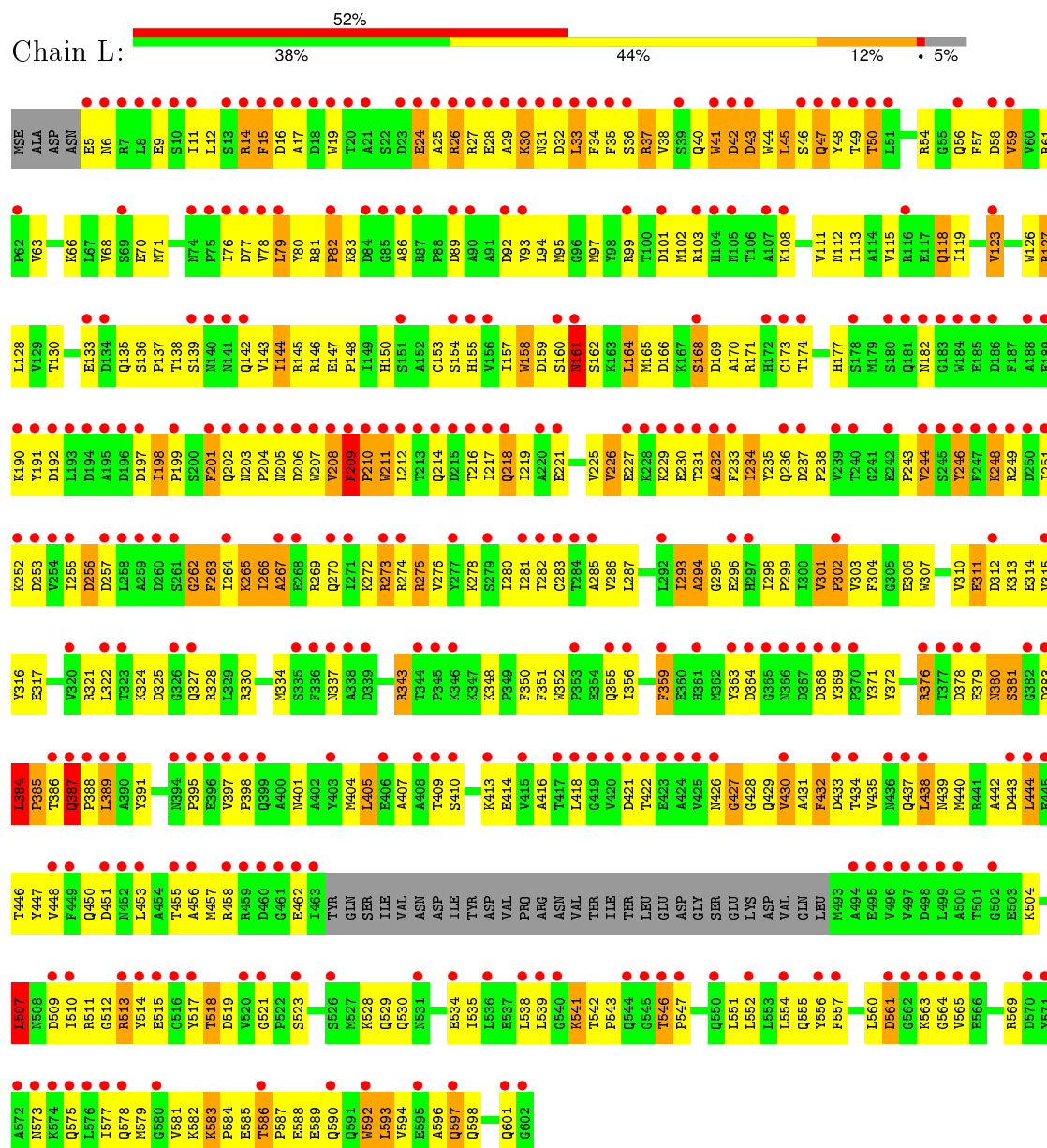




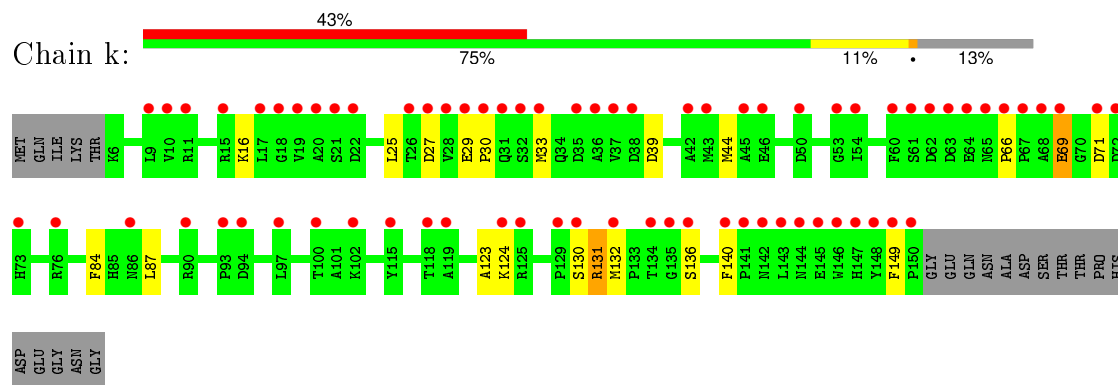
### • Molecule 1: PORTAL PROTEIN



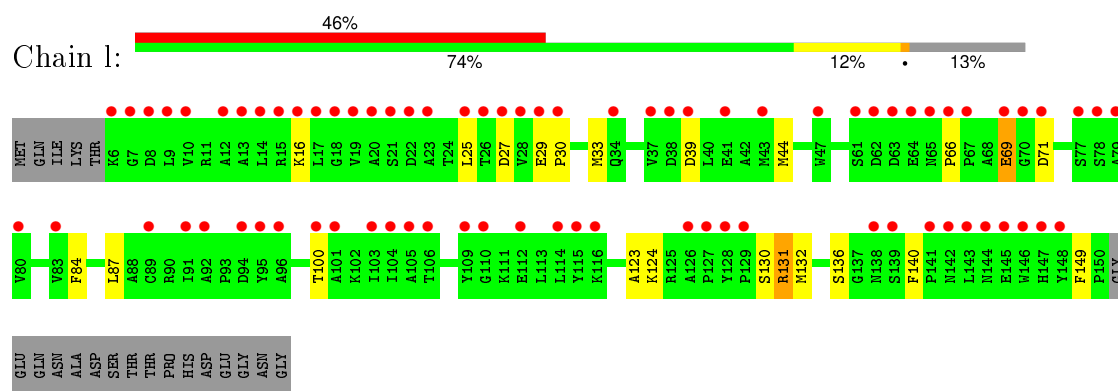
• Molecule 1: PORTAL PROTEIN



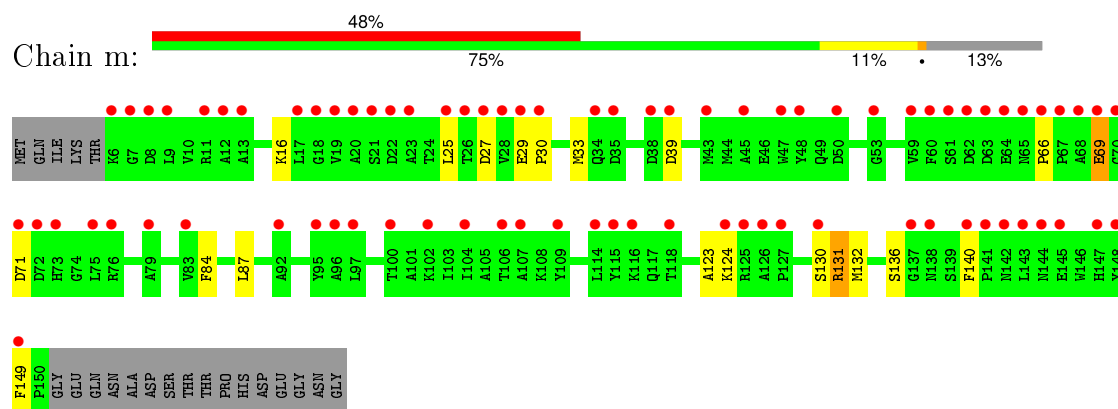
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



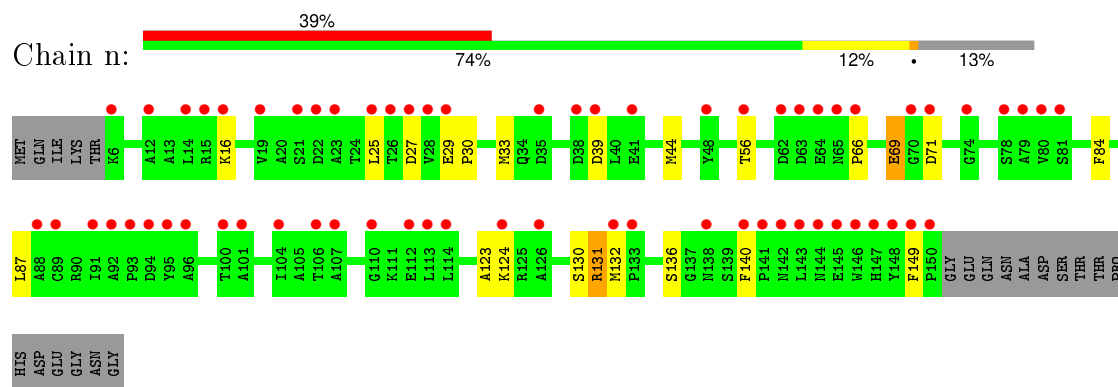
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



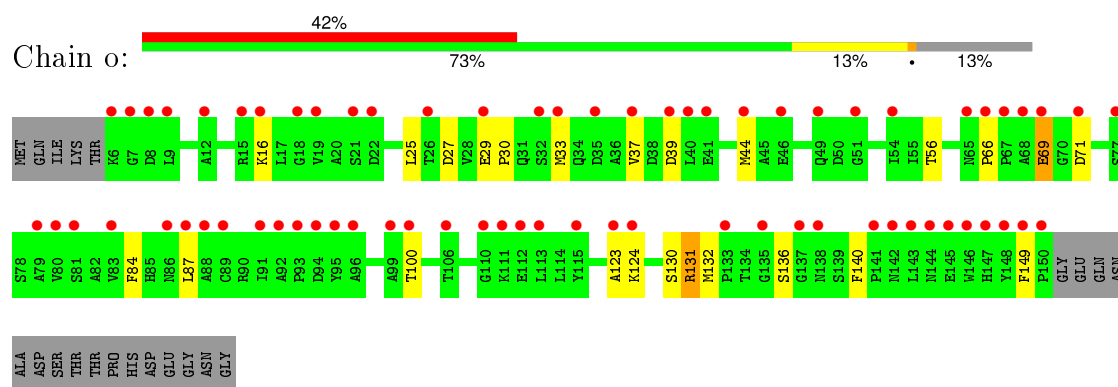
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



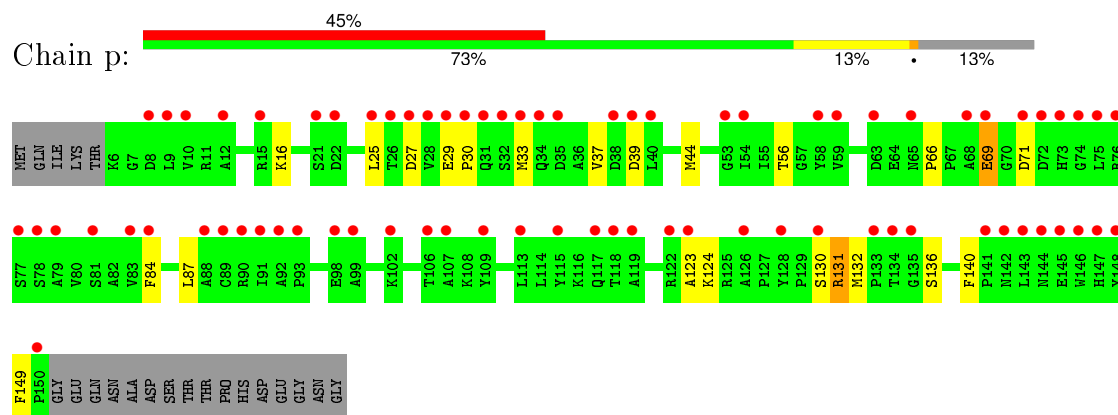
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



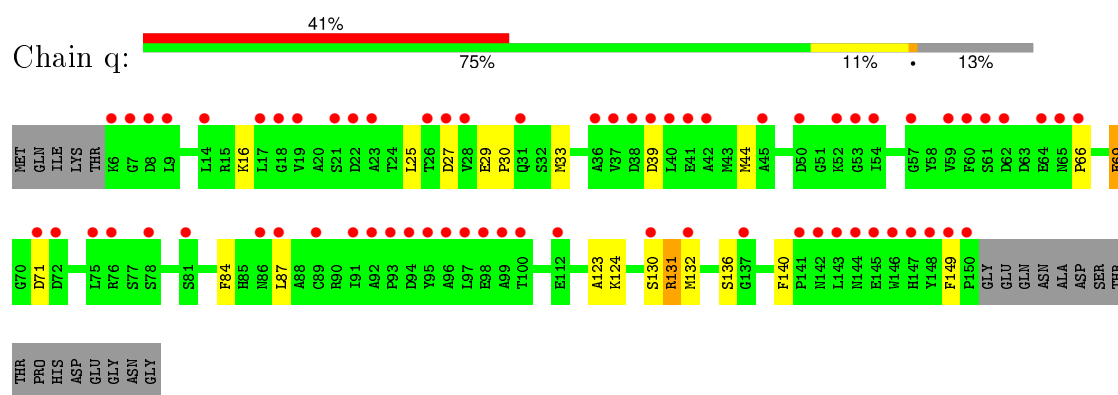
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



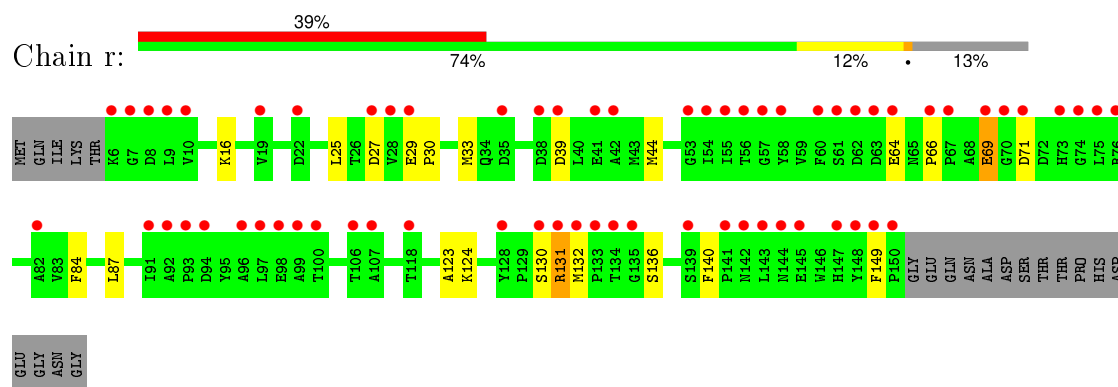
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



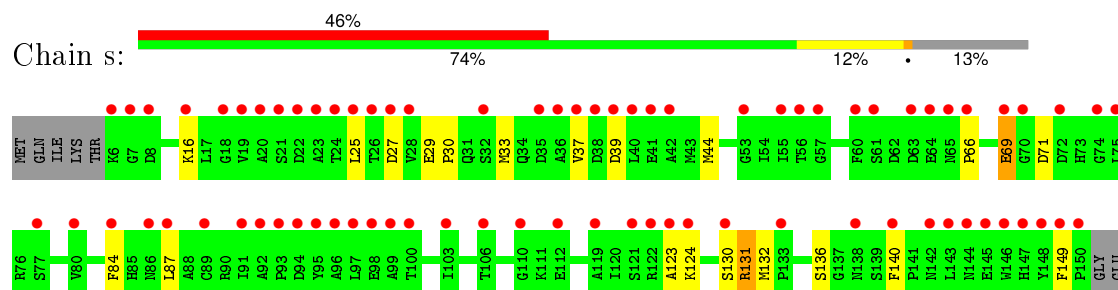
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4




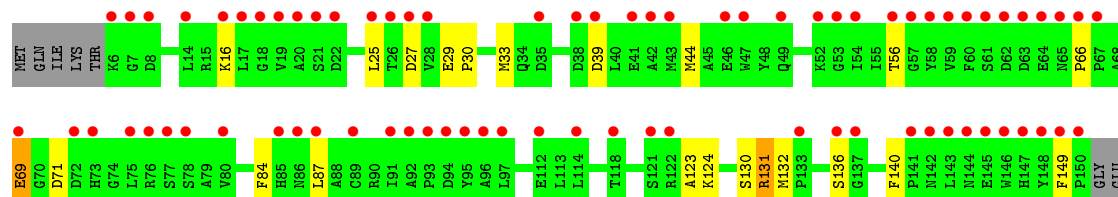
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



GLN  
ASN  
ALA  
ASP  
SER  
THR  
THR  
PRO  
HIS  
ASP  
GLU  
GLY  
ASN  
GLY


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

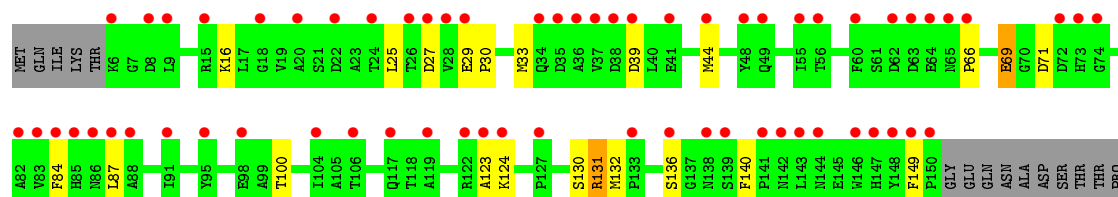
Chain t: 



GLN  
ASN  
ALA  
ASP  
SER  
THR  
THR  
PRO  
HIS  
ASP  
GLU  
GLY  
ASN  
GLY

• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

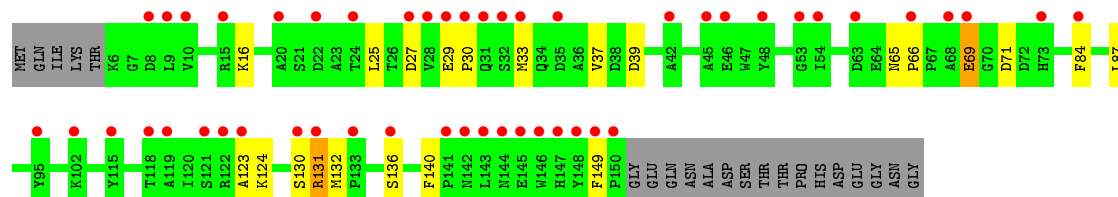
Chain u: 



HIS  
ASP  
GLU  
GLY  
ASN  
GLY

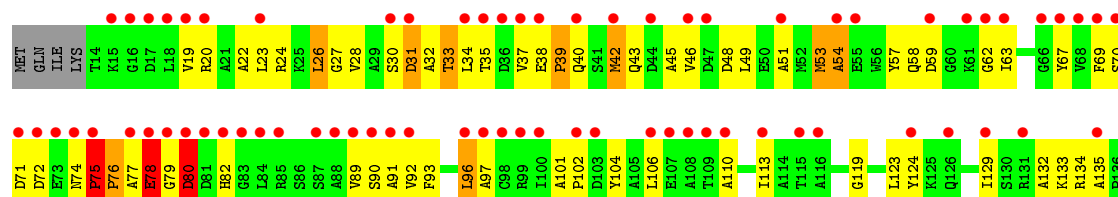
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

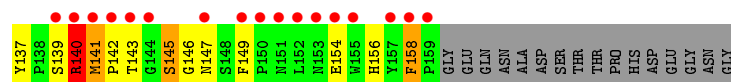
Chain v: 



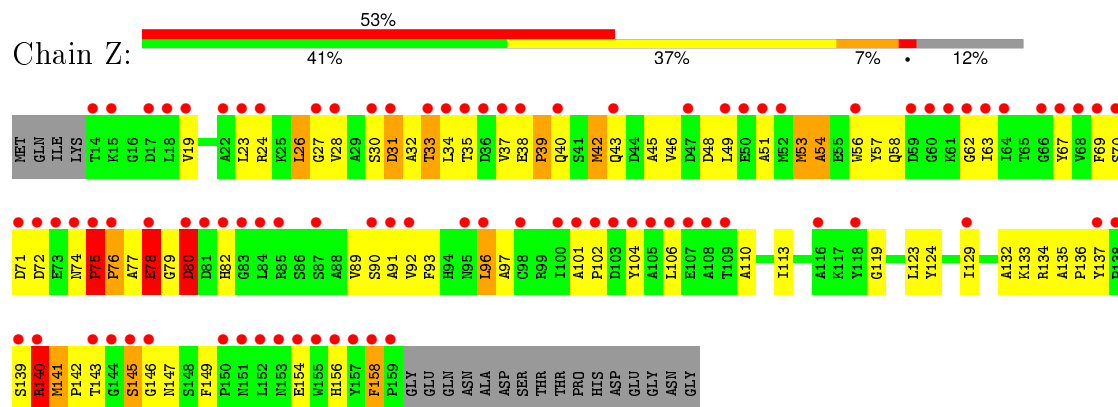
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain Y: 

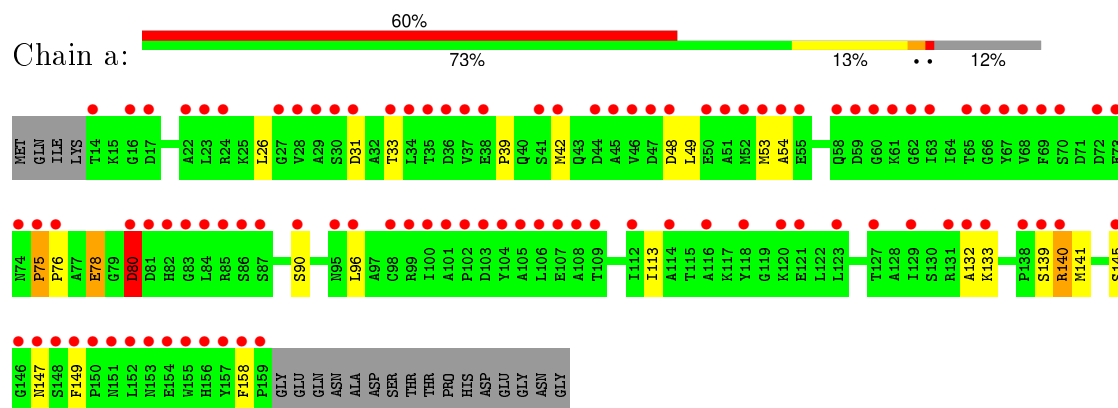




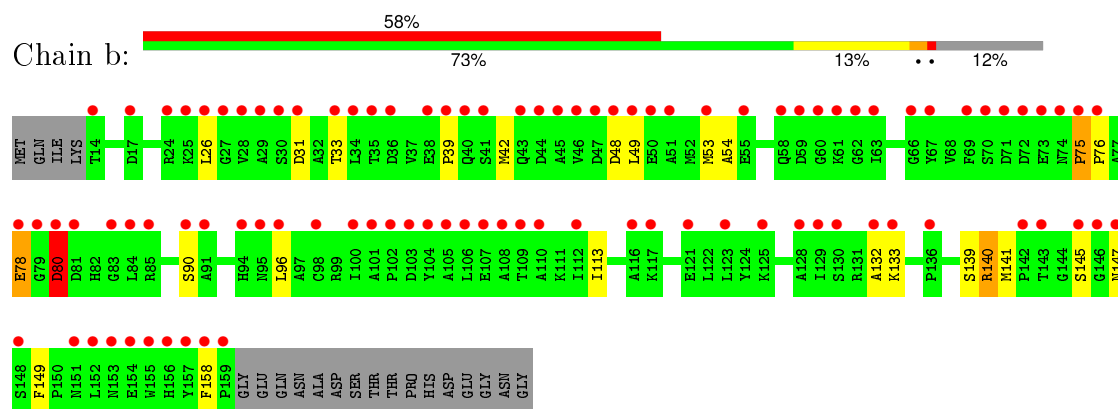
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



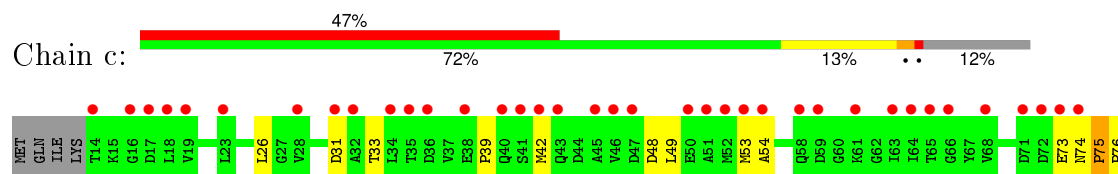
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

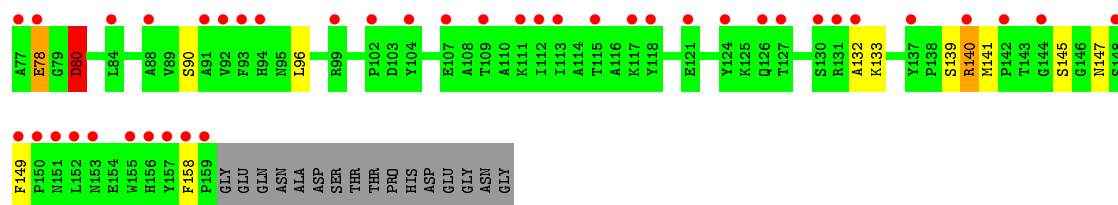


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

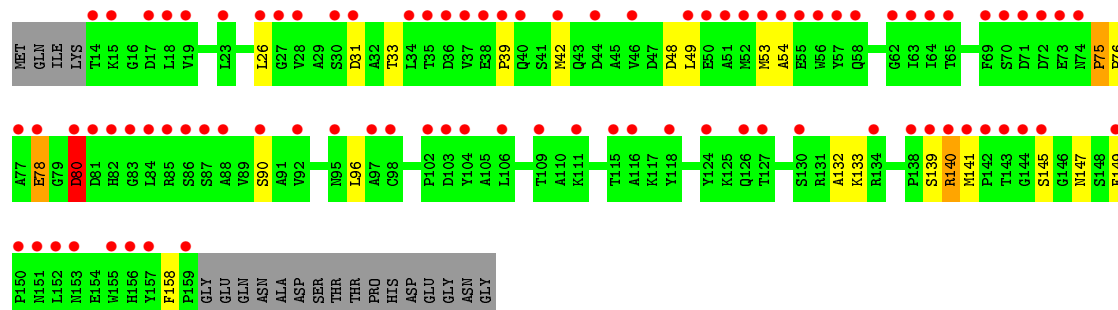
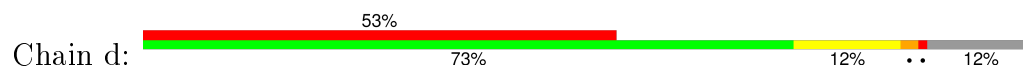


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

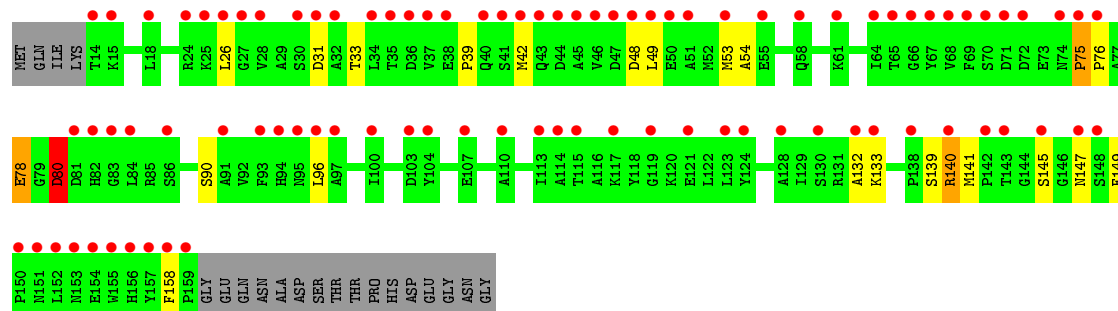
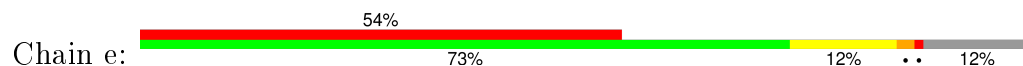




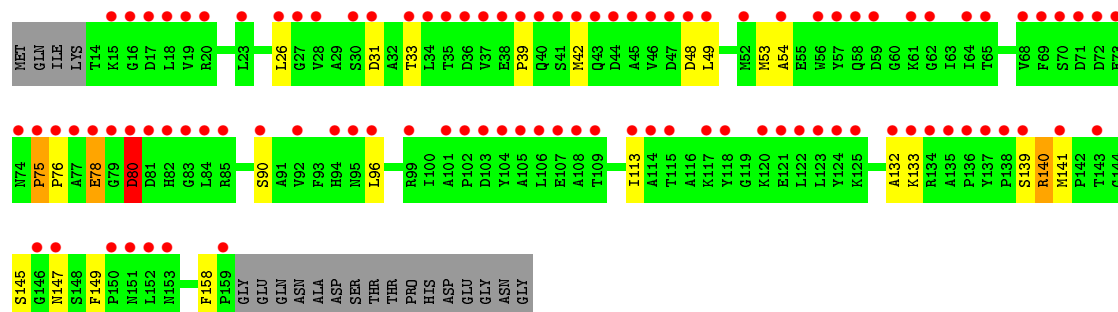
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



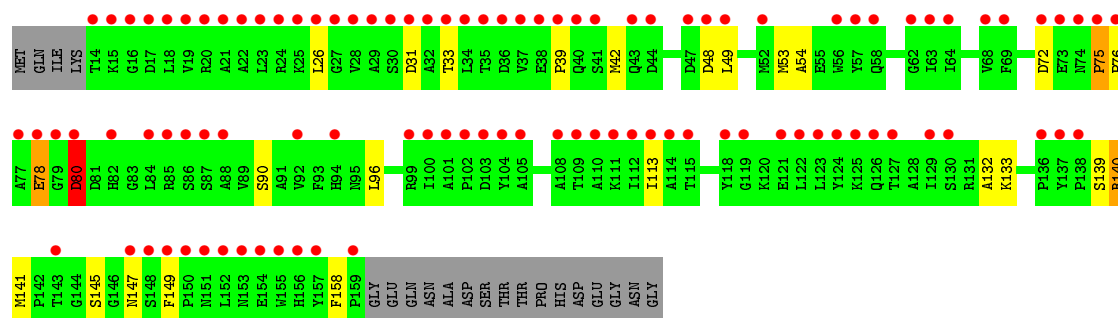
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



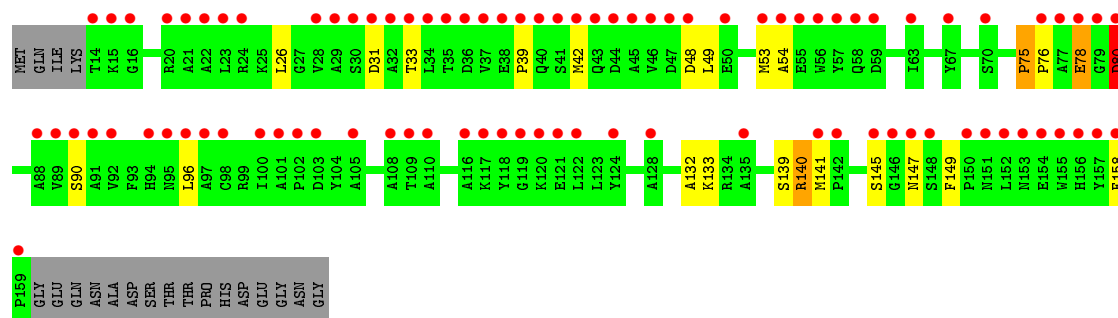
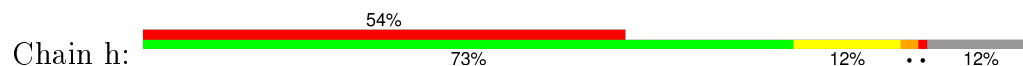
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



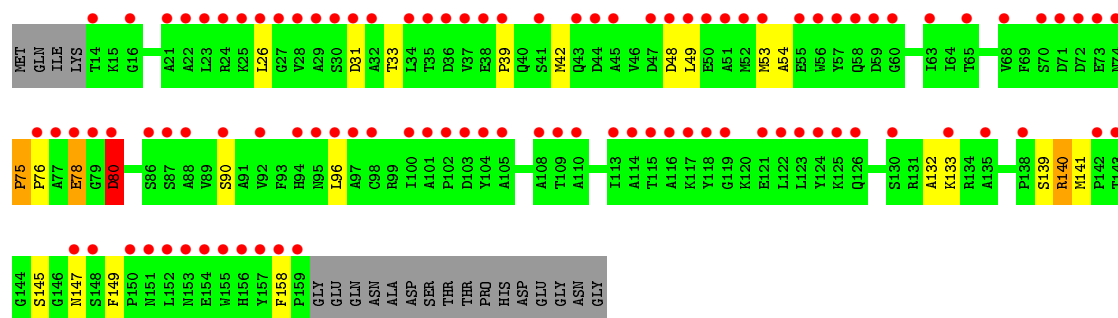
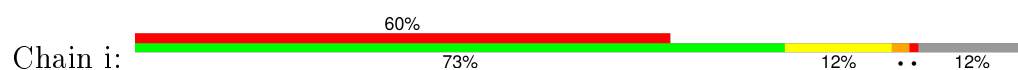




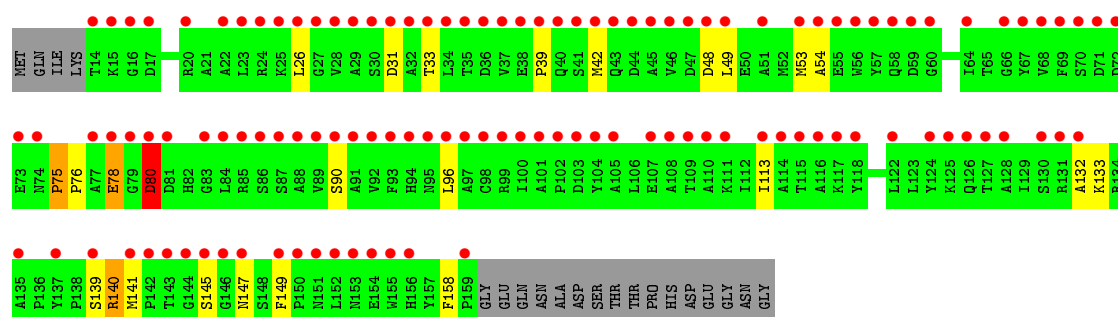
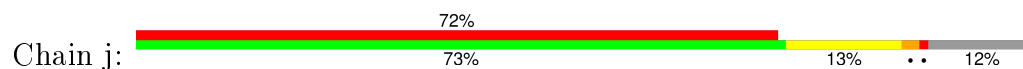
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	170.17Å 253.28Å 282.73Å 90.00° 90.68° 90.00°	Depositor
Resolution (Å)	19.99 – 3.25 78.75 – 3.23	Depositor EDS
% Data completeness (in resolution range)	59.7 (19.99-3.25) 91.6 (78.75-3.23)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 3.26Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.222 , 0.236 0.282 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	65.0	Xtriage
Anisotropy	1.241	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 107.8	EDS
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	36 of 349411 reflections (0.010%)	Xtriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	135120	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.35	0/4635	0.54	0/6265
1	B	0.35	0/4635	0.54	0/6265
1	C	0.35	0/4635	0.54	0/6265
1	D	0.35	0/4635	0.54	0/6265
1	E	0.35	0/4635	0.54	0/6265
1	F	0.35	0/4635	0.54	0/6265
1	G	0.35	0/4635	0.54	0/6265
1	H	0.35	0/4635	0.54	0/6265
1	I	0.35	0/4635	0.54	0/6265
1	J	0.35	0/4635	0.54	0/6265
1	K	0.35	0/4635	0.54	0/6265
1	L	0.35	0/4635	0.54	0/6265
1	M	0.31	0/4646	0.51	0/6278
1	N	0.32	0/4646	0.51	0/6278
1	O	0.32	0/4646	0.50	0/6278
1	P	0.32	0/4646	0.51	0/6278
1	Q	0.32	0/4646	0.51	0/6278
1	R	0.32	0/4646	0.51	0/6278
1	S	0.31	0/4646	0.51	0/6278
1	T	0.31	0/4646	0.50	0/6278
1	U	0.31	0/4646	0.51	0/6278
1	V	0.32	0/4646	0.51	0/6278
1	W	0.31	0/4646	0.55	2/6278 (0.0%)
1	X	0.31	0/4646	0.50	0/6278
2	Y	0.37	0/1067	0.84	4/1452 (0.3%)
2	Z	0.37	0/1067	0.85	4/1452 (0.3%)
2	a	0.37	0/1067	0.84	4/1452 (0.3%)
2	b	0.37	0/1067	0.84	4/1452 (0.3%)
2	c	0.37	0/1067	0.84	4/1452 (0.3%)
2	d	0.37	0/1067	0.84	4/1452 (0.3%)
2	e	0.37	0/1067	0.84	4/1452 (0.3%)
2	f	0.37	0/1067	0.84	4/1452 (0.3%)
2	g	0.37	0/1067	0.84	4/1452 (0.3%)
2	h	0.37	0/1067	0.84	4/1452 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	i	0.37	0/1067	0.85	4/1452 (0.3%)
2	j	0.37	0/1067	0.84	4/1452 (0.3%)
2	k	0.32	0/1071	0.52	0/1455
2	l	0.33	0/1071	0.52	0/1455
2	m	0.33	0/1071	0.51	0/1455
2	n	0.33	0/1071	0.51	0/1455
2	o	0.33	0/1071	0.51	0/1455
2	p	0.33	0/1071	0.51	0/1455
2	q	0.32	0/1071	0.51	0/1455
2	r	0.36	0/1071	0.51	0/1455
2	s	0.32	0/1071	0.52	0/1455
2	t	0.32	0/1071	0.51	0/1455
2	u	0.31	0/1071	0.51	0/1455
2	v	0.32	0/1071	0.51	0/1455
All	All	0.34	0/137028	0.56	50/185400 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
All	All	0	24

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	i	80	ASP	N-CA-CB	17.19	141.54	110.60
2	d	80	ASP	N-CA-CB	17.18	141.52	110.60
2	Z	80	ASP	N-CA-CB	17.17	141.51	110.60
2	Y	80	ASP	N-CA-CB	17.17	141.50	110.60
2	e	80	ASP	N-CA-CB	17.17	141.50	110.60
2	a	80	ASP	N-CA-CB	17.17	141.50	110.60
2	j	80	ASP	N-CA-CB	17.17	141.50	110.60
2	b	80	ASP	N-CA-CB	17.16	141.48	110.60
2	f	80	ASP	N-CA-CB	17.16	141.48	110.60
2	g	80	ASP	N-CA-CB	17.16	141.48	110.60
2	c	80	ASP	N-CA-CB	17.15	141.48	110.60
2	h	80	ASP	N-CA-CB	17.14	141.45	110.60
1	W	249	ARG	NE-CZ-NH2	-15.09	112.75	120.30
2	a	75	PRO	C-N-CD	-9.11	100.57	120.60
2	c	75	PRO	C-N-CD	-9.09	100.60	120.60
2	Z	75	PRO	C-N-CD	-9.09	100.61	120.60
2	f	75	PRO	C-N-CD	-9.08	100.62	120.60
2	i	75	PRO	C-N-CD	-9.08	100.62	120.60
2	Y	75	PRO	C-N-CD	-9.08	100.62	120.60
2	e	75	PRO	C-N-CD	-9.08	100.62	120.60
2	g	75	PRO	C-N-CD	-9.08	100.62	120.60
2	j	75	PRO	C-N-CD	-9.08	100.63	120.60
2	b	75	PRO	C-N-CD	-9.07	100.64	120.60
2	d	75	PRO	C-N-CD	-9.07	100.64	120.60
2	h	75	PRO	C-N-CD	-9.07	100.65	120.60
2	f	80	ASP	N-CA-C	-8.92	86.93	111.00
2	g	80	ASP	N-CA-C	-8.91	86.93	111.00
2	i	80	ASP	N-CA-C	-8.91	86.94	111.00
2	Z	80	ASP	N-CA-C	-8.91	86.95	111.00
2	Y	80	ASP	N-CA-C	-8.90	86.96	111.00
2	e	80	ASP	N-CA-C	-8.90	86.97	111.00
2	c	80	ASP	N-CA-C	-8.90	86.97	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	d	80	ASP	N-CA-C	-8.90	86.98	111.00
2	b	80	ASP	N-CA-C	-8.89	86.98	111.00
2	j	80	ASP	N-CA-C	-8.89	86.99	111.00
2	h	80	ASP	N-CA-C	-8.89	87.00	111.00
2	a	80	ASP	N-CA-C	-8.89	87.00	111.00
1	W	249	ARG	NE-CZ-NH1	7.82	124.21	120.30
2	a	31	ASP	CB-CG-OD2	5.22	123.00	118.30
2	i	31	ASP	CB-CG-OD2	5.22	123.00	118.30
2	Z	31	ASP	CB-CG-OD2	5.21	122.99	118.30
2	c	31	ASP	CB-CG-OD2	5.21	122.99	118.30
2	j	31	ASP	CB-CG-OD2	5.20	122.98	118.30
2	d	31	ASP	CB-CG-OD2	5.20	122.98	118.30
2	Y	31	ASP	CB-CG-OD2	5.18	122.97	118.30
2	g	31	ASP	CB-CG-OD2	5.18	122.97	118.30
2	b	31	ASP	CB-CG-OD2	5.18	122.96	118.30
2	f	31	ASP	CB-CG-OD2	5.17	122.95	118.30
2	e	31	ASP	CB-CG-OD2	5.15	122.94	118.30
2	h	31	ASP	CB-CG-OD2	5.12	122.91	118.30

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	THR	Peptide
1	B	231	THR	Peptide
1	C	231	THR	Peptide
1	D	231	THR	Peptide
1	E	231	THR	Peptide
1	F	231	THR	Peptide
1	G	231	THR	Peptide
1	H	231	THR	Peptide
1	I	231	THR	Peptide
1	J	231	THR	Peptide
1	K	231	THR	Peptide
1	L	231	THR	Peptide
1	M	231	THR	Peptide
1	N	231	THR	Peptide
1	O	231	THR	Peptide
1	P	231	THR	Peptide
1	Q	231	THR	Peptide
1	R	231	THR	Peptide
1	S	231	THR	Peptide

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Mol	Chain	Res	Type	Group
1	T	231	THR	Peptide
1	U	231	THR	Peptide
1	V	231	THR	Peptide
1	W	231	THR	Peptide
1	X	231	THR	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4553	0	4351	430	0
1	B	4553	0	4351	437	2
1	C	4553	0	4351	432	4
1	D	4553	0	4351	423	0
1	E	4553	0	4351	430	0
1	F	4553	0	4351	428	0
1	G	4553	0	4351	430	0
1	H	4553	0	4351	424	0
1	I	4553	0	4351	433	0
1	J	4553	0	4351	430	0
1	K	4553	0	4351	431	0
1	L	4553	0	4351	441	0
1	M	4564	0	4368	365	0
1	N	4564	0	4368	375	5
1	O	4564	0	4368	363	0
1	P	4564	0	4368	371	0
1	Q	4564	0	4368	373	0
1	R	4564	0	4368	385	0
1	S	4564	0	4368	364	3
1	T	4564	0	4368	366	0
1	U	4564	0	4368	374	0
1	V	4564	0	4368	368	0
1	W	4564	0	4368	364	1
1	X	4564	0	4368	364	0
2	Y	1048	0	957	111	0
2	Z	1048	0	957	108	0
2	a	1048	0	957	0	0
2	b	1048	0	957	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	1048	0	957	0	4
2	d	1048	0	957	0	0
2	e	1048	0	957	0	0
2	f	1048	0	957	0	0
2	g	1048	0	957	0	1
2	h	1048	0	957	0	0
2	i	1048	0	957	0	0
2	j	1048	0	957	0	0
2	k	1052	0	975	0	0
2	l	1052	0	975	0	0
2	m	1052	0	975	0	0
2	n	1052	0	975	0	0
2	o	1052	0	975	0	0
2	p	1052	0	975	0	0
2	q	1052	0	975	0	0
2	r	1052	0	975	0	3
2	s	1052	0	975	0	0
2	t	1052	0	975	0	0
2	u	1052	0	975	0	0
2	v	1052	0	975	0	3
3	A	22	0	0	1	0
3	B	22	0	0	1	0
3	C	22	0	0	1	0
3	D	22	0	0	1	0
3	E	22	0	0	2	0
3	F	22	0	0	2	0
3	G	22	0	0	1	0
3	H	22	0	0	2	0
3	I	22	0	0	1	0
3	J	22	0	0	2	0
3	K	22	0	0	2	0
3	L	22	0	0	2	0
3	M	21	0	0	4	0
3	N	21	0	0	4	0
3	O	21	0	0	3	0
3	P	21	0	0	5	0
3	Q	21	0	0	5	0
3	R	21	0	0	4	0
3	S	21	0	0	4	0
3	T	21	0	0	5	0
3	U	21	0	0	3	0
3	V	21	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	W	21	0	0	4	0
3	X	21	0	0	4	0
All	All	135120	0	127812	9241	13

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 42.

All (9241) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:32:ALA:O	2:Z:33:THR:CG2	1.82	1.27
2:Z:32:ALA:O	2:Z:33:THR:HG23	1.12	1.26
2:Y:32:ALA:O	2:Y:33:THR:CG2	1.82	1.26
2:Y:32:ALA:O	2:Y:33:THR:HG23	1.12	1.24
2:Z:28:VAL:HG21	2:Z:96:LEU:CD1	1.68	1.23
2:Y:28:VAL:HG21	2:Y:96:LEU:CD1	1.68	1.21
2:Z:53:MET:CE	2:Z:92:VAL:HG12	1.72	1.20
2:Y:53:MET:CE	2:Y:92:VAL:HG12	1.72	1.18
1:D:78:VAL:HG21	1:D:444:LEU:HD11	1.28	1.16
1:J:78:VAL:HG21	1:J:444:LEU:HD11	1.28	1.16
2:Y:53:MET:CE	2:Y:92:VAL:CG1	2.24	1.15
1:L:78:VAL:HG21	1:L:444:LEU:HD11	1.29	1.15
1:E:78:VAL:HG21	1:E:444:LEU:HD11	1.29	1.15
2:Z:53:MET:CE	2:Z:92:VAL:CG1	2.24	1.15
1:B:78:VAL:HG21	1:B:444:LEU:HD11	1.28	1.15
1:I:78:VAL:HG21	1:I:444:LEU:HD11	1.29	1.15
1:H:78:VAL:HG21	1:H:444:LEU:HD11	1.29	1.15
2:Z:28:VAL:CG1	2:Z:97:ALA:HA	1.77	1.14
2:Y:28:VAL:CG1	2:Y:97:ALA:HA	1.77	1.14
2:Z:42:MET:HG3	2:Z:42:MET:O	1.42	1.13
1:G:78:VAL:HG21	1:G:444:LEU:HD11	1.28	1.13
1:C:78:VAL:HG21	1:C:444:LEU:HD11	1.28	1.12
1:Q:560:LEU:HD13	1:R:82:PRO:HD2	1.31	1.12
2:Y:42:MET:HG3	2:Y:42:MET:O	1.42	1.11
1:K:78:VAL:HG21	1:K:444:LEU:HD11	1.28	1.11
1:K:560:LEU:HD13	1:L:82:PRO:HD2	1.29	1.11
1:A:139:SER:HB3	1:A:455:THR:HG23	1.34	1.10
1:F:139:SER:HB3	1:F:455:THR:HG23	1.34	1.10
1:A:78:VAL:HG21	1:A:444:LEU:HD11	1.29	1.09
1:H:139:SER:HB3	1:H:455:THR:HG23	1.34	1.09
2:Z:28:VAL:HG13	2:Z:97:ALA:CA	1.83	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:14:ARG:HA	1:L:14:ARG:HE	1.19	1.08
2:Z:28:VAL:HG21	2:Z:96:LEU:HD13	1.36	1.08
2:Z:31:ASP:OD2	2:Z:93:PHE:HE2	1.36	1.08
2:Y:53:MET:HE1	2:Y:92:VAL:CG1	1.79	1.08
1:F:78:VAL:HG21	1:F:444:LEU:HD11	1.29	1.08
1:G:139:SER:HB3	1:G:455:THR:HG23	1.34	1.08
1:K:139:SER:HB3	1:K:455:THR:HG23	1.34	1.08
1:E:14:ARG:HE	1:E:14:ARG:HA	1.19	1.07
2:Y:28:VAL:HG13	2:Y:97:ALA:CA	1.83	1.07
1:F:14:ARG:HA	1:F:14:ARG:HE	1.19	1.07
2:Z:53:MET:HE1	2:Z:92:VAL:CG1	1.81	1.07
2:Y:28:VAL:HG21	2:Y:96:LEU:HD13	1.35	1.07
1:L:139:SER:HB3	1:L:455:THR:HG23	1.34	1.07
1:G:14:ARG:HA	1:G:14:ARG:HE	1.19	1.07
1:N:78:VAL:HG21	1:N:444:LEU:HD11	1.37	1.06
1:V:78:VAL:HG21	1:V:444:LEU:HD11	1.35	1.06
1:X:78:VAL:HG21	1:X:444:LEU:HD11	1.38	1.06
1:J:139:SER:HB3	1:J:455:THR:HG23	1.34	1.06
1:I:41:TRP:CZ3	1:I:42:ASP:HB2	1.90	1.06
1:D:41:TRP:CZ3	1:D:42:ASP:HB2	1.91	1.06
1:C:139:SER:HB3	1:C:455:THR:HG23	1.34	1.06
1:U:78:VAL:HG21	1:U:444:LEU:HD11	1.37	1.06
1:J:560:LEU:HD13	1:K:82:PRO:HD2	1.34	1.06
1:K:41:TRP:CZ3	1:K:42:ASP:HB2	1.91	1.06
1:F:41:TRP:CZ3	1:F:42:ASP:HB2	1.91	1.05
1:J:41:TRP:CZ3	1:J:42:ASP:HB2	1.91	1.05
2:Y:28:VAL:CG1	2:Y:97:ALA:CA	2.34	1.05
1:H:41:TRP:CZ3	1:H:42:ASP:HB2	1.90	1.05
1:C:41:TRP:CZ3	1:C:42:ASP:HB2	1.90	1.05
1:K:14:ARG:HE	1:K:14:ARG:HA	1.18	1.05
1:L:41:TRP:CZ3	1:L:42:ASP:HB2	1.91	1.05
1:T:78:VAL:HG21	1:T:444:LEU:HD11	1.37	1.05
1:S:14:ARG:HA	1:S:14:ARG:HE	1.21	1.05
1:A:41:TRP:CZ3	1:A:42:ASP:HB2	1.90	1.05
1:G:41:TRP:CZ3	1:G:42:ASP:HB2	1.91	1.05
1:B:41:TRP:CZ3	1:B:42:ASP:HB2	1.91	1.04
1:B:139:SER:HB3	1:B:455:THR:HG23	1.34	1.04
1:C:14:ARG:HE	1:C:14:ARG:HA	1.19	1.04
1:E:139:SER:HB3	1:E:455:THR:HG23	1.34	1.04
2:Z:28:VAL:CG1	2:Z:97:ALA:CA	2.34	1.04
2:Y:31:ASP:OD2	2:Y:93:PHE:HE2	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:14:ARG:HE	1:M:14:ARG:HA	1.21	1.04
1:O:78:VAL:HG21	1:O:444:LEU:HD11	1.38	1.04
1:X:14:ARG:HA	1:X:14:ARG:HE	1.22	1.04
1:E:41:TRP:CZ3	1:E:42:ASP:HB2	1.90	1.04
1:O:14:ARG:HE	1:O:14:ARG:HA	1.23	1.03
1:A:41:TRP:CE3	1:A:42:ASP:N	2.26	1.03
1:D:41:TRP:CE3	1:D:42:ASP:N	2.26	1.03
1:D:82:PRO:HD2	1:E:560:LEU:HD13	1.37	1.03
1:R:78:VAL:HG21	1:R:444:LEU:HD11	1.36	1.03
1:N:14:ARG:HA	1:N:14:ARG:HE	1.21	1.03
1:I:139:SER:HB3	1:I:455:THR:HG23	1.34	1.03
1:F:41:TRP:CE3	1:F:42:ASP:N	2.26	1.03
1:H:560:LEU:HD13	1:I:82:PRO:HD2	1.40	1.03
1:Q:78:VAL:HG21	1:Q:444:LEU:HD11	1.38	1.03
1:W:78:VAL:HG21	1:W:444:LEU:HD11	1.36	1.03
1:E:41:TRP:CE3	1:E:42:ASP:N	2.26	1.03
1:M:78:VAL:HG21	1:M:444:LEU:HD11	1.37	1.03
1:D:14:ARG:HE	1:D:14:ARG:HA	1.19	1.03
1:P:78:VAL:HG21	1:P:444:LEU:HD11	1.39	1.02
1:W:14:ARG:HA	1:W:14:ARG:HE	1.23	1.02
1:H:41:TRP:CE3	1:H:42:ASP:N	2.26	1.02
1:L:41:TRP:CE3	1:L:42:ASP:N	2.26	1.02
1:G:41:TRP:CE3	1:G:42:ASP:N	2.26	1.02
1:A:82:PRO:HD2	1:L:560:LEU:HD13	1.38	1.02
1:A:14:ARG:HE	1:A:14:ARG:HA	1.19	1.02
1:K:41:TRP:CE3	1:K:42:ASP:N	2.26	1.02
1:B:14:ARG:HA	1:B:14:ARG:HE	1.19	1.02
1:I:41:TRP:CE3	1:I:42:ASP:N	2.26	1.02
1:B:41:TRP:CE3	1:B:42:ASP:N	2.26	1.02
1:N:82:PRO:HD2	1:V:560:LEU:HD13	1.38	1.02
1:F:560:LEU:HD13	1:G:82:PRO:HD2	1.42	1.01
1:J:41:TRP:CE3	1:J:42:ASP:N	2.26	1.01
1:D:139:SER:HB3	1:D:455:THR:HG23	1.34	1.01
1:H:14:ARG:HA	1:H:14:ARG:HE	1.19	1.01
1:C:41:TRP:CE3	1:C:42:ASP:N	2.26	1.01
1:V:82:PRO:HD2	1:W:560:LEU:HD13	1.42	1.01
1:V:14:ARG:HA	1:V:14:ARG:HE	1.21	1.01
1:U:14:ARG:HA	1:U:14:ARG:HE	1.21	1.01
1:R:14:ARG:HA	1:R:14:ARG:HE	1.21	1.01
1:Q:14:ARG:HE	1:Q:14:ARG:HA	1.23	1.01
1:I:14:ARG:HA	1:I:14:ARG:HE	1.19	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:53:MET:HE1	2:Z:92:VAL:HG12	1.01	1.01
1:J:14:ARG:HA	1:J:14:ARG:HE	1.19	1.01
1:T:546:THR:HG23	1:T:547:PRO:HD3	1.43	1.01
1:S:78:VAL:HG21	1:S:444:LEU:HD11	1.38	1.00
1:D:158:TRP:HE3	1:D:173:CYS:HG	1.01	1.00
1:C:58:ASP:O	1:C:59:VAL:HG12	1.62	1.00
1:P:14:ARG:HE	1:P:14:ARG:HA	1.23	1.00
1:T:14:ARG:HE	1:T:14:ARG:HA	1.22	1.00
1:D:560:LEU:HD13	1:F:82:PRO:HD2	1.44	1.00
1:J:58:ASP:O	1:J:59:VAL:HG12	1.62	1.00
1:B:58:ASP:O	1:B:59:VAL:HG12	1.62	1.00
2:Z:24:ARG:O	2:Z:28:VAL:HG23	1.60	1.00
1:Q:546:THR:HG23	1:Q:547:PRO:HD3	1.43	1.00
1:A:58:ASP:O	1:A:59:VAL:HG12	1.62	0.99
1:W:546:THR:HG23	1:W:547:PRO:HD3	1.44	0.99
1:G:158:TRP:HE3	1:G:173:CYS:HG	1.03	0.99
1:K:58:ASP:O	1:K:59:VAL:HG12	1.62	0.99
1:G:58:ASP:O	1:G:59:VAL:HG12	1.62	0.99
1:H:58:ASP:O	1:H:59:VAL:HG12	1.62	0.99
1:F:58:ASP:O	1:F:59:VAL:HG12	1.62	0.99
1:K:158:TRP:HE3	1:K:173:CYS:HG	1.03	0.99
2:Y:24:ARG:O	2:Y:28:VAL:HG23	1.61	0.99
1:L:158:TRP:HE3	1:L:173:CYS:HG	1.05	0.99
1:O:546:THR:HG23	1:O:547:PRO:HD3	1.44	0.99
1:V:546:THR:HG23	1:V:547:PRO:HD3	1.44	0.99
1:E:58:ASP:O	1:E:59:VAL:HG12	1.62	0.99
1:T:560:LEU:HD13	1:W:82:PRO:HD2	1.41	0.99
1:X:248:LYS:HB3	1:X:511:ARG:HH11	1.25	0.98
1:U:82:PRO:HD2	1:X:560:LEU:HD13	1.45	0.98
1:P:560:LEU:HD13	1:Q:82:PRO:HD2	1.43	0.98
1:R:248:LYS:HB3	1:R:511:ARG:HH11	1.27	0.98
1:S:248:LYS:HB3	1:S:511:ARG:HH11	1.29	0.98
1:C:158:TRP:HE3	1:C:173:CYS:HG	1.00	0.98
1:L:58:ASP:O	1:L:59:VAL:HG12	1.62	0.98
1:W:248:LYS:HB3	1:W:511:ARG:HH11	1.28	0.98
1:I:58:ASP:O	1:I:59:VAL:HG12	1.62	0.98
1:M:248:LYS:HB3	1:M:511:ARG:HH11	1.28	0.98
1:O:158:TRP:HB3	1:O:173:CYS:HA	1.46	0.98
1:V:15:PHE:HZ	1:V:283:CYS:HG	1.12	0.98
1:D:58:ASP:O	1:D:59:VAL:HG12	1.62	0.97
2:Y:46:VAL:HG11	2:Y:77:ALA:HB1	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:158:TRP:HE3	1:P:173:CYS:HG	0.98	0.97
1:U:248:LYS:HB3	1:U:511:ARG:HH11	1.28	0.97
1:R:546:THR:HG23	1:R:547:PRO:HD3	1.44	0.97
1:A:158:TRP:HE3	1:A:173:CYS:HG	1.00	0.97
1:M:330:ARG:HH21	1:M:409:THR:HG21	1.29	0.97
1:T:248:LYS:HB3	1:T:511:ARG:HH11	1.27	0.97
2:Z:46:VAL:HG11	2:Z:77:ALA:HB1	1.45	0.97
2:Y:53:MET:HE2	2:Y:92:VAL:HG11	1.47	0.97
1:V:158:TRP:HB3	1:V:173:CYS:HA	1.44	0.97
1:F:34:PHE:HZ	1:F:328:ARG:NH2	1.63	0.96
1:N:546:THR:HG23	1:N:547:PRO:HD3	1.45	0.96
1:A:41:TRP:CZ3	1:A:42:ASP:CB	2.49	0.96
1:H:41:TRP:CZ3	1:H:42:ASP:CB	2.48	0.96
1:E:41:TRP:CZ3	1:E:42:ASP:CB	2.48	0.96
1:H:34:PHE:HZ	1:H:328:ARG:NH2	1.63	0.96
2:Y:53:MET:HE1	2:Y:92:VAL:HG12	0.99	0.96
1:M:546:THR:HG23	1:M:547:PRO:HD3	1.47	0.96
1:J:34:PHE:HZ	1:J:328:ARG:NH2	1.63	0.96
1:S:546:THR:HG23	1:S:547:PRO:HD3	1.45	0.96
2:Z:53:MET:HE2	2:Z:92:VAL:CG1	1.94	0.96
1:W:158:TRP:HB3	1:W:173:CYS:HA	1.45	0.96
1:C:41:TRP:CZ3	1:C:42:ASP:CB	2.49	0.96
1:L:41:TRP:CZ3	1:L:42:ASP:CB	2.49	0.96
1:J:41:TRP:CZ3	1:J:42:ASP:CB	2.49	0.96
1:O:248:LYS:HB3	1:O:511:ARG:HH11	1.29	0.96
1:B:41:TRP:CZ3	1:B:42:ASP:CB	2.49	0.96
1:I:34:PHE:HZ	1:I:328:ARG:NH2	1.63	0.96
1:P:158:TRP:HB3	1:P:173:CYS:HA	1.45	0.96
2:Z:34:LEU:O	2:Z:35:THR:HG23	1.66	0.96
1:S:158:TRP:HB3	1:S:173:CYS:HA	1.47	0.96
1:T:330:ARG:HH21	1:T:409:THR:HG21	1.31	0.96
1:E:158:TRP:HE3	1:E:173:CYS:HG	1.00	0.96
1:B:34:PHE:HZ	1:B:328:ARG:NH2	1.63	0.95
1:K:41:TRP:CZ3	1:K:42:ASP:CB	2.49	0.95
1:E:34:PHE:HZ	1:E:328:ARG:NH2	1.63	0.95
1:F:41:TRP:CZ3	1:F:42:ASP:CB	2.49	0.95
1:V:248:LYS:HB3	1:V:511:ARG:HH11	1.29	0.95
1:X:330:ARG:HH21	1:X:409:THR:HG21	1.30	0.95
1:F:158:TRP:HE3	1:F:173:CYS:HG	1.00	0.95
1:G:34:PHE:HZ	1:G:328:ARG:NH2	1.63	0.95
1:O:330:ARG:HH21	1:O:409:THR:HG21	1.31	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:TRP:CZ3	1:I:42:ASP:CB	2.49	0.95
2:Z:53:MET:HE2	2:Z:92:VAL:HG11	1.46	0.95
1:X:546:THR:HG23	1:X:547:PRO:HD3	1.46	0.95
1:C:34:PHE:HZ	1:C:328:ARG:NH2	1.63	0.95
1:D:41:TRP:CZ3	1:D:42:ASP:CB	2.49	0.95
1:G:41:TRP:CZ3	1:G:42:ASP:CB	2.49	0.95
1:X:158:TRP:HB3	1:X:173:CYS:HA	1.48	0.95
1:U:158:TRP:HB3	1:U:173:CYS:HA	1.49	0.95
1:D:34:PHE:HZ	1:D:328:ARG:NH2	1.63	0.94
1:I:158:TRP:HE3	1:I:173:CYS:HG	1.00	0.94
1:K:561:ASP:HB2	1:L:89:ASP:HA	1.46	0.94
1:Q:248:LYS:HB3	1:Q:511:ARG:HH11	1.29	0.94
1:R:560:LEU:HD13	1:X:82:PRO:HD2	1.49	0.94
1:Q:158:TRP:HB3	1:Q:173:CYS:HA	1.49	0.94
1:L:34:PHE:HZ	1:L:328:ARG:NH2	1.63	0.94
1:K:560:LEU:HD22	1:L:82:PRO:HG2	1.49	0.94
2:Y:34:LEU:O	2:Y:35:THR:HG23	1.65	0.94
1:A:89:ASP:HA	1:L:561:ASP:HB2	1.49	0.94
1:P:248:LYS:HB3	1:P:511:ARG:HH11	1.27	0.94
1:S:330:ARG:HH21	1:S:409:THR:HG21	1.30	0.94
1:A:34:PHE:HZ	1:A:328:ARG:NH2	1.63	0.94
1:T:158:TRP:HB3	1:T:173:CYS:HA	1.44	0.94
2:Z:71:ASP:HB2	2:Z:75:PRO:HD2	1.50	0.94
1:G:560:LEU:HD13	1:H:82:PRO:HD2	1.50	0.94
1:E:546:THR:HG23	1:E:547:PRO:HD3	1.50	0.94
1:V:330:ARG:HH21	1:V:409:THR:HG21	1.28	0.94
1:S:158:TRP:HE3	1:S:173:CYS:HG	0.96	0.94
1:D:546:THR:HG23	1:D:547:PRO:HD3	1.50	0.94
1:R:330:ARG:HH21	1:R:409:THR:HG21	1.32	0.94
1:K:34:PHE:HZ	1:K:328:ARG:NH2	1.63	0.94
1:U:546:THR:HG23	1:U:547:PRO:HD3	1.46	0.94
1:Q:561:ASP:HB2	1:R:89:ASP:HA	1.50	0.93
1:G:139:SER:HB3	1:G:455:THR:CG2	1.98	0.93
1:R:158:TRP:HB3	1:R:173:CYS:HA	1.48	0.93
1:M:158:TRP:HB3	1:M:173:CYS:HA	1.50	0.93
1:P:546:THR:HG23	1:P:547:PRO:HD3	1.46	0.93
1:P:330:ARG:HH21	1:P:409:THR:HG21	1.32	0.93
1:I:139:SER:HB3	1:I:455:THR:CG2	1.98	0.93
1:C:546:THR:HG23	1:C:547:PRO:HD3	1.50	0.93
1:N:158:TRP:HB3	1:N:173:CYS:HA	1.48	0.93
1:M:560:LEU:HD13	1:O:82:PRO:HD2	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:28:VAL:HG21	2:Z:96:LEU:HB3	1.49	0.93
1:C:139:SER:HB3	1:C:455:THR:CG2	1.98	0.93
1:F:546:THR:HG23	1:F:547:PRO:HD3	1.50	0.93
1:J:158:TRP:HE3	1:J:173:CYS:HG	1.01	0.93
1:L:139:SER:HB3	1:L:455:THR:CG2	1.98	0.93
1:F:139:SER:HB3	1:F:455:THR:CG2	1.98	0.93
1:F:14:ARG:NE	1:F:14:ARG:HA	1.83	0.93
1:N:248:LYS:HB3	1:N:511:ARG:HH11	1.30	0.93
1:H:158:TRP:HE3	1:H:173:CYS:HG	1.00	0.93
1:N:15:PHE:HZ	1:N:283:CYS:HG	1.07	0.93
1:U:330:ARG:HH21	1:U:409:THR:HG21	1.29	0.93
1:W:330:ARG:HH21	1:W:409:THR:HG21	1.32	0.93
2:Y:78:GLU:HA	2:Y:78:GLU:OE1	1.69	0.93
2:Y:71:ASP:HB2	2:Y:75:PRO:HD2	1.50	0.93
1:B:546:THR:HG23	1:B:547:PRO:HD3	1.50	0.93
1:E:139:SER:HB3	1:E:455:THR:CG2	1.98	0.92
1:N:158:TRP:HE3	1:N:173:CYS:HG	0.92	0.92
1:A:139:SER:HB3	1:A:455:THR:CG2	1.98	0.92
1:H:139:SER:HB3	1:H:455:THR:CG2	1.98	0.92
1:Q:330:ARG:HH21	1:Q:409:THR:HG21	1.31	0.92
2:Z:78:GLU:HA	2:Z:78:GLU:OE1	1.69	0.92
1:B:139:SER:HB3	1:B:455:THR:CG2	1.98	0.92
2:Y:34:LEU:O	2:Y:35:THR:CG2	2.17	0.92
1:N:330:ARG:HH21	1:N:409:THR:HG21	1.33	0.92
1:G:546:THR:HG23	1:G:547:PRO:HD3	1.50	0.92
1:B:158:TRP:HE3	1:B:173:CYS:HG	1.00	0.92
1:H:14:ARG:HA	1:H:14:ARG:NE	1.83	0.92
1:W:158:TRP:HE3	1:W:173:CYS:HG	0.94	0.92
1:J:139:SER:HB3	1:J:455:THR:CG2	1.98	0.92
1:D:139:SER:HB3	1:D:455:THR:CG2	1.98	0.92
1:N:89:ASP:HA	1:V:561:ASP:HB2	1.48	0.92
1:A:14:ARG:NE	1:A:14:ARG:HA	1.83	0.92
2:Y:31:ASP:OD2	2:Y:93:PHE:CE2	2.22	0.92
1:A:546:THR:HG23	1:A:547:PRO:HD3	1.50	0.92
1:T:158:TRP:HE3	1:T:173:CYS:HG	0.96	0.91
1:W:144:ILE:HG12	1:W:447:TYR:HE1	1.35	0.91
1:G:14:ARG:NE	1:G:14:ARG:HA	1.83	0.91
2:Y:28:VAL:HG21	2:Y:96:LEU:HB3	1.49	0.91
1:K:139:SER:HB3	1:K:455:THR:CG2	1.98	0.91
2:Z:31:ASP:OD2	2:Z:93:PHE:CE2	2.22	0.91
2:Z:34:LEU:O	2:Z:35:THR:CG2	2.17	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:158:TRP:HE3	1:U:173:CYS:HG	0.93	0.91
1:R:158:TRP:HE3	1:R:173:CYS:HG	0.95	0.91
1:D:14:ARG:NE	1:D:14:ARG:HA	1.83	0.91
1:X:158:TRP:HE3	1:X:173:CYS:HG	0.93	0.91
1:H:546:THR:HG23	1:H:547:PRO:HD3	1.50	0.91
1:O:46:SER:H	1:O:48:TYR:HE2	1.19	0.91
1:N:46:SER:H	1:N:48:TYR:HE2	1.19	0.91
1:P:144:ILE:HG12	1:P:447:TYR:HE1	1.35	0.91
2:Z:53:MET:CE	2:Z:92:VAL:HG11	2.00	0.91
1:L:546:THR:HG23	1:L:547:PRO:HD3	1.50	0.91
1:X:46:SER:H	1:X:48:TYR:HE2	1.19	0.91
2:Z:32:ALA:C	2:Z:33:THR:HG23	1.91	0.91
1:O:158:TRP:HE3	1:O:173:CYS:HG	0.94	0.90
1:W:173:CYS:SG	1:W:298:ILE:HD12	2.12	0.90
2:Y:32:ALA:C	2:Y:33:THR:HG23	1.91	0.90
1:S:46:SER:H	1:S:48:TYR:HE2	1.19	0.90
1:X:15:PHE:HZ	1:X:283:CYS:HG	1.14	0.90
1:V:144:ILE:HG12	1:V:447:TYR:HE1	1.34	0.90
1:I:546:THR:HG23	1:I:547:PRO:HD3	1.50	0.90
1:M:144:ILE:HG12	1:M:447:TYR:HE1	1.34	0.90
2:Y:53:MET:CE	2:Y:92:VAL:HG11	2.00	0.90
1:K:546:THR:HG23	1:K:547:PRO:HD3	1.50	0.90
1:N:144:ILE:HG12	1:N:447:TYR:HE1	1.34	0.90
1:V:46:SER:H	1:V:48:TYR:HE2	1.16	0.90
1:J:546:THR:HG23	1:J:547:PRO:HD3	1.50	0.90
1:N:229:LYS:HA	1:N:272:LYS:HA	1.52	0.89
1:C:560:LEU:HD13	1:E:82:PRO:HD2	1.53	0.89
1:K:14:ARG:NE	1:K:14:ARG:HA	1.83	0.89
1:Q:144:ILE:HG12	1:Q:447:TYR:HE1	1.35	0.89
1:U:144:ILE:HG12	1:U:447:TYR:HE1	1.38	0.89
1:E:94:LEU:HA	1:E:97:MSE:HE2	1.55	0.89
1:J:560:LEU:HD22	1:K:82:PRO:HG2	1.52	0.89
1:C:14:ARG:NE	1:C:14:ARG:HA	1.83	0.89
1:I:14:ARG:HA	1:I:14:ARG:NE	1.83	0.89
1:B:94:LEU:HA	1:B:97:MSE:HE2	1.55	0.89
1:D:94:LEU:HA	1:D:97:MSE:HE2	1.55	0.89
1:K:94:LEU:HA	1:K:97:MSE:HE2	1.55	0.89
1:T:46:SER:H	1:T:48:TYR:HE2	1.18	0.89
1:C:94:LEU:HA	1:C:97:MSE:HE2	1.55	0.89
1:F:41:TRP:HE3	1:F:42:ASP:N	1.70	0.89
1:O:144:ILE:HG12	1:O:447:TYR:HE1	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:165:MSE:HG3	1:R:307:TRP:CE3	2.08	0.89
1:C:41:TRP:CE3	1:C:42:ASP:HB2	2.09	0.89
1:G:94:LEU:HA	1:G:97:MSE:HE2	1.55	0.89
1:R:144:ILE:HG12	1:R:447:TYR:HE1	1.36	0.89
1:T:165:MSE:HG3	1:T:307:TRP:CE3	2.07	0.89
1:B:564:GLY:HA2	1:C:554:LEU:HD21	1.53	0.89
1:I:560:LEU:HD13	1:J:82:PRO:HD2	1.53	0.88
1:W:273:ARG:HH22	1:W:453:LEU:HD11	1.38	0.88
1:A:94:LEU:HA	1:A:97:MSE:HE2	1.55	0.88
1:J:561:ASP:HB2	1:K:89:ASP:HA	1.52	0.88
1:M:46:SER:H	1:M:48:TYR:HE2	1.19	0.88
1:K:25:ALA:O	1:K:29:ALA:HB3	1.74	0.88
2:Y:53:MET:HE2	2:Y:92:VAL:CG1	1.96	0.88
1:B:41:TRP:CE3	1:B:42:ASP:HB2	2.09	0.88
1:I:94:LEU:HA	1:I:97:MSE:HE2	1.55	0.88
1:V:158:TRP:HE3	1:V:173:CYS:HG	0.93	0.88
1:Q:229:LYS:HA	1:Q:272:LYS:HA	1.55	0.88
1:R:14:ARG:HA	1:R:14:ARG:NE	1.87	0.88
1:R:46:SER:H	1:R:48:TYR:HE2	1.20	0.88
1:S:144:ILE:HG12	1:S:447:TYR:HE1	1.36	0.88
1:Q:158:TRP:HE3	1:Q:173:CYS:HG	0.92	0.88
1:C:25:ALA:O	1:C:29:ALA:HB3	1.74	0.88
1:E:41:TRP:CE3	1:E:42:ASP:HB2	2.09	0.88
1:I:41:TRP:HE3	1:I:42:ASP:N	1.70	0.88
2:Z:28:VAL:HG21	2:Z:96:LEU:HD12	1.54	0.88
1:D:41:TRP:CE3	1:D:42:ASP:HB2	2.09	0.88
1:H:94:LEU:HA	1:H:97:MSE:HE2	1.55	0.88
1:L:25:ALA:O	1:L:29:ALA:HB3	1.74	0.88
1:J:14:ARG:HA	1:J:14:ARG:NE	1.83	0.88
1:M:158:TRP:HE3	1:M:173:CYS:HG	0.93	0.88
1:P:229:LYS:HA	1:P:272:LYS:HA	1.55	0.88
1:Q:46:SER:H	1:Q:48:TYR:HE2	1.18	0.88
1:W:165:MSE:HG3	1:W:307:TRP:CE3	2.08	0.88
1:B:14:ARG:HA	1:B:14:ARG:NE	1.83	0.88
1:V:173:CYS:SG	1:V:298:ILE:HD12	2.13	0.88
1:L:41:TRP:HE3	1:L:42:ASP:N	1.70	0.88
2:Z:23:LEU:HA	2:Z:26:LEU:HG	1.55	0.88
1:G:41:TRP:CE3	1:G:42:ASP:HB2	2.09	0.87
1:I:37:ARG:HH21	1:I:37:ARG:HB3	1.39	0.87
1:J:25:ALA:O	1:J:29:ALA:HB3	1.74	0.87
1:S:165:MSE:HG3	1:S:307:TRP:CE3	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ARG:HB3	1:A:37:ARG:HH21	1.40	0.87
1:D:41:TRP:HE3	1:D:42:ASP:N	1.70	0.87
1:E:25:ALA:O	1:E:29:ALA:HB3	1.74	0.87
1:F:25:ALA:O	1:F:29:ALA:HB3	1.74	0.87
1:L:41:TRP:CE3	1:L:42:ASP:HB2	2.09	0.87
1:F:94:LEU:HA	1:F:97:MSE:HE2	1.55	0.87
1:J:94:LEU:HA	1:J:97:MSE:HE2	1.55	0.87
1:L:94:LEU:HA	1:L:97:MSE:HE2	1.55	0.87
1:T:144:ILE:HG12	1:T:447:TYR:HE1	1.37	0.87
1:T:229:LYS:HA	1:T:272:LYS:HA	1.56	0.87
1:A:41:TRP:CE3	1:A:42:ASP:HB2	2.09	0.87
1:D:82:PRO:HG2	1:E:560:LEU:HD22	1.57	0.87
1:H:25:ALA:O	1:H:29:ALA:HB3	1.74	0.87
1:J:41:TRP:HE3	1:J:42:ASP:N	1.70	0.87
2:Y:28:VAL:HG21	2:Y:96:LEU:HD12	1.55	0.87
1:W:229:LYS:HA	1:W:272:LYS:HA	1.56	0.87
1:V:229:LYS:HA	1:V:272:LYS:HA	1.55	0.87
1:B:25:ALA:O	1:B:29:ALA:HB3	1.74	0.87
1:A:560:LEU:HD13	1:B:82:PRO:HD2	1.54	0.87
1:G:25:ALA:O	1:G:29:ALA:HB3	1.74	0.87
1:L:14:ARG:HA	1:L:14:ARG:NE	1.83	0.87
1:B:40:GLN:O	1:B:41:TRP:HB2	1.75	0.87
1:E:41:TRP:HE3	1:E:42:ASP:N	1.70	0.87
1:G:37:ARG:HH21	1:G:37:ARG:HB3	1.39	0.87
1:H:41:TRP:CE3	1:H:42:ASP:HB2	2.09	0.87
1:I:40:GLN:O	1:I:41:TRP:HB2	1.75	0.87
1:K:41:TRP:CE3	1:K:42:ASP:HB2	2.09	0.87
1:V:165:MSE:HG3	1:V:307:TRP:CE3	2.10	0.87
1:F:37:ARG:HH21	1:F:37:ARG:HB3	1.40	0.87
1:A:25:ALA:O	1:A:29:ALA:HB3	1.74	0.87
1:F:41:TRP:CE3	1:F:42:ASP:HB2	2.09	0.87
1:E:14:ARG:NE	1:E:14:ARG:HA	1.83	0.87
1:B:37:ARG:HB3	1:B:37:ARG:HH21	1.40	0.87
1:O:165:MSE:HG3	1:O:307:TRP:CE3	2.10	0.87
1:P:46:SER:H	1:P:48:TYR:HE2	1.18	0.87
1:S:173:CYS:SG	1:S:298:ILE:HD12	2.15	0.87
1:Q:173:CYS:SG	1:Q:298:ILE:HD12	2.14	0.87
1:F:40:GLN:O	1:F:41:TRP:HB2	1.75	0.86
1:M:165:MSE:HG3	1:M:307:TRP:CE3	2.10	0.86
1:V:14:ARG:HA	1:V:14:ARG:NE	1.87	0.86
1:N:14:ARG:NE	1:N:14:ARG:HA	1.87	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:173:CYS:SG	1:N:298:ILE:HD12	2.14	0.86
1:Q:273:ARG:HH22	1:Q:453:LEU:HD11	1.39	0.86
1:D:25:ALA:O	1:D:29:ALA:HB3	1.74	0.86
1:D:89:ASP:HA	1:E:561:ASP:HB2	1.56	0.86
1:E:37:ARG:HH21	1:E:37:ARG:HB3	1.39	0.86
1:W:46:SER:H	1:W:48:TYR:HE2	1.18	0.86
1:R:229:LYS:HA	1:R:272:LYS:HA	1.55	0.86
1:I:25:ALA:O	1:I:29:ALA:HB3	1.74	0.86
1:S:15:PHE:HZ	1:S:283:CYS:HG	1.16	0.86
1:I:41:TRP:CE3	1:I:42:ASP:HB2	2.09	0.86
1:S:273:ARG:HH22	1:S:453:LEU:HD11	1.39	0.86
1:C:37:ARG:HH21	1:C:37:ARG:HB3	1.39	0.86
1:U:165:MSE:HG3	1:U:307:TRP:CE3	2.10	0.86
1:J:236:GLN:HB2	1:J:265:LYS:HZ3	1.40	0.86
1:O:273:ARG:HH22	1:O:453:LEU:HD11	1.40	0.86
1:U:46:SER:H	1:U:48:TYR:HE2	1.20	0.86
1:V:273:ARG:HH22	1:V:453:LEU:HD11	1.40	0.86
1:A:41:TRP:HE3	1:A:42:ASP:N	1.70	0.86
1:J:41:TRP:CE3	1:J:42:ASP:HB2	2.09	0.86
1:M:14:ARG:NE	1:M:14:ARG:HA	1.87	0.86
1:U:14:ARG:HA	1:U:14:ARG:NE	1.87	0.86
1:M:273:ARG:HH22	1:M:453:LEU:HD11	1.40	0.86
1:O:173:CYS:SG	1:O:298:ILE:HD12	2.15	0.86
1:X:273:ARG:HH22	1:X:453:LEU:HD11	1.40	0.86
2:Y:23:LEU:HA	2:Y:26:LEU:HG	1.55	0.86
1:G:41:TRP:HE3	1:G:42:ASP:N	1.70	0.86
1:H:41:TRP:HE3	1:H:42:ASP:N	1.70	0.86
2:Y:28:VAL:CG2	2:Y:96:LEU:CD1	2.53	0.86
1:X:248:LYS:CB	1:X:511:ARG:HH11	1.89	0.86
1:G:40:GLN:O	1:G:41:TRP:HB2	1.75	0.86
1:K:236:GLN:HB2	1:K:265:LYS:HZ3	1.40	0.86
1:G:236:GLN:HB2	1:G:265:LYS:HZ3	1.40	0.86
1:H:40:GLN:O	1:H:41:TRP:HB2	1.75	0.86
1:A:564:GLY:HA2	1:B:554:LEU:HD21	1.56	0.86
1:L:40:GLN:O	1:L:41:TRP:HB2	1.75	0.85
1:B:236:GLN:HB2	1:B:265:LYS:HZ3	1.40	0.85
1:U:229:LYS:HA	1:U:272:LYS:HA	1.56	0.85
2:Z:28:VAL:CG2	2:Z:96:LEU:CD1	2.53	0.85
1:R:173:CYS:SG	1:R:298:ILE:HD12	2.16	0.85
1:M:229:LYS:HA	1:M:272:LYS:HA	1.56	0.85
1:O:229:LYS:HA	1:O:272:LYS:HA	1.56	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:89:ASP:HA	1:W:561:ASP:HB2	1.57	0.85
1:S:14:ARG:NE	1:S:14:ARG:HA	1.86	0.85
1:T:15:PHE:HZ	1:T:283:CYS:HG	1.23	0.85
1:S:229:LYS:HA	1:S:272:LYS:HA	1.57	0.85
2:Z:28:VAL:HG13	2:Z:97:ALA:CB	2.06	0.85
1:P:173:CYS:SG	1:P:298:ILE:HD12	2.15	0.85
1:O:14:ARG:HA	1:O:14:ARG:NE	1.88	0.85
1:X:165:MSE:HG3	1:X:307:TRP:CE3	2.11	0.85
1:R:158:TRP:HE3	1:R:173:CYS:SG	2.00	0.85
1:T:273:ARG:HH22	1:T:453:LEU:HD11	1.40	0.85
1:P:273:ARG:HH22	1:P:453:LEU:HD11	1.41	0.85
1:E:40:GLN:O	1:E:41:TRP:HB2	1.75	0.85
1:G:158:TRP:HE3	1:G:173:CYS:SG	2.00	0.85
1:P:165:MSE:HG3	1:P:307:TRP:CE3	2.12	0.85
1:S:82:PRO:HD2	1:U:560:LEU:HD13	1.58	0.85
1:R:248:LYS:CB	1:R:511:ARG:HH11	1.89	0.85
1:U:273:ARG:HH22	1:U:453:LEU:HD11	1.37	0.85
1:C:158:TRP:HE3	1:C:173:CYS:SG	2.00	0.85
1:H:158:TRP:HE3	1:H:173:CYS:SG	2.00	0.85
1:D:236:GLN:HB2	1:D:265:LYS:HZ3	1.42	0.85
1:A:158:TRP:HE3	1:A:173:CYS:SG	2.00	0.85
1:K:40:GLN:O	1:K:41:TRP:HB2	1.75	0.85
1:K:41:TRP:HE3	1:K:42:ASP:N	1.70	0.85
1:U:173:CYS:SG	1:U:298:ILE:HD12	2.17	0.85
2:Y:28:VAL:HG13	2:Y:97:ALA:CB	2.07	0.85
1:N:165:MSE:HG3	1:N:307:TRP:CE3	2.11	0.85
2:Z:34:LEU:HD12	2:Z:104:TYR:CD2	2.11	0.85
1:B:560:LEU:HD13	1:C:82:PRO:HD2	1.59	0.85
1:X:229:LYS:HA	1:X:272:LYS:HA	1.56	0.85
1:H:236:GLN:HB2	1:H:265:LYS:HZ3	1.40	0.85
1:B:158:TRP:HE3	1:B:173:CYS:SG	2.00	0.85
1:D:37:ARG:HB3	1:D:37:ARG:HH21	1.40	0.85
1:S:560:LEU:HD13	1:T:82:PRO:HD2	1.59	0.85
1:R:273:ARG:HH22	1:R:453:LEU:HD11	1.40	0.85
1:J:158:TRP:HE3	1:J:173:CYS:SG	2.00	0.84
1:J:37:ARG:HH21	1:J:37:ARG:HB3	1.40	0.84
1:I:564:GLY:HA2	1:J:554:LEU:HD21	1.59	0.84
1:A:40:GLN:O	1:A:41:TRP:HB2	1.75	0.84
1:L:37:ARG:HB3	1:L:37:ARG:HH21	1.40	0.84
1:Q:165:MSE:HG3	1:Q:307:TRP:CE3	2.11	0.84
1:S:248:LYS:CB	1:S:511:ARG:HH11	1.90	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:158:TRP:HE3	1:W:173:CYS:SG	1.99	0.84
1:Q:158:TRP:HE3	1:Q:173:CYS:SG	1.99	0.84
1:H:37:ARG:HH21	1:H:37:ARG:HB3	1.40	0.84
2:Z:28:VAL:CG2	2:Z:96:LEU:HD13	2.07	0.84
1:B:41:TRP:HE3	1:B:42:ASP:N	1.70	0.84
1:K:158:TRP:HE3	1:K:173:CYS:SG	2.00	0.84
1:L:158:TRP:HE3	1:L:173:CYS:SG	2.00	0.84
1:X:173:CYS:SG	1:X:298:ILE:HD12	2.16	0.84
1:A:212:LEU:HD22	1:B:26:ARG:HG2	1.60	0.84
1:F:158:TRP:HE3	1:F:173:CYS:SG	2.00	0.84
1:S:158:TRP:HE3	1:S:173:CYS:SG	2.00	0.84
2:Y:34:LEU:HD12	2:Y:104:TYR:CD2	2.11	0.84
1:V:330:ARG:HD2	1:V:409:THR:HG22	1.58	0.84
1:D:158:TRP:HE3	1:D:173:CYS:SG	2.00	0.84
1:X:144:ILE:HG12	1:X:447:TYR:HE1	1.39	0.84
1:A:236:GLN:HB2	1:A:265:LYS:HZ3	1.41	0.84
1:A:41:TRP:CE3	1:A:42:ASP:CB	2.61	0.84
1:C:40:GLN:O	1:C:41:TRP:HB2	1.75	0.84
1:F:41:TRP:CE3	1:F:42:ASP:CB	2.61	0.84
1:N:273:ARG:HH22	1:N:453:LEU:HD11	1.41	0.84
1:E:41:TRP:CE3	1:E:42:ASP:CB	2.61	0.84
2:Y:28:VAL:HG13	2:Y:97:ALA:N	1.92	0.84
1:B:41:TRP:CE3	1:B:42:ASP:CB	2.61	0.84
1:I:158:TRP:HE3	1:I:173:CYS:SG	2.00	0.84
1:I:41:TRP:CE3	1:I:42:ASP:CB	2.61	0.84
1:J:40:GLN:O	1:J:41:TRP:HB2	1.75	0.84
1:L:41:TRP:CE3	1:L:42:ASP:CB	2.61	0.84
1:T:14:ARG:NE	1:T:14:ARG:HA	1.87	0.84
1:V:158:TRP:HE3	1:V:173:CYS:SG	2.00	0.84
2:Z:28:VAL:HG13	2:Z:97:ALA:N	1.91	0.84
1:W:14:ARG:HA	1:W:14:ARG:NE	1.88	0.84
1:T:330:ARG:HD2	1:T:409:THR:HG22	1.60	0.84
1:J:41:TRP:CE3	1:J:42:ASP:CB	2.61	0.83
1:K:37:ARG:HH21	1:K:37:ARG:HB3	1.40	0.83
1:K:41:TRP:CE3	1:K:42:ASP:CB	2.61	0.83
1:T:561:ASP:HB2	1:W:89:ASP:HA	1.59	0.83
1:D:40:GLN:O	1:D:41:TRP:HB2	1.75	0.83
1:E:158:TRP:HE3	1:E:173:CYS:SG	2.00	0.83
1:H:41:TRP:CE3	1:H:42:ASP:CB	2.61	0.83
1:T:173:CYS:SG	1:T:298:ILE:HD12	2.18	0.83
1:N:158:TRP:HE3	1:N:173:CYS:SG	2.00	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:236:GLN:HB2	1:I:265:LYS:HZ3	1.41	0.83
1:D:41:TRP:CE3	1:D:42:ASP:CB	2.61	0.83
1:M:82:PRO:HD2	1:N:560:LEU:HD13	1.60	0.83
1:X:14:ARG:HA	1:X:14:ARG:NE	1.87	0.83
1:U:15:PHE:HZ	1:U:283:CYS:HG	1.23	0.83
1:X:158:TRP:HE3	1:X:173:CYS:SG	2.00	0.83
1:X:330:ARG:HD2	1:X:409:THR:HG22	1.61	0.83
1:Q:14:ARG:NE	1:Q:14:ARG:HA	1.88	0.83
1:O:248:LYS:CB	1:O:511:ARG:HH11	1.92	0.83
1:G:41:TRP:CE3	1:G:42:ASP:CB	2.61	0.83
1:M:330:ARG:HD2	1:M:409:THR:HG22	1.61	0.83
1:O:330:ARG:HD2	1:O:409:THR:HG22	1.60	0.83
1:W:330:ARG:HD2	1:W:409:THR:HG22	1.61	0.83
1:P:158:TRP:HE3	1:P:173:CYS:SG	2.00	0.83
2:Y:28:VAL:HG12	2:Y:97:ALA:HA	1.59	0.83
1:A:139:SER:CB	1:A:455:THR:HG23	2.09	0.83
1:T:158:TRP:HE3	1:T:173:CYS:SG	2.01	0.83
1:H:139:SER:CB	1:H:455:THR:HG23	2.09	0.83
1:K:139:SER:CB	1:K:455:THR:HG23	2.09	0.83
1:B:139:SER:CB	1:B:455:THR:HG23	2.09	0.83
1:O:158:TRP:HE3	1:O:173:CYS:SG	2.01	0.83
1:U:158:TRP:HE3	1:U:173:CYS:SG	2.00	0.83
1:C:236:GLN:HB2	1:C:265:LYS:HZ3	1.42	0.83
1:M:158:TRP:HE3	1:M:173:CYS:SG	2.02	0.82
1:N:228:LYS:HA	1:N:228:LYS:HE2	1.61	0.82
1:C:41:TRP:HE3	1:C:42:ASP:N	1.70	0.82
1:Q:560:LEU:HD22	1:R:82:PRO:HG2	1.60	0.82
1:J:139:SER:CB	1:J:455:THR:HG23	2.09	0.82
2:Y:28:VAL:CG2	2:Y:96:LEU:HD13	2.07	0.82
1:T:35:PHE:HE2	1:T:324:LYS:HZ3	1.26	0.82
1:P:14:ARG:HA	1:P:14:ARG:NE	1.88	0.82
1:M:248:LYS:CB	1:M:511:ARG:HH11	1.92	0.82
1:U:248:LYS:CB	1:U:511:ARG:HH11	1.91	0.82
1:R:330:ARG:HD2	1:R:409:THR:HG22	1.62	0.82
1:E:236:GLN:HB2	1:E:265:LYS:HZ3	1.43	0.82
1:B:325:ASP:OD2	2:Y:145:SER:HB3	1.79	0.82
1:P:248:LYS:CB	1:P:511:ARG:HH11	1.91	0.82
1:C:139:SER:CB	1:C:455:THR:HG23	2.09	0.82
1:F:236:GLN:HB2	1:F:265:LYS:HZ3	1.45	0.82
1:T:248:LYS:CB	1:T:511:ARG:HH11	1.91	0.82
1:C:41:TRP:CE3	1:C:42:ASP:CB	2.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:SER:CB	1:F:455:THR:HG23	2.09	0.82
1:M:173:CYS:SG	1:M:298:ILE:HD12	2.18	0.82
1:S:554:LEU:HD21	1:U:564:GLY:HA2	1.61	0.82
1:L:139:SER:CB	1:L:455:THR:HG23	2.09	0.82
1:H:560:LEU:HD22	1:I:82:PRO:HG2	1.60	0.82
1:R:11:ILE:HD12	1:R:285:ALA:HA	1.62	0.81
2:Z:28:VAL:HG12	2:Z:97:ALA:HA	1.59	0.81
1:G:139:SER:CB	1:G:455:THR:HG23	2.09	0.81
1:I:139:SER:CB	1:I:455:THR:HG23	2.09	0.81
1:L:236:GLN:HB2	1:L:265:LYS:HZ3	1.44	0.81
1:E:139:SER:CB	1:E:455:THR:HG23	2.09	0.81
1:Q:248:LYS:CB	1:Q:511:ARG:HH11	1.93	0.81
1:S:330:ARG:HD2	1:S:409:THR:HG22	1.60	0.81
1:N:248:LYS:CB	1:N:511:ARG:HH11	1.94	0.81
1:I:212:LEU:HD22	1:J:26:ARG:HG2	1.62	0.81
1:R:208:VAL:HG12	1:R:210:PRO:HD3	1.63	0.81
1:N:208:VAL:HG12	1:N:210:PRO:HD3	1.63	0.81
2:Z:28:VAL:HG13	2:Z:97:ALA:HB2	1.63	0.81
1:D:139:SER:CB	1:D:455:THR:HG23	2.09	0.81
1:Q:228:LYS:HA	1:Q:228:LYS:HE2	1.62	0.81
1:D:560:LEU:HD22	1:F:82:PRO:HG2	1.62	0.81
1:F:560:LEU:HD22	1:G:82:PRO:HG2	1.60	0.81
1:Q:15:PHE:HZ	1:Q:283:CYS:HG	1.27	0.81
1:R:228:LYS:HA	1:R:228:LYS:HE2	1.63	0.81
1:Q:208:VAL:HG12	1:Q:210:PRO:HD3	1.63	0.81
1:O:560:LEU:HD13	1:P:82:PRO:HD2	1.61	0.81
1:V:63:VAL:HG21	1:V:416:ALA:HB1	1.63	0.81
1:W:208:VAL:HG12	1:W:210:PRO:HD3	1.62	0.81
1:U:330:ARG:HD2	1:U:409:THR:HG22	1.63	0.81
1:X:208:VAL:HG12	1:X:210:PRO:HD3	1.63	0.81
1:U:228:LYS:HA	1:U:228:LYS:HE2	1.63	0.81
1:X:228:LYS:HE2	1:X:228:LYS:HA	1.63	0.81
1:P:376:ARG:O	1:P:383:ASP:HB3	1.81	0.81
1:V:208:VAL:HG12	1:V:210:PRO:HD3	1.63	0.81
1:V:228:LYS:HE2	1:V:228:LYS:HA	1.62	0.81
1:K:35:PHE:HE2	1:K:324:LYS:HZ3	1.28	0.80
2:Y:28:VAL:CG1	2:Y:97:ALA:N	2.44	0.80
1:S:63:VAL:HG21	1:S:416:ALA:HB1	1.63	0.80
1:C:564:GLY:HA2	1:E:554:LEU:HD21	1.62	0.80
1:W:248:LYS:CB	1:W:511:ARG:HH11	1.92	0.80
1:M:228:LYS:HE2	1:M:228:LYS:HA	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:228:LYS:HE2	1:W:228:LYS:HA	1.63	0.80
1:S:564:GLY:HA2	1:T:554:LEU:HD21	1.64	0.80
1:Q:63:VAL:HG21	1:Q:416:ALA:HB1	1.61	0.80
1:C:58:ASP:O	1:C:59:VAL:CG1	2.30	0.80
1:S:228:LYS:HE2	1:S:228:LYS:HA	1.64	0.80
1:Q:11:ILE:HD12	1:Q:285:ALA:HA	1.64	0.80
1:W:303:VAL:HA	1:W:439:ASN:OD1	1.82	0.80
1:Q:330:ARG:HD2	1:Q:409:THR:HG22	1.64	0.80
1:U:35:PHE:HE2	1:U:324:LYS:HZ3	1.28	0.80
1:C:15:PHE:HZ	1:C:283:CYS:HG	1.27	0.80
1:F:561:ASP:HB2	1:G:89:ASP:HA	1.63	0.80
1:M:24:GLU:C	1:M:26:ARG:H	1.85	0.80
1:G:282:THR:HG23	1:G:287:LEU:HD11	1.64	0.80
1:M:208:VAL:HG12	1:M:210:PRO:HD3	1.63	0.80
1:E:282:THR:HG23	1:E:287:LEU:HD11	1.64	0.80
1:I:58:ASP:O	1:I:59:VAL:CG1	2.30	0.80
1:T:228:LYS:HE2	1:T:228:LYS:HA	1.63	0.80
1:F:282:THR:HG23	1:F:287:LEU:HD11	1.64	0.80
1:T:208:VAL:HG12	1:T:210:PRO:HD3	1.63	0.80
1:A:82:PRO:HG2	1:L:560:LEU:HD22	1.62	0.80
1:J:58:ASP:O	1:J:59:VAL:CG1	2.30	0.80
1:H:561:ASP:HB2	1:I:89:ASP:HA	1.62	0.79
1:B:282:THR:HG23	1:B:287:LEU:HD11	1.64	0.79
1:I:282:THR:HG23	1:I:287:LEU:HD11	1.64	0.79
1:P:208:VAL:HG12	1:P:210:PRO:HD3	1.63	0.79
1:V:303:VAL:HA	1:V:439:ASN:OD1	1.81	0.79
1:S:208:VAL:HG12	1:S:210:PRO:HD3	1.63	0.79
1:N:303:VAL:HA	1:N:439:ASN:OD1	1.82	0.79
1:A:282:THR:HG23	1:A:287:LEU:HD11	1.64	0.79
1:U:11:ILE:HD12	1:U:285:ALA:HA	1.64	0.79
1:D:58:ASP:O	1:D:59:VAL:CG1	2.30	0.79
1:F:58:ASP:O	1:F:59:VAL:CG1	2.30	0.79
1:N:11:ILE:HD12	1:N:285:ALA:HA	1.63	0.79
1:S:11:ILE:HD12	1:S:285:ALA:HA	1.64	0.79
1:C:282:THR:HG23	1:C:287:LEU:HD11	1.64	0.79
1:D:282:THR:HG23	1:D:287:LEU:HD11	1.64	0.79
1:G:58:ASP:O	1:G:59:VAL:CG1	2.30	0.79
1:E:58:ASP:O	1:E:59:VAL:CG1	2.30	0.79
1:O:63:VAL:HG21	1:O:416:ALA:HB1	1.64	0.79
1:H:282:THR:HG23	1:H:287:LEU:HD11	1.64	0.79
1:V:11:ILE:HD12	1:V:285:ALA:HA	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:28:VAL:HG13	2:Y:97:ALA:HB2	1.63	0.79
1:V:248:LYS:CB	1:V:511:ARG:HH11	1.94	0.79
1:J:248:LYS:H	1:J:248:LYS:HD2	1.48	0.79
1:O:228:LYS:HA	1:O:228:LYS:HE2	1.63	0.79
1:E:248:LYS:HD2	1:E:248:LYS:H	1.48	0.79
1:O:208:VAL:HG12	1:O:210:PRO:HD3	1.63	0.79
1:Q:35:PHE:HE2	1:Q:324:LYS:HZ3	1.27	0.79
1:A:58:ASP:O	1:A:59:VAL:CG1	2.30	0.79
1:P:63:VAL:HG21	1:P:416:ALA:HB1	1.63	0.79
1:N:248:LYS:HD2	1:N:248:LYS:H	1.47	0.79
1:W:63:VAL:HG21	1:W:416:ALA:HB1	1.64	0.79
1:N:330:ARG:HD2	1:N:409:THR:HG22	1.65	0.79
1:X:11:ILE:HD12	1:X:285:ALA:HA	1.65	0.79
1:D:248:LYS:H	1:D:248:LYS:HD2	1.48	0.79
1:L:248:LYS:HD2	1:L:248:LYS:H	1.48	0.79
1:R:24:GLU:C	1:R:26:ARG:H	1.85	0.79
1:O:334:MSE:SE	1:P:404:MSE:HE1	2.32	0.79
1:P:228:LYS:HA	1:P:228:LYS:HE2	1.64	0.79
1:K:248:LYS:HD2	1:K:248:LYS:H	1.48	0.79
1:G:564:GLY:HA2	1:H:554:LEU:HD21	1.64	0.79
1:W:376:ARG:O	1:W:383:ASP:HB3	1.83	0.79
1:W:11:ILE:HD12	1:W:285:ALA:HA	1.63	0.79
1:P:35:PHE:HE2	1:P:324:LYS:HZ3	1.31	0.79
1:H:58:ASP:O	1:H:59:VAL:CG1	2.30	0.79
1:P:303:VAL:HA	1:P:439:ASN:OD1	1.83	0.79
2:Z:143:THR:HB	2:Z:154:GLU:H	1.48	0.79
1:L:282:THR:HG23	1:L:287:LEU:HD11	1.64	0.79
1:B:212:LEU:HD22	1:C:26:ARG:HG2	1.65	0.79
1:T:303:VAL:HA	1:T:439:ASN:OD1	1.83	0.79
1:V:35:PHE:HE2	1:V:324:LYS:HZ3	1.30	0.79
1:K:58:ASP:O	1:K:59:VAL:CG1	2.30	0.79
1:M:63:VAL:HG21	1:M:416:ALA:HB1	1.64	0.79
1:C:248:LYS:HD2	1:C:248:LYS:H	1.48	0.78
1:P:11:ILE:HD12	1:P:285:ALA:HA	1.64	0.78
1:U:208:VAL:HG12	1:U:210:PRO:HD3	1.62	0.78
1:X:24:GLU:C	1:X:26:ARG:H	1.85	0.78
1:Q:561:ASP:OD2	1:R:92:ASP:HB3	1.81	0.78
1:M:554:LEU:HD21	1:N:564:GLY:HA2	1.63	0.78
1:P:144:ILE:HG12	1:P:447:TYR:CE1	2.19	0.78
1:Q:303:VAL:HA	1:Q:439:ASN:OD1	1.83	0.78
1:B:248:LYS:HD2	1:B:248:LYS:H	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:236:GLN:HB2	1:Q:265:LYS:HG2	1.65	0.78
1:N:376:ARG:O	1:N:383:ASP:HB3	1.84	0.78
1:N:24:GLU:C	1:N:26:ARG:H	1.85	0.78
1:V:144:ILE:HG12	1:V:447:TYR:CE1	2.18	0.78
1:O:35:PHE:HE2	1:O:324:LYS:HZ3	1.27	0.78
2:Z:28:VAL:CG1	2:Z:97:ALA:N	2.44	0.78
1:D:334:MSE:HE1	1:F:407:ALA:HB1	1.63	0.78
1:J:35:PHE:CZ	1:J:321:ARG:NE	2.52	0.78
1:O:24:GLU:C	1:O:26:ARG:H	1.86	0.78
1:T:63:VAL:HG21	1:T:416:ALA:HB1	1.65	0.78
1:N:63:VAL:HG21	1:N:416:ALA:HB1	1.65	0.78
1:A:248:LYS:H	1:A:248:LYS:HD2	1.48	0.78
1:T:11:ILE:HD12	1:T:285:ALA:HA	1.62	0.78
1:J:282:THR:HG23	1:J:287:LEU:HD11	1.64	0.78
2:Y:28:VAL:CG2	2:Y:96:LEU:HB3	2.14	0.78
1:S:24:GLU:C	1:S:26:ARG:H	1.86	0.78
1:S:303:VAL:HA	1:S:439:ASN:OD1	1.84	0.78
1:W:236:GLN:HB2	1:W:265:LYS:HG2	1.66	0.78
1:W:24:GLU:C	1:W:26:ARG:H	1.85	0.78
1:L:58:ASP:O	1:L:59:VAL:CG1	2.30	0.78
1:I:248:LYS:H	1:I:248:LYS:HD2	1.48	0.78
1:O:236:GLN:HB2	1:O:265:LYS:HG2	1.66	0.78
1:A:35:PHE:CZ	1:A:321:ARG:NE	2.52	0.78
1:C:35:PHE:CZ	1:C:321:ARG:NE	2.52	0.78
1:D:561:ASP:HB2	1:F:89:ASP:HA	1.64	0.78
1:M:11:ILE:HD12	1:M:285:ALA:HA	1.64	0.78
1:B:58:ASP:O	1:B:59:VAL:CG1	2.30	0.78
1:A:334:MSE:HE1	1:B:407:ALA:HB1	1.64	0.78
1:B:35:PHE:CZ	1:B:321:ARG:NE	2.52	0.78
1:H:35:PHE:CZ	1:H:321:ARG:NE	2.52	0.78
1:K:35:PHE:CZ	1:K:321:ARG:NE	2.52	0.78
1:M:144:ILE:HG12	1:M:447:TYR:CE1	2.19	0.78
1:N:35:PHE:HE2	1:N:324:LYS:HZ3	1.30	0.78
1:V:82:PRO:HG2	1:W:560:LEU:HD22	1.66	0.78
1:R:303:VAL:HA	1:R:439:ASN:OD1	1.83	0.78
1:R:236:GLN:HB2	1:R:265:LYS:HG2	1.66	0.78
1:V:376:ARG:O	1:V:383:ASP:HB3	1.84	0.78
1:D:35:PHE:CZ	1:D:321:ARG:NE	2.52	0.77
1:O:303:VAL:HA	1:O:439:ASN:OD1	1.83	0.77
1:K:282:THR:HG23	1:K:287:LEU:HD11	1.64	0.77
1:M:236:GLN:HB2	1:M:265:LYS:HG2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:11:ILE:HD12	1:F:285:ALA:HA	1.66	0.77
1:I:35:PHE:CZ	1:I:321:ARG:NE	2.52	0.77
2:Z:28:VAL:CG2	2:Z:96:LEU:HB3	2.14	0.77
1:X:35:PHE:HE2	1:X:324:LYS:HZ3	1.30	0.77
1:O:564:GLY:HA2	1:P:554:LEU:HD21	1.65	0.77
1:G:35:PHE:CZ	1:G:321:ARG:NE	2.52	0.77
1:W:248:LYS:HD2	1:W:248:LYS:H	1.48	0.77
1:X:303:VAL:HA	1:X:439:ASN:OD1	1.83	0.77
1:M:303:VAL:HA	1:M:439:ASN:OD1	1.85	0.77
1:P:236:GLN:HB2	1:P:265:LYS:HG2	1.66	0.77
2:Y:143:THR:HB	2:Y:154:GLU:H	1.48	0.77
1:N:236:GLN:HB2	1:N:265:LYS:HG2	1.65	0.77
1:E:35:PHE:CZ	1:E:321:ARG:NE	2.52	0.77
1:I:334:MSE:HE1	1:J:407:ALA:HB1	1.66	0.77
1:N:144:ILE:HG12	1:N:447:TYR:CE1	2.19	0.77
1:V:236:GLN:HB2	1:V:265:LYS:HG2	1.67	0.77
1:R:376:ARG:O	1:R:383:ASP:HB3	1.84	0.77
1:A:182:ASN:ND2	1:B:171:ARG:HH21	1.81	0.77
1:G:11:ILE:HD12	1:G:285:ALA:HA	1.66	0.77
1:H:11:ILE:HD12	1:H:285:ALA:HA	1.66	0.77
1:L:35:PHE:CZ	1:L:321:ARG:NE	2.52	0.77
1:T:24:GLU:C	1:T:26:ARG:H	1.86	0.77
1:X:37:ARG:NH2	1:X:37:ARG:HB3	2.00	0.77
2:Y:78:GLU:CG	2:Y:79:GLY:H	1.98	0.77
1:O:376:ARG:O	1:O:383:ASP:HB3	1.84	0.77
1:Q:376:ARG:O	1:Q:383:ASP:HB3	1.84	0.77
1:D:11:ILE:HD12	1:D:285:ALA:HA	1.66	0.77
1:L:11:ILE:HD12	1:L:285:ALA:HA	1.66	0.77
1:R:35:PHE:HE2	1:R:324:LYS:HZ3	1.30	0.77
1:R:144:ILE:HG12	1:R:447:TYR:CE1	2.20	0.77
1:H:15:PHE:HZ	1:H:283:CYS:HG	1.27	0.77
1:Q:144:ILE:HG12	1:Q:447:TYR:CE1	2.20	0.77
1:W:35:PHE:HE2	1:W:324:LYS:HZ3	1.31	0.77
1:B:11:ILE:HD12	1:B:285:ALA:HA	1.66	0.77
1:U:63:VAL:HG21	1:U:416:ALA:HB1	1.65	0.77
1:E:273:ARG:HH22	1:E:453:LEU:HD21	1.50	0.77
1:F:248:LYS:HD2	1:F:248:LYS:H	1.48	0.77
1:M:35:PHE:HE2	1:M:324:LYS:HZ3	1.30	0.77
1:O:248:LYS:H	1:O:248:LYS:HD2	1.50	0.77
1:Q:334:MSE:SE	1:R:404:MSE:HE1	2.35	0.77
1:H:248:LYS:HD2	1:H:248:LYS:H	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:35:PHE:CZ	1:F:321:ARG:NE	2.52	0.77
1:N:82:PRO:HG2	1:V:560:LEU:HD22	1.66	0.77
1:T:376:ARG:O	1:T:383:ASP:HB3	1.82	0.77
1:O:144:ILE:HG12	1:O:447:TYR:CE1	2.20	0.76
1:U:24:GLU:C	1:U:26:ARG:H	1.86	0.76
1:X:34:PHE:HZ	1:X:328:ARG:NH2	1.83	0.76
1:M:248:LYS:HD2	1:M:248:LYS:H	1.50	0.76
1:G:248:LYS:HD2	1:G:248:LYS:H	1.48	0.76
1:H:273:ARG:HH22	1:H:453:LEU:HD21	1.50	0.76
1:I:273:ARG:HH22	1:I:453:LEU:HD21	1.50	0.76
1:F:273:ARG:HH22	1:F:453:LEU:HD21	1.50	0.76
1:K:11:ILE:HD12	1:K:285:ALA:HA	1.66	0.76
1:K:273:ARG:HH22	1:K:453:LEU:HD21	1.50	0.76
1:U:236:GLN:HB2	1:U:265:LYS:HG2	1.66	0.76
1:A:35:PHE:HE2	1:A:324:LYS:HZ3	1.33	0.76
1:Q:24:GLU:C	1:Q:26:ARG:H	1.87	0.76
1:G:273:ARG:HH22	1:G:453:LEU:HD21	1.50	0.76
1:A:273:ARG:HH22	1:A:453:LEU:HD21	1.50	0.76
1:T:236:GLN:HB2	1:T:265:LYS:HG2	1.66	0.76
1:A:11:ILE:HD12	1:A:285:ALA:HA	1.66	0.76
1:V:24:GLU:C	1:V:26:ARG:H	1.87	0.76
1:C:11:ILE:HD12	1:C:285:ALA:HA	1.66	0.76
1:O:34:PHE:HZ	1:O:328:ARG:NH2	1.83	0.76
1:P:560:LEU:HD22	1:Q:82:PRO:HG2	1.66	0.76
1:V:248:LYS:HD2	1:V:248:LYS:H	1.50	0.76
1:P:24:GLU:C	1:P:26:ARG:H	1.87	0.76
1:X:376:ARG:O	1:X:383:ASP:HB3	1.84	0.76
1:O:35:PHE:CZ	1:O:321:ARG:NE	2.54	0.76
1:U:303:VAL:HA	1:U:439:ASN:OD1	1.84	0.76
2:Z:78:GLU:CG	2:Z:79:GLY:H	1.98	0.76
1:P:44:TRP:O	1:P:45:LEU:HD13	1.86	0.76
1:Q:44:TRP:O	1:Q:45:LEU:HD13	1.86	0.76
1:U:248:LYS:H	1:U:248:LYS:HD2	1.49	0.76
1:X:63:VAL:HG21	1:X:416:ALA:HB1	1.65	0.76
1:O:11:ILE:HD12	1:O:285:ALA:HA	1.67	0.76
1:S:236:GLN:HB2	1:S:265:LYS:HG2	1.66	0.76
1:G:49:THR:HG22	1:G:49:THR:O	1.86	0.76
1:I:11:ILE:HD12	1:I:285:ALA:HA	1.66	0.76
1:M:35:PHE:CZ	1:M:321:ARG:NE	2.54	0.76
1:D:273:ARG:HH22	1:D:453:LEU:HD21	1.50	0.76
1:U:376:ARG:O	1:U:383:ASP:HB3	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:139:SER:HB3	1:V:455:THR:HG23	1.67	0.76
1:Q:35:PHE:CZ	1:Q:321:ARG:NE	2.54	0.76
1:T:34:PHE:HZ	1:T:328:ARG:NH2	1.84	0.76
1:T:248:LYS:HD2	1:T:248:LYS:H	1.50	0.76
1:S:35:PHE:CZ	1:S:321:ARG:NE	2.54	0.75
1:S:144:ILE:HG12	1:S:447:TYR:CE1	2.20	0.75
1:V:92:ASP:HB3	1:W:561:ASP:OD2	1.86	0.75
1:S:376:ARG:O	1:S:383:ASP:HB3	1.84	0.75
1:F:15:PHE:HZ	1:F:283:CYS:HG	1.33	0.75
1:S:35:PHE:HE2	1:S:324:LYS:HZ3	1.32	0.75
1:U:93:VAL:HG11	1:U:458:ARG:HG3	1.68	0.75
1:W:511:ARG:HA	1:W:513:ARG:HD2	1.68	0.75
1:J:273:ARG:HH22	1:J:453:LEU:HD21	1.50	0.75
1:U:282:THR:HG23	1:U:287:LEU:HD11	1.69	0.75
1:P:35:PHE:CZ	1:P:321:ARG:NE	2.55	0.75
2:Y:78:GLU:HG3	2:Y:79:GLY:H	1.52	0.75
1:Q:248:LYS:H	1:Q:248:LYS:HD2	1.49	0.75
1:R:63:VAL:HG21	1:R:416:ALA:HB1	1.66	0.75
1:P:282:THR:HG23	1:P:287:LEU:HD11	1.68	0.75
1:X:93:VAL:HG11	1:X:458:ARG:HG3	1.69	0.75
1:E:11:ILE:HD12	1:E:285:ALA:HA	1.66	0.75
1:F:49:THR:O	1:F:49:THR:HG22	1.86	0.75
1:J:11:ILE:HD12	1:J:285:ALA:HA	1.66	0.75
1:X:34:PHE:CZ	1:X:328:ARG:NH2	2.55	0.75
1:X:282:THR:HG23	1:X:287:LEU:HD11	1.69	0.75
1:P:232:ALA:HB2	1:P:269:ARG:H	1.51	0.75
1:E:49:THR:O	1:E:49:THR:HG22	1.86	0.75
1:X:236:GLN:HB2	1:X:265:LYS:HG2	1.66	0.75
1:E:5:GLU:HG2	1:E:6:ASN:H	1.52	0.75
1:D:49:THR:O	1:D:49:THR:HG22	1.86	0.75
1:T:44:TRP:O	1:T:45:LEU:HD13	1.87	0.75
1:W:144:ILE:HG12	1:W:447:TYR:CE1	2.20	0.75
1:T:511:ARG:HA	1:T:513:ARG:HD2	1.68	0.75
1:L:273:ARG:HH22	1:L:453:LEU:HD21	1.50	0.75
1:N:232:ALA:HB2	1:N:269:ARG:H	1.51	0.75
1:P:561:ASP:HB2	1:Q:89:ASP:HA	1.67	0.75
2:Z:34:LEU:HD12	2:Z:104:TYR:HD2	1.51	0.75
1:C:273:ARG:HH22	1:C:453:LEU:HD21	1.50	0.75
1:D:5:GLU:HG2	1:D:6:ASN:H	1.52	0.75
1:M:232:ALA:HB2	1:M:269:ARG:H	1.51	0.75
1:M:44:TRP:O	1:M:45:LEU:HD13	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:44:TRP:O	1:S:45:LEU:HD13	1.86	0.75
1:S:248:LYS:HD2	1:S:248:LYS:H	1.49	0.75
1:F:236:GLN:HB2	1:F:265:LYS:HG2	1.68	0.75
1:P:34:PHE:HZ	1:P:328:ARG:NH2	1.84	0.75
1:K:236:GLN:HB2	1:K:265:LYS:HG2	1.68	0.75
1:G:273:ARG:HH22	1:G:453:LEU:CD2	2.00	0.75
1:A:5:GLU:HG2	1:A:6:ASN:H	1.52	0.75
1:K:15:PHE:HZ	1:K:283:CYS:HG	1.33	0.74
1:N:93:VAL:HG11	1:N:458:ARG:HG3	1.68	0.74
1:X:330:ARG:HH21	1:X:409:THR:CG2	2.00	0.74
1:Q:511:ARG:HA	1:Q:513:ARG:HD2	1.69	0.74
1:P:330:ARG:HD2	1:P:409:THR:HG22	1.68	0.74
1:F:273:ARG:HH22	1:F:453:LEU:CD2	2.00	0.74
1:N:282:THR:HG23	1:N:287:LEU:HD11	1.67	0.74
1:A:78:VAL:CG2	1:A:444:LEU:HD11	2.15	0.74
1:M:34:PHE:HZ	1:M:328:ARG:NH2	1.84	0.74
1:R:93:VAL:HG11	1:R:458:ARG:HG3	1.69	0.74
1:S:93:VAL:HG11	1:S:458:ARG:HG3	1.68	0.74
1:T:34:PHE:CZ	1:T:328:ARG:NH2	2.56	0.74
1:D:236:GLN:HB2	1:D:265:LYS:HG2	1.68	0.74
1:G:5:GLU:HG2	1:G:6:ASN:H	1.52	0.74
1:C:49:THR:O	1:C:49:THR:HG22	1.86	0.74
1:F:34:PHE:CZ	1:F:328:ARG:NH2	2.47	0.74
1:J:49:THR:HG22	1:J:49:THR:O	1.86	0.74
1:M:37:ARG:NH2	1:M:37:ARG:HB3	2.03	0.74
1:B:273:ARG:HH22	1:B:453:LEU:CD2	2.00	0.74
1:E:273:ARG:HH22	1:E:453:LEU:CD2	2.00	0.74
1:I:35:PHE:HE2	1:I:324:LYS:HZ3	1.34	0.74
1:O:34:PHE:CZ	1:O:328:ARG:NH2	2.56	0.74
1:X:248:LYS:HD2	1:X:248:LYS:H	1.51	0.74
1:R:248:LYS:H	1:R:248:LYS:HD2	1.51	0.74
1:H:5:GLU:HG2	1:H:6:ASN:H	1.52	0.74
1:F:564:GLY:HA2	1:G:554:LEU:HD21	1.70	0.74
1:A:560:LEU:HD22	1:B:82:PRO:HG2	1.69	0.74
1:C:212:LEU:HD22	1:E:26:ARG:HG2	1.70	0.74
1:K:49:THR:O	1:K:49:THR:HG22	1.86	0.74
1:K:273:ARG:HH22	1:K:453:LEU:CD2	2.00	0.74
1:A:273:ARG:HH22	1:A:453:LEU:CD2	2.00	0.74
1:L:577:ILE:HG12	1:L:582:LYS:HG2	1.69	0.74
1:W:282:THR:HG23	1:W:287:LEU:HD11	1.69	0.74
1:R:282:THR:HG23	1:R:287:LEU:HD11	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:577:ILE:HG12	1:E:582:LYS:HG2	1.69	0.74
1:O:93:VAL:HG11	1:O:458:ARG:HG3	1.68	0.74
2:Z:78:GLU:CA	2:Z:78:GLU:OE1	2.36	0.74
1:R:34:PHE:HZ	1:R:328:ARG:NH2	1.85	0.74
1:T:144:ILE:HG12	1:T:447:TYR:CE1	2.21	0.74
1:U:34:PHE:HZ	1:U:328:ARG:NH2	1.85	0.74
1:U:144:ILE:HG12	1:U:447:TYR:CE1	2.21	0.74
1:V:44:TRP:O	1:V:45:LEU:HD13	1.88	0.74
1:U:330:ARG:HH21	1:U:409:THR:CG2	2.01	0.74
1:H:273:ARG:HH22	1:H:453:LEU:CD2	2.00	0.74
1:A:236:GLN:HB2	1:A:265:LYS:HG2	1.68	0.74
1:R:139:SER:HB3	1:R:455:THR:HG23	1.69	0.74
1:K:577:ILE:HG12	1:K:582:LYS:HG2	1.69	0.74
1:M:282:THR:HG23	1:M:287:LEU:HD11	1.69	0.74
1:L:49:THR:HG22	1:L:49:THR:O	1.86	0.74
1:N:35:PHE:HE1	1:N:321:ARG:HH11	1.36	0.74
1:P:93:VAL:HG11	1:P:458:ARG:HG3	1.69	0.74
1:Q:93:VAL:HG11	1:Q:458:ARG:HG3	1.69	0.74
1:S:35:PHE:HE1	1:S:321:ARG:HH11	1.36	0.74
1:X:35:PHE:CZ	1:X:321:ARG:NE	2.55	0.74
1:G:236:GLN:HB2	1:G:265:LYS:HG2	1.68	0.74
1:B:236:GLN:HB2	1:B:265:LYS:HG2	1.68	0.74
1:H:564:GLY:HA2	1:I:554:LEU:HD21	1.69	0.74
1:A:577:ILE:HG12	1:A:582:LYS:HG2	1.69	0.74
1:W:232:ALA:HB2	1:W:269:ARG:H	1.53	0.74
1:J:577:ILE:HG12	1:J:582:LYS:HG2	1.69	0.74
1:M:35:PHE:HE1	1:M:321:ARG:HH11	1.35	0.74
1:O:44:TRP:O	1:O:45:LEU:HD13	1.88	0.74
1:L:78:VAL:CG2	1:L:444:LEU:HD11	2.15	0.74
1:N:34:PHE:HZ	1:N:328:ARG:NH2	1.86	0.74
1:Q:34:PHE:HZ	1:Q:328:ARG:NH2	1.86	0.74
1:R:34:PHE:CZ	1:R:328:ARG:NH2	2.56	0.74
1:B:273:ARG:HH22	1:B:453:LEU:HD21	1.50	0.74
1:H:236:GLN:HB2	1:H:265:LYS:HG2	1.68	0.74
1:L:236:GLN:HB2	1:L:265:LYS:HG2	1.69	0.74
1:L:273:ARG:HH22	1:L:453:LEU:CD2	2.00	0.74
1:B:577:ILE:HG12	1:B:582:LYS:HG2	1.69	0.74
1:L:5:GLU:HG2	1:L:6:ASN:H	1.52	0.74
1:G:560:LEU:HD22	1:H:82:PRO:HG2	1.69	0.74
1:T:34:PHE:HZ	1:T:328:ARG:HH22	1.35	0.74
1:U:35:PHE:CZ	1:U:321:ARG:NE	2.55	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:44:TRP:O	1:W:45:LEU:HD13	1.87	0.74
1:P:248:LYS:H	1:P:248:LYS:HD2	1.51	0.74
1:V:330:ARG:HH21	1:V:409:THR:CG2	2.00	0.74
1:I:273:ARG:HH22	1:I:453:LEU:CD2	2.00	0.74
1:C:236:GLN:HB2	1:C:265:LYS:HG2	1.68	0.74
1:E:236:GLN:HB2	1:E:265:LYS:HG2	1.68	0.74
1:M:93:VAL:HG11	1:M:458:ARG:HG3	1.68	0.74
1:O:35:PHE:HE1	1:O:321:ARG:HH11	1.36	0.74
1:P:34:PHE:CZ	1:P:328:ARG:NH2	2.56	0.74
1:S:37:ARG:HB3	1:S:37:ARG:NH2	2.03	0.74
1:A:554:LEU:HD21	1:L:564:GLY:HA2	1.70	0.74
1:H:49:THR:O	1:H:49:THR:HG22	1.86	0.73
1:J:35:PHE:HE2	1:J:324:LYS:HZ3	1.34	0.73
1:T:35:PHE:CZ	1:T:321:ARG:NE	2.56	0.73
1:M:139:SER:HB3	1:M:455:THR:HG23	1.70	0.73
1:S:282:THR:HG23	1:S:287:LEU:HD11	1.70	0.73
1:F:78:VAL:CG2	1:F:444:LEU:HD11	2.15	0.73
1:G:34:PHE:CZ	1:G:328:ARG:NH2	2.48	0.73
1:I:560:LEU:HD22	1:J:82:PRO:HG2	1.70	0.73
1:M:34:PHE:HZ	1:M:328:ARG:HH22	1.36	0.73
1:N:136:SER:HB3	1:Q:325:ASP:OD2	87.72	0.73
1:R:35:PHE:CZ	1:R:321:ARG:NE	2.56	0.73
1:U:136:SER:HB3	1:V:325:ASP:OD2	87.87	0.73
1:V:34:PHE:CZ	1:V:328:ARG:NH2	2.57	0.73
1:V:93:VAL:HG11	1:V:458:ARG:HG3	1.69	0.73
1:C:5:GLU:HG2	1:C:6:ASN:H	1.52	0.73
1:K:5:GLU:HG2	1:K:6:ASN:H	1.52	0.73
1:A:74:ASN:CB	1:A:75:PRO:HD3	4.11	0.73
1:J:273:ARG:HH22	1:J:453:LEU:CD2	2.00	0.73
1:W:93:VAL:HG11	1:W:458:ARG:HG3	1.68	0.73
1:C:577:ILE:HG12	1:C:582:LYS:HG2	1.69	0.73
1:B:49:THR:O	1:B:49:THR:HG22	1.86	0.73
1:S:34:PHE:HZ	1:S:328:ARG:NH2	1.85	0.73
1:N:92:ASP:HB3	1:V:561:ASP:OD2	1.88	0.73
1:X:144:ILE:HG12	1:X:447:TYR:CE1	2.22	0.73
1:M:15:PHE:HZ	1:M:283:CYS:HG	1.34	0.73
1:T:560:LEU:HD22	1:W:82:PRO:HG2	1.68	0.73
1:O:282:THR:HG23	1:O:287:LEU:HD11	1.69	0.73
1:M:376:ARG:O	1:M:383:ASP:HB3	1.87	0.73
1:A:49:THR:HG22	1:A:49:THR:O	1.86	0.73
1:G:35:PHE:HE2	1:G:324:LYS:HZ3	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:74:ASN:CB	1:G:75:PRO:HD3	4.11	0.73
1:I:74:ASN:CB	1:I:75:PRO:HD3	4.11	0.73
1:X:34:PHE:HZ	1:X:328:ARG:HH22	1.35	0.73
2:Y:34:LEU:HD12	2:Y:104:TYR:HD2	1.52	0.73
1:J:236:GLN:HB2	1:J:265:LYS:HG2	1.69	0.73
1:F:577:ILE:HG12	1:F:582:LYS:HG2	1.69	0.73
1:D:44:TRP:O	1:D:45:LEU:HD13	1.89	0.73
1:C:560:LEU:HD22	1:E:82:PRO:HG2	1.69	0.73
1:H:74:ASN:CB	1:H:75:PRO:HD3	4.11	0.73
1:J:74:ASN:CB	1:J:75:PRO:HD3	4.11	0.73
1:L:44:TRP:O	1:L:45:LEU:HD13	1.89	0.73
1:U:89:ASP:HA	1:X:561:ASP:HB2	1.69	0.73
2:Y:34:LEU:C	2:Y:35:THR:HG23	2.09	0.73
1:U:232:ALA:HB2	1:U:269:ARG:H	1.54	0.73
1:I:577:ILE:HG12	1:I:582:LYS:HG2	1.69	0.73
1:S:231:THR:HG21	1:S:249:ARG:HH11	1.53	0.73
1:C:74:ASN:CB	1:C:75:PRO:HD3	4.11	0.73
1:I:49:THR:O	1:I:49:THR:HG22	1.86	0.73
2:Y:78:GLU:OE1	2:Y:78:GLU:CA	2.36	0.73
1:D:273:ARG:HH22	1:D:453:LEU:CD2	2.00	0.73
1:I:236:GLN:HB2	1:I:265:LYS:HG2	1.69	0.73
1:G:577:ILE:HG12	1:G:582:LYS:HG2	1.69	0.73
1:Q:282:THR:HG23	1:Q:287:LEU:HD11	1.71	0.73
1:V:34:PHE:HZ	1:V:328:ARG:NH2	1.86	0.73
1:T:561:ASP:OD2	1:W:92:ASP:HB3	1.89	0.73
1:R:511:ARG:HA	1:R:513:ARG:HD2	1.70	0.73
1:R:561:ASP:HB2	1:X:89:ASP:HA	1.70	0.73
1:T:232:ALA:HB2	1:T:269:ARG:H	1.54	0.73
1:E:74:ASN:CB	1:E:75:PRO:HD3	4.11	0.73
1:J:334:MSE:HE1	1:K:407:ALA:HB1	1.69	0.73
2:Z:74:ASN:CB	2:Z:75:PRO:HD3	2.18	0.73
1:O:139:SER:HB3	1:O:455:THR:HG23	1.71	0.73
1:J:5:GLU:HG2	1:J:6:ASN:H	1.52	0.73
1:X:44:TRP:O	1:X:45:LEU:HD13	1.88	0.73
1:C:44:TRP:O	1:C:45:LEU:HD13	1.89	0.72
1:G:44:TRP:O	1:G:45:LEU:HD13	1.89	0.72
1:K:44:TRP:O	1:K:45:LEU:HD13	1.89	0.72
2:Z:78:GLU:HG3	2:Z:79:GLY:H	1.52	0.72
1:M:511:ARG:HA	1:M:513:ARG:HD2	1.70	0.72
2:Z:34:LEU:C	2:Z:35:THR:HG23	2.09	0.72
1:Q:139:SER:HB3	1:Q:455:THR:HG23	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:232:ALA:HB2	1:R:269:ARG:H	1.54	0.72
1:H:577:ILE:HG12	1:H:582:LYS:HG2	1.69	0.72
1:D:577:ILE:HG12	1:D:582:LYS:HG2	1.69	0.72
1:S:232:ALA:HB2	1:S:269:ARG:H	1.53	0.72
1:C:405:LEU:O	1:C:409:THR:HG23	1.90	0.72
1:E:158:TRP:HB3	1:E:173:CYS:HA	1.71	0.72
1:G:158:TRP:HB3	1:G:173:CYS:HA	1.72	0.72
1:I:44:TRP:O	1:I:45:LEU:HD13	1.89	0.72
1:Q:37:ARG:HB3	1:Q:37:ARG:NH2	2.04	0.72
1:U:511:ARG:HA	1:U:513:ARG:HD2	1.71	0.72
1:B:74:ASN:CB	1:B:75:PRO:HD3	4.11	0.72
1:D:158:TRP:HB3	1:D:173:CYS:HA	1.72	0.72
1:E:405:LEU:O	1:E:409:THR:HG23	1.90	0.72
1:F:405:LEU:O	1:F:409:THR:HG23	1.90	0.72
1:M:34:PHE:CZ	1:M:328:ARG:NH2	2.56	0.72
1:V:35:PHE:CZ	1:V:321:ARG:NE	2.58	0.72
1:B:5:GLU:HG2	1:B:6:ASN:H	1.52	0.72
1:B:34:PHE:CZ	1:B:328:ARG:NH2	2.47	0.72
1:D:74:ASN:CB	1:D:75:PRO:HD3	4.11	0.72
1:F:334:MSE:HE1	1:G:407:ALA:HB1	1.71	0.72
1:H:44:TRP:O	1:H:45:LEU:HD13	1.89	0.72
1:R:44:TRP:O	1:R:45:LEU:HD13	1.89	0.72
1:T:93:VAL:HG11	1:T:458:ARG:HG3	1.70	0.72
1:U:34:PHE:CZ	1:U:328:ARG:NH2	2.56	0.72
1:U:554:LEU:HD21	1:X:564:GLY:HA2	1.72	0.72
1:B:44:TRP:O	1:B:45:LEU:HD13	1.89	0.72
1:F:158:TRP:HB3	1:F:173:CYS:HA	1.71	0.72
1:J:44:TRP:O	1:J:45:LEU:HD13	1.89	0.72
1:K:158:TRP:HB3	1:K:173:CYS:HA	1.71	0.72
1:L:34:PHE:CZ	1:L:328:ARG:NH2	2.48	0.72
1:R:37:ARG:NH2	1:R:37:ARG:HB3	2.04	0.72
1:U:44:TRP:O	1:U:45:LEU:HD13	1.89	0.72
1:W:34:PHE:HZ	1:W:328:ARG:NH2	1.85	0.72
1:V:511:ARG:HA	1:V:513:ARG:HD2	1.70	0.72
1:N:511:ARG:HA	1:N:513:ARG:HD2	1.70	0.72
1:F:5:GLU:HG2	1:F:6:ASN:H	1.52	0.72
1:V:232:ALA:HB2	1:V:269:ARG:H	1.54	0.72
1:A:405:LEU:O	1:A:409:THR:HG23	1.90	0.72
1:B:158:TRP:HB3	1:B:173:CYS:HA	1.71	0.72
1:C:325:ASP:OD2	2:Z:145:SER:HB3	1.89	0.72
1:I:158:TRP:HB3	1:I:173:CYS:HA	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:325:ASP:OD2	1:K:136:SER:HB3	208.06	0.72
1:U:37:ARG:NH2	1:U:37:ARG:HB3	2.04	0.72
2:Y:74:ASN:CB	2:Y:75:PRO:HD3	2.18	0.72
1:K:405:LEU:O	1:K:409:THR:HG23	1.90	0.72
1:A:44:TRP:O	1:A:45:LEU:HD13	1.89	0.72
1:F:44:TRP:O	1:F:45:LEU:HD13	1.89	0.72
1:A:26:ARG:HG2	1:L:212:LEU:HD22	1.71	0.72
1:V:577:ILE:HG12	1:V:582:LYS:HG2	1.72	0.72
1:O:232:ALA:HB2	1:O:269:ARG:H	1.52	0.72
1:A:457:MSE:O	1:A:457:MSE:HG3	1.90	0.72
1:N:34:PHE:HZ	1:N:328:ARG:HH22	1.38	0.72
1:O:330:ARG:HH21	1:O:409:THR:CG2	2.02	0.72
1:C:273:ARG:HH22	1:C:453:LEU:CD2	2.00	0.72
1:I:5:GLU:HG2	1:I:6:ASN:H	1.52	0.72
1:V:282:THR:HG23	1:V:287:LEU:HD11	1.70	0.72
1:G:212:LEU:HD22	1:H:26:ARG:HG2	1.71	0.72
1:J:34:PHE:CZ	1:J:328:ARG:NH2	2.47	0.72
1:O:37:ARG:NH2	1:O:37:ARG:HB3	2.04	0.72
1:N:34:PHE:CZ	1:N:328:ARG:NH2	2.58	0.72
1:S:330:ARG:NH2	1:S:409:THR:HG21	2.05	0.72
1:X:232:ALA:HB2	1:X:269:ARG:H	1.53	0.72
1:D:405:LEU:O	1:D:409:THR:HG23	1.90	0.72
1:C:182:ASN:ND2	1:E:171:ARG:HH21	1.88	0.72
1:L:158:TRP:HB3	1:L:173:CYS:HA	1.71	0.72
1:N:44:TRP:O	1:N:45:LEU:HD13	1.89	0.72
1:W:34:PHE:HZ	1:W:328:ARG:HH22	1.38	0.72
1:N:139:SER:HB3	1:N:455:THR:HG23	1.70	0.72
1:W:450:GLN:HG2	1:W:450:GLN:O	1.90	0.72
1:Q:232:ALA:HB2	1:Q:269:ARG:H	1.54	0.72
1:R:564:GLY:HA2	1:X:554:LEU:HD21	1.70	0.72
1:A:303:VAL:HA	1:A:439:ASN:ND2	2.05	0.71
1:N:35:PHE:CZ	1:N:321:ARG:NE	2.57	0.71
1:X:35:PHE:HE1	1:X:321:ARG:HH11	1.37	0.71
1:C:246:TYR:HD2	1:C:511:ARG:HB3	1.55	0.71
1:E:246:TYR:HD2	1:E:511:ARG:HB3	1.55	0.71
1:C:334:MSE:HE1	1:E:407:ALA:HB1	1.70	0.71
1:I:78:VAL:CG2	1:I:444:LEU:HD11	2.15	0.71
1:P:78:VAL:HG12	1:P:79:LEU:N	2.05	0.71
1:W:35:PHE:HE1	1:W:321:ARG:HH11	1.37	0.71
1:V:246:TYR:HD2	1:V:511:ARG:HB2	1.54	0.71
1:E:44:TRP:O	1:E:45:LEU:HD13	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:303:VAL:HA	1:G:439:ASN:ND2	2.05	0.71
1:J:303:VAL:HA	1:J:439:ASN:ND2	2.05	0.71
1:J:405:LEU:O	1:J:409:THR:HG23	1.89	0.71
1:S:139:SER:HB3	1:S:455:THR:HG23	1.73	0.71
1:B:457:MSE:HG3	1:B:457:MSE:O	1.90	0.71
1:C:158:TRP:HB3	1:C:173:CYS:HA	1.71	0.71
1:F:212:LEU:HD22	1:G:26:ARG:HG2	1.72	0.71
1:H:405:LEU:O	1:H:409:THR:HG23	1.90	0.71
1:I:405:LEU:O	1:I:409:THR:HG23	1.90	0.71
1:K:457:MSE:HG3	1:K:457:MSE:O	1.90	0.71
1:P:35:PHE:HE1	1:P:321:ARG:HH11	1.38	0.71
1:Q:34:PHE:CZ	1:Q:328:ARG:NH2	2.57	0.71
1:P:561:ASP:OD2	1:Q:92:ASP:HB3	1.90	0.71
1:S:136:SER:HB3	1:W:325:ASP:OD2	57.15	0.71
1:X:248:LYS:HB3	1:X:511:ARG:NH1	2.02	0.71
1:P:330:ARG:HH21	1:P:409:THR:CG2	2.01	0.71
1:B:246:TYR:HD2	1:B:511:ARG:HB3	1.55	0.71
1:L:303:VAL:HA	1:L:439:ASN:ND2	2.05	0.71
1:W:34:PHE:CZ	1:W:328:ARG:NH2	2.57	0.71
1:M:564:GLY:HA2	1:O:554:LEU:HD21	1.72	0.71
1:M:450:GLN:HG2	1:M:450:GLN:O	1.90	0.71
1:B:405:LEU:O	1:B:409:THR:HG23	1.90	0.71
1:C:35:PHE:HE2	1:C:324:LYS:HZ3	1.39	0.71
1:K:303:VAL:HA	1:K:439:ASN:ND2	2.05	0.71
1:U:82:PRO:HG2	1:X:560:LEU:HD22	1.71	0.71
1:V:37:ARG:HB3	1:V:37:ARG:NH2	2.05	0.71
1:S:511:ARG:HA	1:S:513:ARG:HD2	1.73	0.71
1:P:246:TYR:HD2	1:P:511:ARG:HB2	1.55	0.71
1:T:577:ILE:HG12	1:T:582:LYS:HG2	1.73	0.71
1:B:78:VAL:CG2	1:B:444:LEU:HD11	2.15	0.71
1:C:303:VAL:HA	1:C:439:ASN:ND2	2.05	0.71
1:D:34:PHE:CZ	1:D:328:ARG:NH2	2.47	0.71
1:D:78:VAL:CG2	1:D:444:LEU:HD11	2.15	0.71
1:K:78:VAL:CG2	1:K:444:LEU:HD11	2.15	0.71
1:W:35:PHE:CZ	1:W:321:ARG:NE	2.59	0.71
1:W:78:VAL:HG12	1:W:79:LEU:N	2.05	0.71
1:O:511:ARG:HA	1:O:513:ARG:HD2	1.71	0.71
1:R:330:ARG:HH21	1:R:409:THR:CG2	2.02	0.71
1:Q:330:ARG:HH21	1:Q:409:THR:CG2	2.02	0.71
1:H:158:TRP:HB3	1:H:173:CYS:HA	1.71	0.71
1:H:303:VAL:HA	1:H:439:ASN:ND2	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:35:PHE:HE2	1:H:324:LYS:HZ3	1.38	0.71
1:J:158:TRP:HB3	1:J:173:CYS:HA	1.72	0.71
1:K:99:ARG:HH12	1:K:530:GLN:HE21	1.39	0.71
1:O:34:PHE:HZ	1:O:328:ARG:HH22	1.34	0.71
2:Z:46:VAL:CG1	2:Z:77:ALA:HB1	2.19	0.71
1:R:15:PHE:HZ	1:R:283:CYS:HG	1.39	0.71
1:D:246:TYR:HD2	1:D:511:ARG:HB3	1.55	0.71
1:A:108:LYS:HD2	1:B:438:LEU:HD11	1.71	0.71
1:D:564:GLY:HA2	1:F:554:LEU:HD21	1.72	0.71
1:G:405:LEU:O	1:G:409:THR:HG23	1.90	0.71
1:M:330:ARG:NH2	1:M:409:THR:HG21	2.06	0.71
1:S:330:ARG:HH21	1:S:409:THR:CG2	2.01	0.71
1:S:450:GLN:O	1:S:450:GLN:HG2	1.91	0.71
1:U:450:GLN:HG2	1:U:450:GLN:O	1.90	0.71
1:G:561:ASP:HB2	1:H:89:ASP:HA	1.70	0.71
1:H:78:VAL:CG2	1:H:444:LEU:HD11	2.15	0.71
1:S:34:PHE:CZ	1:S:328:ARG:NH2	2.56	0.71
1:T:136:SER:HB3	1:T:325:ASP:OD2	52.59	0.71
1:X:37:ARG:HB3	1:X:37:ARG:HH21	1.56	0.71
1:X:246:TYR:HD2	1:X:511:ARG:HB2	1.56	0.71
1:M:330:ARG:HH21	1:M:409:THR:CG2	2.03	0.71
1:J:246:TYR:HD2	1:J:511:ARG:HB3	1.56	0.71
1:K:246:TYR:HD2	1:K:511:ARG:HB3	1.55	0.71
1:F:246:TYR:HD2	1:F:511:ARG:HB3	1.55	0.71
1:O:113:ILE:HD13	1:O:150:HIS:CE1	2.26	0.71
1:C:99:ARG:HH12	1:C:530:GLN:HE21	1.39	0.70
1:F:303:VAL:HA	1:F:439:ASN:ND2	2.05	0.70
1:F:74:ASN:CB	1:F:75:PRO:HD3	4.11	0.70
1:I:34:PHE:CZ	1:I:328:ARG:NH2	2.48	0.70
1:J:78:VAL:CG2	1:J:444:LEU:HD11	2.15	0.70
1:G:246:TYR:HD2	1:G:511:ARG:HB3	1.55	0.70
1:A:246:TYR:HD2	1:A:511:ARG:HB3	1.55	0.70
1:J:457:MSE:HG3	1:J:457:MSE:O	1.90	0.70
1:E:41:TRP:CZ3	1:E:42:ASP:HB3	2.26	0.70
1:E:303:VAL:HA	1:E:439:ASN:ND2	2.05	0.70
1:I:303:VAL:HA	1:I:439:ASN:ND2	2.05	0.70
1:I:457:MSE:HG3	1:I:457:MSE:O	1.90	0.70
1:I:99:ARG:HH12	1:I:530:GLN:HE21	1.39	0.70
1:K:34:PHE:CZ	1:K:328:ARG:NH2	2.48	0.70
1:P:334:MSE:SE	1:Q:404:MSE:HE1	2.41	0.70
1:L:405:LEU:O	1:L:409:THR:HG23	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:575:GLN:O	1:T:579:MSE:HG2	1.92	0.70
1:M:238:PRO:HG3	1:M:263:PHE:HB3	1.73	0.70
1:N:113:ILE:HD13	1:N:150:HIS:CE1	2.26	0.70
1:Q:35:PHE:HE1	1:Q:321:ARG:HH11	1.39	0.70
1:T:37:ARG:HB3	1:T:37:ARG:NH2	2.07	0.70
1:U:35:PHE:HE1	1:U:321:ARG:HH11	1.37	0.70
1:O:246:TYR:HD2	1:O:511:ARG:HB2	1.55	0.70
1:V:330:ARG:NH2	1:V:409:THR:HG21	2.04	0.70
1:R:577:ILE:HG12	1:R:582:LYS:HG2	1.73	0.70
1:S:577:ILE:HG12	1:S:582:LYS:HG2	1.71	0.70
1:X:450:GLN:HG2	1:X:450:GLN:O	1.91	0.70
1:T:238:PRO:HG3	1:T:263:PHE:HB3	1.73	0.70
1:B:41:TRP:CZ3	1:B:42:ASP:HB3	2.26	0.70
1:C:78:VAL:CG2	1:C:444:LEU:HD11	2.15	0.70
1:F:34:PHE:HE1	1:F:324:LYS:HZ2	1.39	0.70
1:Q:246:TYR:HD2	1:Q:511:ARG:HB2	1.56	0.70
1:U:330:ARG:NH2	1:U:409:THR:HG21	2.05	0.70
1:N:577:ILE:HG12	1:N:582:LYS:HG2	1.73	0.70
1:R:94:LEU:HA	1:R:97:MSE:HE2	1.74	0.70
1:Q:450:GLN:HG2	1:Q:450:GLN:O	1.92	0.70
1:E:457:MSE:HG3	1:E:457:MSE:O	1.90	0.70
1:A:158:TRP:HB3	1:A:173:CYS:HA	1.72	0.70
1:E:99:ARG:HH12	1:E:530:GLN:HE21	1.39	0.70
1:N:246:TYR:HD2	1:N:511:ARG:HB2	1.56	0.70
1:D:457:MSE:O	1:D:457:MSE:HG3	1.90	0.70
1:F:457:MSE:O	1:F:457:MSE:HG3	1.90	0.70
1:A:26:ARG:HH21	1:A:30:LYS:HB2	1.57	0.70
1:F:41:TRP:CZ3	1:F:42:ASP:HB3	2.26	0.70
1:I:26:ARG:HH21	1:I:30:LYS:HB2	1.57	0.70
1:K:26:ARG:HH21	1:K:30:LYS:HB2	1.57	0.70
1:W:37:ARG:HB3	1:W:37:ARG:NH2	2.07	0.70
1:J:26:ARG:HH21	1:J:30:LYS:HB2	1.57	0.70
1:T:282:THR:HG23	1:T:287:LEU:HD11	1.73	0.70
1:U:577:ILE:HG12	1:U:582:LYS:HG2	1.73	0.70
1:B:99:ARG:HH12	1:B:530:GLN:HE21	1.39	0.70
1:C:41:TRP:CZ3	1:C:42:ASP:HB3	2.26	0.70
1:D:303:VAL:HA	1:D:439:ASN:ND2	2.05	0.70
1:G:26:ARG:HH21	1:G:30:LYS:HB2	1.57	0.70
1:G:334:MSE:HE1	1:H:407:ALA:HB1	1.72	0.70
1:H:26:ARG:HH21	1:H:30:LYS:HB2	1.57	0.70
1:L:99:ARG:HH12	1:L:530:GLN:HE21	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:577:ILE:HG12	1:X:582:LYS:HG2	1.73	0.70
1:B:303:VAL:HA	1:B:439:ASN:ND2	2.05	0.70
1:G:78:VAL:CG2	1:G:444:LEU:HD11	2.15	0.70
1:H:212:LEU:HD22	1:I:26:ARG:HG2	1.72	0.70
2:Y:46:VAL:CG1	2:Y:77:ALA:HB1	2.19	0.70
1:S:246:TYR:HD2	1:S:511:ARG:HB2	1.56	0.70
1:M:246:TYR:HD2	1:M:511:ARG:HB2	1.56	0.70
1:U:248:LYS:HD3	1:U:251:ILE:HB	1.74	0.70
1:T:330:ARG:HH21	1:T:409:THR:CG2	2.03	0.70
1:P:511:ARG:HA	1:P:513:ARG:HD2	1.72	0.70
1:M:404:MSE:HE1	1:N:334:MSE:SE	2.41	0.70
1:H:246:TYR:HD2	1:H:511:ARG:HB3	1.55	0.70
1:F:26:ARG:HH21	1:F:30:LYS:HB2	1.57	0.70
1:I:35:PHE:C	1:I:37:ARG:H	1.95	0.70
1:O:15:PHE:HZ	1:O:283:CYS:HG	1.39	0.70
1:P:37:ARG:HB3	1:P:37:ARG:NH2	2.06	0.70
1:T:35:PHE:HE1	1:T:321:ARG:HH11	1.37	0.70
1:A:567:MSE:SE	1:B:576:LEU:HD13	2.42	0.70
1:L:246:TYR:HD2	1:L:511:ARG:HB3	1.55	0.70
1:P:238:PRO:HG3	1:P:263:PHE:HB3	1.73	0.70
1:S:384:LEU:HD22	1:S:384:LEU:H	1.57	0.70
1:O:556:TYR:OH	1:P:542:THR:HG21	1.92	0.70
1:L:457:MSE:O	1:L:457:MSE:HG3	1.90	0.70
1:G:457:MSE:O	1:G:457:MSE:HG3	1.90	0.70
1:A:35:PHE:C	1:A:37:ARG:H	1.95	0.70
1:D:99:ARG:HH12	1:D:530:GLN:HE21	1.39	0.70
1:L:26:ARG:HH21	1:L:30:LYS:HB2	1.57	0.70
1:X:511:ARG:HA	1:X:513:ARG:HD2	1.73	0.70
1:W:330:ARG:HH21	1:W:409:THR:CG2	2.05	0.70
1:N:330:ARG:HH21	1:N:409:THR:CG2	2.03	0.70
1:P:384:LEU:H	1:P:384:LEU:HD22	1.57	0.70
1:B:182:ASN:ND2	1:C:171:ARG:HH21	1.90	0.69
1:G:35:PHE:C	1:G:37:ARG:H	1.95	0.69
1:U:139:SER:HB3	1:U:455:THR:HG23	1.73	0.69
1:X:139:SER:HB3	1:X:455:THR:HG23	1.73	0.69
1:Q:238:PRO:HG3	1:Q:263:PHE:HB3	1.73	0.69
1:F:99:ARG:HH12	1:F:530:GLN:HE21	1.39	0.69
1:J:99:ARG:HH12	1:J:530:GLN:HE21	1.39	0.69
1:U:246:TYR:HD2	1:U:511:ARG:HB2	1.56	0.69
1:O:248:LYS:HD3	1:O:251:ILE:HB	1.74	0.69
1:I:376:ARG:O	1:I:383:ASP:HB3	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:41:TRP:CZ3	1:G:42:ASP:HB3	2.26	0.69
1:I:182:ASN:ND2	1:J:171:ARG:HH21	1.90	0.69
1:K:35:PHE:C	1:K:37:ARG:H	1.95	0.69
1:L:41:TRP:CZ3	1:L:42:ASP:HB3	2.26	0.69
1:V:78:VAL:HG12	1:V:79:LEU:N	2.07	0.69
1:P:248:LYS:HB3	1:P:511:ARG:NH1	2.04	0.69
1:N:158:TRP:CD1	1:N:158:TRP:N	2.60	0.69
1:H:457:MSE:HG3	1:H:457:MSE:O	1.90	0.69
1:P:113:ILE:HD13	1:P:150:HIS:CE1	2.28	0.69
1:T:113:ILE:HD13	1:T:150:HIS:CE1	2.27	0.69
1:O:238:PRO:HG3	1:O:263:PHE:HB3	1.74	0.69
2:Z:28:VAL:HG21	2:Z:96:LEU:CB	2.22	0.69
1:S:334:MSE:SE	1:T:404:MSE:HE1	2.42	0.69
1:A:376:ARG:O	1:A:383:ASP:HB3	1.93	0.69
1:G:376:ARG:O	1:G:383:ASP:HB3	1.92	0.69
1:P:450:GLN:O	1:P:450:GLN:HG2	1.92	0.69
1:J:376:ARG:O	1:J:383:ASP:HB3	1.92	0.69
1:L:35:PHE:C	1:L:37:ARG:H	1.95	0.69
1:R:248:LYS:HB3	1:R:511:ARG:NH1	2.03	0.69
1:I:246:TYR:HD2	1:I:511:ARG:HB3	1.55	0.69
1:K:376:ARG:O	1:K:383:ASP:HB3	1.93	0.69
1:Q:577:ILE:HG12	1:Q:582:LYS:HG2	1.74	0.69
1:B:26:ARG:HH21	1:B:30:LYS:HB2	1.57	0.69
1:C:26:ARG:HH21	1:C:30:LYS:HB2	1.57	0.69
1:E:35:PHE:C	1:E:37:ARG:H	1.95	0.69
1:F:35:PHE:C	1:F:37:ARG:H	1.95	0.69
1:H:99:ARG:HH12	1:H:530:GLN:HE21	1.39	0.69
1:S:248:LYS:HB3	1:S:511:ARG:NH1	2.04	0.69
1:M:248:LYS:HB3	1:M:511:ARG:NH1	2.05	0.69
2:Y:34:LEU:CD1	2:Y:104:TYR:CD2	2.76	0.69
1:C:457:MSE:HG3	1:C:457:MSE:O	1.90	0.69
1:O:577:ILE:HG12	1:O:582:LYS:HG2	1.74	0.69
1:D:554:LEU:HD21	1:E:564:GLY:HA2	1.75	0.69
1:A:99:ARG:HH12	1:A:530:GLN:HE21	1.39	0.69
1:F:376:ARG:O	1:F:383:ASP:HB3	1.92	0.69
1:B:35:PHE:C	1:B:37:ARG:H	1.95	0.69
1:H:41:TRP:CZ3	1:H:42:ASP:HB3	2.26	0.69
1:L:158:TRP:CD1	1:L:158:TRP:N	2.60	0.69
1:V:35:PHE:HE1	1:V:321:ARG:HH11	1.38	0.69
1:C:554:LEU:HD12	1:C:557:PHE:HD2	1.58	0.69
1:D:26:ARG:HH21	1:D:30:LYS:HB2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:212:LEU:HD22	1:L:26:ARG:HG2	1.75	0.69
1:C:561:ASP:HB2	1:E:89:ASP:HA	1.75	0.69
1:E:15:PHE:HZ	1:E:283:CYS:HG	1.40	0.69
2:Y:28:VAL:CG2	2:Y:96:LEU:HD12	2.22	0.69
2:Y:28:VAL:HG21	2:Y:96:LEU:CB	2.22	0.69
1:W:246:TYR:HD2	1:W:511:ARG:HB2	1.57	0.69
1:J:554:LEU:HD12	1:J:557:PHE:HD2	1.58	0.69
1:D:554:LEU:HD12	1:D:557:PHE:HD2	1.58	0.69
1:U:238:PRO:HG3	1:U:263:PHE:HB3	1.74	0.69
1:W:577:ILE:HG12	1:W:582:LYS:HG2	1.74	0.69
1:L:209:PHE:N	1:L:210:PRO:HD3	2.08	0.69
1:B:376:ARG:O	1:B:383:ASP:HB3	1.92	0.69
1:V:384:LEU:HD22	1:V:384:LEU:H	1.57	0.69
1:N:450:GLN:HG2	1:N:450:GLN:O	1.92	0.69
1:P:577:ILE:HG12	1:P:582:LYS:HG2	1.73	0.69
1:S:534:GLU:O	1:S:538:LEU:HD23	1.92	0.69
1:N:37:ARG:NH2	1:N:37:ARG:HB3	2.07	0.69
1:R:246:TYR:HD2	1:R:511:ARG:HB2	1.57	0.69
1:K:593:LEU:O	1:K:597:GLN:HG2	1.93	0.69
1:M:577:ILE:HG12	1:M:582:LYS:HG2	1.74	0.69
1:I:209:PHE:N	1:I:210:PRO:HD3	2.08	0.69
1:D:209:PHE:N	1:D:210:PRO:HD3	2.08	0.69
1:E:78:VAL:CG2	1:E:444:LEU:HD11	2.15	0.69
1:K:41:TRP:CZ3	1:K:42:ASP:HB3	2.26	0.69
1:S:78:VAL:HG12	1:S:79:LEU:N	2.08	0.69
1:T:384:LEU:H	1:T:384:LEU:HD22	1.58	0.69
1:G:209:PHE:N	1:G:210:PRO:HD3	2.08	0.69
1:R:238:PRO:HG3	1:R:263:PHE:HB3	1.73	0.69
1:S:238:PRO:HG3	1:S:263:PHE:HB3	1.75	0.69
1:J:209:PHE:N	1:J:210:PRO:HD3	2.08	0.69
1:H:158:TRP:CD1	1:H:158:TRP:N	2.60	0.68
1:J:41:TRP:CZ3	1:J:42:ASP:HB3	2.26	0.68
1:T:78:VAL:HG12	1:T:79:LEU:N	2.08	0.68
1:S:404:MSE:HE1	1:U:334:MSE:SE	2.43	0.68
1:L:593:LEU:O	1:L:597:GLN:HG2	1.93	0.68
1:W:238:PRO:HG3	1:W:263:PHE:HB3	1.74	0.68
1:H:209:PHE:N	1:H:210:PRO:HD3	2.08	0.68
1:D:376:ARG:O	1:D:383:ASP:HB3	1.92	0.68
1:T:139:SER:HB3	1:T:455:THR:HG23	1.75	0.68
1:G:593:LEU:O	1:G:597:GLN:HG2	1.93	0.68
1:B:158:TRP:N	1:B:158:TRP:CD1	2.60	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:554:LEU:HD12	1:F:557:PHE:HD2	1.58	0.68
1:A:593:LEU:O	1:A:597:GLN:HG2	1.93	0.68
1:T:450:GLN:O	1:T:450:GLN:HG2	1.93	0.68
1:B:593:LEU:O	1:B:597:GLN:HG2	1.93	0.68
1:K:209:PHE:N	1:K:210:PRO:HD3	2.08	0.68
1:B:37:ARG:HB3	1:B:37:ARG:NH2	2.09	0.68
1:D:41:TRP:CZ3	1:D:42:ASP:HB3	2.26	0.68
1:F:158:TRP:CD1	1:F:158:TRP:N	2.60	0.68
1:M:561:ASP:HB2	1:O:89:ASP:HA	1.75	0.68
1:V:78:VAL:CG2	1:V:444:LEU:HD11	2.20	0.68
1:O:330:ARG:NH2	1:O:409:THR:HG21	2.07	0.68
1:H:376:ARG:O	1:H:383:ASP:HB3	1.92	0.68
1:C:376:ARG:O	1:C:383:ASP:HB3	1.92	0.68
1:G:99:ARG:HH12	1:G:530:GLN:HE21	1.39	0.68
1:J:593:LEU:O	1:J:597:GLN:HG2	1.93	0.68
1:N:238:PRO:HG3	1:N:263:PHE:HB3	1.75	0.68
1:C:35:PHE:C	1:C:37:ARG:H	1.95	0.68
1:I:158:TRP:CD1	1:I:158:TRP:N	2.60	0.68
1:J:37:ARG:NH2	1:J:37:ARG:HB3	2.09	0.68
1:Q:78:VAL:HG12	1:Q:79:LEU:N	2.08	0.68
1:R:35:PHE:HE1	1:R:321:ARG:HH11	1.38	0.68
1:M:248:LYS:HD3	1:M:251:ILE:HB	1.74	0.68
1:N:248:LYS:HD3	1:N:251:ILE:HB	1.75	0.68
1:G:554:LEU:HD12	1:G:557:PHE:HD2	1.58	0.68
1:M:113:ILE:HD13	1:M:150:HIS:CE1	2.28	0.68
1:T:534:GLU:O	1:T:538:LEU:HD23	1.94	0.68
1:L:37:ARG:HB3	1:L:37:ARG:NH2	2.09	0.68
1:B:334:MSE:HE1	1:C:407:ALA:HB1	1.75	0.68
1:O:384:LEU:H	1:O:384:LEU:HD22	1.57	0.68
1:A:209:PHE:N	1:A:210:PRO:HD3	2.08	0.68
1:D:593:LEU:O	1:D:597:GLN:HG2	1.93	0.68
1:D:212:LEU:HD22	1:F:26:ARG:HG2	1.75	0.68
1:E:34:PHE:CZ	1:E:328:ARG:NH2	2.47	0.68
1:K:334:MSE:HE1	1:L:407:ALA:HB1	1.73	0.68
1:C:108:LYS:HD2	1:E:438:LEU:HD11	1.76	0.68
1:I:593:LEU:O	1:I:597:GLN:HG2	1.93	0.68
1:J:108:LYS:HD2	1:K:438:LEU:HD11	1.75	0.68
1:Q:575:GLN:O	1:Q:579:MSE:HG2	1.94	0.68
1:P:139:SER:HB3	1:P:455:THR:HG23	1.74	0.68
1:B:158:TRP:CH2	1:B:302:PRO:HG3	2.29	0.68
1:D:35:PHE:C	1:D:37:ARG:H	1.95	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:158:TRP:CH2	1:J:302:PRO:HG3	2.29	0.68
1:K:37:ARG:HB3	1:K:37:ARG:NH2	2.09	0.68
1:R:78:VAL:HG12	1:R:79:LEU:N	2.07	0.68
1:B:351:PHE:CD2	1:B:356:ILE:HD11	2.29	0.68
1:H:225:VAL:HG22	1:H:276:VAL:HG12	1.76	0.68
1:K:108:LYS:HD2	1:L:438:LEU:HD11	1.75	0.68
1:C:34:PHE:CZ	1:C:328:ARG:NH2	2.47	0.68
1:H:158:TRP:CH2	1:H:302:PRO:HG3	2.29	0.68
1:I:41:TRP:CZ3	1:I:42:ASP:HB3	2.26	0.68
1:L:158:TRP:CH2	1:L:302:PRO:HG3	2.29	0.68
1:W:248:LYS:HB3	1:W:511:ARG:NH1	2.05	0.68
1:O:564:GLY:HA3	1:P:535:ILE:HD11	1.76	0.68
1:W:139:SER:HB3	1:W:455:THR:HG23	1.73	0.68
1:I:108:LYS:HD3	1:I:112:ASN:HD21	1.59	0.68
1:E:376:ARG:O	1:E:383:ASP:HB3	1.93	0.68
1:K:158:TRP:N	1:K:158:TRP:CD1	2.60	0.68
2:Z:34:LEU:CD1	2:Z:104:TYR:CD2	2.76	0.68
1:V:450:GLN:O	1:V:450:GLN:HG2	1.92	0.68
1:I:225:VAL:HG22	1:I:276:VAL:HG12	1.76	0.68
1:F:225:VAL:HG22	1:F:276:VAL:HG12	1.76	0.68
1:D:158:TRP:CH2	1:D:302:PRO:HG3	2.29	0.68
1:E:158:TRP:N	1:E:158:TRP:CD1	2.60	0.68
1:E:26:ARG:HH21	1:E:30:LYS:HB2	1.57	0.68
1:M:78:VAL:HG12	1:M:79:LEU:N	2.09	0.68
1:O:136:SER:HB3	1:R:325:ASP:OD2	71.98	0.68
1:P:158:TRP:HB3	1:P:173:CYS:CA	2.24	0.68
1:I:108:LYS:HD2	1:J:438:LEU:HD11	1.76	0.68
1:V:238:PRO:HG3	1:V:263:PHE:HB3	1.75	0.68
1:J:351:PHE:CD2	1:J:356:ILE:HD11	2.29	0.68
1:Q:384:LEU:H	1:Q:384:LEU:HD22	1.59	0.68
1:H:108:LYS:HD3	1:H:112:ASN:HD21	1.59	0.68
1:K:225:VAL:HG22	1:K:276:VAL:HG12	1.76	0.68
1:P:575:GLN:O	1:P:579:MSE:HG2	1.94	0.68
1:F:158:TRP:CH2	1:F:302:PRO:HG3	2.29	0.67
1:I:237:ASP:H	1:I:243:PRO:HA	1.60	0.67
1:S:209:PHE:CZ	1:S:214:GLN:HG2	2.29	0.67
1:E:209:PHE:N	1:E:210:PRO:HD3	2.08	0.67
1:W:534:GLU:O	1:W:538:LEU:HD23	1.94	0.67
1:F:209:PHE:N	1:F:210:PRO:HD3	2.08	0.67
1:A:585:GLU:C	1:A:587:PRO:HD3	2.15	0.67
1:K:351:PHE:CD2	1:K:356:ILE:HD11	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:575:GLN:O	1:U:579:MSE:HG2	1.95	0.67
1:X:238:PRO:HG3	1:X:263:PHE:HB3	1.74	0.67
1:F:351:PHE:CD2	1:F:356:ILE:HD11	2.29	0.67
1:K:585:GLU:C	1:K:587:PRO:HD3	2.15	0.67
1:B:35:PHE:HE2	1:B:324:LYS:HZ3	1.41	0.67
1:D:37:ARG:HB3	1:D:37:ARG:NH2	2.09	0.67
1:O:158:TRP:N	1:O:158:TRP:CD1	2.62	0.67
1:T:246:TYR:HD2	1:T:511:ARG:HB2	1.59	0.67
1:V:248:LYS:HD3	1:V:251:ILE:HB	1.75	0.67
1:B:554:LEU:HD12	1:B:557:PHE:HD2	1.58	0.67
1:I:554:LEU:HD12	1:I:557:PHE:HD2	1.58	0.67
1:F:585:GLU:C	1:F:587:PRO:HD3	2.15	0.67
1:I:442:ALA:HB1	3:I:702:HOH:O	1.95	0.67
1:G:191:TYR:HE1	1:G:278:LYS:HZ3	1.41	0.67
1:H:585:GLU:C	1:H:587:PRO:HD3	2.15	0.67
1:I:585:GLU:C	1:I:587:PRO:HD3	2.15	0.67
1:L:351:PHE:CD2	1:L:356:ILE:HD11	2.29	0.67
1:C:593:LEU:O	1:C:597:GLN:HG2	1.93	0.67
1:A:351:PHE:CD2	1:A:356:ILE:HD11	2.29	0.67
1:B:442:ALA:HB1	3:B:702:HOH:O	1.95	0.67
1:C:158:TRP:CH2	1:C:302:PRO:HG3	2.29	0.67
1:I:158:TRP:CH2	1:I:302:PRO:HG3	2.29	0.67
1:R:248:LYS:HD3	1:R:251:ILE:HB	1.76	0.67
1:X:330:ARG:NH2	1:X:409:THR:HG21	2.05	0.67
1:X:158:TRP:CD1	1:X:158:TRP:N	2.62	0.67
1:K:237:ASP:H	1:K:243:PRO:HA	1.59	0.67
1:A:108:LYS:HD3	1:A:112:ASN:HD21	1.59	0.67
1:G:585:GLU:C	1:G:587:PRO:HD3	2.15	0.67
1:X:384:LEU:HD22	1:X:384:LEU:H	1.59	0.67
1:A:442:ALA:HB1	3:A:702:HOH:O	1.95	0.67
1:E:585:GLU:C	1:E:587:PRO:HD3	2.15	0.67
1:D:158:TRP:CD1	1:D:158:TRP:N	2.60	0.67
1:J:158:TRP:N	1:J:158:TRP:CD1	2.60	0.67
1:N:78:VAL:HG12	1:N:79:LEU:N	2.09	0.67
1:O:209:PHE:CZ	1:O:214:GLN:HG2	2.30	0.67
1:H:554:LEU:HD12	1:H:557:PHE:HD2	1.58	0.67
1:O:450:GLN:O	1:O:450:GLN:HG2	1.94	0.67
1:H:593:LEU:O	1:H:597:GLN:HG2	1.93	0.67
1:B:585:GLU:C	1:B:587:PRO:HD3	2.15	0.67
1:E:351:PHE:CD2	1:E:356:ILE:HD11	2.29	0.67
1:L:376:ARG:O	1:L:383:ASP:HB3	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:225:VAL:HG22	1:G:276:VAL:HG12	1.76	0.67
1:A:158:TRP:CH2	1:A:302:PRO:HG3	2.29	0.67
1:A:41:TRP:CZ3	1:A:42:ASP:HB3	2.26	0.67
1:G:37:ARG:NH2	1:G:37:ARG:HB3	2.09	0.67
1:I:37:ARG:NH2	1:I:37:ARG:HB3	2.09	0.67
1:O:158:TRP:HB3	1:O:173:CYS:CA	2.24	0.67
1:U:273:ARG:HH22	1:U:453:LEU:CD1	2.08	0.67
1:C:237:ASP:H	1:C:243:PRO:HA	1.59	0.67
1:J:108:LYS:HD3	1:J:112:ASN:HD21	1.59	0.67
1:K:108:LYS:HD3	1:K:112:ASN:HD21	1.59	0.67
1:J:225:VAL:HG22	1:J:276:VAL:HG12	1.76	0.67
1:K:554:LEU:HD12	1:K:557:PHE:HD2	1.58	0.67
1:D:407:ALA:HB1	1:E:334:MSE:HE1	1.77	0.67
1:H:35:PHE:C	1:H:37:ARG:H	1.95	0.67
1:K:158:TRP:CH2	1:K:302:PRO:HG3	2.29	0.67
1:O:78:VAL:HG12	1:O:79:LEU:N	2.09	0.67
1:Q:248:LYS:HD3	1:Q:251:ILE:HB	1.77	0.67
1:M:158:TRP:N	1:M:158:TRP:CD1	2.60	0.67
1:P:209:PHE:CZ	1:P:214:GLN:HG2	2.30	0.67
1:U:534:GLU:O	1:U:538:LEU:HD23	1.95	0.67
1:F:593:LEU:O	1:F:597:GLN:HG2	1.93	0.67
1:G:351:PHE:CD2	1:G:356:ILE:HD11	2.29	0.67
1:U:113:ILE:HD13	1:U:150:HIS:CE1	2.29	0.67
1:A:561:ASP:HB2	1:B:89:ASP:HA	1.77	0.67
1:C:158:TRP:CD1	1:C:158:TRP:N	2.60	0.67
1:U:37:ARG:HH21	1:U:37:ARG:HB3	1.60	0.67
1:U:78:VAL:HG12	1:U:79:LEU:N	2.09	0.67
1:S:248:LYS:HD3	1:S:251:ILE:HB	1.75	0.67
1:W:248:LYS:HD3	1:W:251:ILE:HB	1.76	0.67
1:W:158:TRP:N	1:W:158:TRP:CD1	2.62	0.67
1:Q:248:LYS:HB3	1:Q:511:ARG:NH1	2.06	0.67
1:J:237:ASP:H	1:J:243:PRO:HA	1.60	0.67
1:G:108:LYS:HD3	1:G:112:ASN:HD21	1.59	0.67
1:J:442:ALA:HB1	3:J:702:HOH:O	1.95	0.67
1:R:450:GLN:HG2	1:R:450:GLN:O	1.94	0.67
1:K:379:GLU:O	1:K:380:ASN:HB2	1.95	0.67
1:E:593:LEU:O	1:E:597:GLN:HG2	1.93	0.67
1:G:158:TRP:CH2	1:G:302:PRO:HG3	2.29	0.67
1:M:37:ARG:HB3	1:M:37:ARG:HH21	1.60	0.67
1:R:158:TRP:N	1:R:158:TRP:CD1	2.63	0.67
1:D:237:ASP:H	1:D:243:PRO:HA	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ASP:H	1:A:243:PRO:HA	1.59	0.67
1:N:209:PHE:CZ	1:N:214:GLN:HG2	2.29	0.67
1:Q:209:PHE:CZ	1:Q:214:GLN:HG2	2.30	0.67
1:N:232:ALA:CB	1:N:269:ARG:H	2.08	0.67
1:I:351:PHE:CD2	1:I:356:ILE:HD11	2.29	0.67
1:C:442:ALA:HB1	3:C:702:HOH:O	1.95	0.67
1:C:209:PHE:N	1:C:210:PRO:HD3	2.08	0.67
1:L:237:ASP:H	1:L:243:PRO:HA	1.59	0.67
1:H:442:ALA:HB1	3:H:702:HOH:O	1.95	0.67
1:J:561:ASP:OD2	1:K:92:ASP:HB3	1.95	0.67
1:K:561:ASP:OD2	1:L:92:ASP:HB3	1.93	0.67
1:T:248:LYS:HD3	1:T:251:ILE:HB	1.76	0.67
1:B:237:ASP:H	1:B:243:PRO:HA	1.59	0.67
1:X:209:PHE:CZ	1:X:214:GLN:HG2	2.30	0.67
1:E:554:LEU:HD12	1:E:557:PHE:HD2	1.58	0.67
1:U:384:LEU:HD22	1:U:384:LEU:H	1.59	0.67
1:D:108:LYS:HD3	1:D:112:ASN:HD21	1.59	0.67
1:D:585:GLU:C	1:D:587:PRO:HD3	2.15	0.67
1:L:379:GLU:O	1:L:380:ASN:HB2	1.95	0.67
1:G:379:GLU:O	1:G:380:ASN:HB2	1.95	0.67
1:H:165:MSE:HG3	1:H:307:TRP:CE3	2.30	0.67
1:L:165:MSE:HG3	1:L:307:TRP:CE3	2.30	0.67
1:R:560:LEU:HD22	1:X:82:PRO:HG2	1.75	0.67
1:X:113:ILE:HD13	1:X:150:HIS:CE1	2.31	0.67
1:C:351:PHE:CD2	1:C:356:ILE:HD11	2.29	0.67
1:D:351:PHE:CD2	1:D:356:ILE:HD11	2.29	0.67
1:C:585:GLU:C	1:C:587:PRO:HD3	2.15	0.67
1:M:534:GLU:O	1:M:538:LEU:HD23	1.95	0.67
1:D:379:GLU:O	1:D:380:ASN:HB2	1.95	0.66
1:E:165:MSE:HG3	1:E:307:TRP:CE3	2.30	0.66
1:J:35:PHE:C	1:J:37:ARG:H	1.95	0.66
1:M:560:LEU:HD22	1:O:82:PRO:HG2	1.78	0.66
1:M:209:PHE:CZ	1:M:214:GLN:HG2	2.29	0.66
1:A:554:LEU:HD12	1:A:557:PHE:HD2	1.58	0.66
1:B:379:GLU:O	1:B:380:ASN:HB2	1.95	0.66
1:W:384:LEU:HD22	1:W:384:LEU:H	1.59	0.66
1:R:534:GLU:O	1:R:538:LEU:HD23	1.95	0.66
1:H:351:PHE:CD2	1:H:356:ILE:HD11	2.29	0.66
1:A:34:PHE:CZ	1:A:328:ARG:NH2	2.47	0.66
1:A:78:VAL:HG22	1:A:444:LEU:HD21	1.78	0.66
1:D:34:PHE:HE1	1:D:324:LYS:HZ2	1.39	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:78:VAL:HG22	1:D:444:LEU:HD21	1.78	0.66
1:E:379:GLU:O	1:E:380:ASN:HB2	1.95	0.66
1:E:78:VAL:HG22	1:E:444:LEU:HD21	1.78	0.66
1:H:37:ARG:NH2	1:H:37:ARG:HB3	2.09	0.66
1:O:248:LYS:HB3	1:O:511:ARG:NH1	2.06	0.66
1:N:330:ARG:NH2	1:N:409:THR:HG21	2.08	0.66
1:C:108:LYS:HD3	1:C:112:ASN:HD21	1.59	0.66
1:C:225:VAL:HG22	1:C:276:VAL:HG12	1.76	0.66
1:J:379:GLU:O	1:J:380:ASN:HB2	1.95	0.66
1:A:182:ASN:HD22	1:B:171:ARG:HH21	1.42	0.66
1:G:165:MSE:HG3	1:G:307:TRP:CE3	2.30	0.66
1:H:78:VAL:HG22	1:H:444:LEU:HD21	1.78	0.66
1:R:78:VAL:CG2	1:R:444:LEU:HD11	2.22	0.66
1:K:227:GLU:HA	1:K:274:ARG:HA	1.78	0.66
1:W:209:PHE:CZ	1:W:214:GLN:HG2	2.30	0.66
1:Q:94:LEU:HA	1:Q:97:MSE:HE2	1.77	0.66
1:H:379:GLU:O	1:H:380:ASN:HB2	1.95	0.66
1:B:225:VAL:HG22	1:B:276:VAL:HG12	1.76	0.66
1:R:231:THR:HG21	1:R:249:ARG:HH11	1.60	0.66
1:N:384:LEU:H	1:N:384:LEU:HD22	1.58	0.66
1:L:554:LEU:HD12	1:L:557:PHE:HD2	1.58	0.66
1:N:575:GLN:O	1:N:579:MSE:HG2	1.95	0.66
1:L:225:VAL:HG22	1:L:276:VAL:HG12	1.76	0.66
1:C:37:ARG:NH2	1:C:37:ARG:HB3	2.09	0.66
1:D:182:ASN:ND2	1:F:171:ARG:HH21	1.94	0.66
1:F:78:VAL:HG22	1:F:444:LEU:HD21	1.78	0.66
1:I:165:MSE:HG3	1:I:307:TRP:CE3	2.30	0.66
1:J:165:MSE:HG3	1:J:307:TRP:CE3	2.30	0.66
1:S:158:TRP:N	1:S:158:TRP:CD1	2.62	0.66
1:Q:158:TRP:N	1:Q:158:TRP:CD1	2.62	0.66
1:N:248:LYS:HB3	1:N:511:ARG:NH1	2.07	0.66
1:G:237:ASP:H	1:G:243:PRO:HA	1.60	0.66
1:A:227:GLU:HA	1:A:274:ARG:HA	1.78	0.66
1:W:231:THR:HG21	1:W:249:ARG:HH11	1.60	0.66
1:W:113:ILE:HD13	1:W:150:HIS:CE1	2.31	0.66
1:Q:534:GLU:O	1:Q:538:LEU:HD23	1.95	0.66
1:M:94:LEU:HA	1:M:97:MSE:HE2	1.77	0.66
1:Q:113:ILE:HD13	1:Q:150:HIS:CE1	2.30	0.66
1:C:78:VAL:HG22	1:C:444:LEU:HD21	1.78	0.66
1:E:158:TRP:CH2	1:E:302:PRO:HG3	2.29	0.66
1:F:37:ARG:NH2	1:F:37:ARG:HB3	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:158:TRP:CD1	1:G:158:TRP:N	2.60	0.66
1:I:41:TRP:HZ3	1:I:42:ASP:HB3	1.61	0.66
1:L:41:TRP:HZ3	1:L:42:ASP:HB3	1.61	0.66
1:Q:330:ARG:NH2	1:Q:409:THR:HG21	2.06	0.66
1:L:227:GLU:HA	1:L:274:ARG:HA	1.78	0.66
1:F:108:LYS:HD3	1:F:112:ASN:HD21	1.59	0.66
1:L:585:GLU:C	1:L:587:PRO:HD3	2.15	0.66
1:N:94:LEU:HA	1:N:97:MSE:HE2	1.76	0.66
1:B:165:MSE:HG3	1:B:307:TRP:CE3	2.30	0.66
1:K:41:TRP:HZ3	1:K:42:ASP:HB3	1.61	0.66
1:O:560:LEU:O	1:O:565:VAL:HG21	1.96	0.66
1:T:158:TRP:N	1:T:158:TRP:CD1	2.62	0.66
1:P:248:LYS:HD3	1:P:251:ILE:HB	1.77	0.66
1:B:227:GLU:HA	1:B:274:ARG:HA	1.78	0.66
1:H:227:GLU:HA	1:H:274:ARG:HA	1.78	0.66
1:T:209:PHE:CZ	1:T:214:GLN:HG2	2.30	0.66
1:W:94:LEU:HA	1:W:97:MSE:HE2	1.78	0.66
1:O:534:GLU:O	1:O:538:LEU:HD23	1.96	0.66
1:S:575:GLN:O	1:S:579:MSE:HG2	1.94	0.66
1:E:225:VAL:HG22	1:E:276:VAL:HG12	1.76	0.66
1:C:379:GLU:O	1:C:380:ASN:HB2	1.95	0.66
1:G:442:ALA:HB1	3:G:702:HOH:O	1.95	0.66
1:T:158:TRP:HB3	1:T:173:CYS:CA	2.24	0.66
1:U:248:LYS:HB3	1:U:511:ARG:NH1	2.05	0.66
1:W:330:ARG:NH2	1:W:409:THR:HG21	2.09	0.66
1:J:227:GLU:HA	1:J:274:ARG:HA	1.78	0.66
1:H:237:ASP:H	1:H:243:PRO:HA	1.60	0.66
1:R:209:PHE:CZ	1:R:214:GLN:HG2	2.29	0.66
1:M:575:GLN:O	1:M:579:MSE:HG2	1.96	0.66
1:G:110:ALA:O	1:G:113:ILE:HG13	4.33	0.66
1:K:442:ALA:HB1	3:K:702:HOH:O	1.95	0.66
2:Z:110:ALA:O	2:Z:113:ILE:HG13	1.96	0.66
1:O:231:THR:HG21	1:O:249:ARG:HH11	1.61	0.66
1:F:379:GLU:O	1:F:380:ASN:HB2	1.95	0.66
1:E:37:ARG:NH2	1:E:37:ARG:HB3	2.09	0.66
1:J:110:ALA:O	1:J:113:ILE:HG13	4.33	0.66
1:J:41:TRP:HZ3	1:J:42:ASP:HB3	1.61	0.66
1:L:34:PHE:HE1	1:L:324:LYS:HZ2	1.37	0.66
1:R:330:ARG:NH2	1:R:409:THR:HG21	2.06	0.66
1:S:273:ARG:HH22	1:S:453:LEU:CD1	2.09	0.66
1:P:232:ALA:CB	1:P:269:ARG:H	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:LYS:HD3	1:B:112:ASN:HD21	1.59	0.66
1:E:108:LYS:HD3	1:E:112:ASN:HD21	1.59	0.66
1:I:110:ALA:O	1:I:113:ILE:HG13	4.33	0.66
1:J:585:GLU:C	1:J:587:PRO:HD3	2.15	0.66
1:L:108:LYS:HD3	1:L:112:ASN:HD21	1.59	0.66
1:A:165:MSE:HG3	1:A:307:TRP:CE3	2.30	0.66
1:K:165:MSE:HG3	1:K:307:TRP:CE3	2.30	0.66
1:K:41:TRP:CE3	1:K:42:ASP:CA	2.79	0.66
1:K:78:VAL:HG22	1:K:444:LEU:HD21	1.78	0.66
1:P:325:ASP:OD2	1:L:136:SER:HB3	165.06	0.66
1:X:248:LYS:HD3	1:X:251:ILE:HB	1.77	0.66
1:V:248:LYS:HB3	1:V:511:ARG:NH1	2.07	0.66
1:B:561:ASP:HB2	1:C:89:ASP:HA	1.78	0.66
1:O:232:ALA:CB	1:O:269:ARG:H	2.09	0.66
1:B:209:PHE:N	1:B:210:PRO:HD3	2.08	0.66
1:F:237:ASP:H	1:F:243:PRO:HA	1.60	0.66
1:A:225:VAL:HG22	1:A:276:VAL:HG12	1.76	0.66
1:B:41:TRP:HZ3	1:B:42:ASP:HB3	1.61	0.66
1:J:212:LEU:HD22	1:K:26:ARG:HG2	1.78	0.66
1:O:94:LEU:HA	1:O:97:MSE:HE2	1.77	0.66
1:M:334:MSE:SE	1:O:404:MSE:HE1	2.46	0.66
1:E:227:GLU:HA	1:E:274:ARG:HA	1.78	0.66
1:W:26:ARG:NH2	1:W:30:LYS:HD3	2.11	0.66
1:P:534:GLU:O	1:P:538:LEU:HD23	1.96	0.66
1:S:94:LEU:HA	1:S:97:MSE:HE2	1.76	0.66
1:E:442:ALA:HB1	3:E:702:HOH:O	1.95	0.66
1:D:442:ALA:HB1	3:D:702:HOH:O	1.95	0.66
1:C:556:TYR:OH	1:E:542:THR:HG21	1.96	0.66
1:V:575:GLN:O	1:V:579:MSE:HG2	1.96	0.66
1:V:94:LEU:HA	1:V:97:MSE:HE2	1.77	0.66
1:C:165:MSE:HG3	1:C:307:TRP:CE3	2.30	0.65
1:D:58:ASP:O	1:D:59:VAL:CB	2.45	0.65
1:H:41:TRP:CE3	1:H:42:ASP:CA	2.79	0.65
1:E:58:ASP:O	1:E:59:VAL:CB	2.45	0.65
1:W:158:TRP:HB3	1:W:173:CYS:CA	2.23	0.65
1:P:330:ARG:NH2	1:P:409:THR:HG21	2.07	0.65
1:E:237:ASP:H	1:E:243:PRO:HA	1.59	0.65
1:F:227:GLU:HA	1:F:274:ARG:HA	1.78	0.65
1:W:575:GLN:O	1:W:579:MSE:HG2	1.96	0.65
1:R:575:GLN:O	1:R:579:MSE:HG2	1.96	0.65
1:A:37:ARG:HB3	1:A:37:ARG:NH2	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:58:ASP:O	1:G:59:VAL:CB	2.45	0.65
1:I:561:ASP:HB2	1:J:89:ASP:HA	1.78	0.65
2:Y:32:ALA:O	2:Y:33:THR:HG22	1.92	0.65
1:N:26:ARG:NH2	1:N:30:LYS:HD3	2.11	0.65
1:P:78:VAL:CG2	1:P:444:LEU:HD11	2.23	0.65
1:I:227:GLU:HA	1:I:274:ARG:HA	1.78	0.65
1:M:232:ALA:CB	1:M:269:ARG:H	2.08	0.65
1:A:352:TRP:CG	1:L:376:ARG:HB2	2.31	0.65
1:F:110:ALA:O	1:F:113:ILE:HG13	4.33	0.65
1:W:15:PHE:HZ	1:W:283:CYS:HG	1.42	0.65
1:F:442:ALA:HB1	3:F:702:HOH:O	1.95	0.65
1:D:26:ARG:HG2	1:E:212:LEU:HD22	1.77	0.65
1:G:78:VAL:HG22	1:G:444:LEU:HD21	1.78	0.65
1:J:78:VAL:HG22	1:J:444:LEU:HD21	1.78	0.65
2:Z:32:ALA:O	2:Z:33:THR:HG22	1.92	0.65
1:R:37:ARG:HB3	1:R:37:ARG:HH21	1.60	0.65
1:S:158:TRP:HB3	1:S:173:CYS:CA	2.25	0.65
1:U:158:TRP:N	1:U:158:TRP:CD1	2.64	0.65
1:I:379:GLU:O	1:I:380:ASN:HB2	1.95	0.65
1:U:404:MSE:HE1	1:X:334:MSE:SE	2.47	0.65
1:H:58:ASP:O	1:H:59:VAL:CB	2.45	0.65
1:S:232:ALA:CB	1:S:269:ARG:H	2.10	0.65
2:Y:110:ALA:O	2:Y:113:ILE:HG13	1.96	0.65
1:I:556:TYR:OH	1:J:542:THR:HG21	1.95	0.65
1:B:41:TRP:CE3	1:B:42:ASP:CA	2.79	0.65
1:F:165:MSE:HG3	1:F:307:TRP:CE3	2.30	0.65
1:X:78:VAL:CG2	1:X:444:LEU:HD11	2.23	0.65
1:X:560:LEU:O	1:X:565:VAL:HG21	1.97	0.65
1:P:158:TRP:N	1:P:158:TRP:CD1	2.63	0.65
1:T:248:LYS:HB3	1:T:511:ARG:NH1	2.04	0.65
1:D:227:GLU:HA	1:D:274:ARG:HA	1.78	0.65
1:B:560:LEU:HD22	1:C:82:PRO:HG2	1.78	0.65
1:U:209:PHE:CZ	1:U:214:GLN:HG2	2.30	0.65
1:A:379:GLU:O	1:A:380:ASN:HB2	1.95	0.65
1:X:231:THR:HG21	1:X:249:ARG:HH11	1.61	0.65
1:O:575:GLN:O	1:O:579:MSE:HG2	1.97	0.65
1:E:41:TRP:CE3	1:E:42:ASP:CA	2.79	0.65
1:H:41:TRP:HZ3	1:H:42:ASP:HB3	1.61	0.65
1:I:78:VAL:HG22	1:I:444:LEU:HD21	1.78	0.65
1:S:34:PHE:HZ	1:S:328:ARG:HH22	1.38	0.65
1:S:37:ARG:HB3	1:S:37:ARG:HH21	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:209:PHE:CZ	1:V:214:GLN:HG2	2.30	0.65
1:D:225:VAL:HG22	1:D:276:VAL:HG12	1.76	0.65
1:L:442:ALA:HB1	3:L:702:HOH:O	1.95	0.65
1:F:41:TRP:CE3	1:F:42:ASP:CA	2.79	0.65
1:S:158:TRP:CH2	1:S:302:PRO:HG3	2.31	0.65
1:R:561:ASP:OD2	1:X:92:ASP:HB3	1.97	0.65
1:T:273:ARG:HH22	1:T:453:LEU:CD1	2.09	0.65
1:C:227:GLU:HA	1:C:274:ARG:HA	1.78	0.65
1:C:58:ASP:O	1:C:59:VAL:CB	2.45	0.65
1:L:58:ASP:O	1:L:59:VAL:CB	2.45	0.65
2:Z:28:VAL:CG2	2:Z:96:LEU:HD12	2.22	0.65
1:S:431:ALA:O	1:S:435:VAL:HG22	1.96	0.65
1:Q:158:TRP:CH2	1:Q:302:PRO:HG3	2.31	0.65
1:F:108:LYS:HD2	1:G:438:LEU:HD11	1.79	0.65
1:D:438:LEU:HD11	1:E:108:LYS:HD2	1.79	0.65
1:Q:231:THR:HG21	1:Q:249:ARG:HH11	1.62	0.65
1:P:94:LEU:HA	1:P:97:MSE:HE2	1.79	0.65
1:A:158:TRP:CD1	1:A:158:TRP:N	2.60	0.65
1:C:41:TRP:HZ3	1:C:42:ASP:HB3	1.61	0.65
1:D:41:TRP:CE3	1:D:42:ASP:CA	2.79	0.65
1:F:58:ASP:O	1:F:59:VAL:CB	2.45	0.65
1:G:41:TRP:HZ3	1:G:42:ASP:HB3	1.61	0.65
1:H:47:GLN:N	1:H:47:GLN:OE1	2.30	0.65
1:I:47:GLN:OE1	1:I:47:GLN:N	2.30	0.65
1:J:47:GLN:OE1	1:J:47:GLN:N	2.30	0.65
1:K:158:TRP:CE3	1:K:173:CYS:SG	2.88	0.65
1:S:26:ARG:NH2	1:S:30:LYS:HD3	2.11	0.65
1:N:12:LEU:O	1:N:16:ASP:HB2	1.97	0.65
1:A:58:ASP:O	1:A:59:VAL:CB	2.45	0.65
1:G:227:GLU:HA	1:G:274:ARG:HA	1.78	0.65
1:R:273:ARG:HH22	1:R:453:LEU:CD1	2.10	0.65
1:G:5:GLU:HG2	1:G:6:ASN:N	2.12	0.65
1:T:287:LEU:HD12	1:T:287:LEU:N	2.12	0.65
1:B:110:ALA:O	1:B:113:ILE:HG13	4.33	0.65
1:A:41:TRP:HZ3	1:A:42:ASP:HB3	1.61	0.65
1:E:74:ASN:HB2	1:E:75:PRO:HD3	4.60	0.65
1:G:182:ASN:ND2	1:H:171:ARG:HH21	1.95	0.65
1:G:41:TRP:CE3	1:G:42:ASP:CA	2.79	0.65
1:W:273:ARG:HH22	1:W:453:LEU:CD1	2.09	0.65
1:D:5:GLU:HG2	1:D:6:ASN:N	2.12	0.65
1:A:144:ILE:HG12	1:A:447:TYR:HE1	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:165:MSE:HG3	1:D:307:TRP:CE3	2.30	0.64
1:N:560:LEU:O	1:N:565:VAL:HG21	1.97	0.64
1:T:330:ARG:NH2	1:T:409:THR:HG21	2.07	0.64
1:O:212:LEU:HD22	1:P:26:ARG:HG2	1.79	0.64
1:B:5:GLU:HG2	1:B:6:ASN:N	2.12	0.64
1:M:384:LEU:HD22	1:M:384:LEU:H	1.61	0.64
1:A:41:TRP:CE3	1:A:42:ASP:CA	2.79	0.64
1:B:95:MSE:HE1	1:B:99:ARG:CZ	2.27	0.64
1:C:74:ASN:HB2	1:C:75:PRO:HD3	4.59	0.64
1:H:57:PHE:HD2	1:H:330:ARG:CB	2.10	0.64
1:I:57:PHE:HD2	1:I:330:ARG:CB	2.10	0.64
1:I:41:TRP:CE3	1:I:42:ASP:CA	2.79	0.64
1:J:71:MSE:HE2	1:J:119:ILE:HD11	1.80	0.64
1:J:95:MSE:HE1	1:J:99:ARG:CZ	2.28	0.64
1:K:95:MSE:HE1	1:K:99:ARG:CZ	2.27	0.64
1:L:41:TRP:CE3	1:L:42:ASP:CA	2.79	0.64
1:U:26:ARG:NH2	1:U:30:LYS:HD3	2.13	0.64
1:K:58:ASP:O	1:K:59:VAL:CB	2.45	0.64
1:R:158:TRP:CE3	1:R:173:CYS:SG	2.86	0.64
1:L:5:GLU:HG2	1:L:6:ASN:N	2.13	0.64
1:D:110:ALA:O	1:D:113:ILE:HG13	4.33	0.64
1:C:41:TRP:CE3	1:C:42:ASP:CA	2.79	0.64
1:D:74:ASN:HB2	1:D:75:PRO:HD3	4.60	0.64
1:E:57:PHE:HD2	1:E:330:ARG:CB	2.10	0.64
1:F:15:PHE:CE1	1:F:283:CYS:HA	2.33	0.64
1:F:57:PHE:HD2	1:F:330:ARG:CB	2.10	0.64
1:J:41:TRP:CE3	1:J:42:ASP:CA	2.79	0.64
1:N:128:LEU:HD12	1:N:446:THR:HG23	1.79	0.64
1:N:78:VAL:CG2	1:N:444:LEU:HD11	2.22	0.64
1:V:37:ARG:HH21	1:V:37:ARG:HB3	1.62	0.64
1:I:58:ASP:O	1:I:59:VAL:CB	2.45	0.64
1:V:158:TRP:HB3	1:V:173:CYS:CA	2.23	0.64
1:I:5:GLU:HG2	1:I:6:ASN:N	2.12	0.64
1:B:57:PHE:HD2	1:B:330:ARG:CB	2.11	0.64
1:H:110:ALA:O	1:H:113:ILE:HG13	4.33	0.64
1:R:384:LEU:H	1:R:384:LEU:HD22	1.63	0.64
1:O:567:MSE:SE	1:P:576:LEU:HD13	2.47	0.64
1:D:144:ILE:HG12	1:D:447:TYR:HE1	1.63	0.64
1:H:15:PHE:CE1	1:H:283:CYS:HA	2.33	0.64
1:H:35:PHE:HE1	1:H:321:ARG:HH11	1.46	0.64
1:K:71:MSE:HE2	1:K:119:ILE:HD11	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:528:LYS:NZ	1:L:560:LEU:HD21	2.13	0.64
1:L:78:VAL:HG22	1:L:444:LEU:HD21	1.78	0.64
1:Q:136:SER:HB3	1:S:325:ASP:OD2	88.03	0.64
1:T:158:TRP:CH2	1:T:302:PRO:HG3	2.33	0.64
1:U:92:ASP:HB3	1:X:561:ASP:OD2	1.97	0.64
1:P:15:PHE:CE1	1:P:283:CYS:HA	2.32	0.64
1:V:113:ILE:HD13	1:V:150:HIS:CE1	2.33	0.64
1:V:231:THR:HG21	1:V:249:ARG:HH11	1.62	0.64
1:E:35:PHE:HE1	1:E:321:ARG:HH11	1.46	0.64
1:E:95:MSE:HE1	1:E:99:ARG:CZ	2.28	0.64
1:G:15:PHE:CE1	1:G:283:CYS:HA	2.33	0.64
1:I:15:PHE:CE1	1:I:283:CYS:HA	2.33	0.64
1:I:35:PHE:HE1	1:I:321:ARG:HH11	1.46	0.64
1:I:528:LYS:NZ	1:I:560:LEU:HD21	2.13	0.64
1:X:158:TRP:CH2	1:X:302:PRO:HG3	2.33	0.64
1:X:273:ARG:HH22	1:X:453:LEU:CD1	2.09	0.64
1:A:95:MSE:HE1	1:A:99:ARG:CZ	2.28	0.64
1:G:95:MSE:HE1	1:G:99:ARG:CZ	2.28	0.64
1:N:585:GLU:C	1:N:587:PRO:HD3	2.17	0.64
1:U:585:GLU:C	1:U:587:PRO:HD3	2.18	0.64
1:S:113:ILE:HD13	1:S:150:HIS:CE1	2.32	0.64
1:A:57:PHE:HD2	1:A:330:ARG:CB	2.10	0.64
1:B:78:VAL:HG22	1:B:444:LEU:HD21	1.78	0.64
1:D:15:PHE:CE1	1:D:283:CYS:HA	2.33	0.64
1:E:47:GLN:N	1:E:47:GLN:OE1	2.30	0.64
1:H:95:MSE:HE1	1:H:99:ARG:CZ	2.27	0.64
1:L:95:MSE:HE1	1:L:99:ARG:CZ	2.28	0.64
1:S:561:ASP:HB2	1:T:89:ASP:HA	1.80	0.64
1:N:158:TRP:CH2	1:N:302:PRO:HG3	2.33	0.64
1:B:528:LYS:NZ	1:B:560:LEU:HD21	2.13	0.64
1:H:236:GLN:HA	1:H:244:VAL:H	1.63	0.64
1:J:5:GLU:HG2	1:J:6:ASN:N	2.12	0.64
1:M:585:GLU:C	1:M:587:PRO:HD3	2.18	0.64
1:O:585:GLU:C	1:O:587:PRO:HD3	2.18	0.64
1:N:534:GLU:O	1:N:538:LEU:HD23	1.98	0.64
1:A:71:MSE:HE2	1:A:119:ILE:HD11	1.80	0.64
1:A:528:LYS:NZ	1:A:560:LEU:HD21	2.13	0.64
1:E:15:PHE:CE1	1:E:283:CYS:HA	2.33	0.64
1:E:34:PHE:HE1	1:E:324:LYS:HZ2	1.43	0.64
1:E:144:ILE:HG12	1:E:447:TYR:HE1	1.63	0.64
1:H:71:MSE:HE2	1:H:119:ILE:HD11	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:74:ASN:HB2	1:H:75:PRO:HD3	4.59	0.64
1:J:58:ASP:O	1:J:59:VAL:CB	2.45	0.64
1:O:26:ARG:NH2	1:O:30:LYS:HD3	2.13	0.64
1:O:37:ARG:HH21	1:O:37:ARG:HB3	1.61	0.64
1:N:37:ARG:NH2	1:N:41:TRP:HB3	2.13	0.64
1:X:78:VAL:HG12	1:X:79:LEU:N	2.12	0.64
1:G:546:THR:CG2	1:G:547:PRO:HD3	2.28	0.64
1:Q:273:ARG:HH22	1:Q:453:LEU:CD1	2.09	0.64
1:B:236:GLN:HA	1:B:244:VAL:H	1.63	0.64
1:A:236:GLN:HA	1:A:244:VAL:H	1.63	0.64
1:W:232:ALA:CB	1:W:269:ARG:H	2.10	0.64
1:X:534:GLU:O	1:X:538:LEU:HD23	1.97	0.64
1:U:94:LEU:HA	1:U:97:MSE:HE2	1.80	0.64
1:W:585:GLU:C	1:W:587:PRO:HD3	2.18	0.64
1:Q:585:GLU:C	1:Q:587:PRO:HD3	2.18	0.64
1:A:47:GLN:OE1	1:A:47:GLN:N	2.30	0.64
1:B:144:ILE:HG12	1:B:447:TYR:HE1	1.62	0.64
1:B:15:PHE:CE1	1:B:283:CYS:HA	2.33	0.64
1:F:47:GLN:N	1:F:47:GLN:OE1	2.30	0.64
1:G:47:GLN:N	1:G:47:GLN:OE1	2.30	0.64
1:G:528:LYS:NZ	1:G:560:LEU:HD21	2.13	0.64
1:I:144:ILE:HG12	1:I:447:TYR:HE1	1.62	0.64
1:K:78:VAL:HG12	1:K:79:LEU:N	2.13	0.64
1:Q:560:LEU:O	1:Q:565:VAL:HG21	1.98	0.64
2:Y:42:MET:CG	2:Y:42:MET:O	2.30	0.64
1:V:273:ARG:HH22	1:V:453:LEU:CD1	2.10	0.64
1:S:585:GLU:C	1:S:587:PRO:HD3	2.18	0.64
1:A:15:PHE:CE1	1:A:283:CYS:HA	2.33	0.64
1:B:15:PHE:HZ	1:B:283:CYS:HG	1.45	0.64
1:C:528:LYS:NZ	1:C:560:LEU:HD21	2.13	0.64
1:D:528:LYS:NZ	1:D:560:LEU:HD21	2.13	0.64
1:E:528:LYS:NZ	1:E:560:LEU:HD21	2.13	0.64
1:I:71:MSE:HE2	1:I:119:ILE:HD11	1.80	0.64
1:Q:37:ARG:HH21	1:Q:37:ARG:HB3	1.61	0.64
1:V:560:LEU:O	1:V:565:VAL:HG21	1.97	0.64
1:P:136:SER:HB3	1:X:325:ASP:OD2	72.27	0.64
1:R:560:LEU:O	1:R:565:VAL:HG21	1.98	0.64
1:G:236:GLN:HA	1:G:244:VAL:H	1.63	0.64
1:R:273:ARG:NH2	1:R:453:LEU:HD21	2.13	0.64
1:I:236:GLN:HA	1:I:244:VAL:H	1.63	0.64
1:C:236:GLN:HA	1:C:244:VAL:H	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:113:ILE:HD13	1:R:150:HIS:CE1	2.32	0.64
1:V:534:GLU:O	1:V:538:LEU:HD23	1.98	0.64
1:A:110:ALA:O	1:A:113:ILE:HG13	4.33	0.64
1:E:110:ALA:O	1:E:113:ILE:HG13	4.33	0.64
1:C:71:MSE:HE2	1:C:119:ILE:HD11	1.80	0.64
1:E:78:VAL:HG12	1:E:79:LEU:N	2.13	0.64
1:F:71:MSE:HE2	1:F:119:ILE:HD11	1.80	0.64
1:F:78:VAL:HG12	1:F:79:LEU:N	2.13	0.64
1:G:48:TYR:O	1:G:49:THR:HB	1.98	0.64
1:H:144:ILE:HG12	1:H:447:TYR:HE1	1.62	0.64
1:J:15:PHE:CE1	1:J:283:CYS:HA	2.33	0.64
1:K:15:PHE:CE1	1:K:283:CYS:HA	2.33	0.64
1:Q:26:ARG:NH2	1:Q:30:LYS:HD3	2.13	0.64
1:U:560:LEU:O	1:U:565:VAL:HG21	1.98	0.64
1:J:564:GLY:HA2	1:K:554:LEU:HD21	1.80	0.64
1:X:585:GLU:C	1:X:587:PRO:HD3	2.18	0.64
1:M:231:THR:HG21	1:M:249:ARG:HH11	1.63	0.64
1:B:71:MSE:HE2	1:B:119:ILE:HD11	1.80	0.63
1:E:41:TRP:HZ3	1:E:42:ASP:HB3	1.61	0.63
1:F:48:TYR:O	1:F:49:THR:HB	1.99	0.63
1:G:158:TRP:CE3	1:G:173:CYS:SG	2.88	0.63
1:G:74:ASN:HB2	1:G:75:PRO:HD3	4.59	0.63
1:H:34:PHE:CZ	1:H:328:ARG:NH2	2.48	0.63
1:J:35:PHE:HE1	1:J:321:ARG:HH11	1.46	0.63
1:J:74:ASN:HB2	1:J:75:PRO:HD3	4.59	0.63
2:Z:42:MET:CG	2:Z:42:MET:O	2.30	0.63
1:P:560:LEU:O	1:P:565:VAL:HG21	1.97	0.63
1:W:128:LEU:HD12	1:W:446:THR:HG23	1.80	0.63
1:B:58:ASP:O	1:B:59:VAL:CB	2.45	0.63
1:A:546:THR:CG2	1:A:547:PRO:HD3	2.27	0.63
1:J:546:THR:CG2	1:J:547:PRO:HD3	2.28	0.63
1:Q:273:ARG:NH2	1:Q:453:LEU:HD11	2.12	0.63
1:U:232:ALA:CB	1:U:269:ARG:H	2.12	0.63
1:K:57:PHE:HD2	1:K:330:ARG:CB	2.10	0.63
1:H:108:LYS:HD2	1:I:438:LEU:HD11	1.80	0.63
1:T:585:GLU:C	1:T:587:PRO:HD3	2.18	0.63
1:P:231:THR:HG21	1:P:249:ARG:HH11	1.63	0.63
1:I:48:TYR:O	1:I:49:THR:HB	1.98	0.63
1:J:78:VAL:HG12	1:J:79:LEU:N	2.13	0.63
1:N:15:PHE:CE1	1:N:283:CYS:HA	2.33	0.63
1:P:158:TRP:CE3	1:P:173:CYS:SG	2.86	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:158:TRP:HB3	1:X:173:CYS:CA	2.26	0.63
2:Y:74:ASN:HB2	2:Y:75:PRO:HD3	1.79	0.63
1:J:236:GLN:HA	1:J:244:VAL:H	1.63	0.63
1:R:273:ARG:NH2	1:R:453:LEU:HD11	2.12	0.63
1:F:246:TYR:CD2	1:F:511:ARG:HB3	2.34	0.63
1:L:57:PHE:HD2	1:L:330:ARG:CB	2.10	0.63
1:B:556:TYR:OH	1:C:542:THR:HG21	1.99	0.63
1:C:110:ALA:O	1:C:113:ILE:HG13	4.33	0.63
1:P:585:GLU:C	1:P:587:PRO:HD3	2.18	0.63
1:D:71:MSE:HE2	1:D:119:ILE:HD11	1.80	0.63
1:D:35:PHE:HE1	1:D:321:ARG:HH11	1.46	0.63
1:D:95:MSE:HE1	1:D:99:ARG:CZ	2.28	0.63
1:F:95:MSE:HE1	1:F:99:ARG:CZ	2.28	0.63
1:G:78:VAL:HG12	1:G:79:LEU:N	2.13	0.63
1:I:78:VAL:HG12	1:I:79:LEU:N	2.13	0.63
1:K:144:ILE:HG12	1:K:447:TYR:CE1	2.34	0.63
1:M:12:LEU:O	1:M:16:ASP:HB2	1.99	0.63
1:H:5:GLU:HG2	1:H:6:ASN:N	2.12	0.63
1:X:12:LEU:O	1:X:16:ASP:HB2	1.98	0.63
1:C:144:ILE:HG12	1:C:447:TYR:CE1	2.34	0.63
1:C:95:MSE:HE1	1:C:99:ARG:CZ	2.28	0.63
1:D:57:PHE:HD2	1:D:330:ARG:CB	2.11	0.63
1:F:144:ILE:HG12	1:F:447:TYR:CE1	2.34	0.63
1:G:144:ILE:HG12	1:G:447:TYR:HE1	1.63	0.63
1:J:528:LYS:NZ	1:J:560:LEU:HD21	2.13	0.63
1:K:12:LEU:O	1:K:16:ASP:HB2	1.99	0.63
1:O:12:LEU:O	1:O:16:ASP:HB2	1.98	0.63
1:N:325:ASP:OD2	1:V:136:SER:HB3	48.62	0.63
1:P:12:LEU:O	1:P:16:ASP:HB2	1.98	0.63
1:T:12:LEU:O	1:T:16:ASP:HB2	1.98	0.63
1:C:15:PHE:CE1	1:C:283:CYS:HA	2.33	0.63
1:E:236:GLN:HA	1:E:244:VAL:H	1.63	0.63
1:L:236:GLN:HA	1:L:244:VAL:H	1.63	0.63
1:E:5:GLU:HG2	1:E:6:ASN:N	2.12	0.63
1:C:5:GLU:HG2	1:C:6:ASN:N	2.12	0.63
1:K:5:GLU:HG2	1:K:6:ASN:N	2.12	0.63
1:V:232:ALA:CB	1:V:269:ARG:H	2.11	0.63
1:G:12:LEU:O	1:G:16:ASP:HB2	1.99	0.63
1:H:12:LEU:O	1:H:16:ASP:HB2	1.99	0.63
1:A:144:ILE:HG12	1:A:447:TYR:CE1	2.34	0.63
1:D:41:TRP:HZ3	1:D:42:ASP:HB3	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:144:ILE:HG12	1:E:447:TYR:CE1	2.34	0.63
1:E:71:MSE:HE2	1:E:119:ILE:HD11	1.80	0.63
1:F:74:ASN:HB2	1:F:75:PRO:HD3	4.59	0.63
1:G:57:PHE:HD2	1:G:330:ARG:CB	2.10	0.63
1:I:15:PHE:HZ	1:I:283:CYS:HG	1.45	0.63
1:I:95:MSE:HE1	1:I:99:ARG:CZ	2.28	0.63
1:J:48:TYR:O	1:J:49:THR:HB	1.98	0.63
1:K:144:ILE:HG12	1:K:447:TYR:HE1	1.63	0.63
1:L:78:VAL:HG12	1:L:79:LEU:N	2.13	0.63
1:P:34:PHE:HZ	1:P:328:ARG:HH22	1.36	0.63
1:C:246:TYR:CD2	1:C:511:ARG:HB3	2.34	0.63
1:E:246:TYR:CD2	1:E:511:ARG:HB3	2.34	0.63
1:F:5:GLU:HG2	1:F:6:ASN:N	2.13	0.63
1:Q:232:ALA:CB	1:Q:269:ARG:H	2.11	0.63
1:V:585:GLU:C	1:V:587:PRO:HD3	2.19	0.63
1:C:57:PHE:HD2	1:C:330:ARG:CB	2.10	0.63
1:C:48:TYR:O	1:C:49:THR:HB	1.98	0.63
1:D:15:PHE:HZ	1:D:283:CYS:HG	1.46	0.63
1:E:35:PHE:HE2	1:E:324:LYS:HZ3	1.42	0.63
1:F:144:ILE:HG12	1:F:447:TYR:HE1	1.62	0.63
1:G:71:MSE:HE2	1:G:119:ILE:HD11	1.80	0.63
1:H:528:LYS:NZ	1:H:560:LEU:HD21	2.13	0.63
1:J:144:ILE:HG12	1:J:447:TYR:HE1	1.63	0.63
1:L:15:PHE:CE1	1:L:283:CYS:HA	2.33	0.63
1:L:47:GLN:OE1	1:L:47:GLN:N	2.30	0.63
1:R:15:PHE:CE1	1:R:283:CYS:HA	2.34	0.63
1:T:26:ARG:NH2	1:T:30:LYS:HD3	2.14	0.63
1:S:12:LEU:O	1:S:16:ASP:HB2	1.98	0.63
1:V:158:TRP:N	1:V:158:TRP:CD1	2.63	0.63
1:V:158:TRP:CH2	1:V:302:PRO:HG3	2.34	0.63
1:K:236:GLN:HA	1:K:244:VAL:H	1.63	0.63
1:R:273:ARG:HH22	1:R:453:LEU:HD21	1.64	0.63
1:N:273:ARG:HH22	1:N:453:LEU:CD1	2.11	0.63
1:F:236:GLN:HA	1:F:244:VAL:H	1.63	0.63
1:T:232:ALA:CB	1:T:269:ARG:H	2.11	0.63
1:V:398:PRO:HB3	1:W:395:PRO:HD2	1.81	0.63
1:X:575:GLN:O	1:X:579:MSE:HG2	1.99	0.63
1:A:35:PHE:HE1	1:A:321:ARG:HH11	1.46	0.63
1:A:48:TYR:O	1:A:49:THR:HB	1.98	0.63
1:C:99:ARG:O	1:C:103:ARG:HG3	1.99	0.63
1:D:99:ARG:O	1:D:103:ARG:HG3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:GLN:OE1	1:D:47:GLN:N	2.30	0.63
1:D:48:TYR:O	1:D:49:THR:HB	1.98	0.63
1:L:158:TRP:CE3	1:L:173:CYS:SG	2.88	0.63
1:M:15:PHE:HZ	1:M:283:CYS:SG	2.21	0.63
1:O:158:TRP:CH2	1:O:302:PRO:HG3	2.34	0.63
2:Z:74:ASN:HB2	2:Z:75:PRO:HD3	1.79	0.63
1:D:546:THR:CG2	1:D:547:PRO:HD3	2.28	0.63
1:P:26:ARG:NH2	1:P:30:LYS:HD3	2.14	0.63
1:F:12:LEU:O	1:F:16:ASP:HB2	1.99	0.63
1:B:78:VAL:HG12	1:B:79:LEU:N	2.13	0.63
1:H:334:MSE:HE3	1:I:404:MSE:CE	2.29	0.63
1:I:74:ASN:HB2	1:I:75:PRO:HD3	4.59	0.63
1:J:57:PHE:HD2	1:J:330:ARG:CB	2.10	0.63
1:O:66:LYS:HZ3	1:O:420:VAL:HG11	1.63	0.63
1:S:560:LEU:O	1:S:565:VAL:HG21	1.99	0.63
1:T:128:LEU:HD12	1:T:446:THR:HG23	1.81	0.63
1:V:15:PHE:CE1	1:V:283:CYS:HA	2.34	0.63
1:V:12:LEU:O	1:V:16:ASP:HB2	1.98	0.63
1:W:37:ARG:NH2	1:W:41:TRP:HB3	2.13	0.63
1:D:236:GLN:HA	1:D:244:VAL:H	1.63	0.63
1:A:5:GLU:HG2	1:A:6:ASN:N	2.12	0.63
1:G:99:ARG:O	1:G:103:ARG:HG3	1.99	0.63
1:L:337:ASN:HD21	1:L:401:ASN:HD22	1.47	0.63
1:B:74:ASN:HB2	1:B:75:PRO:HD3	4.60	0.63
1:E:99:ARG:O	1:E:103:ARG:HG3	1.99	0.63
1:F:528:LYS:NZ	1:F:560:LEU:HD21	2.13	0.63
1:G:144:ILE:HG12	1:G:447:TYR:CE1	2.34	0.63
1:K:528:LYS:NZ	1:K:560:LEU:HD21	2.13	0.63
1:L:99:ARG:O	1:L:103:ARG:HG3	1.99	0.63
1:W:34:PHE:HE2	1:W:45:LEU:HG	1.64	0.63
1:U:12:LEU:O	1:U:16:ASP:HB2	1.99	0.63
1:K:564:GLY:HA2	1:L:554:LEU:HD21	1.80	0.63
1:Q:40:GLN:HG2	1:R:310:VAL:HG22	1.81	0.63
1:W:12:LEU:O	1:W:16:ASP:HB2	1.98	0.63
1:F:35:PHE:HE1	1:F:321:ARG:HH11	1.46	0.62
1:H:144:ILE:HG12	1:H:447:TYR:CE1	2.34	0.62
1:L:12:LEU:O	1:L:16:ASP:HB2	1.99	0.62
1:M:26:ARG:NH2	1:M:30:LYS:HD3	2.13	0.62
1:N:34:PHE:HE2	1:N:45:LEU:HG	1.64	0.62
1:O:560:LEU:HD22	1:P:82:PRO:HG2	1.81	0.62
1:T:440:MSE:O	1:T:444:LEU:HD22	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:431:ALA:O	1:W:435:VAL:HG22	1.98	0.62
1:T:15:PHE:CE1	1:T:283:CYS:HA	2.34	0.62
1:B:246:TYR:CD2	1:B:511:ARG:HB3	2.34	0.62
1:I:246:TYR:CD2	1:I:511:ARG:HB3	2.34	0.62
1:W:287:LEU:N	1:W:287:LEU:HD12	2.14	0.62
1:W:15:PHE:CE1	1:W:283:CYS:HA	2.34	0.62
1:A:158:TRP:CE3	1:A:173:CYS:SG	2.88	0.62
1:B:35:PHE:HE1	1:B:321:ARG:HH11	1.46	0.62
1:B:144:ILE:HG12	1:B:447:TYR:CE1	2.34	0.62
1:B:47:GLN:N	1:B:47:GLN:OE1	2.30	0.62
1:D:144:ILE:HG12	1:D:447:TYR:CE1	2.34	0.62
1:D:78:VAL:HG12	1:D:79:LEU:N	2.13	0.62
1:F:99:ARG:O	1:F:103:ARG:HG3	1.99	0.62
1:J:99:ARG:O	1:J:103:ARG:HG3	1.99	0.62
1:O:34:PHE:HE2	1:O:45:LEU:HG	1.64	0.62
1:N:37:ARG:HB3	1:N:37:ARG:HH21	1.64	0.62
1:P:37:ARG:HB3	1:P:37:ARG:HH21	1.62	0.62
1:U:34:PHE:HE2	1:U:45:LEU:HG	1.64	0.62
1:B:546:THR:CG2	1:B:547:PRO:HD3	2.28	0.62
1:R:585:GLU:C	1:R:587:PRO:HD3	2.18	0.62
1:K:337:ASN:HD21	1:K:401:ASN:HD22	1.47	0.62
1:C:12:LEU:O	1:C:16:ASP:HB2	1.99	0.62
1:E:337:ASN:HD21	1:E:401:ASN:HD22	1.47	0.62
1:A:78:VAL:HG12	1:A:79:LEU:N	2.13	0.62
1:E:48:TYR:O	1:E:49:THR:HB	1.98	0.62
1:H:99:ARG:O	1:H:103:ARG:HG3	1.99	0.62
1:I:161:ASN:C	1:I:161:ASN:HD22	2.03	0.62
1:I:144:ILE:HG12	1:I:447:TYR:CE1	2.34	0.62
1:L:144:ILE:HG12	1:L:447:TYR:CE1	2.34	0.62
1:Q:15:PHE:HZ	1:Q:283:CYS:SG	2.22	0.62
1:U:158:TRP:HB3	1:U:173:CYS:CA	2.27	0.62
1:L:546:THR:CG2	1:L:547:PRO:HD3	2.27	0.62
1:O:273:ARG:HH22	1:O:453:LEU:CD1	2.10	0.62
1:W:15:PHE:HZ	1:W:283:CYS:SG	2.22	0.62
1:X:94:LEU:HA	1:X:97:MSE:HE2	1.81	0.62
1:D:191:TYR:HE1	1:D:278:LYS:HZ3	1.47	0.62
1:K:99:ARG:O	1:K:103:ARG:HG3	1.99	0.62
1:L:35:PHE:HE1	1:L:321:ARG:HH11	1.46	0.62
1:L:48:TYR:O	1:L:49:THR:HB	1.98	0.62
1:O:37:ARG:NH2	1:O:41:TRP:HB3	2.14	0.62
1:Q:15:PHE:CE1	1:Q:283:CYS:HA	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:89:ASP:HA	1:V:561:ASP:CB	2.26	0.62
1:G:246:TYR:CD2	1:G:511:ARG:HB3	2.34	0.62
1:A:74:ASN:HB2	1:A:75:PRO:HD3	4.59	0.62
1:C:158:TRP:CE3	1:C:173:CYS:SG	2.88	0.62
1:C:35:PHE:HE1	1:C:321:ARG:HH11	1.46	0.62
1:I:99:ARG:O	1:I:103:ARG:HG3	1.99	0.62
1:L:144:ILE:HG12	1:L:447:TYR:HE1	1.63	0.62
1:Q:34:PHE:HE2	1:Q:45:LEU:HG	1.65	0.62
1:T:37:ARG:HB3	1:T:37:ARG:HH21	1.63	0.62
1:U:431:ALA:O	1:U:435:VAL:HG22	2.00	0.62
1:W:560:LEU:O	1:W:565:VAL:HG21	1.97	0.62
1:P:15:PHE:CZ	1:P:283:CYS:HA	2.35	0.62
1:H:546:THR:CG2	1:H:547:PRO:HD3	2.27	0.62
1:X:232:ALA:CB	1:X:269:ARG:H	2.12	0.62
1:D:12:LEU:O	1:D:16:ASP:HB2	1.99	0.62
1:D:372:TYR:CE2	1:F:348:LYS:HB2	2.34	0.62
1:B:12:LEU:O	1:B:16:ASP:HB2	1.99	0.62
1:J:144:ILE:HG12	1:J:447:TYR:CE1	2.34	0.62
1:K:48:TYR:O	1:K:49:THR:HB	1.98	0.62
1:P:47:GLN:HG2	1:P:48:TYR:H	1.64	0.62
1:Q:12:LEU:O	1:Q:16:ASP:HB2	1.99	0.62
1:V:78:VAL:HG22	1:V:444:LEU:HD21	1.81	0.62
1:C:546:THR:CG2	1:C:547:PRO:HD3	2.27	0.62
1:J:246:TYR:CD2	1:J:511:ARG:HB3	2.34	0.62
1:R:232:ALA:CB	1:R:269:ARG:H	2.12	0.62
1:A:12:LEU:O	1:A:16:ASP:HB2	1.99	0.62
1:C:337:ASN:HD21	1:C:401:ASN:HD22	1.47	0.62
1:F:161:ASN:C	1:F:161:ASN:HD22	2.03	0.62
1:R:440:MSE:O	1:R:444:LEU:HD22	2.00	0.62
1:V:26:ARG:NH2	1:V:30:LYS:HD3	2.13	0.62
1:W:273:ARG:NH2	1:W:453:LEU:HD11	2.11	0.62
1:A:246:TYR:CD2	1:A:511:ARG:HB3	2.34	0.62
1:A:556:TYR:OH	1:B:542:THR:HG21	2.00	0.62
1:E:12:LEU:O	1:E:16:ASP:HB2	1.99	0.62
1:J:337:ASN:HD21	1:J:401:ASN:HD22	1.47	0.62
1:D:158:TRP:CE3	1:D:173:CYS:SG	2.88	0.62
1:F:182:ASN:ND2	1:G:171:ARG:HH21	1.98	0.62
1:M:34:PHE:HE2	1:M:45:LEU:HG	1.65	0.62
1:R:158:TRP:HB3	1:R:173:CYS:CA	2.27	0.62
1:K:246:TYR:CD2	1:K:511:ARG:HB3	2.34	0.62
1:D:246:TYR:CD2	1:D:511:ARG:HB3	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:246:TYR:CD2	1:H:511:ARG:HB3	2.34	0.62
1:G:287:LEU:N	1:G:287:LEU:HD12	2.15	0.62
1:L:287:LEU:HD12	1:L:287:LEU:N	2.15	0.62
1:A:407:ALA:HB1	1:L:334:MSE:HE1	1.81	0.62
1:D:108:LYS:HD2	1:F:438:LEU:HD11	1.82	0.62
1:U:231:THR:HG21	1:U:249:ARG:HH11	1.64	0.62
1:C:144:ILE:HG12	1:C:447:TYR:HE1	1.63	0.62
1:C:161:ASN:HD22	1:C:161:ASN:C	2.03	0.62
1:F:35:PHE:HE2	1:F:324:LYS:HZ3	1.47	0.62
1:L:71:MSE:HE2	1:L:119:ILE:HD11	1.80	0.62
1:M:431:ALA:O	1:M:435:VAL:HG22	1.99	0.62
2:Z:53:MET:HG2	2:Z:67:TYR:CD1	2.34	0.62
1:P:15:PHE:HZ	1:P:283:CYS:SG	2.22	0.62
2:Y:34:LEU:O	2:Y:35:THR:HG22	2.00	0.62
1:T:231:THR:HG21	1:T:249:ARG:HH11	1.62	0.62
1:J:575:GLN:O	1:J:579:MSE:HG2	2.00	0.62
1:F:330:ARG:O	1:F:334:MSE:HB2	2.00	0.62
1:V:34:PHE:HE2	1:V:45:LEU:HG	1.64	0.62
1:W:37:ARG:HB3	1:W:37:ARG:HH21	1.65	0.62
1:V:210:PRO:HD2	1:V:211:TRP:CE3	2.35	0.62
1:A:287:LEU:HD12	1:A:287:LEU:N	2.15	0.62
1:C:287:LEU:N	1:C:287:LEU:HD12	2.15	0.62
1:I:12:LEU:O	1:I:16:ASP:HB2	1.99	0.62
1:J:12:LEU:O	1:J:16:ASP:HB2	1.99	0.62
1:N:276:VAL:HG23	1:N:293:ILE:HG23	1.81	0.62
1:F:191:TYR:HE1	1:F:278:LYS:HZ3	1.45	0.62
1:D:161:ASN:C	1:D:161:ASN:HD22	2.03	0.61
1:O:440:MSE:O	1:O:444:LEU:HD22	2.00	0.61
2:Y:53:MET:HG2	2:Y:67:TYR:CD1	2.34	0.61
2:Y:53:MET:O	2:Y:69:PHE:HE1	1.83	0.61
1:Q:138:THR:H	1:Q:143:VAL:HG22	1.63	0.61
1:S:444:LEU:C	1:S:446:THR:N	2.53	0.61
1:W:440:MSE:O	1:W:444:LEU:HD22	2.00	0.61
2:Z:34:LEU:O	2:Z:35:THR:HG22	2.00	0.61
1:R:334:MSE:SE	1:X:404:MSE:HE1	2.50	0.61
1:X:210:PRO:HD2	1:X:211:TRP:CE3	2.35	0.61
1:I:287:LEU:HD12	1:I:287:LEU:N	2.15	0.61
1:H:287:LEU:N	1:H:287:LEU:HD12	2.15	0.61
1:L:330:ARG:O	1:L:334:MSE:HB2	2.00	0.61
1:L:575:GLN:O	1:L:579:MSE:HG2	2.00	0.61
1:A:575:GLN:O	1:A:579:MSE:HG2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:276:VAL:HG23	1:W:293:ILE:HG23	1.82	0.61
1:W:5:GLU:HG2	1:W:6:ASN:H	1.65	0.61
1:C:41:TRP:HE3	1:C:42:ASP:CA	2.14	0.61
1:C:47:GLN:OE1	1:C:47:GLN:N	2.30	0.61
1:H:48:TYR:O	1:H:49:THR:HB	1.98	0.61
1:J:158:TRP:CE3	1:J:173:CYS:SG	2.88	0.61
1:M:560:LEU:O	1:M:565:VAL:HG21	1.98	0.61
1:Q:34:PHE:HZ	1:Q:328:ARG:HH22	1.40	0.61
1:S:15:PHE:CE1	1:S:283:CYS:HA	2.35	0.61
1:T:15:PHE:HZ	1:T:283:CYS:SG	2.23	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD11	2.13	0.61
1:E:287:LEU:N	1:E:287:LEU:HD12	2.15	0.61
1:B:287:LEU:HD12	1:B:287:LEU:N	2.15	0.61
1:Q:287:LEU:HD12	1:Q:287:LEU:N	2.16	0.61
1:A:398:PRO:HB3	1:L:395:PRO:HD2	1.81	0.61
1:T:5:GLU:HG2	1:T:6:ASN:H	1.66	0.61
1:N:5:GLU:HG2	1:N:6:ASN:H	1.65	0.61
3:P:719:HOH:O	1:Q:430:VAL:CG1	2.47	0.61
1:T:94:LEU:HA	1:T:97:MSE:HE2	1.81	0.61
1:H:337:ASN:HD21	1:H:401:ASN:HD22	1.47	0.61
1:B:99:ARG:O	1:B:103:ARG:HG3	1.99	0.61
1:C:330:ARG:O	1:C:334:MSE:HB2	2.00	0.61
1:C:78:VAL:HG12	1:C:79:LEU:N	2.13	0.61
1:E:330:ARG:O	1:E:334:MSE:HB2	2.00	0.61
1:M:78:VAL:HG22	1:M:444:LEU:HD21	1.82	0.61
1:M:89:ASP:HA	1:N:561:ASP:HB2	1.82	0.61
1:N:440:MSE:O	1:N:444:LEU:HD22	1.99	0.61
1:N:444:LEU:C	1:N:446:THR:N	2.53	0.61
1:T:158:TRP:CE3	1:T:173:CYS:SG	2.87	0.61
1:V:128:LEU:HD12	1:V:446:THR:HG23	1.82	0.61
1:M:273:ARG:HH22	1:M:453:LEU:CD1	2.10	0.61
1:E:546:THR:CG2	1:E:547:PRO:HD3	2.27	0.61
1:U:210:PRO:HD2	1:U:211:TRP:CE3	2.36	0.61
1:B:575:GLN:O	1:B:579:MSE:HG2	2.00	0.61
1:R:5:GLU:HG2	1:R:6:ASN:H	1.65	0.61
1:F:41:TRP:HZ3	1:F:42:ASP:HB3	1.61	0.61
1:H:78:VAL:HG12	1:H:79:LEU:N	2.13	0.61
1:O:15:PHE:CE1	1:O:283:CYS:HA	2.35	0.61
1:T:34:PHE:HE2	1:T:45:LEU:HG	1.64	0.61
1:U:444:LEU:C	1:U:446:THR:N	2.52	0.61
1:N:273:ARG:NH2	1:N:453:LEU:HD11	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:246:TYR:CD2	1:L:511:ARG:HB3	2.34	0.61
1:I:575:GLN:O	1:I:579:MSE:HG2	2.00	0.61
1:I:337:ASN:HD21	1:I:401:ASN:HD22	1.47	0.61
1:B:48:TYR:O	1:B:49:THR:HB	1.98	0.61
1:G:161:ASN:HD22	1:G:161:ASN:C	2.03	0.61
1:G:35:PHE:HE1	1:G:321:ARG:HH11	1.46	0.61
1:H:158:TRP:CE3	1:H:173:CYS:SG	2.88	0.61
1:K:35:PHE:HE1	1:K:321:ARG:HH11	1.46	0.61
1:O:138:THR:H	1:O:143:VAL:HG22	1.66	0.61
1:O:78:VAL:HG22	1:O:444:LEU:HD21	1.83	0.61
1:R:37:ARG:NH2	1:R:41:TRP:HB3	2.15	0.61
1:R:34:PHE:HE2	1:R:45:LEU:HG	1.64	0.61
1:S:78:VAL:CG2	1:S:444:LEU:HD11	2.22	0.61
1:U:440:MSE:O	1:U:444:LEU:HD22	2.01	0.61
1:U:158:TRP:CH2	1:U:302:PRO:HG3	2.35	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD21	2.15	0.61
1:X:26:ARG:NH2	1:X:30:LYS:HD3	2.15	0.61
1:A:99:ARG:O	1:A:103:ARG:HG3	1.99	0.61
1:F:586:THR:N	1:F:587:PRO:HD3	2.16	0.61
1:E:586:THR:N	1:E:587:PRO:HD3	2.16	0.61
1:B:586:THR:N	1:B:587:PRO:HD3	2.16	0.61
1:F:337:ASN:HD21	1:F:401:ASN:HD22	1.47	0.61
1:A:337:ASN:HD21	1:A:401:ASN:HD22	1.47	0.61
1:B:161:ASN:C	1:B:161:ASN:HD22	2.03	0.61
1:D:330:ARG:O	1:D:334:MSE:HB2	2.00	0.61
1:H:330:ARG:O	1:H:334:MSE:HB2	2.00	0.61
1:K:161:ASN:HD22	1:K:161:ASN:C	2.03	0.61
1:P:440:MSE:O	1:P:444:LEU:HD22	2.00	0.61
1:Q:78:VAL:CG2	1:Q:444:LEU:HD11	2.23	0.61
1:Q:47:GLN:HG2	1:Q:48:TYR:H	1.66	0.61
1:R:12:LEU:O	1:R:16:ASP:HB2	2.00	0.61
1:W:78:VAL:CG2	1:W:444:LEU:HD11	2.21	0.61
1:N:15:PHE:CZ	1:N:283:CYS:HA	2.36	0.61
1:M:273:ARG:NH2	1:M:453:LEU:HD11	2.14	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD11	2.14	0.61
1:I:586:THR:N	1:I:587:PRO:HD3	2.16	0.61
1:D:586:THR:N	1:D:587:PRO:HD3	2.16	0.61
1:C:586:THR:N	1:C:587:PRO:HD3	2.16	0.61
1:L:586:THR:N	1:L:587:PRO:HD3	2.16	0.61
1:S:5:GLU:HG2	1:S:6:ASN:H	1.65	0.61
1:A:191:TYR:HE1	1:A:278:LYS:HZ3	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:ASN:HD21	1:B:401:ASN:HD22	1.47	0.61
1:K:395:PRO:HD2	1:L:398:PRO:HB3	1.83	0.61
1:E:575:GLN:O	1:E:579:MSE:HG2	2.00	0.61
1:K:575:GLN:O	1:K:579:MSE:HG2	2.00	0.61
1:I:330:ARG:O	1:I:334:MSE:HB2	2.00	0.61
1:J:182:ASN:ND2	1:K:171:ARG:HH21	1.98	0.61
1:J:41:TRP:HE3	1:J:42:ASP:CA	2.14	0.61
1:K:47:GLN:OE1	1:K:47:GLN:N	2.30	0.61
1:U:128:LEU:HD12	1:U:446:THR:HG23	1.82	0.61
1:T:15:PHE:CZ	1:T:283:CYS:HA	2.35	0.61
1:T:560:LEU:O	1:T:565:VAL:HG21	1.99	0.61
1:V:158:TRP:CE3	1:V:173:CYS:SG	2.86	0.61
1:Q:210:PRO:HD2	1:Q:211:TRP:CE3	2.36	0.61
1:W:210:PRO:HD2	1:W:211:TRP:CE3	2.36	0.61
1:F:287:LEU:HD12	1:F:287:LEU:N	2.15	0.61
1:S:210:PRO:HD2	1:S:211:TRP:CE3	2.35	0.61
1:K:287:LEU:HD12	1:K:287:LEU:N	2.15	0.61
1:R:287:LEU:N	1:R:287:LEU:HD12	2.15	0.61
1:S:287:LEU:HD12	1:S:287:LEU:N	2.15	0.61
1:G:586:THR:N	1:G:587:PRO:HD3	2.16	0.61
1:U:5:GLU:HG2	1:U:6:ASN:H	1.65	0.61
1:M:5:GLU:HG2	1:M:6:ASN:H	1.66	0.61
1:E:161:ASN:HD22	1:E:161:ASN:C	2.03	0.61
1:H:41:TRP:HE3	1:H:42:ASP:CA	2.14	0.61
1:L:161:ASN:C	1:L:161:ASN:HD22	2.03	0.61
1:N:41:TRP:CE3	1:N:42:ASP:HB3	2.36	0.61
1:N:15:PHE:HZ	1:N:283:CYS:SG	2.18	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD21	2.16	0.61
1:R:158:TRP:CH2	1:R:302:PRO:HG3	2.36	0.61
1:X:273:ARG:NH2	1:X:453:LEU:HD11	2.13	0.61
1:D:337:ASN:HD21	1:D:401:ASN:HD22	1.47	0.61
1:O:5:GLU:HG2	1:O:6:ASN:H	1.65	0.61
1:P:564:GLY:HA2	1:Q:554:LEU:HD21	1.81	0.61
1:D:35:PHE:HE2	1:D:324:LYS:HZ3	1.48	0.61
1:O:128:LEU:HD12	1:O:446:THR:HG23	1.83	0.61
1:N:78:VAL:HG22	1:N:444:LEU:HD21	1.83	0.61
1:Q:444:LEU:C	1:Q:446:THR:N	2.53	0.61
1:V:440:MSE:O	1:V:444:LEU:HD22	2.00	0.61
1:M:15:PHE:CE1	1:M:283:CYS:HA	2.35	0.61
1:M:246:TYR:CD2	1:M:511:ARG:HB2	2.36	0.61
1:T:47:GLN:HG2	1:T:48:TYR:H	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287:LEU:N	1:D:287:LEU:HD12	2.15	0.61
1:J:287:LEU:N	1:J:287:LEU:HD12	2.15	0.61
1:J:233:PHE:CE2	1:J:249:ARG:HD3	2.36	0.61
1:E:233:PHE:CE2	1:E:249:ARG:HD3	2.36	0.61
1:P:5:GLU:HG2	1:P:6:ASN:H	1.65	0.61
1:H:233:PHE:CE2	1:H:249:ARG:HD3	2.36	0.61
1:X:5:GLU:HG2	1:X:6:ASN:H	1.65	0.61
1:A:330:ARG:O	1:A:334:MSE:HB2	2.00	0.61
1:G:330:ARG:O	1:G:334:MSE:HB2	2.00	0.61
1:N:47:GLN:HG2	1:N:48:TYR:H	1.66	0.61
1:P:41:TRP:CE3	1:P:42:ASP:HB3	2.36	0.61
1:R:15:PHE:CZ	1:R:283:CYS:HA	2.36	0.61
1:V:15:PHE:CZ	1:V:283:CYS:HA	2.36	0.61
1:W:444:LEU:C	1:W:446:THR:N	2.54	0.61
1:X:34:PHE:HE2	1:X:45:LEU:HG	1.64	0.61
1:U:15:PHE:CE1	1:U:283:CYS:HA	2.36	0.61
1:S:379:GLU:O	1:S:380:ASN:HB2	2.01	0.61
1:M:128:LEU:HD12	1:M:446:THR:HG23	1.82	0.60
1:M:47:GLN:HG2	1:M:48:TYR:H	1.65	0.60
1:R:78:VAL:HG22	1:R:444:LEU:HD21	1.82	0.60
1:U:41:TRP:CE3	1:U:42:ASP:HB3	2.36	0.60
1:T:334:MSE:SE	1:W:404:MSE:HE1	2.51	0.60
1:M:210:PRO:HD2	1:M:211:TRP:CE3	2.36	0.60
1:X:287:LEU:HD12	1:X:287:LEU:N	2.16	0.60
1:H:575:GLN:O	1:H:579:MSE:HG2	2.00	0.60
1:N:390:ALA:CB	1:V:387:GLN:HB3	2.30	0.60
1:P:34:PHE:HE2	1:P:45:LEU:HG	1.65	0.60
1:T:37:ARG:NH2	1:T:41:TRP:HB3	2.15	0.60
1:T:41:TRP:CE3	1:T:42:ASP:HB3	2.37	0.60
1:V:165:MSE:HE3	1:V:304:PHE:HB2	1.82	0.60
1:B:234:ILE:CG1	1:B:267:ALA:HB3	2.31	0.60
1:A:234:ILE:CG1	1:A:267:ALA:HB3	2.32	0.60
1:L:234:ILE:CG1	1:L:267:ALA:HB3	2.32	0.60
1:R:210:PRO:HD2	1:R:211:TRP:CE3	2.36	0.60
1:P:210:PRO:HD2	1:P:211:TRP:CE3	2.36	0.60
1:O:237:ASP:H	1:O:243:PRO:HA	1.65	0.60
1:P:287:LEU:HD12	1:P:287:LEU:N	2.15	0.60
1:V:287:LEU:N	1:V:287:LEU:HD12	2.16	0.60
1:K:586:THR:N	1:K:587:PRO:HD3	2.16	0.60
1:H:586:THR:N	1:H:587:PRO:HD3	2.16	0.60
1:I:372:TYR:CE2	1:J:348:LYS:HB2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:276:VAL:HG23	1:O:293:ILE:HG23	1.83	0.60
1:S:542:THR:HG21	1:U:556:TYR:OH	2.01	0.60
1:L:233:PHE:CE2	1:L:249:ARG:HD3	2.36	0.60
1:T:564:GLY:HA2	1:W:554:LEU:HD21	1.82	0.60
1:I:233:PHE:CE2	1:I:249:ARG:HD3	2.36	0.60
1:M:542:THR:HG21	1:N:556:TYR:OH	2.01	0.60
1:C:233:PHE:CE2	1:C:249:ARG:HD3	2.36	0.60
1:M:37:ARG:NH2	1:M:41:TRP:HB3	2.16	0.60
1:K:561:ASP:CB	1:L:89:ASP:HA	2.28	0.60
1:Q:37:ARG:NH2	1:Q:41:TRP:HB3	2.17	0.60
1:O:246:TYR:CD2	1:O:511:ARG:HB2	2.36	0.60
1:P:246:TYR:CD2	1:P:511:ARG:HB2	2.36	0.60
1:W:273:ARG:NH2	1:W:453:LEU:HD21	2.16	0.60
1:J:234:ILE:CG1	1:J:267:ALA:HB3	2.31	0.60
1:O:287:LEU:N	1:O:287:LEU:HD12	2.16	0.60
1:B:330:ARG:O	1:B:334:MSE:HB2	2.00	0.60
1:J:586:THR:N	1:J:587:PRO:HD3	2.16	0.60
1:S:276:VAL:HG23	1:S:293:ILE:HG23	1.83	0.60
1:V:276:VAL:HG23	1:V:293:ILE:HG23	1.83	0.60
1:C:154:SER:O	1:C:204:PRO:HB3	2.02	0.60
1:O:15:PHE:CZ	1:O:283:CYS:HA	2.36	0.60
1:Q:15:PHE:CZ	1:Q:283:CYS:HA	2.37	0.60
1:T:78:VAL:CG2	1:T:444:LEU:HD11	2.22	0.60
1:V:246:TYR:CD2	1:V:511:ARG:HB2	2.35	0.60
1:R:158:TRP:O	1:R:160:SER:N	2.34	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD11	2.14	0.60
1:T:577:ILE:HA	1:T:582:LYS:HB3	1.83	0.60
1:F:154:SER:O	1:F:204:PRO:HB3	2.02	0.60
1:G:154:SER:O	1:G:204:PRO:HB3	2.02	0.60
1:I:41:TRP:HE3	1:I:42:ASP:CA	2.14	0.60
1:M:440:MSE:O	1:M:444:LEU:HD22	2.01	0.60
1:R:78:VAL:HG11	1:R:444:LEU:HG	1.83	0.60
1:V:37:ARG:NH2	1:V:41:TRP:HB3	2.15	0.60
1:W:41:TRP:CE3	1:W:42:ASP:HB3	2.37	0.60
1:P:273:ARG:HH22	1:P:453:LEU:CD1	2.11	0.60
1:E:199:PRO:HB3	1:E:282:THR:HG22	1.84	0.60
1:K:330:ARG:O	1:K:334:MSE:HB2	2.00	0.60
1:A:586:THR:N	1:A:587:PRO:HD3	2.16	0.60
1:L:154:SER:O	1:L:204:PRO:HB3	2.02	0.60
1:M:276:VAL:HG23	1:M:293:ILE:HG23	1.82	0.60
1:F:575:GLN:O	1:F:579:MSE:HG2	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:575:GLN:O	1:D:579:MSE:HG2	2.00	0.60
1:B:233:PHE:CE2	1:B:249:ARG:HD3	2.36	0.60
1:B:154:SER:O	1:B:204:PRO:HB3	2.02	0.60
1:E:158:TRP:CE3	1:E:173:CYS:SG	2.88	0.60
1:H:161:ASN:HD22	1:H:161:ASN:C	2.03	0.60
1:H:154:SER:O	1:H:204:PRO:HB3	2.02	0.60
2:Z:53:MET:O	2:Z:69:PHE:HE1	1.83	0.60
1:Q:128:LEU:HD12	1:Q:446:THR:HG23	1.83	0.60
1:R:15:PHE:HZ	1:R:283:CYS:SG	2.24	0.60
1:S:47:GLN:HG2	1:S:48:TYR:H	1.66	0.60
1:T:78:VAL:HG22	1:T:444:LEU:HD21	1.84	0.60
1:X:37:ARG:NH2	1:X:41:TRP:HB3	2.17	0.60
1:X:440:MSE:O	1:X:444:LEU:HD22	2.02	0.60
1:S:246:TYR:CD2	1:S:511:ARG:HB2	2.36	0.60
1:W:47:GLN:HG2	1:W:48:TYR:H	1.67	0.60
1:C:567:MSE:SE	1:E:576:LEU:HD13	2.52	0.60
1:T:210:PRO:HD2	1:T:211:TRP:CE3	2.36	0.60
1:Q:236:GLN:CB	1:Q:265:LYS:HG2	2.32	0.60
1:T:236:GLN:CB	1:T:265:LYS:HG2	2.32	0.60
1:U:577:ILE:HA	1:U:582:LYS:HB3	1.84	0.60
1:O:5:GLU:HG2	1:O:6:ASN:N	2.16	0.60
1:J:598:GLN:HB2	1:J:601:GLN:HB2	1.84	0.60
1:N:379:GLU:O	1:N:380:ASN:HB2	2.02	0.60
1:D:233:PHE:CE2	1:D:249:ARG:HD3	2.36	0.60
1:A:395:PRO:HD2	1:B:398:PRO:HB3	1.84	0.60
1:C:575:GLN:O	1:C:579:MSE:HG2	2.00	0.60
1:A:154:SER:O	1:A:204:PRO:HB3	2.02	0.60
1:A:41:TRP:HE3	1:A:42:ASP:CA	2.14	0.60
1:G:41:TRP:HE3	1:G:42:ASP:CA	2.14	0.60
1:I:154:SER:O	1:I:204:PRO:HB3	2.02	0.60
1:J:161:ASN:C	1:J:161:ASN:HD22	2.03	0.60
1:S:34:PHE:HE2	1:S:45:LEU:HG	1.65	0.60
1:X:431:ALA:O	1:X:435:VAL:HG22	2.02	0.60
1:X:15:PHE:CE1	1:X:283:CYS:HA	2.36	0.60
1:F:234:ILE:CG1	1:F:267:ALA:HB3	2.32	0.60
1:N:210:PRO:HD2	1:N:211:TRP:CE3	2.35	0.60
1:F:199:PRO:HB3	1:F:282:THR:HG22	1.84	0.60
1:S:236:GLN:CB	1:S:265:LYS:HG2	2.32	0.60
1:G:108:LYS:HD2	1:H:438:LEU:HD11	1.82	0.60
1:N:398:PRO:HB3	1:V:395:PRO:HD2	1.84	0.60
1:A:233:PHE:CE2	1:A:249:ARG:HD3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:598:GLN:HB2	1:C:601:GLN:HB2	1.84	0.60
1:G:598:GLN:HB2	1:G:601:GLN:HB2	1.84	0.60
1:D:154:SER:O	1:D:204:PRO:HB3	2.02	0.60
1:O:210:PRO:HD2	1:O:211:TRP:CE3	2.36	0.60
1:N:236:GLN:CB	1:N:265:LYS:HG2	2.32	0.60
1:X:237:ASP:H	1:X:243:PRO:HA	1.67	0.60
1:C:577:ILE:HA	1:C:582:LYS:HB3	1.84	0.60
1:S:577:ILE:HA	1:S:582:LYS:HB3	1.84	0.60
1:U:5:GLU:HG2	1:U:6:ASN:N	2.17	0.60
1:A:89:ASP:HA	1:L:561:ASP:CB	2.25	0.60
1:P:165:MSE:HE3	1:P:304:PHE:HB2	1.84	0.60
1:P:37:ARG:NH2	1:P:41:TRP:HB3	2.17	0.60
1:R:26:ARG:NH2	1:R:30:LYS:HD3	2.16	0.60
1:V:47:GLN:HG2	1:V:48:TYR:H	1.67	0.60
1:X:444:LEU:C	1:X:446:THR:N	2.53	0.60
1:S:158:TRP:CE3	1:S:173:CYS:SG	2.87	0.60
1:N:246:TYR:CD2	1:N:511:ARG:HB2	2.37	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD21	2.16	0.60
1:J:199:PRO:HB3	1:J:282:THR:HG22	1.84	0.60
1:U:236:GLN:CB	1:U:265:LYS:HG2	2.32	0.60
1:W:5:GLU:HG2	1:W:6:ASN:N	2.17	0.60
1:N:390:ALA:HB2	1:V:387:GLN:HB2	1.84	0.60
1:X:154:SER:O	1:X:204:PRO:HB3	2.02	0.60
1:G:575:GLN:O	1:G:579:MSE:HG2	2.00	0.60
1:G:337:ASN:HD21	1:G:401:ASN:HD22	1.47	0.60
1:U:276:VAL:HG23	1:U:293:ILE:HG23	1.83	0.60
1:K:154:SER:O	1:K:204:PRO:HB3	2.02	0.60
1:B:54:ARG:HB2	2:Z:146:GLY:HA3	1.83	0.60
1:O:41:TRP:CE3	1:O:42:ASP:HB3	2.37	0.60
1:O:47:GLN:HG2	1:O:48:TYR:H	1.67	0.60
1:Q:41:TRP:CE3	1:Q:42:ASP:HB3	2.37	0.60
1:R:24:GLU:C	1:R:26:ARG:N	2.55	0.60
1:S:41:TRP:CE3	1:S:42:ASP:HB3	2.36	0.60
1:O:158:TRP:CE3	1:O:173:CYS:SG	2.87	0.60
1:U:246:TYR:CD2	1:U:511:ARG:HB2	2.36	0.60
1:I:199:PRO:HB3	1:I:282:THR:HG22	1.84	0.60
1:M:287:LEU:N	1:M:287:LEU:HD12	2.16	0.60
1:K:598:GLN:HB2	1:K:601:GLN:HB2	1.84	0.60
2:Y:137:TYR:CD1	2:Y:141:MET:HG2	2.37	0.60
1:F:233:PHE:CE2	1:F:249:ARG:HD3	2.36	0.60
1:V:5:GLU:HG2	1:V:6:ASN:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ASN:HD22	1:A:161:ASN:C	2.03	0.59
1:B:444:LEU:O	1:B:448:VAL:HG23	2.02	0.59
1:J:330:ARG:O	1:J:334:MSE:HB2	2.00	0.59
1:L:41:TRP:HE3	1:L:42:ASP:CA	2.14	0.59
1:S:37:ARG:NH2	1:S:41:TRP:HB3	2.16	0.59
1:S:560:LEU:HD22	1:T:82:PRO:HG2	1.84	0.59
1:V:138:THR:H	1:V:143:VAL:HG22	1.67	0.59
1:M:15:PHE:CZ	1:M:283:CYS:HA	2.37	0.59
1:P:15:PHE:HZ	1:P:283:CYS:HG	1.49	0.59
1:V:273:ARG:HH22	1:V:453:LEU:HD21	1.67	0.59
1:N:158:TRP:CE3	1:N:173:CYS:SG	2.86	0.59
1:D:234:ILE:CG1	1:D:267:ALA:HB3	2.32	0.59
1:C:199:PRO:HB3	1:C:282:THR:HG22	1.84	0.59
1:K:199:PRO:HB3	1:K:282:THR:HG22	1.84	0.59
1:P:554:LEU:HD12	1:P:557:PHE:HD2	1.66	0.59
1:P:5:GLU:HG2	1:P:6:ASN:N	2.17	0.59
1:P:237:ASP:H	1:P:243:PRO:HA	1.65	0.59
1:L:598:GLN:HB2	1:L:601:GLN:HB2	1.84	0.59
1:E:598:GLN:HB2	1:E:601:GLN:HB2	1.84	0.59
1:B:598:GLN:HB2	1:B:601:GLN:HB2	1.84	0.59
1:G:233:PHE:CE2	1:G:249:ARG:HD3	2.36	0.59
1:B:26:ARG:NH2	1:B:30:LYS:HD3	2.17	0.59
1:E:154:SER:O	1:E:204:PRO:HB3	2.02	0.59
1:O:15:PHE:HZ	1:O:283:CYS:SG	2.25	0.59
1:N:24:GLU:C	1:N:26:ARG:N	2.56	0.59
1:S:78:VAL:HG22	1:S:444:LEU:HD21	1.84	0.59
1:X:78:VAL:HG11	1:X:444:LEU:HG	1.83	0.59
1:I:234:ILE:CG1	1:I:267:ALA:HB3	2.32	0.59
1:L:199:PRO:HB3	1:L:282:THR:HG22	1.84	0.59
1:U:237:ASP:H	1:U:243:PRO:HA	1.66	0.59
1:W:15:PHE:CZ	1:W:283:CYS:HA	2.36	0.59
1:T:5:GLU:HG2	1:T:6:ASN:N	2.17	0.59
1:X:5:GLU:HG2	1:X:6:ASN:N	2.17	0.59
1:K:233:PHE:CE2	1:K:249:ARG:HD3	2.36	0.59
1:Q:5:GLU:HG2	1:Q:6:ASN:H	1.65	0.59
1:J:154:SER:O	1:J:204:PRO:HB3	2.02	0.59
1:M:165:MSE:HE3	1:M:304:PHE:HB2	1.84	0.59
2:Y:28:VAL:HG22	2:Y:93:PHE:O	2.02	0.59
1:X:128:LEU:HD12	1:X:446:THR:HG23	1.83	0.59
1:H:234:ILE:CG1	1:H:267:ALA:HB3	2.32	0.59
1:O:236:GLN:CB	1:O:265:LYS:HG2	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:287:LEU:HD12	1:U:287:LEU:N	2.16	0.59
1:S:5:GLU:HG2	1:S:6:ASN:N	2.17	0.59
1:Q:5:GLU:HG2	1:Q:6:ASN:N	2.17	0.59
1:F:41:TRP:HE3	1:F:42:ASP:CA	2.14	0.59
1:I:444:LEU:O	1:I:448:VAL:HG23	2.03	0.59
2:Z:28:VAL:HG22	2:Z:93:PHE:O	2.02	0.59
1:P:78:VAL:HG22	1:P:444:LEU:HD21	1.85	0.59
1:W:78:VAL:HG22	1:W:444:LEU:HD21	1.84	0.59
1:S:15:PHE:CZ	1:S:283:CYS:HA	2.38	0.59
1:W:158:TRP:CH2	1:W:302:PRO:HG3	2.36	0.59
1:G:234:ILE:CG1	1:G:267:ALA:HB3	2.32	0.59
1:U:273:ARG:NH2	1:U:453:LEU:HD11	2.11	0.59
1:C:234:ILE:CG1	1:C:267:ALA:HB3	2.32	0.59
1:E:234:ILE:CG1	1:E:267:ALA:HB3	2.32	0.59
1:E:236:GLN:CB	1:E:265:LYS:HZ3	2.15	0.59
1:E:577:ILE:HA	1:E:582:LYS:HB3	1.84	0.59
1:N:5:GLU:HG2	1:N:6:ASN:N	2.17	0.59
1:N:390:ALA:HB2	1:V:387:GLN:CB	2.32	0.59
1:A:26:ARG:NH2	1:A:30:LYS:HD3	2.17	0.59
1:D:26:ARG:NH2	1:D:30:LYS:HD3	2.17	0.59
1:J:444:LEU:O	1:J:448:VAL:HG23	2.02	0.59
1:K:26:ARG:NH2	1:K:30:LYS:HD3	2.17	0.59
1:M:138:THR:H	1:M:143:VAL:HG22	1.67	0.59
1:O:431:ALA:O	1:O:435:VAL:HG22	2.01	0.59
1:S:440:MSE:O	1:S:444:LEU:HD22	2.02	0.59
1:W:78:VAL:HG12	1:W:79:LEU:H	1.67	0.59
1:M:158:TRP:CE3	1:M:173:CYS:SG	2.87	0.59
1:W:273:ARG:HH22	1:W:453:LEU:HD21	1.68	0.59
1:J:26:ARG:NH2	1:J:30:LYS:HD3	2.18	0.59
1:S:273:ARG:NH2	1:S:453:LEU:HD11	2.13	0.59
1:O:273:ARG:NH2	1:O:453:LEU:HD11	2.14	0.59
1:H:264:ILE:O	1:H:265:LYS:HD3	2.03	0.59
1:O:564:GLY:O	1:P:554:LEU:HD21	2.02	0.59
1:R:5:GLU:HG2	1:R:6:ASN:N	2.17	0.59
1:T:379:GLU:O	1:T:380:ASN:HB2	2.03	0.59
1:W:237:ASP:H	1:W:243:PRO:HA	1.67	0.59
1:V:554:LEU:HD21	1:W:564:GLY:HA2	1.84	0.59
1:C:26:ARG:NH2	1:C:30:LYS:HD3	2.17	0.59
1:C:444:LEU:O	1:C:448:VAL:HG23	2.03	0.59
1:E:444:LEU:O	1:E:448:VAL:HG23	2.03	0.59
1:U:138:THR:H	1:U:143:VAL:HG22	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:15:PHE:CZ	1:U:283:CYS:HA	2.38	0.59
1:M:158:TRP:CH2	1:M:302:PRO:HG3	2.38	0.59
1:Q:273:ARG:NH2	1:Q:453:LEU:HD21	2.18	0.59
1:N:287:LEU:HD12	1:N:287:LEU:N	2.16	0.59
1:F:577:ILE:HA	1:F:582:LYS:HB3	1.84	0.59
1:H:577:ILE:HA	1:H:582:LYS:HB3	1.84	0.59
1:Q:99:ARG:O	1:Q:103:ARG:HG3	2.02	0.59
2:Z:137:TYR:CD1	2:Z:141:MET:HG2	2.37	0.59
1:H:598:GLN:HB2	1:H:601:GLN:HB2	1.84	0.59
1:L:384:LEU:O	1:L:386:THR:N	2.36	0.59
1:B:158:TRP:CE3	1:B:173:CYS:SG	2.88	0.59
1:D:444:LEU:O	1:D:448:VAL:HG23	2.03	0.59
1:I:26:ARG:NH2	1:I:30:LYS:HD3	2.17	0.59
1:T:138:THR:H	1:T:143:VAL:HG22	1.67	0.59
1:U:158:TRP:CE3	1:U:173:CYS:SG	2.86	0.59
1:K:234:ILE:CG1	1:K:267:ALA:HB3	2.32	0.59
1:B:264:ILE:O	1:B:265:LYS:HD3	2.03	0.59
1:D:236:GLN:CB	1:D:265:LYS:HZ3	2.15	0.59
1:N:273:ARG:NH2	1:N:453:LEU:HD21	2.18	0.59
1:D:199:PRO:HB3	1:D:282:THR:HG22	1.84	0.59
1:P:236:GLN:CB	1:P:265:LYS:HG2	2.32	0.59
1:A:577:ILE:HA	1:A:582:LYS:HB3	1.84	0.59
1:M:5:GLU:HG2	1:M:6:ASN:N	2.17	0.59
1:N:390:ALA:CB	1:V:387:GLN:CB	2.80	0.59
1:P:86:ALA:HB2	1:P:515:GLU:HG3	1.85	0.59
1:S:237:ASP:H	1:S:243:PRO:HA	1.66	0.59
1:E:191:TYR:HE1	1:E:278:LYS:HZ3	1.50	0.59
1:E:384:LEU:H	1:E:384:LEU:HD22	1.68	0.59
1:F:384:LEU:H	1:F:384:LEU:HD22	1.68	0.59
1:D:158:TRP:O	1:D:160:SER:N	2.36	0.59
1:E:34:PHE:HZ	1:E:328:ARG:HH22	0.80	0.59
1:H:158:TRP:O	1:H:160:SER:N	2.36	0.59
1:H:26:ARG:NH2	1:H:30:LYS:HD3	2.17	0.59
1:H:334:MSE:SE	1:I:404:MSE:HE1	2.53	0.59
1:O:24:GLU:C	1:O:26:ARG:N	2.56	0.59
1:N:431:ALA:O	1:N:435:VAL:HG22	2.03	0.59
1:R:41:TRP:CE3	1:R:42:ASP:HB3	2.37	0.59
1:S:89:ASP:HA	1:U:561:ASP:HB2	1.85	0.59
1:U:78:VAL:HG22	1:U:444:LEU:HD21	1.84	0.59
1:X:41:TRP:CE3	1:X:42:ASP:HB3	2.36	0.59
2:Y:42:MET:HE3	2:Y:78:GLU:OE1	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:15:PHE:HZ	1:U:283:CYS:SG	2.25	0.59
1:M:158:TRP:HB3	1:M:173:CYS:CA	2.28	0.59
1:O:273:ARG:NH2	1:O:453:LEU:HD21	2.17	0.59
1:K:264:ILE:O	1:K:265:LYS:HD3	2.03	0.59
1:X:236:GLN:CB	1:X:265:LYS:HG2	2.32	0.59
1:V:5:GLU:HG2	1:V:6:ASN:H	1.65	0.59
1:G:556:TYR:OH	1:H:542:THR:HG21	2.03	0.59
1:J:384:LEU:O	1:J:386:THR:N	2.36	0.59
1:K:384:LEU:O	1:K:386:THR:N	2.36	0.59
1:R:554:LEU:HD12	1:R:557:PHE:HD2	1.68	0.59
1:B:34:PHE:HE1	1:B:324:LYS:HZ2	1.44	0.59
1:K:49:THR:CG2	1:K:49:THR:O	2.51	0.59
1:M:561:ASP:OD2	1:O:92:ASP:HB3	2.02	0.59
1:M:82:PRO:HG2	1:N:560:LEU:HD22	1.84	0.59
1:N:165:MSE:HE3	1:N:304:PHE:HB2	1.85	0.59
1:W:246:TYR:CD2	1:W:511:ARG:HB2	2.38	0.59
1:Q:237:ASP:H	1:Q:243:PRO:HA	1.67	0.59
1:V:236:GLN:CB	1:V:265:LYS:HG2	2.32	0.59
1:L:384:LEU:HD22	1:L:384:LEU:H	1.68	0.59
1:P:379:GLU:O	1:P:380:ASN:HB2	2.03	0.59
1:D:384:LEU:O	1:D:386:THR:N	2.36	0.59
1:A:49:THR:O	1:A:49:THR:CG2	2.51	0.59
1:C:158:TRP:O	1:C:160:SER:N	2.36	0.59
1:E:173:CYS:SG	1:E:298:ILE:HD13	2.43	0.59
1:D:92:ASP:HB3	1:E:561:ASP:OD2	2.03	0.59
1:F:115:VAL:HA	1:F:118:GLN:HB3	1.85	0.59
1:G:26:ARG:NH2	1:G:30:LYS:HD3	2.17	0.59
1:I:158:TRP:O	1:I:160:SER:N	2.36	0.59
1:J:49:THR:CG2	1:J:49:THR:O	2.51	0.59
1:K:50:THR:HG21	1:K:54:ARG:NH2	2.18	0.59
1:R:128:LEU:HD12	1:R:446:THR:HG23	1.85	0.59
1:U:24:GLU:C	1:U:26:ARG:N	2.56	0.59
1:V:41:TRP:CE3	1:V:42:ASP:HB3	2.38	0.59
1:Q:246:TYR:CD2	1:Q:511:ARG:HB2	2.36	0.59
1:M:236:GLN:CB	1:M:265:LYS:HG2	2.32	0.59
1:G:384:LEU:O	1:G:386:THR:N	2.36	0.59
1:A:384:LEU:O	1:A:386:THR:N	2.36	0.59
3:O:719:HOH:O	1:P:430:VAL:CG1	2.51	0.59
1:H:384:LEU:O	1:H:386:THR:N	2.36	0.59
1:V:390:ALA:HB2	1:W:387:GLN:HB2	1.83	0.59
1:U:379:GLU:O	1:U:380:ASN:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:598:GLN:HB2	1:D:601:GLN:HB2	1.84	0.59
1:E:26:ARG:NH2	1:E:30:LYS:HD3	2.17	0.58
1:G:173:CYS:SG	1:G:298:ILE:HD13	2.43	0.58
1:H:444:LEU:O	1:H:448:VAL:HG23	2.03	0.58
1:J:50:THR:HG21	1:J:54:ARG:NH2	2.18	0.58
1:O:78:VAL:CG2	1:O:444:LEU:HD11	2.23	0.58
1:T:444:LEU:C	1:T:446:THR:N	2.55	0.58
1:X:246:TYR:CD2	1:X:511:ARG:HB2	2.36	0.58
1:F:264:ILE:O	1:F:265:LYS:HD3	2.03	0.58
1:S:554:LEU:HD12	1:S:557:PHE:HD2	1.68	0.58
1:L:264:ILE:O	1:L:265:LYS:HD3	2.03	0.58
1:W:24:GLU:C	1:W:26:ARG:N	2.56	0.58
1:M:199:PRO:HB3	1:M:282:THR:HG22	1.85	0.58
1:D:577:ILE:HA	1:D:582:LYS:HB3	1.84	0.58
1:K:384:LEU:HD22	1:K:384:LEU:H	1.68	0.58
1:B:158:TRP:O	1:B:160:SER:N	2.36	0.58
1:F:158:TRP:O	1:F:160:SER:N	2.36	0.58
1:F:444:LEU:O	1:F:448:VAL:HG23	2.03	0.58
1:G:158:TRP:O	1:G:160:SER:N	2.36	0.58
1:J:115:VAL:HA	1:J:118:GLN:HB3	1.85	0.58
1:J:158:TRP:O	1:J:160:SER:N	2.36	0.58
1:L:26:ARG:NH2	1:L:30:LYS:HD3	2.17	0.58
1:O:444:LEU:C	1:O:446:THR:N	2.55	0.58
1:Q:440:MSE:O	1:Q:444:LEU:HD22	2.03	0.58
1:A:563:LYS:HD3	1:B:557:PHE:CE2	2.38	0.58
1:T:273:ARG:HH22	1:T:453:LEU:HD21	1.66	0.58
1:P:273:ARG:HH22	1:P:453:LEU:HD21	1.66	0.58
1:B:577:ILE:HA	1:B:582:LYS:HB3	1.84	0.58
1:A:438:LEU:HD11	1:L:108:LYS:HD2	1.85	0.58
1:N:586:THR:N	1:N:587:PRO:HD3	2.18	0.58
1:A:598:GLN:HB2	1:A:601:GLN:HB2	1.84	0.58
1:O:379:GLU:O	1:O:380:ASN:HB2	2.03	0.58
1:I:384:LEU:HD22	1:I:384:LEU:H	1.68	0.58
1:I:384:LEU:O	1:I:386:THR:N	2.36	0.58
1:P:276:VAL:HG23	1:P:293:ILE:HG23	1.85	0.58
1:I:598:GLN:HB2	1:I:601:GLN:HB2	1.84	0.58
1:A:158:TRP:O	1:A:160:SER:N	2.36	0.58
1:F:26:ARG:NH2	1:F:30:LYS:HD3	2.17	0.58
1:I:49:THR:O	1:I:49:THR:CG2	2.51	0.58
1:K:158:TRP:O	1:K:160:SER:N	2.36	0.58
1:K:41:TRP:HE3	1:K:42:ASP:CA	2.14	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:136:SER:HB3	1:U:325:ASP:OD2	57.05	0.58
1:X:78:VAL:HG22	1:X:444:LEU:HD21	1.85	0.58
1:V:158:TRP:O	1:V:160:SER:N	2.36	0.58
1:D:264:ILE:O	1:D:265:LYS:HD3	2.03	0.58
1:T:554:LEU:HD12	1:T:557:PHE:HD2	1.69	0.58
1:B:199:PRO:HB3	1:B:282:THR:HG22	1.84	0.58
1:X:24:GLU:C	1:X:26:ARG:N	2.55	0.58
1:E:384:LEU:O	1:E:386:THR:N	2.36	0.58
1:J:384:LEU:H	1:J:384:LEU:HD22	1.68	0.58
1:G:389:LEU:HD12	1:G:389:LEU:H	1.68	0.58
1:F:598:GLN:HB2	1:F:601:GLN:HB2	1.84	0.58
1:P:99:ARG:O	1:P:103:ARG:HG3	2.04	0.58
1:U:430:VAL:CG1	3:X:719:HOH:O	2.51	0.58
1:D:173:CYS:SG	1:D:298:ILE:HD13	2.43	0.58
1:E:50:THR:HG21	1:E:54:ARG:NH2	2.18	0.58
1:L:158:TRP:O	1:L:160:SER:N	2.36	0.58
1:M:41:TRP:CE3	1:M:42:ASP:HB3	2.38	0.58
1:L:444:LEU:O	1:L:448:VAL:HG23	2.03	0.58
1:Q:78:VAL:HG11	1:Q:444:LEU:HG	1.84	0.58
1:T:431:ALA:O	1:T:435:VAL:HG22	2.03	0.58
1:X:47:GLN:HG2	1:X:48:TYR:H	1.67	0.58
1:R:237:ASP:H	1:R:243:PRO:HA	1.68	0.58
1:G:577:ILE:HA	1:G:582:LYS:HB3	1.84	0.58
1:O:577:ILE:HA	1:O:582:LYS:HB3	1.85	0.58
1:K:276:VAL:HG23	1:K:293:ILE:CG2	2.34	0.58
1:J:276:VAL:HG23	1:J:293:ILE:CG2	2.34	0.58
1:C:276:VAL:HG23	1:C:293:ILE:CG2	2.34	0.58
1:Q:554:LEU:HD12	1:Q:557:PHE:HD2	1.69	0.58
1:L:389:LEU:H	1:L:389:LEU:HD12	1.68	0.58
1:H:384:LEU:HD22	1:H:384:LEU:H	1.68	0.58
1:I:389:LEU:HD12	1:I:389:LEU:H	1.68	0.58
1:T:276:VAL:HG23	1:T:293:ILE:HG23	1.85	0.58
1:M:237:ASP:H	1:M:243:PRO:HA	1.68	0.58
1:M:86:ALA:HB2	1:M:515:GLU:HG3	1.85	0.58
1:D:50:THR:HG21	1:D:54:ARG:NH2	2.18	0.58
1:L:115:VAL:HA	1:L:118:GLN:HB3	1.86	0.58
1:L:49:THR:CG2	1:L:49:THR:O	2.51	0.58
1:P:138:THR:H	1:P:143:VAL:HG22	1.67	0.58
1:S:128:LEU:HD12	1:S:446:THR:HG23	1.84	0.58
1:H:199:PRO:HB3	1:H:282:THR:HG22	1.84	0.58
1:J:577:ILE:HA	1:J:582:LYS:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:94:LEU:HA	1:R:97:MSE:CE	2.34	0.58
1:L:276:VAL:HG23	1:L:293:ILE:CG2	2.34	0.58
1:E:276:VAL:HG23	1:E:293:ILE:CG2	2.34	0.58
1:A:276:VAL:HG23	1:A:293:ILE:CG2	2.34	0.58
1:S:586:THR:N	1:S:587:PRO:HD3	2.19	0.58
1:F:384:LEU:O	1:F:386:THR:N	2.36	0.58
1:G:384:LEU:H	1:G:384:LEU:HD22	1.68	0.58
1:A:444:LEU:O	1:A:448:VAL:HG23	2.02	0.58
1:B:173:CYS:SG	1:B:298:ILE:HD13	2.43	0.58
1:B:50:THR:HG21	1:B:54:ARG:NH2	2.18	0.58
1:C:334:MSE:SE	1:E:404:MSE:HE1	2.53	0.58
1:C:47:GLN:CD	1:C:47:GLN:O	2.42	0.58
1:E:115:VAL:HA	1:E:118:GLN:HB3	1.86	0.58
1:F:158:TRP:CE3	1:F:173:CYS:SG	2.88	0.58
1:G:444:LEU:O	1:G:448:VAL:HG23	2.02	0.58
1:G:49:THR:CG2	1:G:49:THR:O	2.51	0.58
1:I:158:TRP:CE3	1:I:173:CYS:SG	2.88	0.58
1:J:173:CYS:SG	1:J:298:ILE:HD13	2.43	0.58
2:Y:28:VAL:HG11	2:Y:97:ALA:N	2.19	0.58
1:G:14:ARG:HH11	1:G:17:ALA:CB	2.17	0.58
1:R:246:TYR:CD2	1:R:511:ARG:HB2	2.38	0.58
1:S:273:ARG:NH2	1:S:453:LEU:HD21	2.19	0.58
1:N:273:ARG:HH22	1:N:453:LEU:HD21	1.68	0.58
1:V:199:PRO:HB3	1:V:282:THR:HG22	1.85	0.58
1:W:577:ILE:HA	1:W:582:LYS:HB3	1.84	0.58
1:M:577:ILE:HA	1:M:582:LYS:HB3	1.85	0.58
1:H:276:VAL:HG23	1:H:293:ILE:CG2	2.34	0.58
1:F:389:LEU:H	1:F:389:LEU:HD12	1.68	0.58
1:S:556:TYR:OH	1:T:542:THR:HG21	2.03	0.58
1:B:384:LEU:HD22	1:B:384:LEU:H	1.68	0.58
1:T:237:ASP:H	1:T:243:PRO:HA	1.68	0.58
1:R:99:ARG:O	1:R:103:ARG:HG3	2.03	0.58
1:C:115:VAL:HA	1:C:118:GLN:HB3	1.86	0.58
1:E:118:GLN:NE2	1:E:303:VAL:HB	2.19	0.58
1:F:173:CYS:SG	1:F:298:ILE:HD13	2.43	0.58
1:I:173:CYS:SG	1:I:298:ILE:HD13	2.43	0.58
1:K:173:CYS:SG	1:K:298:ILE:HD13	2.43	0.58
1:W:138:THR:H	1:W:143:VAL:HG22	1.69	0.58
1:I:14:ARG:HH11	1:I:17:ALA:CB	2.17	0.58
1:V:404:MSE:HE1	1:W:334:MSE:SE	2.52	0.58
1:J:248:LYS:NZ	1:J:513:ARG:HH12	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:264:ILE:O	1:J:265:LYS:HD3	2.03	0.58
1:G:264:ILE:O	1:G:265:LYS:HD3	2.03	0.58
1:A:264:ILE:O	1:A:265:LYS:HD3	2.03	0.58
1:I:264:ILE:O	1:I:265:LYS:HD3	2.03	0.58
1:V:577:ILE:HA	1:V:582:LYS:HB3	1.85	0.58
1:X:554:LEU:HD12	1:X:557:PHE:HD2	1.68	0.58
1:P:66:LYS:HZ3	1:P:420:VAL:HG11	1.67	0.58
3:Q:719:HOH:O	1:R:430:VAL:CG1	2.50	0.58
1:N:237:ASP:H	1:N:243:PRO:HA	1.67	0.58
1:C:118:GLN:NE2	1:C:303:VAL:HB	2.19	0.58
1:B:182:ASN:HD22	1:C:171:ARG:HH21	1.50	0.58
1:E:47:GLN:O	1:E:47:GLN:CD	2.42	0.58
1:K:444:LEU:O	1:K:448:VAL:HG23	2.02	0.58
1:Q:24:GLU:C	1:Q:26:ARG:N	2.57	0.58
1:V:444:LEU:C	1:V:446:THR:N	2.55	0.58
1:D:248:LYS:NZ	1:D:513:ARG:HH12	2.02	0.58
1:L:577:ILE:HA	1:L:582:LYS:HB3	1.84	0.58
1:K:577:ILE:HA	1:K:582:LYS:HB3	1.84	0.58
1:O:199:PRO:HB3	1:O:282:THR:HG22	1.86	0.58
1:I:577:ILE:HA	1:I:582:LYS:HB3	1.84	0.58
1:Q:199:PRO:HB3	1:Q:282:THR:HG22	1.86	0.58
1:U:554:LEU:HD12	1:U:557:PHE:HD2	1.69	0.58
1:F:276:VAL:HG23	1:F:293:ILE:CG2	2.34	0.58
1:G:276:VAL:HG23	1:G:293:ILE:CG2	2.34	0.58
1:B:276:VAL:HG23	1:B:293:ILE:CG2	2.34	0.58
1:Q:586:THR:N	1:Q:587:PRO:HD3	2.19	0.58
1:X:586:THR:N	1:X:587:PRO:HD3	2.19	0.58
1:K:389:LEU:H	1:K:389:LEU:HD12	1.68	0.58
1:C:384:LEU:HD22	1:C:384:LEU:H	1.68	0.58
1:C:384:LEU:O	1:C:386:THR:N	2.36	0.58
1:K:372:TYR:CE2	1:L:348:LYS:HB2	2.39	0.58
1:N:231:THR:HG21	1:N:249:ARG:HH11	1.69	0.58
1:V:237:ASP:H	1:V:243:PRO:HA	1.68	0.58
1:A:118:GLN:NE2	1:A:303:VAL:HB	2.19	0.58
1:A:47:GLN:CD	1:A:47:GLN:O	2.42	0.58
1:A:54:ARG:HB2	2:Y:146:GLY:HA3	1.84	0.58
1:A:50:THR:HG21	1:A:54:ARG:NH2	2.18	0.58
1:C:182:ASN:HD22	1:E:171:ARG:HH21	1.51	0.58
1:D:118:GLN:NE2	1:D:303:VAL:HB	2.19	0.58
1:D:41:TRP:HE3	1:D:42:ASP:CA	2.14	0.58
1:F:50:THR:HG21	1:F:54:ARG:NH2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:334:MSE:HE3	1:H:404:MSE:CE	2.34	0.58
1:G:47:GLN:O	1:G:47:GLN:CD	2.42	0.58
1:H:173:CYS:SG	1:H:298:ILE:HD13	2.43	0.58
1:J:158:TRP:H	1:J:158:TRP:HD1	1.52	0.58
1:K:47:GLN:O	1:K:47:GLN:CD	2.42	0.58
1:A:89:ASP:CA	1:L:561:ASP:HB2	2.30	0.58
1:S:24:GLU:C	1:S:26:ARG:N	2.56	0.58
1:X:158:TRP:O	1:X:160:SER:N	2.37	0.58
1:Q:273:ARG:HH22	1:Q:453:LEU:HD21	1.69	0.58
1:C:248:LYS:NZ	1:C:513:ARG:HH12	2.02	0.58
1:E:248:LYS:NZ	1:E:513:ARG:HH12	2.02	0.58
1:M:586:THR:N	1:M:587:PRO:HD3	2.19	0.58
1:T:586:THR:N	1:T:587:PRO:HD3	2.19	0.58
1:D:389:LEU:H	1:D:389:LEU:HD12	1.68	0.58
1:N:554:LEU:HD12	1:N:557:PHE:HD2	1.69	0.58
1:M:95:MSE:HB3	1:M:527:MSE:HE1	1.85	0.58
1:V:154:SER:O	1:V:204:PRO:HB3	2.03	0.58
1:Q:379:GLU:O	1:Q:380:ASN:HB2	2.03	0.58
1:A:348:LYS:HB2	1:L:372:TYR:CE2	2.39	0.58
1:M:379:GLU:O	1:M:380:ASN:HB2	2.04	0.58
1:A:173:CYS:SG	1:A:298:ILE:HD13	2.43	0.58
1:A:34:PHE:HZ	1:A:328:ARG:HH22	0.80	0.58
1:B:158:TRP:HD1	1:B:158:TRP:H	1.52	0.58
1:C:49:THR:O	1:C:49:THR:CG2	2.51	0.58
1:E:158:TRP:O	1:E:160:SER:N	2.36	0.58
1:F:158:TRP:H	1:F:158:TRP:HD1	1.52	0.58
1:F:47:GLN:CD	1:F:47:GLN:O	2.42	0.58
1:F:49:THR:CG2	1:F:49:THR:O	2.51	0.58
1:H:334:MSE:HE1	1:I:407:ALA:HB1	1.86	0.58
1:I:50:THR:HG21	1:I:54:ARG:NH2	2.18	0.58
1:L:173:CYS:SG	1:L:298:ILE:HD13	2.43	0.58
1:L:50:THR:HG21	1:L:54:ARG:NH2	2.18	0.58
1:M:444:LEU:C	1:M:446:THR:N	2.54	0.58
1:M:136:SER:HB3	1:O:325:ASP:OD2	48.52	0.58
1:F:14:ARG:HH11	1:F:17:ALA:CB	2.17	0.58
1:S:15:PHE:HZ	1:S:283:CYS:SG	2.26	0.58
1:A:14:ARG:HH11	1:A:17:ALA:CB	2.17	0.58
1:H:14:ARG:HH11	1:H:17:ALA:CB	2.17	0.58
1:A:199:PRO:HB3	1:A:282:THR:HG22	1.84	0.58
1:S:66:LYS:HZ3	1:S:420:VAL:HG11	1.69	0.58
1:K:598:GLN:HB2	1:K:601:GLN:CB	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:598:GLN:HB2	1:H:601:GLN:CB	2.34	0.58
1:D:598:GLN:HB2	1:D:601:GLN:CB	2.34	0.58
1:B:384:LEU:O	1:B:386:THR:N	2.36	0.58
1:D:238:PRO:HG3	1:D:263:PHE:HB3	1.86	0.58
1:N:86:ALA:HB2	1:N:515:GLU:HG3	1.85	0.58
1:W:379:GLU:O	1:W:380:ASN:HB2	2.04	0.58
1:V:598:GLN:HB2	1:V:601:GLN:CB	2.34	0.58
1:O:86:ALA:HB2	1:O:515:GLU:HG3	1.84	0.58
1:A:363:TYR:HE1	1:B:350:PHE:HE1	1.52	0.58
1:B:118:GLN:NE2	1:B:303:VAL:HB	2.19	0.57
1:B:47:GLN:CD	1:B:47:GLN:O	2.42	0.57
1:C:173:CYS:SG	1:C:298:ILE:HD13	2.43	0.57
1:E:41:TRP:HE3	1:E:42:ASP:CA	2.14	0.57
1:J:47:GLN:CD	1:J:47:GLN:O	2.42	0.57
1:K:560:LEU:HD13	1:L:82:PRO:CD	2.20	0.57
1:V:15:PHE:HZ	1:V:283:CYS:SG	2.22	0.57
1:Q:158:TRP:CE3	1:Q:173:CYS:SG	2.85	0.57
1:X:15:PHE:CZ	1:X:283:CYS:HA	2.38	0.57
1:R:236:GLN:CB	1:R:265:LYS:HG2	2.33	0.57
1:N:352:TRP:CG	1:V:376:ARG:HB2	2.40	0.57
1:U:586:THR:N	1:U:587:PRO:HD3	2.19	0.57
1:B:598:GLN:HB2	1:B:601:GLN:CB	2.34	0.57
1:J:389:LEU:HD12	1:J:389:LEU:H	1.68	0.57
1:A:384:LEU:HD22	1:A:384:LEU:H	1.68	0.57
1:C:238:PRO:HG3	1:C:263:PHE:HB3	1.86	0.57
1:T:395:PRO:HD2	1:W:398:PRO:HB3	1.86	0.57
1:A:238:PRO:HG3	1:A:263:PHE:HB3	1.86	0.57
1:R:276:VAL:HG23	1:R:293:ILE:HG23	1.85	0.57
1:V:99:ARG:O	1:V:103:ARG:HG3	2.03	0.57
1:A:158:TRP:HD1	1:A:158:TRP:H	1.52	0.57
1:C:144:ILE:HD12	1:C:145:ARG:N	2.20	0.57
1:H:118:GLN:NE2	1:H:303:VAL:HB	2.19	0.57
1:H:50:THR:HG21	1:H:54:ARG:NH2	2.18	0.57
1:M:26:ARG:HG2	1:N:212:LEU:HD22	1.86	0.57
1:N:78:VAL:HG11	1:N:444:LEU:HG	1.86	0.57
1:P:128:LEU:HD12	1:P:446:THR:HG23	1.84	0.57
1:U:47:GLN:HG2	1:U:48:TYR:H	1.69	0.57
1:V:431:ALA:O	1:V:435:VAL:HG22	2.04	0.57
1:U:510:ILE:HG12	1:U:511:ARG:N	2.19	0.57
1:V:510:ILE:HG12	1:V:511:ARG:N	2.19	0.57
1:I:546:THR:CG2	1:I:547:PRO:HD3	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:46:SER:N	1:T:48:TYR:HE2	1.97	0.57
1:G:248:LYS:NZ	1:G:513:ARG:HH12	2.02	0.57
1:C:264:ILE:O	1:C:265:LYS:HD3	2.03	0.57
1:E:264:ILE:O	1:E:265:LYS:HD3	2.03	0.57
1:S:563:LYS:HD3	1:T:557:PHE:CE2	2.38	0.57
1:M:554:LEU:HD12	1:M:557:PHE:HD2	1.69	0.57
1:O:586:THR:N	1:O:587:PRO:HD3	2.18	0.57
1:S:86:ALA:HB2	1:S:515:GLU:HG3	1.86	0.57
1:F:238:PRO:HG3	1:F:263:PHE:HB3	1.86	0.57
1:T:86:ALA:HB2	1:T:515:GLU:HG3	1.86	0.57
2:Y:43:GLN:C	2:Y:45:ALA:H	2.07	0.57
1:B:49:THR:O	1:B:49:THR:CG2	2.51	0.57
1:G:144:ILE:HD12	1:G:145:ARG:N	2.20	0.57
1:H:144:ILE:HD12	1:H:145:ARG:N	2.20	0.57
1:H:34:PHE:HE1	1:H:324:LYS:HZ2	1.47	0.57
1:I:182:ASN:HD22	1:J:171:ARG:HH21	1.51	0.57
2:Y:92:VAL:O	2:Y:96:LEU:HB2	2.04	0.57
1:N:138:THR:H	1:N:143:VAL:HG22	1.67	0.57
1:Q:78:VAL:HG22	1:Q:444:LEU:HD21	1.87	0.57
1:R:47:GLN:HG2	1:R:48:TYR:H	1.67	0.57
1:T:24:GLU:C	1:T:26:ARG:N	2.57	0.57
1:S:82:PRO:HG2	1:U:560:LEU:HD22	1.86	0.57
1:X:138:THR:H	1:X:143:VAL:HG22	1.69	0.57
1:R:510:ILE:HG12	1:R:511:ARG:N	2.20	0.57
1:V:71:MSE:HE2	1:V:119:ILE:HD11	1.85	0.57
1:C:236:GLN:CB	1:C:265:LYS:HZ3	2.15	0.57
1:F:248:LYS:NZ	1:F:513:ARG:HH12	2.02	0.57
1:G:199:PRO:HB3	1:G:282:THR:HG22	1.84	0.57
1:R:577:ILE:HA	1:R:582:LYS:HB3	1.86	0.57
1:I:210:PRO:HD2	1:I:211:TRP:CZ3	2.39	0.57
1:J:210:PRO:HD2	1:J:211:TRP:CZ3	2.39	0.57
1:K:210:PRO:HD2	1:K:211:TRP:CZ3	2.39	0.57
1:G:598:GLN:HB2	1:G:601:GLN:CB	2.34	0.57
1:E:598:GLN:HB2	1:E:601:GLN:CB	2.34	0.57
1:D:384:LEU:H	1:D:384:LEU:HD22	1.68	0.57
1:H:389:LEU:H	1:H:389:LEU:HD12	1.68	0.57
1:C:389:LEU:HD12	1:C:389:LEU:H	1.68	0.57
3:M:719:HOH:O	1:O:430:VAL:CG1	2.52	0.57
1:W:86:ALA:HB2	1:W:515:GLU:HG3	1.86	0.57
2:Y:51:ALA:O	2:Y:54:ALA:HB3	2.04	0.57
2:Z:43:GLN:C	2:Z:45:ALA:H	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:541:LYS:HD3	1:D:542:THR:HG23	1.87	0.57
1:K:238:PRO:HG3	1:K:263:PHE:HB3	1.86	0.57
1:X:276:VAL:HG23	1:X:293:ILE:HG23	1.86	0.57
1:X:379:GLU:O	1:X:380:ASN:HB2	2.04	0.57
1:A:144:ILE:HD12	1:A:145:ARG:N	2.20	0.57
1:G:50:THR:HG21	1:G:54:ARG:NH2	2.18	0.57
1:P:444:LEU:C	1:P:446:THR:N	2.53	0.57
1:R:431:ALA:O	1:R:435:VAL:HG22	2.04	0.57
1:V:78:VAL:HG11	1:V:444:LEU:HG	1.86	0.57
1:C:14:ARG:HH11	1:C:17:ALA:CB	2.17	0.57
1:D:14:ARG:HH11	1:D:17:ALA:CB	2.17	0.57
1:B:14:ARG:HH11	1:B:17:ALA:CB	2.17	0.57
1:N:510:ILE:HG12	1:N:511:ARG:N	2.19	0.57
1:O:273:ARG:HH22	1:O:453:LEU:HD21	1.68	0.57
1:B:248:LYS:NZ	1:B:513:ARG:HH12	2.02	0.57
1:Q:577:ILE:HA	1:Q:582:LYS:HB3	1.86	0.57
1:P:577:ILE:HA	1:P:582:LYS:HB3	1.85	0.57
1:G:210:PRO:HD2	1:G:211:TRP:CZ3	2.39	0.57
1:H:210:PRO:HD2	1:H:211:TRP:CZ3	2.39	0.57
1:A:210:PRO:HD2	1:A:211:TRP:CZ3	2.39	0.57
1:E:210:PRO:HD2	1:E:211:TRP:CZ3	2.39	0.57
1:W:586:THR:N	1:W:587:PRO:HD3	2.19	0.57
1:B:541:LYS:HD3	1:B:542:THR:HG23	1.87	0.57
1:E:389:LEU:HD12	1:E:389:LEU:H	1.68	0.57
1:A:598:GLN:HB2	1:A:601:GLN:CB	2.34	0.57
1:I:166:ASP:OD2	1:I:168:SER:HB3	2.05	0.57
1:X:86:ALA:HB2	1:X:515:GLU:HG3	1.85	0.57
1:V:379:GLU:O	1:V:380:ASN:HB2	2.04	0.57
1:D:395:PRO:HD2	1:F:398:PRO:HB3	1.86	0.57
1:T:598:GLN:HB2	1:T:601:GLN:CB	2.34	0.57
1:B:166:ASP:OD2	1:B:168:SER:HB3	2.05	0.57
1:B:144:ILE:HD12	1:B:145:ARG:N	2.19	0.57
1:B:41:TRP:HE3	1:B:42:ASP:CA	2.14	0.57
1:D:47:GLN:CD	1:D:47:GLN:O	2.42	0.57
1:F:118:GLN:NE2	1:F:303:VAL:HB	2.19	0.57
1:H:49:THR:CG2	1:H:49:THR:O	2.51	0.57
1:J:144:ILE:HD12	1:J:145:ARG:N	2.20	0.57
1:L:118:GLN:NE2	1:L:303:VAL:HB	2.19	0.57
2:Z:28:VAL:HG11	2:Z:97:ALA:N	2.19	0.57
1:S:138:THR:H	1:S:143:VAL:HG22	1.68	0.57
1:J:14:ARG:HH11	1:J:17:ALA:CB	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:546:THR:CG2	1:K:547:PRO:HD3	2.27	0.57
1:X:199:PRO:HB3	1:X:282:THR:HG22	1.86	0.57
1:L:210:PRO:HD2	1:L:211:TRP:CZ3	2.39	0.57
1:F:210:PRO:HD2	1:F:211:TRP:CZ3	2.39	0.57
1:B:108:LYS:HD2	1:C:438:LEU:HD11	1.86	0.57
1:B:238:PRO:HG3	1:B:263:PHE:HB3	1.86	0.57
1:H:191:TYR:HE1	1:H:278:LYS:HZ3	1.51	0.57
1:X:99:ARG:O	1:X:103:ARG:HG3	2.04	0.57
1:D:363:TYR:HE1	1:F:350:PHE:HE1	1.50	0.57
1:A:166:ASP:OD2	1:A:168:SER:HB3	2.05	0.57
1:G:238:PRO:HG3	1:G:263:PHE:HB3	1.86	0.57
1:C:34:PHE:HZ	1:C:328:ARG:HH22	0.80	0.57
1:D:158:TRP:H	1:D:158:TRP:HD1	1.52	0.57
1:F:144:ILE:HD12	1:F:145:ARG:N	2.19	0.57
1:G:118:GLN:NE2	1:G:303:VAL:HB	2.19	0.57
1:I:158:TRP:H	1:I:158:TRP:HD1	1.52	0.57
1:J:118:GLN:NE2	1:J:303:VAL:HB	2.19	0.57
1:I:334:MSE:SE	1:J:404:MSE:HE1	2.55	0.57
1:K:115:VAL:HA	1:K:118:GLN:HB3	1.86	0.57
1:K:14:ARG:HH11	1:K:17:ALA:CB	2.17	0.57
1:J:334:MSE:SE	1:K:404:MSE:HE1	2.55	0.57
1:L:35:PHE:HE2	1:L:324:LYS:HZ3	1.50	0.57
2:Z:78:GLU:CG	2:Z:79:GLY:N	2.63	0.57
1:E:14:ARG:HH11	1:E:17:ALA:CB	2.17	0.57
1:I:248:LYS:NZ	1:I:513:ARG:HH12	2.02	0.57
1:L:236:GLN:CB	1:L:265:LYS:HZ3	2.15	0.57
1:P:199:PRO:HB3	1:P:282:THR:HG22	1.87	0.57
1:O:554:LEU:HD12	1:O:557:PHE:HD2	1.69	0.57
1:X:577:ILE:HA	1:X:582:LYS:HB3	1.85	0.57
1:D:276:VAL:HG23	1:D:293:ILE:CG2	2.34	0.57
1:R:586:THR:N	1:R:587:PRO:HD3	2.19	0.57
1:W:554:LEU:HD12	1:W:557:PHE:HD2	1.68	0.57
1:L:598:GLN:HB2	1:L:601:GLN:CB	2.34	0.57
1:C:166:ASP:OD2	1:C:168:SER:HB3	2.05	0.57
1:I:238:PRO:HG3	1:I:263:PHE:HB3	1.86	0.57
1:D:166:ASP:OD2	1:D:168:SER:HB3	2.05	0.57
1:K:541:LYS:HD3	1:K:542:THR:HG23	1.87	0.57
1:N:99:ARG:O	1:N:103:ARG:HG3	2.05	0.57
1:V:86:ALA:HB2	1:V:515:GLU:HG3	1.86	0.57
1:A:115:VAL:HA	1:A:118:GLN:HB3	1.86	0.57
1:C:50:THR:HG21	1:C:54:ARG:NH2	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:THR:CG2	1:E:49:THR:O	2.51	0.57
1:H:37:ARG:HH21	1:H:37:ARG:CB	2.16	0.57
1:I:144:ILE:HD12	1:I:145:ARG:N	2.20	0.57
1:K:440:MSE:O	1:K:444:LEU:HD22	2.05	0.57
1:L:14:ARG:HH11	1:L:17:ALA:CB	2.17	0.57
1:R:165:MSE:HE3	1:R:304:PHE:HB2	1.87	0.57
1:N:310:VAL:HG22	1:V:40:GLN:HG2	1.86	0.57
1:N:158:TRP:HB3	1:N:173:CYS:CA	2.27	0.57
1:B:563:LYS:HD3	1:C:557:PHE:CE2	2.40	0.57
1:O:564:GLY:CA	1:P:554:LEU:HD21	2.34	0.57
1:D:210:PRO:HD2	1:D:211:TRP:CZ3	2.39	0.57
1:V:390:ALA:CB	1:W:387:GLN:CB	2.83	0.57
1:I:598:GLN:HB2	1:I:601:GLN:CB	2.34	0.57
1:Q:598:GLN:HB2	1:Q:601:GLN:CB	2.35	0.57
1:F:166:ASP:OD2	1:F:168:SER:HB3	2.05	0.57
1:L:238:PRO:HG3	1:L:263:PHE:HB3	1.86	0.57
1:P:154:SER:O	1:P:204:PRO:HB3	2.03	0.57
1:Q:276:VAL:HG23	1:Q:293:ILE:HG23	1.85	0.57
1:C:37:ARG:CB	1:C:37:ARG:HH21	2.16	0.57
1:D:49:THR:O	1:D:49:THR:CG2	2.51	0.57
1:E:144:ILE:HD12	1:E:145:ARG:N	2.20	0.57
1:D:171:ARG:HH21	1:E:182:ASN:ND2	2.02	0.57
1:G:115:VAL:HA	1:G:118:GLN:HB3	1.86	0.57
1:H:47:GLN:O	1:H:47:GLN:CD	2.42	0.57
1:O:165:MSE:HE3	1:O:304:PHE:HB2	1.85	0.57
2:Z:92:VAL:O	2:Z:96:LEU:HB2	2.04	0.57
1:M:273:ARG:NH2	1:M:453:LEU:HD21	2.19	0.57
1:U:273:ARG:NH2	1:U:453:LEU:HD21	2.19	0.57
1:S:199:PRO:HB3	1:S:282:THR:HG22	1.85	0.57
1:K:376:ARG:HB2	1:L:352:TRP:CG	2.40	0.57
1:B:597:GLN:HA	1:B:597:GLN:HE21	1.70	0.57
1:I:276:VAL:HG23	1:I:293:ILE:CG2	2.34	0.57
1:C:597:GLN:HE21	1:C:597:GLN:HA	1.70	0.57
1:V:586:THR:N	1:V:587:PRO:HD3	2.19	0.57
1:F:598:GLN:HB2	1:F:601:GLN:CB	2.34	0.57
1:B:389:LEU:HD12	1:B:389:LEU:H	1.68	0.57
1:W:598:GLN:HB2	1:W:601:GLN:CB	2.35	0.57
2:Z:51:ALA:O	2:Z:54:ALA:HB3	2.04	0.57
1:M:154:SER:O	1:M:204:PRO:HB3	2.04	0.57
1:F:372:TYR:CE2	1:G:348:LYS:HB2	2.40	0.57
1:U:95:MSE:HB3	1:U:527:MSE:HE1	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:379:GLU:O	1:R:380:ASN:HB2	2.04	0.57
1:H:166:ASP:OD2	1:H:168:SER:HB3	2.05	0.57
1:B:440:MSE:O	1:B:444:LEU:HD22	2.05	0.57
1:E:440:MSE:O	1:E:444:LEU:HD22	2.05	0.57
1:H:440:MSE:O	1:H:444:LEU:HD22	2.05	0.57
1:I:47:GLN:CD	1:I:47:GLN:O	2.42	0.57
1:L:47:GLN:O	1:L:47:GLN:CD	2.42	0.57
1:O:99:ARG:O	1:O:103:ARG:HG3	2.05	0.57
1:O:561:ASP:OD2	1:P:92:ASP:HB3	2.04	0.57
1:R:138:THR:H	1:R:143:VAL:HG22	1.69	0.57
1:T:78:VAL:HG11	1:T:444:LEU:HG	1.86	0.57
1:W:78:VAL:HG11	1:W:444:LEU:HG	1.87	0.57
1:A:248:LYS:NZ	1:A:513:ARG:HH12	2.02	0.57
1:V:210:PRO:HD2	1:V:211:TRP:CD2	2.40	0.57
1:W:236:GLN:CB	1:W:265:LYS:HG2	2.32	0.57
1:L:597:GLN:HA	1:L:597:GLN:HE21	1.70	0.57
1:B:210:PRO:HD2	1:B:211:TRP:CZ3	2.39	0.57
1:E:541:LYS:HD3	1:E:542:THR:HG23	1.87	0.57
1:C:541:LYS:HD3	1:C:542:THR:HG23	1.87	0.57
1:P:586:THR:N	1:P:587:PRO:HD3	2.19	0.57
1:C:598:GLN:HB2	1:C:601:GLN:CB	2.34	0.57
1:A:389:LEU:HD12	1:A:389:LEU:H	1.68	0.57
1:V:390:ALA:CB	1:W:387:GLN:HB3	2.35	0.57
1:C:334:MSE:HE3	1:E:404:MSE:CE	2.34	0.57
1:H:115:VAL:HA	1:H:118:GLN:HB3	1.86	0.57
1:I:115:VAL:HA	1:I:118:GLN:HB3	1.86	0.57
2:Z:78:GLU:HG3	2:Z:79:GLY:N	2.20	0.57
1:P:431:ALA:O	1:P:435:VAL:HG22	2.05	0.57
1:T:165:MSE:HE3	1:T:304:PHE:HB2	1.87	0.57
1:K:248:LYS:NZ	1:K:513:ARG:HH12	2.02	0.57
1:B:248:LYS:HG3	1:B:511:ARG:HH11	1.70	0.57
1:D:248:LYS:HG3	1:D:511:ARG:HH11	1.70	0.57
1:J:597:GLN:HE21	1:J:597:GLN:HA	1.70	0.57
1:H:597:GLN:HE21	1:H:597:GLN:HA	1.70	0.57
1:E:597:GLN:HA	1:E:597:GLN:HE21	1.70	0.57
1:J:598:GLN:HB2	1:J:601:GLN:CB	2.34	0.57
1:E:238:PRO:HG3	1:E:263:PHE:HB3	1.86	0.57
1:O:598:GLN:HB2	1:O:601:GLN:CB	2.35	0.57
1:X:598:GLN:HB2	1:X:601:GLN:CB	2.35	0.57
3:S:719:HOH:O	1:T:430:VAL:CG1	2.53	0.57
1:R:598:GLN:HB2	1:R:601:GLN:CB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:VAL:HA	1:D:118:GLN:HB3	1.86	0.56
1:D:144:ILE:HD12	1:D:145:ARG:N	2.19	0.56
1:F:34:PHE:HZ	1:F:328:ARG:HH22	0.80	0.56
1:H:334:MSE:HE3	1:I:404:MSE:HE3	1.86	0.56
1:P:46:SER:N	1:P:48:TYR:HE2	1.97	0.56
1:S:561:ASP:OD2	1:T:92:ASP:HB3	2.03	0.56
1:U:37:ARG:NH2	1:U:41:TRP:HB3	2.20	0.56
1:U:78:VAL:HG11	1:U:444:LEU:HG	1.86	0.56
2:Y:78:GLU:CG	2:Y:79:GLY:N	2.63	0.56
1:M:158:TRP:O	1:M:160:SER:N	2.38	0.56
1:L:248:LYS:NZ	1:L:513:ARG:HH12	2.02	0.56
1:T:209:PHE:HZ	1:T:214:GLN:HG2	1.70	0.56
1:D:597:GLN:HA	1:D:597:GLN:HE21	1.70	0.56
1:U:94:LEU:HA	1:U:97:MSE:CE	2.34	0.56
1:E:166:ASP:OD2	1:E:168:SER:HB3	2.05	0.56
1:B:115:VAL:HA	1:B:118:GLN:HB3	1.86	0.56
1:G:440:MSE:O	1:G:444:LEU:HD22	2.05	0.56
1:I:440:MSE:O	1:I:444:LEU:HD22	2.05	0.56
1:K:118:GLN:NE2	1:K:303:VAL:HB	2.19	0.56
1:L:440:MSE:O	1:L:444:LEU:HD22	2.05	0.56
1:O:158:TRP:O	1:O:160:SER:N	2.37	0.56
1:P:158:TRP:CH2	1:P:302:PRO:HG3	2.39	0.56
1:P:158:TRP:O	1:P:160:SER:N	2.38	0.56
1:V:273:ARG:NH1	1:V:275:ARG:HE	2.03	0.56
1:K:248:LYS:CG	1:K:511:ARG:HH11	2.19	0.56
1:Q:94:LEU:HA	1:Q:97:MSE:CE	2.35	0.56
1:M:598:GLN:HB2	1:M:601:GLN:CB	2.35	0.56
1:L:541:LYS:HD3	1:L:542:THR:HG23	1.87	0.56
1:U:86:ALA:HB2	1:U:515:GLU:HG3	1.86	0.56
1:A:372:TYR:CE2	1:B:348:LYS:HB2	2.39	0.56
1:G:34:PHE:HE1	1:G:324:LYS:HZ2	1.50	0.56
1:I:334:MSE:HE3	1:J:404:MSE:CE	2.35	0.56
1:I:118:GLN:NE2	1:I:303:VAL:HB	2.19	0.56
1:J:440:MSE:O	1:J:444:LEU:HD22	2.05	0.56
1:M:78:VAL:CG2	1:M:444:LEU:HD11	2.23	0.56
1:S:165:MSE:HE3	1:S:304:PHE:HB2	1.86	0.56
1:V:78:VAL:HG12	1:V:79:LEU:H	1.70	0.56
1:W:158:TRP:O	1:W:160:SER:N	2.38	0.56
1:M:71:MSE:HE2	1:M:119:ILE:HD11	1.86	0.56
1:J:248:LYS:HG3	1:J:511:ARG:HH11	1.70	0.56
1:G:236:GLN:CB	1:G:265:LYS:HZ3	2.16	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:248:LYS:HG3	1:K:511:ARG:HH11	1.70	0.56
1:U:273:ARG:HH22	1:U:453:LEU:HD21	1.70	0.56
1:I:567:MSE:SE	1:J:576:LEU:HD13	2.55	0.56
1:F:248:LYS:HG3	1:F:511:ARG:HH11	1.70	0.56
1:L:248:LYS:HG3	1:L:511:ARG:HH11	1.70	0.56
1:X:210:PRO:HD2	1:X:211:TRP:CD2	2.40	0.56
1:X:456:ALA:HB1	1:X:509:ASP:OD1	2.05	0.56
1:N:577:ILE:HA	1:N:582:LYS:HB3	1.85	0.56
1:I:597:GLN:HE21	1:I:597:GLN:HA	1.70	0.56
1:S:598:GLN:HB2	1:S:601:GLN:CB	2.35	0.56
1:V:578:GLN:HG2	1:V:596:ALA:HB2	1.87	0.56
1:M:430:VAL:CG1	3:N:719:HOH:O	2.53	0.56
1:G:166:ASP:OD2	1:G:168:SER:HB3	2.05	0.56
1:M:578:GLN:HG2	1:M:596:ALA:HB2	1.87	0.56
1:J:166:ASP:OD2	1:J:168:SER:HB3	2.05	0.56
1:A:72:ARG:HD2	1:B:434:THR:HG21	1.87	0.56
1:G:37:ARG:HH21	1:G:37:ARG:CB	2.16	0.56
1:H:158:TRP:H	1:H:158:TRP:HD1	1.52	0.56
1:O:144:ILE:HD12	1:O:145:ARG:N	2.20	0.56
1:L:144:ILE:HD12	1:L:145:ARG:N	2.20	0.56
1:Q:46:SER:N	1:Q:48:TYR:HE2	1.98	0.56
1:R:165:MSE:HE1	1:R:435:VAL:HB	1.87	0.56
1:Q:158:TRP:O	1:Q:160:SER:N	2.39	0.56
1:P:510:ILE:HG12	1:P:511:ARG:N	2.20	0.56
1:N:71:MSE:HE2	1:N:119:ILE:HD11	1.85	0.56
1:K:273:ARG:NH2	1:K:453:LEU:HD21	2.21	0.56
1:H:248:LYS:CG	1:H:511:ARG:HH11	2.19	0.56
1:Q:210:PRO:HD2	1:Q:211:TRP:CD2	2.40	0.56
1:V:209:PHE:HZ	1:V:214:GLN:HG2	1.70	0.56
1:M:210:PRO:HD2	1:M:211:TRP:CD2	2.41	0.56
1:S:209:PHE:N	1:S:210:PRO:HD3	2.21	0.56
1:U:210:PRO:HD2	1:U:211:TRP:CD2	2.40	0.56
1:U:199:PRO:HB3	1:U:282:THR:HG22	1.87	0.56
1:I:210:PRO:HD2	1:I:211:TRP:CE3	2.41	0.56
1:J:210:PRO:HD2	1:J:211:TRP:CE3	2.41	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CZ3	2.39	0.56
1:Q:564:GLY:HA2	1:R:554:LEU:HD21	1.87	0.56
1:U:99:ARG:O	1:U:103:ARG:HG3	2.05	0.56
1:N:598:GLN:HB2	1:N:601:GLN:CB	2.35	0.56
1:P:598:GLN:HB2	1:P:601:GLN:CB	2.35	0.56
1:K:166:ASP:OD2	1:K:168:SER:HB3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:MSE:O	1:A:444:LEU:HD22	2.05	0.56
1:B:161:ASN:C	1:B:161:ASN:ND2	2.59	0.56
1:E:158:TRP:H	1:E:158:TRP:HD1	1.52	0.56
1:I:161:ASN:C	1:I:161:ASN:ND2	2.59	0.56
1:K:144:ILE:HD12	1:K:145:ARG:N	2.20	0.56
1:S:510:ILE:HG12	1:S:511:ARG:N	2.20	0.56
1:X:158:TRP:CE3	1:X:173:CYS:SG	2.85	0.56
1:J:236:GLN:CB	1:J:265:LYS:HZ3	2.16	0.56
1:G:248:LYS:HG3	1:G:511:ARG:HH11	1.70	0.56
1:D:248:LYS:CG	1:D:511:ARG:HH11	2.19	0.56
1:E:248:LYS:CG	1:E:511:ARG:HH11	2.19	0.56
1:N:210:PRO:HD2	1:N:211:TRP:CD2	2.41	0.56
1:O:210:PRO:HD2	1:O:211:TRP:CD2	2.41	0.56
1:R:199:PRO:HB3	1:R:282:THR:HG22	1.86	0.56
1:A:597:GLN:HE21	1:A:597:GLN:HA	1.70	0.56
1:E:210:PRO:HD2	1:E:211:TRP:CE3	2.41	0.56
1:N:554:LEU:HD21	1:V:564:GLY:HA2	1.86	0.56
1:U:598:GLN:HB2	1:U:601:GLN:CB	2.35	0.56
2:Z:78:GLU:O	2:Z:80:ASP:OD2	2.24	0.56
1:S:78:VAL:HG11	1:S:444:LEU:HG	1.86	0.56
1:T:158:TRP:O	1:T:160:SER:N	2.39	0.56
1:U:165:MSE:HE3	1:U:304:PHE:HB2	1.87	0.56
1:X:510:ILE:HG12	1:X:511:ARG:N	2.19	0.56
1:W:158:TRP:CE3	1:W:173:CYS:SG	2.85	0.56
1:U:158:TRP:O	1:U:160:SER:N	2.39	0.56
1:S:273:ARG:HH22	1:S:453:LEU:HD21	1.70	0.56
1:J:248:LYS:CG	1:J:511:ARG:HH11	2.19	0.56
1:A:236:GLN:CB	1:A:265:LYS:HZ3	2.16	0.56
1:I:248:LYS:CG	1:I:511:ARG:HH11	2.19	0.56
1:I:248:LYS:HG3	1:I:511:ARG:HH11	1.70	0.56
1:V:209:PHE:N	1:V:210:PRO:HD3	2.21	0.56
1:H:210:PRO:HD2	1:H:211:TRP:CE3	2.41	0.56
1:F:210:PRO:HD2	1:F:211:TRP:CE3	2.41	0.56
1:D:337:ASN:ND2	1:D:401:ASN:HD22	2.04	0.56
1:J:238:PRO:HG3	1:J:263:PHE:HB3	1.86	0.56
1:F:363:TYR:HE1	1:G:350:PHE:HE1	1.53	0.56
1:A:541:LYS:HD3	1:A:542:THR:HG23	1.87	0.56
1:R:578:GLN:HG2	1:R:596:ALA:HB2	1.88	0.56
1:C:158:TRP:HD1	1:C:158:TRP:H	1.52	0.56
1:G:158:TRP:HD1	1:G:158:TRP:H	1.52	0.56
1:G:334:MSE:SE	1:H:404:MSE:HE1	2.55	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:456:ALA:HB1	1:T:509:ASP:OD1	2.05	0.56
1:W:165:MSE:HE3	1:W:304:PHE:HB2	1.86	0.56
1:S:158:TRP:O	1:S:160:SER:N	2.39	0.56
1:O:273:ARG:NH1	1:O:275:ARG:HE	2.04	0.56
1:X:273:ARG:NH1	1:X:275:ARG:HE	2.04	0.56
1:X:273:ARG:NH2	1:X:453:LEU:HD21	2.21	0.56
1:H:248:LYS:NZ	1:H:513:ARG:HH12	2.02	0.56
1:K:597:GLN:HE21	1:K:597:GLN:HA	1.70	0.56
1:G:597:GLN:HE21	1:G:597:GLN:HA	1.70	0.56
1:T:66:LYS:HZ3	1:T:420:VAL:HG11	1.71	0.56
1:A:210:PRO:HD2	1:A:211:TRP:CE3	2.41	0.56
1:A:352:TRP:CD2	1:L:376:ARG:HB2	2.41	0.56
1:F:597:GLN:HA	1:F:597:GLN:HE21	1.70	0.56
1:E:337:ASN:ND2	1:E:401:ASN:HD22	2.04	0.56
1:V:95:MSE:HB3	1:V:527:MSE:HE1	1.88	0.56
1:D:161:ASN:ND2	1:D:161:ASN:C	2.59	0.56
1:K:182:ASN:ND2	1:L:171:ARG:HH21	2.03	0.56
1:O:35:PHE:CE1	1:O:321:ARG:NE	2.73	0.56
2:Y:78:GLU:O	2:Y:80:ASP:OD2	2.24	0.56
1:N:158:TRP:O	1:N:160:SER:N	2.38	0.56
1:F:546:THR:CG2	1:F:547:PRO:HD3	2.27	0.56
1:A:248:LYS:CG	1:A:511:ARG:HH11	2.19	0.56
1:C:248:LYS:CG	1:C:511:ARG:HH11	2.19	0.56
1:S:210:PRO:HD2	1:S:211:TRP:CD2	2.40	0.56
1:O:209:PHE:N	1:O:210:PRO:HD3	2.21	0.56
1:I:541:LYS:HD3	1:I:542:THR:HG23	1.87	0.56
1:T:578:GLN:HG2	1:T:596:ALA:HB2	1.86	0.56
1:S:430:VAL:CG1	3:U:719:HOH:O	2.52	0.56
1:C:440:MSE:O	1:C:444:LEU:HD22	2.05	0.56
1:K:158:TRP:HD1	1:K:158:TRP:H	1.52	0.56
1:K:158:TRP:HB3	1:K:173:CYS:CA	2.36	0.56
1:L:161:ASN:ND2	1:L:161:ASN:C	2.59	0.56
1:Q:431:ALA:O	1:Q:435:VAL:HG22	2.05	0.56
1:S:212:LEU:HD22	1:T:26:ARG:HG2	1.86	0.56
1:U:434:THR:O	1:U:437:GLN:HG2	2.06	0.56
1:Q:510:ILE:HG12	1:Q:511:ARG:N	2.20	0.56
1:Q:158:TRP:HB3	1:Q:173:CYS:CA	2.27	0.56
1:J:273:ARG:NH2	1:J:453:LEU:HD21	2.21	0.56
1:G:248:LYS:CG	1:G:511:ARG:HH11	2.19	0.56
1:B:236:GLN:CB	1:B:265:LYS:HZ3	2.16	0.56
1:N:209:PHE:HZ	1:N:214:GLN:HG2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:209:PHE:N	1:T:210:PRO:HD3	2.21	0.56
1:N:199:PRO:HB3	1:N:282:THR:HG22	1.87	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CE3	2.41	0.56
1:N:94:LEU:HA	1:N:97:MSE:CE	2.36	0.56
1:H:337:ASN:ND2	1:H:401:ASN:HD22	2.04	0.56
1:I:337:ASN:ND2	1:I:401:ASN:HD22	2.04	0.56
1:Q:86:ALA:HB2	1:Q:515:GLU:HG3	1.87	0.56
1:S:578:GLN:HG2	1:S:596:ALA:HB2	1.87	0.56
3:T:719:HOH:O	1:W:430:VAL:CG1	2.53	0.56
1:Q:578:GLN:HG2	1:Q:596:ALA:HB2	1.86	0.56
1:B:27:ARG:HB2	1:B:313:LYS:HE3	1.88	0.56
1:E:380:ASN:O	1:E:381:SER:HB3	2.06	0.56
1:G:34:PHE:HZ	1:G:328:ARG:HH22	0.80	0.56
1:J:161:ASN:ND2	1:J:161:ASN:C	2.59	0.56
1:P:144:ILE:HD12	1:P:145:ARG:N	2.21	0.56
1:Q:101:ASP:HB2	1:Q:144:ILE:O	2.06	0.56
1:Q:41:TRP:HE1	1:R:27:ARG:HH21	1.54	0.56
1:F:248:LYS:CG	1:F:511:ARG:HH11	2.19	0.56
1:R:210:PRO:HD2	1:R:211:TRP:CD2	2.41	0.56
1:Q:209:PHE:N	1:Q:210:PRO:HD3	2.21	0.56
1:W:209:PHE:HZ	1:W:214:GLN:HG2	1.70	0.56
1:W:209:PHE:N	1:W:210:PRO:HD3	2.21	0.56
1:S:564:GLY:CA	1:T:554:LEU:HD21	2.36	0.56
1:W:199:PRO:HB3	1:W:282:THR:HG22	1.87	0.56
1:V:430:VAL:CG1	3:W:719:HOH:O	2.54	0.56
1:O:578:GLN:HG2	1:O:596:ALA:HB2	1.88	0.56
1:P:296:GLU:HG2	1:P:449:PHE:HB3	1.88	0.56
1:A:158:TRP:HB3	1:A:173:CYS:CA	2.36	0.55
1:B:158:TRP:HB3	1:B:173:CYS:CA	2.36	0.55
1:D:440:MSE:O	1:D:444:LEU:HD22	2.05	0.55
1:D:404:MSE:CE	1:E:334:MSE:HE3	2.36	0.55
1:L:158:TRP:H	1:L:158:TRP:HD1	1.52	0.55
1:M:78:VAL:HG11	1:M:444:LEU:HG	1.87	0.55
1:X:101:ASP:HB2	1:X:144:ILE:O	2.07	0.55
1:R:71:MSE:HE2	1:R:119:ILE:HD11	1.86	0.55
1:Q:273:ARG:NH1	1:Q:275:ARG:HE	2.04	0.55
1:H:248:LYS:HG3	1:H:511:ARG:HH11	1.70	0.55
1:E:248:LYS:HG3	1:E:511:ARG:HH11	1.70	0.55
1:L:248:LYS:CG	1:L:511:ARG:HH11	2.19	0.55
1:R:209:PHE:N	1:R:210:PRO:HD3	2.21	0.55
1:R:420:VAL:HG22	1:R:428:GLY:HA3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:PRO:HD2	1:B:211:TRP:CE3	2.41	0.55
1:V:94:LEU:HA	1:V:97:MSE:CE	2.36	0.55
1:I:380:ASN:O	1:I:381:SER:HB3	2.07	0.55
1:P:94:LEU:HA	1:P:97:MSE:CE	2.36	0.55
1:F:541:LYS:HD3	1:F:542:THR:HG23	1.87	0.55
1:U:390:ALA:CB	1:X:387:GLN:HB3	2.36	0.55
1:G:541:LYS:HD3	1:G:542:THR:HG23	1.87	0.55
1:W:593:LEU:O	1:W:597:GLN:HG2	2.06	0.55
1:F:47:GLN:CD	1:F:47:GLN:H	2.10	0.55
1:G:27:ARG:HB2	1:G:313:LYS:HE3	1.89	0.55
1:G:380:ASN:O	1:G:381:SER:HB3	2.07	0.55
1:K:34:PHE:CE1	1:K:324:LYS:NZ	2.72	0.55
1:O:44:TRP:CE2	1:O:54:ARG:HB3	2.41	0.55
1:S:99:ARG:O	1:S:103:ARG:HG3	2.05	0.55
1:U:35:PHE:CE1	1:U:321:ARG:NE	2.74	0.55
1:N:546:THR:CG2	1:N:547:PRO:HD3	2.29	0.55
1:U:71:MSE:HE2	1:U:119:ILE:HD11	1.88	0.55
1:X:273:ARG:HH22	1:X:453:LEU:HD21	1.71	0.55
1:T:210:PRO:HD2	1:T:211:TRP:CD2	2.41	0.55
1:G:210:PRO:HD2	1:G:211:TRP:CE3	2.41	0.55
1:L:337:ASN:ND2	1:L:401:ASN:HD22	2.04	0.55
1:L:589:GLU:HA	1:L:592:TRP:HB2	1.88	0.55
1:R:296:GLU:HG2	1:R:449:PHE:HB3	1.88	0.55
1:T:99:ARG:O	1:T:103:ARG:HG3	2.04	0.55
1:J:395:PRO:HD2	1:K:398:PRO:HB3	1.87	0.55
1:H:238:PRO:HG3	1:H:263:PHE:HB3	1.87	0.55
1:Q:296:GLU:HG2	1:Q:449:PHE:HB3	1.87	0.55
1:X:81:ARG:HB2	1:X:517:TYR:CZ	2.41	0.55
1:X:578:GLN:HG2	1:X:596:ALA:HB2	1.87	0.55
1:D:47:GLN:CD	1:D:47:GLN:H	2.10	0.55
1:F:161:ASN:C	1:F:161:ASN:ND2	2.59	0.55
1:F:440:MSE:O	1:F:444:LEU:HD22	2.05	0.55
1:M:92:ASP:HB3	1:N:561:ASP:OD2	2.06	0.55
1:O:94:LEU:HA	1:O:97:MSE:CE	2.36	0.55
1:Q:165:MSE:HE3	1:Q:304:PHE:HB2	1.87	0.55
1:Q:456:ALA:HB1	1:Q:509:ASP:OD1	2.06	0.55
1:T:246:TYR:CD2	1:T:511:ARG:HB2	2.39	0.55
1:X:15:PHE:HZ	1:X:283:CYS:SG	2.26	0.55
1:R:273:ARG:NH1	1:R:275:ARG:HE	2.05	0.55
1:K:210:PRO:HD2	1:K:211:TRP:CE3	2.41	0.55
1:L:380:ASN:O	1:L:381:SER:HB3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:380:ASN:O	1:J:381:SER:HB3	2.07	0.55
1:S:71:MSE:HE2	1:S:119:ILE:HD11	1.87	0.55
1:S:296:GLU:HG2	1:S:449:PHE:HB3	1.87	0.55
1:W:99:ARG:O	1:W:103:ARG:HG3	2.05	0.55
1:X:296:GLU:HG2	1:X:449:PHE:HB3	1.88	0.55
1:D:589:GLU:HA	1:D:592:TRP:HB2	1.89	0.55
1:E:161:ASN:C	1:E:161:ASN:ND2	2.59	0.55
1:D:404:MSE:HE1	1:E:334:MSE:SE	2.57	0.55
1:H:161:ASN:ND2	1:H:161:ASN:C	2.59	0.55
1:L:158:TRP:HB3	1:L:173:CYS:CA	2.36	0.55
1:W:546:THR:CG2	1:W:547:PRO:HD3	2.29	0.55
1:N:404:MSE:HE1	1:V:334:MSE:SE	2.56	0.55
1:N:413:LYS:HA	1:N:416:ALA:HB3	1.88	0.55
1:R:209:PHE:HZ	1:R:214:GLN:HG2	1.70	0.55
1:A:557:PHE:CE2	1:L:563:LYS:HD3	2.41	0.55
1:L:210:PRO:HD2	1:L:211:TRP:CE3	2.41	0.55
1:L:27:ARG:HB2	1:L:313:LYS:HE3	1.89	0.55
1:T:71:MSE:HE2	1:T:119:ILE:HD11	1.87	0.55
1:H:589:GLU:HA	1:H:592:TRP:HB2	1.89	0.55
1:L:166:ASP:OD2	1:L:168:SER:HB3	2.05	0.55
1:B:589:GLU:HA	1:B:592:TRP:HB2	1.88	0.55
1:J:589:GLU:HA	1:J:592:TRP:HB2	1.89	0.55
1:P:578:GLN:HG2	1:P:596:ALA:HB2	1.87	0.55
1:G:47:GLN:H	1:G:47:GLN:CD	2.10	0.55
1:Q:44:TRP:C	1:Q:45:LEU:HD22	2.26	0.55
1:R:444:LEU:C	1:R:446:THR:N	2.54	0.55
1:V:456:ALA:HB1	1:V:509:ASP:OD1	2.06	0.55
1:R:546:THR:CG2	1:R:547:PRO:HD3	2.29	0.55
1:K:236:GLN:CB	1:K:265:LYS:HZ3	2.17	0.55
1:A:248:LYS:HG3	1:A:511:ARG:HH11	1.70	0.55
1:S:557:PHE:CE2	1:U:563:LYS:HD3	2.42	0.55
1:N:209:PHE:N	1:N:210:PRO:HD3	2.21	0.55
1:D:210:PRO:HD2	1:D:211:TRP:CE3	2.41	0.55
1:K:108:LYS:HD3	1:K:112:ASN:ND2	2.21	0.55
1:C:380:ASN:O	1:C:381:SER:HB3	2.07	0.55
1:X:94:LEU:HA	1:X:97:MSE:CE	2.36	0.55
1:G:337:ASN:ND2	1:G:401:ASN:HD22	2.04	0.55
1:N:296:GLU:HG2	1:N:449:PHE:HB3	1.89	0.55
1:A:27:ARG:HB2	1:A:313:LYS:HE3	1.89	0.55
1:F:80:TYR:CE2	1:F:94:LEU:HD22	2.42	0.55
1:S:78:VAL:HG12	1:S:79:LEU:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:35:PHE:HE1	1:U:321:ARG:NH1	2.05	0.55
1:V:546:THR:CG2	1:V:547:PRO:HD3	2.29	0.55
1:M:273:ARG:HH22	1:M:453:LEU:HD21	1.71	0.55
1:X:46:SER:N	1:X:48:TYR:HE2	1.98	0.55
1:G:235:TYR:HA	1:G:265:LYS:HB3	1.89	0.55
1:L:273:ARG:NH2	1:L:453:LEU:HD21	2.21	0.55
1:W:210:PRO:HD2	1:W:211:TRP:CD2	2.41	0.55
1:B:380:ASN:O	1:B:381:SER:HB3	2.06	0.55
1:J:541:LYS:HD3	1:J:542:THR:HG23	1.87	0.55
1:H:541:LYS:HD3	1:H:542:THR:HG23	1.87	0.55
1:W:95:MSE:HB3	1:W:527:MSE:HE1	1.87	0.55
2:Y:19:VAL:O	2:Y:82:HIS:CD2	2.60	0.55
2:Z:19:VAL:O	2:Z:82:HIS:CD2	2.60	0.55
1:D:27:ARG:HB2	1:D:313:LYS:HE3	1.89	0.55
1:J:47:GLN:H	1:J:47:GLN:CD	2.10	0.55
1:O:510:ILE:HG12	1:O:511:ARG:N	2.21	0.55
1:E:235:TYR:HA	1:E:265:LYS:HB3	1.89	0.55
1:F:235:TYR:HA	1:F:265:LYS:HB3	1.89	0.55
1:F:273:ARG:NH2	1:F:453:LEU:HD21	2.21	0.55
1:X:93:VAL:CG1	1:X:458:ARG:HG3	2.37	0.55
1:K:276:VAL:HG23	1:K:293:ILE:HG23	1.89	0.55
1:B:108:LYS:HD3	1:B:112:ASN:ND2	2.21	0.55
1:M:99:ARG:O	1:M:103:ARG:HG3	2.07	0.55
1:G:311:GLU:O	1:G:312:ASP:HB2	2.07	0.55
1:O:71:MSE:HE2	1:O:119:ILE:HD11	1.87	0.55
1:R:351:PHE:CD2	1:R:356:ILE:HD12	2.41	0.55
1:J:372:TYR:CE2	1:K:348:LYS:HB2	2.41	0.55
1:A:171:ARG:HH21	1:L:182:ASN:ND2	2.05	0.55
1:D:158:TRP:HB3	1:D:173:CYS:CA	2.36	0.55
1:D:306:GLU:O	1:D:316:TYR:HA	2.07	0.55
1:E:27:ARG:HB2	1:E:313:LYS:HE3	1.88	0.55
1:E:80:TYR:CE2	1:E:94:LEU:HD22	2.42	0.55
1:H:47:GLN:H	1:H:47:GLN:CD	2.10	0.55
1:K:161:ASN:ND2	1:K:161:ASN:C	2.59	0.55
1:U:165:MSE:HE1	1:U:435:VAL:HB	1.89	0.55
1:S:273:ARG:NH1	1:S:275:ARG:HE	2.05	0.55
1:K:236:GLN:CB	1:K:265:LYS:HG2	2.37	0.55
1:B:235:TYR:HA	1:B:265:LYS:HB3	1.89	0.55
1:C:248:LYS:HG3	1:C:511:ARG:HH11	1.70	0.55
1:C:235:TYR:HA	1:C:265:LYS:HB3	1.89	0.55
1:P:24:GLU:C	1:P:26:ARG:N	2.57	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:420:VAL:HG22	1:S:428:GLY:HA3	1.88	0.55
1:I:108:LYS:HD3	1:I:112:ASN:ND2	2.21	0.55
1:H:108:LYS:HD3	1:H:112:ASN:ND2	2.21	0.55
1:C:276:VAL:HG23	1:C:293:ILE:HG23	1.89	0.55
1:F:108:LYS:HD3	1:F:112:ASN:ND2	2.21	0.55
1:W:296:GLU:HG2	1:W:449:PHE:HB3	1.89	0.55
1:C:589:GLU:HA	1:C:592:TRP:HB2	1.89	0.55
1:A:306:GLU:O	1:A:316:TYR:HA	2.07	0.55
1:F:158:TRP:HB3	1:F:173:CYS:CA	2.36	0.55
1:F:306:GLU:O	1:F:316:TYR:HA	2.07	0.55
1:K:80:TYR:CE2	1:K:94:LEU:HD22	2.42	0.55
1:Q:47:GLN:HG2	1:Q:48:TYR:N	2.22	0.55
2:Y:34:LEU:C	2:Y:35:THR:CG2	2.73	0.55
1:I:235:TYR:HA	1:I:265:LYS:HB3	1.89	0.55
1:M:209:PHE:N	1:M:210:PRO:HD3	2.21	0.55
1:A:108:LYS:HD3	1:A:112:ASN:ND2	2.21	0.55
1:C:108:LYS:HD3	1:C:112:ASN:ND2	2.21	0.55
1:D:108:LYS:HD3	1:D:112:ASN:ND2	2.21	0.55
1:L:108:LYS:HD3	1:L:112:ASN:ND2	2.21	0.55
1:D:276:VAL:HG23	1:D:293:ILE:HG23	1.89	0.55
1:K:337:ASN:ND2	1:K:401:ASN:HD22	2.04	0.55
1:V:554:LEU:HD12	1:V:557:PHE:HD2	1.70	0.55
1:M:296:GLU:HG2	1:M:449:PHE:HB3	1.89	0.55
1:A:589:GLU:HA	1:A:592:TRP:HB2	1.89	0.55
1:U:578:GLN:HG2	1:U:596:ALA:HB2	1.88	0.55
1:E:589:GLU:HA	1:E:592:TRP:HB2	1.89	0.55
1:C:158:TRP:HB3	1:C:173:CYS:CA	2.36	0.55
1:D:380:ASN:O	1:D:381:SER:HB3	2.07	0.55
1:F:334:MSE:HE3	1:G:404:MSE:CE	2.37	0.55
1:L:34:PHE:HZ	1:L:328:ARG:HH22	0.80	0.55
1:P:44:TRP:C	1:P:45:LEU:HD22	2.27	0.55
1:P:47:GLN:HG2	1:P:48:TYR:N	2.20	0.55
1:W:510:ILE:HG12	1:W:511:ARG:N	2.20	0.55
1:V:302:PRO:O	1:V:439:ASN:ND2	2.40	0.55
1:H:380:ASN:O	1:H:381:SER:HB3	2.06	0.55
1:E:276:VAL:HG23	1:E:293:ILE:HG23	1.89	0.55
1:F:380:ASN:O	1:F:381:SER:HB3	2.06	0.55
1:C:337:ASN:ND2	1:C:401:ASN:HD22	2.04	0.55
1:R:86:ALA:HB2	1:R:515:GLU:HG3	1.87	0.55
3:R:719:HOH:O	1:X:430:VAL:CG1	2.55	0.55
1:I:589:GLU:HA	1:I:592:TRP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:584:PRO:HG2	1:P:593:LEU:HD12	1.89	0.55
1:P:593:LEU:O	1:P:597:GLN:HG2	2.07	0.55
2:Y:27:GLY:HA2	2:Y:30:SER:HB3	1.88	0.55
1:D:311:GLU:O	1:D:312:ASP:HB2	2.07	0.55
1:G:161:ASN:C	1:G:161:ASN:ND2	2.59	0.54
1:H:158:TRP:HB3	1:H:173:CYS:CA	2.36	0.54
1:L:306:GLU:O	1:L:316:TYR:HA	2.07	0.54
1:L:37:ARG:CB	1:L:37:ARG:HH21	2.16	0.54
1:M:35:PHE:HE1	1:M:321:ARG:NH1	2.04	0.54
1:N:93:VAL:CG1	1:N:458:ARG:HG3	2.38	0.54
1:N:78:VAL:HG12	1:N:79:LEU:H	1.72	0.54
1:Q:35:PHE:CE1	1:Q:321:ARG:NE	2.75	0.54
1:S:44:TRP:C	1:S:45:LEU:HD22	2.27	0.54
1:X:44:TRP:CE2	1:X:54:ARG:HB3	2.42	0.54
1:E:236:GLN:CB	1:E:265:LYS:HG2	2.37	0.54
1:P:210:PRO:HD2	1:P:211:TRP:CD2	2.41	0.54
1:T:199:PRO:HB3	1:T:282:THR:HG22	1.87	0.54
1:J:108:LYS:HD3	1:J:112:ASN:ND2	2.21	0.54
1:I:276:VAL:HG23	1:I:293:ILE:HG23	1.89	0.54
1:K:380:ASN:O	1:K:381:SER:HB3	2.06	0.54
1:A:380:ASN:O	1:A:381:SER:HB3	2.07	0.54
1:B:337:ASN:ND2	1:B:401:ASN:HD22	2.04	0.54
1:L:311:GLU:O	1:L:312:ASP:HB2	2.07	0.54
1:P:389:LEU:HD12	1:P:389:LEU:H	1.73	0.54
1:S:593:LEU:O	1:S:597:GLN:HG2	2.06	0.54
1:Q:154:SER:O	1:Q:204:PRO:HB3	2.07	0.54
1:C:80:TYR:CE2	1:C:94:LEU:HD22	2.42	0.54
1:F:27:ARG:HB2	1:F:313:LYS:HE3	1.88	0.54
1:G:80:TYR:CE2	1:G:94:LEU:HD22	2.42	0.54
1:H:80:TYR:CE2	1:H:94:LEU:HD22	2.42	0.54
1:J:306:GLU:O	1:J:316:TYR:HA	2.07	0.54
1:K:34:PHE:HZ	1:K:328:ARG:HH22	0.80	0.54
1:J:72:ARG:HD2	1:K:434:THR:HG21	1.89	0.54
1:M:456:ALA:HB1	1:M:509:ASP:OD1	2.07	0.54
1:O:35:PHE:HE1	1:O:321:ARG:NH1	2.05	0.54
1:S:35:PHE:CE1	1:S:321:ARG:NE	2.75	0.54
1:X:165:MSE:HE3	1:X:304:PHE:HB2	1.88	0.54
1:S:546:THR:CG2	1:S:547:PRO:HD3	2.30	0.54
1:N:158:TRP:HD1	1:N:158:TRP:N	2.06	0.54
1:T:47:GLN:HG2	1:T:48:TYR:N	2.22	0.54
1:B:248:LYS:CG	1:B:511:ARG:HH11	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:236:GLN:CB	1:H:265:LYS:HZ3	2.16	0.54
1:A:235:TYR:HA	1:A:265:LYS:HB3	1.89	0.54
1:C:236:GLN:HE21	1:C:265:LYS:NZ	2.06	0.54
1:U:209:PHE:N	1:U:210:PRO:HD3	2.21	0.54
1:M:557:PHE:CE2	1:N:563:LYS:HD3	2.42	0.54
1:J:276:VAL:HG23	1:J:293:ILE:HG23	1.89	0.54
1:E:108:LYS:HD3	1:E:112:ASN:ND2	2.21	0.54
1:J:337:ASN:ND2	1:J:401:ASN:HD22	2.04	0.54
1:N:578:GLN:HG2	1:N:596:ALA:HB2	1.89	0.54
1:M:593:LEU:O	1:M:597:GLN:HG2	2.07	0.54
1:A:80:TYR:CE2	1:A:94:LEU:HD22	2.42	0.54
1:B:80:TYR:CE2	1:B:94:LEU:HD22	2.42	0.54
1:C:444:LEU:C	1:C:446:THR:N	2.61	0.54
1:E:306:GLU:O	1:E:316:TYR:HA	2.07	0.54
1:F:123:VAL:HG22	1:F:316:TYR:CE2	2.43	0.54
1:G:138:THR:H	1:G:143:VAL:HG22	1.73	0.54
1:I:158:TRP:HB3	1:I:173:CYS:CA	2.36	0.54
1:M:101:ASP:HB2	1:M:144:ILE:O	2.07	0.54
1:P:35:PHE:CE1	1:P:321:ARG:NE	2.76	0.54
1:P:78:VAL:CG1	1:P:79:LEU:N	2.70	0.54
1:U:93:VAL:CG1	1:U:458:ARG:HG3	2.36	0.54
1:T:510:ILE:HG12	1:T:511:ARG:N	2.22	0.54
1:E:236:GLN:HE21	1:E:265:LYS:NZ	2.06	0.54
1:P:209:PHE:N	1:P:210:PRO:HD3	2.21	0.54
1:U:209:PHE:HZ	1:U:214:GLN:HG2	1.71	0.54
1:T:94:LEU:HA	1:T:97:MSE:CE	2.36	0.54
1:F:337:ASN:ND2	1:F:401:ASN:HD22	2.04	0.54
1:C:311:GLU:O	1:C:312:ASP:HB2	2.07	0.54
1:K:589:GLU:HA	1:K:592:TRP:HB2	1.89	0.54
1:A:123:VAL:HG22	1:A:316:TYR:CE2	2.43	0.54
1:B:123:VAL:HG22	1:B:316:TYR:CE2	2.43	0.54
1:B:37:ARG:CB	1:B:37:ARG:HH21	2.16	0.54
1:C:306:GLU:O	1:C:316:TYR:HA	2.07	0.54
1:C:72:ARG:HD2	1:E:434:THR:HG21	1.90	0.54
1:D:444:LEU:C	1:D:446:THR:N	2.61	0.54
1:F:561:ASP:OD2	1:G:92:ASP:HB3	2.07	0.54
1:G:15:PHE:HZ	1:G:283:CYS:SG	2.31	0.54
1:J:123:VAL:HG22	1:J:316:TYR:CE2	2.43	0.54
1:J:80:TYR:CE2	1:J:94:LEU:HD22	2.42	0.54
1:U:26:ARG:HG2	1:X:212:LEU:HD22	1.88	0.54
1:X:35:PHE:CE1	1:X:321:ARG:NE	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:273:ARG:NH1	1:M:275:ARG:HE	2.05	0.54
1:M:158:TRP:N	1:M:158:TRP:HD1	2.04	0.54
1:M:302:PRO:O	1:M:439:ASN:ND2	2.41	0.54
1:C:236:GLN:CB	1:C:265:LYS:HG2	2.37	0.54
1:F:236:GLN:HE21	1:F:265:LYS:NZ	2.06	0.54
1:X:209:PHE:HZ	1:X:214:GLN:HG2	1.70	0.54
1:S:209:PHE:HZ	1:S:214:GLN:HG2	1.70	0.54
1:S:94:LEU:HA	1:S:97:MSE:CE	2.37	0.54
1:A:337:ASN:ND2	1:A:401:ASN:HD22	2.04	0.54
1:V:390:ALA:HB2	1:W:387:GLN:CB	2.38	0.54
1:T:584:PRO:HG2	1:T:593:LEU:HD12	1.90	0.54
1:S:154:SER:O	1:S:204:PRO:HB3	2.07	0.54
1:W:578:GLN:HG2	1:W:596:ALA:HB2	1.87	0.54
1:A:161:ASN:C	1:A:161:ASN:ND2	2.59	0.54
1:A:15:PHE:HZ	1:A:283:CYS:SG	2.31	0.54
1:D:15:PHE:HZ	1:D:283:CYS:SG	2.31	0.54
1:H:138:THR:H	1:H:143:VAL:HG22	1.73	0.54
1:I:47:GLN:H	1:I:47:GLN:CD	2.10	0.54
1:L:15:PHE:HZ	1:L:283:CYS:SG	2.31	0.54
1:L:47:GLN:H	1:L:47:GLN:CD	2.10	0.54
1:M:47:GLN:HG2	1:M:48:TYR:N	2.22	0.54
1:O:101:ASP:HB2	1:O:144:ILE:O	2.07	0.54
2:Z:42:MET:HE3	2:Z:78:GLU:OE1	2.08	0.54
1:P:35:PHE:C	1:P:37:ARG:H	2.11	0.54
1:Q:561:ASP:CB	1:R:89:ASP:HA	2.31	0.54
1:U:144:ILE:HD12	1:U:145:ARG:N	2.22	0.54
1:V:93:VAL:CG1	1:V:458:ARG:HG3	2.37	0.54
1:K:236:GLN:HE21	1:K:265:LYS:NZ	2.06	0.54
1:D:235:TYR:HA	1:D:265:LYS:HB3	1.89	0.54
1:H:235:TYR:HA	1:H:265:LYS:HB3	1.89	0.54
1:I:236:GLN:CB	1:I:265:LYS:HG2	2.37	0.54
1:C:273:ARG:NH2	1:C:453:LEU:HD21	2.21	0.54
1:F:236:GLN:CB	1:F:265:LYS:HZ3	2.16	0.54
1:X:209:PHE:N	1:X:210:PRO:HD3	2.21	0.54
1:R:66:LYS:NZ	1:R:420:VAL:HG11	2.22	0.54
1:T:66:LYS:NZ	1:T:420:VAL:HG11	2.23	0.54
1:M:584:PRO:HG2	1:M:593:LEU:HD12	1.90	0.54
1:F:589:GLU:HA	1:F:592:TRP:HB2	1.89	0.54
1:T:387:GLN:HB2	1:W:390:ALA:HB2	1.90	0.54
1:F:311:GLU:O	1:F:312:ASP:HB2	2.07	0.54
1:I:311:GLU:O	1:I:312:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:44:TRP:C	1:E:45:LEU:HD22	2.28	0.54
1:G:306:GLU:O	1:G:316:TYR:HA	2.07	0.54
1:H:444:LEU:C	1:H:446:THR:N	2.61	0.54
1:H:44:TRP:C	1:H:45:LEU:HD22	2.28	0.54
1:I:306:GLU:O	1:I:316:TYR:HA	2.07	0.54
1:J:138:THR:H	1:J:143:VAL:HG22	1.73	0.54
1:J:34:PHE:HZ	1:J:328:ARG:HH22	0.80	0.54
1:K:306:GLU:O	1:K:316:TYR:HA	2.07	0.54
1:K:37:ARG:HH21	1:K:37:ARG:CB	2.16	0.54
1:Q:78:VAL:HG12	1:Q:79:LEU:H	1.70	0.54
1:S:46:SER:N	1:S:48:TYR:HE2	1.99	0.54
1:V:144:ILE:HD12	1:V:145:ARG:N	2.22	0.54
1:M:510:ILE:HG12	1:M:511:ARG:N	2.22	0.54
1:P:302:PRO:O	1:P:439:ASN:ND2	2.41	0.54
1:P:273:ARG:NH1	1:P:275:ARG:HE	2.06	0.54
1:A:273:ARG:NH2	1:A:453:LEU:HD21	2.21	0.54
1:W:456:ALA:HB1	1:W:509:ASP:OD1	2.08	0.54
1:R:573:ASN:O	1:R:577:ILE:HG13	2.08	0.54
1:T:420:VAL:HG22	1:T:428:GLY:HA3	1.90	0.54
1:N:95:MSE:HB3	1:N:527:MSE:HE1	1.88	0.54
1:Q:593:LEU:O	1:Q:597:GLN:HG2	2.08	0.54
2:Z:27:GLY:HA2	2:Z:30:SER:HB3	1.88	0.54
1:K:311:GLU:O	1:K:312:ASP:HB2	2.07	0.54
1:K:27:ARG:HB2	1:K:313:LYS:HE3	1.89	0.54
1:H:311:GLU:O	1:H:312:ASP:HB2	2.07	0.54
1:G:372:TYR:CE2	1:H:348:LYS:HB2	2.42	0.54
1:X:420:VAL:HG22	1:X:428:GLY:HA3	1.90	0.54
1:A:47:GLN:H	1:A:47:GLN:CD	2.10	0.54
1:C:138:THR:H	1:C:143:VAL:HG22	1.73	0.54
1:D:561:ASP:OD2	1:F:92:ASP:HB3	2.07	0.54
1:H:27:ARG:HB2	1:H:313:LYS:HE3	1.89	0.54
1:O:81:ARG:HB2	1:O:517:TYR:CZ	2.42	0.54
1:S:456:ALA:HB1	1:S:509:ASP:OD1	2.07	0.54
1:U:444:LEU:C	1:U:446:THR:H	2.11	0.54
1:X:71:MSE:HE2	1:X:119:ILE:HD11	1.88	0.54
2:Z:71:ASP:O	2:Z:72:ASP:HB3	2.08	0.54
1:W:46:SER:N	1:W:48:TYR:HE2	1.97	0.54
1:G:236:GLN:CB	1:G:265:LYS:HG2	2.37	0.54
1:D:236:GLN:HE21	1:D:265:LYS:NZ	2.06	0.54
1:H:236:GLN:HE21	1:H:265:LYS:NZ	2.06	0.54
1:L:235:TYR:HA	1:L:265:LYS:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:40:GLN:HG2	1:T:310:VAL:HG22	1.90	0.54
1:D:384:LEU:N	1:D:384:LEU:HD22	2.23	0.54
1:R:154:SER:O	1:R:204:PRO:HB3	2.08	0.54
1:W:66:LYS:NZ	1:W:420:VAL:HG11	2.23	0.54
1:T:296:GLU:HG2	1:T:449:PHE:HB3	1.89	0.54
1:B:306:GLU:O	1:B:316:TYR:HA	2.07	0.54
1:C:44:TRP:C	1:C:45:LEU:HD22	2.28	0.54
1:E:123:VAL:HG22	1:E:316:TYR:CE2	2.43	0.54
1:J:44:TRP:C	1:J:45:LEU:HD22	2.28	0.54
1:J:47:GLN:O	1:J:47:GLN:NE2	2.41	0.54
1:K:15:PHE:HZ	1:K:283:CYS:SG	2.31	0.54
1:K:44:TRP:C	1:K:45:LEU:HD22	2.28	0.54
1:K:47:GLN:O	1:K:47:GLN:NE2	2.41	0.54
1:M:78:VAL:HG12	1:M:79:LEU:H	1.73	0.54
1:S:47:GLN:HG2	1:S:48:TYR:N	2.22	0.54
1:V:101:ASP:HB2	1:V:144:ILE:O	2.08	0.54
1:V:80:TYR:CE1	1:V:448:VAL:HG22	2.43	0.54
1:I:14:ARG:CA	1:I:14:ARG:NE	2.67	0.54
1:G:236:GLN:HE21	1:G:265:LYS:NZ	2.06	0.54
1:X:66:LYS:HZ3	1:X:420:VAL:HG11	1.73	0.54
2:Y:58:GLN:H	2:Y:62:GLY:HA3	1.73	0.54
1:O:593:LEU:O	1:O:597:GLN:HG2	2.07	0.54
1:C:27:ARG:HB2	1:C:313:LYS:HE3	1.89	0.54
1:D:35:PHE:C	1:D:37:ARG:N	2.62	0.54
1:D:47:GLN:O	1:D:47:GLN:NE2	2.41	0.54
1:D:80:TYR:CE2	1:D:94:LEU:HD22	2.42	0.54
1:E:37:ARG:HH21	1:E:37:ARG:CB	2.16	0.54
1:G:35:PHE:C	1:G:37:ARG:N	2.62	0.54
1:G:80:TYR:CE1	1:G:448:VAL:HG22	2.43	0.54
1:H:123:VAL:HG22	1:H:316:TYR:CE2	2.43	0.54
1:I:15:PHE:HZ	1:I:283:CYS:SG	2.31	0.54
1:I:47:GLN:NE2	1:I:47:GLN:O	2.41	0.54
1:K:80:TYR:CE1	1:K:448:VAL:HG22	2.43	0.54
1:M:93:VAL:CG1	1:M:458:ARG:HG3	2.37	0.54
1:L:80:TYR:CE2	1:L:94:LEU:HD22	2.42	0.54
2:Y:78:GLU:CD	2:Y:79:GLY:H	2.11	0.54
1:Q:405:LEU:O	1:Q:409:THR:HG23	2.08	0.54
1:J:235:TYR:HA	1:J:265:LYS:HB3	1.89	0.54
1:J:236:GLN:CB	1:J:265:LYS:HG2	2.37	0.54
1:B:236:GLN:HE21	1:B:265:LYS:NZ	2.06	0.54
1:B:234:ILE:HG13	1:B:267:ALA:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:234:ILE:HG13	1:F:267:ALA:HB3	1.90	0.54
1:Q:209:PHE:HZ	1:Q:214:GLN:HG2	1.70	0.54
1:M:209:PHE:HZ	1:M:214:GLN:HG2	1.70	0.54
1:O:236:GLN:HA	1:O:244:VAL:H	1.73	0.54
1:G:108:LYS:HD3	1:G:112:ASN:ND2	2.21	0.54
1:U:420:VAL:HG22	1:U:428:GLY:HA3	1.89	0.54
1:E:384:LEU:HD22	1:E:384:LEU:N	2.23	0.54
1:W:584:PRO:HG2	1:W:593:LEU:HD12	1.89	0.54
1:O:584:PRO:HG2	1:O:593:LEU:HD12	1.90	0.54
1:W:81:ARG:HB2	1:W:517:TYR:CZ	2.43	0.54
1:B:311:GLU:O	1:B:312:ASP:HB2	2.07	0.54
1:A:528:LYS:HZ2	1:A:560:LEU:HD21	1.72	0.54
1:D:123:VAL:HG22	1:D:316:TYR:CE2	2.43	0.54
1:E:138:THR:H	1:E:143:VAL:HG22	1.73	0.54
1:F:560:LEU:O	1:F:561:ASP:O	2.26	0.54
1:F:80:TYR:CE1	1:F:448:VAL:HG22	2.43	0.54
1:G:158:TRP:HB3	1:G:173:CYS:CA	2.36	0.54
1:G:44:TRP:C	1:G:45:LEU:HD22	2.28	0.54
1:J:15:PHE:HZ	1:J:283:CYS:SG	2.31	0.54
1:J:560:LEU:O	1:J:561:ASP:O	2.26	0.54
1:K:14:ARG:NE	1:K:14:ARG:CA	2.67	0.54
1:K:47:GLN:H	1:K:47:GLN:CD	2.10	0.54
1:L:123:VAL:HG22	1:L:316:TYR:CE2	2.43	0.54
1:Q:344:THR:HG23	1:Q:344:THR:O	2.07	0.54
2:Z:78:GLU:CD	2:Z:79:GLY:H	2.11	0.54
1:N:101:ASP:HB2	1:N:144:ILE:O	2.08	0.54
1:N:47:GLN:HG2	1:N:48:TYR:N	2.22	0.54
1:S:444:LEU:C	1:S:446:THR:H	2.11	0.54
1:T:123:VAL:HG22	1:T:316:TYR:CE2	2.42	0.54
1:G:266:ILE:HG23	1:G:267:ALA:N	2.23	0.54
1:O:563:LYS:HD3	1:P:557:PHE:CE2	2.42	0.54
1:S:66:LYS:NZ	1:S:420:VAL:HG11	2.22	0.54
1:J:579:MSE:HB2	1:J:581:VAL:HG12	1.90	0.54
1:U:390:ALA:HB2	1:X:387:GLN:HB2	1.89	0.54
1:Q:584:PRO:HG2	1:Q:593:LEU:HD12	1.90	0.54
1:X:66:LYS:NZ	1:X:420:VAL:HG11	2.23	0.54
1:U:191:TYR:HE1	1:U:278:LYS:HZ3	1.56	0.54
1:G:589:GLU:HA	1:G:592:TRP:HB2	1.89	0.54
1:B:35:PHE:C	1:B:37:ARG:N	2.61	0.53
1:C:161:ASN:ND2	1:C:161:ASN:C	2.59	0.53
1:C:80:TYR:CE1	1:C:448:VAL:HG22	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:47:GLN:H	1:E:47:GLN:CD	2.10	0.53
1:H:47:GLN:NE2	1:H:47:GLN:O	2.41	0.53
1:H:78:VAL:HG11	1:H:444:LEU:HG	1.90	0.53
1:K:123:VAL:HG22	1:K:316:TYR:CE2	2.43	0.53
1:K:35:PHE:C	1:K:37:ARG:N	2.61	0.53
1:M:444:LEU:O	1:M:448:VAL:HG23	2.08	0.53
1:M:81:ARG:HB2	1:M:517:TYR:CZ	2.43	0.53
1:K:560:LEU:O	1:K:561:ASP:O	2.26	0.53
1:P:101:ASP:HB2	1:P:144:ILE:O	2.08	0.53
1:P:444:LEU:C	1:P:446:THR:H	2.11	0.53
1:U:78:VAL:CG2	1:U:444:LEU:HD11	2.22	0.53
2:Y:78:GLU:HG3	2:Y:79:GLY:N	2.20	0.53
1:K:234:ILE:HG13	1:K:267:ALA:HB3	1.90	0.53
1:H:266:ILE:HG23	1:H:267:ALA:N	2.23	0.53
1:N:273:ARG:NH1	1:N:275:ARG:HE	2.05	0.53
1:E:234:ILE:HG13	1:E:267:ALA:HB3	1.91	0.53
1:F:266:ILE:HG23	1:F:267:ALA:N	2.23	0.53
1:P:209:PHE:HZ	1:P:214:GLN:HG2	1.70	0.53
1:W:94:LEU:HA	1:W:97:MSE:CE	2.37	0.53
1:V:389:LEU:H	1:V:389:LEU:HD12	1.72	0.53
1:F:384:LEU:N	1:F:384:LEU:HD22	2.23	0.53
1:G:384:LEU:N	1:G:384:LEU:HD22	2.23	0.53
1:N:535:ILE:HD13	1:N:554:LEU:HG	1.89	0.53
1:U:390:ALA:HB2	1:X:387:GLN:CB	2.38	0.53
1:U:58:ASP:HA	1:U:327:GLN:NE2	2.23	0.53
1:M:389:LEU:H	1:M:389:LEU:HD12	1.72	0.53
1:O:296:GLU:HG2	1:O:449:PHE:HB3	1.89	0.53
1:N:389:LEU:HD12	1:N:389:LEU:H	1.72	0.53
1:A:37:ARG:HH21	1:A:37:ARG:CB	2.16	0.53
1:B:47:GLN:NE2	1:B:47:GLN:O	2.41	0.53
1:C:35:PHE:C	1:C:37:ARG:N	2.62	0.53
1:C:47:GLN:H	1:C:47:GLN:CD	2.10	0.53
1:C:47:GLN:NE2	1:C:47:GLN:O	2.41	0.53
1:E:80:TYR:CE1	1:E:448:VAL:HG22	2.43	0.53
1:G:444:LEU:C	1:G:446:THR:N	2.61	0.53
1:G:560:LEU:O	1:G:561:ASP:O	2.26	0.53
1:G:78:VAL:HG11	1:G:444:LEU:HG	1.90	0.53
1:H:306:GLU:O	1:H:316:TYR:HA	2.07	0.53
1:I:78:VAL:HG11	1:I:444:LEU:HG	1.90	0.53
1:I:560:LEU:O	1:I:561:ASP:O	2.26	0.53
1:I:80:TYR:CE1	1:I:448:VAL:HG22	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:35:PHE:C	1:J:37:ARG:N	2.61	0.53
1:J:78:VAL:HG11	1:J:444:LEU:HG	1.90	0.53
1:O:434:THR:HA	1:O:437:GLN:HG2	1.90	0.53
1:B:328:ARG:HB3	2:Y:142:PRO:HG3	1.90	0.53
1:O:344:THR:O	1:O:344:THR:HG23	2.08	0.53
1:N:456:ALA:HB1	1:N:509:ASP:OD1	2.08	0.53
1:N:46:SER:N	1:N:48:TYR:HE2	1.98	0.53
1:Q:66:LYS:NZ	1:Q:420:VAL:HG11	2.23	0.53
1:U:35:PHE:C	1:U:37:ARG:H	2.11	0.53
1:W:434:THR:O	1:W:437:GLN:HG2	2.08	0.53
1:X:37:ARG:HH21	1:X:37:ARG:CB	2.20	0.53
1:P:405:LEU:O	1:P:409:THR:HG23	2.08	0.53
1:B:273:ARG:NH2	1:B:453:LEU:HD21	2.21	0.53
1:A:236:GLN:CB	1:A:265:LYS:HG2	2.37	0.53
1:A:236:GLN:HE21	1:A:265:LYS:NZ	2.06	0.53
1:I:236:GLN:HE21	1:I:265:LYS:NZ	2.06	0.53
1:L:234:ILE:HG13	1:L:267:ALA:HB3	1.90	0.53
1:G:177:HIS:O	1:G:218:GLN:HA	2.08	0.53
1:S:584:PRO:HG2	1:S:593:LEU:HD12	1.89	0.53
1:E:311:GLU:O	1:E:312:ASP:HB2	2.07	0.53
1:M:398:PRO:HB3	1:N:395:PRO:HD2	1.90	0.53
1:W:154:SER:O	1:W:204:PRO:HB3	2.08	0.53
1:J:191:TYR:HE1	1:J:278:LYS:HZ3	1.54	0.53
1:L:177:HIS:O	1:L:218:GLN:HA	2.09	0.53
1:C:123:VAL:HG22	1:C:316:TYR:CE2	2.43	0.53
1:E:35:PHE:C	1:E:37:ARG:N	2.62	0.53
1:F:138:THR:H	1:F:143:VAL:HG22	1.73	0.53
1:F:78:VAL:HG11	1:F:444:LEU:HG	1.90	0.53
1:G:123:VAL:HG22	1:G:316:TYR:CE2	2.43	0.53
1:I:80:TYR:CE2	1:I:94:LEU:HD22	2.42	0.53
1:K:78:VAL:HG11	1:K:444:LEU:HG	1.91	0.53
1:N:81:ARG:HB2	1:N:517:TYR:CZ	2.44	0.53
1:R:47:GLN:HG2	1:R:48:TYR:N	2.23	0.53
1:S:35:PHE:C	1:S:37:ARG:H	2.12	0.53
1:S:80:TYR:CE1	1:S:448:VAL:HG22	2.43	0.53
1:S:26:ARG:HG2	1:U:212:LEU:HD22	1.90	0.53
1:V:66:LYS:NZ	1:V:420:VAL:HG11	2.22	0.53
1:W:344:THR:O	1:W:344:THR:HG23	2.08	0.53
1:W:273:ARG:NH1	1:W:275:ARG:HE	2.06	0.53
1:J:266:ILE:HG23	1:J:267:ALA:N	2.23	0.53
1:D:266:ILE:HG23	1:D:267:ALA:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:ILE:HG23	1:A:267:ALA:N	2.23	0.53
1:N:236:GLN:HA	1:N:244:VAL:H	1.74	0.53
1:P:66:LYS:NZ	1:P:420:VAL:HG11	2.24	0.53
1:H:276:VAL:HG23	1:H:293:ILE:HG23	1.89	0.53
1:L:276:VAL:HG23	1:L:293:ILE:HG23	1.89	0.53
1:B:384:LEU:HD22	1:B:384:LEU:N	2.23	0.53
1:C:384:LEU:HD22	1:C:384:LEU:N	2.23	0.53
1:T:593:LEU:O	1:T:597:GLN:HG2	2.08	0.53
1:X:593:LEU:O	1:X:597:GLN:HG2	2.08	0.53
1:J:311:GLU:O	1:J:312:ASP:HB2	2.07	0.53
1:O:154:SER:O	1:O:204:PRO:HB3	2.07	0.53
1:A:560:LEU:O	1:A:561:ASP:O	2.26	0.53
1:B:138:THR:H	1:B:143:VAL:HG22	1.73	0.53
1:B:15:PHE:HZ	1:B:283:CYS:SG	2.31	0.53
1:B:47:GLN:H	1:B:47:GLN:CD	2.10	0.53
1:D:78:VAL:HG11	1:D:444:LEU:HG	1.90	0.53
1:D:44:TRP:C	1:D:45:LEU:HD22	2.28	0.53
1:C:334:MSE:HE3	1:E:404:MSE:HE3	1.90	0.53
1:E:47:GLN:O	1:E:47:GLN:NE2	2.41	0.53
1:H:560:LEU:O	1:H:561:ASP:O	2.26	0.53
1:I:27:ARG:HB2	1:I:313:LYS:HE3	1.89	0.53
1:I:44:TRP:C	1:I:45:LEU:HD22	2.28	0.53
1:K:138:THR:H	1:K:143:VAL:HG22	1.73	0.53
1:M:44:TRP:CE2	1:M:54:ARG:HB3	2.43	0.53
1:O:444:LEU:O	1:O:448:VAL:HG23	2.08	0.53
1:L:78:VAL:HG11	1:L:444:LEU:HG	1.90	0.53
1:L:80:TYR:CE1	1:L:448:VAL:HG22	2.43	0.53
1:N:44:TRP:CE2	1:N:54:ARG:HB3	2.43	0.53
1:T:158:TRP:HD1	1:T:158:TRP:N	2.07	0.53
1:T:44:TRP:C	1:T:45:LEU:HD22	2.29	0.53
1:V:420:VAL:HG22	1:V:428:GLY:HA3	1.90	0.53
1:W:35:PHE:HE1	1:W:321:ARG:NH1	2.05	0.53
1:W:44:TRP:C	1:W:45:LEU:HD22	2.28	0.53
1:W:78:VAL:CG1	1:W:79:LEU:N	2.71	0.53
1:K:235:TYR:HA	1:K:265:LYS:HB3	1.89	0.53
1:K:266:ILE:HG23	1:K:267:ALA:N	2.23	0.53
1:G:273:ARG:NH2	1:G:453:LEU:HD21	2.21	0.53
1:H:236:GLN:CB	1:H:265:LYS:HG2	2.37	0.53
1:E:266:ILE:HG23	1:E:267:ALA:N	2.23	0.53
1:Q:236:GLN:HA	1:Q:244:VAL:H	1.74	0.53
1:P:236:GLN:HA	1:P:244:VAL:H	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:276:VAL:HG23	1:F:293:ILE:HG23	1.89	0.53
1:G:276:VAL:HG23	1:G:293:ILE:HG23	1.89	0.53
1:F:177:HIS:O	1:F:218:GLN:HA	2.09	0.53
1:K:579:MSE:HB2	1:K:581:VAL:HG12	1.91	0.53
1:A:384:LEU:N	1:A:384:LEU:HD22	2.23	0.53
1:P:58:ASP:HA	1:P:327:GLN:NE2	2.24	0.53
1:N:584:PRO:HG2	1:N:593:LEU:HD12	1.91	0.53
3:Q:718:HOH:O	1:R:438:LEU:HD22	2.08	0.53
1:B:177:HIS:O	1:B:218:GLN:HA	2.09	0.53
1:V:584:PRO:HG2	1:V:593:LEU:HD12	1.90	0.53
1:O:427:GLY:C	1:O:429:GLN:H	2.12	0.53
1:R:395:PRO:HD2	1:X:398:PRO:HB3	1.90	0.53
1:A:80:TYR:CE1	1:A:448:VAL:HG22	2.43	0.53
1:C:78:VAL:HG11	1:C:444:LEU:HG	1.90	0.53
1:E:15:PHE:HZ	1:E:283:CYS:SG	2.31	0.53
1:F:15:PHE:HZ	1:F:283:CYS:SG	2.31	0.53
1:F:78:VAL:CG1	1:F:79:LEU:N	2.72	0.53
1:L:44:TRP:C	1:L:45:LEU:HD22	2.28	0.53
1:O:66:LYS:NZ	1:O:420:VAL:HG11	2.23	0.53
1:P:78:VAL:HG12	1:P:79:LEU:H	1.69	0.53
1:Q:444:LEU:C	1:Q:446:THR:H	2.12	0.53
1:S:44:TRP:CE2	1:S:54:ARG:HB3	2.44	0.53
1:T:444:LEU:O	1:T:448:VAL:HG23	2.09	0.53
1:T:78:VAL:HG12	1:T:79:LEU:H	1.72	0.53
1:W:123:VAL:HG22	1:W:316:TYR:CE2	2.43	0.53
1:L:266:ILE:HG23	1:L:267:ALA:N	2.23	0.53
1:U:380:ASN:O	1:U:381:SER:HB3	2.08	0.53
1:H:177:HIS:O	1:H:218:GLN:HA	2.09	0.53
1:N:593:LEU:O	1:N:597:GLN:HG2	2.08	0.53
1:G:229:LYS:HA	1:G:272:LYS:HA	1.90	0.53
1:T:344:THR:HG23	1:T:344:THR:O	2.06	0.53
1:A:35:PHE:C	1:A:37:ARG:N	2.62	0.53
1:A:44:TRP:C	1:A:45:LEU:HD22	2.28	0.53
1:A:78:VAL:CG1	1:A:79:LEU:N	2.72	0.53
1:B:444:LEU:C	1:B:446:THR:N	2.61	0.53
1:D:138:THR:H	1:D:143:VAL:HG22	1.73	0.53
1:E:158:TRP:HB3	1:E:173:CYS:CA	2.36	0.53
1:H:35:PHE:C	1:H:37:ARG:N	2.62	0.53
1:H:78:VAL:CG1	1:H:79:LEU:N	2.72	0.53
1:J:444:LEU:C	1:J:446:THR:N	2.61	0.53
1:O:47:GLN:HG2	1:O:48:TYR:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:LEU:HD22	2:Y:142:PRO:HG2	1.89	0.53
1:Q:44:TRP:CE2	1:Q:54:ARG:HB3	2.44	0.53
1:R:101:ASP:HB2	1:R:144:ILE:O	2.08	0.53
1:U:101:ASP:HB2	1:U:144:ILE:O	2.09	0.53
1:U:81:ARG:HB2	1:U:517:TYR:CZ	2.44	0.53
1:W:144:ILE:HD12	1:W:145:ARG:N	2.24	0.53
1:X:47:GLN:HG2	1:X:48:TYR:N	2.24	0.53
1:J:27:ARG:HB2	1:J:313:LYS:HE3	1.89	0.53
1:J:236:GLN:HE21	1:J:265:LYS:NZ	2.06	0.53
1:I:511:ARG:HA	1:I:513:ARG:HD2	1.91	0.53
1:C:511:ARG:HA	1:C:513:ARG:HD2	1.91	0.53
1:F:236:GLN:CB	1:F:265:LYS:HG2	2.37	0.53
1:M:236:GLN:HA	1:M:244:VAL:H	1.74	0.53
1:S:236:GLN:HA	1:S:244:VAL:H	1.74	0.53
1:B:276:VAL:HG23	1:B:293:ILE:HG23	1.89	0.53
1:M:94:LEU:HA	1:M:97:MSE:CE	2.38	0.53
1:I:579:MSE:HB2	1:I:581:VAL:HG12	1.90	0.53
1:F:579:MSE:HB2	1:F:581:VAL:HG12	1.90	0.53
1:T:380:ASN:O	1:T:381:SER:HB3	2.09	0.53
1:I:384:LEU:N	1:I:384:LEU:HD22	2.23	0.53
1:R:380:ASN:O	1:R:381:SER:HB3	2.09	0.53
1:J:177:HIS:O	1:J:218:GLN:HA	2.09	0.53
1:X:584:PRO:HG2	1:X:593:LEU:HD12	1.90	0.53
1:V:593:LEU:O	1:V:597:GLN:HG2	2.08	0.53
1:J:229:LYS:HA	1:J:272:LYS:HA	1.90	0.53
1:B:80:TYR:CE1	1:B:448:VAL:HG22	2.43	0.53
1:E:32:ASP:HA	1:E:35:PHE:CE1	2.44	0.53
1:E:78:VAL:HG11	1:E:444:LEU:HG	1.91	0.53
1:G:78:VAL:CG1	1:G:79:LEU:N	2.72	0.53
1:I:123:VAL:HG22	1:I:316:TYR:CE2	2.43	0.53
1:J:80:TYR:CE1	1:J:448:VAL:HG22	2.43	0.53
1:N:66:LYS:NZ	1:N:420:VAL:HG11	2.23	0.53
1:Q:35:PHE:C	1:Q:37:ARG:H	2.12	0.53
1:Q:165:MSE:HE1	1:Q:435:VAL:HB	1.91	0.53
1:R:78:VAL:HG12	1:R:79:LEU:H	1.72	0.53
1:S:123:VAL:HG22	1:S:316:TYR:CE2	2.44	0.53
1:T:80:TYR:CE1	1:T:448:VAL:HG22	2.44	0.53
1:V:81:ARG:HB2	1:V:517:TYR:CZ	2.44	0.53
1:W:35:PHE:C	1:W:37:ARG:H	2.10	0.53
1:W:44:TRP:CE2	1:W:54:ARG:HB3	2.44	0.53
1:W:47:GLN:HG2	1:W:48:TYR:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:511:ARG:HA	1:J:513:ARG:HD2	1.91	0.53
1:K:511:ARG:HA	1:K:513:ARG:HD2	1.91	0.53
1:C:234:ILE:HG13	1:C:267:ALA:HB3	1.91	0.53
1:L:236:GLN:HE21	1:L:265:LYS:NZ	2.06	0.53
1:U:236:GLN:HA	1:U:244:VAL:H	1.73	0.53
1:V:598:GLN:HB2	1:V:601:GLN:HB2	1.91	0.53
1:X:380:ASN:O	1:X:381:SER:HB3	2.07	0.53
1:T:58:ASP:HA	1:T:327:GLN:NE2	2.24	0.53
1:I:177:HIS:O	1:I:218:GLN:HA	2.09	0.53
1:A:311:GLU:O	1:A:312:ASP:HB2	2.07	0.53
1:U:348:LYS:HB2	1:X:372:TYR:CE2	2.43	0.53
1:C:177:HIS:O	1:C:218:GLN:HA	2.09	0.53
1:U:389:LEU:HD12	1:U:389:LEU:H	1.73	0.53
1:B:32:ASP:HA	1:B:35:PHE:CE1	2.44	0.53
1:B:44:TRP:C	1:B:45:LEU:HD22	2.28	0.53
1:F:32:ASP:HA	1:F:35:PHE:CE1	2.44	0.53
1:H:32:ASP:HA	1:H:35:PHE:CE1	2.44	0.53
1:L:47:GLN:NE2	1:L:47:GLN:O	2.41	0.53
1:M:35:PHE:CE1	1:M:321:ARG:NE	2.75	0.53
1:M:344:THR:O	1:M:344:THR:HG23	2.07	0.53
1:P:456:ALA:HB1	1:P:509:ASP:OD1	2.09	0.53
1:Q:41:TRP:HE1	1:R:27:ARG:NH2	2.07	0.53
1:R:35:PHE:C	1:R:37:ARG:H	2.11	0.53
1:R:456:ALA:HB1	1:R:509:ASP:OD1	2.08	0.53
1:V:35:PHE:HE1	1:V:321:ARG:NH1	2.06	0.53
1:X:44:TRP:C	1:X:45:LEU:HD22	2.29	0.53
2:Y:71:ASP:O	2:Y:72:ASP:HB3	2.08	0.53
1:A:234:ILE:HG13	1:A:267:ALA:HB3	1.90	0.53
1:A:511:ARG:HA	1:A:513:ARG:HD2	1.91	0.53
1:F:511:ARG:HA	1:F:513:ARG:HD2	1.91	0.53
1:U:352:TRP:CG	1:X:376:ARG:HB2	2.44	0.53
1:U:66:LYS:NZ	1:U:420:VAL:HG11	2.23	0.53
1:A:276:VAL:HG23	1:A:293:ILE:HG23	1.89	0.53
1:D:177:HIS:O	1:D:218:GLN:HA	2.09	0.53
1:A:177:HIS:O	1:A:218:GLN:HA	2.09	0.53
1:E:177:HIS:O	1:E:218:GLN:HA	2.09	0.53
1:H:384:LEU:HD22	1:H:384:LEU:N	2.23	0.53
1:R:593:LEU:O	1:R:597:GLN:HG2	2.08	0.53
1:F:395:PRO:HD2	1:G:398:PRO:HB3	1.91	0.53
1:V:351:PHE:CD2	1:V:356:ILE:HD12	2.44	0.53
2:Z:58:GLN:H	2:Z:62:GLY:HA3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:229:LYS:HA	1:H:272:LYS:HA	1.90	0.53
1:U:593:LEU:O	1:U:597:GLN:HG2	2.08	0.53
1:I:229:LYS:HA	1:I:272:LYS:HA	1.90	0.53
1:A:138:THR:H	1:A:143:VAL:HG22	1.73	0.53
1:A:47:GLN:NE2	1:A:47:GLN:O	2.41	0.53
1:C:560:LEU:O	1:C:561:ASP:O	2.26	0.53
1:D:560:LEU:O	1:D:561:ASP:O	2.26	0.53
1:H:80:TYR:CE1	1:H:448:VAL:HG22	2.43	0.53
1:L:35:PHE:C	1:L:37:ARG:N	2.61	0.53
1:M:444:LEU:C	1:M:446:THR:H	2.13	0.53
1:N:35:PHE:HE1	1:N:321:ARG:NH1	2.05	0.53
1:N:434:THR:HA	1:N:437:GLN:HG2	1.90	0.53
1:N:434:THR:O	1:N:437:GLN:HG2	2.09	0.53
1:Q:420:VAL:HG22	1:Q:428:GLY:HA3	1.91	0.53
1:Q:81:ARG:HB2	1:Q:517:TYR:CZ	2.44	0.53
1:V:158:TRP:HD1	1:V:158:TRP:N	2.07	0.53
1:N:302:PRO:O	1:N:439:ASN:ND2	2.41	0.53
1:H:511:ARG:HA	1:H:513:ARG:HD2	1.91	0.53
1:E:511:ARG:HA	1:E:513:ARG:HD2	1.91	0.53
1:Q:427:GLY:C	1:Q:429:GLN:H	2.12	0.53
1:P:55:GLY:HA3	1:P:57:PHE:CE1	2.44	0.53
1:E:229:LYS:HA	1:E:272:LYS:HA	1.90	0.53
1:L:229:LYS:HA	1:L:272:LYS:HA	1.90	0.53
1:M:351:PHE:CD2	1:M:356:ILE:HD12	2.43	0.53
1:D:34:PHE:HZ	1:D:328:ARG:HH22	0.80	0.53
1:D:80:TYR:CE1	1:D:448:VAL:HG22	2.43	0.53
1:E:35:PHE:HE2	1:E:324:LYS:NZ	2.07	0.53
1:H:15:PHE:HZ	1:H:283:CYS:SG	2.31	0.53
1:S:101:ASP:HB2	1:S:144:ILE:O	2.09	0.53
1:T:35:PHE:CE1	1:T:321:ARG:NE	2.76	0.53
1:V:325:ASP:O	1:V:329:LEU:HD23	2.09	0.53
1:V:35:PHE:C	1:V:37:ARG:H	2.11	0.53
1:W:80:TYR:CE1	1:W:448:VAL:HG22	2.44	0.53
1:X:325:ASP:O	1:X:329:LEU:HD23	2.09	0.53
1:X:80:TYR:CE1	1:X:448:VAL:HG22	2.44	0.53
1:P:71:MSE:HE2	1:P:119:ILE:HD11	1.90	0.53
1:W:302:PRO:O	1:W:439:ASN:ND2	2.42	0.53
1:Q:71:MSE:HE2	1:Q:119:ILE:HD11	1.91	0.53
1:D:511:ARG:HA	1:D:513:ARG:HD2	1.91	0.53
1:B:560:LEU:O	1:B:561:ASP:O	2.26	0.53
1:I:266:ILE:HG23	1:I:267:ALA:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:511:ARG:HA	1:L:513:ARG:HD2	1.91	0.53
1:V:236:GLN:HA	1:V:244:VAL:H	1.73	0.53
1:B:334:MSE:HE3	1:C:404:MSE:CE	2.39	0.53
1:M:380:ASN:O	1:M:381:SER:HB3	2.09	0.53
1:X:389:LEU:H	1:X:389:LEU:HD12	1.74	0.53
1:B:78:VAL:HG11	1:B:444:LEU:HG	1.90	0.52
1:F:35:PHE:C	1:F:37:ARG:N	2.62	0.52
1:F:47:GLN:NE2	1:F:47:GLN:O	2.41	0.52
1:G:32:ASP:HA	1:G:35:PHE:CE1	2.44	0.52
1:I:138:THR:H	1:I:143:VAL:HG22	1.73	0.52
1:I:15:PHE:CZ	1:I:283:CYS:HA	2.45	0.52
1:I:72:ARG:HD2	1:J:434:THR:HG21	1.91	0.52
1:K:32:ASP:HA	1:K:35:PHE:CE1	2.44	0.52
1:O:78:VAL:HG11	1:O:444:LEU:HG	1.90	0.52
1:N:444:LEU:C	1:N:446:THR:H	2.13	0.52
1:R:164:LEU:HD22	1:R:169:ASP:CG	2.29	0.52
1:R:46:SER:N	1:R:48:TYR:HE2	1.98	0.52
1:V:34:PHE:HZ	1:V:328:ARG:HH22	1.40	0.52
1:X:434:THR:HA	1:X:437:GLN:HG2	1.91	0.52
1:R:302:PRO:O	1:R:439:ASN:ND2	2.42	0.52
1:J:234:ILE:HG13	1:J:267:ALA:HB3	1.90	0.52
1:B:511:ARG:HA	1:B:513:ARG:HD2	1.91	0.52
1:D:273:ARG:NH2	1:D:453:LEU:HD21	2.21	0.52
1:I:563:LYS:HD3	1:J:557:PHE:CE2	2.44	0.52
1:R:344:THR:O	1:R:344:THR:HG23	2.08	0.52
1:N:154:SER:O	1:N:204:PRO:HB3	2.09	0.52
1:B:78:VAL:CG1	1:B:79:LEU:N	2.72	0.52
1:F:15:PHE:CZ	1:F:283:CYS:HA	2.45	0.52
1:J:158:TRP:HB3	1:J:173:CYS:CA	2.36	0.52
1:K:78:VAL:CG1	1:K:79:LEU:N	2.72	0.52
1:M:123:VAL:HG22	1:M:316:TYR:CE2	2.45	0.52
1:M:66:LYS:NZ	1:M:420:VAL:HG11	2.24	0.52
1:O:420:VAL:HG22	1:O:428:GLY:HA3	1.90	0.52
1:L:138:THR:H	1:L:143:VAL:HG22	1.73	0.52
1:R:93:VAL:CG1	1:R:458:ARG:HG3	2.38	0.52
1:R:81:ARG:HB2	1:R:517:TYR:CZ	2.45	0.52
1:S:434:THR:HA	1:S:437:GLN:HG2	1.91	0.52
1:T:81:ARG:HB2	1:T:517:TYR:CZ	2.44	0.52
1:V:47:GLN:HG2	1:V:48:TYR:N	2.23	0.52
1:T:546:THR:CG2	1:T:547:PRO:HD3	2.28	0.52
1:G:265:LYS:O	1:G:266:ILE:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:15:PHE:CZ	1:C:283:CYS:HA	2.45	0.52
1:L:236:GLN:CB	1:L:265:LYS:HG2	2.37	0.52
1:L:265:LYS:O	1:L:266:ILE:HG12	2.10	0.52
1:T:573:ASN:O	1:T:577:ILE:HG13	2.09	0.52
1:L:209:PHE:HA	1:L:211:TRP:NE1	2.24	0.52
1:S:380:ASN:O	1:S:381:SER:HB3	2.10	0.52
1:G:579:MSE:HB2	1:G:581:VAL:HG12	1.91	0.52
1:L:384:LEU:HD22	1:L:384:LEU:N	2.23	0.52
1:K:384:LEU:HD22	1:K:384:LEU:N	2.23	0.52
1:D:556:TYR:OH	1:F:542:THR:HG21	2.09	0.52
1:R:584:PRO:HG2	1:R:593:LEU:HD12	1.90	0.52
1:K:229:LYS:HA	1:K:272:LYS:HA	1.90	0.52
1:R:427:GLY:C	1:R:429:GLN:H	2.12	0.52
1:C:229:LYS:HA	1:C:272:LYS:HA	1.90	0.52
1:X:427:GLY:C	1:X:429:GLN:H	2.12	0.52
1:D:229:LYS:HA	1:D:272:LYS:HA	1.90	0.52
1:A:78:VAL:HG11	1:A:444:LEU:HG	1.90	0.52
1:E:560:LEU:O	1:E:561:ASP:O	2.26	0.52
1:G:47:GLN:NE2	1:G:47:GLN:O	2.41	0.52
1:H:429:GLN:HG2	1:H:429:GLN:O	2.10	0.52
1:I:457:MSE:O	1:I:458:ARG:HD2	2.10	0.52
1:L:32:ASP:HA	1:L:35:PHE:CE1	2.44	0.52
1:S:165:MSE:HE1	1:S:435:VAL:HB	1.91	0.52
1:S:95:MSE:HB3	1:S:527:MSE:HE1	1.90	0.52
1:T:144:ILE:HD12	1:T:145:ARG:N	2.25	0.52
1:T:35:PHE:HE1	1:T:321:ARG:NH1	2.06	0.52
1:D:376:ARG:HB2	1:F:352:TRP:CG	2.44	0.52
1:L:579:MSE:HB2	1:L:581:VAL:HG12	1.90	0.52
1:A:579:MSE:HB2	1:A:581:VAL:HG12	1.91	0.52
1:N:380:ASN:O	1:N:381:SER:HB3	2.09	0.52
1:Q:380:ASN:O	1:Q:381:SER:HB3	2.10	0.52
1:U:296:GLU:HG2	1:U:449:PHE:HB3	1.90	0.52
1:U:398:PRO:HB3	1:X:395:PRO:HD2	1.90	0.52
1:B:229:LYS:HA	1:B:272:LYS:HA	1.90	0.52
1:D:379:GLU:O	1:D:380:ASN:CB	2.58	0.52
1:J:334:MSE:HE3	1:K:404:MSE:CE	2.40	0.52
1:L:78:VAL:CG1	1:L:79:LEU:N	2.72	0.52
1:R:434:THR:HA	1:R:437:GLN:HG2	1.90	0.52
1:S:93:VAL:CG1	1:S:458:ARG:HG3	2.37	0.52
1:T:434:THR:HA	1:T:437:GLN:HG2	1.91	0.52
1:T:93:VAL:CG1	1:T:458:ARG:HG3	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:234:ILE:HG13	1:D:267:ALA:HB3	1.90	0.52
1:F:265:LYS:O	1:F:266:ILE:HG12	2.10	0.52
1:D:209:PHE:HA	1:D:211:TRP:NE1	2.24	0.52
1:I:310:VAL:C	1:I:312:ASP:H	2.13	0.52
2:Y:57:TYR:CD2	2:Y:57:TYR:O	2.62	0.52
1:E:444:LEU:C	1:E:446:THR:N	2.61	0.52
1:F:44:TRP:C	1:F:45:LEU:HD22	2.28	0.52
1:F:334:MSE:SE	1:G:404:MSE:HE1	2.60	0.52
1:K:444:LEU:C	1:K:446:THR:N	2.61	0.52
1:L:48:TYR:HD2	1:L:48:TYR:O	4.89	0.52
1:P:93:VAL:CG1	1:P:458:ARG:HG3	2.38	0.52
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG11	1.74	0.52
1:S:144:ILE:HD12	1:S:145:ARG:N	2.24	0.52
1:S:81:ARG:HB2	1:S:517:TYR:CZ	2.44	0.52
1:T:35:PHE:C	1:T:37:ARG:H	2.11	0.52
1:U:344:THR:O	1:U:344:THR:HG23	2.10	0.52
1:U:456:ALA:HB1	1:U:509:ASP:OD1	2.09	0.52
1:U:302:PRO:O	1:U:439:ASN:ND2	2.42	0.52
1:H:273:ARG:NH2	1:H:453:LEU:HD21	2.21	0.52
1:V:352:TRP:CG	1:W:376:ARG:HB2	2.45	0.52
1:R:236:GLN:HA	1:R:244:VAL:H	1.74	0.52
1:W:93:VAL:CG1	1:W:458:ARG:HG3	2.37	0.52
1:J:457:MSE:O	1:J:458:ARG:HD2	2.10	0.52
1:C:457:MSE:O	1:C:458:ARG:HD2	2.10	0.52
1:G:209:PHE:HA	1:G:211:TRP:NE1	2.24	0.52
1:K:209:PHE:HA	1:K:211:TRP:NE1	2.24	0.52
1:F:379:GLU:O	1:F:380:ASN:CB	2.58	0.52
1:M:40:GLN:HG2	1:O:310:VAL:HG22	1.90	0.52
1:W:598:GLN:HB2	1:W:601:GLN:HB2	1.92	0.52
1:G:310:VAL:C	1:G:312:ASP:H	2.13	0.52
1:J:310:VAL:C	1:J:312:ASP:H	2.13	0.52
1:V:296:GLU:HG2	1:V:449:PHE:HB3	1.91	0.52
1:F:229:LYS:HA	1:F:272:LYS:HA	1.90	0.52
1:M:556:TYR:OH	1:O:542:THR:HG21	2.10	0.52
1:A:15:PHE:CZ	1:A:283:CYS:HA	2.45	0.52
1:C:32:ASP:HA	1:C:35:PHE:CE1	2.44	0.52
1:D:32:ASP:HA	1:D:35:PHE:CE1	2.44	0.52
1:H:15:PHE:CZ	1:H:283:CYS:HA	2.45	0.52
1:I:78:VAL:CG1	1:I:79:LEU:N	2.72	0.52
1:J:78:VAL:CG1	1:J:79:LEU:N	2.72	0.52
1:M:165:MSE:HE1	1:M:435:VAL:HB	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:44:TRP:C	1:N:45:LEU:HD22	2.30	0.52
1:P:165:MSE:HE1	1:P:435:VAL:HB	1.91	0.52
1:P:44:TRP:CE2	1:P:54:ARG:HB3	2.44	0.52
1:T:434:THR:O	1:T:437:GLN:HG2	2.10	0.52
1:U:434:THR:HA	1:U:437:GLN:HG2	1.91	0.52
1:U:44:TRP:CE2	1:U:54:ARG:HB3	2.45	0.52
1:V:24:GLU:C	1:V:26:ARG:N	2.57	0.52
1:V:329:LEU:HD21	1:W:53:TYR:OH	2.10	0.52
1:V:444:LEU:O	1:V:448:VAL:HG23	2.10	0.52
1:W:165:MSE:HG3	1:W:307:TRP:CD2	2.44	0.52
1:W:165:MSE:HE1	1:W:435:VAL:HB	1.91	0.52
1:G:234:ILE:HG13	1:G:267:ALA:HB3	1.91	0.52
1:B:266:ILE:HG23	1:B:267:ALA:N	2.23	0.52
1:H:234:ILE:HG13	1:H:267:ALA:HB3	1.90	0.52
1:C:266:ILE:HG23	1:C:267:ALA:N	2.23	0.52
1:E:265:LYS:O	1:E:266:ILE:HG12	2.10	0.52
1:I:209:PHE:HA	1:I:211:TRP:NE1	2.24	0.52
1:J:209:PHE:HA	1:J:211:TRP:NE1	2.24	0.52
1:A:209:PHE:HA	1:A:211:TRP:NE1	2.24	0.52
1:A:379:GLU:O	1:A:380:ASN:CB	2.58	0.52
1:E:113:ILE:HD13	1:E:150:HIS:CE1	2.45	0.52
1:C:113:ILE:HD13	1:C:150:HIS:CE1	2.45	0.52
1:D:221:GLU:OE2	1:D:278:LYS:HD2	2.10	0.52
1:J:384:LEU:N	1:J:384:LEU:HD22	2.23	0.52
1:P:380:ASN:O	1:P:381:SER:HB3	2.09	0.52
1:W:380:ASN:O	1:W:381:SER:HB3	2.10	0.52
1:I:221:GLU:OE2	1:I:278:LYS:HD2	2.10	0.52
1:B:363:TYR:HE1	1:C:350:PHE:HE1	1.56	0.52
1:K:177:HIS:O	1:K:218:GLN:HA	2.09	0.52
1:A:350:PHE:HE1	1:L:363:TYR:HE1	1.57	0.52
1:K:113:ILE:HD13	1:K:150:HIS:CE1	2.45	0.52
1:A:32:ASP:HA	1:A:35:PHE:CE1	2.44	0.52
1:F:444:LEU:C	1:F:446:THR:N	2.61	0.52
1:I:32:ASP:HA	1:I:35:PHE:CE1	2.44	0.52
1:J:113:ILE:HD13	1:J:150:HIS:CE1	2.45	0.52
1:L:113:ILE:HD13	1:L:150:HIS:CE1	2.45	0.52
1:O:53:TYR:OH	1:P:329:LEU:HD21	2.07	0.52
1:N:165:MSE:HE1	1:N:435:VAL:HB	1.92	0.52
1:Q:144:ILE:HD12	1:Q:145:ARG:N	2.25	0.52
1:R:80:TYR:CE1	1:R:448:VAL:HG22	2.43	0.52
1:S:434:THR:O	1:S:437:GLN:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:35:PHE:CE1	1:W:321:ARG:NE	2.78	0.52
1:L:139:SER:CB	1:L:455:THR:CG2	2.80	0.52
1:U:273:ARG:NH1	1:U:275:ARG:HE	2.07	0.52
1:D:265:LYS:O	1:D:266:ILE:HG12	2.10	0.52
1:N:352:TRP:CD1	1:V:376:ARG:HB2	2.45	0.52
1:T:236:GLN:HA	1:T:244:VAL:H	1.74	0.52
1:L:457:MSE:O	1:L:458:ARG:HD2	2.10	0.52
1:G:457:MSE:O	1:G:458:ARG:HD2	2.10	0.52
1:C:209:PHE:HA	1:C:211:TRP:NE1	2.24	0.52
1:A:438:LEU:HD22	3:L:719:HOH:O	2.09	0.52
1:S:389:LEU:HD12	1:S:389:LEU:H	1.75	0.52
1:I:363:TYR:HE1	1:J:350:PHE:HE1	1.56	0.52
1:T:427:GLY:C	1:T:429:GLN:H	2.13	0.52
1:Q:55:GLY:HA3	1:Q:57:PHE:CE1	2.45	0.52
1:J:32:ASP:HA	1:J:35:PHE:CE1	2.44	0.52
1:K:457:MSE:O	1:K:458:ARG:HD2	2.10	0.52
1:M:48:TYR:O	1:M:48:TYR:HD2	5.13	0.52
1:P:344:THR:HG23	1:P:344:THR:O	2.08	0.52
1:R:35:PHE:HE1	1:R:321:ARG:NH1	2.07	0.52
1:D:139:SER:CB	1:D:455:THR:CG2	2.80	0.52
1:O:546:THR:CG2	1:O:547:PRO:HD3	2.29	0.52
1:T:273:ARG:NH1	1:T:275:ARG:HE	2.08	0.52
1:O:209:PHE:HZ	1:O:214:GLN:HG2	1.70	0.52
1:E:457:MSE:O	1:E:458:ARG:HD2	2.10	0.52
1:B:379:GLU:O	1:B:380:ASN:CB	2.58	0.52
1:J:379:GLU:O	1:J:380:ASN:CB	2.58	0.52
1:B:113:ILE:HD13	1:B:150:HIS:CE1	2.45	0.52
1:B:579:MSE:HB2	1:B:581:VAL:HG12	1.91	0.52
1:E:579:MSE:HB2	1:E:581:VAL:HG12	1.91	0.52
1:P:95:MSE:HB3	1:P:527:MSE:HE1	1.90	0.52
1:T:598:GLN:HB2	1:T:601:GLN:HB2	1.91	0.52
1:M:598:GLN:HB2	1:M:601:GLN:HB2	1.92	0.52
1:N:598:GLN:HB2	1:N:601:GLN:HB2	1.92	0.52
1:H:556:TYR:OH	1:I:542:THR:HG21	2.09	0.52
1:Q:58:ASP:HA	1:Q:327:GLN:NE2	2.24	0.52
1:F:310:VAL:C	1:F:312:ASP:H	2.13	0.52
1:B:310:VAL:C	1:B:312:ASP:H	2.13	0.52
1:D:35:PHE:HE2	1:D:324:LYS:NZ	2.07	0.52
1:E:15:PHE:CZ	1:E:283:CYS:HA	2.45	0.52
1:J:15:PHE:CZ	1:J:283:CYS:HA	2.45	0.52
1:L:560:LEU:O	1:L:561:ASP:O	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:93:VAL:CG1	1:O:458:ARG:HG3	2.38	0.52
1:M:325:ASP:O	1:M:329:LEU:HD23	2.10	0.52
1:R:325:ASP:O	1:R:329:LEU:HD23	2.09	0.52
1:E:273:ARG:NH2	1:E:453:LEU:HD21	2.21	0.52
1:W:236:GLN:HA	1:W:244:VAL:H	1.74	0.52
1:A:573:ASN:O	1:A:577:ILE:HG13	2.10	0.52
1:A:457:MSE:O	1:A:458:ARG:HD2	2.10	0.52
1:P:420:VAL:HG22	1:P:428:GLY:HA3	1.91	0.52
1:G:113:ILE:HD13	1:G:150:HIS:CE1	2.45	0.52
1:I:113:ILE:HD13	1:I:150:HIS:CE1	2.45	0.52
1:B:209:PHE:HA	1:B:211:TRP:NE1	2.24	0.52
1:F:113:ILE:HD13	1:F:150:HIS:CE1	2.45	0.52
1:A:221:GLU:OE2	1:A:278:LYS:HD2	2.10	0.52
1:H:579:MSE:HB2	1:H:581:VAL:HG12	1.90	0.52
1:D:579:MSE:HB2	1:D:581:VAL:HG12	1.90	0.52
1:C:310:VAL:C	1:C:312:ASP:H	2.13	0.52
1:V:427:GLY:C	1:V:429:GLN:H	2.13	0.52
1:I:395:PRO:HD2	1:J:398:PRO:HB3	1.92	0.52
1:Q:389:LEU:H	1:Q:389:LEU:HD12	1.74	0.52
1:A:561:ASP:OD2	1:B:92:ASP:HB3	2.10	0.52
1:B:15:PHE:CZ	1:B:283:CYS:HA	2.45	0.52
1:B:35:PHE:CE2	1:B:321:ARG:HG3	2.45	0.52
1:D:78:VAL:CG1	1:D:79:LEU:N	2.72	0.52
1:E:78:VAL:CG1	1:E:79:LEU:N	2.72	0.52
1:F:35:PHE:CE2	1:F:321:ARG:HG3	2.45	0.52
1:G:35:PHE:HE2	1:G:324:LYS:NZ	2.07	0.52
1:G:334:MSE:HE3	1:H:404:MSE:HE3	1.92	0.52
1:L:15:PHE:CZ	1:L:283:CYS:HA	2.45	0.52
2:Z:53:MET:O	2:Z:69:PHE:CE1	2.63	0.52
1:U:325:ASP:O	1:U:329:LEU:HD23	2.10	0.52
1:U:34:PHE:CE2	1:U:45:LEU:HG	2.45	0.52
1:W:444:LEU:O	1:W:448:VAL:HG23	2.10	0.52
2:Y:77:ALA:O	2:Y:78:GLU:HB3	2.10	0.52
1:E:14:ARG:NE	1:E:14:ARG:CA	2.67	0.52
1:J:14:ARG:NE	1:J:14:ARG:CA	2.67	0.52
1:J:248:LYS:HZ1	1:J:513:ARG:HH12	1.58	0.52
1:I:265:LYS:O	1:I:266:ILE:HG12	2.10	0.52
1:K:573:ASN:O	1:K:577:ILE:HG13	2.11	0.52
1:C:573:ASN:O	1:C:577:ILE:HG13	2.10	0.52
1:X:535:ILE:HD13	1:X:554:LEU:HG	1.92	0.52
1:H:457:MSE:O	1:H:458:ARG:HD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:719:HOH:O	1:L:438:LEU:HD22	2.10	0.52
1:C:379:GLU:O	1:C:380:ASN:CB	2.58	0.52
3:P:719:HOH:O	1:Q:430:VAL:HG11	2.10	0.52
1:D:310:VAL:C	1:D:312:ASP:H	2.13	0.52
1:K:310:VAL:C	1:K:312:ASP:H	2.13	0.52
1:C:221:GLU:OE2	1:C:278:LYS:HD2	2.10	0.52
2:Z:57:TYR:O	2:Z:57:TYR:CD2	2.62	0.52
2:Z:57:TYR:O	2:Z:57:TYR:HD2	1.92	0.52
1:R:387:GLN:HB3	1:X:390:ALA:CB	2.40	0.52
1:A:229:LYS:HA	1:A:272:LYS:HA	1.90	0.52
1:A:35:PHE:CE2	1:A:321:ARG:HG3	2.45	0.51
1:B:302:PRO:O	1:B:439:ASN:CG	2.49	0.51
1:B:443:ASP:C	1:B:444:LEU:HD13	2.31	0.51
1:B:457:MSE:O	1:B:458:ARG:HD2	2.10	0.51
1:C:35:PHE:CE2	1:C:321:ARG:HG3	2.45	0.51
1:C:429:GLN:O	1:C:429:GLN:HG2	2.10	0.51
1:F:160:SER:O	1:F:161:ASN:ND2	2.43	0.51
1:G:160:SER:O	1:G:161:ASN:ND2	2.44	0.51
1:J:35:PHE:CE2	1:J:321:ARG:HG3	2.45	0.51
1:J:37:ARG:HH21	1:J:37:ARG:CB	2.16	0.51
1:L:35:PHE:CE2	1:L:321:ARG:HG3	2.45	0.51
1:O:164:LEU:HD22	1:O:169:ASP:CG	2.31	0.51
1:O:434:THR:O	1:O:437:GLN:HG2	2.10	0.51
1:O:78:VAL:HG12	1:O:79:LEU:H	1.74	0.51
2:Z:77:ALA:O	2:Z:78:GLU:HB3	2.10	0.51
1:P:78:VAL:HG11	1:P:444:LEU:HG	1.91	0.51
1:R:434:THR:O	1:R:437:GLN:HG2	2.10	0.51
1:V:164:LEU:HD22	1:V:169:ASP:CG	2.30	0.51
1:X:35:PHE:C	1:X:37:ARG:H	2.12	0.51
1:X:444:LEU:C	1:X:446:THR:H	2.13	0.51
1:C:14:ARG:NE	1:C:14:ARG:CA	2.67	0.51
1:O:334:MSE:HE1	1:P:407:ALA:HB1	1.91	0.51
1:G:511:ARG:HA	1:G:513:ARG:HD2	1.91	0.51
1:C:265:LYS:O	1:C:266:ILE:HG12	2.10	0.51
1:X:236:GLN:HA	1:X:244:VAL:H	1.74	0.51
1:P:573:ASN:O	1:P:577:ILE:HG13	2.10	0.51
1:F:209:PHE:HA	1:F:211:TRP:NE1	2.24	0.51
1:D:113:ILE:HD13	1:D:150:HIS:CE1	2.45	0.51
3:O:719:HOH:O	1:P:430:VAL:HG11	2.10	0.51
1:V:380:ASN:O	1:V:381:SER:HB3	2.10	0.51
1:P:427:GLY:C	1:P:429:GLN:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:456:ALA:HB1	1:O:509:ASP:OD1	2.09	0.51
1:D:15:PHE:CZ	1:D:283:CYS:HA	2.45	0.51
1:D:160:SER:O	1:D:161:ASN:ND2	2.44	0.51
1:D:334:MSE:HE3	1:F:404:MSE:CE	2.40	0.51
1:E:379:GLU:O	1:E:380:ASN:CB	2.58	0.51
1:E:443:ASP:C	1:E:444:LEU:HD13	2.31	0.51
1:H:182:ASN:ND2	1:I:171:ARG:HH21	2.08	0.51
1:I:443:ASP:C	1:I:444:LEU:HD13	2.31	0.51
1:K:443:ASP:C	1:K:444:LEU:HD13	2.31	0.51
1:M:37:ARG:CB	1:M:37:ARG:HH21	2.23	0.51
1:N:34:PHE:CE2	1:N:45:LEU:HG	2.46	0.51
1:N:80:TYR:CE1	1:N:448:VAL:HG22	2.45	0.51
1:U:44:TRP:C	1:U:45:LEU:HD22	2.30	0.51
1:V:123:VAL:HG22	1:V:316:TYR:CE2	2.45	0.51
1:X:123:VAL:HG22	1:X:316:TYR:CE2	2.45	0.51
1:K:265:LYS:O	1:K:266:ILE:HG12	2.10	0.51
1:C:563:LYS:HD3	1:E:557:PHE:CE2	2.45	0.51
1:D:573:ASN:O	1:D:577:ILE:HG13	2.10	0.51
1:W:389:LEU:HD12	1:W:389:LEU:H	1.75	0.51
1:M:95:MSE:HE1	1:M:99:ARG:CZ	2.41	0.51
1:Q:598:GLN:HB2	1:Q:601:GLN:HB2	1.92	0.51
1:F:556:TYR:OH	1:G:542:THR:HG21	2.09	0.51
1:B:221:GLU:OE2	1:B:278:LYS:HD2	2.10	0.51
1:R:389:LEU:HD12	1:R:389:LEU:H	1.74	0.51
1:B:372:TYR:CE2	1:C:348:LYS:HB2	2.45	0.51
1:U:154:SER:O	1:U:204:PRO:HB3	2.10	0.51
1:N:427:GLY:C	1:N:429:GLN:H	2.13	0.51
1:A:302:PRO:O	1:A:439:ASN:CG	2.49	0.51
1:A:443:ASP:C	1:A:444:LEU:HD13	2.31	0.51
1:C:302:PRO:O	1:C:439:ASN:CG	2.49	0.51
1:C:63:VAL:HG21	1:C:416:ALA:HB1	1.93	0.51
1:D:37:ARG:HH21	1:D:37:ARG:CB	2.16	0.51
1:D:63:VAL:HG21	1:D:416:ALA:HB1	1.93	0.51
1:F:63:VAL:HG21	1:F:416:ALA:HB1	1.93	0.51
1:I:160:SER:O	1:I:161:ASN:ND2	2.44	0.51
1:I:35:PHE:C	1:I:37:ARG:N	2.62	0.51
1:I:35:PHE:HE2	1:I:324:LYS:NZ	2.08	0.51
1:J:443:ASP:C	1:J:444:LEU:HD13	2.31	0.51
1:P:164:LEU:HD22	1:P:169:ASP:CG	2.31	0.51
1:Q:164:LEU:HD22	1:Q:169:ASP:CG	2.31	0.51
1:Q:434:THR:HA	1:Q:437:GLN:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:35:PHE:HE1	1:S:321:ARG:NH1	2.06	0.51
1:H:139:SER:CB	1:H:455:THR:CG2	2.80	0.51
1:X:158:TRP:HD1	1:X:158:TRP:N	2.07	0.51
1:Q:158:TRP:HD1	1:Q:158:TRP:N	2.07	0.51
1:J:265:LYS:O	1:J:266:ILE:HG12	2.10	0.51
1:H:265:LYS:O	1:H:266:ILE:HG12	2.10	0.51
1:I:236:GLN:CB	1:I:265:LYS:HZ3	2.16	0.51
1:I:573:ASN:O	1:I:577:ILE:HG13	2.10	0.51
1:G:221:GLU:OE2	1:G:278:LYS:HD2	2.10	0.51
1:H:113:ILE:HD13	1:H:150:HIS:CE1	2.45	0.51
1:S:379:GLU:O	1:S:380:ASN:CB	2.58	0.51
1:C:579:MSE:HB2	1:C:581:VAL:HG12	1.91	0.51
1:E:221:GLU:OE2	1:E:278:LYS:HD2	2.10	0.51
1:O:598:GLN:HB2	1:O:601:GLN:HB2	1.92	0.51
1:U:390:ALA:CB	1:X:387:GLN:CB	2.88	0.51
1:L:310:VAL:C	1:L:312:ASP:H	2.13	0.51
1:O:58:ASP:HA	1:O:327:GLN:NE2	2.26	0.51
2:Y:57:TYR:HD2	2:Y:57:TYR:O	1.92	0.51
1:M:322:LEU:HD22	1:M:322:LEU:N	2.25	0.51
1:B:395:PRO:HD2	1:C:398:PRO:HB3	1.92	0.51
1:N:351:PHE:CD2	1:N:356:ILE:HD12	2.46	0.51
1:A:63:VAL:HG21	1:A:416:ALA:HB1	1.93	0.51
1:C:78:VAL:CG1	1:C:79:LEU:N	2.72	0.51
1:D:111:VAL:O	1:D:115:VAL:HG13	2.11	0.51
1:D:302:PRO:O	1:D:439:ASN:CG	2.49	0.51
1:E:302:PRO:O	1:E:439:ASN:CG	2.49	0.51
1:F:111:VAL:O	1:F:115:VAL:HG13	2.11	0.51
1:G:429:GLN:O	1:G:429:GLN:HG2	2.10	0.51
1:H:35:PHE:CE2	1:H:321:ARG:HG3	2.45	0.51
1:I:35:PHE:CE2	1:I:321:ARG:HG3	2.45	0.51
1:J:63:VAL:HG21	1:J:416:ALA:HB1	1.93	0.51
1:M:434:THR:O	1:M:437:GLN:HG2	2.09	0.51
1:O:46:SER:N	1:O:48:TYR:HE2	1.98	0.51
1:P:81:ARG:HB2	1:P:517:TYR:CZ	2.45	0.51
1:L:443:ASP:C	1:L:444:LEU:HD13	2.31	0.51
1:N:35:PHE:C	1:N:37:ARG:H	2.14	0.51
1:N:66:LYS:HZ3	1:N:420:VAL:HG11	1.75	0.51
1:P:434:THR:HA	1:P:437:GLN:HG2	1.92	0.51
1:R:34:PHE:CE2	1:R:45:LEU:HG	2.44	0.51
1:T:101:ASP:HB2	1:T:144:ILE:O	2.11	0.51
1:V:44:TRP:CE2	1:V:54:ARG:HB3	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:44:TRP:C	1:V:45:LEU:HD22	2.31	0.51
1:X:144:ILE:HD12	1:X:145:ARG:N	2.25	0.51
1:Q:546:THR:CG2	1:Q:547:PRO:HD3	2.29	0.51
1:O:302:PRO:O	1:O:439:ASN:ND2	2.43	0.51
1:Q:302:PRO:O	1:Q:439:ASN:ND2	2.44	0.51
1:L:573:ASN:O	1:L:577:ILE:HG13	2.10	0.51
1:E:573:ASN:O	1:E:577:ILE:HG13	2.11	0.51
1:F:573:ASN:O	1:F:577:ILE:HG13	2.11	0.51
1:D:457:MSE:O	1:D:458:ARG:HD2	2.10	0.51
1:K:379:GLU:O	1:K:380:ASN:CB	2.58	0.51
1:I:379:GLU:O	1:I:380:ASN:CB	2.58	0.51
1:W:535:ILE:HD13	1:W:554:LEU:HG	1.93	0.51
1:A:348:LYS:HB3	1:L:371:TYR:HA	1.92	0.51
1:U:598:GLN:HB2	1:U:601:GLN:HB2	1.92	0.51
1:T:95:MSE:HB3	1:T:527:MSE:HE1	1.91	0.51
1:U:351:PHE:CD2	1:U:356:ILE:HD12	2.44	0.51
1:V:348:LYS:HB2	1:W:372:TYR:CE2	2.46	0.51
1:K:363:TYR:HE1	1:L:350:PHE:HE1	1.57	0.51
1:T:154:SER:O	1:T:204:PRO:HB3	2.09	0.51
1:P:395:PRO:HD2	1:Q:398:PRO:HB3	1.91	0.51
1:A:101:ASP:HB3	1:A:138:THR:HG21	1.93	0.51
1:A:160:SER:O	1:A:161:ASN:ND2	2.44	0.51
1:A:444:LEU:C	1:A:446:THR:N	2.61	0.51
1:B:34:PHE:HZ	1:B:328:ARG:HH22	0.80	0.51
1:C:111:VAL:O	1:C:115:VAL:HG13	2.11	0.51
1:F:429:GLN:HG2	1:F:429:GLN:O	2.10	0.51
1:H:443:ASP:C	1:H:444:LEU:HD13	2.31	0.51
1:H:561:ASP:OD2	1:I:92:ASP:HB3	2.10	0.51
1:J:101:ASP:HB3	1:J:138:THR:HG21	1.93	0.51
1:L:528:LYS:HZ2	1:L:560:LEU:HD21	1.75	0.51
1:M:420:VAL:HG22	1:M:428:GLY:HA3	1.92	0.51
1:N:344:THR:HG23	1:N:344:THR:O	2.09	0.51
1:R:44:TRP:C	1:R:45:LEU:HD22	2.30	0.51
1:U:123:VAL:HG22	1:U:316:TYR:CE2	2.46	0.51
1:X:344:THR:HG23	1:X:344:THR:O	2.09	0.51
1:X:434:THR:O	1:X:437:GLN:HG2	2.10	0.51
1:E:14:ARG:HH11	1:E:17:ALA:HB2	1.76	0.51
1:F:14:ARG:NE	1:F:14:ARG:CA	2.67	0.51
1:G:14:ARG:HH11	1:G:17:ALA:HB2	1.76	0.51
1:I:234:ILE:HG13	1:I:267:ALA:HB3	1.90	0.51
1:B:573:ASN:O	1:B:577:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:598:GLN:HB2	1:P:601:GLN:HB2	1.92	0.51
1:A:310:VAL:C	1:A:312:ASP:H	2.13	0.51
1:U:584:PRO:HG2	1:U:593:LEU:HD12	1.91	0.51
1:N:430:VAL:CG1	3:V:719:HOH:O	2.59	0.51
1:N:438:LEU:HD22	3:V:718:HOH:O	2.09	0.51
1:K:63:VAL:HG21	1:K:416:ALA:HB1	1.93	0.51
1:B:35:PHE:HE2	1:B:324:LYS:NZ	2.07	0.51
1:E:63:VAL:HG21	1:E:416:ALA:HB1	1.93	0.51
1:G:15:PHE:CZ	1:G:283:CYS:HA	2.45	0.51
1:H:101:ASP:HB3	1:H:138:THR:HG21	1.93	0.51
1:H:160:SER:O	1:H:161:ASN:ND2	2.44	0.51
1:J:111:VAL:O	1:J:115:VAL:HG13	2.11	0.51
1:J:160:SER:O	1:J:161:ASN:ND2	2.44	0.51
1:J:302:PRO:O	1:J:439:ASN:CG	2.49	0.51
1:K:15:PHE:CZ	1:K:283:CYS:HA	2.45	0.51
1:M:48:TYR:O	1:M:48:TYR:CD2	5.16	0.51
1:O:35:PHE:C	1:O:37:ARG:H	2.12	0.51
2:Y:53:MET:O	2:Y:69:PHE:CE1	2.63	0.51
1:N:164:LEU:HD22	1:N:169:ASP:CG	2.30	0.51
1:Q:37:ARG:HH21	1:Q:37:ARG:CB	2.24	0.51
1:S:48:TYR:O	1:S:48:TYR:CD2	5.17	0.51
1:S:48:TYR:O	1:S:48:TYR:HD2	5.14	0.51
1:V:344:THR:HG23	1:V:344:THR:O	2.09	0.51
1:W:434:THR:HA	1:W:437:GLN:HG2	1.92	0.51
1:F:14:ARG:HH11	1:F:17:ALA:HB2	1.76	0.51
1:X:302:PRO:O	1:X:439:ASN:ND2	2.43	0.51
1:H:573:ASN:O	1:H:577:ILE:HG13	2.10	0.51
1:H:209:PHE:HA	1:H:211:TRP:NE1	2.24	0.51
1:E:209:PHE:HA	1:E:211:TRP:NE1	2.24	0.51
1:H:221:GLU:OE2	1:H:278:LYS:HD2	2.10	0.51
1:R:598:GLN:HB2	1:R:601:GLN:HB2	1.92	0.51
1:V:58:ASP:HA	1:V:327:GLN:NE2	2.25	0.51
1:K:221:GLU:OE2	1:K:278:LYS:HD2	2.10	0.51
1:O:456:ALA:O	1:O:457:MSE:HB2	2.11	0.51
1:S:351:PHE:CD2	1:S:356:ILE:HD12	2.45	0.51
1:A:111:VAL:O	1:A:115:VAL:HG13	2.11	0.51
1:C:528:LYS:HZ2	1:C:560:LEU:HD21	1.76	0.51
1:F:37:ARG:HH21	1:F:37:ARG:CB	2.16	0.51
1:G:35:PHE:CE2	1:G:321:ARG:HG3	2.45	0.51
1:G:379:GLU:O	1:G:380:ASN:CB	2.58	0.51
1:K:302:PRO:O	1:K:439:ASN:CG	2.49	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:160:SER:O	1:L:161:ASN:ND2	2.44	0.51
1:L:35:PHE:HE2	1:L:324:LYS:NZ	2.07	0.51
1:L:444:LEU:C	1:L:446:THR:N	2.61	0.51
1:P:80:TYR:CE1	1:P:448:VAL:HG22	2.45	0.51
1:R:443:ASP:C	1:R:446:THR:HG22	2.31	0.51
1:R:44:TRP:CE2	1:R:54:ARG:HB3	2.46	0.51
1:R:78:VAL:CG1	1:R:79:LEU:N	2.73	0.51
1:T:34:PHE:CE2	1:T:45:LEU:HG	2.45	0.51
1:V:35:PHE:CE1	1:V:321:ARG:NE	2.76	0.51
1:D:14:ARG:CA	1:D:14:ARG:NE	2.67	0.51
1:P:546:THR:CG2	1:P:547:PRO:HD3	2.31	0.51
1:A:564:GLY:CA	1:B:554:LEU:HD21	2.35	0.51
1:H:251:ILE:O	1:H:507:LEU:HD13	2.11	0.51
1:F:457:MSE:O	1:F:458:ARG:HD2	2.10	0.51
1:X:573:ASN:O	1:X:577:ILE:HG13	2.10	0.51
1:A:113:ILE:HD13	1:A:150:HIS:CE1	2.45	0.51
1:O:380:ASN:O	1:O:381:SER:HB3	2.11	0.51
1:S:58:ASP:HA	1:S:327:GLN:NE2	2.25	0.51
1:O:389:LEU:HD12	1:O:389:LEU:H	1.75	0.51
1:X:351:PHE:CD2	1:X:356:ILE:HD12	2.45	0.51
1:B:111:VAL:O	1:B:115:VAL:HG13	2.11	0.51
1:B:37:ARG:HH22	1:B:45:LEU:CD1	2.24	0.51
1:F:101:ASP:HB3	1:F:138:THR:HG21	1.93	0.51
1:H:302:PRO:O	1:H:439:ASN:CG	2.49	0.51
1:I:37:ARG:HH22	1:I:45:LEU:CD1	2.24	0.51
1:I:302:PRO:O	1:I:439:ASN:CG	2.49	0.51
1:L:111:VAL:O	1:L:115:VAL:HG13	2.11	0.51
1:L:37:ARG:HH22	1:L:45:LEU:CD1	2.24	0.51
1:M:144:ILE:HD12	1:M:145:ARG:N	2.26	0.51
1:O:165:MSE:HE1	1:O:435:VAL:HB	1.93	0.51
1:O:78:VAL:CG1	1:O:79:LEU:N	2.74	0.51
1:N:325:ASP:O	1:N:329:LEU:HD23	2.10	0.51
1:N:456:ALA:O	1:N:457:MSE:HB2	2.11	0.51
1:Q:80:TYR:CE1	1:Q:448:VAL:HG22	2.46	0.51
1:R:123:VAL:HG22	1:R:316:TYR:CE2	2.45	0.51
1:R:456:ALA:O	1:R:457:MSE:HB2	2.11	0.51
1:S:37:ARG:CB	1:S:37:ARG:HH21	2.24	0.51
1:U:78:VAL:HG12	1:U:79:LEU:H	1.75	0.51
1:W:34:PHE:CE2	1:W:45:LEU:HG	2.45	0.51
1:X:34:PHE:CE2	1:X:45:LEU:HG	2.45	0.51
1:X:405:LEU:O	1:X:409:THR:HG23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:273:ARG:NH2	1:I:453:LEU:HD21	2.21	0.51
1:C:248:LYS:HD3	1:C:251:ILE:HB	1.93	0.51
1:F:251:ILE:O	1:F:507:LEU:HD13	2.11	0.51
1:J:573:ASN:O	1:J:577:ILE:HG13	2.10	0.51
1:U:535:ILE:HD13	1:U:554:LEU:HG	1.93	0.51
1:D:376:ARG:HB2	1:F:352:TRP:CD2	2.46	0.51
1:U:66:LYS:HZ3	1:U:420:VAL:HG11	1.74	0.51
1:L:379:GLU:O	1:L:380:ASN:CB	2.58	0.51
1:H:379:GLU:O	1:H:380:ASN:CB	2.58	0.51
1:R:95:MSE:HB3	1:R:527:MSE:HE1	1.93	0.51
1:X:95:MSE:HB3	1:X:527:MSE:HE1	1.92	0.51
1:M:430:VAL:HG11	3:N:719:HOH:O	2.11	0.51
1:R:58:ASP:HA	1:R:327:GLN:NE2	2.26	0.51
1:J:221:GLU:OE2	1:J:278:LYS:HD2	2.10	0.51
1:A:427:GLY:C	1:A:429:GLN:H	2.15	0.51
1:V:399:GLN:OE1	1:W:396:GLU:O	2.29	0.51
1:C:160:SER:O	1:C:161:ASN:ND2	2.44	0.51
1:C:35:PHE:HE2	1:C:324:LYS:NZ	2.08	0.51
1:G:443:ASP:C	1:G:444:LEU:HD13	2.31	0.51
1:I:444:LEU:C	1:I:446:THR:N	2.61	0.51
1:L:14:ARG:CA	1:L:14:ARG:NE	2.67	0.51
1:L:48:TYR:O	1:L:48:TYR:CD2	5.23	0.51
1:L:101:ASP:HB3	1:L:138:THR:HG21	1.93	0.51
1:N:144:ILE:HD12	1:N:145:ARG:N	2.26	0.51
1:N:420:VAL:HG22	1:N:428:GLY:HA3	1.92	0.51
1:T:302:PRO:O	1:T:439:ASN:ND2	2.44	0.51
1:T:44:TRP:CE2	1:T:54:ARG:HB3	2.46	0.51
1:D:14:ARG:HH11	1:D:17:ALA:HB2	1.76	0.51
1:J:14:ARG:HH11	1:J:17:ALA:HB2	1.76	0.51
1:A:265:LYS:O	1:A:266:ILE:HG12	2.10	0.51
1:W:456:ALA:O	1:W:457:MSE:HB2	2.11	0.51
1:F:221:GLU:OE2	1:F:278:LYS:HD2	2.10	0.51
1:R:535:ILE:HD13	1:R:554:LEU:HG	1.92	0.51
1:L:221:GLU:OE2	1:L:278:LYS:HD2	2.10	0.51
1:L:191:TYR:HE1	1:L:278:LYS:HZ3	1.57	0.51
1:S:55:GLY:HA3	1:S:57:PHE:CE1	2.46	0.51
1:E:429:GLN:O	1:E:429:GLN:HG2	2.10	0.51
1:B:160:SER:O	1:B:161:ASN:ND2	2.44	0.51
1:C:101:ASP:HB3	1:C:138:THR:HG21	1.93	0.51
1:E:160:SER:O	1:E:161:ASN:ND2	2.44	0.51
1:F:560:LEU:O	1:F:565:VAL:HG21	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:560:LEU:O	1:G:565:VAL:HG21	2.11	0.51
1:H:560:LEU:O	1:H:565:VAL:HG21	2.11	0.51
1:I:429:GLN:O	1:I:429:GLN:HG2	2.10	0.51
1:M:434:THR:HA	1:M:437:GLN:HG2	1.92	0.51
1:M:456:ALA:O	1:M:457:MSE:HB2	2.11	0.51
1:O:444:LEU:C	1:O:446:THR:H	2.13	0.51
1:K:72:ARG:HD2	1:L:434:THR:HG21	1.93	0.51
1:S:456:ALA:O	1:S:457:MSE:HB2	2.10	0.51
1:T:78:VAL:CG1	1:T:79:LEU:N	2.74	0.51
1:U:80:TYR:CE1	1:U:448:VAL:HG22	2.45	0.51
1:O:158:TRP:N	1:O:158:TRP:HD1	2.07	0.51
1:W:413:LYS:HA	1:W:416:ALA:HB3	1.93	0.51
1:B:251:ILE:O	1:B:507:LEU:HD13	2.11	0.51
1:D:236:GLN:CB	1:D:265:LYS:HG2	2.37	0.51
1:F:248:LYS:HD3	1:F:251:ILE:HB	1.93	0.51
1:R:212:LEU:HD22	1:X:26:ARG:HG2	1.93	0.51
1:B:63:VAL:HG21	1:B:416:ALA:HB1	1.93	0.51
3:M:719:HOH:O	1:O:430:VAL:HG11	2.11	0.51
1:H:310:VAL:C	1:H:312:ASP:H	2.13	0.51
1:E:310:VAL:C	1:E:312:ASP:H	2.13	0.51
1:M:429:GLN:HG2	1:M:429:GLN:O	2.11	0.51
1:B:429:GLN:HG2	1:B:429:GLN:O	2.10	0.51
1:A:37:ARG:HH22	1:A:45:LEU:CD1	2.24	0.50
1:D:35:PHE:CE2	1:D:321:ARG:HG3	2.45	0.50
1:E:35:PHE:CE2	1:E:321:ARG:HG3	2.45	0.50
1:G:111:VAL:O	1:G:115:VAL:HG13	2.11	0.50
1:G:63:VAL:HG21	1:G:416:ALA:HB1	1.93	0.50
1:H:35:PHE:HE2	1:H:324:LYS:NZ	2.08	0.50
1:H:63:VAL:HG21	1:H:416:ALA:HB1	1.93	0.50
1:I:111:VAL:O	1:I:115:VAL:HG13	2.11	0.50
1:I:427:GLY:C	1:I:429:GLN:H	2.14	0.50
1:I:63:VAL:HG21	1:I:416:ALA:HB1	1.93	0.50
1:J:560:LEU:O	1:J:565:VAL:HG21	2.11	0.50
1:K:101:ASP:HB3	1:K:138:THR:HG21	1.93	0.50
1:K:160:SER:O	1:K:161:ASN:ND2	2.44	0.50
1:K:35:PHE:CE2	1:K:321:ARG:HG3	2.45	0.50
1:L:81:ARG:HB2	1:L:517:TYR:CE2	2.46	0.50
1:O:80:TYR:CE1	1:O:448:VAL:HG22	2.46	0.50
1:K:81:ARG:HB2	1:K:517:TYR:CE2	2.46	0.50
1:N:35:PHE:CE1	1:N:321:ARG:NE	2.78	0.50
1:Q:78:VAL:CG1	1:Q:79:LEU:N	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:35:PHE:CE1	1:R:321:ARG:NE	2.77	0.50
1:V:46:SER:N	1:V:48:TYR:HE2	1.96	0.50
1:W:444:LEU:C	1:W:446:THR:H	2.13	0.50
1:X:413:LYS:HA	1:X:416:ALA:HB3	1.92	0.50
1:B:265:LYS:O	1:B:266:ILE:HG12	2.10	0.50
1:A:248:LYS:HD3	1:A:251:ILE:HB	1.93	0.50
1:I:513:ARG:H	1:I:513:ARG:HD3	1.77	0.50
1:K:376:ARG:HB2	1:L:352:TRP:CD2	2.46	0.50
1:N:58:ASP:HA	1:N:327:GLN:NE2	2.26	0.50
1:T:389:LEU:HD12	1:T:389:LEU:H	1.76	0.50
2:Z:38:GLU:N	2:Z:39:PRO:HD3	2.26	0.50
1:K:427:GLY:C	1:K:429:GLN:H	2.15	0.50
1:O:171:ARG:O	1:O:224:GLU:HA	2.11	0.50
1:A:92:ASP:HB3	1:L:561:ASP:OD2	2.10	0.50
1:C:443:ASP:C	1:C:444:LEU:HD13	2.31	0.50
1:G:427:GLY:C	1:G:429:GLN:H	2.15	0.50
1:H:111:VAL:O	1:H:115:VAL:HG13	2.11	0.50
1:Q:325:ASP:O	1:Q:329:LEU:HD23	2.11	0.50
1:T:456:ALA:O	1:T:457:MSE:HB2	2.11	0.50
1:M:405:LEU:O	1:M:409:THR:HG23	2.12	0.50
2:Z:70:SER:HB2	2:Z:75:PRO:O	2.12	0.50
1:R:405:LEU:O	1:R:409:THR:HG23	2.12	0.50
1:J:246:TYR:HE2	1:J:512:GLY:N	2.10	0.50
1:B:248:LYS:HD3	1:B:251:ILE:HB	1.93	0.50
1:B:560:LEU:O	1:B:565:VAL:HG21	2.11	0.50
1:A:251:ILE:O	1:A:507:LEU:HD13	2.11	0.50
1:C:513:ARG:HD3	1:C:513:ARG:H	1.77	0.50
1:F:586:THR:N	1:F:587:PRO:CD	2.74	0.50
1:J:586:THR:N	1:J:587:PRO:CD	2.75	0.50
1:A:429:GLN:O	1:A:429:GLN:HG2	2.10	0.50
1:D:429:GLN:O	1:D:429:GLN:HG2	2.10	0.50
1:L:429:GLN:HG2	1:L:429:GLN:O	2.10	0.50
1:F:418:LEU:HB2	1:F:428:GLY:O	2.12	0.50
1:S:427:GLY:C	1:S:429:GLN:H	2.14	0.50
1:J:81:ARG:HB2	1:J:517:TYR:CE2	2.46	0.50
1:U:427:GLY:C	1:U:429:GLN:H	2.15	0.50
1:I:418:LEU:HB2	1:I:428:GLY:O	2.12	0.50
1:B:101:ASP:HB3	1:B:138:THR:HG21	1.93	0.50
1:D:37:ARG:HH22	1:D:45:LEU:CD1	2.24	0.50
1:D:404:MSE:HE3	1:E:334:MSE:HE3	1.93	0.50
1:D:560:LEU:O	1:D:565:VAL:HG21	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:302:PRO:O	1:F:439:ASN:CG	2.49	0.50
1:G:302:PRO:O	1:G:439:ASN:CG	2.49	0.50
1:G:37:ARG:HH22	1:G:45:LEU:CD1	2.24	0.50
1:I:101:ASP:HB3	1:I:138:THR:HG21	1.93	0.50
1:I:34:PHE:HE1	1:I:324:LYS:HZ2	1.50	0.50
1:L:113:ILE:HD12	1:L:148:PRO:HB3	1.94	0.50
1:P:325:ASP:O	1:P:329:LEU:HD23	2.11	0.50
1:V:9:GLU:HG3	1:V:12:LEU:H	1.77	0.50
1:U:546:THR:CG2	1:U:547:PRO:HD3	2.31	0.50
1:R:158:TRP:N	1:R:158:TRP:HD1	2.08	0.50
1:J:251:ILE:O	1:J:507:LEU:HD13	2.11	0.50
1:B:246:TYR:HE2	1:B:512:GLY:N	2.10	0.50
1:E:513:ARG:HD3	1:E:513:ARG:H	1.76	0.50
1:L:251:ILE:O	1:L:507:LEU:HD13	2.11	0.50
1:G:563:LYS:HD3	1:H:557:PHE:CE2	2.47	0.50
1:G:573:ASN:O	1:G:577:ILE:HG13	2.10	0.50
1:I:586:THR:N	1:I:587:PRO:CD	2.75	0.50
1:E:586:THR:N	1:E:587:PRO:CD	2.75	0.50
1:W:420:VAL:HG22	1:W:428:GLY:HA3	1.91	0.50
1:I:191:TYR:HE1	1:I:278:LYS:HZ3	1.57	0.50
1:K:418:LEU:HB2	1:K:428:GLY:O	2.12	0.50
1:G:81:ARG:HB2	1:G:517:TYR:CE2	2.46	0.50
1:O:135:GLN:NE2	1:P:514:TYR:HE2	2.09	0.50
1:T:396:GLU:O	1:W:399:GLN:OE1	2.29	0.50
1:N:174:THR:N	3:N:705:HOH:O	2.44	0.50
1:C:81:ARG:HB2	1:C:517:TYR:CE2	2.46	0.50
1:C:418:LEU:HB2	1:C:428:GLY:O	2.12	0.50
1:A:126:TRP:CD1	1:A:146:ARG:HG3	2.46	0.50
1:D:443:ASP:C	1:D:444:LEU:HD13	2.31	0.50
1:G:15:PHE:HZ	1:G:283:CYS:HG	1.60	0.50
1:H:126:TRP:CD1	1:H:146:ARG:HG3	2.46	0.50
1:I:126:TRP:CD1	1:I:146:ARG:HG3	2.46	0.50
1:Q:34:PHE:CE2	1:Q:45:LEU:HG	2.46	0.50
1:R:37:ARG:CB	1:R:37:ARG:HH21	2.24	0.50
1:V:26:ARG:HG2	1:W:212:LEU:HD22	1.94	0.50
1:X:164:LEU:HD22	1:X:169:ASP:CG	2.32	0.50
1:A:14:ARG:NE	1:A:14:ARG:CA	2.67	0.50
1:H:14:ARG:HH11	1:H:17:ALA:HB2	1.76	0.50
1:I:14:ARG:HH11	1:I:17:ALA:HB2	1.76	0.50
2:Z:104:TYR:HB2	2:Z:106:LEU:HD12	1.93	0.50
1:S:302:PRO:O	1:S:439:ASN:ND2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:246:TYR:HE2	1:K:512:GLY:N	2.10	0.50
1:K:251:ILE:O	1:K:507:LEU:HD13	2.11	0.50
1:K:510:ILE:O	1:K:513:ARG:HD2	2.12	0.50
1:L:246:TYR:HE2	1:L:512:GLY:N	2.10	0.50
1:L:248:LYS:HD3	1:L:251:ILE:HB	1.93	0.50
1:E:535:ILE:HD11	1:E:554:LEU:HG	1.94	0.50
1:M:535:ILE:HD13	1:M:554:LEU:HG	1.93	0.50
1:Q:266:ILE:HG23	1:Q:267:ALA:N	2.26	0.50
1:V:266:ILE:HG23	1:V:267:ALA:N	2.26	0.50
1:T:235:TYR:HA	1:T:265:LYS:HB3	1.94	0.50
1:S:235:TYR:HA	1:S:265:LYS:HB3	1.94	0.50
1:B:409:THR:O	1:B:413:LYS:HG2	2.12	0.50
1:L:409:THR:O	1:L:413:LYS:HG2	2.12	0.50
1:C:584:PRO:HG2	1:C:593:LEU:HD12	1.94	0.50
1:L:535:ILE:HD11	1:L:554:LEU:HG	1.94	0.50
1:X:598:GLN:HB2	1:X:601:GLN:HB2	1.92	0.50
1:K:429:GLN:O	1:K:429:GLN:HG2	2.10	0.50
1:G:198:ILE:HG22	1:G:198:ILE:O	2.12	0.50
1:A:81:ARG:HB2	1:A:517:TYR:CE2	2.46	0.50
1:C:409:THR:O	1:C:413:LYS:HG2	2.12	0.50
1:E:37:ARG:HH22	1:E:45:LEU:CD1	2.24	0.50
1:E:94:LEU:HA	1:E:97:MSE:CE	2.37	0.50
1:F:35:PHE:HE2	1:F:324:LYS:NZ	2.08	0.50
1:F:443:ASP:C	1:F:444:LEU:HD13	2.31	0.50
1:H:37:ARG:HH22	1:H:45:LEU:CD1	2.24	0.50
1:K:126:TRP:CD1	1:K:146:ARG:HG3	2.46	0.50
1:K:14:ARG:HH11	1:K:17:ALA:HB2	1.76	0.50
1:L:302:PRO:O	1:L:439:ASN:CG	2.49	0.50
1:K:560:LEU:O	1:K:565:VAL:HG21	2.11	0.50
1:R:48:TYR:CD2	1:R:48:TYR:O	5.16	0.50
1:S:344:THR:O	1:S:344:THR:HG23	2.11	0.50
1:U:37:ARG:CB	1:U:37:ARG:HH21	2.24	0.50
1:U:443:ASP:C	1:U:446:THR:HG22	2.32	0.50
1:V:34:PHE:CE2	1:V:45:LEU:HG	2.46	0.50
1:W:434:THR:HG23	1:W:435:VAL:N	2.26	0.50
1:P:158:TRP:N	1:P:158:TRP:HD1	2.07	0.50
1:C:535:ILE:HD11	1:C:554:LEU:HG	1.94	0.50
1:D:248:LYS:HD3	1:D:251:ILE:HB	1.93	0.50
1:D:251:ILE:O	1:D:507:LEU:HD13	2.11	0.50
1:H:510:ILE:O	1:H:513:ARG:HD2	2.12	0.50
1:A:246:TYR:HE2	1:A:512:GLY:N	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:246:TYR:HE2	1:F:512:GLY:N	2.10	0.50
1:T:535:ILE:HD13	1:T:554:LEU:HG	1.93	0.50
1:L:57:PHE:CD2	1:L:330:ARG:CB	2.95	0.50
1:Q:573:ASN:O	1:Q:577:ILE:HG13	2.12	0.50
1:D:535:ILE:HD11	1:D:554:LEU:HG	1.94	0.50
1:G:586:THR:N	1:G:587:PRO:CD	2.75	0.50
1:F:113:ILE:HD12	1:F:148:PRO:HB3	1.94	0.50
1:E:113:ILE:HD12	1:E:148:PRO:HB3	1.94	0.50
1:N:379:GLU:O	1:N:380:ASN:CB	2.59	0.50
1:S:598:GLN:HB2	1:S:601:GLN:HB2	1.92	0.50
1:U:55:GLY:HA3	1:U:57:PHE:CE1	2.46	0.50
1:E:81:ARG:HB2	1:E:517:TYR:CE2	2.46	0.50
1:D:81:ARG:HB2	1:D:517:TYR:CE2	2.46	0.50
1:W:351:PHE:CD2	1:W:356:ILE:HD12	2.46	0.50
2:Y:89:VAL:C	2:Y:91:ALA:H	2.15	0.50
1:H:81:ARG:HB2	1:H:517:TYR:CE2	2.46	0.50
1:C:34:PHE:HE1	1:C:324:LYS:HZ2	1.46	0.50
1:D:101:ASP:HB3	1:D:138:THR:HG21	1.93	0.50
1:D:136:SER:N	1:D:137:PRO:HD3	2.27	0.50
1:D:126:TRP:CD1	1:D:146:ARG:HG3	2.46	0.50
1:D:409:THR:O	1:D:413:LYS:HG2	2.12	0.50
1:E:560:LEU:O	1:E:565:VAL:HG21	2.11	0.50
1:F:57:PHE:CD2	1:F:330:ARG:CB	2.95	0.50
1:H:427:GLY:C	1:H:429:GLN:H	2.15	0.50
1:J:126:TRP:CD1	1:J:146:ARG:HG3	2.46	0.50
1:L:560:LEU:O	1:L:565:VAL:HG21	2.11	0.50
1:Q:9:GLU:HG3	1:Q:12:LEU:H	1.77	0.50
1:V:165:MSE:HE1	1:V:435:VAL:HB	1.94	0.50
1:B:14:ARG:HH11	1:B:17:ALA:HB2	1.76	0.50
2:Z:72:ASP:OD1	2:Z:72:ASP:O	2.30	0.50
2:Y:70:SER:HB2	2:Y:75:PRO:O	2.12	0.50
2:Y:72:ASP:O	2:Y:72:ASP:OD1	2.30	0.50
1:K:513:ARG:HD3	1:K:513:ARG:H	1.77	0.50
1:B:513:ARG:HD3	1:B:513:ARG:H	1.77	0.50
1:D:246:TYR:HE2	1:D:512:GLY:N	2.10	0.50
1:D:510:ILE:O	1:D:513:ARG:HD2	2.12	0.50
1:H:248:LYS:HD3	1:H:251:ILE:HB	1.93	0.50
1:A:513:ARG:HD3	1:A:513:ARG:H	1.76	0.50
1:A:510:ILE:O	1:A:513:ARG:HD2	2.12	0.50
1:C:251:ILE:O	1:C:507:LEU:HD13	2.11	0.50
1:E:251:ILE:O	1:E:507:LEU:HD13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:235:TYR:HA	1:U:265:LYS:HB3	1.94	0.50
1:I:535:ILE:HD11	1:I:554:LEU:HG	1.94	0.50
1:K:409:THR:O	1:K:413:LYS:HG2	2.12	0.50
1:S:573:ASN:O	1:S:577:ILE:HG13	2.12	0.50
1:B:113:ILE:HD12	1:B:148:PRO:HB3	1.94	0.50
1:N:586:THR:N	1:N:587:PRO:CD	2.75	0.50
1:K:113:ILE:HD12	1:K:148:PRO:HB3	1.94	0.50
1:M:322:LEU:H	1:M:322:LEU:HD22	1.77	0.50
1:D:418:LEU:HB2	1:D:428:GLY:O	2.12	0.50
1:B:81:ARG:HB2	1:B:517:TYR:CE2	2.46	0.50
1:A:136:SER:N	1:A:137:PRO:HD3	2.27	0.50
1:A:160:SER:HB3	1:A:171:ARG:NH2	2.27	0.50
1:C:37:ARG:HH22	1:C:45:LEU:CD1	2.24	0.50
1:E:126:TRP:CD1	1:E:146:ARG:HG3	2.46	0.50
1:E:409:THR:O	1:E:413:LYS:HG2	2.12	0.50
1:C:561:ASP:OD2	1:E:92:ASP:HB3	2.12	0.50
1:G:126:TRP:CD1	1:G:146:ARG:HG3	2.46	0.50
1:G:409:THR:O	1:G:413:LYS:HG2	2.12	0.50
1:I:334:MSE:HE3	1:J:404:MSE:HE3	1.93	0.50
1:I:560:LEU:O	1:I:565:VAL:HG21	2.11	0.50
1:J:128:LEU:HD12	1:J:446:THR:HG23	1.94	0.50
2:Z:28:VAL:HG21	2:Z:96:LEU:CG	2.40	0.50
1:P:34:PHE:CE2	1:P:45:LEU:HG	2.46	0.50
1:R:444:LEU:O	1:R:448:VAL:HG23	2.11	0.50
1:U:47:GLN:HG2	1:U:48:TYR:N	2.26	0.50
1:U:78:VAL:CG1	1:U:79:LEU:N	2.74	0.50
1:V:343:ARG:O	1:V:344:THR:HB	2.12	0.50
1:N:27:ARG:NH2	1:V:41:TRP:HE1	2.10	0.50
1:S:14:ARG:NE	1:S:14:ARG:CA	2.69	0.50
1:S:9:GLU:HG3	1:S:12:LEU:H	1.77	0.50
1:D:513:ARG:HD3	1:D:513:ARG:H	1.77	0.50
1:R:235:TYR:HA	1:R:265:LYS:HB3	1.94	0.50
1:A:352:TRP:CD1	1:L:376:ARG:HB2	2.47	0.50
1:D:586:THR:N	1:D:587:PRO:CD	2.75	0.50
1:L:586:THR:N	1:L:587:PRO:CD	2.75	0.50
1:U:379:GLU:O	1:U:380:ASN:CB	2.59	0.50
1:C:136:SER:N	1:C:137:PRO:HD3	2.27	0.50
1:E:418:LEU:HB2	1:E:428:GLY:O	2.12	0.50
1:V:322:LEU:N	1:V:322:LEU:HD22	2.27	0.50
1:G:418:LEU:HB2	1:G:428:GLY:O	2.12	0.50
1:E:111:VAL:O	1:E:115:VAL:HG13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:160:SER:HB3	1:E:171:ARG:NH2	2.27	0.50
1:F:160:SER:HB3	1:F:171:ARG:NH2	2.27	0.50
1:F:409:THR:O	1:F:413:LYS:HG2	2.12	0.50
1:I:160:SER:HB3	1:I:171:ARG:NH2	2.27	0.50
1:J:409:THR:O	1:J:413:LYS:HG2	2.12	0.50
1:L:14:ARG:HH11	1:L:17:ALA:HB2	1.76	0.50
1:O:48:TYR:O	1:O:48:TYR:HD2	5.13	0.50
1:L:126:TRP:CD1	1:L:146:ARG:HG3	2.46	0.50
1:Q:434:THR:O	1:Q:437:GLN:HG2	2.11	0.50
1:Q:444:LEU:O	1:Q:448:VAL:HG23	2.11	0.50
1:R:27:ARG:HB2	1:R:313:LYS:HE3	1.94	0.50
1:S:434:THR:HG23	1:S:435:VAL:N	2.26	0.50
1:X:35:PHE:HE1	1:X:321:ARG:NH1	2.06	0.50
1:X:78:VAL:CG1	1:X:444:LEU:HG	2.42	0.50
1:M:413:LYS:HA	1:M:416:ALA:HB3	1.93	0.50
1:V:248:LYS:HG3	1:V:511:ARG:HE	1.77	0.50
1:G:251:ILE:O	1:G:507:LEU:HD13	2.11	0.50
1:I:248:LYS:HD3	1:I:251:ILE:HB	1.93	0.50
1:L:513:ARG:HD3	1:L:513:ARG:H	1.77	0.50
1:H:535:ILE:HD11	1:H:554:LEU:HG	1.94	0.50
1:B:57:PHE:CD2	1:B:330:ARG:CB	2.95	0.50
1:C:586:THR:N	1:C:587:PRO:CD	2.75	0.50
1:Q:535:ILE:HD13	1:Q:554:LEU:HG	1.94	0.50
1:T:387:GLN:CB	1:W:390:ALA:CB	2.89	0.50
1:E:427:GLY:C	1:E:429:GLN:H	2.15	0.50
1:M:427:GLY:C	1:M:429:GLN:H	2.15	0.50
1:E:198:ILE:O	1:E:198:ILE:HG22	2.12	0.50
1:I:81:ARG:HB2	1:I:517:TYR:CE2	2.46	0.50
1:A:128:LEU:HD12	1:A:446:THR:HG23	1.94	0.50
1:B:160:SER:HB3	1:B:171:ARG:NH2	2.27	0.50
1:C:126:TRP:CD1	1:C:146:ARG:HG3	2.46	0.50
1:D:160:SER:HB3	1:D:171:ARG:NH2	2.27	0.50
1:F:126:TRP:CD1	1:F:146:ARG:HG3	2.46	0.50
1:G:160:SER:HB3	1:G:171:ARG:NH2	2.27	0.50
1:H:119:ILE:HA	1:H:432:PHE:HE2	1.77	0.50
1:I:57:PHE:CD2	1:I:330:ARG:CB	2.95	0.50
1:J:15:PHE:HZ	1:J:283:CYS:HG	1.60	0.50
1:J:57:PHE:CD2	1:J:330:ARG:CB	2.95	0.50
1:J:37:ARG:HH22	1:J:45:LEU:CD1	2.24	0.50
1:K:160:SER:HB3	1:K:171:ARG:NH2	2.27	0.50
1:O:95:MSE:HE1	1:O:99:ARG:CZ	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:34:PHE:CE2	1:S:45:LEU:HG	2.46	0.50
1:T:27:ARG:HB2	1:T:313:LYS:HE3	1.94	0.50
1:V:444:LEU:C	1:V:446:THR:H	2.16	0.50
1:V:89:ASP:HA	1:W:561:ASP:CB	2.37	0.50
1:X:78:VAL:HG12	1:X:79:LEU:H	1.74	0.50
1:A:14:ARG:HH11	1:A:17:ALA:HB2	1.76	0.50
1:G:510:ILE:O	1:G:513:ARG:HD2	2.12	0.50
1:G:513:ARG:H	1:G:513:ARG:HD3	1.77	0.50
1:E:248:LYS:HD3	1:E:251:ILE:HB	1.93	0.50
1:E:280:ILE:HG22	1:E:287:LEU:HD13	1.94	0.50
1:A:280:ILE:HG22	1:A:287:LEU:HD13	1.94	0.50
1:D:280:ILE:HG22	1:D:287:LEU:HD13	1.94	0.50
1:L:280:ILE:HG22	1:L:287:LEU:HD13	1.94	0.50
1:K:198:ILE:O	1:K:198:ILE:HG22	2.12	0.50
1:G:584:PRO:HG2	1:G:593:LEU:HD12	1.94	0.50
1:B:584:PRO:HG2	1:B:593:LEU:HD12	1.94	0.50
1:D:584:PRO:CG	1:D:593:LEU:HD12	2.42	0.50
1:I:584:PRO:HG2	1:I:593:LEU:HD12	1.94	0.50
1:K:586:THR:N	1:K:587:PRO:CD	2.75	0.50
1:B:586:THR:N	1:B:587:PRO:CD	2.75	0.50
1:C:113:ILE:HD12	1:C:148:PRO:HB3	1.94	0.50
1:P:95:MSE:HE1	1:P:99:ARG:CZ	2.42	0.50
1:L:427:GLY:C	1:L:429:GLN:H	2.15	0.50
1:J:451:ASP:O	1:J:456:ALA:N	2.41	0.50
1:A:418:LEU:HB2	1:A:428:GLY:O	2.12	0.50
1:H:418:LEU:HB2	1:H:428:GLY:O	2.12	0.50
1:B:44:TRP:CE2	1:B:54:ARG:HB3	2.48	0.49
1:C:427:GLY:C	1:C:429:GLN:H	2.15	0.49
1:D:334:MSE:SE	1:F:404:MSE:HE1	2.61	0.49
1:H:160:SER:HB3	1:H:171:ARG:NH2	2.27	0.49
1:H:409:THR:O	1:H:413:LYS:HG2	2.12	0.49
1:K:111:VAL:O	1:K:115:VAL:HG13	2.11	0.49
2:Y:28:VAL:HG11	2:Y:96:LEU:C	2.33	0.49
1:L:128:LEU:HD12	1:L:446:THR:HG23	1.94	0.49
1:Q:456:ALA:O	1:Q:457:MSE:HB2	2.12	0.49
1:Q:48:TYR:CD2	1:Q:48:TYR:O	5.17	0.49
1:U:27:ARG:HB2	1:U:313:LYS:HE3	1.94	0.49
1:W:164:LEU:HD22	1:W:169:ASP:CG	2.33	0.49
1:X:343:ARG:O	1:X:344:THR:HB	2.12	0.49
1:C:14:ARG:HH11	1:C:17:ALA:HB2	1.76	0.49
1:T:9:GLU:HG3	1:T:12:LEU:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248:LYS:H	1:O:248:LYS:CD	2.17	0.49
1:I:248:LYS:HZ1	1:I:513:ARG:HH12	1.59	0.49
1:A:535:ILE:HD11	1:A:554:LEU:HG	1.94	0.49
1:L:584:PRO:HG2	1:L:593:LEU:HD12	1.94	0.49
1:H:584:PRO:HG2	1:H:593:LEU:HD12	1.94	0.49
1:M:379:GLU:O	1:M:380:ASN:CB	2.60	0.49
1:V:322:LEU:H	1:V:322:LEU:HD22	1.77	0.49
1:W:58:ASP:HA	1:W:327:GLN:NE2	2.27	0.49
1:F:81:ARG:HB2	1:F:517:TYR:CE2	2.46	0.49
1:L:255:ILE:O	1:L:257:ASP:N	2.45	0.49
1:A:44:TRP:CE2	1:A:54:ARG:HB3	2.48	0.49
1:C:128:LEU:HD12	1:C:446:THR:HG23	1.94	0.49
1:E:80:TYR:CE1	1:E:444:LEU:HB3	2.48	0.49
1:F:119:ILE:HA	1:F:432:PHE:HE2	1.78	0.49
1:G:182:ASN:HD22	1:H:171:ARG:HH21	1.58	0.49
1:I:136:SER:N	1:I:137:PRO:HD3	2.27	0.49
1:J:160:SER:HB3	1:J:171:ARG:NH2	2.27	0.49
1:J:429:GLN:O	1:J:429:GLN:HG2	2.10	0.49
1:K:128:LEU:HD12	1:K:446:THR:HG23	1.94	0.49
1:M:164:LEU:HA	1:M:307:TRP:HH2	1.77	0.49
2:Y:28:VAL:HG21	2:Y:96:LEU:CG	2.40	0.49
1:T:444:LEU:C	1:T:446:THR:H	2.14	0.49
1:U:164:LEU:HD22	1:U:169:ASP:CG	2.32	0.49
1:U:46:SER:N	1:U:48:TYR:HE2	1.99	0.49
1:V:434:THR:HA	1:V:437:GLN:HG2	1.93	0.49
1:N:82:PRO:CD	1:V:560:LEU:HD13	2.27	0.49
1:W:443:ASP:C	1:W:446:THR:HG22	2.32	0.49
2:Y:104:TYR:HB2	2:Y:106:LEU:HD12	1.93	0.49
1:N:405:LEU:O	1:N:409:THR:HG23	2.11	0.49
1:J:248:LYS:HD3	1:J:251:ILE:HB	1.93	0.49
1:J:510:ILE:O	1:J:513:ARG:HD2	2.12	0.49
1:I:510:ILE:O	1:I:513:ARG:HD2	2.12	0.49
1:C:246:TYR:HE2	1:C:512:GLY:N	2.10	0.49
1:I:280:ILE:HG22	1:I:287:LEU:HD13	1.94	0.49
1:H:280:ILE:HG22	1:H:287:LEU:HD13	1.94	0.49
1:M:573:ASN:O	1:M:577:ILE:HG13	2.12	0.49
1:L:584:PRO:CG	1:L:593:LEU:HD12	2.42	0.49
1:J:584:PRO:CG	1:J:593:LEU:HD12	2.42	0.49
1:D:584:PRO:HG2	1:D:593:LEU:HD12	1.94	0.49
1:A:586:THR:N	1:A:587:PRO:CD	2.75	0.49
1:C:584:PRO:CG	1:C:593:LEU:HD12	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:584:PRO:HG2	1:E:593:LEU:HD12	1.94	0.49
1:W:586:THR:N	1:W:587:PRO:CD	2.75	0.49
1:T:40:GLN:HG2	1:W:310:VAL:HG22	1.93	0.49
1:P:95:MSE:HE1	1:P:99:ARG:NH2	2.26	0.49
1:W:66:LYS:HZ3	1:W:420:VAL:HG11	1.77	0.49
1:Q:387:GLN:CB	1:R:390:ALA:CB	2.90	0.49
1:B:427:GLY:C	1:B:429:GLN:H	2.15	0.49
1:I:255:ILE:O	1:I:257:ASP:N	2.45	0.49
1:L:418:LEU:HB2	1:L:428:GLY:O	2.12	0.49
1:H:578:GLN:HG2	1:H:596:ALA:HB2	1.94	0.49
2:Y:38:GLU:N	2:Y:39:PRO:HD3	2.26	0.49
1:A:409:THR:O	1:A:413:LYS:HG2	2.12	0.49
1:B:126:TRP:CD1	1:B:146:ARG:HG3	2.46	0.49
1:C:328:ARG:HB3	2:Z:142:PRO:HG3	1.94	0.49
1:D:119:ILE:HA	1:D:432:PHE:HE2	1.78	0.49
1:G:119:ILE:HA	1:G:432:PHE:HE2	1.77	0.49
1:K:37:ARG:HH22	1:K:45:LEU:CD1	2.24	0.49
1:L:160:SER:HB3	1:L:171:ARG:NH2	2.27	0.49
1:N:443:ASP:C	1:N:446:THR:HG22	2.33	0.49
1:Q:93:VAL:CG1	1:Q:458:ARG:HG3	2.38	0.49
1:S:78:VAL:CG1	1:S:79:LEU:N	2.74	0.49
1:J:535:ILE:HD11	1:J:554:LEU:HG	1.94	0.49
1:G:280:ILE:HG22	1:G:287:LEU:HD13	1.94	0.49
1:X:235:TYR:HA	1:X:265:LYS:HB3	1.94	0.49
1:G:584:PRO:CG	1:G:593:LEU:HD12	2.42	0.49
1:B:584:PRO:CG	1:B:593:LEU:HD12	2.42	0.49
1:H:586:THR:N	1:H:587:PRO:CD	2.75	0.49
1:H:584:PRO:CG	1:H:593:LEU:HD12	2.42	0.49
1:K:535:ILE:HD11	1:K:554:LEU:HG	1.94	0.49
1:L:386:THR:O	1:L:387:GLN:O	2.31	0.49
1:X:95:MSE:HE1	1:X:99:ARG:CZ	2.42	0.49
1:D:427:GLY:C	1:D:429:GLN:H	2.14	0.49
1:C:456:ALA:HB1	1:C:509:ASP:OD2	2.13	0.49
1:X:58:ASP:HA	1:X:327:GLN:NE2	2.27	0.49
1:L:359:PHE:HD1	2:Z:129:ILE:HD11	1.76	0.49
1:A:255:ILE:O	1:A:257:ASP:N	2.45	0.49
1:A:456:ALA:HB1	1:A:509:ASP:OD2	2.13	0.49
1:A:560:LEU:O	1:A:565:VAL:HG21	2.11	0.49
1:B:119:ILE:HA	1:B:432:PHE:HE2	1.77	0.49
1:C:34:PHE:O	1:C:34:PHE:CG	2.66	0.49
1:E:101:ASP:HB3	1:E:138:THR:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:SER:N	1:E:137:PRO:HD3	2.27	0.49
1:G:101:ASP:HB3	1:G:138:THR:HG21	1.93	0.49
1:G:47:GLN:HG3	1:G:54:ARG:NH1	2.28	0.49
1:H:128:LEU:HD12	1:H:446:THR:HG23	1.94	0.49
1:I:34:PHE:HZ	1:I:328:ARG:HH22	0.80	0.49
1:J:113:ILE:HD12	1:J:148:PRO:HB3	1.94	0.49
1:J:427:GLY:C	1:J:429:GLN:H	2.15	0.49
1:K:44:TRP:CE2	1:K:54:ARG:HB3	2.47	0.49
1:L:119:ILE:HA	1:L:432:PHE:HE2	1.77	0.49
1:L:44:TRP:CE2	1:L:54:ARG:HB3	2.48	0.49
1:M:46:SER:N	1:M:48:TYR:HE2	1.98	0.49
1:M:80:TYR:CE1	1:M:448:VAL:HG22	2.48	0.49
1:O:48:TYR:O	1:O:48:TYR:CD2	5.16	0.49
1:O:95:MSE:HB3	1:O:527:MSE:HE1	1.93	0.49
1:K:136:SER:N	1:K:137:PRO:HD3	2.27	0.49
1:U:123:VAL:CG1	1:U:304:PHE:CE1	2.95	0.49
1:V:434:THR:O	1:V:437:GLN:HG2	2.11	0.49
1:Q:409:THR:O	1:Q:413:LYS:HG2	2.12	0.49
1:H:246:TYR:HE2	1:H:512:GLY:N	2.10	0.49
1:H:513:ARG:HD3	1:H:513:ARG:H	1.77	0.49
1:I:246:TYR:HE2	1:I:512:GLY:N	2.10	0.49
1:B:280:ILE:HG22	1:B:287:LEU:HD13	1.94	0.49
1:H:198:ILE:O	1:H:198:ILE:HG22	2.12	0.49
1:J:280:ILE:HG22	1:J:287:LEU:HD13	1.94	0.49
1:K:280:ILE:HG22	1:K:287:LEU:HD13	1.95	0.49
1:M:266:ILE:HG23	1:M:267:ALA:N	2.27	0.49
1:P:235:TYR:HA	1:P:265:LYS:HB3	1.95	0.49
1:P:266:ILE:HG23	1:P:267:ALA:N	2.27	0.49
1:G:535:ILE:HD11	1:G:554:LEU:HG	1.94	0.49
1:J:584:PRO:HG2	1:J:593:LEU:HD12	1.94	0.49
1:O:384:LEU:HD22	1:O:384:LEU:N	2.27	0.49
1:O:586:THR:N	1:O:587:PRO:CD	2.75	0.49
1:V:586:THR:N	1:V:587:PRO:CD	2.76	0.49
1:K:386:THR:O	1:K:387:GLN:O	2.31	0.49
1:D:386:THR:O	1:D:387:GLN:O	2.31	0.49
1:Q:379:GLU:O	1:Q:380:ASN:CB	2.60	0.49
1:V:95:MSE:HE1	1:V:99:ARG:CZ	2.42	0.49
1:X:95:MSE:HE1	1:X:99:ARG:NH2	2.28	0.49
1:J:456:ALA:HB1	1:J:509:ASP:OD2	2.13	0.49
1:D:456:ALA:HB1	1:D:509:ASP:OD2	2.13	0.49
1:K:456:ALA:HB1	1:K:509:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:63:VAL:HG21	1:L:416:ALA:HB1	1.93	0.49
1:E:451:ASP:O	1:E:456:ALA:N	2.41	0.49
1:J:578:GLN:HG2	1:J:596:ALA:HB2	1.94	0.49
1:F:456:ALA:HB1	1:F:509:ASP:OD2	2.13	0.49
1:R:191:TYR:HE1	1:R:278:LYS:HZ3	1.60	0.49
1:G:456:ALA:HB1	1:G:509:ASP:OD2	2.13	0.49
1:B:34:PHE:O	1:B:34:PHE:CG	2.66	0.49
1:C:160:SER:HB3	1:C:171:ARG:NH2	2.27	0.49
1:F:37:ARG:HH22	1:F:45:LEU:CD1	2.24	0.49
1:J:44:TRP:CE2	1:J:54:ARG:HB3	2.47	0.49
1:J:334:MSE:HE3	1:K:404:MSE:HE3	1.94	0.49
1:M:443:ASP:C	1:M:446:THR:HG22	2.32	0.49
1:O:443:ASP:C	1:O:444:LEU:HD13	2.32	0.49
1:P:456:ALA:O	1:P:457:MSE:HB2	2.11	0.49
1:P:48:TYR:O	1:P:48:TYR:CD2	5.17	0.49
1:R:48:TYR:HD2	1:R:48:TYR:O	5.13	0.49
1:W:101:ASP:HB2	1:W:144:ILE:O	2.11	0.49
1:S:407:ALA:HB1	1:U:334:MSE:HE1	1.94	0.49
1:T:48:TYR:O	1:T:48:TYR:CD2	5.17	0.49
1:I:251:ILE:O	1:I:507:LEU:HD13	2.11	0.49
1:F:513:ARG:H	1:F:513:ARG:HD3	1.76	0.49
1:A:198:ILE:O	1:A:198:ILE:HG22	2.12	0.49
1:C:198:ILE:HG22	1:C:198:ILE:O	2.12	0.49
1:Q:235:TYR:HA	1:Q:265:LYS:HB3	1.94	0.49
1:F:535:ILE:HD11	1:F:554:LEU:HG	1.94	0.49
1:Q:586:THR:N	1:Q:587:PRO:CD	2.76	0.49
1:S:586:THR:N	1:S:587:PRO:CD	2.76	0.49
1:A:113:ILE:HD12	1:A:148:PRO:HB3	1.94	0.49
1:P:586:THR:N	1:P:587:PRO:CD	2.76	0.49
1:V:386:THR:O	1:V:387:GLN:C	2.51	0.49
1:O:379:GLU:O	1:O:380:ASN:CB	2.60	0.49
1:M:390:ALA:HB2	1:N:387:GLN:HB2	1.95	0.49
1:J:418:LEU:HB2	1:J:428:GLY:O	2.12	0.49
1:J:255:ILE:O	1:J:257:ASP:N	2.45	0.49
1:D:348:LYS:HB2	1:E:372:TYR:CE2	2.47	0.49
1:D:255:ILE:O	1:D:257:ASP:N	2.45	0.49
1:B:418:LEU:HB2	1:B:428:GLY:O	2.12	0.49
1:B:136:SER:N	1:B:137:PRO:HD3	2.27	0.49
1:C:44:TRP:CE2	1:C:54:ARG:HB3	2.47	0.49
1:C:560:LEU:O	1:C:565:VAL:HG21	2.11	0.49
1:E:44:TRP:CE2	1:E:54:ARG:HB3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:528:LYS:HZ3	1:E:560:LEU:HD21	1.77	0.49
1:F:34:PHE:O	1:F:34:PHE:CG	2.65	0.49
1:I:119:ILE:HA	1:I:432:PHE:HE2	1.77	0.49
1:I:37:ARG:HH21	1:I:37:ARG:CB	2.16	0.49
1:I:47:GLN:HG3	1:I:54:ARG:NH1	2.28	0.49
1:L:47:GLN:HG3	1:L:54:ARG:NH1	2.28	0.49
1:O:34:PHE:CE2	1:O:45:LEU:HG	2.45	0.49
1:L:80:TYR:CE1	1:L:444:LEU:HB3	2.48	0.49
1:N:48:TYR:HD2	1:N:48:TYR:O	5.13	0.49
1:R:165:MSE:HG3	1:R:307:TRP:CD2	2.47	0.49
1:V:78:VAL:CG1	1:V:79:LEU:N	2.73	0.49
1:X:33:LEU:HD12	1:X:34:PHE:N	2.28	0.49
1:O:405:LEU:O	1:O:409:THR:HG23	2.12	0.49
1:B:535:ILE:HD11	1:B:554:LEU:HG	1.94	0.49
1:B:236:GLN:CB	1:B:265:LYS:HG2	2.37	0.49
1:I:226:VAL:O	1:I:274:ARG:HA	2.13	0.49
1:P:418:LEU:HB2	1:P:428:GLY:O	2.13	0.49
1:A:584:PRO:CG	1:A:593:LEU:HD12	2.42	0.49
1:G:113:ILE:HD12	1:G:148:PRO:HB3	1.94	0.49
1:Q:95:MSE:HB3	1:Q:527:MSE:HE1	1.93	0.49
1:E:386:THR:O	1:E:387:GLN:O	2.31	0.49
1:M:95:MSE:HE1	1:M:99:ARG:NH2	2.28	0.49
1:E:255:ILE:O	1:E:257:ASP:N	2.45	0.49
1:O:372:TYR:CE2	1:P:348:LYS:HB2	2.47	0.49
1:P:191:TYR:HE1	1:P:278:LYS:HZ3	1.61	0.49
1:D:398:PRO:HB3	1:E:395:PRO:HD2	1.93	0.49
1:D:578:GLN:HG2	1:D:596:ALA:HB2	1.94	0.49
1:B:255:ILE:O	1:B:257:ASP:N	2.45	0.49
1:C:94:LEU:HA	1:C:97:MSE:CE	2.37	0.49
1:E:128:LEU:HD12	1:E:446:THR:HG23	1.94	0.49
1:E:34:PHE:O	1:E:34:PHE:CG	2.66	0.49
1:F:427:GLY:C	1:F:429:GLN:H	2.15	0.49
1:G:80:TYR:CE1	1:G:444:LEU:HB3	2.48	0.49
1:I:44:TRP:CE2	1:I:54:ARG:HB3	2.48	0.49
1:M:24:GLU:C	1:M:26:ARG:N	2.55	0.49
1:O:27:ARG:HB2	1:O:313:LYS:HE3	1.94	0.49
1:O:418:LEU:HB2	1:O:428:GLY:O	2.13	0.49
1:O:95:MSE:HE1	1:O:99:ARG:NH2	2.28	0.49
1:K:561:ASP:HB2	1:L:89:ASP:CA	2.32	0.49
1:Q:123:VAL:HG22	1:Q:316:TYR:CE2	2.48	0.49
1:S:92:ASP:HB3	1:U:561:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:14:ARG:NE	1:X:14:ARG:CA	2.71	0.49
1:U:248:LYS:HG3	1:U:511:ARG:HE	1.78	0.49
1:P:248:LYS:HG3	1:P:511:ARG:HE	1.77	0.49
2:Z:23:LEU:HD23	2:Z:26:LEU:HD11	1.94	0.49
1:G:226:VAL:O	1:G:274:ARG:HA	2.13	0.49
1:B:510:ILE:O	1:B:513:ARG:HD2	2.12	0.49
1:L:510:ILE:O	1:L:513:ARG:HD2	2.12	0.49
1:J:198:ILE:O	1:J:198:ILE:HG22	2.12	0.49
1:V:235:TYR:HA	1:V:265:LYS:HB3	1.93	0.49
1:R:586:THR:N	1:R:587:PRO:CD	2.76	0.49
1:P:379:GLU:O	1:P:380:ASN:CB	2.60	0.49
1:N:95:MSE:HE1	1:N:99:ARG:NH2	2.27	0.49
1:R:379:GLU:O	1:R:380:ASN:CB	2.61	0.49
1:S:430:VAL:HG11	3:U:719:HOH:O	2.10	0.49
1:E:456:ALA:HB1	1:E:509:ASP:OD2	2.13	0.49
1:I:578:GLN:HG2	1:I:596:ALA:HB2	1.94	0.49
1:H:255:ILE:O	1:H:257:ASP:N	2.45	0.49
1:T:351:PHE:CD2	1:T:356:ILE:HD12	2.47	0.49
1:F:80:TYR:CE1	1:F:444:LEU:HB3	2.48	0.49
1:G:136:SER:N	1:G:137:PRO:HD3	2.27	0.49
1:H:47:GLN:HG3	1:H:54:ARG:NH1	2.28	0.49
1:I:409:THR:O	1:I:413:LYS:HG2	2.12	0.49
1:I:80:TYR:CE1	1:I:444:LEU:HB3	2.48	0.49
1:J:80:TYR:CE1	1:J:444:LEU:HB3	2.47	0.49
1:K:119:ILE:HA	1:K:432:PHE:HE2	1.78	0.49
1:K:48:TYR:HD2	1:K:48:TYR:O	4.89	0.49
1:P:37:ARG:HH21	1:P:37:ARG:CB	2.26	0.49
1:T:37:ARG:C	1:T:39:SER:N	2.66	0.49
1:U:9:GLU:HG3	1:U:12:LEU:H	1.78	0.49
1:T:451:ASP:C	1:T:453:LEU:H	2.15	0.49
1:C:15:PHE:CE2	1:C:19:TRP:NE1	2.81	0.49
1:E:246:TYR:HE2	1:E:512:GLY:N	2.10	0.49
1:L:226:VAL:O	1:L:274:ARG:HA	2.13	0.49
1:C:577:ILE:HG12	1:C:582:LYS:CG	2.41	0.49
1:G:577:ILE:HG12	1:G:582:LYS:CG	2.41	0.49
1:O:535:ILE:HD13	1:O:554:LEU:HG	1.95	0.49
1:R:66:LYS:HZ3	1:R:420:VAL:HG21	1.77	0.49
1:K:584:PRO:CG	1:K:593:LEU:HD12	2.42	0.49
3:H:719:HOH:O	1:I:438:LEU:HD22	2.12	0.49
1:D:113:ILE:HD12	1:D:148:PRO:HB3	1.94	0.49
1:W:9:GLU:HG3	1:W:12:LEU:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:535:ILE:HD13	1:V:554:LEU:HG	1.94	0.49
1:F:386:THR:O	1:F:387:GLN:O	2.31	0.49
1:I:386:THR:O	1:I:387:GLN:O	2.31	0.49
1:V:598:GLN:HB2	1:V:601:GLN:HB3	1.94	0.49
3:R:719:HOH:O	1:X:430:VAL:HG11	2.13	0.49
1:W:427:GLY:C	1:W:429:GLN:H	2.14	0.49
1:V:55:GLY:HA3	1:V:57:PHE:CE1	2.48	0.49
1:M:171:ARG:O	1:M:224:GLU:HA	2.13	0.49
1:B:80:TYR:CE1	1:B:444:LEU:HB3	2.48	0.49
1:C:47:GLN:HG3	1:C:54:ARG:NH1	2.28	0.49
1:E:15:PHE:CE2	1:E:19:TRP:NE1	2.81	0.49
1:H:80:TYR:CE1	1:H:444:LEU:HB3	2.47	0.49
1:I:34:PHE:CG	1:I:34:PHE:O	2.66	0.49
1:J:47:GLN:HG3	1:J:54:ARG:NH1	2.28	0.49
1:K:80:TYR:CE1	1:K:444:LEU:HB3	2.48	0.49
1:K:48:TYR:O	1:K:48:TYR:CD2	5.23	0.49
1:M:44:TRP:C	1:M:45:LEU:HD22	2.33	0.49
1:P:443:ASP:C	1:P:446:THR:HG22	2.33	0.49
1:Q:27:ARG:HB2	1:Q:313:LYS:HE3	1.94	0.49
1:T:443:ASP:C	1:T:446:THR:HG22	2.34	0.49
1:S:405:LEU:O	1:S:409:THR:HG23	2.12	0.49
1:J:513:ARG:H	1:J:513:ARG:HD3	1.77	0.49
1:K:248:LYS:HD3	1:K:251:ILE:HB	1.93	0.49
1:G:246:TYR:HE2	1:G:512:GLY:N	2.10	0.49
1:C:15:PHE:HZ	1:C:283:CYS:SG	2.31	0.49
1:C:510:ILE:O	1:C:513:ARG:HD2	2.12	0.49
1:F:510:ILE:O	1:F:513:ARG:HD2	2.12	0.49
1:F:280:ILE:HG22	1:F:287:LEU:HD13	1.94	0.49
1:L:198:ILE:O	1:L:198:ILE:HG22	2.12	0.49
1:M:554:LEU:HD21	1:N:564:GLY:CA	2.38	0.49
1:X:266:ILE:HG23	1:X:267:ALA:N	2.26	0.49
1:K:334:MSE:SE	1:L:404:MSE:HE1	2.62	0.49
1:H:113:ILE:HD12	1:H:148:PRO:HB3	1.94	0.49
1:T:586:THR:N	1:T:587:PRO:CD	2.75	0.49
1:H:386:THR:O	1:H:387:GLN:O	2.31	0.49
1:B:386:THR:O	1:B:387:GLN:O	2.31	0.49
1:F:578:GLN:HG2	1:F:596:ALA:HB2	1.94	0.49
1:B:456:ALA:HB1	1:B:509:ASP:OD2	2.13	0.49
1:L:578:GLN:HG2	1:L:596:ALA:HB2	1.94	0.49
1:C:578:GLN:HG2	1:C:596:ALA:HB2	1.94	0.49
1:W:71:MSE:HE2	1:W:119:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:GLN:HG3	1:D:54:ARG:NH1	2.28	0.49
1:F:136:SER:N	1:F:137:PRO:HD3	2.27	0.49
1:H:136:SER:N	1:H:137:PRO:HD3	2.27	0.49
1:M:78:VAL:CG1	1:M:79:LEU:N	2.75	0.49
1:P:443:ASP:C	1:P:444:LEU:HD13	2.34	0.49
1:Q:443:ASP:C	1:Q:446:THR:HG22	2.34	0.49
1:R:164:LEU:HA	1:R:307:TRP:HH2	1.78	0.49
1:R:78:VAL:CG1	1:R:444:LEU:HG	2.43	0.49
1:V:31:ASN:O	1:V:34:PHE:HB3	2.12	0.49
1:V:456:ALA:O	1:V:457:MSE:HB2	2.13	0.49
1:N:14:ARG:CA	1:N:14:ARG:NE	2.70	0.49
1:B:14:ARG:CA	1:B:14:ARG:NE	2.67	0.49
1:S:413:LYS:HA	1:S:416:ALA:HB3	1.94	0.49
1:E:510:ILE:O	1:E:513:ARG:HD2	2.12	0.49
1:S:535:ILE:HD13	1:S:554:LEU:HG	1.95	0.49
1:P:535:ILE:HD13	1:P:554:LEU:HG	1.95	0.49
1:N:235:TYR:OH	1:N:252:LYS:NZ	2.45	0.49
1:Q:95:MSE:HE1	1:Q:99:ARG:NH2	2.28	0.49
1:T:386:THR:O	1:T:387:GLN:C	2.51	0.49
1:R:387:GLN:HB2	1:X:390:ALA:HB2	1.94	0.49
1:O:55:GLY:HA3	1:O:57:PHE:CE1	2.48	0.49
1:H:456:ALA:HB1	1:H:509:ASP:OD2	2.13	0.49
1:G:255:ILE:O	1:G:257:ASP:N	2.45	0.49
1:K:255:ILE:O	1:K:257:ASP:N	2.45	0.49
1:A:34:PHE:CG	1:A:34:PHE:O	2.66	0.48
1:C:329:LEU:HD22	2:Z:142:PRO:HG2	1.94	0.48
1:C:80:TYR:CE1	1:C:444:LEU:HB3	2.48	0.48
1:E:47:GLN:HG3	1:E:54:ARG:NH1	2.28	0.48
1:F:44:TRP:CE2	1:F:54:ARG:HB3	2.47	0.48
1:G:142:GLN:O	1:G:143:VAL:HG23	2.13	0.48
1:G:15:PHE:CE2	1:G:19:TRP:NE1	2.81	0.48
1:G:57:PHE:CD2	1:G:330:ARG:CB	2.95	0.48
1:I:15:PHE:CE2	1:I:19:TRP:NE1	2.81	0.48
1:L:15:PHE:CE2	1:L:19:TRP:NE1	2.81	0.48
1:M:31:ASN:O	1:M:34:PHE:HB3	2.12	0.48
1:M:35:PHE:C	1:M:37:ARG:H	2.16	0.48
1:N:343:ARG:O	1:N:344:THR:HB	2.13	0.48
1:P:434:THR:O	1:P:437:GLN:HG2	2.12	0.48
1:R:444:LEU:C	1:R:446:THR:H	2.15	0.48
1:W:37:ARG:C	1:W:39:SER:N	2.67	0.48
1:T:48:TYR:O	1:T:48:TYR:HD2	5.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:226:VAL:O	1:K:274:ARG:HA	2.13	0.48
1:G:248:LYS:HD3	1:G:251:ILE:HB	1.93	0.48
1:C:226:VAL:O	1:C:274:ARG:HA	2.13	0.48
1:F:236:GLN:HE21	1:F:265:LYS:HZ3	1.61	0.48
1:Q:235:TYR:OH	1:Q:252:LYS:NZ	2.46	0.48
1:M:235:TYR:OH	1:M:252:LYS:NZ	2.45	0.48
1:X:456:ALA:O	1:X:457:MSE:HB2	2.12	0.48
1:V:573:ASN:O	1:V:577:ILE:HG13	2.13	0.48
1:I:584:PRO:CG	1:I:593:LEU:HD12	2.42	0.48
1:N:384:LEU:N	1:N:384:LEU:HD22	2.28	0.48
1:X:586:THR:N	1:X:587:PRO:CD	2.76	0.48
1:X:293:ILE:HD13	1:X:294:ALA:N	2.28	0.48
1:V:379:GLU:O	1:V:380:ASN:CB	2.61	0.48
1:T:598:GLN:HB2	1:T:601:GLN:HB3	1.95	0.48
1:W:598:GLN:HB2	1:W:601:GLN:HB3	1.95	0.48
1:S:598:GLN:HB2	1:S:601:GLN:HB3	1.95	0.48
1:W:95:MSE:HE1	1:W:99:ARG:CZ	2.43	0.48
1:A:578:GLN:HG2	1:A:596:ALA:HB2	1.94	0.48
1:I:456:ALA:HB1	1:I:509:ASP:OD2	2.13	0.48
1:A:15:PHE:CE2	1:A:19:TRP:NE1	2.81	0.48
1:E:11:ILE:O	1:E:15:PHE:HB2	2.13	0.48
1:G:34:PHE:CG	1:G:34:PHE:O	2.66	0.48
1:H:44:TRP:CE2	1:H:54:ARG:HB3	2.47	0.48
1:J:34:PHE:CG	1:J:34:PHE:O	2.65	0.48
1:K:142:GLN:O	1:K:143:VAL:HG23	2.13	0.48
1:K:47:GLN:HG3	1:K:54:ARG:NH1	2.28	0.48
1:M:164:LEU:HD22	1:M:169:ASP:CG	2.33	0.48
1:M:212:LEU:HD22	1:O:26:ARG:HG2	1.95	0.48
1:O:325:ASP:O	1:O:329:LEU:HD23	2.12	0.48
1:U:560:LEU:O	1:U:561:ASP:O	2.32	0.48
1:X:164:LEU:HA	1:X:307:TRP:CH2	2.48	0.48
1:M:9:GLU:HG3	1:M:12:LEU:H	1.77	0.48
1:T:561:ASP:CB	1:W:89:ASP:HA	2.38	0.48
1:W:405:LEU:O	1:W:409:THR:HG23	2.13	0.48
1:C:11:ILE:O	1:C:15:PHE:HB2	2.13	0.48
1:I:567:MSE:HE2	1:J:554:LEU:HD22	1.94	0.48
1:B:198:ILE:HG22	1:B:198:ILE:O	2.12	0.48
1:F:376:ARG:HB2	1:G:352:TRP:CG	2.48	0.48
1:E:584:PRO:CG	1:E:593:LEU:HD12	2.42	0.48
1:U:586:THR:N	1:U:587:PRO:CD	2.76	0.48
1:V:293:ILE:HD13	1:V:294:ALA:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:386:THR:O	1:J:387:GLN:O	2.31	0.48
1:U:378:ASP:O	1:U:381:SER:O	2.31	0.48
1:N:95:MSE:HE1	1:N:99:ARG:CZ	2.44	0.48
1:R:387:GLN:CB	1:X:390:ALA:CB	2.91	0.48
1:N:429:GLN:HG2	1:N:429:GLN:O	2.13	0.48
1:S:398:PRO:HB3	1:U:395:PRO:HD2	1.95	0.48
1:U:322:LEU:N	1:U:322:LEU:HD22	2.29	0.48
2:Z:89:VAL:C	2:Z:91:ALA:H	2.15	0.48
1:D:198:ILE:O	1:D:198:ILE:HG22	2.12	0.48
1:F:255:ILE:O	1:F:257:ASP:N	2.45	0.48
1:A:119:ILE:HA	1:A:432:PHE:HE2	1.77	0.48
1:B:128:LEU:HD12	1:B:446:THR:HG23	1.94	0.48
1:B:11:ILE:O	1:B:15:PHE:HB2	2.13	0.48
1:D:72:ARG:HD2	1:F:434:THR:HG21	1.96	0.48
1:D:89:ASP:HA	1:E:561:ASP:CB	2.36	0.48
1:F:47:GLN:HG3	1:F:54:ARG:NH1	2.28	0.48
1:G:128:LEU:HD12	1:G:446:THR:HG23	1.94	0.48
1:F:72:ARG:HD2	1:G:434:THR:HG21	1.95	0.48
1:K:94:LEU:HA	1:K:97:MSE:CE	2.37	0.48
1:M:164:LEU:HA	1:M:307:TRP:CH2	2.48	0.48
1:O:443:ASP:C	1:O:446:THR:HG22	2.34	0.48
1:N:123:VAL:CG1	1:N:304:PHE:CE1	2.96	0.48
1:N:27:ARG:HH21	1:V:41:TRP:HE1	1.61	0.48
1:P:123:VAL:HG22	1:P:316:TYR:CE2	2.48	0.48
1:P:444:LEU:O	1:P:448:VAL:HG23	2.13	0.48
1:S:443:ASP:C	1:S:444:LEU:HD13	2.34	0.48
1:T:164:LEU:HD22	1:T:169:ASP:CG	2.33	0.48
1:U:48:TYR:CD2	1:U:48:TYR:O	5.17	0.48
1:V:37:ARG:HH21	1:V:37:ARG:CB	2.25	0.48
1:W:164:LEU:HA	1:W:307:TRP:HH2	1.79	0.48
1:W:248:LYS:HG3	1:W:511:ARG:HE	1.78	0.48
1:W:158:TRP:N	1:W:158:TRP:HD1	2.07	0.48
1:B:567:MSE:SE	1:C:576:LEU:HD13	2.63	0.48
1:H:248:LYS:CD	1:H:248:LYS:H	2.16	0.48
1:R:451:ASP:C	1:R:453:LEU:H	2.17	0.48
1:W:235:TYR:OH	1:W:252:LYS:NZ	2.45	0.48
1:N:266:ILE:HG23	1:N:267:ALA:N	2.29	0.48
1:U:266:ILE:HG23	1:U:267:ALA:N	2.28	0.48
1:S:266:ILE:HG23	1:S:267:ALA:N	2.28	0.48
1:H:563:LYS:HD3	1:I:557:PHE:CE2	2.48	0.48
1:M:563:LYS:HD3	1:O:557:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:208:VAL:HG12	1:L:210:PRO:HD3	1.95	0.48
1:I:208:VAL:HG12	1:I:210:PRO:HD3	1.95	0.48
1:D:208:VAL:HG12	1:D:210:PRO:HD3	1.96	0.48
1:J:208:VAL:HG12	1:J:210:PRO:HD3	1.96	0.48
1:A:584:PRO:HG2	1:A:593:LEU:HD12	1.94	0.48
1:F:584:PRO:CG	1:F:593:LEU:HD12	2.42	0.48
1:A:386:THR:O	1:A:387:GLN:O	2.31	0.48
1:T:293:ILE:HD13	1:T:294:ALA:N	2.29	0.48
3:Q:719:HOH:O	1:R:430:VAL:HG13	2.12	0.48
1:V:95:MSE:HE1	1:V:99:ARG:NH2	2.29	0.48
1:G:395:PRO:HD2	1:H:398:PRO:HB3	1.94	0.48
1:P:351:PHE:CD2	1:P:356:ILE:HD12	2.48	0.48
1:A:80:TYR:CE1	1:A:444:LEU:HB3	2.47	0.48
1:D:15:PHE:CE2	1:D:19:TRP:NE1	2.81	0.48
1:D:34:PHE:O	1:D:34:PHE:CG	2.66	0.48
1:D:334:MSE:SE	1:D:405:LEU:HD11	2.64	0.48
1:D:80:TYR:CE1	1:D:444:LEU:HB3	2.48	0.48
1:E:119:ILE:HA	1:E:432:PHE:HE2	1.77	0.48
1:F:142:GLN:O	1:F:143:VAL:HG23	2.13	0.48
1:H:15:PHE:CE2	1:H:19:TRP:NE1	2.81	0.48
1:J:119:ILE:HA	1:J:432:PHE:HE2	1.77	0.48
1:J:136:SER:N	1:J:137:PRO:HD3	2.27	0.48
2:Z:28:VAL:HG11	2:Z:96:LEU:C	2.33	0.48
1:L:142:GLN:O	1:L:143:VAL:HG23	2.13	0.48
1:P:47:GLN:H	1:P:48:TYR:HD2	1.61	0.48
1:S:41:TRP:HE1	1:T:27:ARG:HH21	1.62	0.48
1:U:434:THR:HG23	1:U:435:VAL:N	2.28	0.48
1:V:66:LYS:HZ3	1:V:420:VAL:HG21	1.77	0.48
1:B:226:VAL:O	1:B:274:ARG:HA	2.13	0.48
1:F:198:ILE:O	1:F:198:ILE:HG22	2.12	0.48
1:I:198:ILE:HG22	1:I:198:ILE:O	2.12	0.48
1:C:280:ILE:HG22	1:C:287:LEU:HD13	1.94	0.48
1:K:584:PRO:HG2	1:K:593:LEU:HD12	1.94	0.48
1:T:418:LEU:HB2	1:T:428:GLY:O	2.13	0.48
1:U:407:ALA:HB1	1:X:334:MSE:HE1	1.96	0.48
1:M:586:THR:N	1:M:587:PRO:CD	2.76	0.48
1:O:293:ILE:HD13	1:O:294:ALA:N	2.28	0.48
1:T:379:GLU:O	1:T:380:ASN:CB	2.60	0.48
1:Q:95:MSE:HE1	1:Q:99:ARG:CZ	2.43	0.48
1:K:191:TYR:HE1	1:K:278:LYS:HZ3	1.60	0.48
1:R:387:GLN:CB	1:X:390:ALA:HB2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:322:LEU:N	1:O:322:LEU:HD22	2.28	0.48
1:B:47:GLN:HG3	1:B:54:ARG:NH1	2.28	0.48
1:D:44:TRP:CE2	1:D:54:ARG:HB3	2.48	0.48
1:D:434:THR:HG21	1:E:72:ARG:HD2	1.96	0.48
1:G:334:MSE:SE	1:G:405:LEU:HD11	2.64	0.48
1:I:128:LEU:HD12	1:I:446:THR:HG23	1.94	0.48
1:K:15:PHE:CE2	1:K:19:TRP:NE1	2.81	0.48
1:M:37:ARG:C	1:M:39:SER:N	2.67	0.48
1:O:37:ARG:CB	1:O:37:ARG:HH21	2.24	0.48
1:P:48:TYR:O	1:P:48:TYR:HD2	5.14	0.48
1:O:561:ASP:HB2	1:P:89:ASP:HA	1.95	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:HH2	1.79	0.48
1:Q:35:PHE:HE1	1:Q:321:ARG:NH1	2.08	0.48
1:Q:37:ARG:C	1:Q:39:SER:H	2.16	0.48
1:S:325:ASP:O	1:S:329:LEU:HD23	2.13	0.48
1:S:444:LEU:O	1:S:446:THR:N	2.46	0.48
1:U:444:LEU:O	1:U:446:THR:N	2.46	0.48
1:V:164:LEU:HA	1:V:307:TRP:CH2	2.49	0.48
1:W:78:VAL:CG1	1:W:79:LEU:H	2.26	0.48
1:X:37:ARG:C	1:X:39:SER:N	2.66	0.48
1:M:248:LYS:HG3	1:M:511:ARG:HE	1.79	0.48
1:O:413:LYS:HA	1:O:416:ALA:HB3	1.95	0.48
1:J:226:VAL:O	1:J:274:ARG:HA	2.13	0.48
1:T:266:ILE:HG23	1:T:267:ALA:N	2.29	0.48
1:D:577:ILE:HG12	1:D:582:LYS:CG	2.41	0.48
1:S:418:LEU:HB2	1:S:428:GLY:O	2.13	0.48
1:J:376:ARG:HB2	1:K:352:TRP:CG	2.48	0.48
1:F:208:VAL:HG12	1:F:210:PRO:HD3	1.95	0.48
1:B:208:VAL:HG12	1:B:210:PRO:HD3	1.95	0.48
1:X:9:GLU:HG3	1:X:12:LEU:H	1.79	0.48
1:J:386:THR:O	1:J:387:GLN:C	2.52	0.48
1:G:386:THR:O	1:G:387:GLN:O	2.31	0.48
1:C:386:THR:CG2	1:C:389:LEU:HD21	2.44	0.48
1:X:379:GLU:O	1:X:380:ASN:CB	2.61	0.48
1:Q:293:ILE:HD13	1:Q:294:ALA:N	2.29	0.48
1:U:95:MSE:HE1	1:U:99:ARG:NH2	2.28	0.48
1:Q:386:THR:O	1:Q:387:GLN:C	2.52	0.48
1:B:343:ARG:NH1	2:Z:135:ALA:O	2.41	0.48
1:B:578:GLN:HG2	1:B:596:ALA:HB2	1.94	0.48
1:A:57:PHE:CD2	1:A:330:ARG:CB	2.95	0.48
1:A:94:LEU:HA	1:A:97:MSE:CE	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:PHE:CE2	1:B:19:TRP:NE1	2.81	0.48
1:E:142:GLN:O	1:E:143:VAL:HG23	2.13	0.48
1:F:334:MSE:SE	1:F:405:LEU:HD11	2.64	0.48
1:H:34:PHE:O	1:H:34:PHE:CG	2.66	0.48
1:K:34:PHE:CG	1:K:34:PHE:O	2.66	0.48
1:L:34:PHE:O	1:L:34:PHE:CG	2.66	0.48
1:P:560:LEU:O	1:P:561:ASP:O	2.32	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:CH2	2.49	0.48
1:Q:82:PRO:O	1:Q:516:CYS:HA	2.13	0.48
1:U:164:LEU:HA	1:U:307:TRP:HH2	1.79	0.48
1:U:48:TYR:O	1:U:48:TYR:HD2	5.14	0.48
1:X:164:LEU:HA	1:X:307:TRP:HH2	1.78	0.48
1:E:139:SER:CB	1:E:455:THR:CG2	2.80	0.48
1:P:71:MSE:CE	1:P:115:VAL:HB	2.44	0.48
1:V:118:GLN:OE1	1:V:303:VAL:HB	2.13	0.48
1:V:413:LYS:HA	1:V:416:ALA:HB3	1.95	0.48
2:Y:23:LEU:HD23	2:Y:26:LEU:HD11	1.94	0.48
1:R:273:ARG:HH22	1:R:453:LEU:CD2	2.27	0.48
1:N:273:ARG:CZ	1:N:275:ARG:HE	2.27	0.48
1:F:227:GLU:HA	1:F:274:ARG:CA	2.44	0.48
1:F:226:VAL:O	1:F:274:ARG:HA	2.13	0.48
1:O:573:ASN:O	1:O:577:ILE:HG13	2.13	0.48
1:H:208:VAL:HG12	1:H:210:PRO:HD3	1.96	0.48
1:F:584:PRO:HG2	1:F:593:LEU:HD12	1.94	0.48
1:K:386:THR:O	1:K:387:GLN:C	2.52	0.48
1:B:386:THR:O	1:B:387:GLN:C	2.52	0.48
1:W:379:GLU:O	1:W:380:ASN:CB	2.61	0.48
1:X:598:GLN:HB2	1:X:601:GLN:HB3	1.95	0.48
1:M:58:ASP:HA	1:M:327:GLN:NE2	2.28	0.48
1:W:418:LEU:HB2	1:W:428:GLY:O	2.13	0.48
1:M:386:THR:O	1:M:387:GLN:C	2.51	0.48
1:E:578:GLN:HG2	1:E:596:ALA:HB2	1.94	0.48
1:C:255:ILE:O	1:C:257:ASP:N	2.45	0.48
1:G:578:GLN:HG2	1:G:596:ALA:HB2	1.94	0.48
1:N:322:LEU:HD22	1:N:322:LEU:H	1.78	0.48
1:Q:351:PHE:CD2	1:Q:356:ILE:HD12	2.49	0.48
1:A:11:ILE:O	1:A:15:PHE:HB2	2.13	0.48
1:C:142:GLN:O	1:C:143:VAL:HG23	2.13	0.48
1:D:11:ILE:O	1:D:15:PHE:HB2	2.13	0.48
1:H:11:ILE:O	1:H:15:PHE:HB2	2.13	0.48
1:H:142:GLN:O	1:H:143:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:334:MSE:SE	1:H:405:LEU:HD11	2.64	0.48
1:I:142:GLN:O	1:I:143:VAL:HG23	2.13	0.48
1:J:15:PHE:CE2	1:J:19:TRP:NE1	2.81	0.48
1:J:334:MSE:SE	1:J:405:LEU:HD11	2.64	0.48
1:B:42:ASP:OD2	2:Z:145:SER:O	2.31	0.48
1:N:443:ASP:C	1:N:444:LEU:HD13	2.34	0.48
1:N:48:TYR:CD2	1:N:48:TYR:O	5.16	0.48
1:Q:48:TYR:HD2	1:Q:48:TYR:O	5.14	0.48
1:R:164:LEU:HA	1:R:307:TRP:CH2	2.48	0.48
1:T:434:THR:HG23	1:T:435:VAL:N	2.28	0.48
1:U:456:ALA:O	1:U:457:MSE:HB2	2.12	0.48
1:X:165:MSE:HE1	1:X:435:VAL:HB	1.95	0.48
1:O:248:LYS:HG3	1:O:511:ARG:HE	1.79	0.48
1:N:158:TRP:HD1	1:N:158:TRP:H	1.62	0.48
1:K:248:LYS:CD	1:K:248:LYS:H	2.16	0.48
1:W:235:TYR:HA	1:W:265:LYS:HB3	1.96	0.48
1:W:266:ILE:HG23	1:W:267:ALA:N	2.28	0.48
1:O:266:ILE:HG23	1:O:267:ALA:N	2.27	0.48
1:R:235:TYR:OH	1:R:252:LYS:NZ	2.46	0.48
1:S:235:TYR:OH	1:S:252:LYS:NZ	2.47	0.48
1:A:577:ILE:HG12	1:A:582:LYS:CG	2.41	0.48
1:H:577:ILE:HG12	1:H:582:LYS:CG	2.41	0.48
1:S:384:LEU:HD22	1:S:384:LEU:N	2.28	0.48
1:E:208:VAL:HG12	1:E:210:PRO:HD3	1.96	0.48
1:C:208:VAL:HG12	1:C:210:PRO:HD3	1.95	0.48
1:K:386:THR:CG2	1:K:389:LEU:HD21	2.44	0.48
1:W:386:THR:O	1:W:387:GLN:C	2.52	0.48
1:P:386:THR:O	1:P:387:GLN:C	2.51	0.48
1:T:387:GLN:HB3	1:W:390:ALA:CB	2.44	0.48
1:N:322:LEU:N	1:N:322:LEU:HD22	2.29	0.48
1:S:322:LEU:HD22	1:S:322:LEU:N	2.28	0.48
1:R:322:LEU:N	1:R:322:LEU:HD22	2.29	0.48
1:U:310:VAL:HG22	1:X:40:GLN:HG2	1.96	0.48
1:R:371:TYR:HE2	1:R:373:LEU:HD21	1.79	0.48
1:A:165:MSE:HG3	1:A:307:TRP:CD2	2.49	0.48
1:A:47:GLN:HG3	1:A:54:ARG:NH1	2.28	0.48
1:C:165:MSE:HG3	1:C:307:TRP:CD2	2.49	0.48
1:F:11:ILE:O	1:F:15:PHE:HB2	2.13	0.48
1:G:11:ILE:O	1:G:15:PHE:HB2	2.13	0.48
1:G:44:TRP:CE2	1:G:54:ARG:HB3	2.48	0.48
1:H:165:MSE:HG3	1:H:307:TRP:CD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:34:PHE:HZ	1:H:328:ARG:HH22	0.80	0.48
1:I:11:ILE:O	1:I:15:PHE:HB2	2.13	0.48
1:I:34:PHE:CE1	1:I:324:LYS:NZ	2.72	0.48
1:P:35:PHE:HE1	1:P:321:ARG:NH1	2.08	0.48
1:Q:37:ARG:C	1:Q:39:SER:N	2.66	0.48
1:S:27:ARG:HB2	1:S:313:LYS:HE3	1.95	0.48
1:S:560:LEU:O	1:S:561:ASP:O	2.31	0.48
1:U:164:LEU:HA	1:U:307:TRP:CH2	2.49	0.48
1:U:329:LEU:HD21	1:X:53:TYR:OH	2.13	0.48
1:V:27:ARG:HB2	1:V:313:LYS:HE3	1.96	0.48
1:V:443:ASP:C	1:V:446:THR:HG22	2.34	0.48
1:V:48:TYR:O	1:V:48:TYR:CD2	5.17	0.48
1:N:89:ASP:CA	1:V:561:ASP:HB2	2.31	0.48
1:W:123:VAL:HG22	1:W:316:TYR:HE2	1.79	0.48
1:G:14:ARG:NE	1:G:14:ARG:CA	2.67	0.48
1:N:9:GLU:HG3	1:N:12:LEU:H	1.77	0.48
1:V:248:LYS:CD	1:V:248:LYS:H	2.18	0.48
1:N:248:LYS:HG3	1:N:511:ARG:HE	1.79	0.48
1:E:227:GLU:HA	1:E:274:ARG:CA	2.44	0.48
1:E:226:VAL:O	1:E:274:ARG:HA	2.13	0.48
1:K:334:MSE:HE3	1:L:404:MSE:CE	2.44	0.48
1:A:376:ARG:HB2	1:B:352:TRP:CG	2.49	0.48
1:V:384:LEU:HD22	1:V:384:LEU:N	2.27	0.48
1:J:386:THR:CG2	1:J:389:LEU:HD21	2.44	0.48
1:D:386:THR:CG2	1:D:389:LEU:HD21	2.44	0.48
1:A:386:THR:CG2	1:A:389:LEU:HD21	2.44	0.48
1:C:386:THR:O	1:C:387:GLN:C	2.52	0.48
1:N:598:GLN:HB2	1:N:601:GLN:HB3	1.96	0.48
1:C:372:TYR:CE2	1:E:348:LYS:HB2	2.49	0.48
1:Q:395:PRO:HD2	1:R:398:PRO:HB3	1.95	0.48
1:K:578:GLN:HG2	1:K:596:ALA:HB2	1.94	0.48
1:B:165:MSE:HG3	1:B:307:TRP:CD2	2.49	0.48
1:E:334:MSE:SE	1:E:405:LEU:HD11	2.64	0.48
1:D:182:ASN:HD22	1:F:171:ARG:HH21	1.62	0.48
1:F:165:MSE:HG3	1:F:307:TRP:CD2	2.49	0.48
1:J:165:MSE:HG3	1:J:307:TRP:CD2	2.49	0.48
1:K:11:ILE:O	1:K:15:PHE:HB2	2.13	0.48
1:K:165:MSE:HG3	1:K:307:TRP:CD2	2.49	0.48
1:M:47:GLN:H	1:M:48:TYR:HD2	1.62	0.48
1:O:123:VAL:HG22	1:O:316:TYR:CE2	2.49	0.48
1:N:123:VAL:HG22	1:N:316:TYR:CE2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:78:VAL:CG1	1:P:79:LEU:H	2.27	0.48
1:Q:443:ASP:C	1:Q:444:LEU:HD13	2.34	0.48
1:S:164:LEU:HD22	1:S:169:ASP:CG	2.34	0.48
1:S:47:GLN:CG	1:S:48:TYR:H	2.27	0.48
1:S:95:MSE:HE1	1:S:99:ARG:NH2	2.29	0.48
1:T:33:LEU:HD12	1:T:34:PHE:N	2.29	0.48
1:W:31:ASN:O	1:W:34:PHE:HB3	2.14	0.48
1:X:78:VAL:CG1	1:X:79:LEU:N	2.77	0.48
1:P:9:GLU:HG3	1:P:12:LEU:H	1.77	0.48
1:T:14:ARG:NE	1:T:14:ARG:CA	2.70	0.48
1:X:248:LYS:HG3	1:X:511:ARG:HE	1.77	0.48
1:S:248:LYS:CD	1:S:248:LYS:H	2.17	0.48
1:S:158:TRP:HD1	1:S:158:TRP:N	2.07	0.48
1:L:227:GLU:HA	1:L:274:ARG:CA	2.44	0.48
1:K:577:ILE:HG12	1:K:582:LYS:CG	2.41	0.48
1:B:334:MSE:SE	1:C:404:MSE:HE1	2.64	0.48
1:T:384:LEU:HD22	1:T:384:LEU:N	2.28	0.48
1:S:293:ILE:HD13	1:S:294:ALA:N	2.28	0.48
1:L:386:THR:CG2	1:L:389:LEU:HD21	2.44	0.48
1:F:386:THR:CG2	1:F:389:LEU:HD21	2.44	0.48
1:B:386:THR:CG2	1:B:389:LEU:HD21	2.44	0.48
1:C:386:THR:O	1:C:387:GLN:O	2.31	0.48
1:T:95:MSE:HE1	1:T:99:ARG:CZ	2.44	0.48
1:O:155:HIS:CE1	1:O:204:PRO:HB2	2.49	0.48
1:U:386:THR:O	1:U:387:GLN:C	2.52	0.48
1:X:127:ARG:HG2	1:X:147:GLU:HB2	1.96	0.48
1:A:334:MSE:SE	1:A:405:LEU:HD11	2.64	0.48
1:C:119:ILE:HA	1:C:432:PHE:HE2	1.77	0.48
1:D:128:LEU:HD12	1:D:446:THR:HG23	1.94	0.48
1:D:40:GLN:O	1:D:41:TRP:CB	2.54	0.48
1:F:128:LEU:HD12	1:F:446:THR:HG23	1.94	0.48
1:F:15:PHE:CE2	1:F:19:TRP:NE1	2.81	0.48
1:J:561:ASP:CB	1:K:89:ASP:HA	2.33	0.48
1:L:136:SER:N	1:L:137:PRO:HD3	2.27	0.48
1:L:101:ASP:HB2	1:L:144:ILE:O	2.14	0.48
1:L:164:LEU:HA	1:L:307:TRP:HH2	1.79	0.48
1:M:329:LEU:HD21	1:N:53:TYR:OH	2.13	0.48
1:N:47:GLN:CG	1:N:48:TYR:H	2.27	0.48
1:P:444:LEU:O	1:P:446:THR:N	2.46	0.48
1:P:82:PRO:O	1:P:516:CYS:HA	2.13	0.48
1:R:37:ARG:C	1:R:39:SER:N	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:38:VAL:HG21	1:T:324:LYS:HD2	1.96	0.48
1:T:165:MSE:HE1	1:T:435:VAL:HB	1.95	0.48
1:U:444:LEU:O	1:U:448:VAL:HG23	2.14	0.48
1:V:48:TYR:O	1:V:48:TYR:HD2	5.14	0.48
1:W:164:LEU:HA	1:W:307:TRP:CH2	2.49	0.48
1:X:444:LEU:O	1:X:446:THR:N	2.47	0.48
1:W:451:ASP:C	1:W:453:LEU:H	2.18	0.48
1:K:227:GLU:HA	1:K:274:ARG:CA	2.44	0.48
1:K:248:LYS:HZ1	1:K:513:ARG:HH12	1.60	0.48
1:D:227:GLU:HA	1:D:274:ARG:CA	2.44	0.48
1:A:234:ILE:HG12	1:A:267:ALA:HB3	1.96	0.48
1:C:227:GLU:HA	1:C:274:ARG:CA	2.44	0.48
1:R:266:ILE:HG23	1:R:267:ALA:N	2.28	0.48
1:M:235:TYR:HA	1:M:265:LYS:HB3	1.94	0.48
1:L:334:MSE:SE	1:L:405:LEU:HD11	2.64	0.48
1:P:238:PRO:HD3	1:P:263:PHE:HB2	1.95	0.48
1:L:386:THR:O	1:L:387:GLN:C	2.52	0.48
1:H:386:THR:CG2	1:H:389:LEU:HD21	2.44	0.48
1:X:386:THR:O	1:X:387:GLN:C	2.52	0.48
1:Q:322:LEU:N	1:Q:322:LEU:HD22	2.29	0.48
1:D:539:LEU:HD21	1:D:551:LEU:HB3	1.96	0.48
1:R:55:GLY:HA3	1:R:57:PHE:CE1	2.48	0.48
1:A:434:THR:HA	1:A:437:GLN:CD	2.35	0.47
1:G:165:MSE:HG3	1:G:307:TRP:CD2	2.49	0.47
1:G:26:ARG:NH2	1:G:30:LYS:HB2	2.28	0.47
1:G:58:ASP:O	1:G:59:VAL:HB	2.14	0.47
1:I:165:MSE:HG3	1:I:307:TRP:CD2	2.49	0.47
1:I:334:MSE:SE	1:I:405:LEU:HD11	2.64	0.47
1:J:142:GLN:O	1:J:143:VAL:HG23	2.13	0.47
1:J:101:ASP:HB2	1:J:144:ILE:O	2.14	0.47
1:M:66:LYS:HZ3	1:M:420:VAL:HG11	1.79	0.47
1:O:14:ARG:NE	1:O:14:ARG:CA	2.71	0.47
1:O:434:THR:HG23	1:O:435:VAL:N	2.28	0.47
1:Q:165:MSE:HG3	1:Q:307:TRP:CD2	2.48	0.47
1:R:9:GLU:HG3	1:R:12:LEU:H	1.78	0.47
1:S:123:VAL:CG1	1:S:304:PHE:CE1	2.97	0.47
1:K:58:ASP:O	1:K:59:VAL:HB	2.14	0.47
1:P:71:MSE:HE3	1:P:115:VAL:HB	1.95	0.47
1:T:248:LYS:HG3	1:T:511:ARG:HE	1.79	0.47
2:Z:75:PRO:HA	2:Z:76:PRO:HD3	1.42	0.47
1:V:330:ARG:HD2	1:V:409:THR:CG2	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:ILE:HG12	1:B:267:ALA:HB3	1.96	0.47
1:D:226:VAL:O	1:D:274:ARG:HA	2.13	0.47
1:H:226:VAL:O	1:H:274:ARG:HA	2.13	0.47
1:A:226:VAL:O	1:A:274:ARG:HA	2.13	0.47
1:F:230:GLU:HG2	1:F:273:ARG:HB2	1.96	0.47
1:L:230:GLU:HG2	1:L:273:ARG:HB2	1.96	0.47
1:B:577:ILE:HG12	1:B:582:LYS:CG	2.41	0.47
1:K:334:MSE:SE	1:K:405:LEU:HD11	2.64	0.47
1:K:208:VAL:HG12	1:K:210:PRO:HD3	1.96	0.47
1:X:86:ALA:CB	1:X:515:GLU:HG3	2.44	0.47
1:Q:387:GLN:HB2	1:R:390:ALA:HB2	1.94	0.47
1:Q:387:GLN:HB3	1:R:390:ALA:CB	2.44	0.47
1:J:539:LEU:HD21	1:J:551:LEU:CB	2.44	0.47
1:L:86:ALA:HB2	1:L:515:GLU:HG3	1.96	0.47
1:S:127:ARG:HG2	1:S:147:GLU:HB2	1.96	0.47
1:L:456:ALA:HB1	1:L:509:ASP:OD2	2.13	0.47
1:L:539:LEU:HD21	1:L:551:LEU:HB3	1.96	0.47
1:H:101:ASP:HB2	1:H:144:ILE:O	2.14	0.47
1:K:101:ASP:HB2	1:K:144:ILE:O	2.14	0.47
1:L:11:ILE:O	1:L:15:PHE:HB2	2.13	0.47
1:M:434:THR:HG23	1:M:435:VAL:N	2.29	0.47
1:O:123:VAL:CG1	1:O:304:PHE:CE1	2.97	0.47
1:P:434:THR:HG23	1:P:435:VAL:N	2.29	0.47
1:S:35:PHE:HZ	1:S:321:ARG:NE	2.11	0.47
1:U:127:ARG:HG2	1:U:147:GLU:HB2	1.96	0.47
1:U:31:ASN:O	1:U:34:PHE:HB3	2.14	0.47
1:X:443:ASP:C	1:X:444:LEU:HD13	2.35	0.47
1:X:444:LEU:O	1:X:448:VAL:HG23	2.13	0.47
1:O:451:ASP:C	1:O:453:LEU:H	2.17	0.47
1:D:230:GLU:HG2	1:D:273:ARG:HB2	1.96	0.47
1:I:227:GLU:HA	1:I:274:ARG:CA	2.44	0.47
1:E:535:ILE:CD1	1:E:554:LEU:HG	2.44	0.47
1:W:27:ARG:HB2	1:W:313:LYS:HE3	1.96	0.47
1:N:573:ASN:O	1:N:577:ILE:HG13	2.14	0.47
1:T:193:LEU:HD22	1:T:287:LEU:HB3	1.96	0.47
1:I:113:ILE:HD12	1:I:148:PRO:HB3	1.94	0.47
1:U:598:GLN:HB2	1:U:601:GLN:HB3	1.95	0.47
1:W:95:MSE:HE1	1:W:99:ARG:NH2	2.29	0.47
1:C:81:ARG:HB2	1:C:517:TYR:CZ	2.50	0.47
1:K:539:LEU:HD21	1:K:551:LEU:HB3	1.96	0.47
1:I:86:ALA:HB2	1:I:515:GLU:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ALA:HB2	1:B:515:GLU:HG3	1.96	0.47
1:A:334:MSE:SE	1:B:404:MSE:HE1	2.64	0.47
1:D:142:GLN:O	1:D:143:VAL:HG23	2.13	0.47
1:H:40:GLN:O	1:H:41:TRP:CB	2.55	0.47
1:I:101:ASP:HB2	1:I:144:ILE:O	2.14	0.47
1:M:27:ARG:HB2	1:M:313:LYS:HE3	1.94	0.47
1:N:78:VAL:CG1	1:N:444:LEU:HG	2.44	0.47
1:Q:35:PHE:HZ	1:Q:321:ARG:NE	2.10	0.47
1:S:95:MSE:HE1	1:S:99:ARG:CZ	2.45	0.47
1:T:325:ASP:O	1:T:329:LEU:HD23	2.14	0.47
1:T:409:THR:O	1:T:413:LYS:HG2	2.15	0.47
1:X:47:GLN:H	1:X:48:TYR:HD2	1.61	0.47
1:K:273:ARG:HH22	1:K:453:LEU:CD1	2.28	0.47
1:B:273:ARG:HH22	1:B:453:LEU:CD1	2.28	0.47
1:S:564:GLY:HA3	1:T:535:ILE:HD11	1.96	0.47
1:A:198:ILE:HA	1:A:199:PRO:HD3	1.64	0.47
1:G:567:MSE:HE2	1:H:554:LEU:HD22	1.96	0.47
1:X:27:ARG:HB2	1:X:313:LYS:HE3	1.95	0.47
1:I:535:ILE:CD1	1:I:554:LEU:HG	2.44	0.47
1:A:535:ILE:CD1	1:A:554:LEU:HG	2.44	0.47
1:X:238:PRO:HD3	1:X:263:PHE:HB2	1.96	0.47
1:N:293:ILE:HD13	1:N:294:ALA:N	2.29	0.47
1:E:386:THR:CG2	1:E:389:LEU:HD21	2.44	0.47
1:U:430:VAL:HG11	3:X:719:HOH:O	2.13	0.47
1:R:378:ASP:O	1:R:381:SER:O	2.33	0.47
1:R:386:THR:O	1:R:387:GLN:C	2.51	0.47
1:K:539:LEU:HD21	1:K:551:LEU:CB	2.44	0.47
1:E:162:SER:HB2	1:E:170:ALA:HB2	1.97	0.47
1:E:86:ALA:HB2	1:E:515:GLU:HG3	1.96	0.47
1:O:227:GLU:O	1:O:227:GLU:CG	2.63	0.47
1:B:35:PHE:HE1	1:B:321:ARG:NH1	2.13	0.47
1:D:164:LEU:HA	1:D:307:TRP:HH2	1.79	0.47
1:E:34:PHE:O	1:E:34:PHE:CD2	2.68	0.47
1:F:434:THR:HA	1:F:437:GLN:CD	2.35	0.47
1:G:101:ASP:HB2	1:G:144:ILE:O	2.14	0.47
1:H:130:THR:HG22	1:H:144:ILE:HA	1.97	0.47
1:H:57:PHE:CD2	1:H:330:ARG:CB	2.95	0.47
1:I:115:VAL:O	1:I:119:ILE:HG13	2.15	0.47
1:J:164:LEU:HA	1:J:307:TRP:HH2	1.79	0.47
1:J:35:PHE:HE2	1:J:324:LYS:NZ	2.08	0.47
1:L:81:ARG:HB2	1:L:517:TYR:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:164:LEU:HA	1:O:307:TRP:CH2	2.50	0.47
1:O:37:ARG:C	1:O:39:SER:N	2.67	0.47
1:L:165:MSE:HG3	1:L:307:TRP:CD2	2.49	0.47
1:N:38:VAL:HG21	1:N:324:LYS:HD2	1.96	0.47
1:P:35:PHE:HZ	1:P:321:ARG:NE	2.11	0.47
1:Q:560:LEU:O	1:Q:561:ASP:O	2.33	0.47
1:V:33:LEU:HD12	1:V:34:PHE:N	2.30	0.47
1:X:123:VAL:CG1	1:X:304:PHE:CE1	2.97	0.47
1:H:58:ASP:O	1:H:59:VAL:HB	2.14	0.47
1:I:58:ASP:O	1:I:59:VAL:HB	2.14	0.47
1:Q:158:TRP:HD1	1:Q:158:TRP:H	1.62	0.47
1:N:118:GLN:OE1	1:N:303:VAL:HB	2.14	0.47
1:U:413:LYS:HA	1:U:416:ALA:HB3	1.96	0.47
1:I:230:GLU:HG2	1:I:273:ARG:HB2	1.96	0.47
1:C:567:MSE:HE2	1:E:554:LEU:HD22	1.95	0.47
1:R:376:ARG:HB2	1:X:352:TRP:CG	2.49	0.47
1:R:563:LYS:HD3	1:X:557:PHE:CE2	2.49	0.47
1:R:418:LEU:HB2	1:R:428:GLY:O	2.14	0.47
1:K:535:ILE:CD1	1:K:554:LEU:HG	2.44	0.47
1:W:293:ILE:HD13	1:W:294:ALA:N	2.29	0.47
1:G:386:THR:O	1:G:387:GLN:C	2.52	0.47
1:I:386:THR:O	1:I:387:GLN:C	2.52	0.47
1:T:95:MSE:HE1	1:T:99:ARG:NH2	2.29	0.47
1:L:451:ASP:O	1:L:456:ALA:N	2.41	0.47
1:K:86:ALA:HB2	1:K:515:GLU:HG3	1.96	0.47
1:S:227:GLU:CG	1:S:227:GLU:O	2.62	0.47
1:O:568:MSE:HG3	1:P:551:LEU:CD2	2.44	0.47
1:E:539:LEU:HD21	1:E:551:LEU:CB	2.45	0.47
1:A:130:THR:HG22	1:A:144:ILE:HA	1.97	0.47
1:B:101:ASP:HB2	1:B:144:ILE:O	2.14	0.47
1:B:434:THR:HA	1:B:437:GLN:CD	2.35	0.47
1:C:101:ASP:HB2	1:C:144:ILE:O	2.14	0.47
1:G:29:ALA:O	1:G:33:LEU:HG	2.15	0.47
1:H:34:PHE:CD2	1:H:34:PHE:O	2.68	0.47
1:M:443:ASP:C	1:M:444:LEU:HD13	2.35	0.47
1:L:434:THR:HA	1:L:437:GLN:CD	2.35	0.47
1:N:444:LEU:O	1:N:446:THR:N	2.48	0.47
1:P:316:TYR:O	1:P:321:ARG:NH1	2.48	0.47
1:Q:34:PHE:O	1:Q:37:ARG:HB2	2.14	0.47
1:Q:78:VAL:CG1	1:Q:444:LEU:HG	2.44	0.47
1:R:434:THR:HG23	1:R:435:VAL:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:443:ASP:C	1:S:446:THR:HG22	2.34	0.47
1:W:325:ASP:O	1:W:329:LEU:HD23	2.13	0.47
1:U:451:ASP:C	1:U:453:LEU:H	2.18	0.47
1:N:235:TYR:HA	1:N:265:LYS:HB3	1.95	0.47
1:F:535:ILE:CD1	1:F:554:LEU:HG	2.44	0.47
1:M:238:PRO:HD3	1:M:263:PHE:HB2	1.97	0.47
1:A:208:VAL:HG12	1:A:210:PRO:HD3	1.96	0.47
1:L:535:ILE:CD1	1:L:554:LEU:HG	2.44	0.47
1:P:86:ALA:CB	1:P:515:GLU:HG3	2.44	0.47
1:N:386:THR:O	1:N:387:GLN:C	2.52	0.47
1:J:81:ARG:HB2	1:J:517:TYR:CZ	2.50	0.47
1:G:81:ARG:HB2	1:G:517:TYR:CZ	2.50	0.47
1:F:81:ARG:HB2	1:F:517:TYR:CZ	2.50	0.47
1:L:539:LEU:HD21	1:L:551:LEU:CB	2.45	0.47
1:H:539:LEU:HD21	1:H:551:LEU:CB	2.44	0.47
1:B:539:LEU:HD21	1:B:551:LEU:HB3	1.96	0.47
1:P:260:ASP:HA	1:P:264:ILE:HB	1.97	0.47
1:Q:260:ASP:HA	1:Q:264:ILE:HB	1.97	0.47
1:F:86:ALA:HB2	1:F:515:GLU:HG3	1.96	0.47
1:A:86:ALA:HB2	1:A:515:GLU:HG3	1.96	0.47
1:A:34:PHE:CD2	1:A:34:PHE:O	2.68	0.47
1:A:42:ASP:OD2	2:Y:145:SER:O	2.32	0.47
1:B:142:GLN:O	1:B:143:VAL:HG23	2.13	0.47
1:B:164:LEU:HA	1:B:307:TRP:HH2	1.80	0.47
1:C:334:MSE:SE	1:C:405:LEU:HD11	2.64	0.47
1:C:434:THR:HA	1:C:437:GLN:CD	2.35	0.47
1:D:58:ASP:O	1:D:59:VAL:HB	2.14	0.47
1:E:165:MSE:HG3	1:E:307:TRP:CD2	2.49	0.47
1:F:130:THR:HG22	1:F:144:ILE:HA	1.97	0.47
1:F:101:ASP:HB2	1:F:144:ILE:O	2.14	0.47
1:F:164:LEU:HA	1:F:307:TRP:HH2	1.80	0.47
1:F:29:ALA:O	1:F:33:LEU:HG	2.15	0.47
1:J:71:MSE:CE	1:J:115:VAL:HB	2.45	0.47
1:J:34:PHE:CD2	1:J:34:PHE:O	2.68	0.47
1:L:35:PHE:HE1	1:L:321:ARG:NH1	2.13	0.47
1:O:44:TRP:C	1:O:45:LEU:HD22	2.35	0.47
1:L:130:THR:HG22	1:L:144:ILE:HA	1.97	0.47
1:N:37:ARG:CB	1:N:37:ARG:HH21	2.28	0.47
1:N:444:LEU:O	1:N:447:TYR:N	2.47	0.47
1:N:444:LEU:O	1:N:448:VAL:HG23	2.14	0.47
1:P:212:LEU:HD22	1:Q:26:ARG:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:164:LEU:HD22	1:R:169:ASP:OD1	2.15	0.47
1:V:434:THR:HG23	1:V:435:VAL:N	2.29	0.47
1:U:14:ARG:CA	1:U:14:ARG:NE	2.70	0.47
1:S:248:LYS:HG3	1:S:511:ARG:HE	1.78	0.47
1:T:405:LEU:O	1:T:409:THR:HG23	2.14	0.47
1:O:330:ARG:HD2	1:O:409:THR:CG2	2.40	0.47
1:X:82:PRO:O	1:X:516:CYS:HA	2.14	0.47
1:P:413:LYS:HA	1:P:416:ALA:HB3	1.97	0.47
1:X:47:GLN:N	1:X:48:TYR:HD2	2.13	0.47
1:J:26:ARG:NH2	1:J:30:LYS:HB2	2.28	0.47
1:Q:451:ASP:C	1:Q:453:LEU:H	2.17	0.47
1:J:230:GLU:HG2	1:J:273:ARG:HB2	1.96	0.47
1:C:197:ASP:O	1:C:198:ILE:HB	2.15	0.47
1:L:197:ASP:O	1:L:198:ILE:HB	2.15	0.47
1:O:235:TYR:HA	1:O:265:LYS:HB3	1.95	0.47
1:P:235:TYR:OH	1:P:252:LYS:NZ	2.48	0.47
1:V:235:TYR:OH	1:V:252:LYS:NZ	2.47	0.47
1:F:563:LYS:HD3	1:G:557:PHE:CE2	2.49	0.47
1:B:334:MSE:SE	1:B:405:LEU:HD11	2.64	0.47
1:S:420:VAL:HA	1:S:428:GLY:HA2	1.96	0.47
1:W:238:PRO:HD3	1:W:263:PHE:HB2	1.96	0.47
1:T:454:ALA:O	1:T:455:THR:C	2.53	0.47
1:P:40:GLN:HG2	1:Q:310:VAL:HG22	1.95	0.47
1:D:386:THR:O	1:D:387:GLN:C	2.52	0.47
1:A:386:THR:O	1:A:387:GLN:C	2.52	0.47
1:H:386:THR:O	1:H:387:GLN:C	2.52	0.47
1:R:598:GLN:HB2	1:R:601:GLN:HB3	1.95	0.47
1:W:171:ARG:O	1:W:224:GLU:HA	2.15	0.47
1:O:260:ASP:HA	1:O:264:ILE:HB	1.97	0.47
1:V:260:ASP:HA	1:V:264:ILE:HB	1.96	0.47
1:R:556:TYR:OH	1:X:542:THR:HG21	2.13	0.47
1:M:371:TYR:HE2	1:M:373:LEU:HD21	1.79	0.47
1:G:539:LEU:HD21	1:G:551:LEU:CB	2.44	0.47
1:D:101:ASP:HB2	1:D:144:ILE:O	2.14	0.47
1:D:29:ALA:O	1:D:33:LEU:HG	2.15	0.47
1:D:57:PHE:CD2	1:D:330:ARG:CB	2.95	0.47
1:G:115:VAL:O	1:G:119:ILE:HG13	2.15	0.47
1:I:130:THR:HG22	1:I:144:ILE:HA	1.97	0.47
1:J:11:ILE:O	1:J:15:PHE:HB2	2.13	0.47
1:K:34:PHE:CD2	1:K:34:PHE:O	2.68	0.47
1:M:418:LEU:HB2	1:M:428:GLY:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:164:LEU:HA	1:O:307:TRP:HH2	1.80	0.47
1:O:31:ASN:O	1:O:34:PHE:HB3	2.14	0.47
1:O:47:GLN:H	1:O:48:TYR:HD2	1.63	0.47
1:C:115:VAL:O	1:C:119:ILE:HG13	2.15	0.47
1:C:57:PHE:CD2	1:C:330:ARG:CB	2.95	0.47
1:E:71:MSE:CE	1:E:115:VAL:HB	2.45	0.47
1:E:115:VAL:O	1:E:119:ILE:HG13	2.15	0.47
1:E:130:THR:HG22	1:E:144:ILE:HA	1.97	0.47
1:F:115:VAL:O	1:F:119:ILE:HG13	2.15	0.47
1:F:34:PHE:CD2	1:F:34:PHE:O	2.68	0.47
1:F:334:MSE:HE3	1:G:404:MSE:HE3	1.96	0.47
1:G:565:VAL:O	1:G:569:ARG:HB3	2.15	0.47
1:J:130:THR:HG22	1:J:144:ILE:HA	1.97	0.47
1:K:130:THR:HG22	1:K:144:ILE:HA	1.97	0.47
1:N:164:LEU:HA	1:N:307:TRP:CH2	2.50	0.47
1:N:27:ARG:HB2	1:N:313:LYS:HE3	1.96	0.47
1:Q:14:ARG:NE	1:Q:14:ARG:CA	2.71	0.47
1:Q:561:ASP:HB2	1:R:89:ASP:CA	2.35	0.47
1:V:29:ALA:O	1:V:33:LEU:HG	2.15	0.47
1:W:528:LYS:CD	1:W:560:LEU:HD21	2.45	0.47
1:N:47:GLN:H	1:N:48:TYR:HD2	1.62	0.47
1:P:136:SER:N	1:P:137:PRO:HD3	2.30	0.47
1:T:123:VAL:HG22	1:T:316:TYR:HE2	1.79	0.47
1:X:31:ASN:O	1:X:34:PHE:HB3	2.15	0.47
1:X:37:ARG:C	1:X:39:SER:H	2.18	0.47
1:X:560:LEU:O	1:X:561:ASP:O	2.33	0.47
1:B:58:ASP:O	1:B:59:VAL:HB	2.14	0.47
1:R:248:LYS:HG3	1:R:511:ARG:HE	1.78	0.47
1:M:248:LYS:CD	1:M:248:LYS:H	2.17	0.47
1:O:158:TRP:HH2	1:O:302:PRO:HG3	1.80	0.47
1:M:451:ASP:C	1:M:453:LEU:H	2.17	0.47
1:W:47:GLN:CG	1:W:48:TYR:H	2.28	0.47
1:G:230:GLU:HG2	1:G:273:ARG:HB2	1.96	0.47
1:B:535:ILE:CD1	1:B:554:LEU:HG	2.44	0.47
1:J:535:ILE:CD1	1:J:554:LEU:HG	2.44	0.47
1:A:273:ARG:HH22	1:A:453:LEU:CD1	2.28	0.47
1:E:230:GLU:HG2	1:E:273:ARG:HB2	1.96	0.47
1:B:197:ASP:O	1:B:198:ILE:HB	2.15	0.47
1:P:554:LEU:O	1:P:557:PHE:HB3	2.14	0.47
1:V:454:ALA:O	1:V:455:THR:C	2.53	0.47
1:F:577:ILE:HG12	1:F:582:LYS:CG	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:573:ASN:O	1:U:577:ILE:HG13	2.13	0.47
1:Q:238:PRO:HD3	1:Q:263:PHE:HB2	1.95	0.47
1:G:208:VAL:HG12	1:G:210:PRO:HD3	1.95	0.47
1:R:238:PRO:HD3	1:R:263:PHE:HB2	1.97	0.47
1:U:66:LYS:HZ3	1:U:420:VAL:HG21	1.79	0.47
1:U:418:LEU:HB2	1:U:428:GLY:O	2.14	0.47
1:K:563:LYS:HD3	1:L:557:PHE:CE2	2.50	0.47
1:W:293:ILE:HG12	1:W:294:ALA:H	1.80	0.47
1:X:155:HIS:CE1	1:X:204:PRO:HB2	2.50	0.47
1:O:386:THR:O	1:O:387:GLN:C	2.52	0.47
1:A:81:ARG:HB2	1:A:517:TYR:CZ	2.50	0.47
1:D:81:ARG:HB2	1:D:517:TYR:CZ	2.50	0.47
1:B:451:ASP:O	1:B:456:ALA:N	2.41	0.47
1:S:322:LEU:H	1:S:322:LEU:HD22	1.79	0.47
1:E:539:LEU:HD21	1:E:551:LEU:HB3	1.96	0.47
1:D:162:SER:HB2	1:D:170:ALA:HB2	1.97	0.47
1:G:86:ALA:HB2	1:G:515:GLU:HG3	1.96	0.47
1:I:162:SER:HB2	1:I:170:ALA:HB2	1.96	0.47
1:X:260:ASP:HA	1:X:264:ILE:HB	1.96	0.47
1:G:162:SER:HB2	1:G:170:ALA:HB2	1.97	0.47
1:V:438:LEU:HD22	3:W:718:HOH:O	2.13	0.47
1:N:348:LYS:HB2	1:V:372:TYR:CE2	2.50	0.47
1:B:162:SER:HB2	1:B:170:ALA:HB2	1.97	0.47
1:A:142:GLN:O	1:A:143:VAL:HG23	2.13	0.47
1:B:130:THR:HG22	1:B:144:ILE:HA	1.97	0.47
1:C:92:ASP:OD2	1:C:92:ASP:N	2.48	0.47
1:D:26:ARG:NH2	1:D:30:LYS:HB2	2.28	0.47
1:H:29:ALA:O	1:H:33:LEU:HG	2.15	0.47
1:I:29:ALA:O	1:I:33:LEU:HG	2.15	0.47
1:I:34:PHE:CD2	1:I:34:PHE:O	2.68	0.47
1:J:565:VAL:O	1:J:569:ARG:HB3	2.15	0.47
1:M:343:ARG:O	1:M:344:THR:HB	2.15	0.47
1:M:47:GLN:CG	1:M:48:TYR:H	2.27	0.47
1:M:66:LYS:HZ3	1:M:420:VAL:HG21	1.78	0.47
1:Q:434:THR:HG23	1:Q:435:VAL:N	2.29	0.47
1:Q:47:GLN:H	1:Q:48:TYR:HD2	1.62	0.47
1:V:47:GLN:N	1:V:48:TYR:HD2	2.13	0.47
1:M:511:ARG:HA	1:M:513:ARG:CD	2.44	0.47
1:M:546:THR:CG2	1:M:547:PRO:HD3	2.31	0.47
1:T:413:LYS:HA	1:T:416:ALA:HB3	1.96	0.47
1:V:273:ARG:CZ	1:V:275:ARG:HE	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:535:ILE:CD1	1:C:554:LEU:HG	2.44	0.47
1:J:234:ILE:HG12	1:J:267:ALA:HB3	1.96	0.47
1:G:234:ILE:HG12	1:G:267:ALA:HB3	1.96	0.47
1:H:273:ARG:HH22	1:H:453:LEU:CD1	2.28	0.47
1:I:273:ARG:HH22	1:I:453:LEU:CD1	2.28	0.47
1:T:554:LEU:O	1:T:557:PHE:HB3	2.15	0.47
1:J:577:ILE:HG12	1:J:582:LYS:CG	2.41	0.47
1:L:207:TRP:O	1:L:208:VAL:C	2.53	0.47
1:C:207:TRP:O	1:C:208:VAL:C	2.54	0.47
1:I:386:THR:CG2	1:I:389:LEU:HD21	2.44	0.47
1:P:293:ILE:HD13	1:P:294:ALA:N	2.30	0.47
1:Q:598:GLN:HB2	1:Q:601:GLN:HB3	1.95	0.47
1:S:386:THR:O	1:S:387:GLN:C	2.52	0.47
1:E:81:ARG:HB2	1:E:517:TYR:CZ	2.50	0.47
1:H:81:ARG:HB2	1:H:517:TYR:CZ	2.50	0.47
1:E:197:ASP:O	1:E:198:ILE:HB	2.15	0.47
1:D:197:ASP:O	1:D:198:ILE:HB	2.15	0.47
1:V:245:SER:HG	1:V:247:PHE:HE1	1.62	0.47
1:T:191:TYR:HE1	1:T:278:LYS:HZ3	1.63	0.47
1:A:101:ASP:HB2	1:A:144:ILE:O	2.14	0.47
1:B:115:VAL:O	1:B:119:ILE:HG13	2.15	0.47
1:D:528:LYS:HZ3	1:D:560:LEU:HD21	1.78	0.47
1:H:164:LEU:HA	1:H:307:TRP:HH2	1.80	0.47
1:K:434:THR:HA	1:K:437:GLN:CD	2.35	0.47
1:L:34:PHE:CD2	1:L:34:PHE:O	2.68	0.47
1:M:38:VAL:HG21	1:M:324:LYS:HD2	1.97	0.47
1:O:9:GLU:HG3	1:O:12:LEU:H	1.78	0.47
1:P:37:ARG:C	1:P:39:SER:N	2.68	0.47
1:Q:444:LEU:O	1:Q:446:THR:N	2.47	0.47
1:S:444:LEU:O	1:S:448:VAL:HG23	2.15	0.47
1:S:528:LYS:CD	1:S:560:LEU:HD21	2.45	0.47
1:T:158:TRP:HH2	1:T:302:PRO:HG3	1.80	0.47
1:U:123:VAL:HG13	1:U:304:PHE:CE1	2.50	0.47
1:U:37:ARG:C	1:U:39:SER:N	2.68	0.47
1:U:78:VAL:CG1	1:U:444:LEU:HG	2.44	0.47
1:M:273:ARG:CZ	1:M:275:ARG:HE	2.27	0.47
1:O:160:SER:O	1:O:161:ASN:ND2	2.44	0.47
1:N:71:MSE:HE3	1:N:115:VAL:HB	1.97	0.47
1:B:248:LYS:HB3	1:B:511:ARG:NH1	2.30	0.47
1:U:273:ARG:CZ	1:U:275:ARG:HE	2.28	0.47
1:A:248:LYS:HZ1	1:A:513:ARG:HH12	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:GLU:HG2	1:C:273:ARG:HB2	1.96	0.47
1:S:554:LEU:O	1:S:557:PHE:HB3	2.14	0.47
1:L:227:GLU:OE2	1:L:227:GLU:N	2.47	0.47
1:H:535:ILE:CD1	1:H:554:LEU:HG	2.44	0.47
1:K:201:PHE:HE2	1:K:281:ILE:HG22	1.80	0.47
1:M:232:ALA:HB2	1:M:269:ARG:O	2.15	0.47
1:D:535:ILE:CD1	1:D:554:LEU:HG	2.44	0.47
1:J:207:TRP:O	1:J:208:VAL:C	2.53	0.47
3:P:719:HOH:O	1:Q:430:VAL:HG13	2.13	0.47
1:R:293:ILE:HG12	1:R:294:ALA:H	1.80	0.47
1:P:155:HIS:CE1	1:P:204:PRO:HB2	2.50	0.47
1:M:598:GLN:HB2	1:M:601:GLN:HB3	1.96	0.47
1:W:66:LYS:HZ3	1:W:420:VAL:HG21	1.80	0.47
1:G:197:ASP:O	1:G:198:ILE:HB	2.15	0.47
1:O:568:MSE:SE	1:P:550:GLN:HB3	2.65	0.47
1:G:539:LEU:HD21	1:G:551:LEU:HB3	1.96	0.47
1:R:171:ARG:O	1:R:224:GLU:HA	2.14	0.47
1:W:322:LEU:HD22	1:W:322:LEU:N	2.30	0.47
1:R:227:GLU:CG	1:R:227:GLU:O	2.63	0.47
1:U:76:ILE:HD12	1:U:433:ASP:OD1	2.15	0.47
1:F:539:LEU:HD21	1:F:551:LEU:CB	2.44	0.47
1:K:162:SER:HB2	1:K:170:ALA:HB2	1.97	0.47
1:C:35:PHE:HE1	1:C:321:ARG:NH1	2.13	0.47
1:D:130:THR:HG22	1:D:144:ILE:HA	1.97	0.47
1:D:165:MSE:HG3	1:D:307:TRP:CD2	2.49	0.47
1:E:434:THR:HA	1:E:437:GLN:CD	2.35	0.47
1:E:57:PHE:CD2	1:E:330:ARG:CB	2.95	0.47
1:F:92:ASP:N	1:F:92:ASP:OD2	2.48	0.47
1:G:434:THR:HA	1:G:437:GLN:CD	2.35	0.47
1:H:434:THR:HA	1:H:437:GLN:CD	2.35	0.47
1:I:164:LEU:HA	1:I:307:TRP:HH2	1.80	0.47
1:I:434:THR:HA	1:I:437:GLN:CD	2.35	0.47
1:J:28:GLU:HG3	1:J:32:ASP:OD2	2.15	0.47
1:J:29:ALA:O	1:J:33:LEU:HG	2.15	0.47
1:K:115:VAL:O	1:K:119:ILE:HG13	2.15	0.47
1:N:78:VAL:CG1	1:N:79:LEU:N	2.75	0.47
1:Q:444:LEU:N	1:Q:444:LEU:HD13	2.30	0.47
1:S:38:VAL:HG21	1:S:324:LYS:HD2	1.97	0.47
1:S:41:TRP:HE1	1:T:27:ARG:NH2	2.13	0.47
1:T:37:ARG:CB	1:T:37:ARG:HH21	2.28	0.47
1:W:343:ARG:O	1:W:344:THR:HB	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:ASP:O	1:E:59:VAL:HB	2.14	0.47
1:W:118:GLN:OE1	1:W:303:VAL:HB	2.14	0.47
1:R:560:LEU:O	1:R:561:ASP:O	2.32	0.47
1:V:409:THR:O	1:V:413:LYS:HG2	2.15	0.47
1:B:227:GLU:OE2	1:B:227:GLU:N	2.47	0.47
1:B:565:VAL:O	1:B:569:ARG:HB3	2.15	0.47
1:A:248:LYS:HB3	1:A:511:ARG:NH1	2.30	0.47
1:E:248:LYS:HB3	1:E:511:ARG:NH1	2.30	0.47
1:F:273:ARG:HH22	1:F:453:LEU:CD1	2.28	0.47
1:A:197:ASP:O	1:A:198:ILE:HB	2.15	0.47
1:H:201:PHE:HE2	1:H:281:ILE:HG22	1.80	0.47
1:U:235:TYR:OH	1:U:252:LYS:NZ	2.48	0.47
1:T:235:TYR:OH	1:T:252:LYS:NZ	2.48	0.47
1:T:266:ILE:O	1:T:267:ALA:HB2	2.16	0.47
1:W:193:LEU:HD22	1:W:287:LEU:HB3	1.97	0.47
1:U:557:PHE:CE2	1:X:563:LYS:HD3	2.49	0.47
1:S:577:ILE:HG12	1:S:582:LYS:CG	2.43	0.47
1:S:238:PRO:HD3	1:S:263:PHE:HB2	1.97	0.47
1:E:207:TRP:O	1:E:208:VAL:C	2.53	0.47
1:U:384:LEU:N	1:U:384:LEU:HD22	2.29	0.47
1:E:386:THR:O	1:E:387:GLN:C	2.52	0.47
1:F:386:THR:O	1:F:387:GLN:C	2.52	0.47
1:R:293:ILE:HD13	1:R:294:ALA:N	2.29	0.47
1:S:86:ALA:CB	1:S:515:GLU:HG3	2.45	0.47
1:D:542:THR:HG21	1:E:556:TYR:OH	2.15	0.47
1:B:81:ARG:HB2	1:B:517:TYR:CZ	2.50	0.47
1:C:451:ASP:O	1:C:456:ALA:N	2.41	0.47
1:F:539:LEU:HD21	1:F:551:LEU:HB3	1.96	0.47
1:M:55:GLY:HA3	1:M:57:PHE:CE1	2.49	0.47
1:C:539:LEU:HD21	1:C:551:LEU:HB3	1.96	0.47
1:Q:245:SER:HG	1:Q:247:PHE:HE1	1.62	0.47
1:X:227:GLU:O	1:X:227:GLU:CG	2.63	0.47
1:J:86:ALA:HB2	1:J:515:GLU:HG3	1.96	0.47
1:A:29:ALA:O	1:A:33:LEU:HG	2.15	0.46
1:B:94:LEU:HA	1:B:97:MSE:CE	2.37	0.46
1:D:71:MSE:CE	1:D:115:VAL:HB	2.45	0.46
1:D:115:VAL:O	1:D:119:ILE:HG13	2.15	0.46
1:D:92:ASP:OD2	1:D:92:ASP:N	2.48	0.46
1:H:92:ASP:N	1:H:92:ASP:OD2	2.48	0.46
1:I:565:VAL:O	1:I:569:ARG:HB3	2.15	0.46
1:J:58:ASP:O	1:J:59:VAL:HB	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:92:ASP:OD2	1:J:92:ASP:N	2.48	0.46
1:M:78:VAL:CG1	1:M:444:LEU:HG	2.45	0.46
1:L:444:LEU:C	1:L:446:THR:H	2.19	0.46
1:N:165:MSE:HG3	1:N:307:TRP:CD2	2.49	0.46
1:P:343:ARG:O	1:P:344:THR:HB	2.14	0.46
1:P:47:GLN:N	1:P:48:TYR:HD2	2.13	0.46
1:R:47:GLN:N	1:R:48:TYR:HD2	2.13	0.46
1:S:78:VAL:CG1	1:S:444:LEU:HG	2.45	0.46
1:U:80:TYR:OH	1:U:444:LEU:HD12	2.15	0.46
1:U:82:PRO:O	1:U:516:CYS:HA	2.15	0.46
1:W:123:VAL:CG1	1:W:304:PHE:CE1	2.98	0.46
1:U:405:LEU:O	1:U:409:THR:HG23	2.15	0.46
1:K:230:GLU:HG2	1:K:273:ARG:HB2	1.96	0.46
1:H:248:LYS:HB3	1:H:511:ARG:NH1	2.30	0.46
1:R:273:ARG:CZ	1:R:275:ARG:HE	2.28	0.46
1:F:197:ASP:O	1:F:198:ILE:HB	2.15	0.46
1:L:201:PHE:HE2	1:L:281:ILE:HG22	1.80	0.46
1:P:27:ARG:HB2	1:P:313:LYS:HE3	1.96	0.46
1:N:198:ILE:HG22	1:N:198:ILE:O	2.15	0.46
1:L:577:ILE:HG12	1:L:582:LYS:CG	2.41	0.46
1:M:198:ILE:HG22	1:M:198:ILE:O	2.14	0.46
1:B:376:ARG:HB2	1:C:352:TRP:CG	2.50	0.46
1:F:207:TRP:O	1:F:208:VAL:C	2.54	0.46
1:G:386:THR:CG2	1:G:389:LEU:HD21	2.44	0.46
1:U:95:MSE:HE1	1:U:99:ARG:CZ	2.44	0.46
1:O:598:GLN:HB2	1:O:601:GLN:HB3	1.95	0.46
1:U:86:ALA:CB	1:U:515:GLU:HG3	2.45	0.46
1:R:343:ARG:O	1:R:344:THR:HB	2.15	0.46
1:H:539:LEU:HD21	1:H:551:LEU:HB3	1.96	0.46
1:N:348:LYS:HE2	1:V:369:TYR:O	2.15	0.46
1:D:86:ALA:HB2	1:D:515:GLU:HG3	1.96	0.46
1:I:539:LEU:HD21	1:I:551:LEU:HB3	1.96	0.46
1:C:395:PRO:HD2	1:E:398:PRO:HB3	1.96	0.46
1:H:86:ALA:HB2	1:H:515:GLU:HG3	1.96	0.46
1:M:260:ASP:HA	1:M:264:ILE:HB	1.98	0.46
1:T:260:ASP:HA	1:T:264:ILE:HB	1.96	0.46
1:D:317:GLU:HB3	1:D:321:ARG:CZ	2.46	0.46
1:D:34:PHE:CD2	1:D:34:PHE:O	2.68	0.46
1:E:444:LEU:C	1:E:446:THR:H	2.19	0.46
1:E:565:VAL:O	1:E:569:ARG:HB3	2.15	0.46
1:G:164:LEU:HA	1:G:307:TRP:HH2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:317:GLU:HB3	1:G:321:ARG:CZ	2.46	0.46
1:G:34:PHE:O	1:G:34:PHE:CD2	2.68	0.46
1:G:413:LYS:HB3	1:G:413:LYS:HE2	1.74	0.46
1:H:565:VAL:O	1:H:569:ARG:HB3	2.15	0.46
1:I:444:LEU:C	1:I:446:THR:H	2.19	0.46
1:J:317:GLU:HB3	1:J:321:ARG:CZ	2.46	0.46
1:K:434:THR:HA	1:K:437:GLN:HG2	1.97	0.46
1:M:560:LEU:O	1:M:561:ASP:O	2.33	0.46
1:N:37:ARG:C	1:N:39:SER:N	2.67	0.46
1:O:560:LEU:O	1:O:561:ASP:O	2.33	0.46
1:R:47:GLN:H	1:R:48:TYR:HD2	1.62	0.46
1:R:82:PRO:O	1:R:516:CYS:HA	2.15	0.46
1:S:37:ARG:C	1:S:39:SER:N	2.68	0.46
1:X:165:MSE:HG3	1:X:307:TRP:CD2	2.49	0.46
1:X:434:THR:HG23	1:X:435:VAL:N	2.30	0.46
1:U:71:MSE:HE3	1:U:115:VAL:HB	1.96	0.46
1:R:413:LYS:HA	1:R:416:ALA:HB3	1.96	0.46
1:T:47:GLN:CG	1:T:48:TYR:H	2.27	0.46
1:T:47:GLN:H	1:T:48:TYR:HD2	1.64	0.46
1:J:227:GLU:HA	1:J:274:ARG:CA	2.44	0.46
1:G:273:ARG:HH22	1:G:453:LEU:CD1	2.28	0.46
1:B:230:GLU:HG2	1:B:273:ARG:HB2	1.96	0.46
1:T:451:ASP:C	1:T:453:LEU:N	2.69	0.46
1:A:201:PHE:HE2	1:A:281:ILE:HG22	1.80	0.46
1:M:193:LEU:HD22	1:M:287:LEU:HB3	1.97	0.46
1:H:567:MSE:HE2	1:I:554:LEU:HD22	1.96	0.46
1:R:564:GLY:CA	1:X:554:LEU:HD21	2.42	0.46
1:R:420:VAL:HA	1:R:428:GLY:HA2	1.98	0.46
1:F:376:ARG:HB2	1:G:352:TRP:CD2	2.50	0.46
1:D:207:TRP:O	1:D:208:VAL:C	2.54	0.46
1:A:207:TRP:O	1:A:208:VAL:C	2.53	0.46
1:D:438:LEU:HD22	3:E:719:HOH:O	2.15	0.46
1:M:293:ILE:HD13	1:M:294:ALA:N	2.31	0.46
1:X:378:ASP:O	1:X:381:SER:O	2.33	0.46
1:J:343:ARG:H	1:J:343:ARG:HG2	1.52	0.46
1:P:598:GLN:HB2	1:P:601:GLN:HB3	1.95	0.46
1:I:343:ARG:H	1:I:343:ARG:HG2	1.52	0.46
1:O:322:LEU:H	1:O:322:LEU:HD22	1.79	0.46
1:D:539:LEU:HD21	1:D:551:LEU:CB	2.44	0.46
1:I:539:LEU:HD21	1:I:551:LEU:CB	2.44	0.46
1:A:539:LEU:HD21	1:A:551:LEU:CB	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:SER:HB2	1:C:170:ALA:HB2	1.97	0.46
1:U:542:THR:HG21	1:X:556:TYR:OH	2.14	0.46
1:O:395:PRO:HD2	1:P:398:PRO:HB3	1.96	0.46
1:M:127:ARG:HG2	1:M:147:GLU:HB2	1.96	0.46
1:N:171:ARG:O	1:N:224:GLU:HA	2.15	0.46
1:C:86:ALA:HB2	1:C:515:GLU:HG3	1.96	0.46
1:A:164:LEU:HA	1:A:307:TRP:HH2	1.80	0.46
1:C:28:GLU:HG3	1:C:32:ASP:OD2	2.15	0.46
1:C:29:ALA:O	1:C:33:LEU:HG	2.15	0.46
1:C:34:PHE:O	1:C:34:PHE:CD2	2.68	0.46
1:D:444:LEU:HD13	1:D:444:LEU:N	2.31	0.46
1:F:565:VAL:O	1:F:569:ARG:HB3	2.15	0.46
1:H:28:GLU:HG3	1:H:32:ASP:OD2	2.15	0.46
1:H:444:LEU:HD13	1:H:444:LEU:N	2.31	0.46
1:I:71:MSE:CE	1:I:115:VAL:HB	2.45	0.46
1:J:434:THR:HA	1:J:437:GLN:CD	2.35	0.46
1:K:28:GLU:HG3	1:K:32:ASP:OD2	2.15	0.46
1:K:29:ALA:O	1:K:33:LEU:HG	2.15	0.46
1:K:92:ASP:N	1:K:92:ASP:OD2	2.48	0.46
1:K:81:ARG:HB2	1:K:517:TYR:CZ	2.50	0.46
1:Q:560:LEU:HD13	1:R:82:PRO:CD	2.22	0.46
1:T:164:LEU:HA	1:T:307:TRP:CH2	2.51	0.46
1:T:165:MSE:HG3	1:T:307:TRP:CD2	2.49	0.46
1:U:165:MSE:HG3	1:U:307:TRP:CD2	2.50	0.46
1:U:33:LEU:HD12	1:U:34:PHE:N	2.30	0.46
1:N:26:ARG:HG2	1:V:212:LEU:HD22	1.98	0.46
1:V:418:LEU:HB2	1:V:428:GLY:O	2.15	0.46
1:V:443:ASP:C	1:V:444:LEU:HD13	2.35	0.46
1:V:78:VAL:CG1	1:V:444:LEU:HG	2.45	0.46
1:X:41:TRP:HE3	1:X:42:ASP:HB3	1.81	0.46
1:B:139:SER:CB	1:B:455:THR:CG2	2.80	0.46
1:R:510:ILE:O	1:R:513:ARG:HD2	2.15	0.46
1:M:510:ILE:O	1:M:513:ARG:HD2	2.15	0.46
1:X:546:THR:CG2	1:X:547:PRO:HD3	2.30	0.46
1:M:158:TRP:H	1:M:158:TRP:HD1	1.61	0.46
1:J:273:ARG:HH22	1:J:453:LEU:CD1	2.28	0.46
1:X:273:ARG:CZ	1:X:275:ARG:HE	2.28	0.46
1:K:234:ILE:HG12	1:K:267:ALA:HB3	1.96	0.46
1:A:227:GLU:HA	1:A:274:ARG:CA	2.44	0.46
1:E:273:ARG:HH22	1:E:453:LEU:CD1	2.28	0.46
1:J:197:ASP:O	1:J:198:ILE:HB	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:454:ALA:O	1:Q:455:THR:C	2.53	0.46
1:V:280:ILE:HG22	1:V:287:LEU:HD13	1.97	0.46
1:I:376:ARG:HB2	1:J:352:TRP:CG	2.51	0.46
1:O:238:PRO:HD3	1:O:263:PHE:HB2	1.96	0.46
1:N:238:PRO:HD3	1:N:263:PHE:HB2	1.97	0.46
2:Z:140:ARG:O	2:Z:141:MET:HB3	2.16	0.46
1:R:95:MSE:HE1	1:R:99:ARG:NH2	2.31	0.46
1:V:378:ASP:O	1:V:381:SER:O	2.34	0.46
1:T:387:GLN:HG2	1:T:387:GLN:H	1.57	0.46
1:T:429:GLN:HG2	1:T:429:GLN:O	2.15	0.46
1:J:539:LEU:HD21	1:J:551:LEU:HB3	1.96	0.46
1:B:539:LEU:HD21	1:B:551:LEU:CB	2.44	0.46
1:C:539:LEU:HD21	1:C:551:LEU:CB	2.44	0.46
1:J:410:SER:O	1:J:414:GLU:HG2	2.16	0.46
1:U:260:ASP:HA	1:U:264:ILE:HB	1.97	0.46
1:Q:127:ARG:HG2	1:Q:147:GLU:HB2	1.96	0.46
1:E:410:SER:O	1:E:414:GLU:HG2	2.16	0.46
1:P:322:LEU:N	1:P:322:LEU:HD22	2.29	0.46
1:W:227:GLU:O	1:W:227:GLU:CG	2.63	0.46
1:Q:174:THR:N	3:Q:705:HOH:O	2.47	0.46
1:F:162:SER:HB2	1:F:170:ALA:HB2	1.96	0.46
1:O:127:ARG:HG2	1:O:147:GLU:HB2	1.96	0.46
1:A:162:SER:HB2	1:A:170:ALA:HB2	1.96	0.46
1:I:410:SER:O	1:I:414:GLU:HG2	2.16	0.46
1:A:565:VAL:O	1:A:569:ARG:HB3	2.15	0.46
1:B:48:TYR:O	1:B:49:THR:CB	2.64	0.46
1:C:26:ARG:NH2	1:C:30:LYS:HB2	2.28	0.46
1:E:101:ASP:HB2	1:E:144:ILE:O	2.14	0.46
1:E:28:GLU:HG3	1:E:32:ASP:OD2	2.15	0.46
1:E:434:THR:HA	1:E:437:GLN:HG2	1.98	0.46
1:E:444:LEU:N	1:E:444:LEU:HD13	2.31	0.46
1:G:71:MSE:CE	1:G:115:VAL:HB	2.45	0.46
1:H:115:VAL:O	1:H:119:ILE:HG13	2.15	0.46
1:H:71:MSE:CE	1:H:115:VAL:HB	2.45	0.46
1:I:317:GLU:HB3	1:I:321:ARG:CZ	2.46	0.46
1:I:77:ASP:HB2	1:I:523:SER:HB2	1.98	0.46
1:J:78:VAL:CG2	1:J:444:LEU:HD21	2.46	0.46
1:L:565:VAL:O	1:L:569:ARG:HB3	2.15	0.46
1:O:164:LEU:HD22	1:O:169:ASP:OD1	2.15	0.46
1:P:164:LEU:HA	1:P:307:TRP:CH2	2.51	0.46
1:Q:316:TYR:O	1:Q:321:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:33:LEU:HD12	1:S:34:PHE:N	2.31	0.46
1:T:37:ARG:C	1:T:39:SER:H	2.18	0.46
1:T:80:TYR:OH	1:T:444:LEU:HD12	2.16	0.46
1:V:47:GLN:CG	1:V:48:TYR:H	2.28	0.46
1:V:560:LEU:O	1:V:561:ASP:O	2.33	0.46
1:W:443:ASP:C	1:W:444:LEU:HD13	2.36	0.46
1:T:330:ARG:O	1:T:334:MSE:HB2	2.16	0.46
1:P:409:THR:O	1:P:413:LYS:HG2	2.15	0.46
1:W:409:THR:O	1:W:413:LYS:HG2	2.16	0.46
1:W:47:GLN:N	1:W:48:TYR:HD2	2.14	0.46
1:K:248:LYS:HB3	1:K:511:ARG:NH1	2.30	0.46
1:B:227:GLU:HA	1:B:274:ARG:CA	2.44	0.46
1:D:248:LYS:HB3	1:D:511:ARG:NH1	2.30	0.46
1:H:230:GLU:HG2	1:H:273:ARG:HB2	1.96	0.46
1:A:230:GLU:HG2	1:A:273:ARG:HB2	1.96	0.46
1:C:273:ARG:HH22	1:C:453:LEU:CD1	2.28	0.46
1:L:248:LYS:HB3	1:L:511:ARG:NH1	2.30	0.46
1:L:273:ARG:HH22	1:L:453:LEU:CD1	2.28	0.46
1:F:219:ILE:HD12	1:F:281:ILE:O	2.16	0.46
1:X:193:LEU:HD22	1:X:287:LEU:HB3	1.97	0.46
1:W:198:ILE:O	1:W:198:ILE:HG22	2.14	0.46
1:T:577:ILE:HG12	1:T:582:LYS:CG	2.45	0.46
1:U:238:PRO:HD3	1:U:263:PHE:HB2	1.98	0.46
1:I:207:TRP:O	1:I:208:VAL:C	2.53	0.46
1:B:207:TRP:O	1:B:208:VAL:C	2.53	0.46
1:A:238:PRO:HG3	1:A:263:PHE:CB	2.46	0.46
1:T:86:ALA:CB	1:T:515:GLU:HG3	2.45	0.46
3:S:719:HOH:O	1:T:430:VAL:HG11	2.15	0.46
1:U:322:LEU:H	1:U:322:LEU:HD22	1.80	0.46
1:A:539:LEU:HD21	1:A:551:LEU:HB3	1.96	0.46
1:T:227:GLU:O	1:T:227:GLU:CG	2.63	0.46
1:G:410:SER:O	1:G:414:GLU:HG2	2.16	0.46
1:L:162:SER:HB2	1:L:170:ALA:HB2	1.96	0.46
3:T:718:HOH:O	1:W:438:LEU:HD22	2.15	0.46
1:A:34:PHE:HE1	1:A:324:LYS:HZ2	1.52	0.46
1:A:35:PHE:HE1	1:A:321:ARG:NH1	2.13	0.46
1:B:71:MSE:CE	1:B:115:VAL:HB	2.45	0.46
1:B:28:GLU:HG3	1:B:32:ASP:OD2	2.15	0.46
1:B:92:ASP:N	1:B:92:ASP:OD2	2.48	0.46
1:E:92:ASP:OD2	1:E:92:ASP:N	2.48	0.46
1:F:71:MSE:CE	1:F:115:VAL:HB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:444:LEU:C	1:F:446:THR:H	2.19	0.46
1:J:115:VAL:O	1:J:119:ILE:HG13	2.15	0.46
1:J:77:ASP:HB2	1:J:523:SER:HB2	1.98	0.46
1:K:164:LEU:HA	1:K:307:TRP:HH2	1.80	0.46
1:L:28:GLU:HG3	1:L:32:ASP:OD2	2.15	0.46
1:M:80:TYR:OH	1:M:444:LEU:HD12	2.16	0.46
1:N:560:LEU:O	1:N:561:ASP:O	2.33	0.46
2:Z:28:VAL:CB	2:Z:96:LEU:HD13	2.45	0.46
2:Y:28:VAL:CB	2:Y:96:LEU:HD13	2.45	0.46
1:N:29:ALA:O	1:N:33:LEU:HG	2.16	0.46
1:N:47:GLN:N	1:N:48:TYR:HD2	2.14	0.46
1:P:165:MSE:HG3	1:P:307:TRP:CD2	2.50	0.46
1:R:144:ILE:HD12	1:R:145:ARG:N	2.30	0.46
1:S:31:ASN:O	1:S:34:PHE:HB3	2.15	0.46
1:T:82:PRO:O	1:T:516:CYS:HA	2.15	0.46
1:T:78:VAL:CG1	1:T:444:LEU:HG	2.45	0.46
1:V:66:LYS:HZ3	1:V:420:VAL:HG11	1.80	0.46
1:W:100:THR:HG22	1:W:138:THR:HG22	1.96	0.46
1:W:560:LEU:O	1:W:561:ASP:O	2.32	0.46
1:W:47:GLN:H	1:W:48:TYR:HD2	1.63	0.46
1:J:273:ARG:O	1:J:274:ARG:CB	2.64	0.46
1:H:234:ILE:HG22	1:H:246:TYR:HB3	1.98	0.46
1:C:248:LYS:HB3	1:C:511:ARG:NH1	2.30	0.46
1:F:234:ILE:HG12	1:F:267:ALA:HB3	1.96	0.46
1:B:201:PHE:HE2	1:B:281:ILE:HG22	1.80	0.46
1:A:219:ILE:HD12	1:A:281:ILE:O	2.16	0.46
1:D:219:ILE:HD12	1:D:281:ILE:O	2.16	0.46
1:N:193:LEU:HD22	1:N:287:LEU:HB3	1.97	0.46
1:G:535:ILE:CD1	1:G:554:LEU:HG	2.44	0.46
1:W:232:ALA:HB2	1:W:269:ARG:O	2.15	0.46
1:O:198:ILE:HG22	1:O:198:ILE:O	2.14	0.46
1:U:554:LEU:O	1:U:557:PHE:HB3	2.15	0.46
1:V:193:LEU:HD22	1:V:287:LEU:HB3	1.98	0.46
1:T:238:PRO:HD3	1:T:263:PHE:HB2	1.96	0.46
1:D:557:PHE:CE2	1:E:563:LYS:HD3	2.50	0.46
1:N:262:GLY:O	1:N:263:PHE:HB3	2.14	0.46
1:W:554:LEU:O	1:W:557:PHE:HB3	2.16	0.46
1:U:293:ILE:HD13	1:U:294:ALA:N	2.30	0.46
1:N:86:ALA:CB	1:N:515:GLU:HG3	2.44	0.46
1:X:293:ILE:HG12	1:X:294:ALA:H	1.81	0.46
1:P:387:GLN:HB2	1:Q:390:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:387:GLN:CB	1:W:390:ALA:HB2	2.46	0.46
1:I:81:ARG:HB2	1:I:517:TYR:CZ	2.50	0.46
1:R:422:THR:HG22	1:R:423:GLU:N	2.31	0.46
1:O:108:LYS:HD2	1:P:438:LEU:HD11	1.97	0.46
1:J:162:SER:HB2	1:J:170:ALA:HB2	1.97	0.46
1:W:422:THR:HG22	1:W:423:GLU:N	2.31	0.46
1:O:191:TYR:HE1	1:O:278:LYS:HZ3	1.62	0.46
1:P:556:TYR:OH	1:Q:542:THR:HG21	2.15	0.46
1:S:348:LYS:HB2	1:U:372:TYR:CE2	2.50	0.46
1:U:438:LEU:HD22	3:X:718:HOH:O	2.15	0.46
1:D:434:THR:HA	1:D:437:GLN:CD	2.35	0.46
1:E:164:LEU:HA	1:E:307:TRP:CH2	2.51	0.46
1:E:317:GLU:HB3	1:E:321:ARG:CZ	2.46	0.46
1:F:28:GLU:HG3	1:F:32:ASP:OD2	2.15	0.46
1:I:26:ARG:NH2	1:I:30:LYS:HB2	2.28	0.46
1:J:434:THR:HA	1:J:437:GLN:HG2	1.98	0.46
1:M:34:PHE:CE2	1:M:45:LEU:HG	2.46	0.46
1:M:528:LYS:CD	1:M:560:LEU:HD21	2.46	0.46
1:O:29:ALA:O	1:O:33:LEU:HG	2.16	0.46
1:O:37:ARG:C	1:O:39:SER:H	2.19	0.46
1:O:528:LYS:CD	1:O:560:LEU:HD21	2.46	0.46
1:P:47:GLN:CG	1:P:48:TYR:H	2.26	0.46
1:S:41:TRP:HE3	1:S:42:ASP:HB3	1.81	0.46
1:V:164:LEU:HA	1:V:307:TRP:HH2	1.79	0.46
1:V:82:PRO:O	1:V:516:CYS:HA	2.16	0.46
1:X:123:VAL:HG22	1:X:316:TYR:HE2	1.81	0.46
1:X:528:LYS:CD	1:X:560:LEU:HD21	2.46	0.46
1:M:409:THR:O	1:M:413:LYS:HG2	2.16	0.46
1:Q:71:MSE:CE	1:Q:115:VAL:HB	2.46	0.46
1:N:71:MSE:CE	1:N:115:VAL:HB	2.46	0.46
1:G:248:LYS:HB3	1:G:511:ARG:NH1	2.30	0.46
1:A:227:GLU:OE2	1:A:227:GLU:N	2.47	0.46
1:I:234:ILE:HG12	1:I:267:ALA:HB3	1.96	0.46
1:I:248:LYS:HB3	1:I:511:ARG:NH1	2.30	0.46
1:F:273:ARG:O	1:F:274:ARG:CB	2.64	0.46
1:L:234:ILE:HG12	1:L:267:ALA:HB3	1.96	0.46
1:F:201:PHE:HE2	1:F:281:ILE:HG22	1.80	0.46
1:H:198:ILE:HA	1:H:199:PRO:HD3	1.64	0.46
1:L:219:ILE:HD12	1:L:281:ILE:O	2.16	0.46
1:W:266:ILE:O	1:W:267:ALA:HB2	2.15	0.46
1:K:219:ILE:HD12	1:K:281:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:573:ASN:O	1:W:577:ILE:HG13	2.16	0.46
1:W:577:ILE:HG12	1:W:582:LYS:CG	2.44	0.46
1:W:454:ALA:O	1:W:455:THR:C	2.52	0.46
1:M:378:ASP:O	1:M:381:SER:O	2.34	0.46
1:Q:293:ILE:HG12	1:Q:294:ALA:H	1.81	0.46
1:S:390:ALA:HB2	1:U:387:GLN:HB2	1.98	0.46
1:S:429:GLN:O	1:S:429:GLN:HG2	2.16	0.46
1:W:429:GLN:O	1:W:429:GLN:HG2	2.16	0.46
1:H:162:SER:HB2	1:H:170:ALA:HB2	1.97	0.46
1:K:77:ASP:HB2	1:K:523:SER:HB2	1.98	0.46
1:A:48:TYR:O	1:A:49:THR:CB	2.64	0.46
1:B:34:PHE:CD2	1:B:34:PHE:O	2.68	0.46
1:C:164:LEU:HA	1:C:307:TRP:HH2	1.80	0.46
1:D:28:GLU:HG3	1:D:32:ASP:OD2	2.15	0.46
1:D:434:THR:HA	1:D:437:GLN:HG2	1.98	0.46
1:D:444:LEU:C	1:D:446:THR:H	2.19	0.46
1:E:164:LEU:HA	1:E:307:TRP:HH2	1.79	0.46
1:E:29:ALA:O	1:E:33:LEU:HG	2.15	0.46
1:G:130:THR:HG22	1:G:144:ILE:HA	1.97	0.46
1:G:72:ARG:HD2	1:H:434:THR:HG21	1.98	0.46
1:J:164:LEU:HA	1:J:307:TRP:CH2	2.51	0.46
1:J:82:PRO:HB2	1:J:83:LYS:H	1.58	0.46
1:L:115:VAL:O	1:L:119:ILE:HG13	2.15	0.46
1:L:317:GLU:HB3	1:L:321:ARG:CZ	2.46	0.46
1:M:47:GLN:N	1:M:48:TYR:HD2	2.14	0.46
1:O:47:GLN:CG	1:O:48:TYR:H	2.28	0.46
1:L:78:VAL:CG2	1:L:444:LEU:HD21	2.46	0.46
1:N:434:THR:HG23	1:N:435:VAL:N	2.30	0.46
1:Q:528:LYS:CD	1:Q:560:LEU:HD21	2.46	0.46
1:T:123:VAL:CG1	1:T:304:PHE:CE1	2.99	0.46
1:V:37:ARG:C	1:V:39:SER:N	2.68	0.46
1:V:420:VAL:HA	1:V:428:GLY:HA2	1.98	0.46
1:Q:71:MSE:HE3	1:Q:115:VAL:HB	1.97	0.46
1:V:405:LEU:O	1:V:409:THR:HG23	2.16	0.46
1:K:273:ARG:O	1:K:274:ARG:CB	2.64	0.46
1:B:248:LYS:HZ1	1:B:513:ARG:HH12	1.63	0.46
1:D:234:ILE:HG12	1:D:267:ALA:HB3	1.96	0.46
1:F:248:LYS:HB3	1:F:511:ARG:NH1	2.30	0.46
1:I:219:ILE:HD12	1:I:281:ILE:O	2.16	0.46
1:M:535:ILE:HD11	1:N:564:GLY:HA3	1.98	0.46
1:M:554:LEU:O	1:M:557:PHE:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:280:ILE:HD12	1:R:280:ILE:N	2.31	0.46
1:L:413:LYS:HE2	1:L:413:LYS:HB3	1.74	0.46
1:J:542:THR:HA	1:J:543:PRO:HD3	1.82	0.46
1:M:86:ALA:CB	1:M:515:GLU:HG3	2.45	0.46
1:W:378:ASP:O	1:W:381:SER:O	2.34	0.46
1:E:238:PRO:HG3	1:E:263:PHE:CB	2.46	0.46
1:P:387:GLN:CB	1:Q:390:ALA:CB	2.94	0.46
1:T:155:HIS:CE1	1:T:204:PRO:HB2	2.51	0.46
1:V:422:THR:HG22	1:V:423:GLU:N	2.31	0.46
1:X:77:ASP:HB2	1:X:523:SER:HB2	1.98	0.46
1:L:343:ARG:HG2	1:L:343:ARG:H	1.52	0.46
1:T:322:LEU:HD22	1:T:322:LEU:N	2.31	0.46
1:V:227:GLU:O	1:V:227:GLU:CG	2.64	0.46
1:S:174:THR:N	3:S:705:HOH:O	2.49	0.46
1:S:171:ARG:O	1:S:224:GLU:HA	2.15	0.46
1:A:115:VAL:O	1:A:119:ILE:HG13	2.15	0.46
1:A:28:GLU:HG3	1:A:32:ASP:OD2	2.15	0.46
1:D:565:VAL:O	1:D:569:ARG:HB3	2.15	0.46
1:F:58:ASP:O	1:F:59:VAL:HB	2.14	0.46
1:F:94:LEU:HA	1:F:97:MSE:CE	2.37	0.46
1:G:92:ASP:OD2	1:G:92:ASP:N	2.48	0.46
1:I:561:ASP:OD2	1:J:92:ASP:HB3	2.16	0.46
1:K:444:LEU:C	1:K:446:THR:H	2.19	0.46
1:K:528:LYS:HZ3	1:K:560:LEU:HD21	1.80	0.46
1:N:82:PRO:O	1:N:516:CYS:HA	2.16	0.46
1:P:123:VAL:CG1	1:P:304:PHE:CE1	2.99	0.46
1:Q:31:ASN:O	1:Q:34:PHE:HB3	2.15	0.46
1:R:47:GLN:CG	1:R:48:TYR:H	2.28	0.46
1:S:340:ILE:O	1:S:344:THR:HG21	2.16	0.46
1:T:164:LEU:HA	1:T:307:TRP:HH2	1.81	0.46
1:W:444:LEU:O	1:W:446:THR:N	2.49	0.46
1:F:139:SER:CB	1:F:455:THR:CG2	2.80	0.46
1:P:160:SER:O	1:P:161:ASN:ND2	2.44	0.46
1:S:118:GLN:OE1	1:S:303:VAL:HB	2.15	0.46
1:T:330:ARG:HD2	1:T:409:THR:CG2	2.39	0.46
1:V:451:ASP:C	1:V:453:LEU:H	2.19	0.46
1:J:248:LYS:HB3	1:J:511:ARG:NH1	2.30	0.46
1:O:273:ARG:CZ	1:O:275:ARG:HE	2.29	0.46
1:R:274:ARG:O	1:R:275:ARG:HD2	2.15	0.46
1:G:201:PHE:HE2	1:G:281:ILE:HG22	1.80	0.46
1:G:219:ILE:HD12	1:G:281:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:ILE:HD12	1:B:281:ILE:O	2.16	0.46
1:I:197:ASP:O	1:I:198:ILE:HB	2.15	0.46
1:J:219:ILE:HD12	1:J:281:ILE:O	2.16	0.46
1:K:197:ASP:O	1:K:198:ILE:HB	2.15	0.46
1:Q:376:ARG:HB2	1:R:352:TRP:CG	2.50	0.46
1:F:567:MSE:HE2	1:G:554:LEU:HD22	1.97	0.46
1:B:413:LYS:HE2	1:B:413:LYS:HB3	1.73	0.46
1:R:95:MSE:HE1	1:R:99:ARG:CZ	2.46	0.46
1:R:343:ARG:H	1:R:343:ARG:HG2	1.56	0.46
1:N:155:HIS:CE1	1:N:204:PRO:HB2	2.50	0.46
1:S:396:GLU:O	1:T:399:GLN:OE1	2.34	0.46
1:W:260:ASP:HA	1:W:264:ILE:HB	1.97	0.46
1:R:260:ASP:HA	1:R:264:ILE:HB	1.97	0.46
1:O:76:ILE:HD12	1:O:433:ASP:OD1	2.16	0.46
1:F:410:SER:O	1:F:414:GLU:HG2	2.16	0.46
1:W:55:GLY:HA3	1:W:57:PHE:CE1	2.50	0.46
1:S:260:ASP:HA	1:S:264:ILE:HB	1.96	0.46
1:X:55:GLY:HA3	1:X:57:PHE:CE1	2.50	0.46
1:G:363:TYR:HE1	1:H:350:PHE:HE1	1.64	0.46
1:A:171:ARG:HH21	1:L:182:ASN:HD22	1.64	0.46
1:B:164:LEU:HA	1:B:307:TRP:CH2	2.51	0.46
1:B:317:GLU:HB3	1:B:321:ARG:CZ	2.46	0.46
1:B:77:ASP:HB2	1:B:523:SER:HB2	1.98	0.46
1:G:35:PHE:HE1	1:G:321:ARG:NH1	2.13	0.46
1:I:35:PHE:CE1	1:I:321:ARG:NH1	2.84	0.46
1:L:29:ALA:O	1:L:33:LEU:HG	2.15	0.46
1:M:444:LEU:N	1:M:444:LEU:HD13	2.30	0.46
1:O:24:GLU:O	1:O:26:ARG:N	2.49	0.46
1:O:82:PRO:O	1:O:516:CYS:HA	2.16	0.46
1:K:565:VAL:O	1:K:569:ARG:HB3	2.15	0.46
1:U:26:ARG:HG3	1:U:27:ARG:N	2.31	0.46
1:U:437:GLN:HA	1:U:440:MSE:HB2	1.98	0.46
1:W:35:PHE:C	1:W:37:ARG:N	2.69	0.46
1:S:158:TRP:HD1	1:S:158:TRP:H	1.63	0.46
1:S:451:ASP:C	1:S:453:LEU:H	2.19	0.46
1:G:273:ARG:O	1:G:274:ARG:CB	2.64	0.46
1:P:273:ARG:HH22	1:P:453:LEU:CD2	2.29	0.46
1:D:273:ARG:O	1:D:274:ARG:CB	2.64	0.46
1:H:234:ILE:HG12	1:H:267:ALA:HB3	1.96	0.46
1:R:451:ASP:C	1:R:453:LEU:N	2.69	0.46
1:C:234:ILE:HG22	1:C:246:TYR:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:234:ILE:HG22	1:F:246:TYR:HB3	1.98	0.46
1:E:219:ILE:HD12	1:E:281:ILE:O	2.16	0.46
1:H:197:ASP:O	1:H:198:ILE:HB	2.15	0.46
1:Q:198:ILE:O	1:Q:198:ILE:HG22	2.16	0.46
1:D:567:MSE:HE2	1:F:554:LEU:HD22	1.97	0.46
1:T:575:GLN:O	1:T:579:MSE:CG	2.63	0.46
1:G:207:TRP:O	1:G:208:VAL:C	2.53	0.46
1:T:66:LYS:HZ3	1:T:420:VAL:HG21	1.81	0.46
1:V:238:PRO:HD3	1:V:263:PHE:HB2	1.98	0.46
1:K:293:ILE:HD13	1:K:294:ALA:N	2.31	0.46
1:Q:378:ASP:O	1:Q:381:SER:O	2.34	0.46
1:W:86:ALA:CB	1:W:515:GLU:HG3	2.45	0.46
1:W:322:LEU:HD22	1:W:322:LEU:H	1.80	0.46
1:O:371:TYR:HE2	1:O:373:LEU:HD21	1.81	0.46
1:M:227:GLU:CG	1:M:227:GLU:O	2.64	0.46
1:L:410:SER:O	1:L:414:GLU:HG2	2.16	0.46
1:A:410:SER:O	1:A:414:GLU:HG2	2.16	0.46
1:N:77:ASP:HB2	1:N:523:SER:HB2	1.98	0.46
1:A:317:GLU:HB3	1:A:321:ARG:CZ	2.46	0.46
1:A:334:MSE:HE3	1:B:404:MSE:CE	2.46	0.46
1:C:71:MSE:CE	1:C:115:VAL:HB	2.45	0.46
1:D:78:VAL:HG21	1:D:444:LEU:CD1	2.21	0.46
1:F:48:TYR:O	1:F:49:THR:CB	2.64	0.46
1:G:35:PHE:CE1	1:G:321:ARG:NH1	2.84	0.46
1:I:28:GLU:HG3	1:I:32:ASP:OD2	2.15	0.46
1:I:92:ASP:OD2	1:I:92:ASP:N	2.48	0.46
1:K:71:MSE:CE	1:K:115:VAL:HB	2.45	0.46
1:K:78:VAL:CG2	1:K:444:LEU:HD21	2.46	0.46
1:M:165:MSE:HG3	1:M:307:TRP:CD2	2.51	0.46
1:M:35:PHE:CE1	1:M:321:ARG:NH1	2.83	0.46
1:O:33:LEU:HD12	1:O:34:PHE:N	2.31	0.46
1:N:35:PHE:CE1	1:N:321:ARG:NH1	2.84	0.46
1:P:528:LYS:CD	1:P:560:LEU:HD21	2.46	0.46
1:Q:38:VAL:HG21	1:Q:324:LYS:HD2	1.98	0.46
1:Q:78:VAL:CG1	1:Q:79:LEU:H	2.29	0.46
1:Q:80:TYR:OH	1:Q:444:LEU:HD12	2.16	0.46
1:R:316:TYR:O	1:R:321:ARG:NH1	2.49	0.46
1:S:37:ARG:C	1:S:39:SER:H	2.20	0.46
1:W:37:ARG:CB	1:W:37:ARG:HH21	2.28	0.46
1:W:37:ARG:C	1:W:39:SER:H	2.19	0.46
1:W:78:VAL:CG1	1:W:444:LEU:HG	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:437:GLN:HA	1:X:440:MSE:HB2	1.98	0.46
1:M:14:ARG:NE	1:M:14:ARG:CA	2.70	0.46
1:T:560:LEU:O	1:T:561:ASP:O	2.33	0.46
1:X:248:LYS:CD	1:X:248:LYS:H	2.17	0.46
1:V:71:MSE:HE3	1:V:115:VAL:HB	1.98	0.46
1:H:234:ILE:CG2	1:H:246:TYR:HB3	2.46	0.46
1:A:273:ARG:O	1:A:274:ARG:CB	2.64	0.46
1:I:234:ILE:HG22	1:I:246:TYR:HB3	1.98	0.46
1:C:219:ILE:HD12	1:C:281:ILE:O	2.16	0.46
1:S:236:GLN:HG3	1:S:265:LYS:HG2	1.98	0.46
1:R:454:ALA:O	1:R:455:THR:C	2.54	0.46
1:O:232:ALA:HB2	1:O:269:ARG:O	2.16	0.46
1:A:376:ARG:HB2	1:B:352:TRP:CD2	2.51	0.46
1:J:293:ILE:HD13	1:J:294:ALA:N	2.31	0.46
1:S:71:MSE:HE3	1:S:115:VAL:HB	1.97	0.46
1:N:554:LEU:O	1:N:557:PHE:HB3	2.15	0.46
1:K:238:PRO:HG3	1:K:263:PHE:CB	2.46	0.46
1:V:86:ALA:CB	1:V:515:GLU:HG3	2.45	0.46
1:M:390:ALA:CB	1:N:387:GLN:CB	2.94	0.46
1:R:429:GLN:HG2	1:R:429:GLN:O	2.16	0.46
1:P:422:THR:HG22	1:P:423:GLU:N	2.31	0.46
1:T:55:GLY:HA3	1:T:57:PHE:CE1	2.51	0.46
1:N:227:GLU:CG	1:N:227:GLU:O	2.64	0.46
1:M:270:GLN:OE1	1:M:270:GLN:HA	2.16	0.46
1:T:171:ARG:O	1:T:224:GLU:HA	2.16	0.46
1:V:310:VAL:HG22	1:W:40:GLN:HG2	1.98	0.46
1:M:349:PRO:HG3	1:M:391:TYR:CE1	2.51	0.46
1:X:422:THR:HG22	1:X:423:GLU:N	2.31	0.46
1:P:171:ARG:O	1:P:224:GLU:HA	2.15	0.46
1:A:71:MSE:CE	1:A:115:VAL:HB	2.45	0.45
1:A:434:THR:HA	1:A:437:GLN:HG2	1.98	0.45
1:A:444:LEU:HD13	1:A:444:LEU:N	2.31	0.45
1:A:92:ASP:OD2	1:A:92:ASP:N	2.48	0.45
1:C:130:THR:HG22	1:C:144:ILE:HA	1.97	0.45
1:C:565:VAL:O	1:C:569:ARG:HB3	2.15	0.45
1:D:48:TYR:O	1:D:49:THR:CB	2.64	0.45
1:D:528:LYS:HD2	1:D:560:LEU:HD21	1.99	0.45
1:F:444:LEU:N	1:F:444:LEU:HD13	2.31	0.45
1:G:164:LEU:HA	1:G:307:TRP:CH2	2.51	0.45
1:K:40:GLN:O	1:K:41:TRP:CB	2.54	0.45
1:O:34:PHE:O	1:O:37:ARG:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:164:LEU:HA	1:L:307:TRP:CH2	2.51	0.45
1:N:418:LEU:HB2	1:N:428:GLY:O	2.15	0.45
1:Q:47:GLN:CG	1:Q:48:TYR:H	2.28	0.45
1:R:26:ARG:HG3	1:R:27:ARG:N	2.31	0.45
1:R:443:ASP:C	1:R:444:LEU:HD13	2.36	0.45
1:S:343:ARG:O	1:S:344:THR:HB	2.16	0.45
1:U:37:ARG:C	1:U:39:SER:H	2.19	0.45
1:U:41:TRP:HE3	1:U:42:ASP:HB3	1.81	0.45
1:V:38:VAL:HG21	1:V:324:LYS:HD2	1.98	0.45
1:V:47:GLN:H	1:V:48:TYR:HD2	1.62	0.45
1:V:160:SER:O	1:V:161:ASN:ND2	2.46	0.45
1:Q:248:LYS:HG3	1:Q:511:ARG:HE	1.81	0.45
1:R:409:THR:O	1:R:413:LYS:HG2	2.16	0.45
1:N:160:SER:O	1:N:161:ASN:ND2	2.46	0.45
1:J:234:ILE:CG2	1:J:246:TYR:HB3	2.46	0.45
1:K:234:ILE:HG22	1:K:246:TYR:HB3	1.98	0.45
1:K:273:ARG:O	1:K:274:ARG:HB3	2.17	0.45
1:D:234:ILE:CG2	1:D:246:TYR:HB3	2.47	0.45
1:D:273:ARG:HH22	1:D:453:LEU:CD1	2.28	0.45
1:C:246:TYR:HD2	1:C:511:ARG:CB	2.28	0.45
1:E:234:ILE:HG12	1:E:267:ALA:HB3	1.96	0.45
1:E:201:PHE:HE2	1:E:281:ILE:HG22	1.80	0.45
1:X:24:GLU:O	1:X:26:ARG:N	2.48	0.45
1:S:231:THR:CG2	1:S:249:ARG:HH11	2.23	0.45
1:D:563:LYS:HD3	1:F:557:PHE:CE2	2.51	0.45
1:I:293:ILE:HD13	1:I:294:ALA:N	2.31	0.45
1:S:378:ASP:O	1:S:381:SER:O	2.34	0.45
1:V:554:LEU:O	1:V:557:PHE:HB3	2.16	0.45
1:T:293:ILE:HG12	1:T:294:ALA:H	1.81	0.45
1:F:238:PRO:HG3	1:F:263:PHE:CB	2.46	0.45
1:B:238:PRO:HG3	1:B:263:PHE:CB	2.46	0.45
1:P:429:GLN:HG2	1:P:429:GLN:O	2.17	0.45
1:K:590:GLN:O	1:K:594:VAL:HG23	2.16	0.45
1:H:590:GLN:O	1:H:594:VAL:HG23	2.16	0.45
1:I:590:GLN:O	1:I:594:VAL:HG23	2.16	0.45
1:A:35:PHE:CE1	1:A:321:ARG:NH1	2.84	0.45
1:B:29:ALA:O	1:B:33:LEU:HG	2.15	0.45
1:B:434:THR:HA	1:B:437:GLN:HG2	1.97	0.45
1:C:413:LYS:HE2	1:C:413:LYS:HB3	1.74	0.45
1:E:77:ASP:HB2	1:E:523:SER:HB2	1.98	0.45
1:G:78:VAL:HG21	1:G:444:LEU:CD1	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:82:PRO:HB2	1:G:83:LYS:H	1.58	0.45
1:I:427:GLY:C	1:I:429:GLN:N	2.70	0.45
1:J:444:LEU:N	1:J:444:LEU:HD13	2.31	0.45
1:K:35:PHE:CE1	1:K:321:ARG:NH1	2.84	0.45
1:M:37:ARG:C	1:M:39:SER:H	2.19	0.45
1:O:101:ASP:HB3	1:O:138:THR:HG21	1.98	0.45
1:N:444:LEU:HD13	1:N:444:LEU:N	2.31	0.45
1:O:136:SER:N	1:O:137:PRO:HD3	2.31	0.45
1:Q:47:GLN:N	1:Q:48:TYR:HD2	2.14	0.45
1:R:136:SER:N	1:R:137:PRO:HD3	2.31	0.45
1:R:444:LEU:HD13	1:R:444:LEU:N	2.31	0.45
1:S:316:TYR:O	1:S:321:ARG:NH1	2.50	0.45
1:T:118:GLN:OE1	1:T:303:VAL:HB	2.16	0.45
1:T:26:ARG:HG3	1:T:27:ARG:N	2.30	0.45
1:W:38:VAL:HG21	1:W:324:LYS:HD2	1.99	0.45
1:S:158:TRP:HH2	1:S:302:PRO:HG3	1.78	0.45
1:W:273:ARG:CZ	1:W:275:ARG:HE	2.29	0.45
1:G:227:GLU:HA	1:G:274:ARG:CA	2.44	0.45
1:G:234:ILE:HG22	1:G:246:TYR:HB3	1.98	0.45
1:B:234:ILE:HG22	1:B:246:TYR:HB3	1.98	0.45
1:B:234:ILE:CG2	1:B:246:TYR:HB3	2.47	0.45
1:H:273:ARG:O	1:H:274:ARG:HB3	2.17	0.45
1:L:236:GLN:HE21	1:L:265:LYS:HZ3	1.63	0.45
1:H:219:ILE:HD12	1:H:281:ILE:O	2.16	0.45
1:U:193:LEU:HD22	1:U:287:LEU:HB3	1.98	0.45
1:S:40:GLN:HE21	1:S:40:GLN:HB2	1.58	0.45
2:Y:140:ARG:O	2:Y:141:MET:HB3	2.16	0.45
1:I:238:PRO:HG3	1:I:263:PHE:CB	2.46	0.45
1:M:155:HIS:CE1	1:M:204:PRO:HB2	2.52	0.45
1:Q:86:ALA:CB	1:Q:515:GLU:HG3	2.45	0.45
1:R:86:ALA:CB	1:R:515:GLU:HG3	2.46	0.45
1:G:451:ASP:O	1:G:456:ALA:N	2.40	0.45
1:P:127:ARG:HG2	1:P:147:GLU:HB2	1.97	0.45
1:W:136:SER:N	1:W:137:PRO:HD3	2.31	0.45
1:V:171:ARG:O	1:V:224:GLU:HA	2.15	0.45
1:S:395:PRO:HD2	1:T:398:PRO:HB3	1.99	0.45
1:Q:227:GLU:O	1:Q:227:GLU:CG	2.64	0.45
1:O:422:THR:HG22	1:O:423:GLU:N	2.31	0.45
1:A:78:VAL:CG2	1:A:444:LEU:HD21	2.46	0.45
1:C:317:GLU:HB3	1:C:321:ARG:CZ	2.46	0.45
1:C:444:LEU:HD13	1:C:444:LEU:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:LEU:HA	1:D:307:TRP:CH2	2.51	0.45
1:E:45:LEU:HD21	1:E:328:ARG:HH21	1.82	0.45
1:F:35:PHE:CE1	1:F:321:ARG:NH1	2.84	0.45
1:G:444:LEU:N	1:G:444:LEU:HD13	2.31	0.45
1:H:317:GLU:HB3	1:H:321:ARG:CZ	2.46	0.45
1:K:317:GLU:HB3	1:K:321:ARG:CZ	2.46	0.45
1:K:444:LEU:HD13	1:K:444:LEU:N	2.31	0.45
1:M:123:VAL:HG22	1:M:316:TYR:HE2	1.82	0.45
1:N:31:ASN:O	1:N:34:PHE:HB3	2.15	0.45
1:N:66:LYS:HZ3	1:N:420:VAL:HG21	1.81	0.45
1:U:528:LYS:CD	1:U:560:LEU:HD21	2.46	0.45
1:K:139:SER:CB	1:K:455:THR:CG2	2.80	0.45
1:O:118:GLN:OE1	1:O:303:VAL:HB	2.15	0.45
1:U:71:MSE:CE	1:U:115:VAL:HB	2.46	0.45
1:R:334:MSE:HE1	1:X:407:ALA:HB1	1.99	0.45
1:U:409:THR:O	1:U:413:LYS:HG2	2.16	0.45
1:Q:413:LYS:HA	1:Q:416:ALA:HB3	1.99	0.45
1:Q:273:ARG:CZ	1:Q:275:ARG:HE	2.30	0.45
1:J:234:ILE:HG22	1:J:246:TYR:HB3	1.98	0.45
1:G:234:ILE:CG2	1:G:246:TYR:HB3	2.47	0.45
1:D:251:ILE:HG23	1:D:507:LEU:HD22	1.98	0.45
1:A:234:ILE:HG22	1:A:246:TYR:HB3	1.98	0.45
1:A:273:ARG:O	1:A:274:ARG:HB3	2.17	0.45
1:I:273:ARG:O	1:I:274:ARG:CB	2.64	0.45
1:F:246:TYR:HD2	1:F:511:ARG:CB	2.28	0.45
1:P:282:THR:HG23	1:P:287:LEU:CD1	2.44	0.45
1:P:232:ALA:HB2	1:P:269:ARG:O	2.16	0.45
1:I:577:ILE:HG12	1:I:582:LYS:CG	2.41	0.45
1:A:293:ILE:HD13	1:A:294:ALA:N	2.31	0.45
1:P:564:GLY:HA3	1:Q:535:ILE:HD11	1.99	0.45
1:C:232:ALA:N	1:C:269:ARG:O	2.50	0.45
1:O:86:ALA:CB	1:O:515:GLU:HG3	2.44	0.45
2:Y:43:GLN:C	2:Y:45:ALA:N	2.70	0.45
1:K:262:GLY:O	1:K:263:PHE:HB3	2.17	0.45
1:O:71:MSE:HE3	1:O:115:VAL:HB	1.98	0.45
1:X:66:LYS:HZ3	1:X:420:VAL:HG21	1.82	0.45
1:W:71:MSE:HE3	1:W:115:VAL:HB	1.98	0.45
1:O:351:PHE:CD2	1:O:356:ILE:HD12	2.51	0.45
1:N:371:TYR:HE2	1:N:373:LEU:HD21	1.82	0.45
1:H:232:ALA:N	1:H:269:ARG:O	2.50	0.45
1:A:35:PHE:HE2	1:A:324:LYS:NZ	2.08	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ARG:NH2	1:B:30:LYS:HB2	2.28	0.45
1:C:164:LEU:HA	1:C:307:TRP:CH2	2.51	0.45
1:F:164:LEU:HA	1:F:307:TRP:CH2	2.51	0.45
1:G:28:GLU:HG3	1:G:32:ASP:OD2	2.15	0.45
1:G:427:GLY:C	1:G:429:GLN:N	2.70	0.45
1:G:528:LYS:HD2	1:G:560:LEU:HD21	1.99	0.45
1:G:561:ASP:OD2	1:H:92:ASP:HB3	2.16	0.45
1:H:164:LEU:HA	1:H:307:TRP:CH2	2.51	0.45
1:H:78:VAL:CG2	1:H:444:LEU:HD21	2.46	0.45
1:J:182:ASN:HD22	1:K:171:ARG:HH21	1.65	0.45
1:M:29:ALA:O	1:M:33:LEU:HG	2.16	0.45
1:M:34:PHE:O	1:M:37:ARG:HB2	2.17	0.45
1:L:92:ASP:OD2	1:L:92:ASP:N	2.48	0.45
1:O:343:ARG:O	1:O:344:THR:HB	2.16	0.45
1:R:443:ASP:O	1:R:446:THR:HG22	2.17	0.45
1:S:164:LEU:HA	1:S:307:TRP:CH2	2.51	0.45
1:T:41:TRP:HE3	1:T:42:ASP:HB3	1.82	0.45
1:U:34:PHE:O	1:U:37:ARG:HB2	2.16	0.45
1:V:26:ARG:HG3	1:V:27:ARG:N	2.31	0.45
1:V:316:TYR:O	1:V:321:ARG:NH1	2.50	0.45
1:V:528:LYS:CD	1:V:560:LEU:HD21	2.46	0.45
1:W:444:LEU:HD13	1:W:444:LEU:N	2.32	0.45
1:P:14:ARG:CA	1:P:14:ARG:NE	2.71	0.45
1:W:82:PRO:O	1:W:516:CYS:HA	2.17	0.45
1:X:409:THR:O	1:X:413:LYS:HG2	2.16	0.45
1:B:273:ARG:O	1:B:274:ARG:HB3	2.17	0.45
1:C:273:ARG:O	1:C:274:ARG:CB	2.64	0.45
1:L:273:ARG:O	1:L:274:ARG:HB3	2.17	0.45
1:J:201:PHE:HE2	1:J:281:ILE:HG22	1.80	0.45
1:W:24:GLU:HG3	1:W:313:LYS:HE2	1.98	0.45
1:W:198:ILE:HA	1:W:199:PRO:HD3	1.71	0.45
1:R:66:LYS:HZ3	1:R:420:VAL:HG11	1.79	0.45
1:K:207:TRP:O	1:K:208:VAL:C	2.53	0.45
1:H:293:ILE:HD13	1:H:294:ALA:N	2.31	0.45
1:L:293:ILE:HD13	1:L:294:ALA:N	2.31	0.45
1:F:9:GLU:HG3	1:F:12:LEU:H	1.82	0.45
1:A:9:GLU:HG3	1:A:12:LEU:H	1.81	0.45
3:Q:719:HOH:O	1:R:430:VAL:HG11	2.15	0.45
1:A:262:GLY:O	1:A:263:PHE:HB3	2.17	0.45
1:B:262:GLY:O	1:B:263:PHE:HB3	2.17	0.45
1:E:262:GLY:O	1:E:263:PHE:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:262:GLY:O	1:H:263:PHE:HB3	2.17	0.45
1:X:429:GLN:O	1:X:429:GLN:HG2	2.16	0.45
1:D:86:ALA:CB	1:D:515:GLU:HG3	2.47	0.45
1:D:410:SER:O	1:D:414:GLU:HG2	2.16	0.45
1:E:590:GLN:O	1:E:594:VAL:HG23	2.16	0.45
1:U:174:THR:N	3:U:705:HOH:O	2.50	0.45
1:P:76:ILE:HD12	1:P:433:ASP:OD1	2.16	0.45
1:X:136:SER:N	1:X:137:PRO:HD3	2.32	0.45
1:P:396:GLU:O	1:Q:399:GLN:OE1	2.34	0.45
1:V:127:ARG:HG2	1:V:147:GLU:HB2	1.98	0.45
1:A:26:ARG:NH2	1:A:30:LYS:HB2	2.28	0.45
1:A:77:ASP:HB2	1:A:523:SER:HB2	1.98	0.45
1:B:444:LEU:N	1:B:444:LEU:HD13	2.31	0.45
1:C:77:ASP:HB2	1:C:523:SER:HB2	1.98	0.45
1:F:434:THR:HA	1:F:437:GLN:HG2	1.97	0.45
1:F:528:LYS:HD2	1:F:560:LEU:HD21	1.99	0.45
1:F:182:ASN:HD22	1:G:171:ARG:HH21	1.61	0.45
1:G:77:ASP:HB2	1:G:523:SER:HB2	1.98	0.45
1:L:71:MSE:CE	1:L:115:VAL:HB	2.45	0.45
1:N:343:ARG:H	1:N:343:ARG:HG2	1.53	0.45
1:N:528:LYS:CD	1:N:560:LEU:HD21	2.46	0.45
1:O:165:MSE:HG3	1:O:307:TRP:CD2	2.49	0.45
1:O:26:ARG:HG3	1:O:27:ARG:N	2.32	0.45
1:P:53:TYR:OH	1:Q:329:LEU:HD21	2.16	0.45
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG21	1.82	0.45
1:R:24:GLU:O	1:R:26:ARG:N	2.50	0.45
1:T:31:ASN:O	1:T:34:PHE:HB3	2.16	0.45
1:V:136:SER:N	1:V:137:PRO:HD3	2.31	0.45
1:R:53:TYR:OH	1:X:329:LEU:HD21	2.16	0.45
1:T:528:LYS:CD	1:T:560:LEU:HD21	2.47	0.45
1:S:273:ARG:CZ	1:S:275:ARG:HE	2.29	0.45
1:C:234:ILE:HG12	1:C:267:ALA:HB3	1.96	0.45
1:C:251:ILE:HG23	1:C:507:LEU:HD22	1.98	0.45
1:E:251:ILE:HG23	1:E:507:LEU:HD22	1.98	0.45
1:F:234:ILE:CG2	1:F:246:TYR:HB3	2.47	0.45
1:F:251:ILE:HG23	1:F:507:LEU:HD22	1.98	0.45
1:U:198:ILE:HA	1:U:199:PRO:HD3	1.71	0.45
1:F:567:MSE:SE	1:G:576:LEU:HD13	2.66	0.45
1:S:193:LEU:HD22	1:S:287:LEU:HB3	1.97	0.45
1:K:57:PHE:CD2	1:K:330:ARG:CB	2.95	0.45
1:X:384:LEU:HD22	1:X:384:LEU:N	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:293:ILE:HD13	1:E:294:ALA:N	2.31	0.45
1:D:293:ILE:HD13	1:D:294:ALA:N	2.31	0.45
1:N:378:ASP:O	1:N:381:SER:O	2.34	0.45
1:W:420:VAL:HA	1:W:428:GLY:HA2	1.98	0.45
1:E:427:GLY:C	1:E:429:GLN:N	2.70	0.45
1:D:427:GLY:C	1:D:429:GLN:N	2.70	0.45
1:Q:322:LEU:H	1:Q:322:LEU:HD22	1.82	0.45
1:A:86:ALA:CB	1:A:515:GLU:HG3	2.47	0.45
1:U:227:GLU:O	1:U:227:GLU:CG	2.64	0.45
1:G:232:ALA:N	1:G:269:ARG:O	2.50	0.45
1:L:232:ALA:N	1:L:269:ARG:O	2.50	0.45
1:B:410:SER:O	1:B:414:GLU:HG2	2.16	0.45
1:F:232:ALA:N	1:F:269:ARG:O	2.50	0.45
1:G:590:GLN:O	1:G:594:VAL:HG23	2.16	0.45
1:C:410:SER:O	1:C:414:GLU:HG2	2.16	0.45
1:Q:396:GLU:O	1:R:399:GLN:OE1	2.34	0.45
1:A:47:GLN:CG	1:A:47:GLN:O	2.65	0.45
1:B:444:LEU:C	1:B:446:THR:H	2.19	0.45
1:C:58:ASP:O	1:C:59:VAL:HB	2.15	0.45
1:E:35:PHE:CE1	1:E:321:ARG:NH1	2.84	0.45
1:F:45:LEU:HD21	1:F:328:ARG:HH21	1.82	0.45
1:F:427:GLY:C	1:F:429:GLN:N	2.70	0.45
1:G:48:TYR:O	1:G:49:THR:CB	2.64	0.45
1:K:47:GLN:O	1:K:47:GLN:CG	2.65	0.45
1:K:9:GLU:HG3	1:K:12:LEU:H	1.82	0.45
1:R:31:ASN:O	1:R:34:PHE:HB3	2.16	0.45
1:R:35:PHE:C	1:R:37:ARG:N	2.70	0.45
1:R:37:ARG:C	1:R:39:SER:H	2.18	0.45
1:T:160:SER:O	1:T:161:ASN:ND2	2.43	0.45
1:T:443:ASP:C	1:T:444:LEU:HD13	2.36	0.45
1:U:136:SER:N	1:U:137:PRO:HD3	2.31	0.45
1:U:35:PHE:C	1:U:37:ARG:N	2.69	0.45
1:U:443:ASP:C	1:U:444:LEU:HD13	2.37	0.45
1:V:165:MSE:HG3	1:V:307:TRP:CD2	2.49	0.45
1:V:343:ARG:HG2	1:V:343:ARG:H	1.55	0.45
1:T:511:ARG:HA	1:T:513:ARG:CD	2.44	0.45
1:T:334:MSE:HE1	1:W:407:ALA:HB1	1.98	0.45
1:X:158:TRP:HH2	1:X:302:PRO:HG3	1.80	0.45
1:Q:510:ILE:O	1:Q:513:ARG:HD2	2.17	0.45
2:Y:71:ASP:O	2:Y:72:ASP:CB	2.65	0.45
2:Y:75:PRO:HA	2:Y:76:PRO:HD3	1.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:47:GLN:N	1:T:48:TYR:HD2	2.15	0.45
1:H:273:ARG:O	1:H:274:ARG:CB	2.64	0.45
1:I:227:GLU:OE2	1:I:227:GLU:N	2.47	0.45
1:C:273:ARG:O	1:C:274:ARG:HB3	2.17	0.45
1:E:234:ILE:HG22	1:E:246:TYR:HB3	1.98	0.45
1:I:201:PHE:HE2	1:I:281:ILE:HG22	1.80	0.45
1:O:193:LEU:HD22	1:O:287:LEU:HB3	1.98	0.45
1:O:554:LEU:O	1:O:557:PHE:HB3	2.16	0.45
1:H:207:TRP:O	1:H:208:VAL:C	2.54	0.45
1:R:40:GLN:HG2	1:X:310:VAL:HG22	1.98	0.45
1:G:9:GLU:HG3	1:G:12:LEU:H	1.82	0.45
1:D:238:PRO:HG3	1:D:263:PHE:CB	2.46	0.45
1:D:262:GLY:O	1:D:263:PHE:HB3	2.17	0.45
1:L:427:GLY:C	1:L:429:GLN:N	2.70	0.45
1:J:86:ALA:CB	1:J:515:GLU:HG3	2.47	0.45
1:K:410:SER:O	1:K:414:GLU:HG2	2.16	0.45
1:X:171:ARG:O	1:X:224:GLU:HA	2.17	0.45
1:F:590:GLN:O	1:F:594:VAL:HG23	2.16	0.45
1:T:270:GLN:OE1	1:T:270:GLN:HA	2.17	0.45
1:R:127:ARG:HG2	1:R:147:GLU:HB2	1.97	0.45
1:B:590:GLN:O	1:B:594:VAL:HG23	2.17	0.45
1:A:232:ALA:N	1:A:269:ARG:O	2.50	0.45
1:N:422:THR:HG22	1:N:423:GLU:N	2.32	0.45
1:E:47:GLN:O	1:E:47:GLN:CG	2.65	0.45
1:H:72:ARG:HD2	1:I:434:THR:HG21	1.99	0.45
1:I:528:LYS:HZ3	1:I:560:LEU:HD21	1.80	0.45
1:I:94:LEU:HA	1:I:97:MSE:CE	2.37	0.45
1:J:48:TYR:O	1:J:49:THR:CB	2.64	0.45
1:M:24:GLU:O	1:M:26:ARG:N	2.49	0.45
1:M:41:TRP:HE1	1:O:27:ARG:NH2	2.14	0.45
1:O:316:TYR:O	1:O:321:ARG:NH1	2.49	0.45
1:O:35:PHE:CE1	1:O:321:ARG:NH1	2.84	0.45
1:Q:343:ARG:O	1:Q:344:THR:HB	2.16	0.45
1:L:444:LEU:N	1:L:444:LEU:HD13	2.31	0.45
1:R:444:LEU:O	1:R:446:THR:N	2.49	0.45
1:T:316:TYR:O	1:T:321:ARG:NH1	2.50	0.45
1:V:123:VAL:CG1	1:V:304:PHE:CE1	3.00	0.45
1:V:35:PHE:C	1:V:37:ARG:N	2.70	0.45
1:X:444:LEU:HD13	1:X:444:LEU:N	2.30	0.45
1:O:510:ILE:O	1:O:513:ARG:HD2	2.17	0.45
2:Z:71:ASP:O	2:Z:72:ASP:CB	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:298:ILE:HA	1:M:299:PRO:HD3	1.79	0.45
1:P:334:MSE:HE1	1:Q:407:ALA:HB1	1.99	0.45
1:G:273:ARG:O	1:G:274:ARG:HB3	2.16	0.45
1:T:451:ASP:O	1:T:453:LEU:N	2.49	0.45
1:A:234:ILE:CG2	1:A:246:TYR:HB3	2.46	0.45
1:E:234:ILE:CG2	1:E:246:TYR:HB3	2.47	0.45
1:E:273:ARG:O	1:E:274:ARG:CB	2.64	0.45
1:E:273:ARG:O	1:E:274:ARG:HB3	2.17	0.45
1:E:248:LYS:HZ1	1:E:513:ARG:HH12	1.64	0.45
1:L:273:ARG:O	1:L:274:ARG:CB	2.64	0.45
1:C:201:PHE:HE2	1:C:281:ILE:HG22	1.80	0.45
1:X:26:ARG:HG3	1:X:27:ARG:N	2.31	0.45
1:X:235:TYR:OH	1:X:252:LYS:NZ	2.48	0.45
1:X:232:ALA:HB2	1:X:269:ARG:O	2.17	0.45
3:J:719:HOH:O	1:K:438:LEU:HD22	2.16	0.45
1:F:293:ILE:HD13	1:F:294:ALA:N	2.31	0.45
1:U:420:VAL:HA	1:U:428:GLY:HA2	1.98	0.45
1:B:293:ILE:HD13	1:B:294:ALA:N	2.31	0.45
1:S:310:VAL:HG22	1:U:40:GLN:HG2	1.99	0.45
1:M:276:VAL:CG2	1:M:293:ILE:HG23	2.47	0.45
1:E:177:HIS:HE1	1:E:221:GLU:OE1	2.00	0.45
1:P:378:ASP:O	1:P:381:SER:O	2.35	0.45
1:C:238:PRO:HG3	1:C:263:PHE:CB	2.46	0.45
1:L:262:GLY:O	1:L:263:PHE:HB3	2.17	0.45
1:K:451:ASP:O	1:K:456:ALA:N	2.41	0.45
1:B:456:ALA:CB	1:B:509:ASP:OD2	2.65	0.45
1:L:456:ALA:CB	1:L:509:ASP:OD2	2.65	0.45
1:B:86:ALA:CB	1:B:515:GLU:HG3	2.47	0.45
1:G:534:GLU:O	1:G:538:LEU:HD23	2.17	0.45
1:Q:171:ARG:O	1:Q:224:GLU:HA	2.17	0.45
1:N:55:GLY:HA3	1:N:57:PHE:CE1	2.51	0.45
1:U:371:TYR:HE2	1:U:373:LEU:HD21	1.81	0.45
1:P:227:GLU:CG	1:P:227:GLU:O	2.64	0.45
1:M:422:THR:HG22	1:M:423:GLU:N	2.32	0.45
1:H:410:SER:O	1:H:414:GLU:HG2	2.16	0.45
1:J:590:GLN:O	1:J:594:VAL:HG23	2.17	0.45
1:I:232:ALA:N	1:I:269:ARG:O	2.50	0.45
1:U:422:THR:HG22	1:U:423:GLU:N	2.31	0.45
1:A:45:LEU:HD21	1:A:328:ARG:HH21	1.82	0.45
1:B:47:GLN:CG	1:B:47:GLN:O	2.65	0.45
1:C:35:PHE:CE1	1:C:321:ARG:NH1	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:GLU:HB3	1:F:321:ARG:CZ	2.46	0.45
1:G:434:THR:HA	1:G:437:GLN:HG2	1.98	0.45
1:H:413:LYS:HE2	1:H:413:LYS:HB3	1.74	0.45
1:H:77:ASP:HB2	1:H:523:SER:HB2	1.98	0.45
1:I:48:TYR:O	1:I:49:THR:CB	2.64	0.45
1:I:528:LYS:HD2	1:I:560:LEU:HD21	1.99	0.45
1:J:528:LYS:HZ3	1:J:560:LEU:HD21	1.80	0.45
1:J:78:VAL:HG21	1:J:444:LEU:CD1	2.21	0.45
1:L:35:PHE:CE1	1:L:321:ARG:NH1	2.84	0.45
1:M:100:THR:HG22	1:M:138:THR:HG22	1.97	0.45
1:M:82:PRO:O	1:M:516:CYS:HA	2.17	0.45
1:O:420:VAL:HA	1:O:428:GLY:HA2	1.98	0.45
1:O:444:LEU:O	1:O:446:THR:N	2.50	0.45
1:N:164:LEU:HA	1:N:307:TRP:HH2	1.81	0.45
1:N:41:TRP:HE3	1:N:42:ASP:HB3	1.80	0.45
1:P:31:ASN:O	1:P:34:PHE:HB3	2.15	0.45
1:P:37:ARG:C	1:P:39:SER:H	2.20	0.45
1:Q:26:ARG:HG3	1:Q:27:ARG:N	2.31	0.45
1:Q:41:TRP:HE3	1:Q:42:ASP:HB3	1.82	0.45
1:S:123:VAL:HG22	1:S:316:TYR:HE2	1.80	0.45
1:U:47:GLN:H	1:U:48:TYR:HD2	1.65	0.45
1:W:443:ASP:O	1:W:446:THR:HG22	2.17	0.45
1:X:164:LEU:HD22	1:X:169:ASP:OD1	2.17	0.45
1:W:511:ARG:HA	1:W:513:ARG:CD	2.44	0.45
1:S:301:VAL:HA	1:S:302:PRO:HD3	1.80	0.45
1:O:409:THR:O	1:O:413:LYS:HG2	2.16	0.45
1:X:118:GLN:OE1	1:X:303:VAL:HB	2.17	0.45
1:R:301:VAL:HA	1:R:302:PRO:HD3	1.79	0.45
1:Q:451:ASP:C	1:Q:453:LEU:N	2.70	0.45
1:K:234:ILE:CG2	1:K:246:TYR:HB3	2.47	0.45
1:B:246:TYR:HD2	1:B:511:ARG:CB	2.28	0.45
1:B:273:ARG:O	1:B:274:ARG:CB	2.64	0.45
1:T:273:ARG:HH22	1:T:453:LEU:CD2	2.28	0.45
1:I:251:ILE:HG23	1:I:507:LEU:HD22	1.98	0.45
1:L:251:ILE:HG23	1:L:507:LEU:HD22	1.99	0.45
1:E:577:ILE:HG12	1:E:582:LYS:CG	2.41	0.45
1:A:404:MSE:CE	1:L:334:MSE:HE3	2.47	0.45
1:U:454:ALA:O	1:U:455:THR:C	2.54	0.45
1:G:293:ILE:HD13	1:G:294:ALA:N	2.31	0.45
1:D:177:HIS:HE1	1:D:221:GLU:OE1	2.00	0.45
1:E:9:GLU:HG3	1:E:12:LEU:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:177:HIS:HE1	1:H:221:GLU:OE1	2.00	0.45
1:A:427:GLY:C	1:A:429:GLN:N	2.70	0.45
1:R:322:LEU:HD22	1:R:322:LEU:H	1.81	0.45
1:K:534:GLU:O	1:K:538:LEU:HD23	2.17	0.45
1:M:348:LYS:HB2	1:N:372:TYR:CE2	2.52	0.45
1:N:191:TYR:HE1	1:N:278:LYS:HZ3	1.63	0.45
1:Q:422:THR:HG22	1:Q:423:GLU:N	2.32	0.45
1:O:190:LYS:HE3	1:O:190:LYS:HA	1.99	0.45
1:R:77:ASP:HB2	1:R:523:SER:HB2	1.98	0.45
1:T:76:ILE:HD12	1:T:433:ASP:OD1	2.16	0.45
1:D:590:GLN:O	1:D:594:VAL:HG23	2.17	0.45
1:A:444:LEU:C	1:A:446:THR:H	2.19	0.45
1:C:444:LEU:C	1:C:446:THR:H	2.19	0.45
1:E:48:TYR:O	1:E:49:THR:CB	2.64	0.45
1:H:47:GLN:O	1:H:47:GLN:CG	2.65	0.45
1:I:164:LEU:HA	1:I:307:TRP:CH2	2.51	0.45
1:I:434:THR:HA	1:I:437:GLN:HG2	1.98	0.45
1:O:444:LEU:HD13	1:O:444:LEU:N	2.31	0.45
1:L:434:THR:HA	1:L:437:GLN:HG2	1.98	0.45
1:S:123:VAL:HG13	1:S:304:PHE:CE1	2.52	0.45
1:S:78:VAL:CG1	1:S:79:LEU:H	2.30	0.45
1:X:35:PHE:C	1:X:37:ARG:N	2.70	0.45
1:I:273:ARG:O	1:I:274:ARG:HB3	2.16	0.45
1:L:234:ILE:HG22	1:L:246:TYR:HB3	1.98	0.45
1:G:567:MSE:SE	1:H:576:LEU:HD13	2.67	0.45
1:P:26:ARG:HG3	1:P:27:ARG:N	2.31	0.45
1:S:266:ILE:O	1:S:267:ALA:HB2	2.17	0.45
1:P:193:LEU:HD22	1:P:287:LEU:HB3	1.98	0.45
1:U:232:ALA:HB1	1:U:233:PHE:H	1.57	0.45
1:J:563:LYS:HD3	1:K:557:PHE:CE2	2.52	0.45
1:A:177:HIS:HE1	1:A:221:GLU:OE1	2.00	0.45
1:I:177:HIS:HE1	1:I:221:GLU:OE1	2.00	0.45
1:U:429:GLN:O	1:U:429:GLN:HG2	2.16	0.45
1:C:456:ALA:CB	1:C:509:ASP:OD2	2.65	0.45
1:D:456:ALA:CB	1:D:509:ASP:OD2	2.65	0.45
1:F:456:ALA:CB	1:F:509:ASP:OD2	2.65	0.45
1:I:451:ASP:O	1:I:456:ALA:N	2.41	0.45
1:L:534:GLU:O	1:L:538:LEU:HD23	2.17	0.45
1:H:534:GLU:O	1:H:538:LEU:HD23	2.17	0.45
1:G:86:ALA:CB	1:G:515:GLU:HG3	2.47	0.45
1:A:534:GLU:O	1:A:538:LEU:HD23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:127:ARG:HG2	1:W:147:GLU:HB2	1.98	0.45
1:X:76:ILE:HD12	1:X:433:ASP:OD1	2.17	0.45
1:B:232:ALA:N	1:B:269:ARG:O	2.50	0.45
1:W:77:ASP:HB2	1:W:523:SER:HB2	1.99	0.45
1:N:260:ASP:HA	1:N:264:ILE:HB	1.97	0.45
1:C:434:THR:HA	1:C:437:GLN:HG2	1.98	0.45
1:D:45:LEU:HD21	1:D:328:ARG:HH21	1.82	0.45
1:F:31:ASN:HD22	1:F:31:ASN:HA	1.62	0.45
1:H:434:THR:HA	1:H:437:GLN:HG2	1.97	0.45
1:I:45:LEU:HD22	1:I:45:LEU:N	2.32	0.45
1:J:427:GLY:C	1:J:429:GLN:N	2.70	0.45
1:K:164:LEU:HA	1:K:307:TRP:CH2	2.51	0.45
1:K:26:ARG:NH2	1:K:30:LYS:HB2	2.28	0.45
1:L:47:GLN:CG	1:L:47:GLN:O	2.65	0.45
1:M:26:ARG:HG3	1:M:27:ARG:N	2.31	0.45
1:O:35:PHE:HZ	1:O:321:ARG:NE	2.11	0.45
1:O:35:PHE:C	1:O:37:ARG:N	2.70	0.45
1:P:444:LEU:N	1:P:444:LEU:HD13	2.30	0.45
1:P:80:TYR:OH	1:P:444:LEU:HD12	2.17	0.45
1:Q:136:SER:N	1:Q:137:PRO:HD3	2.33	0.45
1:U:343:ARG:O	1:U:344:THR:HB	2.16	0.45
1:W:33:LEU:HD12	1:W:34:PHE:N	2.31	0.45
1:C:139:SER:CB	1:C:455:THR:CG2	2.80	0.45
1:S:15:PHE:CE2	1:S:19:TRP:NE1	2.85	0.45
1:X:158:TRP:H	1:X:158:TRP:HD1	1.65	0.45
1:U:330:ARG:O	1:U:334:MSE:HB2	2.17	0.45
1:W:330:ARG:HD2	1:W:409:THR:CG2	2.40	0.45
1:P:273:ARG:CZ	1:P:275:ARG:HE	2.30	0.45
1:H:227:GLU:HA	1:H:274:ARG:CA	2.44	0.45
1:N:451:ASP:C	1:N:453:LEU:H	2.19	0.45
1:C:234:ILE:CG2	1:C:246:TYR:HB3	2.47	0.45
1:L:246:TYR:HD2	1:L:511:ARG:CB	2.28	0.45
1:D:201:PHE:HE2	1:D:281:ILE:HG22	1.80	0.45
1:N:198:ILE:HA	1:N:199:PRO:HD3	1.70	0.45
1:W:280:ILE:HD12	1:W:280:ILE:N	2.32	0.45
1:T:232:ALA:HB2	1:T:269:ARG:O	2.17	0.45
1:B:334:MSE:HE3	1:C:404:MSE:HE3	1.99	0.45
1:G:376:ARG:HB2	1:H:352:TRP:CG	2.52	0.45
1:D:554:LEU:HD22	1:E:567:MSE:HE2	1.99	0.45
1:B:9:GLU:HG3	1:B:12:LEU:H	1.81	0.45
1:T:378:ASP:O	1:T:381:SER:O	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:542:THR:HA	1:H:543:PRO:HD3	1.82	0.45
1:A:348:LYS:HB2	1:L:372:TYR:CD2	2.50	0.45
1:G:238:PRO:HG3	1:G:263:PHE:CB	2.46	0.45
1:X:418:LEU:HB2	1:X:428:GLY:O	2.16	0.45
1:D:534:GLU:O	1:D:538:LEU:HD23	2.17	0.45
1:E:86:ALA:CB	1:E:515:GLU:HG3	2.47	0.45
1:F:86:ALA:CB	1:F:515:GLU:HG3	2.47	0.45
1:H:372:TYR:CE2	1:I:348:LYS:HB2	2.51	0.45
1:V:198:ILE:HG22	1:V:198:ILE:O	2.17	0.45
1:A:45:LEU:HD22	1:A:45:LEU:N	2.32	0.44
1:B:35:PHE:CE1	1:B:321:ARG:NH1	2.84	0.44
1:B:78:VAL:HG21	1:B:444:LEU:CD1	2.21	0.44
1:C:427:GLY:C	1:C:429:GLN:N	2.70	0.44
1:C:78:VAL:HG21	1:C:444:LEU:CD1	2.21	0.44
1:E:434:THR:O	1:E:437:GLN:HG2	2.17	0.44
1:E:528:LYS:HD2	1:E:560:LEU:HD21	1.99	0.44
1:F:47:GLN:CG	1:F:47:GLN:O	2.65	0.44
1:G:434:THR:O	1:G:437:GLN:HG2	2.17	0.44
1:G:444:LEU:C	1:G:446:THR:H	2.19	0.44
1:J:444:LEU:C	1:J:446:THR:H	2.19	0.44
1:J:45:LEU:N	1:J:45:LEU:HD22	2.32	0.44
1:J:528:LYS:HD2	1:J:560:LEU:HD21	1.99	0.44
1:L:45:LEU:HD21	1:L:328:ARG:HH21	1.82	0.44
1:M:41:TRP:HE1	1:O:27:ARG:HH21	1.63	0.44
1:M:437:GLN:HA	1:M:440:MSE:HB2	1.97	0.44
1:N:136:SER:N	1:N:137:PRO:HD3	2.31	0.44
1:N:37:ARG:C	1:N:39:SER:H	2.19	0.44
1:R:123:VAL:CG1	1:R:304:PHE:CE1	3.00	0.44
1:S:82:PRO:O	1:S:516:CYS:HA	2.17	0.44
1:T:158:TRP:HD1	1:T:158:TRP:H	1.64	0.44
1:U:100:THR:HG22	1:U:138:THR:HG22	1.98	0.44
1:U:147:GLU:HA	1:U:148:PRO:HD3	1.81	0.44
1:U:316:TYR:O	1:U:321:ARG:NH1	2.50	0.44
1:V:444:LEU:HD13	1:V:444:LEU:N	2.32	0.44
1:X:34:PHE:O	1:X:37:ARG:HB2	2.17	0.44
1:R:511:ARG:HA	1:R:513:ARG:CD	2.45	0.44
1:M:274:ARG:O	1:M:275:ARG:HD2	2.18	0.44
1:R:71:MSE:HE3	1:R:115:VAL:HB	1.98	0.44
1:M:118:GLN:OE1	1:M:303:VAL:HB	2.17	0.44
1:Q:273:ARG:HH22	1:Q:453:LEU:CD2	2.30	0.44
1:J:273:ARG:NH2	1:J:453:LEU:HD11	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:273:ARG:NH2	1:K:453:LEU:HD11	2.33	0.44
1:R:236:GLN:H	1:R:265:LYS:HB2	1.82	0.44
1:N:236:GLN:H	1:N:265:LYS:HB2	1.82	0.44
1:Q:193:LEU:HD22	1:Q:287:LEU:HB3	1.97	0.44
1:N:577:ILE:HG12	1:N:582:LYS:CG	2.45	0.44
1:T:420:VAL:HA	1:T:428:GLY:HA2	1.98	0.44
1:H:9:GLU:HG3	1:H:12:LEU:H	1.81	0.44
1:J:9:GLU:HG3	1:J:12:LEU:H	1.81	0.44
1:F:177:HIS:HE1	1:F:221:GLU:OE1	2.00	0.44
1:G:262:GLY:O	1:G:263:PHE:HB3	2.17	0.44
1:J:238:PRO:HG3	1:J:263:PHE:CB	2.46	0.44
1:Q:429:GLN:O	1:Q:429:GLN:HG2	2.17	0.44
1:Q:57:PHE:N	1:Q:57:PHE:CD1	2.84	0.44
2:Z:39:PRO:HB2	2:Z:40:GLN:H	1.51	0.44
1:K:86:ALA:CB	1:K:515:GLU:HG3	2.47	0.44
1:F:534:GLU:O	1:F:538:LEU:HD23	2.17	0.44
1:D:232:ALA:N	1:D:269:ARG:O	2.50	0.44
1:K:232:ALA:N	1:K:269:ARG:O	2.50	0.44
1:Q:280:ILE:HD12	1:Q:280:ILE:N	2.33	0.44
1:L:77:ASP:HB2	1:L:523:SER:HB2	1.98	0.44
1:D:77:ASP:HB2	1:D:523:SER:HB2	1.98	0.44
1:E:78:VAL:CG2	1:E:444:LEU:HD21	2.46	0.44
1:F:45:LEU:N	1:F:45:LEU:HD22	2.32	0.44
1:G:47:GLN:CG	1:G:47:GLN:O	2.65	0.44
1:H:45:LEU:HD21	1:H:328:ARG:HH21	1.82	0.44
1:K:45:LEU:N	1:K:45:LEU:HD22	2.32	0.44
1:L:26:ARG:NH2	1:L:30:LYS:HB2	2.28	0.44
1:L:9:GLU:HG3	1:L:12:LEU:H	1.81	0.44
1:M:136:SER:N	1:M:137:PRO:HD3	2.32	0.44
1:O:78:VAL:CG1	1:O:444:LEU:HG	2.47	0.44
1:O:47:GLN:N	1:O:48:TYR:HD2	2.15	0.44
1:P:164:LEU:HA	1:P:307:TRP:HH2	1.81	0.44
1:Q:418:LEU:HB2	1:Q:428:GLY:O	2.16	0.44
1:X:340:ILE:O	1:X:344:THR:HG21	2.16	0.44
1:X:38:VAL:HG21	1:X:324:LYS:HD2	1.99	0.44
1:X:443:ASP:C	1:X:446:THR:HG22	2.36	0.44
1:X:71:MSE:HE3	1:X:115:VAL:HB	1.99	0.44
1:R:528:LYS:CD	1:R:560:LEU:HD21	2.47	0.44
1:R:118:GLN:OE1	1:R:303:VAL:HB	2.16	0.44
1:B:251:ILE:HG23	1:B:507:LEU:HD22	1.98	0.44
1:H:251:ILE:HG23	1:H:507:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:234:ILE:CG2	1:I:246:TYR:HB3	2.47	0.44
1:E:246:TYR:HD2	1:E:511:ARG:CB	2.28	0.44
1:F:227:GLU:OE2	1:F:227:GLU:N	2.47	0.44
1:F:273:ARG:O	1:F:274:ARG:HB3	2.17	0.44
1:L:234:ILE:CG2	1:L:246:TYR:HB3	2.47	0.44
1:S:564:GLY:O	1:T:554:LEU:HD21	2.17	0.44
1:W:236:GLN:HG3	1:W:265:LYS:HG2	1.99	0.44
1:W:24:GLU:O	1:W:26:ARG:N	2.49	0.44
1:M:236:GLN:H	1:M:265:LYS:HB2	1.83	0.44
1:Q:383:ASP:C	1:Q:385:PRO:HD3	2.38	0.44
1:S:236:GLN:H	1:S:265:LYS:HB2	1.82	0.44
1:P:198:ILE:O	1:P:198:ILE:HG22	2.16	0.44
1:V:387:GLN:H	1:V:387:GLN:HG2	1.57	0.44
1:T:71:MSE:HE3	1:T:115:VAL:HB	1.98	0.44
1:S:155:HIS:CE1	1:S:204:PRO:HB2	2.52	0.44
1:J:177:HIS:HE1	1:J:221:GLU:OE1	2.00	0.44
1:L:177:HIS:HE1	1:L:221:GLU:OE1	2.00	0.44
1:P:57:PHE:N	1:P:57:PHE:CD1	2.86	0.44
2:Z:37:VAL:C	2:Z:39:PRO:HD3	2.38	0.44
1:F:451:ASP:O	1:F:456:ALA:N	2.41	0.44
1:G:456:ALA:CB	1:G:509:ASP:OD2	2.65	0.44
1:B:343:ARG:H	1:B:343:ARG:HG2	1.52	0.44
1:K:538:LEU:HB3	1:K:551:LEU:HD13	2.00	0.44
1:P:322:LEU:H	1:P:322:LEU:HD22	1.81	0.44
1:V:190:LYS:HE3	1:V:190:LYS:HA	2.00	0.44
1:X:322:LEU:N	1:X:322:LEU:HD22	2.32	0.44
1:C:590:GLN:O	1:C:594:VAL:HG23	2.16	0.44
1:A:590:GLN:O	1:A:594:VAL:HG23	2.16	0.44
1:C:48:TYR:O	1:C:49:THR:CB	2.64	0.44
1:D:45:LEU:N	1:D:45:LEU:HD22	2.32	0.44
1:E:26:ARG:NH2	1:E:30:LYS:HB2	2.28	0.44
1:F:15:PHE:HE2	1:F:19:TRP:HE1	1.66	0.44
1:F:528:LYS:HZ2	1:F:560:LEU:HD21	1.79	0.44
1:H:334:MSE:HE3	1:I:404:MSE:HE1	1.99	0.44
1:I:25:ALA:O	1:I:29:ALA:CB	2.58	0.44
1:I:444:LEU:N	1:I:444:LEU:HD13	2.31	0.44
1:J:34:PHE:CE1	1:J:324:LYS:NZ	2.72	0.44
1:P:35:PHE:C	1:P:37:ARG:N	2.70	0.44
1:Q:420:VAL:HA	1:Q:428:GLY:HA2	1.99	0.44
1:S:26:ARG:HG3	1:S:27:ARG:N	2.31	0.44
1:S:444:LEU:HD13	1:S:444:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:136:SER:N	1:T:137:PRO:HD3	2.32	0.44
1:U:164:LEU:HD22	1:U:169:ASP:OD1	2.17	0.44
1:W:316:TYR:O	1:W:321:ARG:NH1	2.50	0.44
1:W:34:PHE:O	1:W:37:ARG:HB2	2.18	0.44
1:X:316:TYR:O	1:X:321:ARG:NH1	2.50	0.44
1:P:118:GLN:OE1	1:P:303:VAL:HB	2.17	0.44
1:J:273:ARG:O	1:J:274:ARG:HB3	2.17	0.44
1:O:273:ARG:HH22	1:O:453:LEU:CD2	2.30	0.44
1:G:251:ILE:HG23	1:G:507:LEU:HD22	1.99	0.44
1:P:451:ASP:C	1:P:453:LEU:H	2.18	0.44
1:D:273:ARG:NH2	1:D:453:LEU:HD11	2.32	0.44
1:Q:236:GLN:H	1:Q:265:LYS:HB2	1.82	0.44
1:W:26:ARG:HG3	1:W:27:ARG:N	2.32	0.44
1:O:236:GLN:HG3	1:O:265:LYS:HG2	2.00	0.44
1:N:232:ALA:HB2	1:N:269:ARG:O	2.18	0.44
1:N:454:ALA:O	1:N:455:THR:C	2.54	0.44
1:S:454:ALA:O	1:S:455:THR:C	2.54	0.44
1:A:400:ALA:HB3	1:L:395:PRO:HB2	1.99	0.44
1:C:262:GLY:O	1:C:263:PHE:HB3	2.17	0.44
1:C:343:ARG:HG2	1:C:343:ARG:H	1.52	0.44
2:Y:57:TYR:H	2:Y:63:ILE:H	1.65	0.44
1:K:177:HIS:HE1	1:K:221:GLU:OE1	2.00	0.44
1:B:427:GLY:C	1:B:429:GLN:N	2.70	0.44
2:Y:39:PRO:HB2	2:Y:40:GLN:H	1.51	0.44
1:D:451:ASP:O	1:D:456:ALA:N	2.41	0.44
1:E:456:ALA:CB	1:E:509:ASP:OD2	2.65	0.44
1:I:456:ALA:CB	1:I:509:ASP:OD2	2.65	0.44
1:I:86:ALA:CB	1:I:515:GLU:HG3	2.47	0.44
1:H:86:ALA:CB	1:H:515:GLU:HG3	2.47	0.44
1:J:232:ALA:N	1:J:269:ARG:O	2.50	0.44
1:V:77:ASP:HB2	1:V:523:SER:HB2	1.98	0.44
1:S:422:THR:HG22	1:S:423:GLU:N	2.32	0.44
1:T:422:THR:HG22	1:T:423:GLU:N	2.31	0.44
1:X:191:TYR:HE1	1:X:278:LYS:HZ3	1.66	0.44
1:C:47:GLN:CG	1:C:47:GLN:O	2.65	0.44
1:D:66:LYS:O	1:D:70:GLU:HG3	2.18	0.44
1:E:45:LEU:N	1:E:45:LEU:HD22	2.32	0.44
1:F:77:ASP:HB2	1:F:523:SER:HB2	1.98	0.44
1:G:45:LEU:N	1:G:45:LEU:HD22	2.32	0.44
1:H:182:ASN:HD22	1:I:171:ARG:HH21	1.65	0.44
1:I:434:THR:O	1:I:437:GLN:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:45:LEU:HD21	1:K:328:ARG:HH21	1.82	0.44
1:M:443:ASP:O	1:M:446:THR:HG22	2.18	0.44
1:L:434:THR:O	1:L:437:GLN:HG2	2.18	0.44
1:P:38:VAL:HG21	1:P:324:LYS:HD2	1.98	0.44
1:P:33:LEU:HD12	1:P:34:PHE:N	2.32	0.44
1:P:437:GLN:HA	1:P:440:MSE:HB2	2.00	0.44
1:P:78:VAL:CG1	1:P:444:LEU:HG	2.47	0.44
1:R:100:THR:HG22	1:R:138:THR:HG22	1.98	0.44
1:S:437:GLN:HA	1:S:440:MSE:HB2	1.99	0.44
1:S:80:TYR:OH	1:S:444:LEU:HD12	2.18	0.44
1:U:29:ALA:O	1:U:33:LEU:HG	2.18	0.44
1:V:34:PHE:O	1:V:37:ARG:HB2	2.17	0.44
1:W:35:PHE:CE1	1:W:321:ARG:NH1	2.85	0.44
1:Q:118:GLN:OE1	1:Q:303:VAL:HB	2.17	0.44
2:Y:104:TYR:N	2:Y:104:TYR:CD1	2.85	0.44
1:P:510:ILE:O	1:P:513:ARG:HD2	2.16	0.44
1:J:251:ILE:HG23	1:J:507:LEU:HD22	1.98	0.44
1:P:274:ARG:O	1:P:275:ARG:HD2	2.18	0.44
1:L:273:ARG:NH2	1:L:453:LEU:HD11	2.33	0.44
1:D:219:ILE:HD13	1:D:282:THR:HG22	2.00	0.44
2:Z:143:THR:N	2:Z:154:GLU:HA	2.32	0.44
1:T:236:GLN:H	1:T:265:LYS:HB2	1.82	0.44
1:X:236:GLN:H	1:X:265:LYS:HB2	1.83	0.44
1:Q:40:GLN:HE21	1:Q:40:GLN:HB2	1.58	0.44
1:N:276:VAL:CG2	1:N:293:ILE:HG23	2.47	0.44
1:W:276:VAL:CG2	1:W:293:ILE:HG23	2.47	0.44
1:F:262:GLY:O	1:F:263:PHE:HB3	2.17	0.44
1:O:429:GLN:HG2	1:O:429:GLN:O	2.18	0.44
1:W:71:MSE:CE	1:W:115:VAL:HB	2.47	0.44
1:H:456:ALA:CB	1:H:509:ASP:OD2	2.65	0.44
1:L:86:ALA:CB	1:L:515:GLU:HG3	2.47	0.44
1:B:538:LEU:HB3	1:B:551:LEU:HD13	2.00	0.44
1:C:538:LEU:HB3	1:C:551:LEU:HD13	2.00	0.44
1:I:538:LEU:HB3	1:I:551:LEU:HD13	2.00	0.44
1:Q:190:LYS:HA	1:Q:190:LYS:HE3	2.00	0.44
1:X:190:LYS:HA	1:X:190:LYS:HE3	2.00	0.44
1:R:174:THR:N	3:R:705:HOH:O	2.50	0.44
1:M:191:TYR:HE1	1:M:278:LYS:HZ3	1.64	0.44
1:A:164:LEU:HA	1:A:307:TRP:CH2	2.51	0.44
1:A:443:ASP:C	1:A:446:THR:HG22	2.38	0.44
1:C:78:VAL:CG2	1:C:444:LEU:HD21	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:THR:O	1:D:437:GLN:HG2	2.18	0.44
1:D:78:VAL:CG2	1:D:444:LEU:HD21	2.46	0.44
1:E:444:LEU:HD23	1:E:518:THR:OG1	2.18	0.44
1:F:40:GLN:O	1:F:41:TRP:CB	2.55	0.44
1:F:444:LEU:HD23	1:F:518:THR:OG1	2.18	0.44
1:G:45:LEU:HD21	1:G:328:ARG:HH21	1.82	0.44
1:G:444:LEU:HD23	1:G:518:THR:OG1	2.18	0.44
1:H:427:GLY:C	1:H:429:GLN:N	2.70	0.44
1:H:434:THR:O	1:H:437:GLN:HG2	2.18	0.44
1:H:443:ASP:C	1:H:446:THR:HG22	2.38	0.44
1:H:528:LYS:HD2	1:H:560:LEU:HD21	1.99	0.44
1:I:444:LEU:HD23	1:I:518:THR:OG1	2.18	0.44
1:J:35:PHE:CE1	1:J:321:ARG:NH1	2.84	0.44
1:J:434:THR:O	1:J:437:GLN:HG2	2.18	0.44
1:M:444:LEU:O	1:M:446:THR:N	2.50	0.44
1:L:94:LEU:HA	1:L:97:MSE:CE	2.37	0.44
1:Q:35:PHE:C	1:Q:37:ARG:N	2.71	0.44
1:S:444:LEU:O	1:S:447:TYR:N	2.50	0.44
1:U:35:PHE:CE1	1:U:321:ARG:NH1	2.85	0.44
1:W:80:TYR:OH	1:W:444:LEU:HD12	2.18	0.44
1:X:160:SER:O	1:X:161:ASN:ND2	2.46	0.44
1:U:301:VAL:HG23	1:U:439:ASN:HB3	2.00	0.44
1:U:301:VAL:HA	1:U:302:PRO:HD3	1.79	0.44
1:J:227:GLU:OE2	1:J:227:GLU:N	2.47	0.44
1:D:234:ILE:HG22	1:D:246:TYR:HB3	1.98	0.44
1:A:251:ILE:HG23	1:A:507:LEU:HD22	1.99	0.44
1:O:266:ILE:O	1:O:267:ALA:HB2	2.17	0.44
1:U:266:ILE:O	1:U:267:ALA:HB2	2.18	0.44
1:X:383:ASP:C	1:X:385:PRO:HD3	2.38	0.44
1:S:198:ILE:HG22	1:S:198:ILE:O	2.16	0.44
1:V:232:ALA:HB2	1:V:269:ARG:O	2.17	0.44
1:X:577:ILE:HG12	1:X:582:LYS:CG	2.45	0.44
1:F:383:ASP:C	1:F:385:PRO:CD	2.86	0.44
1:P:454:ALA:O	1:P:455:THR:C	2.56	0.44
1:M:310:VAL:HG22	1:N:40:GLN:HG2	1.98	0.44
1:C:9:GLU:HG3	1:C:12:LEU:H	1.81	0.44
2:Z:43:GLN:C	2:Z:45:ALA:N	2.70	0.44
1:H:238:PRO:HG3	1:H:263:PHE:CB	2.46	0.44
1:Q:155:HIS:CE1	1:Q:204:PRO:HB2	2.53	0.44
1:M:387:GLN:HG2	1:M:387:GLN:H	1.58	0.44
1:T:343:ARG:O	1:T:344:THR:HB	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:ALA:CB	1:A:509:ASP:OD2	2.65	0.44
1:K:456:ALA:CB	1:K:509:ASP:OD2	2.65	0.44
1:V:57:PHE:N	1:V:57:PHE:CD1	2.85	0.44
1:D:538:LEU:HB3	1:D:551:LEU:HD13	2.00	0.44
1:J:534:GLU:O	1:J:538:LEU:HD23	2.17	0.44
1:C:86:ALA:CB	1:C:515:GLU:HG3	2.47	0.44
1:L:590:GLN:O	1:L:594:VAL:HG23	2.17	0.44
1:U:77:ASP:HB2	1:U:523:SER:HB2	1.99	0.44
1:W:76:ILE:HD12	1:W:433:ASP:OD1	2.18	0.44
1:X:107:ALA:HA	1:X:146:ARG:HB3	2.00	0.44
1:U:399:GLN:OE1	1:X:396:GLU:O	2.35	0.44
1:B:434:THR:O	1:B:437:GLN:HG2	2.18	0.44
1:B:45:LEU:HD22	1:B:45:LEU:N	2.32	0.44
1:B:95:MSE:HE1	1:B:99:ARG:NH2	2.33	0.44
1:D:155:HIS:CE1	1:D:204:PRO:HB2	2.53	0.44
1:F:298:ILE:HA	1:F:299:PRO:HD3	1.82	0.44
1:I:45:LEU:HD21	1:I:328:ARG:HH21	1.82	0.44
1:L:35:PHE:CE2	1:L:324:LYS:NZ	2.80	0.44
1:L:528:LYS:HD2	1:L:560:LEU:HD21	1.99	0.44
1:M:528:LYS:NZ	1:M:560:LEU:HD21	2.32	0.44
1:M:78:VAL:CG1	1:M:79:LEU:H	2.31	0.44
1:O:38:VAL:HG21	1:O:324:LYS:HD2	1.99	0.44
1:N:420:VAL:HA	1:N:428:GLY:HA2	2.00	0.44
1:S:164:LEU:HA	1:S:307:TRP:HH2	1.83	0.44
1:S:165:MSE:HG3	1:S:307:TRP:CD2	2.51	0.44
1:U:444:LEU:O	1:U:447:TYR:N	2.49	0.44
1:U:47:GLN:CG	1:U:48:TYR:H	2.30	0.44
1:A:58:ASP:O	1:A:59:VAL:HB	2.14	0.44
1:V:407:ALA:HB1	1:W:334:MSE:HE1	1.99	0.44
1:O:451:ASP:C	1:O:453:LEU:N	2.70	0.44
1:O:451:ASP:O	1:O:453:LEU:N	2.51	0.44
1:P:451:ASP:C	1:P:453:LEU:N	2.71	0.44
1:U:451:ASP:C	1:U:453:LEU:N	2.70	0.44
1:C:273:ARG:NH2	1:C:453:LEU:HD11	2.33	0.44
1:L:248:LYS:HZ1	1:L:513:ARG:HH12	1.64	0.44
1:H:219:ILE:HD13	1:H:282:THR:HG22	2.00	0.44
1:J:219:ILE:HD13	1:J:282:THR:HG22	2.00	0.44
1:M:236:GLN:HG3	1:M:265:LYS:HG2	1.99	0.44
1:X:236:GLN:HG3	1:X:265:LYS:HG2	2.00	0.44
1:X:554:LEU:O	1:X:557:PHE:HB3	2.18	0.44
1:X:454:ALA:O	1:X:455:THR:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:383:ASP:C	1:G:385:PRO:CD	2.86	0.44
1:M:577:ILE:HG12	1:M:582:LYS:CG	2.45	0.44
1:D:352:TRP:CG	1:E:376:ARG:HB2	2.53	0.44
1:C:293:ILE:HD13	1:C:294:ALA:N	2.31	0.44
1:D:9:GLU:HG3	1:D:12:LEU:H	1.81	0.44
1:I:9:GLU:HG3	1:I:12:LEU:H	1.81	0.44
1:V:387:GLN:O	1:V:389:LEU:HG	2.18	0.44
1:V:293:ILE:HG12	1:V:294:ALA:H	1.82	0.44
1:V:155:HIS:CE1	1:V:204:PRO:HB2	2.52	0.44
1:A:348:LYS:HE2	1:L:369:TYR:O	2.18	0.44
1:R:155:HIS:CE1	1:R:204:PRO:HB2	2.52	0.44
1:W:155:HIS:CE1	1:W:204:PRO:HB2	2.52	0.44
1:J:456:ALA:CB	1:J:509:ASP:OD2	2.65	0.44
2:Y:37:VAL:C	2:Y:39:PRO:HD3	2.38	0.44
1:A:451:ASP:O	1:A:456:ALA:N	2.41	0.44
1:E:534:GLU:O	1:E:538:LEU:HD23	2.17	0.44
1:A:444:LEU:HD23	1:A:518:THR:OG1	2.18	0.44
1:C:45:LEU:N	1:C:45:LEU:HD22	2.32	0.44
1:D:47:GLN:CG	1:D:47:GLN:O	2.65	0.44
1:D:94:LEU:HA	1:D:97:MSE:CE	2.37	0.44
1:E:413:LYS:HB3	1:E:413:LYS:HE2	1.74	0.44
1:E:95:MSE:HE1	1:E:99:ARG:NH2	2.33	0.44
1:F:413:LYS:HB3	1:F:413:LYS:HE2	1.74	0.44
1:F:95:MSE:HE1	1:F:99:ARG:NH2	2.33	0.44
1:G:443:ASP:C	1:G:446:THR:HG22	2.38	0.44
1:H:444:LEU:C	1:H:446:THR:H	2.19	0.44
1:I:443:ASP:C	1:I:446:THR:HG22	2.38	0.44
1:J:47:GLN:CG	1:J:47:GLN:O	2.65	0.44
1:J:444:LEU:HD23	1:J:518:THR:OG1	2.18	0.44
1:K:434:THR:O	1:K:437:GLN:HG2	2.18	0.44
1:L:15:PHE:HE2	1:L:19:TRP:HE1	1.66	0.44
1:O:80:TYR:OH	1:O:444:LEU:HD12	2.18	0.44
2:Z:28:VAL:HG11	2:Z:97:ALA:HA	1.88	0.44
1:N:33:LEU:HD12	1:N:34:PHE:N	2.33	0.44
1:N:34:PHE:O	1:N:37:ARG:HB2	2.17	0.44
1:V:100:THR:HG22	1:V:138:THR:HG22	2.00	0.44
1:S:510:ILE:O	1:S:513:ARG:HD2	2.18	0.44
1:M:248:LYS:HE2	1:M:513:ARG:HH12	1.83	0.44
1:O:158:TRP:HD1	1:O:158:TRP:H	1.64	0.44
1:V:71:MSE:CE	1:V:115:VAL:HB	2.48	0.44
1:U:158:TRP:HD1	1:U:158:TRP:H	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:330:ARG:O	1:S:334:MSE:HB2	2.17	0.44
1:R:71:MSE:CE	1:R:115:VAL:HB	2.48	0.44
1:W:273:ARG:HH22	1:W:453:LEU:CD2	2.30	0.44
1:Q:135:GLN:OE1	1:R:273:ARG:HG2	2.18	0.44
1:G:282:THR:HG23	1:G:287:LEU:CD1	2.43	0.44
1:Q:236:GLN:HG3	1:Q:265:LYS:HG2	2.00	0.44
1:P:236:GLN:HG3	1:P:265:LYS:HG2	2.00	0.44
2:Y:143:THR:N	2:Y:154:GLU:HA	2.32	0.44
1:V:236:GLN:HG3	1:V:265:LYS:HG2	1.99	0.44
1:P:24:GLU:HG3	1:P:313:LYS:HE2	2.00	0.44
1:S:66:LYS:HZ3	1:S:420:VAL:HG21	1.82	0.44
1:J:383:ASP:C	1:J:385:PRO:CD	2.86	0.44
1:G:95:MSE:HE1	1:G:99:ARG:NH2	2.33	0.44
1:E:232:ALA:N	1:E:269:ARG:O	2.50	0.44
1:I:534:GLU:O	1:I:538:LEU:HD23	2.17	0.44
1:M:190:LYS:HA	1:M:190:LYS:HE3	2.00	0.44
1:R:372:TYR:CE2	1:X:348:LYS:HB2	2.53	0.44
1:N:127:ARG:HG2	1:N:147:GLU:HB2	2.00	0.44
3:P:718:HOH:O	1:Q:438:LEU:HD22	2.15	0.44
1:S:352:TRP:O	1:S:355:GLN:HG2	2.18	0.44
1:B:45:LEU:HD21	1:B:328:ARG:HH21	1.82	0.44
1:B:66:LYS:O	1:B:70:GLU:HG3	2.18	0.44
1:D:334:MSE:HE3	1:F:404:MSE:HE3	1.99	0.44
1:D:444:LEU:HD23	1:D:518:THR:OG1	2.18	0.44
1:E:35:PHE:HZ	1:E:321:ARG:NE	2.12	0.44
1:E:35:PHE:HE1	1:E:321:ARG:NH1	2.13	0.44
1:F:78:VAL:CG2	1:F:444:LEU:HD21	2.46	0.44
1:H:35:PHE:CE1	1:H:321:ARG:NH1	2.84	0.44
1:H:45:LEU:HD22	1:H:45:LEU:N	2.32	0.44
1:I:49:THR:O	1:I:50:THR:C	2.56	0.44
1:J:443:ASP:C	1:J:446:THR:HG22	2.38	0.44
1:L:45:LEU:N	1:L:45:LEU:HD22	2.32	0.44
1:N:101:ASP:HB3	1:N:138:THR:HG21	1.99	0.44
1:P:34:PHE:O	1:P:37:ARG:HB2	2.17	0.44
1:Q:33:LEU:HD12	1:Q:34:PHE:N	2.32	0.44
1:R:26:ARG:O	1:R:27:ARG:C	2.56	0.44
1:T:35:PHE:CE1	1:T:321:ARG:NH1	2.85	0.44
1:U:78:VAL:CG1	1:U:79:LEU:H	2.31	0.44
1:V:37:ARG:C	1:V:39:SER:H	2.20	0.44
1:V:82:PRO:HB2	1:V:83:LYS:H	1.62	0.44
1:X:71:MSE:CE	1:X:115:VAL:HB	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:158:TRP:HD1	1:U:158:TRP:N	2.11	0.44
1:W:451:ASP:C	1:W:453:LEU:N	2.70	0.44
1:I:273:ARG:NH2	1:I:453:LEU:HD11	2.32	0.44
1:C:248:LYS:HZ1	1:C:513:ARG:HH12	1.64	0.44
1:O:236:GLN:H	1:O:265:LYS:HB2	1.83	0.44
1:R:236:GLN:HG3	1:R:265:LYS:HG2	2.00	0.44
1:N:236:GLN:HG3	1:N:265:LYS:HG2	2.00	0.44
1:P:198:ILE:HA	1:P:199:PRO:HD3	1.70	0.44
1:X:266:ILE:O	1:X:267:ALA:HB2	2.17	0.44
1:K:334:MSE:HE3	1:L:404:MSE:HE3	2.00	0.44
1:H:383:ASP:C	1:H:385:PRO:CD	2.86	0.44
1:U:293:ILE:HG12	1:U:294:ALA:H	1.83	0.44
1:K:155:HIS:CE1	1:K:204:PRO:HB2	2.53	0.44
1:D:542:THR:HA	1:D:543:PRO:HD3	1.82	0.44
1:Q:584:PRO:CG	1:Q:593:LEU:HD12	2.48	0.44
1:M:390:ALA:CB	1:N:387:GLN:HB3	2.47	0.44
1:B:177:HIS:HE1	1:B:221:GLU:OE1	2.00	0.44
1:R:57:PHE:CD1	1:R:57:PHE:N	2.86	0.44
1:S:399:GLN:OE1	1:U:396:GLU:O	2.36	0.44
1:M:589:GLU:HA	1:M:592:TRP:HB2	1.99	0.44
1:S:77:ASP:HB2	1:S:523:SER:HB2	2.00	0.44
1:R:76:ILE:HD12	1:R:433:ASP:OD1	2.17	0.44
1:U:589:GLU:HA	1:U:592:TRP:HB2	1.99	0.44
1:N:399:GLN:OE1	1:V:396:GLU:O	2.36	0.44
1:A:79:LEU:N	1:A:519:ASP:O	2.51	0.44
1:B:155:HIS:CE1	1:B:204:PRO:HB2	2.53	0.44
1:D:15:PHE:HE2	1:D:19:TRP:HE1	1.66	0.44
1:E:15:PHE:HE2	1:E:19:TRP:HE1	1.66	0.44
1:E:49:THR:O	1:E:50:THR:C	2.56	0.44
1:E:79:LEU:N	1:E:519:ASP:O	2.51	0.44
1:F:434:THR:O	1:F:437:GLN:HG2	2.17	0.44
1:G:66:LYS:O	1:G:70:GLU:HG3	2.18	0.44
1:H:94:LEU:HA	1:H:97:MSE:CE	2.37	0.44
1:H:561:ASP:CB	1:I:89:ASP:HA	2.41	0.44
1:L:58:ASP:O	1:L:59:VAL:HB	2.14	0.44
1:M:316:TYR:O	1:M:321:ARG:NH1	2.51	0.44
1:M:344:THR:CG2	1:M:344:THR:O	2.66	0.44
1:M:420:VAL:HA	1:M:428:GLY:HA2	2.00	0.44
1:Q:344:THR:O	1:Q:344:THR:CG2	2.66	0.44
1:K:528:LYS:HD2	1:K:560:LEU:HD21	1.99	0.44
1:L:443:ASP:C	1:L:446:THR:HG22	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:79:LEU:N	1:L:519:ASP:O	2.51	0.44
1:N:437:GLN:HA	1:N:440:MSE:HB2	1.99	0.44
1:P:101:ASP:HB3	1:P:138:THR:HG21	1.99	0.44
1:P:344:THR:O	1:P:344:THR:CG2	2.66	0.44
1:Q:101:ASP:HB3	1:Q:138:THR:HG21	2.00	0.44
1:S:29:ALA:O	1:S:33:LEU:HG	2.18	0.44
1:S:47:GLN:N	1:S:48:TYR:HD2	2.15	0.44
1:T:127:ARG:HG2	1:T:147:GLU:HB2	1.98	0.44
1:U:38:VAL:HG21	1:U:324:LYS:HD2	1.98	0.44
1:X:100:THR:HG22	1:X:138:THR:HG22	1.99	0.44
1:P:301:VAL:HA	1:P:302:PRO:HD3	1.79	0.44
1:U:248:LYS:CD	1:U:248:LYS:H	2.17	0.44
1:V:451:ASP:C	1:V:453:LEU:N	2.71	0.44
1:V:511:ARG:HA	1:V:513:ARG:CD	2.45	0.44
1:S:409:THR:O	1:S:413:LYS:HG2	2.18	0.44
1:Q:334:MSE:SE	1:Q:405:LEU:HD11	2.67	0.44
1:K:251:ILE:HG23	1:K:507:LEU:HD22	1.98	0.44
1:P:265:LYS:O	1:P:266:ILE:HG12	2.18	0.44
1:X:265:LYS:O	1:X:266:ILE:HG12	2.17	0.44
1:V:577:ILE:HG12	1:V:582:LYS:CG	2.44	0.44
1:U:575:GLN:O	1:U:579:MSE:CG	2.65	0.44
1:G:177:HIS:HE1	1:G:221:GLU:OE1	2.00	0.44
1:L:383:ASP:C	1:L:385:PRO:CD	2.86	0.44
1:L:238:PRO:HG3	1:L:263:PHE:CB	2.46	0.44
1:T:344:THR:CG2	1:T:344:THR:O	2.66	0.44
1:U:387:GLN:O	1:U:389:LEU:HG	2.18	0.44
1:X:322:LEU:H	1:X:322:LEU:HD22	1.83	0.44
1:X:589:GLU:HA	1:X:592:TRP:HB2	1.99	0.44
1:R:245:SER:HG	1:R:247:PHE:HE1	1.61	0.44
1:T:198:ILE:O	1:T:198:ILE:HG22	2.16	0.44
1:R:107:ALA:HA	1:R:146:ARG:HB3	1.99	0.44
1:X:371:TYR:HE2	1:X:373:LEU:HD21	1.82	0.44
1:A:71:MSE:HE3	1:A:115:VAL:HB	2.00	0.43
1:B:71:MSE:HE3	1:B:115:VAL:HB	2.00	0.43
1:C:434:THR:O	1:C:437:GLN:HG2	2.18	0.43
1:D:99:ARG:NH1	1:D:530:GLN:HE21	2.13	0.43
1:E:78:VAL:HG21	1:E:444:LEU:CD1	2.21	0.43
1:G:24:GLU:CD	1:G:24:GLU:N	2.71	0.43
1:H:15:PHE:HE2	1:H:19:TRP:HE1	1.66	0.43
1:H:26:ARG:NH2	1:H:30:LYS:HB2	2.28	0.43
1:J:79:LEU:N	1:J:519:ASP:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:95:MSE:HE1	1:J:99:ARG:NH2	2.33	0.43
1:M:33:LEU:HD12	1:M:34:PHE:N	2.33	0.43
1:N:35:PHE:C	1:N:37:ARG:N	2.71	0.43
1:P:458:ARG:HA	1:P:458:ARG:HD3	1.83	0.43
1:R:34:PHE:O	1:R:37:ARG:HB2	2.18	0.43
1:T:35:PHE:HZ	1:T:321:ARG:NE	2.14	0.43
1:U:47:GLN:N	1:U:48:TYR:HD2	2.15	0.43
1:W:123:VAL:HG13	1:W:304:PHE:CE1	2.53	0.43
1:X:343:ARG:H	1:X:343:ARG:HG2	1.53	0.43
1:M:451:ASP:C	1:M:453:LEU:N	2.71	0.43
1:W:158:TRP:H	1:W:158:TRP:HD1	1.65	0.43
1:P:248:LYS:HE2	1:P:513:ARG:HH12	1.83	0.43
1:X:47:GLN:CG	1:X:48:TYR:H	2.28	0.43
1:D:273:ARG:O	1:D:274:ARG:HB3	2.17	0.43
1:H:273:ARG:NH2	1:H:453:LEU:HD11	2.33	0.43
1:O:235:TYR:OH	1:O:252:LYS:NZ	2.50	0.43
1:L:66:LYS:O	1:L:70:GLU:HG3	2.18	0.43
1:Q:575:GLN:O	1:Q:579:MSE:CG	2.65	0.43
1:E:383:ASP:C	1:E:385:PRO:CD	2.86	0.43
1:P:575:GLN:O	1:P:579:MSE:CG	2.64	0.43
1:P:567:MSE:HE2	1:Q:554:LEU:HD22	2.00	0.43
1:S:390:ALA:CB	1:U:387:GLN:CB	2.96	0.43
1:E:538:LEU:HB3	1:E:551:LEU:HD13	2.00	0.43
1:A:127:ARG:HA	1:A:299:PRO:O	2.18	0.43
1:N:190:LYS:HE3	1:N:190:LYS:HA	2.00	0.43
1:S:245:SER:HG	1:S:247:PHE:HE1	1.65	0.43
1:Q:349:PRO:HG3	1:Q:391:TYR:CE1	2.53	0.43
1:V:179:MSE:O	1:V:217:ILE:HD12	2.18	0.43
3:S:718:HOH:O	1:T:438:LEU:HD22	2.17	0.43
1:C:155:HIS:CE1	1:C:204:PRO:HB2	2.53	0.43
1:C:45:LEU:HD21	1:C:328:ARG:HH21	1.82	0.43
1:C:528:LYS:HD2	1:C:560:LEU:HD21	1.99	0.43
1:D:35:PHE:CE1	1:D:321:ARG:NH1	2.84	0.43
1:D:443:ASP:C	1:D:446:THR:HG22	2.38	0.43
1:D:79:LEU:N	1:D:519:ASP:O	2.51	0.43
1:E:155:HIS:CE1	1:E:204:PRO:HB2	2.53	0.43
1:F:443:ASP:C	1:F:446:THR:HG22	2.38	0.43
1:F:82:PRO:HB2	1:F:83:LYS:H	1.58	0.43
1:G:155:HIS:CE1	1:G:204:PRO:HB2	2.53	0.43
1:G:94:LEU:HA	1:G:97:MSE:CE	2.37	0.43
1:H:155:HIS:CE1	1:H:204:PRO:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:49:THR:O	1:H:50:THR:C	2.56	0.43
1:H:82:PRO:HB2	1:H:83:LYS:H	1.58	0.43
1:I:95:MSE:HE1	1:I:99:ARG:NH2	2.33	0.43
1:J:79:LEU:HD23	1:J:521:GLY:HA3	2.00	0.43
1:K:444:LEU:HD23	1:K:518:THR:OG1	2.18	0.43
1:K:79:LEU:N	1:K:519:ASP:O	2.51	0.43
1:K:66:LYS:O	1:K:70:GLU:HG3	2.18	0.43
1:L:298:ILE:HA	1:L:299:PRO:HD3	1.82	0.43
1:L:444:LEU:HD23	1:L:518:THR:OG1	2.18	0.43
1:L:79:LEU:HD23	1:L:521:GLY:HA3	2.00	0.43
1:S:35:PHE:CE1	1:S:321:ARG:NH1	2.85	0.43
1:V:78:VAL:CG1	1:V:79:LEU:H	2.29	0.43
1:X:80:TYR:OH	1:X:444:LEU:HD12	2.18	0.43
1:V:274:ARG:O	1:V:275:ARG:HD2	2.18	0.43
1:N:228:LYS:CE	1:N:228:LYS:HA	2.42	0.43
1:X:451:ASP:C	1:X:453:LEU:N	2.71	0.43
1:B:273:ARG:NH2	1:B:453:LEU:HD11	2.32	0.43
1:C:266:ILE:O	1:C:267:ALA:HB2	2.19	0.43
1:E:273:ARG:NH2	1:E:453:LEU:HD11	2.33	0.43
1:F:266:ILE:O	1:F:267:ALA:HB2	2.19	0.43
1:L:266:ILE:O	1:L:267:ALA:HB2	2.18	0.43
1:B:198:ILE:HA	1:B:199:PRO:HD3	1.64	0.43
1:I:219:ILE:HD13	1:I:282:THR:HG22	2.00	0.43
1:Q:266:ILE:O	1:Q:267:ALA:HB2	2.18	0.43
1:W:265:LYS:O	1:W:266:ILE:HG12	2.18	0.43
1:K:219:ILE:HD13	1:K:282:THR:HG22	2.00	0.43
1:K:282:THR:HG23	1:K:287:LEU:CD1	2.43	0.43
1:M:265:LYS:O	1:M:266:ILE:HG12	2.18	0.43
1:U:198:ILE:O	1:U:198:ILE:HG22	2.17	0.43
1:O:454:ALA:O	1:O:455:THR:C	2.56	0.43
1:A:404:MSE:HE1	1:L:334:MSE:SE	2.67	0.43
1:I:383:ASP:C	1:I:385:PRO:CD	2.86	0.43
1:K:383:ASP:C	1:K:385:PRO:HD3	2.39	0.43
1:F:383:ASP:C	1:F:385:PRO:HD3	2.39	0.43
1:L:583:LYS:HA	1:L:584:PRO:HD3	1.85	0.43
1:O:276:VAL:CG2	1:O:293:ILE:HG23	2.47	0.43
1:L:155:HIS:CE1	1:L:204:PRO:HB2	2.53	0.43
1:U:276:VAL:CG2	1:U:293:ILE:HG23	2.47	0.43
1:O:378:ASP:O	1:O:381:SER:O	2.36	0.43
1:J:262:GLY:O	1:J:263:PHE:HB3	2.17	0.43
1:F:542:THR:HA	1:F:543:PRO:HD3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:584:PRO:CG	1:W:593:LEU:HD12	2.48	0.43
1:P:584:PRO:CG	1:P:593:LEU:HD12	2.47	0.43
1:C:177:HIS:HE1	1:C:221:GLU:OE1	2.00	0.43
1:V:429:GLN:O	1:V:429:GLN:HG2	2.18	0.43
1:L:538:LEU:HB3	1:L:551:LEU:HD13	2.00	0.43
1:B:534:GLU:O	1:B:538:LEU:HD23	2.17	0.43
1:C:534:GLU:O	1:C:538:LEU:HD23	2.17	0.43
1:H:391:TYR:CD2	1:H:391:TYR:N	2.87	0.43
1:N:76:ILE:HD12	1:N:433:ASP:OD1	2.18	0.43
1:A:528:LYS:HD2	1:A:560:LEU:HD21	1.99	0.43
1:C:71:MSE:HE3	1:C:115:VAL:HB	2.01	0.43
1:I:155:HIS:CE1	1:I:204:PRO:HB2	2.53	0.43
1:I:47:GLN:CG	1:I:47:GLN:O	2.65	0.43
1:J:15:PHE:HE2	1:J:19:TRP:HE1	1.66	0.43
1:K:71:MSE:HE3	1:K:115:VAL:HB	2.01	0.43
1:L:127:ARG:HA	1:L:299:PRO:O	2.18	0.43
1:M:340:ILE:O	1:M:344:THR:HG21	2.19	0.43
1:N:24:GLU:O	1:N:26:ARG:N	2.50	0.43
1:Q:53:TYR:OH	1:R:329:LEU:HD21	2.18	0.43
1:Q:92:ASP:N	1:Q:92:ASP:OD2	2.52	0.43
1:R:92:ASP:N	1:R:92:ASP:OD2	2.51	0.43
1:S:34:PHE:O	1:S:37:ARG:HB2	2.19	0.43
1:T:123:VAL:HG13	1:T:304:PHE:CE1	2.52	0.43
1:W:344:THR:CG2	1:W:344:THR:O	2.66	0.43
1:I:139:SER:CB	1:I:455:THR:CG2	2.80	0.43
1:V:273:ARG:HH22	1:V:453:LEU:CD2	2.29	0.43
1:M:71:MSE:HE3	1:M:115:VAL:HB	1.99	0.43
1:K:266:ILE:O	1:K:267:ALA:HB2	2.19	0.43
1:U:273:ARG:HH22	1:U:453:LEU:CD2	2.32	0.43
1:D:266:ILE:O	1:D:267:ALA:HB2	2.19	0.43
1:X:24:GLU:HG3	1:X:313:LYS:HE2	2.01	0.43
1:V:236:GLN:H	1:V:265:LYS:HB2	1.83	0.43
1:T:236:GLN:HG3	1:T:265:LYS:HG2	2.00	0.43
1:R:198:ILE:O	1:R:198:ILE:HG22	2.17	0.43
1:S:232:ALA:HB2	1:S:269:ARG:O	2.18	0.43
1:J:383:ASP:C	1:J:385:PRO:HD3	2.39	0.43
1:B:383:ASP:C	1:B:385:PRO:CD	2.86	0.43
1:C:383:ASP:C	1:C:385:PRO:HD3	2.39	0.43
1:I:262:GLY:O	1:I:263:PHE:HB3	2.17	0.43
1:U:155:HIS:CE1	1:U:204:PRO:HB2	2.53	0.43
1:O:387:GLN:O	1:O:389:LEU:HG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:589:GLU:HA	1:T:592:TRP:HB2	2.00	0.43
1:P:174:THR:N	3:P:705:HOH:O	2.51	0.43
1:T:77:ASP:HB2	1:T:523:SER:HB2	1.99	0.43
1:M:174:THR:N	3:M:705:HOH:O	2.50	0.43
1:A:155:HIS:CE1	1:A:204:PRO:HB2	2.53	0.43
1:B:79:LEU:N	1:B:519:ASP:O	2.51	0.43
1:C:437:GLN:HA	1:C:440:MSE:HB2	2.01	0.43
1:D:24:GLU:N	1:D:24:GLU:CD	2.71	0.43
1:D:79:LEU:HD23	1:D:521:GLY:HA3	2.00	0.43
1:F:24:GLU:N	1:F:24:GLU:CD	2.71	0.43
1:F:127:ARG:HA	1:F:299:PRO:O	2.18	0.43
1:G:34:PHE:CE1	1:G:324:LYS:NZ	2.72	0.43
1:H:444:LEU:HD23	1:H:518:THR:OG1	2.18	0.43
1:H:79:LEU:HD23	1:H:521:GLY:HA3	2.00	0.43
1:I:437:GLN:HA	1:I:440:MSE:HB2	2.00	0.43
1:I:79:LEU:N	1:I:519:ASP:O	2.51	0.43
1:K:35:PHE:HE2	1:K:324:LYS:NZ	2.08	0.43
1:L:35:PHE:CZ	1:L:321:ARG:CZ	3.02	0.43
1:Q:164:LEU:HD22	1:Q:169:ASP:OD1	2.17	0.43
1:S:329:LEU:HD21	1:U:53:TYR:OH	2.17	0.43
1:S:35:PHE:C	1:S:37:ARG:N	2.71	0.43
1:S:451:ASP:C	1:S:453:LEU:N	2.72	0.43
1:O:228:LYS:HA	1:O:228:LYS:CE	2.43	0.43
1:I:266:ILE:O	1:I:267:ALA:HB2	2.19	0.43
1:C:227:GLU:OE2	1:C:227:GLU:N	2.47	0.43
1:E:236:GLN:HE21	1:E:265:LYS:HZ3	1.65	0.43
1:F:273:ARG:NH2	1:F:453:LEU:HD11	2.32	0.43
1:V:352:TRP:CD1	1:W:376:ARG:HB2	2.53	0.43
1:V:266:ILE:O	1:V:267:ALA:HB2	2.18	0.43
1:R:376:ARG:HB2	1:X:352:TRP:CD1	2.54	0.43
1:R:383:ASP:C	1:R:385:PRO:HD3	2.39	0.43
1:G:383:ASP:C	1:G:385:PRO:HD3	2.39	0.43
1:K:383:ASP:C	1:K:385:PRO:CD	2.86	0.43
1:A:99:ARG:NH1	1:A:530:GLN:HE21	2.13	0.43
1:A:95:MSE:HE1	1:A:99:ARG:NH2	2.33	0.43
1:B:383:ASP:C	1:B:385:PRO:HD3	2.39	0.43
1:P:420:VAL:HA	1:P:428:GLY:HA2	2.00	0.43
1:D:383:ASP:C	1:D:385:PRO:CD	2.86	0.43
1:V:387:GLN:HA	1:V:388:PRO:HD3	1.92	0.43
1:S:293:ILE:HG12	1:S:294:ALA:H	1.83	0.43
1:O:71:MSE:CE	1:O:115:VAL:HB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:229:LYS:HD2	1:I:270:GLN:HG3	2.01	0.43
1:L:229:LYS:HD2	1:L:270:GLN:HG3	2.01	0.43
1:R:344:THR:CG2	1:R:344:THR:O	2.67	0.43
1:Q:387:GLN:CB	1:R:390:ALA:HB2	2.49	0.43
1:J:538:LEU:HB3	1:J:551:LEU:HD13	2.00	0.43
1:K:343:ARG:HG2	1:K:343:ARG:H	1.52	0.43
1:P:190:LYS:HE3	1:P:190:LYS:HA	2.00	0.43
1:I:391:TYR:N	1:I:391:TYR:CD2	2.87	0.43
1:L:391:TYR:CD2	1:L:391:TYR:N	2.86	0.43
1:A:343:ARG:NH2	2:Y:134:ARG:HD3	2.33	0.43
1:O:245:SER:HG	1:O:247:PHE:HE1	1.62	0.43
1:A:437:GLN:HA	1:A:440:MSE:HB2	2.01	0.43
1:A:66:LYS:O	1:A:70:GLU:HG3	2.18	0.43
1:B:79:LEU:HD23	1:B:521:GLY:HA3	2.00	0.43
1:C:66:LYS:O	1:C:70:GLU:HG3	2.18	0.43
1:D:71:MSE:HE3	1:D:115:VAL:HB	2.00	0.43
1:E:127:ARG:HA	1:E:299:PRO:O	2.18	0.43
1:E:43:ASP:OD2	1:E:43:ASP:N	2.52	0.43
1:E:82:PRO:HB2	1:E:83:LYS:H	1.58	0.43
1:I:43:ASP:N	1:I:43:ASP:OD2	2.52	0.43
1:I:78:VAL:CG2	1:I:444:LEU:HD21	2.46	0.43
1:J:155:HIS:CE1	1:J:204:PRO:HB2	2.53	0.43
1:M:123:VAL:CG1	1:M:304:PHE:CE1	3.00	0.43
1:Q:343:ARG:H	1:Q:343:ARG:HG2	1.53	0.43
1:L:95:MSE:HE1	1:L:99:ARG:NH2	2.33	0.43
1:N:458:ARG:HD3	1:N:458:ARG:HA	1.82	0.43
1:P:92:ASP:N	1:P:92:ASP:OD2	2.51	0.43
1:Q:15:PHE:CE2	1:Q:19:TRP:NE1	2.86	0.43
1:T:444:LEU:O	1:T:446:THR:N	2.50	0.43
1:U:26:ARG:O	1:U:27:ARG:C	2.56	0.43
1:V:340:ILE:O	1:V:344:THR:HG21	2.18	0.43
1:V:437:GLN:HA	1:V:440:MSE:HB2	2.00	0.43
1:V:444:LEU:O	1:V:446:THR:N	2.51	0.43
1:V:80:TYR:OH	1:V:444:LEU:HD12	2.18	0.43
1:V:92:ASP:N	1:V:92:ASP:OD2	2.51	0.43
1:X:123:VAL:HG13	1:X:304:PHE:CE1	2.53	0.43
1:X:35:PHE:CE1	1:X:321:ARG:NH1	2.85	0.43
1:X:440:MSE:O	1:X:443:ASP:HB3	2.18	0.43
1:N:15:PHE:CE2	1:N:19:TRP:NE1	2.87	0.43
1:X:510:ILE:O	1:X:513:ARG:HD2	2.18	0.43
1:O:334:MSE:CG	1:P:404:MSE:HE1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:413:LYS:HB3	1:W:413:LYS:HE2	1.87	0.43
1:G:273:ARG:NH2	1:G:453:LEU:HD11	2.33	0.43
1:B:528:LYS:HD2	1:B:560:LEU:HD21	1.99	0.43
1:C:82:PRO:HB2	1:C:83:LYS:H	1.58	0.43
1:H:246:TYR:HD2	1:H:511:ARG:CB	2.28	0.43
1:H:248:LYS:HZ2	1:H:251:ILE:HD12	1.84	0.43
1:A:273:ARG:NH2	1:A:453:LEU:HD11	2.33	0.43
1:N:451:ASP:C	1:N:453:LEU:N	2.71	0.43
1:N:266:ILE:O	1:N:267:ALA:HB2	2.19	0.43
1:U:236:GLN:H	1:U:265:LYS:HB2	1.83	0.43
1:M:280:ILE:HG22	1:M:287:LEU:HD13	2.00	0.43
1:U:232:ALA:HB2	1:U:269:ARG:O	2.18	0.43
1:D:383:ASP:C	1:D:385:PRO:HD3	2.39	0.43
1:W:384:LEU:HD22	1:W:384:LEU:N	2.29	0.43
1:I:378:ASP:O	1:I:381:SER:O	2.37	0.43
1:O:40:GLN:HB2	1:O:40:GLN:HE21	1.57	0.43
1:T:343:ARG:H	1:T:343:ARG:HG2	1.58	0.43
1:K:427:GLY:C	1:K:429:GLN:N	2.70	0.43
1:H:343:ARG:H	1:H:343:ARG:HG2	1.52	0.43
1:M:576:LEU:HD13	1:N:567:MSE:SE	2.68	0.43
1:O:369:TYR:HA	1:O:370:PRO:HD3	1.83	0.43
1:R:270:GLN:HA	1:R:270:GLN:OE1	2.18	0.43
1:A:252:LYS:O	1:A:252:LYS:HE3	2.19	0.43
1:X:198:ILE:HG22	1:X:198:ILE:O	2.18	0.43
1:R:190:LYS:HE3	1:R:190:LYS:HA	1.99	0.43
1:E:391:TYR:CD2	1:E:391:TYR:N	2.87	0.43
1:A:391:TYR:N	1:A:391:TYR:CD2	2.87	0.43
1:W:589:GLU:HA	1:W:592:TRP:HB2	2.00	0.43
1:S:371:TYR:HE2	1:S:373:LEU:HD21	1.83	0.43
1:A:24:GLU:N	1:A:24:GLU:CD	2.71	0.43
1:A:434:THR:O	1:A:437:GLN:HG2	2.18	0.43
1:A:49:THR:O	1:A:50:THR:C	2.56	0.43
1:B:78:VAL:CG2	1:B:444:LEU:HD21	2.46	0.43
1:B:49:THR:O	1:B:50:THR:C	2.56	0.43
1:C:443:ASP:C	1:C:446:THR:HG22	2.38	0.43
1:D:127:ARG:HA	1:D:299:PRO:O	2.18	0.43
1:D:95:MSE:HE1	1:D:99:ARG:NH2	2.33	0.43
1:E:443:ASP:C	1:E:446:THR:HG22	2.38	0.43
1:F:155:HIS:CE1	1:F:204:PRO:HB2	2.53	0.43
1:F:35:PHE:CZ	1:F:321:ARG:CZ	3.02	0.43
1:I:24:GLU:CD	1:I:24:GLU:N	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:71:MSE:HE3	1:I:115:VAL:HB	2.00	0.43
1:J:47:GLN:CD	1:J:47:GLN:N	2.72	0.43
1:K:24:GLU:N	1:K:24:GLU:CD	2.71	0.43
1:L:71:MSE:HE3	1:L:115:VAL:HB	2.00	0.43
1:N:26:ARG:HG3	1:N:27:ARG:N	2.32	0.43
1:S:47:GLN:H	1:S:48:TYR:HD2	1.65	0.43
1:T:100:THR:HG22	1:T:138:THR:HG22	2.00	0.43
1:T:24:GLU:O	1:T:26:ARG:N	2.50	0.43
1:T:78:VAL:CG1	1:T:79:LEU:H	2.30	0.43
1:U:24:GLU:O	1:U:26:ARG:N	2.50	0.43
1:T:510:ILE:O	1:T:513:ARG:HD2	2.18	0.43
1:T:413:LYS:HE2	1:T:413:LYS:HB3	1.85	0.43
1:V:510:ILE:O	1:V:513:ARG:HD2	2.19	0.43
1:X:301:VAL:HG23	1:X:439:ASN:HB3	2.01	0.43
1:R:334:MSE:SE	1:R:405:LEU:HD11	2.69	0.43
1:G:266:ILE:O	1:G:267:ALA:HB2	2.19	0.43
1:F:219:ILE:HD13	1:F:282:THR:HG22	2.00	0.43
1:B:219:ILE:HD13	1:B:282:THR:HG22	2.00	0.43
1:I:198:ILE:HA	1:I:199:PRO:HD3	1.64	0.43
1:Q:265:LYS:O	1:Q:266:ILE:HG12	2.18	0.43
1:R:265:LYS:O	1:R:266:ILE:HG12	2.18	0.43
1:N:352:TRP:CD2	1:V:376:ARG:HB2	2.53	0.43
1:D:567:MSE:SE	1:F:576:LEU:HD13	2.68	0.43
1:P:542:THR:HA	1:P:543:PRO:HD3	1.88	0.43
1:A:383:ASP:C	1:A:385:PRO:HD3	2.39	0.43
1:I:127:ARG:HA	1:I:299:PRO:O	2.18	0.43
1:P:380:ASN:O	1:P:381:SER:CB	2.66	0.43
1:D:598:GLN:O	1:D:601:GLN:HB2	2.19	0.43
1:P:293:ILE:HG12	1:P:294:ALA:H	1.82	0.43
1:X:420:VAL:HA	1:X:428:GLY:HA2	2.00	0.43
1:S:57:PHE:N	1:S:57:PHE:CD1	2.87	0.43
1:H:538:LEU:HB3	1:H:551:LEU:HD13	2.00	0.43
1:K:391:TYR:CD2	1:K:391:TYR:N	2.87	0.43
1:D:350:PHE:HE1	1:E:363:TYR:HE1	1.67	0.43
1:M:345:PRO:HB2	1:M:392:TYR:CE1	2.54	0.43
1:V:589:GLU:HA	1:V:592:TRP:HB2	2.00	0.43
1:A:15:PHE:HE2	1:A:19:TRP:HE1	1.66	0.43
1:A:35:PHE:CZ	1:A:321:ARG:CZ	3.02	0.43
1:A:43:ASP:OD2	1:A:43:ASP:N	2.52	0.43
1:B:212:LEU:HD12	1:B:212:LEU:N	2.34	0.43
1:B:37:ARG:HA	1:B:37:ARG:HD2	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:GLN:HA	1:B:440:MSE:HB2	2.00	0.43
1:C:38:VAL:HG21	1:C:324:LYS:HD2	2.01	0.43
1:C:49:THR:O	1:C:50:THR:C	2.56	0.43
1:D:35:PHE:CZ	1:D:321:ARG:CZ	3.02	0.43
1:D:43:ASP:OD2	1:D:43:ASP:N	2.52	0.43
1:F:25:ALA:O	1:F:29:ALA:CB	2.58	0.43
1:F:437:GLN:HA	1:F:440:MSE:HB2	2.00	0.43
1:F:66:LYS:O	1:F:70:GLU:HG3	2.18	0.43
1:G:79:LEU:N	1:G:519:ASP:O	2.51	0.43
1:H:95:MSE:HE1	1:H:99:ARG:NH2	2.33	0.43
1:I:413:LYS:HB3	1:I:413:LYS:HE2	1.73	0.43
1:I:80:TYR:CZ	1:I:448:VAL:HG22	2.54	0.43
1:I:79:LEU:HD23	1:I:521:GLY:HA3	2.00	0.43
1:J:45:LEU:HD21	1:J:328:ARG:HH21	1.82	0.43
1:K:15:PHE:HE2	1:K:19:TRP:HE1	1.66	0.43
1:K:80:TYR:CZ	1:K:448:VAL:HG22	2.54	0.43
1:K:95:MSE:HE1	1:K:99:ARG:NH2	2.33	0.43
1:N:212:LEU:HD12	1:N:212:LEU:N	2.34	0.43
1:R:38:VAL:HG21	1:R:324:LYS:HD2	1.99	0.43
1:R:78:VAL:CG1	1:R:79:LEU:H	2.30	0.43
1:S:101:ASP:HB3	1:S:138:THR:HG21	2.01	0.43
1:S:431:ALA:HA	1:S:434:THR:HG22	2.01	0.43
1:M:330:ARG:O	1:M:334:MSE:HB2	2.18	0.43
1:Q:274:ARG:O	1:Q:275:ARG:HD2	2.19	0.43
1:J:266:ILE:O	1:J:267:ALA:HB2	2.19	0.43
1:D:246:TYR:HD2	1:D:511:ARG:CB	2.28	0.43
1:G:219:ILE:HD13	1:G:282:THR:HG22	2.00	0.43
1:P:384:LEU:N	1:P:384:LEU:HD22	2.27	0.43
1:A:383:ASP:C	1:A:385:PRO:CD	2.86	0.43
1:K:378:ASP:O	1:K:381:SER:O	2.37	0.43
1:L:378:ASP:O	1:L:381:SER:O	2.37	0.43
1:E:598:GLN:O	1:E:601:GLN:HB2	2.19	0.43
1:U:584:PRO:CG	1:U:593:LEU:HD12	2.49	0.43
1:B:229:LYS:HD2	1:B:270:GLN:HG3	2.01	0.43
1:F:538:LEU:HB3	1:F:551:LEU:HD13	2.00	0.43
1:Q:542:THR:HA	1:Q:543:PRO:HD3	1.88	0.43
1:B:391:TYR:N	1:B:391:TYR:CD2	2.87	0.43
1:T:212:LEU:HD12	1:T:212:LEU:N	2.33	0.43
1:W:190:LYS:HA	1:W:190:LYS:HE3	2.00	0.43
1:J:391:TYR:N	1:J:391:TYR:CD2	2.87	0.43
1:G:391:TYR:N	1:G:391:TYR:CD2	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:191:TYR:HE1	1:V:278:LYS:HZ3	1.65	0.43
1:A:80:TYR:CZ	1:A:448:VAL:HG22	2.54	0.43
1:A:94:LEU:HD23	1:A:94:LEU:O	2.19	0.43
1:B:35:PHE:CZ	1:B:321:ARG:CZ	3.02	0.43
1:B:444:LEU:O	1:B:447:TYR:N	2.52	0.43
1:C:79:LEU:N	1:C:519:ASP:O	2.51	0.43
1:C:95:MSE:HE1	1:C:99:ARG:NH2	2.33	0.43
1:D:35:PHE:HZ	1:D:321:ARG:NE	2.12	0.43
1:D:378:ASP:O	1:D:381:SER:O	2.37	0.43
1:F:43:ASP:OD2	1:F:43:ASP:N	2.52	0.43
1:H:212:LEU:N	1:H:212:LEU:HD12	2.34	0.43
1:H:24:GLU:N	1:H:24:GLU:CD	2.71	0.43
1:H:444:LEU:O	1:H:447:TYR:N	2.52	0.43
1:H:66:LYS:O	1:H:70:GLU:HG3	2.18	0.43
1:I:123:VAL:HG13	1:I:304:PHE:CE1	2.54	0.43
1:I:99:ARG:NH1	1:I:530:GLN:HE21	2.13	0.43
1:I:94:LEU:HD23	1:I:94:LEU:O	2.19	0.43
1:J:35:PHE:CZ	1:J:321:ARG:CZ	3.02	0.43
1:J:560:LEU:HD13	1:K:82:PRO:CD	2.25	0.43
1:O:78:VAL:CG1	1:O:79:LEU:H	2.31	0.43
1:N:26:ARG:O	1:N:27:ARG:C	2.57	0.43
1:N:316:TYR:O	1:N:321:ARG:NH1	2.52	0.43
1:Q:35:PHE:CE1	1:Q:321:ARG:NH1	2.87	0.43
1:R:437:GLN:HA	1:R:440:MSE:HB2	1.99	0.43
1:T:443:ASP:O	1:T:446:THR:HG22	2.19	0.43
1:U:340:ILE:O	1:U:344:THR:HG21	2.19	0.43
1:X:431:ALA:HA	1:X:434:THR:HG22	2.01	0.43
1:X:444:LEU:O	1:X:447:TYR:N	2.52	0.43
1:O:180:SER:OG	1:P:161:ASN:HB3	2.19	0.43
1:V:248:LYS:HE2	1:V:513:ARG:HH12	1.83	0.43
1:R:158:TRP:H	1:R:158:TRP:HD1	1.65	0.43
1:N:298:ILE:HA	1:N:299:PRO:HD3	1.78	0.43
1:X:15:PHE:CE2	1:X:19:TRP:NE1	2.87	0.43
1:I:212:LEU:N	1:I:212:LEU:HD12	2.34	0.43
1:U:451:ASP:O	1:U:453:LEU:N	2.52	0.43
1:C:15:PHE:HE2	1:C:19:TRP:HE1	1.66	0.43
1:A:266:ILE:O	1:A:267:ALA:HB2	2.19	0.43
1:L:274:ARG:HD3	1:L:296:GLU:O	2.19	0.43
1:E:282:THR:HG23	1:E:287:LEU:CD1	2.44	0.43
1:L:219:ILE:HD13	1:L:282:THR:HG22	2.00	0.43
1:U:383:ASP:C	1:U:385:PRO:HD3	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:583:LYS:HA	1:J:584:PRO:HD3	1.85	0.43
1:L:383:ASP:C	1:L:385:PRO:HD3	2.39	0.43
1:F:378:ASP:O	1:F:381:SER:O	2.37	0.43
1:S:71:MSE:CE	1:S:115:VAL:HB	2.48	0.43
1:T:71:MSE:CE	1:T:115:VAL:HB	2.49	0.43
1:M:387:GLN:O	1:M:389:LEU:HG	2.18	0.43
1:T:340:ILE:O	1:T:344:THR:HG21	2.19	0.43
1:B:371:TYR:HA	1:C:348:LYS:HB3	2.01	0.43
1:U:179:MSE:O	1:U:217:ILE:HD12	2.19	0.43
1:M:395:PRO:HD2	1:O:398:PRO:HB3	2.00	0.43
1:N:270:GLN:HA	1:N:270:GLN:OE1	2.19	0.43
1:N:179:MSE:O	1:N:217:ILE:HD12	2.19	0.43
3:R:718:HOH:O	1:X:438:LEU:HD22	2.19	0.43
1:O:589:GLU:HA	1:O:592:TRP:HB2	2.00	0.43
1:B:252:LYS:HE3	1:B:252:LYS:O	2.19	0.43
1:Q:589:GLU:HA	1:Q:592:TRP:HB2	2.00	0.43
1:A:49:THR:O	1:A:50:THR:O	2.37	0.43
1:C:444:LEU:HD23	1:C:518:THR:OG1	2.18	0.43
1:E:66:LYS:O	1:E:70:GLU:HG3	2.18	0.43
1:G:71:MSE:HE3	1:G:115:VAL:HB	2.00	0.43
1:H:127:ARG:HA	1:H:299:PRO:O	2.18	0.43
1:H:38:VAL:HG21	1:H:324:LYS:HD2	2.01	0.43
1:I:35:PHE:CZ	1:I:321:ARG:CZ	3.02	0.43
1:J:80:TYR:CZ	1:J:448:VAL:HG22	2.54	0.43
1:J:49:THR:O	1:J:50:THR:O	2.37	0.43
1:J:66:LYS:O	1:J:70:GLU:HG3	2.18	0.43
1:J:94:LEU:O	1:J:94:LEU:HD23	2.19	0.43
1:K:35:PHE:CZ	1:K:321:ARG:CZ	3.02	0.43
1:K:182:ASN:HD22	1:L:171:ARG:HH21	1.65	0.43
1:N:340:ILE:O	1:N:344:THR:HG21	2.19	0.43
1:N:164:LEU:HD22	1:N:169:ASP:OD1	2.19	0.43
1:R:35:PHE:CE1	1:R:321:ARG:NH1	2.86	0.43
1:S:136:SER:N	1:S:137:PRO:HD3	2.33	0.43
1:T:35:PHE:C	1:T:37:ARG:N	2.70	0.43
1:T:53:TYR:OH	1:W:329:LEU:HD21	2.19	0.43
1:V:164:LEU:HD22	1:V:169:ASP:OD1	2.18	0.43
1:W:212:LEU:HD12	1:W:212:LEU:N	2.34	0.43
1:W:92:ASP:OD2	1:W:92:ASP:N	2.51	0.43
1:R:248:LYS:HE2	1:R:513:ARG:HH12	1.84	0.43
1:W:510:ILE:O	1:W:513:ARG:HD2	2.19	0.43
1:W:160:SER:O	1:W:161:ASN:ND2	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248:LYS:HE2	1:O:513:ARG:HH12	1.83	0.43
1:N:248:LYS:CD	1:N:248:LYS:H	2.15	0.43
1:X:273:ARG:HH22	1:X:453:LEU:CD2	2.32	0.43
1:K:274:ARG:HD3	1:K:296:GLU:O	2.19	0.43
1:N:273:ARG:HH22	1:N:453:LEU:CD2	2.30	0.43
1:C:219:ILE:HD13	1:C:282:THR:HG22	2.00	0.43
1:P:236:GLN:H	1:P:265:LYS:HB2	1.83	0.43
1:H:383:ASP:C	1:H:385:PRO:HD3	2.39	0.43
1:R:575:GLN:O	1:R:579:MSE:CG	2.67	0.43
1:F:598:GLN:O	1:F:601:GLN:HB2	2.19	0.43
1:Q:380:ASN:O	1:Q:381:SER:CB	2.67	0.43
1:T:387:GLN:HA	1:T:388:PRO:HD3	1.93	0.43
1:F:229:LYS:HD2	1:F:270:GLN:HG3	2.01	0.43
1:N:191:TYR:O	1:N:288:LYS:HE2	2.19	0.43
1:T:372:TYR:CE2	1:W:348:LYS:HB2	2.53	0.43
1:V:174:THR:N	3:V:705:HOH:O	2.51	0.43
1:W:174:THR:N	3:W:705:HOH:O	2.51	0.43
1:G:252:LYS:HE3	1:G:252:LYS:O	2.19	0.43
1:T:245:SER:HG	1:T:247:PHE:HE1	1.65	0.43
1:A:35:PHE:HZ	1:A:321:ARG:NE	2.12	0.43
1:A:38:VAL:HG21	1:A:324:LYS:HD2	2.01	0.43
1:C:79:LEU:HD23	1:C:521:GLY:HA3	2.00	0.43
1:C:80:TYR:CZ	1:C:448:VAL:HG22	2.54	0.43
1:D:31:ASN:HD22	1:D:31:ASN:HA	1.62	0.43
1:E:79:LEU:HD23	1:E:521:GLY:HA3	2.00	0.43
1:E:94:LEU:O	1:E:94:LEU:HD23	2.19	0.43
1:F:79:LEU:N	1:F:519:ASP:O	2.51	0.43
1:G:378:ASP:O	1:G:381:SER:O	2.37	0.43
1:G:94:LEU:HD23	1:G:94:LEU:O	2.19	0.43
1:H:49:THR:O	1:H:50:THR:O	2.37	0.43
1:I:49:THR:O	1:I:50:THR:O	2.37	0.43
1:J:127:ARG:HA	1:J:299:PRO:O	2.18	0.43
1:J:34:PHE:HE1	1:J:324:LYS:HZ2	1.50	0.43
1:J:444:LEU:O	1:J:447:TYR:N	2.52	0.43
1:K:94:LEU:O	1:K:94:LEU:HD23	2.19	0.43
1:L:43:ASP:OD2	1:L:43:ASP:N	2.52	0.43
1:L:49:THR:O	1:L:50:THR:O	2.37	0.43
1:N:528:LYS:NZ	1:N:560:LEU:HD21	2.33	0.43
1:O:437:GLN:HA	1:O:440:MSE:HB2	2.01	0.43
1:L:78:VAL:HG21	1:L:444:LEU:CD1	2.21	0.43
1:O:528:LYS:HD2	1:O:560:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:164:LEU:HD22	1:P:169:ASP:OD1	2.18	0.43
1:Q:123:VAL:CG1	1:Q:304:PHE:CE1	3.02	0.43
1:Q:437:GLN:HA	1:Q:440:MSE:HB2	2.01	0.43
1:S:92:ASP:OD2	1:S:92:ASP:N	2.52	0.43
1:U:306:GLU:O	1:U:316:TYR:HA	2.19	0.43
1:A:139:SER:CB	1:A:455:THR:CG2	2.80	0.43
1:P:158:TRP:H	1:P:158:TRP:HD1	1.66	0.43
1:W:298:ILE:HA	1:W:299:PRO:HD3	1.80	0.43
1:N:510:ILE:O	1:N:513:ARG:HD2	2.19	0.43
1:J:274:ARG:HD3	1:J:296:GLU:O	2.19	0.43
1:G:251:ILE:HD11	1:G:275:ARG:NH2	2.34	0.43
1:A:282:THR:HG23	1:A:287:LEU:CD1	2.43	0.43
1:C:198:ILE:HA	1:C:199:PRO:HD3	1.64	0.43
1:T:236:GLN:H	1:T:265:LYS:CB	2.32	0.43
1:T:262:GLY:O	1:T:263:PHE:HB3	2.19	0.43
1:I:583:LYS:HA	1:I:584:PRO:HD3	1.85	0.43
1:H:583:LYS:HA	1:H:584:PRO:HD3	1.85	0.43
1:R:231:THR:CG2	1:R:249:ARG:HH11	2.31	0.43
1:U:430:VAL:HG13	3:X:719:HOH:O	2.17	0.43
1:M:387:GLN:CB	1:O:390:ALA:CB	2.97	0.43
1:M:387:GLN:HB3	1:O:390:ALA:CB	2.49	0.43
1:N:387:GLN:O	1:N:389:LEU:HG	2.19	0.43
1:R:179:MSE:O	1:R:217:ILE:HD12	2.19	0.43
1:S:567:MSE:SE	1:T:576:LEU:HD13	2.67	0.43
1:L:252:LYS:HE3	1:L:252:LYS:O	2.19	0.43
1:F:252:LYS:HE3	1:F:252:LYS:O	2.19	0.43
1:D:391:TYR:N	1:D:391:TYR:CD2	2.87	0.43
1:S:270:GLN:HA	1:S:270:GLN:OE1	2.18	0.43
1:S:190:LYS:HA	1:S:190:LYS:HE3	2.00	0.43
1:F:391:TYR:N	1:F:391:TYR:CD2	2.87	0.43
1:U:280:ILE:HD12	1:U:280:ILE:N	2.33	0.43
1:U:171:ARG:O	1:U:224:GLU:HA	2.18	0.43
1:A:34:PHE:CE1	1:A:324:LYS:NZ	2.72	0.42
1:A:79:LEU:HD23	1:A:521:GLY:HA3	2.00	0.42
1:B:127:ARG:HA	1:B:299:PRO:O	2.18	0.42
1:C:123:VAL:HG13	1:C:304:PHE:CE1	2.54	0.42
1:C:212:LEU:N	1:C:212:LEU:HD12	2.34	0.42
1:D:123:VAL:HG13	1:D:304:PHE:CE1	2.54	0.42
1:D:38:VAL:HG21	1:D:324:LYS:HD2	2.01	0.42
1:D:80:TYR:CZ	1:D:448:VAL:HG22	2.54	0.42
1:F:123:VAL:HG13	1:F:304:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:THR:O	1:F:50:THR:O	2.37	0.42
1:G:49:THR:O	1:G:50:THR:C	2.56	0.42
1:H:71:MSE:HE3	1:H:115:VAL:HB	2.00	0.42
1:H:35:PHE:CZ	1:H:321:ARG:CZ	3.02	0.42
1:H:437:GLN:HA	1:H:440:MSE:HB2	2.01	0.42
1:I:15:PHE:HE2	1:I:19:TRP:HE1	1.66	0.42
1:J:212:LEU:N	1:J:212:LEU:HD12	2.34	0.42
1:J:123:VAL:HG13	1:J:304:PHE:CE1	2.54	0.42
1:K:212:LEU:HD12	1:K:212:LEU:N	2.34	0.42
1:K:123:VAL:HG13	1:K:304:PHE:CE1	2.54	0.42
1:K:79:LEU:HD23	1:K:521:GLY:HA3	2.00	0.42
1:K:99:ARG:NH1	1:K:530:GLN:HE21	2.13	0.42
1:L:24:GLU:CD	1:L:24:GLU:N	2.71	0.42
1:P:29:ALA:O	1:P:33:LEU:HG	2.19	0.42
1:R:306:GLU:O	1:R:316:TYR:HA	2.19	0.42
1:T:444:LEU:HD13	1:T:444:LEU:N	2.34	0.42
1:H:14:ARG:CA	1:H:14:ARG:NE	2.67	0.42
1:U:15:PHE:CE2	1:U:19:TRP:NE1	2.87	0.42
1:U:118:GLN:OE1	1:U:303:VAL:HB	2.19	0.42
1:R:330:ARG:O	1:R:334:MSE:HB2	2.19	0.42
1:O:274:ARG:O	1:O:275:ARG:HD2	2.19	0.42
1:G:227:GLU:N	1:G:227:GLU:OE2	2.47	0.42
1:B:274:ARG:HD3	1:B:296:GLU:O	2.19	0.42
1:H:266:ILE:O	1:H:267:ALA:HB2	2.19	0.42
1:E:227:GLU:OE2	1:E:227:GLU:N	2.47	0.42
1:E:266:ILE:O	1:E:267:ALA:HB2	2.19	0.42
1:F:274:ARG:HD3	1:F:296:GLU:O	2.19	0.42
1:E:219:ILE:HD13	1:E:282:THR:HG22	2.00	0.42
1:A:219:ILE:HD13	1:A:282:THR:HG22	2.00	0.42
1:O:212:LEU:HD12	1:O:212:LEU:N	2.34	0.42
1:R:282:THR:HG23	1:R:287:LEU:CD1	2.46	0.42
1:Q:232:ALA:HB2	1:Q:269:ARG:O	2.19	0.42
1:W:575:GLN:O	1:W:579:MSE:CG	2.66	0.42
1:A:579:MSE:CB	1:A:581:VAL:HG12	2.49	0.42
1:E:232:ALA:HB1	1:E:233:PHE:H	1.71	0.42
1:V:386:THR:CG2	1:V:389:LEU:HD21	2.49	0.42
1:S:276:VAL:CG2	1:S:293:ILE:HG23	2.48	0.42
1:A:598:GLN:O	1:A:601:GLN:HB2	2.19	0.42
1:G:229:LYS:HD2	1:G:270:GLN:HG3	2.01	0.42
1:K:229:LYS:HD2	1:K:270:GLN:HG3	2.01	0.42
1:D:229:LYS:HD2	1:D:270:GLN:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:538:LEU:HB3	1:G:551:LEU:HD13	2.00	0.42
1:A:538:LEU:HB3	1:A:551:LEU:HD13	2.00	0.42
1:O:147:GLU:HA	1:O:148:PRO:HD3	1.81	0.42
1:O:179:MSE:O	1:O:217:ILE:HD12	2.19	0.42
1:W:245:SER:HG	1:W:247:PHE:HE1	1.65	0.42
1:C:252:LYS:O	1:C:252:LYS:HE3	2.19	0.42
1:Q:76:ILE:HD12	1:Q:433:ASP:OD1	2.18	0.42
1:G:127:ARG:HA	1:G:299:PRO:O	2.18	0.42
1:X:179:MSE:O	1:X:217:ILE:HD12	2.19	0.42
1:O:107:ALA:HA	1:O:146:ARG:HB3	2.00	0.42
1:B:15:PHE:HE2	1:B:19:TRP:HE1	1.66	0.42
1:B:123:VAL:HG13	1:B:304:PHE:CE1	2.54	0.42
1:C:43:ASP:OD2	1:C:43:ASP:N	2.52	0.42
1:C:94:LEU:HD23	1:C:94:LEU:O	2.19	0.42
1:D:212:LEU:HD12	1:D:212:LEU:N	2.34	0.42
1:D:444:LEU:O	1:D:447:TYR:N	2.52	0.42
1:D:94:LEU:HD23	1:D:94:LEU:O	2.19	0.42
1:E:24:GLU:N	1:E:24:GLU:CD	2.71	0.42
1:E:38:VAL:HG21	1:E:324:LYS:HD2	2.01	0.42
1:F:79:LEU:HD23	1:F:521:GLY:HA3	2.00	0.42
1:H:123:VAL:HG13	1:H:304:PHE:CE1	2.54	0.42
1:I:66:LYS:O	1:I:70:GLU:HG3	2.18	0.42
1:J:43:ASP:N	1:J:43:ASP:OD2	2.52	0.42
1:K:443:ASP:C	1:K:446:THR:HG22	2.38	0.42
1:K:49:THR:O	1:K:50:THR:O	2.37	0.42
1:M:444:LEU:O	1:M:447:TYR:N	2.52	0.42
1:O:344:THR:O	1:O:344:THR:CG2	2.67	0.42
1:N:92:ASP:OD2	1:N:92:ASP:N	2.53	0.42
1:R:29:ALA:O	1:R:33:LEU:HG	2.19	0.42
1:S:100:THR:HG22	1:S:138:THR:HG22	2.00	0.42
1:S:24:GLU:O	1:S:26:ARG:N	2.50	0.42
1:T:29:ALA:O	1:T:33:LEU:HG	2.18	0.42
1:V:344:THR:O	1:V:344:THR:CG2	2.66	0.42
1:W:29:ALA:O	1:W:33:LEU:HG	2.19	0.42
1:X:528:LYS:NZ	1:X:560:LEU:HD21	2.34	0.42
1:B:251:ILE:HD11	1:B:275:ARG:NH2	2.34	0.42
1:B:273:ARG:HH22	1:B:453:LEU:HD11	1.85	0.42
1:T:273:ARG:CZ	1:T:275:ARG:HE	2.31	0.42
1:E:273:ARG:HD2	1:E:275:ARG:HD2	2.02	0.42
1:F:251:ILE:HD11	1:F:275:ARG:NH2	2.34	0.42
1:W:236:GLN:H	1:W:265:LYS:HB2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:266:ILE:O	1:R:267:ALA:HB2	2.19	0.42
1:V:265:LYS:O	1:V:266:ILE:HG12	2.19	0.42
1:O:383:ASP:C	1:O:385:PRO:HD3	2.39	0.42
1:T:376:ARG:HB2	1:W:352:TRP:CG	2.54	0.42
1:C:383:ASP:C	1:C:385:PRO:CD	2.86	0.42
1:J:378:ASP:O	1:J:381:SER:O	2.37	0.42
1:K:598:GLN:O	1:K:601:GLN:HB2	2.19	0.42
1:L:598:GLN:O	1:L:601:GLN:HB2	2.19	0.42
1:B:598:GLN:O	1:B:601:GLN:HB2	2.19	0.42
1:A:390:ALA:HB2	1:L:387:GLN:HG3	1.99	0.42
1:P:387:GLN:HB3	1:Q:390:ALA:CB	2.49	0.42
1:T:584:PRO:CG	1:T:593:LEU:HD12	2.49	0.42
1:X:584:PRO:CG	1:X:593:LEU:HD12	2.49	0.42
2:Z:57:TYR:H	2:Z:63:ILE:H	1.65	0.42
1:U:57:PHE:CD1	1:U:57:PHE:N	2.87	0.42
1:S:589:GLU:HA	1:S:592:TRP:HB2	2.00	0.42
1:M:77:ASP:HB2	1:M:523:SER:HB2	2.02	0.42
1:E:252:LYS:O	1:E:252:LYS:HE3	2.19	0.42
1:D:252:LYS:O	1:D:252:LYS:HE3	2.19	0.42
1:Q:371:TYR:HE2	1:Q:373:LEU:HD21	1.84	0.42
1:T:179:MSE:O	1:T:217:ILE:HD12	2.20	0.42
1:R:349:PRO:HG3	1:R:391:TYR:CE1	2.54	0.42
1:A:25:ALA:O	1:A:29:ALA:CB	2.58	0.42
1:D:171:ARG:HH21	1:E:182:ASN:HD22	1.65	0.42
1:D:35:PHE:HE1	1:D:321:ARG:NH1	2.13	0.42
1:F:26:ARG:NH2	1:F:30:LYS:HB2	2.28	0.42
1:F:38:VAL:HG21	1:F:324:LYS:HD2	2.01	0.42
1:G:15:PHE:HE2	1:G:19:TRP:HE1	1.66	0.42
1:G:35:PHE:CZ	1:G:321:ARG:CZ	3.02	0.42
1:H:79:LEU:N	1:H:519:ASP:O	2.51	0.42
1:I:35:PHE:HE1	1:I:321:ARG:NH1	2.13	0.42
1:J:49:THR:O	1:J:50:THR:C	2.56	0.42
1:K:43:ASP:N	1:K:43:ASP:OD2	2.52	0.42
1:K:444:LEU:O	1:K:447:TYR:N	2.52	0.42
1:K:48:TYR:O	1:K:49:THR:CB	2.64	0.42
1:L:49:THR:O	1:L:50:THR:C	2.56	0.42
1:M:24:GLU:CD	1:M:24:GLU:N	2.73	0.42
1:L:82:PRO:HB2	1:L:83:LYS:H	1.58	0.42
1:Q:431:ALA:HA	1:Q:434:THR:HG22	2.01	0.42
1:T:101:ASP:HB3	1:T:138:THR:HG21	2.01	0.42
1:V:15:PHE:CE2	1:V:19:TRP:NE1	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:407:ALA:HB1	1:N:334:MSE:HE1	2.00	0.42
1:G:246:TYR:HD2	1:G:511:ARG:CB	2.28	0.42
1:B:248:LYS:CD	1:B:248:LYS:H	2.16	0.42
1:D:273:ARG:HD2	1:D:275:ARG:HD2	2.01	0.42
1:B:528:LYS:HZ3	1:B:560:LEU:HD21	1.83	0.42
1:C:273:ARG:HD2	1:C:275:ARG:HD2	2.02	0.42
1:F:273:ARG:HH22	1:F:453:LEU:HD11	1.85	0.42
1:L:251:ILE:HD11	1:L:275:ARG:NH2	2.35	0.42
1:S:280:ILE:HG22	1:S:287:LEU:HD13	2.01	0.42
1:O:280:ILE:HG22	1:O:287:LEU:HD13	2.02	0.42
1:Q:198:ILE:HA	1:Q:199:PRO:HD3	1.72	0.42
1:E:383:ASP:C	1:E:385:PRO:HD3	2.39	0.42
1:C:378:ASP:O	1:C:381:SER:O	2.37	0.42
1:L:542:THR:HA	1:L:543:PRO:HD3	1.82	0.42
1:T:578:GLN:HG2	1:T:596:ALA:CB	2.49	0.42
1:S:584:PRO:CG	1:S:593:LEU:HD12	2.49	0.42
1:O:584:PRO:CG	1:O:593:LEU:HD12	2.49	0.42
1:J:229:LYS:HD2	1:J:270:GLN:HG3	2.01	0.42
1:T:322:LEU:HD22	1:T:322:LEU:H	1.83	0.42
1:X:191:TYR:O	1:X:288:LYS:HE2	2.19	0.42
1:W:191:TYR:O	1:W:288:LYS:HE2	2.20	0.42
1:P:589:GLU:HA	1:P:592:TRP:HB2	2.01	0.42
1:A:528:LYS:CD	1:A:560:LEU:HD21	2.50	0.42
1:B:444:LEU:HD23	1:B:518:THR:OG1	2.18	0.42
1:C:35:PHE:CZ	1:C:321:ARG:CZ	3.02	0.42
1:C:47:GLN:CD	1:C:47:GLN:N	2.72	0.42
1:E:444:LEU:O	1:E:447:TYR:N	2.52	0.42
1:G:123:VAL:HG13	1:G:304:PHE:CE1	2.54	0.42
1:G:78:VAL:CG2	1:G:444:LEU:HD21	2.46	0.42
1:H:528:LYS:CD	1:H:560:LEU:HD21	2.50	0.42
1:J:71:MSE:HE3	1:J:115:VAL:HB	2.01	0.42
1:K:434:THR:HG23	1:K:435:VAL:N	2.35	0.42
1:K:49:THR:O	1:K:50:THR:C	2.56	0.42
1:O:123:VAL:HG13	1:O:304:PHE:CE1	2.54	0.42
1:N:24:GLU:HG3	1:N:313:LYS:HE2	2.00	0.42
1:P:444:LEU:O	1:P:447:TYR:N	2.52	0.42
1:T:437:GLN:HA	1:T:440:MSE:HB2	2.02	0.42
1:T:528:LYS:NZ	1:T:560:LEU:HD21	2.35	0.42
1:Q:301:VAL:HA	1:Q:302:PRO:HD3	1.79	0.42
1:N:158:TRP:HH2	1:N:302:PRO:HG3	1.80	0.42
1:J:251:ILE:HD11	1:J:275:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:251:ILE:HD11	1:H:275:ARG:NH2	2.34	0.42
1:A:274:ARG:HD3	1:A:296:GLU:O	2.19	0.42
1:X:26:ARG:O	1:X:27:ARG:C	2.56	0.42
1:G:208:VAL:HB	1:G:209:PHE:H	1.69	0.42
1:B:378:ASP:O	1:B:381:SER:O	2.37	0.42
1:V:575:GLN:O	1:V:579:MSE:CG	2.66	0.42
1:L:579:MSE:CB	1:L:581:VAL:HG12	2.50	0.42
1:W:554:LEU:HD12	1:W:557:PHE:CD2	2.53	0.42
1:J:598:GLN:O	1:J:601:GLN:HB2	2.19	0.42
1:C:579:MSE:CB	1:C:581:VAL:HG12	2.49	0.42
1:G:598:GLN:O	1:G:601:GLN:HB2	2.19	0.42
1:H:598:GLN:O	1:H:601:GLN:HB2	2.19	0.42
1:G:552:LEU:O	1:G:556:TYR:HD2	2.03	0.42
1:J:556:TYR:OH	1:K:542:THR:HG21	2.20	0.42
1:R:584:PRO:CG	1:R:593:LEU:HD12	2.50	0.42
1:X:227:GLU:O	1:X:227:GLU:HG2	2.20	0.42
1:N:589:GLU:HA	1:N:592:TRP:HB2	2.01	0.42
1:U:190:LYS:HA	1:U:190:LYS:HE3	2.00	0.42
1:C:127:ARG:HA	1:C:299:PRO:O	2.18	0.42
1:E:369:TYR:HA	1:E:370:PRO:HD3	1.84	0.42
1:A:444:LEU:O	1:A:447:TYR:N	2.52	0.42
1:B:94:LEU:O	1:B:94:LEU:HD23	2.19	0.42
1:E:49:THR:O	1:E:50:THR:O	2.37	0.42
1:G:80:TYR:CZ	1:G:448:VAL:HG22	2.54	0.42
1:G:93:VAL:O	1:G:97:MSE:HG3	2.20	0.42
1:H:68:VAL:HG22	1:H:119:ILE:HD12	2.02	0.42
1:H:94:LEU:O	1:H:94:LEU:HD23	2.19	0.42
1:I:47:GLN:N	1:I:47:GLN:CD	2.72	0.42
1:J:24:GLU:CD	1:J:24:GLU:N	2.71	0.42
1:J:99:ARG:NH1	1:J:530:GLN:HE21	2.13	0.42
1:J:528:LYS:CD	1:J:560:LEU:HD21	2.50	0.42
1:M:212:LEU:HD12	1:M:212:LEU:N	2.34	0.42
1:M:35:PHE:HZ	1:M:321:ARG:NE	2.12	0.42
1:M:35:PHE:C	1:M:37:ARG:N	2.73	0.42
1:L:434:THR:HG23	1:L:435:VAL:N	2.35	0.42
1:L:437:GLN:HA	1:L:440:MSE:HB2	2.01	0.42
1:L:94:LEU:HD23	1:L:94:LEU:O	2.19	0.42
1:Q:24:GLU:O	1:Q:26:ARG:N	2.50	0.42
1:Q:528:LYS:NZ	1:Q:560:LEU:HD21	2.34	0.42
1:R:33:LEU:HD12	1:R:34:PHE:N	2.34	0.42
1:T:34:PHE:O	1:T:37:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:79:LEU:N	1:T:519:ASP:O	2.53	0.42
1:U:101:ASP:HB3	1:U:138:THR:HG21	2.02	0.42
1:U:443:ASP:O	1:U:446:THR:HG22	2.20	0.42
1:V:306:GLU:O	1:V:316:TYR:HA	2.19	0.42
1:W:306:GLU:O	1:W:316:TYR:HA	2.20	0.42
1:W:343:ARG:HG2	1:W:343:ARG:H	1.56	0.42
1:V:158:TRP:HH2	1:V:302:PRO:HG3	1.81	0.42
1:Q:160:SER:O	1:Q:161:ASN:ND2	2.44	0.42
1:B:266:ILE:O	1:B:267:ALA:HB2	2.19	0.42
1:I:246:TYR:HD2	1:I:511:ARG:CB	2.28	0.42
1:O:265:LYS:O	1:O:266:ILE:HG12	2.19	0.42
1:U:236:GLN:HG3	1:U:265:LYS:HG2	2.00	0.42
1:I:383:ASP:C	1:I:385:PRO:HD3	2.39	0.42
1:U:61:ARG:CB	1:U:62:PRO:HD3	2.49	0.42
1:I:552:LEU:O	1:I:556:TYR:HD2	2.03	0.42
1:B:579:MSE:CB	1:B:581:VAL:HG12	2.50	0.42
1:D:363:TYR:HE1	1:F:350:PHE:CE1	2.35	0.42
1:H:552:LEU:O	1:H:556:TYR:HD2	2.03	0.42
1:H:229:LYS:HD2	1:H:270:GLN:HG3	2.01	0.42
3:M:718:HOH:O	1:O:438:LEU:HD22	2.19	0.42
1:C:391:TYR:N	1:C:391:TYR:CD2	2.87	0.42
1:X:280:ILE:HD12	1:X:280:ILE:N	2.34	0.42
1:W:179:MSE:O	1:W:217:ILE:HD12	2.19	0.42
1:B:43:ASP:OD2	1:B:43:ASP:N	2.52	0.42
1:B:443:ASP:C	1:B:446:THR:HG22	2.38	0.42
1:B:49:THR:O	1:B:50:THR:O	2.37	0.42
1:C:24:GLU:C	1:C:26:ARG:N	2.73	0.42
1:C:444:LEU:O	1:C:447:TYR:N	2.52	0.42
1:D:93:VAL:O	1:D:97:MSE:HG3	2.20	0.42
1:E:123:VAL:HG13	1:E:304:PHE:CE1	2.54	0.42
1:E:71:MSE:HE3	1:E:115:VAL:HB	2.01	0.42
1:F:80:TYR:CZ	1:F:448:VAL:HG22	2.54	0.42
1:F:93:VAL:O	1:F:97:MSE:HG3	2.20	0.42
1:G:444:LEU:O	1:G:447:TYR:N	2.52	0.42
1:H:93:VAL:O	1:H:97:MSE:HG3	2.20	0.42
1:I:434:THR:HG23	1:I:435:VAL:N	2.35	0.42
1:K:127:ARG:HA	1:K:299:PRO:O	2.19	0.42
1:O:92:ASP:N	1:O:92:ASP:OD2	2.52	0.42
1:P:528:LYS:NZ	1:P:560:LEU:HD21	2.34	0.42
1:S:212:LEU:HD12	1:S:212:LEU:N	2.34	0.42
1:T:92:ASP:N	1:T:92:ASP:OD2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:212:LEU:N	1:U:212:LEU:HD12	2.34	0.42
1:U:344:THR:O	1:U:344:THR:CG2	2.68	0.42
1:V:123:VAL:HG22	1:V:316:TYR:HE2	1.83	0.42
1:V:24:GLU:HG3	1:V:313:LYS:HE2	2.00	0.42
1:V:528:LYS:NZ	1:V:560:LEU:HD21	2.34	0.42
1:W:41:TRP:HE3	1:W:42:ASP:HB3	1.82	0.42
1:S:248:LYS:HE2	1:S:513:ARG:HH12	1.85	0.42
1:S:248:LYS:CG	1:S:511:ARG:HH11	2.31	0.42
1:U:115:VAL:HA	1:U:118:GLN:HB3	2.02	0.42
1:X:92:ASP:OD2	1:X:92:ASP:N	2.52	0.42
1:N:301:VAL:HG23	1:N:439:ASN:HB3	2.01	0.42
1:Q:334:MSE:HE1	1:R:407:ALA:HB1	2.01	0.42
1:J:273:ARG:HD2	1:J:275:ARG:HD2	2.02	0.42
1:S:554:LEU:HD21	1:U:564:GLY:CA	2.39	0.42
1:N:280:ILE:HG22	1:N:287:LEU:HD13	2.02	0.42
1:M:383:ASP:C	1:M:385:PRO:HD3	2.40	0.42
1:S:575:GLN:O	1:S:579:MSE:CG	2.66	0.42
1:M:40:GLN:HE21	1:M:40:GLN:HB2	1.57	0.42
1:A:229:LYS:HD2	1:A:270:GLN:HG3	2.01	0.42
1:U:369:TYR:HA	1:U:370:PRO:HD3	1.83	0.42
1:X:270:GLN:OE1	1:X:270:GLN:HA	2.19	0.42
1:T:503:GLU:HB3	1:T:508:ASN:HB3	2.02	0.42
1:A:123:VAL:HG13	1:A:304:PHE:CE1	2.54	0.42
1:C:301:VAL:HG23	1:C:439:ASN:HB3	2.02	0.42
1:D:24:GLU:C	1:D:26:ARG:N	2.73	0.42
1:E:34:PHE:CE1	1:E:324:LYS:NZ	2.72	0.42
1:E:80:TYR:CZ	1:E:448:VAL:HG22	2.54	0.42
1:F:24:GLU:C	1:F:26:ARG:N	2.73	0.42
1:F:528:LYS:CD	1:F:560:LEU:HD21	2.50	0.42
1:D:561:ASP:CB	1:F:89:ASP:HA	2.43	0.42
1:G:68:VAL:HG22	1:G:119:ILE:HD12	2.02	0.42
1:H:80:TYR:CZ	1:H:448:VAL:HG22	2.54	0.42
1:J:437:GLN:HA	1:J:440:MSE:HB2	2.00	0.42
1:K:35:PHE:HZ	1:K:321:ARG:NE	2.12	0.42
1:K:68:VAL:HG22	1:K:119:ILE:HD12	2.02	0.42
1:L:123:VAL:HG13	1:L:304:PHE:CE1	2.54	0.42
1:L:48:TYR:O	1:L:49:THR:CB	2.64	0.42
1:R:80:TYR:OH	1:R:444:LEU:HD12	2.19	0.42
1:T:306:GLU:O	1:T:316:TYR:HA	2.19	0.42
1:T:301:VAL:HG23	1:T:439:ASN:HB3	2.01	0.42
1:U:444:LEU:N	1:U:444:LEU:HD13	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:340:ILE:O	1:W:344:THR:HG21	2.20	0.42
1:X:101:ASP:HB3	1:X:138:THR:HG21	2.01	0.42
1:X:306:GLU:O	1:X:316:TYR:HA	2.20	0.42
1:X:248:LYS:HE2	1:X:513:ARG:HH12	1.85	0.42
1:W:248:LYS:HE2	1:W:513:ARG:HH12	1.84	0.42
2:Z:104:TYR:CD1	2:Z:104:TYR:N	2.85	0.42
1:R:528:LYS:HD2	1:R:560:LEU:HD21	2.02	0.42
1:N:409:THR:O	1:N:413:LYS:HG2	2.20	0.42
1:B:567:MSE:HE2	1:C:554:LEU:HD22	2.00	0.42
1:W:451:ASP:O	1:W:453:LEU:N	2.52	0.42
1:Q:451:ASP:O	1:Q:453:LEU:N	2.53	0.42
1:X:451:ASP:C	1:X:453:LEU:H	2.20	0.42
1:B:528:LYS:CD	1:B:560:LEU:HD21	2.50	0.42
1:H:227:GLU:OE2	1:H:227:GLU:N	2.47	0.42
1:A:248:LYS:CD	1:A:248:LYS:H	2.16	0.42
1:A:251:ILE:HD11	1:A:275:ARG:NH2	2.35	0.42
1:F:248:LYS:HZ2	1:F:251:ILE:HD12	1.85	0.42
1:P:383:ASP:C	1:P:385:PRO:HD3	2.40	0.42
1:R:212:LEU:N	1:R:212:LEU:HD12	2.35	0.42
1:Q:376:ARG:HB2	1:R:352:TRP:CD1	2.55	0.42
1:U:234:ILE:HG12	1:U:267:ALA:O	2.20	0.42
1:S:383:ASP:C	1:S:385:PRO:HD3	2.40	0.42
1:R:564:GLY:HA3	1:X:535:ILE:HD11	2.00	0.42
1:P:262:GLY:O	1:P:263:PHE:HB3	2.20	0.42
1:C:457:MSE:CG	1:C:457:MSE:O	2.63	0.42
1:E:583:LYS:HA	1:E:584:PRO:HD3	1.85	0.42
1:E:579:MSE:CB	1:E:581:VAL:HG12	2.50	0.42
1:O:293:ILE:HG12	1:O:294:ALA:H	1.84	0.42
1:C:598:GLN:O	1:C:601:GLN:HB2	2.19	0.42
1:B:332:MSE:SE	2:Y:141:MET:HA	2.69	0.42
1:I:598:GLN:O	1:I:601:GLN:HB2	2.19	0.42
1:U:191:TYR:O	1:U:288:LYS:HE2	2.19	0.42
1:V:584:PRO:CG	1:V:593:LEU:HD12	2.50	0.42
1:R:394:ASN:HA	1:R:395:PRO:HD3	1.93	0.42
1:C:229:LYS:HD2	1:C:270:GLN:HG3	2.01	0.42
1:S:227:GLU:HG2	1:S:227:GLU:O	2.18	0.42
1:R:589:GLU:HA	1:R:592:TRP:HB2	2.00	0.42
1:P:77:ASP:HB2	1:P:523:SER:HB2	2.02	0.42
1:K:252:LYS:O	1:K:252:LYS:HE3	2.19	0.42
1:M:179:MSE:O	1:M:217:ILE:HD12	2.20	0.42
1:B:430:VAL:HG12	1:B:431:ALA:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:61:ARG:CB	1:X:62:PRO:HD3	2.49	0.42
1:A:37:ARG:HD2	1:A:37:ARG:HA	1.79	0.42
1:D:528:LYS:CD	1:D:560:LEU:HD21	2.50	0.42
1:E:212:LEU:HD12	1:E:212:LEU:N	2.34	0.42
1:F:71:MSE:HE3	1:F:115:VAL:HB	2.00	0.42
1:G:212:LEU:HD12	1:G:212:LEU:N	2.34	0.42
1:G:165:MSE:HE1	1:G:435:VAL:HB	2.02	0.42
1:G:79:LEU:HD23	1:G:521:GLY:HA3	2.00	0.42
1:I:35:PHE:HZ	1:I:321:ARG:NE	2.12	0.42
1:I:444:LEU:O	1:I:447:TYR:N	2.52	0.42
1:J:434:THR:HG23	1:J:435:VAL:N	2.35	0.42
1:O:41:TRP:HE3	1:O:42:ASP:HB3	1.83	0.42
1:O:431:ALA:HA	1:O:434:THR:HG22	2.02	0.42
1:N:431:ALA:HA	1:N:434:THR:HG22	2.01	0.42
1:P:212:LEU:HD12	1:P:212:LEU:N	2.34	0.42
1:P:443:ASP:O	1:P:446:THR:HG22	2.20	0.42
1:Q:528:LYS:HD2	1:Q:560:LEU:HD21	2.02	0.42
1:R:24:GLU:HG3	1:R:313:LYS:HE2	2.01	0.42
1:S:27:ARG:HH21	1:U:41:TRP:HE1	1.67	0.42
1:S:528:LYS:NZ	1:S:560:LEU:HD21	2.35	0.42
1:T:431:ALA:HA	1:T:434:THR:HG22	2.01	0.42
1:T:458:ARG:HA	1:T:458:ARG:HD3	1.84	0.42
1:U:528:LYS:HD2	1:U:560:LEU:HD21	2.02	0.42
1:V:443:ASP:O	1:V:446:THR:HG22	2.20	0.42
1:W:437:GLN:HA	1:W:440:MSE:HB2	2.01	0.42
1:M:15:PHE:CE2	1:M:19:TRP:NE1	2.88	0.42
1:T:15:PHE:CE2	1:T:19:TRP:NE1	2.88	0.42
1:X:510:ILE:HG12	1:X:511:ARG:H	1.84	0.42
1:V:158:TRP:HD1	1:V:158:TRP:H	1.66	0.42
1:X:115:VAL:HA	1:X:118:GLN:HB3	2.02	0.42
1:R:158:TRP:HH2	1:R:302:PRO:HG3	1.84	0.42
1:S:451:ASP:O	1:S:453:LEU:N	2.53	0.42
1:L:198:ILE:HA	1:L:199:PRO:HD3	1.64	0.42
1:T:265:LYS:O	1:T:266:ILE:HG12	2.19	0.42
1:S:265:LYS:O	1:S:266:ILE:HG12	2.20	0.42
1:M:262:GLY:O	1:M:263:PHE:HB3	2.20	0.42
1:Q:384:LEU:HD22	1:Q:384:LEU:N	2.29	0.42
1:F:209:PHE:N	1:F:210:PRO:CD	2.82	0.42
1:C:147:GLU:HA	1:C:148:PRO:HD3	1.86	0.42
1:J:386:THR:HG21	1:J:389:LEU:HD21	2.02	0.42
1:H:386:THR:HG21	1:H:389:LEU:HD21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:386:THR:HG21	1:I:389:LEU:HD21	2.02	0.42
1:M:578:GLN:HG2	1:M:596:ALA:CB	2.50	0.42
1:F:552:LEU:O	1:F:556:TYR:HD2	2.03	0.42
1:P:387:GLN:O	1:P:389:LEU:HG	2.20	0.42
1:I:229:LYS:HG2	1:I:272:LYS:CG	2.50	0.42
1:K:426:ASN:O	1:K:427:GLY:C	2.58	0.42
1:O:227:GLU:HG2	1:O:227:GLU:O	2.20	0.42
1:V:438:LEU:HD12	1:V:441:ARG:NH1	2.35	0.42
1:I:369:TYR:HA	1:I:370:PRO:HD3	1.84	0.42
1:V:270:GLN:OE1	1:V:270:GLN:HA	2.20	0.42
1:H:252:LYS:O	1:H:252:LYS:HE3	2.19	0.42
1:I:252:LYS:HE3	1:I:252:LYS:O	2.19	0.42
1:V:542:THR:HA	1:V:543:PRO:HD3	1.87	0.42
1:Q:372:TYR:CE2	1:R:348:LYS:HB2	2.55	0.42
1:U:503:GLU:HB3	1:U:508:ASN:HB3	2.02	0.42
1:A:212:LEU:N	1:A:212:LEU:HD12	2.34	0.42
1:B:24:GLU:C	1:B:26:ARG:N	2.73	0.42
1:C:434:THR:HG23	1:C:435:VAL:N	2.35	0.42
1:D:165:MSE:HE1	1:D:435:VAL:HB	2.02	0.42
1:D:47:GLN:CD	1:D:47:GLN:N	2.72	0.42
1:D:49:THR:O	1:D:50:THR:O	2.37	0.42
1:E:68:VAL:HG22	1:E:119:ILE:HD12	2.02	0.42
1:E:35:PHE:CZ	1:E:321:ARG:CZ	3.02	0.42
1:E:378:ASP:O	1:E:381:SER:O	2.37	0.42
1:F:130:THR:HG23	1:F:450:GLN:NE2	2.35	0.42
1:G:528:LYS:CD	1:G:560:LEU:HD21	2.50	0.42
1:H:130:THR:HG23	1:H:450:GLN:NE2	2.35	0.42
1:H:165:MSE:HE1	1:H:435:VAL:HB	2.02	0.42
1:I:93:VAL:O	1:I:97:MSE:HG3	2.20	0.42
1:K:38:VAL:HG21	1:K:324:LYS:HD2	2.01	0.42
1:L:212:LEU:N	1:L:212:LEU:HD12	2.34	0.42
1:M:306:GLU:O	1:M:316:TYR:HA	2.19	0.42
1:M:92:ASP:N	1:M:92:ASP:OD2	2.53	0.42
1:N:457:MSE:O	1:N:458:ARG:CD	2.68	0.42
1:Q:443:ASP:O	1:Q:446:THR:HG22	2.19	0.42
1:R:15:PHE:CE2	1:R:19:TRP:NE1	2.88	0.42
1:V:123:VAL:HG13	1:V:304:PHE:CE1	2.55	0.42
1:V:35:PHE:CE1	1:V:321:ARG:NH1	2.86	0.42
1:X:344:THR:CG2	1:X:344:THR:O	2.68	0.42
1:V:301:VAL:HG23	1:V:439:ASN:HB3	2.01	0.42
1:O:511:ARG:HA	1:O:513:ARG:CD	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:248:LYS:HE2	1:Q:513:ARG:HH12	1.84	0.42
1:R:160:SER:O	1:R:161:ASN:ND2	2.46	0.42
1:M:301:VAL:HG23	1:M:439:ASN:HB3	2.00	0.42
1:N:301:VAL:HA	1:N:302:PRO:HD3	1.77	0.42
1:N:228:LYS:O	1:N:229:LYS:HB3	2.20	0.42
1:I:273:ARG:HH22	1:I:453:LEU:HD11	1.85	0.42
1:E:273:ARG:HH22	1:E:453:LEU:HD11	1.85	0.42
1:D:282:THR:HG23	1:D:287:LEU:CD1	2.43	0.42
1:P:554:LEU:HD12	1:P:557:PHE:CD2	2.52	0.42
1:P:24:GLU:O	1:P:26:ARG:N	2.51	0.42
1:S:61:ARG:CB	1:S:62:PRO:HD3	2.49	0.42
1:K:209:PHE:N	1:K:210:PRO:CD	2.82	0.42
1:C:552:LEU:O	1:C:556:TYR:HD2	2.03	0.42
1:T:40:GLN:HB2	1:T:40:GLN:HE21	1.58	0.42
1:C:386:THR:HG21	1:C:389:LEU:HD21	2.02	0.42
1:E:552:LEU:O	1:E:556:TYR:HD2	2.03	0.42
1:V:578:GLN:HG2	1:V:596:ALA:CB	2.50	0.42
3:T:719:HOH:O	1:W:430:VAL:HG13	2.18	0.42
1:E:229:LYS:HD2	1:E:270:GLN:HG3	2.01	0.42
1:K:229:LYS:HG2	1:K:272:LYS:CG	2.50	0.42
2:Y:101:ALA:N	2:Y:102:PRO:CD	2.82	0.42
1:W:107:ALA:HA	1:W:146:ARG:HB3	2.01	0.42
1:X:311:GLU:O	1:X:312:ASP:HB2	2.20	0.42
1:T:591:GLN:HA	1:T:594:VAL:CG2	2.50	0.42
1:A:130:THR:HG23	1:A:450:GLN:NE2	2.35	0.42
1:A:68:VAL:HG22	1:A:119:ILE:HD12	2.02	0.42
1:A:93:VAL:O	1:A:97:MSE:HG3	2.20	0.42
1:C:68:VAL:HG22	1:C:119:ILE:HD12	2.02	0.42
1:D:130:THR:HG23	1:D:450:GLN:NE2	2.35	0.42
1:D:301:VAL:HG23	1:D:439:ASN:HB3	2.02	0.42
1:G:130:THR:HG23	1:G:450:GLN:NE2	2.35	0.42
1:G:437:GLN:HA	1:G:440:MSE:HB2	2.01	0.42
1:H:434:THR:HG23	1:H:435:VAL:N	2.35	0.42
1:H:48:TYR:O	1:H:49:THR:CB	2.64	0.42
1:I:528:LYS:CD	1:I:560:LEU:HD21	2.50	0.42
1:J:35:PHE:HE1	1:J:321:ARG:NH1	2.13	0.42
1:J:301:VAL:HG23	1:J:439:ASN:HB3	2.02	0.42
1:L:528:LYS:CD	1:L:560:LEU:HD21	2.50	0.42
1:M:431:ALA:HA	1:M:434:THR:HG22	2.02	0.42
1:N:344:THR:CG2	1:N:344:THR:O	2.67	0.42
1:L:93:VAL:O	1:L:97:MSE:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:306:GLU:O	1:S:316:TYR:HA	2.20	0.42
1:U:24:GLU:CD	1:U:24:GLU:N	2.73	0.42
1:V:212:LEU:HD12	1:V:212:LEU:N	2.35	0.42
1:W:528:LYS:HD2	1:W:560:LEU:HD21	2.01	0.42
1:X:78:VAL:CG1	1:X:79:LEU:H	2.33	0.42
1:P:115:VAL:HA	1:P:118:GLN:HB3	2.02	0.42
1:S:330:ARG:HD2	1:S:409:THR:CG2	2.41	0.42
1:M:160:SER:O	1:M:161:ASN:ND2	2.45	0.42
1:Q:330:ARG:O	1:Q:334:MSE:HB2	2.20	0.42
1:G:265:LYS:HA	1:G:265:LYS:HD2	1.96	0.42
1:D:274:ARG:HD3	1:D:296:GLU:O	2.19	0.42
1:D:248:LYS:HZ1	1:D:513:ARG:HH12	1.66	0.42
1:H:274:ARG:HD3	1:H:296:GLU:O	2.19	0.42
1:C:274:ARG:HD3	1:C:296:GLU:O	2.19	0.42
1:E:251:ILE:HD11	1:E:275:ARG:NH2	2.34	0.42
1:E:274:ARG:HD3	1:E:296:GLU:O	2.19	0.42
1:B:282:THR:HG23	1:B:287:LEU:CD1	2.43	0.42
1:Q:266:ILE:HA	1:Q:266:ILE:HD13	1.89	0.42
1:P:266:ILE:O	1:P:267:ALA:HB2	2.18	0.42
1:N:265:LYS:O	1:N:266:ILE:HG12	2.20	0.42
1:V:236:GLN:H	1:V:265:LYS:CB	2.33	0.42
1:T:383:ASP:C	1:T:385:PRO:HD3	2.40	0.42
1:X:252:LYS:HZ1	1:X:256:ASP:HB3	1.83	0.42
1:N:280:ILE:HD12	1:N:280:ILE:N	2.35	0.42
1:W:280:ILE:HG22	1:W:287:LEU:HD13	2.01	0.42
1:R:232:ALA:HB2	1:R:269:ARG:O	2.19	0.42
1:I:376:ARG:HB2	1:J:352:TRP:CD2	2.55	0.42
1:J:567:MSE:SE	1:K:576:LEU:HD13	2.69	0.42
2:Z:101:ALA:N	2:Z:102:PRO:CD	2.82	0.42
1:F:386:THR:HG21	1:F:389:LEU:HD21	2.02	0.42
1:X:380:ASN:O	1:X:381:SER:CB	2.68	0.42
1:M:387:GLN:HB2	1:O:390:ALA:HB2	2.01	0.42
1:C:229:LYS:HG2	1:C:272:LYS:CG	2.50	0.42
1:F:229:LYS:HG2	1:F:272:LYS:CG	2.50	0.42
1:L:426:ASN:O	1:L:427:GLY:C	2.58	0.42
1:H:451:ASP:O	1:H:456:ALA:N	2.41	0.42
1:T:191:TYR:O	1:T:288:LYS:HE2	2.20	0.42
1:T:190:LYS:HA	1:T:190:LYS:HE3	2.00	0.42
1:U:270:GLN:HA	1:U:270:GLN:OE1	2.19	0.42
1:O:270:GLN:HA	1:O:270:GLN:OE1	2.20	0.42
1:W:542:THR:HA	1:W:543:PRO:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:76:ILE:HD12	1:M:433:ASP:OD1	2.20	0.42
1:L:368:ASP:O	2:Z:134:ARG:HG3	2.20	0.42
1:A:430:VAL:HG12	1:A:431:ALA:N	2.35	0.42
1:V:76:ILE:HD12	1:V:433:ASP:OD1	2.18	0.42
1:P:591:GLN:HA	1:P:594:VAL:CG2	2.50	0.42
1:S:219:ILE:HG13	1:S:220:ALA:N	2.35	0.42
1:V:503:GLU:HB3	1:V:508:ASN:HB3	2.02	0.42
1:B:130:THR:HG23	1:B:450:GLN:NE2	2.35	0.41
1:B:80:TYR:CZ	1:B:448:VAL:HG22	2.54	0.41
1:C:35:PHE:HZ	1:C:321:ARG:NE	2.12	0.41
1:C:49:THR:O	1:C:50:THR:O	2.37	0.41
1:D:68:VAL:HG22	1:D:119:ILE:HD12	2.02	0.41
1:D:437:GLN:HA	1:D:440:MSE:HB2	2.01	0.41
1:E:434:THR:HG23	1:E:435:VAL:N	2.35	0.41
1:G:38:VAL:HG21	1:G:324:LYS:HD2	2.01	0.41
1:G:434:THR:HG23	1:G:435:VAL:N	2.35	0.41
1:G:43:ASP:OD2	1:G:43:ASP:N	2.52	0.41
1:I:15:PHE:HE2	1:I:19:TRP:NE1	2.18	0.41
1:I:78:VAL:HG21	1:I:444:LEU:CD1	2.21	0.41
1:I:99:ARG:HH12	1:I:530:GLN:NE2	2.14	0.41
1:J:165:MSE:HE1	1:J:435:VAL:HB	2.02	0.41
1:J:93:VAL:O	1:J:97:MSE:HG3	2.20	0.41
1:K:127:ARG:HG2	1:K:147:GLU:HB2	2.02	0.41
1:K:130:THR:HG23	1:K:450:GLN:NE2	2.35	0.41
1:K:437:GLN:HA	1:K:440:MSE:HB2	2.00	0.41
1:L:127:ARG:HG2	1:L:147:GLU:HB2	2.02	0.41
1:M:26:ARG:O	1:M:27:ARG:C	2.58	0.41
1:M:458:ARG:HD3	1:M:458:ARG:HA	1.83	0.41
1:O:24:GLU:HG3	1:O:313:LYS:HE2	2.01	0.41
1:K:528:LYS:CD	1:K:560:LEU:HD21	2.50	0.41
1:L:165:MSE:HE1	1:L:435:VAL:HB	2.02	0.41
1:O:528:LYS:NZ	1:O:560:LEU:HD21	2.35	0.41
1:R:101:ASP:HB3	1:R:138:THR:HG21	2.01	0.41
1:R:35:PHE:HZ	1:R:321:ARG:NE	2.13	0.41
1:S:24:GLU:HG3	1:S:313:LYS:HE2	2.02	0.41
1:S:443:ASP:O	1:S:446:THR:HG22	2.20	0.41
1:S:27:ARG:NH2	1:U:41:TRP:HE1	2.18	0.41
1:U:528:LYS:NZ	1:U:560:LEU:HD21	2.34	0.41
1:U:92:ASP:N	1:U:92:ASP:OD2	2.53	0.41
1:V:528:LYS:HD2	1:V:560:LEU:HD21	2.01	0.41
1:W:101:ASP:HB3	1:W:138:THR:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:15:PHE:CE2	1:P:19:TRP:NE1	2.88	0.41
1:O:298:ILE:HA	1:O:299:PRO:HD3	1.79	0.41
1:U:511:ARG:HA	1:U:513:ARG:CD	2.47	0.41
1:Q:115:VAL:HA	1:Q:118:GLN:HB3	2.02	0.41
1:S:334:MSE:HE1	1:T:407:ALA:HB1	2.02	0.41
1:R:301:VAL:HG23	1:R:439:ASN:HB3	2.02	0.41
1:H:273:ARG:HH22	1:H:453:LEU:HD11	1.85	0.41
1:I:251:ILE:HD11	1:I:275:ARG:NH2	2.35	0.41
1:I:274:ARG:HD3	1:I:296:GLU:O	2.19	0.41
1:F:273:ARG:HD2	1:F:275:ARG:HD2	2.01	0.41
1:L:273:ARG:HD2	1:L:275:ARG:HD2	2.02	0.41
1:F:198:ILE:HA	1:F:199:PRO:HD3	1.64	0.41
1:L:282:THR:HG23	1:L:287:LEU:CD1	2.43	0.41
1:M:266:ILE:O	1:M:267:ALA:HB2	2.19	0.41
1:N:236:GLN:H	1:N:265:LYS:CB	2.33	0.41
1:U:554:LEU:HD21	1:X:564:GLY:CA	2.46	0.41
1:G:209:PHE:N	1:G:210:PRO:CD	2.82	0.41
1:W:262:GLY:O	1:W:263:PHE:HB3	2.21	0.41
1:U:579:MSE:HB2	1:U:581:VAL:HG12	2.02	0.41
1:M:575:GLN:O	1:M:579:MSE:CG	2.66	0.41
1:R:384:LEU:HD22	1:R:384:LEU:N	2.33	0.41
1:Q:554:LEU:O	1:Q:557:PHE:HB3	2.20	0.41
1:V:557:PHE:CE2	1:W:563:LYS:HD3	2.55	0.41
1:W:387:GLN:HG2	1:W:387:GLN:H	1.58	0.41
1:A:598:GLN:HB2	1:A:601:GLN:HB3	2.02	0.41
1:R:380:ASN:O	1:R:381:SER:CB	2.68	0.41
1:V:430:VAL:HG11	3:W:719:HOH:O	2.16	0.41
1:G:229:LYS:HG2	1:G:272:LYS:CG	2.50	0.41
1:L:229:LYS:HG2	1:L:272:LYS:CG	2.50	0.41
1:D:229:LYS:HG2	1:D:272:LYS:CG	2.50	0.41
1:D:426:ASN:O	1:D:427:GLY:C	2.58	0.41
1:C:568:MSE:HG3	1:E:551:LEU:CD2	2.50	0.41
1:Q:147:GLU:HA	1:Q:148:PRO:HD3	1.81	0.41
1:N:57:PHE:N	1:N:57:PHE:CD1	2.88	0.41
1:V:191:TYR:O	1:V:288:LYS:HE2	2.19	0.41
1:T:280:ILE:HD12	1:T:280:ILE:N	2.35	0.41
1:J:252:LYS:O	1:J:252:LYS:HE3	2.19	0.41
1:K:430:VAL:HG12	1:K:431:ALA:N	2.35	0.41
1:E:430:VAL:HG12	1:E:431:ALA:N	2.35	0.41
1:B:123:VAL:HG21	1:B:153:CYS:HB3	2.02	0.41
1:B:434:THR:HG23	1:B:435:VAL:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:VAL:O	1:B:97:MSE:HG3	2.20	0.41
1:D:440:MSE:O	1:D:444:LEU:CD2	2.69	0.41
1:D:49:THR:O	1:D:50:THR:C	2.56	0.41
1:F:212:LEU:N	1:F:212:LEU:HD12	2.34	0.41
1:F:440:MSE:O	1:F:444:LEU:CD2	2.69	0.41
1:F:94:LEU:HD23	1:F:94:LEU:O	2.19	0.41
1:G:24:GLU:C	1:G:26:ARG:N	2.73	0.41
1:G:528:LYS:HZ2	1:G:560:LEU:HD21	1.82	0.41
1:I:130:THR:HG23	1:I:450:GLN:NE2	2.35	0.41
1:I:68:VAL:HG22	1:I:119:ILE:HD12	2.02	0.41
1:J:130:THR:HG23	1:J:450:GLN:NE2	2.35	0.41
1:J:316:TYR:O	1:J:321:ARG:NH1	2.54	0.41
1:L:68:VAL:HG22	1:L:119:ILE:HD12	2.02	0.41
1:R:41:TRP:HE3	1:R:42:ASP:HB3	1.82	0.41
1:R:444:LEU:O	1:R:445:GLU:C	2.58	0.41
1:S:457:MSE:O	1:S:458:ARG:CD	2.69	0.41
1:Q:301:VAL:HG23	1:Q:439:ASN:HB3	2.02	0.41
1:X:11:ILE:O	1:X:15:PHE:HB2	2.20	0.41
1:S:273:ARG:HH22	1:S:453:LEU:CD2	2.31	0.41
1:K:251:ILE:HD11	1:K:275:ARG:NH2	2.35	0.41
1:R:236:GLN:H	1:R:265:LYS:CB	2.33	0.41
1:U:236:GLN:H	1:U:265:LYS:CB	2.33	0.41
1:S:236:GLN:H	1:S:265:LYS:CB	2.33	0.41
1:R:193:LEU:HD22	1:R:287:LEU:HB3	2.01	0.41
1:V:280:ILE:N	1:V:280:ILE:HD12	2.34	0.41
1:B:376:ARG:HB2	1:C:352:TRP:CD2	2.55	0.41
1:H:378:ASP:O	1:H:381:SER:O	2.37	0.41
1:V:276:VAL:CG2	1:V:293:ILE:HG23	2.49	0.41
1:G:579:MSE:CB	1:G:581:VAL:HG12	2.50	0.41
1:T:380:ASN:O	1:T:381:SER:CB	2.68	0.41
1:W:380:ASN:O	1:W:381:SER:CB	2.68	0.41
1:D:552:LEU:O	1:D:556:TYR:HD2	2.03	0.41
1:U:583:LYS:HA	1:U:584:PRO:HD3	1.92	0.41
1:R:340:ILE:O	1:R:344:THR:HG21	2.20	0.41
1:B:229:LYS:HG2	1:B:272:LYS:CG	2.50	0.41
1:A:229:LYS:HG2	1:A:272:LYS:CG	2.50	0.41
1:N:430:VAL:HG11	3:V:719:HOH:O	2.19	0.41
1:T:349:PRO:HB2	1:T:351:PHE:CE2	2.55	0.41
1:P:245:SER:HG	1:P:247:PHE:HE1	1.62	0.41
1:P:280:ILE:N	1:P:280:ILE:HD12	2.35	0.41
1:L:397:VAL:HG12	1:L:397:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:395:PRO:HD2	1:I:398:PRO:HB3	2.02	0.41
2:Z:156:HIS:C	2:Z:158:PHE:H	2.23	0.41
1:P:310:VAL:HB	1:P:311:GLU:H	1.64	0.41
1:A:434:THR:HG23	1:A:435:VAL:N	2.35	0.41
1:C:130:THR:HG23	1:C:450:GLN:NE2	2.35	0.41
1:C:426:ASN:O	1:C:427:GLY:C	2.58	0.41
1:C:528:LYS:CD	1:C:560:LEU:HD21	2.50	0.41
1:D:434:THR:HG23	1:D:435:VAL:N	2.35	0.41
1:E:130:THR:HG23	1:E:450:GLN:NE2	2.35	0.41
1:E:437:GLN:HA	1:E:440:MSE:HB2	2.00	0.41
1:F:434:THR:HG23	1:F:435:VAL:N	2.35	0.41
1:F:444:LEU:O	1:F:447:TYR:N	2.52	0.41
1:G:426:ASN:O	1:G:427:GLY:C	2.59	0.41
1:G:49:THR:O	1:G:50:THR:O	2.37	0.41
1:I:38:VAL:HG21	1:I:324:LYS:HD2	2.01	0.41
1:J:68:VAL:HG22	1:J:119:ILE:HD12	2.02	0.41
1:K:93:VAL:O	1:K:97:MSE:HG3	2.20	0.41
1:L:47:GLN:CD	1:L:47:GLN:N	2.72	0.41
1:N:528:LYS:HD2	1:N:560:LEU:HD21	2.03	0.41
2:Y:28:VAL:HG11	2:Y:97:ALA:HA	1.88	0.41
1:L:444:LEU:O	1:L:447:TYR:N	2.52	0.41
1:N:123:VAL:HG22	1:N:316:TYR:HE2	1.84	0.41
1:P:41:TRP:HE1	1:Q:27:ARG:HH21	1.67	0.41
1:Q:212:LEU:HD22	1:R:26:ARG:HG2	2.03	0.41
1:S:24:GLU:CD	1:S:24:GLU:N	2.74	0.41
1:T:24:GLU:HG3	1:T:313:LYS:HE2	2.02	0.41
1:U:79:LEU:N	1:U:519:ASP:O	2.53	0.41
1:W:431:ALA:HA	1:W:434:THR:HG22	2.01	0.41
1:X:29:ALA:O	1:X:33:LEU:HG	2.19	0.41
1:X:528:LYS:HD2	1:X:560:LEU:HD21	2.02	0.41
1:S:511:ARG:HA	1:S:513:ARG:CD	2.47	0.41
1:O:301:VAL:HG23	1:O:439:ASN:HB3	2.02	0.41
1:T:248:LYS:HE2	1:T:513:ARG:HH12	1.85	0.41
1:R:298:ILE:HA	1:R:299:PRO:HD3	1.78	0.41
1:U:413:LYS:HE2	1:U:413:LYS:HB3	1.84	0.41
1:K:227:GLU:OE2	1:K:227:GLU:N	2.47	0.41
1:G:274:ARG:HD3	1:G:296:GLU:O	2.19	0.41
1:G:248:LYS:HZ1	1:G:513:ARG:HH12	1.67	0.41
1:B:273:ARG:HD2	1:B:275:ARG:HD2	2.02	0.41
1:C:15:PHE:HE2	1:C:19:TRP:NE1	2.18	0.41
1:A:246:TYR:HD2	1:A:511:ARG:CB	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:HD2	1:A:275:ARG:HD2	2.02	0.41
1:C:251:ILE:HD11	1:C:275:ARG:NH2	2.35	0.41
1:S:554:LEU:HD12	1:S:557:PHE:CD2	2.53	0.41
1:U:265:LYS:O	1:U:266:ILE:HG12	2.19	0.41
1:M:454:ALA:O	1:M:455:THR:C	2.58	0.41
1:S:282:THR:HG23	1:S:287:LEU:CD1	2.47	0.41
1:W:457:MSE:O	1:W:458:ARG:CD	2.68	0.41
1:R:61:ARG:CB	1:R:62:PRO:HD3	2.51	0.41
1:L:209:PHE:N	1:L:210:PRO:CD	2.82	0.41
1:P:66:LYS:HZ3	1:P:420:VAL:HG21	1.85	0.41
1:B:552:LEU:O	1:B:556:TYR:HD2	2.03	0.41
1:J:579:MSE:CB	1:J:581:VAL:HG12	2.49	0.41
1:K:579:MSE:CB	1:K:581:VAL:HG12	2.50	0.41
1:J:229:LYS:HG2	1:J:272:LYS:CG	2.50	0.41
1:R:583:LYS:HA	1:R:584:PRO:HD3	1.91	0.41
2:Y:63:ILE:CG2	2:Y:123:LEU:HB3	2.51	0.41
1:E:426:ASN:O	1:E:427:GLY:C	2.59	0.41
1:A:255:ILE:O	1:A:258:LEU:N	2.53	0.41
1:I:568:MSE:HG3	1:J:551:LEU:CD2	2.50	0.41
1:A:568:MSE:HG3	1:B:551:LEU:CD2	2.50	0.41
1:R:227:GLU:HG2	1:R:227:GLU:O	2.20	0.41
1:W:227:GLU:O	1:W:227:GLU:HG2	2.20	0.41
1:P:147:GLU:HA	1:P:148:PRO:HD3	1.82	0.41
1:T:371:TYR:HE2	1:T:373:LEU:HD21	1.85	0.41
1:O:174:THR:N	3:O:705:HOH:O	2.53	0.41
1:B:397:VAL:O	1:B:397:VAL:HG12	2.20	0.41
2:Z:124:TYR:O	2:Z:124:TYR:CG	2.73	0.41
1:A:157:ILE:CG1	1:A:157:ILE:O	2.69	0.41
1:B:157:ILE:O	1:B:157:ILE:CG1	2.69	0.41
1:I:157:ILE:O	1:I:157:ILE:CG1	2.69	0.41
1:M:591:GLN:HA	1:M:594:VAL:CG2	2.50	0.41
1:O:177:HIS:O	1:O:218:GLN:HA	2.21	0.41
1:Q:591:GLN:HA	1:Q:594:VAL:CG2	2.50	0.41
1:A:165:MSE:HE1	1:A:435:VAL:HB	2.02	0.41
1:A:24:GLU:C	1:A:26:ARG:N	2.73	0.41
1:A:313:LYS:HD3	1:A:314:GLU:N	2.36	0.41
1:A:316:TYR:O	1:A:321:ARG:NH1	2.54	0.41
1:B:24:GLU:CD	1:B:24:GLU:N	2.71	0.41
1:B:316:TYR:O	1:B:321:ARG:NH1	2.53	0.41
1:B:165:MSE:HE1	1:B:435:VAL:HB	2.02	0.41
1:D:316:TYR:O	1:D:321:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:PHE:HE2	1:E:19:TRP:NE1	2.18	0.41
1:E:24:GLU:C	1:E:26:ARG:N	2.73	0.41
1:F:118:GLN:HB2	1:F:118:GLN:HE21	1.77	0.41
1:F:32:ASP:CG	1:F:316:TYR:CE2	2.94	0.41
1:G:123:VAL:HG21	1:G:153:CYS:HB3	2.02	0.41
1:G:316:TYR:O	1:G:321:ARG:NH1	2.54	0.41
1:J:32:ASP:CG	1:J:316:TYR:CE2	2.94	0.41
1:L:301:VAL:HG23	1:L:439:ASN:HB3	2.02	0.41
1:M:24:GLU:OE1	1:M:24:GLU:N	2.54	0.41
1:M:528:LYS:HD2	1:M:560:LEU:HD21	2.02	0.41
1:O:444:LEU:O	1:O:447:TYR:N	2.53	0.41
1:L:80:TYR:CZ	1:L:448:VAL:HG22	2.54	0.41
1:N:310:VAL:HB	1:N:311:GLU:H	1.67	0.41
1:Q:100:THR:HG22	1:Q:138:THR:HG22	2.02	0.41
1:Q:24:GLU:CD	1:Q:24:GLU:N	2.74	0.41
1:Q:72:ARG:HG2	1:R:434:THR:HG21	2.03	0.41
1:R:78:VAL:HG11	1:R:444:LEU:CG	2.50	0.41
1:S:343:ARG:HG2	1:S:343:ARG:H	1.54	0.41
1:S:444:LEU:O	1:S:445:GLU:C	2.57	0.41
1:T:457:MSE:O	1:T:458:ARG:CD	2.68	0.41
1:V:101:ASP:HB3	1:V:138:THR:HG21	2.01	0.41
1:W:164:LEU:HD22	1:W:169:ASP:OD1	2.20	0.41
1:K:236:GLN:HE21	1:K:265:LYS:HZ1	1.68	0.41
1:G:273:ARG:HH22	1:G:453:LEU:HD11	1.85	0.41
1:R:451:ASP:O	1:R:453:LEU:N	2.53	0.41
1:I:273:ARG:HD2	1:I:275:ARG:HD2	2.01	0.41
1:W:458:ARG:HA	1:W:458:ARG:HD3	1.83	0.41
1:B:352:TRP:HB2	1:B:355:GLN:HG2	2.03	0.41
1:G:209:PHE:CE2	1:G:214:GLN:HG2	2.56	0.41
1:S:262:GLY:O	1:S:263:PHE:HB3	2.20	0.41
1:A:209:PHE:N	1:A:210:PRO:CD	2.82	0.41
1:D:352:TRP:HB2	1:D:355:GLN:HG2	2.03	0.41
1:E:209:PHE:CE2	1:E:214:GLN:HG2	2.56	0.41
1:X:575:GLN:O	1:X:579:MSE:CG	2.68	0.41
1:T:310:VAL:HB	1:T:311:GLU:H	1.70	0.41
1:M:293:ILE:HG12	1:M:294:ALA:H	1.85	0.41
1:D:579:MSE:CB	1:D:581:VAL:HG12	2.49	0.41
1:F:598:GLN:HB2	1:F:601:GLN:HB3	2.03	0.41
1:R:387:GLN:O	1:R:389:LEU:HG	2.20	0.41
1:P:191:TYR:O	1:P:288:LYS:HE2	2.20	0.41
1:K:255:ILE:O	1:K:258:LEU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:191:TYR:O	1:O:288:LYS:HE2	2.21	0.41
1:S:76:ILE:HD12	1:S:433:ASP:OD1	2.19	0.41
1:E:157:ILE:CG1	1:E:157:ILE:O	2.68	0.41
1:P:270:GLN:HA	1:P:270:GLN:OE1	2.19	0.41
2:Z:56:TRP:N	2:Z:56:TRP:CD1	2.89	0.41
1:P:371:TYR:HE2	1:P:373:LEU:HD21	1.85	0.41
1:M:399:GLN:OE1	1:N:396:GLU:O	2.38	0.41
2:Y:156:HIS:C	2:Y:158:PHE:H	2.23	0.41
1:W:371:TYR:HE2	1:W:373:LEU:HD21	1.86	0.41
1:P:372:TYR:CE2	1:Q:348:LYS:HB2	2.56	0.41
1:M:438:LEU:HD12	1:M:441:ARG:NH1	2.35	0.41
1:X:349:PRO:HG3	1:X:391:TYR:CE1	2.55	0.41
1:A:15:PHE:HE2	1:A:19:TRP:NE1	2.18	0.41
1:B:15:PHE:HE2	1:B:19:TRP:NE1	2.18	0.41
1:C:99:ARG:HH12	1:C:530:GLN:NE2	2.14	0.41
1:E:165:MSE:HE1	1:E:435:VAL:HB	2.02	0.41
1:E:313:LYS:HD3	1:E:314:GLU:N	2.36	0.41
1:E:93:VAL:O	1:E:97:MSE:HG3	2.20	0.41
1:F:35:PHE:HZ	1:F:321:ARG:NE	2.12	0.41
1:G:313:LYS:HD3	1:G:314:GLU:N	2.36	0.41
1:H:301:VAL:HG23	1:H:439:ASN:HB3	2.02	0.41
1:H:80:TYR:HB2	1:H:95:MSE:HG2	2.03	0.41
1:I:165:MSE:HE1	1:I:435:VAL:HB	2.02	0.41
1:K:316:TYR:O	1:K:321:ARG:NH1	2.54	0.41
1:L:316:TYR:O	1:L:321:ARG:NH1	2.54	0.41
1:L:38:VAL:HG21	1:L:324:LYS:HD2	2.01	0.41
1:L:40:GLN:O	1:L:41:TRP:CB	2.55	0.41
1:M:164:LEU:HD22	1:M:169:ASP:OD1	2.20	0.41
1:L:80:TYR:HB2	1:L:95:MSE:HG2	2.03	0.41
2:Z:78:GLU:O	2:Z:79:GLY:C	2.59	0.41
1:N:440:MSE:O	1:N:443:ASP:HB3	2.20	0.41
1:N:80:TYR:OH	1:N:444:LEU:HD12	2.20	0.41
1:Q:444:LEU:O	1:Q:445:GLU:C	2.58	0.41
1:R:24:GLU:CD	1:R:24:GLU:N	2.74	0.41
1:R:431:ALA:HA	1:R:434:THR:HG22	2.01	0.41
1:R:458:ARG:HA	1:R:458:ARG:HD3	1.83	0.41
1:W:528:LYS:NZ	1:W:560:LEU:HD21	2.35	0.41
1:X:443:ASP:O	1:X:446:THR:HG22	2.21	0.41
1:U:510:ILE:O	1:U:513:ARG:HD2	2.20	0.41
1:W:301:VAL:HG23	1:W:439:ASN:HB3	2.02	0.41
1:M:301:VAL:HA	1:M:302:PRO:HD3	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:71:MSE:CE	1:M:115:VAL:HB	2.50	0.41
1:K:273:ARG:HH22	1:K:453:LEU:HD11	1.85	0.41
1:B:273:ARG:NH1	1:B:275:ARG:HE	2.19	0.41
1:U:274:ARG:O	1:U:275:ARG:HD2	2.20	0.41
1:H:273:ARG:NH1	1:H:275:ARG:HE	2.19	0.41
1:J:198:ILE:HA	1:J:199:PRO:HD3	1.64	0.41
1:L:209:PHE:CE2	1:L:214:GLN:HG2	2.56	0.41
1:P:577:ILE:HG12	1:P:582:LYS:CG	2.45	0.41
1:B:276:VAL:HG23	1:B:293:ILE:HG22	2.03	0.41
1:A:378:ASP:O	1:A:381:SER:O	2.37	0.41
1:P:563:LYS:HD3	1:Q:557:PHE:CE2	2.55	0.41
1:C:598:GLN:HB2	1:C:601:GLN:HB3	2.03	0.41
1:G:598:GLN:HB2	1:G:601:GLN:HB3	2.02	0.41
1:K:598:GLN:HB2	1:K:601:GLN:HB3	2.02	0.41
1:D:386:THR:HG21	1:D:389:LEU:HD21	2.02	0.41
1:O:380:ASN:O	1:O:381:SER:CB	2.69	0.41
1:K:542:THR:HA	1:K:543:PRO:HD3	1.82	0.41
1:L:313:LYS:HD3	1:L:314:GLU:N	2.36	0.41
1:T:387:GLN:O	1:T:389:LEU:HG	2.20	0.41
1:K:313:LYS:HD3	1:K:314:GLU:N	2.36	0.41
1:H:310:VAL:HB	1:H:311:GLU:H	1.78	0.41
1:M:390:ALA:HB2	1:N:387:GLN:CB	2.50	0.41
1:A:426:ASN:O	1:A:427:GLY:C	2.58	0.41
1:Q:394:ASN:HA	1:Q:395:PRO:HD3	1.93	0.41
1:M:59:VAL:CG2	1:M:59:VAL:O	2.69	0.41
1:O:77:ASP:HB2	1:O:523:SER:HB2	2.02	0.41
1:P:179:MSE:O	1:P:217:ILE:HD12	2.21	0.41
1:W:270:GLN:HA	1:W:270:GLN:OE1	2.20	0.41
1:Q:270:GLN:OE1	1:Q:270:GLN:HA	2.20	0.41
1:D:397:VAL:HG12	1:D:397:VAL:O	2.20	0.41
1:V:591:GLN:HA	1:V:594:VAL:CG2	2.51	0.41
1:S:191:TYR:O	1:S:288:LYS:HE2	2.20	0.41
1:B:313:LYS:HD3	1:B:314:GLU:N	2.36	0.41
1:B:38:VAL:HG21	1:B:324:LYS:HD2	2.01	0.41
1:B:68:VAL:HG22	1:B:119:ILE:HD12	2.02	0.41
1:C:93:VAL:O	1:C:97:MSE:HG3	2.20	0.41
1:C:80:TYR:HB2	1:C:95:MSE:HG2	2.03	0.41
1:D:123:VAL:HG21	1:D:153:CYS:HB3	2.02	0.41
1:E:528:LYS:CD	1:E:560:LEU:HD21	2.50	0.41
1:F:313:LYS:HD3	1:F:314:GLU:N	2.36	0.41
1:F:165:MSE:HE1	1:F:435:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:80:TYR:HB2	1:F:95:MSE:HG2	2.03	0.41
1:I:301:VAL:HA	1:I:302:PRO:HD3	1.84	0.41
1:I:316:TYR:O	1:I:321:ARG:NH1	2.54	0.41
1:I:426:ASN:O	1:I:427:GLY:C	2.58	0.41
1:L:528:LYS:HD2	1:L:560:LEU:HD11	2.03	0.41
1:M:82:PRO:HB2	1:M:83:LYS:H	1.63	0.41
1:N:123:VAL:HG13	1:N:304:PHE:CE1	2.56	0.41
1:N:78:VAL:CG1	1:N:79:LEU:H	2.31	0.41
1:P:528:LYS:HD2	1:P:560:LEU:HD21	2.02	0.41
1:Q:212:LEU:N	1:Q:212:LEU:HD12	2.35	0.41
1:Q:29:ALA:O	1:Q:33:LEU:HG	2.20	0.41
1:Q:65:ARG:HG2	1:R:306:GLU:OE2	2.21	0.41
1:T:126:TRP:NE1	1:T:301:VAL:HG13	2.36	0.41
1:T:24:GLU:CD	1:T:24:GLU:N	2.74	0.41
1:V:35:PHE:O	1:V:37:ARG:N	2.46	0.41
1:V:431:ALA:HA	1:V:434:THR:HG22	2.02	0.41
1:V:444:LEU:O	1:V:447:TYR:N	2.53	0.41
1:X:444:LEU:O	1:X:445:GLU:C	2.58	0.41
2:Y:78:GLU:O	2:Y:79:GLY:C	2.59	0.41
1:M:273:ARG:HH22	1:M:453:LEU:CD2	2.31	0.41
1:M:451:ASP:O	1:M:453:LEU:N	2.53	0.41
1:P:298:ILE:HA	1:P:299:PRO:HD3	1.77	0.41
1:P:330:ARG:O	1:P:334:MSE:HB2	2.20	0.41
1:N:115:VAL:HA	1:N:118:GLN:HB3	2.03	0.41
1:N:413:LYS:HB3	1:N:413:LYS:HE2	1.87	0.41
1:P:228:LYS:O	1:P:229:LYS:HB3	2.21	0.41
1:J:236:GLN:CG	1:J:243:PRO:HB2	2.51	0.41
1:D:251:ILE:HD11	1:D:275:ARG:NH2	2.35	0.41
1:N:451:ASP:O	1:N:453:LEU:N	2.54	0.41
1:C:265:LYS:HA	1:C:265:LYS:HD2	1.96	0.41
1:C:273:ARG:NH1	1:C:275:ARG:HE	2.19	0.41
1:Q:236:GLN:H	1:Q:265:LYS:CB	2.33	0.41
1:M:198:ILE:HA	1:M:199:PRO:HD3	1.70	0.41
1:V:232:ALA:HB1	1:V:233:PHE:H	1.58	0.41
1:I:209:PHE:CE2	1:I:214:GLN:HG2	2.56	0.41
1:T:61:ARG:CB	1:T:62:PRO:HD3	2.50	0.41
1:C:583:LYS:HA	1:C:584:PRO:HD3	1.85	0.41
1:G:276:VAL:HG23	1:G:293:ILE:HG22	2.03	0.41
1:C:276:VAL:HG23	1:C:293:ILE:HG22	2.03	0.41
1:W:249:ARG:HH21	1:W:249:ARG:HD2	1.52	0.41
1:I:127:ARG:HG2	1:I:147:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:PHE:CE2	1:B:214:GLN:HG2	2.56	0.41
1:W:15:PHE:CE2	1:W:19:TRP:NE1	2.88	0.41
1:M:384:LEU:HD22	1:M:384:LEU:N	2.31	0.41
1:D:372:TYR:CD2	1:F:348:LYS:HB2	2.56	0.41
1:H:579:MSE:CB	1:H:581:VAL:HG12	2.49	0.41
2:Z:63:ILE:CG2	2:Z:123:LEU:HB3	2.51	0.41
1:W:57:PHE:CD1	1:W:57:PHE:N	2.88	0.41
1:R:156:VAL:O	1:R:156:VAL:CG2	2.69	0.41
1:J:157:ILE:O	1:J:157:ILE:CG1	2.68	0.41
1:Q:369:TYR:HA	1:Q:370:PRO:HD3	1.84	0.41
1:U:107:ALA:HA	1:U:146:ARG:HB3	2.02	0.41
1:W:591:GLN:HA	1:W:594:VAL:CG2	2.50	0.41
1:A:32:ASP:CG	1:A:316:TYR:CE2	2.94	0.41
1:A:301:VAL:HG23	1:A:439:ASN:HB3	2.02	0.41
1:B:127:ARG:HG2	1:B:147:GLU:HB2	2.03	0.41
1:D:32:ASP:CG	1:D:316:TYR:CE2	2.94	0.41
1:E:301:VAL:HG23	1:E:439:ASN:HB3	2.02	0.41
1:H:313:LYS:HD3	1:H:314:GLU:N	2.36	0.41
1:J:15:PHE:HE2	1:J:19:TRP:NE1	2.18	0.41
1:L:301:VAL:HA	1:L:302:PRO:HD3	1.85	0.41
1:N:306:GLU:O	1:N:316:TYR:HA	2.21	0.41
1:N:443:ASP:O	1:N:446:THR:HG22	2.20	0.41
1:R:14:ARG:CA	1:R:14:ARG:NE	2.70	0.41
1:U:123:VAL:HG22	1:U:316:TYR:HE2	1.83	0.41
1:O:159:ASP:OD2	1:O:161:ASN:N	2.51	0.41
1:G:236:GLN:CG	1:G:243:PRO:HB2	2.51	0.41
1:G:273:ARG:HD2	1:G:275:ARG:HD2	2.02	0.41
1:D:227:GLU:N	1:D:227:GLU:OE2	2.47	0.41
1:H:236:GLN:CG	1:H:243:PRO:HB2	2.51	0.41
1:I:273:ARG:NH1	1:I:275:ARG:HE	2.19	0.41
1:W:352:TRP:HB2	1:W:355:GLN:HG2	2.03	0.41
1:U:352:TRP:O	1:U:355:GLN:HG2	2.20	0.41
1:R:577:ILE:HG12	1:R:582:LYS:CG	2.45	0.41
1:J:567:MSE:HE2	1:K:554:LEU:HD22	2.02	0.41
1:R:231:THR:HG23	1:R:249:ARG:HE	1.85	0.41
1:U:404:MSE:HE1	1:X:334:MSE:HG3	2.02	0.41
1:W:311:GLU:HG3	1:W:311:GLU:H	1.76	0.41
1:P:564:GLY:O	1:Q:554:LEU:HD21	2.19	0.41
1:F:579:MSE:CB	1:F:581:VAL:HG12	2.49	0.41
1:F:343:ARG:HG2	1:F:343:ARG:H	1.52	0.41
1:P:276:VAL:CG2	1:P:293:ILE:HG23	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:387:GLN:O	1:X:389:LEU:HG	2.20	0.41
1:M:584:PRO:CG	1:M:593:LEU:HD12	2.48	0.41
1:N:387:GLN:HA	1:N:388:PRO:HD3	1.93	0.41
1:X:427:GLY:C	1:X:429:GLN:N	2.74	0.41
2:Y:119:GLY:O	2:Y:123:LEU:HD13	2.21	0.41
1:O:387:GLN:HB2	1:P:390:ALA:HB2	2.03	0.41
2:Z:135:ALA:HA	2:Z:136:PRO:HD3	1.92	0.41
1:S:108:LYS:HD2	1:T:438:LEU:HD11	2.01	0.41
1:T:369:TYR:HA	1:T:370:PRO:HD3	1.83	0.41
1:I:397:VAL:HG12	1:I:397:VAL:O	2.20	0.41
1:C:397:VAL:HG12	1:C:397:VAL:O	2.20	0.41
1:P:156:VAL:CG2	1:P:156:VAL:O	2.69	0.41
1:O:396:GLU:O	1:P:399:GLN:OE1	2.38	0.41
1:N:107:ALA:HA	1:N:146:ARG:HB3	2.02	0.41
1:G:430:VAL:HG12	1:G:431:ALA:N	2.35	0.41
1:Q:107:ALA:HA	1:Q:146:ARG:HB3	2.03	0.41
1:W:61:ARG:CB	1:W:62:PRO:HD3	2.50	0.41
1:T:174:THR:N	3:T:705:HOH:O	2.53	0.41
1:B:298:ILE:HA	1:B:299:PRO:HD3	1.82	0.41
1:C:24:GLU:CD	1:C:24:GLU:N	2.71	0.41
1:C:165:MSE:HE1	1:C:435:VAL:HB	2.02	0.41
1:F:301:VAL:HG23	1:F:439:ASN:HB3	2.02	0.41
1:F:316:TYR:O	1:F:321:ARG:NH1	2.53	0.41
1:F:426:ASN:O	1:F:427:GLY:C	2.58	0.41
1:G:32:ASP:CG	1:G:316:TYR:CE2	2.94	0.41
1:I:313:LYS:HD3	1:I:314:GLU:N	2.36	0.41
1:J:127:ARG:HG2	1:J:147:GLU:HB2	2.03	0.41
1:J:528:LYS:HD2	1:J:560:LEU:HD11	2.03	0.41
1:J:80:TYR:HB2	1:J:95:MSE:HG2	2.03	0.41
1:O:93:VAL:O	1:O:97:MSE:HG3	2.21	0.41
1:Q:340:ILE:O	1:Q:344:THR:HG21	2.21	0.41
1:L:130:THR:HG23	1:L:450:GLN:NE2	2.35	0.41
1:P:123:VAL:HG13	1:P:304:PHE:CE1	2.56	0.41
1:Q:444:LEU:O	1:Q:447:TYR:N	2.54	0.41
1:U:27:ARG:HH21	1:X:41:TRP:HE1	1.68	0.41
1:M:248:LYS:HZ1	1:M:513:ARG:HH12	1.69	0.41
1:U:248:LYS:HE2	1:U:513:ARG:HH12	1.84	0.41
1:T:248:LYS:HZ1	1:T:513:ARG:HH12	1.68	0.41
1:V:115:VAL:HA	1:V:118:GLN:HB3	2.02	0.41
1:Q:158:TRP:HH2	1:Q:302:PRO:HG3	1.80	0.41
1:X:274:ARG:O	1:X:275:ARG:HD2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:236:GLN:CG	1:K:243:PRO:HB2	2.51	0.41
1:B:236:GLN:CG	1:B:243:PRO:HB2	2.51	0.41
1:D:273:ARG:HH22	1:D:453:LEU:HD11	1.85	0.41
1:A:273:ARG:HH22	1:A:453:LEU:HD11	1.85	0.41
1:T:266:ILE:HD13	1:T:266:ILE:HA	1.90	0.41
1:X:457:MSE:O	1:X:458:ARG:CD	2.69	0.41
1:S:280:ILE:HD12	1:S:280:ILE:N	2.35	0.41
1:Q:262:GLY:O	1:Q:263:PHE:HB3	2.20	0.41
1:J:376:ARG:NE	1:K:354:GLU:OE2	2.51	0.41
1:I:147:GLU:HA	1:I:148:PRO:HD3	1.86	0.41
1:U:40:GLN:HB2	1:U:40:GLN:HE21	1.58	0.41
1:A:552:LEU:O	1:A:556:TYR:HD2	2.03	0.41
1:L:386:THR:HG21	1:L:389:LEU:HD21	2.02	0.41
1:G:386:THR:HG21	1:G:389:LEU:HD21	2.02	0.41
1:W:387:GLN:O	1:W:389:LEU:HG	2.20	0.41
1:T:276:VAL:CG2	1:T:293:ILE:HG23	2.49	0.41
1:R:276:VAL:CG2	1:R:293:ILE:HG23	2.49	0.41
1:N:584:PRO:CG	1:N:593:LEU:HD12	2.49	0.41
1:R:438:LEU:HD12	1:R:441:ARG:NH1	2.36	0.41
1:W:40:GLN:HE21	1:W:40:GLN:HB2	1.61	0.41
1:A:127:ARG:HG2	1:A:147:GLU:HB2	2.02	0.41
1:U:349:PRO:HG3	1:U:391:TYR:CE1	2.55	0.41
1:X:591:GLN:HA	1:X:594:VAL:CG2	2.50	0.41
1:S:349:PRO:HG3	1:S:391:TYR:CE1	2.55	0.41
1:J:430:VAL:HG12	1:J:431:ALA:N	2.35	0.41
1:F:157:ILE:O	1:F:157:ILE:CG1	2.68	0.41
1:C:322:LEU:N	1:C:322:LEU:HD22	2.36	0.41
1:K:322:LEU:N	1:K:322:LEU:HD22	2.36	0.41
1:Q:156:VAL:O	1:Q:156:VAL:CG2	2.69	0.41
1:V:107:ALA:HA	1:V:146:ARG:HB3	2.03	0.41
1:Q:77:ASP:HB2	1:Q:523:SER:HB2	2.03	0.41
1:B:301:VAL:HG23	1:B:439:ASN:HB3	2.02	0.41
1:C:61:ARG:N	1:C:62:PRO:CD	2.84	0.41
1:D:313:LYS:HD3	1:D:314:GLU:N	2.36	0.41
1:E:298:ILE:HA	1:E:299:PRO:HD3	1.82	0.41
1:E:301:VAL:HA	1:E:302:PRO:HD3	1.84	0.41
1:F:123:VAL:HG21	1:F:153:CYS:HB3	2.02	0.41
1:F:68:VAL:HG22	1:F:119:ILE:HD12	2.02	0.41
1:H:164:LEU:HD22	1:H:169:ASP:CG	2.42	0.41
1:H:426:ASN:O	1:H:427:GLY:C	2.58	0.41
1:H:43:ASP:OD2	1:H:43:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:80:TYR:HB2	1:I:95:MSE:HG2	2.03	0.41
1:J:164:LEU:HD22	1:J:169:ASP:CG	2.42	0.41
1:J:298:ILE:HA	1:J:299:PRO:HD3	1.82	0.41
1:J:426:ASN:O	1:J:427:GLY:C	2.58	0.41
1:K:165:MSE:HE1	1:K:435:VAL:HB	2.02	0.41
1:K:24:GLU:C	1:K:26:ARG:N	2.73	0.41
1:O:103:ARG:NH1	1:P:517:TYR:HB2	2.36	0.41
1:B:32:ASP:CG	1:B:316:TYR:CE2	2.94	0.41
1:C:123:VAL:HG21	1:C:153:CYS:HB3	2.02	0.41
1:C:528:LYS:HD2	1:C:560:LEU:HD11	2.03	0.41
1:E:32:ASP:CG	1:E:316:TYR:CE2	2.94	0.41
1:E:80:TYR:HB2	1:E:95:MSE:HG2	2.03	0.41
1:F:528:LYS:HD2	1:F:560:LEU:HD11	2.03	0.41
1:G:164:LEU:HD22	1:G:169:ASP:CG	2.42	0.41
1:J:38:VAL:HG21	1:J:324:LYS:HD2	2.01	0.41
1:J:440:MSE:O	1:J:444:LEU:CD2	2.69	0.41
1:J:61:ARG:N	1:J:62:PRO:CD	2.84	0.41
1:J:94:LEU:HA	1:J:97:MSE:CE	2.37	0.41
1:K:32:ASP:CG	1:K:316:TYR:CE2	2.94	0.41
1:K:35:PHE:HE1	1:K:321:ARG:NH1	2.13	0.41
1:K:440:MSE:O	1:K:444:LEU:CD2	2.69	0.41
1:L:24:GLU:C	1:L:26:ARG:N	2.73	0.41
1:M:101:ASP:HB3	1:M:138:THR:HG21	2.02	0.41
1:M:440:MSE:O	1:M:443:ASP:HB3	2.21	0.41
1:N:311:GLU:O	1:N:312:ASP:HB2	2.21	0.41
1:P:41:TRP:HE3	1:P:42:ASP:HB3	1.80	0.41
1:Q:440:MSE:O	1:Q:443:ASP:HB3	2.21	0.41
1:R:79:LEU:N	1:R:519:ASP:O	2.53	0.41
1:T:298:ILE:HA	1:T:299:PRO:HD3	1.80	0.41
1:V:26:ARG:O	1:V:27:ARG:C	2.58	0.41
1:W:35:PHE:O	1:W:37:ARG:N	2.46	0.41
1:N:123:VAL:HG23	3:N:709:HOH:O	2.21	0.41
1:P:35:PHE:CE1	1:P:321:ARG:NH1	2.87	0.41
1:Q:61:ARG:CB	1:Q:62:PRO:HD3	2.50	0.41
1:R:123:VAL:HG22	1:R:316:TYR:HE2	1.84	0.41
1:U:24:GLU:HG3	1:U:313:LYS:HE2	2.03	0.41
1:U:35:PHE:HZ	1:U:321:ARG:NE	2.13	0.41
1:W:444:LEU:O	1:W:447:TYR:N	2.53	0.41
1:X:78:VAL:HG11	1:X:444:LEU:CG	2.48	0.41
1:M:11:ILE:O	1:M:15:PHE:HB2	2.21	0.41
1:V:298:ILE:HA	1:V:299:PRO:HD3	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:330:ARG:O	1:O:334:MSE:HB2	2.20	0.41
1:V:334:MSE:SE	1:V:405:LEU:HD11	2.71	0.41
1:M:115:VAL:HA	1:M:118:GLN:HB3	2.02	0.41
1:N:330:ARG:O	1:N:334:MSE:HB2	2.21	0.41
1:W:274:ARG:O	1:W:275:ARG:HD2	2.21	0.41
1:Q:228:LYS:O	1:Q:229:LYS:HB3	2.21	0.41
1:V:228:LYS:O	1:V:229:LYS:HB3	2.21	0.41
1:J:313:LYS:HD3	1:J:314:GLU:N	2.36	0.41
1:K:273:ARG:NH1	1:K:275:ARG:HE	2.19	0.41
1:B:265:LYS:HA	1:B:265:LYS:HD2	1.96	0.41
1:P:451:ASP:O	1:P:453:LEU:N	2.54	0.41
1:D:236:GLN:CG	1:D:243:PRO:HB2	2.51	0.41
1:H:273:ARG:HD2	1:H:275:ARG:HD2	2.02	0.41
1:A:236:GLN:CG	1:A:243:PRO:HB2	2.51	0.41
1:I:236:GLN:CG	1:I:243:PRO:HB2	2.51	0.41
1:C:236:GLN:CG	1:C:243:PRO:HB2	2.51	0.41
1:C:273:ARG:HH22	1:C:453:LEU:HD11	1.85	0.41
1:P:376:ARG:HB2	1:Q:352:TRP:CG	2.56	0.41
1:M:554:LEU:HD12	1:M:557:PHE:CD2	2.54	0.41
1:Q:236:GLN:CG	1:Q:243:PRO:HB2	2.51	0.41
1:N:383:ASP:C	1:N:385:PRO:HD3	2.40	0.41
1:W:236:GLN:H	1:W:265:LYS:CB	2.34	0.41
1:W:24:GLU:N	1:W:24:GLU:CD	2.74	0.41
1:M:236:GLN:H	1:M:265:LYS:CB	2.34	0.41
1:O:564:GLY:HA2	1:P:554:LEU:CD2	2.43	0.41
1:U:282:THR:HG23	1:U:287:LEU:CD1	2.46	0.41
1:X:236:GLN:H	1:X:265:LYS:CB	2.34	0.41
1:K:413:LYS:HB3	1:K:413:LYS:HE2	1.74	0.41
1:M:564:GLY:CA	1:O:554:LEU:HD21	2.48	0.41
1:U:577:ILE:HG12	1:U:582:LYS:CG	2.46	0.41
1:F:383:ASP:CB	1:F:385:PRO:HD3	2.51	0.41
1:C:352:TRP:HB2	1:C:355:GLN:HG2	2.03	0.41
1:K:209:PHE:CE2	1:K:214:GLN:HG2	2.56	0.41
1:C:383:ASP:CB	1:C:385:PRO:HD3	2.51	0.41
1:V:262:GLY:O	1:V:263:PHE:HB3	2.20	0.41
1:E:276:VAL:HG23	1:E:293:ILE:HG22	2.03	0.41
1:N:293:ILE:HG12	1:N:294:ALA:H	1.85	0.41
1:B:598:GLN:HB2	1:B:601:GLN:HB3	2.03	0.41
1:E:386:THR:HG21	1:E:389:LEU:HD21	2.02	0.41
1:I:598:GLN:HB2	1:I:601:GLN:HB3	2.03	0.41
1:B:386:THR:HG21	1:B:389:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:394:ASN:HA	1:T:395:PRO:HD3	1.91	0.41
1:J:552:LEU:O	1:J:556:TYR:HD2	2.03	0.41
1:P:578:GLN:HG2	1:P:596:ALA:CB	2.50	0.41
1:H:229:LYS:HG2	1:H:272:LYS:CG	2.50	0.41
1:S:387:GLN:O	1:S:389:LEU:HG	2.21	0.41
1:Q:387:GLN:O	1:Q:389:LEU:HG	2.21	0.41
1:B:426:ASN:O	1:B:427:GLY:C	2.59	0.41
1:R:191:TYR:O	1:R:288:LYS:HE2	2.20	0.41
1:V:227:GLU:HG2	1:V:227:GLU:O	2.21	0.41
1:M:227:GLU:HG2	1:M:227:GLU:O	2.21	0.41
1:P:227:GLU:HG2	1:P:227:GLU:O	2.21	0.41
1:M:191:TYR:O	1:M:288:LYS:HE2	2.21	0.41
1:X:438:LEU:HD12	1:X:441:ARG:NH1	2.35	0.41
1:R:177:HIS:O	1:R:218:GLN:HA	2.21	0.41
1:P:349:PRO:HG3	1:P:391:TYR:CE1	2.55	0.41
1:G:157:ILE:O	1:G:157:ILE:CG1	2.69	0.41
1:J:322:LEU:HD22	1:J:322:LEU:N	2.36	0.41
1:W:349:PRO:HG3	1:W:391:TYR:CE1	2.56	0.41
1:O:591:GLN:HA	1:O:594:VAL:CG2	2.51	0.41
1:W:503:GLU:HB3	1:W:508:ASN:HB3	2.02	0.41
1:J:397:VAL:HG12	1:J:397:VAL:O	2.20	0.41
1:N:349:PRO:HG3	1:N:391:TYR:CE1	2.56	0.41
1:K:359:PHE:HD1	2:Y:129:ILE:HD11	1.86	0.41
1:F:430:VAL:HG12	1:F:431:ALA:N	2.35	0.41
1:C:369:TYR:HA	1:C:370:PRO:HD3	1.84	0.41
1:K:552:LEU:O	1:K:556:TYR:HD2	2.03	0.41
1:U:591:GLN:HA	1:U:594:VAL:CG2	2.51	0.41
1:O:503:GLU:HB3	1:O:508:ASN:HB3	2.03	0.41
1:P:219:ILE:HG13	1:P:220:ALA:N	2.36	0.41
1:B:78:VAL:CG1	1:B:444:LEU:HG	2.51	0.41
1:B:80:TYR:HB2	1:B:95:MSE:HG2	2.03	0.41
1:C:118:GLN:HB2	1:C:118:GLN:HE21	1.77	0.41
1:C:316:TYR:O	1:C:321:ARG:NH1	2.53	0.41
1:C:440:MSE:O	1:C:444:LEU:CD2	2.69	0.41
1:G:301:VAL:HG23	1:G:439:ASN:HB3	2.02	0.41
1:H:316:TYR:O	1:H:321:ARG:NH1	2.54	0.41
1:I:24:GLU:C	1:I:26:ARG:N	2.73	0.41
1:I:301:VAL:HG23	1:I:439:ASN:HB3	2.02	0.41
1:I:93:VAL:HG11	1:I:458:ARG:HG2	2.03	0.41
1:K:47:GLN:CD	1:K:47:GLN:N	2.72	0.41
1:N:61:ARG:CB	1:N:62:PRO:HD3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:340:ILE:O	1:P:344:THR:HG21	2.20	0.41
1:Q:306:GLU:O	1:Q:316:TYR:HA	2.21	0.41
1:Q:457:MSE:O	1:Q:458:ARG:CD	2.69	0.41
1:X:212:LEU:N	1:X:212:LEU:HD12	2.35	0.41
1:J:273:ARG:HH22	1:J:453:LEU:HD11	1.85	0.41
1:D:273:ARG:NH1	1:D:275:ARG:HE	2.19	0.41
1:L:273:ARG:HH22	1:L:453:LEU:HD11	1.85	0.41
1:S:210:PRO:HD2	1:S:211:TRP:CZ3	2.56	0.41
1:W:24:GLU:N	1:W:24:GLU:OE1	2.54	0.41
1:V:383:ASP:C	1:V:385:PRO:HD3	2.41	0.41
1:K:198:ILE:HA	1:K:199:PRO:HD3	1.64	0.41
1:R:198:ILE:HA	1:R:199:PRO:HD3	1.71	0.41
1:I:383:ASP:CB	1:I:385:PRO:HD3	2.51	0.41
1:H:352:TRP:HB2	1:H:355:GLN:HG2	2.03	0.41
1:U:262:GLY:O	1:U:263:PHE:HB3	2.21	0.41
1:R:262:GLY:O	1:R:263:PHE:HB3	2.21	0.41
1:H:383:ASP:CB	1:H:385:PRO:HD3	2.51	0.41
1:E:383:ASP:CB	1:E:385:PRO:HD3	2.51	0.41
1:S:579:MSE:HB2	1:S:581:VAL:HG12	2.03	0.41
1:Q:231:THR:CG2	1:Q:249:ARG:HH11	2.32	0.41
1:R:578:GLN:HG2	1:R:596:ALA:CB	2.51	0.41
2:Z:119:GLY:O	2:Z:123:LEU:HD13	2.21	0.41
1:H:322:LEU:HD22	1:H:322:LEU:N	2.36	0.41
1:I:322:LEU:N	1:I:322:LEU:HD22	2.36	0.41
1:H:459:ARG:HD2	1:H:459:ARG:C	2.42	0.41
1:D:157:ILE:CG1	1:D:157:ILE:O	2.68	0.41
1:O:349:PRO:HG3	1:O:391:TYR:CE1	2.56	0.41
1:S:107:ALA:HA	1:S:146:ARG:HB3	2.02	0.41
1:Q:191:TYR:O	1:Q:288:LYS:HE2	2.21	0.41
1:T:202:GLN:O	1:T:203:ASN:HB3	2.21	0.41
1:S:177:HIS:O	1:S:218:GLN:HA	2.21	0.41
1:H:430:VAL:HG12	1:H:431:ALA:N	2.35	0.41
1:B:440:MSE:O	1:B:444:LEU:CD2	2.69	0.40
1:C:164:LEU:HD22	1:C:169:ASP:CG	2.42	0.40
1:D:528:LYS:HD2	1:D:560:LEU:HD11	2.03	0.40
1:E:440:MSE:O	1:E:444:LEU:CD2	2.69	0.40
1:E:99:ARG:NH1	1:E:530:GLN:HE21	2.13	0.40
1:F:15:PHE:HE2	1:F:19:TRP:NE1	2.18	0.40
1:F:61:ARG:N	1:F:62:PRO:CD	2.84	0.40
1:G:31:ASN:HA	1:G:31:ASN:HD22	1.62	0.40
1:H:127:ARG:HG2	1:H:147:GLU:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:15:PHE:HE2	1:H:19:TRP:NE1	2.18	0.40
1:H:440:MSE:O	1:H:444:LEU:CD2	2.69	0.40
1:I:123:VAL:HG21	1:I:153:CYS:HB3	2.02	0.40
1:J:35:PHE:HZ	1:J:321:ARG:NE	2.12	0.40
1:K:80:TYR:HB2	1:K:95:MSE:HG2	2.03	0.40
1:L:35:PHE:HZ	1:L:321:ARG:NE	2.12	0.40
1:M:123:VAL:HG13	1:M:304:PHE:CE1	2.56	0.40
1:O:340:ILE:O	1:O:344:THR:HG21	2.22	0.40
1:N:444:LEU:O	1:N:445:GLU:C	2.60	0.40
1:N:82:PRO:HB2	1:N:83:LYS:H	1.63	0.40
1:Q:79:LEU:N	1:Q:519:ASP:O	2.54	0.40
1:S:80:TYR:CE1	1:S:448:VAL:CG2	3.05	0.40
1:T:26:ARG:O	1:T:27:ARG:C	2.59	0.40
1:U:457:MSE:O	1:U:458:ARG:CD	2.69	0.40
1:U:458:ARG:HD3	1:U:458:ARG:HA	1.84	0.40
1:T:528:LYS:HD2	1:T:560:LEU:HD21	2.02	0.40
1:V:251:ILE:HD11	1:V:275:ARG:HH21	1.86	0.40
1:V:451:ASP:O	1:V:453:LEU:N	2.54	0.40
1:P:248:LYS:H	1:P:248:LYS:CD	2.18	0.40
1:P:511:ARG:HA	1:P:513:ARG:CD	2.46	0.40
1:R:330:ARG:HD2	1:R:409:THR:CG2	2.42	0.40
1:U:334:MSE:SE	1:U:405:LEU:HD11	2.71	0.40
1:K:273:ARG:HD2	1:K:275:ARG:HD2	2.02	0.40
1:G:248:LYS:HZ2	1:G:251:ILE:HD12	1.86	0.40
1:G:273:ARG:NH1	1:G:275:ARG:HE	2.19	0.40
1:P:236:GLN:H	1:P:265:LYS:CB	2.34	0.40
1:K:383:ASP:CB	1:K:385:PRO:HD3	2.51	0.40
1:D:576:LEU:HD13	1:E:567:MSE:SE	2.71	0.40
1:G:352:TRP:HB2	1:G:355:GLN:HG2	2.03	0.40
1:D:209:PHE:CE2	1:D:214:GLN:HG2	2.56	0.40
1:A:209:PHE:CE2	1:A:214:GLN:HG2	2.56	0.40
1:F:351:PHE:CD2	1:F:356:ILE:CD1	3.04	0.40
1:L:108:LYS:HE2	1:L:108:LYS:HB3	4.41	0.40
1:R:310:VAL:HB	1:R:311:GLU:H	1.66	0.40
1:C:232:ALA:HB1	1:C:233:PHE:H	1.71	0.40
1:L:598:GLN:HB2	1:L:601:GLN:HB3	2.02	0.40
1:K:386:THR:HG21	1:K:389:LEU:HD21	2.02	0.40
1:U:380:ASN:O	1:U:381:SER:CB	2.69	0.40
1:N:386:THR:CG2	1:N:389:LEU:HD21	2.51	0.40
1:E:229:LYS:HG2	1:E:272:LYS:CG	2.50	0.40
1:J:255:ILE:O	1:J:258:LEU:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:394:ASN:HA	1:U:395:PRO:HD3	1.93	0.40
1:V:438:LEU:HD11	1:W:108:LYS:HD2	2.02	0.40
1:N:227:GLU:HG2	1:N:227:GLU:O	2.21	0.40
1:X:370:PRO:HB2	1:X:371:TYR:CD1	2.56	0.40
1:G:127:ARG:HG2	1:G:147:GLU:HB2	2.03	0.40
1:I:352:TRP:HB2	1:I:355:GLN:HG2	2.03	0.40
1:H:397:VAL:HG12	1:H:397:VAL:O	2.20	0.40
1:E:397:VAL:O	1:E:397:VAL:HG12	2.20	0.40
1:A:459:ARG:HD2	1:A:459:ARG:C	2.42	0.40
1:D:322:LEU:HD22	1:D:322:LEU:N	2.36	0.40
1:E:322:LEU:HD22	1:E:322:LEU:N	2.36	0.40
1:S:503:GLU:HB3	1:S:508:ASN:HB3	2.03	0.40
1:N:591:GLN:HA	1:N:594:VAL:CG2	2.51	0.40
1:S:179:MSE:O	1:S:217:ILE:HD12	2.21	0.40
1:L:552:LEU:O	1:L:556:TYR:HD2	2.03	0.40
1:W:219:ILE:HG13	1:W:220:ALA:N	2.36	0.40
1:A:528:LYS:HD2	1:A:560:LEU:HD11	2.03	0.40
1:B:93:VAL:HG11	1:B:458:ARG:HG2	2.03	0.40
1:C:32:ASP:CG	1:C:316:TYR:CE2	2.94	0.40
1:D:61:ARG:N	1:D:62:PRO:CD	2.84	0.40
1:E:164:LEU:HD22	1:E:169:ASP:CG	2.42	0.40
1:H:123:VAL:HG21	1:H:153:CYS:HB3	2.02	0.40
1:H:528:LYS:HD2	1:H:560:LEU:HD11	2.03	0.40
1:L:123:VAL:HG21	1:L:153:CYS:HB3	2.02	0.40
1:L:32:ASP:CG	1:L:316:TYR:CE2	2.94	0.40
1:M:24:GLU:HG3	1:M:313:LYS:HE2	2.03	0.40
1:M:457:MSE:O	1:M:458:ARG:CD	2.70	0.40
1:O:24:GLU:CD	1:O:24:GLU:N	2.74	0.40
1:P:457:MSE:O	1:P:458:ARG:CD	2.69	0.40
1:U:444:LEU:O	1:U:445:GLU:C	2.58	0.40
1:V:457:MSE:O	1:V:458:ARG:CD	2.69	0.40
1:A:61:ARG:N	1:A:62:PRO:CD	2.84	0.40
1:P:301:VAL:HG23	1:P:439:ASN:HB3	2.02	0.40
1:N:248:LYS:HE2	1:N:513:ARG:HH12	1.85	0.40
1:N:229:LYS:CG	1:N:229:LYS:O	2.69	0.40
1:T:228:LYS:O	1:T:229:LYS:HB3	2.22	0.40
1:A:567:MSE:HE2	1:B:554:LEU:HD22	2.03	0.40
1:E:236:GLN:CG	1:E:243:PRO:HB2	2.51	0.40
1:Q:210:PRO:HD2	1:Q:211:TRP:CZ3	2.56	0.40
1:X:24:GLU:CD	1:X:24:GLU:N	2.75	0.40
1:X:236:GLN:CG	1:X:243:PRO:HB2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:198:ILE:HA	1:O:199:PRO:HD3	1.69	0.40
1:Q:282:THR:HG23	1:Q:287:LEU:CD1	2.47	0.40
1:J:352:TRP:HB2	1:J:355:GLN:HG2	2.03	0.40
1:A:383:ASP:CB	1:A:385:PRO:HD3	2.51	0.40
1:K:376:ARG:HB2	1:L:352:TRP:CD1	2.56	0.40
1:L:352:TRP:HB2	1:L:355:GLN:HG2	2.03	0.40
1:H:209:PHE:CE2	1:H:214:GLN:HG2	2.56	0.40
1:B:351:PHE:CD2	1:B:356:ILE:CD1	3.04	0.40
1:I:293:ILE:HD13	1:I:294:ALA:H	1.86	0.40
1:F:276:VAL:HG23	1:F:293:ILE:HG22	2.03	0.40
1:L:383:ASP:CB	1:L:385:PRO:HD3	2.51	0.40
1:C:351:PHE:CD2	1:C:356:ILE:CD1	3.04	0.40
1:O:538:LEU:HB3	1:O:551:LEU:HD13	2.02	0.40
1:X:231:THR:HG23	1:X:249:ARG:HE	1.86	0.40
1:R:311:GLU:O	1:R:312:ASP:HB2	2.21	0.40
1:W:310:VAL:HB	1:W:311:GLU:H	1.68	0.40
1:K:372:TYR:CD2	1:L:348:LYS:HB2	2.55	0.40
1:X:387:GLN:HA	1:X:388:PRO:HD3	1.93	0.40
1:W:578:GLN:HG2	1:W:596:ALA:CB	2.50	0.40
1:M:386:THR:CG2	1:M:389:LEU:HD21	2.51	0.40
1:N:583:LYS:HA	1:N:584:PRO:HD3	1.91	0.40
1:C:191:TYR:HE1	1:C:278:LYS:HZ3	1.66	0.40
1:S:390:ALA:CB	1:U:387:GLN:HB3	2.51	0.40
1:R:147:GLU:HA	1:R:148:PRO:HD3	1.80	0.40
1:X:177:HIS:O	1:X:218:GLN:HA	2.21	0.40
1:L:322:LEU:HD22	1:L:322:LEU:N	2.36	0.40
1:G:459:ARG:C	1:G:459:ARG:HD2	2.42	0.40
1:C:157:ILE:O	1:C:157:ILE:CG1	2.69	0.40
1:B:459:ARG:C	1:B:459:ARG:HD2	2.42	0.40
1:A:397:VAL:O	1:A:397:VAL:HG12	2.20	0.40
2:Y:124:TYR:O	2:Y:124:TYR:CG	2.73	0.40
1:N:216:THR:HB	1:N:218:GLN:OE1	2.21	0.40
1:E:352:TRP:HB2	1:E:355:GLN:HG2	2.02	0.40
1:N:503:GLU:HB3	1:N:508:ASN:HB3	2.03	0.40
1:B:35:PHE:HZ	1:B:321:ARG:NE	2.12	0.40
1:C:313:LYS:HD3	1:C:314:GLU:N	2.36	0.40
1:D:80:TYR:HB2	1:D:95:MSE:HG2	2.03	0.40
1:E:316:TYR:O	1:E:321:ARG:NH1	2.53	0.40
1:E:528:LYS:HD2	1:E:560:LEU:HD11	2.03	0.40
1:G:40:GLN:NE2	1:G:120:GLU:OE1	2.46	0.40
1:H:71:MSE:HG2	1:H:429:GLN:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:99:ARG:NH1	1:H:530:GLN:HE21	2.13	0.40
1:I:32:ASP:CG	1:I:316:TYR:CE2	2.94	0.40
1:I:71:MSE:HG2	1:I:429:GLN:HG3	2.04	0.40
1:I:45:LEU:O	1:I:46:SER:HB3	2.22	0.40
1:J:147:GLU:HA	1:J:148:PRO:HD3	1.86	0.40
1:J:71:MSE:HG2	1:J:429:GLN:HG3	2.03	0.40
1:K:93:VAL:HG11	1:K:458:ARG:HG2	2.03	0.40
1:O:440:MSE:O	1:O:443:ASP:HB3	2.22	0.40
1:O:458:ARG:HD3	1:O:458:ARG:HA	1.83	0.40
1:R:123:VAL:HG13	1:R:304:PHE:CE1	2.57	0.40
1:R:457:MSE:O	1:R:458:ARG:CD	2.69	0.40
1:E:61:ARG:N	1:E:62:PRO:CD	2.84	0.40
1:U:160:SER:O	1:U:161:ASN:ND2	2.46	0.40
1:U:298:ILE:HA	1:U:299:PRO:HD3	1.77	0.40
1:Q:510:ILE:HG12	1:Q:511:ARG:H	1.86	0.40
1:O:228:LYS:O	1:O:229:LYS:HB3	2.20	0.40
1:A:273:ARG:NH1	1:A:275:ARG:HE	2.19	0.40
1:O:236:GLN:H	1:O:265:LYS:CB	2.34	0.40
1:R:236:GLN:CG	1:R:243:PRO:HB2	2.51	0.40
1:G:383:ASP:CB	1:G:385:PRO:HD3	2.51	0.40
1:C:209:PHE:CE2	1:C:214:GLN:HG2	2.56	0.40
1:L:293:ILE:HD13	1:L:294:ALA:H	1.87	0.40
1:I:579:MSE:CB	1:I:581:VAL:HG12	2.49	0.40
1:J:598:GLN:HB2	1:J:601:GLN:HB3	2.02	0.40
1:E:598:GLN:HB2	1:E:601:GLN:HB3	2.02	0.40
1:I:542:THR:HA	1:I:543:PRO:HD3	1.82	0.40
1:X:578:GLN:HG2	1:X:596:ALA:CB	2.50	0.40
1:L:255:ILE:O	1:L:256:ASP:C	2.60	0.40
1:O:57:PHE:CD1	1:O:57:PHE:N	2.88	0.40
1:R:202:GLN:O	1:R:203:ASN:HB3	2.22	0.40
1:D:430:VAL:HG12	1:D:431:ALA:N	2.35	0.40
1:R:503:GLU:HB3	1:R:508:ASN:HB3	2.03	0.40
1:M:219:ILE:HG13	1:M:220:ALA:N	2.35	0.40
1:L:430:VAL:HG12	1:L:431:ALA:N	2.35	0.40
1:M:245:SER:HG	1:M:247:PHE:HE1	1.64	0.40
1:L:364:ASP:CG	2:Y:135:ALA:HB2	2.42	0.40
2:Y:20:ARG:C	2:Y:22:ALA:N	2.74	0.40
1:S:311:GLU:O	1:S:312:ASP:HB2	2.22	0.40
1:A:123:VAL:HG21	1:A:153:CYS:HB3	2.02	0.40
1:A:40:GLN:O	1:A:41:TRP:CB	2.55	0.40
1:C:71:MSE:HG2	1:C:429:GLN:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:ILE:HA	1:D:299:PRO:HD3	1.82	0.40
1:E:123:VAL:HG21	1:E:153:CYS:HB3	2.02	0.40
1:F:71:MSE:HG2	1:F:429:GLN:HG3	2.03	0.40
1:G:45:LEU:O	1:G:46:SER:HB3	2.22	0.40
1:G:528:LYS:HD2	1:G:560:LEU:HD11	2.03	0.40
1:H:102:MSE:CE	1:H:144:ILE:HD11	2.52	0.40
1:H:24:GLU:C	1:H:26:ARG:N	2.73	0.40
1:H:37:ARG:HA	1:H:37:ARG:HD2	1.79	0.40
1:I:528:LYS:HD2	1:I:560:LEU:HD11	2.03	0.40
1:J:45:LEU:O	1:J:46:SER:HB3	2.22	0.40
1:K:78:VAL:CG1	1:K:444:LEU:HG	2.51	0.40
1:K:45:LEU:O	1:K:46:SER:HB3	2.22	0.40
2:Y:28:VAL:HG22	2:Y:93:PHE:CA	2.52	0.40
1:K:528:LYS:HD2	1:K:560:LEU:HD11	2.03	0.40
1:P:306:GLU:O	1:P:316:TYR:HA	2.22	0.40
1:R:444:LEU:O	1:R:447:TYR:N	2.54	0.40
1:T:164:LEU:HD22	1:T:169:ASP:OD1	2.22	0.40
1:T:440:MSE:O	1:T:443:ASP:HB3	2.21	0.40
1:V:14:ARG:NE	1:V:14:ARG:CA	2.69	0.40
1:J:139:SER:CB	1:J:455:THR:CG2	2.80	0.40
1:N:11:ILE:O	1:N:15:PHE:HB2	2.22	0.40
1:H:61:ARG:N	1:H:62:PRO:CD	2.84	0.40
1:S:160:SER:O	1:S:161:ASN:ND2	2.46	0.40
1:R:115:VAL:HA	1:R:118:GLN:HB3	2.04	0.40
1:B:528:LYS:HZ2	1:B:560:LEU:HD21	1.87	0.40
1:I:248:LYS:H	1:I:248:LYS:CD	2.16	0.40
1:E:273:ARG:NH1	1:E:275:ARG:HE	2.19	0.40
1:W:383:ASP:C	1:W:385:PRO:HD3	2.40	0.40
1:O:236:GLN:CG	1:O:243:PRO:HB2	2.51	0.40
1:T:252:LYS:HE3	1:T:252:LYS:O	2.22	0.40
1:P:24:GLU:N	1:P:24:GLU:CD	2.74	0.40
1:R:280:ILE:HG22	1:R:287:LEU:HD13	2.03	0.40
1:S:198:ILE:HA	1:S:199:PRO:HD3	1.71	0.40
1:S:232:ALA:HB1	1:S:233:PHE:H	1.56	0.40
1:O:232:ALA:HB1	1:O:233:PHE:H	1.58	0.40
1:P:61:ARG:CB	1:P:62:PRO:HD3	2.52	0.40
1:B:583:LYS:HA	1:B:584:PRO:HD3	1.85	0.40
1:L:380:ASN:O	1:L:381:SER:CB	2.70	0.40
3:F:719:HOH:O	1:G:438:LEU:HD22	2.20	0.40
1:T:311:GLU:O	1:T:312:ASP:HB2	2.21	0.40
1:A:386:THR:HG21	1:A:389:LEU:HD21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:371:TYR:HA	1:L:348:LYS:HB3	2.03	0.40
1:O:578:GLN:HG2	1:O:596:ALA:CB	2.51	0.40
1:T:386:THR:CG2	1:T:389:LEU:HD21	2.51	0.40
1:M:387:GLN:CB	1:O:390:ALA:HB2	2.52	0.40
1:E:255:ILE:O	1:E:258:LEU:N	2.53	0.40
1:G:255:ILE:O	1:G:256:ASP:C	2.60	0.40
1:F:255:ILE:O	1:F:256:ASP:C	2.60	0.40
1:U:310:VAL:HB	1:U:311:GLU:H	1.66	0.40
1:M:371:TYR:CE2	1:M:373:LEU:HD21	2.56	0.40
1:T:227:GLU:HG2	1:T:227:GLU:O	2.20	0.40
1:B:252:LYS:HZ1	1:B:256:ASP:HB3	1.86	0.40
1:I:430:VAL:HG12	1:I:431:ALA:N	2.35	0.40
1:F:322:LEU:HD22	1:F:322:LEU:N	2.36	0.40
1:G:322:LEU:HD22	1:G:322:LEU:N	2.36	0.40
1:E:459:ARG:C	1:E:459:ARG:HD2	2.42	0.40
1:F:459:ARG:C	1:F:459:ARG:HD2	2.42	0.40
1:W:156:VAL:O	1:W:156:VAL:CG2	2.68	0.40
1:V:177:HIS:O	1:V:218:GLN:HA	2.22	0.40
1:B:164:LEU:HD22	1:B:169:ASP:CG	2.42	0.40
1:B:47:GLN:N	1:B:47:GLN:CD	2.72	0.40
1:C:47:GLN:C	1:C:48:TYR:CD2	2.95	0.40
1:E:127:ARG:HG2	1:E:147:GLU:HB2	2.02	0.40
1:E:37:ARG:HA	1:E:37:ARG:HD2	1.79	0.40
1:F:127:ARG:HG2	1:F:147:GLU:HB2	2.02	0.40
1:G:35:PHE:HZ	1:G:321:ARG:NE	2.12	0.40
1:G:71:MSE:HG2	1:G:429:GLN:HG3	2.03	0.40
1:G:440:MSE:O	1:G:444:LEU:CD2	2.69	0.40
1:G:47:GLN:C	1:G:48:TYR:CD2	2.95	0.40
1:H:298:ILE:HA	1:H:299:PRO:HD3	1.82	0.40
1:I:78:VAL:CG1	1:I:444:LEU:HG	2.51	0.40
1:J:123:VAL:HG21	1:J:153:CYS:HB3	2.02	0.40
1:J:99:ARG:HH12	1:J:530:GLN:NE2	2.14	0.40
1:K:123:VAL:HG21	1:K:153:CYS:HB3	2.02	0.40
1:L:147:GLU:HA	1:L:148:PRO:HD3	1.86	0.40
1:L:45:LEU:O	1:L:46:SER:HB3	2.22	0.40
1:L:102:MSE:CE	1:L:144:ILE:HD11	2.52	0.40
1:L:164:LEU:HD22	1:L:169:ASP:CG	2.41	0.40
1:G:139:SER:CB	1:G:455:THR:CG2	2.80	0.40
1:B:61:ARG:N	1:B:62:PRO:CD	2.84	0.40
1:M:251:ILE:HD11	1:M:275:ARG:HH21	1.86	0.40
1:S:301:VAL:HG23	1:S:439:ASN:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:334:MSE:SE	1:W:405:LEU:HD11	2.71	0.40
1:J:246:TYR:HD2	1:J:511:ARG:CB	2.28	0.40
1:H:248:LYS:HZ1	1:H:513:ARG:HH12	1.70	0.40
1:N:210:PRO:HD2	1:N:211:TRP:CZ3	2.56	0.40
1:X:210:PRO:HD2	1:X:211:TRP:CZ3	2.56	0.40
1:U:236:GLN:CG	1:U:243:PRO:HB2	2.52	0.40
1:P:26:ARG:O	1:P:27:ARG:C	2.59	0.40
1:N:232:ALA:N	1:N:269:ARG:O	2.54	0.40
1:Q:577:ILE:HG12	1:Q:582:LYS:CG	2.45	0.40
1:G:99:ARG:NH1	1:G:530:GLN:HE21	2.13	0.40
1:K:276:VAL:HG23	1:K:293:ILE:HG22	2.03	0.40
1:A:352:TRP:HB2	1:A:355:GLN:HG2	2.03	0.40
1:J:380:ASN:O	1:J:381:SER:CB	2.70	0.40
1:H:380:ASN:O	1:H:381:SER:CB	2.70	0.40
3:T:719:HOH:O	1:W:430:VAL:HG11	2.17	0.40
2:Y:57:TYR:O	2:Y:59:ASP:N	2.54	0.40
1:N:438:LEU:HD12	1:N:441:ARG:NH1	2.37	0.40
1:K:255:ILE:O	1:K:256:ASP:C	2.60	0.40
1:X:260:ASP:CA	1:X:264:ILE:HB	2.52	0.40
1:P:107:ALA:HA	1:P:146:ARG:HB3	2.03	0.40
1:R:591:GLN:HA	1:R:594:VAL:CG2	2.51	0.40
1:V:349:PRO:HG3	1:V:391:TYR:CE1	2.56	0.40
1:S:514:TYR:HE2	1:U:135:GLN:NE2	2.19	0.40
1:O:219:ILE:HG13	1:O:220:ALA:N	2.37	0.40
1:P:216:THR:HB	1:P:218:GLN:OE1	2.22	0.40
1:R:396:GLU:O	1:X:399:GLN:OE1	2.39	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:GLU:OE2	2:c:74:ASN:ND2[2_546]	1.06	1.14
1:N:230:GLU:N	2:r:64:GLU:OE2[2_455]	1.79	0.41
1:N:260:ASP:OD2	1:B:601:GLN:NE2[2_555]	1.79	0.41
1:C:250:ASP:OD2	2:c:74:ASN:OD1[2_546]	1.83	0.37
1:N:228:LYS:CG	2:r:64:GLU:OE1[2_455]	1.89	0.31
1:N:229:LYS:C	2:r:64:GLU:OE2[2_455]	1.92	0.28
1:S:249:ARG:NH1	2:v:65:ASN:CB[2_445]	1.94	0.26
1:S:249:ARG:NH2	2:v:65:ASN:ND2[2_445]	1.99	0.21
1:C:277:TYR:OH	2:c:73:GLU:CG[2_546]	2.05	0.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:262:GLY:O	1:B:594:VAL:CG1[2_555]	2.08	0.12
1:C:230:GLU:CD	2:c:74:ASN:ND2[2_546]	2.08	0.12
1:S:249:ARG:NH1	2:v:65:ASN:ND2[2_445]	2.09	0.11
1:W:249:ARG:NH1	2:g:72:ASP:CG[1_454]	2.10	0.10

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	B	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	8
1	C	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	8
1	D	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	E	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	F	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	G	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	H	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	I	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	J	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	K	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	9
1	L	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	8
1	M	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	12
1	N	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	11
1	O	565/602 (94%)	447 (79%)	80 (14%)	38 (7%)	1	12
1	P	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	12
1	Q	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	11
1	R	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	565/602 (94%)	443 (78%)	83 (15%)	39 (7%)	1	11
1	T	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	12
1	U	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	11
1	V	565/602 (94%)	445 (79%)	82 (14%)	38 (7%)	1	12
1	W	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	11
1	X	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	11
2	Y	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	Z	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	a	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	b	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	c	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	d	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	e	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	f	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	g	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	h	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	i	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	j	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	6
2	k	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	9
2	l	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	9
2	m	143/166 (86%)	115 (80%)	18 (13%)	10 (7%)	1	10
2	n	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	9
2	o	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	9
2	p	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	9
2	q	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	9
2	r	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	9
2	s	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	9
2	t	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	9
2	u	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	9
2	v	143/166 (86%)	114 (80%)	19 (13%)	10 (7%)	1	10
All	All	17004/18432 (92%)	13318 (78%)	2419 (14%)	1267 (8%)	1	9

All (1267) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	82	PRO
1	M	263	PHE
1	M	294	ALA
1	M	462	GLU
1	M	514	TYR
1	M	561	ASP
1	M	586	THR
1	M	588	GLU
1	N	82	PRO
1	N	263	PHE
1	N	294	ALA
1	N	462	GLU
1	N	514	TYR
1	N	561	ASP
1	N	586	THR
1	N	588	GLU
1	O	82	PRO
1	O	263	PHE
1	O	294	ALA
1	O	462	GLU
1	O	514	TYR
1	O	561	ASP
1	O	586	THR
1	O	588	GLU
1	P	82	PRO
1	P	263	PHE
1	P	294	ALA
1	P	462	GLU
1	P	514	TYR
1	P	561	ASP
1	P	586	THR
1	P	588	GLU
1	Q	82	PRO
1	Q	263	PHE
1	Q	294	ALA
1	Q	462	GLU
1	Q	514	TYR
1	Q	561	ASP
1	Q	586	THR
1	Q	588	GLU
1	R	82	PRO
1	R	263	PHE

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Mol	Chain	Res	Type
1	R	294	ALA
1	R	462	GLU
1	R	514	TYR
1	R	561	ASP
1	R	586	THR
1	R	588	GLU
1	S	82	PRO
1	S	263	PHE
1	S	294	ALA
1	S	462	GLU
1	S	514	TYR
1	S	561	ASP
1	S	586	THR
1	S	588	GLU
1	T	82	PRO
1	T	263	PHE
1	T	294	ALA
1	T	462	GLU
1	T	514	TYR
1	T	561	ASP
1	T	586	THR
1	T	588	GLU
1	U	82	PRO
1	U	263	PHE
1	U	294	ALA
1	U	462	GLU
1	U	514	TYR
1	U	561	ASP
1	U	586	THR
1	U	588	GLU
1	V	82	PRO
1	V	263	PHE
1	V	294	ALA
1	V	462	GLU
1	V	514	TYR
1	V	561	ASP
1	V	586	THR
1	V	588	GLU
1	W	82	PRO
1	W	263	PHE
1	W	294	ALA
1	W	462	GLU

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Mol	Chain	Res	Type
1	W	514	TYR
1	W	561	ASP
1	W	586	THR
1	W	588	GLU
1	X	82	PRO
1	X	263	PHE
1	X	294	ALA
1	X	462	GLU
1	X	514	TYR
1	X	561	ASP
1	X	586	THR
1	X	588	GLU
2	k	25	LEU
2	k	30	PRO
2	k	123	ALA
2	l	25	LEU
2	l	30	PRO
2	l	123	ALA
2	m	25	LEU
2	m	30	PRO
2	m	123	ALA
2	n	25	LEU
2	n	30	PRO
2	n	123	ALA
2	o	25	LEU
2	o	30	PRO
2	o	123	ALA
2	p	25	LEU
2	p	30	PRO
2	p	123	ALA
2	q	25	LEU
2	q	30	PRO
2	q	123	ALA
2	r	25	LEU
2	r	30	PRO
2	r	123	ALA
2	s	25	LEU
2	s	30	PRO
2	s	123	ALA
2	t	25	LEU
2	t	30	PRO
2	t	123	ALA

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Mol	Chain	Res	Type
2	u	25	LEU
2	u	30	PRO
2	u	123	ALA
2	v	25	LEU
2	v	30	PRO
2	v	123	ALA
1	A	41	TRP
1	A	50	THR
1	A	59	VAL
1	A	82	PRO
1	A	159	ASP
1	A	208	VAL
1	A	256	ASP
1	A	263	PHE
1	A	294	ALA
1	A	387	GLN
1	A	462	GLU
1	A	504	LYS
1	A	514	TYR
1	A	561	ASP
1	A	586	THR
1	B	41	TRP
1	B	50	THR
1	B	59	VAL
1	B	82	PRO
1	B	159	ASP
1	B	208	VAL
1	B	256	ASP
1	B	263	PHE
1	B	294	ALA
1	B	387	GLN
1	B	462	GLU
1	B	504	LYS
1	B	514	TYR
1	B	561	ASP
1	B	586	THR
1	C	41	TRP
1	C	50	THR
1	C	59	VAL
1	C	82	PRO
1	C	159	ASP
1	C	208	VAL

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Mol	Chain	Res	Type
1	C	256	ASP
1	C	263	PHE
1	C	294	ALA
1	C	387	GLN
1	C	462	GLU
1	C	504	LYS
1	C	514	TYR
1	C	561	ASP
1	C	586	THR
1	D	41	TRP
1	D	50	THR
1	D	59	VAL
1	D	82	PRO
1	D	159	ASP
1	D	208	VAL
1	D	256	ASP
1	D	263	PHE
1	D	294	ALA
1	D	387	GLN
1	D	462	GLU
1	D	504	LYS
1	D	514	TYR
1	D	561	ASP
1	D	586	THR
1	E	41	TRP
1	E	50	THR
1	E	59	VAL
1	E	82	PRO
1	E	159	ASP
1	E	208	VAL
1	E	256	ASP
1	E	263	PHE
1	E	294	ALA
1	E	387	GLN
1	E	462	GLU
1	E	504	LYS
1	E	514	TYR
1	E	561	ASP
1	E	586	THR
1	F	41	TRP
1	F	50	THR
1	F	59	VAL

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Mol	Chain	Res	Type
1	F	82	PRO
1	F	159	ASP
1	F	208	VAL
1	F	256	ASP
1	F	263	PHE
1	F	294	ALA
1	F	387	GLN
1	F	462	GLU
1	F	504	LYS
1	F	514	TYR
1	F	561	ASP
1	F	586	THR
1	G	41	TRP
1	G	50	THR
1	G	59	VAL
1	G	82	PRO
1	G	159	ASP
1	G	208	VAL
1	G	256	ASP
1	G	263	PHE
1	G	294	ALA
1	G	387	GLN
1	G	462	GLU
1	G	504	LYS
1	G	514	TYR
1	G	561	ASP
1	G	586	THR
1	H	41	TRP
1	H	50	THR
1	H	59	VAL
1	H	82	PRO
1	H	159	ASP
1	H	208	VAL
1	H	256	ASP
1	H	263	PHE
1	H	294	ALA
1	H	387	GLN
1	H	462	GLU
1	H	504	LYS
1	H	514	TYR
1	H	561	ASP
1	H	586	THR

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Mol	Chain	Res	Type
1	I	41	TRP
1	I	50	THR
1	I	59	VAL
1	I	82	PRO
1	I	159	ASP
1	I	208	VAL
1	I	256	ASP
1	I	263	PHE
1	I	294	ALA
1	I	387	GLN
1	I	462	GLU
1	I	504	LYS
1	I	514	TYR
1	I	561	ASP
1	I	586	THR
1	J	41	TRP
1	J	50	THR
1	J	59	VAL
1	J	82	PRO
1	J	159	ASP
1	J	208	VAL
1	J	256	ASP
1	J	263	PHE
1	J	294	ALA
1	J	387	GLN
1	J	462	GLU
1	J	504	LYS
1	J	514	TYR
1	J	561	ASP
1	J	586	THR
1	K	41	TRP
1	K	50	THR
1	K	59	VAL
1	K	82	PRO
1	K	208	VAL
1	K	256	ASP
1	K	263	PHE
1	K	294	ALA
1	K	387	GLN
1	K	462	GLU
1	K	504	LYS
1	K	514	TYR

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Mol	Chain	Res	Type
1	K	561	ASP
1	K	586	THR
1	L	41	TRP
1	L	50	THR
1	L	59	VAL
1	L	82	PRO
1	L	159	ASP
1	L	208	VAL
1	L	256	ASP
1	L	263	PHE
1	L	294	ALA
1	L	387	GLN
1	L	462	GLU
1	L	504	LYS
1	L	514	TYR
1	L	561	ASP
1	L	586	THR
2	Y	33	THR
2	Y	39	PRO
2	Y	75	PRO
2	Y	76	PRO
2	Y	133	LYS
2	Z	33	THR
2	Z	39	PRO
2	Z	75	PRO
2	Z	76	PRO
2	Z	133	LYS
2	a	33	THR
2	a	39	PRO
2	a	75	PRO
2	a	76	PRO
2	a	133	LYS
2	b	33	THR
2	b	39	PRO
2	b	75	PRO
2	b	76	PRO
2	b	133	LYS
2	c	33	THR
2	c	39	PRO
2	c	75	PRO
2	c	76	PRO
2	c	133	LYS

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Mol	Chain	Res	Type
2	d	33	THR
2	d	39	PRO
2	d	75	PRO
2	d	76	PRO
2	d	133	LYS
2	e	33	THR
2	e	39	PRO
2	e	75	PRO
2	e	76	PRO
2	e	133	LYS
2	f	33	THR
2	f	39	PRO
2	f	75	PRO
2	f	76	PRO
2	f	133	LYS
2	g	33	THR
2	g	39	PRO
2	g	75	PRO
2	g	76	PRO
2	g	133	LYS
2	h	33	THR
2	h	39	PRO
2	h	75	PRO
2	h	76	PRO
2	h	133	LYS
2	i	33	THR
2	i	39	PRO
2	i	75	PRO
2	i	76	PRO
2	i	133	LYS
2	j	33	THR
2	j	39	PRO
2	j	75	PRO
2	j	76	PRO
2	j	133	LYS
1	M	25	ALA
1	M	159	ASP
1	M	205	ASN
1	M	267	ALA
1	M	500	ALA
1	N	25	ALA
1	N	159	ASP

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Mol	Chain	Res	Type
1	N	205	ASN
1	N	267	ALA
1	N	295	GLY
1	N	500	ALA
1	N	513	ARG
1	O	25	ALA
1	O	76	ILE
1	O	159	ASP
1	O	205	ASN
1	O	267	ALA
1	O	295	GLY
1	O	500	ALA
1	O	513	ARG
1	P	25	ALA
1	P	49	THR
1	P	159	ASP
1	P	205	ASN
1	P	267	ALA
1	P	500	ALA
1	P	513	ARG
1	Q	25	ALA
1	Q	159	ASP
1	Q	205	ASN
1	Q	267	ALA
1	Q	500	ALA
1	R	25	ALA
1	R	159	ASP
1	R	205	ASN
1	R	267	ALA
1	R	295	GLY
1	R	500	ALA
1	S	25	ALA
1	S	49	THR
1	S	159	ASP
1	S	205	ASN
1	S	267	ALA
1	S	295	GLY
1	S	500	ALA
1	S	513	ARG
1	T	25	ALA
1	T	159	ASP
1	T	205	ASN

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Mol	Chain	Res	Type
1	T	267	ALA
1	T	500	ALA
1	T	513	ARG
1	U	25	ALA
1	U	159	ASP
1	U	205	ASN
1	U	267	ALA
1	U	295	GLY
1	U	500	ALA
1	U	513	ARG
1	V	25	ALA
1	V	159	ASP
1	V	205	ASN
1	V	267	ALA
1	V	295	GLY
1	V	500	ALA
1	W	25	ALA
1	W	159	ASP
1	W	205	ASN
1	W	267	ALA
1	W	295	GLY
1	W	500	ALA
1	X	25	ALA
1	X	76	ILE
1	X	159	ASP
1	X	205	ASN
1	X	267	ALA
1	X	295	GLY
1	X	500	ALA
2	k	66	PRO
2	k	69	GLU
2	k	124	LYS
2	k	149	PHE
2	l	66	PRO
2	l	69	GLU
2	l	124	LYS
2	l	131	ARG
2	l	149	PHE
2	m	66	PRO
2	m	124	LYS
2	m	149	PHE
2	n	66	PRO

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Mol	Chain	Res	Type
2	n	124	LYS
2	n	131	ARG
2	n	149	PHE
2	o	66	PRO
2	o	124	LYS
2	o	149	PHE
2	p	66	PRO
2	p	124	LYS
2	p	149	PHE
2	q	66	PRO
2	q	69	GLU
2	q	124	LYS
2	q	149	PHE
2	r	66	PRO
2	r	69	GLU
2	r	124	LYS
2	r	131	ARG
2	r	149	PHE
2	s	66	PRO
2	s	124	LYS
2	s	149	PHE
2	t	66	PRO
2	t	124	LYS
2	t	149	PHE
2	u	66	PRO
2	u	69	GLU
2	u	124	LYS
2	u	149	PHE
2	v	66	PRO
2	v	69	GLU
2	v	124	LYS
2	v	149	PHE
1	A	267	ALA
1	A	381	SER
1	A	388	PRO
1	A	588	GLU
1	B	267	ALA
1	B	381	SER
1	B	388	PRO
1	B	588	GLU
1	C	267	ALA
1	C	381	SER

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Mol	Chain	Res	Type
1	C	388	PRO
1	C	588	GLU
1	D	267	ALA
1	D	381	SER
1	D	388	PRO
1	D	588	GLU
1	E	267	ALA
1	E	381	SER
1	E	388	PRO
1	E	588	GLU
1	F	267	ALA
1	F	381	SER
1	F	388	PRO
1	F	588	GLU
1	G	267	ALA
1	G	381	SER
1	G	388	PRO
1	G	588	GLU
1	H	267	ALA
1	H	381	SER
1	H	388	PRO
1	H	588	GLU
1	I	267	ALA
1	I	381	SER
1	I	388	PRO
1	I	588	GLU
1	J	267	ALA
1	J	381	SER
1	J	388	PRO
1	J	588	GLU
1	K	159	ASP
1	K	267	ALA
1	K	381	SER
1	K	388	PRO
1	K	588	GLU
1	L	267	ALA
1	L	381	SER
1	L	388	PRO
1	L	588	GLU
2	Y	80	ASP
2	Y	132	ALA
2	Y	140	ARG

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Mol	Chain	Res	Type
2	Y	158	PHE
2	Z	80	ASP
2	Z	132	ALA
2	Z	140	ARG
2	Z	158	PHE
2	a	80	ASP
2	a	132	ALA
2	a	140	ARG
2	a	158	PHE
2	b	80	ASP
2	b	132	ALA
2	b	140	ARG
2	b	158	PHE
2	c	80	ASP
2	c	132	ALA
2	c	140	ARG
2	c	158	PHE
2	d	80	ASP
2	d	132	ALA
2	d	140	ARG
2	d	158	PHE
2	e	80	ASP
2	e	132	ALA
2	e	140	ARG
2	e	158	PHE
2	f	80	ASP
2	f	132	ALA
2	f	140	ARG
2	f	158	PHE
2	g	80	ASP
2	g	132	ALA
2	g	140	ARG
2	g	158	PHE
2	h	80	ASP
2	h	132	ALA
2	h	140	ARG
2	h	158	PHE
2	i	80	ASP
2	i	132	ALA
2	i	140	ARG
2	i	158	PHE
2	j	80	ASP

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Mol	Chain	Res	Type
2	j	132	ALA
2	j	140	ARG
2	j	158	PHE
1	M	8	LEU
1	M	49	THR
1	M	76	ILE
1	M	210	PRO
1	M	216	THR
1	M	295	GLY
1	M	302	PRO
1	M	381	SER
1	M	388	PRO
1	M	452	ASN
1	M	513	ARG
1	N	8	LEU
1	N	49	THR
1	N	76	ILE
1	N	210	PRO
1	N	216	THR
1	N	302	PRO
1	N	388	PRO
1	N	457	MSE
1	O	8	LEU
1	O	49	THR
1	O	210	PRO
1	O	216	THR
1	O	302	PRO
1	O	381	SER
1	O	388	PRO
1	O	452	ASN
1	O	457	MSE
1	P	8	LEU
1	P	76	ILE
1	P	210	PRO
1	P	216	THR
1	P	295	GLY
1	P	302	PRO
1	P	381	SER
1	P	388	PRO
1	P	452	ASN
1	P	457	MSE
1	Q	8	LEU

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Mol	Chain	Res	Type
1	Q	49	THR
1	Q	76	ILE
1	Q	210	PRO
1	Q	216	THR
1	Q	295	GLY
1	Q	302	PRO
1	Q	381	SER
1	Q	388	PRO
1	Q	457	MSE
1	Q	513	ARG
1	R	8	LEU
1	R	49	THR
1	R	76	ILE
1	R	210	PRO
1	R	216	THR
1	R	302	PRO
1	R	388	PRO
1	R	457	MSE
1	R	513	ARG
1	S	8	LEU
1	S	76	ILE
1	S	210	PRO
1	S	216	THR
1	S	302	PRO
1	S	381	SER
1	S	388	PRO
1	S	452	ASN
1	S	457	MSE
1	T	8	LEU
1	T	49	THR
1	T	76	ILE
1	T	210	PRO
1	T	216	THR
1	T	295	GLY
1	T	302	PRO
1	T	381	SER
1	T	388	PRO
1	T	452	ASN
1	U	8	LEU
1	U	49	THR
1	U	76	ILE
1	U	210	PRO

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Mol	Chain	Res	Type
1	U	216	THR
1	U	302	PRO
1	U	388	PRO
1	U	452	ASN
1	V	8	LEU
1	V	36	SER
1	V	49	THR
1	V	76	ILE
1	V	210	PRO
1	V	216	THR
1	V	302	PRO
1	V	388	PRO
1	V	513	ARG
1	W	8	LEU
1	W	49	THR
1	W	76	ILE
1	W	210	PRO
1	W	216	THR
1	W	302	PRO
1	W	388	PRO
1	W	452	ASN
1	W	457	MSE
1	W	513	ARG
1	X	8	LEU
1	X	49	THR
1	X	210	PRO
1	X	216	THR
1	X	302	PRO
1	X	381	SER
1	X	388	PRO
1	X	457	MSE
1	X	513	ARG
2	k	131	ARG
2	m	69	GLU
2	m	131	ARG
2	n	69	GLU
2	o	69	GLU
2	o	131	ARG
2	p	69	GLU
2	p	131	ARG
2	q	131	ARG
2	s	69	GLU

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Mol	Chain	Res	Type
2	s	131	ARG
2	t	69	GLU
2	t	131	ARG
2	u	131	ARG
2	v	131	ARG
1	A	26	ARG
1	A	36	SER
1	A	205	ASN
1	A	262	GLY
1	B	26	ARG
1	B	36	SER
1	B	205	ASN
1	B	262	GLY
1	C	26	ARG
1	C	36	SER
1	C	205	ASN
1	C	262	GLY
1	D	26	ARG
1	D	36	SER
1	D	205	ASN
1	D	262	GLY
1	E	26	ARG
1	E	36	SER
1	E	205	ASN
1	E	262	GLY
1	F	26	ARG
1	F	36	SER
1	F	205	ASN
1	F	262	GLY
1	G	26	ARG
1	G	36	SER
1	G	205	ASN
1	G	262	GLY
1	H	26	ARG
1	H	36	SER
1	H	205	ASN
1	H	262	GLY
1	I	26	ARG
1	I	36	SER
1	I	205	ASN
1	I	262	GLY
1	J	26	ARG

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Mol	Chain	Res	Type
1	J	36	SER
1	J	205	ASN
1	J	262	GLY
1	K	26	ARG
1	K	36	SER
1	K	205	ASN
1	K	262	GLY
1	L	26	ARG
1	L	36	SER
1	L	205	ASN
1	L	262	GLY
2	Y	54	ALA
2	Y	78	GLU
2	Z	54	ALA
2	Z	78	GLU
2	a	54	ALA
2	a	78	GLU
2	b	54	ALA
2	b	78	GLU
2	c	54	ALA
2	c	78	GLU
2	d	54	ALA
2	d	78	GLU
2	e	54	ALA
2	e	78	GLU
2	f	54	ALA
2	f	78	GLU
2	g	54	ALA
2	g	78	GLU
2	h	54	ALA
2	h	78	GLU
2	i	54	ALA
2	i	78	GLU
2	j	54	ALA
2	j	78	GLU
1	M	192	ASP
1	M	198	ILE
1	M	244	VAL
1	M	457	MSE
1	M	583	LYS
1	N	36	SER
1	N	192	ASP

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Mol	Chain	Res	Type
1	N	198	ILE
1	N	244	VAL
1	N	381	SER
1	N	452	ASN
1	N	583	LYS
1	O	36	SER
1	O	192	ASP
1	O	198	ILE
1	O	244	VAL
1	O	508	ASN
1	O	583	LYS
1	P	192	ASP
1	P	198	ILE
1	P	244	VAL
1	P	583	LYS
1	Q	36	SER
1	Q	192	ASP
1	Q	198	ILE
1	Q	244	VAL
1	Q	452	ASN
1	Q	583	LYS
1	R	36	SER
1	R	198	ILE
1	R	244	VAL
1	R	381	SER
1	R	452	ASN
1	R	583	LYS
1	S	36	SER
1	S	192	ASP
1	S	198	ILE
1	S	244	VAL
1	S	450	GLN
1	S	583	LYS
1	T	192	ASP
1	T	198	ILE
1	T	244	VAL
1	T	457	MSE
1	T	583	LYS
1	U	36	SER
1	U	192	ASP
1	U	198	ILE
1	U	244	VAL

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Mol	Chain	Res	Type
1	U	381	SER
1	U	457	MSE
1	U	583	LYS
1	V	192	ASP
1	V	198	ILE
1	V	244	VAL
1	V	381	SER
1	V	452	ASN
1	V	457	MSE
1	V	583	LYS
1	W	36	SER
1	W	192	ASP
1	W	198	ILE
1	W	244	VAL
1	W	381	SER
1	W	583	LYS
1	X	36	SER
1	X	192	ASP
1	X	198	ILE
1	X	244	VAL
1	X	452	ASN
1	X	583	LYS
2	k	132	MET
2	l	132	MET
2	m	132	MET
2	n	132	MET
2	o	132	MET
2	p	132	MET
2	q	132	MET
2	r	132	MET
2	s	132	MET
2	t	132	MET
2	u	132	MET
2	v	132	MET
1	A	161	ASN
1	A	198	ILE
1	A	209	PHE
1	A	216	THR
1	A	244	VAL
1	A	253	ASP
1	A	380	ASN
1	A	583	LYS

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Mol	Chain	Res	Type
1	B	161	ASN
1	B	198	ILE
1	B	209	PHE
1	B	216	THR
1	B	244	VAL
1	B	253	ASP
1	B	380	ASN
1	B	583	LYS
1	C	161	ASN
1	C	198	ILE
1	C	209	PHE
1	C	216	THR
1	C	244	VAL
1	C	253	ASP
1	C	380	ASN
1	C	583	LYS
1	D	161	ASN
1	D	198	ILE
1	D	209	PHE
1	D	216	THR
1	D	244	VAL
1	D	253	ASP
1	D	380	ASN
1	D	583	LYS
1	E	161	ASN
1	E	198	ILE
1	E	209	PHE
1	E	216	THR
1	E	244	VAL
1	E	253	ASP
1	E	380	ASN
1	E	583	LYS
1	F	161	ASN
1	F	198	ILE
1	F	209	PHE
1	F	216	THR
1	F	244	VAL
1	F	253	ASP
1	F	380	ASN
1	F	583	LYS
1	G	161	ASN
1	G	198	ILE

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Mol	Chain	Res	Type
1	G	209	PHE
1	G	216	THR
1	G	244	VAL
1	G	253	ASP
1	G	380	ASN
1	G	583	LYS
1	H	161	ASN
1	H	198	ILE
1	H	209	PHE
1	H	216	THR
1	H	244	VAL
1	H	253	ASP
1	H	380	ASN
1	H	583	LYS
1	I	161	ASN
1	I	198	ILE
1	I	209	PHE
1	I	216	THR
1	I	244	VAL
1	I	253	ASP
1	I	380	ASN
1	I	583	LYS
1	J	161	ASN
1	J	198	ILE
1	J	209	PHE
1	J	216	THR
1	J	244	VAL
1	J	253	ASP
1	J	380	ASN
1	J	583	LYS
1	K	161	ASN
1	K	198	ILE
1	K	209	PHE
1	K	216	THR
1	K	244	VAL
1	K	253	ASP
1	K	380	ASN
1	K	583	LYS
1	L	161	ASN
1	L	198	ILE
1	L	209	PHE
1	L	216	THR

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Mol	Chain	Res	Type
1	L	244	VAL
1	L	253	ASP
1	L	380	ASN
1	L	583	LYS
2	Y	141	MET
2	Y	149	PHE
2	Z	141	MET
2	Z	149	PHE
2	a	141	MET
2	a	149	PHE
2	b	141	MET
2	b	149	PHE
2	c	141	MET
2	c	149	PHE
2	d	141	MET
2	d	149	PHE
2	e	141	MET
2	e	149	PHE
2	f	141	MET
2	f	149	PHE
2	g	141	MET
2	g	149	PHE
2	h	141	MET
2	h	149	PHE
2	i	141	MET
2	i	149	PHE
2	j	141	MET
2	j	149	PHE
1	M	36	SER
1	M	344	THR
1	M	450	GLN
1	M	508	ASN
1	N	262	GLY
1	N	344	THR
1	N	508	ASN
1	O	217	ILE
1	O	344	THR
1	P	445	GLU
1	P	450	GLN
1	P	508	ASN
1	Q	262	GLY
1	Q	450	GLN

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Mol	Chain	Res	Type
1	Q	508	ASN
1	R	192	ASP
1	R	217	ILE
1	R	450	GLN
1	R	508	ASN
1	S	445	GLU
1	S	508	ASN
1	T	36	SER
1	T	217	ILE
1	T	262	GLY
1	T	450	GLN
1	T	508	ASN
1	U	262	GLY
1	U	344	THR
1	U	445	GLU
1	U	450	GLN
1	U	508	ASN
1	V	344	THR
1	V	450	GLN
1	V	508	ASN
1	W	217	ILE
1	W	344	THR
1	W	450	GLN
1	W	508	ASN
1	X	344	THR
1	X	445	GLU
1	X	508	ASN
2	k	44	MET
2	l	44	MET
2	n	44	MET
2	p	44	MET
2	q	44	MET
2	r	44	MET
1	A	76	ILE
1	A	192	ASP
1	A	206	ASP
1	A	232	ALA
1	A	295	GLY
1	A	302	PRO
1	B	76	ILE
1	B	192	ASP
1	B	206	ASP

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Mol	Chain	Res	Type
1	B	232	ALA
1	B	295	GLY
1	B	302	PRO
1	C	76	ILE
1	C	192	ASP
1	C	206	ASP
1	C	232	ALA
1	C	295	GLY
1	C	302	PRO
1	D	76	ILE
1	D	192	ASP
1	D	232	ALA
1	D	295	GLY
1	D	302	PRO
1	E	76	ILE
1	E	192	ASP
1	E	206	ASP
1	E	232	ALA
1	E	295	GLY
1	E	302	PRO
1	F	76	ILE
1	F	192	ASP
1	F	206	ASP
1	F	232	ALA
1	F	295	GLY
1	F	302	PRO
1	G	76	ILE
1	G	192	ASP
1	G	206	ASP
1	G	232	ALA
1	G	295	GLY
1	G	302	PRO
1	H	76	ILE
1	H	192	ASP
1	H	206	ASP
1	H	232	ALA
1	H	295	GLY
1	H	302	PRO
1	I	76	ILE
1	I	192	ASP
1	I	232	ALA
1	I	295	GLY

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Mol	Chain	Res	Type
1	I	302	PRO
1	J	76	ILE
1	J	192	ASP
1	J	206	ASP
1	J	232	ALA
1	J	295	GLY
1	J	302	PRO
1	K	76	ILE
1	K	192	ASP
1	K	206	ASP
1	K	232	ALA
1	K	295	GLY
1	K	302	PRO
1	L	76	ILE
1	L	192	ASP
1	L	206	ASP
1	L	232	ALA
1	L	295	GLY
1	L	302	PRO
1	M	203	ASN
1	M	217	ILE
1	M	262	GLY
1	M	397	VAL
1	N	203	ASN
1	N	217	ILE
1	N	445	GLU
1	N	450	GLN
1	O	203	ASN
1	O	262	GLY
1	O	397	VAL
1	O	450	GLN
1	P	203	ASN
1	P	262	GLY
1	P	344	THR
1	Q	203	ASN
1	Q	217	ILE
1	Q	344	THR
1	Q	397	VAL
1	Q	498	ASP
1	R	203	ASN
1	R	262	GLY
1	R	344	THR

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Mol	Chain	Res	Type
1	R	397	VAL
1	S	203	ASN
1	S	217	ILE
1	S	262	GLY
1	T	203	ASN
1	T	344	THR
1	U	203	ASN
1	U	217	ILE
1	V	203	ASN
1	V	217	ILE
1	V	262	GLY
1	W	203	ASN
1	W	262	GLY
1	W	445	GLU
1	X	203	ASN
1	X	217	ILE
1	X	262	GLY
1	X	397	VAL
1	X	450	GLN
2	o	44	MET
2	s	44	MET
2	t	44	MET
2	u	44	MET
1	A	311	GLU
1	A	384	LEU
1	B	311	GLU
1	B	384	LEU
1	B	507	LEU
1	C	311	GLU
1	C	384	LEU
1	C	507	LEU
1	D	206	ASP
1	D	311	GLU
1	D	384	LEU
1	E	311	GLU
1	E	384	LEU
1	F	311	GLU
1	F	384	LEU
1	G	311	GLU
1	G	384	LEU
1	H	311	GLU
1	H	384	LEU

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Mol	Chain	Res	Type
1	I	206	ASP
1	I	311	GLU
1	I	384	LEU
1	J	311	GLU
1	J	384	LEU
1	K	311	GLU
1	K	384	LEU
1	L	311	GLU
1	L	384	LEU
1	L	507	LEU
1	N	397	VAL
1	P	217	ILE
1	S	344	THR
1	S	397	VAL
1	T	397	VAL
1	V	397	VAL
1	W	397	VAL
2	k	140	PHE
2	l	140	PHE
2	m	140	PHE
2	n	140	PHE
2	s	140	PHE
2	t	140	PHE
2	v	140	PHE
1	A	203	ASN
1	B	203	ASN
1	C	203	ASN
1	D	203	ASN
1	E	203	ASN
1	F	203	ASN
1	G	203	ASN
1	H	203	ASN
1	I	203	ASN
1	J	203	ASN
1	K	203	ASN
1	L	203	ASN
1	P	397	VAL
2	o	140	PHE
2	p	140	PHE
2	q	140	PHE
2	r	140	PHE
2	u	140	PHE

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Mol	Chain	Res	Type
1	A	385	PRO
1	A	427	GLY
1	B	385	PRO
1	B	427	GLY
1	C	385	PRO
1	C	427	GLY
1	D	385	PRO
1	D	427	GLY
1	E	385	PRO
1	E	427	GLY
1	F	385	PRO
1	F	427	GLY
1	G	385	PRO
1	G	427	GLY
1	H	385	PRO
1	H	427	GLY
1	I	385	PRO
1	I	427	GLY
1	J	385	PRO
1	J	427	GLY
1	K	385	PRO
1	K	427	GLY
1	L	385	PRO
1	L	427	GLY
1	U	397	VAL
1	M	310	VAL
1	N	310	VAL
1	O	310	VAL
1	P	310	VAL
1	Q	310	VAL
1	R	310	VAL
1	S	310	VAL
1	T	310	VAL
1	U	310	VAL
1	V	310	VAL
1	W	310	VAL
1	X	310	VAL
1	A	210	PRO
1	B	210	PRO
1	C	210	PRO
1	D	210	PRO
1	E	210	PRO

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Mol	Chain	Res	Type
1	F	210	PRO
1	G	210	PRO
1	H	210	PRO
1	I	210	PRO
1	J	210	PRO
1	K	210	PRO
1	L	210	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	B	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	C	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	D	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	E	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	F	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	G	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	H	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	I	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	J	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	K	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	L	483/510 (95%)	412 (85%)	71 (15%)	4	18
1	M	485/510 (95%)	412 (85%)	73 (15%)	3	17
1	N	485/510 (95%)	412 (85%)	73 (15%)	3	17
1	O	485/510 (95%)	413 (85%)	72 (15%)	4	18
1	P	485/510 (95%)	413 (85%)	72 (15%)	4	18
1	Q	485/510 (95%)	412 (85%)	73 (15%)	3	17
1	R	485/510 (95%)	411 (85%)	74 (15%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	485/510 (95%)	411 (85%)	74 (15%)	3	17
1	T	485/510 (95%)	412 (85%)	73 (15%)	3	17
1	U	485/510 (95%)	413 (85%)	72 (15%)	4	18
1	V	485/510 (95%)	413 (85%)	72 (15%)	4	18
1	W	485/510 (95%)	413 (85%)	72 (15%)	4	18
1	X	485/510 (95%)	411 (85%)	74 (15%)	3	17
2	Y	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	Z	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	a	98/132 (74%)	84 (86%)	14 (14%)	4	19
2	b	98/132 (74%)	84 (86%)	14 (14%)	4	19
2	c	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	d	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	e	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	f	98/132 (74%)	84 (86%)	14 (14%)	4	19
2	g	98/132 (74%)	84 (86%)	14 (14%)	4	19
2	h	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	i	98/132 (74%)	85 (87%)	13 (13%)	5	23
2	j	98/132 (74%)	84 (86%)	14 (14%)	4	19
2	k	100/132 (76%)	88 (88%)	12 (12%)	6	28
2	l	100/132 (76%)	87 (87%)	13 (13%)	5	24
2	m	100/132 (76%)	88 (88%)	12 (12%)	6	28
2	n	100/132 (76%)	87 (87%)	13 (13%)	5	24
2	o	100/132 (76%)	85 (85%)	15 (15%)	3	17
2	p	100/132 (76%)	86 (86%)	14 (14%)	4	20
2	q	100/132 (76%)	88 (88%)	12 (12%)	6	28
2	r	100/132 (76%)	88 (88%)	12 (12%)	6	28
2	s	100/132 (76%)	87 (87%)	13 (13%)	5	24
2	t	100/132 (76%)	87 (87%)	13 (13%)	5	24
2	u	100/132 (76%)	87 (87%)	13 (13%)	5	24
2	v	100/132 (76%)	87 (87%)	13 (13%)	5	24
All	All	13992/15408 (91%)	11950 (85%)	2042 (15%)	4	19

All (2042) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	14	ARG
1	M	15	PHE
1	M	24	GLU
1	M	30	LYS
1	M	31	ASN
1	M	33	LEU
1	M	40	GLN
1	M	42	ASP
1	M	47	GLN
1	M	49	THR
1	M	50	THR
1	M	56	GLN
1	M	59	VAL
1	M	61	ARG
1	M	69	SER
1	M	79	LEU
1	M	94	LEU
1	M	101	ASP
1	M	123	VAL
1	M	127	ARG
1	M	133	GLU
1	M	135	GLN
1	M	144	ILE
1	M	156	VAL
1	M	157	ILE
1	M	158	TRP
1	M	161	ASN
1	M	164	LEU
1	M	174	THR
1	M	175	VAL
1	M	190	LYS
1	M	201	PHE
1	M	202	GLN
1	M	209	PHE
1	M	211	TRP
1	M	217	ILE
1	M	218	GLN
1	M	226	VAL
1	M	228	LYS
1	M	231	THR
1	M	234	ILE
1	M	246	TYR

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Mol	Chain	Res	Type
1	M	248	LYS
1	M	265	LYS
1	M	266	ILE
1	M	275	ARG
1	M	286	VAL
1	M	293	ILE
1	M	298	ILE
1	M	301	VAL
1	M	311	GLU
1	M	327	GLN
1	M	343	ARG
1	M	356	ILE
1	M	359	PHE
1	M	376	ARG
1	M	378	ASP
1	M	384	LEU
1	M	387	GLN
1	M	389	LEU
1	M	405	LEU
1	M	430	VAL
1	M	433	ASP
1	M	444	LEU
1	M	451	ASP
1	M	510	ILE
1	M	513	ARG
1	M	518	THR
1	M	541	LYS
1	M	546	THR
1	M	558	THR
1	M	592	TRP
1	M	593	LEU
1	N	14	ARG
1	N	15	PHE
1	N	24	GLU
1	N	30	LYS
1	N	31	ASN
1	N	33	LEU
1	N	40	GLN
1	N	42	ASP
1	N	47	GLN
1	N	49	THR
1	N	50	THR

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Mol	Chain	Res	Type
1	N	56	GLN
1	N	59	VAL
1	N	61	ARG
1	N	69	SER
1	N	79	LEU
1	N	94	LEU
1	N	101	ASP
1	N	123	VAL
1	N	127	ARG
1	N	133	GLU
1	N	135	GLN
1	N	144	ILE
1	N	156	VAL
1	N	157	ILE
1	N	158	TRP
1	N	161	ASN
1	N	164	LEU
1	N	174	THR
1	N	175	VAL
1	N	190	LYS
1	N	201	PHE
1	N	202	GLN
1	N	209	PHE
1	N	211	TRP
1	N	217	ILE
1	N	218	GLN
1	N	226	VAL
1	N	228	LYS
1	N	231	THR
1	N	234	ILE
1	N	246	TYR
1	N	248	LYS
1	N	265	LYS
1	N	266	ILE
1	N	273	ARG
1	N	275	ARG
1	N	286	VAL
1	N	293	ILE
1	N	298	ILE
1	N	301	VAL
1	N	327	GLN
1	N	343	ARG

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Mol	Chain	Res	Type
1	N	356	ILE
1	N	359	PHE
1	N	376	ARG
1	N	378	ASP
1	N	384	LEU
1	N	387	GLN
1	N	389	LEU
1	N	405	LEU
1	N	430	VAL
1	N	433	ASP
1	N	444	LEU
1	N	451	ASP
1	N	510	ILE
1	N	513	ARG
1	N	518	THR
1	N	541	LYS
1	N	546	THR
1	N	558	THR
1	N	592	TRP
1	N	593	LEU
1	O	14	ARG
1	O	15	PHE
1	O	24	GLU
1	O	30	LYS
1	O	31	ASN
1	O	33	LEU
1	O	40	GLN
1	O	42	ASP
1	O	47	GLN
1	O	49	THR
1	O	50	THR
1	O	56	GLN
1	O	59	VAL
1	O	61	ARG
1	O	69	SER
1	O	79	LEU
1	O	94	LEU
1	O	101	ASP
1	O	123	VAL
1	O	127	ARG
1	O	133	GLU
1	O	135	GLN

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Mol	Chain	Res	Type
1	O	144	ILE
1	O	156	VAL
1	O	157	ILE
1	O	158	TRP
1	O	161	ASN
1	O	164	LEU
1	O	174	THR
1	O	175	VAL
1	O	190	LYS
1	O	201	PHE
1	O	202	GLN
1	O	209	PHE
1	O	211	TRP
1	O	217	ILE
1	O	218	GLN
1	O	225	VAL
1	O	226	VAL
1	O	228	LYS
1	O	231	THR
1	O	234	ILE
1	O	246	TYR
1	O	248	LYS
1	O	265	LYS
1	O	266	ILE
1	O	275	ARG
1	O	286	VAL
1	O	293	ILE
1	O	298	ILE
1	O	301	VAL
1	O	327	GLN
1	O	343	ARG
1	O	356	ILE
1	O	359	PHE
1	O	376	ARG
1	O	378	ASP
1	O	384	LEU
1	O	387	GLN
1	O	389	LEU
1	O	405	LEU
1	O	433	ASP
1	O	444	LEU
1	O	451	ASP

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Mol	Chain	Res	Type
1	O	510	ILE
1	O	513	ARG
1	O	518	THR
1	O	541	LYS
1	O	546	THR
1	O	558	THR
1	O	592	TRP
1	O	593	LEU
1	P	14	ARG
1	P	15	PHE
1	P	24	GLU
1	P	30	LYS
1	P	31	ASN
1	P	33	LEU
1	P	40	GLN
1	P	42	ASP
1	P	47	GLN
1	P	49	THR
1	P	50	THR
1	P	56	GLN
1	P	59	VAL
1	P	61	ARG
1	P	69	SER
1	P	79	LEU
1	P	94	LEU
1	P	101	ASP
1	P	123	VAL
1	P	127	ARG
1	P	133	GLU
1	P	135	GLN
1	P	144	ILE
1	P	156	VAL
1	P	157	ILE
1	P	158	TRP
1	P	161	ASN
1	P	164	LEU
1	P	174	THR
1	P	175	VAL
1	P	190	LYS
1	P	201	PHE
1	P	202	GLN
1	P	209	PHE

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Mol	Chain	Res	Type
1	P	211	TRP
1	P	217	ILE
1	P	218	GLN
1	P	225	VAL
1	P	226	VAL
1	P	228	LYS
1	P	231	THR
1	P	234	ILE
1	P	246	TYR
1	P	248	LYS
1	P	265	LYS
1	P	266	ILE
1	P	275	ARG
1	P	286	VAL
1	P	293	ILE
1	P	298	ILE
1	P	301	VAL
1	P	327	GLN
1	P	343	ARG
1	P	356	ILE
1	P	359	PHE
1	P	376	ARG
1	P	378	ASP
1	P	384	LEU
1	P	387	GLN
1	P	389	LEU
1	P	430	VAL
1	P	433	ASP
1	P	444	LEU
1	P	451	ASP
1	P	510	ILE
1	P	513	ARG
1	P	518	THR
1	P	541	LYS
1	P	546	THR
1	P	558	THR
1	P	592	TRP
1	P	593	LEU
1	Q	14	ARG
1	Q	15	PHE
1	Q	24	GLU
1	Q	30	LYS

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Mol	Chain	Res	Type
1	Q	31	ASN
1	Q	33	LEU
1	Q	40	GLN
1	Q	42	ASP
1	Q	47	GLN
1	Q	49	THR
1	Q	50	THR
1	Q	56	GLN
1	Q	59	VAL
1	Q	61	ARG
1	Q	69	SER
1	Q	79	LEU
1	Q	94	LEU
1	Q	101	ASP
1	Q	123	VAL
1	Q	127	ARG
1	Q	133	GLU
1	Q	135	GLN
1	Q	144	ILE
1	Q	156	VAL
1	Q	157	ILE
1	Q	158	TRP
1	Q	161	ASN
1	Q	164	LEU
1	Q	174	THR
1	Q	175	VAL
1	Q	190	LYS
1	Q	201	PHE
1	Q	202	GLN
1	Q	209	PHE
1	Q	211	TRP
1	Q	217	ILE
1	Q	218	GLN
1	Q	225	VAL
1	Q	226	VAL
1	Q	228	LYS
1	Q	231	THR
1	Q	234	ILE
1	Q	246	TYR
1	Q	248	LYS
1	Q	265	LYS
1	Q	266	ILE

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Mol	Chain	Res	Type
1	Q	275	ARG
1	Q	286	VAL
1	Q	293	ILE
1	Q	298	ILE
1	Q	301	VAL
1	Q	327	GLN
1	Q	343	ARG
1	Q	356	ILE
1	Q	359	PHE
1	Q	376	ARG
1	Q	378	ASP
1	Q	384	LEU
1	Q	387	GLN
1	Q	389	LEU
1	Q	405	LEU
1	Q	430	VAL
1	Q	433	ASP
1	Q	444	LEU
1	Q	451	ASP
1	Q	510	ILE
1	Q	513	ARG
1	Q	518	THR
1	Q	541	LYS
1	Q	546	THR
1	Q	558	THR
1	Q	592	TRP
1	Q	593	LEU
1	R	14	ARG
1	R	15	PHE
1	R	24	GLU
1	R	30	LYS
1	R	31	ASN
1	R	33	LEU
1	R	40	GLN
1	R	42	ASP
1	R	47	GLN
1	R	49	THR
1	R	50	THR
1	R	56	GLN
1	R	59	VAL
1	R	69	SER
1	R	79	LEU

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Mol	Chain	Res	Type
1	R	94	LEU
1	R	101	ASP
1	R	123	VAL
1	R	127	ARG
1	R	133	GLU
1	R	135	GLN
1	R	144	ILE
1	R	156	VAL
1	R	157	ILE
1	R	158	TRP
1	R	161	ASN
1	R	164	LEU
1	R	174	THR
1	R	175	VAL
1	R	190	LYS
1	R	201	PHE
1	R	202	GLN
1	R	209	PHE
1	R	211	TRP
1	R	217	ILE
1	R	218	GLN
1	R	225	VAL
1	R	226	VAL
1	R	228	LYS
1	R	231	THR
1	R	234	ILE
1	R	246	TYR
1	R	248	LYS
1	R	265	LYS
1	R	266	ILE
1	R	275	ARG
1	R	286	VAL
1	R	293	ILE
1	R	298	ILE
1	R	301	VAL
1	R	311	GLU
1	R	315	VAL
1	R	327	GLN
1	R	343	ARG
1	R	356	ILE
1	R	359	PHE
1	R	376	ARG

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Mol	Chain	Res	Type
1	R	378	ASP
1	R	384	LEU
1	R	387	GLN
1	R	389	LEU
1	R	405	LEU
1	R	430	VAL
1	R	433	ASP
1	R	444	LEU
1	R	451	ASP
1	R	510	ILE
1	R	513	ARG
1	R	518	THR
1	R	541	LYS
1	R	546	THR
1	R	558	THR
1	R	592	TRP
1	R	593	LEU
1	S	14	ARG
1	S	15	PHE
1	S	24	GLU
1	S	30	LYS
1	S	31	ASN
1	S	33	LEU
1	S	40	GLN
1	S	42	ASP
1	S	47	GLN
1	S	49	THR
1	S	50	THR
1	S	56	GLN
1	S	59	VAL
1	S	61	ARG
1	S	69	SER
1	S	79	LEU
1	S	94	LEU
1	S	101	ASP
1	S	123	VAL
1	S	127	ARG
1	S	133	GLU
1	S	135	GLN
1	S	144	ILE
1	S	156	VAL
1	S	157	ILE

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Mol	Chain	Res	Type
1	S	158	TRP
1	S	161	ASN
1	S	164	LEU
1	S	174	THR
1	S	175	VAL
1	S	190	LYS
1	S	201	PHE
1	S	202	GLN
1	S	209	PHE
1	S	211	TRP
1	S	217	ILE
1	S	218	GLN
1	S	225	VAL
1	S	226	VAL
1	S	228	LYS
1	S	231	THR
1	S	234	ILE
1	S	246	TYR
1	S	248	LYS
1	S	265	LYS
1	S	266	ILE
1	S	275	ARG
1	S	286	VAL
1	S	293	ILE
1	S	298	ILE
1	S	301	VAL
1	S	311	GLU
1	S	327	GLN
1	S	343	ARG
1	S	356	ILE
1	S	359	PHE
1	S	376	ARG
1	S	378	ASP
1	S	384	LEU
1	S	387	GLN
1	S	389	LEU
1	S	405	LEU
1	S	430	VAL
1	S	433	ASP
1	S	444	LEU
1	S	451	ASP
1	S	510	ILE

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Mol	Chain	Res	Type
1	S	513	ARG
1	S	518	THR
1	S	541	LYS
1	S	546	THR
1	S	558	THR
1	S	592	TRP
1	S	593	LEU
1	T	14	ARG
1	T	15	PHE
1	T	24	GLU
1	T	30	LYS
1	T	31	ASN
1	T	33	LEU
1	T	40	GLN
1	T	42	ASP
1	T	47	GLN
1	T	49	THR
1	T	50	THR
1	T	56	GLN
1	T	59	VAL
1	T	61	ARG
1	T	69	SER
1	T	79	LEU
1	T	94	LEU
1	T	101	ASP
1	T	123	VAL
1	T	127	ARG
1	T	133	GLU
1	T	135	GLN
1	T	144	ILE
1	T	156	VAL
1	T	157	ILE
1	T	158	TRP
1	T	161	ASN
1	T	164	LEU
1	T	174	THR
1	T	175	VAL
1	T	190	LYS
1	T	201	PHE
1	T	202	GLN
1	T	209	PHE
1	T	211	TRP

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Mol	Chain	Res	Type
1	T	217	ILE
1	T	218	GLN
1	T	225	VAL
1	T	226	VAL
1	T	228	LYS
1	T	231	THR
1	T	234	ILE
1	T	246	TYR
1	T	248	LYS
1	T	265	LYS
1	T	266	ILE
1	T	275	ARG
1	T	286	VAL
1	T	293	ILE
1	T	298	ILE
1	T	301	VAL
1	T	327	GLN
1	T	343	ARG
1	T	356	ILE
1	T	359	PHE
1	T	376	ARG
1	T	378	ASP
1	T	384	LEU
1	T	387	GLN
1	T	389	LEU
1	T	405	LEU
1	T	430	VAL
1	T	433	ASP
1	T	444	LEU
1	T	451	ASP
1	T	510	ILE
1	T	513	ARG
1	T	518	THR
1	T	541	LYS
1	T	546	THR
1	T	558	THR
1	T	592	TRP
1	T	593	LEU
1	U	14	ARG
1	U	15	PHE
1	U	24	GLU
1	U	30	LYS

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Mol	Chain	Res	Type
1	U	31	ASN
1	U	33	LEU
1	U	40	GLN
1	U	42	ASP
1	U	47	GLN
1	U	49	THR
1	U	50	THR
1	U	56	GLN
1	U	59	VAL
1	U	61	ARG
1	U	69	SER
1	U	79	LEU
1	U	94	LEU
1	U	101	ASP
1	U	123	VAL
1	U	127	ARG
1	U	133	GLU
1	U	135	GLN
1	U	144	ILE
1	U	156	VAL
1	U	157	ILE
1	U	158	TRP
1	U	161	ASN
1	U	164	LEU
1	U	174	THR
1	U	175	VAL
1	U	190	LYS
1	U	201	PHE
1	U	202	GLN
1	U	209	PHE
1	U	211	TRP
1	U	217	ILE
1	U	218	GLN
1	U	226	VAL
1	U	228	LYS
1	U	231	THR
1	U	234	ILE
1	U	246	TYR
1	U	248	LYS
1	U	265	LYS
1	U	266	ILE
1	U	275	ARG

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Mol	Chain	Res	Type
1	U	286	VAL
1	U	293	ILE
1	U	298	ILE
1	U	301	VAL
1	U	327	GLN
1	U	343	ARG
1	U	356	ILE
1	U	359	PHE
1	U	376	ARG
1	U	378	ASP
1	U	384	LEU
1	U	387	GLN
1	U	389	LEU
1	U	405	LEU
1	U	430	VAL
1	U	433	ASP
1	U	444	LEU
1	U	451	ASP
1	U	510	ILE
1	U	513	ARG
1	U	518	THR
1	U	541	LYS
1	U	546	THR
1	U	558	THR
1	U	592	TRP
1	U	593	LEU
1	V	14	ARG
1	V	15	PHE
1	V	24	GLU
1	V	30	LYS
1	V	31	ASN
1	V	33	LEU
1	V	40	GLN
1	V	42	ASP
1	V	47	GLN
1	V	49	THR
1	V	50	THR
1	V	56	GLN
1	V	59	VAL
1	V	61	ARG
1	V	69	SER
1	V	79	LEU

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Mol	Chain	Res	Type
1	V	94	LEU
1	V	101	ASP
1	V	123	VAL
1	V	127	ARG
1	V	133	GLU
1	V	135	GLN
1	V	144	ILE
1	V	156	VAL
1	V	157	ILE
1	V	158	TRP
1	V	161	ASN
1	V	164	LEU
1	V	174	THR
1	V	175	VAL
1	V	190	LYS
1	V	201	PHE
1	V	202	GLN
1	V	209	PHE
1	V	211	TRP
1	V	217	ILE
1	V	218	GLN
1	V	226	VAL
1	V	228	LYS
1	V	231	THR
1	V	234	ILE
1	V	246	TYR
1	V	248	LYS
1	V	265	LYS
1	V	266	ILE
1	V	275	ARG
1	V	286	VAL
1	V	293	ILE
1	V	298	ILE
1	V	301	VAL
1	V	327	GLN
1	V	343	ARG
1	V	356	ILE
1	V	359	PHE
1	V	376	ARG
1	V	378	ASP
1	V	384	LEU
1	V	387	GLN

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Mol	Chain	Res	Type
1	V	389	LEU
1	V	405	LEU
1	V	430	VAL
1	V	433	ASP
1	V	444	LEU
1	V	451	ASP
1	V	510	ILE
1	V	513	ARG
1	V	518	THR
1	V	541	LYS
1	V	546	THR
1	V	558	THR
1	V	592	TRP
1	V	593	LEU
1	W	14	ARG
1	W	15	PHE
1	W	24	GLU
1	W	30	LYS
1	W	31	ASN
1	W	33	LEU
1	W	40	GLN
1	W	42	ASP
1	W	47	GLN
1	W	49	THR
1	W	50	THR
1	W	56	GLN
1	W	59	VAL
1	W	61	ARG
1	W	69	SER
1	W	79	LEU
1	W	94	LEU
1	W	101	ASP
1	W	123	VAL
1	W	127	ARG
1	W	133	GLU
1	W	135	GLN
1	W	144	ILE
1	W	156	VAL
1	W	157	ILE
1	W	158	TRP
1	W	161	ASN
1	W	164	LEU

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Mol	Chain	Res	Type
1	W	174	THR
1	W	175	VAL
1	W	190	LYS
1	W	201	PHE
1	W	202	GLN
1	W	209	PHE
1	W	211	TRP
1	W	217	ILE
1	W	218	GLN
1	W	225	VAL
1	W	226	VAL
1	W	228	LYS
1	W	231	THR
1	W	234	ILE
1	W	246	TYR
1	W	248	LYS
1	W	265	LYS
1	W	266	ILE
1	W	275	ARG
1	W	286	VAL
1	W	293	ILE
1	W	298	ILE
1	W	301	VAL
1	W	327	GLN
1	W	343	ARG
1	W	356	ILE
1	W	359	PHE
1	W	376	ARG
1	W	378	ASP
1	W	384	LEU
1	W	387	GLN
1	W	389	LEU
1	W	430	VAL
1	W	433	ASP
1	W	444	LEU
1	W	451	ASP
1	W	510	ILE
1	W	513	ARG
1	W	518	THR
1	W	541	LYS
1	W	546	THR
1	W	558	THR

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Mol	Chain	Res	Type
1	W	592	TRP
1	W	593	LEU
1	X	14	ARG
1	X	15	PHE
1	X	24	GLU
1	X	30	LYS
1	X	31	ASN
1	X	33	LEU
1	X	40	GLN
1	X	42	ASP
1	X	47	GLN
1	X	49	THR
1	X	50	THR
1	X	56	GLN
1	X	59	VAL
1	X	69	SER
1	X	79	LEU
1	X	94	LEU
1	X	101	ASP
1	X	123	VAL
1	X	127	ARG
1	X	133	GLU
1	X	135	GLN
1	X	144	ILE
1	X	156	VAL
1	X	157	ILE
1	X	158	TRP
1	X	161	ASN
1	X	164	LEU
1	X	174	THR
1	X	175	VAL
1	X	190	LYS
1	X	201	PHE
1	X	202	GLN
1	X	209	PHE
1	X	211	TRP
1	X	217	ILE
1	X	218	GLN
1	X	225	VAL
1	X	226	VAL
1	X	228	LYS
1	X	231	THR

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Mol	Chain	Res	Type
1	X	234	ILE
1	X	246	TYR
1	X	248	LYS
1	X	265	LYS
1	X	266	ILE
1	X	275	ARG
1	X	286	VAL
1	X	293	ILE
1	X	298	ILE
1	X	301	VAL
1	X	311	GLU
1	X	327	GLN
1	X	343	ARG
1	X	356	ILE
1	X	359	PHE
1	X	376	ARG
1	X	378	ASP
1	X	384	LEU
1	X	387	GLN
1	X	389	LEU
1	X	405	LEU
1	X	430	VAL
1	X	433	ASP
1	X	444	LEU
1	X	451	ASP
1	X	510	ILE
1	X	513	ARG
1	X	518	THR
1	X	541	LYS
1	X	546	THR
1	X	558	THR
1	X	561	ASP
1	X	592	TRP
1	X	593	LEU
2	k	16	LYS
2	k	27	ASP
2	k	29	GLU
2	k	33	MET
2	k	39	ASP
2	k	69	GLU
2	k	71	ASP
2	k	84	PHE

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Mol	Chain	Res	Type
2	k	87	LEU
2	k	130	SER
2	k	131	ARG
2	k	136	SER
2	l	16	LYS
2	l	27	ASP
2	l	29	GLU
2	l	33	MET
2	l	39	ASP
2	l	69	GLU
2	l	71	ASP
2	l	84	PHE
2	l	87	LEU
2	l	100	THR
2	l	130	SER
2	l	131	ARG
2	l	136	SER
2	m	16	LYS
2	m	27	ASP
2	m	29	GLU
2	m	33	MET
2	m	39	ASP
2	m	69	GLU
2	m	71	ASP
2	m	84	PHE
2	m	87	LEU
2	m	130	SER
2	m	131	ARG
2	m	136	SER
2	n	16	LYS
2	n	27	ASP
2	n	29	GLU
2	n	33	MET
2	n	39	ASP
2	n	56	THR
2	n	69	GLU
2	n	71	ASP
2	n	84	PHE
2	n	87	LEU
2	n	130	SER
2	n	131	ARG
2	n	136	SER

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Mol	Chain	Res	Type
2	o	16	LYS
2	o	27	ASP
2	o	29	GLU
2	o	33	MET
2	o	37	VAL
2	o	39	ASP
2	o	56	THR
2	o	69	GLU
2	o	71	ASP
2	o	84	PHE
2	o	87	LEU
2	o	100	THR
2	o	130	SER
2	o	131	ARG
2	o	136	SER
2	p	16	LYS
2	p	27	ASP
2	p	29	GLU
2	p	33	MET
2	p	37	VAL
2	p	39	ASP
2	p	56	THR
2	p	69	GLU
2	p	71	ASP
2	p	84	PHE
2	p	87	LEU
2	p	130	SER
2	p	131	ARG
2	p	136	SER
2	q	16	LYS
2	q	27	ASP
2	q	29	GLU
2	q	33	MET
2	q	39	ASP
2	q	69	GLU
2	q	71	ASP
2	q	84	PHE
2	q	87	LEU
2	q	130	SER
2	q	131	ARG
2	q	136	SER
2	r	16	LYS

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Mol	Chain	Res	Type
2	r	27	ASP
2	r	29	GLU
2	r	33	MET
2	r	39	ASP
2	r	69	GLU
2	r	71	ASP
2	r	84	PHE
2	r	87	LEU
2	r	130	SER
2	r	131	ARG
2	r	136	SER
2	s	16	LYS
2	s	27	ASP
2	s	29	GLU
2	s	33	MET
2	s	37	VAL
2	s	39	ASP
2	s	69	GLU
2	s	71	ASP
2	s	84	PHE
2	s	87	LEU
2	s	130	SER
2	s	131	ARG
2	s	136	SER
2	t	16	LYS
2	t	27	ASP
2	t	29	GLU
2	t	33	MET
2	t	39	ASP
2	t	56	THR
2	t	69	GLU
2	t	71	ASP
2	t	84	PHE
2	t	87	LEU
2	t	130	SER
2	t	131	ARG
2	t	136	SER
2	u	16	LYS
2	u	27	ASP
2	u	29	GLU
2	u	33	MET
2	u	39	ASP

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Mol	Chain	Res	Type
2	u	69	GLU
2	u	71	ASP
2	u	84	PHE
2	u	87	LEU
2	u	100	THR
2	u	130	SER
2	u	131	ARG
2	u	136	SER
2	v	16	LYS
2	v	27	ASP
2	v	29	GLU
2	v	33	MET
2	v	37	VAL
2	v	39	ASP
2	v	69	GLU
2	v	71	ASP
2	v	84	PHE
2	v	87	LEU
2	v	130	SER
2	v	131	ARG
2	v	136	SER
1	A	14	ARG
1	A	15	PHE
1	A	24	GLU
1	A	30	LYS
1	A	31	ASN
1	A	33	LEU
1	A	37	ARG
1	A	42	ASP
1	A	43	ASP
1	A	45	LEU
1	A	47	GLN
1	A	56	GLN
1	A	61	ARG
1	A	79	LEU
1	A	118	GLN
1	A	123	VAL
1	A	127	ARG
1	A	133	GLU
1	A	135	GLN
1	A	144	ILE
1	A	157	ILE

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Mol	Chain	Res	Type
1	A	158	TRP
1	A	161	ASN
1	A	164	LEU
1	A	168	SER
1	A	174	THR
1	A	190	LYS
1	A	201	PHE
1	A	202	GLN
1	A	209	PHE
1	A	211	TRP
1	A	217	ILE
1	A	218	GLN
1	A	226	VAL
1	A	234	ILE
1	A	246	TYR
1	A	248	LYS
1	A	265	LYS
1	A	266	ILE
1	A	273	ARG
1	A	275	ARG
1	A	286	VAL
1	A	293	ILE
1	A	301	VAL
1	A	315	VAL
1	A	325	ASP
1	A	327	GLN
1	A	343	ARG
1	A	359	PHE
1	A	376	ARG
1	A	384	LEU
1	A	387	GLN
1	A	389	LEU
1	A	405	LEU
1	A	421	ASP
1	A	422	THR
1	A	430	VAL
1	A	432	PHE
1	A	433	ASP
1	A	438	LEU
1	A	444	LEU
1	A	507	LEU
1	A	513	ARG

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Mol	Chain	Res	Type
1	A	518	THR
1	A	529	GLN
1	A	541	LYS
1	A	546	THR
1	A	555	GLN
1	A	592	TRP
1	A	593	LEU
1	A	597	GLN
1	B	14	ARG
1	B	15	PHE
1	B	24	GLU
1	B	30	LYS
1	B	31	ASN
1	B	33	LEU
1	B	37	ARG
1	B	42	ASP
1	B	43	ASP
1	B	45	LEU
1	B	47	GLN
1	B	56	GLN
1	B	61	ARG
1	B	79	LEU
1	B	118	GLN
1	B	123	VAL
1	B	127	ARG
1	B	133	GLU
1	B	135	GLN
1	B	144	ILE
1	B	157	ILE
1	B	158	TRP
1	B	161	ASN
1	B	164	LEU
1	B	168	SER
1	B	174	THR
1	B	190	LYS
1	B	201	PHE
1	B	202	GLN
1	B	209	PHE
1	B	211	TRP
1	B	217	ILE
1	B	218	GLN
1	B	226	VAL

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Mol	Chain	Res	Type
1	B	234	ILE
1	B	246	TYR
1	B	248	LYS
1	B	265	LYS
1	B	266	ILE
1	B	273	ARG
1	B	275	ARG
1	B	286	VAL
1	B	293	ILE
1	B	301	VAL
1	B	315	VAL
1	B	325	ASP
1	B	327	GLN
1	B	343	ARG
1	B	359	PHE
1	B	376	ARG
1	B	384	LEU
1	B	387	GLN
1	B	389	LEU
1	B	405	LEU
1	B	421	ASP
1	B	422	THR
1	B	430	VAL
1	B	432	PHE
1	B	433	ASP
1	B	438	LEU
1	B	444	LEU
1	B	507	LEU
1	B	513	ARG
1	B	518	THR
1	B	529	GLN
1	B	541	LYS
1	B	546	THR
1	B	555	GLN
1	B	592	TRP
1	B	593	LEU
1	B	597	GLN
1	C	14	ARG
1	C	15	PHE
1	C	24	GLU
1	C	30	LYS
1	C	31	ASN

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Mol	Chain	Res	Type
1	C	33	LEU
1	C	37	ARG
1	C	42	ASP
1	C	43	ASP
1	C	45	LEU
1	C	47	GLN
1	C	56	GLN
1	C	61	ARG
1	C	79	LEU
1	C	118	GLN
1	C	123	VAL
1	C	127	ARG
1	C	133	GLU
1	C	135	GLN
1	C	144	ILE
1	C	157	ILE
1	C	158	TRP
1	C	161	ASN
1	C	164	LEU
1	C	168	SER
1	C	174	THR
1	C	190	LYS
1	C	201	PHE
1	C	202	GLN
1	C	209	PHE
1	C	211	TRP
1	C	217	ILE
1	C	218	GLN
1	C	226	VAL
1	C	234	ILE
1	C	246	TYR
1	C	248	LYS
1	C	265	LYS
1	C	266	ILE
1	C	273	ARG
1	C	275	ARG
1	C	286	VAL
1	C	293	ILE
1	C	301	VAL
1	C	315	VAL
1	C	325	ASP
1	C	327	GLN

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Mol	Chain	Res	Type
1	C	343	ARG
1	C	359	PHE
1	C	376	ARG
1	C	384	LEU
1	C	387	GLN
1	C	389	LEU
1	C	405	LEU
1	C	421	ASP
1	C	422	THR
1	C	430	VAL
1	C	432	PHE
1	C	433	ASP
1	C	438	LEU
1	C	444	LEU
1	C	507	LEU
1	C	513	ARG
1	C	518	THR
1	C	529	GLN
1	C	541	LYS
1	C	546	THR
1	C	555	GLN
1	C	592	TRP
1	C	593	LEU
1	C	597	GLN
1	D	14	ARG
1	D	15	PHE
1	D	24	GLU
1	D	30	LYS
1	D	31	ASN
1	D	33	LEU
1	D	37	ARG
1	D	42	ASP
1	D	43	ASP
1	D	45	LEU
1	D	47	GLN
1	D	56	GLN
1	D	61	ARG
1	D	79	LEU
1	D	118	GLN
1	D	123	VAL
1	D	127	ARG
1	D	133	GLU

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Mol	Chain	Res	Type
1	D	135	GLN
1	D	144	ILE
1	D	157	ILE
1	D	158	TRP
1	D	161	ASN
1	D	164	LEU
1	D	168	SER
1	D	174	THR
1	D	190	LYS
1	D	201	PHE
1	D	202	GLN
1	D	209	PHE
1	D	211	TRP
1	D	217	ILE
1	D	218	GLN
1	D	226	VAL
1	D	234	ILE
1	D	246	TYR
1	D	248	LYS
1	D	265	LYS
1	D	266	ILE
1	D	273	ARG
1	D	275	ARG
1	D	286	VAL
1	D	293	ILE
1	D	301	VAL
1	D	315	VAL
1	D	325	ASP
1	D	327	GLN
1	D	343	ARG
1	D	359	PHE
1	D	376	ARG
1	D	384	LEU
1	D	387	GLN
1	D	389	LEU
1	D	405	LEU
1	D	421	ASP
1	D	422	THR
1	D	430	VAL
1	D	432	PHE
1	D	433	ASP
1	D	438	LEU

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Mol	Chain	Res	Type
1	D	444	LEU
1	D	507	LEU
1	D	513	ARG
1	D	518	THR
1	D	529	GLN
1	D	541	LYS
1	D	546	THR
1	D	555	GLN
1	D	592	TRP
1	D	593	LEU
1	D	597	GLN
1	E	14	ARG
1	E	15	PHE
1	E	24	GLU
1	E	30	LYS
1	E	31	ASN
1	E	33	LEU
1	E	37	ARG
1	E	42	ASP
1	E	43	ASP
1	E	45	LEU
1	E	47	GLN
1	E	56	GLN
1	E	61	ARG
1	E	79	LEU
1	E	118	GLN
1	E	123	VAL
1	E	127	ARG
1	E	133	GLU
1	E	135	GLN
1	E	144	ILE
1	E	157	ILE
1	E	158	TRP
1	E	161	ASN
1	E	164	LEU
1	E	168	SER
1	E	174	THR
1	E	190	LYS
1	E	201	PHE
1	E	202	GLN
1	E	209	PHE
1	E	211	TRP

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Mol	Chain	Res	Type
1	E	217	ILE
1	E	218	GLN
1	E	226	VAL
1	E	234	ILE
1	E	246	TYR
1	E	248	LYS
1	E	265	LYS
1	E	266	ILE
1	E	273	ARG
1	E	275	ARG
1	E	286	VAL
1	E	293	ILE
1	E	301	VAL
1	E	315	VAL
1	E	325	ASP
1	E	327	GLN
1	E	343	ARG
1	E	359	PHE
1	E	376	ARG
1	E	384	LEU
1	E	387	GLN
1	E	389	LEU
1	E	405	LEU
1	E	421	ASP
1	E	422	THR
1	E	430	VAL
1	E	432	PHE
1	E	433	ASP
1	E	438	LEU
1	E	444	LEU
1	E	507	LEU
1	E	513	ARG
1	E	518	THR
1	E	529	GLN
1	E	541	LYS
1	E	546	THR
1	E	555	GLN
1	E	592	TRP
1	E	593	LEU
1	E	597	GLN
1	F	14	ARG
1	F	15	PHE

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Mol	Chain	Res	Type
1	F	24	GLU
1	F	30	LYS
1	F	31	ASN
1	F	33	LEU
1	F	37	ARG
1	F	42	ASP
1	F	43	ASP
1	F	45	LEU
1	F	47	GLN
1	F	56	GLN
1	F	61	ARG
1	F	79	LEU
1	F	118	GLN
1	F	123	VAL
1	F	127	ARG
1	F	133	GLU
1	F	135	GLN
1	F	144	ILE
1	F	157	ILE
1	F	158	TRP
1	F	161	ASN
1	F	164	LEU
1	F	168	SER
1	F	174	THR
1	F	190	LYS
1	F	201	PHE
1	F	202	GLN
1	F	209	PHE
1	F	211	TRP
1	F	217	ILE
1	F	218	GLN
1	F	226	VAL
1	F	234	ILE
1	F	246	TYR
1	F	248	LYS
1	F	265	LYS
1	F	266	ILE
1	F	273	ARG
1	F	275	ARG
1	F	286	VAL
1	F	293	ILE
1	F	301	VAL

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Mol	Chain	Res	Type
1	F	315	VAL
1	F	325	ASP
1	F	327	GLN
1	F	343	ARG
1	F	359	PHE
1	F	376	ARG
1	F	384	LEU
1	F	387	GLN
1	F	389	LEU
1	F	405	LEU
1	F	421	ASP
1	F	422	THR
1	F	430	VAL
1	F	432	PHE
1	F	433	ASP
1	F	438	LEU
1	F	444	LEU
1	F	507	LEU
1	F	513	ARG
1	F	518	THR
1	F	529	GLN
1	F	541	LYS
1	F	546	THR
1	F	555	GLN
1	F	592	TRP
1	F	593	LEU
1	F	597	GLN
1	G	14	ARG
1	G	15	PHE
1	G	24	GLU
1	G	30	LYS
1	G	31	ASN
1	G	33	LEU
1	G	37	ARG
1	G	42	ASP
1	G	43	ASP
1	G	45	LEU
1	G	47	GLN
1	G	56	GLN
1	G	61	ARG
1	G	79	LEU
1	G	118	GLN

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Mol	Chain	Res	Type
1	G	123	VAL
1	G	127	ARG
1	G	133	GLU
1	G	135	GLN
1	G	144	ILE
1	G	157	ILE
1	G	158	TRP
1	G	161	ASN
1	G	164	LEU
1	G	168	SER
1	G	174	THR
1	G	190	LYS
1	G	201	PHE
1	G	202	GLN
1	G	209	PHE
1	G	211	TRP
1	G	217	ILE
1	G	218	GLN
1	G	226	VAL
1	G	234	ILE
1	G	246	TYR
1	G	248	LYS
1	G	265	LYS
1	G	266	ILE
1	G	273	ARG
1	G	275	ARG
1	G	286	VAL
1	G	293	ILE
1	G	301	VAL
1	G	315	VAL
1	G	325	ASP
1	G	327	GLN
1	G	343	ARG
1	G	359	PHE
1	G	376	ARG
1	G	384	LEU
1	G	387	GLN
1	G	389	LEU
1	G	405	LEU
1	G	421	ASP
1	G	422	THR
1	G	430	VAL

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Mol	Chain	Res	Type
1	G	432	PHE
1	G	433	ASP
1	G	438	LEU
1	G	444	LEU
1	G	507	LEU
1	G	513	ARG
1	G	518	THR
1	G	529	GLN
1	G	541	LYS
1	G	546	THR
1	G	555	GLN
1	G	592	TRP
1	G	593	LEU
1	G	597	GLN
1	H	14	ARG
1	H	15	PHE
1	H	24	GLU
1	H	30	LYS
1	H	31	ASN
1	H	33	LEU
1	H	37	ARG
1	H	42	ASP
1	H	43	ASP
1	H	45	LEU
1	H	47	GLN
1	H	56	GLN
1	H	61	ARG
1	H	79	LEU
1	H	118	GLN
1	H	123	VAL
1	H	127	ARG
1	H	133	GLU
1	H	135	GLN
1	H	144	ILE
1	H	157	ILE
1	H	158	TRP
1	H	161	ASN
1	H	164	LEU
1	H	168	SER
1	H	174	THR
1	H	190	LYS
1	H	201	PHE

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Mol	Chain	Res	Type
1	H	202	GLN
1	H	209	PHE
1	H	211	TRP
1	H	217	ILE
1	H	218	GLN
1	H	226	VAL
1	H	234	ILE
1	H	246	TYR
1	H	248	LYS
1	H	265	LYS
1	H	266	ILE
1	H	273	ARG
1	H	275	ARG
1	H	286	VAL
1	H	293	ILE
1	H	301	VAL
1	H	315	VAL
1	H	325	ASP
1	H	327	GLN
1	H	343	ARG
1	H	359	PHE
1	H	376	ARG
1	H	384	LEU
1	H	387	GLN
1	H	389	LEU
1	H	405	LEU
1	H	421	ASP
1	H	422	THR
1	H	430	VAL
1	H	432	PHE
1	H	433	ASP
1	H	438	LEU
1	H	444	LEU
1	H	507	LEU
1	H	513	ARG
1	H	518	THR
1	H	529	GLN
1	H	541	LYS
1	H	546	THR
1	H	555	GLN
1	H	592	TRP
1	H	593	LEU

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Mol	Chain	Res	Type
1	H	597	GLN
1	I	14	ARG
1	I	15	PHE
1	I	24	GLU
1	I	30	LYS
1	I	31	ASN
1	I	33	LEU
1	I	37	ARG
1	I	42	ASP
1	I	43	ASP
1	I	45	LEU
1	I	47	GLN
1	I	56	GLN
1	I	61	ARG
1	I	79	LEU
1	I	118	GLN
1	I	123	VAL
1	I	127	ARG
1	I	133	GLU
1	I	135	GLN
1	I	144	ILE
1	I	157	ILE
1	I	158	TRP
1	I	161	ASN
1	I	164	LEU
1	I	168	SER
1	I	174	THR
1	I	190	LYS
1	I	201	PHE
1	I	202	GLN
1	I	209	PHE
1	I	211	TRP
1	I	217	ILE
1	I	218	GLN
1	I	226	VAL
1	I	234	ILE
1	I	246	TYR
1	I	248	LYS
1	I	265	LYS
1	I	266	ILE
1	I	273	ARG
1	I	275	ARG

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Mol	Chain	Res	Type
1	I	286	VAL
1	I	293	ILE
1	I	301	VAL
1	I	315	VAL
1	I	325	ASP
1	I	327	GLN
1	I	343	ARG
1	I	359	PHE
1	I	376	ARG
1	I	384	LEU
1	I	387	GLN
1	I	389	LEU
1	I	405	LEU
1	I	421	ASP
1	I	422	THR
1	I	430	VAL
1	I	432	PHE
1	I	433	ASP
1	I	438	LEU
1	I	444	LEU
1	I	507	LEU
1	I	513	ARG
1	I	518	THR
1	I	529	GLN
1	I	541	LYS
1	I	546	THR
1	I	555	GLN
1	I	592	TRP
1	I	593	LEU
1	I	597	GLN
1	J	14	ARG
1	J	15	PHE
1	J	24	GLU
1	J	30	LYS
1	J	31	ASN
1	J	33	LEU
1	J	37	ARG
1	J	42	ASP
1	J	43	ASP
1	J	45	LEU
1	J	47	GLN
1	J	56	GLN

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Mol	Chain	Res	Type
1	J	61	ARG
1	J	79	LEU
1	J	118	GLN
1	J	123	VAL
1	J	127	ARG
1	J	133	GLU
1	J	135	GLN
1	J	144	ILE
1	J	157	ILE
1	J	158	TRP
1	J	161	ASN
1	J	164	LEU
1	J	168	SER
1	J	174	THR
1	J	190	LYS
1	J	201	PHE
1	J	202	GLN
1	J	209	PHE
1	J	211	TRP
1	J	217	ILE
1	J	218	GLN
1	J	226	VAL
1	J	234	ILE
1	J	246	TYR
1	J	248	LYS
1	J	265	LYS
1	J	266	ILE
1	J	273	ARG
1	J	275	ARG
1	J	286	VAL
1	J	293	ILE
1	J	301	VAL
1	J	315	VAL
1	J	325	ASP
1	J	327	GLN
1	J	343	ARG
1	J	359	PHE
1	J	376	ARG
1	J	384	LEU
1	J	387	GLN
1	J	389	LEU
1	J	405	LEU

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Mol	Chain	Res	Type
1	J	421	ASP
1	J	422	THR
1	J	430	VAL
1	J	432	PHE
1	J	433	ASP
1	J	438	LEU
1	J	444	LEU
1	J	507	LEU
1	J	513	ARG
1	J	518	THR
1	J	529	GLN
1	J	541	LYS
1	J	546	THR
1	J	555	GLN
1	J	592	TRP
1	J	593	LEU
1	J	597	GLN
1	K	14	ARG
1	K	15	PHE
1	K	24	GLU
1	K	30	LYS
1	K	31	ASN
1	K	33	LEU
1	K	37	ARG
1	K	42	ASP
1	K	43	ASP
1	K	45	LEU
1	K	47	GLN
1	K	56	GLN
1	K	61	ARG
1	K	79	LEU
1	K	118	GLN
1	K	123	VAL
1	K	127	ARG
1	K	133	GLU
1	K	135	GLN
1	K	144	ILE
1	K	157	ILE
1	K	158	TRP
1	K	161	ASN
1	K	164	LEU
1	K	168	SER

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Mol	Chain	Res	Type
1	K	174	THR
1	K	190	LYS
1	K	201	PHE
1	K	202	GLN
1	K	209	PHE
1	K	211	TRP
1	K	217	ILE
1	K	218	GLN
1	K	226	VAL
1	K	234	ILE
1	K	246	TYR
1	K	248	LYS
1	K	265	LYS
1	K	266	ILE
1	K	273	ARG
1	K	275	ARG
1	K	286	VAL
1	K	293	ILE
1	K	301	VAL
1	K	315	VAL
1	K	325	ASP
1	K	327	GLN
1	K	343	ARG
1	K	359	PHE
1	K	376	ARG
1	K	384	LEU
1	K	387	GLN
1	K	389	LEU
1	K	405	LEU
1	K	421	ASP
1	K	422	THR
1	K	430	VAL
1	K	432	PHE
1	K	433	ASP
1	K	438	LEU
1	K	444	LEU
1	K	507	LEU
1	K	513	ARG
1	K	518	THR
1	K	529	GLN
1	K	541	LYS
1	K	546	THR

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Mol	Chain	Res	Type
1	K	555	GLN
1	K	592	TRP
1	K	593	LEU
1	K	597	GLN
1	L	14	ARG
1	L	15	PHE
1	L	24	GLU
1	L	30	LYS
1	L	31	ASN
1	L	33	LEU
1	L	37	ARG
1	L	42	ASP
1	L	43	ASP
1	L	45	LEU
1	L	47	GLN
1	L	56	GLN
1	L	61	ARG
1	L	79	LEU
1	L	118	GLN
1	L	123	VAL
1	L	127	ARG
1	L	133	GLU
1	L	135	GLN
1	L	144	ILE
1	L	157	ILE
1	L	158	TRP
1	L	161	ASN
1	L	164	LEU
1	L	168	SER
1	L	174	THR
1	L	190	LYS
1	L	201	PHE
1	L	202	GLN
1	L	209	PHE
1	L	211	TRP
1	L	217	ILE
1	L	218	GLN
1	L	226	VAL
1	L	234	ILE
1	L	246	TYR
1	L	248	LYS
1	L	265	LYS

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Mol	Chain	Res	Type
1	L	266	ILE
1	L	273	ARG
1	L	275	ARG
1	L	286	VAL
1	L	293	ILE
1	L	301	VAL
1	L	315	VAL
1	L	325	ASP
1	L	327	GLN
1	L	343	ARG
1	L	359	PHE
1	L	376	ARG
1	L	384	LEU
1	L	387	GLN
1	L	389	LEU
1	L	405	LEU
1	L	421	ASP
1	L	422	THR
1	L	430	VAL
1	L	432	PHE
1	L	433	ASP
1	L	438	LEU
1	L	444	LEU
1	L	507	LEU
1	L	513	ARG
1	L	518	THR
1	L	529	GLN
1	L	541	LYS
1	L	546	THR
1	L	555	GLN
1	L	592	TRP
1	L	593	LEU
1	L	597	GLN
2	Y	26	LEU
2	Y	42	MET
2	Y	48	ASP
2	Y	49	LEU
2	Y	53	MET
2	Y	78	GLU
2	Y	80	ASP
2	Y	90	SER
2	Y	96	LEU

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Mol	Chain	Res	Type
2	Y	139	SER
2	Y	140	ARG
2	Y	145	SER
2	Y	147	ASN
2	Z	26	LEU
2	Z	42	MET
2	Z	48	ASP
2	Z	49	LEU
2	Z	53	MET
2	Z	78	GLU
2	Z	80	ASP
2	Z	90	SER
2	Z	96	LEU
2	Z	139	SER
2	Z	140	ARG
2	Z	145	SER
2	Z	147	ASN
2	a	26	LEU
2	a	42	MET
2	a	48	ASP
2	a	49	LEU
2	a	53	MET
2	a	78	GLU
2	a	80	ASP
2	a	90	SER
2	a	96	LEU
2	a	113	ILE
2	a	139	SER
2	a	140	ARG
2	a	145	SER
2	a	147	ASN
2	b	26	LEU
2	b	42	MET
2	b	48	ASP
2	b	49	LEU
2	b	53	MET
2	b	78	GLU
2	b	80	ASP
2	b	90	SER
2	b	96	LEU
2	b	113	ILE
2	b	139	SER

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Mol	Chain	Res	Type
2	b	140	ARG
2	b	145	SER
2	b	147	ASN
2	c	26	LEU
2	c	42	MET
2	c	48	ASP
2	c	49	LEU
2	c	53	MET
2	c	78	GLU
2	c	80	ASP
2	c	90	SER
2	c	96	LEU
2	c	139	SER
2	c	140	ARG
2	c	145	SER
2	c	147	ASN
2	d	26	LEU
2	d	42	MET
2	d	48	ASP
2	d	49	LEU
2	d	53	MET
2	d	78	GLU
2	d	80	ASP
2	d	90	SER
2	d	96	LEU
2	d	139	SER
2	d	140	ARG
2	d	145	SER
2	d	147	ASN
2	e	26	LEU
2	e	42	MET
2	e	48	ASP
2	e	49	LEU
2	e	53	MET
2	e	78	GLU
2	e	80	ASP
2	e	90	SER
2	e	96	LEU
2	e	139	SER
2	e	140	ARG
2	e	145	SER
2	e	147	ASN

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Mol	Chain	Res	Type
2	f	26	LEU
2	f	42	MET
2	f	48	ASP
2	f	49	LEU
2	f	53	MET
2	f	78	GLU
2	f	80	ASP
2	f	90	SER
2	f	96	LEU
2	f	113	ILE
2	f	139	SER
2	f	140	ARG
2	f	145	SER
2	f	147	ASN
2	g	26	LEU
2	g	42	MET
2	g	48	ASP
2	g	49	LEU
2	g	53	MET
2	g	78	GLU
2	g	80	ASP
2	g	90	SER
2	g	96	LEU
2	g	113	ILE
2	g	139	SER
2	g	140	ARG
2	g	145	SER
2	g	147	ASN
2	h	26	LEU
2	h	42	MET
2	h	48	ASP
2	h	49	LEU
2	h	53	MET
2	h	78	GLU
2	h	80	ASP
2	h	90	SER
2	h	96	LEU
2	h	139	SER
2	h	140	ARG
2	h	145	SER
2	h	147	ASN
2	i	26	LEU

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Mol	Chain	Res	Type
2	i	42	MET
2	i	48	ASP
2	i	49	LEU
2	i	53	MET
2	i	78	GLU
2	i	80	ASP
2	i	90	SER
2	i	96	LEU
2	i	139	SER
2	i	140	ARG
2	i	145	SER
2	i	147	ASN
2	j	26	LEU
2	j	42	MET
2	j	48	ASP
2	j	49	LEU
2	j	53	MET
2	j	78	GLU
2	j	80	ASP
2	j	90	SER
2	j	96	LEU
2	j	113	ILE
2	j	139	SER
2	j	140	ARG
2	j	145	SER
2	j	147	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (319) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	31	ASN
1	M	40	GLN
1	M	508	ASN
1	M	575	GLN
1	N	31	ASN
1	N	142	GLN
1	N	508	ASN
1	N	575	GLN
1	O	31	ASN
1	O	40	GLN
1	O	135	GLN
1	O	142	GLN

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Mol	Chain	Res	Type
1	O	450	GLN
1	O	575	GLN
1	P	31	ASN
1	P	40	GLN
1	P	575	GLN
1	Q	31	ASN
1	Q	40	GLN
1	Q	508	ASN
1	Q	575	GLN
1	R	31	ASN
1	R	508	ASN
1	R	575	GLN
1	S	31	ASN
1	S	40	GLN
1	S	135	GLN
1	S	508	ASN
1	S	575	GLN
1	T	40	GLN
1	T	450	GLN
1	T	508	ASN
1	T	575	GLN
1	U	31	ASN
1	U	40	GLN
1	U	135	GLN
1	U	142	GLN
1	U	450	GLN
1	U	508	ASN
1	U	575	GLN
1	V	31	ASN
1	V	40	GLN
1	V	508	ASN
1	V	575	GLN
1	W	31	ASN
1	W	40	GLN
1	W	508	ASN
1	W	575	GLN
1	X	31	ASN
1	X	40	GLN
1	X	142	GLN
1	X	508	ASN
1	X	575	GLN
1	A	31	ASN

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Mol	Chain	Res	Type
1	A	56	GLN
1	A	73	GLN
1	A	112	ASN
1	A	118	GLN
1	A	135	GLN
1	A	161	ASN
1	A	177	HIS
1	A	182	ASN
1	A	202	GLN
1	A	214	GLN
1	A	218	GLN
1	A	236	GLN
1	A	291	GLN
1	A	297	HIS
1	A	327	GLN
1	A	337	ASN
1	A	439	ASN
1	A	529	GLN
1	A	530	GLN
1	A	555	GLN
1	A	597	GLN
1	B	31	ASN
1	B	56	GLN
1	B	73	GLN
1	B	112	ASN
1	B	118	GLN
1	B	135	GLN
1	B	161	ASN
1	B	177	HIS
1	B	182	ASN
1	B	202	GLN
1	B	214	GLN
1	B	218	GLN
1	B	236	GLN
1	B	291	GLN
1	B	297	HIS
1	B	337	ASN
1	B	439	ASN
1	B	529	GLN
1	B	530	GLN
1	B	555	GLN
1	B	597	GLN

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Mol	Chain	Res	Type
1	C	31	ASN
1	C	56	GLN
1	C	73	GLN
1	C	112	ASN
1	C	118	GLN
1	C	135	GLN
1	C	161	ASN
1	C	177	HIS
1	C	182	ASN
1	C	202	GLN
1	C	214	GLN
1	C	218	GLN
1	C	236	GLN
1	C	291	GLN
1	C	297	HIS
1	C	337	ASN
1	C	439	ASN
1	C	529	GLN
1	C	530	GLN
1	C	555	GLN
1	C	597	GLN
1	D	31	ASN
1	D	56	GLN
1	D	73	GLN
1	D	112	ASN
1	D	118	GLN
1	D	135	GLN
1	D	161	ASN
1	D	177	HIS
1	D	182	ASN
1	D	202	GLN
1	D	214	GLN
1	D	218	GLN
1	D	236	GLN
1	D	291	GLN
1	D	297	HIS
1	D	337	ASN
1	D	439	ASN
1	D	529	GLN
1	D	530	GLN
1	D	555	GLN
1	D	597	GLN

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Mol	Chain	Res	Type
1	E	31	ASN
1	E	56	GLN
1	E	73	GLN
1	E	112	ASN
1	E	118	GLN
1	E	135	GLN
1	E	161	ASN
1	E	177	HIS
1	E	182	ASN
1	E	202	GLN
1	E	214	GLN
1	E	218	GLN
1	E	236	GLN
1	E	291	GLN
1	E	297	HIS
1	E	337	ASN
1	E	439	ASN
1	E	529	GLN
1	E	530	GLN
1	E	555	GLN
1	E	597	GLN
1	F	31	ASN
1	F	56	GLN
1	F	73	GLN
1	F	112	ASN
1	F	118	GLN
1	F	135	GLN
1	F	161	ASN
1	F	177	HIS
1	F	182	ASN
1	F	202	GLN
1	F	214	GLN
1	F	218	GLN
1	F	236	GLN
1	F	291	GLN
1	F	297	HIS
1	F	327	GLN
1	F	337	ASN
1	F	439	ASN
1	F	529	GLN
1	F	530	GLN
1	F	555	GLN

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Mol	Chain	Res	Type
1	F	597	GLN
1	G	31	ASN
1	G	73	GLN
1	G	112	ASN
1	G	118	GLN
1	G	135	GLN
1	G	161	ASN
1	G	177	HIS
1	G	182	ASN
1	G	202	GLN
1	G	214	GLN
1	G	218	GLN
1	G	236	GLN
1	G	291	GLN
1	G	297	HIS
1	G	337	ASN
1	G	439	ASN
1	G	529	GLN
1	G	530	GLN
1	G	555	GLN
1	G	597	GLN
1	H	31	ASN
1	H	73	GLN
1	H	112	ASN
1	H	118	GLN
1	H	135	GLN
1	H	161	ASN
1	H	177	HIS
1	H	182	ASN
1	H	202	GLN
1	H	214	GLN
1	H	218	GLN
1	H	236	GLN
1	H	291	GLN
1	H	297	HIS
1	H	337	ASN
1	H	439	ASN
1	H	529	GLN
1	H	530	GLN
1	H	555	GLN
1	H	597	GLN
1	I	31	ASN

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Mol	Chain	Res	Type
1	I	56	GLN
1	I	73	GLN
1	I	112	ASN
1	I	118	GLN
1	I	135	GLN
1	I	161	ASN
1	I	177	HIS
1	I	182	ASN
1	I	202	GLN
1	I	214	GLN
1	I	218	GLN
1	I	236	GLN
1	I	291	GLN
1	I	297	HIS
1	I	337	ASN
1	I	439	ASN
1	I	529	GLN
1	I	530	GLN
1	I	555	GLN
1	I	597	GLN
1	J	31	ASN
1	J	73	GLN
1	J	112	ASN
1	J	118	GLN
1	J	135	GLN
1	J	161	ASN
1	J	177	HIS
1	J	182	ASN
1	J	202	GLN
1	J	214	GLN
1	J	218	GLN
1	J	236	GLN
1	J	291	GLN
1	J	297	HIS
1	J	337	ASN
1	J	439	ASN
1	J	529	GLN
1	J	530	GLN
1	J	555	GLN
1	J	597	GLN
1	K	31	ASN
1	K	56	GLN

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Mol	Chain	Res	Type
1	K	73	GLN
1	K	112	ASN
1	K	118	GLN
1	K	135	GLN
1	K	161	ASN
1	K	177	HIS
1	K	182	ASN
1	K	202	GLN
1	K	214	GLN
1	K	218	GLN
1	K	236	GLN
1	K	291	GLN
1	K	297	HIS
1	K	327	GLN
1	K	337	ASN
1	K	439	ASN
1	K	529	GLN
1	K	530	GLN
1	K	555	GLN
1	K	597	GLN
1	L	31	ASN
1	L	56	GLN
1	L	73	GLN
1	L	112	ASN
1	L	118	GLN
1	L	135	GLN
1	L	161	ASN
1	L	177	HIS
1	L	182	ASN
1	L	202	GLN
1	L	214	GLN
1	L	218	GLN
1	L	236	GLN
1	L	291	GLN
1	L	297	HIS
1	L	337	ASN
1	L	439	ASN
1	L	529	GLN
1	L	530	GLN
1	L	555	GLN
1	L	597	GLN
2	Y	94	HIS

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Mol	Chain	Res	Type
2	Z	94	HIS
2	a	94	HIS
2	b	94	HIS
2	c	40	GLN
2	c	94	HIS
2	d	40	GLN
2	d	94	HIS
2	e	94	HIS
2	f	94	HIS
2	g	94	HIS
2	h	94	HIS
2	i	94	HIS
2	j	94	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	552/602 (91%)	2.81	288 (52%)	0	0	22, 84, 246, 379	0
1	B	552/602 (91%)	2.87	311 (56%)	0	0	23, 85, 246, 379	0
1	C	552/602 (91%)	2.84	303 (54%)	0	0	26, 84, 246, 379	0
1	D	552/602 (91%)	2.59	266 (48%)	0	0	25, 84, 246, 379	0
1	E	552/602 (91%)	2.79	285 (51%)	0	0	25, 84, 246, 379	0
1	F	552/602 (91%)	2.72	265 (48%)	0	0	25, 84, 246, 379	0
1	G	552/602 (91%)	2.75	278 (50%)	0	0	30, 84, 246, 379	0
1	H	552/602 (91%)	2.89	288 (52%)	0	0	26, 86, 246, 379	0
1	I	552/602 (91%)	2.90	300 (54%)	0	0	31, 88, 246, 379	0
1	J	552/602 (91%)	3.00	329 (59%)	0	0	33, 96, 246, 379	0
1	K	552/602 (91%)	3.05	304 (55%)	0	0	26, 88, 245, 379	0
1	L	552/602 (91%)	3.05	312 (56%)	0	0	24, 87, 246, 379	0
1	M	552/602 (91%)	2.33	236 (42%)	0	0	15, 70, 209, 327	0
1	N	552/602 (91%)	2.19	215 (38%)	0	1	18, 69, 209, 327	0
1	O	552/602 (91%)	2.16	224 (40%)	0	1	15, 69, 209, 326	0
1	P	552/602 (91%)	2.22	236 (42%)	0	0	15, 70, 209, 327	0
1	Q	552/602 (91%)	2.25	226 (40%)	0	1	15, 69, 209, 326	0
1	R	552/602 (91%)	2.29	219 (39%)	0	1	17, 69, 209, 327	0
1	S	552/602 (91%)	2.39	248 (44%)	0	0	19, 70, 209, 326	0
1	T	552/602 (91%)	2.46	241 (43%)	0	0	15, 70, 208, 326	0
1	U	552/602 (91%)	2.61	278 (50%)	0	0	17, 69, 209, 327	0
1	V	552/602 (91%)	2.49	230 (41%)	0	0	18, 70, 209, 327	0
1	W	552/602 (91%)	2.32	249 (45%)	0	0	17, 70, 209, 326	0
1	X	552/602 (91%)	2.50	242 (43%)	0	0	14, 69, 209, 326	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
2	Y	146/166 (87%)	3.81	88 (60%) 0 0	38, 75, 221, 304	0
2	Z	146/166 (87%)	3.67	88 (60%) 0 0	37, 73, 222, 304	0
2	a	146/166 (87%)	3.64	100 (68%) 0 0	37, 77, 221, 304	0
2	b	146/166 (87%)	3.64	96 (65%) 0 0	39, 72, 221, 304	0
2	c	146/166 (87%)	2.66	78 (53%) 0 0	39, 72, 222, 305	0
2	d	146/166 (87%)	3.07	88 (60%) 0 0	35, 72, 222, 304	0
2	e	146/166 (87%)	3.12	89 (60%) 0 0	37, 73, 220, 304	0
2	f	146/166 (87%)	3.68	100 (68%) 0 0	39, 74, 222, 304	0
2	g	146/166 (87%)	3.69	101 (69%) 0 0	44, 75, 221, 304	0
2	h	146/166 (87%)	3.67	89 (60%) 0 0	38, 75, 221, 305	0
2	i	146/166 (87%)	3.52	100 (68%) 0 0	40, 75, 221, 304	0
2	j	146/166 (87%)	4.19	119 (81%) 0 0	36, 75, 222, 305	0
2	k	145/166 (87%)	2.88	72 (49%) 0 0	25, 57, 204, 314	0
2	l	145/166 (87%)	2.82	77 (53%) 0 0	28, 56, 204, 314	0
2	m	145/166 (87%)	3.28	79 (54%) 0 0	30, 59, 203, 314	0
2	n	145/166 (87%)	2.75	65 (44%) 0 0	23, 55, 204, 314	0
2	o	145/166 (87%)	2.58	70 (48%) 0 0	26, 57, 204, 314	0
2	p	145/166 (87%)	2.96	75 (51%) 0 0	27, 57, 204, 314	0
2	q	145/166 (87%)	2.75	68 (46%) 0 0	29, 58, 204, 314	0
2	r	145/166 (87%)	2.65	65 (44%) 0 0	26, 57, 205, 314	0
2	s	145/166 (87%)	2.80	77 (53%) 0 0	30, 58, 204, 314	0
2	t	145/166 (87%)	2.90	76 (52%) 0 0	31, 58, 204, 314	0
2	u	145/166 (87%)	2.54	64 (44%) 0 0	30, 58, 204, 314	0
2	v	145/166 (87%)	1.99	49 (33%) 0 1	29, 57, 204, 314	0
All	All	16740/18432 (90%)	2.71	8346 (49%) 0 0	14, 76, 228, 379	0

All (8346) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Y	151	ASN	38.0
2	Y	152	LEU	36.1
1	D	240	THR	33.9
1	K	210	PRO	31.5
2	Y	150	PRO	30.5

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Mol	Chain	Res	Type	RSRZ
2	n	142	ASN	29.5
2	Z	152	LEU	28.4
1	G	495	GLU	28.3
2	s	150	PRO	27.7
1	V	240	THR	27.0
2	m	142	ASN	26.7
2	k	143	LEU	26.7
1	I	211	TRP	26.6
2	a	36	ASP	26.5
1	X	210	PRO	26.2
1	F	240	THR	26.1
2	t	149	PHE	26.1
2	k	141	PRO	25.8
1	V	496	VAL	25.3
2	p	144	ASN	25.1
1	A	210	PRO	24.3
2	n	150	PRO	24.2
2	j	153	ASN	23.5
1	G	211	TRP	23.0
1	V	586	THR	22.5
2	b	158	PHE	22.1
1	V	497	VAL	21.8
1	H	209	PHE	21.7
1	L	211	TRP	21.5
1	C	260	ASP	21.5
2	f	37	VAL	21.5
2	k	142	ASN	21.5
2	u	142	ASN	21.4
1	E	240	THR	21.1
1	F	495	GLU	21.0
2	Z	151	ASN	21.0
1	U	240	THR	20.8
2	g	152	LEU	20.7
1	C	495	GLU	20.7
1	F	211	TRP	20.5
1	Q	564	GLY	20.5
2	m	28	VAL	20.5
2	h	152	LEU	20.4
2	v	142	ASN	20.3
2	m	143	LEU	20.1
2	j	152	LEU	20.1
2	p	142	ASN	20.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	n	149	PHE	19.9
1	R	214	GLN	19.6
1	N	602	GLY	19.5
1	N	240	THR	19.4
2	q	28	VAL	19.4
2	g	151	ASN	19.1
2	r	142	ASN	19.0
1	H	208	VAL	18.9
2	m	141	PRO	18.8
2	q	144	ASN	18.8
1	J	253	ASP	18.7
2	g	153	ASN	18.6
1	V	211	TRP	18.6
1	X	211	TRP	18.6
2	r	141	PRO	18.5
1	S	564	GLY	18.5
2	o	143	LEU	18.2
1	H	585	GLU	18.1
2	b	35	THR	18.0
2	e	14	THR	17.9
1	A	209	PHE	17.8
1	J	504	LYS	17.8
2	t	148	TYR	17.8
2	m	144	ASN	17.7
1	W	211	TRP	17.6
2	h	159	PRO	17.5
1	M	424	ALA	17.5
2	t	150	PRO	17.4
2	d	150	PRO	17.3
1	N	207	TRP	17.1
1	V	602	GLY	17.1
2	l	142	ASN	17.1
1	L	240	THR	16.9
1	I	424	ALA	16.9
2	b	159	PRO	16.9
1	N	422	THR	16.6
1	G	586	THR	16.5
2	n	143	LEU	16.4
1	V	498	ASP	16.4
2	c	159	PRO	16.4
1	O	240	THR	16.4
1	A	186	ASP	16.3

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Mol	Chain	Res	Type	RSRZ
2	l	144	ASN	16.3
2	g	37	VAL	16.2
1	G	498	ASP	16.2
2	g	150	PRO	16.2
1	I	495	GLU	16.2
2	Y	153	ASN	16.1
1	N	494	ALA	16.1
2	q	142	ASN	16.0
2	u	143	LEU	16.0
2	t	28	VAL	15.9
2	b	157	TYR	15.7
1	P	253	ASP	15.7
1	A	462	GLU	15.6
1	M	602	GLY	15.6
1	P	242	GLU	15.5
2	d	151	ASN	15.5
1	C	494	ALA	15.5
1	L	564	GLY	15.5
1	I	421	ASP	15.5
2	j	154	GLU	15.5
1	A	211	TRP	15.4
1	M	421	ASP	15.4
1	E	204	PRO	15.4
1	I	210	PRO	15.4
1	G	210	PRO	15.3
1	H	422	THR	15.2
1	H	242	GLU	15.2
1	D	421	ASP	15.2
2	f	153	ASN	15.1
1	H	49	THR	15.1
1	A	246	TYR	15.0
2	Z	153	ASN	15.0
1	K	501	THR	15.0
1	X	461	GLY	15.0
2	Y	35	THR	14.9
1	K	240	THR	14.8
2	r	150	PRO	14.7
2	n	141	PRO	14.7
1	M	601	GLN	14.6
2	l	141	PRO	14.6
2	q	141	PRO	14.5
1	J	421	ASP	14.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	W	502	GLY	14.3
1	V	601	GLN	14.3
1	L	208	VAL	14.3
1	E	499	LEU	14.3
1	J	238	PRO	14.2
1	B	417	THR	14.2
2	i	71	ASP	14.2
1	X	6	ASN	14.1
1	C	425	VAL	14.0
1	M	211	TRP	14.0
1	L	183	GLY	13.9
1	V	585	GLU	13.9
1	B	211	TRP	13.9
1	E	261	SER	13.9
1	G	602	GLY	13.8
2	k	144	ASN	13.7
1	I	422	THR	13.6
1	U	260	ASP	13.6
1	C	92	ASP	13.6
1	M	210	PRO	13.6
2	f	36	ASP	13.6
2	o	147	HIS	13.6
1	K	216	THR	13.6
2	g	36	ASP	13.5
1	V	210	PRO	13.5
2	l	143	LEU	13.5
1	M	6	ASN	13.5
2	m	8	ASP	13.5
1	X	547	PRO	13.4
1	L	194	ASP	13.4
1	M	207	TRP	13.4
2	i	157	TYR	13.4
1	T	564	GLY	13.3
1	A	214	GLN	13.3
2	s	149	PHE	13.3
1	J	239	VAL	13.3
1	I	253	ASP	13.2
1	T	422	THR	13.2
1	H	237	ASP	13.1
1	T	211	TRP	13.1
1	C	385	PRO	13.0
1	L	206	ASP	13.0

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Mol	Chain	Res	Type	RSRZ
1	V	424	ALA	13.0
1	B	213	THR	12.9
1	H	424	ALA	12.8
1	K	494	ALA	12.8
1	K	211	TRP	12.8
2	f	38	GLU	12.8
2	j	159	PRO	12.8
2	q	94	ASP	12.8
1	J	197	ASP	12.7
2	p	28	VAL	12.7
1	W	214	GLN	12.7
1	U	386	THR	12.7
2	f	152	LEU	12.7
1	W	192	ASP	12.7
1	H	197	ASP	12.7
2	o	150	PRO	12.7
1	C	209	PHE	12.7
2	c	151	ASN	12.6
1	B	260	ASP	12.6
2	Y	36	ASP	12.6
2	c	17	ASP	12.6
1	K	386	THR	12.6
1	D	598	GLN	12.6
1	J	240	THR	12.5
1	J	6	ASN	12.5
2	b	74	ASN	12.5
1	O	424	ALA	12.5
2	b	151	ASN	12.5
1	R	89	ASP	12.4
1	O	208	VAL	12.4
1	X	207	TRP	12.3
1	N	495	GLU	12.3
2	b	48	ASP	12.3
1	B	209	PHE	12.3
1	J	130	THR	12.3
2	e	159	PRO	12.3
2	n	148	TYR	12.3
2	Z	72	ASP	12.3
1	Q	211	TRP	12.2
1	Q	495	GLU	12.2
2	h	153	ASN	12.2
1	O	211	TRP	12.2

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Mol	Chain	Res	Type	RSRZ
2	i	151	ASN	12.2
1	U	208	VAL	12.2
1	Q	210	PRO	12.1
2	h	151	ASN	12.1
2	p	143	LEU	12.1
1	E	260	ASP	12.1
1	Q	255	ILE	12.1
1	A	50	THR	12.1
1	J	211	TRP	12.1
2	e	28	VAL	12.1
1	F	494	ALA	12.0
1	S	196	ASP	12.0
1	T	423	GLU	12.0
1	T	586	THR	11.9
1	L	210	PRO	11.9
1	I	209	PHE	11.8
1	A	561	ASP	11.8
1	C	207	TRP	11.8
2	a	74	ASN	11.8
2	r	149	PHE	11.8
1	V	239	VAL	11.8
2	a	152	LEU	11.8
1	E	424	ALA	11.8
1	W	561	ASP	11.8
1	N	283	CYS	11.7
2	r	8	ASP	11.7
1	E	546	THR	11.7
1	X	213	THR	11.7
1	R	207	TRP	11.7
1	L	540	GLY	11.7
1	U	595	GLU	11.7
1	F	496	VAL	11.6
1	L	89	ASP	11.6
1	F	500	ALA	11.6
1	I	268	GLU	11.6
1	F	423	GLU	11.6
1	L	563	LYS	11.6
1	H	386	THR	11.6
1	H	591	GLN	11.6
1	R	463	ILE	11.6
1	E	242	GLU	11.6
1	R	564	GLY	11.5

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Mol	Chain	Res	Type	RSRZ
1	M	497	VAL	11.5
1	D	239	VAL	11.5
1	S	213	THR	11.5
1	W	424	ALA	11.5
2	u	149	PHE	11.4
1	M	586	THR	11.4
1	X	240	THR	11.4
1	G	186	ASP	11.4
2	o	142	ASN	11.4
1	F	589	GLU	11.4
1	J	210	PRO	11.3
2	d	38	GLU	11.3
1	G	267	ALA	11.3
1	J	505	GLN	11.3
1	B	215	ASP	11.3
1	S	565	VAL	11.3
1	D	494	ALA	11.3
1	H	496	VAL	11.2
1	S	500	ALA	11.2
2	b	34	LEU	11.2
1	K	50	THR	11.2
2	o	149	PHE	11.2
2	h	158	PHE	11.2
1	T	502	GLY	11.2
1	W	421	ASP	11.2
2	e	35	THR	11.2
1	L	550	GLN	11.1
2	Z	35	THR	11.1
1	J	252	LYS	11.1
2	i	153	ASN	11.1
2	e	153	ASN	11.1
1	F	501	THR	11.1
2	d	37	VAL	11.1
1	F	504	LYS	11.1
1	W	586	THR	11.1
1	S	260	ASP	11.1
1	S	240	THR	11.1
2	s	89	CYS	11.1
2	v	141	PRO	11.1
1	E	262	GLY	11.0
1	F	192	ASP	11.0
1	P	424	ALA	11.0

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Mol	Chain	Res	Type	RSRZ
1	C	550	GLN	11.0
2	l	28	VAL	11.0
1	N	601	GLN	11.0
2	j	34	LEU	11.0
1	D	241	GLY	11.0
1	A	559	LEU	11.0
1	N	6	ASN	11.0
2	d	77	ALA	10.9
2	q	145	GLU	10.9
1	G	499	LEU	10.9
2	a	154	GLU	10.9
1	F	424	ALA	10.9
1	A	417	THR	10.9
2	h	35	THR	10.9
2	g	16	GLY	10.9
1	B	385	PRO	10.9
1	Q	240	THR	10.8
1	W	602	GLY	10.8
1	P	501	THR	10.8
1	Q	245	SER	10.8
1	T	238	PRO	10.8
1	Q	242	GLU	10.8
1	N	421	ASP	10.8
2	i	36	ASP	10.8
1	K	367	ASP	10.8
1	V	207	TRP	10.8
2	e	44	ASP	10.8
1	H	425	VAL	10.8
1	D	422	THR	10.7
1	U	587	PRO	10.7
2	i	35	THR	10.7
1	M	5	GLU	10.7
1	R	205	ASN	10.7
1	L	207	TRP	10.7
2	a	151	ASN	10.7
1	U	211	TRP	10.7
1	E	589	GLU	10.6
1	R	255	ILE	10.6
1	M	253	ASP	10.6
1	H	260	ASP	10.6
1	E	601	GLN	10.6
2	h	155	TRP	10.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	R	208	VAL	10.5
1	V	192	ASP	10.5
1	C	462	GLU	10.5
1	L	271	ILE	10.5
1	H	495	GLU	10.5
1	H	423	GLU	10.5
1	J	460	ASP	10.5
1	D	601	GLN	10.4
1	F	422	THR	10.4
2	j	155	TRP	10.4
2	l	8	ASP	10.4
1	T	585	GLU	10.4
1	D	32	ASP	10.4
1	V	234	ILE	10.4
2	Z	73	GLU	10.3
1	B	550	GLN	10.3
2	i	154	GLU	10.3
1	D	426	ASN	10.3
2	i	28	VAL	10.3
1	K	510	ILE	10.3
1	T	494	ALA	10.3
1	G	209	PHE	10.3
2	h	156	HIS	10.3
2	t	89	CYS	10.3
1	U	417	THR	10.2
1	V	205	ASN	10.2
2	a	47	ASP	10.2
1	J	462	GLU	10.2
1	I	591	GLN	10.2
1	P	505	GLN	10.2
1	M	543	PRO	10.2
1	B	210	PRO	10.2
2	k	9	LEU	10.2
1	P	214	GLN	10.1
2	a	35	THR	10.1
1	H	601	GLN	10.1
2	Y	16	GLY	10.1
1	U	426	ASN	10.1
2	f	35	THR	10.1
2	Z	103	ASP	10.1
2	j	38	GLU	10.1
1	T	240	THR	10.1

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Mol	Chain	Res	Type	RSRZ
1	B	191	TYR	10.1
1	E	13	SER	10.1
1	E	214	GLN	10.1
1	L	205	ASN	10.1
1	E	561	ASP	10.1
2	v	143	LEU	10.1
1	V	214	GLN	10.0
1	O	6	ASN	10.0
1	G	421	ASP	10.0
1	U	425	VAL	10.0
1	F	502	GLY	10.0
1	A	546	THR	10.0
1	G	240	THR	10.0
1	R	462	GLU	10.0
1	B	559	LEU	10.0
1	T	420	VAL	10.0
1	I	84	ASP	10.0
2	l	6	LYS	9.9
1	N	242	GLU	9.9
1	A	564	GLY	9.9
1	C	595	GLU	9.9
1	P	504	LYS	9.9
1	C	240	THR	9.9
2	u	150	PRO	9.8
2	a	37	VAL	9.8
1	E	6	ASN	9.8
2	h	37	VAL	9.8
1	H	6	ASN	9.8
1	I	232	ALA	9.8
1	W	242	GLU	9.8
1	B	248	LYS	9.8
2	q	143	LEU	9.8
2	j	37	VAL	9.8
1	R	602	GLY	9.8
1	V	215	ASP	9.8
1	C	259	ALA	9.8
1	E	463	ILE	9.7
1	F	542	THR	9.7
2	g	38	GLU	9.7
1	O	253	ASP	9.7
2	j	100	ILE	9.7
1	B	597	GLN	9.7

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Mol	Chain	Res	Type	RSRZ
2	r	28	VAL	9.7
1	X	546	THR	9.7
1	W	585	GLU	9.7
1	F	601	GLN	9.7
1	F	203	ASN	9.7
1	P	50	THR	9.7
1	T	424	ALA	9.7
1	A	183	GLY	9.7
1	U	92	ASP	9.7
1	A	6	ASN	9.7
1	F	602	GLY	9.7
1	U	214	GLN	9.6
1	V	558	THR	9.6
1	I	85	GLY	9.6
1	M	587	PRO	9.6
1	X	209	PHE	9.6
1	S	587	PRO	9.6
1	O	212	LEU	9.6
2	a	28	VAL	9.6
1	G	237	ASP	9.6
1	E	565	VAL	9.6
1	A	245	SER	9.6
2	j	108	ALA	9.6
1	K	230	GLU	9.6
2	l	34	GLN	9.5
1	X	424	ALA	9.5
1	Q	214	GLN	9.5
1	T	210	PRO	9.5
1	Q	228	LYS	9.5
2	Z	34	LEU	9.5
2	h	150	PRO	9.5
2	u	27	ASP	9.5
2	u	141	PRO	9.5
1	H	602	GLY	9.5
1	S	558	THR	9.5
1	X	597	GLN	9.5
2	c	36	ASP	9.5
1	Q	494	ALA	9.5
2	a	153	ASN	9.5
1	L	215	ASP	9.5
1	K	253	ASP	9.5
1	R	245	SER	9.4

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Mol	Chain	Res	Type	RSRZ
1	L	188	ALA	9.4
1	H	7	ARG	9.4
1	I	386	THR	9.4
2	s	35	ASP	9.4
1	O	422	THR	9.4
1	K	130	THR	9.4
2	k	10	VAL	9.4
1	W	240	THR	9.4
2	b	28	VAL	9.4
1	D	424	ALA	9.4
1	H	253	ASP	9.4
1	A	338	ALA	9.4
1	M	197	ASP	9.4
1	A	386	THR	9.3
1	F	32	ASP	9.3
1	A	547	PRO	9.3
1	J	424	ALA	9.3
1	T	584	PRO	9.3
1	E	501	THR	9.3
2	h	44	ASP	9.3
1	D	420	VAL	9.3
1	T	599	ALA	9.3
1	F	234	ILE	9.3
1	X	495	GLU	9.3
1	J	10	SER	9.3
2	j	151	ASN	9.3
1	H	509	ASP	9.3
1	M	496	VAL	9.2
1	L	239	VAL	9.2
1	G	587	PRO	9.2
1	L	285	ALA	9.2
2	f	17	ASP	9.2
1	T	284	THR	9.2
1	J	386	THR	9.2
1	R	421	ASP	9.2
1	P	246	TYR	9.2
1	X	239	VAL	9.2
1	G	494	ALA	9.2
1	K	31	ASN	9.2
2	s	144	ASN	9.2
1	X	499	LEU	9.2
2	r	134	THR	9.2

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Mol	Chain	Res	Type	RSRZ
1	N	250	ASP	9.1
1	W	213	THR	9.1
1	K	208	VAL	9.1
1	E	257	ASP	9.1
2	i	48	ASP	9.1
1	M	231	THR	9.1
1	O	543	PRO	9.1
1	D	170	ALA	9.1
1	R	592	TRP	9.1
1	B	208	VAL	9.1
2	q	27	ASP	9.1
1	F	212	LEU	9.1
1	C	49	THR	9.1
1	L	420	VAL	9.1
2	r	148	TYR	9.1
2	u	55	ILE	9.1
2	f	71	ASP	9.1
1	V	423	GLU	9.0
1	N	547	PRO	9.0
1	T	602	GLY	9.0
1	F	213	THR	9.0
1	V	505	GLN	9.0
2	h	36	ASP	9.0
1	C	426	ASN	9.0
1	C	211	TRP	9.0
1	R	206	ASP	8.9
2	b	95	ASN	8.9
1	H	8	LEU	8.9
1	R	211	TRP	8.9
2	Z	150	PRO	8.9
1	L	417	THR	8.9
2	e	37	VAL	8.9
1	E	588	GLU	8.9
1	G	206	ASP	8.9
1	K	592	TRP	8.9
1	L	246	TYR	8.9
1	L	268	GLU	8.9
1	T	506	VAL	8.9
2	i	110	ALA	8.9
1	S	424	ALA	8.9
1	G	49	THR	8.9
1	C	424	ALA	8.9

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Mol	Chain	Res	Type	RSRZ
1	B	192	ASP	8.9
1	X	48	TYR	8.9
1	X	462	GLU	8.9
1	I	585	GLU	8.9
1	D	496	VAL	8.8
1	R	386	THR	8.8
1	O	210	PRO	8.8
1	I	86	ALA	8.8
1	F	420	VAL	8.8
1	T	601	GLN	8.8
1	G	8	LEU	8.8
1	A	545	GLY	8.8
2	f	74	ASN	8.8
1	N	211	TRP	8.8
1	I	207	TRP	8.8
1	O	503	GLU	8.8
2	j	58	GLN	8.8
1	B	594	VAL	8.8
1	L	203	ASN	8.8
1	V	8	LEU	8.8
1	D	498	ASP	8.8
1	U	5	GLU	8.8
2	l	145	GLU	8.8
1	F	210	PRO	8.7
1	C	538	LEU	8.7
2	Z	14	THR	8.7
1	K	548	GLU	8.7
1	Q	253	ASP	8.7
1	F	92	ASP	8.7
1	L	245	SER	8.7
1	E	461	GLY	8.7
1	N	267	ALA	8.7
2	Z	19	VAL	8.7
1	S	259	ALA	8.7
1	W	496	VAL	8.7
2	h	48	ASP	8.7
1	Q	8	LEU	8.7
2	u	28	VAL	8.6
1	L	386	THR	8.6
1	D	497	VAL	8.6
1	M	232	ALA	8.6
1	J	50	THR	8.6

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Mol	Chain	Res	Type	RSRZ
1	T	162	SER	8.6
1	F	503	GLU	8.6
2	t	64	GLU	8.6
1	X	425	VAL	8.6
1	J	506	VAL	8.6
1	B	92	ASP	8.6
2	e	48	ASP	8.6
1	H	396	GLU	8.6
1	O	207	TRP	8.6
1	G	177	HIS	8.6
2	Z	157	TYR	8.6
1	K	540	GLY	8.5
1	J	208	VAL	8.5
1	W	241	GLY	8.5
2	e	15	LYS	8.5
1	L	15	PHE	8.5
1	L	463	ILE	8.5
2	v	144	ASN	8.5
2	Z	74	ASN	8.5
1	B	249	ARG	8.5
1	T	561	ASP	8.5
2	g	31	ASP	8.5
2	b	104	TYR	8.5
2	j	47	ASP	8.5
2	v	9	LEU	8.5
1	T	598	GLN	8.5
1	H	211	TRP	8.5
1	I	584	PRO	8.5
2	h	16	GLY	8.5
1	W	595	GLU	8.5
1	Q	6	ASN	8.5
1	R	561	ASP	8.4
1	J	138	THR	8.4
2	j	33	THR	8.4
2	Y	70	SER	8.4
2	f	75	PRO	8.4
1	B	32	ASP	8.4
1	J	269	ARG	8.4
2	n	22	ASP	8.4
1	W	598	GLN	8.4
1	L	242	GLU	8.4
1	S	245	SER	8.4

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Mol	Chain	Res	Type	RSRZ
1	C	384	LEU	8.4
1	F	499	LEU	8.4
1	T	208	VAL	8.3
1	K	444	LEU	8.3
1	M	523	SER	8.3
1	R	256	ASP	8.3
1	A	597	GLN	8.3
1	U	499	LEU	8.3
2	d	17	ASP	8.3
1	X	208	VAL	8.3
2	s	143	LEU	8.3
2	k	150	PRO	8.3
1	Q	213	THR	8.3
1	K	284	THR	8.3
1	P	585	GLU	8.3
1	I	561	ASP	8.3
1	C	594	VAL	8.3
1	A	339	ASP	8.3
1	B	261	SER	8.3
1	W	239	VAL	8.3
1	A	208	VAL	8.3
1	D	13	SER	8.3
1	O	558	THR	8.3
2	Z	70	SER	8.3
1	I	238	PRO	8.3
2	d	39	PRO	8.3
1	A	423	GLU	8.3
1	H	283	CYS	8.3
1	T	563	LYS	8.3
1	K	32	ASP	8.3
1	K	461	GLY	8.2
2	a	155	TRP	8.2
1	H	212	LEU	8.2
2	b	75	PRO	8.2
1	L	515	GLU	8.2
1	E	259	ALA	8.2
1	T	565	VAL	8.2
1	Q	563	LYS	8.2
1	K	15	PHE	8.2
1	L	460	ASP	8.2
1	W	284	THR	8.2
1	B	259	ALA	8.2

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Mol	Chain	Res	Type	RSRZ
1	O	502	GLY	8.2
1	T	590	GLN	8.2
1	D	563	LYS	8.2
2	s	27	ASP	8.2
2	Y	37	VAL	8.1
2	l	66	PRO	8.1
1	K	545	GLY	8.1
1	X	421	ASP	8.1
1	Q	283	CYS	8.1
1	A	283	CYS	8.1
1	D	259	ALA	8.1
2	j	44	ASP	8.1
1	F	561	ASP	8.1
1	U	597	GLN	8.1
1	C	559	LEU	8.1
2	p	145	GLU	8.1
1	G	283	CYS	8.1
1	R	7	ARG	8.1
1	S	559	LEU	8.0
1	C	262	GLY	8.0
1	K	160	SER	8.0
1	P	564	GLY	8.0
1	G	426	ASN	8.0
1	E	498	ASP	8.0
2	Z	31	ASP	8.0
1	V	233	PHE	8.0
1	P	537	GLU	8.0
1	Q	503	GLU	8.0
1	D	245	SER	8.0
1	H	499	LEU	8.0
1	I	252	LYS	8.0
1	N	8	LEU	8.0
1	Q	540	GLY	8.0
1	R	246	TYR	8.0
1	K	495	GLU	8.0
2	f	77	ALA	8.0
1	C	549	TYR	8.0
2	e	38	GLU	7.9
1	U	216	THR	7.9
1	E	58	ASP	7.9
1	I	501	THR	7.9
1	N	210	PRO	7.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	b	98	CYS	7.9
1	A	8	LEU	7.9
1	D	162	SER	7.9
1	K	515	GLU	7.9
1	A	42	ASP	7.9
1	N	209	PHE	7.9
1	R	565	VAL	7.9
1	I	524	PHE	7.9
1	L	546	THR	7.9
2	Y	158	PHE	7.9
1	M	585	GLU	7.9
1	L	575	GLN	7.9
2	v	32	SER	7.9
1	W	587	PRO	7.9
1	L	500	ALA	7.9
2	Z	62	GLY	7.9
1	S	253	ASP	7.9
1	U	563	LYS	7.9
1	G	205	ASN	7.9
1	M	451	ASP	7.9
1	K	186	ASP	7.9
2	e	24	ARG	7.9
1	D	590	GLN	7.9
1	D	548	GLU	7.9
1	K	198	ILE	7.9
1	X	214	GLN	7.9
1	H	500	ALA	7.9
1	P	240	THR	7.8
1	C	496	VAL	7.8
2	u	35	ASP	7.8
1	F	590	GLN	7.8
1	L	85	GLY	7.8
1	E	460	ASP	7.8
2	t	38	ASP	7.8
2	d	153	ASN	7.8
1	N	424	ALA	7.8
2	d	14	THR	7.8
1	K	235	TYR	7.8
1	J	207	TRP	7.8
1	J	389	LEU	7.8
1	G	260	ASP	7.8
1	F	595	GLU	7.8

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Mol	Chain	Res	Type	RSRZ
1	H	241	GLY	7.8
2	b	84	LEU	7.8
1	F	260	ASP	7.8
1	S	596	ALA	7.8
1	B	421	ASP	7.8
1	P	6	ASN	7.8
1	C	421	ASP	7.8
1	I	260	ASP	7.8
1	V	420	VAL	7.8
1	W	259	ALA	7.8
1	E	558	THR	7.8
1	R	575	GLN	7.8
2	a	73	GLU	7.8
1	B	383	ASP	7.8
2	v	31	GLN	7.7
1	J	451	ASP	7.7
2	m	61	SER	7.7
1	S	501	THR	7.7
1	C	531	ASN	7.7
1	L	77	ASP	7.7
1	W	420	VAL	7.7
1	A	205	ASN	7.7
1	I	202	GLN	7.7
1	U	48	TYR	7.7
2	o	148	TYR	7.7
1	M	242	GLU	7.7
2	t	65	ASN	7.7
1	D	599	ALA	7.7
2	Y	71	ASP	7.7
2	f	103	ASP	7.7
1	I	504	LYS	7.7
1	K	13	SER	7.7
1	I	7	ARG	7.7
1	P	422	THR	7.7
2	o	35	ASP	7.7
2	b	156	HIS	7.7
1	J	584	PRO	7.7
1	S	211	TRP	7.7
1	H	210	PRO	7.7
1	Q	449	PHE	7.7
1	A	312	ASP	7.7
1	X	246	TYR	7.7

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Mol	Chain	Res	Type	RSRZ
2	Y	139	SER	7.7
2	Z	83	GLY	7.7
1	O	213	THR	7.7
1	J	237	ASP	7.6
1	G	547	PRO	7.6
1	G	28	GLU	7.6
1	J	437	GLN	7.6
1	R	215	ASP	7.6
2	r	9	LEU	7.6
1	P	545	GLY	7.6
1	A	267	ALA	7.6
1	H	256	ASP	7.6
2	i	31	ASP	7.6
1	T	426	ASN	7.6
1	T	421	ASP	7.6
1	X	422	THR	7.6
1	B	587	PRO	7.6
1	J	601	GLN	7.6
1	H	133	GLU	7.6
1	W	558	THR	7.6
1	G	32	ASP	7.6
1	B	48	TYR	7.6
2	h	101	ALA	7.6
1	U	259	ALA	7.6
1	E	599	ALA	7.6
1	B	8	LEU	7.6
2	e	104	TYR	7.6
1	Q	545	GLY	7.6
1	G	580	GLY	7.6
2	q	148	TYR	7.5
2	r	143	LEU	7.5
1	B	196	ASP	7.5
1	J	131	ASP	7.5
1	K	16	ASP	7.5
1	M	423	GLU	7.5
1	A	41	TRP	7.5
1	X	8	LEU	7.5
1	E	339	ASP	7.5
1	K	185	GLU	7.5
1	R	188	ALA	7.5
1	F	204	PRO	7.5
2	s	146	TRP	7.5

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Mol	Chain	Res	Type	RSRZ
2	e	155	TRP	7.5
1	C	15	PHE	7.5
2	Y	38	GLU	7.5
2	Z	154	GLU	7.5
1	V	195	ALA	7.5
1	D	558	THR	7.5
1	T	244	VAL	7.5
2	l	18	GLY	7.5
1	U	47	GLN	7.5
1	C	214	GLN	7.5
2	k	28	VAL	7.5
2	Z	155	TRP	7.5
2	i	158	PHE	7.5
2	t	27	ASP	7.5
1	M	209	PHE	7.5
1	D	531	ASN	7.5
1	N	386	THR	7.5
1	L	282	THR	7.5
1	Q	386	THR	7.5
1	H	264	ILE	7.5
1	Q	515	GLU	7.5
1	U	588	GLU	7.5
1	K	422	THR	7.5
1	L	423	GLU	7.5
2	b	73	GLU	7.5
1	R	239	VAL	7.5
1	X	571	TYR	7.4
2	c	14	THR	7.4
1	S	601	GLN	7.4
1	I	239	VAL	7.4
1	U	585	GLU	7.4
2	i	156	HIS	7.4
1	U	525	GLN	7.4
1	D	495	GLU	7.4
1	T	214	GLN	7.4
1	P	252	LYS	7.4
1	H	584	PRO	7.4
1	P	425	VAL	7.4
1	X	256	ASP	7.4
1	B	570	ASP	7.4
1	G	31	ASN	7.4
1	Q	75	PRO	7.4

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Mol	Chain	Res	Type	RSRZ
1	C	91	ALA	7.4
1	C	587	PRO	7.4
1	J	25	ALA	7.4
1	R	339	ASP	7.4
2	Z	15	LYS	7.4
1	S	499	LEU	7.4
1	I	50	THR	7.4
1	G	29	ALA	7.4
2	a	159	PRO	7.4
1	N	498	ASP	7.4
1	I	131	ASP	7.4
1	O	261	SER	7.4
1	P	550	GLN	7.4
1	U	263	PHE	7.4
1	V	209	PHE	7.4
1	G	50	THR	7.4
1	K	188	ALA	7.4
2	Y	143	THR	7.4
1	R	547	PRO	7.4
1	X	498	ASP	7.4
1	H	523	SER	7.4
2	s	147	HIS	7.4
1	J	375	ASN	7.4
1	T	558	THR	7.3
1	U	264	ILE	7.3
1	I	237	ASP	7.3
1	Q	25	ALA	7.3
1	X	572	ALA	7.3
1	N	423	GLU	7.3
1	T	495	GLU	7.3
1	U	213	THR	7.3
1	J	410	SER	7.3
1	U	11	ILE	7.3
1	G	250	ASP	7.3
1	K	539	LEU	7.3
1	T	13	SER	7.3
1	J	263	PHE	7.3
1	A	461	GLY	7.3
2	o	146	TRP	7.3
1	F	581	VAL	7.3
1	U	6	ASN	7.3
1	B	190	LYS	7.3

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Mol	Chain	Res	Type	RSRZ
2	h	88	ALA	7.3
2	a	84	LEU	7.3
2	d	138	PRO	7.3
1	V	89	ASP	7.3
1	J	422	THR	7.3
1	U	590	GLN	7.3
2	c	35	THR	7.3
1	B	242	GLU	7.3
2	t	142	ASN	7.3
1	G	378	ASP	7.3
1	E	566	GLU	7.2
1	L	25	ALA	7.2
1	R	573	ASN	7.2
1	B	214	GLN	7.2
2	m	70	GLY	7.2
1	O	197	ASP	7.2
1	E	538	LEU	7.2
1	E	598	GLN	7.2
1	L	597	GLN	7.2
1	D	262	GLY	7.2
1	D	602	GLY	7.2
1	C	213	THR	7.2
1	L	173	CYS	7.2
2	f	18	LEU	7.2
1	V	182	ASN	7.2
1	I	203	ASN	7.2
1	D	575	GLN	7.2
2	i	72	ASP	7.2
1	D	595	GLU	7.2
1	J	185	GLU	7.2
1	R	270	GLN	7.2
1	O	421	ASP	7.2
1	X	339	ASP	7.2
2	r	94	ASP	7.2
1	A	213	THR	7.2
1	X	139	SER	7.2
1	Q	424	ALA	7.2
1	X	215	ASP	7.2
1	E	547	PRO	7.2
1	R	189	GLU	7.2
1	H	451	ASP	7.2
1	J	236	GLN	7.2

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Mol	Chain	Res	Type	RSRZ
1	L	255	ILE	7.2
1	R	597	GLN	7.2
1	L	189	GLU	7.1
2	Y	34	LEU	7.1
1	H	421	ASP	7.1
2	o	22	ASP	7.1
1	S	533	ALA	7.1
2	q	72	ASP	7.1
1	H	268	GLU	7.1
1	K	550	GLN	7.1
1	I	261	SER	7.1
1	G	182	ASN	7.1
1	B	575	GLN	7.1
1	I	581	VAL	7.1
1	J	548	GLU	7.1
1	K	246	TYR	7.1
1	L	456	ALA	7.1
1	U	586	THR	7.1
1	Q	173	CYS	7.1
1	J	503	GLU	7.1
1	X	7	ARG	7.1
2	k	147	HIS	7.1
1	X	141	ASN	7.1
1	E	253	ASP	7.1
2	o	8	ASP	7.1
1	W	210	PRO	7.1
2	b	69	PHE	7.1
2	u	56	THR	7.1
2	n	79	ALA	7.1
1	V	31	ASN	7.1
1	E	16	ASP	7.1
2	r	62	ASP	7.1
2	h	78	GLU	7.1
1	A	550	GLN	7.1
1	L	367	ASP	7.1
1	U	600	LYS	7.1
1	F	565	VAL	7.1
1	I	543	PRO	7.1
2	j	150	PRO	7.1
2	s	7	GLY	7.0
1	P	20	THR	7.0
1	B	216	THR	7.0

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Mol	Chain	Res	Type	RSRZ
1	Q	575	GLN	7.0
1	A	139	SER	7.0
1	J	428	GLY	7.0
2	a	158	PHE	7.0
1	Q	548	GLU	7.0
1	G	194	ASP	7.0
1	F	205	ASN	7.0
1	H	595	GLU	7.0
1	J	445	GLU	7.0
1	J	270	GLN	7.0
1	H	378	ASP	7.0
1	A	337	ASN	7.0
1	W	279	SER	7.0
1	C	32	ASP	7.0
1	N	31	ASN	7.0
2	t	97	LEU	7.0
2	i	23	LEU	7.0
1	D	214	GLN	7.0
2	g	149	PHE	7.0
1	Q	570	ASP	7.0
2	e	47	ASP	7.0
2	a	46	VAL	7.0
1	B	26	ARG	7.0
2	d	35	THR	7.0
2	m	96	ALA	7.0
1	C	546	THR	7.0
1	F	186	ASP	7.0
1	K	202	GLN	7.0
2	k	145	GLU	7.0
1	C	499	LEU	7.0
1	H	549	TYR	7.0
1	S	497	VAL	7.0
1	D	565	VAL	7.0
1	C	46	SER	7.0
1	D	564	GLY	7.0
1	G	556	TYR	7.0
1	V	547	PRO	6.9
2	p	141	PRO	6.9
1	A	32	ASP	6.9
1	B	580	GLY	6.9
1	H	32	ASP	6.9
2	h	157	TYR	6.9

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Mol	Chain	Res	Type	RSRZ
1	C	588	GLU	6.9
2	k	30	PRO	6.9
1	B	563	LYS	6.9
1	V	250	ASP	6.9
1	I	197	ASP	6.9
1	G	584	PRO	6.9
1	F	218	GLN	6.9
1	S	425	VAL	6.9
1	D	561	ASP	6.9
1	K	241	GLY	6.9
1	J	387	GLN	6.9
1	N	420	VAL	6.9
2	g	124	TYR	6.9
2	a	107	GLU	6.9
1	F	161	ASN	6.9
2	d	28	VAL	6.9
1	O	238	PRO	6.9
1	M	260	ASP	6.9
2	a	81	ASP	6.9
1	B	573	ASN	6.9
1	V	267	ALA	6.9
1	A	259	ALA	6.9
1	E	220	ALA	6.9
1	H	114	ALA	6.9
2	Y	154	GLU	6.9
1	J	162	SER	6.8
2	a	150	PRO	6.8
2	f	45	ALA	6.8
1	F	580	GLY	6.8
1	E	32	ASP	6.8
1	D	25	ALA	6.8
2	p	35	ASP	6.8
1	S	209	PHE	6.8
2	p	147	HIS	6.8
1	O	239	VAL	6.8
1	E	542	THR	6.8
1	I	6	ASN	6.8
1	O	89	ASP	6.8
1	E	50	THR	6.8
1	P	254	VAL	6.8
1	V	212	LEU	6.8
1	W	426	ASN	6.8

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Mol	Chain	Res	Type	RSRZ
1	I	198	ILE	6.8
1	F	367	ASP	6.8
1	L	190	LYS	6.8
1	E	205	ASN	6.8
1	V	581	VAL	6.8
1	U	241	GLY	6.8
1	E	279	SER	6.8
1	O	86	ALA	6.8
1	H	387	GLN	6.8
1	M	495	GLU	6.8
1	P	421	ASP	6.8
1	D	39	SER	6.8
1	K	10	SER	6.8
1	G	496	VAL	6.7
1	J	23	ASP	6.7
1	R	264	ILE	6.7
2	b	152	LEU	6.7
1	C	434	THR	6.7
1	S	93	VAL	6.7
1	G	311	GLU	6.7
1	B	41	TRP	6.7
1	K	89	ASP	6.7
2	Z	47	ASP	6.7
1	E	170	ALA	6.7
1	J	533	ALA	6.7
2	e	46	VAL	6.7
1	U	570	ASP	6.7
1	P	180	SER	6.7
1	Q	26	ARG	6.7
1	T	460	ASP	6.7
1	U	509	ASP	6.7
2	i	155	TRP	6.7
1	S	238	PRO	6.7
2	s	28	VAL	6.7
2	j	101	ALA	6.7
1	N	216	THR	6.7
1	R	383	ASP	6.7
1	T	209	PHE	6.7
1	T	505	GLN	6.7
2	j	43	GLN	6.7
1	R	576	LEU	6.7
1	E	502	GLY	6.7

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Mol	Chain	Res	Type	RSRZ
1	V	584	PRO	6.7
1	X	563	LYS	6.7
1	B	591	GLN	6.7
1	D	501	THR	6.7
1	J	602	GLY	6.7
2	t	147	HIS	6.7
2	h	23	LEU	6.7
1	N	260	ASP	6.7
1	B	424	ALA	6.7
2	m	75	LEU	6.7
2	h	34	LEU	6.7
1	C	208	VAL	6.7
1	V	206	ASP	6.7
1	K	197	ASP	6.7
1	M	566	GLU	6.7
1	L	495	GLU	6.7
1	K	143	VAL	6.6
1	U	500	ALA	6.6
1	W	207	TRP	6.6
1	C	261	SER	6.6
1	P	183	GLY	6.6
1	K	271	ILE	6.6
2	v	150	PRO	6.6
1	C	242	GLU	6.6
1	H	42	ASP	6.6
1	U	572	ALA	6.6
1	K	280	ILE	6.6
1	O	263	PHE	6.6
1	T	39	SER	6.6
1	A	452	ASN	6.6
2	m	38	ASP	6.6
2	f	72	ASP	6.6
1	T	589	GLU	6.6
1	F	558	THR	6.6
1	U	519	ASP	6.6
1	J	261	SER	6.6
1	R	8	LEU	6.6
1	P	503	GLU	6.6
1	G	242	GLU	6.6
1	U	591	GLN	6.6
1	A	420	VAL	6.6
1	A	422	THR	6.6

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Mol	Chain	Res	Type	RSRZ
1	F	497	VAL	6.6
1	L	344	THR	6.6
1	I	173	CYS	6.6
1	I	259	ALA	6.6
2	r	7	GLY	6.6
1	D	586	THR	6.6
2	j	80	ASP	6.6
1	J	230	GLU	6.6
1	H	202	GLN	6.6
2	u	148	TYR	6.6
1	S	423	GLU	6.6
1	D	58	ASP	6.6
2	l	38	ASP	6.6
1	V	194	ASP	6.6
1	A	602	GLY	6.6
1	E	250	ASP	6.6
1	W	497	VAL	6.6
2	t	145	GLU	6.6
1	M	252	LYS	6.5
1	A	49	THR	6.5
1	B	256	ASP	6.5
1	K	20	THR	6.5
1	S	214	GLN	6.5
1	S	580	GLY	6.5
1	C	313	LYS	6.5
1	E	543	PRO	6.5
1	G	420	VAL	6.5
1	L	565	VAL	6.5
1	G	519	ASP	6.5
1	S	598	GLN	6.5
2	o	144	ASN	6.5
2	m	69	GLU	6.5
1	C	357	ALA	6.5
1	T	425	VAL	6.5
2	m	19	VAL	6.5
1	U	559	LEU	6.5
1	L	213	THR	6.5
1	K	252	LYS	6.5
2	g	19	VAL	6.5
1	S	599	ALA	6.5
1	J	444	LEU	6.5
1	X	103	ARG	6.5

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Mol	Chain	Res	Type	RSRZ
1	Q	421	ASP	6.5
1	V	387	GLN	6.5
1	K	433	ASP	6.5
2	r	63	ASP	6.5
2	f	27	GLY	6.5
1	V	161	ASN	6.5
1	F	460	ASP	6.5
2	f	16	GLY	6.5
1	R	213	THR	6.5
2	b	14	THR	6.5
1	P	375	ASN	6.5
1	T	587	PRO	6.5
1	F	578	GLN	6.5
1	S	254	VAL	6.5
1	J	452	ASN	6.5
1	V	516	CYS	6.5
1	C	41	TRP	6.5
1	X	186	ASP	6.5
1	E	586	THR	6.5
1	L	49	THR	6.5
2	q	61	SER	6.5
1	G	292	LEU	6.5
1	G	456	ALA	6.5
2	i	52	MET	6.5
1	B	526	SER	6.5
1	T	461	GLY	6.4
1	V	503	GLU	6.4
1	O	271	ILE	6.4
1	K	546	THR	6.4
1	K	437	GLN	6.4
1	P	283	CYS	6.4
1	A	256	ASP	6.4
1	U	461	GLY	6.4
1	P	592	TRP	6.4
1	E	587	PRO	6.4
1	L	209	PHE	6.4
1	C	191	TYR	6.4
1	R	494	ALA	6.4
1	E	5	GLU	6.4
1	L	513	ARG	6.4
2	c	153	ASN	6.4
1	R	540	GLY	6.4

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Mol	Chain	Res	Type	RSRZ
1	J	583	LYS	6.4
2	g	18	LEU	6.4
1	N	586	THR	6.4
1	T	239	VAL	6.4
1	L	17	ALA	6.4
2	t	66	PRO	6.4
1	L	516	CYS	6.4
1	U	580	GLY	6.4
2	b	47	ASP	6.4
2	j	36	ASP	6.4
1	K	17	ALA	6.4
1	A	388	PRO	6.4
1	X	200	SER	6.4
1	B	531	ASN	6.4
1	R	25	ALA	6.4
1	F	282	THR	6.4
1	F	419	GLY	6.4
1	K	420	VAL	6.4
1	L	531	ASN	6.4
2	r	97	LEU	6.4
2	r	144	ASN	6.4
2	f	70	SER	6.4
1	N	325	ASP	6.4
1	I	204	PRO	6.4
1	P	389	LEU	6.4
1	U	79	LEU	6.4
1	A	206	ASP	6.4
2	j	156	HIS	6.4
1	U	204	PRO	6.4
1	F	388	PRO	6.4
2	Y	144	GLY	6.4
1	W	503	GLU	6.4
1	E	462	GLU	6.4
1	H	161	ASN	6.4
2	e	157	TYR	6.4
1	O	199	PRO	6.3
1	F	588	GLU	6.3
2	k	42	ALA	6.3
2	s	20	ALA	6.3
1	C	339	ASP	6.3
1	K	203	ASN	6.3
1	I	548	GLU	6.3

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Mol	Chain	Res	Type	RSRZ
2	i	24	ARG	6.3
1	T	339	ASP	6.3
1	L	498	ASP	6.3
1	M	589	GLU	6.3
1	P	444	LEU	6.3
1	E	241	GLY	6.3
1	I	537	GLU	6.3
1	S	542	THR	6.3
1	X	216	THR	6.3
1	C	566	GLU	6.3
1	D	550	GLN	6.3
1	J	143	VAL	6.3
2	Y	98	CYS	6.3
2	a	70	SER	6.3
2	m	22	ASP	6.3
1	N	543	PRO	6.3
1	O	270	GLN	6.3
1	S	563	LYS	6.3
1	S	590	GLN	6.3
1	K	283	CYS	6.3
1	V	203	ASN	6.3
1	A	216	THR	6.3
1	B	150	HIS	6.3
1	U	159	ASP	6.3
1	V	587	PRO	6.3
2	s	97	LEU	6.3
2	g	123	LEU	6.3
2	p	33	MET	6.3
1	V	542	THR	6.3
1	L	191	TYR	6.3
2	m	71	ASP	6.3
1	C	361	HIS	6.3
1	C	596	ALA	6.3
1	J	546	THR	6.3
1	G	543	PRO	6.3
1	L	561	ASP	6.3
2	t	94	ASP	6.3
1	R	550	GLN	6.3
1	T	530	GLN	6.3
1	L	592	TRP	6.3
1	V	216	THR	6.3
1	W	380	ASN	6.3

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Mol	Chain	Res	Type	RSRZ
1	K	542	THR	6.3
1	I	257	ASP	6.3
1	F	387	GLN	6.3
1	T	566	GLU	6.2
2	b	106	LEU	6.2
1	T	257	ASP	6.2
1	F	257	ASP	6.2
1	B	28	GLU	6.2
1	I	553	LEU	6.2
1	U	254	VAL	6.2
1	E	504	LYS	6.2
1	J	49	THR	6.2
2	j	109	THR	6.2
1	W	590	GLN	6.2
1	S	462	GLU	6.2
2	g	24	ARG	6.2
1	R	420	VAL	6.2
1	T	235	TYR	6.2
1	P	386	THR	6.2
1	B	574	LYS	6.2
1	V	168	SER	6.2
1	I	389	LEU	6.2
1	H	541	LYS	6.2
1	J	134	ASP	6.2
2	r	61	SER	6.2
2	v	130	SER	6.2
1	M	49	THR	6.2
1	F	152	ALA	6.2
1	U	221	GLU	6.2
1	E	534	GLU	6.2
1	W	243	PRO	6.2
1	A	410	SER	6.2
1	B	204	PRO	6.2
1	E	92	ASP	6.2
1	I	331	ASN	6.2
1	J	241	GLY	6.2
2	g	28	VAL	6.2
1	X	494	ALA	6.2
1	H	207	TRP	6.2
2	h	77	ALA	6.2
1	B	588	GLU	6.2
1	B	13	SER	6.2

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Mol	Chain	Res	Type	RSRZ
1	K	439	ASN	6.2
1	I	499	LEU	6.2
2	d	152	LEU	6.2
1	A	58	ASP	6.2
1	B	159	ASP	6.2
1	M	386	THR	6.2
1	U	501	THR	6.2
1	D	6	ASN	6.2
1	I	180	SER	6.2
1	J	187	PHE	6.2
2	p	65	ASN	6.2
2	t	136	SER	6.2
1	R	88	PRO	6.2
1	D	380	ASN	6.2
1	G	207	TRP	6.2
1	K	84	ASP	6.2
2	d	73	GLU	6.2
1	F	258	LEU	6.2
2	d	157	TYR	6.2
2	a	52	MET	6.2
1	F	243	PRO	6.2
1	B	282	THR	6.1
1	B	586	THR	6.1
1	C	409	THR	6.1
2	j	35	THR	6.1
1	Q	500	ALA	6.1
1	W	495	GLU	6.1
1	J	235	TYR	6.1
1	B	264	ILE	6.1
1	K	187	PHE	6.1
1	U	242	GLU	6.1
1	C	386	THR	6.1
1	G	424	ALA	6.1
2	a	106	LEU	6.1
2	b	27	GLY	6.1
1	S	417	THR	6.1
1	K	601	GLN	6.1
1	V	456	ALA	6.1
1	E	193	LEU	6.1
1	U	385	PRO	6.1
1	S	459	ARG	6.1
2	j	71	ASP	6.1

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Mol	Chain	Res	Type	RSRZ
1	T	261	SER	6.1
2	Y	88	ALA	6.1
2	c	132	ALA	6.1
2	Z	61	LYS	6.1
2	j	92	VAL	6.1
1	E	41	TRP	6.1
1	E	196	ASP	6.1
2	a	59	ASP	6.1
1	X	205	ASN	6.1
1	H	236	GLN	6.1
1	M	422	THR	6.1
1	G	422	THR	6.1
2	Z	108	ALA	6.1
2	p	150	PRO	6.1
1	B	42	ASP	6.1
1	P	494	ALA	6.1
1	R	47	GLN	6.1
1	I	151	SER	6.1
1	K	228	LYS	6.1
2	h	110	ALA	6.1
1	T	594	VAL	6.1
1	G	233	PHE	6.1
1	I	388	PRO	6.1
1	N	212	LEU	6.1
1	P	84	ASP	6.1
1	P	211	TRP	6.1
1	V	367	ASP	6.1
1	E	19	TRP	6.1
1	F	89	ASP	6.1
1	L	212	LEU	6.1
2	r	38	ASP	6.1
1	N	284	THR	6.1
1	L	284	THR	6.1
1	K	462	GLU	6.1
1	H	576	LEU	6.1
1	L	26	ARG	6.1
2	d	134	ARG	6.1
1	W	387	GLN	6.1
1	B	47	GLN	6.1
1	H	259	ALA	6.1
1	A	141	ASN	6.1
1	J	5	GLU	6.1

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Mol	Chain	Res	Type	RSRZ
1	R	456	ALA	6.1
2	g	114	ALA	6.1
2	i	88	ALA	6.1
1	H	134	ASP	6.1
2	p	130	SER	6.1
1	V	543	PRO	6.1
1	V	506	VAL	6.0
1	A	519	ASP	6.0
2	i	98	CYS	6.0
1	H	252	LYS	6.0
1	O	7	ARG	6.0
1	A	580	GLY	6.0
2	d	19	VAL	6.0
2	u	9	LEU	6.0
1	Q	31	ASN	6.0
1	E	531	ASN	6.0
2	g	101	ALA	6.0
1	I	423	GLU	6.0
1	T	58	ASP	6.0
1	T	246	TYR	6.0
2	h	92	VAL	6.0
1	J	537	GLU	6.0
1	X	206	ASP	6.0
2	s	39	ASP	6.0
1	S	6	ASN	6.0
1	L	75	PRO	6.0
1	E	550	GLN	6.0
1	A	212	LEU	6.0
2	a	69	PHE	6.0
2	h	121	GLU	6.0
2	i	87	SER	6.0
1	H	389	LEU	6.0
1	Q	169	ASP	6.0
1	O	5	GLU	6.0
1	H	397	VAL	6.0
1	A	575	GLN	6.0
1	H	33	LEU	6.0
1	J	180	SER	6.0
2	g	87	SER	6.0
2	j	102	PRO	6.0
1	B	501	THR	6.0
1	F	50	THR	6.0

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Mol	Chain	Res	Type	RSRZ
1	W	498	ASP	6.0
1	D	540	GLY	6.0
1	H	494	ALA	6.0
2	m	7	GLY	6.0
1	H	87	ARG	6.0
1	L	87	ARG	6.0
1	S	422	THR	6.0
1	B	252	LYS	6.0
2	i	73	GLU	6.0
1	C	237	ASP	6.0
1	K	424	ALA	6.0
1	B	270	GLN	6.0
1	E	203	ASN	6.0
2	i	16	GLY	6.0
1	H	510	ILE	6.0
1	V	186	ASP	6.0
2	j	98	CYS	6.0
1	L	445	GLU	5.9
1	B	219	ILE	5.9
2	g	21	ALA	5.9
1	F	530	GLN	5.9
2	p	27	ASP	5.9
2	q	50	ASP	5.9
1	X	263	PHE	5.9
1	L	547	PRO	5.9
1	D	242	GLU	5.9
1	B	139	SER	5.9
1	R	260	ASP	5.9
1	K	497	VAL	5.9
1	L	230	GLU	5.9
2	h	28	VAL	5.9
1	S	15	PHE	5.9
1	G	563	LYS	5.9
2	k	64	GLU	5.9
1	K	516	CYS	5.9
2	f	80	ASP	5.9
1	F	463	ILE	5.9
1	G	381	SER	5.9
1	M	509	ASP	5.9
1	X	260	ASP	5.9
1	X	385	PRO	5.9
1	B	538	LEU	5.9

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Mol	Chain	Res	Type	RSRZ
1	T	557	PHE	5.9
1	P	506	VAL	5.9
1	A	565	VAL	5.9
1	R	516	CYS	5.9
2	k	125	ARG	5.9
1	L	16	ASP	5.9
2	h	33	THR	5.9
1	S	600	LYS	5.9
1	J	24	GLU	5.9
2	a	85	ARG	5.9
2	e	158	PHE	5.9
1	X	565	VAL	5.9
1	Q	246	TYR	5.9
1	M	510	ILE	5.9
1	Q	192	ASP	5.9
2	a	22	ALA	5.9
2	b	105	ALA	5.9
1	E	35	PHE	5.9
1	U	575	GLN	5.9
1	V	597	GLN	5.9
1	J	436	ASN	5.9
1	L	182	ASN	5.9
1	K	25	ALA	5.9
2	l	62	ASP	5.9
2	p	26	THR	5.9
1	V	515	GLU	5.9
1	A	81	ARG	5.9
1	O	8	LEU	5.9
1	X	41	TRP	5.9
1	W	26	ARG	5.9
1	R	209	PHE	5.9
1	X	460	ASP	5.9
1	B	227	GLU	5.9
1	D	260	ASP	5.9
1	K	596	ALA	5.9
1	W	162	SER	5.8
1	D	10	SER	5.8
1	K	14	ARG	5.9
1	U	15	PHE	5.8
1	H	137	PRO	5.8
1	H	388	PRO	5.8
1	N	266	ILE	5.8

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Mol	Chain	Res	Type	RSRZ
1	P	19	TRP	5.8
1	Q	463	ILE	5.8
1	Q	203	ASN	5.8
1	B	91	ALA	5.8
1	I	426	ASN	5.8
2	g	73	GLU	5.8
1	E	497	VAL	5.8
2	c	150	PRO	5.8
1	I	601	GLN	5.8
2	u	95	TYR	5.8
1	G	537	GLU	5.8
1	E	161	ASN	5.8
1	C	586	THR	5.8
1	K	268	GLU	5.8
1	A	421	ASP	5.8
2	f	52	MET	5.8
1	H	91	ALA	5.8
1	G	241	GLY	5.8
2	i	27	GLY	5.8
1	B	423	GLU	5.8
1	E	386	THR	5.8
2	o	92	ALA	5.8
1	G	506	VAL	5.8
1	K	538	LEU	5.8
1	T	439	ASN	5.8
1	O	516	CYS	5.8
1	U	458	ARG	5.8
1	L	214	GLN	5.8
2	n	28	VAL	5.8
1	K	85	GLY	5.8
2	d	144	GLY	5.8
1	G	217	ILE	5.8
1	I	269	ARG	5.8
1	F	237	ASP	5.8
1	H	383	ASP	5.8
2	h	53	MET	5.8
1	V	422	THR	5.8
1	S	204	PRO	5.8
1	P	192	ASP	5.8
1	K	496	VAL	5.8
1	S	434	THR	5.8
1	K	434	THR	5.8

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Mol	Chain	Res	Type	RSRZ
1	O	15	PHE	5.8
1	X	557	PHE	5.8
1	P	200	SER	5.8
1	S	92	ASP	5.8
2	n	62	ASP	5.8
1	U	155	HIS	5.8
1	D	600	LYS	5.8
1	G	266	ILE	5.8
1	L	595	GLU	5.8
1	C	204	PRO	5.8
1	E	425	VAL	5.8
1	L	270	GLN	5.8
1	C	583	LYS	5.8
1	K	602	GLY	5.8
1	S	386	THR	5.7
1	M	208	VAL	5.7
1	A	576	LEU	5.7
1	G	137	PRO	5.7
1	J	246	TYR	5.7
1	J	456	ALA	5.7
2	Y	68	VAL	5.7
2	a	102	PRO	5.7
2	c	28	VAL	5.7
1	Q	85	GLY	5.7
1	T	253	ASP	5.7
1	H	561	ASP	5.7
1	K	451	ASP	5.7
2	l	63	ASP	5.7
2	u	144	ASN	5.7
2	Z	158	PHE	5.7
1	M	500	ALA	5.7
2	Z	159	PRO	5.7
1	T	592	TRP	5.7
1	H	48	TYR	5.7
1	N	264	ILE	5.7
1	E	139	SER	5.7
1	S	560	LEU	5.7
2	f	28	VAL	5.7
2	i	37	VAL	5.7
1	G	86	ALA	5.7
2	f	146	GLY	5.7
2	i	43	GLN	5.7

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Mol	Chain	Res	Type	RSRZ
2	j	114	ALA	5.7
1	C	585	GLU	5.7
1	M	498	ASP	5.7
1	B	509	ASP	5.7
2	Z	82	HIS	5.7
2	d	72	ASP	5.7
2	g	17	ASP	5.7
1	I	420	VAL	5.7
1	S	597	GLN	5.7
1	L	29	ALA	5.7
2	s	123	ALA	5.7
1	A	563	LYS	5.7
1	M	565	VAL	5.7
2	a	139	SER	5.7
1	O	556	TYR	5.7
1	T	259	ALA	5.7
2	j	67	TYR	5.7
1	M	388	PRO	5.7
1	V	92	ASP	5.7
1	X	92	ASP	5.7
1	A	426	ASN	5.7
2	j	72	ASP	5.7
1	R	26	ARG	5.7
1	F	549	TYR	5.7
1	I	246	TYR	5.7
2	p	29	GLU	5.7
2	l	19	VAL	5.7
2	Y	84	LEU	5.7
1	C	206	ASP	5.7
1	S	261	SER	5.7
2	f	83	GLY	5.7
2	c	152	LEU	5.7
1	Q	502	GLY	5.7
1	S	561	ASP	5.7
1	T	170	ALA	5.7
2	m	68	ALA	5.7
1	C	139	SER	5.7
1	F	591	GLN	5.7
2	c	74	ASN	5.7
1	J	7	ARG	5.7
2	m	76	ARG	5.7
2	e	34	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
1	M	240	THR	5.7
1	U	546	THR	5.7
1	L	557	PHE	5.7
2	l	22	ASP	5.7
1	U	576	LEU	5.7
1	P	5	GLU	5.7
2	k	38	ASP	5.6
2	s	38	ASP	5.6
2	f	31	ASP	5.6
1	W	458	ARG	5.6
1	V	208	VAL	5.6
1	C	565	VAL	5.6
2	r	10	VAL	5.6
1	N	5	GLU	5.6
1	O	25	ALA	5.6
1	S	339	ASP	5.6
1	L	544	GLN	5.6
1	W	28	GLU	5.6
1	O	547	PRO	5.6
1	U	547	PRO	5.6
2	q	53	GLY	5.6
1	W	195	ALA	5.6
1	H	558	THR	5.6
2	i	101	ALA	5.6
1	X	576	LEU	5.6
1	P	451	ASP	5.6
1	C	215	ASP	5.6
1	C	461	GLY	5.6
1	F	151	SER	5.6
2	s	110	GLY	5.6
1	P	210	PRO	5.6
1	K	75	PRO	5.6
2	f	85	ARG	5.6
1	F	25	ALA	5.6
2	l	79	ALA	5.6
1	Q	216	THR	5.6
1	R	100	THR	5.6
1	X	284	THR	5.6
1	F	597	GLN	5.6
1	J	536	LEU	5.6
1	T	169	ASP	5.6
1	A	185	GLU	5.6

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Mol	Chain	Res	Type	RSRZ
1	H	519	ASP	5.6
1	K	42	ASP	5.6
2	u	146	TRP	5.6
1	M	261	SER	5.6
1	H	205	ASN	5.6
1	J	494	ALA	5.6
2	p	12	ALA	5.6
1	B	386	THR	5.6
1	V	242	GLU	5.6
1	B	566	GLU	5.6
1	J	550	GLN	5.6
2	n	64	GLU	5.6
2	a	24	ARG	5.6
1	L	576	LEU	5.6
2	h	142	PRO	5.6
2	g	125	LYS	5.6
2	k	94	ASP	5.6
1	U	599	ALA	5.6
1	D	337	ASN	5.6
1	U	594	VAL	5.6
2	Y	78	GLU	5.6
2	Y	92	VAL	5.6
2	f	19	VAL	5.6
1	Q	501	THR	5.6
1	E	15	PHE	5.6
1	T	497	VAL	5.6
1	K	375	ASN	5.6
2	v	48	TYR	5.6
1	K	564	GLY	5.6
1	E	383	ASP	5.6
1	H	251	ILE	5.6
2	s	22	ASP	5.6
2	Z	80	ASP	5.6
2	d	155	TRP	5.6
1	Q	420	VAL	5.6
2	m	145	GLU	5.6
1	B	151	SER	5.6
2	f	151	ASN	5.6
1	B	202	GLN	5.6
1	O	551	LEU	5.6
1	B	546	THR	5.6
1	S	32	ASP	5.6

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Mol	Chain	Res	Type	RSRZ
1	I	206	ASP	5.6
2	e	72	ASP	5.6
1	M	268	GLU	5.6
1	H	589	GLU	5.6
1	F	235	TYR	5.6
1	A	525	GLN	5.6
1	E	162	SER	5.6
1	H	563	LYS	5.6
1	V	232	ALA	5.6
1	F	259	ALA	5.6
1	I	570	ASP	5.6
2	a	157	TYR	5.6
2	f	104	TYR	5.6
1	B	241	GLY	5.6
1	C	547	PRO	5.6
1	I	578	GLN	5.6
1	N	215	ASP	5.5
1	E	89	ASP	5.5
2	h	14	THR	5.5
1	D	88	PRO	5.5
1	V	266	ILE	5.5
1	W	551	LEU	5.5
1	C	572	ALA	5.5
2	a	44	ASP	5.5
1	C	212	LEU	5.5
1	L	76	ILE	5.5
1	L	462	GLU	5.5
1	F	289	ASP	5.5
1	K	192	ASP	5.5
2	c	72	ASP	5.5
1	S	385	PRO	5.5
1	C	575	GLN	5.5
2	a	75	PRO	5.5
1	O	180	SER	5.5
1	U	34	PHE	5.5
1	P	186	ASP	5.5
1	Q	271	ILE	5.5
1	G	451	ASP	5.5
1	I	558	THR	5.5
1	G	136	SER	5.5
1	K	245	SER	5.5
1	M	84	ASP	5.5

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Mol	Chain	Res	Type	RSRZ
1	B	70	GLU	5.5
1	G	601	GLN	5.5
2	p	91	ILE	5.5
2	q	38	ASP	5.5
2	f	159	PRO	5.5
1	R	563	LYS	5.5
1	S	246	TYR	5.5
1	N	7	ARG	5.5
1	R	443	ASP	5.5
1	C	598	GLN	5.5
2	k	15	ARG	5.5
1	M	576	LEU	5.5
1	X	36	SER	5.5
1	D	585	GLU	5.5
1	I	425	VAL	5.5
1	O	209	PHE	5.5
1	O	87	ARG	5.5
1	T	180	SER	5.5
1	S	550	GLN	5.5
1	H	325	ASP	5.5
1	S	586	THR	5.5
1	W	408	ALA	5.5
1	D	29	ALA	5.5
2	Z	84	LEU	5.5
1	R	595	GLU	5.5
1	C	6	ASN	5.5
1	U	381	SER	5.5
1	W	425	VAL	5.5
1	K	448	VAL	5.5
1	O	428	GLY	5.5
1	S	210	PRO	5.5
1	W	169	ASP	5.5
1	C	58	ASP	5.5
2	q	60	PHE	5.5
2	b	44	ASP	5.5
1	U	462	GLU	5.5
1	E	600	LYS	5.5
2	j	64	ILE	5.5
2	j	28	VAL	5.5
1	H	89	ASP	5.4
1	K	421	ASP	5.4
1	L	259	ALA	5.5

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Mol	Chain	Res	Type	RSRZ
1	P	388	PRO	5.4
1	R	210	PRO	5.4
1	U	196	ASP	5.4
1	E	238	PRO	5.4
2	f	138	PRO	5.4
1	P	463	ILE	5.4
1	X	264	ILE	5.4
1	S	236	GLN	5.4
1	D	597	GLN	5.4
2	t	18	GLY	5.4
1	I	546	THR	5.4
1	M	597	GLN	5.4
1	O	557	PHE	5.4
1	P	387	GLN	5.4
1	D	578	GLN	5.4
1	E	575	GLN	5.4
1	X	241	GLY	5.4
1	C	508	ASN	5.4
1	Q	592	TRP	5.4
1	E	14	ARG	5.4
1	T	591	GLN	5.4
1	B	525	GLN	5.4
1	W	188	ALA	5.4
1	T	207	TRP	5.4
1	I	510	ILE	5.4
1	J	209	PHE	5.4
1	S	591	GLN	5.4
1	I	240	THR	5.4
1	U	566	GLU	5.4
2	s	41	GLU	5.4
2	v	29	GLU	5.4
1	U	565	VAL	5.4
1	N	197	ASP	5.4
1	D	173	CYS	5.4
1	H	258	LEU	5.4
1	H	580	GLY	5.4
2	r	6	LYS	5.4
1	I	205	ASN	5.4
1	K	239	VAL	5.4
1	W	139	SER	5.4
2	Y	142	PRO	5.4
2	Y	159	PRO	5.4

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Mol	Chain	Res	Type	RSRZ
2	Z	36	ASP	5.4
1	A	544	GLN	5.4
1	K	406	GLU	5.4
2	q	75	LEU	5.4
2	Z	144	GLY	5.4
1	D	294	ALA	5.4
2	h	105	ALA	5.4
2	p	134	THR	5.4
1	N	496	VAL	5.4
1	M	215	ASP	5.4
1	N	237	ASP	5.4
1	O	237	ASP	5.4
1	O	553	LEU	5.4
1	R	258	LEU	5.4
1	G	196	ASP	5.4
2	h	146	GLY	5.4
1	L	274	ARG	5.4
2	c	104	TYR	5.4
1	E	258	LEU	5.4
1	T	550	GLN	5.4
1	E	368	ASP	5.4
2	t	53	GLY	5.4
2	c	77	ALA	5.4
1	H	313	LYS	5.4
1	K	129	VAL	5.4
1	E	540	GLY	5.4
1	O	256	ASP	5.4
1	X	550	GLN	5.4
1	G	180	SER	5.4
1	K	234	ILE	5.4
2	j	59	ASP	5.4
1	X	91	ALA	5.3
1	X	510	ILE	5.3
1	D	31	ASN	5.3
1	H	182	ASN	5.3
1	S	335	SER	5.3
1	F	136	SER	5.3
1	J	285	ALA	5.3
1	J	196	ASP	5.3
1	T	542	THR	5.3
1	V	386	THR	5.3
1	D	209	PHE	5.3

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Mol	Chain	Res	Type	RSRZ
1	S	595	GLU	5.3
1	T	540	GLY	5.3
1	H	416	ALA	5.3
1	U	317	GLU	5.3
1	K	396	GLU	5.3
2	g	78	GLU	5.3
1	Q	205	ASN	5.3
1	B	367	ASP	5.3
1	F	31	ASN	5.3
2	j	48	ASP	5.3
2	d	57	TYR	5.3
1	W	456	ALA	5.3
1	I	407	ALA	5.3
2	Z	51	ALA	5.3
2	j	88	ALA	5.3
2	f	136	PRO	5.3
1	R	5	GLU	5.3
1	C	85	GLY	5.3
1	H	556	TYR	5.3
2	l	21	SER	5.3
1	M	251	ILE	5.3
1	B	500	ALA	5.3
1	O	601	GLN	5.3
1	K	49	THR	5.3
2	i	109	THR	5.3
1	R	237	ASP	5.3
1	H	200	SER	5.3
1	J	153	CYS	5.3
2	Y	91	ALA	5.3
1	A	495	GLU	5.3
1	M	542	THR	5.3
2	p	146	TRP	5.3
1	J	545	GLY	5.3
1	R	58	ASP	5.3
1	R	531	ASN	5.3
1	S	498	ASP	5.3
1	B	105	ASN	5.3
1	N	425	VAL	5.3
2	a	148	SER	5.3
1	S	400	ALA	5.3
1	X	5	GLU	5.3
1	T	262	GLY	5.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	M	563	LYS	5.3
1	O	84	ASP	5.3
1	I	496	VAL	5.3
2	m	62	ASP	5.3
1	F	162	SER	5.3
1	H	456	ALA	5.3
1	N	576	LEU	5.3
1	B	547	PRO	5.3
1	H	41	TRP	5.3
1	K	297	HIS	5.3
2	a	66	GLY	5.3
2	u	106	THR	5.3
1	U	421	ASP	5.3
1	L	13	SER	5.3
1	A	265	LYS	5.3
1	M	420	VAL	5.3
1	B	284	THR	5.3
1	J	271	ILE	5.3
1	N	456	ALA	5.3
1	O	460	ASP	5.3
1	D	539	LEU	5.3
1	G	110	ALA	5.3
1	E	324	LYS	5.2
2	j	23	LEU	5.3
1	U	601	GLN	5.2
1	H	39	SER	5.2
1	I	505	GLN	5.2
1	S	548	GLU	5.2
1	W	133	GLU	5.2
1	H	230	GLU	5.2
1	G	400	ALA	5.2
1	H	390	ALA	5.2
1	A	443	ASP	5.2
1	P	540	GLY	5.2
1	A	326	GLY	5.2
1	G	291	GLN	5.2
1	D	571	TYR	5.2
2	j	142	PRO	5.2
1	Q	367	ASP	5.2
1	C	89	ASP	5.2
1	N	202	GLN	5.2
1	V	366	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	236	GLN	5.2
1	J	283	CYS	5.2
1	K	242	GLU	5.2
2	a	100	ILE	5.2
2	Z	156	HIS	5.2
1	J	16	ASP	5.2
2	r	27	ASP	5.2
1	I	263	PHE	5.2
1	G	576	LEU	5.2
1	I	114	ALA	5.2
1	O	130	THR	5.2
1	B	240	THR	5.2
1	L	419	GLY	5.2
2	p	38	ASP	5.2
2	Y	99	ARG	5.2
1	O	499	LEU	5.2
1	F	51	LEU	5.2
1	L	139	SER	5.2
1	P	243	PRO	5.2
1	A	456	ALA	5.2
1	I	357	ALA	5.2
1	M	558	THR	5.2
1	A	383	ASP	5.2
1	B	409	THR	5.2
1	J	214	GLN	5.2
1	L	387	GLN	5.2
2	n	26	THR	5.2
2	Y	69	PHE	5.2
2	e	69	PHE	5.2
2	n	145	GLU	5.2
2	b	67	TYR	5.2
1	U	288	LYS	5.2
1	W	136	SER	5.2
2	n	147	HIS	5.2
2	u	123	ALA	5.2
2	g	159	PRO	5.2
1	J	93	VAL	5.2
1	K	589	GLU	5.2
2	i	78	GLU	5.2
1	E	559	LEU	5.2
1	G	374	LEU	5.2
1	X	452	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
1	S	547	PRO	5.2
1	U	151	SER	5.2
1	B	55	GLY	5.2
1	T	35	PHE	5.2
1	H	239	VAL	5.2
1	L	422	THR	5.2
2	Y	80	ASP	5.2
2	p	92	ALA	5.2
2	l	78	SER	5.2
2	e	156	HIS	5.2
2	g	41	SER	5.2
2	g	103	ASP	5.2
2	s	138	ASN	5.2
1	W	423	GLU	5.2
1	B	324	LYS	5.2
2	l	29	GLU	5.2
2	m	34	GLN	5.2
2	g	43	GLN	5.2
1	N	213	THR	5.2
1	Q	498	ASP	5.2
1	K	368	ASP	5.2
2	p	118	THR	5.2
1	Q	252	LYS	5.2
1	S	414	GLU	5.2
1	T	531	ASN	5.2
1	A	26	ARG	5.2
1	M	517	TYR	5.1
1	D	16	ASP	5.1
2	c	51	ALA	5.1
1	D	319	VAL	5.1
2	g	56	TRP	5.1
2	g	148	SER	5.1
1	P	235	TYR	5.1
1	B	313	LYS	5.1
1	W	170	ALA	5.1
1	B	96	GLY	5.1
1	G	263	PHE	5.1
2	a	55	GLU	5.1
1	A	538	LEU	5.1
2	Z	139	SER	5.1
1	Q	15	PHE	5.1
1	V	580	GLY	5.1

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Mol	Chain	Res	Type	RSRZ
1	G	382	GLY	5.1
2	i	29	ALA	5.1
1	S	581	VAL	5.1
1	T	41	TRP	5.1
1	V	449	PHE	5.1
2	q	95	TYR	5.1
2	Y	157	TYR	5.1
1	P	538	LEU	5.1
1	E	422	THR	5.1
1	S	381	SER	5.1
1	A	5	GLU	5.1
1	E	602	GLY	5.1
1	A	29	ALA	5.1
2	t	60	PHE	5.1
2	Y	107	GLU	5.1
2	h	21	ALA	5.1
2	i	135	ALA	5.1
1	E	420	VAL	5.1
1	K	76	ILE	5.1
1	X	58	ASP	5.1
1	W	542	THR	5.1
2	Y	109	THR	5.1
1	R	566	GLU	5.1
2	g	110	ALA	5.1
1	Q	510	ILE	5.1
1	T	570	ASP	5.1
1	G	312	ASP	5.1
1	J	84	ASP	5.1
1	B	207	TRP	5.1
2	f	73	GLU	5.1
1	Q	425	VAL	5.1
1	W	258	LEU	5.1
1	X	140	ASN	5.1
1	X	497	VAL	5.1
1	B	258	LEU	5.1
1	C	420	VAL	5.1
2	p	9	LEU	5.1
1	Q	505	GLN	5.1
1	T	541	LYS	5.1
1	F	562	GLY	5.1
1	R	232	ALA	5.1
1	K	220	ALA	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	b	155	TRP	5.1
1	D	161	ASN	5.1
1	H	217	ILE	5.1
1	I	523	SER	5.1
1	S	578	GLN	5.1
1	X	505	GLN	5.1
1	A	299	PRO	5.1
1	V	25	ALA	5.1
1	I	599	ALA	5.1
2	n	146	TRP	5.1
2	t	143	LEU	5.1
2	k	65	ASN	5.1
1	P	583	LYS	5.1
1	H	526	SER	5.1
1	I	502	GLY	5.1
1	L	202	GLN	5.1
2	u	62	ASP	5.1
2	f	82	HIS	5.1
1	N	556	TYR	5.1
1	K	595	GLU	5.1
2	u	44	MET	5.1
2	d	139	SER	5.1
1	M	387	GLN	5.1
1	M	506	VAL	5.1
1	S	191	TYR	5.1
1	U	238	PRO	5.1
1	U	533	ALA	5.1
1	W	12	LEU	5.1
1	C	584	PRO	5.1
1	E	191	TYR	5.1
1	I	451	ASP	5.1
1	K	93	VAL	5.1
1	X	573	ASN	5.0
2	g	52	MET	5.0
1	T	193	LEU	5.0
1	B	576	LEU	5.0
1	F	13	SER	5.0
1	M	48	TYR	5.0
1	S	421	ASP	5.0
1	X	443	ASP	5.0
1	A	257	ASP	5.0
2	b	81	ASP	5.0

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Mol	Chain	Res	Type	RSRZ
2	g	47	ASP	5.0
1	I	600	LYS	5.0
1	R	267	ALA	5.0
1	K	450	GLN	5.0
1	T	243	PRO	5.0
1	D	89	ASP	5.0
2	m	67	PRO	5.0
1	E	459	ARG	5.0
1	B	318	GLY	5.0
2	u	24	THR	5.0
2	d	62	GLY	5.0
2	c	46	VAL	5.0
1	O	550	GLN	5.0
1	W	494	ALA	5.0
1	T	260	ASP	5.0
2	f	78	GLU	5.0
2	a	60	GLY	5.0
1	R	422	THR	5.0
2	u	37	VAL	5.0
1	W	544	GLN	5.0
1	L	337	ASN	5.0
1	Q	168	SER	5.0
2	j	124	TYR	5.0
1	W	388	PRO	5.0
1	D	192	ASP	5.0
1	G	497	VAL	5.0
1	J	374	LEU	5.0
1	J	553	LEU	5.0
1	P	31	ASN	5.0
1	K	270	GLN	5.0
1	A	48	TYR	5.0
2	l	92	ALA	5.0
2	g	121	GLU	5.0
1	L	388	PRO	5.0
1	G	92	ASP	5.0
1	K	18	ASP	5.0
1	L	92	ASP	5.0
2	a	140	ARG	5.0
1	P	546	THR	5.0
1	U	327	GLN	5.0
1	P	548	GLU	5.0
1	R	6	ASN	5.0

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Mol	Chain	Res	Type	RSRZ
1	N	177	HIS	5.0
2	g	23	LEU	5.0
2	h	76	PRO	5.0
1	W	460	ASP	5.0
1	K	87	ARG	5.0
1	K	364	ASP	5.0
1	L	458	ARG	5.0
1	W	589	GLU	5.0
1	A	387	GLN	5.0
1	C	599	ALA	5.0
1	J	357	ALA	5.0
2	l	126	ALA	5.0
1	D	542	THR	5.0
2	b	33	THR	5.0
1	X	564	GLY	5.0
1	F	587	PRO	5.0
1	C	498	ASP	5.0
1	P	234	ILE	5.0
1	X	47	GLN	5.0
1	I	416	ALA	5.0
1	K	173	CYS	5.0
1	C	539	LEU	5.0
1	I	49	THR	5.0
1	J	279	SER	5.0
2	c	148	SER	5.0
1	D	41	TRP	5.0
1	J	312	ASP	5.0
1	J	502	GLY	5.0
2	Z	106	LEU	5.0
1	C	141	ASN	5.0
1	K	344	THR	5.0
1	J	75	PRO	5.0
1	K	255	ILE	5.0
1	K	577	ILE	5.0
2	Y	73	GLU	5.0
2	h	41	SER	5.0
1	R	192	ASP	5.0
1	S	42	ASP	5.0
1	Q	557	PHE	5.0
1	A	424	ALA	5.0
1	B	338	ALA	5.0
1	K	209	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
1	L	86	ALA	5.0
1	K	229	LYS	5.0
2	d	34	LEU	5.0
2	e	27	GLY	5.0
1	W	283	CYS	5.0
1	B	299	PRO	4.9
2	o	141	PRO	4.9
2	f	76	PRO	4.9
1	Q	197	ASP	4.9
1	S	526	SER	4.9
1	K	509	ASP	4.9
1	K	600	LYS	4.9
1	F	461	GLY	4.9
1	S	463	ILE	4.9
1	D	28	GLU	4.9
1	K	361	HIS	4.9
1	J	388	PRO	4.9
2	b	50	GLU	4.9
1	U	35	PHE	4.9
1	C	602	GLY	4.9
1	D	530	GLN	4.9
1	I	517	TYR	4.9
2	a	34	LEU	4.9
1	S	531	ASN	4.9
1	A	409	THR	4.9
1	G	524	PHE	4.9
1	M	169	ASP	4.9
1	C	335	SER	4.9
1	E	206	ASP	4.9
1	G	151	SER	4.9
1	L	237	ASP	4.9
1	F	425	VAL	4.9
1	I	115	VAL	4.9
1	O	548	GLU	4.9
1	C	5	GLU	4.9
1	N	400	ALA	4.9
1	F	456	ALA	4.9
1	H	232	ALA	4.9
1	I	559	LEU	4.9
1	P	244	VAL	4.9
1	T	458	ARG	4.9
1	C	249	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
1	I	437	GLN	4.9
2	d	31	ASP	4.9
1	G	379	GLU	4.9
2	n	92	ALA	4.9
2	q	45	ALA	4.9
2	b	91	ALA	4.9
2	h	45	ALA	4.9
1	E	290	LYS	4.9
1	I	387	GLN	4.9
1	Q	230	GLU	4.9
1	V	32	ASP	4.9
1	A	367	ASP	4.9
1	T	203	ASN	4.9
1	T	386	THR	4.9
1	N	378	ASP	4.9
1	T	537	GLU	4.9
2	f	59	ASP	4.9
1	X	187	PHE	4.9
1	O	183	GLY	4.9
2	m	20	ALA	4.9
1	M	88	PRO	4.9
2	q	59	VAL	4.9
1	B	595	GLU	4.9
1	J	592	TRP	4.9
1	W	16	ASP	4.9
1	Q	212	LEU	4.9
1	B	564	GLY	4.9
1	E	597	GLN	4.9
2	m	29	GLU	4.9
1	V	26	ARG	4.9
1	E	377	THR	4.9
2	o	91	ILE	4.9
1	E	508	ASN	4.9
1	I	41	TRP	4.9
1	S	242	GLU	4.9
1	E	252	LYS	4.9
1	F	52	GLN	4.9
2	g	76	PRO	4.9
1	X	417	THR	4.9
1	K	131	ASP	4.9
2	Y	23	LEU	4.9
2	j	31	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
1	N	261	SER	4.9
1	V	540	GLY	4.9
2	m	21	SER	4.9
2	t	20	ALA	4.9
1	E	248	LYS	4.9
1	E	280	ILE	4.9
1	V	283	CYS	4.9
1	C	576	LEU	4.9
1	D	8	LEU	4.9
2	f	84	LEU	4.9
1	B	452	ASN	4.9
1	D	134	ASP	4.9
1	F	546	THR	4.9
1	G	508	ASN	4.9
2	t	96	ALA	4.9
2	k	61	SER	4.9
2	g	154	GLU	4.9
2	d	63	ILE	4.8
2	b	49	LEU	4.8
1	I	503	GLU	4.8
1	K	249	ARG	4.8
2	m	59	VAL	4.8
2	h	147	ASN	4.8
2	d	156	HIS	4.8
1	U	552	LEU	4.8
1	T	305	GLY	4.8
1	G	114	ALA	4.8
2	a	45	ALA	4.8
1	Q	422	THR	4.8
1	T	213	THR	4.8
1	H	452	ASN	4.8
1	H	46	SER	4.8
1	K	39	SER	4.8
1	Q	444	LEU	4.8
1	F	539	LEU	4.8
1	S	87	ARG	4.8
2	b	62	GLY	4.8
1	N	234	ILE	4.8
1	T	205	ASN	4.8
1	C	100	THR	4.8
1	E	237	ASP	4.8
1	A	327	GLN	4.8

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Mol	Chain	Res	Type	RSRZ
1	I	212	LEU	4.8
2	l	16	LYS	4.8
2	t	114	LEU	4.8
2	u	139	SER	4.8
1	G	238	PRO	4.8
1	O	230	GLU	4.8
1	L	267	ALA	4.8
1	O	535	ILE	4.8
1	B	288	LYS	4.8
1	O	501	THR	4.8
1	X	384	LEU	4.8
2	Z	33	THR	4.8
2	r	147	HIS	4.8
2	d	18	LEU	4.8
1	O	420	VAL	4.8
2	h	38	GLU	4.8
1	X	259	ALA	4.8
1	C	35	PHE	4.8
1	P	237	ASP	4.8
1	T	43	ASP	4.8
2	e	152	LEU	4.8
1	C	591	GLN	4.8
1	H	578	GLN	4.8
1	P	230	GLU	4.8
1	G	168	SER	4.8
2	j	144	GLY	4.8
1	J	265	LYS	4.8
1	I	309	PHE	4.8
2	i	56	TRP	4.8
1	S	141	ASN	4.8
2	v	27	ASP	4.8
2	j	17	ASP	4.8
1	F	183	GLY	4.8
1	L	586	THR	4.8
2	j	55	GLU	4.8
1	X	34	PHE	4.8
1	D	188	ALA	4.8
1	K	449	PHE	4.8
1	C	571	TYR	4.8
1	M	452	ASN	4.8
1	U	326	GLY	4.8
1	W	31	ASN	4.8

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Mol	Chain	Res	Type	RSRZ
1	X	105	ASN	4.8
1	F	531	ASN	4.8
2	b	24	ARG	4.8
1	B	335	SER	4.8
1	B	353	PRO	4.8
1	I	500	ALA	4.8
2	h	145	SER	4.8
1	J	535	ILE	4.8
1	M	595	GLU	4.8
1	V	565	VAL	4.8
1	X	396	GLU	4.8
1	B	317	GLU	4.8
1	D	314	GLU	4.8
1	D	459	ARG	4.8
1	H	550	GLN	4.8
1	K	233	PHE	4.8
1	Q	160	SER	4.8
1	S	536	LEU	4.8
1	T	595	GLU	4.8
1	K	445	GLU	4.8
1	Q	254	VAL	4.8
1	G	131	ASP	4.8
1	I	92	ASP	4.8
1	J	42	ASP	4.8
2	Z	95	ASN	4.8
1	P	238	PRO	4.8
2	Z	102	PRO	4.8
1	F	242	GLU	4.8
2	h	50	GLU	4.8
1	X	270	GLN	4.8
1	X	580	GLY	4.8
1	B	35	PHE	4.7
1	Q	443	ASP	4.7
1	F	582	LYS	4.7
2	p	72	ASP	4.7
2	d	103	ASP	4.7
1	M	499	LEU	4.7
1	P	205	ASN	4.7
2	i	50	GLU	4.7
1	G	208	VAL	4.7
1	H	254	VAL	4.7
1	C	601	GLN	4.7

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Mol	Chain	Res	Type	RSRZ
1	V	289	ASP	4.7
1	I	576	LEU	4.7
2	k	29	GLU	4.7
2	s	65	ASN	4.7
1	N	208	VAL	4.7
1	V	502	GLY	4.7
1	G	63	VAL	4.7
2	e	70	SER	4.7
2	g	30	SER	4.7
1	E	211	TRP	4.7
2	t	146	TRP	4.7
1	G	7	ARG	4.7
1	S	368	ASP	4.7
2	e	36	ASP	4.7
1	S	96	GLY	4.7
1	V	213	THR	4.7
1	W	582	LYS	4.7
1	C	558	THR	4.7
1	I	231	THR	4.7
1	G	236	GLN	4.7
1	I	283	CYS	4.7
2	g	20	ARG	4.7
1	S	237	ASP	4.7
1	S	534	GLU	4.7
1	B	519	ASP	4.7
1	H	23	ASP	4.7
2	e	71	ASP	4.7
1	A	96	GLY	4.7
1	E	199	PRO	4.7
2	n	65	ASN	4.7
2	d	124	TYR	4.7
1	R	37	ARG	4.7
2	j	93	PHE	4.7
1	U	279	SER	4.7
2	h	58	GLN	4.7
1	S	19	TRP	4.7
1	B	384	LEU	4.7
1	G	234	ILE	4.7
2	l	64	GLU	4.7
2	j	94	HIS	4.7
1	V	421	ASP	4.7
2	d	80	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
2	q	150	PRO	4.7
1	C	597	GLN	4.7
1	G	47	GLN	4.7
1	J	566	GLU	4.7
1	Q	208	VAL	4.7
1	B	7	ARG	4.7
1	G	62	PRO	4.7
1	T	499	LEU	4.7
1	G	501	THR	4.7
1	P	423	GLU	4.7
1	U	154	SER	4.7
1	L	396	GLU	4.7
1	N	169	ASP	4.7
1	U	248	LYS	4.7
1	M	357	ALA	4.7
1	N	416	ALA	4.7
1	H	501	THR	4.7
1	J	596	ALA	4.7
1	O	389	LEU	4.7
1	S	566	GLU	4.7
1	V	47	GLN	4.7
1	E	515	GLU	4.7
1	K	436	ASN	4.7
1	R	417	THR	4.7
1	L	448	VAL	4.7
2	m	26	THR	4.7
1	D	502	GLY	4.7
2	n	110	GLY	4.7
2	Y	67	TYR	4.7
1	P	134	ASP	4.7
1	O	214	GLN	4.7
1	C	388	PRO	4.7
1	F	325	ASP	4.7
1	R	424	ALA	4.7
1	A	494	ALA	4.7
2	a	27	GLY	4.7
1	N	46	SER	4.7
1	P	269	ARG	4.7
1	M	227	GLU	4.7
1	Q	186	ASP	4.7
1	V	589	GLU	4.7
1	C	519	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
1	F	28	GLU	4.7
1	D	529	GLN	4.7
1	D	547	PRO	4.7
2	p	79	ALA	4.7
2	b	72	ASP	4.7
2	d	71	ASP	4.7
2	j	42	MET	4.7
1	N	182	ASN	4.6
1	W	49	THR	4.6
1	L	50	THR	4.6
2	f	123	LEU	4.6
2	m	115	TYR	4.6
1	S	543	PRO	4.6
1	B	228	LYS	4.6
1	G	169	ASP	4.6
1	H	47	GLN	4.6
1	I	390	ALA	4.6
1	J	443	ASP	4.6
1	K	387	GLN	4.6
2	p	8	ASP	4.6
2	v	42	ALA	4.6
1	P	539	LEU	4.6
1	T	242	GLU	4.6
2	s	26	THR	4.6
2	s	16	LYS	4.6
2	b	154	GLU	4.6
1	M	494	ALA	4.6
1	T	367	ASP	4.6
1	U	93	VAL	4.6
1	D	52	GLN	4.6
1	B	459	ARG	4.6
1	B	554	LEU	4.6
1	W	234	ILE	4.6
1	B	50	THR	4.6
1	H	586	THR	4.6
1	L	231	THR	4.6
2	p	78	SER	4.6
1	X	336	PHE	4.6
1	A	497	VAL	4.6
2	b	51	ALA	4.6
1	B	58	ASP	4.6
1	L	32	ASP	4.6

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Mol	Chain	Res	Type	RSRZ
2	o	110	GLY	4.6
2	i	34	LEU	4.6
1	M	230	GLU	4.6
1	V	380	ASN	4.6
1	A	592	TRP	4.6
1	L	216	THR	4.6
2	t	118	THR	4.6
2	h	109	THR	4.6
1	T	56	GLN	4.6
1	G	342	ALA	4.6
1	L	195	ALA	4.6
2	p	77	SER	4.6
1	T	283	CYS	4.6
1	F	228	LYS	4.6
1	O	423	GLU	4.6
1	S	28	GLU	4.6
2	i	104	TYR	4.6
1	M	87	ARG	4.6
1	O	27	ARG	4.6
1	S	575	GLN	4.6
1	G	578	GLN	4.6
1	X	570	ASP	4.6
1	D	243	PRO	4.6
1	N	233	PHE	4.6
1	C	430	VAL	4.6
2	c	158	PHE	4.6
1	X	218	GLN	4.6
1	G	558	THR	4.6
1	F	46	SER	4.6
2	q	14	LEU	4.6
1	V	238	PRO	4.6
1	G	462	GLU	4.6
1	S	134	ASP	4.6
1	V	460	ASP	4.6
1	U	239	VAL	4.6
1	W	263	PHE	4.6
1	F	182	ASN	4.6
1	K	267	ALA	4.6
2	j	66	GLY	4.6
1	X	529	GLN	4.6
1	A	323	THR	4.6
1	F	200	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	P	76	ILE	4.6
1	X	42	ASP	4.6
2	k	63	ASP	4.6
1	K	225	VAL	4.6
1	K	407	ALA	4.6
1	T	538	LEU	4.6
2	d	82	HIS	4.6
1	K	296	GLU	4.6
1	T	204	PRO	4.6
1	A	62	PRO	4.6
1	G	284	THR	4.6
1	L	229	LYS	4.6
2	u	66	PRO	4.6
1	D	92	ASP	4.6
1	W	581	VAL	4.6
1	E	246	TYR	4.6
1	C	79	LEU	4.6
1	F	195	ALA	4.6
1	P	534	GLU	4.6
1	T	575	GLN	4.6
1	H	537	GLU	4.6
1	I	555	GLN	4.6
2	m	73	HIS	4.6
1	T	366	ASN	4.6
1	P	251	ILE	4.6
2	g	86	SER	4.6
1	U	449	PHE	4.6
1	W	215	ASP	4.6
1	A	556	TYR	4.6
1	G	549	TYR	4.6
1	H	84	ASP	4.6
2	k	148	TYR	4.6
2	m	63	ASP	4.6
1	E	51	LEU	4.6
1	L	554	LEU	4.6
2	g	105	ALA	4.6
1	U	70	GLU	4.6
1	V	563	LYS	4.6
1	X	508	ASN	4.6
1	G	516	CYS	4.6
1	J	356	ILE	4.6
1	N	136	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	X	506	VAL	4.6
1	H	50	THR	4.6
1	J	129	VAL	4.6
1	K	557	PHE	4.6
2	o	26	THR	4.6
1	R	183	GLY	4.5
1	O	504	LYS	4.5
1	Q	537	GLU	4.5
1	D	515	GLU	4.5
1	R	337	ASN	4.5
1	I	31	ASN	4.5
1	O	246	TYR	4.5
2	h	117	LYS	4.5
1	P	206	ASP	4.5
1	B	77	ASP	4.5
2	q	39	ASP	4.5
1	W	52	GLN	4.5
2	f	58	GLN	4.5
1	J	461	GLY	4.5
1	I	344	THR	4.5
1	K	389	LEU	4.5
1	L	602	GLY	4.5
2	s	148	TYR	4.5
1	Q	86	ALA	4.5
1	B	518	THR	4.5
2	a	98	CYS	4.5
1	S	41	TRP	4.5
1	P	263	PHE	4.5
2	j	46	VAL	4.5
1	T	380	ASN	4.5
1	A	398	PRO	4.5
2	m	97	LEU	4.5
2	o	65	ASN	4.5
2	f	101	ALA	4.5
1	O	134	ASP	4.5
1	V	523	SER	4.5
1	C	410	SER	4.5
2	t	26	THR	4.5
1	P	555	GLN	4.5
1	S	529	GLN	4.5
1	X	15	PHE	4.5
1	H	34	PHE	4.5

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Mol	Chain	Res	Type	RSRZ
1	L	41	TRP	4.5
1	G	589	GLU	4.5
2	u	87	LEU	4.5
1	W	599	ALA	4.5
1	M	313	LYS	4.5
1	W	47	GLN	4.5
2	u	39	ASP	4.5
2	i	30	SER	4.5
1	H	420	VAL	4.5
1	L	156	VAL	4.5
1	B	560	LEU	4.5
2	i	152	LEU	4.5
1	G	25	ALA	4.5
2	p	148	TYR	4.5
1	J	199	PRO	4.5
2	i	22	ALA	4.5
1	P	255	ILE	4.5
1	X	217	ILE	4.5
1	W	186	ASP	4.5
1	I	506	VAL	4.5
2	t	19	VAL	4.5
1	O	545	GLY	4.5
1	P	26	ARG	4.5
1	W	253	ASP	4.5
1	A	142	GLN	4.5
1	H	263	PHE	4.5
1	M	8	LEU	4.5
1	B	81	ARG	4.5
1	C	553	LEU	4.5
1	I	213	THR	4.5
1	I	519	ASP	4.5
1	I	545	GLY	4.5
1	K	24	GLU	4.5
1	L	160	SER	4.5
2	a	103	ASP	4.5
1	U	313	LYS	4.5
1	L	580	GLY	4.5
1	C	220	ALA	4.5
1	C	219	ILE	4.5
1	H	198	ILE	4.5
1	Q	50	THR	4.5
1	T	5	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
1	U	538	LEU	4.5
1	D	339	ASP	4.5
1	D	589	GLU	4.5
1	L	28	GLU	4.5
2	r	75	LEU	4.5
2	u	64	GLU	4.5
1	L	155	HIS	4.5
1	R	338	ALA	4.5
2	f	105	ALA	4.5
1	F	255	ILE	4.5
1	I	535	ILE	4.5
2	Y	100	ILE	4.5
1	Q	229	LYS	4.5
1	E	532	ARG	4.5
1	A	560	LEU	4.5
1	L	590	GLN	4.5
1	Q	434	THR	4.5
1	U	498	ASP	4.5
2	j	81	ASP	4.5
1	X	19	TRP	4.5
1	U	243	PRO	4.5
1	E	395	PRO	4.5
1	I	27	ARG	4.5
1	N	502	GLY	4.5
1	O	31	ASN	4.5
1	O	439	ASN	4.5
2	n	94	ASP	4.5
2	a	31	ASP	4.5
1	V	46	SER	4.5
1	K	36	SER	4.5
1	D	249	ARG	4.5
1	K	582	LYS	4.5
1	V	12	LEU	4.4
2	f	62	GLY	4.4
2	Z	98	CYS	4.4
1	S	572	ALA	4.4
1	X	456	ALA	4.4
2	b	132	ALA	4.4
2	Y	19	VAL	4.4
1	T	529	GLN	4.4
1	U	83	LYS	4.4
2	n	6	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
2	g	85	ARG	4.4
1	T	533	ALA	4.4
1	U	220	ALA	4.4
1	B	131	ASP	4.4
1	C	263	PHE	4.4
1	E	21	ALA	4.4
1	I	234	ILE	4.4
1	I	498	ASP	4.4
1	R	546	THR	4.4
1	U	558	THR	4.4
1	I	542	THR	4.4
2	m	53	GLY	4.4
1	M	584	PRO	4.4
1	I	199	PRO	4.4
2	t	16	LYS	4.4
2	r	55	ILE	4.4
2	a	108	ALA	4.4
1	Q	89	ASP	4.4
1	R	506	VAL	4.4
1	U	506	VAL	4.4
1	A	192	ASP	4.4
1	T	501	THR	4.4
2	l	14	LEU	4.4
2	Y	96	LEU	4.4
1	B	160	SER	4.4
1	F	290	LYS	4.4
1	H	532	ARG	4.4
2	f	133	LYS	4.4
1	H	199	PRO	4.4
1	P	233	PHE	4.4
1	R	187	PHE	4.4
1	X	255	ILE	4.4
1	N	133	GLU	4.4
1	P	129	VAL	4.4
1	Q	507	LEU	4.4
1	C	177	HIS	4.4
1	R	269	ARG	4.4
1	V	27	ARG	4.4
1	P	245	SER	4.4
1	K	410	SER	4.4
1	Q	550	GLN	4.4
1	J	107	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
2	h	22	ALA	4.4
1	R	574	LYS	4.4
1	F	459	ARG	4.4
2	v	28	VAL	4.4
1	H	498	ASP	4.4
2	e	74	ASN	4.4
2	h	31	ASP	4.4
1	U	100	THR	4.4
1	X	558	THR	4.4
1	C	270	GLN	4.4
1	H	36	SER	4.4
1	H	327	GLN	4.4
1	M	238	PRO	4.4
1	K	88	PRO	4.4
2	m	140	PHE	4.4
1	A	156	VAL	4.4
1	A	258	LEU	4.4
1	C	294	ALA	4.4
1	F	246	TYR	4.4
2	h	119	GLY	4.4
2	Y	72	ASP	4.4
1	M	291	GLN	4.4
1	S	546	THR	4.4
1	C	543	PRO	4.4
1	D	248	LYS	4.4
2	m	66	PRO	4.4
2	o	6	LYS	4.4
1	R	296	GLU	4.4
1	W	534	GLU	4.4
1	D	274	ARG	4.4
1	S	244	VAL	4.4
1	K	285	ALA	4.4
2	i	118	TYR	4.4
1	P	197	ASP	4.4
1	C	573	ASN	4.4
1	C	248	LYS	4.4
1	L	383	ASP	4.4
1	L	449	PHE	4.4
1	N	36	SER	4.4
2	f	134	ARG	4.4
1	P	93	VAL	4.4
1	R	388	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	V	400	ALA	4.4
1	E	190	LYS	4.4
2	m	6	LYS	4.4
1	I	256	ASP	4.4
1	K	561	ASP	4.4
1	L	273	ARG	4.4
2	g	48	ASP	4.4
1	O	198	ILE	4.4
1	B	11	ILE	4.4
1	Q	17	ALA	4.4
1	C	533	ALA	4.4
1	H	560	LEU	4.4
1	J	438	LEU	4.4
1	U	191	TYR	4.4
1	X	318	GLY	4.4
1	J	108	LYS	4.4
1	P	15	PHE	4.4
1	N	194	ASP	4.4
1	P	270	GLN	4.4
1	R	194	ASP	4.4
1	S	58	ASP	4.4
1	U	134	ASP	4.4
1	X	227	GLU	4.4
1	D	253	ASP	4.4
1	G	366	ASN	4.4
1	G	561	ASP	4.4
1	K	41	TRP	4.4
1	J	390	ALA	4.4
1	Q	586	THR	4.4
1	X	96	GLY	4.4
1	D	386	THR	4.4
2	Y	90	SER	4.4
1	H	361	HIS	4.4
2	b	94	HIS	4.4
1	A	271	ILE	4.4
1	F	573	ASN	4.3
1	G	73	GLN	4.4
1	L	197	ASP	4.3
1	L	394	ASN	4.3
2	n	144	ASN	4.3
1	R	96	GLY	4.3
1	S	279	SER	4.3

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Mol	Chain	Res	Type	RSRZ
1	H	417	THR	4.3
1	L	7	ARG	4.3
1	T	597	GLN	4.3
1	B	337	ASN	4.3
2	a	101	ALA	4.3
2	j	27	GLY	4.3
2	b	102	PRO	4.3
1	P	542	THR	4.3
1	F	160	SER	4.3
1	M	198	ILE	4.3
1	Q	536	LEU	4.3
1	S	594	VAL	4.3
1	A	590	GLN	4.3
1	B	420	VAL	4.3
1	L	499	LEU	4.3
1	K	391	TYR	4.3
1	A	395	PRO	4.3
2	g	39	PRO	4.3
1	U	33	LEU	4.3
1	A	173	CYS	4.3
1	E	541	LYS	4.3
1	L	410	SER	4.3
1	C	280	ILE	4.3
2	Y	18	LEU	4.3
2	g	35	THR	4.3
2	i	14	THR	4.3
2	j	126	GLN	4.3
1	W	101	ASP	4.3
2	m	72	ASP	4.3
1	O	449	PHE	4.3
1	B	34	PHE	4.3
1	C	537	GLU	4.3
2	n	133	PRO	4.3
2	g	75	PRO	4.3
1	S	284	THR	4.3
1	I	11	ILE	4.3
1	K	279	SER	4.3
1	X	591	GLN	4.3
2	h	98	CYS	4.3
2	k	68	ALA	4.3
1	F	207	TRP	4.3
2	k	62	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
2	k	146	TRP	4.3
1	K	79	LEU	4.3
2	m	127	PRO	4.3
1	N	47	GLN	4.3
1	A	591	GLN	4.3
1	E	295	GLY	4.3
1	U	207	TRP	4.3
2	t	95	TYR	4.3
1	X	509	ASP	4.3
1	D	534	GLU	4.3
1	K	169	ASP	4.3
2	Z	56	TRP	4.3
1	P	213	THR	4.3
1	R	387	GLN	4.3
1	T	220	ALA	4.3
1	A	236	GLN	4.3
1	C	338	ALA	4.3
1	K	236	GLN	4.3
2	f	30	SER	4.3
1	O	406	GLU	4.3
1	L	185	GLU	4.3
2	p	15	ARG	4.3
1	A	51	LEU	4.3
1	K	237	ASP	4.3
2	n	27	ASP	4.3
2	u	38	ASP	4.3
2	f	47	ASP	4.3
2	i	49	LEU	4.3
1	V	286	VAL	4.3
1	B	182	ASN	4.3
1	C	210	PRO	4.3
1	K	320	VAL	4.3
1	A	25	ALA	4.3
1	G	590	GLN	4.3
1	A	28	GLU	4.3
2	a	104	TYR	4.3
1	O	581	VAL	4.3
1	E	134	ASP	4.3
1	E	496	VAL	4.3
1	I	383	ASP	4.3
2	p	133	PRO	4.3
1	M	540	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	O	387	GLN	4.3
1	Q	459	ARG	4.3
1	T	263	PHE	4.3
1	B	15	PHE	4.3
1	V	455	THR	4.3
1	D	261	SER	4.3
1	E	178	SER	4.3
1	E	414	GLU	4.3
2	m	149	PHE	4.3
2	h	90	SER	4.3
1	L	8	LEU	4.3
1	L	538	LEU	4.3
2	t	17	LEU	4.3
1	J	266	ILE	4.3
1	W	260	ASP	4.3
2	t	39	ASP	4.3
2	c	71	ASP	4.3
1	R	29	ALA	4.3
1	S	35	PHE	4.3
1	U	195	ALA	4.3
1	E	439	ASN	4.3
1	G	585	GLU	4.3
1	G	507	LEU	4.3
1	K	281	ILE	4.3
1	X	32	ASP	4.3
2	q	71	ASP	4.3
1	P	533	ALA	4.3
1	E	313	LYS	4.3
1	J	15	PHE	4.3
1	L	452	ASN	4.3
2	l	20	ALA	4.3
2	f	121	GLU	4.3
1	E	235	TYR	4.3
1	I	8	LEU	4.3
1	P	143	VAL	4.2
1	D	546	THR	4.2
1	L	20	THR	4.2
1	U	564	GLY	4.2
1	U	32	ASP	4.2
1	W	237	ASP	4.2
1	B	398	PRO	4.2
1	K	23	ASP	4.2

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Mol	Chain	Res	Type	RSRZ
2	p	69	GLU	4.2
2	s	8	ASP	4.2
1	U	549	TYR	4.2
1	D	549	TYR	4.2
1	F	556	TYR	4.2
2	t	78	SER	4.2
1	H	308	GLY	4.2
1	N	304	PHE	4.2
1	S	147	GLU	4.2
1	X	338	ALA	4.2
1	I	230	GLU	4.2
1	J	543	PRO	4.2
1	P	551	LEU	4.2
1	H	507	LEU	4.2
1	G	161	ASN	4.2
1	I	244	VAL	4.2
2	f	113	ILE	4.2
2	h	15	LYS	4.2
2	o	89	CYS	4.2
2	Z	109	THR	4.2
1	G	51	LEU	4.2
1	L	42	ASP	4.2
2	j	103	ASP	4.2
1	J	425	VAL	4.2
2	o	33	MET	4.2
1	R	268	GLU	4.2
1	F	515	GLU	4.2
1	M	114	ALA	4.2
1	R	586	THR	4.2
1	H	136	SER	4.2
1	H	160	SER	4.2
2	n	21	SER	4.2
1	U	91	ALA	4.2
1	B	504	LYS	4.2
1	C	570	ASP	4.2
1	L	260	ASP	4.2
2	n	91	ILE	4.2
1	M	439	ASN	4.2
1	N	28	GLU	4.2
1	E	564	GLY	4.2
2	j	16	GLY	4.2
1	C	19	TRP	4.2

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Mol	Chain	Res	Type	RSRZ
1	G	386	THR	4.2
1	Q	506	VAL	4.2
1	T	32	ASP	4.2
1	V	312	ASP	4.2
1	A	92	ASP	4.2
1	D	367	ASP	4.2
1	E	421	ASP	4.2
1	F	173	CYS	4.2
1	G	64	VAL	4.2
1	H	214	GLN	4.2
1	J	498	ASP	4.2
1	L	192	ASP	4.2
2	i	44	ASP	4.2
1	M	31	ASN	4.2
1	M	205	ASN	4.2
1	D	537	GLU	4.2
1	L	161	ASN	4.2
2	p	76	ARG	4.2
2	Z	66	GLY	4.2
1	H	229	LYS	4.2
2	a	96	LEU	4.2
1	E	82	PRO	4.2
1	L	323	THR	4.2
1	O	16	ASP	4.2
1	R	253	ASP	4.2
2	p	71	ASP	4.2
2	Y	31	ASP	4.2
1	H	304	PHE	4.2
2	o	7	GLY	4.2
1	Q	74	ASN	4.2
1	B	140	ASN	4.2
1	L	252	LYS	4.2
1	Q	533	ALA	4.2
1	Q	76	ILE	4.2
1	W	41	TRP	4.2
1	K	184	TRP	4.2
2	s	37	VAL	4.2
1	W	446	THR	4.2
1	D	584	PRO	4.2
1	T	368	ASP	4.2
1	E	215	ASP	4.2
1	J	359	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
1	S	426	ASN	4.2
1	A	407	ALA	4.2
1	G	285	ALA	4.2
1	J	267	ALA	4.2
1	L	573	ASN	4.2
2	a	29	ALA	4.2
1	O	26	ARG	4.2
1	B	517	TYR	4.2
1	F	600	LYS	4.2
2	e	142	PRO	4.2
2	b	31	ASP	4.2
1	V	551	LEU	4.2
1	X	51	LEU	4.2
1	L	536	LEU	4.2
1	Q	565	VAL	4.2
1	U	508	ASN	4.2
1	E	25	ALA	4.2
2	Y	110	ALA	4.2
2	b	153	ASN	4.2
1	L	248	LYS	4.2
1	I	227	GLU	4.2
2	b	43	GLN	4.2
1	P	160	SER	4.2
1	X	35	PHE	4.2
1	A	261	SER	4.2
1	B	326	GLY	4.2
2	m	130	SER	4.2
2	f	124	TYR	4.2
1	W	501	THR	4.2
1	A	377	THR	4.2
2	j	127	THR	4.2
1	T	61	ARG	4.2
1	F	569	ARG	4.2
1	V	600	LYS	4.2
1	D	594	VAL	4.2
2	p	119	ALA	4.2
1	E	535	ILE	4.2
2	u	65	ASN	4.2
1	M	396	GLU	4.2
1	C	358	GLY	4.2
2	s	145	GLU	4.2
1	K	8	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
2	n	14	LEU	4.2
2	c	102	PRO	4.2
2	i	130	SER	4.2
1	T	250	ASP	4.2
1	K	174	THR	4.2
1	K	257	ASP	4.2
1	U	30	LYS	4.1
1	O	331	ASN	4.1
1	Q	437	GLN	4.1
1	C	540	GLY	4.1
1	G	6	ASN	4.1
1	G	505	GLN	4.1
2	d	104	TYR	4.1
1	O	173	CYS	4.1
1	E	173	CYS	4.1
1	F	12	LEU	4.1
2	c	142	PRO	4.1
2	a	87	SER	4.1
1	M	325	ASP	4.1
1	A	107	ALA	4.1
1	K	21	ALA	4.1
1	L	58	ASP	4.1
1	G	423	GLU	4.1
1	C	337	ASN	4.1
1	E	554	LEU	4.1
2	q	132	MET	4.1
2	f	56	TRP	4.1
1	X	543	PRO	4.1
1	G	82	PRO	4.1
2	h	42	MET	4.1
1	U	176	ILE	4.1
1	D	244	VAL	4.1
1	E	367	ASP	4.1
1	J	63	VAL	4.1
2	q	96	ALA	4.1
2	Y	81	ASP	4.1
1	W	515	GLU	4.1
1	O	524	PHE	4.1
1	B	557	PHE	4.1
1	O	163	LYS	4.1
1	A	31	ASN	4.1
1	H	331	ASN	4.1

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Mol	Chain	Res	Type	RSRZ
2	v	33	MET	4.1
1	U	543	PRO	4.1
1	O	500	ALA	4.1
1	U	294	ALA	4.1
1	C	11	ILE	4.1
2	p	88	ALA	4.1
2	Y	108	ALA	4.1
1	R	283	CYS	4.1
1	X	159	ASP	4.1
1	H	240	THR	4.1
2	i	119	GLY	4.1
1	O	517	TYR	4.1
1	B	181	GLN	4.1
2	g	49	LEU	4.1
1	J	331	ASN	4.1
1	M	11	ILE	4.1
2	r	133	PRO	4.1
1	O	599	ALA	4.1
1	G	232	ALA	4.1
2	n	88	ALA	4.1
2	d	64	ILE	4.1
2	e	91	ALA	4.1
1	M	206	ASP	4.1
1	D	101	ASP	4.1
1	F	528	LYS	4.1
1	H	582	LYS	4.1
2	c	111	LYS	4.1
1	S	56	GLN	4.1
1	W	597	GLN	4.1
2	h	43	GLN	4.1
1	N	87	ARG	4.1
1	B	510	ILE	4.1
1	J	184	TRP	4.1
2	j	95	ASN	4.1
1	I	288	LYS	4.1
1	C	350	PHE	4.1
1	A	570	ASP	4.1
1	F	194	ASP	4.1
1	G	258	LEU	4.1
1	G	323	THR	4.1
1	J	538	LEU	4.1
1	U	598	GLN	4.1

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Mol	Chain	Res	Type	RSRZ
2	n	89	CYS	4.1
2	c	53	MET	4.1
1	M	239	VAL	4.1
2	e	154	GLU	4.1
2	j	29	ALA	4.1
1	R	79	LEU	4.1
1	B	193	LEU	4.1
1	P	261	SER	4.1
1	W	257	ASP	4.1
2	o	39	ASP	4.1
1	Q	387	GLN	4.1
1	G	387	GLN	4.1
1	U	60	VAL	4.1
1	J	38	VAL	4.1
2	a	68	VAL	4.1
2	c	52	MET	4.1
1	A	406	GLU	4.1
1	C	463	ILE	4.1
2	e	50	GLU	4.1
1	N	114	ALA	4.1
2	s	93	PRO	4.1
1	M	98	TYR	4.1
1	N	206	ASP	4.1
1	B	36	SER	4.1
1	E	591	GLN	4.1
1	G	103	ARG	4.1
2	b	148	SER	4.1
1	H	506	VAL	4.1
1	K	300	ILE	4.1
2	c	64	ILE	4.1
2	s	36	ALA	4.1
1	O	241	GLY	4.1
1	E	545	GLY	4.1
1	L	339	ASP	4.1
1	N	503	GLU	4.1
1	M	524	PHE	4.1
1	R	247	PHE	4.1
1	H	557	PHE	4.1
1	K	390	ALA	4.1
1	S	461	GLY	4.1
1	V	388	PRO	4.1
1	A	193	LEU	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	41	TRP	4.1
2	d	85	ARG	4.1
2	f	20	ARG	4.1
1	A	573	ASN	4.1
1	L	31	ASN	4.1
1	T	314	GLU	4.1
1	W	218	GLN	4.1
1	F	571	TYR	4.1
1	I	117	GLU	4.1
1	I	155	HIS	4.1
1	I	550	GLN	4.1
1	V	255	ILE	4.1
1	A	89	ASP	4.1
1	C	13	SER	4.1
1	G	162	SER	4.1
2	a	105	ALA	4.1
1	F	8	LEU	4.1
1	X	426	ASN	4.0
1	H	315	VAL	4.0
1	I	189	GLU	4.0
2	g	92	VAL	4.0
1	R	519	ASP	4.0
1	S	535	ILE	4.0
1	M	91	ALA	4.0
1	M	151	SER	4.0
1	W	32	ASP	4.0
1	W	134	ASP	4.0
1	H	173	CYS	4.0
1	J	255	ILE	4.0
1	I	87	ARG	4.0
1	J	364	ASP	4.0
2	m	104	ILE	4.0
2	Y	17	ASP	4.0
1	E	342	ALA	4.0
2	k	18	GLY	4.0
2	p	99	ALA	4.0
2	d	30	SER	4.0
2	e	41	SER	4.0
1	P	586	THR	4.0
1	L	409	THR	4.0
1	J	41	TRP	4.0
1	M	581	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
1	X	31	ASN	4.0
1	J	244	VAL	4.0
1	K	38	VAL	4.0
1	G	264	ILE	4.0
1	H	235	TYR	4.0
1	N	519	ASP	4.0
1	P	196	ASP	4.0
1	G	257	ASP	4.0
1	A	46	SER	4.0
1	G	130	THR	4.0
1	F	584	PRO	4.0
1	G	398	PRO	4.0
2	e	121	GLU	4.0
1	V	246	TYR	4.0
1	N	508	ASN	4.0
1	X	449	PHE	4.0
1	I	452	ASN	4.0
1	K	590	GLN	4.0
2	Y	42	MET	4.0
2	i	95	ASN	4.0
1	Q	215	ASP	4.0
1	J	499	LEU	4.0
2	l	39	ASP	4.0
2	f	114	ALA	4.0
1	M	50	THR	4.0
1	M	588	GLU	4.0
1	V	595	GLU	4.0
1	B	5	GLU	4.0
1	E	423	GLU	4.0
1	G	445	GLU	4.0
1	A	11	ILE	4.0
1	F	575	GLN	4.0
1	I	399	GLN	4.0
1	B	426	ASN	4.0
1	C	170	ALA	4.0
1	N	196	ASP	4.0
2	v	8	ASP	4.0
2	Z	71	ASP	4.0
1	P	268	GLU	4.0
1	D	14	ARG	4.0
1	E	245	SER	4.0
1	O	323	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	U	80	TYR	4.0
1	X	109	ILE	4.0
2	p	89	CYS	4.0
2	h	118	TYR	4.0
1	W	193	LEU	4.0
1	D	427	GLY	4.0
2	b	110	ALA	4.0
2	d	74	ASN	4.0
2	e	66	GLY	4.0
2	k	22	ASP	4.0
2	h	47	ASP	4.0
1	O	410	SER	4.0
1	W	46	SER	4.0
1	I	13	SER	4.0
2	t	61	SER	4.0
2	Z	37	VAL	4.0
1	M	553	LEU	4.0
1	O	41	TRP	4.0
1	V	571	TYR	4.0
1	F	592	TRP	4.0
1	G	213	THR	4.0
2	j	143	THR	4.0
2	l	96	ALA	4.0
2	d	15	LYS	4.0
2	i	77	ALA	4.0
1	C	401	ASN	4.0
1	O	585	GLU	4.0
1	Q	364	ASP	4.0
1	R	423	GLU	4.0
1	V	237	ASP	4.0
1	G	253	ASP	4.0
1	K	215	ASP	4.0
2	i	121	GLU	4.0
1	D	310	VAL	4.0
1	P	410	SER	4.0
1	D	264	ILE	4.0
1	H	356	ILE	4.0
2	e	130	SER	4.0
1	V	183	GLY	4.0
1	K	218	GLN	4.0
2	o	67	PRO	4.0
1	P	436	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
2	e	147	ASN	4.0
1	F	206	ASP	4.0
1	R	410	SER	4.0
1	W	261	SER	4.0
1	B	549	TYR	4.0
1	I	376	ARG	4.0
2	Y	62	GLY	4.0
2	e	65	THR	4.0
2	g	115	THR	4.0
2	j	110	ALA	4.0
1	B	537	GLU	4.0
1	T	59	VAL	4.0
1	M	541	LYS	4.0
1	P	203	ASN	4.0
1	D	30	LYS	4.0
2	k	124	LYS	4.0
2	l	65	ASN	4.0
2	u	124	LYS	4.0
1	M	33	LEU	4.0
1	I	287	LEU	4.0
2	l	114	LEU	4.0
2	f	106	LEU	4.0
1	J	191	TYR	4.0
1	S	5	GLU	4.0
2	f	108	ALA	4.0
1	G	282	THR	4.0
1	J	115	VAL	4.0
2	o	19	VAL	4.0
1	U	459	ARG	4.0
1	V	7	ARG	4.0
1	N	256	ASP	4.0
1	R	32	ASP	4.0
1	G	383	ASP	4.0
1	J	89	ASP	4.0
2	g	84	LEU	4.0
1	O	189	GLU	4.0
1	F	529	GLN	4.0
2	f	43	GLN	4.0
1	Q	49	THR	4.0
1	I	63	VAL	4.0
1	V	34	PHE	4.0
1	B	569	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	577	ILE	4.0
1	O	42	ASP	4.0
1	L	253	ASP	4.0
1	C	563	LYS	3.9
1	J	311	GLU	4.0
2	q	99	ALA	3.9
2	s	98	GLU	4.0
1	Q	207	TRP	3.9
1	D	64	VAL	3.9
1	X	386	THR	3.9
1	B	155	HIS	3.9
1	B	344	THR	3.9
1	I	172	HIS	3.9
2	l	17	LEU	3.9
1	S	556	TYR	3.9
1	T	192	ASP	3.9
1	W	58	ASP	3.9
1	B	257	ASP	3.9
1	C	288	LYS	3.9
1	E	337	ASN	3.9
1	H	196	ASP	3.9
1	Q	259	ALA	3.9
1	R	254	VAL	3.9
1	S	239	VAL	3.9
1	W	184	TRP	3.9
1	D	506	VAL	3.9
2	Z	30	SER	3.9
2	f	69	PHE	3.9
1	R	217	ILE	3.9
1	W	538	LEU	3.9
1	K	155	HIS	3.9
1	K	535	ILE	3.9
2	g	33	THR	3.9
1	U	277	TYR	3.9
1	V	590	GLN	3.9
1	A	458	ARG	3.9
1	C	314	GLU	3.9
1	C	561	ASP	3.9
1	G	433	ASP	3.9
1	A	425	VAL	3.9
1	A	574	LYS	3.9
1	I	262	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	E	131	ASP	3.9
2	g	126	GLN	3.9
1	S	582	LYS	3.9
2	s	66	PRO	3.9
1	W	13	SER	3.9
1	J	13	SER	3.9
2	a	145	SER	3.9
1	O	386	THR	3.9
1	D	591	GLN	3.9
1	H	309	PHE	3.9
1	T	51	LEU	3.9
1	H	394	ASN	3.9
1	K	92	ASP	3.9
1	K	141	ASN	3.9
1	N	249	ARG	3.9
1	K	19	TRP	3.9
1	P	589	GLU	3.9
1	R	160	SER	3.9
1	I	160	SER	3.9
1	U	571	TYR	3.9
2	a	67	TYR	3.9
1	V	425	VAL	3.9
1	A	225	VAL	3.9
1	F	598	GLN	3.9
1	F	599	ALA	3.9
1	H	497	VAL	3.9
1	J	420	VAL	3.9
1	J	516	CYS	3.9
1	U	554	LEU	3.9
1	E	570	ASP	3.9
1	G	61	ARG	3.9
2	e	31	ASP	3.9
1	N	388	PRO	3.9
1	A	147	GLU	3.9
1	C	564	GLY	3.9
2	r	53	GLY	3.9
1	G	39	SER	3.9
2	s	95	TYR	3.9
1	O	416	ALA	3.9
1	S	507	LEU	3.9
1	T	234	ILE	3.9
1	F	283	CYS	3.9

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Mol	Chain	Res	Type	RSRZ
1	S	337	ASN	3.9
1	V	196	ASP	3.9
1	P	41	TRP	3.9
1	P	75	PRO	3.9
1	E	401	ASN	3.9
2	Y	66	GLY	3.9
1	P	187	PHE	3.9
1	X	191	TYR	3.9
1	C	187	PHE	3.9
2	h	108	ALA	3.9
1	S	384	LEU	3.9
1	D	234	ILE	3.9
1	E	284	THR	3.9
1	P	199	PRO	3.9
1	S	197	ASP	3.9
1	T	337	ASN	3.9
1	V	295	GLY	3.9
1	J	337	ASN	3.9
1	J	589	GLU	3.9
1	K	583	LYS	3.9
1	R	458	ARG	3.9
1	M	107	ALA	3.9
1	P	408	ALA	3.9
1	I	98	TYR	3.9
1	V	180	SER	3.9
1	M	202	GLN	3.9
1	B	552	LEU	3.9
1	I	236	GLN	3.9
1	U	534	GLU	3.9
1	G	9	GLU	3.9
1	P	215	ASP	3.9
2	i	47	ASP	3.9
1	O	269	ARG	3.9
1	S	207	TRP	3.9
1	O	12	LEU	3.9
1	V	235	TYR	3.9
1	J	259	ALA	3.9
1	K	536	LEU	3.9
2	n	101	ALA	3.9
1	U	139	SER	3.9
1	V	136	SER	3.9
1	K	505	GLN	3.9

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Mol	Chain	Res	Type	RSRZ
1	Q	546	THR	3.9
1	J	344	THR	3.9
1	D	237	ASP	3.9
1	I	254	VAL	3.9
2	f	44	ASP	3.9
1	P	141	ASN	3.9
1	S	361	HIS	3.9
1	S	592	TRP	3.9
1	U	592	TRP	3.9
1	A	105	ASN	3.9
1	C	551	LEU	3.9
2	k	115	TYR	3.9
1	V	160	SER	3.9
1	W	530	GLN	3.9
1	B	109	ILE	3.9
1	M	462	GLU	3.9
1	B	396	GLU	3.9
1	E	590	GLN	3.9
2	r	64	GLU	3.9
2	t	7	GLY	3.9
2	d	78	GLU	3.9
1	U	284	THR	3.8
1	M	129	VAL	3.8
1	O	506	VAL	3.8
1	P	169	ASP	3.8
1	R	385	PRO	3.8
1	A	498	ASP	3.8
1	F	62	PRO	3.8
1	L	186	ASP	3.8
1	M	401	ASN	3.8
1	O	252	LYS	3.8
1	P	195	ALA	3.8
1	R	90	ALA	3.8
1	S	205	ASN	3.8
1	V	539	LEU	3.8
1	L	424	ALA	3.8
1	L	444	LEU	3.8
2	t	75	LEU	3.8
2	b	96	LEU	3.8
2	b	129	ILE	3.8
2	d	54	ALA	3.8
1	U	135	GLN	3.8

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Mol	Chain	Res	Type	RSRZ
1	V	495	GLU	3.8
1	J	495	GLU	3.8
2	j	24	ARG	3.8
2	j	107	GLU	3.8
1	I	410	SER	3.8
1	O	254	VAL	3.8
1	U	409	THR	3.8
1	B	558	THR	3.8
1	G	216	THR	3.8
1	H	35	PHE	3.8
1	I	130	THR	3.8
1	N	48	TYR	3.8
1	Q	134	ASP	3.8
1	N	203	ASN	3.8
1	X	411	ALA	3.8
1	X	416	ALA	3.8
1	S	555	GLN	3.8
1	V	525	GLN	3.8
1	W	564	GLY	3.8
1	W	575	GLN	3.8
1	C	327	GLN	3.8
1	C	578	GLN	3.8
1	L	14	ARG	3.8
2	l	7	GLY	3.8
1	L	247	PHE	3.8
1	E	560	LEU	3.8
1	G	455	THR	3.8
1	N	32	ASP	3.8
1	V	325	ASP	3.8
1	L	421	ASP	3.8
2	Z	75	PRO	3.8
1	U	19	TRP	3.8
2	j	78	GLU	3.8
1	N	387	GLN	3.8
1	U	387	GLN	3.8
1	G	375	ASN	3.8
1	H	141	ASN	3.8
1	J	202	GLN	3.8
1	L	141	ASN	3.8
1	Q	600	LYS	3.8
1	K	33	LEU	3.8
1	L	335	SER	3.8

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Mol	Chain	Res	Type	RSRZ
2	v	10	VAL	3.8
2	h	89	VAL	3.8
1	M	27	ARG	3.8
1	M	283	CYS	3.8
1	O	407	ALA	3.8
1	R	271	ILE	3.8
1	A	264	ILE	3.8
1	O	519	ASP	3.8
1	U	367	ASP	3.8
1	C	28	GLU	3.8
1	F	217	ILE	3.8
1	J	195	ALA	3.8
2	s	96	ALA	3.8
2	Z	63	ILE	3.8
2	Z	17	ASP	3.8
2	c	50	GLU	3.8
1	J	183	GLY	3.8
1	M	426	ASN	3.8
1	J	233	PHE	3.8
1	B	287	LEU	3.8
1	Q	139	SER	3.8
1	F	168	SER	3.8
1	X	147	GLU	3.8
1	B	230	GLU	3.8
1	F	596	ALA	3.8
2	m	92	ALA	3.8
2	n	126	ALA	3.8
2	g	113	ILE	3.8
1	Q	516	CYS	3.8
1	R	186	ASP	3.8
2	s	53	GLY	3.8
1	D	236	GLN	3.8
1	P	552	LEU	3.8
1	X	559	LEU	3.8
1	W	541	LYS	3.8
1	K	195	ALA	3.8
2	c	32	ALA	3.8
1	M	398	PRO	3.8
1	O	584	PRO	3.8
2	a	16	GLY	3.8
1	N	451	ASP	3.8
1	U	550	GLN	3.8

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Mol	Chain	Res	Type	RSRZ
1	E	249	ARG	3.8
1	G	327	GLN	3.8
2	k	73	HIS	3.8
1	R	389	LEU	3.8
1	L	453	LEU	3.8
2	g	74	ASN	3.8
1	X	595	GLU	3.8
1	U	424	ALA	3.8
1	I	356	ILE	3.8
1	L	281	ILE	3.8
1	C	48	TYR	3.8
1	C	160	SER	3.8
2	i	97	ALA	3.8
1	M	34	PHE	3.8
1	U	249	ARG	3.8
1	F	88	PRO	3.8
2	k	67	PRO	3.8
1	U	41	TRP	3.8
1	V	236	GLN	3.8
1	C	196	ASP	3.8
1	E	20	THR	3.8
1	J	250	ASP	3.8
2	b	123	LEU	3.8
2	i	92	VAL	3.8
1	Q	572	ALA	3.8
1	P	513	ARG	3.8
1	V	200	SER	3.8
1	D	200	SER	3.8
2	q	78	SER	3.8
1	O	559	LEU	3.8
1	Q	601	GLN	3.8
1	I	33	LEU	3.8
1	I	574	LYS	3.8
1	K	498	ASP	3.8
2	k	102	LYS	3.8
1	D	588	GLU	3.8
1	I	5	GLU	3.8
2	i	55	GLU	3.8
1	J	510	ILE	3.8
2	o	138	ASN	3.8
1	M	591	GLN	3.8
1	P	547	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	U	270	GLN	3.8
1	A	47	GLN	3.8
1	G	52	GLN	3.8
1	G	214	GLN	3.8
1	H	63	VAL	3.8
1	I	547	PRO	3.8
1	K	552	LEU	3.8
2	e	75	PRO	3.8
2	f	90	SER	3.8
2	j	26	LEU	3.8
1	M	216	THR	3.8
1	O	264	ILE	3.8
1	S	50	THR	3.8
1	T	534	GLU	3.8
1	C	281	ILE	3.8
2	p	53	GLY	3.8
2	e	83	GLY	3.8
2	n	140	PHE	3.8
1	H	299	PRO	3.8
1	H	384	LEU	3.8
2	f	68	VAL	3.8
1	S	523	SER	3.8
1	J	381	SER	3.8
1	J	399	GLN	3.8
1	G	296	GLU	3.8
2	b	121	GLU	3.8
2	r	71	ASP	3.8
1	F	417	THR	3.8
1	M	267	ALA	3.8
1	N	580	GLY	3.8
1	E	533	ALA	3.8
1	G	183	GLY	3.8
1	H	90	ALA	3.8
1	H	419	GLY	3.8
2	r	135	GLY	3.8
2	d	83	GLY	3.8
2	e	45	ALA	3.8
1	X	337	ASN	3.7
1	I	301	VAL	3.7
2	k	19	VAL	3.7
1	Q	22	SER	3.7
1	C	26	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	G	249	ARG	3.7
1	H	40	GLN	3.7
1	L	227	GLU	3.7
1	X	383	ASP	3.7
1	C	518	THR	3.7
1	Q	233	PHE	3.7
1	W	209	PHE	3.7
1	E	263	PHE	3.7
1	N	239	VAL	3.7
1	T	64	VAL	3.7
1	W	445	GLU	3.7
1	A	529	GLN	3.7
1	C	379	GLU	3.7
1	T	582	LYS	3.7
1	V	582	LYS	3.7
1	D	587	PRO	3.7
1	D	381	SER	3.7
1	F	139	SER	3.7
1	J	200	SER	3.7
1	L	283	CYS	3.7
2	Z	100	ILE	3.7
2	i	90	SER	3.7
1	T	19	TRP	3.7
1	B	572	ALA	3.7
1	E	382	GLY	3.7
1	F	352	TRP	3.7
1	J	188	ALA	3.7
1	J	192	ASP	3.7
1	R	216	THR	3.7
1	K	323	THR	3.7
2	e	53	MET	3.7
2	Z	92	VAL	3.7
1	M	578	GLN	3.7
1	T	600	LYS	3.7
1	V	290	LYS	3.7
1	B	327	GLN	3.7
2	u	117	GLN	3.7
2	g	58	GLN	3.7
1	M	570	ASP	3.7
1	P	42	ASP	3.7
1	P	383	ASP	3.7
1	R	197	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	S	194	ASP	3.7
1	S	220	ALA	3.7
2	k	53	GLY	3.7
1	T	237	ASP	3.7
1	W	222	PHE	3.7
1	J	368	ASP	3.7
1	L	134	ASP	3.7
2	s	119	ALA	3.7
1	S	571	TYR	3.7
1	T	60	VAL	3.7
1	B	372	TYR	3.7
1	B	422	THR	3.7
1	B	553	LEU	3.7
1	E	49	THR	3.7
1	M	122	GLY	3.7
1	M	580	GLY	3.7
1	F	545	GLY	3.7
1	G	152	ALA	3.7
1	K	168	SER	3.7
1	K	500	ALA	3.7
2	k	136	SER	3.7
2	p	122	ARG	3.7
1	R	265	LYS	3.7
1	T	554	LEU	3.7
1	W	341	VAL	3.7
1	J	163	LYS	3.7
1	L	364	ASP	3.7
2	b	103	ASP	3.7
1	Q	462	GLU	3.7
1	N	100	THR	3.7
1	J	409	THR	3.7
2	k	26	THR	3.7
1	T	6	ASN	3.7
1	B	118	GLN	3.7
1	B	508	ASN	3.7
1	G	203	ASN	3.7
1	J	141	ASN	3.7
2	n	138	ASN	3.7
2	t	54	ILE	3.7
1	N	180	SER	3.7
1	D	207	TRP	3.7
1	D	560	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
2	b	46	VAL	3.7
1	N	383	ASP	3.7
1	N	445	GLU	3.7
1	D	566	GLU	3.7
1	I	534	GLU	3.7
1	L	5	GLU	3.7
2	q	8	ASP	3.7
2	s	94	ASP	3.7
2	d	70	SER	3.7
1	P	11	ILE	3.7
1	S	293	ILE	3.7
1	M	163	LYS	3.7
1	C	252	LYS	3.7
1	H	55	GLY	3.7
2	a	83	GLY	3.7
2	j	83	GLY	3.7
1	J	369	TYR	3.7
1	D	196	ASP	3.7
2	c	41	SER	3.7
1	N	541	LYS	3.7
1	P	446	THR	3.7
1	T	583	LYS	3.7
1	Q	34	PHE	3.7
1	D	562	GLY	3.7
1	I	291	GLN	3.7
2	j	117	LYS	3.7
1	U	596	ALA	3.7
1	V	204	PRO	3.7
1	W	543	PRO	3.7
1	X	125	ALA	3.7
1	X	232	ALA	3.7
1	E	552	LEU	3.7
2	Y	135	ALA	3.7
1	Q	24	GLU	3.7
1	Q	509	ASP	3.7
1	T	279	SER	3.7
1	H	261	SER	3.7
2	l	15	ARG	3.7
2	l	77	SER	3.7
2	j	30	SER	3.7
1	O	505	GLN	3.7
1	U	55	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	U	209	PHE	3.7
1	X	262	GLY	3.7
1	D	365	GLY	3.7
2	k	149	PHE	3.7
2	Y	126	GLN	3.7
2	b	60	GLY	3.7
1	F	193	LEU	3.7
2	f	115	THR	3.7
1	Q	439	ASN	3.7
1	Q	497	VAL	3.7
1	U	105	ASN	3.7
1	W	60	VAL	3.7
1	X	331	ASN	3.7
1	B	220	ALA	3.7
1	I	143	VAL	3.7
1	J	423	GLU	3.7
2	t	144	ASN	3.7
2	b	142	PRO	3.7
1	N	367	ASP	3.7
1	S	460	ASP	3.7
1	T	245	SER	3.7
1	U	58	ASP	3.7
1	X	561	ASP	3.7
1	G	261	SER	3.7
1	Q	450	GLN	3.7
1	V	73	GLN	3.7
1	D	580	GLY	3.7
1	G	247	PHE	3.7
1	R	425	VAL	3.7
1	S	94	LEU	3.7
1	X	586	THR	3.7
1	E	17	ALA	3.7
1	I	129	VAL	3.7
2	o	29	GLU	3.7
2	q	37	VAL	3.7
1	A	366	ASN	3.7
1	F	313	LYS	3.7
1	G	532	ARG	3.7
2	Y	82	HIS	3.7
2	f	39	PRO	3.7
1	O	206	ASP	3.7
1	Q	460	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	U	237	ASP	3.7
1	W	151	SER	3.7
1	B	279	SER	3.7
1	C	42	ASP	3.7
1	F	359	PHE	3.7
1	H	186	ASP	3.7
2	c	93	PHE	3.7
1	I	397	VAL	3.7
1	K	221	GLU	3.7
1	I	108	LYS	3.7
1	L	232	ALA	3.7
2	e	117	LYS	3.7
2	j	25	LYS	3.7
1	R	141	ASN	3.7
1	S	401	ASN	3.7
1	L	366	ASN	3.7
2	o	93	PRO	3.7
2	o	133	PRO	3.7
1	P	207	TRP	3.7
1	R	11	ILE	3.7
1	D	19	TRP	3.7
1	J	198	ILE	3.7
1	E	194	ASP	3.6
1	U	569	ARG	3.6
1	B	565	VAL	3.6
1	C	381	SER	3.6
1	E	548	GLU	3.6
1	J	145	ARG	3.6
2	q	40	LEU	3.6
2	d	84	LEU	3.6
1	L	228	LYS	3.6
1	L	296	GLU	3.6
2	a	50	GLU	3.6
2	g	68	VAL	3.6
2	j	90	SER	3.6
2	j	145	SER	3.6
1	M	213	THR	3.6
1	P	426	ASN	3.6
1	B	177	HIS	3.6
1	L	74	ASN	3.6
2	q	54	ILE	3.6
1	B	418	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	W	200	SER	3.6
1	A	397	VAL	3.6
1	C	589	GLU	3.6
1	E	202	GLN	3.6
1	H	581	VAL	3.6
1	I	327	GLN	3.6
1	N	200	SER	3.6
1	Q	408	ALA	3.6
1	B	29	ALA	3.6
2	b	30	SER	3.6
1	C	50	THR	3.6
1	D	353	PRO	3.6
1	E	293	ILE	3.6
1	K	204	PRO	3.6
1	S	31	ASN	3.6
1	B	203	ASN	3.6
1	C	532	ARG	3.6
1	F	374	LEU	3.6
1	K	499	LEU	3.6
1	L	461	GLY	3.6
1	M	319	VAL	3.6
1	D	211	TRP	3.6
1	F	341	VAL	3.6
1	H	379	GLU	3.6
1	K	355	GLN	3.6
2	p	10	VAL	3.6
2	e	58	GLN	3.6
1	I	192	ASP	3.6
1	J	416	ALA	3.6
2	p	39	ASP	3.6
1	Q	10	SER	3.6
1	X	279	SER	3.6
2	g	88	ALA	3.6
2	j	45	ALA	3.6
2	j	91	ALA	3.6
1	I	447	TYR	3.6
1	I	549	TYR	3.6
1	H	88	PRO	3.6
2	h	100	ILE	3.6
1	O	205	ASN	3.6
1	R	203	ASN	3.6
1	U	560	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	J	172	HIS	3.6
2	c	115	THR	3.6
1	E	595	GLU	3.6
2	s	86	ASN	3.6
1	Q	93	VAL	3.6
1	X	142	GLN	3.6
1	J	320	VAL	3.6
2	i	58	GLN	3.6
1	O	451	ASP	3.6
1	A	166	ASP	3.6
1	I	533	ALA	3.6
1	J	43	ASP	3.6
2	j	97	ALA	3.6
1	M	108	LYS	3.6
1	O	187	PHE	3.6
1	R	48	TYR	3.6
2	m	95	TYR	3.6
1	T	55	GLY	3.6
1	P	462	GLU	3.6
1	B	543	PRO	3.6
1	O	375	ASN	3.6
1	P	420	VAL	3.6
1	U	7	ARG	3.6
1	C	582	LYS	3.6
1	H	163	LYS	3.6
2	q	52	LYS	3.6
2	j	128	ALA	3.6
1	I	250	ASP	3.6
1	F	35	PHE	3.6
1	N	584	PRO	3.6
1	R	587	PRO	3.6
1	T	395	PRO	3.6
1	U	396	GLU	3.6
1	A	70	GLU	3.6
1	C	548	GLU	3.6
1	U	173	CYS	3.6
1	U	518	THR	3.6
1	A	239	VAL	3.6
1	T	578	GLN	3.6
1	B	269	ARG	3.6
1	T	92	ASP	3.6
1	V	293	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	E	233	PHE	3.6
1	K	144	ILE	3.6
2	h	80	ASP	3.6
1	U	160	SER	3.6
1	U	227	GLU	3.6
1	H	559	LEU	3.6
1	J	262	GLY	3.6
1	L	10	SER	3.6
2	e	96	LEU	3.6
2	j	70	SER	3.6
1	G	565	VAL	3.6
2	u	147	HIS	3.6
2	Z	68	VAL	3.6
1	O	50	THR	3.6
1	I	174	THR	3.6
2	h	24	ARG	3.6
2	p	54	ILE	3.6
1	P	339	ASP	3.6
1	P	507	LEU	3.6
1	S	512	GLY	3.6
1	X	423	GLU	3.6
1	A	444	LEU	3.6
1	B	585	GLU	3.6
1	G	58	ASP	3.6
2	s	40	LEU	3.6
1	T	254	VAL	3.6
1	T	343	ARG	3.6
1	C	458	ARG	3.6
2	k	90	ARG	3.6
1	U	399	GLN	3.6
1	W	386	THR	3.6
1	F	294	ALA	3.6
1	K	138	THR	3.6
1	D	255	ILE	3.6
1	K	74	ASN	3.6
1	M	191	TYR	3.6
1	P	512	GLY	3.6
1	S	540	GLY	3.6
2	t	25	LEU	3.6
1	N	581	VAL	3.6
1	D	208	VAL	3.6
1	H	27	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
2	k	71	ASP	3.6
2	n	39	ASP	3.6
2	t	62	ASP	3.6
2	r	139	SER	3.6
1	Q	41	TRP	3.6
1	A	217	ILE	3.6
1	M	445	GLU	3.6
1	Q	576	LEU	3.6
1	B	221	GLU	3.6
1	H	98	TYR	3.6
1	H	112	ASN	3.6
2	r	145	GLU	3.6
2	i	123	LEU	3.6
1	L	27	ARG	3.6
2	h	67	TYR	3.6
1	M	320	VAL	3.6
1	M	561	ASP	3.6
1	M	594	VAL	3.6
1	P	364	ASP	3.6
1	H	215	ASP	3.6
1	I	565	VAL	3.6
2	c	19	VAL	3.6
1	G	200	SER	3.6
2	k	66	PRO	3.6
2	e	145	SER	3.6
1	W	25	ALA	3.6
1	C	304	PHE	3.6
1	H	350	PHE	3.6
2	c	58	GLN	3.6
1	T	49	THR	3.6
1	B	100	THR	3.6
2	m	114	LEU	3.6
1	B	439	ASN	3.6
1	S	43	ASP	3.6
1	V	378	ASP	3.6
1	X	173	CYS	3.6
1	B	339	ASP	3.6
1	N	291	GLN	3.6
1	Q	13	SER	3.6
1	J	243	PRO	3.6
2	f	150	PRO	3.6
1	W	560	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	384	LEU	3.5
1	D	5	GLU	3.5
2	Z	18	LEU	3.5
1	K	541	LYS	3.5
1	L	346	LYS	3.5
2	m	27	ASP	3.5
2	m	50	ASP	3.5
1	M	327	GLN	3.5
1	M	530	GLN	3.5
1	M	555	GLN	3.5
1	B	187	PHE	3.5
1	C	359	PHE	3.5
1	U	224	GLU	3.5
1	U	230	GLU	3.5
1	E	39	SER	3.5
1	I	530	GLN	3.5
1	L	204	PRO	3.5
2	b	136	PRO	3.5
1	O	425	VAL	3.5
2	h	56	TRP	3.5
1	R	452	ASN	3.5
2	t	22	ASP	3.5
1	N	299	PRO	3.5
1	O	537	GLU	3.5
1	O	587	PRO	3.5
1	U	536	LEU	3.5
1	H	577	ILE	3.5
1	P	502	GLY	3.5
1	W	262	GLY	3.5
1	I	243	PRO	3.5
1	J	547	PRO	3.5
2	r	130	SER	3.5
2	u	85	HIS	3.5
1	C	190	LYS	3.5
2	g	104	TYR	3.5
2	i	124	TYR	3.5
1	R	31	ASN	3.5
1	R	557	PHE	3.5
1	U	573	ASN	3.5
1	C	377	THR	3.5
1	V	247	PHE	3.5
1	B	263	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	J	161	ASN	3.5
1	M	356	ILE	3.5
1	W	110	ALA	3.5
1	A	79	LEU	3.5
1	C	134	ASP	3.5
1	C	408	ALA	3.5
1	D	271	ILE	3.5
1	J	333	ILE	3.5
2	o	79	ALA	3.5
2	u	41	GLU	3.5
2	e	107	GLU	3.5
2	j	73	GLU	3.5
1	P	318	GLY	3.5
1	W	562	GLY	3.5
1	W	584	PRO	3.5
1	T	581	VAL	3.5
1	J	319	VAL	3.5
1	X	249	ARG	3.5
1	E	48	TYR	3.5
1	R	15	PHE	3.5
1	R	182	ASN	3.5
1	D	50	THR	3.5
1	D	503	GLU	3.5
1	C	250	ASP	3.5
1	C	400	ALA	3.5
1	E	456	ALA	3.5
1	P	181	GLN	3.5
2	o	49	GLN	3.5
2	s	74	GLY	3.5
2	d	36	ASP	3.5
1	N	62	PRO	3.5
1	G	361	HIS	3.5
2	v	147	HIS	3.5
1	X	98	TYR	3.5
1	Q	209	PHE	3.5
1	B	449	PHE	3.5
2	c	155	TRP	3.5
1	H	342	ALA	3.5
1	L	174	THR	3.5
2	o	96	ALA	3.5
2	h	63	ILE	3.5
2	j	84	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	O	215	ASP	3.5
1	X	525	GLN	3.5
1	C	378	ASP	3.5
1	D	26	ARG	3.5
2	t	141	PRO	3.5
2	Z	138	PRO	3.5
2	d	141	MET	3.5
1	I	201	PHE	3.5
1	J	22	SER	3.5
1	T	553	LEU	3.5
1	L	193	LEU	3.5
2	t	41	GLU	3.5
1	H	431	ALA	3.5
1	L	251	ILE	3.5
2	j	96	LEU	3.5
1	X	402	ALA	3.5
1	P	7	ARG	3.5
1	R	496	VAL	3.5
1	W	459	ARG	3.5
1	D	425	VAL	3.5
1	D	458	ARG	3.5
1	V	253	ASP	3.5
1	H	597	GLN	3.5
1	J	186	ASP	3.5
1	M	556	TYR	3.5
1	B	388	PRO	3.5
2	b	76	PRO	3.5
1	F	245	SER	3.5
1	F	247	PHE	3.5
2	s	124	LYS	3.5
2	Z	38	GLU	3.5
1	T	285	ALA	3.5
1	T	459	ARG	3.5
1	K	29	ALA	3.5
1	U	505	GLN	3.5
1	N	16	ASP	3.5
1	N	205	ASN	3.5
1	W	516	CYS	3.5
1	D	323	THR	3.5
1	H	31	ASN	3.5
2	u	86	ASN	3.5
1	N	137	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	P	224	GLU	3.5
1	S	185	GLU	3.5
1	B	247	PHE	3.5
1	W	51	LEU	3.5
1	K	423	GLU	3.5
2	q	9	LEU	3.5
2	f	49	LEU	3.5
2	h	55	GLU	3.5
1	R	416	ALA	3.5
1	U	335	SER	3.5
1	W	533	ALA	3.5
1	D	152	ALA	3.5
1	E	207	TRP	3.5
1	G	520	VAL	3.5
1	L	437	GLN	3.5
1	O	452	ASN	3.5
1	C	140	ASN	3.5
1	E	331	ASN	3.5
1	F	191	TYR	3.5
2	m	60	PHE	3.5
2	f	81	ASP	3.5
1	E	551	LEU	3.5
1	I	264	ILE	3.5
2	e	64	ILE	3.5
2	i	100	ILE	3.5
2	d	51	ALA	3.5
2	e	86	SER	3.5
1	M	549	TYR	3.5
1	O	312	ASP	3.5
1	P	439	ASN	3.5
1	P	445	GLU	3.5
1	R	495	GLU	3.5
1	S	514	TYR	3.5
1	S	537	GLU	3.5
1	A	336	PHE	3.5
1	U	353	PRO	3.5
1	B	361	HIS	3.5
1	C	311	GLU	3.5
1	I	587	PRO	3.5
2	o	145	GLU	3.5
1	P	541	LYS	3.5
1	S	86	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	461	GLY	3.5
1	L	494	ALA	3.5
2	g	22	ALA	3.5
1	J	335	SER	3.5
1	M	218	GLN	3.5
1	S	530	GLN	3.5
1	T	236	GLN	3.5
1	B	529	GLN	3.5
1	J	598	GLN	3.5
1	Q	552	LEU	3.5
1	C	534	GLU	3.5
1	H	462	GLU	3.5
1	L	336	PHE	3.5
1	A	455	THR	3.4
1	B	169	ASP	3.4
1	B	443	ASP	3.4
1	D	570	ASP	3.4
2	Y	47	ASP	3.4
2	b	112	ILE	3.4
1	S	208	VAL	3.4
1	P	437	GLN	3.4
1	E	537	GLU	3.4
1	L	389	LEU	3.4
1	X	388	PRO	3.4
1	G	112	ASN	3.4
1	G	289	ASP	3.4
1	H	238	PRO	3.4
1	J	166	ASP	3.4
1	L	140	ASN	3.4
2	t	63	ASP	3.4
2	i	143	THR	3.4
1	W	56	GLN	3.4
1	F	222	PHE	3.4
1	E	553	LEU	3.4
1	F	576	LEU	3.4
1	K	178	SER	3.4
2	Z	107	GLU	3.4
2	b	58	GLN	3.4
1	T	571	TYR	3.4
1	U	164	LEU	3.4
1	L	514	TYR	3.4
1	P	535	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	N	257	ASP	3.4
1	N	407	ALA	3.4
1	O	546	THR	3.4
1	P	29	ALA	3.4
1	S	195	ALA	3.4
1	T	161	ASN	3.4
1	X	312	ASP	3.4
1	G	502	GLY	3.4
2	m	13	ALA	3.4
2	q	42	ALA	3.4
2	s	56	THR	3.4
2	Z	81	ASP	3.4
2	a	109	THR	3.4
2	h	97	ALA	3.4
1	N	591	GLN	3.4
1	A	449	PHE	3.4
1	V	193	LEU	3.4
1	C	52	GLN	3.4
1	G	449	PHE	3.4
2	e	93	PHE	3.4
1	F	10	SER	3.4
2	i	41	SER	3.4
1	R	340	ILE	3.4
1	G	300	ILE	3.4
1	J	11	ILE	3.4
1	L	577	ILE	3.4
2	g	27	GLY	3.4
1	M	250	ASP	3.4
1	N	357	ALA	3.4
1	R	312	ASP	3.4
1	U	232	ALA	3.4
1	W	112	ASN	3.4
1	D	408	ALA	3.4
2	n	96	ALA	3.4
1	J	20	THR	3.4
1	N	563	LYS	3.4
1	U	24	GLU	3.4
1	W	537	GLU	3.4
1	X	28	GLU	3.4
2	Z	69	PHE	3.4
1	V	184	TRP	3.4
2	q	17	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
2	h	96	LEU	3.4
1	J	517	TYR	3.4
1	M	199	PRO	3.4
1	U	150	HIS	3.4
1	V	276	VAL	3.4
1	F	239	VAL	3.4
1	H	115	VAL	3.4
1	H	565	VAL	3.4
1	I	602	GLY	3.4
2	f	125	LYS	3.4
1	X	189	GLU	3.4
1	A	311	GLU	3.4
1	L	436	ASN	3.4
2	t	122	ARG	3.4
1	P	549	TYR	3.4
1	H	447	TYR	3.4
1	V	526	SER	3.4
1	B	154	SER	3.4
1	F	180	SER	3.4
2	p	59	VAL	3.4
2	f	15	LYS	3.4
1	H	522	PRO	3.4
1	M	256	ASP	3.4
1	D	169	ASP	3.4
1	F	386	THR	3.4
2	i	74	ASN	3.4
1	M	264	ILE	3.4
1	Q	202	GLN	3.4
1	X	124	GLY	3.4
2	j	56	TRP	3.4
2	n	80	VAL	3.4
1	B	39	SER	3.4
1	N	595	GLU	3.4
1	P	204	PRO	3.4
1	A	187	PHE	3.4
1	J	524	PHE	3.4
2	b	55	GLU	3.4
1	C	289	ASP	3.4
1	J	51	LEU	3.4
2	e	81	ASP	3.4
1	U	434	THR	3.4
1	X	598	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	X	601	GLN	3.4
1	A	578	GLN	3.4
1	F	426	ASN	3.4
1	K	6	ASN	3.4
2	d	95	ASN	3.4
1	F	514	TYR	3.4
1	G	315	VAL	3.4
2	l	148	TYR	3.4
1	M	90	ALA	3.4
1	Q	390	ALA	3.4
1	A	247	PHE	3.4
1	A	379	GLU	3.4
1	D	35	PHE	3.4
1	E	57	PHE	3.4
1	H	151	SER	3.4
2	o	41	GLU	3.4
1	V	499	LEU	3.4
1	H	587	PRO	3.4
1	P	18	ASP	3.4
1	Q	270	GLN	3.4
1	T	573	ASN	3.4
1	E	216	THR	3.4
1	I	508	ASN	3.4
1	F	44	TRP	3.4
2	v	148	TYR	3.4
2	h	124	TYR	3.4
1	T	26	ARG	3.4
1	G	304	PHE	3.4
1	H	572	ALA	3.4
1	I	107	ALA	3.4
1	J	201	PHE	3.4
2	p	98	GLU	3.4
1	R	526	SER	3.4
1	U	405	LEU	3.4
1	L	180	SER	3.4
2	v	30	PRO	3.4
2	e	150	PRO	3.4
1	N	356	ILE	3.4
1	U	109	ILE	3.4
1	B	590	GLN	3.4
1	K	134	ASP	3.4
2	l	104	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
2	n	35	ASP	3.4
1	O	235	TYR	3.4
1	G	447	TYR	3.4
1	Q	187	PHE	3.4
1	D	596	ALA	3.4
2	e	97	ALA	3.4
1	D	313	LYS	3.4
1	J	346	LYS	3.4
1	T	142	GLN	3.4
1	W	378	ASP	3.4
1	E	96	GLY	3.4
1	L	11	ILE	3.4
2	e	42	MET	3.4
1	E	343	ARG	3.4
1	J	570	ASP	3.4
1	K	339	ASP	3.4
1	K	511	ARG	3.4
1	K	594	VAL	3.4
2	j	131	ARG	3.4
1	A	282	THR	3.4
1	A	589	GLU	3.4
1	F	24	GLU	3.4
2	k	140	PHE	3.4
2	f	107	GLU	3.4
1	N	86	ALA	3.4
1	S	338	ALA	3.4
1	I	536	LEU	3.4
2	c	54	ALA	3.4
1	H	153	CYS	3.3
1	A	370	PRO	3.3
1	F	238	PRO	3.3
1	F	308	GLY	3.3
1	F	327	GLN	3.3
1	J	321	ARG	3.3
2	k	93	PRO	3.3
1	R	38	VAL	3.3
1	U	303	VAL	3.3
2	h	20	ARG	3.3
1	N	23	ASP	3.3
1	H	257	ASP	3.3
1	Q	20	THR	3.3
1	U	329	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	W	212	LEU	3.3
1	W	573	ASN	3.3
1	K	508	ASN	3.3
2	l	105	ALA	3.3
2	c	18	LEU	3.3
1	R	13	SER	3.3
1	V	575	GLN	3.3
1	B	180	SER	3.3
1	F	153	CYS	3.3
1	J	160	SER	3.3
1	F	537	GLU	3.3
1	J	229	LYS	3.3
1	Q	206	ASP	3.3
1	X	131	ASP	3.3
1	E	277	TYR	3.3
1	G	89	ASP	3.3
1	G	367	ASP	3.3
1	O	390	ALA	3.3
1	G	259	ALA	3.3
2	u	88	ALA	3.3
2	e	26	LEU	3.3
1	V	282	THR	3.3
1	E	573	ASN	3.3
1	J	254	VAL	3.3
2	q	57	GLY	3.3
1	P	360	GLU	3.3
1	M	132	TYR	3.3
1	E	10	SER	3.3
1	G	178	SER	3.3
2	c	38	GLU	3.3
1	N	285	ALA	3.3
1	N	509	ASP	3.3
1	P	23	ASP	3.3
1	J	173	CYS	3.3
1	Q	145	ARG	3.3
1	D	343	ARG	3.3
1	J	19	TRP	3.3
1	O	455	THR	3.3
1	F	248	LYS	3.3
1	N	308	GLY	3.3
1	Q	239	VAL	3.3
1	G	308	GLY	3.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	75	PRO	3.3
1	I	557	PHE	3.3
2	o	66	PRO	3.3
1	R	444	LEU	3.3
1	T	292	LEU	3.3
1	F	384	LEU	3.3
1	H	453	LEU	3.3
2	p	75	LEU	3.3
2	f	23	LEU	3.3
1	N	42	ASP	3.3
1	X	26	ARG	3.3
2	l	94	ASP	3.3
2	c	88	ALA	3.3
1	M	161	ASN	3.3
1	U	510	ILE	3.3
1	X	412	VAL	3.3
1	D	112	ASN	3.3
2	l	103	ILE	3.3
1	D	9	GLU	3.3
1	F	360	GLU	3.3
1	L	434	THR	3.3
1	R	449	PHE	3.3
1	I	15	PHE	3.3
1	U	299	PRO	3.3
1	W	48	TYR	3.3
1	X	75	PRO	3.3
1	C	137	PRO	3.3
1	L	363	TYR	3.3
2	o	15	ARG	3.3
2	p	34	GLN	3.3
1	P	500	ALA	3.3
1	C	279	SER	3.3
1	P	89	ASP	3.3
1	P	443	ASP	3.3
1	F	312	ASP	3.3
2	q	62	ASP	3.3
2	u	72	ASP	3.3
1	T	306	GLU	3.3
1	T	588	GLU	3.3
1	U	158	TRP	3.3
1	I	217	ILE	3.3
1	K	319	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	Q	508	ASN	3.3
1	W	439	ASN	3.3
1	A	182	ASN	3.3
2	s	142	ASN	3.3
2	t	86	ASN	3.3
2	a	147	ASN	3.3
2	t	76	ARG	3.3
2	j	69	PHE	3.3
1	C	556	TYR	3.3
1	E	291	GLN	3.3
1	G	48	TYR	3.3
1	H	400	ALA	3.3
2	b	145	SER	3.3
1	V	217	ILE	3.3
1	A	196	ASP	3.3
1	C	367	ASP	3.3
2	k	35	ASP	3.3
2	m	35	ASP	3.3
1	U	262	GLY	3.3
1	H	158	TRP	3.3
2	q	98	GLU	3.3
2	h	154	GLU	3.3
1	O	49	THR	3.3
1	S	541	LYS	3.3
1	J	542	THR	3.3
1	L	574	LYS	3.3
1	A	218	GLN	3.3
2	l	106	THR	3.3
1	E	232	ALA	3.3
1	K	62	PRO	3.3
2	g	77	ALA	3.3
1	N	151	SER	3.3
1	B	200	SER	3.3
1	X	27	ARG	3.3
1	B	315	VAL	3.3
1	F	16	ASP	3.3
1	H	445	GLU	3.3
1	L	18	ASP	3.3
2	j	99	ARG	3.3
1	R	252	LYS	3.3
1	A	15	PHE	3.3
1	C	405	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	I	313	LYS	3.3
1	I	384	LEU	3.3
1	U	177	HIS	3.3
1	C	422	THR	3.3
2	l	26	THR	3.3
1	H	267	ALA	3.3
1	M	115	VAL	3.3
1	O	255	ILE	3.3
1	B	293	ILE	3.3
1	W	30	LYS	3.3
1	B	314	GLU	3.3
2	c	130	SER	3.3
1	B	33	LEU	3.3
1	U	118	GLN	3.3
1	X	556	TYR	3.3
1	H	375	ASN	3.3
1	H	517	TYR	3.3
2	j	57	TYR	3.3
1	M	400	ALA	3.3
1	R	62	PRO	3.3
1	T	532	ARG	3.3
1	W	238	PRO	3.3
1	A	103	ARG	3.3
1	B	434	THR	3.3
1	C	86	ALA	3.3
1	G	81	ARG	3.3
1	J	106	THR	3.3
1	S	133	GLU	3.3
1	B	226	VAL	3.3
1	Q	368	ASP	3.3
1	R	536	LEU	3.3
1	S	51	LEU	3.3
1	A	389	LEU	3.3
1	D	256	ASP	3.3
2	l	9	LEU	3.3
2	p	32	SER	3.3
2	j	141	MET	3.3
1	S	26	ARG	3.3
1	T	65	ARG	3.3
2	p	31	GLN	3.3
1	U	454	ALA	3.3
1	Q	388	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	W	290	LYS	3.3
1	J	439	ASN	3.3
1	B	395	PRO	3.3
1	I	93	VAL	3.3
1	J	448	VAL	3.3
2	o	137	GLY	3.3
2	c	107	GLU	3.3
2	j	14	THR	3.3
1	N	131	ASP	3.3
1	S	136	SER	3.3
1	D	158	TRP	3.2
1	F	458	ARG	3.2
1	K	127	ARG	3.2
2	v	115	TYR	3.2
1	M	425	VAL	3.2
1	V	419	GLY	3.2
1	W	531	ASN	3.2
1	X	226	VAL	3.2
1	A	124	GLY	3.2
1	E	251	ILE	3.2
1	H	147	GLU	3.2
1	E	584	PRO	3.2
1	I	183	GLY	3.2
2	r	70	GLY	3.2
2	q	100	THR	3.2
2	g	136	PRO	3.2
1	C	593	LEU	3.2
1	S	289	ASP	3.2
1	T	101	ASP	3.2
2	v	102	LYS	3.2
2	h	103	ASP	3.2
1	L	184	TRP	3.2
1	R	259	ALA	3.2
1	U	357	ALA	3.2
1	F	285	ALA	3.2
1	I	40	GLN	3.2
2	l	23	ALA	3.2
2	f	94	HIS	3.2
2	i	60	GLY	3.2
1	Q	539	LEU	3.2
1	Q	573	ASN	3.2
1	J	74	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	377	THR	3.2
2	n	15	ARG	3.2
2	n	100	THR	3.2
1	P	556	TYR	3.2
1	T	191	TYR	3.2
1	U	494	ALA	3.2
1	A	279	SER	3.2
1	I	406	GLU	3.2
1	I	516	CYS	3.2
1	I	556	TYR	3.2
2	n	63	ASP	3.2
2	o	69	GLU	3.2
2	Z	101	ALA	3.2
1	M	15	PHE	3.2
1	Q	183	GLY	3.2
1	U	51	LEU	3.2
1	C	287	LEU	3.2
1	D	507	LEU	3.2
1	K	438	LEU	3.2
1	L	418	LEU	3.2
2	p	113	LEU	3.2
1	K	394	ASN	3.2
1	B	323	THR	3.2
1	I	106	THR	3.2
1	R	364	ASP	3.2
1	N	241	GLY	3.2
1	R	529	GLN	3.2
1	T	178	SER	3.2
1	U	526	SER	3.2
1	V	256	ASP	3.2
1	E	571	TYR	3.2
1	F	197	ASP	3.2
1	F	421	ASP	3.2
1	I	462	GLU	3.2
2	l	115	TYR	3.2
2	a	121	GLU	3.2
1	I	10	SER	3.2
1	J	449	PHE	3.2
1	G	539	LEU	3.2
1	F	105	ASN	3.2
1	X	133	GLU	3.2
1	Q	556	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	M	592	TRP	3.2
1	N	218	GLN	3.2
1	Q	272	LYS	3.2
1	V	294	ALA	3.2
1	B	325	ASP	3.2
1	C	256	ASP	3.2
1	G	341	VAL	3.2
1	H	234	ILE	3.2
2	l	95	TYR	3.2
2	v	68	ALA	3.2
1	T	507	LEU	3.2
1	F	39	SER	3.2
1	W	88	PRO	3.2
1	N	426	ASN	3.2
1	D	439	ASN	3.2
1	M	109	ILE	3.2
1	M	305	GLY	3.2
1	P	202	GLN	3.2
1	Q	461	GLY	3.2
1	U	602	GLY	3.2
1	C	497	VAL	3.2
1	G	363	TYR	3.2
1	I	342	ALA	3.2
2	l	10	VAL	3.2
2	h	120	LYS	3.2
1	O	92	ASP	3.2
1	F	453	LEU	3.2
1	C	155	HIS	3.2
1	M	583	LYS	3.2
1	N	585	GLU	3.2
1	I	375	ASN	3.2
1	K	504	LYS	3.2
2	e	95	ASN	3.2
1	S	387	GLN	3.2
1	U	455	THR	3.2
1	W	529	GLN	3.2
1	W	596	ALA	3.2
1	B	49	THR	3.2
1	B	455	THR	3.2
1	F	34	PHE	3.2
1	F	209	PHE	3.2
1	F	315	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	J	310	VAL	3.2
1	T	12	LEU	3.2
1	C	202	GLN	3.2
1	F	214	GLN	3.2
1	G	437	GLN	3.2
1	K	586	THR	3.2
2	k	36	ALA	3.2
2	g	157	TYR	3.2
1	M	237	ASP	3.2
2	f	48	ASP	3.2
1	X	150	HIS	3.2
1	R	230	GLU	3.2
1	B	103	ARG	3.2
1	B	120	GLU	3.2
1	D	423	GLU	3.2
1	T	319	VAL	3.2
1	N	214	GLN	3.2
1	R	530	GLN	3.2
1	U	402	ALA	3.2
1	W	6	ASN	3.2
1	W	203	ASN	3.2
1	I	59	VAL	3.2
1	G	357	ALA	3.2
2	t	91	ILE	3.2
2	u	82	ALA	3.2
2	a	54	ALA	3.2
2	b	66	GLY	3.2
1	L	142	GLN	3.2
2	a	58	GLN	3.2
1	P	250	ASP	3.2
1	R	257	ASP	3.2
1	C	443	ASP	3.2
2	h	59	ASP	3.2
1	O	515	GLU	3.2
1	U	172	HIS	3.2
1	V	162	SER	3.2
1	B	46	SER	3.2
1	I	9	GLU	3.2
1	R	34	PHE	3.2
1	T	535	ILE	3.2
1	I	338	ALA	3.2
2	m	48	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
2	a	123	LEU	3.2
1	O	530	GLN	3.2
1	Q	590	GLN	3.2
1	F	544	GLN	3.2
2	e	151	ASN	3.2
1	V	451	ASP	3.2
1	A	24	GLU	3.2
1	A	194	ASP	3.2
1	A	215	ASP	3.2
1	A	249	ARG	3.2
1	B	542	THR	3.2
1	J	434	THR	3.2
1	K	282	THR	3.2
1	P	367	ASP	3.2
1	T	23	ASP	3.2
1	U	215	ASP	3.2
1	A	396	GLU	3.2
2	Y	103	ASP	3.2
1	W	381	SER	3.2
2	d	130	SER	3.2
1	X	587	PRO	3.2
1	A	266	ILE	3.2
1	C	557	PHE	3.2
1	I	594	VAL	3.2
2	n	66	PRO	3.2
2	d	159	PRO	3.2
1	M	94	LEU	3.2
1	M	390	ALA	3.2
1	P	267	ALA	3.2
1	B	292	LEU	3.2
1	I	538	LEU	3.2
1	L	107	ALA	3.2
2	d	97	ALA	3.2
1	U	531	ASN	3.2
1	E	380	ASN	3.2
1	H	504	LYS	3.2
1	I	14	ARG	3.2
1	K	140	ASN	3.2
1	X	434	THR	3.2
1	A	434	THR	3.2
1	O	383	ASP	3.2
1	Q	32	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	V	18	ASP	3.2
1	W	166	ASP	3.2
1	B	534	GLU	3.2
1	E	503	GLU	3.2
2	t	8	ASP	3.2
2	t	47	TRP	3.2
2	b	71	ASP	3.2
1	N	385	PRO	3.2
1	P	212	LEU	3.2
1	A	577	ILE	3.2
1	W	248	LYS	3.2
1	W	554	LEU	3.2
1	E	563	LYS	3.2
1	I	12	LEU	3.2
1	I	385	PRO	3.2
1	J	559	LEU	3.2
2	o	16	LYS	3.2
2	h	102	PRO	3.2
1	U	338	ALA	3.2
1	B	456	ALA	3.2
1	L	277	TYR	3.2
2	v	123	ALA	3.2
2	f	135	ALA	3.2
1	B	462	GLU	3.1
1	M	32	ASP	3.1
1	O	63	VAL	3.1
1	Q	155	HIS	3.1
1	T	498	ASP	3.1
1	W	545	GLY	3.1
1	A	172	HIS	3.1
1	C	264	ILE	3.1
1	F	166	ASP	3.1
1	J	300	ILE	3.1
2	t	73	HIS	3.1
2	t	137	GLY	3.1
2	Y	79	GLY	3.1
2	e	82	HIS	3.1
1	P	249	ARG	3.1
1	Q	188	ALA	3.1
1	T	21	ALA	3.1
1	U	316	TYR	3.1
1	E	90	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
2	o	115	TYR	3.1
2	e	110	ALA	3.1
1	T	291	GLN	3.1
1	P	74	ASN	3.1
1	V	227	GLU	3.1
1	X	120	GLU	3.1
1	S	324	LYS	3.1
1	M	318	GLY	3.1
1	Q	234	ILE	3.1
1	U	89	ASP	3.1
1	U	253	ASP	3.1
1	X	37	ARG	3.1
1	C	72	ARG	3.1
1	C	271	ILE	3.1
1	E	93	VAL	3.1
1	H	174	THR	3.1
1	H	243	PRO	3.1
1	O	283	CYS	3.1
2	f	137	TYR	3.1
1	S	47	GLN	3.1
1	A	202	GLN	3.1
1	E	236	GLN	3.1
1	K	598	GLN	3.1
2	Y	55	GLU	3.1
2	c	73	GLU	3.1
1	N	449	PHE	3.1
1	S	63	VAL	3.1
1	U	276	VAL	3.1
1	U	439	ASN	3.1
2	j	111	LYS	3.1
1	D	535	ILE	3.1
1	E	350	PHE	3.1
1	U	551	LEU	3.1
1	W	295	GLY	3.1
1	A	207	TRP	3.1
1	J	8	LEU	3.1
2	k	33	MET	3.1
2	s	70	GLY	3.1
1	L	104	HIS	3.1
1	L	196	ASP	3.1
1	L	297	HIS	3.1
2	d	115	THR	3.1

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Mol	Chain	Res	Type	RSRZ
2	g	155	TRP	3.1
1	M	86	ALA	3.1
1	S	549	TYR	3.1
1	H	403	TYR	3.1
2	o	68	ALA	3.1
2	m	30	PRO	3.1
1	X	387	GLN	3.1
1	G	218	GLN	3.1
2	Z	145	SER	3.1
1	N	61	ARG	3.1
1	S	263	PHE	3.1
1	W	247	PHE	3.1
1	A	496	VAL	3.1
1	D	60	VAL	3.1
1	K	269	ARG	3.1
2	s	60	PHE	3.1
1	V	241	GLY	3.1
1	D	461	GLY	3.1
2	p	135	GLY	3.1
1	O	196	ASP	3.1
1	P	561	ASP	3.1
1	R	409	THR	3.1
1	W	29	ALA	3.1
1	B	107	ALA	3.1
1	H	77	ASP	3.1
1	L	368	ASP	3.1
2	v	24	THR	3.1
1	M	414	GLU	3.1
1	Q	299	PRO	3.1
1	B	589	GLU	3.1
1	F	391	TYR	3.1
1	H	5	GLU	3.1
1	J	585	GLU	3.1
1	M	10	SER	3.1
1	I	178	SER	3.1
1	M	560	LEU	3.1
1	D	57	PHE	3.1
1	Q	333	ILE	3.1
1	S	340	ILE	3.1
1	H	38	VAL	3.1
1	I	310	VAL	3.1
1	L	326	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
2	e	84	LEU	3.1
1	U	337	ASN	3.1
2	f	147	ASN	3.1
1	M	89	ASP	3.1
1	N	572	ALA	3.1
1	O	533	ALA	3.1
1	B	250	ASP	3.1
2	e	25	LYS	3.1
1	B	445	GLU	3.1
1	O	327	GLN	3.1
1	P	587	PRO	3.1
2	f	102	PRO	3.1
1	U	217	ILE	3.1
1	C	93	VAL	3.1
1	X	602	GLY	3.1
2	j	122	LEU	3.1
2	f	61	LYS	3.1
1	M	416	ALA	3.1
1	S	494	ALA	3.1
1	U	445	GLU	3.1
1	A	184	TRP	3.1
1	E	140	ASN	3.1
1	L	534	GLU	3.1
2	k	86	ASN	3.1
1	K	274	ARG	3.1
2	l	89	CYS	3.1
2	m	47	TRP	3.1
2	m	64	GLU	3.1
1	I	525	GLN	3.1
1	N	520	VAL	3.1
1	L	552	LEU	3.1
2	a	23	LEU	3.1
2	f	46	VAL	3.1
1	F	358	GLY	3.1
2	d	42	MET	3.1
1	S	91	ALA	3.1
1	A	534	GLU	3.1
1	F	380	ASN	3.1
1	K	191	TYR	3.1
2	g	137	TYR	3.1
1	M	449	PHE	3.1
1	R	367	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	I	560	LEU	3.1
1	L	236	GLN	3.1
2	s	100	THR	3.1
2	i	59	ASP	3.1
1	X	418	LEU	3.1
1	C	244	VAL	3.1
1	S	513	ARG	3.1
1	Q	406	GLU	3.1
2	i	21	ALA	3.1
1	G	371	TYR	3.1
2	m	148	TYR	3.1
1	N	34	PHE	3.1
1	K	108	LYS	3.1
1	L	47	GLN	3.1
1	O	305	GLY	3.1
1	T	14	ARG	3.1
1	W	219	ILE	3.1
1	W	280	ILE	3.1
1	X	65	ARG	3.1
1	A	219	ILE	3.1
2	b	146	GLY	3.1
2	f	64	ILE	3.1
2	g	63	ILE	3.1
1	P	495	GLU	3.1
1	V	311	GLU	3.1
1	H	381	SER	3.1
1	K	189	GLU	3.1
1	L	36	SER	3.1
2	Z	90	SER	3.1
1	R	408	ALA	3.1
2	Y	97	ALA	3.1
1	R	277	TYR	3.1
1	O	426	ASN	3.1
1	Q	201	PHE	3.1
1	A	229	LYS	3.1
1	C	600	LYS	3.1
1	L	6	ASN	3.1
1	L	19	TRP	3.1
2	m	124	LYS	3.1
1	Q	389	LEU	3.1
1	T	593	LEU	3.1
2	r	60	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	303	VAL	3.1
1	N	433	ASP	3.1
1	U	124	GLY	3.1
1	R	50	THR	3.1
1	U	584	PRO	3.1
1	A	376	ARG	3.1
1	B	273	ARG	3.1
1	H	318	GLY	3.1
2	s	57	GLY	3.1
2	u	15	ARG	3.1
2	Z	140	ARG	3.1
2	b	100	ILE	3.1
1	J	417	THR	3.1
1	A	9	GLU	3.1
1	C	227	GLU	3.1
1	D	227	GLU	3.1
1	G	189	GLU	3.1
2	v	45	ALA	3.1
2	j	135	ALA	3.1
1	R	12	LEU	3.1
1	W	549	TYR	3.1
1	C	246	TYR	3.1
1	K	164	LEU	3.1
1	N	236	GLN	3.1
1	N	327	GLN	3.1
1	X	439	ASN	3.1
1	E	530	GLN	3.1
1	C	253	ASP	3.1
1	F	101	ASP	3.1
1	U	589	GLU	3.0
1	J	317	GLU	3.0
1	V	494	ALA	3.0
2	d	88	ALA	3.0
2	i	32	ALA	3.0
1	I	513	ARG	3.0
1	K	459	ARG	3.0
2	d	86	SER	3.0
2	d	145	SER	3.0
1	D	538	LEU	3.0
2	i	57	TYR	3.0
1	R	461	GLY	3.0
1	E	427	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	184	TRP	3.0
1	Q	18	ASP	3.0
1	A	75	PRO	3.0
1	B	89	ASP	3.0
1	C	439	ASN	3.0
1	D	257	ASP	3.0
1	E	256	ASP	3.0
2	g	15	LYS	3.0
1	P	282	THR	3.0
1	G	106	THR	3.0
2	d	143	THR	3.0
1	N	263	PHE	3.0
1	Q	38	VAL	3.0
1	C	506	VAL	3.0
1	I	53	TYR	3.0
2	e	49	LEU	3.0
1	O	510	ILE	3.0
1	I	52	GLN	3.0
1	O	589	GLU	3.0
1	D	445	GLU	3.0
1	I	163	LYS	3.0
1	S	570	ASP	3.0
2	v	133	PRO	3.0
2	b	53	MET	3.0
1	M	572	ALA	3.0
1	R	231	THR	3.0
2	l	13	ALA	3.0
2	o	88	ALA	3.0
2	q	23	ALA	3.0
2	e	128	ALA	3.0
2	i	116	ALA	3.0
1	W	8	LEU	3.0
1	W	539	LEU	3.0
1	B	363	TYR	3.0
1	H	45	LEU	3.0
1	H	94	LEU	3.0
1	X	271	ILE	3.0
1	D	160	SER	3.0
2	a	30	SER	3.0
2	b	63	ILE	3.0
2	b	70	SER	3.0
2	h	30	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	M	19	TRP	3.0
1	N	117	GLU	3.0
1	W	224	GLU	3.0
1	H	117	GLU	3.0
2	l	147	HIS	3.0
1	A	385	PRO	3.0
1	C	7	ARG	3.0
1	B	312	ASP	3.0
1	D	238	PRO	3.0
1	I	32	ASP	3.0
1	I	105	ASN	3.0
2	u	138	ASN	3.0
2	a	138	PRO	3.0
2	t	14	LEU	3.0
2	b	29	ALA	3.0
1	P	216	THR	3.0
1	W	506	VAL	3.0
1	B	175	VAL	3.0
1	D	213	THR	3.0
1	J	174	THR	3.0
2	Z	60	GLY	3.0
1	O	598	GLN	3.0
1	T	445	GLU	3.0
1	D	387	GLN	3.0
1	J	525	GLN	3.0
2	p	117	GLN	3.0
1	U	257	ASP	3.0
1	X	367	ASP	3.0
1	L	395	PRO	3.0
1	C	541	LYS	3.0
1	D	541	LYS	3.0
2	o	94	ASP	3.0
2	r	96	ALA	3.0
2	a	61	LYS	3.0
2	a	116	ALA	3.0
2	e	18	LEU	3.0
2	h	54	ALA	3.0
1	E	276	VAL	3.0
1	N	130	THR	3.0
1	S	11	ILE	3.0
1	S	55	GLY	3.0
1	A	277	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	W	5	GLU	3.0
1	M	399	GLN	3.0
1	P	13	SER	3.0
1	S	181	GLN	3.0
1	S	202	GLN	3.0
1	D	569	ARG	3.0
1	G	5	GLU	3.0
1	F	104	HIS	3.0
1	K	575	GLN	3.0
2	j	85	ARG	3.0
2	c	156	HIS	3.0
1	R	35	PHE	3.0
1	U	557	PHE	3.0
1	A	543	PRO	3.0
1	B	63	VAL	3.0
1	F	353	PRO	3.0
1	I	89	ASP	3.0
1	I	448	VAL	3.0
1	K	12	LEU	3.0
1	L	220	ALA	3.0
2	o	87	LEU	3.0
2	h	122	LEU	3.0
1	L	570	ASP	3.0
1	P	132	TYR	3.0
1	W	330	ARG	3.0
1	W	571	TYR	3.0
1	R	49	THR	3.0
1	B	147	GLU	3.0
1	E	28	GLU	3.0
1	E	580	GLY	3.0
1	H	305	GLY	3.0
1	K	340	ILE	3.0
2	k	135	GLY	3.0
2	p	74	GLY	3.0
2	v	46	GLU	3.0
2	Z	24	ARG	3.0
2	v	118	THR	3.0
2	e	43	GLN	3.0
1	G	336	PHE	3.0
1	H	247	PHE	3.0
1	K	139	SER	3.0
2	g	82	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
2	k	45	ALA	3.0
2	d	26	LEU	3.0
1	E	581	VAL	3.0
2	r	93	PRO	3.0
1	P	194	ASP	3.0
1	M	246	TYR	3.0
1	U	423	GLU	3.0
1	W	246	TYR	3.0
1	A	296	GLU	3.0
1	F	196	ASP	3.0
1	H	105	ASN	3.0
1	H	250	ASP	3.0
1	L	571	TYR	3.0
2	f	95	ASN	3.0
1	Q	504	LYS	3.0
1	U	49	THR	3.0
1	W	291	GLN	3.0
1	A	174	THR	3.0
1	D	49	THR	3.0
1	E	355	GLN	3.0
1	J	446	THR	3.0
2	m	116	LYS	3.0
2	Y	40	GLN	3.0
1	X	247	PHE	3.0
1	H	104	HIS	3.0
1	M	259	ALA	3.0
1	M	397	VAL	3.0
1	P	170	ALA	3.0
1	P	390	ALA	3.0
1	T	412	VAL	3.0
1	U	46	SER	3.0
1	V	110	ALA	3.0
1	X	407	ALA	3.0
1	C	63	VAL	3.0
1	I	200	SER	3.0
2	p	126	ALA	3.0
2	s	42	ALA	3.0
2	j	116	ALA	3.0
1	N	217	ILE	3.0
1	U	280	ILE	3.0
1	E	169	ASP	3.0
1	G	325	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	J	306	GLU	3.0
1	L	264	ILE	3.0
1	L	382	GLY	3.0
2	m	18	GLY	3.0
1	K	337	ASN	3.0
2	r	22	ASP	3.0
2	b	147	ASN	3.0
1	N	201	PHE	3.0
1	H	284	THR	3.0
1	G	559	LEU	3.0
1	K	201	PHE	3.0
2	Z	143	THR	3.0
1	S	532	ARG	3.0
1	A	507	LEU	3.0
1	Q	200	SER	3.0
1	W	319	VAL	3.0
1	G	111	VAL	3.0
1	K	430	VAL	3.0
2	k	130	SER	3.0
2	s	23	ALA	3.0
2	v	119	ALA	3.0
2	b	108	ALA	3.0
1	S	588	GLU	3.0
1	C	545	GLY	3.0
1	F	167	LYS	3.0
1	F	219	ILE	3.0
2	m	137	GLY	3.0
2	s	18	GLY	3.0
2	s	133	PRO	3.0
2	u	74	GLY	3.0
2	u	98	GLU	3.0
2	Z	146	GLY	3.0
2	d	55	GLU	3.0
1	U	289	ASP	3.0
1	K	112	ASN	3.0
2	v	22	ASP	3.0
1	O	202	GLN	3.0
1	O	93	VAL	3.0
1	O	155	HIS	3.0
1	T	446	THR	3.0
1	V	459	ARG	3.0
1	E	26	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	555	GLN	3.0
1	L	601	GLN	3.0
2	s	25	LEU	3.0
2	c	43	GLN	3.0
1	W	173	CYS	3.0
1	A	232	ALA	3.0
1	A	315	VAL	3.0
1	E	130	THR	3.0
1	G	409	THR	3.0
1	I	377	THR	3.0
1	L	338	ALA	3.0
2	k	20	ALA	3.0
2	m	43	MET	3.0
2	r	73	HIS	3.0
1	M	217	ILE	3.0
1	S	190	LYS	3.0
1	G	534	GLU	3.0
1	H	185	GLU	3.0
2	p	21	SER	3.0
1	R	75	PRO	3.0
1	A	571	TYR	3.0
1	Q	269	ARG	3.0
1	K	443	ASP	3.0
2	r	35	ASP	3.0
1	R	218	GLN	3.0
1	S	350	PHE	3.0
1	F	375	ASN	3.0
2	i	147	ASN	3.0
1	M	138	THR	3.0
1	P	208	VAL	3.0
1	S	348	LYS	3.0
1	U	520	VAL	3.0
1	U	361	HIS	3.0
1	U	422	THR	3.0
1	A	520	VAL	3.0
1	G	581	VAL	3.0
1	F	406	GLU	3.0
1	J	400	ALA	3.0
1	J	496	VAL	3.0
1	K	170	ALA	3.0
2	o	37	VAL	3.0
2	o	106	THR	3.0

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Mol	Chain	Res	Type	RSRZ
2	r	92	ALA	3.0
2	t	52	LYS	3.0
2	h	141	MET	3.0
1	M	41	TRP	3.0
1	H	113	ILE	3.0
1	H	516	CYS	3.0
1	J	293	ILE	3.0
2	s	103	ILE	3.0
2	Z	64	ILE	3.0
2	h	79	GLY	3.0
1	T	372	TYR	2.9
1	B	62	PRO	2.9
1	F	369	TYR	2.9
1	K	299	PRO	2.9
2	h	57	TYR	2.9
2	j	39	PRO	2.9
1	N	561	ASP	2.9
2	s	63	ASP	2.9
1	M	600	LYS	2.9
1	U	205	ASN	2.9
1	W	228	LYS	2.9
1	B	74	ASN	2.9
1	H	291	GLN	2.9
1	J	31	ASN	2.9
1	J	324	LYS	2.9
1	L	244	VAL	2.9
2	s	19	VAL	2.9
2	a	95	ASN	2.9
1	P	296	GLU	2.9
1	N	417	THR	2.9
1	N	542	THR	2.9
1	E	155	HIS	2.9
1	E	585	GLU	2.9
2	a	62	GLY	2.9
2	i	114	ALA	2.9
1	G	100	THR	2.9
1	D	532	ARG	2.9
1	R	173	CYS	2.9
1	S	388	PRO	2.9
1	S	395	PRO	2.9
1	A	526	SER	2.9
1	L	370	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	L	526	SER	2.9
2	p	115	TYR	2.9
2	Y	124	TYR	2.9
2	c	157	TYR	2.9
2	v	149	PHE	2.9
2	j	139	SER	2.9
1	R	384	LEU	2.9
1	Q	182	ASN	2.9
1	R	236	GLN	2.9
1	F	140	ASN	2.9
1	I	588	GLU	2.9
2	l	43	MET	2.9
2	q	41	GLU	2.9
1	F	251	ILE	2.9
1	S	269	ARG	2.9
1	D	246	TYR	2.9
2	r	58	TYR	2.9
2	Y	155	TRP	2.9
1	U	261	SER	2.9
1	E	557	PHE	2.9
1	G	30	LYS	2.9
1	G	33	LEU	2.9
1	G	551	LEU	2.9
1	M	516	CYS	2.9
1	N	115	VAL	2.9
1	P	368	ASP	2.9
1	S	437	GLN	2.9
1	X	192	ASP	2.9
1	B	56	GLN	2.9
1	G	594	VAL	2.9
1	V	152	ALA	2.9
1	A	87	ARG	2.9
1	A	195	ALA	2.9
1	A	416	ALA	2.9
1	J	21	ALA	2.9
2	v	122	ARG	2.9
1	P	417	THR	2.9
1	U	138	THR	2.9
1	A	351	PHE	2.9
1	A	453	LEU	2.9
1	C	67	LEU	2.9
1	F	199	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	G	385	PRO	2.9
1	L	33	LEU	2.9
1	L	258	LEU	2.9
1	L	556	TYR	2.9
2	s	75	LEU	2.9
2	i	76	PRO	2.9
1	X	245	SER	2.9
1	A	160	SER	2.9
1	L	279	SER	2.9
1	R	534	GLU	2.9
1	M	196	ASP	2.9
1	O	192	ASP	2.9
1	V	544	GLN	2.9
1	S	173	CYS	2.9
1	T	596	ALA	2.9
1	C	90	ALA	2.9
1	C	459	ARG	2.9
1	J	52	GLN	2.9
2	f	99	ARG	2.9
2	g	72	ASP	2.9
2	h	91	ALA	2.9
1	P	248	LYS	2.9
1	U	401	ASN	2.9
1	J	228	LYS	2.9
2	q	65	ASN	2.9
1	S	155	HIS	2.9
1	N	549	TYR	2.9
1	S	8	LEU	2.9
1	V	191	TYR	2.9
1	W	422	THR	2.9
1	X	507	LEU	2.9
1	C	344	THR	2.9
1	K	417	THR	2.9
1	F	370	PRO	2.9
1	G	595	GLU	2.9
1	I	175	VAL	2.9
1	N	523	SER	2.9
1	J	171	ARG	2.9
2	o	32	SER	2.9
2	t	46	GLU	2.9
1	Q	220	ALA	2.9
1	U	324	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	596	ALA	2.9
1	F	368	ASP	2.9
1	L	433	ASP	2.9
2	j	53	MET	2.9
2	m	138	ASN	2.9
2	j	74	ASN	2.9
1	M	389	LEU	2.9
1	A	191	TYR	2.9
1	D	12	LEU	2.9
2	j	149	PHE	2.9
1	S	589	GLU	2.9
1	T	496	VAL	2.9
1	U	495	GLU	2.9
1	X	377	THR	2.9
1	F	208	VAL	2.9
2	l	67	PRO	2.9
2	p	83	VAL	2.9
2	d	102	PRO	2.9
1	O	381	SER	2.9
1	F	295	GLY	2.9
1	L	218	GLN	2.9
1	U	400	ALA	2.9
2	u	104	ILE	2.9
2	Y	113	ILE	2.9
2	i	70	SER	2.9
2	i	86	SER	2.9
1	M	433	ASP	2.9
1	N	368	ASP	2.9
1	E	42	ASP	2.9
1	U	593	LEU	2.9
1	A	516	CYS	2.9
1	D	48	TYR	2.9
1	E	269	ARG	2.9
1	J	539	LEU	2.9
1	X	288	LYS	2.9
2	n	124	LYS	2.9
2	r	69	GLU	2.9
1	P	419	GLY	2.9
1	T	546	THR	2.9
1	V	262	GLY	2.9
1	C	437	GLN	2.9
1	G	122	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	I	142	GLN	2.9
2	Y	83	GLY	2.9
1	X	335	SER	2.9
2	d	52	MET	2.9
1	N	384	LEU	2.9
1	P	460	ASP	2.9
1	Q	87	ARG	2.9
1	S	77	ASP	2.9
1	H	222	PHE	2.9
1	J	33	LEU	2.9
1	T	503	GLU	2.9
1	W	361	HIS	2.9
1	C	372	TYR	2.9
1	Q	323	THR	2.9
1	S	602	GLY	2.9
1	U	202	GLN	2.9
1	W	216	THR	2.9
1	X	138	THR	2.9
1	X	299	PRO	2.9
1	B	25	ALA	2.9
1	C	535	ILE	2.9
1	I	100	THR	2.9
1	J	349	PRO	2.9
2	k	31	GLN	2.9
2	e	100	ILE	2.9
1	D	151	SER	2.9
1	E	136	SER	2.9
1	L	168	SER	2.9
2	g	130	SER	2.9
1	Q	23	ASP	2.9
1	E	30	LYS	2.9
2	d	111	LYS	2.9
1	N	60	VAL	2.9
1	R	445	GLU	2.9
1	U	175	VAL	2.9
1	I	403	TYR	2.9
1	P	508	ASN	2.9
1	L	361	HIS	2.9
1	A	429	GLN	2.9
1	F	236	GLN	2.9
1	H	575	GLN	2.9
1	N	20	THR	2.9

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Mol	Chain	Res	Type	RSRZ
1	N	409	THR	2.9
1	S	377	THR	2.9
1	B	336	PHE	2.9
1	E	213	THR	2.9
1	J	86	ALA	2.9
2	s	106	THR	2.9
2	d	69	PHE	2.9
2	d	98	CYS	2.9
2	t	6	LYS	2.9
2	j	15	LYS	2.9
1	S	46	SER	2.9
1	V	28	GLU	2.9
1	A	566	GLU	2.9
1	D	159	ASP	2.9
1	K	22	SER	2.9
1	M	85	GLY	2.9
1	N	105	ASN	2.9
1	D	203	ASN	2.9
1	B	54	ARG	2.9
1	N	600	LYS	2.9
1	V	35	PHE	2.9
1	V	188	ALA	2.9
1	H	376	ARG	2.9
1	W	57	PHE	2.9
1	D	199	PRO	2.9
1	F	163	LYS	2.9
1	G	388	PRO	2.9
1	K	349	PRO	2.9
2	s	84	PHE	2.9
2	Z	91	ALA	2.9
2	e	40	GLN	2.9
2	f	141	MET	2.9
1	A	138	THR	2.9
2	a	127	THR	2.9
2	d	49	LEU	2.9
1	C	423	GLU	2.9
2	q	89	CYS	2.9
1	R	42	ASP	2.9
1	V	16	ASP	2.9
1	B	277	TYR	2.9
1	B	571	TYR	2.9
1	E	289	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	58	ASP	2.9
1	V	564	GLY	2.9
1	C	569	ARG	2.9
2	r	54	ILE	2.8
1	M	453	LEU	2.8
1	N	525	GLN	2.8
1	O	388	PRO	2.8
1	R	327	GLN	2.8
1	C	195	ALA	2.8
1	E	505	GLN	2.8
1	H	152	ALA	2.8
1	K	86	ALA	2.8
2	g	29	ALA	2.8
1	T	388	PRO	2.8
1	H	543	PRO	2.8
2	Z	76	PRO	2.8
1	N	589	GLU	2.8
1	V	50	THR	2.8
1	C	138	THR	2.8
2	m	83	VAL	2.8
2	i	38	GLU	2.8
1	N	108	LYS	2.8
1	P	459	ARG	2.8
1	X	237	ASP	2.8
1	B	87	ARG	2.8
1	C	136	SER	2.8
1	Q	172	HIS	2.8
1	D	382	GLY	2.8
1	H	180	SER	2.8
2	q	22	ASP	2.8
1	I	293	ILE	2.8
2	m	147	HIS	2.8
2	i	63	ILE	2.8
1	U	31	ASN	2.8
1	E	426	ASN	2.8
1	F	33	LEU	2.8
1	H	398	PRO	2.8
1	K	238	PRO	2.8
2	l	47	TRP	2.8
1	U	120	GLU	2.8
2	d	142	PRO	2.8
1	N	116	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	W	415	VAL	2.8
1	X	458	ARG	2.8
1	D	446	THR	2.8
1	F	413	LYS	2.8
1	G	20	THR	2.8
2	t	56	THR	2.8
2	u	26	THR	2.8
2	Y	15	LYS	2.8
1	P	16	ASP	2.8
2	l	110	GLY	2.8
2	u	73	HIS	2.8
2	c	63	ILE	2.8
1	T	25	ALA	2.8
1	U	8	LEU	2.8
1	V	164	LEU	2.8
1	D	533	ALA	2.8
1	L	201	PHE	2.8
1	G	598	GLN	2.8
2	q	87	LEU	2.8
2	Y	74	ASN	2.8
1	T	341	VAL	2.8
1	D	341	VAL	2.8
1	F	415	VAL	2.8
1	N	558	THR	2.8
1	U	293	ILE	2.8
1	V	382	GLY	2.8
1	J	282	THR	2.8
2	g	62	GLY	2.8
1	N	539	LEU	2.8
1	R	212	LEU	2.8
1	E	539	LEU	2.8
1	J	222	PHE	2.8
1	J	509	ASP	2.8
1	L	154	SER	2.8
1	X	500	ALA	2.8
1	F	107	ALA	2.8
1	I	125	ALA	2.8
2	b	45	ALA	2.8
1	Q	268	GLU	2.8
1	R	142	GLN	2.8
1	S	52	GLN	2.8
1	C	399	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
2	q	31	GLN	2.8
1	B	19	TRP	2.8
1	D	210	PRO	2.8
1	L	105	ASN	2.8
1	T	545	GLY	2.8
1	S	551	LEU	2.8
1	T	539	LEU	2.8
1	M	537	GLU	2.8
1	O	259	ALA	2.8
1	R	335	SER	2.8
1	A	595	GLU	2.8
1	C	402	ALA	2.8
1	G	133	GLU	2.8
1	H	107	ALA	2.8
2	m	9	LEU	2.8
2	g	122	LEU	2.8
1	H	116	ARG	2.8
1	H	274	ARG	2.8
1	H	588	GLU	2.8
1	J	242	GLU	2.8
2	i	148	SER	2.8
2	j	22	ALA	2.8
1	L	181	GLN	2.8
1	X	111	VAL	2.8
1	B	239	VAL	2.8
1	L	497	VAL	2.8
2	l	80	VAL	2.8
1	O	549	TYR	2.8
1	W	540	GLY	2.8
1	C	580	GLY	2.8
1	L	562	GLY	2.8
1	G	278	LYS	2.8
1	I	539	LEU	2.8
1	Q	21	ALA	2.8
1	P	279	SER	2.8
1	R	178	SER	2.8
1	S	13	SER	2.8
1	S	519	ASP	2.8
1	T	134	ASP	2.8
1	A	104	HIS	2.8
1	V	69	SER	2.8
1	A	136	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	159	ASP	2.8
1	H	29	ALA	2.8
1	H	357	ALA	2.8
1	I	408	ALA	2.8
2	n	41	GLU	2.8
2	t	35	ASP	2.8
2	h	32	ALA	2.8
2	u	83	VAL	2.8
1	W	370	PRO	2.8
1	C	173	CYS	2.8
1	J	157	ILE	2.8
1	C	25	ALA	2.8
1	C	515	GLU	2.8
1	H	407	ALA	2.8
1	R	578	GLN	2.8
1	L	451	ASP	2.8
2	l	27	ASP	2.8
1	W	163	LYS	2.8
1	D	217	ILE	2.8
1	I	19	TRP	2.8
1	E	549	TYR	2.8
2	n	104	ILE	2.8
2	q	66	PRO	2.8
1	I	112	ASN	2.8
1	K	263	PHE	2.8
1	Q	221	GLU	2.8
1	Q	423	GLU	2.8
1	B	173	CYS	2.8
1	C	500	ALA	2.8
1	L	9	GLU	2.8
1	U	181	GLN	2.8
1	F	361	HIS	2.8
1	H	542	THR	2.8
1	I	215	ASP	2.8
2	g	127	THR	2.8
1	D	290	LYS	2.8
1	E	305	GLY	2.8
1	G	564	GLY	2.8
1	I	335	SER	2.8
2	l	139	SER	2.8
1	B	592	TRP	2.8
2	a	118	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	J	294	ALA	2.8
2	g	108	ALA	2.8
1	I	319	VAL	2.8
2	k	37	VAL	2.8
1	P	174	THR	2.8
1	P	228	LYS	2.8
1	W	327	GLN	2.8
1	A	177	HIS	2.8
1	V	383	ASP	2.8
1	B	122	GLY	2.8
1	E	197	ASP	2.8
1	F	383	ASP	2.8
2	c	47	ASP	2.8
2	f	33	THR	2.8
1	V	557	PHE	2.8
1	A	39	SER	2.8
1	J	251	ILE	2.8
1	J	280	ILE	2.8
1	J	512	GLY	2.8
1	J	453	LEU	2.8
2	k	17	LEU	2.8
2	k	97	LEU	2.8
2	l	61	SER	2.8
2	s	21	SER	2.8
2	v	95	TYR	2.8
2	d	23	LEU	2.8
1	U	548	GLU	2.8
1	W	588	GLU	2.8
1	B	379	GLU	2.8
1	G	515	GLU	2.8
1	H	314	GLU	2.8
1	K	70	GLU	2.8
1	M	375	ASN	2.8
1	I	456	ALA	2.8
1	T	504	LYS	2.8
1	A	413	LYS	2.8
1	G	582	LYS	2.8
1	E	181	GLN	2.8
1	M	77	ASP	2.8
1	Q	602	GLY	2.8
1	P	374	LEU	2.8
1	X	283	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	H	255	ILE	2.8
1	I	449	PHE	2.8
2	i	80	ASP	2.8
1	B	389	LEU	2.8
1	C	536	LEU	2.8
1	X	296	GLU	2.8
1	G	46	SER	2.8
1	J	39	SER	2.8
1	K	224	GLU	2.8
2	v	146	TRP	2.8
2	g	138	PRO	2.8
1	N	25	ALA	2.8
1	O	324	LYS	2.8
1	S	458	ARG	2.8
1	V	103	ARG	2.8
1	V	167	LYS	2.8
1	W	366	ASN	2.8
1	F	394	ASN	2.8
1	H	426	ASN	2.8
1	I	401	ASN	2.8
1	J	408	ALA	2.8
2	e	132	ALA	2.8
1	S	270	GLN	2.8
1	P	281	ILE	2.7
1	G	155	HIS	2.7
1	J	382	GLY	2.7
1	J	427	GLY	2.7
1	O	586	THR	2.7
1	V	169	ASP	2.7
1	D	216	THR	2.7
1	D	389	LEU	2.7
1	L	35	PHE	2.7
1	I	134	ASP	2.7
2	c	23	LEU	2.7
2	e	113	ILE	2.7
1	R	242	GLU	2.7
1	M	229	LYS	2.7
1	N	39	SER	2.7
1	S	235	TYR	2.7
1	J	556	TYR	2.7
1	K	360	GLU	2.7
1	K	446	THR	2.7

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Mol	Chain	Res	Type	RSRZ
2	e	115	THR	2.7
1	X	81	ARG	2.7
1	X	190	LYS	2.7
1	A	69	SER	2.7
1	A	335	SER	2.7
1	A	582	LYS	2.7
2	o	21	SER	2.7
2	c	140	ARG	2.7
1	M	407	ALA	2.7
1	A	408	ALA	2.7
2	c	91	ALA	2.7
1	B	6	ASN	2.7
1	D	366	ASN	2.7
1	J	508	ASN	2.7
1	O	555	GLN	2.7
1	D	291	GLN	2.7
1	J	73	GLN	2.7
1	N	258	LEU	2.7
1	N	551	LEU	2.7
1	P	12	LEU	2.7
1	E	266	ILE	2.7
1	L	79	LEU	2.7
1	Q	58	ASP	2.7
1	Q	237	ASP	2.7
1	C	348	LYS	2.7
1	F	296	GLU	2.7
1	K	83	LYS	2.7
1	U	231	THR	2.7
1	J	532	ARG	2.7
1	Q	178	SER	2.7
1	R	442	ALA	2.7
1	X	86	ALA	2.7
1	X	592	TRP	2.7
1	J	62	PRO	2.7
1	J	497	VAL	2.7
2	p	93	PRO	2.7
2	t	43	MET	2.7
1	R	590	GLN	2.7
1	Q	324	LYS	2.7
1	S	495	GLU	2.7
1	T	258	LEU	2.7
1	X	327	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	I	554	LEU	2.7
2	Y	149	PHE	2.7
1	W	249	ARG	2.7
1	E	177	HIS	2.7
2	g	25	LYS	2.7
2	i	125	LYS	2.7
2	j	113	ILE	2.7
1	K	26	ARG	2.7
2	k	69	GLU	2.7
2	b	107	GLU	2.7
1	U	372	TYR	2.7
1	X	519	ASP	2.7
1	G	246	TYR	2.7
1	H	166	ASP	2.7
1	J	215	ASP	2.7
1	P	38	VAL	2.7
1	P	599	ALA	2.7
1	B	303	VAL	2.7
2	c	109	THR	2.7
1	W	592	TRP	2.7
1	A	523	SER	2.7
1	C	243	PRO	2.7
1	F	21	ALA	2.7
1	L	69	SER	2.7
2	o	12	ALA	2.7
2	u	133	PRO	2.7
2	e	148	SER	2.7
1	O	602	GLY	2.7
1	W	580	GLY	2.7
1	A	418	LEU	2.7
1	A	557	PHE	2.7
1	H	218	GLN	2.7
1	I	229	LYS	2.7
1	I	589	GLU	2.7
1	J	577	ILE	2.7
2	v	53	GLY	2.7
1	O	337	ASN	2.7
1	P	112	ASN	2.7
1	T	9	GLU	2.7
2	v	131	ARG	2.7
2	b	26	LEU	2.7
2	t	85	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	383	ASP	2.7
1	G	443	ASP	2.7
1	P	434	THR	2.7
1	W	106	THR	2.7
1	X	107	ALA	2.7
1	H	395	PRO	2.7
1	I	216	THR	2.7
2	r	66	PRO	2.7
2	j	32	ALA	2.7
1	N	336	PHE	2.7
1	C	178	SER	2.7
1	J	178	SER	2.7
2	i	53	MET	2.7
1	S	264	ILE	2.7
1	E	270	GLN	2.7
1	G	202	GLN	2.7
2	a	38	GLU	2.7
2	g	112	ILE	2.7
2	h	94	HIS	2.7
1	U	244	VAL	2.7
1	L	425	VAL	2.7
2	s	80	VAL	2.7
1	V	433	ASP	2.7
1	A	125	ALA	2.7
1	A	285	ALA	2.7
2	b	36	ASP	2.7
2	h	116	ALA	2.7
1	R	370	PRO	2.7
1	U	26	ARG	2.7
1	N	69	SER	2.7
1	B	602	GLY	2.7
2	m	106	THR	2.7
2	a	14	THR	2.7
1	I	445	GLU	2.7
2	t	121	SER	2.7
1	M	141	ASN	2.7
1	I	439	ASN	2.7
1	E	229	LYS	2.7
1	F	516	CYS	2.7
1	H	528	LYS	2.7
1	K	556	TYR	2.7
2	s	6	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	Q	383	ASP	2.7
1	U	250	ASP	2.7
1	W	325	ASP	2.7
1	W	449	PHE	2.7
1	D	77	ASP	2.7
1	F	416	ALA	2.7
1	J	433	ASP	2.7
2	r	107	ALA	2.7
2	l	30	PRO	2.7
2	l	70	GLY	2.7
2	u	84	PHE	2.7
2	b	80	ASP	2.7
1	N	305	GLY	2.7
1	N	499	LEU	2.7
1	C	82	PRO	2.7
1	D	388	PRO	2.7
2	q	146	TRP	2.7
2	r	29	GLU	2.7
2	i	115	THR	2.7
1	S	291	GLN	2.7
1	E	529	GLN	2.7
1	J	47	GLN	2.7
2	d	126	GLN	2.7
2	j	41	SER	2.7
1	W	565	VAL	2.7
1	A	108	LYS	2.7
2	Y	46	VAL	2.7
2	i	133	LYS	2.7
1	E	81	ARG	2.7
2	Z	85	ARG	2.7
1	X	599	ALA	2.7
1	I	195	ALA	2.7
1	M	193	LEU	2.7
1	Q	227	GLU	2.7
1	T	206	ASP	2.7
1	A	540	GLY	2.7
1	L	443	ASP	2.7
2	p	40	LEU	2.7
2	t	87	LEU	2.7
2	c	149	PHE	2.7
1	B	370	PRO	2.7
1	D	406	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	198	ILE	2.7
1	F	299	PRO	2.7
1	R	83	LYS	2.7
1	G	518	THR	2.7
1	A	22	SER	2.7
1	I	218	GLN	2.7
1	U	87	ARG	2.7
1	C	269	ARG	2.7
1	D	171	ARG	2.7
2	Z	104	TYR	2.7
1	G	572	ALA	2.7
2	i	51	ALA	2.7
1	N	251	ILE	2.7
1	G	360	GLU	2.7
1	J	76	ILE	2.7
1	K	585	GLU	2.7
1	S	504	LYS	2.7
1	S	528	LYS	2.7
1	A	260	ASP	2.7
1	J	383	ASP	2.7
1	W	532	ARG	2.7
1	G	530	GLN	2.7
1	X	63	VAL	2.7
2	b	130	SER	2.7
2	j	89	VAL	2.7
1	A	53	TYR	2.7
2	m	65	ASN	2.7
2	o	46	GLU	2.7
2	p	123	ALA	2.7
2	u	119	ALA	2.7
2	i	94	HIS	2.7
1	N	389	LEU	2.7
1	P	140	ASN	2.7
1	P	264	ILE	2.7
1	W	337	ASN	2.7
1	D	295	GLY	2.7
1	D	545	GLY	2.7
2	h	95	ASN	2.7
1	R	92	ASP	2.7
1	C	441	ARG	2.7
1	E	23	ASP	2.7
1	O	129	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	P	138	THR	2.7
1	E	138	THR	2.7
1	H	435	VAL	2.7
1	L	59	VAL	2.7
2	c	65	THR	2.7
1	O	335	SER	2.7
1	E	335	SER	2.7
1	P	418	LEU	2.7
1	F	30	LYS	2.7
1	F	108	LYS	2.7
1	H	128	LEU	2.7
1	I	124	GLY	2.7
1	J	17	ALA	2.7
1	B	113	ILE	2.7
1	D	463	ILE	2.7
1	N	458	ARG	2.7
2	q	86	ASN	2.7
2	f	42	MET	2.7
1	S	243	PRO	2.7
1	S	257	ASP	2.7
1	X	238	PRO	2.7
1	X	364	ASP	2.7
2	n	71	ASP	2.7
2	u	8	ASP	2.7
1	U	497	VAL	2.7
1	E	239	VAL	2.7
1	F	397	VAL	2.7
1	M	447	TYR	2.6
1	P	33	LEU	2.6
1	R	233	PHE	2.6
1	S	313	LYS	2.6
1	W	235	TYR	2.6
1	D	583	LYS	2.6
2	c	127	THR	2.7
2	e	124	TYR	2.6
2	f	143	THR	2.7
1	S	585	GLU	2.6
1	U	96	GLY	2.6
1	W	406	GLU	2.6
1	A	445	GLU	2.6
1	A	562	GLY	2.6
2	Z	27	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
2	f	132	ALA	2.6
2	c	99	ARG	2.6
2	k	132	MET	2.6
1	N	565	VAL	2.6
1	O	236	GLN	2.6
1	T	543	PRO	2.6
1	U	166	ASP	2.6
1	V	202	GLN	2.6
1	W	19	TRP	2.6
1	W	43	ASP	2.6
1	C	353	PRO	2.6
1	D	204	PRO	2.6
1	E	592	TRP	2.6
1	G	591	GLN	2.6
1	I	166	ASP	2.6
1	J	218	GLN	2.6
2	u	22	ASP	2.6
2	j	40	GLN	2.6
1	S	57	PHE	2.6
1	X	233	PHE	2.6
1	R	344	THR	2.6
1	A	122	GLY	2.6
1	A	227	GLU	2.6
1	C	80	TYR	2.6
1	T	580	GLY	2.6
1	C	360	GLU	2.6
1	F	462	GLU	2.6
1	H	20	THR	2.6
1	K	223	TYR	2.6
1	D	298	ILE	2.6
1	E	458	ARG	2.6
2	f	34	LEU	2.6
2	g	143	THR	2.6
1	O	13	SER	2.6
1	D	410	SER	2.6
1	D	516	CYS	2.6
2	k	32	SER	2.6
2	c	94	HIS	2.6
1	N	134	ASP	2.6
1	T	387	GLN	2.6
1	A	59	VAL	2.6
1	F	594	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	T	547	PRO	2.6
1	B	289	ASP	2.6
1	C	194	ASP	2.6
1	C	395	PRO	2.6
1	E	192	ASP	2.6
1	L	578	GLN	2.6
2	b	40	GLN	2.6
1	W	559	LEU	2.6
1	B	403	TYR	2.6
1	K	350	PHE	2.6
2	f	57	TYR	2.6
2	g	57	TYR	2.6
1	V	454	ALA	2.6
1	R	20	THR	2.6
1	I	138	THR	2.6
1	I	586	THR	2.6
2	a	63	ILE	2.6
1	C	39	SER	2.6
2	u	136	SER	2.6
1	O	108	LYS	2.6
1	N	112	ASN	2.6
1	R	366	ASN	2.6
1	N	12	LEU	2.6
1	R	199	PRO	2.6
1	S	7	ARG	2.6
1	Q	19	TRP	2.6
1	S	517	TYR	2.6
1	X	134	ASP	2.6
1	F	534	GLU	2.6
1	I	458	ARG	2.6
1	L	438	LEU	2.6
1	I	109	ILE	2.6
2	u	36	ALA	2.6
2	j	105	ALA	2.6
1	O	156	VAL	2.6
1	U	59	VAL	2.6
1	O	141	ASN	2.6
1	P	359	PHE	2.6
1	R	453	LEU	2.6
1	S	120	GLU	2.6
1	S	525	GLN	2.6
1	V	222	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	V	270	GLN	2.6
1	W	601	GLN	2.6
1	B	513	ARG	2.6
1	J	164	LEU	2.6
1	K	429	GLN	2.6
2	Y	131	ARG	2.6
1	T	401	ASN	2.6
2	o	112	GLU	2.6
2	u	60	PHE	2.6
1	O	131	ASP	2.6
1	T	312	ASP	2.6
1	C	349	PRO	2.6
1	E	385	PRO	2.6
1	V	356	ILE	2.6
1	D	293	ILE	2.6
1	D	514	TYR	2.6
1	G	166	ASP	2.6
1	I	540	GLY	2.6
1	J	540	GLY	2.6
1	O	265	LYS	2.6
1	K	190	LYS	2.6
2	n	16	LYS	2.6
2	q	6	LYS	2.6
2	v	54	ILE	2.6
1	P	320	VAL	2.6
1	Q	344	THR	2.6
1	Q	496	VAL	2.6
1	Q	542	THR	2.6
1	V	341	VAL	2.6
2	e	143	THR	2.6
1	X	538	LEU	2.6
1	I	373	LEU	2.6
1	I	593	LEU	2.6
1	B	502	GLY	2.6
1	J	463	ILE	2.6
1	K	82	PRO	2.6
1	K	388	PRO	2.6
1	K	392	TYR	2.6
2	q	91	ILE	2.6
2	d	81	ASP	2.6
2	e	51	ALA	2.6
2	j	77	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	S	569	ARG	2.6
2	k	43	MET	2.6
1	O	539	LEU	2.6
1	P	10	SER	2.6
1	T	28	GLU	2.6
1	T	406	GLU	2.6
1	U	247	PHE	2.6
1	W	50	THR	2.6
1	A	515	GLU	2.6
1	B	133	GLU	2.6
2	m	100	THR	2.6
1	D	168	SER	2.6
2	o	113	LEU	2.6
2	p	84	PHE	2.6
2	t	21	SER	2.6
2	u	29	GLU	2.6
1	K	578	GLN	2.6
1	P	259	ALA	2.6
1	P	517	TYR	2.6
2	r	67	PRO	2.6
1	V	561	ASP	2.6
1	B	458	ARG	2.6
1	E	43	ASP	2.6
1	K	171	ARG	2.6
1	K	513	ARG	2.6
1	W	507	LEU	2.6
1	C	389	LEU	2.6
1	C	507	LEU	2.6
1	D	263	PHE	2.6
1	D	309	PHE	2.6
1	L	172	HIS	2.6
1	O	160	SER	2.6
1	P	39	SER	2.6
1	Q	284	THR	2.6
1	G	329	LEU	2.6
1	E	450	GLN	2.6
1	H	178	SER	2.6
2	o	100	THR	2.6
1	R	266	ILE	2.6
1	M	137	PRO	2.6
1	M	243	PRO	2.6
1	N	80	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	S	81	ARG	2.6
1	A	76	ILE	2.6
1	B	556	TYR	2.6
1	E	333	ILE	2.6
1	K	330	ARG	2.6
2	j	104	TYR	2.6
1	S	276	VAL	2.6
1	E	63	VAL	2.6
1	I	312	ASP	2.6
1	K	415	VAL	2.6
2	l	71	ASP	2.6
2	o	83	VAL	2.6
2	a	42	MET	2.6
1	N	79	LEU	2.6
1	P	516	CYS	2.6
1	Q	384	LEU	2.6
1	S	418	LEU	2.6
1	V	317	GLU	2.6
1	B	536	LEU	2.6
1	C	336	PHE	2.6
1	G	193	LEU	2.6
1	J	361	HIS	2.6
1	Q	174	THR	2.6
1	U	274	ARG	2.6
1	V	14	ARG	2.6
1	V	428	GLY	2.6
1	W	569	ARG	2.6
1	A	36	SER	2.6
1	B	20	THR	2.6
1	G	427	GLY	2.6
2	o	81	SER	2.6
2	q	76	ARG	2.6
2	d	90	SER	2.6
1	F	547	PRO	2.6
1	O	600	LYS	2.6
1	S	420	VAL	2.6
1	T	528	LYS	2.6
1	W	92	ASP	2.6
1	W	367	ASP	2.6
1	K	43	ASP	2.6
2	l	116	LYS	2.6
2	v	35	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	R	227	GLU	2.6
1	R	515	GLU	2.6
1	W	359	PHE	2.6
1	X	515	GLU	2.6
1	D	444	LEU	2.6
1	E	94	LEU	2.6
1	G	147	GLU	2.6
1	I	35	PHE	2.6
1	K	374	LEU	2.6
1	C	326	GLY	2.6
1	C	427	GLY	2.6
1	I	532	ARG	2.6
1	O	340	ILE	2.6
1	O	356	ILE	2.6
1	B	298	ILE	2.6
2	g	100	ILE	2.6
1	O	178	SER	2.6
1	J	363	TYR	2.6
1	K	456	ALA	2.6
2	Y	54	ALA	2.6
2	j	87	SER	2.6
1	M	554	LEU	2.6
1	O	133	GLU	2.6
1	Q	312	ASP	2.6
1	R	396	GLU	2.6
1	V	374	LEU	2.6
1	W	451	ASP	2.6
1	D	15	PHE	2.6
1	E	84	ASP	2.6
1	E	366	ASN	2.6
1	F	378	ASP	2.6
1	I	453	LEU	2.6
1	K	366	ASN	2.6
1	L	24	GLU	2.6
2	o	9	LEU	2.6
1	R	103	ARG	2.6
2	p	73	HIS	2.6
2	s	122	ARG	2.6
1	B	429	GLN	2.6
1	G	80	TYR	2.6
1	K	324	LYS	2.6
1	L	355	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	O	456	ALA	2.6
1	T	282	THR	2.6
1	W	220	ALA	2.6
2	Y	116	ALA	2.6
2	b	133	LYS	2.6
1	X	69	SER	2.6
1	D	153	CYS	2.6
2	e	67	TYR	2.6
1	E	137	PRO	2.6
1	L	62	PRO	2.6
1	M	519	ASP	2.5
1	O	321	ARG	2.5
1	V	593	LEU	2.5
1	H	553	LEU	2.5
1	P	312	ASP	2.5
1	T	186	ASP	2.5
1	W	42	ASP	2.5
1	A	331	ASN	2.5
1	D	325	ASP	2.5
1	F	433	ASP	2.5
1	G	105	ASN	2.5
1	I	511	ARG	2.5
2	n	38	ASP	2.5
2	g	80	ASP	2.5
1	J	291	GLN	2.5
1	Q	442	ALA	2.5
1	S	369	TYR	2.5
1	C	403	TYR	2.5
1	F	86	ALA	2.5
1	F	316	TYR	2.5
1	K	48	TYR	2.5
2	a	132	ALA	2.5
1	M	311	GLU	2.5
1	X	258	LEU	2.5
1	A	27	ARG	2.5
1	A	330	ARG	2.5
1	B	495	GLU	2.5
1	I	551	LEU	2.5
2	s	112	GLU	2.5
1	S	82	PRO	2.5
1	E	210	PRO	2.5
2	j	86	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	S	562	GLY	2.5
1	T	30	LYS	2.5
1	V	112	ASN	2.5
1	A	203	ASN	2.5
1	F	498	ASP	2.5
1	G	190	LYS	2.5
1	J	205	ASN	2.5
2	j	146	GLY	2.5
1	J	144	ILE	2.5
1	K	172	HIS	2.5
1	R	315	VAL	2.5
1	U	235	TYR	2.5
1	I	267	ALA	2.5
2	r	99	ALA	2.5
1	A	268	GLU	2.5
1	U	418	LEU	2.5
1	D	222	PHE	2.5
1	L	359	PHE	2.5
2	Z	23	LEU	2.5
2	f	122	LEU	2.5
1	H	204	PRO	2.5
1	J	148	PRO	2.5
2	t	77	SER	2.5
2	i	25	LYS	2.5
1	O	427	GLY	2.5
2	q	137	GLY	2.5
1	G	293	ILE	2.5
1	K	194	ASP	2.5
1	N	29	ALA	2.5
1	X	56	GLN	2.5
1	V	64	VAL	2.5
1	J	26	ARG	2.5
2	b	128	ALA	2.5
1	F	449	PHE	2.5
1	O	284	THR	2.5
1	R	200	SER	2.5
1	R	238	PRO	2.5
1	X	231	THR	2.5
1	E	455	THR	2.5
1	I	455	THR	2.5
2	r	74	GLY	2.5
2	u	127	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
2	a	53	MET	2.5
2	a	146	GLY	2.5
1	H	157	ILE	2.5
1	S	131	ASP	2.5
1	L	101	ASP	2.5
1	O	357	ALA	2.5
1	U	420	VAL	2.5
1	C	47	GLN	2.5
1	E	254	VAL	2.5
1	F	177	HIS	2.5
1	F	435	VAL	2.5
1	J	147	GLU	2.5
1	K	408	ALA	2.5
2	r	82	ALA	2.5
1	M	263	PHE	2.5
2	Y	106	LEU	2.5
1	O	522	PRO	2.5
1	T	295	GLY	2.5
1	X	398	PRO	2.5
1	G	295	GLY	2.5
1	J	441	ARG	2.5
1	K	409	THR	2.5
1	L	377	THR	2.5
2	c	144	GLY	2.5
1	Q	513	ARG	2.5
1	M	411	ALA	2.5
1	N	253	ASP	2.5
1	P	147	GLU	2.5
1	X	221	GLU	2.5
1	X	291	GLN	2.5
1	A	414	GLU	2.5
1	D	43	ASP	2.5
1	F	366	ASN	2.5
1	F	566	GLU	2.5
1	G	500	ALA	2.5
1	I	450	GLN	2.5
1	J	412	VAL	2.5
1	K	58	ASP	2.5
2	a	133	LYS	2.5
1	L	403	TYR	2.5
2	f	54	ALA	2.5
1	Q	538	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	N	82	PRO	2.5
1	P	144	ILE	2.5
1	G	510	ILE	2.5
2	l	127	PRO	2.5
2	b	85	ARG	2.5
1	Q	410	SER	2.5
1	U	377	THR	2.5
1	C	417	THR	2.5
1	D	163	LYS	2.5
1	F	381	SER	2.5
2	p	106	THR	2.5
2	u	6	LYS	2.5
1	O	143	VAL	2.5
1	T	52	GLN	2.5
1	T	115	VAL	2.5
1	S	45	LEU	2.5
1	U	256	ASP	2.5
1	W	256	ASP	2.5
1	C	412	VAL	2.5
1	C	460	ASP	2.5
1	F	396	GLU	2.5
1	G	550	GLN	2.5
1	I	18	ASP	2.5
1	I	48	TYR	2.5
1	J	181	GLN	2.5
2	p	68	ALA	2.5
2	Z	116	ALA	2.5
1	I	441	ARG	2.5
1	U	62	PRO	2.5
1	A	88	PRO	2.5
1	C	238	PRO	2.5
1	C	272	LYS	2.5
1	D	333	ILE	2.5
2	a	120	LYS	2.5
2	i	142	PRO	2.5
1	Q	296	GLU	2.5
1	Q	360	GLU	2.5
1	B	268	GLU	2.5
1	O	405	LEU	2.5
1	P	21	ALA	2.5
1	P	209	PHE	2.5
1	D	100	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	554	LEU	2.5
1	J	450	GLN	2.5
1	K	335	SER	2.5
1	L	123	VAL	2.5
2	n	19	VAL	2.5
2	t	80	VAL	2.5
2	Z	78	GLU	2.5
2	d	65	THR	2.5
1	A	94	LEU	2.5
1	P	155	HIS	2.5
1	S	16	ASP	2.5
1	X	84	ASP	2.5
1	B	246	TYR	2.5
2	s	87	LEU	2.5
1	B	364	ASP	2.5
1	B	331	ASN	2.5
2	r	131	ARG	2.5
1	G	413	LYS	2.5
1	K	183	GLY	2.5
2	c	16	GLY	2.5
1	P	271	ILE	2.5
1	N	238	PRO	2.5
1	N	243	PRO	2.5
1	N	286	VAL	2.5
1	S	379	GLU	2.5
1	C	315	VAL	2.5
1	D	370	PRO	2.5
2	q	64	GLU	2.5
1	P	438	LEU	2.5
1	M	139	SER	2.5
1	P	442	ALA	2.5
1	N	364	ASP	2.5
1	Q	48	TYR	2.5
1	Q	56	GLN	2.5
1	W	10	SER	2.5
1	E	294	ALA	2.5
1	G	384	LEU	2.5
1	I	444	LEU	2.5
1	L	233	PHE	2.5
1	E	523	SER	2.5
1	H	454	ALA	2.5
1	J	355	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	J	442	ALA	2.5
1	L	390	ALA	2.5
2	l	12	ALA	2.5
2	q	97	LEU	2.5
2	i	108	ALA	2.5
1	J	392	TYR	2.5
1	K	273	ARG	2.5
1	O	570	ASP	2.5
1	R	77	ASP	2.5
2	c	124	TYR	2.5
1	X	74	ASN	2.5
1	B	521	GLY	2.5
1	V	60	VAL	2.5
1	V	306	GLU	2.5
1	V	360	GLU	2.5
1	D	225	VAL	2.5
1	D	462	GLU	2.5
1	I	395	PRO	2.5
1	J	353	PRO	2.5
1	F	188	ALA	2.5
1	G	212	LEU	2.5
1	G	254	VAL	2.5
1	I	147	GLU	2.5
1	M	522	PRO	2.5
1	P	173	CYS	2.5
1	T	552	LEU	2.5
2	l	129	PRO	2.5
2	t	93	PRO	2.5
2	i	138	PRO	2.5
1	M	582	LYS	2.5
1	P	231	THR	2.5
1	S	48	TYR	2.5
1	D	135	GLN	2.5
2	k	118	THR	2.5
2	u	34	GLN	2.5
2	h	128	ALA	2.5
1	F	284	THR	2.5
1	J	48	TYR	2.5
2	u	48	TYR	2.5
2	g	118	TYR	2.5
1	P	382	GLY	2.5
1	A	394	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	161	ASN	2.5
1	B	311	GLU	2.5
1	V	299	PRO	2.5
1	X	87	ARG	2.5
1	B	496	VAL	2.5
1	H	393	GLU	2.5
1	E	359	PHE	2.5
1	E	569	ARG	2.5
1	J	309	PHE	2.5
1	B	416	ALA	2.5
1	K	345	PRO	2.5
1	L	82	PRO	2.5
2	n	23	ALA	2.5
2	e	76	PRO	2.5
1	S	153	CYS	2.5
1	K	44	TRP	2.5
1	K	403	TYR	2.5
1	W	427	GLY	2.5
1	L	455	THR	2.5
2	j	130	SER	2.5
1	P	217	ILE	2.5
1	I	76	ILE	2.5
1	P	87	ARG	2.5
1	Q	458	ARG	2.5
1	V	445	GLU	2.5
1	S	129	VAL	2.5
1	W	374	LEU	2.5
1	X	193	LEU	2.5
1	B	59	VAL	2.5
1	B	412	VAL	2.5
1	I	116	ARG	2.5
1	G	560	LEU	2.5
1	H	320	VAL	2.5
1	L	292	LEU	2.5
2	e	68	VAL	2.5
1	R	229	LYS	2.5
1	L	413	LYS	2.5
2	c	61	LYS	2.5
1	N	431	ALA	2.4
1	X	408	ALA	2.4
1	B	345	PRO	2.4
1	E	195	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	I	110	ALA	2.4
1	I	220	ALA	2.4
2	m	107	ALA	2.4
1	A	73	GLN	2.4
1	G	525	GLN	2.4
1	H	392	TYR	2.4
1	I	44	TRP	2.4
1	M	180	SER	2.4
1	R	240	THR	2.4
1	U	273	ARG	2.4
1	U	379	GLU	2.4
1	A	328	ARG	2.4
1	B	65	ARG	2.4
1	G	160	SER	2.4
1	K	162	SER	2.4
2	r	41	GLU	2.4
2	Y	140	ARG	2.4
1	I	187	PHE	2.4
1	R	17	ALA	2.4
1	K	353	PRO	2.4
2	j	51	ALA	2.4
1	U	73	GLN	2.4
1	W	73	GLN	2.4
1	C	530	GLN	2.4
2	l	109	TYR	2.4
1	W	293	ILE	2.4
1	A	37	ARG	2.4
1	Q	409	THR	2.4
1	S	252	LYS	2.4
1	W	583	LYS	2.4
1	C	117	GLU	2.4
1	C	176	ILE	2.4
1	C	185	GLU	2.4
1	C	510	ILE	2.4
1	I	352	TRP	2.4
1	X	420	VAL	2.4
1	B	254	VAL	2.4
2	i	122	LEU	2.4
2	u	20	ALA	2.4
1	R	204	PRO	2.4
1	X	116	ARG	2.4
1	B	116	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	J	302	PRO	2.4
1	L	48	TYR	2.4
2	a	99	ARG	2.4
1	O	109	ILE	2.4
1	Q	189	GLU	2.4
1	D	252	LYS	2.4
1	H	288	LYS	2.4
1	L	30	LYS	2.4
2	v	145	GLU	2.4
2	i	117	LYS	2.4
1	T	444	LEU	2.4
1	V	106	THR	2.4
1	W	35	PHE	2.4
1	B	60	VAL	2.4
1	B	329	LEU	2.4
1	D	156	VAL	2.4
1	H	15	PHE	2.4
1	K	34	PHE	2.4
1	L	415	VAL	2.4
1	B	460	ASP	2.4
2	r	56	THR	2.4
2	v	121	SER	2.4
1	M	29	ALA	2.4
1	T	456	ALA	2.4
1	F	114	ALA	2.4
1	J	114	ALA	2.4
1	U	529	GLN	2.4
1	B	30	LYS	2.4
1	G	399	GLN	2.4
1	J	511	ARG	2.4
1	K	372	TYR	2.4
2	k	129	PRO	2.4
2	t	49	GLN	2.4
2	Z	67	TYR	2.4
2	b	117	LYS	2.4
2	j	20	ARG	2.4
1	D	395	PRO	2.4
1	T	198	ILE	2.4
1	D	379	GLU	2.4
1	F	379	GLU	2.4
1	G	227	GLU	2.4
1	L	217	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	M	329	LEU	2.4
1	M	361	HIS	2.4
1	O	594	VAL	2.4
1	V	336	PHE	2.4
1	A	438	LEU	2.4
1	C	319	VAL	2.4
1	P	256	ASP	2.4
1	P	409	THR	2.4
1	S	89	ASP	2.4
1	A	284	THR	2.4
1	D	139	SER	2.4
1	D	282	THR	2.4
1	G	377	THR	2.4
1	H	138	THR	2.4
1	J	77	ASP	2.4
2	q	21	SER	2.4
2	b	90	SER	2.4
1	W	54	ARG	2.4
1	X	265	LYS	2.4
1	J	407	ALA	2.4
2	p	102	LYS	2.4
1	M	236	GLN	2.4
1	Q	512	GLY	2.4
1	B	141	ASN	2.4
2	b	83	GLY	2.4
1	C	144	ILE	2.4
1	F	120	GLU	2.4
1	K	395	PRO	2.4
2	b	78	GLU	2.4
1	K	222	PHE	2.4
1	L	322	LEU	2.4
2	o	80	VAL	2.4
1	J	81	ARG	2.4
2	m	125	ARG	2.4
2	c	131	ARG	2.4
1	O	169	ASP	2.4
1	Q	339	ASP	2.4
1	S	121	ALA	2.4
1	S	378	ASP	2.4
1	T	526	SER	2.4
1	V	411	ALA	2.4
1	X	409	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	J	139	SER	2.4
1	O	85	GLY	2.4
1	E	562	GLY	2.4
1	S	88	PRO	2.4
1	U	182	ASN	2.4
1	W	161	ASN	2.4
1	X	353	PRO	2.4
1	D	401	ASN	2.4
1	M	405	LEU	2.4
1	N	254	VAL	2.4
1	C	351	PHE	2.4
1	I	353	PRO	2.4
1	L	302	PRO	2.4
1	Q	127	ARG	2.4
1	L	376	ARG	2.4
2	j	125	LYS	2.4
1	U	407	ALA	2.4
1	V	285	ALA	2.4
1	W	197	ASP	2.4
1	W	339	ASP	2.4
1	C	416	ALA	2.4
1	I	162	SER	2.4
1	J	18	ASP	2.4
2	q	36	ALA	2.4
2	h	29	ALA	2.4
1	N	221	GLU	2.4
1	O	48	TYR	2.4
1	O	534	GLU	2.4
1	L	221	GLU	2.4
1	L	365	GLY	2.4
1	O	591	GLN	2.4
1	S	277	TYR	2.4
1	A	109	ILE	2.4
1	M	63	VAL	2.4
1	M	331	ASN	2.4
1	T	88	PRO	2.4
1	D	233	PHE	2.4
1	G	429	GLN	2.4
1	H	52	GLN	2.4
1	U	54	ARG	2.4
1	U	61	ARG	2.4
1	E	37	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	444	LEU	2.4
1	H	269	ARG	2.4
2	q	19	VAL	2.4
2	c	117	LYS	2.4
2	f	120	LYS	2.4
1	R	41	TRP	2.4
1	A	155	HIS	2.4
1	N	342	ALA	2.4
2	e	32	ALA	2.4
1	M	18	ASP	2.4
1	O	186	ASP	2.4
1	Q	433	ASP	2.4
1	U	443	ASP	2.4
1	C	84	ASP	2.4
1	C	312	ASP	2.4
1	E	445	GLU	2.4
1	J	206	ASP	2.4
1	L	406	GLU	2.4
2	l	41	GLU	2.4
2	j	79	GLY	2.4
1	P	130	THR	2.4
1	N	33	LEU	2.4
1	P	601	GLN	2.4
1	V	48	TYR	2.4
1	W	578	GLN	2.4
1	A	403	TYR	2.4
1	E	223	TYR	2.4
1	H	323	THR	2.4
1	I	255	ILE	2.4
1	Q	438	LEU	2.4
1	T	513	ARG	2.4
1	B	78	VAL	2.4
1	H	108	LYS	2.4
1	H	351	PHE	2.4
1	L	78	VAL	2.4
1	L	430	VAL	2.4
2	l	83	VAL	2.4
2	d	58	GLN	2.4
1	R	398	PRO	2.4
1	B	380	ASN	2.4
1	L	426	ASN	2.4
2	Y	75	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	P	17	ALA	2.4
1	R	572	ALA	2.4
1	X	585	GLU	2.4
1	B	185	GLU	2.4
1	F	445	GLU	2.4
1	L	408	ALA	2.4
2	c	66	GLY	2.4
1	M	287	LEU	2.4
1	N	159	ASP	2.4
1	V	81	ARG	2.4
1	W	316	TYR	2.4
1	C	198	ILE	2.4
1	U	553	LEU	2.4
1	W	418	LEU	2.4
1	A	118	GLN	2.4
1	D	56	GLN	2.4
1	D	378	ASP	2.4
1	A	412	VAL	2.4
1	A	506	VAL	2.4
1	D	437	GLN	2.4
1	E	187	PHE	2.4
1	F	103	ARG	2.4
1	K	145	ARG	2.4
1	L	99	ARG	2.4
1	L	250	ASP	2.4
1	L	356	ILE	2.4
1	I	154	SER	2.4
1	L	93	VAL	2.4
2	m	25	LEU	2.4
2	n	81	SER	2.4
2	Z	96	LEU	2.4
2	e	30	SER	2.4
1	O	203	ASN	2.4
1	L	345	PRO	2.4
1	R	28	GLU	2.4
1	X	155	HIS	2.4
1	V	265	LYS	2.4
1	C	147	GLU	2.4
1	D	96	GLY	2.4
1	E	133	GLU	2.4
1	H	44	TRP	2.4
2	s	64	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	27	ARG	2.4
1	C	61	ARG	2.4
1	N	578	GLN	2.4
1	N	594	VAL	2.4
1	O	399	GLN	2.4
1	Q	12	LEU	2.4
1	S	80	TYR	2.4
1	S	405	LEU	2.4
1	T	212	LEU	2.4
1	B	79	LEU	2.4
1	C	293	ILE	2.4
1	U	578	GLN	2.4
1	B	111	VAL	2.4
1	C	525	GLN	2.4
1	D	51	LEU	2.4
1	F	538	LEU	2.4
1	G	403	TYR	2.4
1	H	418	LEU	2.4
2	i	113	ILE	2.4
1	H	450	GLN	2.4
1	H	594	VAL	2.4
1	J	303	VAL	2.4
2	v	63	ASP	2.4
2	d	46	VAL	2.4
1	V	417	THR	2.4
1	W	526	SER	2.4
2	f	139	SER	2.4
1	M	74	ASN	2.4
1	N	569	ARG	2.4
1	T	241	GLY	2.4
1	U	297	HIS	2.4
1	A	324	LYS	2.4
1	F	427	GLY	2.4
2	b	25	LYS	2.4
1	N	514	TYR	2.4
1	S	552	LEU	2.4
1	C	254	VAL	2.4
1	K	57	PHE	2.4
1	O	450	GLN	2.4
1	R	437	GLN	2.4
2	o	95	TYR	2.4
1	C	257	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	K	378	ASP	2.3
2	m	39	ASP	2.3
2	s	72	ASP	2.3
2	Z	59	ASP	2.3
2	c	40	GLN	2.4
1	M	265	LYS	2.3
1	O	174	THR	2.3
1	V	153	CYS	2.3
1	X	151	SER	2.3
1	B	138	THR	2.3
1	G	173	CYS	2.3
1	C	83	LYS	2.3
1	D	228	LYS	2.3
1	O	495	GLU	2.3
1	E	7	ARG	2.3
1	J	14	ARG	2.3
1	J	299	PRO	2.3
1	P	182	ASN	2.3
1	S	25	ALA	2.3
1	U	452	ASN	2.3
1	E	394	ASN	2.3
1	H	411	ALA	2.3
2	j	54	ALA	2.3
1	S	292	LEU	2.3
1	T	536	LEU	2.3
1	K	571	TYR	2.3
1	L	397	VAL	2.3
2	l	25	LEU	2.3
1	L	23	ASP	2.3
1	L	108	LYS	2.3
1	L	257	ASP	2.3
2	a	80	ASP	2.3
1	M	269	ARG	2.3
1	A	200	SER	2.3
1	B	410	SER	2.3
1	M	262	GLY	2.3
1	C	230	GLU	2.3
1	E	314	GLU	2.3
1	J	124	GLY	2.3
2	l	101	ALA	2.3
2	q	7	GLY	2.3
2	t	57	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	a	33	THR	2.3
2	b	79	GLY	2.3
2	i	39	PRO	2.3
1	N	164	LEU	2.3
1	R	155	HIS	2.3
1	S	212	LEU	2.3
1	T	352	TRP	2.3
1	V	19	TRP	2.3
1	D	251	ILE	2.3
1	E	507	LEU	2.3
1	K	182	ASN	2.3
1	K	351	PHE	2.3
1	L	21	ALA	2.3
1	D	258	LEU	2.3
2	v	84	PHE	2.3
1	H	129	VAL	2.3
2	j	68	VAL	2.3
1	N	530	GLN	2.3
1	U	514	TYR	2.3
1	V	228	LYS	2.3
1	A	517	TYR	2.3
1	D	181	GLN	2.3
1	G	27	ARG	2.3
1	J	273	ARG	2.3
1	Q	256	ASP	2.3
1	R	378	ASP	2.3
1	F	117	GLU	2.3
1	G	18	ASP	2.3
1	G	256	ASP	2.3
1	I	169	ASP	2.3
2	c	42	MET	2.3
1	W	462	GLU	2.3
1	K	147	GLU	2.3
1	P	370	PRO	2.3
1	P	385	PRO	2.3
1	X	410	SER	2.3
1	B	358	GLY	2.3
1	N	45	LEU	2.3
1	N	152	ALA	2.3
1	O	201	PHE	2.3
1	T	454	ALA	2.3
1	C	151	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	543	PRO	2.3
2	q	18	GLY	2.3
2	m	17	LEU	2.3
2	Z	49	LEU	2.3
2	Z	105	ALA	2.3
2	c	84	LEU	2.3
2	d	106	LEU	2.3
1	N	278	LYS	2.3
1	A	531	ASN	2.3
1	H	203	ASN	2.3
1	F	132	TYR	2.3
1	G	369	TYR	2.3
1	K	549	TYR	2.3
2	e	61	LYS	2.3
2	Z	43	GLN	2.3
1	N	312	ASP	2.3
1	S	70	GLU	2.3
1	I	194	ASP	2.3
2	b	17	ASP	2.3
2	d	50	GLU	2.3
1	O	540	GLY	2.3
1	L	521	GLY	2.3
1	P	536	LEU	2.3
1	M	38	VAL	2.3
1	Q	518	THR	2.3
1	U	36	SER	2.3
1	R	397	VAL	2.3
1	U	163	LYS	2.3
1	B	255	ILE	2.3
1	H	551	LEU	2.3
1	I	417	THR	2.3
1	J	500	ALA	2.3
1	B	541	LYS	2.3
2	a	112	ILE	2.3
2	f	26	LEU	2.3
2	f	117	LYS	2.3
2	j	49	LEU	2.3
1	Q	366	ASN	2.3
1	X	203	ASN	2.3
1	E	61	ARG	2.3
1	F	27	ARG	2.3
1	H	64	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	249	ARG	2.3
1	L	496	VAL	2.3
2	k	76	ARG	2.3
2	l	37	VAL	2.3
2	m	11	ARG	2.3
2	e	140	ARG	2.3
1	H	53	TYR	2.3
2	Z	118	TYR	2.3
1	W	555	GLN	2.3
1	W	591	GLN	2.3
1	H	399	GLN	2.3
1	L	399	GLN	2.3
1	B	414	GLU	2.3
1	J	117	GLU	2.3
1	R	30	LYS	2.3
1	R	289	ASP	2.3
1	A	18	ASP	2.3
2	o	51	GLY	2.3
1	H	574	LYS	2.3
2	Y	59	ASP	2.3
1	U	448	VAL	2.3
1	E	113	ILE	2.3
2	m	12	ALA	2.3
2	p	107	ALA	2.3
2	i	96	LEU	2.3
1	K	310	VAL	2.3
1	L	103	ARG	2.3
1	U	50	THR	2.3
1	L	151	SER	2.3
1	L	178	SER	2.3
2	a	86	SER	2.3
1	O	191	TYR	2.3
1	Q	436	ASN	2.3
1	I	372	TYR	2.3
2	l	138	ASN	2.3
2	o	86	ASN	2.3
2	p	128	TYR	2.3
1	A	588	GLU	2.3
1	I	133	GLU	2.3
1	A	278	LYS	2.3
1	A	600	LYS	2.3
1	C	504	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	J	348	LYS	2.3
1	M	342	ALA	2.3
1	M	559	LEU	2.3
1	W	294	ALA	2.3
1	X	532	ARG	2.3
1	D	559	LEU	2.3
1	G	356	ILE	2.3
1	J	169	ASP	2.3
1	L	84	ASP	2.3
2	u	91	ILE	2.3
1	S	349	PRO	2.3
1	V	395	PRO	2.3
1	L	353	PRO	2.3
1	O	523	SER	2.3
1	X	526	SER	2.3
1	Q	235	TYR	2.3
1	T	177	HIS	2.3
1	A	231	THR	2.3
1	F	227	GLU	2.3
1	J	360	GLU	2.3
2	d	56	TRP	2.3
2	j	118	TYR	2.3
1	Q	52	GLN	2.3
2	u	49	GLN	2.3
1	O	384	LEU	2.3
1	O	532	ARG	2.3
1	S	12	LEU	2.3
1	V	173	CYS	2.3
1	W	389	LEU	2.3
1	J	12	LEU	2.3
1	V	257	ASP	2.3
1	A	581	VAL	2.3
1	B	90	ALA	2.3
1	K	333	ILE	2.3
2	n	107	ALA	2.3
2	Y	129	ILE	2.3
2	b	101	ALA	2.3
2	i	45	ALA	2.3
1	O	370	PRO	2.3
1	W	9	GLU	2.3
1	F	216	THR	2.3
1	H	446	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	I	396	GLU	2.3
2	k	21	SER	2.3
2	k	134	THR	2.3
2	s	121	SER	2.3
1	T	181	GLN	2.3
1	N	573	ASN	2.3
1	T	569	ARG	2.3
1	V	562	GLY	2.3
1	W	44	TRP	2.3
1	X	555	GLN	2.3
1	C	118	GLN	2.3
1	E	352	TRP	2.3
1	G	87	ARG	2.3
1	U	350	PHE	2.3
1	A	536	LEU	2.3
1	B	350	PHE	2.3
1	D	359	PHE	2.3
1	G	35	PHE	2.3
1	J	350	PHE	2.3
1	K	419	GLY	2.3
2	r	57	GLY	2.3
1	T	280	ILE	2.3
1	E	45	LEU	2.3
2	p	25	LEU	2.3
2	s	140	PHE	2.3
2	c	34	LEU	2.3
1	V	416	ALA	2.3
1	E	408	ALA	2.3
1	J	175	VAL	2.3
1	W	89	ASP	2.3
1	W	137	PRO	2.3
1	F	256	ASP	2.3
1	H	206	ASP	2.3
2	n	93	PRO	2.3
2	Y	102	PRO	2.3
2	i	103	ASP	2.3
1	P	185	GLU	2.3
1	X	185	GLU	2.3
1	A	133	GLU	2.3
1	D	7	ARG	2.3
1	D	391	TYR	2.3
1	I	515	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
2	l	112	GLU	2.3
2	t	58	TYR	2.3
2	t	112	GLU	2.3
1	P	449	PHE	2.3
1	Q	558	THR	2.3
1	R	523	SER	2.3
1	X	22	SER	2.3
1	A	399	GLN	2.3
2	Y	85	ARG	2.3
1	E	417	THR	2.3
1	G	540	GLY	2.3
1	H	106	THR	2.3
1	J	501	THR	2.3
2	Y	87	SER	2.3
1	B	366	ASN	2.3
1	C	554	LEU	2.3
1	D	326	GLY	2.3
2	u	18	GLY	2.3
1	O	217	ILE	2.3
1	P	452	ASN	2.3
1	P	577	ILE	2.3
1	T	276	VAL	2.3
2	Y	63	ILE	2.3
2	f	92	VAL	2.3
1	A	30	LYS	2.3
1	V	88	PRO	2.3
1	V	368	ASP	2.3
1	E	311	GLU	2.3
1	J	9	GLU	2.3
2	a	48	ASP	2.3
1	D	235	TYR	2.3
2	m	109	TYR	2.3
1	R	136	SER	2.3
1	S	358	GLY	2.3
1	V	550	GLN	2.3
1	A	35	PHE	2.3
1	B	124	GLY	2.3
1	D	557	PHE	2.3
1	E	351	PHE	2.3
1	I	355	GLN	2.3
2	n	25	LEU	2.3
2	g	119	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	f	65	THR	2.3
1	M	315	VAL	2.3
1	Q	64	VAL	2.3
1	S	439	ASN	2.3
1	D	582	LYS	2.3
1	G	583	LYS	2.3
1	K	563	LYS	2.3
1	P	221	GLU	2.3
1	U	513	ARG	2.3
1	F	133	GLU	2.3
2	d	140	ARG	2.3
1	M	42	ASP	2.3
1	P	433	ASP	2.3
1	R	16	ASP	2.3
1	U	460	ASP	2.3
1	V	166	ASP	2.3
1	W	364	ASP	2.3
1	A	237	ASP	2.3
1	B	206	ASP	2.3
1	C	517	TYR	2.3
1	E	388	PRO	2.3
1	G	509	ASP	2.3
2	r	39	ASP	2.3
2	t	133	PRO	2.3
1	O	576	LEU	2.3
1	P	79	LEU	2.3
1	I	241	GLY	2.3
2	n	132	MET	2.3
1	P	280	ILE	2.3
1	Q	279	SER	2.3
1	C	592	TRP	2.3
1	D	119	ILE	2.3
1	F	106	THR	2.3
1	G	158	TRP	2.3
1	K	272	LYS	2.3
2	m	102	LYS	2.3
2	s	77	SER	2.3
1	O	171	ARG	2.2
1	Q	170	ALA	2.2
1	W	321	ARG	2.2
1	D	357	ALA	2.2
1	I	494	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	r	42	ALA	2.2
2	e	114	ALA	2.2
1	O	380	ASN	2.2
1	S	380	ASN	2.2
1	I	436	ASN	2.2
1	K	5	GLU	2.2
1	N	560	LEU	2.2
1	Q	351	PHE	2.2
1	T	427	GLY	2.2
1	B	253	ASP	2.2
1	C	16	ASP	2.2
1	H	194	ASP	2.2
1	I	235	TYR	2.2
1	I	514	TYR	2.2
1	J	159	ASP	2.2
1	G	45	LEU	2.2
1	I	292	LEU	2.2
1	J	419	GLY	2.2
1	J	561	ASP	2.2
1	L	378	ASP	2.2
2	a	72	ASP	2.2
2	c	118	TYR	2.2
1	U	228	LYS	2.2
1	L	51	LEU	2.2
2	g	34	LEU	2.2
2	Z	52	MET	2.2
2	g	111	LYS	2.2
1	W	417	THR	2.2
1	B	152	ALA	2.2
1	H	216	THR	2.2
1	I	91	ALA	2.2
1	I	294	ALA	2.2
1	J	216	THR	2.2
1	L	39	SER	2.2
2	q	26	THR	2.2
1	M	258	LEU	2.2
1	M	384	LEU	2.2
1	R	336	PHE	2.2
1	V	385	PRO	2.2
1	V	556	TYR	2.2
1	A	447	TYR	2.2
1	G	199	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	222	PHE	2.2
2	i	150	PRO	2.2
2	j	137	TYR	2.2
1	M	146	ARG	2.2
1	M	214	GLN	2.2
1	R	361	HIS	2.2
1	V	530	GLN	2.2
1	B	356	ILE	2.2
1	F	135	GLN	2.2
2	p	90	ARG	2.2
2	r	19	VAL	2.2
2	Z	40	GLN	2.2
2	d	53	MET	2.2
2	h	40	GLN	2.2
1	A	189	GLU	2.2
1	C	24	GLU	2.2
1	E	117	GLU	2.2
1	K	91	ALA	2.2
1	K	537	GLU	2.2
1	H	546	THR	2.2
1	J	231	THR	2.2
2	g	109	THR	2.2
1	C	331	ASN	2.2
2	b	61	LYS	2.2
1	T	326	GLY	2.2
1	U	540	GLY	2.2
1	W	557	PHE	2.2
1	A	233	PHE	2.2
1	B	80	TYR	2.2
2	n	95	TYR	2.2
2	a	149	PHE	2.2
1	O	257	ASP	2.2
1	T	215	ASP	2.2
1	T	271	ILE	2.2
1	W	199	PRO	2.2
1	A	364	ASP	2.2
1	B	84	ASP	2.2
1	D	215	ASP	2.2
1	K	370	PRO	2.2
1	J	142	GLN	2.2
1	L	509	ASP	2.2
2	q	93	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	r	76	ARG	2.2
2	u	63	ASP	2.2
2	u	122	ARG	2.2
2	v	15	ARG	2.2
2	Y	44	ASP	2.2
2	a	129	ILE	2.2
1	C	407	ALA	2.2
1	G	416	ALA	2.2
1	J	221	GLU	2.2
2	r	98	GLU	2.2
2	Y	77	ALA	2.2
1	S	154	SER	2.2
1	W	288	LYS	2.2
1	I	583	LYS	2.2
2	e	133	LYS	2.2
2	n	56	THR	2.2
2	b	143	THR	2.2
2	d	127	THR	2.2
1	M	373	LEU	2.2
1	U	258	LEU	2.2
1	V	426	ASN	2.2
1	F	336	PHE	2.2
1	G	145	ARG	2.2
1	J	223	TYR	2.2
2	l	128	TYR	2.2
2	c	137	TYR	2.2
2	j	147	ASN	2.2
1	O	166	ASP	2.2
1	A	320	VAL	2.2
1	A	353	PRO	2.2
1	D	412	VAL	2.2
2	o	44	MET	2.2
1	M	534	GLU	2.2
1	A	297	HIS	2.2
1	D	456	ALA	2.2
1	E	296	GLU	2.2
1	I	572	ALA	2.2
2	a	82	HIS	2.2
1	H	126	TRP	2.2
1	N	162	SER	2.2
1	P	344	THR	2.2
1	S	61	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	V	569	ARG	2.2
1	E	54	ARG	2.2
1	E	183	GLY	2.2
1	E	326	GLY	2.2
1	F	376	ARG	2.2
1	G	553	LEU	2.2
1	I	57	PHE	2.2
1	J	57	PHE	2.2
2	o	18	GLY	2.2
1	Q	141	ASN	2.2
1	S	303	VAL	2.2
1	M	505	GLN	2.2
1	P	596	ALA	2.2
1	T	383	ASP	2.2
1	U	530	GLN	2.2
1	X	137	PRO	2.2
1	C	387	GLN	2.2
1	F	215	ASP	2.2
1	I	302	PRO	2.2
1	D	17	ALA	2.2
2	k	46	GLU	2.2
2	t	72	ASP	2.2
2	a	17	ASP	2.2
2	e	103	ASP	2.2
1	H	150	HIS	2.2
1	N	37	ARG	2.2
1	R	249	ARG	2.2
1	U	99	ARG	2.2
1	W	171	ARG	2.2
1	B	532	ARG	2.2
1	D	54	ARG	2.2
1	P	154	SER	2.2
1	S	10	SER	2.2
1	S	326	GLY	2.2
1	B	540	GLY	2.2
1	L	46	SER	2.2
1	L	502	GLY	2.2
1	L	539	LEU	2.2
1	C	69	SER	2.2
2	s	61	SER	2.2
2	f	41	SER	2.2
2	f	79	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	P	300	ILE	2.2
1	P	333	ILE	2.2
1	Q	290	LYS	2.2
1	E	448	VAL	2.2
2	o	124	LYS	2.2
2	s	55	ILE	2.2
2	a	65	THR	2.2
1	O	227	GLU	2.2
1	K	331	ASN	2.2
2	d	40	GLN	2.2
1	O	29	ALA	2.2
1	X	77	ASP	2.2
1	A	411	ALA	2.2
1	M	155	HIS	2.2
1	E	376	ARG	2.2
1	G	134	ASP	2.2
1	G	458	ARG	2.2
2	h	135	ALA	2.2
2	g	156	HIS	2.2
1	T	183	GLY	2.2
1	T	382	GLY	2.2
1	X	358	GLY	2.2
1	D	592	TRP	2.2
1	H	554	LEU	2.2
1	J	158	TRP	2.2
2	o	40	LEU	2.2
1	U	281	ILE	2.2
1	X	320	VAL	2.2
1	C	228	LYS	2.2
1	F	229	LYS	2.2
1	F	293	ILE	2.2
1	H	223	TYR	2.2
1	J	154	SER	2.2
1	J	549	TYR	2.2
1	K	149	ILE	2.2
1	K	163	LYS	2.2
1	K	363	TYR	2.2
1	L	254	VAL	2.2
2	p	109	TYR	2.2
2	b	41	SER	2.2
2	d	92	VAL	2.2
2	g	64	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	106	THR	2.2
1	O	24	GLU	2.2
1	S	117	GLU	2.2
1	D	360	GLU	2.2
1	E	231	THR	2.2
2	r	106	THR	2.2
2	b	38	GLU	2.2
2	j	115	THR	2.2
1	S	366	ASN	2.2
1	O	232	ALA	2.2
1	S	402	ALA	2.2
1	U	388	PRO	2.2
1	V	578	GLN	2.2
1	X	569	ARG	2.2
1	A	137	PRO	2.2
1	N	361	HIS	2.2
1	W	23	ASP	2.2
1	G	197	ASP	2.2
1	N	96	GLY	2.2
1	F	521	GLY	2.2
2	n	114	LEU	2.2
1	P	448	VAL	2.2
1	X	175	VAL	2.2
1	K	11	ILE	2.2
2	k	54	ILE	2.2
2	Z	28	VAL	2.2
1	F	523	SER	2.2
1	H	245	SER	2.2
1	K	154	SER	2.2
2	Y	20	ARG	2.2
2	d	87	SER	2.2
2	h	148	SER	2.2
1	M	417	THR	2.2
1	B	73	GLN	2.2
1	M	112	ASN	2.2
1	N	366	ASN	2.2
2	m	45	ALA	2.2
2	i	105	ALA	2.2
1	M	551	LEU	2.2
1	Q	164	LEU	2.2
1	M	295	GLY	2.2
1	N	582	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	V	292	LEU	2.2
1	W	563	LYS	2.2
1	D	172	HIS	2.2
1	J	256	ASP	2.2
2	e	94	HIS	2.2
1	O	307	TRP	2.2
1	X	11	ILE	2.2
1	A	286	VAL	2.2
1	D	38	VAL	2.2
1	N	516	CYS	2.2
1	Q	514	TYR	2.2
1	T	117	GLU	2.2
1	T	311	GLU	2.2
1	T	556	TYR	2.2
1	D	44	TRP	2.2
1	U	28	GLU	2.2
1	D	133	GLU	2.2
1	E	379	GLU	2.2
1	E	510	ILE	2.2
1	H	109	ILE	2.2
1	K	376	ARG	2.2
1	K	447	TYR	2.2
2	k	11	ARG	2.2
2	g	99	ARG	2.2
1	T	154	SER	2.2
1	W	39	SER	2.2
2	a	41	SER	2.2
1	S	342	ALA	2.2
1	M	105	ASN	2.2
1	N	302	PRO	2.2
1	V	6	ASN	2.2
1	X	228	LYS	2.2
1	C	88	PRO	2.2
1	E	344	THR	2.2
2	r	118	THR	2.2
2	i	126	GLN	2.2
1	C	164	LEU	2.2
1	C	229	LYS	2.2
1	F	351	PHE	2.2
1	G	67	LEU	2.2
1	G	573	ASN	2.2
2	i	102	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	194	ASP	2.2
1	N	461	GLY	2.2
1	O	32	ASP	2.2
1	C	131	ASP	2.2
1	T	143	VAL	2.2
1	T	144	ILE	2.2
1	U	328	ARG	2.2
1	D	59	VAL	2.2
1	T	514	TYR	2.2
1	V	534	GLU	2.2
1	V	549	TYR	2.2
1	W	566	GLU	2.2
1	G	14	ARG	2.2
1	H	273	ARG	2.2
2	l	69	GLU	2.2
2	n	48	TYR	2.2
2	n	112	GLU	2.2
1	R	195	ALA	2.2
1	T	118	GLN	2.2
1	W	313	LYS	2.2
1	B	283	CYS	2.2
1	J	411	ALA	2.2
1	J	552	LEU	2.2
1	J	593	LEU	2.2
2	o	99	ALA	2.2
2	p	81	SER	2.2
2	s	130	SER	2.2
2	a	90	SER	2.2
1	T	323	THR	2.2
1	U	210	PRO	2.2
1	A	521	GLY	2.2
1	L	199	PRO	2.2
2	d	27	GLY	2.2
2	f	109	THR	2.2
2	h	39	PRO	2.2
1	M	312	ASP	2.2
1	M	503	GLU	2.1
1	P	319	VAL	2.2
1	A	378	ASP	2.2
1	B	497	VAL	2.2
1	C	197	ASP	2.2
2	c	59	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	Q	9	GLU	2.1
2	v	69	GLU	2.1
1	U	574	LYS	2.1
1	X	44	TRP	2.1
2	Z	137	TYR	2.1
1	M	538	LEU	2.1
1	Q	125	ALA	2.1
1	R	139	SER	2.1
1	S	538	LEU	2.1
1	U	450	GLN	2.1
1	B	304	PHE	2.1
1	G	359	PHE	2.1
1	I	575	GLN	2.1
2	n	113	LEU	2.1
2	s	92	ALA	2.1
2	s	99	ALA	2.1
2	Z	22	ALA	2.1
2	d	149	PHE	2.1
2	v	136	SER	2.1
2	e	123	LEU	2.1
1	M	20	THR	2.1
1	P	284	THR	2.1
1	A	7	ARG	2.1
1	A	441	ARG	2.1
1	H	127	ARG	2.1
2	m	118	THR	2.1
2	s	24	THR	2.1
1	O	172	HIS	2.1
1	O	306	GLU	2.1
1	A	38	VAL	2.1
1	B	189	GLU	2.1
1	D	226	VAL	2.1
1	H	548	GLU	2.1
1	I	208	VAL	2.1
1	K	276	VAL	2.1
1	L	320	VAL	2.1
1	O	229	LYS	2.1
1	P	43	ASP	2.1
1	V	260	ASP	2.1
1	A	43	ASP	2.1
1	D	84	ASP	2.1
1	G	16	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	L	566	GLU	2.1
2	v	73	HIS	2.1
1	W	191	TYR	2.1
1	G	541	LYS	2.1
1	J	277	TYR	2.1
1	L	369	TYR	2.1
1	O	429	GLN	2.1
1	R	27	ARG	2.1
1	R	400	ALA	2.1
1	W	152	ALA	2.1
1	J	56	GLN	2.1
1	X	183	GLY	2.1
1	J	358	GLY	2.1
2	n	70	GLY	2.1
1	O	385	PRO	2.1
1	Q	243	PRO	2.1
2	n	78	SER	2.1
2	n	106	THR	2.1
2	p	30	PRO	2.1
2	v	66	PRO	2.1
2	Y	30	SER	2.1
1	R	426	ASN	2.1
1	W	375	ASN	2.1
1	C	216	THR	2.1
1	C	542	THR	2.1
1	C	574	LYS	2.1
2	r	91	ILE	2.1
2	Y	115	THR	2.1
2	c	113	ILE	2.1
1	C	53	TYR	2.1
1	E	186	ASP	2.1
1	H	43	ASP	2.1
2	r	128	TYR	2.1
1	M	187	PHE	2.1
1	R	554	LEU	2.1
1	X	389	LEU	2.1
1	X	459	ARG	2.1
1	B	44	TRP	2.1
1	F	418	LEU	2.1
1	I	307	TRP	2.1
1	B	195	ALA	2.1
1	K	411	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
2	v	20	ALA	2.1
2	g	32	ALA	2.1
1	D	419	GLY	2.1
1	I	428	GLY	2.1
2	g	40	GLN	2.1
1	U	414	GLU	2.1
1	V	261	SER	2.1
1	V	300	ILE	2.1
1	B	244	VAL	2.1
1	B	515	GLU	2.1
1	C	154	SER	2.1
1	D	117	GLU	2.1
1	G	349	PRO	2.1
1	J	522	PRO	2.1
1	K	227	GLU	2.1
2	o	54	ILE	2.1
2	o	77	SER	2.1
2	q	130	SER	2.1
2	g	129	ILE	2.1
1	A	344	THR	2.1
1	P	509	ASP	2.1
1	Q	451	ASP	2.1
1	Q	519	ASP	2.1
1	V	171	ARG	2.1
1	V	514	TYR	2.1
1	D	205	ASN	2.1
1	H	213	THR	2.1
1	J	194	ASP	2.1
1	L	517	TYR	2.1
2	b	59	ASP	2.1
1	W	201	PHE	2.1
1	C	94	LEU	2.1
1	H	449	PHE	2.1
1	N	411	ALA	2.1
1	P	544	GLN	2.1
1	T	121	ALA	2.1
1	A	188	ALA	2.1
2	l	146	TRP	2.1
1	Q	326	GLY	2.1
1	R	365	GLY	2.1
1	B	348	LYS	2.1
1	G	135	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
2	b	125	LYS	2.1
1	E	224	GLU	2.1
1	H	226	VAL	2.1
1	K	251	ILE	2.1
1	L	510	ILE	2.1
2	n	29	GLU	2.1
1	T	62	PRO	2.1
1	W	160	SER	2.1
1	F	22	SER	2.1
1	F	543	PRO	2.1
2	s	32	SER	2.1
1	Q	275	ARG	2.1
1	X	172	HIS	2.1
1	F	323	THR	2.1
1	J	284	THR	2.1
1	V	159	ASP	2.1
1	J	339	ASP	2.1
1	M	153	CYS	2.1
1	P	229	LYS	2.1
1	V	248	LYS	2.1
1	V	413	LYS	2.1
1	S	241	GLY	2.1
1	X	562	GLY	2.1
1	E	184	TRP	2.1
1	K	599	ALA	2.1
1	L	90	ALA	2.1
2	o	123	ALA	2.1
2	j	132	ALA	2.1
1	S	341	VAL	2.1
1	X	379	GLU	2.1
1	X	340	ILE	2.1
1	A	280	ILE	2.1
1	B	64	VAL	2.1
1	F	5	GLU	2.1
1	L	133	GLU	2.1
1	G	251	ILE	2.1
1	L	520	VAL	2.1
2	Z	129	ILE	2.1
1	R	274	ARG	2.1
1	A	14	ARG	2.1
1	C	81	ARG	2.1
2	e	138	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	P	335	SER	2.1
1	T	389	LEU	2.1
1	C	172	HIS	2.1
1	G	446	THR	2.1
1	I	405	LEU	2.1
2	k	60	PHE	2.1
2	o	111	LYS	2.1
1	N	107	ALA	2.1
1	P	411	ALA	2.1
1	V	519	ASP	2.1
1	X	401	ASN	2.1
1	G	411	ALA	2.1
1	J	426	ASN	2.1
1	K	101	ASP	2.1
2	p	63	ASP	2.1
2	g	44	ASP	2.1
1	S	419	GLY	2.1
1	X	545	GLY	2.1
1	L	545	GLY	2.1
1	R	185	GLU	2.1
1	W	153	CYS	2.1
1	W	271	ILE	2.1
1	A	276	VAL	2.1
2	Y	89	VAL	2.1
2	c	68	VAL	2.1
2	h	46	VAL	2.1
1	D	103	ARG	2.1
1	J	61	ARG	2.1
1	M	83	LYS	2.1
1	R	67	LEU	2.1
1	C	398	PRO	2.1
1	K	248	LYS	2.1
1	B	172	HIS	2.1
1	C	277	TYR	2.1
1	E	172	HIS	2.1
1	F	261	SER	2.1
2	h	70	SER	2.1
2	i	26	LEU	2.1
1	O	417	THR	2.1
1	O	542	THR	2.1
1	W	183	GLY	2.1
1	W	442	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	365	GLY	2.1
1	F	540	GLY	2.1
1	J	170	ALA	2.1
2	m	23	ALA	2.1
2	g	79	GLY	2.1
2	i	79	GLY	2.1
1	O	175	VAL	2.1
1	T	269	ARG	2.1
1	C	218	GLN	2.1
1	D	40	GLN	2.1
1	G	175	VAL	2.1
1	H	525	GLN	2.1
2	i	68	VAL	2.1
1	M	574	LYS	2.1
1	Q	248	LYS	2.1
1	W	108	LYS	2.1
1	S	554	LEU	2.1
1	C	258	LEU	2.1
1	E	373	LEU	2.1
1	F	389	LEU	2.1
1	F	559	LEU	2.1
1	I	258	LEU	2.1
1	J	98	TYR	2.1
1	N	382	GLY	2.1
1	G	338	ALA	2.1
1	F	355	GLN	2.1
1	G	215	ASP	2.1
1	G	221	GLU	2.1
1	H	294	ALA	2.1
1	L	572	ALA	2.1
2	Z	87	SER	2.1
1	O	496	VAL	2.1
1	S	24	GLU	2.1
1	E	185	GLU	2.1
1	H	458	ARG	2.1
1	I	459	ARG	2.1
1	K	397	VAL	2.1
1	L	459	ARG	2.1
2	c	121	GLU	2.1
2	d	116	ALA	2.1
1	Q	544	GLN	2.1
1	R	544	GLN	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	k	27	ASP	2.1
2	d	44	ASP	2.1
2	f	40	GLN	2.1
1	B	290	LYS	2.1
1	E	83	LYS	2.1
1	A	552	LEU	2.1
1	I	359	PHE	2.1
1	J	292	LEU	2.1
1	E	369	TYR	2.1
1	H	547	PRO	2.1
2	p	58	TYR	2.1
1	O	188	ALA	2.1
1	D	330	ARG	2.1
1	B	415	VAL	2.1
1	C	342	ALA	2.1
1	C	442	ALA	2.1
1	H	25	ALA	2.1
2	a	51	ALA	2.1
2	a	156	HIS	2.1
2	b	116	ALA	2.1
1	O	194	ASP	2.1
1	V	49	THR	2.1
1	D	184	TRP	2.1
1	E	112	ASN	2.1
1	E	519	ASP	2.1
1	F	281	ILE	2.1
1	F	429	GLN	2.1
1	H	169	ASP	2.1
1	H	529	GLN	2.1
1	I	77	ASP	2.1
1	L	312	ASP	2.1
2	l	100	THR	2.1
2	b	109	THR	2.1
2	c	112	ILE	2.1
1	O	444	LEU	2.1
1	C	560	LEU	2.1
1	E	536	LEU	2.1
2	q	149	PHE	2.1
1	X	274	ARG	2.1
1	V	462	GLU	2.1
1	A	204	PRO	2.1
1	B	137	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	274	ARG	2.1
1	N	326	GLY	2.1
1	N	537	GLU	2.1
1	Q	382	GLY	2.1
1	M	173	CYS	2.1
1	Q	416	ALA	2.1
1	U	416	ALA	2.1
1	B	183	GLY	2.1
1	C	419	GLY	2.1
1	I	308	GLY	2.1
2	k	119	ALA	2.1
2	n	12	ALA	2.1
2	t	69	GLU	2.1
2	b	39	PRO	2.1
1	V	123	VAL	2.1
1	D	254	VAL	2.1
1	E	91	ALA	2.1
1	J	297	HIS	2.1
2	Y	51	ALA	2.1
1	M	234	ILE	2.1
1	Q	429	GLN	2.1
1	T	168	SER	2.1
1	X	118	GLN	2.1
1	A	180	SER	2.1
1	A	450	GLN	2.1
1	C	162	SER	2.1
1	G	113	ILE	2.1
1	I	113	ILE	2.1
1	K	399	GLN	2.1
2	q	81	SER	2.1
1	S	74	ASN	2.1
1	T	84	ASP	2.1
1	U	312	ASP	2.1
1	W	205	ASN	2.1
1	A	240	THR	2.1
1	C	192	ASP	2.1
1	C	231	THR	2.1
1	T	359	PHE	2.1
1	D	375	ASN	2.1
1	G	41	TRP	2.1
1	J	519	ASP	2.1
1	L	43	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	c	31	ASP	2.1
1	E	292	LEU	2.1
1	J	34	PHE	2.1
1	K	322	LEU	2.1
2	g	26	LEU	2.1
1	E	273	ARG	2.1
1	J	376	ARG	2.1
1	J	459	ARG	2.1
1	O	228	LYS	2.1
1	O	445	GLU	2.1
1	T	248	LYS	2.1
1	U	545	GLY	2.1
1	W	268	GLU	2.1
1	X	403	TYR	2.1
2	o	135	GLY	2.1
2	f	118	TYR	2.1
1	O	342	ALA	2.1
1	Q	62	PRO	2.1
1	Q	238	PRO	2.1
1	Q	302	PRO	2.1
1	X	395	PRO	2.1
1	B	294	ALA	2.1
1	F	59	VAL	2.1
2	c	45	ALA	2.1
2	c	92	VAL	2.1
2	i	159	PRO	2.1
1	M	429	GLN	2.0
1	T	119	ILE	2.0
1	W	463	ILE	2.0
1	X	575	GLN	2.0
1	C	555	GLN	2.0
1	I	544	GLN	2.0
1	J	40	GLN	2.0
1	J	555	GLN	2.0
1	L	56	GLN	2.0
1	M	164	LEU	2.0
1	M	309	PHE	2.0
1	O	511	ARG	2.0
1	R	196	ASP	2.0
1	S	206	ASP	2.0
1	U	101	ASP	2.0
1	B	498	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	561	ASP	2.0
1	I	72	ARG	2.0
1	K	289	ASP	2.0
1	R	394	ASN	2.0
1	S	573	ASN	2.0
1	J	112	ASN	2.0
2	g	14	THR	2.0
1	N	30	LYS	2.0
1	K	346	LYS	2.0
2	Y	61	LYS	2.0
2	Z	50	GLU	2.0
1	N	454	ALA	2.0
1	O	442	ALA	2.0
1	P	220	ALA	2.0
1	R	411	ALA	2.0
1	T	195	ALA	2.0
1	U	581	VAL	2.0
1	W	208	VAL	2.0
1	B	407	ALA	2.0
1	G	60	VAL	2.0
1	K	425	VAL	2.0
1	L	315	VAL	2.0
2	t	59	VAL	2.0
2	g	102	PRO	2.0
1	U	219	ILE	2.0
1	V	177	HIS	2.0
1	E	219	ILE	2.0
1	F	577	ILE	2.0
2	q	147	HIS	2.0
2	g	94	HIS	2.0
1	R	601	GLN	2.0
1	V	142	GLN	2.0
1	N	329	LEU	2.0
1	M	504	LYS	2.0
1	N	248	LYS	2.0
1	N	289	ASP	2.0
1	R	39	SER	2.0
1	B	245	SER	2.0
1	D	275	ARG	2.0
1	I	99	ARG	2.0
1	L	116	ARG	2.0
1	L	327	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	M	436	ASN	2.0
1	R	184	TRP	2.0
1	N	379	GLU	2.0
1	O	105	ASN	2.0
1	P	161	ASN	2.0
1	P	352	TRP	2.0
2	p	22	ASP	2.0
1	S	100	THR	2.0
1	L	379	GLU	2.0
2	d	109	THR	2.0
1	T	96	GLY	2.0
1	V	111	VAL	2.0
1	X	372	TYR	2.0
2	n	74	GLY	2.0
1	N	390	ALA	2.0
1	O	110	ALA	2.0
1	R	407	ALA	2.0
1	U	75	PRO	2.0
1	X	333	ILE	2.0
1	J	232	ALA	2.0
2	l	91	ILE	2.0
2	t	67	PRO	2.0
1	T	40	GLN	2.0
1	T	328	ARG	2.0
1	B	399	GLN	2.0
1	D	99	ARG	2.0
1	F	155	HIS	2.0
1	J	87	ARG	2.0
1	K	321	ARG	2.0
1	W	432	PHE	2.0
1	A	499	LEU	2.0
1	H	538	LEU	2.0
1	I	552	LEU	2.0
1	K	336	PHE	2.0
1	L	34	PHE	2.0
2	f	96	LEU	2.0
1	R	101	ASP	2.0
1	V	537	GLU	2.0
1	C	523	SER	2.0
1	E	410	SER	2.0
1	I	368	ASP	2.0
2	k	50	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
2	k	72	ASP	2.0
2	s	69	GLU	2.0
2	e	55	GLU	2.0
1	N	55	GLY	2.0
1	O	461	GLY	2.0
1	N	435	VAL	2.0
1	O	115	VAL	2.0
1	Q	153	CYS	2.0
1	Q	455	THR	2.0
1	N	198	ILE	2.0
1	Q	431	ALA	2.0
1	Q	448	VAL	2.0
1	T	508	ASN	2.0
1	E	372	TYR	2.0
2	r	100	THR	2.0
2	d	118	TYR	2.0
2	i	65	THR	2.0
1	T	333	ILE	2.0
1	T	385	PRO	2.0
1	U	146	ARG	2.0
1	X	219	ILE	2.0
2	m	79	ALA	2.0
2	m	126	ALA	2.0
2	q	92	ALA	2.0
2	r	132	MET	2.0
1	V	163	LYS	2.0
1	W	82	PRO	2.0
1	W	297	HIS	2.0
1	E	272	LYS	2.0
1	G	600	LYS	2.0
1	T	15	PHE	2.0
1	T	47	GLN	2.0
1	W	453	LEU	2.0
1	X	536	LEU	2.0
1	F	551	LEU	2.0
1	X	534	GLU	2.0
1	P	602	GLY	2.0
1	Q	318	GLY	2.0
1	Q	27	ARG	2.0
1	R	581	VAL	2.0
1	U	206	ASP	2.0
1	D	55	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	G	159	ASP	2.0
1	I	196	ASP	2.0
1	L	523	SER	2.0
1	V	458	ARG	2.0
1	V	517	TYR	2.0
1	X	50	THR	2.0
1	X	156	VAL	2.0
2	o	71	ASP	2.0
1	A	20	THR	2.0
1	A	80	TYR	2.0
1	P	510	ILE	2.0
1	U	272	LYS	2.0
1	C	324	LYS	2.0
1	H	11	ILE	2.0
1	I	119	ILE	2.0
1	J	119	ILE	2.0
1	K	573	ASN	2.0
2	k	100	THR	2.0
2	t	42	ALA	2.0
2	Y	141	MET	2.0
2	a	114	ALA	2.0
1	O	204	PRO	2.0
1	V	359	PHE	2.0
1	W	444	LEU	2.0
1	C	51	LEU	2.0
1	H	444	LEU	2.0
1	L	398	PRO	2.0
2	a	76	PRO	2.0
2	g	69	PHE	2.0
1	M	598	GLN	2.0
1	V	52	GLN	2.0
1	B	450	GLN	2.0
1	K	56	GLN	2.0
2	c	126	GLN	2.0
2	q	112	GLU	2.0
2	c	78	GLU	2.0
1	P	274	ARG	2.0
1	Q	14	ARG	2.0
1	U	269	ARG	2.0
1	M	235	TYR	2.0
1	U	301	VAL	2.0
1	V	391	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
1	W	412	VAL	2.0
1	C	175	VAL	2.0
1	F	310	VAL	2.0
2	a	131	ARG	2.0
2	e	119	GLY	2.0
2	j	60	GLY	2.0
1	E	312	ASP	2.0
1	F	339	ASP	2.0
1	H	391	TYR	2.0
1	H	514	TYR	2.0
1	J	126	TRP	2.0
1	J	367	ASP	2.0
1	L	261	SER	2.0
1	U	20	THR	2.0
1	W	535	ILE	2.0
1	B	340	ILE	2.0
1	G	577	ILE	2.0
1	J	338	ALA	2.0
2	s	91	ILE	2.0
2	t	92	ALA	2.0
2	Y	147	ASN	2.0
2	g	147	ASN	2.0
1	O	57	PHE	2.0
1	C	449	PHE	2.0
1	G	557	PHE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.