



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:43 AM GMT

PDB ID : 3MVO  
Title : Crystal structure of bovine glutamate dehydrogenase complexed with Eu3+  
Authors : Smith, T.J.; Li, M.  
Deposited on : 2010-05-04  
Resolution : 3.23 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

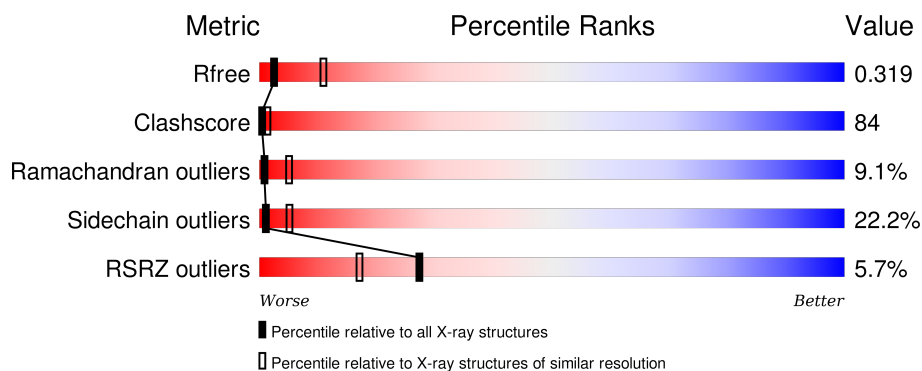
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.23 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))
$R_{free}$	91344	1092 (3.28-3.20)
Clashscore	102246	1227 (3.28-3.20)
Ramachandran outliers	100387	1204 (3.28-3.20)
Sidechain outliers	100360	1203 (3.28-3.20)
RSRZ outliers	91569	1097 (3.28-3.20)

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	501	<div> <div>9%</div> <div>17% 57% 22%</div> <div>..</div> </div>
1	B	501	<div> <div>5%</div> <div>19% 59% 18%</div> <div>..</div> </div>
1	C	501	<div> <div>9%</div> <div>22% 54% 21%</div> <div>..</div> </div>
1	D	501	<div> <div>3%</div> <div>20% 57% 20%</div> <div>..</div> </div>
1	E	501	<div> <div>5%</div> <div>22% 54% 21%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	501	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLU	A	502	-	-	X	-
2	GLU	C	502	-	-	X	-
2	GLU	D	502	-	-	X	-
2	GLU	E	502	-	-	X	-
2	GLU	F	502	-	-	X	-

## 2 Entry composition [i](#)

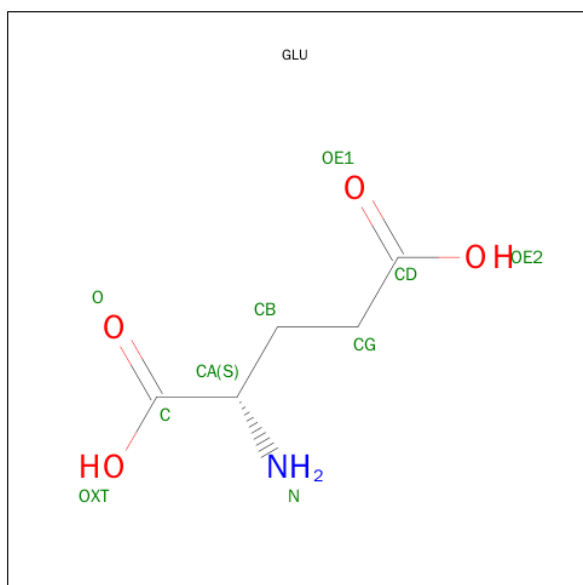
There are 4 unique types of molecules in this entry. The entry contains 23630 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutamate dehydrogenase 1, mitochondrial.

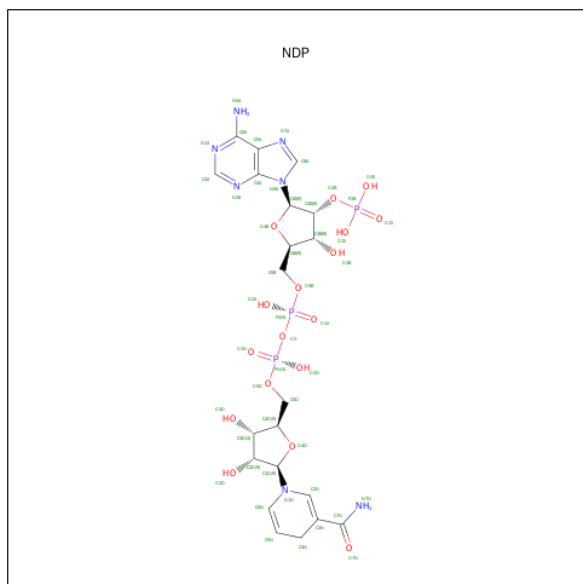
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			
1	B	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			
1	C	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			
1	D	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			
1	E	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			
1	F	495	Total	C	N	O	S	0	0	0
			3880	2449	681	731	19			

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		
2	C	1	Total	C	N	O	0	0
			10	5	1	4		
2	D	1	Total	C	N	O	0	0
			10	5	1	4		
2	E	1	Total	C	N	O	0	0
			10	5	1	4		
2	F	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula:  $C_{21}H_{30}N_7O_{17}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

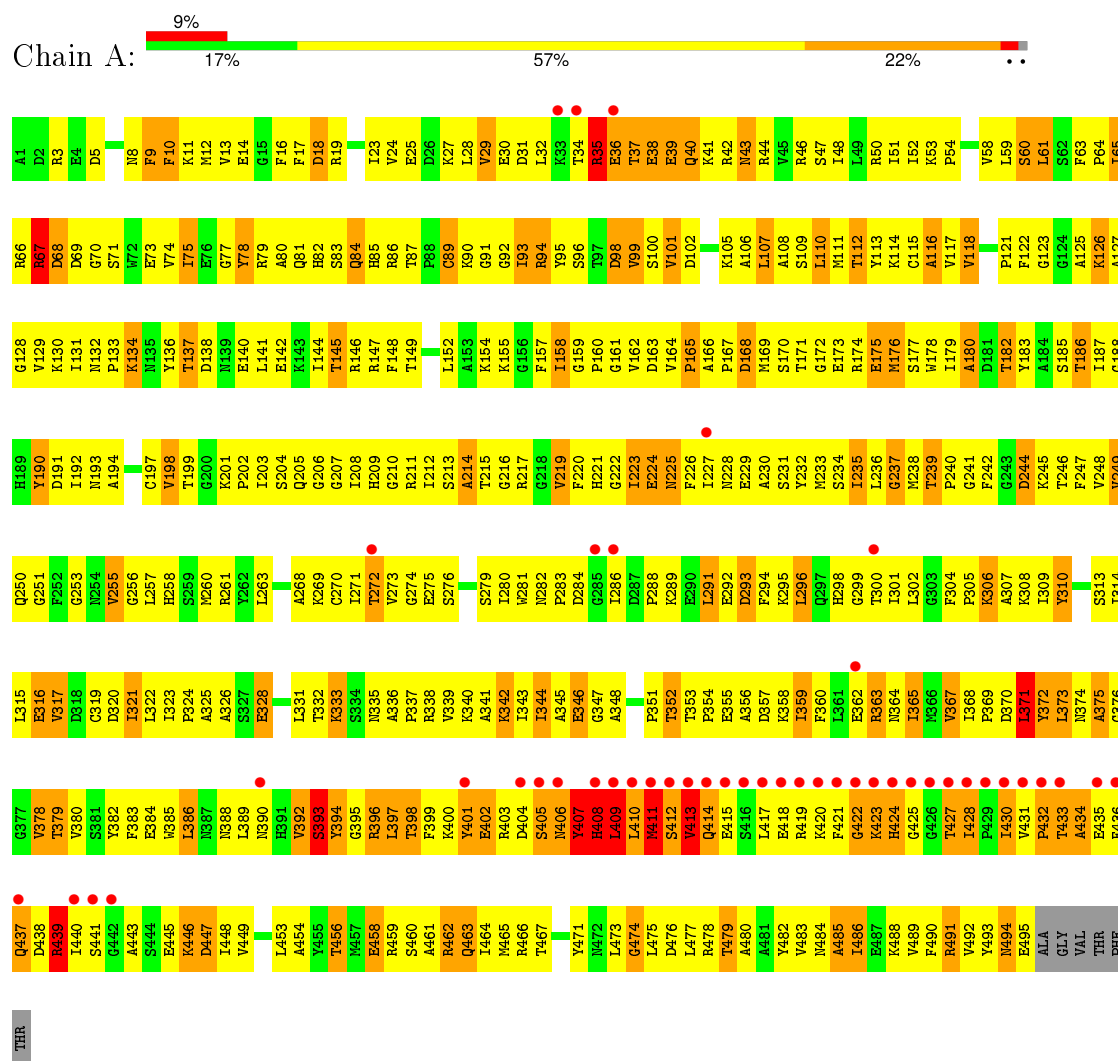
- Molecule 4 is EUROPIUM (III) ION (three-letter code: EU3) (formula: Eu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Eu	0	0
			1	1		
4	D	1	Total	Eu	0	0
			1	1		

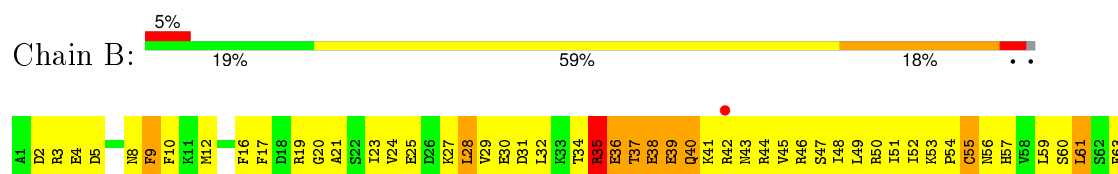
### 3 Residue-property plots

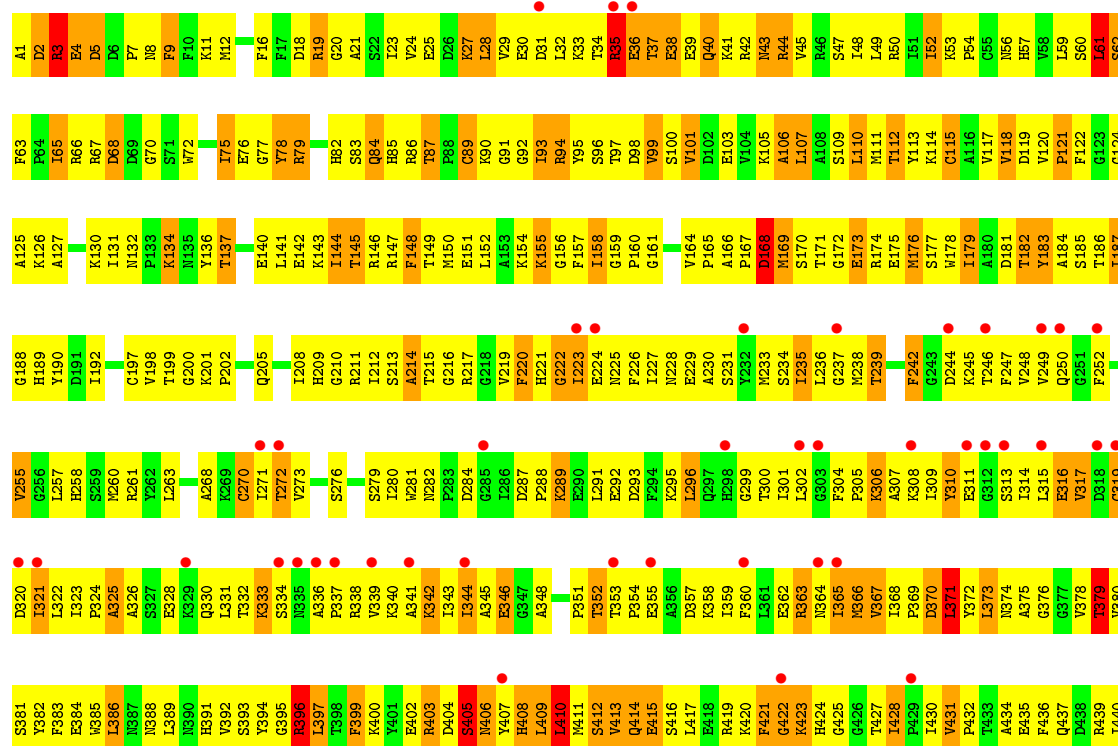
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Glutamate dehydrogenase 1, mitochondrial



- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

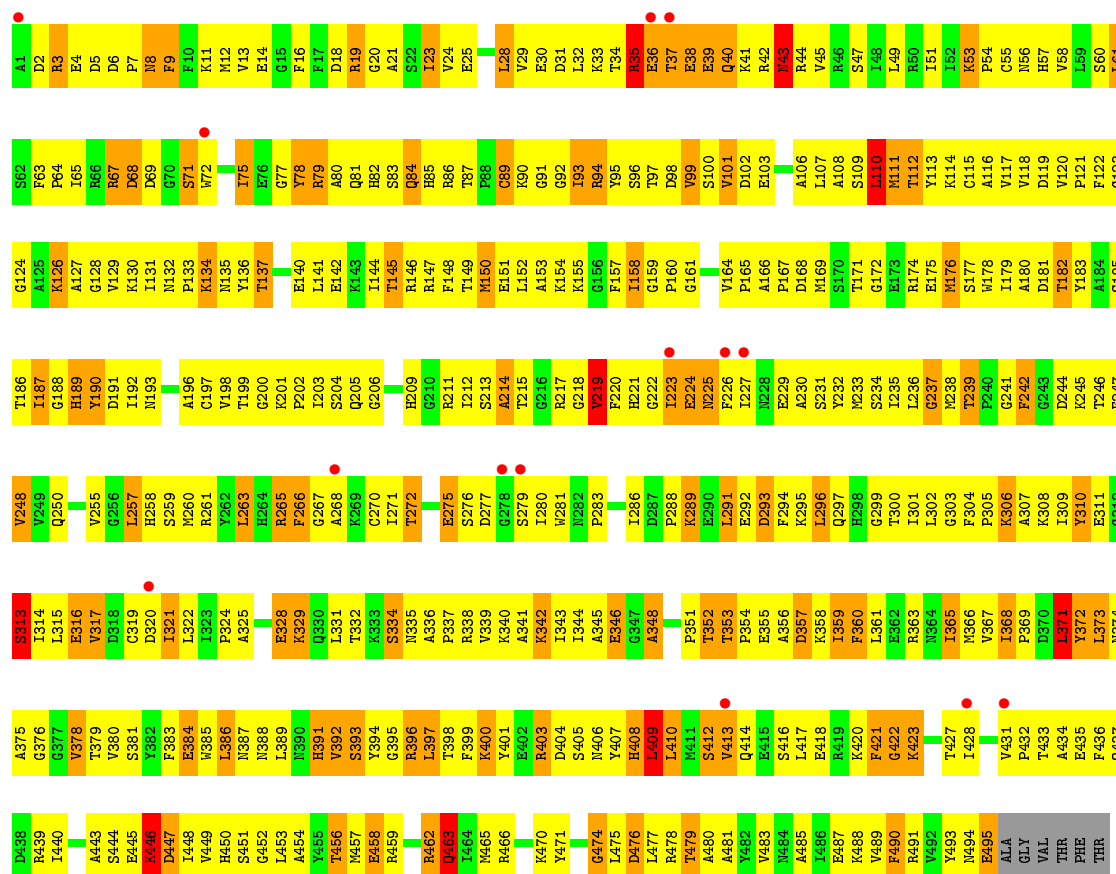




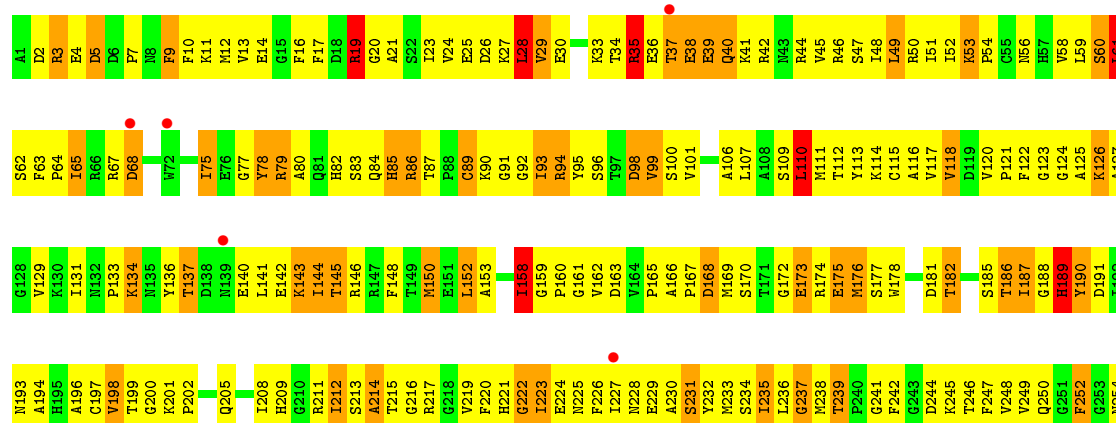


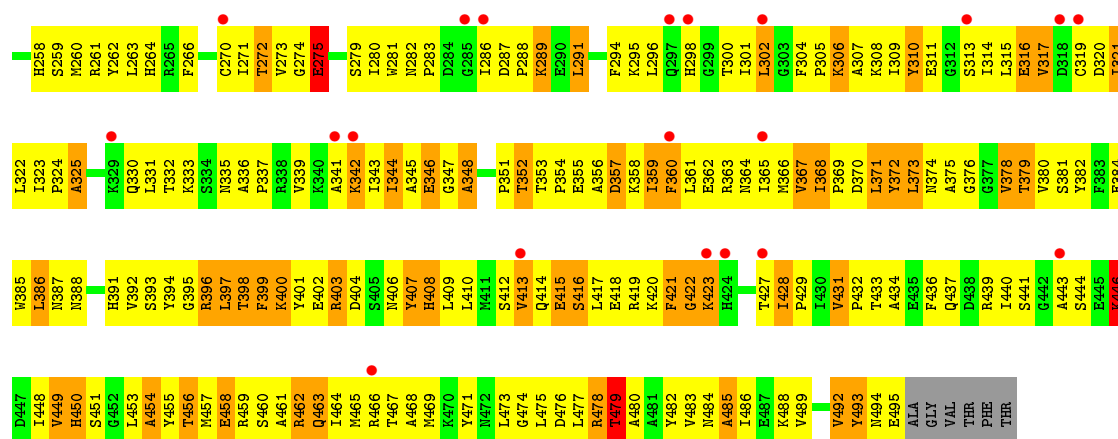


• Molecule 1: Glutamate dehydrogenase 1, mitochondrial

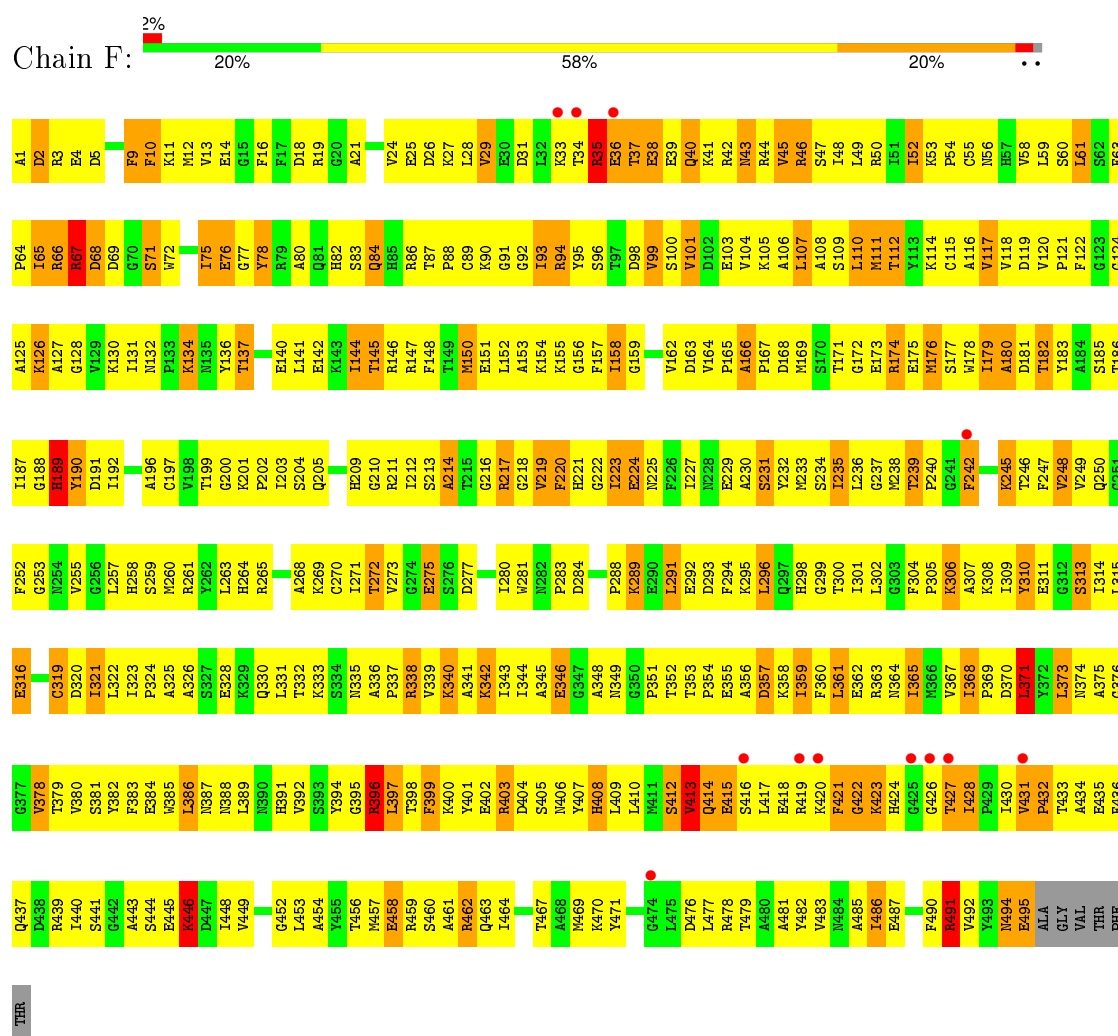


• Molecule 1: Glutamate dehydrogenase 1, mitochondrial





• Molecule 1: Glutamate dehydrogenase 1, mitochondrial



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.11Å 98.76Å 165.64Å 90.00° 101.55° 90.00°	Depositor
Resolution (Å)	43.89 – 3.23 47.44 – 3.23	Depositor EDS
% Data completeness (in resolution range)	90.1 (43.89-3.23) 90.2 (47.44-3.23)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 3.25Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_353)	Depositor
R, $R_{free}$	0.261 , 0.310 0.241 , 0.319	Depositor DCC
$R_{free}$ test set	2840 reflections (5.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 33.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 55739 reflections	Xtriage
$F_o, F_c$ correlation	0.80	EDS
Total number of atoms	23630	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, EU3

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	0.92	11/3962 (0.3%)	0.81	3/5348 (0.1%)
1	B	0.81	7/3962 (0.2%)	0.82	6/5348 (0.1%)
1	C	0.53	1/3962 (0.0%)	0.74	4/5348 (0.1%)
1	D	0.52	1/3962 (0.0%)	0.72	1/5348 (0.0%)
1	E	0.51	1/3962 (0.0%)	0.70	0/5348
1	F	0.54	1/3962 (0.0%)	0.70	1/5348 (0.0%)
All	All	0.66	22/23772 (0.1%)	0.75	15/32088 (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	B	0	1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	401	TYR	CD1-CE1	25.60	1.77	1.39
1	A	401	TYR	CD2-CE2	21.54	1.71	1.39
1	B	436	PHE	CE1-CZ	20.24	1.75	1.37
1	A	401	TYR	CE2-CZ	17.79	1.61	1.38
1	B	436	PHE	CD1-CE1	16.55	1.72	1.39
1	A	401	TYR	CE1-CZ	14.64	1.57	1.38
1	B	436	PHE	CE2-CZ	14.61	1.65	1.37
1	B	436	PHE	CD2-CE2	13.34	1.66	1.39
1	A	408	HIS	N-CA	10.05	1.66	1.46
1	A	401	TYR	CG-CD2	9.58	1.51	1.39
1	B	443	ALA	N-CA	9.56	1.65	1.46
1	A	401	TYR	CG-CD1	9.52	1.51	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	436	PHE	CG-CD1	8.03	1.50	1.38
1	C	89	CYS	CB-SG	-6.52	1.71	1.82
1	F	89	CYS	CB-SG	-6.25	1.71	1.82
1	E	89	CYS	CB-SG	-6.16	1.71	1.82
1	B	436	PHE	CG-CD2	6.07	1.47	1.38
1	A	392	VAL	CB-CG1	-5.54	1.41	1.52
1	A	89	CYS	CB-SG	-5.40	1.73	1.81
1	A	392	VAL	CA-CB	-5.19	1.43	1.54
1	A	393	SER	CA-CB	5.17	1.60	1.52
1	D	89	CYS	CB-SG	-5.04	1.73	1.81

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	TYR	C-N-CA	11.29	149.91	121.70
1	B	442	GLY	C-N-CA	7.76	141.09	121.70
1	A	409	LEU	CA-CB-CG	6.42	130.06	115.30
1	C	61	LEU	CA-CB-CG	6.09	129.32	115.30
1	C	409	LEU	CA-CB-CG	6.05	129.22	115.30
1	B	410	LEU	CB-CG-CD1	5.97	121.15	111.00
1	D	409	LEU	CA-CB-CG	5.94	128.97	115.30
1	F	89	CYS	CA-CB-SG	-5.85	103.46	114.00
1	B	407	TYR	N-CA-C	-5.47	96.24	111.00
1	B	386	LEU	CA-CB-CG	5.35	127.61	115.30
1	C	410	LEU	CB-CG-CD2	5.34	120.09	111.00
1	B	430	ILE	CG1-CB-CG2	-5.33	99.68	111.40
1	C	115	CYS	CA-CB-SG	-5.25	104.55	114.00
1	B	440	ILE	CG1-CB-CG2	5.13	122.70	111.40
1	A	408	HIS	CB-CA-C	-5.04	100.31	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	443	ALA	Peptide

## 5.2 Too-close contacts [i](#)

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	3880	0	3842	1074	0
1	B	3880	0	3842	991	0
1	C	3880	0	3843	684	0
1	D	3880	0	3843	592	0
1	E	3880	0	3843	588	0
1	F	3880	0	3843	576	0
2	A	10	0	5	5	0
2	B	10	0	5	3	0
2	C	10	0	5	12	0
2	D	10	0	5	9	0
2	E	10	0	5	6	0
2	F	10	0	5	6	0
3	A	48	0	26	15	0
3	B	48	0	26	15	0
3	C	48	0	26	19	0
3	D	48	0	26	15	0
3	E	48	0	26	10	0
3	F	48	0	26	13	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
All	All	23630	0	23242	3956	0

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 84.

All (3956) 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)
1:A:414:GLN:HG2	1:B:430:ILE:CG2	1.17	1.61
1:A:401:TYR:CD1	1:A:401:TYR:CE1	1.77	1.55
1:A:409:LEU:CD2	1:B:407:TYR:H	1.24	1.51
1:A:401:TYR:CD1	1:B:443:ALA:CA	1.95	1.47
1:A:414:GLN:CG	1:B:430:ILE:HG22	1.54	1.35
1:A:428:ILE:HG12	1:B:428:ILE:CB	1.53	1.35
1:A:414:GLN:HB3	1:B:431:VAL:CA	1.55	1.35
1:A:409:LEU:HD22	1:B:407:TYR:N	1.35	1.35
1:A:428:ILE:CG1	1:B:428:ILE:HB	1.60	1.31
1:A:401:TYR:CD1	1:B:442:GLY:C	1.93	1.30
1:A:428:ILE:HB	1:B:430:ILE:CG1	1.61	1.29
1:A:412:SER:HB3	1:B:407:TYR:CG	1.67	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:GLU:H	1:B:432:PRO:CD	1.45	1.28
1:A:82:HIS:CD2	1:A:112:THR:HG21	1.68	1.28
1:A:410:LEU:C	1:B:410:LEU:HD13	1.51	1.28
1:A:411:MET:O	1:A:414:GLN:HB2	1.15	1.26
1:A:428:ILE:CB	1:B:430:ILE:HG13	1.66	1.26
1:A:401:TYR:CD1	1:B:442:GLY:O	1.84	1.26
1:A:434:ALA:N	1:C:412:SER:HB2	1.50	1.25
1:A:408:HIS:CE1	1:B:436:PHE:HA	1.74	1.23
1:A:436:PHE:N	1:C:408:HIS:HB3	1.55	1.20
1:A:409:LEU:CD1	1:B:406:ASN:H	1.56	1.19
1:A:410:LEU:N	1:B:406:ASN:HB2	1.57	1.19
1:B:82:HIS:CD2	1:B:112:THR:HG21	1.78	1.17
1:A:411:MET:HE2	1:B:433:THR:HG23	1.20	1.17
1:C:321:ILE:HG22	1:C:343:ILE:HB	1.24	1.16
1:A:414:GLN:CG	1:B:430:ILE:CG2	2.14	1.16
1:C:434:ALA:HA	1:C:437:GLN:HE22	1.08	1.16
1:A:434:ALA:H	1:C:412:SER:CB	1.58	1.15
1:A:410:LEU:CD1	1:B:410:LEU:HD12	1.75	1.15
1:E:52:ILE:HD13	1:E:489:VAL:HG12	1.21	1.15
1:A:414:GLN:HB3	1:B:431:VAL:C	1.67	1.15
1:A:430:ILE:HD12	1:B:430:ILE:HG21	1.17	1.14
1:A:409:LEU:HD13	1:B:406:ASN:N	1.59	1.14
1:A:410:LEU:HD12	1:B:410:LEU:HD12	1.28	1.14
1:A:433:THR:HA	1:C:412:SER:HB2	1.30	1.13
1:A:433:THR:HB	1:C:412:SER:N	1.63	1.13
2:E:502:GLU:HA	3:E:552:NDP:H41N	1.15	1.13
1:A:414:GLN:HG3	1:B:410:LEU:CD2	1.76	1.13
1:A:409:LEU:HG	1:B:403:ARG:HA	1.16	1.12
1:A:412:SER:HB3	1:B:407:TYR:CD2	1.84	1.12
1:A:415:GLU:HG3	1:B:431:VAL:HG23	1.28	1.12
1:A:409:LEU:HD23	1:B:407:TYR:HB2	1.14	1.12
1:A:408:HIS:HB3	1:B:440:ILE:HA	1.27	1.12
1:E:321:ILE:HG22	1:E:343:ILE:HB	1.26	1.12
1:A:406:ASN:O	1:A:410:LEU:HB2	1.46	1.11
1:A:418:GLU:HA	1:B:429:PRO:HB2	1.17	1.11
1:A:430:ILE:CG1	1:B:413:VAL:HB	1.81	1.10
1:A:435:GLU:HB3	1:C:408:HIS:CG	1.86	1.10
1:B:236:LEU:HD21	1:B:342:LYS:HG2	1.34	1.10
1:A:410:LEU:HB3	1:B:436:PHE:CE2	1.87	1.09
1:A:415:GLU:H	1:B:432:PRO:HD2	1.03	1.09
1:A:411:MET:HB2	1:B:436:PHE:CD2	1.88	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:LEU:HG	1:B:403:ARG:CA	1.83	1.09
1:A:433:THR:HA	1:C:412:SER:CB	1.83	1.09
1:A:411:MET:HG3	1:B:432:PRO:HA	1.26	1.08
1:A:401:TYR:CD1	1:B:443:ALA:HA	1.53	1.08
1:A:408:HIS:CE1	1:B:439:ARG:HG2	1.87	1.08
1:A:201:LYS:NZ	1:A:388:ASN:HD21	1.49	1.08
1:A:409:LEU:O	1:A:412:SER:HB2	1.53	1.08
1:A:321:ILE:HG22	1:A:343:ILE:HB	1.33	1.08
1:A:436:PHE:HB2	1:C:405:SER:C	1.73	1.08
1:B:63:PHE:CE1	1:B:75:ILE:HD11	1.89	1.07
1:F:236:LEU:HD21	1:F:342:LYS:HG2	1.34	1.07
1:A:408:HIS:NE2	1:B:438:ASP:N	2.02	1.07
1:A:434:ALA:HA	1:A:437:GLN:HE22	1.14	1.07
1:D:321:ILE:HG22	1:D:343:ILE:HB	1.35	1.07
1:C:173:GLU:OE2	1:C:202:PRO:HA	1.53	1.07
1:A:430:ILE:HG23	1:B:413:VAL:HG21	1.25	1.06
1:B:434:ALA:HA	1:B:437:GLN:HE22	1.17	1.06
1:A:436:PHE:HB3	1:C:409:LEU:H	0.90	1.05
1:A:415:GLU:N	1:B:432:PRO:HD2	1.71	1.05
2:C:502:GLU:HB3	3:C:552:NDP:H41N	1.32	1.05
1:A:436:PHE:HB3	1:C:409:LEU:N	1.71	1.05
1:A:413:VAL:HG23	1:B:410:LEU:CB	1.86	1.04
1:F:148:PHE:O	1:F:152:LEU:HD12	1.55	1.04
1:B:217:ARG:HG2	1:B:217:ARG:HH11	1.22	1.04
1:D:160:PRO:HG3	1:D:193:ASN:O	1.56	1.04
1:A:407:TYR:O	1:B:436:PHE:CD2	2.05	1.04
1:A:414:GLN:HG2	1:B:430:ILE:HG23	1.35	1.03
1:A:411:MET:O	1:A:414:GLN:CB	2.04	1.03
1:D:56:ASN:HD22	1:D:84:GLN:HE21	1.04	1.03
1:D:56:ASN:HD22	1:D:84:GLN:NE2	1.56	1.03
1:F:82:HIS:CD2	1:F:112:THR:HG21	1.94	1.03
1:D:236:LEU:HD21	1:D:342:LYS:HG2	1.40	1.03
1:A:413:VAL:HG23	1:B:410:LEU:HB3	1.35	1.02
1:E:91:GLY:HA3	1:E:125:ALA:O	1.59	1.02
1:A:96:SER:HB3	1:A:99:VAL:HG13	1.40	1.02
1:A:415:GLU:HB3	1:A:419:ARG:NH2	1.74	1.02
1:A:433:THR:CA	1:C:412:SER:HB2	1.89	1.01
1:C:95:TYR:OH	1:C:145:THR:HB	1.59	1.01
1:A:406:ASN:HA	1:B:406:ASN:OD1	1.60	1.01
1:A:433:THR:CG2	1:C:413:VAL:HG23	1.91	1.01
1:C:117:VAL:HG21	1:C:371:LEU:HD22	1.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:HIS:HD2	1:B:261:ARG:NH1	1.58	1.01
1:C:406:ASN:H	1:C:406:ASN:ND2	1.46	1.00
1:A:201:LYS:HZ1	1:A:388:ASN:ND2	1.57	1.00
1:A:413:VAL:CG1	1:B:411:MET:HG2	1.90	1.00
1:B:409:LEU:O	1:B:412:SER:HB2	1.61	1.00
1:A:410:LEU:CD1	1:B:409:LEU:HD22	1.91	1.00
1:D:94:ARG:NH1	1:D:107:LEU:HD21	1.74	1.00
1:B:72:TRP:HB2	1:E:47:SER:HB3	1.42	1.00
1:A:224:GLU:HB2	1:A:242:PHE:HE2	1.25	1.00
1:A:408:HIS:ND1	1:B:439:ARG:HG2	1.74	1.00
1:A:405:SER:HB3	1:B:402:GLU:OE2	1.59	1.00
1:C:458:GLU:HG3	1:C:459:ARG:N	1.77	0.99
1:B:56:ASN:HD22	1:B:84:GLN:NE2	1.61	0.99
1:A:95:TYR:OH	1:A:145:THR:HB	1.63	0.99
1:E:53:LYS:HB3	1:E:54:PRO:HD3	1.41	0.99
1:A:414:GLN:HB3	1:B:431:VAL:N	1.77	0.98
1:E:201:LYS:NZ	1:E:388:ASN:HD21	1.61	0.98
1:C:107:LEU:HB3	1:C:126:LYS:HG2	1.44	0.98
1:A:409:LEU:HB3	1:B:406:ASN:OD1	1.63	0.98
1:A:428:ILE:HD12	1:B:430:ILE:H	1.28	0.98
1:A:414:GLN:CG	1:B:410:LEU:HD21	1.93	0.98
1:A:410:LEU:O	1:B:410:LEU:HD22	1.63	0.97
1:B:272:THR:OG1	1:B:314:ILE:HD11	1.65	0.97
1:B:35:ARG:HD2	1:B:35:ARG:H	1.26	0.97
1:A:434:ALA:HA	1:A:437:GLN:NE2	1.79	0.97
1:A:430:ILE:HG13	1:B:430:ILE:HD13	1.43	0.96
1:A:421:PHE:HB3	1:B:427:THR:OG1	1.63	0.96
1:A:413:VAL:HG11	1:B:411:MET:HG2	1.44	0.96
1:A:433:THR:OG1	1:C:411:MET:N	1.99	0.96
1:C:300:THR:HG22	1:C:302:LEU:H	1.27	0.96
1:A:430:ILE:HG13	1:B:413:VAL:HB	1.45	0.96
1:A:414:GLN:HG3	1:B:410:LEU:HD21	1.00	0.96
1:D:313:SER:HB3	1:D:316:GLU:HB2	1.46	0.96
1:A:63:PHE:CE1	1:A:75:ILE:HD11	1.99	0.96
1:A:433:THR:HG22	1:C:413:VAL:CG2	1.96	0.96
1:A:421:PHE:HB3	1:B:427:THR:HG1	1.30	0.96
1:C:117:VAL:CG2	1:C:371:LEU:HD22	1.95	0.96
1:D:219:VAL:HA	1:D:373:LEU:CD2	1.96	0.96
1:A:411:MET:H	1:B:436:PHE:HE2	1.12	0.96
1:A:141:LEU:O	1:A:145:THR:HG22	1.65	0.96
1:F:63:PHE:CE1	1:F:75:ILE:HD11	2.01	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:HIS:CD2	1:B:439:ARG:H	1.83	0.95
1:D:219:VAL:HA	1:D:373:LEU:HD22	1.47	0.95
1:E:35:ARG:HD2	1:E:35:ARG:H	1.32	0.95
1:A:430:ILE:HD12	1:B:430:ILE:CG2	1.97	0.95
1:B:321:ILE:HG22	1:B:343:ILE:HB	1.45	0.95
1:F:458:GLU:HG3	1:F:459:ARG:N	1.82	0.95
1:A:436:PHE:CD2	1:C:409:LEU:HB3	2.01	0.95
1:A:434:ALA:N	1:C:412:SER:CB	2.24	0.95
1:E:118:VAL:HG11	1:E:375:ALA:CB	1.97	0.95
1:A:428:ILE:HD12	1:B:430:ILE:N	1.80	0.94
1:A:408:HIS:CA	1:B:436:PHE:CG	2.37	0.94
1:A:490:PHE:O	1:A:491:ARG:HD2	1.64	0.94
1:E:175:GLU:HA	1:E:178:TRP:HE3	1.29	0.94
1:A:430:ILE:CB	1:B:410:LEU:HG	1.97	0.94
1:A:418:GLU:HG3	1:B:431:VAL:HB	1.48	0.94
1:A:90:LYS:HB2	1:A:122:PHE:CD1	2.03	0.94
1:B:53:LYS:HB3	1:B:54:PRO:HD3	1.49	0.94
1:A:409:LEU:HB3	1:B:406:ASN:CG	1.89	0.93
1:A:411:MET:HE2	1:B:433:THR:CG2	1.98	0.93
1:A:414:GLN:HE21	1:B:431:VAL:N	1.66	0.93
1:D:244:ASP:HB2	1:D:245:LYS:HD2	1.48	0.93
1:E:131:ILE:O	1:E:133:PRO:HD3	1.68	0.93
1:E:177:SER:HB2	1:E:202:PRO:HG2	1.49	0.93
1:A:433:THR:C	1:C:412:SER:HB2	1.89	0.93
1:E:141:LEU:O	1:E:145:THR:HG22	1.67	0.93
1:A:148:PHE:CE2	1:A:152:LEU:HD11	2.03	0.93
1:A:161:GLY:HA2	1:C:192:ILE:HG13	1.50	0.93
1:F:382:TYR:O	1:F:386:LEU:HD22	1.69	0.93
1:A:411:MET:O	1:B:432:PRO:HD3	1.68	0.93
1:A:433:THR:HG22	1:C:413:VAL:H	1.34	0.93
1:B:437:GLN:HA	1:B:440:ILE:HD12	1.48	0.93
1:D:69:ASP:OD2	1:D:71:SER:HB3	1.69	0.93
1:E:52:ILE:HD13	1:E:489:VAL:CG1	1.99	0.93
1:A:415:GLU:N	1:B:432:PRO:CD	2.30	0.92
1:B:171:THR:HG22	1:B:175:GLU:HG3	1.50	0.92
1:C:24:VAL:CG1	1:C:483:VAL:HG13	1.99	0.92
1:A:410:LEU:HD12	1:B:410:LEU:CD1	1.98	0.92
1:A:146:ARG:HB3	1:A:182:THR:HG21	1.47	0.92
1:A:428:ILE:O	1:B:430:ILE:HA	1.69	0.92
1:B:405:SER:O	1:B:408:HIS:HB2	1.68	0.92
1:A:409:LEU:CD2	1:B:407:TYR:HB2	1.98	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:HIS:CD2	1:D:112:THR:HG21	2.03	0.92
1:A:407:TYR:N	1:B:436:PHE:CE1	2.38	0.92
1:A:409:LEU:CB	1:B:406:ASN:OD1	2.18	0.92
1:A:408:HIS:CD2	1:B:437:GLN:CA	2.53	0.92
1:C:434:ALA:HA	1:C:437:GLN:NE2	1.85	0.92
1:A:412:SER:CB	1:B:407:TYR:CG	2.52	0.92
1:A:436:PHE:CB	1:C:409:LEU:H	1.81	0.92
1:E:175:GLU:HA	1:E:178:TRP:CE3	2.05	0.91
1:A:411:MET:HB2	1:B:436:PHE:HD2	1.34	0.91
1:D:255:VAL:HG12	3:D:552:NDP:O2N	1.70	0.91
1:A:439:ARG:HD2	1:C:405:SER:HA	1.52	0.91
1:A:415:GLU:HB2	1:B:432:PRO:HD2	1.50	0.91
1:B:68:ASP:HB2	1:B:140:GLU:OE1	1.69	0.91
1:F:217:ARG:HH11	1:F:217:ARG:HG2	1.34	0.91
1:A:414:GLN:HE21	1:B:431:VAL:H	0.92	0.91
1:A:409:LEU:HD21	1:B:404:ASP:N	1.86	0.91
1:A:401:TYR:CG	1:B:443:ALA:HB2	2.06	0.91
1:A:224:GLU:HB2	1:A:242:PHE:CE2	2.06	0.91
1:E:244:ASP:HB2	1:E:245:LYS:HD2	1.54	0.90
1:A:236:LEU:HD21	1:A:342:LYS:HG2	1.51	0.90
1:A:401:TYR:CG	1:B:443:ALA:CB	2.52	0.90
1:A:411:MET:CE	1:B:433:THR:HG23	1.99	0.90
1:A:414:GLN:CB	1:B:431:VAL:C	2.39	0.90
1:A:118:VAL:HG11	1:A:375:ALA:CB	2.01	0.90
1:E:107:LEU:HD23	1:E:126:LYS:HE2	1.53	0.90
1:F:470:LYS:HG2	1:F:471:TYR:CE2	2.07	0.90
1:E:93:ILE:HB	1:E:127:ALA:HB3	1.54	0.90
1:A:430:ILE:CG2	1:B:413:VAL:HG21	2.02	0.90
1:A:409:LEU:HD13	1:B:406:ASN:H	0.77	0.90
1:A:430:ILE:CG1	1:B:430:ILE:HD13	2.01	0.90
1:D:272:THR:OG1	1:D:314:ILE:HD11	1.72	0.90
1:A:430:ILE:HG12	1:B:413:VAL:HB	1.50	0.89
1:D:300:THR:HG22	1:D:302:LEU:H	1.35	0.89
1:A:248:VAL:HG23	1:A:272:THR:O	1.71	0.89
1:A:280:ILE:HB	1:A:307:ALA:CB	2.00	0.89
1:C:167:PRO:HG3	1:C:176:MET:HG2	1.54	0.89
1:F:141:LEU:O	1:F:145:THR:HG22	1.71	0.89
1:B:408:HIS:HB3	1:C:436:PHE:HB2	1.54	0.89
1:A:409:LEU:CD2	1:B:407:TYR:N	2.08	0.89
1:C:199:THR:HA	1:C:384:GLU:OE1	1.72	0.89
1:D:417:LEU:HD23	1:F:428:ILE:HG21	1.52	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:GLU:HB3	1:C:408:HIS:CB	2.01	0.89
1:F:169:MET:HA	3:F:552:NDP:O2A	1.72	0.89
1:E:217:ARG:HD2	1:E:262:TYR:CZ	2.08	0.89
1:E:63:PHE:CE1	1:E:75:ILE:HD11	2.08	0.89
1:C:333:LYS:HB2	1:C:355:GLU:HG3	1.55	0.88
1:E:434:ALA:HA	1:E:437:GLN:HE22	1.38	0.88
1:D:201:LYS:HZ1	1:D:388:ASN:HD21	1.13	0.88
1:D:247:PHE:HB3	1:D:321:ILE:HG12	1.55	0.88
1:A:409:LEU:HB3	1:B:406:ASN:CB	2.03	0.88
1:A:409:LEU:HD23	1:B:407:TYR:CB	2.03	0.88
1:A:408:HIS:CD2	1:B:437:GLN:HA	2.08	0.88
1:F:95:TYR:OH	1:F:145:THR:HB	1.73	0.88
1:B:24:VAL:CG1	1:B:483:VAL:HG13	2.03	0.88
1:B:331:LEU:HD23	1:B:360:PHE:HZ	1.38	0.88
1:A:411:MET:CG	1:B:432:PRO:HA	2.02	0.88
1:B:160:PRO:HD3	1:B:197:CYS:HB3	1.56	0.88
1:A:411:MET:N	1:B:436:PHE:HE2	1.71	0.88
1:C:35:ARG:HG2	1:C:36:GLU:H	1.38	0.88
1:B:281:TRP:HB3	1:B:310:TYR:HB2	1.52	0.88
1:A:495:GLU:HG2	1:C:178:TRP:HE1	1.39	0.88
1:C:214:ALA:HB1	1:C:380:VAL:HG21	1.56	0.88
1:A:411:MET:HG3	1:B:432:PRO:CA	2.03	0.88
1:B:167:PRO:HG3	1:B:176:MET:CG	2.04	0.88
2:C:502:GLU:CB	3:C:552:NDP:H41N	2.04	0.87
1:C:19:ARG:HH11	1:C:19:ARG:HG2	1.39	0.87
1:F:35:ARG:H	1:F:35:ARG:HD2	1.38	0.87
1:B:403:ARG:CG	1:B:403:ARG:O	2.21	0.87
1:B:348:ALA:O	1:B:351:PRO:HD3	1.75	0.87
1:E:16:PHE:HE2	1:E:354:PRO:HB3	1.39	0.87
1:A:410:LEU:HD13	1:B:409:LEU:HD22	1.55	0.87
1:F:114:LYS:HA	1:F:371:LEU:HD23	1.56	0.87
1:A:415:GLU:CB	1:B:432:PRO:HD2	2.04	0.87
1:A:253:GLY:HA3	3:A:552:NDP:H52A	1.56	0.87
1:E:281:TRP:CB	1:E:310:TYR:HB2	2.03	0.87
1:F:247:PHE:HB3	1:F:321:ILE:HG12	1.57	0.87
1:F:114:LYS:HA	1:F:371:LEU:CD2	2.04	0.87
1:A:35:ARG:H	1:A:35:ARG:HD2	1.37	0.87
1:B:315:LEU:O	1:B:339:VAL:HG13	1.75	0.87
1:E:82:HIS:CD2	1:E:112:THR:HG21	2.09	0.87
1:A:433:THR:HG22	1:C:413:VAL:HG23	1.53	0.87
1:A:210:GLY:O	1:A:214:ALA:HB2	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:TYR:N	1:B:436:PHE:CZ	2.42	0.86
1:F:90:LYS:NZ	2:F:502:GLU:OE1	2.07	0.86
1:B:199:THR:HA	1:B:384:GLU:OE1	1.74	0.86
1:C:148:PHE:CE2	1:C:152:LEU:HD11	2.11	0.86
1:D:19:ARG:HH11	1:D:19:ARG:HG2	1.40	0.86
1:D:96:SER:O	1:D:130:LYS:HA	1.76	0.86
1:A:408:HIS:ND1	1:B:436:PHE:HA	1.91	0.86
1:E:90:LYS:HD3	1:E:122:PHE:CE1	2.11	0.86
1:A:430:ILE:CD1	1:B:430:ILE:HG21	2.06	0.86
1:C:406:ASN:N	1:C:406:ASN:ND2	2.19	0.86
2:B:502:GLU:HA	3:B:552:NDP:H41N	1.54	0.86
1:C:112:THR:HB	1:C:124:GLY:H	1.40	0.86
1:D:355:GLU:OE2	1:D:358:LYS:HE3	1.76	0.86
1:F:162:VAL:HG23	1:F:163:ASP:N	1.91	0.85
1:A:408:HIS:NE2	1:B:439:ARG:N	2.24	0.85
1:E:199:THR:HA	1:E:384:GLU:OE1	1.76	0.85
1:A:280:ILE:HB	1:A:307:ALA:HB1	1.55	0.85
1:C:63:PHE:CZ	1:C:75:ILE:HD11	2.12	0.85
1:B:116:ALA:O	1:B:488:LYS:HD2	1.76	0.85
1:E:258:HIS:HD2	1:E:261:ARG:NH1	1.74	0.85
1:A:414:GLN:CB	1:B:431:VAL:CA	2.50	0.85
1:A:201:LYS:NZ	1:A:388:ASN:ND2	2.19	0.85
1:C:107:LEU:CB	1:C:126:LYS:HG2	2.07	0.85
1:A:333:LYS:HB2	1:A:355:GLU:HG3	1.58	0.85
1:B:342:LYS:HB2	1:B:342:LYS:NZ	1.91	0.85
1:C:224:GLU:HB2	1:C:242:PHE:HE2	1.39	0.85
1:D:137:THR:HG23	1:D:140:GLU:HG3	1.59	0.85
1:D:95:TYR:OH	1:D:145:THR:HB	1.77	0.85
1:E:91:GLY:O	1:E:165:PRO:HA	1.77	0.84
1:B:217:ARG:NH1	1:B:221:HIS:HE1	1.76	0.84
1:D:434:ALA:HA	1:D:437:GLN:HE22	1.42	0.84
1:C:201:LYS:NZ	1:C:388:ASN:HD21	1.76	0.84
1:D:462:ARG:HG3	1:D:466:ARG:HH12	1.42	0.84
1:D:420:LYS:C	1:D:421:PHE:HD2	1.79	0.84
1:C:305:PRO:HB2	1:C:306:LYS:CD	2.07	0.84
1:A:408:HIS:CB	1:B:440:ILE:HA	2.07	0.84
1:E:150:MET:HE1	1:E:187:ILE:HD11	1.58	0.84
1:E:375:ALA:O	1:E:379:THR:OG1	1.96	0.84
1:A:446:LYS:H	1:A:446:LYS:HD2	1.42	0.84
1:C:63:PHE:CE1	1:C:75:ILE:HD11	2.12	0.84
1:E:224:GLU:HB2	1:E:242:PHE:HE2	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:348:ALA:HB1	3:D:552:NDP:O3D	1.78	0.84
1:B:313:SER:HB3	1:B:316:GLU:HB2	1.60	0.84
1:F:271:ILE:HD12	1:F:272:THR:CG2	2.07	0.84
1:F:281:TRP:HB3	1:F:310:TYR:HB2	1.59	0.84
1:A:417:LEU:HB3	1:B:414:GLN:HE22	1.41	0.83
1:A:404:ASP:HA	1:B:439:ARG:CD	2.08	0.83
1:A:226:PHE:HE2	1:A:465:MET:HG2	1.41	0.83
1:A:415:GLU:N	1:B:431:VAL:HA	1.92	0.83
1:A:197:CYS:SG	1:A:198:VAL:HG12	2.17	0.83
2:E:502:GLU:CA	3:E:552:NDP:H41N	2.05	0.83
1:F:153:ALA:HA	1:F:158:ILE:HG22	1.58	0.83
1:A:410:LEU:HB3	1:B:436:PHE:HE2	1.42	0.83
1:A:414:GLN:NE2	1:B:431:VAL:H	1.76	0.83
1:A:82:HIS:HD2	1:A:112:THR:HG21	1.43	0.83
1:D:111:MET:SD	2:D:502:GLU:HA	2.17	0.83
1:B:434:ALA:HA	1:B:437:GLN:NE2	1.92	0.83
1:C:410:LEU:HD23	1:C:432:PRO:HD3	1.59	0.83
1:C:201:LYS:HZ1	1:C:388:ASN:HD21	1.26	0.83
1:A:425:GLY:HA3	1:B:427:THR:O	1.76	0.83
1:A:315:LEU:HD12	1:A:335:ASN:HD21	1.41	0.83
1:A:281:TRP:HB3	1:A:310:TYR:HB2	1.60	0.83
1:B:255:VAL:HG12	3:B:552:NDP:O2N	1.79	0.83
1:E:332:THR:HG22	1:E:353:THR:HG21	1.59	0.83
1:C:420:LYS:C	1:C:421:PHE:HD2	1.81	0.83
1:E:174:ARG:HB3	1:E:175:GLU:OE2	1.79	0.83
1:E:224:GLU:CB	1:E:242:PHE:HE2	1.92	0.83
1:A:410:LEU:HD11	1:B:409:LEU:HD22	1.58	0.83
1:C:236:LEU:HD21	1:C:342:LYS:CG	2.08	0.83
1:A:433:THR:CB	1:C:412:SER:N	2.41	0.82
1:D:227:ILE:HD12	1:D:233:MET:SD	2.18	0.82
1:B:413:VAL:CG1	1:C:413:VAL:HG11	2.08	0.82
1:C:201:LYS:HZ1	1:C:388:ASN:ND2	1.77	0.82
1:A:458:GLU:HG3	1:A:459:ARG:N	1.93	0.82
1:D:35:ARG:HD2	1:D:35:ARG:H	1.43	0.82
1:B:53:LYS:O	1:B:82:HIS:HE1	1.62	0.82
1:C:434:ALA:CA	1:C:437:GLN:HE22	1.90	0.82
1:B:90:LYS:HZ3	1:B:164:VAL:HG12	1.44	0.82
1:A:436:PHE:HB2	1:C:405:SER:O	1.77	0.82
1:F:63:PHE:CZ	1:F:75:ILE:HD11	2.14	0.82
1:B:403:ARG:HG2	1:B:403:ARG:O	1.76	0.82
1:A:436:PHE:H	1:C:408:HIS:C	1.82	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:ILE:CD1	1:E:489:VAL:HG12	2.07	0.82
1:E:117:VAL:HG12	1:E:118:VAL:HG12	1.60	0.82
1:C:304:PHE:CD1	1:C:305:PRO:HD2	2.15	0.82
1:A:258:HIS:HD2	1:A:261:ARG:HH11	1.28	0.82
1:A:430:ILE:HB	1:B:410:LEU:HG	1.62	0.82
1:F:281:TRP:CB	1:F:310:TYR:HB2	2.10	0.82
1:B:160:PRO:HG3	1:B:193:ASN:O	1.80	0.82
1:C:405:SER:HB3	1:C:406:ASN:ND2	1.94	0.82
1:A:260:MET:HG2	1:A:288:PRO:HG3	1.60	0.82
1:D:29:VAL:HG21	1:D:42:ARG:HE	1.44	0.81
1:C:344:ILE:HB	1:C:367:VAL:HG12	1.61	0.81
1:B:63:PHE:CZ	1:B:75:ILE:HD11	2.14	0.81
1:A:435:GLU:O	1:A:438:ASP:HB2	1.77	0.81
1:A:131:ILE:O	1:A:133:PRO:HD3	1.79	0.81
1:F:201:LYS:HD2	1:F:205:GLN:O	1.80	0.81
1:B:68:ASP:OD1	1:B:137:THR:HG21	1.81	0.81
1:A:410:LEU:CG	1:B:410:LEU:HD12	2.10	0.81
1:A:408:HIS:NE2	1:B:437:GLN:N	2.29	0.81
1:E:219:VAL:HG11	1:E:259:SER:OG	1.81	0.81
1:F:167:PRO:HG3	1:F:176:MET:HE3	1.63	0.81
1:E:224:GLU:HB2	1:E:242:PHE:CE2	2.15	0.81
1:E:247:PHE:HB3	1:E:321:ILE:HG12	1.63	0.81
1:D:433:THR:HG23	1:E:412:SER:OG	1.79	0.81
1:A:410:LEU:CA	1:B:410:LEU:HD13	2.11	0.81
1:E:281:TRP:HB3	1:E:310:TYR:HB2	1.61	0.81
1:A:249:VAL:HB	1:A:323:ILE:HB	1.62	0.81
1:F:59:LEU:HD22	1:F:157:PHE:CD1	2.16	0.81
1:A:279:SER:CB	1:A:314:ILE:HD13	2.11	0.81
1:D:332:THR:HG22	1:D:353:THR:HG21	1.62	0.81
1:F:345:ALA:HB1	1:F:373:LEU:HD11	1.62	0.81
1:F:12:MET:HG3	1:F:354:PRO:HD3	1.63	0.81
1:D:225:ASN:HD21	1:D:458:GLU:HB2	1.44	0.81
1:F:348:ALA:HB1	3:F:552:NDP:O3D	1.81	0.81
1:A:164:VAL:HG13	1:A:197:CYS:O	1.81	0.80
1:A:90:LYS:HD3	1:A:122:PHE:CE1	2.16	0.80
1:D:63:PHE:CE1	1:D:75:ILE:HD11	2.16	0.80
1:E:368:ILE:HG22	1:E:373:LEU:HG	1.63	0.80
1:F:346:GLU:HG2	1:F:351:PRO:HG2	1.63	0.80
1:E:382:TYR:O	1:E:386:LEU:HD22	1.81	0.80
1:F:434:ALA:HA	1:F:437:GLN:HE22	1.46	0.80
1:A:411:MET:CG	1:B:433:THR:H	1.95	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:343:ILE:HG23	1:D:366:MET:HE3	1.62	0.80
1:F:199:THR:HA	1:F:384:GLU:OE1	1.80	0.80
1:B:222:GLY:HA3	1:B:373:LEU:HD21	1.62	0.80
1:C:405:SER:O	1:C:408:HIS:N	2.13	0.80
1:D:281:TRP:CZ2	1:D:283:PRO:HG3	2.17	0.80
1:E:332:THR:O	1:E:336:ALA:HB2	1.80	0.80
1:D:289:LYS:HE2	1:D:293:ASP:OD1	1.81	0.80
1:A:412:SER:HB3	1:B:407:TYR:CD1	2.17	0.80
1:A:435:GLU:C	1:C:408:HIS:HB3	2.00	0.80
1:F:363:ARG:NH1	1:F:365:ILE:HD11	1.97	0.80
1:C:244:ASP:HB2	1:C:245:LYS:HD2	1.63	0.80
1:A:323:ILE:HD13	1:A:345:ALA:HB3	1.64	0.79
1:D:82:HIS:CG	1:D:112:THR:HG21	2.16	0.79
1:A:476:ASP:OD2	1:A:479:THR:HG23	1.81	0.79
1:C:3:ARG:CZ	1:C:4:GLU:HG3	2.12	0.79
1:D:148:PHE:CE2	1:D:152:LEU:HD11	2.16	0.79
1:D:400:LYS:HD3	1:D:400:LYS:O	1.83	0.79
1:B:167:PRO:HG3	1:B:176:MET:HG3	1.65	0.79
1:D:315:LEU:HD13	1:D:331:LEU:CD1	2.12	0.79
1:D:35:ARG:HG2	1:D:36:GLU:H	1.46	0.79
1:E:382:TYR:CZ	1:E:386:LEU:HD21	2.17	0.79
1:A:411:MET:HG3	1:B:433:THR:N	1.96	0.79
1:E:372:TYR:CE1	1:E:461:ALA:HB2	2.17	0.79
1:C:90:LYS:HD2	1:C:164:VAL:HB	1.65	0.79
1:A:411:MET:HG3	1:B:433:THR:H	1.45	0.79
1:C:72:TRP:HB2	1:F:47:SER:HB3	1.63	0.79
1:A:414:GLN:HB3	1:B:431:VAL:HA	1.63	0.79
1:E:372:TYR:CZ	1:E:461:ALA:HB2	2.18	0.79
1:A:428:ILE:HB	1:B:430:ILE:HG13	0.83	0.79
1:B:258:HIS:HD2	1:B:261:ARG:HH11	1.25	0.79
1:E:44:ARG:NH2	1:E:494:ASN:HB2	1.98	0.79
1:F:1:ALA:O	1:F:2:ASP:HB2	1.81	0.79
1:F:420:LYS:C	1:F:421:PHE:HD2	1.86	0.79
1:A:410:LEU:C	1:B:410:LEU:CD1	2.45	0.79
1:B:399:PHE:HA	1:B:441:SER:HB3	1.65	0.79
1:B:444:SER:OG	1:B:446:LYS:HD3	1.82	0.79
1:B:274:GLY:O	1:B:275:GLU:HB2	1.81	0.79
1:E:115:CYS:SG	1:E:378:VAL:HG11	2.22	0.79
1:A:402:GLU:O	1:A:406:ASN:OD1	2.00	0.78
1:E:211:ARG:O	1:E:214:ALA:HB3	1.83	0.78
1:B:16:PHE:CD1	1:B:478:ARG:HD3	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:281:TRP:HB3	1:D:310:TYR:HB2	1.63	0.78
1:D:107:LEU:HD23	1:D:126:LYS:HE2	1.65	0.78
1:A:410:LEU:H	1:B:406:ASN:HB2	1.48	0.78
1:B:420:LYS:C	1:B:421:PHE:HD2	1.85	0.78
1:A:408:HIS:HA	1:B:436:PHE:CG	1.78	0.78
1:A:226:PHE:CE2	1:A:465:MET:HG2	2.18	0.78
1:A:118:VAL:HG11	1:A:375:ALA:HB3	1.63	0.78
1:D:109:SER:O	1:D:112:THR:HG23	1.83	0.78
1:D:90:LYS:HZ1	1:D:166:ALA:HB2	1.47	0.78
1:E:45:VAL:O	1:E:49:LEU:HB2	1.84	0.78
1:D:391:HIS:O	1:D:392:VAL:HG23	1.84	0.78
1:D:439:ARG:NH1	1:E:404:ASP:HB3	1.99	0.78
1:A:443:ALA:HB1	1:A:448:ILE:HG12	1.64	0.78
1:A:324:PRO:HD2	1:A:347:GLY:H	1.48	0.78
1:E:444:SER:OG	1:E:446:LYS:HD3	1.84	0.78
1:A:414:GLN:C	1:B:430:ILE:O	2.21	0.78
1:C:236:LEU:HD21	1:C:342:LYS:HG2	1.64	0.78
1:A:224:GLU:CB	1:A:242:PHE:HE2	1.96	0.78
1:B:35:ARG:HG2	1:B:36:GLU:H	1.49	0.78
1:E:35:ARG:HG2	1:E:36:GLU:H	1.45	0.78
1:F:333:LYS:HB2	1:F:355:GLU:HG3	1.65	0.78
1:A:417:LEU:HB3	1:B:414:GLN:NE2	1.99	0.78
1:B:406:ASN:C	1:B:408:HIS:H	1.84	0.77
1:B:323:ILE:HD13	1:B:345:ALA:HB3	1.65	0.77
1:E:458:GLU:HG3	1:E:459:ARG:N	1.98	0.77
2:C:502:GLU:HB3	3:C:552:NDP:C4N	2.13	0.77
1:A:414:GLN:CB	1:B:431:VAL:N	2.47	0.77
1:A:415:GLU:H	1:B:432:PRO:HD3	1.45	0.77
1:A:82:HIS:CG	1:A:112:THR:HG21	2.19	0.77
1:C:79:ARG:HD2	1:C:127:ALA:HB2	1.65	0.77
1:A:242:PHE:CE1	1:A:263:LEU:HD22	2.18	0.77
1:F:255:VAL:HG13	1:F:325:ALA:HB1	1.67	0.77
1:B:107:LEU:HB3	1:B:126:LYS:HG2	1.67	0.77
1:C:368:ILE:CG2	1:C:373:LEU:HG	2.15	0.77
1:E:476:ASP:OD2	1:E:479:THR:HG23	1.84	0.77
1:A:436:PHE:CE1	1:A:440:ILE:HA	2.19	0.77
1:C:406:ASN:N	1:C:406:ASN:HD22	1.81	0.77
1:B:72:TRP:HB2	1:E:47:SER:CB	2.14	0.77
1:A:129:VAL:HG12	1:A:131:ILE:HG12	1.66	0.77
1:B:35:ARG:HG2	1:B:36:GLU:HG3	1.66	0.77
1:E:86:ARG:NH2	1:F:204:SER:O	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:ALA:HB1	3:A:552:NDP:O3D	1.83	0.77
1:A:233:MET:HB3	1:A:238:MET:O	1.84	0.77
1:A:35:ARG:CD	1:A:35:ARG:H	1.97	0.77
1:F:437:GLN:HA	1:F:440:ILE:HB	1.65	0.77
1:D:160:PRO:HD3	1:D:197:CYS:HB3	1.66	0.77
1:D:65:ILE:HG13	1:D:144:ILE:HD13	1.67	0.77
1:D:260:MET:HG2	1:D:288:PRO:HG3	1.67	0.77
1:B:82:HIS:HD2	1:B:112:THR:HG21	1.49	0.76
1:F:211:ARG:HD2	1:F:211:ARG:O	1.85	0.76
1:D:488:LYS:HA	1:D:491:ARG:HD2	1.67	0.76
1:C:358:LYS:HG3	1:C:359:ILE:N	2.00	0.76
1:A:421:PHE:CB	1:B:427:THR:HG1	1.97	0.76
1:F:75:ILE:O	1:F:75:ILE:HD13	1.84	0.76
1:E:79:ARG:HD2	1:E:127:ALA:HB2	1.67	0.76
1:C:131:ILE:HB	1:C:136:TYR:HE2	1.49	0.76
1:E:64:PRO:O	1:E:65:ILE:HD13	1.86	0.76
1:A:401:TYR:O	1:A:404:ASP:HB2	1.85	0.76
1:A:414:GLN:CB	1:B:430:ILE:HG22	2.14	0.76
3:C:552:NDP:H2N	3:C:552:NDP:O5D	1.84	0.76
1:F:394:TYR:HE2	1:F:443:ALA:HB3	1.48	0.76
1:A:12:MET:HG3	1:A:354:PRO:HD3	1.68	0.76
1:C:53:LYS:HB3	1:C:54:PRO:HD3	1.67	0.76
1:B:413:VAL:HG11	1:C:413:VAL:HG11	1.68	0.76
1:B:258:HIS:CD2	1:B:261:ARG:NH1	2.50	0.76
1:A:408:HIS:ND1	1:B:436:PHE:CD1	2.54	0.76
1:A:434:ALA:H	1:C:412:SER:HB2	1.13	0.76
1:B:391:HIS:CD2	1:C:385:TRP:HH2	2.03	0.76
1:B:95:TYR:OH	1:B:145:THR:HB	1.86	0.76
1:F:162:VAL:CG2	1:F:163:ASP:N	2.49	0.76
1:F:399:PHE:HE2	1:F:443:ALA:O	1.69	0.76
1:C:131:ILE:HB	1:C:136:TYR:CE2	2.21	0.76
1:A:403:ARG:O	1:A:407:TYR:HB2	1.86	0.76
1:A:17:PHE:CE1	1:A:486:ILE:HG12	2.20	0.76
1:A:279:SER:HB3	1:A:314:ILE:HD13	1.67	0.76
1:A:414:GLN:O	1:B:430:ILE:O	2.04	0.76
1:C:406:ASN:H	1:C:406:ASN:HD22	1.34	0.76
1:A:436:PHE:H	1:C:408:HIS:HB3	1.49	0.76
1:D:348:ALA:HA	3:D:552:NDP:H1D	1.66	0.76
1:D:25:GLU:O	1:D:29:VAL:HG23	1.86	0.76
1:F:3:ARG:HG2	1:F:4:GLU:HG3	1.68	0.76
1:A:410:LEU:CB	1:B:436:PHE:CE2	2.69	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:TYR:CZ	1:A:461:ALA:HB2	2.21	0.76
1:E:201:LYS:HZ2	1:E:388:ASN:HD21	1.32	0.76
1:B:35:ARG:CD	1:B:35:ARG:H	1.99	0.76
1:B:174:ARG:HD2	1:B:178:TRP:CH2	2.19	0.76
1:A:436:PHE:N	1:C:408:HIS:CB	2.45	0.75
1:A:407:TYR:C	1:B:436:PHE:CG	2.44	0.75
1:A:406:ASN:C	1:B:436:PHE:CZ	2.59	0.75
1:A:5:ASP:HB3	1:A:332:THR:HB	1.69	0.75
1:D:224:GLU:HB2	1:D:242:PHE:HE2	1.50	0.75
1:C:255:VAL:HG22	1:C:325:ALA:HB1	1.69	0.75
1:F:443:ALA:HB1	1:F:448:ILE:HG12	1.67	0.75
1:C:321:ILE:CG2	1:C:343:ILE:HB	2.13	0.75
1:B:247:PHE:HB3	1:B:321:ILE:HG12	1.66	0.75
1:D:153:ALA:HA	1:D:158:ILE:HG22	1.68	0.75
1:B:331:LEU:HD23	1:B:360:PHE:CZ	2.20	0.75
1:C:16:PHE:HE2	1:C:354:PRO:HB3	1.52	0.75
1:D:92:GLY:HA2	1:D:166:ALA:O	1.85	0.75
1:C:37:THR:HA	1:C:40:GLN:HG3	1.67	0.75
1:A:414:GLN:NE2	1:B:431:VAL:O	2.19	0.75
1:C:248:VAL:HG12	1:C:319:CYS:SG	2.26	0.75
1:E:236:LEU:HD21	1:E:342:LYS:CG	2.16	0.75
1:A:428:ILE:HB	1:B:430:ILE:CD1	2.16	0.75
1:B:248:VAL:HG12	1:B:319:CYS:SG	2.26	0.75
1:A:146:ARG:CB	1:A:182:THR:HG21	2.16	0.75
1:A:175:GLU:HA	1:A:178:TRP:CE3	2.21	0.75
1:E:109:SER:O	1:E:112:THR:HG22	1.87	0.75
1:C:397:LEU:HD12	1:C:397:LEU:H	1.52	0.75
1:E:114:LYS:HA	1:E:371:LEU:HD23	1.69	0.75
1:E:63:PHE:CZ	1:E:75:ILE:HD11	2.22	0.75
1:D:37:THR:HA	1:D:40:GLN:HG3	1.68	0.75
1:F:322:LEU:O	1:F:324:PRO:HD3	1.86	0.75
1:B:90:LYS:HD2	1:B:164:VAL:O	1.87	0.75
1:D:247:PHE:CB	1:D:321:ILE:HG12	2.16	0.75
1:D:417:LEU:HD21	1:F:417:LEU:HD13	1.69	0.75
1:D:476:ASP:OD2	1:D:479:THR:HG23	1.87	0.75
1:A:430:ILE:CG2	1:B:410:LEU:HG	2.17	0.75
1:C:281:TRP:O	1:C:307:ALA:HA	1.87	0.75
1:A:98:ASP:O	1:A:100:SER:N	2.20	0.75
1:F:214:ALA:HB1	1:F:380:VAL:HG21	1.68	0.75
1:A:35:ARG:HG2	1:A:36:GLU:H	1.50	0.75
1:A:408:HIS:CE1	1:B:436:PHE:CA	2.64	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48:ILE:O	1:C:52:ILE:HG13	1.88	0.74
1:A:409:LEU:HD22	1:B:406:ASN:N	2.02	0.74
2:A:502:GLU:HA	3:A:552:NDP:H41N	1.68	0.74
1:C:247:PHE:CZ	1:C:270:CYS:HB2	2.22	0.74
1:C:211:ARG:HH22	2:C:502:GLU:HG3	1.50	0.74
1:E:344:ILE:HB	1:E:367:VAL:HG12	1.70	0.74
1:E:188:GLY:O	1:E:190:TYR:N	2.21	0.74
1:A:410:LEU:CD1	1:B:410:LEU:CD1	2.62	0.74
1:A:409:LEU:HD22	1:B:407:TYR:H	0.60	0.74
1:C:103:GLU:O	1:C:106:ALA:HB3	1.88	0.74
1:A:29:VAL:HG13	1:A:41:LYS:HB3	1.68	0.74
1:F:304:PHE:CE2	1:F:306:LYS:HB2	2.23	0.74
1:A:410:LEU:O	1:B:410:LEU:CD2	2.35	0.74
1:A:413:VAL:HG22	1:B:407:TYR:CA	2.16	0.74
1:A:430:ILE:HG12	1:B:413:VAL:CB	2.16	0.74
1:B:363:ARG:NH1	1:B:365:ILE:HD11	2.02	0.74
1:F:171:THR:HB	1:F:175:GLU:HG3	1.69	0.74
1:C:35:ARG:H	1:C:35:ARG:HD2	1.51	0.74
1:D:85:HIS:CD2	1:D:489:VAL:HG13	2.22	0.74
2:F:502:GLU:N	3:F:552:NDP:H41N	2.03	0.74
1:A:430:ILE:HD13	1:B:410:LEU:CG	2.18	0.74
1:A:313:SER:HB3	1:A:316:GLU:HB2	1.70	0.74
1:D:79:ARG:HD3	1:D:152:LEU:HD22	1.67	0.74
1:D:305:PRO:HB2	1:D:306:LYS:HD3	1.68	0.74
1:B:188:GLY:O	1:B:190:TYR:N	2.20	0.74
1:E:158:ILE:HG12	1:E:159:GLY:H	1.52	0.74
1:F:335:ASN:C	1:F:337:PRO:HD2	2.07	0.74
1:C:247:PHE:CE1	1:C:270:CYS:HB2	2.23	0.74
1:E:247:PHE:O	1:E:271:ILE:HG13	1.87	0.74
1:C:313:SER:HB3	1:C:316:GLU:HB2	1.70	0.73
2:C:502:GLU:OE1	3:C:552:NDP:H42N	1.87	0.73
1:F:358:LYS:HG3	1:F:359:ILE:N	2.00	0.73
1:A:385:TRP:HH2	1:C:391:HIS:CD2	2.05	0.73
1:A:433:THR:CG2	1:C:413:VAL:H	2.00	0.73
1:A:433:THR:CG2	1:C:413:VAL:CG2	2.59	0.73
1:B:394:TYR:CE2	1:B:443:ALA:HB3	2.23	0.73
1:C:300:THR:HG22	1:C:302:LEU:N	2.02	0.73
1:B:322:LEU:O	1:B:324:PRO:HD3	1.89	0.73
1:A:36:GLU:O	1:A:37:THR:HG23	1.89	0.73
1:D:98:ASP:O	1:D:130:LYS:HE3	1.87	0.73
1:F:162:VAL:CG2	1:F:163:ASP:H	2.02	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ILE:HD13	1:E:64:PRO:HB3	1.68	0.73
1:A:414:GLN:C	1:B:431:VAL:HA	2.08	0.73
1:A:258:HIS:HD2	1:A:261:ARG:NH1	1.84	0.73
1:E:221:HIS:O	1:E:225:ASN:HB2	1.87	0.73
1:E:453:LEU:CD1	1:E:457:MET:HG2	2.18	0.73
1:E:44:ARG:HH22	1:E:494:ASN:HB2	1.51	0.73
1:B:306:LYS:N	1:B:306:LYS:HD3	2.03	0.73
1:C:410:LEU:HD23	1:C:432:PRO:CD	2.19	0.73
1:E:199:THR:CA	1:E:384:GLU:OE1	2.36	0.73
1:E:281:TRP:HB2	1:E:310:TYR:HB2	1.69	0.73
1:A:201:LYS:HZ1	1:A:388:ASN:HD21	0.76	0.73
1:A:409:LEU:HD21	1:B:404:ASP:CA	2.18	0.73
1:A:412:SER:HA	1:B:432:PRO:HG3	1.71	0.73
1:D:53:LYS:HB3	1:D:54:PRO:HD3	1.70	0.73
1:A:418:GLU:HG3	1:B:431:VAL:CB	2.19	0.73
1:A:406:ASN:ND2	1:B:402:GLU:OE2	2.22	0.73
1:F:230:ALA:O	1:F:231:SER:C	2.27	0.73
1:C:5:ASP:HB3	1:C:332:THR:HB	1.69	0.73
1:A:94:ARG:O	1:A:128:GLY:HA2	1.88	0.73
1:F:380:VAL:HA	1:F:383:PHE:HD2	1.53	0.73
1:A:409:LEU:CG	1:B:403:ARG:HA	2.09	0.73
1:A:271:ILE:HD11	1:A:319:CYS:HB3	1.71	0.73
1:E:118:VAL:HG11	1:E:375:ALA:HB1	1.70	0.73
1:C:24:VAL:HG11	1:C:483:VAL:HG13	1.71	0.73
1:A:236:LEU:HD22	1:A:238:MET:HB2	1.71	0.73
1:A:48:ILE:O	1:A:52:ILE:HG13	1.89	0.73
1:E:114:LYS:HA	1:E:371:LEU:CD2	2.19	0.73
1:A:109:SER:O	1:A:113:TYR:CD1	2.42	0.72
1:E:85:HIS:HB2	1:E:492:VAL:HG21	1.71	0.72
1:E:250:GLN:HG3	1:E:314:ILE:HG21	1.71	0.72
1:B:271:ILE:HD12	1:B:272:THR:HG23	1.71	0.72
1:F:132:ASN:OD1	1:F:134:LYS:HB2	1.89	0.72
1:A:414:GLN:CG	1:B:410:LEU:CD2	2.58	0.72
1:C:326:ALA:O	3:C:552:NDP:H4D	1.88	0.72
1:D:47:SER:O	1:D:51:ILE:HG13	1.89	0.72
1:D:200:GLY:H	1:D:384:GLU:CD	1.93	0.72
1:E:161:GLY:HA2	1:F:192:ILE:HG13	1.70	0.72
1:A:413:VAL:H	1:B:407:TYR:HA	1.54	0.72
1:A:414:GLN:HG2	1:B:430:ILE:HG22	0.73	0.72
1:A:407:TYR:CD1	1:A:440:ILE:CD1	2.72	0.72
1:C:405:SER:O	1:C:408:HIS:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:90:LYS:HB2	1:E:122:PHE:CD1	2.24	0.72
1:B:321:ILE:CG2	1:B:343:ILE:HB	2.18	0.72
1:D:24:VAL:CG1	1:D:483:VAL:HG13	2.20	0.72
1:D:167:PRO:HG3	1:D:176:MET:HG2	1.70	0.72
1:A:436:PHE:H	1:C:409:LEU:N	1.87	0.72
1:D:331:LEU:HD23	1:D:360:PHE:HZ	1.54	0.72
1:F:250:GLN:HG3	1:F:314:ILE:HG21	1.71	0.72
1:A:413:VAL:HG22	1:B:407:TYR:HA	1.69	0.72
1:B:462:ARG:HG3	1:B:466:ARG:HH22	1.53	0.72
1:C:248:VAL:HG23	1:C:272:THR:O	1.90	0.72
1:C:175:GLU:CD	1:C:175:GLU:H	1.90	0.72
1:E:117:VAL:HG21	1:E:371:LEU:HD22	1.70	0.72
1:C:306:LYS:HD3	1:C:306:LYS:N	2.05	0.72
1:D:118:VAL:HG11	1:D:375:ALA:CB	2.19	0.72
1:A:433:THR:HG21	1:C:413:VAL:HG23	1.72	0.72
3:C:552:NDP:O2N	3:C:552:NDP:H52A	1.89	0.72
1:F:247:PHE:CB	1:F:321:ILE:HG12	2.19	0.72
1:C:476:ASP:OD2	1:C:479:THR:HG23	1.90	0.72
1:C:431:VAL:HG23	1:C:432:PRO:HD2	1.71	0.72
1:A:495:GLU:HG2	1:C:178:TRP:NE1	2.04	0.72
1:F:167:PRO:CG	1:F:176:MET:HE3	2.20	0.72
1:C:282:ASN:OD1	1:C:284:ASP:HB2	1.89	0.72
1:E:382:TYR:OH	1:F:392:VAL:HG22	1.89	0.72
1:D:306:LYS:N	1:D:306:LYS:HD3	2.03	0.72
1:A:410:LEU:HG	1:B:410:LEU:CD1	2.18	0.71
1:C:272:THR:OG1	1:C:314:ILE:HD11	1.90	0.71
1:F:5:ASP:HB3	1:F:332:THR:HB	1.71	0.71
1:F:491:ARG:HH11	1:F:491:ARG:HB2	1.55	0.71
1:A:407:TYR:O	1:B:436:PHE:CG	2.44	0.71
1:A:315:LEU:HD12	1:A:335:ASN:ND2	2.04	0.71
1:D:271:ILE:HD12	1:D:272:THR:HG23	1.71	0.71
1:C:177:SER:HB2	1:C:202:PRO:HG2	1.72	0.71
1:F:458:GLU:HG3	1:F:459:ARG:H	1.54	0.71
1:F:271:ILE:HD12	1:F:272:THR:HG22	1.70	0.71
1:C:36:GLU:O	1:C:37:THR:HG23	1.90	0.71
1:B:300:THR:HG22	1:B:302:LEU:H	1.55	0.71
1:C:437:GLN:HA	1:C:440:ILE:HB	1.71	0.71
1:C:175:GLU:HA	1:C:178:TRP:CE3	2.25	0.71
1:E:196:ALA:HA	1:E:388:ASN:HD22	1.55	0.71
1:D:409:LEU:HB2	1:F:436:PHE:CZ	2.25	0.71
1:D:183:TYR:O	1:D:183:TYR:CD2	2.43	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:PRO:HB3	1:C:172:GLY:HA2	1.73	0.71
1:E:201:LYS:HZ1	1:E:388:ASN:HD21	1.38	0.71
1:D:413:VAL:HG11	1:F:413:VAL:HG11	1.72	0.71
1:A:404:ASP:CB	1:B:442:GLY:O	2.38	0.71
1:E:211:ARG:HA	1:E:380:VAL:HG11	1.72	0.71
1:D:360:PHE:HA	1:D:365:ILE:HG13	1.72	0.71
1:B:38:GLU:HG2	1:B:39:GLU:N	2.03	0.71
1:F:414:GLN:O	1:F:416:SER:N	2.23	0.71
1:D:96:SER:HB3	1:D:99:VAL:HG13	1.72	0.71
1:E:457:MET:CE	1:E:457:MET:HA	2.21	0.71
1:B:217:ARG:HG2	1:B:217:ARG:NH1	2.02	0.71
1:E:53:LYS:O	1:E:82:HIS:HE1	1.72	0.71
1:F:137:THR:O	1:F:140:GLU:N	2.23	0.71
1:B:16:PHE:CE1	1:B:478:ARG:HD3	2.25	0.71
1:B:132:ASN:OD1	1:B:134:LYS:HB2	1.91	0.71
1:B:421:PHE:N	1:B:421:PHE:CD2	2.58	0.71
1:A:430:ILE:CD1	1:B:430:ILE:HD13	2.20	0.71
1:A:408:HIS:CD2	1:B:437:GLN:N	2.59	0.71
1:D:164:VAL:HG13	1:D:198:VAL:HA	1.72	0.71
1:F:35:ARG:H	1:F:35:ARG:CD	2.02	0.71
1:D:320:ASP:O	1:D:341:ALA:HB1	1.91	0.71
1:C:281:TRP:HB3	1:C:310:TYR:HB2	1.71	0.71
1:C:186:THR:O	1:C:189:HIS:HB3	1.91	0.71
1:F:34:THR:HG23	1:F:35:ARG:HD3	1.73	0.71
1:E:3:ARG:HG2	1:E:4:GLU:N	2.03	0.71
1:A:415:GLU:HB3	1:A:419:ARG:HH21	1.55	0.71
1:F:188:GLY:O	1:F:190:TYR:N	2.24	0.71
1:D:280:ILE:HD11	1:D:291:LEU:HD11	1.71	0.71
1:B:217:ARG:NH1	1:B:221:HIS:CE1	2.59	0.71
1:B:72:TRP:CB	1:E:47:SER:HB3	2.19	0.71
1:E:177:SER:HB2	1:E:202:PRO:CG	2.18	0.71
1:E:332:THR:O	1:E:336:ALA:CB	2.38	0.71
1:C:305:PRO:HB2	1:C:306:LYS:HD2	1.69	0.71
1:F:306:LYS:HD3	1:F:306:LYS:N	2.06	0.71
1:C:96:SER:O	1:C:130:LYS:HA	1.90	0.71
1:A:401:TYR:CD1	1:B:443:ALA:CB	2.74	0.70
1:C:211:ARG:HH22	2:C:502:GLU:CG	2.03	0.70
1:B:148:PHE:CE2	1:B:152:LEU:HD11	2.25	0.70
1:C:47:SER:HB3	1:F:72:TRP:HB2	1.73	0.70
1:C:493:TYR:O	1:C:495:GLU:N	2.24	0.70
1:C:412:SER:O	1:C:413:VAL:C	2.30	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:VAL:O	1:C:413:VAL:HG22	1.92	0.70
1:F:29:VAL:HG21	1:F:42:ARG:HE	1.56	0.70
1:B:346:GLU:HG2	1:B:351:PRO:CG	2.21	0.70
1:D:93:ILE:HB	1:D:127:ALA:HB3	1.73	0.70
1:A:16:PHE:HD1	1:A:482:TYR:HH	1.35	0.70
1:A:375:ALA:O	1:A:379:THR:OG1	2.08	0.70
1:C:331:LEU:HD23	1:C:360:PHE:HZ	1.57	0.70
1:A:281:TRP:CB	1:A:310:TYR:HB2	2.21	0.70
1:C:9:PHE:CD2	1:C:106:ALA:HB1	2.26	0.70
1:F:336:ALA:O	1:F:339:VAL:HG23	1.92	0.70
1:E:437:GLN:HA	1:E:440:ILE:HB	1.73	0.70
1:B:24:VAL:O	1:B:27:LYS:N	2.24	0.70
1:B:24:VAL:HG11	1:B:483:VAL:HG13	1.73	0.70
1:D:45:VAL:O	1:D:49:LEU:HB2	1.91	0.70
1:A:415:GLU:CA	1:B:432:PRO:HD2	2.21	0.70
1:C:279:SER:OG	1:C:314:ILE:HB	1.91	0.70
1:B:279:SER:HB3	1:B:314:ILE:HD13	1.73	0.70
1:C:147:ARG:O	1:C:150:MET:N	2.25	0.70
1:A:446:LYS:H	1:A:446:LYS:CD	2.03	0.70
1:B:277:ASP:OD1	1:B:302:LEU:HG	1.92	0.70
1:A:418:GLU:HA	1:B:429:PRO:CB	2.10	0.70
1:A:430:ILE:HG21	1:B:410:LEU:HG	1.73	0.70
1:A:434:ALA:CA	1:A:437:GLN:HE22	1.98	0.70
1:A:114:LYS:HA	1:A:371:LEU:HD23	1.72	0.70
1:D:480:ALA:O	1:D:483:VAL:HB	1.90	0.70
1:B:199:THR:CA	1:B:384:GLU:OE1	2.38	0.70
1:A:409:LEU:N	1:B:440:ILE:HG13	2.07	0.70
1:A:436:PHE:HB2	1:C:405:SER:CA	2.21	0.70
1:D:83:SER:O	1:D:84:GLN:HG3	1.92	0.70
1:A:436:PHE:O	1:A:436:PHE:CD1	2.45	0.70
1:E:321:ILE:CG2	1:E:343:ILE:HB	2.15	0.70
1:B:239:THR:HG23	1:B:245:LYS:NZ	2.06	0.70
1:A:434:ALA:H	1:C:412:SER:CA	2.04	0.70
1:A:428:ILE:HG13	1:B:429:PRO:N	2.05	0.70
1:A:52:ILE:HD13	1:A:489:VAL:HG12	1.73	0.70
1:E:220:PHE:HE1	1:E:266:PHE:HB2	1.55	0.70
1:E:248:VAL:HG21	1:E:314:ILE:HD11	1.72	0.70
1:D:238:MET:CE	1:D:245:LYS:HZ2	2.05	0.70
1:F:459:ARG:O	1:F:462:ARG:HB3	1.91	0.70
1:E:117:VAL:CG2	1:E:371:LEU:HD22	2.21	0.70
1:F:336:ALA:N	1:F:337:PRO:HD2	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:281:TRP:CB	1:D:310:TYR:HB2	2.21	0.70
1:D:315:LEU:O	1:D:339:VAL:HG13	1.92	0.70
1:C:382:TYR:O	1:C:386:LEU:HD22	1.92	0.70
1:B:281:TRP:CB	1:B:310:TYR:HB2	2.21	0.70
1:E:358:LYS:HG3	1:E:359:ILE:N	2.07	0.70
1:E:368:ILE:CG2	1:E:373:LEU:HG	2.21	0.70
1:C:169:MET:HG2	3:C:552:NDP:H52N	1.74	0.70
1:C:25:GLU:O	1:C:29:VAL:HG23	1.92	0.70
1:C:271:ILE:HD12	1:C:272:THR:HG23	1.73	0.69
1:F:150:MET:SD	1:F:186:THR:HG21	2.32	0.69
1:E:304:PHE:CD1	1:E:305:PRO:HD2	2.27	0.69
1:A:436:PHE:CB	1:C:405:SER:C	2.55	0.69
1:A:272:THR:HB	1:A:281:TRP:HA	1.73	0.69
1:F:363:ARG:HH11	1:F:365:ILE:HD11	1.57	0.69
1:F:323:ILE:HD13	1:F:345:ALA:HB3	1.72	0.69
1:D:410:LEU:O	1:D:413:VAL:HG23	1.92	0.69
1:C:308:LYS:HG2	1:C:308:LYS:O	1.92	0.69
1:E:214:ALA:HB1	1:E:380:VAL:HG21	1.74	0.69
1:F:302:LEU:HD22	1:F:309:ILE:HG23	1.73	0.69
1:D:246:THR:O	1:D:320:ASP:HB2	1.91	0.69
1:E:3:ARG:HG2	1:E:4:GLU:H	1.55	0.69
1:A:90:LYS:HB2	1:A:122:PHE:HD1	1.55	0.69
1:C:281:TRP:N	1:C:307:ALA:HB1	2.07	0.69
1:A:281:TRP:CZ2	1:A:283:PRO:HG3	2.28	0.69
1:A:417:LEU:HD11	1:B:411:MET:SD	2.32	0.69
1:A:490:PHE:CD2	1:A:491:ARG:N	2.61	0.69
1:D:462:ARG:HG3	1:D:466:ARG:NH1	2.07	0.69
1:D:399:PHE:O	1:D:401:TYR:N	2.26	0.69
1:E:107:LEU:HB3	1:E:126:LYS:HG2	1.73	0.69
1:F:29:VAL:CG2	1:F:42:ARG:HG2	2.22	0.69
1:F:35:ARG:HG2	1:F:36:GLU:H	1.57	0.69
1:F:394:TYR:CE2	1:F:443:ALA:HB3	2.28	0.69
1:A:385:TRP:O	1:A:389:LEU:HG	1.92	0.69
1:A:428:ILE:HG12	1:B:428:ILE:CA	2.21	0.69
1:C:416:SER:HA	1:C:419:ARG:NH1	2.08	0.69
1:C:242:PHE:CE1	1:C:263:LEU:HD22	2.28	0.69
1:C:202:PRO:HB2	1:C:205:GLN:HG2	1.74	0.69
1:F:109:SER:O	1:F:112:THR:HG23	1.92	0.69
1:A:161:GLY:CA	1:C:192:ILE:HG13	2.21	0.69
1:D:409:LEU:HB2	1:F:436:PHE:CE2	2.27	0.69
1:D:431:VAL:HG23	1:D:432:PRO:HD2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:LEU:HD22	1:B:406:ASN:C	2.11	0.69
1:F:211:ARG:HH22	3:F:552:NDP:H71N	1.39	0.69
1:A:410:LEU:CG	1:B:410:LEU:CD1	2.70	0.69
1:A:433:THR:OG1	1:C:408:HIS:O	2.09	0.69
1:A:400:LYS:NZ	1:B:439:ARG:HH12	1.91	0.69
1:E:166:ALA:HB1	1:E:167:PRO:CD	2.23	0.69
1:F:179:ILE:O	1:F:180:ALA:C	2.29	0.69
1:E:24:VAL:HG23	1:E:28:LEU:HD22	1.75	0.69
1:F:431:VAL:HG23	1:F:432:PRO:HD2	1.73	0.69
1:E:95:TYR:OH	1:E:145:THR:HB	1.93	0.69
1:C:372:TYR:CZ	1:C:461:ALA:HB2	2.28	0.69
1:F:169:MET:HG2	3:F:552:NDP:H52N	1.75	0.69
1:E:453:LEU:HD12	1:E:457:MET:HG2	1.74	0.69
1:A:473:LEU:HB3	1:A:476:ASP:HB3	1.75	0.69
1:F:304:PHE:CD1	1:F:305:PRO:HD2	2.27	0.69
1:B:61:LEU:HB3	1:B:77:GLY:O	1.93	0.69
1:C:462:ARG:HG3	1:C:466:ARG:HH12	1.58	0.69
1:A:411:MET:N	1:B:410:LEU:HD13	2.08	0.69
1:E:248:VAL:HG23	1:E:272:THR:O	1.92	0.69
1:B:12:MET:HG3	1:B:354:PRO:HD3	1.75	0.69
1:B:222:GLY:HA3	1:B:373:LEU:CD2	2.22	0.69
1:D:68:ASP:OD1	1:D:137:THR:HG21	1.93	0.69
1:E:449:VAL:HG12	1:E:450:HIS:N	2.07	0.69
1:A:323:ILE:CD1	1:A:345:ALA:HB3	2.23	0.68
1:A:96:SER:HB3	1:A:99:VAL:CG1	2.22	0.68
1:B:485:ALA:O	1:B:489:VAL:HG23	1.94	0.68
1:E:99:VAL:HG23	1:E:99:VAL:O	1.92	0.68
1:A:408:HIS:CE1	1:B:435:GLU:O	2.46	0.68
1:A:410:LEU:O	1:B:410:LEU:HD13	1.91	0.68
1:A:408:HIS:HD2	1:B:437:GLN:HA	1.58	0.68
1:B:209:HIS:CD2	1:B:446:LYS:HA	2.29	0.68
1:F:167:PRO:HG3	1:F:176:MET:HG2	1.74	0.68
1:A:490:PHE:O	1:A:491:ARG:CD	2.40	0.68
1:E:345:ALA:HB1	1:E:373:LEU:HD11	1.75	0.68
1:B:279:SER:OG	1:B:314:ILE:HB	1.93	0.68
1:D:37:THR:O	1:D:38:GLU:HB2	1.94	0.68
1:D:132:ASN:CG	1:D:135:ASN:ND2	2.47	0.68
1:A:409:LEU:HD12	1:B:402:GLU:C	2.12	0.68
1:B:118:VAL:HG11	1:B:375:ALA:HB1	1.76	0.68
1:D:115:CYS:SG	1:D:378:VAL:HG11	2.33	0.68
1:F:174:ARG:O	1:F:177:SER:N	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:ARG:HH21	1:B:169:MET:HG3	1.58	0.68
1:A:27:LYS:HE2	1:A:31:ASP:OD1	1.93	0.68
1:A:428:ILE:C	1:B:430:ILE:HG12	2.12	0.68
1:C:224:GLU:CB	1:C:242:PHE:HE2	2.07	0.68
1:D:315:LEU:HD13	1:D:331:LEU:HD12	1.74	0.68
1:C:210:GLY:O	1:C:214:ALA:HB2	1.93	0.68
1:C:5:ASP:C	1:C:7:PRO:HD3	2.13	0.68
1:E:53:LYS:CB	1:E:54:PRO:HD3	2.19	0.68
1:B:281:TRP:CZ2	1:B:283:PRO:HG3	2.29	0.68
1:D:93:ILE:HD11	1:D:95:TYR:CE1	2.28	0.68
1:F:150:MET:HE1	1:F:187:ILE:HD11	1.76	0.68
1:D:34:THR:HG23	1:D:35:ARG:HD3	1.76	0.68
1:A:64:PRO:O	1:A:65:ILE:HD13	1.93	0.68
1:A:409:LEU:HB3	1:B:406:ASN:HB2	1.74	0.68
1:B:314:ILE:HD12	1:B:317:VAL:HG21	1.74	0.68
1:F:236:LEU:HD21	1:F:342:LYS:CG	2.19	0.68
1:B:56:ASN:HD22	1:B:84:GLN:HE21	1.40	0.68
1:E:226:PHE:O	1:E:229:GLU:HB3	1.94	0.68
1:D:420:LYS:C	1:D:421:PHE:CD2	2.66	0.68
1:B:126:LYS:HG3	1:B:127:ALA:H	1.57	0.68
1:A:406:ASN:O	1:A:410:LEU:CB	2.34	0.68
1:A:430:ILE:HD13	1:B:410:LEU:HD23	1.76	0.68
1:A:413:VAL:CG2	1:B:411:MET:H	2.07	0.68
1:D:126:LYS:HE3	1:D:168:ASP:OD2	1.94	0.68
1:E:118:VAL:O	1:E:118:VAL:HG23	1.94	0.68
1:B:167:PRO:HG3	1:B:176:MET:HG2	1.76	0.68
1:E:158:ILE:HG12	1:E:159:GLY:N	2.08	0.68
1:D:331:LEU:HD23	1:D:360:PHE:CZ	2.29	0.68
1:F:375:ALA:O	1:F:379:THR:OG1	2.12	0.68
1:A:34:THR:HG23	1:A:35:ARG:HD3	1.74	0.68
1:E:315:LEU:HD13	1:E:331:LEU:CD1	2.24	0.68
1:A:428:ILE:CD1	1:B:414:GLN:CD	2.62	0.68
1:C:402:GLU:HA	1:C:405:SER:HB2	1.75	0.68
1:F:346:GLU:HG2	1:F:351:PRO:CG	2.24	0.68
1:B:174:ARG:HD2	1:B:178:TRP:CZ2	2.28	0.68
1:E:12:MET:HG3	1:E:354:PRO:HD3	1.76	0.68
1:F:305:PRO:HB2	1:F:306:LYS:HD3	1.75	0.68
1:C:209:HIS:CD2	1:C:446:LYS:HA	2.29	0.68
1:B:118:VAL:O	1:B:118:VAL:HG23	1.94	0.67
1:D:247:PHE:CE2	1:D:263:LEU:HB3	2.30	0.67
1:C:4:GLU:O	1:C:5:ASP:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:335:ASN:OD1	1:F:336:ALA:N	2.27	0.67
1:B:204:SER:O	1:C:86:ARG:NH2	2.27	0.67
1:A:352:THR:OG1	1:A:478:ARG:NH2	2.27	0.67
1:A:300:THR:CG2	1:A:302:LEU:HB2	2.24	0.67
1:A:410:LEU:CD1	1:B:409:LEU:CD2	2.72	0.67
1:A:411:MET:CB	1:B:436:PHE:HD2	2.06	0.67
1:A:435:GLU:O	1:A:438:ASP:N	2.26	0.67
1:A:430:ILE:HB	1:B:410:LEU:CG	2.24	0.67
1:A:433:THR:HG22	1:C:413:VAL:HG22	1.77	0.67
1:C:224:GLU:HB2	1:C:242:PHE:CE2	2.26	0.67
1:B:236:LEU:HD21	1:B:342:LYS:CG	2.19	0.67
1:C:332:THR:HG22	1:C:353:THR:HG21	1.75	0.67
1:C:258:HIS:HD2	1:C:261:ARG:NH1	1.92	0.67
1:A:408:HIS:CB	1:B:436:PHE:CD1	2.67	0.67
1:A:436:PHE:CB	1:C:405:SER:O	2.42	0.67
1:D:392:VAL:HG22	1:F:382:TYR:OH	1.95	0.67
1:F:397:LEU:H	1:F:397:LEU:HD12	1.59	0.67
1:F:305:PRO:HB2	1:F:306:LYS:CD	2.24	0.67
1:C:165:PRO:O	1:C:198:VAL:HG23	1.94	0.67
1:C:95:TYR:HH	1:C:145:THR:HB	1.59	0.67
1:E:482:TYR:O	1:E:486:ILE:HG13	1.93	0.67
1:E:407:TYR:CE1	1:E:440:ILE:HD13	2.29	0.67
1:C:20:GLY:HA2	1:C:23:ILE:HD12	1.77	0.67
1:A:148:PHE:CZ	1:A:152:LEU:HD11	2.28	0.67
1:E:177:SER:CB	1:E:202:PRO:HG2	2.24	0.67
1:A:244:ASP:HB2	1:A:245:LYS:HD2	1.77	0.67
1:F:470:LYS:HG2	1:F:471:TYR:CD2	2.29	0.67
1:B:98:ASP:O	1:B:100:SER:N	2.28	0.67
1:E:431:VAL:HG23	1:E:432:PRO:HD2	1.75	0.67
1:C:37:THR:CG2	1:C:41:LYS:HG3	2.24	0.67
1:F:414:GLN:O	1:F:417:LEU:N	2.27	0.67
1:C:112:THR:HB	1:C:124:GLY:N	2.10	0.67
1:D:167:PRO:HB3	1:D:172:GLY:HA2	1.77	0.67
1:E:394:TYR:HE2	1:E:443:ALA:HB3	1.58	0.67
1:D:416:SER:HB3	1:F:430:ILE:HA	1.76	0.67
1:C:302:LEU:HD22	1:C:309:ILE:HG23	1.77	0.67
1:B:244:ASP:HB2	1:B:245:LYS:HD2	1.75	0.67
1:C:289:LYS:HE2	1:C:293:ASP:OD1	1.95	0.67
1:B:394:TYR:HE2	1:B:443:ALA:HB3	1.57	0.67
1:B:371:LEU:HD12	1:B:482:TYR:CD1	2.29	0.67
1:A:111:MET:HE1	1:A:378:VAL:HG13	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:PHE:HB3	1:C:321:ILE:HG12	1.75	0.67
1:E:167:PRO:HG3	1:E:176:MET:HG2	1.76	0.67
1:B:344:ILE:HB	1:B:367:VAL:HG12	1.75	0.67
1:D:148:PHE:CZ	1:D:152:LEU:HD11	2.30	0.67
1:D:90:LYS:HB2	1:D:122:PHE:CD1	2.29	0.67
1:D:457:MET:HA	1:D:457:MET:CE	2.24	0.67
1:F:37:THR:HA	1:F:40:GLN:HG3	1.77	0.67
1:E:98:ASP:O	1:E:100:SER:N	2.28	0.67
1:B:421:PHE:N	1:B:421:PHE:HD2	1.92	0.67
1:A:421:PHE:HB2	1:B:429:PRO:HB3	1.75	0.67
1:E:90:LYS:CB	1:E:122:PHE:CD1	2.78	0.67
1:B:363:ARG:HH11	1:B:365:ILE:HD11	1.57	0.67
1:B:56:ASN:HD22	1:B:84:GLN:HE22	1.42	0.67
1:A:209:HIS:CD2	1:A:446:LYS:HA	2.30	0.67
1:E:186:THR:OG1	1:E:187:ILE:N	2.28	0.67
1:B:258:HIS:CD2	1:B:261:ARG:HH11	2.09	0.67
1:F:280:ILE:HB	1:F:307:ALA:CB	2.25	0.67
1:E:19:ARG:HH11	1:E:19:ARG:HG2	1.59	0.67
1:A:433:THR:OG1	1:C:409:LEU:HA	1.95	0.66
1:A:428:ILE:HG23	1:B:428:ILE:HG21	1.75	0.66
1:C:482:TYR:O	1:C:486:ILE:HG13	1.95	0.66
1:A:142:GLU:HB2	1:A:178:TRP:CZ2	2.30	0.66
1:E:392:VAL:HG12	1:E:393:SER:O	1.95	0.66
1:A:304:PHE:CD1	1:A:305:PRO:HD2	2.30	0.66
1:A:404:ASP:CG	1:B:439:ARG:HD3	2.15	0.66
1:A:428:ILE:CG1	1:B:428:ILE:C	2.64	0.66
1:E:323:ILE:CD1	1:E:345:ALA:HB3	2.25	0.66
1:D:56:ASN:ND2	1:D:84:GLN:HE21	1.85	0.66
1:D:201:LYS:NZ	1:D:388:ASN:HD21	1.90	0.66
1:A:476:ASP:CG	1:A:479:THR:HG23	2.15	0.66
1:E:148:PHE:CE2	1:E:152:LEU:HD11	2.30	0.66
1:E:226:PHE:CE2	1:E:465:MET:SD	2.88	0.66
1:F:224:GLU:HB2	1:F:242:PHE:HE2	1.60	0.66
1:D:171:THR:CB	1:D:175:GLU:HG3	2.25	0.66
1:A:116:ALA:HB1	1:A:485:ALA:HA	1.76	0.66
1:F:112:THR:HB	1:F:124:GLY:H	1.60	0.66
1:C:41:LYS:O	1:C:45:VAL:HG23	1.94	0.66
1:C:292:GLU:O	1:C:296:LEU:HB2	1.96	0.66
1:A:400:LYS:HD2	1:B:451:SER:HB3	1.77	0.66
1:A:407:TYR:CD1	1:A:440:ILE:HD13	2.29	0.66
1:C:160:PRO:HG2	1:C:161:GLY:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:502:GLU:CA	3:B:552:NDP:H41N	2.25	0.66
1:B:260:MET:HG2	1:B:288:PRO:HG3	1.77	0.66
1:B:396:ARG:NH2	1:C:456:THR:HG21	2.11	0.66
1:E:214:ALA:CB	1:E:380:VAL:HG21	2.26	0.66
1:B:220:PHE:O	1:B:224:GLU:HB2	1.94	0.66
1:A:308:LYS:HG2	1:A:308:LYS:O	1.94	0.66
1:E:280:ILE:HB	1:E:307:ALA:CB	2.26	0.66
1:E:314:ILE:HD12	1:E:317:VAL:HG21	1.77	0.66
1:A:247:PHE:HB3	1:A:321:ILE:HG12	1.78	0.66
1:C:63:PHE:HD1	1:C:147:ARG:HG2	1.60	0.66
1:C:337:PRO:HA	1:C:359:ILE:HG21	1.76	0.66
1:C:330:GLN:HA	1:C:330:GLN:HE21	1.59	0.66
1:A:411:MET:N	1:B:436:PHE:CE2	2.51	0.66
1:C:227:ILE:HD12	1:C:233:MET:SD	2.35	0.66
1:A:433:THR:HA	1:C:412:SER:HB3	1.77	0.66
1:C:120:VAL:HG22	1:C:382:TYR:CD2	2.30	0.66
1:F:247:PHE:CE2	1:F:263:LEU:HB3	2.31	0.66
1:B:107:LEU:HG	1:B:126:LYS:HE2	1.78	0.66
1:E:315:LEU:HD13	1:E:331:LEU:HD12	1.77	0.66
1:A:404:ASP:HA	1:B:439:ARG:HD2	1.77	0.65
1:E:199:THR:HG21	1:E:381:SER:O	1.95	0.65
1:B:271:ILE:HD12	1:B:272:THR:CG2	2.25	0.65
1:E:196:ALA:HB2	1:E:388:ASN:HB3	1.77	0.65
1:B:330:GLN:HA	1:B:330:GLN:HE21	1.61	0.65
1:D:434:ALA:HA	1:D:437:GLN:NE2	2.09	0.65
1:F:434:ALA:HA	1:F:437:GLN:NE2	2.11	0.65
1:F:66:ARG:O	1:F:67:ARG:O	2.14	0.65
1:D:244:ASP:HB2	1:D:245:LYS:CD	2.25	0.65
1:B:5:ASP:HB3	1:B:332:THR:HB	1.78	0.65
1:B:177:SER:HB2	1:B:202:PRO:HG2	1.79	0.65
1:D:147:ARG:NE	1:D:151:GLU:OE2	2.23	0.65
1:C:239:THR:O	1:C:245:LYS:HE2	1.96	0.65
1:A:436:PHE:CD2	1:C:406:ASN:HA	2.31	0.65
1:B:414:GLN:O	1:B:418:GLU:HG3	1.95	0.65
1:E:26:ASP:O	1:E:29:VAL:HG13	1.97	0.65
1:F:217:ARG:NH1	1:F:217:ARG:HG2	2.06	0.65
1:A:406:ASN:HA	1:B:406:ASN:CG	2.17	0.65
1:A:82:HIS:CD2	1:A:112:THR:CG2	2.63	0.65
3:E:552:NDP:H2N	3:E:552:NDP:O1N	1.97	0.65
1:C:458:GLU:HG3	1:C:459:ARG:H	1.59	0.65
1:F:353:THR:HB	1:F:354:PRO:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:LEU:O	1:D:145:THR:CG2	2.44	0.65
1:A:409:LEU:HB2	1:B:406:ASN:OD1	1.95	0.65
1:B:90:LYS:NZ	1:B:164:VAL:HG12	2.11	0.65
1:A:410:LEU:HG	1:B:410:LEU:HD12	1.75	0.65
1:A:412:SER:OG	1:B:440:ILE:HD11	1.95	0.65
1:C:396:ARG:HG3	1:C:397:LEU:HG	1.78	0.65
1:A:373:LEU:O	1:A:373:LEU:HD22	1.96	0.65
1:F:148:PHE:CE2	1:F:152:LEU:HD11	2.31	0.65
1:F:248:VAL:HB	1:F:272:THR:HG23	1.78	0.65
1:D:99:VAL:O	1:D:99:VAL:HG23	1.97	0.65
1:B:444:SER:CB	1:B:446:LYS:HD3	2.27	0.65
2:C:502:GLU:CG	3:C:552:NDP:H41N	2.26	0.65
1:F:29:VAL:HG21	1:F:42:ARG:HG2	1.79	0.65
1:A:346:GLU:OE1	1:A:351:PRO:HD2	1.97	0.65
1:A:407:TYR:CD1	1:A:440:ILE:HD11	2.31	0.65
1:B:65:ILE:HG13	1:B:144:ILE:HG12	1.78	0.65
1:D:16:PHE:HE2	1:D:354:PRO:HB3	1.60	0.65
1:B:458:GLU:HG3	1:B:459:ARG:N	2.11	0.65
1:B:371:LEU:HD12	1:B:482:TYR:CE1	2.32	0.65
1:B:394:TYR:CD2	1:B:394:TYR:C	2.70	0.65
1:B:403:ARG:O	1:B:403:ARG:HG3	1.96	0.65
1:A:428:ILE:CD1	1:B:430:ILE:N	2.58	0.65
1:E:197:CYS:SG	1:E:198:VAL:HG12	2.37	0.65
1:C:249:VAL:HA	1:C:323:ILE:HB	1.78	0.65
1:E:456:THR:HA	1:E:459:ARG:HB3	1.79	0.65
1:A:16:PHE:HE2	1:A:354:PRO:HB3	1.60	0.65
1:A:412:SER:CB	1:B:407:TYR:CD1	2.78	0.65
1:B:410:LEU:O	1:B:411:MET:C	2.34	0.65
1:E:169:MET:HG2	3:E:552:NDP:C5D	2.27	0.65
1:C:345:ALA:HB1	1:C:373:LEU:HD11	1.78	0.65
1:D:399:PHE:HE2	1:D:443:ALA:O	1.78	0.65
1:C:473:LEU:HD22	1:C:476:ASP:HB3	1.77	0.65
1:D:131:ILE:HB	1:D:136:TYR:HE2	1.62	0.65
1:D:295:LYS:O	1:D:299:GLY:HA2	1.97	0.65
1:D:160:PRO:CG	1:D:193:ASN:O	2.41	0.65
1:B:152:LEU:HD23	1:B:157:PHE:HB2	1.79	0.65
1:E:161:GLY:CA	1:F:192:ILE:HG13	2.27	0.65
1:D:24:VAL:HG11	1:D:483:VAL:HG13	1.78	0.65
1:A:405:SER:OG	1:B:402:GLU:HB3	1.96	0.64
1:A:91:GLY:HA3	1:A:125:ALA:O	1.96	0.64
1:B:217:ARG:CG	1:B:217:ARG:HH11	2.01	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:GLU:O	1:E:29:VAL:HG12	1.97	0.64
1:A:81:GLN:NE2	1:A:157:PHE:CD2	2.66	0.64
1:B:117:VAL:HG12	1:B:118:VAL:HG12	1.80	0.64
1:B:224:GLU:HA	1:B:242:PHE:HE2	1.61	0.64
2:D:502:GLU:OXT	3:D:552:NDP:H41N	1.97	0.64
1:B:37:THR:HA	1:B:40:GLN:HG3	1.79	0.64
1:D:118:VAL:HG11	1:D:375:ALA:HB1	1.79	0.64
1:A:414:GLN:HA	1:B:430:ILE:C	2.18	0.64
1:A:279:SER:OG	1:A:314:ILE:HD13	1.97	0.64
1:C:443:ALA:HB1	1:C:448:ILE:HG12	1.79	0.64
1:F:202:PRO:HB2	1:F:205:GLN:CG	2.28	0.64
1:C:44:ARG:HH22	1:C:494:ASN:CB	2.10	0.64
1:B:99:VAL:HG23	1:B:99:VAL:O	1.98	0.64
1:C:132:ASN:OD1	1:C:134:LYS:HB2	1.97	0.64
1:E:90:LYS:HD3	1:E:122:PHE:HE1	1.57	0.64
1:C:150:MET:HE2	1:C:150:MET:HA	1.80	0.64
1:C:448:ILE:HG22	1:C:449:VAL:N	2.13	0.64
1:F:214:ALA:CB	1:F:380:VAL:HG21	2.27	0.64
1:F:248:VAL:HG21	1:F:314:ILE:HD11	1.79	0.64
1:E:403:ARG:HG3	1:E:407:TYR:HD1	1.63	0.64
1:A:29:VAL:HG21	1:A:42:ARG:HG2	1.79	0.64
1:A:410:LEU:HD11	1:B:409:LEU:CD2	2.27	0.64
1:B:451:SER:OG	1:B:452:GLY:N	2.31	0.64
1:D:236:LEU:HD22	1:D:238:MET:HB2	1.79	0.64
1:A:353:THR:O	1:A:357:ASP:N	2.29	0.64
1:E:148:PHE:CZ	1:E:152:LEU:HD11	2.32	0.64
1:D:188:GLY:O	1:D:191:ASP:N	2.30	0.64
1:A:413:VAL:HG23	1:B:410:LEU:HB2	1.75	0.64
1:C:247:PHE:CB	1:C:321:ILE:HG12	2.28	0.64
1:C:250:GLN:HG3	1:C:314:ILE:HG21	1.79	0.64
1:E:52:ILE:HG12	1:E:493:TYR:CE1	2.33	0.64
1:E:153:ALA:HA	1:E:158:ILE:HG22	1.80	0.64
1:B:336:ALA:N	1:B:337:PRO:HD2	2.13	0.64
1:C:348:ALA:HA	3:C:552:NDP:H1D	1.79	0.64
1:D:107:LEU:HB3	1:D:126:LYS:HG2	1.78	0.64
1:A:65:ILE:HG12	1:A:144:ILE:HD13	1.78	0.64
1:A:409:LEU:HD13	1:B:406:ASN:CG	2.18	0.64
1:C:248:VAL:HG21	1:C:314:ILE:HD11	1.79	0.64
1:E:272:THR:HB	1:E:281:TRP:HA	1.80	0.64
1:A:494:ASN:O	1:A:495:GLU:HB2	1.98	0.64
1:A:208:ILE:HG22	1:A:384:GLU:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:436:PHE:CZ	1:F:409:LEU:HD12	2.32	0.64
1:F:313:SER:HB3	1:F:316:GLU:HB2	1.79	0.64
1:E:404:ASP:O	1:E:408:HIS:HB2	1.98	0.64
1:D:35:ARG:CD	1:D:35:ARG:H	2.10	0.64
1:D:39:GLU:HG2	1:D:39:GLU:O	1.96	0.64
1:A:414:GLN:CD	1:B:431:VAL:O	2.36	0.64
1:A:90:LYS:NZ	1:A:164:VAL:O	2.30	0.64
1:C:280:ILE:HB	1:C:307:ALA:CB	2.27	0.64
1:D:224:GLU:HA	1:D:227:ILE:HG22	1.80	0.64
1:C:214:ALA:CB	1:C:380:VAL:HG21	2.26	0.64
1:D:420:LYS:O	1:D:421:PHE:HD2	1.80	0.64
1:B:349:ASN:N	3:B:552:NDP:O2D	2.28	0.64
1:D:141:LEU:O	1:D:145:THR:HG23	1.97	0.64
1:A:191:ASP:O	1:A:194:ALA:HB2	1.98	0.64
1:D:236:LEU:HD23	1:D:237:GLY:N	2.12	0.64
1:B:225:ASN:HD21	1:B:458:GLU:HB2	1.63	0.64
1:E:271:ILE:HD12	1:E:272:THR:HG23	1.80	0.64
1:B:323:ILE:CD1	1:B:345:ALA:HB3	2.28	0.64
1:E:36:GLU:O	1:E:37:THR:HG23	1.97	0.64
1:E:372:TYR:HE1	1:E:461:ALA:H	1.46	0.64
1:F:248:VAL:CG2	1:F:314:ILE:HD11	2.28	0.64
1:F:380:VAL:O	1:F:383:PHE:N	2.31	0.64
1:D:221:HIS:O	1:D:225:ASN:HB2	1.98	0.64
1:A:300:THR:HG22	1:A:302:LEU:N	2.13	0.64
1:C:414:GLN:CG	1:C:428:ILE:O	2.46	0.63
1:E:421:PHE:CD2	1:E:421:PHE:N	2.64	0.63
1:D:211:ARG:NE	1:D:381:SER:OG	2.30	0.63
1:E:331:LEU:HD23	1:E:360:PHE:CZ	2.32	0.63
1:A:409:LEU:CD1	1:B:402:GLU:C	2.66	0.63
1:A:382:TYR:O	1:A:386:LEU:HD22	1.98	0.63
1:A:211:ARG:HD2	1:A:211:ARG:O	1.97	0.63
1:C:112:THR:H	1:C:124:GLY:HA3	1.61	0.63
1:C:330:GLN:HA	1:C:330:GLN:NE2	2.13	0.63
1:C:183:TYR:C	1:C:183:TYR:CD2	2.71	0.63
1:C:91:GLY:O	1:C:165:PRO:HA	1.98	0.63
1:E:305:PRO:HB2	1:E:306:LYS:CD	2.28	0.63
1:B:427:THR:O	1:B:427:THR:OG1	2.16	0.63
1:A:414:GLN:CA	1:B:430:ILE:O	2.46	0.63
1:C:224:GLU:HA	1:C:227:ILE:HG22	1.79	0.63
1:B:246:THR:O	1:B:320:ASP:HB2	1.98	0.63
1:E:35:ARG:CD	1:E:35:ARG:H	2.08	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:ARG:HA	1:F:182:THR:HG21	1.81	0.63
1:D:369:PRO:HG3	1:D:478:ARG:HA	1.81	0.63
1:C:382:TYR:CE1	1:C:386:LEU:HD21	2.33	0.63
1:B:29:VAL:O	1:B:41:LYS:HD3	1.98	0.63
1:D:225:ASN:HD21	1:D:458:GLU:CB	2.09	0.63
1:C:68:ASP:HB2	1:C:140:GLU:OE1	1.97	0.63
1:A:433:THR:HB	1:C:412:SER:CA	2.27	0.63
1:C:344:ILE:HD11	1:C:360:PHE:CE1	2.33	0.63
1:C:403:ARG:O	1:C:407:TYR:HB2	1.99	0.63
1:E:34:THR:HG23	1:E:35:ARG:HD3	1.81	0.63
1:E:371:LEU:HD12	1:E:482:TYR:CD1	2.33	0.63
1:D:437:GLN:HA	1:D:440:ILE:HB	1.79	0.63
1:D:224:GLU:CB	1:D:242:PHE:HE2	2.11	0.63
1:C:371:LEU:HD13	1:C:481:ALA:HB1	1.81	0.63
1:B:172:GLY:O	1:B:176:MET:HG2	1.99	0.63
1:C:374:ASN:C	1:C:376:GLY:H	2.01	0.63
1:A:430:ILE:HG12	1:B:413:VAL:CG2	2.29	0.63
1:D:219:VAL:HA	1:D:373:LEU:HD21	1.79	0.63
1:C:19:ARG:CG	1:C:19:ARG:HH11	2.11	0.63
1:C:82:HIS:CD2	1:C:112:THR:HG21	2.33	0.63
1:E:342:LYS:NZ	1:E:342:LYS:HB2	2.14	0.63
1:C:230:ALA:HA	1:C:233:MET:HB2	1.81	0.62
1:B:315:LEU:HA	1:B:322:LEU:HD11	1.81	0.62
1:A:345:ALA:HB1	1:A:373:LEU:HD11	1.79	0.62
1:D:328:GLU:O	1:D:329:LYS:C	2.37	0.62
1:A:78:TYR:N	1:A:78:TYR:CD1	2.67	0.62
1:F:90:LYS:HE3	1:F:381:SER:HB3	1.80	0.62
1:F:221:HIS:NE2	1:F:454:ALA:HB2	2.14	0.62
1:C:59:LEU:HD22	1:C:157:PHE:CD1	2.33	0.62
1:A:397:LEU:HD23	1:B:383:PHE:CE1	2.33	0.62
1:B:405:SER:O	1:B:408:HIS:CB	2.45	0.62
1:A:414:GLN:HA	1:B:430:ILE:O	1.98	0.62
1:C:300:THR:CG2	1:C:302:LEU:HB2	2.29	0.62
1:A:154:LYS:HD3	1:E:189:HIS:CD2	2.34	0.62
1:B:272:THR:HG1	1:B:314:ILE:HD11	1.64	0.62
1:C:382:TYR:O	1:C:385:TRP:HB3	1.97	0.62
1:D:219:VAL:HG22	1:D:373:LEU:HD13	1.80	0.62
1:E:300:THR:CG2	1:E:302:LEU:HB2	2.28	0.62
1:A:428:ILE:HD11	1:B:428:ILE:C	2.20	0.62
1:E:169:MET:HG2	3:E:552:NDP:H51N	1.81	0.62
1:A:126:LYS:HG3	1:A:127:ALA:H	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:ASN:OD1	1:D:134:LYS:HB2	1.98	0.62
1:B:23:ILE:HG22	1:B:471:TYR:HD1	1.64	0.62
1:A:409:LEU:HD21	1:B:404:ASP:C	2.19	0.62
1:E:281:TRP:CZ2	1:E:283:PRO:HG3	2.33	0.62
1:B:315:LEU:HD13	1:B:331:LEU:HD12	1.81	0.62
1:C:252:PHE:CZ	1:C:257:LEU:HD13	2.35	0.62
1:A:235:ILE:O	1:A:235:ILE:HG22	1.99	0.62
1:F:231:SER:O	1:F:235:ILE:HD13	1.99	0.62
1:F:348:ALA:O	1:F:351:PRO:HD3	2.00	0.62
1:E:417:LEU:HB3	1:E:428:ILE:HD13	1.81	0.62
1:E:394:TYR:CE2	1:E:443:ALA:HB3	2.35	0.62
1:D:146:ARG:HA	1:D:182:THR:HG21	1.82	0.62
1:A:399:PHE:O	1:A:441:SER:HB3	1.99	0.62
1:A:201:LYS:HE3	1:A:206:GLY:HA3	1.82	0.62
1:D:281:TRP:N	1:D:307:ALA:HB1	2.14	0.62
1:C:94:ARG:HH21	1:C:169:MET:HG3	1.65	0.62
1:D:94:ARG:NH1	1:D:107:LEU:CD2	2.58	0.62
1:D:397:LEU:H	1:D:397:LEU:HD12	1.63	0.62
1:F:242:PHE:CE1	1:F:263:LEU:HD22	2.35	0.62
1:D:137:THR:HG23	1:D:140:GLU:CG	2.28	0.62
1:D:458:GLU:HG3	1:D:459:ARG:N	2.15	0.62
1:F:491:ARG:NH1	1:F:491:ARG:HB2	2.14	0.62
1:D:183:TYR:CD2	1:D:183:TYR:C	2.73	0.62
1:B:252:PHE:CZ	1:B:291:LEU:HD13	2.34	0.62
1:A:85:HIS:CE1	1:A:489:VAL:HG22	2.35	0.62
1:E:223:ILE:HA	1:E:368:ILE:HD12	1.82	0.62
1:A:315:LEU:HA	1:A:322:LEU:HD11	1.81	0.62
1:C:118:VAL:HG11	1:C:375:ALA:CB	2.29	0.62
1:E:140:GLU:O	1:E:143:LYS:HB2	1.99	0.62
1:F:260:MET:HG2	1:F:288:PRO:HG3	1.82	0.62
1:B:117:VAL:HG12	1:B:118:VAL:CG1	2.30	0.62
1:C:148:PHE:CD2	1:C:152:LEU:HD11	2.35	0.62
1:C:178:TRP:O	1:C:182:THR:HG23	1.99	0.62
1:C:150:MET:SD	1:C:186:THR:HG21	2.40	0.62
1:C:213:SER:O	1:C:215:THR:N	2.33	0.62
1:E:35:ARG:HD2	1:E:35:ARG:N	2.11	0.62
1:F:137:THR:HG23	1:F:140:GLU:CD	2.20	0.62
1:D:93:ILE:HD11	1:D:95:TYR:HE1	1.64	0.62
1:D:35:ARG:HG2	1:D:36:GLU:HG3	1.81	0.62
1:F:418:GLU:O	1:F:422:GLY:HA2	2.00	0.62
1:A:362:GLU:C	1:A:364:ASN:H	2.01	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:PHE:HA	1:A:441:SER:HB3	1.81	0.62
1:E:246:THR:O	1:E:320:ASP:HB2	1.99	0.62
1:A:273:VAL:HG21	1:A:291:LEU:CD1	2.29	0.62
1:A:358:LYS:HG3	1:A:359:ILE:N	2.15	0.62
1:D:332:THR:CA	1:D:356:ALA:HB2	2.30	0.62
1:F:167:PRO:HD3	1:F:200:GLY:HA3	1.82	0.62
1:D:131:ILE:HB	1:D:136:TYR:CE2	2.35	0.62
1:E:274:GLY:O	1:E:275:GLU:HB2	2.00	0.62
1:A:409:LEU:HD11	1:B:405:SER:N	2.15	0.61
1:A:428:ILE:HD11	1:B:428:ILE:O	1.99	0.61
1:A:117:VAL:HG21	1:A:371:LEU:HD22	1.82	0.61
1:E:230:ALA:HA	1:E:233:MET:HB2	1.81	0.61
1:F:174:ARG:HB3	1:F:175:GLU:OE2	1.99	0.61
1:C:479:THR:O	1:C:483:VAL:HG23	2.00	0.61
1:E:382:TYR:CE1	1:E:386:LEU:HD21	2.35	0.61
1:A:158:ILE:HA	1:A:163:ASP:O	2.00	0.61
1:E:333:LYS:HB2	1:E:355:GLU:HG3	1.81	0.61
1:C:101:VAL:O	1:C:105:LYS:HG3	2.00	0.61
1:A:118:VAL:HG11	1:A:375:ALA:HB1	1.82	0.61
1:D:314:ILE:HD12	1:D:317:VAL:HG21	1.81	0.61
1:C:107:LEU:HB3	1:C:126:LYS:CG	2.23	0.61
1:F:63:PHE:CD1	1:F:75:ILE:HD11	2.35	0.61
1:B:171:THR:CG2	1:B:175:GLU:HG3	2.29	0.61
1:A:37:THR:O	1:A:38:GLU:HB2	1.99	0.61
1:E:258:HIS:CD2	1:E:261:ARG:NH1	2.64	0.61
1:A:353:THR:HB	1:A:354:PRO:HD2	1.82	0.61
1:A:269:LYS:HD3	1:A:284:ASP:C	2.21	0.61
1:E:300:THR:HG22	1:E:302:LEU:H	1.65	0.61
1:F:258:HIS:HD2	1:F:261:ARG:HH11	1.46	0.61
1:A:408:HIS:HD1	1:B:436:PHE:HD1	1.44	0.61
1:B:247:PHE:HB3	1:B:321:ILE:CG1	2.30	0.61
1:F:342:LYS:HA	1:F:365:ILE:HG23	1.83	0.61
1:C:117:VAL:HG23	1:C:371:LEU:HD22	1.80	0.61
1:F:142:GLU:HA	1:F:178:TRP:CZ3	2.35	0.61
1:F:35:ARG:HG2	1:F:36:GLU:HG3	1.82	0.61
1:D:403:ARG:HA	1:D:440:ILE:O	2.01	0.61
1:C:306:LYS:CD	1:C:306:LYS:N	2.63	0.61
1:E:330:GLN:HA	1:E:330:GLN:NE2	2.14	0.61
1:A:410:LEU:O	1:B:410:LEU:CG	2.49	0.61
1:A:413:VAL:HG21	1:B:411:MET:H	1.65	0.61
1:B:110:LEU:O	1:B:112:THR:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:271:ILE:HD11	1:C:319:CYS:HB3	1.82	0.61
1:C:217:ARG:CZ	1:C:450:HIS:CD2	2.84	0.61
1:C:276:SER:HB2	3:C:552:NDP:O2X	2.00	0.61
1:F:93:ILE:HD11	1:F:95:TYR:HE1	1.65	0.61
1:F:421:PHE:N	1:F:421:PHE:CD2	2.68	0.61
1:D:171:THR:HB	1:D:175:GLU:HG3	1.82	0.61
1:A:295:LYS:O	1:A:299:GLY:HA2	2.00	0.61
1:E:402:GLU:HB2	1:E:441:SER:O	1.99	0.61
1:B:459:ARG:O	1:B:462:ARG:HB3	2.00	0.61
1:B:239:THR:O	1:B:245:LYS:HE2	2.00	0.61
1:A:404:ASP:HB2	1:B:442:GLY:O	2.00	0.61
1:B:399:PHE:HA	1:B:441:SER:O	2.01	0.61
1:E:129:VAL:HG12	1:E:131:ILE:HG23	1.82	0.61
1:C:222:GLY:HA3	1:C:373:LEU:HD21	1.83	0.61
1:D:92:GLY:CA	1:D:166:ALA:O	2.48	0.61
1:C:421:PHE:CD2	1:C:421:PHE:N	2.67	0.61
1:C:457:MET:CE	1:C:457:MET:HA	2.31	0.61
1:A:413:VAL:HB	1:B:411:MET:H	1.66	0.61
1:A:414:GLN:HA	1:B:430:ILE:HG22	1.83	0.61
1:A:428:ILE:H	1:B:429:PRO:C	2.03	0.61
1:A:430:ILE:HD13	1:B:410:LEU:CB	2.31	0.61
1:A:433:THR:HB	1:C:411:MET:C	2.20	0.61
1:A:247:PHE:HB3	1:A:321:ILE:CG1	2.31	0.61
1:F:233:MET:HE2	1:F:233:MET:HA	1.83	0.61
1:D:114:LYS:HA	1:D:371:LEU:CD2	2.30	0.61
1:C:372:TYR:CE1	1:C:461:ALA:HB2	2.36	0.61
1:A:146:ARG:NH2	1:A:182:THR:HG22	2.16	0.61
1:F:271:ILE:HD12	1:F:272:THR:HG23	1.81	0.61
1:C:421:PHE:HD2	1:C:421:PHE:N	1.97	0.61
1:B:461:ALA:O	1:B:465:MET:HG3	2.00	0.61
1:C:362:GLU:C	1:C:364:ASN:H	2.02	0.61
1:D:106:ALA:O	1:D:109:SER:OG	2.16	0.61
1:C:481:ALA:O	1:C:484:ASN:N	2.33	0.61
1:A:79:ARG:HG3	1:A:126:LYS:O	2.01	0.61
1:B:29:VAL:HG21	1:B:42:ARG:HG2	1.82	0.61
1:F:247:PHE:HB3	1:F:321:ILE:CG1	2.29	0.61
1:D:445:GLU:O	1:D:446:LYS:C	2.38	0.61
1:B:120:VAL:HG22	1:B:382:TYR:CD2	2.35	0.61
1:A:417:LEU:HD11	1:B:411:MET:CE	2.31	0.61
1:B:227:ILE:HD12	1:B:233:MET:SD	2.41	0.61
1:F:316:GLU:O	1:F:340:LYS:HE2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:236:LEU:HD21	1:E:342:LYS:HG2	1.81	0.61
1:D:171:THR:HG22	1:D:175:GLU:HG3	1.82	0.61
1:B:287:ASP:OD1	1:B:290:GLU:HG3	2.00	0.61
1:A:116:ALA:O	1:A:488:LYS:HD2	2.01	0.61
1:A:85:HIS:HB2	1:A:492:VAL:HG11	1.82	0.61
1:D:224:GLU:HB2	1:D:242:PHE:CE2	2.35	0.61
1:E:353:THR:HB	1:E:354:PRO:HD2	1.83	0.61
1:A:16:PHE:O	1:A:19:ARG:HB3	2.01	0.61
1:A:409:LEU:HD21	1:B:403:ARG:C	2.22	0.60
1:A:404:ASP:O	1:B:439:ARG:HG3	2.00	0.60
1:B:316:GLU:O	1:B:340:LYS:HE2	2.01	0.60
1:D:114:LYS:HZ2	2:D:502:GLU:N	1.99	0.60
1:C:117:VAL:HG12	1:C:118:VAL:HG12	1.83	0.60
1:B:346:GLU:HG2	1:B:351:PRO:HD2	1.83	0.60
1:A:25:GLU:O	1:A:29:VAL:HG23	2.01	0.60
1:A:204:SER:OG	1:B:495:GLU:HG2	2.01	0.60
1:B:385:TRP:CE3	1:B:386:LEU:HD13	2.36	0.60
1:A:118:VAL:O	1:A:118:VAL:HG23	2.01	0.60
1:B:34:THR:HG23	1:B:35:ARG:HD3	1.82	0.60
1:F:379:THR:HG22	1:F:383:PHE:CE2	2.36	0.60
1:E:392:VAL:CG1	1:E:393:SER:N	2.64	0.60
1:F:258:HIS:HD2	1:F:261:ARG:NH1	2.00	0.60
1:A:217:ARG:O	1:A:220:PHE:HB3	2.00	0.60
1:A:408:HIS:HE1	1:B:435:GLU:O	1.83	0.60
1:D:53:LYS:O	1:D:82:HIS:HE1	1.84	0.60
1:E:37:THR:CG2	1:E:41:LYS:HG3	2.31	0.60
1:B:480:ALA:O	1:B:483:VAL:HB	2.01	0.60
1:C:82:HIS:C	1:C:82:HIS:CD2	2.74	0.60
1:B:239:THR:O	1:B:245:LYS:CE	2.49	0.60
1:C:462:ARG:HG3	1:C:466:ARG:NH1	2.16	0.60
1:A:101:VAL:O	1:A:105:LYS:HG3	2.02	0.60
1:C:436:PHE:O	1:C:436:PHE:CG	2.55	0.60
1:C:44:ARG:HH22	1:C:494:ASN:HB2	1.65	0.60
1:F:400:LYS:HD3	1:F:400:LYS:O	2.01	0.60
1:B:462:ARG:HG3	1:B:466:ARG:HH12	1.66	0.60
1:E:294:PHE:CE2	1:E:298:HIS:CE1	2.89	0.60
1:F:239:THR:HG23	1:F:245:LYS:HZ1	1.66	0.60
1:A:396:ARG:HG3	1:A:397:LEU:N	2.15	0.60
1:A:417:LEU:HD13	1:B:414:GLN:CD	2.22	0.60
1:A:409:LEU:O	1:B:406:ASN:C	2.39	0.60
1:C:168:ASP:HA	3:C:552:NDP:O7N	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:192:ILE:HG23	1:D:193:ASN:OD1	2.01	0.60
1:E:5:ASP:HB3	1:E:332:THR:HB	1.83	0.60
1:F:61:LEU:O	1:F:76:GLU:HA	2.01	0.60
1:A:406:ASN:ND2	1:B:402:GLU:OE1	2.35	0.60
1:A:404:ASP:O	1:A:408:HIS:HB2	2.02	0.60
1:A:436:PHE:HD2	1:C:409:LEU:HB3	1.60	0.60
1:B:406:ASN:C	1:B:408:HIS:N	2.55	0.60
1:A:425:GLY:CA	1:B:427:THR:O	2.48	0.60
1:A:411:MET:CG	1:B:433:THR:N	2.60	0.60
1:D:247:PHE:HB3	1:D:321:ILE:CG1	2.29	0.60
1:D:332:THR:HG22	1:D:353:THR:CG2	2.30	0.60
1:D:409:LEU:C	1:D:409:LEU:HD12	2.22	0.60
2:F:502:GLU:OE2	2:F:502:GLU:N	2.35	0.60
1:D:305:PRO:HB2	1:D:306:LYS:CD	2.31	0.60
1:E:58:VAL:HG22	1:E:80:ALA:CB	2.31	0.60
1:C:400:LYS:HD3	1:C:400:LYS:O	2.01	0.60
1:A:404:ASP:HA	1:B:439:ARG:HD3	1.81	0.60
1:C:336:ALA:O	1:C:339:VAL:HG23	2.01	0.60
1:E:29:VAL:O	1:E:41:LYS:HD3	2.02	0.60
1:F:223:ILE:HD13	1:F:345:ALA:CB	2.32	0.60
1:A:409:LEU:C	1:B:406:ASN:HB2	2.22	0.60
1:C:394:TYR:HE2	1:C:443:ALA:HB3	1.66	0.60
1:A:238:MET:HG2	1:A:245:LYS:HZ1	1.67	0.60
1:E:63:PHE:CD1	1:E:75:ILE:HD11	2.36	0.60
1:B:410:LEU:O	1:B:412:SER:N	2.34	0.60
1:A:418:GLU:CA	1:B:429:PRO:HB2	2.11	0.60
1:C:414:GLN:HG2	1:C:428:ILE:O	2.00	0.60
1:B:84:GLN:C	1:B:86:ARG:N	2.53	0.60
1:A:146:ARG:HE	1:A:182:THR:CG2	2.14	0.60
1:B:36:GLU:O	1:B:37:THR:HG23	2.02	0.60
1:B:177:SER:HB2	1:B:202:PRO:CG	2.31	0.60
1:A:235:ILE:CG2	1:A:235:ILE:O	2.49	0.60
1:A:258:HIS:CD2	1:A:261:ARG:NH1	2.68	0.60
1:C:315:LEU:HD22	1:C:331:LEU:HD11	1.84	0.60
1:A:300:THR:HG22	1:A:302:LEU:H	1.66	0.60
1:B:195:HIS:HE1	1:C:87:THR:HG21	1.67	0.60
1:F:476:ASP:OD2	1:F:479:THR:HG23	2.01	0.60
1:A:249:VAL:CB	1:A:323:ILE:HB	2.32	0.59
1:A:242:PHE:HE1	1:A:263:LEU:HD22	1.63	0.59
1:E:37:THR:HA	1:E:40:GLN:HG3	1.83	0.59
1:C:44:ARG:HH22	1:C:494:ASN:CA	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ILE:HD13	1:B:410:LEU:CD2	2.32	0.59
1:D:280:ILE:HG22	1:D:309:ILE:HD13	1.84	0.59
1:D:319:CYS:SG	1:D:341:ALA:HB2	2.42	0.59
1:C:462:ARG:HG3	1:C:466:ARG:HH22	1.66	0.59
1:A:251:GLY:O	1:A:256:GLY:HA3	2.01	0.59
1:E:61:LEU:HB3	1:E:77:GLY:O	2.02	0.59
1:D:470:LYS:HG2	1:D:471:TYR:CE2	2.37	0.59
1:A:420:LYS:C	1:A:421:PHE:HD2	2.04	0.59
1:C:281:TRP:CB	1:C:310:TYR:HB2	2.31	0.59
1:D:495:GLU:OE2	1:E:205:GLN:HG2	2.02	0.59
1:F:162:VAL:HG23	1:F:163:ASP:H	1.63	0.59
1:C:272:THR:HG22	1:C:281:TRP:HD1	1.66	0.59
1:C:344:ILE:HD11	1:C:360:PHE:CZ	2.38	0.59
1:E:200:GLY:N	1:E:384:GLU:OE1	2.35	0.59
1:D:259:SER:O	1:D:263:LEU:HG	2.02	0.59
1:D:3:ARG:O	1:D:5:ASP:N	2.26	0.59
1:C:147:ARG:O	1:C:148:PHE:C	2.40	0.59
1:D:117:VAL:HG21	1:D:371:LEU:HD13	1.84	0.59
1:F:16:PHE:HE2	1:F:354:PRO:HB3	1.67	0.59
1:B:60:SER:HA	1:B:78:TYR:HD2	1.68	0.59
1:F:88:PRO:HD2	1:F:122:PHE:CE2	2.37	0.59
1:D:95:TYR:HB3	1:D:133:PRO:HG3	1.83	0.59
1:B:372:TYR:CZ	1:B:461:ALA:HB2	2.36	0.59
1:A:408:HIS:CG	1:B:436:PHE:CD1	2.91	0.59
1:A:428:ILE:HG12	1:B:428:ILE:HB	0.68	0.59
1:A:408:HIS:NE2	1:B:437:GLN:C	2.56	0.59
1:A:408:HIS:CD2	1:B:440:ILE:N	2.70	0.59
1:E:220:PHE:CE1	1:E:266:PHE:HB2	2.35	0.59
1:D:248:VAL:HG23	1:D:272:THR:O	2.02	0.59
1:D:334:SER:O	1:D:337:PRO:HD2	2.03	0.59
1:B:56:ASN:ND2	1:B:84:GLN:NE2	2.43	0.59
1:A:107:LEU:HB3	1:A:126:LYS:HG2	1.85	0.59
1:F:357:ASP:OD2	1:F:478:ARG:NE	2.35	0.59
1:C:52:ILE:HG12	1:C:493:TYR:CE2	2.37	0.59
1:B:19:ARG:HH11	1:B:19:ARG:HG2	1.68	0.59
1:A:158:ILE:HG13	1:A:165:PRO:HD2	1.84	0.59
1:A:412:SER:OG	1:B:407:TYR:CD1	2.55	0.59
1:B:247:PHE:CZ	1:B:270:CYS:HB2	2.37	0.59
1:D:308:LYS:O	1:D:308:LYS:HG2	2.02	0.59
1:C:222:GLY:HA3	1:C:373:LEU:CD2	2.33	0.59
1:C:93:ILE:HD11	1:C:95:TYR:HE1	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:HIS:CD2	1:A:446:LYS:HB3	2.37	0.59
1:B:51:ILE:CD1	1:E:64:PRO:HB3	2.33	0.59
1:B:51:ILE:HD13	1:E:64:PRO:CB	2.33	0.59
1:D:304:PHE:CE2	1:D:306:LYS:HB2	2.38	0.59
1:B:183:TYR:CD2	1:B:183:TYR:C	2.76	0.59
1:B:214:ALA:HB1	1:B:380:VAL:HG21	1.84	0.59
1:E:175:GLU:CD	1:E:175:GLU:H	2.05	0.59
1:E:239:THR:O	1:E:245:LYS:HE2	2.02	0.59
1:C:346:GLU:HB2	1:C:368:ILE:O	2.02	0.59
1:D:169:MET:HG2	3:D:552:NDP:H51N	1.84	0.59
1:F:167:PRO:CA	1:F:176:MET:HE3	2.31	0.59
1:F:416:SER:HA	1:F:419:ARG:NH1	2.18	0.59
1:E:209:HIS:CD2	1:E:446:LYS:HA	2.37	0.59
1:D:436:PHE:O	1:D:436:PHE:CG	2.54	0.59
1:A:310:TYR:CZ	1:A:317:VAL:HG22	2.37	0.59
1:A:336:ALA:O	1:A:339:VAL:HG23	2.03	0.59
1:B:224:GLU:HA	1:B:242:PHE:CE2	2.38	0.59
1:A:354:PRO:HA	1:A:357:ASP:HB2	1.83	0.59
1:B:23:ILE:HG22	1:B:471:TYR:CD1	2.37	0.59
1:E:116:ALA:O	1:E:488:LYS:HD2	2.03	0.59
1:A:58:VAL:HG22	1:A:80:ALA:CB	2.33	0.59
1:A:400:LYS:O	1:A:404:ASP:OD1	2.20	0.59
1:A:401:TYR:HA	1:A:404:ASP:CG	2.23	0.59
1:A:52:ILE:HD13	1:A:489:VAL:CG1	2.32	0.59
1:F:36:GLU:O	1:F:37:THR:HG23	2.03	0.59
1:B:94:ARG:NH1	1:B:107:LEU:HD21	2.18	0.59
1:E:42:ARG:O	1:E:46:ARG:HB2	2.03	0.59
1:A:409:LEU:HD22	1:B:406:ASN:CA	2.33	0.59
1:F:217:ARG:O	1:F:220:PHE:HB3	2.02	0.59
1:D:421:PHE:N	1:D:421:PHE:CD2	2.69	0.59
1:A:413:VAL:CB	1:B:411:MET:H	2.16	0.58
1:E:244:ASP:HB2	1:E:245:LYS:CD	2.30	0.58
1:D:271:ILE:HD12	1:D:272:THR:CG2	2.33	0.58
1:C:95:TYR:OH	1:C:145:THR:CB	2.43	0.58
1:A:239:THR:O	1:A:245:LYS:HE2	2.03	0.58
1:E:225:ASN:HD21	1:E:458:GLU:HB2	1.68	0.58
1:A:402:GLU:HB2	1:A:441:SER:O	2.03	0.58
1:A:430:ILE:CG1	1:B:410:LEU:HG	2.31	0.58
1:C:344:ILE:HB	1:C:367:VAL:CG1	2.33	0.58
1:C:165:PRO:HD2	1:C:197:CYS:O	2.03	0.58
1:B:37:THR:HB	1:B:41:LYS:HG3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:LYS:HE2	1:C:31:ASP:OD1	2.03	0.58
1:F:396:ARG:HG3	1:F:397:LEU:HG	1.85	0.58
1:D:153:ALA:CA	1:D:158:ILE:HG22	2.32	0.58
1:A:430:ILE:HG13	1:B:430:ILE:CD1	2.25	0.58
1:A:434:ALA:N	1:C:412:SER:H	2.02	0.58
1:A:374:ASN:HD22	3:A:552:NDP:H6N	1.68	0.58
1:F:224:GLU:CB	1:F:242:PHE:HE2	2.17	0.58
1:A:43:ASN:O	1:A:44:ARG:C	2.41	0.58
1:E:476:ASP:CG	1:E:479:THR:HG23	2.22	0.58
1:A:351:PRO:HG2	1:A:352:THR:HG23	1.84	0.58
1:B:192:ILE:HG13	1:C:161:GLY:HA2	1.84	0.58
1:E:247:PHE:CZ	1:E:270:CYS:HB2	2.37	0.58
1:E:248:VAL:CG2	1:E:314:ILE:HD11	2.33	0.58
1:D:160:PRO:HD3	1:D:197:CYS:CB	2.34	0.58
1:D:215:THR:HG21	3:D:552:NDP:O7N	2.03	0.58
1:E:53:LYS:O	1:E:82:HIS:CE1	2.55	0.58
1:F:175:GLU:CD	1:F:175:GLU:H	2.05	0.58
1:A:412:SER:O	1:A:414:GLN:N	2.36	0.58
1:A:146:ARG:CZ	1:A:182:THR:HG22	2.34	0.58
1:B:148:PHE:CZ	1:B:152:LEU:HD11	2.39	0.58
1:E:9:PHE:CD2	1:E:12:MET:HE2	2.38	0.58
1:A:294:PHE:CE2	1:A:298:HIS:CE1	2.92	0.58
1:D:275:GLU:HB2	1:D:301:ILE:CD1	2.34	0.58
1:A:489:VAL:O	1:A:492:VAL:HG12	2.04	0.58
1:C:368:ILE:HG22	1:C:373:LEU:HG	1.85	0.58
1:B:219:VAL:HA	1:B:373:LEU:HD22	1.86	0.58
1:C:99:VAL:O	1:C:99:VAL:HG23	2.02	0.58
1:A:401:TYR:CB	1:B:443:ALA:HB2	2.32	0.58
1:B:398:THR:O	1:B:399:PHE:C	2.42	0.58
1:A:111:MET:HE1	1:A:378:VAL:CG1	2.32	0.58
1:A:321:ILE:HG22	1:A:343:ILE:CB	2.23	0.58
1:C:348:ALA:O	1:C:351:PRO:HD3	2.04	0.58
1:F:281:TRP:HB2	1:F:310:TYR:HB2	1.84	0.58
1:A:37:THR:C	1:A:40:GLN:HG3	2.24	0.58
1:C:209:HIS:CG	1:C:446:LYS:HG3	2.37	0.58
1:B:392:VAL:HG22	1:C:382:TYR:OH	2.04	0.58
1:D:90:LYS:HD2	1:D:164:VAL:HB	1.86	0.58
1:E:201:LYS:HZ2	1:E:388:ASN:ND2	2.00	0.58
1:B:408:HIS:O	1:B:409:LEU:C	2.41	0.58
1:A:408:HIS:CD2	1:B:437:GLN:C	2.77	0.58
1:B:342:LYS:HB2	1:B:342:LYS:HZ3	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:196:ALA:HB2	1:E:388:ASN:CB	2.33	0.58
1:F:175:GLU:O	1:F:179:ILE:HG13	2.03	0.58
1:D:385:TRP:CE3	1:D:386:LEU:HD13	2.38	0.58
1:C:90:LYS:HD3	1:C:122:PHE:CE1	2.39	0.58
1:E:188:GLY:O	1:E:191:ASP:N	2.37	0.58
1:A:68:ASP:OD2	1:A:140:GLU:HG3	2.04	0.58
1:A:406:ASN:HB3	1:B:406:ASN:ND2	2.19	0.58
1:A:406:ASN:C	1:B:436:PHE:HZ	2.04	0.58
1:A:117:VAL:CG2	1:A:371:LEU:HD22	2.34	0.58
1:D:321:ILE:CG2	1:D:343:ILE:HB	2.22	0.58
1:F:56:ASN:ND2	1:F:82:HIS:O	2.37	0.58
1:D:417:LEU:HB3	1:D:428:ILE:CD1	2.34	0.58
1:B:272:THR:OG1	1:B:314:ILE:CD1	2.48	0.57
1:D:316:GLU:OE2	1:D:338:ARG:HG3	2.03	0.57
1:E:109:SER:O	1:E:113:TYR:CD1	2.56	0.57
1:E:118:VAL:HG11	1:E:375:ALA:HB3	1.85	0.57
1:C:35:ARG:HG2	1:C:36:GLU:N	2.14	0.57
1:D:418:GLU:O	1:D:422:GLY:HA2	2.04	0.57
1:B:92:GLY:HA2	1:B:166:ALA:O	2.04	0.57
1:F:88:PRO:HD2	1:F:122:PHE:CD2	2.39	0.57
1:D:171:THR:CG2	1:D:175:GLU:HG3	2.34	0.57
1:C:423:LYS:N	1:C:423:LYS:HD2	2.18	0.57
1:A:411:MET:CB	1:B:432:PRO:HA	2.34	0.57
1:A:409:LEU:CG	1:B:403:ARG:CA	2.71	0.57
1:B:408:HIS:O	1:B:410:LEU:N	2.37	0.57
1:A:93:ILE:HD12	1:A:148:PHE:CE2	2.39	0.57
1:D:399:PHE:C	1:D:401:TYR:H	2.06	0.57
1:F:118:VAL:HG11	1:F:375:ALA:HB3	1.85	0.57
1:F:321:ILE:CG2	1:F:343:ILE:HB	2.34	0.57
1:D:32:LEU:HD12	1:D:33:LYS:N	2.18	0.57
1:A:24:VAL:HG11	1:A:483:VAL:HG13	1.86	0.57
1:A:402:GLU:OE1	1:A:402:GLU:HA	2.04	0.57
1:A:397:LEU:HD23	1:B:383:PHE:CD1	2.39	0.57
1:B:90:LYS:HB2	1:B:122:PHE:CD1	2.38	0.57
1:C:409:LEU:HD23	1:C:409:LEU:O	2.03	0.57
1:C:280:ILE:HG21	1:C:301:ILE:O	2.04	0.57
1:D:270:CYS:O	1:D:286:ILE:N	2.36	0.57
1:D:245:LYS:N	1:D:245:LYS:HD2	2.19	0.57
1:A:37:THR:HA	1:A:40:GLN:HG3	1.85	0.57
1:A:209:HIS:CD2	1:A:446:LYS:CB	2.87	0.57
1:C:260:MET:HG2	1:C:288:PRO:HG3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:GLY:O	1:A:191:ASP:N	2.36	0.57
1:A:413:VAL:HG11	1:B:411:MET:CG	2.25	0.57
1:A:410:LEU:HD13	1:B:409:LEU:HB3	1.87	0.57
1:E:230:ALA:O	1:E:232:TYR:N	2.37	0.57
1:C:118:VAL:O	1:C:118:VAL:HG23	2.04	0.57
1:A:342:LYS:NZ	1:A:342:LYS:HB2	2.19	0.57
1:A:42:ARG:O	1:A:46:ARG:HB2	2.05	0.57
1:A:257:LEU:HD11	1:A:292:GLU:OE2	2.04	0.57
1:E:439:ARG:HG3	1:E:439:ARG:O	2.03	0.57
1:C:435:GLU:N	1:C:435:GLU:OE1	2.37	0.57
1:A:433:THR:O	1:A:435:GLU:N	2.32	0.57
1:A:400:LYS:HZ2	1:B:439:ARG:HH12	1.52	0.57
1:E:227:ILE:CG2	1:E:228:ASN:N	2.67	0.57
1:B:315:LEU:HD22	1:B:331:LEU:HD11	1.86	0.57
1:F:167:PRO:HA	1:F:176:MET:CE	2.34	0.57
1:F:142:GLU:HB2	1:F:178:TRP:CZ2	2.40	0.57
1:F:339:VAL:C	1:F:341:ALA:H	2.08	0.57
1:A:64:PRO:HD2	1:A:147:ARG:NH2	2.18	0.57
1:F:53:LYS:HB3	1:F:54:PRO:HD3	1.86	0.57
1:A:436:PHE:CE2	1:C:409:LEU:HD22	2.40	0.57
1:B:118:VAL:HG11	1:B:375:ALA:CB	2.34	0.57
1:B:208:ILE:CD1	1:B:383:PHE:HB3	2.34	0.57
1:A:428:ILE:C	1:B:430:ILE:CG1	2.73	0.57
2:A:502:GLU:HA	3:A:552:NDP:C4N	2.34	0.57
1:C:403:ARG:HA	1:C:440:ILE:O	2.04	0.57
1:E:160:PRO:HD3	1:E:197:CYS:HB3	1.86	0.57
1:A:227:ILE:HD13	1:A:343:ILE:CD1	2.34	0.57
1:C:9:PHE:CG	1:C:106:ALA:CB	2.88	0.57
1:E:372:TYR:OH	1:E:461:ALA:HB2	2.04	0.57
1:F:280:ILE:HB	1:F:307:ALA:HB1	1.87	0.57
1:B:107:LEU:CB	1:B:126:LYS:HG2	2.33	0.57
1:B:464:ILE:O	1:B:468:ALA:N	2.35	0.57
1:A:68:ASP:HB2	1:A:140:GLU:OE1	2.05	0.57
1:A:24:VAL:CG1	1:A:483:VAL:HG13	2.34	0.57
1:A:430:ILE:CG1	1:B:413:VAL:CB	2.68	0.57
1:A:410:LEU:CA	1:B:406:ASN:HB2	2.32	0.57
1:E:136:TYR:HB2	1:E:141:LEU:HD21	1.86	0.57
1:B:331:LEU:O	1:B:353:THR:HG23	2.05	0.57
1:C:169:MET:HE1	3:C:552:NDP:H8A	1.86	0.57
1:A:59:LEU:HD21	1:A:61:LEU:HD22	1.86	0.57
1:A:59:LEU:O	1:A:78:TYR:HA	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:36:GLU:O	1:D:37:THR:HG23	2.04	0.57
1:D:489:VAL:HG12	1:D:493:TYR:HE1	1.69	0.57
1:F:137:THR:HG23	1:F:140:GLU:HG3	1.86	0.57
1:F:201:LYS:HB2	1:F:384:GLU:OE1	2.05	0.57
1:C:480:ALA:O	1:C:483:VAL:HB	2.04	0.57
1:B:346:GLU:HG2	1:B:351:PRO:CD	2.33	0.57
1:E:258:HIS:HD2	1:E:261:ARG:HH12	1.51	0.57
1:F:3:ARG:HG2	1:F:4:GLU:N	2.19	0.57
1:B:416:SER:HB3	1:C:430:ILE:HA	1.87	0.57
1:C:229:GLU:HG3	1:C:231:SER:HB3	1.87	0.57
1:E:348:ALA:HA	3:E:552:NDP:H1D	1.85	0.57
1:D:346:GLU:HG2	1:D:351:PRO:HG2	1.85	0.57
1:A:234:SER:O	1:A:236:LEU:N	2.38	0.57
1:D:439:ARG:NH1	1:E:404:ASP:CB	2.67	0.57
1:B:107:LEU:HB3	1:B:126:LYS:CG	2.34	0.57
1:E:16:PHE:CE2	1:E:354:PRO:HB3	2.30	0.57
1:C:82:HIS:CG	1:C:112:THR:HG21	2.39	0.57
1:E:477:LEU:O	1:E:480:ALA:HB3	2.05	0.57
1:A:400:LYS:HZ2	1:B:439:ARG:NH1	2.02	0.57
1:A:408:HIS:NE2	1:B:437:GLN:CA	2.67	0.57
1:B:401:TYR:O	1:B:404:ASP:N	2.36	0.57
1:E:159:GLY:O	1:E:162:VAL:HG22	2.04	0.57
1:E:346:GLU:OE1	1:E:352:THR:HG23	2.04	0.57
1:E:89:CYS:HB3	1:E:125:ALA:HB2	1.86	0.57
1:A:314:ILE:HG23	1:A:315:LEU:HD23	1.86	0.57
1:C:178:TRP:O	1:C:179:ILE:C	2.41	0.57
1:B:24:VAL:O	1:B:27:LYS:HB3	2.05	0.57
1:A:69:ASP:OD2	1:A:71:SER:HB3	2.04	0.57
1:A:432:PRO:HA	1:C:409:LEU:HG	1.87	0.56
1:A:409:LEU:HD12	1:B:402:GLU:O	2.05	0.56
1:A:414:GLN:CA	1:B:430:ILE:C	2.74	0.56
1:A:226:PHE:CE2	1:A:465:MET:CG	2.87	0.56
1:A:91:GLY:HA2	1:A:111:MET:HE2	1.87	0.56
1:A:248:VAL:HG23	1:A:272:THR:C	2.24	0.56
1:F:247:PHE:CZ	1:F:263:LEU:HB2	2.40	0.56
1:E:409:LEU:O	1:E:412:SER:HB2	2.05	0.56
1:C:155:LYS:O	1:C:157:PHE:CD1	2.58	0.56
1:A:409:LEU:O	1:B:407:TYR:N	2.38	0.56
1:D:250:GLN:HG3	1:D:314:ILE:HG21	1.87	0.56
1:D:450:HIS:O	1:D:453:LEU:HB3	2.05	0.56
1:E:107:LEU:CB	1:E:126:LYS:HG2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:ASP:O	1:E:99:VAL:C	2.44	0.56
1:D:58:VAL:HA	1:D:80:ALA:HA	1.87	0.56
1:B:90:LYS:HD3	1:B:122:PHE:CE1	2.41	0.56
1:B:379:THR:O	1:B:382:TYR:HB3	2.05	0.56
1:C:402:GLU:O	1:C:405:SER:CB	2.53	0.56
1:A:412:SER:O	1:A:415:GLU:N	2.38	0.56
1:A:169:MET:HG2	3:A:552:NDP:H52N	1.86	0.56
1:B:53:LYS:O	1:B:82:HIS:CE1	2.52	0.56
1:C:321:ILE:HG22	1:C:343:ILE:CB	2.16	0.56
1:B:315:LEU:HD13	1:B:331:LEU:CD1	2.35	0.56
1:B:344:ILE:HD11	1:B:360:PHE:CE1	2.41	0.56
1:F:342:LYS:HB2	1:F:342:LYS:NZ	2.19	0.56
1:C:186:THR:OG1	1:C:187:ILE:HG12	2.04	0.56
1:A:93:ILE:HD11	1:A:95:TYR:HE1	1.71	0.56
1:F:10:PHE:CE2	1:F:14:GLU:HG3	2.40	0.56
1:C:19:ARG:NH1	1:C:19:ARG:HG2	2.14	0.56
1:B:174:ARG:CD	1:B:178:TRP:CH2	2.88	0.56
1:B:479:THR:O	1:B:483:VAL:HG23	2.05	0.56
1:B:280:ILE:HB	1:B:307:ALA:CB	2.35	0.56
1:E:258:HIS:HD2	1:E:261:ARG:HH11	1.50	0.56
1:E:385:TRP:CZ2	1:F:192:ILE:HD11	2.40	0.56
1:E:209:HIS:CG	1:E:446:LYS:HG3	2.41	0.56
1:B:462:ARG:HG3	1:B:466:ARG:NH2	2.21	0.56
1:A:282:ASN:OD1	1:A:284:ASP:HB2	2.06	0.56
1:A:488:LYS:O	1:A:490:PHE:O	2.24	0.56
1:E:271:ILE:HD11	1:E:319:CYS:HB3	1.86	0.56
1:C:323:ILE:CD1	1:C:345:ALA:HB3	2.35	0.56
1:A:148:PHE:CD2	1:A:152:LEU:HD11	2.40	0.56
1:B:149:THR:O	1:B:152:LEU:HB2	2.06	0.56
1:D:435:GLU:HB3	1:E:408:HIS:NE2	2.21	0.56
1:D:37:THR:CA	1:D:40:GLN:HG3	2.35	0.56
1:D:479:THR:O	1:D:483:VAL:HG23	2.05	0.56
1:B:459:ARG:HG2	1:B:459:ARG:HH11	1.70	0.56
1:C:61:LEU:HD21	1:C:151:GLU:HB2	1.88	0.56
1:F:308:LYS:HG2	1:F:308:LYS:O	2.05	0.56
1:A:408:HIS:ND1	1:B:439:ARG:CG	2.58	0.56
1:B:399:PHE:CA	1:B:441:SER:HB3	2.34	0.56
1:E:142:GLU:O	1:E:146:ARG:HG3	2.05	0.56
1:B:221:HIS:HA	1:B:224:GLU:HB3	1.87	0.56
1:C:93:ILE:HD11	1:C:95:TYR:CE1	2.39	0.56
1:B:64:PRO:HB3	1:E:51:ILE:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:ARG:HG2	1:E:36:GLU:HG3	1.88	0.56
1:E:418:GLU:CG	1:E:428:ILE:HD12	2.36	0.56
2:B:502:GLU:HA	3:B:552:NDP:C4N	2.31	0.56
1:A:209:HIS:HD2	1:A:446:LYS:HA	1.71	0.56
1:E:315:LEU:HD12	1:E:335:ASN:ND2	2.20	0.56
1:B:369:PRO:HG3	1:B:477:LEU:O	2.06	0.56
1:D:57:HIS:HB2	1:D:81:GLN:HB2	1.88	0.56
1:B:403:ARG:HG3	1:B:407:TYR:HD1	1.70	0.56
1:C:379:THR:O	1:C:382:TYR:HB3	2.06	0.56
1:E:421:PHE:N	1:E:421:PHE:HD2	2.03	0.56
1:E:386:LEU:HG	1:F:392:VAL:CG2	2.36	0.56
1:A:16:PHE:CE2	1:A:354:PRO:HB3	2.40	0.56
1:F:239:THR:O	1:F:245:LYS:HE2	2.06	0.56
1:E:289:LYS:HA	1:E:289:LYS:HE3	1.87	0.56
1:A:404:ASP:HB3	1:B:442:GLY:O	2.05	0.56
1:C:413:VAL:O	1:C:417:LEU:HB2	2.05	0.56
1:C:412:SER:O	1:C:414:GLN:C	2.45	0.56
1:D:315:LEU:HD12	1:D:335:ASN:ND2	2.21	0.56
1:B:391:HIS:CD2	1:C:385:TRP:CH2	2.91	0.56
1:C:165:PRO:CD	1:C:197:CYS:O	2.54	0.56
1:F:354:PRO:HA	1:F:357:ASP:HB2	1.87	0.56
1:F:209:HIS:CD2	1:F:446:LYS:HA	2.40	0.56
1:A:306:LYS:HD3	1:A:306:LYS:N	2.21	0.56
1:C:61:LEU:HD21	1:C:151:GLU:CB	2.36	0.56
1:C:246:THR:O	1:C:320:ASP:N	2.36	0.56
1:A:436:PHE:CD1	1:C:405:SER:OG	2.52	0.56
1:A:372:TYR:OH	1:A:461:ALA:HB2	2.06	0.56
1:E:271:ILE:HD12	1:E:272:THR:CG2	2.35	0.56
1:D:271:ILE:O	1:D:272:THR:HG22	2.05	0.56
1:D:279:SER:OG	1:D:314:ILE:HB	2.06	0.56
1:A:146:ARG:NE	1:A:182:THR:HG22	2.19	0.56
1:B:38:GLU:CG	1:B:39:GLU:H	2.19	0.56
1:F:167:PRO:HA	1:F:176:MET:HE1	1.87	0.56
1:B:126:LYS:HG3	1:B:127:ALA:N	2.20	0.56
1:E:306:LYS:HD3	1:E:306:LYS:N	2.21	0.56
1:A:404:ASP:CB	1:B:439:ARG:HD3	2.35	0.56
1:D:394:TYR:HE2	1:D:443:ALA:HB3	1.71	0.56
1:C:37:THR:O	1:C:38:GLU:HB2	2.06	0.56
1:E:11:LYS:O	1:E:12:MET:C	2.44	0.56
1:C:457:MET:HA	1:C:457:MET:HE2	1.88	0.56
1:F:460:SER:O	1:F:464:ILE:HG13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:GLU:OE2	1:A:229:GLU:HA	2.06	0.56
1:D:423:LYS:N	1:D:423:LYS:HD2	2.21	0.56
1:E:222:GLY:HA3	1:E:373:LEU:CD2	2.36	0.56
1:D:248:VAL:HG21	1:D:314:ILE:HD11	1.87	0.56
1:C:167:PRO:HA	1:C:176:MET:HE3	1.87	0.56
1:D:393:SER:O	1:D:394:TYR:C	2.42	0.56
1:D:485:ALA:O	1:D:489:VAL:HG23	2.06	0.56
1:B:466:ARG:NH1	1:B:466:ARG:HB2	2.21	0.56
1:B:464:ILE:HD13	1:B:481:ALA:HB2	1.87	0.56
1:E:60:SER:O	1:E:61:LEU:HB2	2.06	0.56
1:A:418:GLU:HG2	1:B:429:PRO:O	2.06	0.55
1:A:47:SER:HB3	1:D:72:TRP:HB2	1.86	0.55
1:E:199:THR:HG22	1:E:384:GLU:HG2	1.88	0.55
1:B:217:ARG:HH12	1:B:221:HIS:CE1	2.23	0.55
1:D:100:SER:O	1:D:101:VAL:C	2.43	0.55
1:D:166:ALA:CB	2:D:502:GLU:OE2	2.54	0.55
1:B:85:HIS:CD2	1:B:489:VAL:HG13	2.41	0.55
1:D:211:ARG:HA	1:D:380:VAL:HG11	1.88	0.55
1:D:19:ARG:CG	1:D:19:ARG:HH11	2.14	0.55
1:E:392:VAL:HG12	1:E:393:SER:N	2.20	0.55
1:F:78:TYR:N	1:F:78:TYR:CD1	2.74	0.55
1:A:374:ASN:C	1:A:376:GLY:H	2.09	0.55
1:F:224:GLU:HA	1:F:227:ILE:HG22	1.89	0.55
1:A:234:SER:C	1:A:236:LEU:H	2.10	0.55
1:F:47:SER:O	1:F:50:ARG:N	2.39	0.55
1:A:446:LYS:O	1:A:447:ASP:C	2.42	0.55
1:D:24:VAL:HG23	1:D:28:LEU:HD22	1.88	0.55
1:A:433:THR:HG22	1:C:413:VAL:N	2.14	0.55
1:A:409:LEU:HD11	1:B:404:ASP:H	1.70	0.55
1:C:230:ALA:O	1:C:231:SER:C	2.44	0.55
1:C:166:ALA:HB2	1:C:199:THR:OG1	2.06	0.55
1:B:37:THR:CA	1:B:40:GLN:HG3	2.36	0.55
1:F:63:PHE:CD1	1:F:147:ARG:HG3	2.41	0.55
1:F:339:VAL:O	1:F:341:ALA:N	2.40	0.55
1:B:196:ALA:HB2	1:B:388:ASN:CB	2.37	0.55
1:D:176:MET:N	1:D:176:MET:HE1	2.21	0.55
1:B:372:TYR:CE1	1:B:461:ALA:HB2	2.42	0.55
1:D:58:VAL:HG22	1:D:80:ALA:CB	2.37	0.55
1:E:120:VAL:HG13	1:E:121:PRO:HD2	1.89	0.55
1:A:404:ASP:OD1	1:B:439:ARG:HD3	2.06	0.55
1:A:415:GLU:HB2	1:B:432:PRO:CD	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:VAL:HG22	1:B:197:CYS:HA	1.88	0.55
1:A:413:VAL:HB	1:B:411:MET:N	2.22	0.55
1:B:90:LYS:HG3	1:B:91:GLY:N	2.22	0.55
1:C:280:ILE:HB	1:C:307:ALA:HB3	1.86	0.55
1:D:331:LEU:O	1:D:353:THR:HG23	2.06	0.55
1:D:332:THR:HA	1:D:356:ALA:HB2	1.89	0.55
1:D:90:LYS:HE2	1:D:164:VAL:HG12	1.88	0.55
1:B:346:GLU:OE1	1:B:352:THR:HG23	2.06	0.55
1:F:96:SER:O	1:F:130:LYS:HA	2.06	0.55
1:D:354:PRO:HA	1:D:357:ASP:HB2	1.89	0.55
1:E:453:LEU:HD11	1:E:457:MET:HG2	1.88	0.55
1:A:435:GLU:HB3	1:C:408:HIS:CA	2.36	0.55
1:A:414:GLN:CA	1:B:430:ILE:HG22	2.37	0.55
1:A:118:VAL:CG1	1:A:375:ALA:CB	2.81	0.55
1:E:90:LYS:HG3	1:E:91:GLY:H	1.71	0.55
1:C:458:GLU:O	1:C:460:SER:N	2.39	0.55
1:A:208:ILE:CG2	1:A:384:GLU:HB2	2.36	0.55
1:B:332:THR:O	1:B:334:SER:N	2.39	0.55
1:F:91:GLY:HA3	1:F:125:ALA:O	2.07	0.55
1:D:175:GLU:HA	1:D:178:TRP:CE3	2.42	0.55
1:A:113:TYR:O	1:A:116:ALA:HB3	2.05	0.55
1:A:382:TYR:OH	1:C:392:VAL:HG22	2.07	0.55
1:D:229:GLU:HG3	1:D:231:SER:HB3	1.88	0.55
1:E:41:LYS:O	1:E:45:VAL:HG23	2.07	0.55
1:D:395:GLY:O	1:D:399:PHE:CD2	2.60	0.55
1:F:95:TYR:HH	1:F:145:THR:HB	1.68	0.55
1:F:309:ILE:O	1:F:310:TYR:C	2.44	0.55
1:A:183:TYR:C	1:A:183:TYR:CD2	2.79	0.55
1:D:94:ARG:CZ	1:D:107:LEU:HD21	2.36	0.55
1:E:464:ILE:O	1:E:468:ALA:N	2.38	0.55
1:E:173:GLU:OE2	1:E:202:PRO:HA	2.05	0.55
1:F:167:PRO:CB	1:F:176:MET:HE3	2.36	0.55
1:F:271:ILE:C	1:F:272:THR:HG22	2.27	0.55
1:B:346:GLU:HG2	1:B:351:PRO:HG2	1.88	0.55
1:E:336:ALA:N	1:E:337:PRO:HD2	2.22	0.55
1:D:176:MET:CE	1:D:176:MET:N	2.69	0.55
1:B:245:LYS:HD2	1:B:245:LYS:N	2.21	0.55
1:D:220:PHE:CE1	1:D:266:PHE:HB2	2.42	0.55
1:A:430:ILE:HG23	1:B:413:VAL:CG2	2.17	0.55
1:A:433:THR:OG1	1:C:410:LEU:N	2.40	0.55
1:C:402:GLU:O	1:C:405:SER:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:281:TRP:O	1:D:307:ALA:HA	2.06	0.55
1:C:368:ILE:HG21	1:C:373:LEU:HG	1.88	0.55
1:D:37:THR:O	1:D:38:GLU:CB	2.54	0.55
1:E:305:PRO:HB2	1:E:306:LYS:HD3	1.88	0.55
1:F:485:ALA:O	1:F:486:ILE:C	2.43	0.55
1:B:405:SER:O	1:B:409:LEU:N	2.34	0.55
1:E:233:MET:HB3	1:E:238:MET:O	2.06	0.55
1:E:247:PHE:CB	1:E:321:ILE:HG12	2.35	0.55
1:D:336:ALA:N	1:D:337:PRO:HD2	2.20	0.55
1:E:455:TYR:HB2	1:F:400:LYS:HB2	1.88	0.55
1:C:238:MET:HG2	1:C:245:LYS:HZ1	1.72	0.55
1:B:99:VAL:CG2	1:B:130:LYS:HA	2.37	0.55
1:B:374:ASN:C	1:B:376:GLY:H	2.10	0.55
1:A:409:LEU:CD2	1:B:403:ARG:C	2.76	0.55
1:A:409:LEU:HD13	1:B:406:ASN:ND2	2.22	0.55
1:A:411:MET:O	1:B:432:PRO:CD	2.51	0.55
1:A:412:SER:CA	1:B:432:PRO:HG3	2.36	0.55
1:C:173:GLU:O	1:C:202:PRO:HD3	2.07	0.55
1:F:118:VAL:HG11	1:F:375:ALA:CB	2.36	0.55
1:E:84:GLN:C	1:E:86:ARG:N	2.60	0.55
1:D:404:ASP:O	1:D:408:HIS:HB2	2.07	0.55
1:A:430:ILE:HD12	1:B:430:ILE:CB	2.37	0.54
1:C:331:LEU:HD23	1:C:360:PHE:CZ	2.41	0.54
1:E:202:PRO:O	1:E:205:GLN:HB2	2.06	0.54
1:F:114:LYS:CA	1:F:371:LEU:HD23	2.35	0.54
1:E:385:TRP:HH2	1:F:391:HIS:CD2	2.25	0.54
1:E:382:TYR:OH	1:F:391:HIS:O	2.23	0.54
1:A:269:LYS:HD3	1:A:284:ASP:O	2.07	0.54
1:E:300:THR:HG22	1:E:302:LEU:HB2	1.88	0.54
1:A:177:SER:HB2	1:A:202:PRO:CD	2.36	0.54
1:B:247:PHE:O	1:B:271:ILE:HG13	2.07	0.54
1:A:406:ASN:ND2	1:B:402:GLU:CD	2.61	0.54
1:B:164:VAL:HG13	1:B:198:VAL:HA	1.89	0.54
1:C:392:VAL:HG11	1:C:397:LEU:HD11	1.90	0.54
1:B:112:THR:HB	1:B:124:GLY:H	1.72	0.54
1:D:83:SER:C	1:D:84:GLN:HG3	2.25	0.54
1:A:208:ILE:CD1	1:A:383:PHE:HB3	2.38	0.54
1:D:300:THR:HG22	1:D:302:LEU:N	2.14	0.54
1:E:217:ARG:HD2	1:E:262:TYR:CE2	2.42	0.54
1:D:98:ASP:O	1:D:99:VAL:C	2.45	0.54
1:E:457:MET:HE1	1:E:457:MET:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:423:LYS:N	1:F:423:LYS:HD2	2.22	0.54
1:F:330:GLN:NE2	1:F:330:GLN:HA	2.22	0.54
1:C:235:ILE:O	1:C:235:ILE:CG2	2.55	0.54
1:F:246:THR:O	1:F:320:ASP:HB2	2.06	0.54
1:A:406:ASN:O	1:A:410:LEU:HD22	2.07	0.54
1:B:401:TYR:OH	1:C:442:GLY:O	2.21	0.54
1:A:336:ALA:N	1:A:337:PRO:HD2	2.22	0.54
1:D:343:ILE:CG2	1:D:366:MET:HE3	2.36	0.54
1:F:148:PHE:CD2	1:F:152:LEU:HD11	2.42	0.54
1:E:202:PRO:HB2	1:E:205:GLN:CG	2.38	0.54
1:D:396:ARG:HG3	1:D:397:LEU:HG	1.89	0.54
1:C:52:ILE:HD13	1:C:489:VAL:HG12	1.89	0.54
1:F:29:VAL:HG21	1:F:42:ARG:NE	2.19	0.54
1:F:25:GLU:O	1:F:29:VAL:HG23	2.07	0.54
1:B:79:ARG:HG3	1:B:126:LYS:O	2.08	0.54
1:F:444:SER:OG	1:F:446:LYS:HB2	2.06	0.54
1:B:456:THR:HA	1:B:459:ARG:HB3	1.87	0.54
1:C:12:MET:HG3	1:C:354:PRO:HD3	1.90	0.54
1:C:394:TYR:CE2	1:C:443:ALA:HB3	2.42	0.54
1:D:197:CYS:SG	1:D:198:VAL:HG12	2.47	0.54
1:F:321:ILE:HG22	1:F:343:ILE:HB	1.88	0.54
1:E:434:ALA:HA	1:E:437:GLN:NE2	2.16	0.54
1:A:430:ILE:HD12	1:B:430:ILE:HD13	1.89	0.54
1:A:146:ARG:NE	1:A:182:THR:CG2	2.71	0.54
1:E:461:ALA:O	1:E:465:MET:HG3	2.07	0.54
1:F:137:THR:HG23	1:F:140:GLU:CG	2.38	0.54
1:F:250:GLN:O	1:F:326:ALA:HB2	2.08	0.54
1:C:98:ASP:O	1:C:100:SER:N	2.41	0.54
1:C:261:ARG:CZ	1:C:261:ARG:HB3	2.37	0.54
1:E:443:ALA:HB1	1:E:448:ILE:HG12	1.90	0.54
1:E:362:GLU:C	1:E:364:ASN:H	2.11	0.54
1:B:432:PRO:HB3	1:B:437:GLN:HB3	1.89	0.54
1:A:492:VAL:CG1	1:A:493:TYR:N	2.70	0.54
1:C:248:VAL:HG13	1:C:322:LEU:HD12	1.89	0.54
1:E:211:ARG:HH22	3:E:552:NDP:H72N	1.52	0.54
1:D:247:PHE:CZ	1:D:270:CYS:HB2	2.43	0.54
1:C:1:ALA:O	1:C:2:ASP:HB3	2.07	0.54
1:C:382:TYR:CZ	1:C:386:LEU:HD21	2.43	0.54
1:D:409:LEU:C	1:D:409:LEU:CD1	2.76	0.54
1:F:332:THR:O	1:F:336:ALA:CB	2.56	0.54
1:A:238:MET:CE	1:A:245:LYS:HZ1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:37:THR:O	1:F:38:GLU:HB2	2.08	0.54
1:A:456:THR:HA	1:A:459:ARG:HB3	1.88	0.54
1:F:421:PHE:N	1:F:421:PHE:HD2	2.04	0.54
1:C:137:THR:HG23	1:C:140:GLU:CD	2.28	0.54
1:C:462:ARG:HG3	1:C:466:ARG:NH2	2.22	0.54
1:C:289:LYS:HE3	1:C:289:LYS:HA	1.90	0.54
1:B:380:VAL:O	1:B:383:PHE:HB2	2.07	0.54
1:F:232:TYR:OH	1:F:477:LEU:HD21	2.08	0.54
1:C:201:LYS:CE	1:C:388:ASN:HD21	2.20	0.54
1:D:169:MET:HG2	3:D:552:NDP:C5D	2.38	0.54
1:A:412:SER:C	1:A:414:GLN:N	2.61	0.54
1:B:399:PHE:O	1:B:401:TYR:N	2.41	0.54
1:A:428:ILE:CG1	1:B:428:ILE:CB	2.45	0.54
1:B:336:ALA:O	1:B:339:VAL:HG23	2.08	0.54
1:B:337:PRO:HD3	1:B:359:ILE:CD1	2.38	0.54
1:C:217:ARG:NE	1:C:450:HIS:CD2	2.76	0.54
1:A:138:ASP:O	1:A:141:LEU:N	2.41	0.54
1:C:30:GLU:HG2	1:C:31:ASP:N	2.23	0.54
1:D:213:SER:O	1:D:214:ALA:C	2.46	0.54
1:F:42:ARG:O	1:F:46:ARG:HB2	2.07	0.54
1:E:337:PRO:HA	1:E:359:ILE:HG21	1.89	0.54
1:A:35:ARG:CD	1:A:35:ARG:N	2.69	0.54
1:C:463:GLN:HA	1:C:466:ARG:HB3	1.90	0.54
1:B:44:ARG:O	1:B:48:ILE:HG13	2.07	0.54
1:A:411:MET:HG3	1:B:432:PRO:C	2.27	0.54
1:A:435:GLU:O	1:A:438:ASP:CB	2.52	0.54
1:C:176:MET:HG3	1:C:199:THR:O	2.08	0.54
1:C:443:ALA:CB	1:C:448:ILE:HG12	2.39	0.54
1:C:63:PHE:CE2	1:C:75:ILE:HD11	2.43	0.54
1:B:37:THR:CG2	1:B:41:LYS:HG3	2.37	0.54
1:D:222:GLY:HA2	1:D:372:TYR:OH	2.08	0.54
1:C:40:GLN:HA	1:C:43:ASN:HB2	1.90	0.54
1:D:417:LEU:HD21	1:F:417:LEU:CD1	2.36	0.54
1:D:383:PHE:O	1:D:385:TRP:N	2.41	0.54
1:B:97:THR:CG2	1:B:132:ASN:HB2	2.37	0.54
1:A:346:GLU:OE1	1:A:352:THR:HG23	2.07	0.54
2:D:502:GLU:N	3:D:552:NDP:H5N	2.22	0.53
1:F:112:THR:HB	1:F:124:GLY:N	2.23	0.53
1:A:98:ASP:O	1:A:99:VAL:C	2.46	0.53
1:F:10:PHE:O	1:F:10:PHE:HD2	1.90	0.53
1:F:137:THR:O	1:F:140:GLU:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:68:ASP:HB2	1:F:140:GLU:CG	2.38	0.53
1:D:445:GLU:O	1:D:446:LYS:O	2.25	0.53
1:C:66:ARG:NH2	1:C:70:GLY:O	2.41	0.53
1:A:428:ILE:CB	1:B:428:ILE:HB	2.34	0.53
1:E:272:THR:OG1	1:E:314:ILE:HD11	2.09	0.53
1:B:271:ILE:HD11	1:B:319:CYS:HB3	1.90	0.53
1:B:339:VAL:O	1:B:341:ALA:N	2.41	0.53
1:D:336:ALA:O	1:D:339:VAL:HG23	2.08	0.53
1:F:84:GLN:C	1:F:86:ARG:N	2.62	0.53
1:A:95:TYR:HH	1:A:145:THR:HB	1.67	0.53
1:D:373:LEU:HD22	1:D:373:LEU:O	2.08	0.53
1:F:211:ARG:O	1:F:214:ALA:HB3	2.08	0.53
1:B:19:ARG:NH1	1:B:479:THR:HG21	2.24	0.53
1:A:29:VAL:HG13	1:A:41:LYS:CB	2.36	0.53
1:F:165:PRO:HD2	1:F:197:CYS:O	2.08	0.53
1:A:221:HIS:O	1:A:225:ASN:HB2	2.08	0.53
1:C:272:THR:CG2	1:C:281:TRP:HD1	2.21	0.53
1:C:175:GLU:HA	1:C:178:TRP:HE3	1.71	0.53
1:E:38:GLU:HG2	1:E:39:GLU:N	2.22	0.53
1:B:8:ASN:O	1:B:9:PHE:C	2.47	0.53
1:A:433:THR:CA	1:C:412:SER:CB	2.63	0.53
1:B:405:SER:HA	1:C:439:ARG:HD2	1.89	0.53
1:A:114:LYS:HA	1:A:371:LEU:CD2	2.38	0.53
1:D:315:LEU:HD13	1:D:331:LEU:HD11	1.89	0.53
1:F:29:VAL:HG22	1:F:42:ARG:HG2	1.90	0.53
1:A:101:VAL:HG22	1:A:105:LYS:HD2	1.91	0.53
1:A:186:THR:OG1	1:A:187:ILE:N	2.41	0.53
1:E:308:LYS:HG2	1:E:308:LYS:O	2.07	0.53
1:A:410:LEU:HB3	1:B:436:PHE:CZ	2.43	0.53
1:A:415:GLU:O	1:A:419:ARG:HB2	2.08	0.53
1:A:436:PHE:O	1:A:436:PHE:CG	2.62	0.53
1:A:213:SER:O	1:A:215:THR:N	2.42	0.53
1:C:167:PRO:CB	1:C:172:GLY:HA2	2.39	0.53
1:B:38:GLU:HG2	1:B:39:GLU:H	1.73	0.53
1:F:177:SER:HB2	1:F:202:PRO:CG	2.38	0.53
1:C:82:HIS:CD2	1:C:83:SER:N	2.76	0.53
1:A:428:ILE:HD11	1:B:414:GLN:NE2	2.23	0.53
1:E:238:MET:HE3	1:E:320:ASP:OD2	2.09	0.53
1:E:320:ASP:HB3	1:E:321:ILE:HD13	1.90	0.53
1:D:255:VAL:HG11	3:D:552:NDP:O4D	2.08	0.53
1:E:173:GLU:O	1:E:202:PRO:HD3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:171:THR:CB	1:F:175:GLU:HG3	2.36	0.53
1:A:236:LEU:HD23	1:A:237:GLY:N	2.23	0.53
1:C:82:HIS:ND1	1:C:109:SER:HA	2.24	0.53
1:C:155:LYS:O	1:C:157:PHE:HD1	1.90	0.53
1:E:282:ASN:HB2	1:E:306:LYS:O	2.08	0.53
1:E:331:LEU:HD23	1:E:360:PHE:HZ	1.73	0.53
1:E:260:MET:HG2	1:E:288:PRO:HG3	1.91	0.53
1:F:457:MET:CE	1:F:457:MET:HA	2.38	0.53
1:C:412:SER:O	1:C:414:GLN:N	2.41	0.53
1:A:379:THR:O	1:A:382:TYR:HB3	2.09	0.53
1:E:92:GLY:HA2	1:E:166:ALA:H	1.72	0.53
1:B:339:VAL:C	1:B:341:ALA:H	2.11	0.53
1:D:303:GLY:H	1:D:309:ILE:CD1	2.22	0.53
1:C:147:ARG:O	1:C:149:THR:N	2.41	0.53
1:B:219:VAL:HG12	1:B:220:PHE:N	2.22	0.53
1:A:93:ILE:HD12	1:A:148:PHE:HE2	1.73	0.53
1:F:247:PHE:CE2	1:F:263:LEU:CB	2.91	0.53
1:E:395:GLY:O	1:E:399:PHE:CD2	2.61	0.53
1:F:45:VAL:O	1:F:47:SER:N	2.41	0.53
1:F:99:VAL:O	1:F:99:VAL:HG23	2.09	0.53
1:B:99:VAL:HG22	1:B:130:LYS:HA	1.91	0.53
1:D:209:HIS:CD2	1:D:446:LYS:HA	2.44	0.53
1:D:275:GLU:HB2	1:D:301:ILE:HD11	1.91	0.53
1:C:216:GLY:HA2	1:C:219:VAL:HB	1.89	0.53
1:A:404:ASP:O	1:B:436:PHE:CE1	2.61	0.53
1:A:53:LYS:O	1:A:82:HIS:HE1	1.92	0.53
1:F:248:VAL:HG12	1:F:319:CYS:SG	2.48	0.53
1:F:368:ILE:CG2	1:F:373:LEU:HG	2.38	0.53
1:D:397:LEU:HD23	1:F:383:PHE:CD1	2.44	0.53
1:F:380:VAL:HA	1:F:383:PHE:CD2	2.37	0.53
1:F:114:LYS:NZ	2:F:502:GLU:O	2.35	0.53
1:B:95:TYR:HB3	1:B:133:PRO:HG3	1.90	0.53
1:B:196:ALA:HB2	1:B:388:ASN:HB3	1.89	0.53
1:A:385:TRP:CZ2	1:A:389:LEU:HD11	2.44	0.53
1:F:48:ILE:HG21	1:F:490:PHE:CD1	2.44	0.53
1:F:131:ILE:HG13	1:F:131:ILE:O	2.07	0.53
1:A:400:LYS:NZ	1:B:439:ARG:NH1	2.56	0.53
1:A:430:ILE:HD13	1:B:410:LEU:HG	1.90	0.53
1:A:434:ALA:H	1:C:412:SER:N	2.06	0.53
1:A:374:ASN:HB2	3:A:552:NDP:H5N	1.91	0.53
1:E:313:SER:HB3	1:E:316:GLU:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:VAL:HG11	1:E:317:VAL:HG11	1.91	0.53
1:C:167:PRO:HD3	1:C:200:GLY:HA3	1.91	0.53
1:D:164:VAL:HG13	1:D:198:VAL:CA	2.38	0.53
1:B:258:HIS:HD2	1:B:261:ARG:HH12	1.49	0.53
1:F:166:ALA:HA	1:F:199:THR:O	2.09	0.53
1:F:281:TRP:CZ2	1:F:283:PRO:HG3	2.44	0.53
1:E:478:ARG:O	1:E:480:ALA:N	2.42	0.53
1:F:306:LYS:N	1:F:306:LYS:CD	2.72	0.53
1:B:491:ARG:O	1:B:494:ASN:N	2.25	0.53
1:F:104:VAL:HG12	1:F:104:VAL:O	2.09	0.53
1:A:408:HIS:CE1	1:B:439:ARG:N	2.78	0.53
1:A:436:PHE:HD2	1:C:406:ASN:HA	1.73	0.53
1:A:433:THR:CB	1:C:412:SER:H	2.18	0.53
1:E:162:VAL:HG23	1:E:163:ASP:N	2.23	0.53
1:F:234:SER:C	1:F:236:LEU:H	2.12	0.53
1:C:5:ASP:O	1:C:7:PRO:HD3	2.09	0.53
1:B:37:THR:C	1:B:40:GLN:HG3	2.30	0.53
1:A:10:PHE:HA	1:A:106:ALA:HB2	1.90	0.53
1:A:410:LEU:O	1:B:410:LEU:CB	2.57	0.52
1:A:51:ILE:O	1:A:54:PRO:HD2	2.08	0.52
1:C:392:VAL:HG12	1:C:393:SER:O	2.09	0.52
1:E:211:ARG:HD2	1:E:211:ARG:O	2.08	0.52
1:E:280:ILE:HB	1:E:307:ALA:HB1	1.91	0.52
1:C:16:PHE:CE2	1:C:354:PRO:HB3	2.38	0.52
1:D:90:LYS:CB	1:D:122:PHE:CD1	2.92	0.52
1:F:275:GLU:HG3	3:F:552:NDP:O2X	2.09	0.52
1:E:483:VAL:HG12	1:E:484:ASN:N	2.23	0.52
1:A:301:ILE:HG13	1:A:302:LEU:N	2.25	0.52
1:A:392:VAL:HG11	1:A:397:LEU:HD11	1.90	0.52
1:A:412:SER:N	1:B:432:PRO:HG3	2.24	0.52
1:B:220:PHE:CZ	1:B:224:GLU:HG3	2.45	0.52
1:E:236:LEU:HD21	1:E:342:LYS:HG3	1.89	0.52
1:B:292:GLU:O	1:B:294:PHE:N	2.42	0.52
1:C:444:SER:O	1:C:445:GLU:C	2.48	0.52
1:C:374:ASN:C	1:C:376:GLY:N	2.63	0.52
1:B:444:SER:HB2	1:B:446:LYS:HD3	1.91	0.52
1:A:222:GLY:HA3	1:A:373:LEU:HD23	1.90	0.52
1:D:314:ILE:HD12	1:D:317:VAL:CG2	2.39	0.52
1:D:53:LYS:O	1:D:82:HIS:CE1	2.62	0.52
1:B:400:LYS:HB2	1:C:455:TYR:HB2	1.90	0.52
1:F:183:TYR:CD2	1:F:183:TYR:O	2.61	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:257:LEU:HD12	1:D:257:LEU:O	2.08	0.52
1:A:411:MET:CE	1:A:414:GLN:OE1	2.57	0.52
1:B:413:VAL:O	1:B:417:LEU:HG	2.10	0.52
1:A:412:SER:HA	1:B:432:PRO:CG	2.39	0.52
1:C:404:ASP:O	1:C:408:HIS:HB2	2.08	0.52
1:A:339:VAL:C	1:A:341:ALA:H	2.12	0.52
1:A:77:GLY:C	1:A:78:TYR:CD1	2.83	0.52
1:E:201:LYS:NZ	1:E:388:ASN:ND2	2.44	0.52
1:A:238:MET:HE1	1:A:320:ASP:HB3	1.92	0.52
1:E:421:PHE:O	1:E:422:GLY:O	2.27	0.52
1:C:109:SER:O	1:C:112:THR:HG23	2.09	0.52
1:A:423:LYS:HD2	1:A:423:LYS:N	2.25	0.52
1:B:114:LYS:HA	1:B:371:LEU:HD23	1.91	0.52
1:B:431:VAL:HG22	1:B:432:PRO:O	2.08	0.52
1:C:366:MET:HG3	1:C:475:LEU:HD22	1.89	0.52
1:E:90:LYS:HG3	1:E:91:GLY:N	2.24	0.52
1:A:247:PHE:O	1:A:271:ILE:HG13	2.08	0.52
1:C:173:GLU:CD	1:C:202:PRO:HA	2.28	0.52
1:F:316:GLU:OE2	1:F:338:ARG:HG3	2.09	0.52
1:F:371:LEU:HD13	1:F:481:ALA:HB1	1.91	0.52
1:B:280:ILE:HB	1:B:307:ALA:HB1	1.91	0.52
1:B:94:ARG:HG2	1:B:94:ARG:O	2.10	0.52
1:E:23:ILE:HG22	1:E:471:TYR:HD1	1.74	0.52
1:D:18:ASP:O	1:D:21:ALA:HB3	2.10	0.52
1:B:410:LEU:C	1:B:412:SER:N	2.59	0.52
1:A:490:PHE:CG	1:A:491:ARG:N	2.78	0.52
1:C:247:PHE:CE2	1:C:263:LEU:HB3	2.44	0.52
1:C:346:GLU:OE1	1:C:352:THR:HG23	2.10	0.52
1:C:353:THR:HB	1:C:354:PRO:HD2	1.90	0.52
1:C:211:ARG:HH22	2:C:502:GLU:CD	2.13	0.52
1:D:94:ARG:HE	1:D:169:MET:HG3	1.75	0.52
1:E:53:LYS:HB3	1:E:54:PRO:CD	2.28	0.52
1:F:126:LYS:HG3	1:F:127:ALA:H	1.74	0.52
1:F:214:ALA:HB1	1:F:380:VAL:CG2	2.39	0.52
1:B:172:GLY:H	1:B:175:GLU:HG2	1.75	0.52
1:E:420:LYS:C	1:E:421:PHE:HD2	2.13	0.52
1:D:64:PRO:O	1:D:65:ILE:HD13	2.09	0.52
1:D:29:VAL:HG21	1:D:42:ARG:NE	2.20	0.52
1:D:444:SER:H	1:D:447:ASP:HB2	1.74	0.52
1:A:24:VAL:HG13	1:A:483:VAL:HG22	1.91	0.52
1:A:409:LEU:HA	1:A:412:SER:OG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:ALA:O	1:A:488:LYS:N	2.43	0.52
1:C:363:ARG:NH1	1:C:365:ILE:HD11	2.25	0.52
1:A:219:VAL:HA	1:A:373:LEU:HD22	1.90	0.52
1:F:236:LEU:HD22	1:F:238:MET:HB2	1.92	0.52
1:C:63:PHE:CD1	1:C:147:ARG:CG	2.92	0.52
1:D:186:THR:OG1	1:D:187:ILE:N	2.42	0.52
1:B:64:PRO:O	1:B:65:ILE:HD13	2.08	0.52
1:B:29:VAL:CG2	1:B:42:ARG:HG2	2.40	0.52
1:D:453:LEU:HG	1:D:454:ALA:N	2.25	0.52
1:F:93:ILE:HB	1:F:127:ALA:HB3	1.90	0.52
1:F:172:GLY:H	1:F:175:GLU:HG2	1.74	0.52
1:A:37:THR:CG2	1:A:41:LYS:HG3	2.40	0.52
1:A:459:ARG:O	1:A:462:ARG:HB3	2.09	0.52
1:E:446:LYS:CD	1:E:446:LYS:H	2.22	0.52
1:F:304:PHE:HE2	1:F:306:LYS:HB2	1.72	0.52
1:A:404:ASP:CA	1:B:439:ARG:CD	2.86	0.52
1:E:492:VAL:CG2	1:E:493:TYR:N	2.73	0.52
1:B:230:ALA:O	1:B:231:SER:C	2.48	0.52
1:D:272:THR:OG1	1:D:314:ILE:CD1	2.54	0.52
1:C:91:GLY:HA3	1:C:125:ALA:O	2.10	0.52
1:C:385:TRP:CE2	1:C:389:LEU:HD11	2.45	0.52
1:C:63:PHE:CD1	1:C:75:ILE:HD11	2.44	0.52
1:E:112:THR:HG23	1:E:113:TYR:N	2.24	0.52
1:D:409:LEU:HD21	1:F:409:LEU:HD22	1.90	0.52
1:F:41:LYS:O	1:F:45:VAL:HG23	2.09	0.52
1:A:305:PRO:HB2	1:A:306:LYS:CD	2.40	0.52
1:A:463:GLN:HB3	1:A:466:ARG:HH21	1.74	0.52
1:A:409:LEU:CD2	1:B:407:TYR:CB	2.76	0.52
1:B:411:MET:O	1:B:414:GLN:HB3	2.10	0.52
1:D:150:MET:CE	1:D:187:ILE:HD11	2.39	0.52
1:D:392:VAL:HG11	1:D:397:LEU:HD11	1.90	0.52
1:C:34:THR:HG23	1:C:35:ARG:HD3	1.92	0.52
1:B:239:THR:HG23	1:B:245:LYS:HZ3	1.74	0.52
1:C:216:GLY:O	1:C:219:VAL:HB	2.10	0.52
1:E:339:VAL:HG12	1:E:341:ALA:HB3	1.92	0.52
1:A:410:LEU:CB	1:B:436:PHE:CZ	2.92	0.52
1:A:413:VAL:HG22	1:B:406:ASN:O	2.10	0.52
1:B:339:VAL:O	1:B:339:VAL:HG12	2.09	0.52
1:C:168:ASP:O	1:C:171:THR:O	2.28	0.52
1:C:198:VAL:O	1:C:201:LYS:NZ	2.32	0.52
1:B:25:GLU:O	1:B:29:VAL:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:164:VAL:HG13	1:F:197:CYS:C	2.30	0.52
1:F:362:GLU:C	1:F:364:ASN:H	2.12	0.52
1:B:93:ILE:O	1:B:93:ILE:HG12	2.07	0.52
1:A:435:GLU:N	1:A:437:GLN:OE1	2.43	0.51
1:B:412:SER:O	1:B:414:GLN:N	2.42	0.51
1:C:414:GLN:O	1:C:416:SER:N	2.43	0.51
1:B:212:ILE:HG13	1:B:213:SER:N	2.25	0.51
1:A:171:THR:HB	1:A:175:GLU:HG3	1.92	0.51
1:D:211:ARG:O	1:D:214:ALA:HB3	2.10	0.51
1:F:37:THR:O	1:F:38:GLU:CB	2.57	0.51
1:D:355:GLU:CD	1:D:358:LYS:HE3	2.31	0.51
1:C:59:LEU:HD21	1:C:155:LYS:HB2	1.92	0.51
1:D:24:VAL:HG23	1:D:28:LEU:CD2	2.40	0.51
1:D:446:LYS:O	1:D:447:ASP:C	2.48	0.51
1:A:66:ARG:NH2	1:A:70:GLY:O	2.43	0.51
1:B:9:PHE:CD2	1:B:106:ALA:HB1	2.45	0.51
1:C:344:ILE:CD1	1:C:360:PHE:CZ	2.93	0.51
1:C:383:PHE:O	1:C:386:LEU:N	2.43	0.51
1:F:201:LYS:HZ1	1:F:388:ASN:ND2	2.08	0.51
1:B:175:GLU:HA	1:B:178:TRP:CE3	2.45	0.51
1:C:30:GLU:HG2	1:C:31:ASP:H	1.74	0.51
1:E:433:THR:CG2	1:F:412:SER:HA	2.40	0.51
1:F:37:THR:CG2	1:F:41:LYS:HG3	2.40	0.51
1:D:289:LYS:CE	1:D:293:ASP:OD1	2.56	0.51
1:A:394:TYR:HE2	1:A:443:ALA:HB3	1.74	0.51
1:B:96:SER:O	1:B:99:VAL:HG22	2.09	0.51
1:A:420:LYS:HG3	1:A:421:PHE:CE2	2.46	0.51
1:C:412:SER:C	1:C:414:GLN:N	2.60	0.51
1:E:95:TYR:HB3	1:E:133:PRO:HG3	1.92	0.51
1:B:358:LYS:HG3	1:B:359:ILE:N	2.24	0.51
1:C:174:ARG:O	1:C:177:SER:HB3	2.10	0.51
1:D:90:LYS:NZ	1:D:166:ALA:HB2	2.23	0.51
1:D:391:HIS:O	1:D:392:VAL:CG2	2.58	0.51
1:E:5:ASP:C	1:E:7:PRO:HD3	2.30	0.51
1:A:428:ILE:CG1	1:B:430:ILE:HG13	2.36	0.51
1:C:280:ILE:HB	1:C:307:ALA:HB1	1.91	0.51
1:C:309:ILE:O	1:C:310:TYR:C	2.48	0.51
1:B:316:GLU:OE2	1:B:338:ARG:HG3	2.10	0.51
1:D:336:ALA:HB3	1:D:359:ILE:HD12	1.92	0.51
1:C:199:THR:HG21	1:C:381:SER:O	2.10	0.51
1:D:117:VAL:HG21	1:D:371:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:GLU:O	1:A:224:GLU:OE1	2.28	0.51
1:E:226:PHE:HE2	1:E:465:MET:HG2	1.75	0.51
1:F:10:PHE:O	1:F:10:PHE:CD2	2.63	0.51
1:F:219:VAL:HG11	1:F:259:SER:OG	2.10	0.51
1:F:478:ARG:O	1:F:481:ALA:N	2.43	0.51
1:C:43:ASN:O	1:C:44:ARG:C	2.48	0.51
1:A:238:MET:CG	1:A:245:LYS:HZ1	2.23	0.51
1:D:417:LEU:CD2	1:F:428:ILE:HG21	2.33	0.51
1:D:380:VAL:HG22	1:D:449:VAL:HG13	1.92	0.51
1:F:399:PHE:CE2	1:F:443:ALA:O	2.58	0.51
1:A:473:LEU:O	1:A:475:LEU:N	2.44	0.51
1:B:304:PHE:CD1	1:B:305:PRO:HD2	2.45	0.51
1:A:173:GLU:O	1:A:174:ARG:C	2.48	0.51
1:D:30:GLU:HG2	1:D:31:ASP:N	2.24	0.51
1:A:409:LEU:CD1	1:B:406:ASN:CG	2.78	0.51
1:A:409:LEU:HD11	1:B:404:ASP:N	2.25	0.51
1:A:228:ASN:OD1	1:A:241:GLY:HA2	2.10	0.51
1:F:232:TYR:O	1:F:235:ILE:N	2.43	0.51
1:C:175:GLU:O	1:C:178:TRP:N	2.44	0.51
1:C:154:LYS:HE2	1:D:185:SER:O	2.10	0.51
1:D:109:SER:O	1:D:113:TYR:CD1	2.64	0.51
1:D:78:TYR:CD1	1:D:78:TYR:N	2.79	0.51
1:D:392:VAL:O	1:D:394:TYR:N	2.43	0.51
1:F:202:PRO:HB2	1:F:205:GLN:HG2	1.91	0.51
1:B:30:GLU:HG2	1:B:31:ASP:N	2.26	0.51
1:F:43:ASN:O	1:F:44:ARG:C	2.48	0.51
1:F:153:ALA:CA	1:F:158:ILE:HG22	2.34	0.51
1:D:220:PHE:HE1	1:D:266:PHE:HB2	1.73	0.51
1:A:23:ILE:HG22	1:A:471:TYR:CD1	2.46	0.51
1:A:410:LEU:CB	1:B:436:PHE:HE2	2.14	0.51
1:E:313:SER:HB3	1:E:316:GLU:OE1	2.11	0.51
1:D:303:GLY:H	1:D:309:ILE:HD11	1.74	0.51
1:D:186:THR:OG1	1:D:187:ILE:HG12	2.11	0.51
1:F:56:ASN:HD21	1:F:83:SER:HA	1.76	0.51
1:B:149:THR:OG1	1:B:179:ILE:HG23	2.11	0.51
1:B:107:LEU:CG	1:B:126:LYS:HE2	2.40	0.51
1:F:433:THR:O	1:F:437:GLN:OE1	2.29	0.51
1:F:1:ALA:O	1:F:2:ASP:CB	2.57	0.51
1:A:90:LYS:CB	1:A:122:PHE:HD1	2.23	0.51
1:D:316:GLU:OE2	1:D:338:ARG:NH1	2.43	0.51
1:C:217:ARG:O	1:C:220:PHE:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:150:MET:O	1:F:154:LYS:HG3	2.11	0.51
1:D:289:LYS:HA	1:D:289:LYS:HE3	1.92	0.51
1:B:20:GLY:HA2	1:B:23:ILE:HD12	1.92	0.51
1:A:158:ILE:HG12	1:A:159:GLY:N	2.25	0.51
1:D:205:GLN:NE2	1:F:495:GLU:HB2	2.26	0.51
1:B:406:ASN:HA	1:B:409:LEU:CB	2.41	0.51
1:C:439:ARG:O	1:C:439:ARG:HG3	2.10	0.51
1:A:324:PRO:HD2	1:A:345:ALA:O	2.11	0.51
1:F:335:ASN:O	1:F:338:ARG:HG2	2.10	0.51
1:C:494:ASN:O	1:C:495:GLU:HG2	2.10	0.51
1:F:24:VAL:CG1	1:F:483:VAL:HG13	2.41	0.51
1:C:112:THR:N	1:C:124:GLY:HA3	2.26	0.51
1:D:406:ASN:O	1:D:410:LEU:HB2	2.11	0.51
1:A:300:THR:HG22	1:A:302:LEU:HB2	1.92	0.51
1:D:203:ILE:CG2	1:D:204:SER:N	2.73	0.51
1:A:9:PHE:O	1:A:10:PHE:C	2.46	0.51
1:E:23:ILE:HG22	1:E:471:TYR:CD1	2.46	0.51
1:C:158:ILE:HG12	1:C:159:GLY:N	2.25	0.51
1:B:423:LYS:CD	1:B:423:LYS:N	2.74	0.51
1:A:430:ILE:CD1	1:B:410:LEU:HD23	2.40	0.51
1:E:212:ILE:HG13	1:E:213:SER:N	2.24	0.51
1:B:337:PRO:HA	1:B:359:ILE:HG21	1.92	0.51
1:A:280:ILE:HB	1:A:307:ALA:HB3	1.87	0.51
1:D:325:ALA:HA	1:D:348:ALA:H	1.75	0.51
1:A:458:GLU:CG	1:A:459:ARG:N	2.71	0.51
1:D:37:THR:CG2	1:D:41:LYS:HG3	2.40	0.51
1:A:346:GLU:HG2	1:A:351:PRO:CG	2.40	0.51
1:A:8:ASN:CG	1:A:11:LYS:HG3	2.31	0.51
1:A:52:ILE:CD1	1:A:489:VAL:HG12	2.39	0.51
1:B:316:GLU:O	1:B:317:VAL:C	2.49	0.51
1:B:216:GLY:HA2	1:B:219:VAL:HB	1.93	0.51
1:D:255:VAL:HG22	1:D:325:ALA:HB1	1.92	0.51
1:E:300:THR:HG21	1:E:302:LEU:HB2	1.92	0.51
1:E:68:ASP:HB2	1:E:140:GLU:OE1	2.10	0.51
1:A:408:HIS:CD2	1:B:436:PHE:C	2.84	0.50
1:A:410:LEU:O	1:B:410:LEU:CD1	2.56	0.50
1:C:300:THR:HG21	1:C:302:LEU:HB2	1.93	0.50
2:F:502:GLU:CA	2:F:502:GLU:OE2	2.59	0.50
1:B:142:GLU:HB2	1:B:178:TRP:CZ2	2.46	0.50
1:B:59:LEU:HD22	1:B:157:PHE:CD1	2.46	0.50
1:C:19:ARG:CG	1:C:19:ARG:NH1	2.69	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:84:GLN:C	1:C:86:ARG:N	2.63	0.50
1:C:306:LYS:HD3	1:C:306:LYS:H	1.76	0.50
1:F:186:THR:O	1:F:189:HIS:HB3	2.12	0.50
1:A:344:ILE:HB	1:A:367:VAL:HG12	1.94	0.50
1:B:88:PRO:HB3	1:B:161:GLY:C	2.31	0.50
1:B:113:TYR:C	1:B:371:LEU:HD21	2.31	0.50
1:A:430:ILE:CG2	1:B:410:LEU:CD1	2.90	0.50
1:C:342:LYS:O	1:C:365:ILE:HG23	2.11	0.50
1:E:175:GLU:O	1:E:178:TRP:HB2	2.10	0.50
1:C:63:PHE:O	1:C:75:ILE:HD13	2.10	0.50
2:D:502:GLU:N	3:D:552:NDP:C5N	2.75	0.50
1:A:224:GLU:HG2	1:A:224:GLU:O	2.12	0.50
1:F:406:ASN:O	1:F:410:LEU:HB2	2.11	0.50
1:E:397:LEU:H	1:E:397:LEU:HD12	1.75	0.50
1:A:413:VAL:CG2	1:B:406:ASN:O	2.59	0.50
1:A:404:ASP:CA	1:B:439:ARG:HD3	2.41	0.50
1:B:445:GLU:O	1:B:446:LYS:C	2.49	0.50
1:C:160:PRO:CG	1:C:161:GLY:H	2.22	0.50
1:A:169:MET:O	1:A:170:SER:HB2	2.12	0.50
1:C:300:THR:HG22	1:C:302:LEU:HB2	1.93	0.50
1:E:172:GLY:O	1:E:176:MET:HB2	2.11	0.50
1:B:342:LYS:HB2	1:B:342:LYS:HZ2	1.75	0.50
1:D:280:ILE:HB	1:D:307:ALA:HB3	1.93	0.50
1:C:324:PRO:HB2	1:C:351:PRO:CB	2.40	0.50
1:B:37:THR:O	1:B:38:GLU:HB2	2.11	0.50
1:D:345:ALA:HB1	1:D:373:LEU:HD11	1.92	0.50
1:F:75:ILE:CD1	1:F:75:ILE:O	2.57	0.50
1:D:200:GLY:N	1:D:384:GLU:OE1	2.45	0.50
1:D:63:PHE:CZ	1:D:75:ILE:HD11	2.46	0.50
1:E:473:LEU:O	1:E:475:LEU:N	2.44	0.50
1:E:315:LEU:HD12	1:E:335:ASN:HD21	1.75	0.50
1:B:96:SER:O	1:B:130:LYS:HA	2.11	0.50
1:A:158:ILE:HG13	1:A:165:PRO:CD	2.42	0.50
1:A:10:PHE:O	1:A:13:VAL:HB	2.11	0.50
1:A:258:HIS:CD2	1:A:261:ARG:HH11	2.19	0.50
1:C:271:ILE:HD12	1:C:272:THR:CG2	2.41	0.50
1:D:230:ALA:HA	1:D:233:MET:HB2	1.93	0.50
1:D:107:LEU:CD2	1:D:126:LYS:HE2	2.38	0.50
1:D:276:SER:OG	3:D:552:NDP:O3X	2.29	0.50
1:D:78:TYR:O	1:D:79:ARG:HB2	2.12	0.50
1:F:459:ARG:O	1:F:462:ARG:CB	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:PHE:CD2	1:E:106:ALA:HB1	2.46	0.50
1:D:19:ARG:NH1	1:D:19:ARG:HG2	2.19	0.50
1:D:99:VAL:HA	1:D:103:GLU:OE1	2.11	0.50
1:C:445:GLU:O	1:C:446:LYS:C	2.49	0.50
1:E:59:LEU:O	1:E:78:TYR:HA	2.12	0.50
1:E:60:SER:HA	1:E:78:TYR:HD2	1.75	0.50
1:A:401:TYR:CE1	1:B:444:SER:N	2.79	0.50
1:A:411:MET:O	1:A:414:GLN:N	2.44	0.50
1:B:417:LEU:HB3	1:B:428:ILE:CD1	2.42	0.50
1:C:236:LEU:HD21	1:C:342:LYS:HG3	1.92	0.50
1:E:136:TYR:HB2	1:E:141:LEU:CD2	2.42	0.50
1:B:230:ALA:HA	1:B:233:MET:HB2	1.93	0.50
1:B:337:PRO:HD3	1:B:359:ILE:HD12	1.93	0.50
1:D:291:LEU:O	1:D:292:GLU:C	2.50	0.50
1:D:90:LYS:HD3	1:D:122:PHE:CE1	2.46	0.50
1:A:129:VAL:O	1:A:131:ILE:N	2.44	0.50
1:C:48:ILE:HG21	1:C:490:PHE:HD1	1.77	0.50
1:B:137:THR:HG23	1:B:140:GLU:HG3	1.94	0.50
1:F:26:ASP:OD1	1:F:42:ARG:NH2	2.45	0.50
1:A:29:VAL:CG2	1:A:42:ARG:HG2	2.41	0.50
1:D:175:GLU:HA	1:D:178:TRP:HE3	1.76	0.50
1:F:19:ARG:NH1	1:F:479:THR:HG21	2.26	0.50
1:F:77:GLY:HA2	1:F:128:GLY:O	2.10	0.50
1:B:53:LYS:CB	1:B:54:PRO:HD3	2.22	0.50
1:E:47:SER:O	1:E:51:ILE:HG13	2.11	0.50
1:D:396:ARG:O	1:D:396:ARG:HD2	2.12	0.50
1:F:177:SER:HB2	1:F:202:PRO:HG2	1.93	0.50
1:F:211:ARG:NH2	3:F:552:NDP:N7N	2.48	0.50
1:F:92:GLY:HA2	1:F:166:ALA:H	1.76	0.50
1:F:217:ARG:NH1	1:F:221:HIS:HE1	2.10	0.50
1:B:253:GLY:N	3:B:552:NDP:H4B	2.26	0.50
1:B:239:THR:HG23	1:B:245:LYS:HZ1	1.74	0.50
1:A:409:LEU:CD1	1:B:406:ASN:N	2.41	0.50
1:A:414:GLN:NE2	1:B:431:VAL:N	2.48	0.50
1:A:411:MET:C	1:B:432:PRO:HD3	2.31	0.50
1:C:402:GLU:CA	1:C:405:SER:HB2	2.41	0.50
1:A:491:ARG:HG2	1:A:492:VAL:N	2.27	0.50
1:A:271:ILE:C	1:A:272:THR:HG22	2.32	0.50
1:A:316:GLU:O	1:A:317:VAL:C	2.49	0.50
1:D:321:ILE:N	1:D:321:ILE:HD13	2.27	0.50
1:B:38:GLU:HB3	1:B:40:GLN:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:ARG:CD	1:E:35:ARG:N	2.73	0.50
1:F:35:ARG:N	1:F:35:ARG:CD	2.74	0.50
1:F:457:MET:HA	1:F:457:MET:HE2	1.93	0.50
1:E:215:THR:HG23	1:E:216:GLY:N	2.26	0.50
1:A:412:SER:HB3	1:B:407:TYR:CE2	2.44	0.50
1:A:421:PHE:CB	1:B:429:PRO:HB3	2.41	0.50
1:A:436:PHE:CD2	1:C:409:LEU:HD22	2.47	0.50
1:E:220:PHE:O	1:E:224:GLU:HB3	2.12	0.50
1:A:272:THR:HA	1:A:286:ILE:HD12	1.93	0.50
1:C:323:ILE:HD13	1:C:345:ALA:HB3	1.94	0.50
1:F:115:CYS:SG	1:F:378:VAL:HG11	2.52	0.50
1:F:172:GLY:H	1:F:175:GLU:CG	2.24	0.50
1:A:27:LYS:HE2	1:A:31:ASP:CG	2.31	0.50
1:C:90:LYS:HE2	1:C:164:VAL:CG1	2.42	0.50
1:D:167:PRO:CG	1:D:176:MET:HG2	2.39	0.50
1:B:239:THR:CG2	1:B:245:LYS:NZ	2.74	0.50
1:B:372:TYR:C	1:B:372:TYR:CD2	2.85	0.50
1:D:174:ARG:O	1:D:177:SER:HB3	2.12	0.50
1:D:177:SER:HB2	1:D:202:PRO:CG	2.42	0.50
1:D:181:ASP:O	1:D:181:ASP:OD1	2.29	0.50
1:A:339:VAL:O	1:A:341:ALA:N	2.45	0.50
1:E:399:PHE:C	1:E:401:TYR:H	2.14	0.50
1:F:91:GLY:O	1:F:165:PRO:HA	2.12	0.50
1:D:204:SER:O	1:F:492:VAL:HG13	2.11	0.50
1:F:49:LEU:HA	1:F:52:ILE:HD12	1.94	0.50
1:A:409:LEU:CD2	1:B:406:ASN:N	2.71	0.49
1:A:436:PHE:HB2	1:C:405:SER:HA	1.93	0.49
1:E:182:THR:O	1:E:186:THR:HG23	2.12	0.49
1:C:255:VAL:HG22	1:C:325:ALA:CB	2.40	0.49
1:B:219:VAL:HG22	1:B:373:LEU:HD13	1.93	0.49
1:D:90:LYS:HE2	1:D:164:VAL:CG1	2.42	0.49
1:D:451:SER:C	1:D:453:LEU:N	2.63	0.49
1:F:414:GLN:O	1:F:415:GLU:C	2.50	0.49
1:D:196:ALA:HB2	1:D:388:ASN:HB3	1.94	0.49
1:C:97:THR:CG2	1:C:132:ASN:HB2	2.42	0.49
1:A:137:THR:O	1:A:140:GLU:HB2	2.12	0.49
1:C:414:GLN:O	1:C:417:LEU:N	2.44	0.49
1:A:50:ARG:O	1:A:54:PRO:HD3	2.11	0.49
1:C:271:ILE:C	1:C:272:THR:HG22	2.32	0.49
1:E:247:PHE:HB3	1:E:321:ILE:CG1	2.40	0.49
1:B:234:SER:C	1:B:236:LEU:H	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:ALA:HB2	1:D:356:ALA:HB1	1.94	0.49
1:A:146:ARG:O	1:A:149:THR:HB	2.12	0.49
1:E:173:GLU:CD	1:E:202:PRO:HA	2.32	0.49
1:D:385:TRP:O	1:D:389:LEU:HG	2.11	0.49
1:B:348:ALA:HA	3:B:552:NDP:H1D	1.94	0.49
1:B:202:PRO:HD2	1:B:205:GLN:HB2	1.94	0.49
1:F:444:SER:O	1:F:445:GLU:C	2.48	0.49
1:D:85:HIS:NE2	1:D:489:VAL:HG13	2.27	0.49
1:B:300:THR:HG22	1:B:302:LEU:N	2.25	0.49
1:D:57:HIS:O	1:D:81:GLN:N	2.37	0.49
1:A:402:GLU:HA	1:A:405:SER:HB2	1.92	0.49
1:A:415:GLU:HG3	1:B:431:VAL:CG2	2.20	0.49
1:A:428:ILE:HG23	1:B:428:ILE:CG2	2.41	0.49
1:D:230:ALA:O	1:D:231:SER:C	2.51	0.49
1:D:150:MET:HE1	1:D:187:ILE:HD11	1.93	0.49
1:F:272:THR:OG1	1:F:314:ILE:HD11	2.12	0.49
1:C:476:ASP:CG	1:C:479:THR:HG23	2.32	0.49
1:D:99:VAL:HG22	1:D:130:LYS:HA	1.95	0.49
1:F:403:ARG:O	1:F:404:ASP:C	2.50	0.49
1:D:487:GLU:O	1:D:490:PHE:HB3	2.12	0.49
1:B:208:ILE:HD13	1:B:383:PHE:CB	2.43	0.49
1:C:316:GLU:O	1:C:340:LYS:HE2	2.12	0.49
1:B:247:PHE:CB	1:B:321:ILE:HG12	2.38	0.49
1:B:360:PHE:HD1	1:B:365:ILE:HG13	1.78	0.49
1:B:83:SER:O	1:B:84:GLN:HG3	2.12	0.49
1:F:374:ASN:C	1:F:376:GLY:H	2.15	0.49
1:F:24:VAL:O	1:F:25:GLU:C	2.50	0.49
1:F:44:ARG:O	1:F:45:VAL:C	2.49	0.49
1:B:78:TYR:O	1:B:127:ALA:HB1	2.11	0.49
1:F:422:GLY:O	1:F:426:GLY:O	2.30	0.49
1:A:405:SER:OG	1:B:402:GLU:CB	2.61	0.49
1:B:412:SER:C	1:B:414:GLN:N	2.66	0.49
1:A:374:ASN:ND2	3:A:552:NDP:H6N	2.27	0.49
1:A:281:TRP:O	1:A:307:ALA:HA	2.13	0.49
1:F:148:PHE:CZ	1:F:152:LEU:HD11	2.47	0.49
1:F:10:PHE:CD2	1:F:14:GLU:HG3	2.47	0.49
1:F:281:TRP:H	1:F:307:ALA:HB1	1.77	0.49
1:A:29:VAL:O	1:A:32:LEU:HB3	2.13	0.49
1:E:453:LEU:O	1:E:456:THR:N	2.46	0.49
1:F:2:ASP:CG	1:F:3:ARG:H	2.16	0.49
1:A:467:THR:HG21	1:A:483:VAL:CG1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:ILE:HG13	1:B:161:GLY:HA2	1.92	0.49
1:A:430:ILE:CD1	1:B:430:ILE:CD1	2.89	0.49
1:A:417:LEU:HD11	1:B:411:MET:HE3	1.95	0.49
1:C:234:SER:C	1:C:236:LEU:H	2.15	0.49
1:C:339:VAL:O	1:C:340:LYS:HB2	2.12	0.49
1:E:89:CYS:HB2	1:E:163:ASP:CG	2.32	0.49
1:E:219:VAL:O	1:E:223:ILE:HG12	2.12	0.49
1:E:227:ILE:HG23	1:E:228:ASN:N	2.26	0.49
1:A:321:ILE:CG2	1:A:343:ILE:HB	2.24	0.49
1:C:346:GLU:HG2	1:C:351:PRO:HD2	1.94	0.49
1:D:236:LEU:HD21	1:D:342:LYS:CG	2.27	0.49
1:E:47:SER:HA	1:E:50:ARG:HB2	1.94	0.49
1:F:281:TRP:O	1:F:307:ALA:HA	2.12	0.49
1:F:349:ASN:ND2	3:F:552:NDP:O2D	2.45	0.49
1:B:137:THR:HG23	1:B:140:GLU:CG	2.42	0.49
1:B:202:PRO:O	1:B:203:ILE:C	2.50	0.49
1:C:111:MET:HB3	1:C:124:GLY:HA2	1.95	0.49
1:F:19:ARG:HG2	1:F:479:THR:HG21	1.94	0.49
1:B:308:LYS:HG2	1:B:308:LYS:O	2.10	0.49
1:E:169:MET:HG2	3:E:552:NDP:H52N	1.95	0.49
1:E:348:ALA:HB1	3:E:552:NDP:O3D	2.12	0.49
1:E:220:PHE:CE1	1:E:266:PHE:CD1	3.01	0.49
1:F:229:GLU:HG3	1:F:231:SER:HB3	1.94	0.49
1:B:84:GLN:O	1:B:86:ARG:N	2.45	0.49
1:A:77:GLY:C	1:A:78:TYR:CG	2.85	0.49
1:D:399:PHE:C	1:D:401:TYR:N	2.65	0.49
1:A:230:ALA:HA	1:A:233:MET:HB2	1.95	0.49
1:E:2:ASP:HB3	1:E:5:ASP:O	2.11	0.49
1:D:9:PHE:O	1:D:9:PHE:HD2	1.95	0.49
1:E:455:TYR:HH	1:F:399:PHE:HD1	1.61	0.49
1:C:136:TYR:HA	1:C:140:GLU:OE2	2.12	0.49
1:C:246:THR:O	1:C:320:ASP:HB2	2.13	0.49
1:A:409:LEU:O	1:B:406:ASN:O	2.31	0.49
1:B:412:SER:C	1:B:414:GLN:H	2.16	0.49
1:A:401:TYR:CG	1:B:442:GLY:O	2.47	0.49
1:D:271:ILE:C	1:D:272:THR:HG22	2.32	0.49
1:D:164:VAL:HA	1:D:197:CYS:O	2.13	0.49
1:B:65:ILE:HG12	1:B:144:ILE:HD13	1.95	0.49
1:E:109:SER:O	1:E:112:THR:CG2	2.60	0.49
1:E:82:HIS:CG	1:E:109:SER:HA	2.47	0.49
1:F:224:GLU:HB2	1:F:242:PHE:CE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:GLU:CG	1:C:31:ASP:N	2.75	0.49
1:F:98:ASP:O	1:F:100:SER:N	2.45	0.49
1:F:407:TYR:CE1	1:F:440:ILE:HD13	2.48	0.49
1:D:188:GLY:O	1:D:190:TYR:N	2.45	0.49
1:C:183:TYR:CE2	1:C:188:GLY:HA3	2.48	0.49
1:C:295:LYS:O	1:C:299:GLY:HA2	2.13	0.49
1:A:415:GLU:CG	1:B:431:VAL:HG23	2.20	0.49
1:A:332:THR:CA	1:A:356:ALA:HB2	2.43	0.49
1:D:315:LEU:HD12	1:D:335:ASN:HD21	1.76	0.49
1:C:150:MET:HA	1:C:150:MET:CE	2.42	0.49
1:C:35:ARG:CD	1:C:35:ARG:H	2.23	0.49
1:E:418:GLU:HG3	1:E:428:ILE:HD12	1.94	0.49
1:E:479:THR:O	1:E:483:VAL:HG23	2.13	0.49
1:C:68:ASP:OD1	1:C:137:THR:HG21	2.12	0.49
1:E:148:PHE:O	1:E:152:LEU:HD12	2.13	0.49
1:B:48:ILE:O	1:B:52:ILE:HG13	2.13	0.49
1:A:396:ARG:HG3	1:A:397:LEU:HG	1.94	0.49
1:B:208:ILE:HG21	1:B:380:VAL:HG12	1.94	0.49
1:A:430:ILE:HG21	1:B:410:LEU:CD1	2.43	0.49
1:A:413:VAL:HG12	1:B:411:MET:HG2	1.85	0.49
1:A:433:THR:CB	1:C:413:VAL:H	2.26	0.49
1:E:176:MET:SD	1:E:198:VAL:HG21	2.53	0.49
1:E:223:ILE:HD13	1:E:345:ALA:CB	2.43	0.49
1:B:234:SER:C	1:B:236:LEU:N	2.66	0.49
1:D:255:VAL:HG22	1:D:325:ALA:CB	2.43	0.49
1:E:114:LYS:O	1:E:117:VAL:HB	2.13	0.49
1:C:37:THR:HG21	1:C:41:LYS:HG3	1.94	0.49
1:F:420:LYS:C	1:F:421:PHE:CD2	2.76	0.49
1:E:400:LYS:O	1:E:400:LYS:HD3	2.13	0.49
1:B:131:ILE:HB	1:B:136:TYR:CE2	2.48	0.49
1:A:410:LEU:HD13	1:B:409:LEU:CD2	2.35	0.48
1:A:413:VAL:HG13	1:B:407:TYR:O	2.13	0.48
1:B:435:GLU:OE1	1:B:435:GLU:N	2.46	0.48
1:A:404:ASP:O	1:B:436:PHE:HE1	1.96	0.48
1:E:213:SER:OG	1:E:214:ALA:N	2.45	0.48
1:E:345:ALA:HB1	1:E:373:LEU:CD1	2.43	0.48
1:B:236:LEU:HD22	1:B:238:MET:HB2	1.95	0.48
1:F:300:THR:HG22	1:F:302:LEU:H	1.79	0.48
1:F:331:LEU:HA	1:F:335:ASN:HD21	1.78	0.48
1:F:417:LEU:HB3	1:F:428:ILE:HD13	1.94	0.48
1:A:37:THR:CA	1:A:40:GLN:HG3	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:GLU:C	1:B:294:PHE:H	2.16	0.48
1:B:394:TYR:C	1:B:394:TYR:HD2	2.13	0.48
1:A:108:ALA:O	1:A:112:THR:HG22	2.12	0.48
1:E:272:THR:HG22	1:E:281:TRP:HD1	1.78	0.48
1:E:246:THR:HG23	1:E:319:CYS:HB2	1.94	0.48
1:A:250:GLN:HG3	1:A:314:ILE:HG21	1.95	0.48
1:F:219:VAL:HG11	1:F:259:SER:CB	2.43	0.48
1:F:114:LYS:CA	1:F:371:LEU:CD2	2.86	0.48
1:A:246:THR:O	1:A:320:ASP:HB2	2.13	0.48
1:D:201:LYS:HZ1	1:D:388:ASN:ND2	1.95	0.48
1:E:12:MET:CG	1:E:354:PRO:HD3	2.42	0.48
1:D:134:LYS:HE2	1:D:134:LYS:HB3	1.55	0.48
1:A:300:THR:HG21	1:A:302:LEU:HB2	1.93	0.48
1:E:208:ILE:HD12	1:E:387:ASN:HB2	1.94	0.48
1:B:473:LEU:HD22	1:B:476:ASP:HB3	1.95	0.48
1:D:20:GLY:HA2	1:D:23:ILE:HD12	1.95	0.48
1:B:200:GLY:N	1:B:384:GLU:OE1	2.46	0.48
1:B:272:THR:HG1	1:B:314:ILE:CD1	2.26	0.48
1:A:248:VAL:HG12	1:A:319:CYS:SG	2.54	0.48
1:E:202:PRO:HB2	1:E:205:GLN:HG2	1.95	0.48
1:F:118:VAL:HG23	1:F:118:VAL:O	2.13	0.48
1:F:332:THR:HG22	1:F:353:THR:HG21	1.96	0.48
1:F:255:VAL:HG12	3:F:552:NDP:O2N	2.14	0.48
1:E:385:TRP:HZ2	1:F:192:ILE:HD11	1.75	0.48
1:E:96:SER:HB3	1:E:99:VAL:HG13	1.95	0.48
1:B:158:ILE:O	1:B:158:ILE:CG2	2.58	0.48
1:A:436:PHE:H	1:C:408:HIS:CB	2.18	0.48
1:A:413:VAL:HG13	1:B:407:TYR:C	2.33	0.48
1:A:418:GLU:CG	1:B:431:VAL:HB	2.32	0.48
1:E:228:ASN:OD1	1:E:241:GLY:HA2	2.13	0.48
1:D:342:LYS:NZ	1:D:342:LYS:HB2	2.28	0.48
1:C:118:VAL:HG11	1:C:375:ALA:HB1	1.94	0.48
1:D:345:ALA:HA	1:D:368:ILE:HB	1.94	0.48
1:F:136:TYR:HB2	1:F:141:LEU:CD2	2.42	0.48
1:F:98:ASP:O	1:F:99:VAL:C	2.52	0.48
1:A:409:LEU:CD2	1:B:404:ASP:N	2.68	0.48
1:B:217:ARG:CG	1:B:217:ARG:NH1	2.65	0.48
1:F:11:LYS:O	1:F:14:GLU:HB2	2.13	0.48
1:F:168:ASP:O	1:F:169:MET:C	2.50	0.48
1:C:29:VAL:O	1:C:41:LYS:HD3	2.13	0.48
1:B:330:GLN:O	1:B:332:THR:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:ARG:HB3	1:C:121:PRO:O	2.13	0.48
1:F:444:SER:OG	1:F:446:LYS:HD3	2.13	0.48
1:C:245:LYS:N	1:C:245:LYS:HD2	2.29	0.48
1:E:83:SER:O	1:E:84:GLN:HG3	2.14	0.48
1:F:482:TYR:O	1:F:486:ILE:HG13	2.14	0.48
1:D:232:TYR:HE1	1:D:474:GLY:O	1.97	0.48
1:A:232:TYR:HE1	1:A:474:GLY:O	1.95	0.48
1:E:363:ARG:NH1	1:E:365:ILE:HD11	2.28	0.48
1:A:405:SER:N	1:B:442:GLY:HA2	2.28	0.48
1:B:233:MET:O	1:B:237:GLY:N	2.41	0.48
1:D:242:PHE:CE1	1:D:263:LEU:HD22	2.49	0.48
1:C:213:SER:OG	1:C:214:ALA:N	2.45	0.48
1:A:99:VAL:HG23	1:A:99:VAL:O	2.12	0.48
1:A:63:PHE:CE1	1:A:75:ILE:CD1	2.86	0.48
1:D:409:LEU:O	1:D:409:LEU:CD1	2.62	0.48
1:A:346:GLU:OE2	1:A:369:PRO:HA	2.14	0.48
1:A:81:GLN:HG3	1:A:157:PHE:CE2	2.48	0.48
1:E:463:GLN:O	1:E:467:THR:HB	2.12	0.48
1:B:382:TYR:CZ	1:B:386:LEU:HD21	2.49	0.48
1:A:428:ILE:CD1	1:B:428:ILE:C	2.82	0.48
1:A:436:PHE:N	1:C:409:LEU:N	2.59	0.48
1:E:309:ILE:O	1:E:310:TYR:C	2.52	0.48
1:A:216:GLY:HA2	1:A:219:VAL:HB	1.96	0.48
1:A:272:THR:OG1	1:A:314:ILE:HD11	2.14	0.48
1:C:167:PRO:HG3	1:C:176:MET:HE2	1.96	0.48
1:C:2:ASP:OD2	1:C:3:ARG:NH2	2.46	0.48
1:D:82:HIS:N	1:D:124:GLY:O	2.45	0.48
1:A:99:VAL:HG22	1:A:130:LYS:HA	1.96	0.48
1:F:270:CYS:SG	1:F:272:THR:O	2.72	0.48
1:C:45:VAL:O	1:C:47:SER:N	2.46	0.48
1:D:29:VAL:CG2	1:D:42:ARG:HG2	2.44	0.48
1:F:399:PHE:O	1:F:401:TYR:N	2.47	0.48
1:B:305:PRO:HB2	1:B:306:LYS:HD3	1.95	0.48
1:B:396:ARG:HH21	1:C:456:THR:HG21	1.78	0.48
1:A:67:ARG:HD2	1:A:140:GLU:OE1	2.13	0.48
1:A:67:ARG:N	1:A:71:SER:O	2.47	0.48
1:F:49:LEU:HD12	1:F:52:ILE:HD12	1.95	0.48
1:A:437:GLN:OE1	1:A:438:ASP:N	2.47	0.48
1:A:410:LEU:O	1:B:410:LEU:HB2	2.14	0.48
1:A:421:PHE:CB	1:B:427:THR:OG1	2.47	0.48
1:B:443:ALA:CB	1:B:448:ILE:HG12	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:405:SER:O	1:C:408:HIS:CB	2.58	0.48
1:C:417:LEU:HB3	1:C:428:ILE:HD13	1.94	0.48
1:C:236:LEU:CD2	1:C:342:LYS:HG2	2.37	0.48
1:E:90:LYS:HE3	2:E:502:GLU:OE1	2.14	0.48
1:B:229:GLU:OE2	1:B:229:GLU:HA	2.14	0.48
1:C:3:ARG:C	1:C:5:ASP:H	2.16	0.48
1:D:223:ILE:HA	1:D:368:ILE:HD12	1.95	0.48
1:F:346:GLU:HB2	1:F:368:ILE:O	2.14	0.48
1:B:295:LYS:NZ	3:B:552:NDP:O1X	2.47	0.48
1:C:305:PRO:HB2	1:C:306:LYS:HD3	1.91	0.48
1:A:19:ARG:HG2	1:A:19:ARG:HH11	1.78	0.48
1:B:292:GLU:C	1:B:294:PHE:N	2.66	0.48
1:E:315:LEU:HD22	1:E:331:LEU:HD11	1.95	0.48
1:C:321:ILE:H	1:C:321:ILE:HD13	1.77	0.48
1:C:63:PHE:HD1	1:C:147:ARG:CG	2.23	0.48
1:A:166:ALA:HB1	1:A:167:PRO:CD	2.43	0.48
1:F:339:VAL:HG12	1:F:341:ALA:HB3	1.95	0.48
1:B:19:ARG:HH11	1:B:479:THR:HG21	1.79	0.48
1:F:154:LYS:C	1:F:156:GLY:H	2.17	0.48
1:F:315:LEU:HD22	1:F:322:LEU:HD21	1.96	0.48
1:A:305:PRO:HB2	1:A:306:LYS:HD3	1.96	0.48
1:A:203:ILE:HA	1:A:207:GLY:HA3	1.95	0.48
1:A:409:LEU:HG	1:B:402:GLU:C	2.34	0.48
1:A:430:ILE:CD1	1:B:410:LEU:HG	2.44	0.48
1:B:443:ALA:HB1	1:B:448:ILE:HG12	1.96	0.48
1:A:433:THR:CB	1:C:411:MET:N	2.77	0.48
1:A:110:LEU:O	1:A:111:MET:C	2.51	0.48
1:E:248:VAL:HG23	1:E:272:THR:C	2.33	0.48
1:A:248:VAL:HG22	1:A:249:VAL:N	2.29	0.48
1:C:202:PRO:HB2	1:C:205:GLN:CG	2.41	0.48
1:B:56:ASN:ND2	1:B:84:GLN:HE22	2.11	0.48
1:A:59:LEU:CD2	1:A:61:LEU:HD22	2.44	0.48
1:D:372:TYR:C	1:D:372:TYR:CD2	2.86	0.48
1:F:248:VAL:HG21	1:F:314:ILE:CD1	2.43	0.48
1:E:19:ARG:HA	1:E:19:ARG:HD2	1.57	0.48
1:F:78:TYR:CD2	1:F:101:VAL:HB	2.49	0.48
1:B:214:ALA:CB	1:B:380:VAL:HG21	2.43	0.47
1:A:430:ILE:HG21	1:B:410:LEU:HD12	1.96	0.47
1:A:436:PHE:CG	1:C:409:LEU:HB3	2.48	0.47
1:A:115:CYS:O	1:A:116:ALA:C	2.52	0.47
1:A:82:HIS:CD2	1:A:83:SER:HB2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:SER:O	1:B:110:LEU:O	2.31	0.47
1:C:315:LEU:O	1:C:339:VAL:HG13	2.13	0.47
1:B:314:ILE:HD12	1:B:317:VAL:CG2	2.42	0.47
1:A:331:LEU:N	1:A:331:LEU:HD12	2.29	0.47
1:D:238:MET:HE3	1:D:245:LYS:NZ	2.29	0.47
1:C:372:TYR:CD2	1:C:372:TYR:C	2.88	0.47
1:E:461:ALA:O	1:E:462:ARG:C	2.52	0.47
1:F:382:TYR:CE1	1:F:386:LEU:HD21	2.49	0.47
1:D:9:PHE:CD2	1:D:12:MET:HE2	2.49	0.47
1:E:193:ASN:O	1:E:194:ALA:C	2.53	0.47
1:C:462:ARG:CG	1:C:466:ARG:HH22	2.25	0.47
1:A:66:ARG:O	1:A:67:ARG:O	2.32	0.47
1:E:264:HIS:O	1:E:264:HIS:ND1	2.47	0.47
1:A:409:LEU:O	1:B:407:TYR:CA	2.61	0.47
1:A:428:ILE:CA	1:B:430:ILE:HG13	2.41	0.47
1:C:3:ARG:NH1	1:C:4:GLU:HG3	2.28	0.47
1:D:94:ARG:O	1:D:94:ARG:HG2	2.14	0.47
1:D:239:THR:O	1:D:245:LYS:HE2	2.15	0.47
1:E:226:PHE:CE2	1:E:465:MET:HG2	2.49	0.47
1:D:396:ARG:O	1:D:396:ARG:CD	2.62	0.47
1:F:210:GLY:O	1:F:214:ALA:HB2	2.14	0.47
1:F:196:ALA:HB2	1:F:388:ASN:HB2	1.95	0.47
1:B:145:THR:O	1:B:148:PHE:N	2.46	0.47
1:D:277:ASP:O	1:D:302:LEU:HD11	2.14	0.47
1:D:201:LYS:HE2	1:D:206:GLY:O	2.14	0.47
1:B:202:PRO:HB2	1:B:205:GLN:HG2	1.95	0.47
1:B:202:PRO:O	1:B:205:GLN:N	2.38	0.47
1:E:456:THR:HG21	1:F:396:ARG:NH2	2.29	0.47
1:C:374:ASN:O	1:C:376:GLY:N	2.47	0.47
1:F:490:PHE:O	1:F:492:VAL:N	2.46	0.47
1:A:409:LEU:HG	1:B:403:ARG:N	2.28	0.47
1:B:164:VAL:HG13	1:B:198:VAL:CA	2.44	0.47
1:E:230:ALA:C	1:E:232:TYR:N	2.66	0.47
1:E:323:ILE:HD12	1:E:345:ALA:HB3	1.94	0.47
1:A:219:VAL:O	1:A:223:ILE:HG12	2.14	0.47
1:A:332:THR:HA	1:A:356:ALA:HB2	1.97	0.47
1:D:316:GLU:O	1:D:317:VAL:C	2.52	0.47
1:D:241:GLY:O	1:D:245:LYS:HD3	2.14	0.47
1:C:114:LYS:HA	1:C:371:LEU:HD23	1.95	0.47
1:E:371:LEU:HD12	1:E:482:TYR:CE1	2.49	0.47
1:F:178:TRP:O	1:F:179:ILE:C	2.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:380:VAL:O	1:F:381:SER:C	2.53	0.47
1:D:28:LEU:HD13	1:D:28:LEU:H	1.79	0.47
1:A:16:PHE:HD1	1:A:482:TYR:OH	1.95	0.47
1:A:89:CYS:HB2	1:A:163:ASP:OD2	2.14	0.47
1:C:411:MET:O	1:C:414:GLN:CB	2.63	0.47
1:A:90:LYS:HG3	1:A:91:GLY:H	1.79	0.47
1:E:90:LYS:NZ	2:E:502:GLU:OE1	2.47	0.47
1:A:271:ILE:O	1:A:272:THR:HG22	2.15	0.47
1:C:167:PRO:HD3	1:C:199:THR:O	2.14	0.47
1:D:238:MET:CE	1:D:245:LYS:NZ	2.77	0.47
1:F:63:PHE:O	1:F:75:ILE:CD1	2.62	0.47
1:D:454:ALA:HA	1:D:457:MET:HB2	1.95	0.47
1:F:336:ALA:N	1:F:337:PRO:CD	2.77	0.47
1:F:217:ARG:NH1	1:F:217:ARG:CG	2.70	0.47
1:B:24:VAL:HG12	1:B:483:VAL:HG13	1.91	0.47
1:B:332:THR:C	1:B:334:SER:N	2.68	0.47
1:D:132:ASN:CG	1:D:135:ASN:HD22	2.16	0.47
1:E:60:SER:HA	1:E:78:TYR:CD2	2.50	0.47
1:B:309:ILE:O	1:B:309:ILE:HG22	2.15	0.47
1:F:269:LYS:HD3	1:F:284:ASP:C	2.35	0.47
1:B:199:THR:HG22	1:B:384:GLU:HB3	1.96	0.47
1:E:211:ARG:NE	1:E:381:SER:OG	2.46	0.47
1:E:249:VAL:HA	1:E:323:ILE:HB	1.96	0.47
1:B:331:LEU:HD12	1:B:331:LEU:N	2.30	0.47
1:D:236:LEU:CD2	1:D:237:GLY:N	2.78	0.47
1:D:451:SER:O	1:D:453:LEU:N	2.48	0.47
1:D:63:PHE:CD1	1:D:147:ARG:HG3	2.50	0.47
1:D:406:ASN:C	1:D:408:HIS:N	2.68	0.47
1:A:66:ARG:O	1:A:67:ARG:C	2.52	0.47
1:B:32:LEU:HD13	1:B:494:ASN:OD1	2.13	0.47
1:A:398:THR:HG22	1:B:394:TYR:OH	2.14	0.47
1:A:405:SER:CA	1:B:442:GLY:HA2	2.44	0.47
1:C:281:TRP:H	1:C:307:ALA:HB1	1.78	0.47
1:E:131:ILE:HG13	1:E:133:PRO:HG3	1.96	0.47
1:E:153:ALA:CA	1:E:158:ILE:HG22	2.44	0.47
1:E:162:VAL:CG2	1:E:163:ASP:N	2.77	0.47
1:A:224:GLU:O	1:A:224:GLU:CG	2.62	0.47
1:F:10:PHE:CD1	1:F:105:LYS:HE2	2.49	0.47
1:C:37:THR:HB	1:C:41:LYS:HG3	1.97	0.47
1:E:412:SER:O	1:E:416:SER:OG	2.23	0.47
1:E:406:ASN:OD1	1:E:440:ILE:O	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:346:GLU:CG	1:B:351:PRO:HG2	2.45	0.47
1:D:141:LEU:O	1:D:145:THR:HG22	2.14	0.47
1:A:446:LYS:N	1:A:446:LYS:CD	2.74	0.47
1:A:454:ALA:O	1:A:458:GLU:HB3	2.14	0.47
1:E:344:ILE:N	1:E:366:MET:O	2.42	0.47
1:B:372:TYR:OH	1:B:461:ALA:HB2	2.14	0.47
1:A:202:PRO:HG2	1:A:205:GLN:HG3	1.97	0.47
1:B:473:LEU:HB3	1:B:476:ASP:HB3	1.96	0.47
1:B:17:PHE:CD1	1:B:113:TYR:CZ	3.02	0.47
1:A:169:MET:CG	3:A:552:NDP:H52N	2.44	0.47
1:A:324:PRO:CD	1:A:345:ALA:O	2.62	0.47
1:A:250:GLN:HA	1:A:274:GLY:HA3	1.96	0.47
1:D:247:PHE:O	1:D:271:ILE:HG13	2.13	0.47
1:D:77:GLY:HA2	1:D:128:GLY:O	2.14	0.47
1:C:154:LYS:HD3	1:D:189:HIS:CD2	2.50	0.47
1:D:238:MET:HE3	1:D:245:LYS:HZ2	1.77	0.47
1:E:53:LYS:CB	1:E:54:PRO:CD	2.91	0.47
1:F:294:PHE:CE2	1:F:298:HIS:CE1	3.03	0.47
1:D:443:ALA:HB1	1:D:448:ILE:HG12	1.96	0.47
1:F:202:PRO:HG2	1:F:205:GLN:HG3	1.96	0.47
1:D:420:LYS:NZ	1:F:427:THR:O	2.41	0.47
1:A:214:ALA:HB1	1:A:380:VAL:HG21	1.96	0.47
1:D:140:GLU:O	1:D:144:ILE:HG12	2.15	0.47
1:C:90:LYS:HA	1:C:164:VAL:O	2.14	0.47
1:D:490:PHE:C	1:D:490:PHE:HD1	2.18	0.47
1:D:488:LYS:O	1:D:489:VAL:C	2.52	0.47
1:E:236:LEU:CD2	1:E:342:LYS:HG2	2.45	0.47
1:E:137:THR:HG23	1:E:140:GLU:CD	2.35	0.47
1:F:9:PHE:CD2	1:F:106:ALA:HB1	2.48	0.47
1:C:8:ASN:HB3	1:C:11:LYS:HG3	1.96	0.47
1:B:395:GLY:O	1:B:399:PHE:CD2	2.67	0.47
1:A:436:PHE:HE2	1:B:409:LEU:CD1	2.28	0.47
1:C:160:PRO:HG2	1:C:161:GLY:N	2.28	0.47
1:D:360:PHE:HD1	1:D:365:ILE:HG13	1.79	0.47
1:C:9:PHE:CD2	1:C:106:ALA:CB	2.97	0.47
1:C:324:PRO:C	1:C:326:ALA:H	2.17	0.47
1:D:234:SER:O	1:D:236:LEU:N	2.48	0.47
1:A:126:LYS:HE3	1:A:168:ASP:OD2	2.14	0.47
1:A:75:ILE:HG12	1:A:75:ILE:O	2.14	0.47
1:F:331:LEU:HD23	1:F:360:PHE:CZ	2.50	0.47
1:F:331:LEU:HD23	1:F:360:PHE:HZ	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:ARG:HH22	1:C:494:ASN:HA	1.80	0.47
1:B:281:TRP:CD1	1:B:282:ASN:N	2.83	0.47
1:F:29:VAL:HG13	1:F:41:LYS:HB3	1.96	0.47
1:E:86:ARG:O	1:E:123:GLY:N	2.47	0.47
1:C:463:GLN:HB3	1:C:466:ARG:HH21	1.80	0.47
1:C:320:ASP:O	1:C:341:ALA:HB1	2.15	0.47
1:B:55:CYS:O	1:E:62:SER:HB2	2.14	0.47
1:A:160:PRO:HD3	1:A:197:CYS:HB3	1.97	0.47
1:A:111:MET:CE	2:A:502:GLU:HG3	2.45	0.47
1:A:90:LYS:HG3	1:A:91:GLY:N	2.30	0.47
1:E:150:MET:CE	1:E:150:MET:HA	2.45	0.47
1:E:158:ILE:HA	1:E:163:ASP:O	2.14	0.47
1:D:352:THR:OG1	1:D:478:ARG:NH2	2.48	0.47
1:D:107:LEU:HB3	1:D:126:LYS:CG	2.45	0.47
1:C:141:LEU:HA	1:C:141:LEU:HD23	1.52	0.47
1:D:9:PHE:CD2	1:D:12:MET:CE	2.98	0.47
1:E:382:TYR:CE2	1:E:386:LEU:HD21	2.49	0.47
1:F:448:ILE:HG22	1:F:449:VAL:N	2.29	0.47
1:F:315:LEU:HD23	1:F:322:LEU:HD11	1.97	0.47
1:B:277:ASP:O	1:B:302:LEU:HD11	2.14	0.47
1:C:209:HIS:CD2	1:C:446:LYS:HG3	2.50	0.47
1:A:102:ASP:HA	1:A:105:LYS:HD3	1.95	0.47
1:A:409:LEU:CG	1:B:402:GLU:O	2.63	0.47
1:A:435:GLU:CB	1:C:408:HIS:CG	2.79	0.47
1:A:309:ILE:O	1:A:310:TYR:C	2.54	0.47
1:C:372:TYR:OH	1:C:461:ALA:HB2	2.15	0.47
1:A:129:VAL:CG1	1:A:131:ILE:HG12	2.42	0.47
1:F:326:ALA:O	3:F:552:NDP:H51N	2.15	0.47
1:F:159:GLY:O	1:F:163:ASP:O	2.33	0.47
1:D:40:GLN:HA	1:D:43:ASN:HB2	1.97	0.47
1:F:395:GLY:O	1:F:398:THR:N	2.45	0.47
1:E:24:VAL:CG1	1:E:483:VAL:HG13	2.45	0.47
1:E:120:VAL:CG1	1:E:121:PRO:HD2	2.45	0.47
1:A:435:GLU:HB2	1:C:408:HIS:O	2.15	0.46
1:A:413:VAL:HG22	1:B:407:TYR:C	2.34	0.46
1:A:433:THR:OG1	1:C:409:LEU:CA	2.62	0.46
1:A:90:LYS:HD3	1:A:122:PHE:CD1	2.49	0.46
1:B:238:MET:CE	1:B:320:ASP:HB3	2.45	0.46
1:D:110:LEU:HA	1:D:110:LEU:HD12	1.78	0.46
1:F:213:SER:O	1:F:214:ALA:C	2.53	0.46
1:D:420:LYS:HG3	1:D:421:PHE:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:SER:O	1:C:113:TYR:CD1	2.68	0.46
1:E:300:THR:HG22	1:E:302:LEU:N	2.29	0.46
1:C:32:LEU:HD12	1:C:33:LYS:N	2.30	0.46
1:D:6:ASP:N	1:D:7:PRO:HD3	2.30	0.46
1:A:403:ARG:HB2	1:A:441:SER:OG	2.15	0.46
1:A:408:HIS:C	1:B:440:ILE:HG13	2.35	0.46
1:C:404:ASP:O	1:C:405:SER:O	2.34	0.46
1:A:247:PHE:CZ	1:A:270:CYS:HB2	2.51	0.46
1:A:279:SER:OG	1:A:314:ILE:HB	2.15	0.46
1:D:90:LYS:HG3	1:D:91:GLY:N	2.31	0.46
1:B:42:ARG:O	1:B:46:ARG:HB2	2.15	0.46
1:D:167:PRO:CB	1:D:172:GLY:HA2	2.44	0.46
1:D:176:MET:HG3	1:D:199:THR:O	2.13	0.46
1:E:413:VAL:HG11	1:F:413:VAL:HG11	1.98	0.46
1:C:453:LEU:CD1	1:C:457:MET:HG2	2.44	0.46
1:D:61:LEU:C	1:D:61:LEU:HD12	2.35	0.46
1:A:427:THR:HA	1:B:429:PRO:HG2	1.98	0.46
1:B:90:LYS:N	1:B:123:GLY:O	2.40	0.46
1:A:428:ILE:HD13	1:B:414:GLN:CD	2.35	0.46
1:A:428:ILE:CD1	1:B:414:GLN:NE2	2.78	0.46
1:C:395:GLY:O	1:C:397:LEU:N	2.48	0.46
1:C:396:ARG:O	1:C:396:ARG:HD2	2.15	0.46
1:E:146:ARG:HH22	1:E:181:ASP:CG	2.18	0.46
1:E:245:LYS:N	1:E:245:LYS:HD2	2.30	0.46
1:B:336:ALA:HB3	1:B:337:PRO:HD3	1.97	0.46
1:D:271:ILE:HG13	1:D:271:ILE:H	1.56	0.46
1:C:171:THR:HB	1:C:175:GLU:HG3	1.96	0.46
1:C:369:PRO:O	1:C:370:ASP:C	2.53	0.46
1:A:132:ASN:O	1:A:136:TYR:HD2	1.99	0.46
1:A:178:TRP:O	1:A:182:THR:HG23	2.15	0.46
1:F:65:ILE:HG13	1:F:144:ILE:HG12	1.98	0.46
1:E:25:GLU:O	1:E:29:VAL:CG1	2.62	0.46
1:E:117:VAL:HG12	1:E:118:VAL:CG1	2.40	0.46
1:F:174:ARG:O	1:F:177:SER:HB3	2.15	0.46
1:B:275:GLU:HB2	1:B:301:ILE:HD11	1.96	0.46
1:E:209:HIS:ND1	1:E:446:LYS:HG3	2.30	0.46
1:A:17:PHE:HE1	1:A:486:ILE:HG12	1.77	0.46
1:A:407:TYR:CE1	1:A:440:ILE:HD13	2.50	0.46
1:B:406:ASN:HA	1:B:409:LEU:HB2	1.97	0.46
1:A:372:TYR:CE1	1:A:461:ALA:HB2	2.49	0.46
1:E:166:ALA:HB1	1:E:167:PRO:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:GLU:HB2	1:C:334:SER:OG	2.16	0.46
1:C:201:LYS:NZ	1:C:384:GLU:OE1	2.46	0.46
1:D:110:LEU:O	1:D:113:TYR:N	2.49	0.46
1:D:152:LEU:HD23	1:D:157:PHE:HB2	1.97	0.46
1:D:77:GLY:C	1:D:78:TYR:CD1	2.89	0.46
1:F:94:ARG:HG2	1:F:94:ARG:O	2.16	0.46
1:C:19:ARG:NH1	1:C:479:THR:HG21	2.31	0.46
1:F:96:SER:HB3	1:F:99:VAL:HG13	1.98	0.46
1:C:421:PHE:O	1:C:422:GLY:O	2.33	0.46
1:A:64:PRO:HD2	1:A:147:ARG:HH22	1.80	0.46
1:E:58:VAL:HG22	1:E:80:ALA:HA	1.96	0.46
1:B:32:LEU:HD21	1:B:44:ARG:NH1	2.30	0.46
1:A:404:ASP:O	1:B:439:ARG:O	2.34	0.46
1:A:371:LEU:HA	1:A:371:LEU:HD23	1.72	0.46
1:E:214:ALA:HB1	1:E:380:VAL:CG2	2.43	0.46
1:B:233:MET:HA	1:B:233:MET:HE2	1.98	0.46
1:D:255:VAL:HG13	1:D:325:ALA:HB1	1.97	0.46
1:D:276:SER:OG	3:D:552:NDP:P2B	2.74	0.46
1:A:98:ASP:N	1:A:98:ASP:OD2	2.48	0.46
1:D:451:SER:O	1:D:452:GLY:C	2.52	0.46
1:F:281:TRP:N	1:F:307:ALA:HB1	2.31	0.46
1:F:436:PHE:HA	1:F:439:ARG:HG2	1.96	0.46
1:D:386:LEU:O	1:D:387:ASN:C	2.54	0.46
1:B:295:LYS:HG3	1:B:295:LYS:O	2.14	0.46
1:A:453:LEU:O	1:A:456:THR:N	2.48	0.46
1:D:29:VAL:HG21	1:D:42:ARG:HG2	1.97	0.46
1:C:61:LEU:O	1:C:76:GLU:HA	2.15	0.46
1:C:235:ILE:O	1:C:235:ILE:HG22	2.15	0.46
1:F:69:ASP:OD2	1:F:71:SER:HB3	2.16	0.46
1:B:397:LEU:H	1:B:397:LEU:HD12	1.80	0.46
1:D:475:LEU:HA	1:D:475:LEU:HD23	1.62	0.46
1:A:399:PHE:O	1:A:441:SER:CB	2.64	0.46
1:A:428:ILE:CG1	1:B:429:PRO:N	2.74	0.46
1:B:421:PHE:O	1:B:422:GLY:C	2.53	0.46
1:E:150:MET:O	1:E:153:ALA:HB3	2.14	0.46
1:E:166:ALA:HB1	1:E:167:PRO:HD2	1.97	0.46
1:B:12:MET:CG	1:B:354:PRO:HD3	2.45	0.46
1:A:248:VAL:CG2	1:A:249:VAL:N	2.79	0.46
1:F:230:ALA:HA	1:F:233:MET:HB2	1.98	0.46
1:C:166:ALA:HA	1:C:199:THR:O	2.16	0.46
1:D:91:GLY:HA2	2:D:502:GLU:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:217:ARG:O	1:F:218:GLY:C	2.52	0.46
1:F:217:ARG:O	1:F:220:PHE:N	2.49	0.46
1:E:399:PHE:O	1:E:401:TYR:N	2.48	0.46
1:E:453:LEU:O	1:E:454:ALA:C	2.53	0.46
1:F:420:LYS:O	1:F:421:PHE:HD2	1.99	0.46
1:E:209:HIS:O	1:E:449:VAL:HG21	2.16	0.46
1:F:188:GLY:O	1:F:191:ASP:N	2.34	0.46
1:A:294:PHE:O	1:A:298:HIS:N	2.46	0.46
1:A:39:GLU:HG2	1:A:39:GLU:O	2.14	0.46
1:A:84:GLN:C	1:A:86:ARG:N	2.67	0.46
1:A:477:LEU:HD23	1:A:477:LEU:HA	1.53	0.46
1:A:403:ARG:O	1:A:407:TYR:CB	2.61	0.46
1:A:47:SER:HA	1:A:50:ARG:HB2	1.97	0.46
1:C:271:ILE:H	1:C:271:ILE:HG13	1.48	0.46
1:C:172:GLY:O	1:C:175:GLU:HG2	2.16	0.46
1:F:414:GLN:C	1:F:416:SER:N	2.68	0.46
1:D:118:VAL:O	1:D:118:VAL:HG23	2.14	0.46
1:E:96:SER:O	1:E:99:VAL:HG22	2.15	0.46
1:D:205:GLN:HE21	1:F:495:GLU:HB2	1.80	0.46
1:B:420:LYS:C	1:B:421:PHE:CD2	2.77	0.46
1:E:280:ILE:HB	1:E:307:ALA:HB3	1.95	0.46
1:B:272:THR:HG21	1:B:317:VAL:HG11	1.97	0.46
1:C:211:ARG:HD2	1:C:211:ARG:O	2.16	0.46
1:F:10:PHE:C	1:F:10:PHE:CD2	2.86	0.46
1:F:118:VAL:HG23	1:F:120:VAL:HG23	1.98	0.46
1:F:178:TRP:O	1:F:179:ILE:O	2.33	0.46
1:F:5:ASP:OD2	1:F:355:GLU:HB3	2.16	0.46
1:A:37:THR:HB	1:A:41:LYS:HG3	1.96	0.46
1:E:258:HIS:CD2	1:E:261:ARG:HH11	2.29	0.46
1:F:395:GLY:O	1:F:396:ARG:C	2.53	0.46
1:F:403:ARG:HG3	1:F:407:TYR:HD1	1.81	0.46
1:E:111:MET:HE1	1:E:378:VAL:HG13	1.97	0.46
1:C:406:ASN:O	1:C:410:LEU:HB2	2.15	0.46
1:E:233:MET:O	1:E:237:GLY:N	2.49	0.46
1:B:233:MET:O	1:B:236:LEU:HB3	2.16	0.46
1:D:363:ARG:NH1	1:D:365:ILE:HD11	2.31	0.46
1:C:94:ARG:NH1	1:C:103:GLU:OE2	2.49	0.46
2:C:502:GLU:OE2	3:C:552:NDP:N7N	2.49	0.46
1:B:217:ARG:HH11	1:B:221:HIS:HE1	1.58	0.46
1:D:86:ARG:HB2	1:D:122:PHE:C	2.36	0.46
1:C:107:LEU:HA	1:C:107:LEU:HD12	1.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:THR:CB	1:B:41:LYS:HG3	2.46	0.46
1:C:24:VAL:O	1:C:27:LYS:HB3	2.15	0.46
1:C:44:ARG:NH2	1:C:494:ASN:HA	2.31	0.46
1:A:306:LYS:HD3	1:A:306:LYS:H	1.80	0.46
1:D:203:ILE:HG23	1:D:204:SER:N	2.31	0.46
1:B:418:GLU:O	1:B:422:GLY:HA2	2.16	0.46
1:B:437:GLN:N	1:B:437:GLN:OE1	2.49	0.46
1:A:117:VAL:HG12	1:A:118:VAL:HG12	1.98	0.46
1:A:121:PRO:O	1:A:122:PHE:HD2	1.98	0.46
1:A:372:TYR:C	1:A:372:TYR:CD2	2.89	0.46
1:A:90:LYS:HD3	1:A:122:PHE:HE1	1.76	0.46
1:B:248:VAL:HG13	1:B:322:LEU:HD12	1.97	0.46
1:D:5:ASP:HB3	1:D:332:THR:HB	1.98	0.46
1:B:391:HIS:HB3	1:C:385:TRP:HZ3	1.81	0.46
1:D:198:VAL:O	1:D:198:VAL:HG13	2.16	0.46
1:C:370:ASP:OD1	1:C:370:ASP:N	2.48	0.46
1:B:37:THR:O	1:B:38:GLU:CB	2.63	0.46
1:D:222:GLY:O	1:D:226:PHE:HD1	1.98	0.46
1:F:339:VAL:C	1:F:341:ALA:N	2.69	0.46
1:C:43:ASN:O	1:C:45:VAL:N	2.49	0.46
1:B:30:GLU:CG	1:B:31:ASP:N	2.79	0.46
1:A:30:GLU:HG2	1:A:31:ASP:N	2.30	0.46
1:D:19:ARG:CG	1:D:19:ARG:NH1	2.76	0.46
1:B:201:LYS:HZ1	1:B:388:ASN:ND2	2.14	0.46
1:C:82:HIS:HD2	1:C:83:SER:N	2.14	0.46
1:D:36:GLU:H	1:D:36:GLU:HG3	1.56	0.46
1:F:403:ARG:HA	1:F:440:ILE:O	2.15	0.46
1:E:478:ARG:O	1:E:479:THR:C	2.54	0.46
1:E:480:ALA:O	1:E:483:VAL:HB	2.16	0.46
1:D:116:ALA:O	1:D:488:LYS:HD2	2.15	0.46
1:D:490:PHE:C	1:D:490:PHE:CD1	2.88	0.46
1:C:463:GLN:HG2	1:C:463:GLN:H	1.49	0.46
1:E:331:LEU:O	1:E:356:ALA:CB	2.64	0.46
1:A:282:ASN:HB2	1:A:306:LYS:O	2.16	0.46
1:A:362:GLU:C	1:A:364:ASN:N	2.70	0.46
1:A:292:GLU:C	1:A:294:PHE:H	2.18	0.46
1:C:143:LYS:O	1:C:144:ILE:C	2.53	0.46
1:A:400:LYS:HZ1	1:B:439:ARG:HH12	1.63	0.45
1:C:9:PHE:HD1	1:C:103:GLU:HG3	1.80	0.45
1:B:217:ARG:NE	1:B:450:HIS:CD2	2.85	0.45
1:E:37:THR:O	1:E:38:GLU:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:107:LEU:O	1:E:110:LEU:HB2	2.16	0.45
1:B:255:VAL:HG11	3:B:552:NDP:O4D	2.16	0.45
1:B:332:THR:O	1:B:333:LYS:C	2.54	0.45
1:F:494:ASN:O	1:F:495:GLU:HG3	2.16	0.45
1:B:153:ALA:HA	1:B:158:ILE:HG22	1.98	0.45
1:B:199:THR:CG2	1:B:384:GLU:HB3	2.46	0.45
1:B:429:PRO:O	1:B:429:PRO:CG	2.64	0.45
1:A:117:VAL:HG11	1:A:372:TYR:HB2	1.98	0.45
1:B:110:LEU:O	1:B:111:MET:C	2.53	0.45
1:E:270:CYS:O	1:E:286:ILE:N	2.48	0.45
1:E:316:GLU:O	1:E:317:VAL:C	2.54	0.45
1:B:353:THR:HB	1:B:354:PRO:HD2	1.96	0.45
1:A:175:GLU:HA	1:A:178:TRP:HE3	1.75	0.45
1:F:371:LEU:HA	1:F:371:LEU:HD23	1.74	0.45
1:F:379:THR:O	1:F:382:TYR:HB3	2.17	0.45
1:F:37:THR:HB	1:F:41:LYS:HG3	1.97	0.45
1:B:348:ALA:HB1	3:B:552:NDP:O3D	2.16	0.45
1:D:65:ILE:HG12	1:D:75:ILE:HD12	1.98	0.45
1:A:475:LEU:HA	1:A:475:LEU:HD23	1.75	0.45
1:E:56:ASN:HD22	1:E:84:GLN:HE21	1.62	0.45
1:E:78:TYR:CD1	1:E:78:TYR:N	2.85	0.45
1:A:409:LEU:HG	1:B:402:GLU:O	2.16	0.45
1:A:438:ASP:C	1:A:439:ARG:CG	2.84	0.45
1:A:164:VAL:HA	1:A:197:CYS:O	2.17	0.45
1:A:154:LYS:HE3	1:E:185:SER:O	2.16	0.45
1:B:315:LEU:HB3	1:B:322:LEU:HD21	1.97	0.45
1:D:346:GLU:CD	1:D:478:ARG:HH22	2.20	0.45
1:C:148:PHE:CD2	1:C:152:LEU:CD1	3.00	0.45
1:D:448:ILE:O	1:D:452:GLY:N	2.45	0.45
1:F:142:GLU:HA	1:F:178:TRP:CH2	2.51	0.45
1:F:331:LEU:O	1:F:353:THR:HG23	2.17	0.45
1:E:402:GLU:O	1:E:403:ARG:C	2.54	0.45
1:D:136:TYR:HB2	1:D:141:LEU:HD21	1.98	0.45
1:E:475:LEU:HD23	1:E:475:LEU:HA	1.77	0.45
1:B:239:THR:CG2	1:B:245:LYS:HZ1	2.29	0.45
1:B:98:ASP:O	1:B:99:VAL:C	2.54	0.45
1:B:491:ARG:HA	1:B:491:ARG:HD2	1.65	0.45
1:B:309:ILE:HD13	1:B:309:ILE:N	2.31	0.45
1:E:174:ARG:HG2	1:E:178:TRP:CH2	2.51	0.45
1:D:456:THR:O	1:D:457:MET:C	2.55	0.45
1:F:136:TYR:HA	1:F:140:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:ILE:HD13	1:F:345:ALA:HB2	1.98	0.45
1:F:379:THR:O	1:F:383:PHE:CD2	2.70	0.45
1:E:406:ASN:C	1:E:408:HIS:N	2.70	0.45
1:F:387:ASN:ND2	1:F:445:GLU:OE1	2.46	0.45
1:A:482:TYR:O	1:A:486:ILE:HG13	2.17	0.45
1:D:97:THR:HG22	1:D:132:ASN:N	2.31	0.45
1:C:423:LYS:C	1:C:425:GLY:N	2.70	0.45
1:F:293:ASP:HA	1:F:296:LEU:HB2	1.99	0.45
1:E:235:ILE:O	1:E:235:ILE:CG2	2.64	0.45
1:E:273:VAL:HG21	1:E:291:LEU:HD12	1.96	0.45
1:A:400:LYS:HD2	1:B:451:SER:CB	2.47	0.45
1:B:90:LYS:NZ	1:B:199:THR:OG1	2.47	0.45
1:A:433:THR:N	1:C:409:LEU:HG	2.31	0.45
1:E:259:SER:O	1:E:263:LEU:HG	2.17	0.45
1:A:222:GLY:HA3	1:A:373:LEU:CD2	2.46	0.45
1:F:234:SER:O	1:F:236:LEU:N	2.49	0.45
1:D:309:ILE:O	1:D:310:TYR:C	2.54	0.45
1:C:214:ALA:HB1	1:C:380:VAL:CG2	2.37	0.45
1:D:159:GLY:C	1:D:161:GLY:N	2.70	0.45
1:B:41:LYS:O	1:B:45:VAL:HG23	2.17	0.45
1:F:458:GLU:O	1:F:459:ARG:C	2.55	0.45
1:F:211:ARG:HD2	1:F:211:ARG:C	2.33	0.45
1:F:272:THR:OG1	1:F:273:VAL:N	2.48	0.45
1:C:24:VAL:HG23	1:C:28:LEU:HD22	1.97	0.45
1:A:234:SER:C	1:A:236:LEU:N	2.70	0.45
1:E:399:PHE:C	1:E:401:TYR:N	2.70	0.45
1:F:98:ASP:O	1:F:130:LYS:HE3	2.17	0.45
1:B:117:VAL:CG2	1:B:371:LEU:HD22	2.46	0.45
1:A:414:GLN:CG	1:B:430:ILE:HG23	2.13	0.45
1:A:411:MET:CB	1:B:436:PHE:CD2	2.77	0.45
1:E:238:MET:HG2	1:E:245:LYS:HZ1	1.81	0.45
1:B:314:ILE:O	1:B:317:VAL:HG23	2.16	0.45
1:B:336:ALA:HB3	1:B:359:ILE:HD12	1.99	0.45
1:C:167:PRO:CD	1:C:200:GLY:HA3	2.46	0.45
1:C:62:SER:HB2	1:F:55:CYS:O	2.16	0.45
1:F:108:ALA:O	1:F:112:THR:HG22	2.17	0.45
1:C:226:PHE:HE2	1:C:465:MET:HG2	1.81	0.45
1:C:370:ASP:O	1:C:371:LEU:C	2.55	0.45
1:F:202:PRO:HB2	1:F:205:GLN:CB	2.46	0.45
1:F:35:ARG:HG2	1:F:36:GLU:N	2.30	0.45
1:C:57:HIS:CE1	1:C:84:GLN:HE22	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:VAL:O	1:D:28:LEU:N	2.45	0.45
1:B:477:LEU:HD23	1:B:477:LEU:HA	1.62	0.45
1:E:339:VAL:C	1:E:341:ALA:H	2.19	0.45
1:E:415:GLU:O	1:E:419:ARG:HB2	2.16	0.45
1:E:361:LEU:HD23	1:E:361:LEU:O	2.16	0.45
1:C:410:LEU:HD12	1:C:410:LEU:HA	1.72	0.45
1:C:395:GLY:O	1:C:396:ARG:C	2.55	0.45
1:E:176:MET:HG3	1:E:199:THR:O	2.16	0.45
1:B:315:LEU:HD12	1:B:335:ASN:HD21	1.80	0.45
1:F:234:SER:C	1:F:236:LEU:N	2.69	0.45
1:D:280:ILE:HB	1:D:307:ALA:CB	2.47	0.45
1:D:107:LEU:CB	1:D:126:LYS:HG2	2.45	0.45
1:D:159:GLY:O	1:D:161:GLY:N	2.50	0.45
1:E:37:THR:O	1:E:38:GLU:HB2	2.17	0.45
1:F:167:PRO:CD	1:F:200:GLY:HA3	2.45	0.45
1:F:373:LEU:HD23	1:F:373:LEU:HA	1.83	0.45
1:A:35:ARG:HG2	1:A:36:GLU:HG3	1.98	0.45
1:B:150:MET:SD	1:B:186:THR:HG21	2.57	0.45
1:B:459:ARG:HG2	1:B:459:ARG:NH1	2.31	0.45
1:A:293:ASP:HA	1:A:296:LEU:HB2	1.99	0.45
1:E:59:LEU:O	1:E:78:TYR:HB3	2.17	0.45
1:F:183:TYR:CD2	1:F:183:TYR:C	2.90	0.45
1:C:411:MET:O	1:C:415:GLU:N	2.48	0.45
1:C:247:PHE:O	1:C:270:CYS:HA	2.16	0.45
1:E:323:ILE:HG22	1:E:325:ALA:HB2	1.99	0.45
1:D:279:SER:HB3	1:D:314:ILE:HD13	1.98	0.45
1:A:176:MET:HG3	1:A:199:THR:O	2.16	0.45
1:A:175:GLU:O	1:A:179:ILE:HG13	2.17	0.45
1:A:199:THR:HG22	1:A:384:GLU:HG2	1.98	0.45
1:B:35:ARG:N	1:B:35:ARG:CD	2.71	0.45
1:F:173:GLU:OE2	1:F:202:PRO:HA	2.17	0.45
1:F:173:GLU:O	1:F:202:PRO:HD3	2.17	0.45
1:F:219:VAL:O	1:F:223:ILE:HG12	2.17	0.45
1:E:436:PHE:HZ	1:F:409:LEU:HD12	1.80	0.45
1:B:141:LEU:HA	1:B:141:LEU:HD23	1.61	0.45
1:D:444:SER:O	1:D:445:GLU:C	2.54	0.45
1:A:406:ASN:O	1:A:410:LEU:CD2	2.64	0.45
1:B:165:PRO:HD2	1:B:197:CYS:O	2.17	0.45
1:B:429:PRO:HG2	1:B:429:PRO:O	2.17	0.45
1:D:280:ILE:HG13	1:D:280:ILE:O	2.16	0.45
1:D:321:ILE:HD13	1:D:321:ILE:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3:ARG:HG3	1:D:3:ARG:H	1.58	0.45
1:D:109:SER:HA	1:D:112:THR:CG2	2.47	0.45
1:B:86:ARG:HB3	1:B:121:PRO:O	2.16	0.45
1:F:301:ILE:HG13	1:F:302:LEU:N	2.32	0.45
1:C:494:ASN:C	1:C:495:GLU:CG	2.85	0.45
1:E:353:THR:O	1:E:357:ASP:N	2.48	0.45
1:B:202:PRO:HG2	1:B:205:GLN:HG3	1.99	0.45
1:A:209:HIS:CD2	1:A:446:LYS:CA	2.99	0.45
1:A:306:LYS:N	1:A:306:LYS:CD	2.80	0.45
1:A:435:GLU:HB3	1:C:408:HIS:CD2	2.44	0.45
1:B:208:ILE:HB	1:B:384:GLU:HA	1.98	0.45
1:B:208:ILE:CG2	1:B:380:VAL:HG12	2.47	0.45
1:B:427:THR:O	1:B:429:PRO:HD3	2.17	0.45
1:E:90:LYS:NZ	1:E:166:ALA:HB2	2.32	0.45
1:E:169:MET:O	1:E:170:SER:HB2	2.17	0.45
2:C:502:GLU:CD	3:C:552:NDP:H42N	2.37	0.45
1:E:382:TYR:CZ	1:F:392:VAL:HG22	2.52	0.45
1:B:396:ARG:HG2	1:B:396:ARG:NH1	2.31	0.45
1:F:385:TRP:O	1:F:389:LEU:HG	2.17	0.45
1:A:409:LEU:HD12	1:B:402:GLU:HA	1.99	0.44
1:A:428:ILE:CD1	1:B:430:ILE:H	2.14	0.44
1:B:404:ASP:HB3	1:C:439:ARG:NH1	2.33	0.44
1:B:246:THR:OG1	1:B:271:ILE:HG12	2.17	0.44
1:C:146:ARG:HA	1:C:182:THR:HG21	1.98	0.44
1:C:146:ARG:CB	1:C:182:THR:HG21	2.47	0.44
1:C:379:THR:O	1:C:380:VAL:C	2.55	0.44
1:C:448:ILE:HA	1:C:448:ILE:HD13	1.51	0.44
1:F:82:HIS:CD2	1:F:83:SER:N	2.85	0.44
1:A:172:GLY:H	1:A:175:GLU:CG	2.30	0.44
1:E:82:HIS:CD2	1:E:112:THR:CG2	2.93	0.44
1:E:372:TYR:CD1	1:E:464:ILE:HD12	2.53	0.44
1:F:202:PRO:HB2	1:F:205:GLN:HB2	1.99	0.44
1:F:211:ARG:HH22	3:F:552:NDP:H72N	1.57	0.44
1:D:381:SER:O	1:D:384:GLU:HB3	2.17	0.44
1:B:328:GLU:HA	1:B:351:PRO:HA	1.99	0.44
1:A:32:LEU:HD21	1:A:44:ARG:NH1	2.32	0.44
1:C:421:PHE:O	1:C:422:GLY:C	2.56	0.44
1:C:50:ARG:O	1:C:54:PRO:HD3	2.16	0.44
1:F:181:ASP:O	1:F:185:SER:N	2.44	0.44
1:C:471:TYR:N	1:C:471:TYR:CD2	2.85	0.44
1:F:265:ARG:HB2	1:F:265:ARG:HE	1.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:GLN:HB2	1:B:432:PRO:HD3	1.99	0.44
1:B:370:ASP:O	1:B:371:LEU:C	2.56	0.44
1:A:430:ILE:HD12	1:B:430:ILE:CD1	2.46	0.44
1:A:428:ILE:CB	1:B:430:ILE:CG1	2.53	0.44
2:A:502:GLU:HA	3:A:552:NDP:C3N	2.47	0.44
1:C:407:TYR:CE1	1:C:440:ILE:HD13	2.52	0.44
1:B:229:GLU:HG3	1:B:231:SER:HB3	1.98	0.44
1:B:336:ALA:O	1:B:338:ARG:N	2.49	0.44
1:A:201:LYS:HZ2	1:A:388:ASN:ND2	2.12	0.44
1:A:335:ASN:C	1:A:337:PRO:HD2	2.38	0.44
1:D:332:THR:C	1:D:356:ALA:HB2	2.37	0.44
1:C:148:PHE:O	1:C:152:LEU:HD12	2.17	0.44
1:C:175:GLU:O	1:C:176:MET:C	2.56	0.44
1:E:93:ILE:O	1:E:93:ILE:HG12	2.18	0.44
1:E:418:GLU:HG2	1:E:428:ILE:HD12	2.00	0.44
1:D:420:LYS:HG2	1:F:428:ILE:HG23	2.00	0.44
1:D:63:PHE:O	1:D:75:ILE:HD13	2.17	0.44
1:E:385:TRP:HZ3	1:F:391:HIS:HB3	1.82	0.44
1:D:260:MET:CG	1:D:288:PRO:HG3	2.41	0.44
1:D:45:VAL:HG13	1:D:490:PHE:HE2	1.83	0.44
1:C:362:GLU:C	1:C:364:ASN:N	2.71	0.44
1:B:491:ARG:O	1:B:492:VAL:C	2.55	0.44
1:F:405:SER:O	1:F:408:HIS:HB2	2.16	0.44
1:F:69:ASP:OD2	1:F:69:ASP:O	2.35	0.44
1:A:363:ARG:NH1	1:A:365:ILE:HD11	2.32	0.44
1:E:95:TYR:HH	1:E:145:THR:HB	1.81	0.44
1:E:219:VAL:HG12	1:E:220:PHE:N	2.32	0.44
1:D:272:THR:HG22	1:D:281:TRP:HD1	1.82	0.44
1:D:165:PRO:HD2	1:D:197:CYS:O	2.17	0.44
1:B:57:HIS:CE1	1:B:84:GLN:OE1	2.69	0.44
1:F:94:ARG:NE	1:F:168:ASP:OD1	2.46	0.44
1:D:420:LYS:CG	1:D:421:PHE:HE2	2.30	0.44
1:C:110:LEU:HA	1:C:110:LEU:HD12	1.64	0.44
1:F:76:GLU:OE1	1:F:130:LYS:HD3	2.18	0.44
1:B:186:THR:OG1	1:B:187:ILE:N	2.50	0.44
1:E:344:ILE:HG13	1:E:367:VAL:HG13	1.98	0.44
1:E:301:ILE:HG13	1:E:302:LEU:N	2.32	0.44
1:F:104:VAL:CG1	1:F:104:VAL:O	2.64	0.44
1:A:430:ILE:HG21	1:B:410:LEU:CG	2.44	0.44
1:B:115:CYS:SG	1:B:378:VAL:HG11	2.58	0.44
1:A:400:LYS:HB3	1:B:451:SER:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:THR:OG1	3:A:552:NDP:H42N	2.18	0.44
1:E:186:THR:O	1:E:189:HIS:HB3	2.16	0.44
1:E:220:PHE:O	1:E:224:GLU:CB	2.66	0.44
1:E:238:MET:CE	1:E:320:ASP:OD2	2.66	0.44
1:B:238:MET:HE3	1:B:320:ASP:HB3	1.99	0.44
1:B:75:ILE:O	1:B:75:ILE:HG12	2.16	0.44
1:C:226:PHE:HE2	1:C:465:MET:CG	2.30	0.44
1:A:132:ASN:O	1:A:136:TYR:CD2	2.70	0.44
1:E:418:GLU:O	1:E:422:GLY:HA2	2.17	0.44
1:D:35:ARG:CD	1:D:35:ARG:N	2.80	0.44
1:C:462:ARG:CG	1:C:466:ARG:HH12	2.28	0.44
1:A:480:ALA:O	1:A:483:VAL:HB	2.16	0.44
1:A:430:ILE:HA	1:B:413:VAL:HG11	2.00	0.44
1:C:431:VAL:HA	1:C:432:PRO:HD3	1.92	0.44
1:C:342:LYS:O	1:C:365:ILE:CG2	2.64	0.44
1:C:150:MET:HE1	1:C:186:THR:OG1	2.17	0.44
1:B:219:VAL:O	1:B:222:GLY:N	2.51	0.44
1:D:238:MET:HG2	1:D:245:LYS:NZ	2.32	0.44
1:A:92:GLY:O	1:A:126:LYS:HD2	2.18	0.44
1:D:219:VAL:O	1:D:373:LEU:HD21	2.18	0.44
1:F:167:PRO:CA	1:F:176:MET:CE	2.91	0.44
1:C:29:VAL:HG21	1:C:42:ARG:HE	1.83	0.44
1:B:251:GLY:HA2	3:B:552:NDP:H1B	2.00	0.44
1:F:150:MET:CE	1:F:150:MET:HA	2.47	0.44
1:E:456:THR:O	1:E:457:MET:C	2.55	0.44
1:D:412:SER:OG	1:F:433:THR:HG23	2.17	0.44
1:E:191:ASP:HB3	1:E:194:ALA:HB2	1.98	0.44
1:A:193:ASN:O	1:A:194:ALA:C	2.56	0.44
1:D:423:LYS:N	1:D:423:LYS:CD	2.79	0.44
1:D:258:HIS:HD2	1:D:261:ARG:HH11	1.65	0.44
1:A:417:LEU:HA	1:A:417:LEU:HD23	1.84	0.44
1:A:427:THR:CA	1:B:429:PRO:HD2	2.48	0.44
1:B:90:LYS:HD3	1:B:122:PHE:CD1	2.53	0.44
1:B:421:PHE:O	1:B:422:GLY:O	2.35	0.44
1:A:428:ILE:O	1:B:430:ILE:HG12	2.16	0.44
1:A:401:TYR:CD1	1:B:443:ALA:HB2	2.48	0.44
1:A:401:TYR:HB2	1:B:443:ALA:HB2	2.00	0.44
1:A:432:PRO:HA	1:C:409:LEU:CG	2.47	0.44
1:A:48:ILE:HA	1:A:51:ILE:HD12	1.99	0.44
1:C:316:GLU:OE2	1:C:338:ARG:NH1	2.51	0.44
1:E:142:GLU:HB2	1:E:178:TRP:CZ2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:145:THR:HG21	1:E:178:TRP:CE3	2.52	0.44
1:E:249:VAL:HG23	1:E:325:ALA:HB3	1.99	0.44
1:A:249:VAL:HA	1:A:323:ILE:O	2.18	0.44
1:F:233:MET:HB3	1:F:238:MET:O	2.17	0.44
1:C:169:MET:O	1:C:170:SER:HB2	2.18	0.44
1:B:38:GLU:OE1	1:B:39:GLU:OE1	2.35	0.44
1:D:462:ARG:CG	1:D:466:ARG:HH12	2.22	0.44
1:F:166:ALA:HB1	1:F:167:PRO:CD	2.47	0.44
1:F:332:THR:O	1:F:336:ALA:N	2.44	0.44
1:D:433:THR:CG2	1:E:412:SER:HA	2.47	0.44
1:A:38:GLU:HB3	1:A:40:GLN:HG2	2.00	0.44
1:F:395:GLY:O	1:F:397:LEU:N	2.51	0.44
1:C:462:ARG:HG3	1:C:466:ARG:CZ	2.48	0.44
1:A:188:GLY:O	1:A:190:TYR:N	2.51	0.44
1:D:475:LEU:O	1:D:477:LEU:N	2.48	0.44
1:B:47:SER:HA	1:B:50:ARG:HB2	1.98	0.44
1:A:420:LYS:O	1:A:421:PHE:HD2	2.00	0.44
1:B:420:LYS:CG	1:B:421:PHE:HE2	2.30	0.44
1:A:169:MET:HG3	3:A:552:NDP:H3D	1.99	0.44
1:E:224:GLU:HA	1:E:227:ILE:HG22	2.00	0.44
1:A:223:ILE:H	1:A:223:ILE:HG12	1.69	0.44
1:B:345:ALA:HB1	1:B:373:LEU:HD11	2.00	0.44
1:D:462:ARG:HG3	1:D:466:ARG:HH22	1.82	0.44
1:F:63:PHE:CD1	1:F:147:ARG:CG	3.01	0.44
1:F:177:SER:CB	1:F:202:PRO:HG2	2.48	0.44
1:D:439:ARG:HB2	1:E:401:TYR:OH	2.18	0.44
1:C:85:HIS:CD2	1:C:86:ARG:HG2	2.52	0.44
1:B:154:LYS:HD3	1:F:189:HIS:HB2	2.00	0.44
1:C:420:LYS:O	1:C:420:LYS:HG3	2.17	0.44
1:F:3:ARG:CG	1:F:4:GLU:HG3	2.45	0.44
1:A:17:PHE:O	1:A:18:ASP:C	2.56	0.44
1:A:12:MET:CG	1:A:354:PRO:HD3	2.45	0.44
1:E:342:LYS:HZ3	1:E:342:LYS:HB2	1.83	0.44
1:E:392:VAL:HG12	1:E:393:SER:C	2.37	0.44
1:B:208:ILE:HD13	1:B:383:PHE:HB3	2.00	0.44
1:B:446:LYS:H	1:B:446:LYS:CD	2.31	0.44
1:A:370:ASP:O	1:A:374:ASN:OD1	2.35	0.44
1:E:227:ILE:CG2	1:E:228:ASN:H	2.31	0.44
1:B:248:VAL:HG21	1:B:314:ILE:HD11	2.00	0.44
1:C:115:CYS:HB3	1:C:120:VAL:O	2.17	0.44
1:C:211:ARG:HH12	2:C:502:GLU:CD	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:399:PHE:HE2	1:C:443:ALA:O	2.01	0.44
2:C:502:GLU:CD	3:C:552:NDP:C4N	2.86	0.44
1:C:478:ARG:O	1:C:481:ALA:N	2.50	0.44
1:A:172:GLY:O	1:A:175:GLU:HG2	2.18	0.44
1:D:398:THR:O	1:D:399:PHE:C	2.56	0.44
1:D:453:LEU:CD1	1:D:457:MET:HG2	2.47	0.44
1:F:120:VAL:HA	1:F:121:PRO:HD2	1.52	0.44
1:F:321:ILE:HD13	1:F:321:ILE:N	2.33	0.44
1:C:40:GLN:H	1:C:40:GLN:HG2	1.40	0.44
1:C:45:VAL:C	1:C:47:SER:N	2.71	0.44
1:C:493:TYR:C	1:C:495:GLU:H	2.15	0.44
1:B:16:PHE:CD2	1:B:16:PHE:N	2.83	0.44
1:C:420:LYS:C	1:C:421:PHE:CD2	2.73	0.44
1:A:443:ALA:CB	1:A:448:ILE:HG12	2.41	0.44
1:C:183:TYR:O	1:C:183:TYR:CD2	2.71	0.44
1:A:412:SER:O	1:B:432:PRO:HD3	2.18	0.44
1:C:248:VAL:HG21	1:C:314:ILE:CD1	2.45	0.44
1:E:220:PHE:C	1:E:220:PHE:CD2	2.91	0.44
1:D:79:ARG:HA	1:D:126:LYS:O	2.18	0.44
1:D:78:TYR:CE2	1:D:101:VAL:HG12	2.53	0.44
1:E:372:TYR:C	1:E:372:TYR:CD2	2.91	0.44
1:F:271:ILE:HG22	1:F:283:PRO:O	2.18	0.44
1:F:159:GLY:N	1:F:163:ASP:O	2.47	0.44
1:D:132:ASN:HB3	1:D:135:ASN:ND2	2.33	0.44
1:D:44:ARG:HH12	1:D:494:ASN:HD21	1.66	0.44
1:B:9:PHE:O	1:B:10:PHE:C	2.56	0.44
1:B:267:GLY:O	1:B:268:ALA:O	2.36	0.44
1:E:410:LEU:HA	1:E:410:LEU:HD12	1.83	0.44
1:A:395:GLY:O	1:A:396:ARG:C	2.57	0.43
1:A:382:TYR:CZ	1:A:386:LEU:HD21	2.53	0.43
1:B:279:SER:CB	1:B:314:ILE:HD13	2.46	0.43
1:C:146:ARG:HB3	1:C:182:THR:HG21	2.00	0.43
1:D:13:VAL:O	1:D:14:GLU:C	2.56	0.43
1:D:55:CYS:HA	1:D:82:HIS:HA	2.00	0.43
1:E:462:ARG:HG3	1:E:466:ARG:HH12	1.83	0.43
1:E:226:PHE:CD2	1:E:465:MET:SD	3.11	0.43
1:F:300:THR:HG22	1:F:302:LEU:N	2.33	0.43
1:B:27:LYS:HG3	1:B:31:ASP:HB2	2.00	0.43
1:B:104:VAL:HG11	1:B:127:ALA:HA	2.00	0.43
1:A:35:ARG:HG2	1:A:36:GLU:N	2.27	0.43
1:B:150:MET:CE	1:B:187:ILE:HD11	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:396:ARG:HB2	1:F:396:ARG:HH11	1.83	0.43
1:F:209:HIS:CE1	1:F:446:LYS:HG3	2.52	0.43
1:E:305:PRO:HB2	1:E:306:LYS:HD2	1.98	0.43
1:A:255:VAL:HG22	1:A:325:ALA:HB1	2.00	0.43
1:F:295:LYS:O	1:F:299:GLY:HA2	2.17	0.43
1:A:428:ILE:HG13	1:A:428:ILE:H	1.68	0.43
1:B:114:LYS:HD2	1:B:378:VAL:HG21	2.00	0.43
1:E:165:PRO:HD2	1:E:197:CYS:O	2.18	0.43
1:E:223:ILE:H	1:E:223:ILE:HG12	1.58	0.43
1:E:250:GLN:N	1:E:323:ILE:O	2.41	0.43
1:C:63:PHE:CD1	1:C:147:ARG:HG3	2.53	0.43
1:D:148:PHE:O	1:D:149:THR:C	2.56	0.43
1:B:85:HIS:HB3	1:B:493:TYR:CE2	2.53	0.43
1:D:397:LEU:HD23	1:F:383:PHE:CE1	2.52	0.43
1:F:136:TYR:HB2	1:F:141:LEU:HD21	1.98	0.43
1:D:12:MET:HG3	1:D:354:PRO:HD3	1.99	0.43
1:F:421:PHE:O	1:F:422:GLY:C	2.56	0.43
1:D:85:HIS:CG	1:D:489:VAL:HG13	2.53	0.43
1:B:462:ARG:HG3	1:B:466:ARG:NH1	2.30	0.43
1:C:258:HIS:HD2	1:C:261:ARG:HH11	1.66	0.43
1:A:68:ASP:CG	1:A:140:GLU:HG3	2.39	0.43
1:C:61:LEU:N	1:C:77:GLY:O	2.51	0.43
1:E:423:LYS:HD2	1:E:423:LYS:N	2.33	0.43
1:E:168:ASP:O	1:E:169:MET:C	2.56	0.43
1:D:247:PHE:CE1	1:D:270:CYS:HB2	2.53	0.43
1:D:324:PRO:HB2	1:D:351:PRO:HG3	2.00	0.43
1:B:84:GLN:O	1:B:85:HIS:C	2.55	0.43
1:F:199:THR:HG1	1:F:381:SER:HG	1.63	0.43
1:C:112:THR:N	1:C:124:GLY:CA	2.82	0.43
1:C:56:ASN:HD22	1:C:84:GLN:HE21	1.66	0.43
1:D:11:LYS:O	1:D:12:MET:C	2.56	0.43
1:E:366:MET:HG3	1:E:475:LEU:HD22	2.00	0.43
1:F:203:ILE:CG2	1:F:204:SER:N	2.81	0.43
1:B:294:PHE:CD2	1:B:304:PHE:HD1	2.36	0.43
1:B:244:ASP:HB2	1:B:245:LYS:HZ3	1.84	0.43
1:A:13:VAL:O	1:A:14:GLU:C	2.57	0.43
1:F:289:LYS:HE2	1:F:293:ASP:OD1	2.17	0.43
1:E:14:GLU:O	1:E:17:PHE:HB3	2.19	0.43
1:A:411:MET:HE1	1:A:414:GLN:OE1	2.17	0.43
1:B:404:ASP:O	1:B:405:SER:C	2.55	0.43
1:B:414:GLN:O	1:B:415:GLU:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:409:LEU:O	1:C:410:LEU:CD1	2.66	0.43
1:A:121:PRO:CG	1:A:382:TYR:CE1	3.02	0.43
1:A:201:LYS:HE2	1:A:201:LYS:HB2	1.81	0.43
1:C:167:PRO:CG	1:C:176:MET:HG2	2.38	0.43
1:A:179:ILE:O	1:A:180:ALA:C	2.55	0.43
1:D:219:VAL:HG22	1:D:373:LEU:CD1	2.47	0.43
1:D:226:PHE:HE2	1:D:465:MET:HG2	1.82	0.43
1:E:436:PHE:CG	1:E:436:PHE:O	2.72	0.43
1:F:271:ILE:HG13	1:F:271:ILE:H	1.66	0.43
1:C:29:VAL:HG21	1:C:42:ARG:HG2	2.00	0.43
1:D:386:LEU:C	1:D:388:ASN:N	2.70	0.43
1:B:16:PHE:O	1:B:19:ARG:HB3	2.19	0.43
1:C:110:LEU:O	1:C:111:MET:C	2.56	0.43
1:C:59:LEU:HA	1:F:58:VAL:O	2.18	0.43
1:C:98:ASP:O	1:C:99:VAL:C	2.57	0.43
1:A:353:THR:CB	1:A:354:PRO:HD2	2.46	0.43
1:B:43:ASN:O	1:B:44:ARG:C	2.57	0.43
1:A:409:LEU:N	1:B:436:PHE:CZ	2.87	0.43
1:A:434:ALA:CA	1:A:437:GLN:NE2	2.64	0.43
1:A:121:PRO:HD2	1:A:382:TYR:CE1	2.54	0.43
1:B:336:ALA:HB3	1:B:337:PRO:CD	2.47	0.43
1:C:220:PHE:O	1:C:222:GLY:N	2.52	0.43
1:D:192:ILE:CG2	1:D:193:ASN:N	2.82	0.43
1:F:82:HIS:CG	1:F:112:THR:HG21	2.45	0.43
1:F:11:LYS:HA	1:F:14:GLU:HB2	2.01	0.43
1:D:428:ILE:HG21	1:E:417:LEU:HD23	1.99	0.43
1:E:344:ILE:HG13	1:E:367:VAL:CG1	2.49	0.43
1:D:476:ASP:CG	1:D:479:THR:HG23	2.39	0.43
1:F:406:ASN:C	1:F:408:HIS:N	2.71	0.43
1:B:81:GLN:NE2	1:B:163:ASP:OD1	2.28	0.43
1:B:490:PHE:C	1:B:490:PHE:CD2	2.92	0.43
1:A:411:MET:O	1:A:414:GLN:CA	2.63	0.43
1:A:430:ILE:HD11	1:B:410:LEU:O	2.19	0.43
1:B:211:ARG:O	1:B:214:ALA:HB3	2.18	0.43
1:C:160:PRO:CG	1:C:161:GLY:N	2.80	0.43
1:B:82:HIS:N	1:B:124:GLY:O	2.37	0.43
1:E:52:ILE:HG12	1:E:493:TYR:CD1	2.53	0.43
1:B:63:PHE:CD1	1:B:75:ILE:HD11	2.48	0.43
1:C:146:ARG:O	1:C:149:THR:HB	2.19	0.43
1:C:171:THR:CB	1:C:175:GLU:HG3	2.49	0.43
1:C:323:ILE:HG22	1:C:325:ALA:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:552:NDP:PN	3:C:552:NDP:H2N	2.59	0.43
1:F:56:ASN:ND2	1:F:83:SER:HA	2.32	0.43
1:D:238:MET:HG2	1:D:245:LYS:HZ2	1.83	0.43
1:B:213:SER:O	1:B:215:THR:N	2.52	0.43
1:D:217:ARG:NH2	1:D:450:HIS:HB3	2.33	0.43
1:F:116:ALA:O	1:F:117:VAL:C	2.56	0.43
1:B:95:TYR:CD2	1:B:171:THR:CG2	3.01	0.43
1:C:56:ASN:O	1:F:61:LEU:HD13	2.18	0.43
1:A:209:HIS:NE2	1:A:446:LYS:HB3	2.33	0.43
1:D:132:ASN:CG	1:D:135:ASN:HD21	2.21	0.43
1:E:68:ASP:HB2	1:E:140:GLU:CG	2.48	0.43
1:B:372:TYR:CG	1:B:372:TYR:O	2.71	0.43
1:F:423:LYS:CD	1:F:423:LYS:N	2.81	0.43
1:E:339:VAL:HG12	1:E:341:ALA:CB	2.49	0.43
1:D:202:PRO:HB2	1:D:205:GLN:CG	2.48	0.43
1:D:23:ILE:HG13	1:D:23:ILE:H	1.70	0.43
1:B:223:ILE:HG12	1:B:223:ILE:H	1.58	0.43
1:F:18:ASP:O	1:F:21:ALA:HB3	2.18	0.43
1:A:424:HIS:CD2	1:B:427:THR:HG21	2.53	0.43
1:B:439:ARG:HG3	1:B:439:ARG:O	2.19	0.43
1:C:322:LEU:N	1:C:343:ILE:O	2.36	0.43
1:B:272:THR:CG2	1:B:317:VAL:HG11	2.49	0.43
1:D:308:LYS:O	1:D:309:ILE:C	2.57	0.43
1:C:142:GLU:O	1:C:146:ARG:HG3	2.18	0.43
1:D:111:MET:SD	1:D:114:LYS:NZ	2.92	0.43
1:C:481:ALA:O	1:C:484:ASN:HB2	2.18	0.43
1:A:60:SER:HA	1:A:78:TYR:CD2	2.53	0.43
1:F:107:LEU:HB3	1:F:126:LYS:HG2	2.00	0.43
1:F:94:ARG:HB2	1:F:168:ASP:HB3	2.00	0.43
1:D:420:LYS:HG3	1:D:421:PHE:HE2	1.82	0.43
1:C:72:TRP:HB2	1:F:47:SER:CB	2.41	0.43
1:F:153:ALA:HB1	1:F:187:ILE:HG13	2.01	0.43
1:D:459:ARG:HH11	1:D:459:ARG:HG2	1.84	0.43
1:E:236:LEU:C	1:E:236:LEU:HD23	2.39	0.43
1:B:396:ARG:HH11	1:B:396:ARG:CG	2.31	0.43
1:A:372:TYR:CE1	1:A:461:ALA:N	2.86	0.43
1:E:245:LYS:HA	1:E:320:ASP:OD1	2.19	0.43
1:E:223:ILE:HG22	1:E:368:ILE:CD1	2.49	0.43
1:F:233:MET:HA	1:F:233:MET:CE	2.48	0.43
1:C:79:ARG:NH2	1:C:125:ALA:CB	2.82	0.43
1:C:4:GLU:O	1:C:5:ASP:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:LYS:CB	1:D:122:PHE:HD1	2.31	0.43
1:F:222:GLY:HA3	1:F:373:LEU:CD2	2.48	0.43
1:F:378:VAL:HG13	2:F:502:GLU:HG3	1.99	0.43
1:B:330:GLN:N	1:B:351:PRO:O	2.50	0.43
1:A:17:PHE:C	1:A:19:ARG:N	2.69	0.43
1:A:65:ILE:HA	1:A:65:ILE:HD12	1.76	0.43
1:F:181:ASP:O	1:F:182:THR:C	2.57	0.43
1:F:239:THR:O	1:F:245:LYS:CE	2.66	0.43
1:A:408:HIS:CD2	1:B:439:ARG:N	2.68	0.43
1:B:258:HIS:CD2	1:B:261:ARG:HH12	2.30	0.43
1:F:332:THR:HA	1:F:356:ALA:HB2	2.01	0.43
1:E:110:LEU:HA	1:E:110:LEU:HD12	1.68	0.43
1:F:100:SER:O	1:F:103:GLU:HB3	2.18	0.43
1:D:95:TYR:HH	1:D:145:THR:HB	1.82	0.43
1:B:186:THR:O	1:B:189:HIS:HB3	2.19	0.43
1:A:369:PRO:HG3	1:A:478:ARG:HA	1.99	0.43
1:A:58:VAL:HG22	1:A:80:ALA:HB2	2.01	0.43
1:C:423:LYS:N	1:C:423:LYS:CD	2.81	0.43
1:A:401:TYR:HA	1:A:404:ASP:HB2	2.01	0.43
1:A:432:PRO:HA	1:C:409:LEU:CD1	2.49	0.43
1:A:461:ALA:O	1:A:465:MET:HG3	2.19	0.43
1:E:346:GLU:OE2	1:E:369:PRO:HA	2.18	0.43
1:E:346:GLU:HG2	1:E:351:PRO:HG2	2.01	0.43
1:E:246:THR:O	1:E:320:ASP:N	2.43	0.43
1:A:216:GLY:O	1:A:219:VAL:HB	2.19	0.43
1:F:230:ALA:O	1:F:234:SER:N	2.39	0.43
1:C:220:PHE:O	1:C:221:HIS:C	2.56	0.43
1:D:401:TYR:CE1	1:F:439:ARG:NH1	2.87	0.43
1:E:403:ARG:HG3	1:E:407:TYR:CD1	2.48	0.43
1:B:273:VAL:HG12	1:B:301:ILE:HD13	2.00	0.43
1:B:201:LYS:NZ	1:B:388:ASN:HD21	2.17	0.43
1:D:137:THR:HG23	1:D:140:GLU:CD	2.38	0.43
1:D:440:ILE:HG23	1:D:440:ILE:O	2.18	0.43
1:D:410:LEU:HA	1:D:410:LEU:HD12	1.74	0.43
1:D:265:ARG:O	1:D:267:GLY:N	2.52	0.43
1:A:109:SER:O	1:A:112:THR:HG23	2.19	0.42
1:A:374:ASN:C	1:A:376:GLY:N	2.72	0.42
1:C:230:ALA:O	1:C:234:SER:N	2.41	0.42
1:C:271:ILE:O	1:C:272:THR:HG22	2.18	0.42
1:C:247:PHE:HB2	1:C:321:ILE:HG12	2.01	0.42
1:A:227:ILE:CG2	1:A:228:ASN:N	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:ASP:OD2	1:A:332:THR:HB	2.19	0.42
1:D:186:THR:O	1:D:189:HIS:HB3	2.19	0.42
1:E:37:THR:HB	1:E:41:LYS:HG3	2.01	0.42
1:F:355:GLU:OE2	1:F:355:GLU:HA	2.18	0.42
1:A:230:ALA:O	1:A:231:SER:C	2.55	0.42
1:A:30:GLU:C	1:A:32:LEU:N	2.73	0.42
1:E:386:LEU:HG	1:F:392:VAL:HG23	2.01	0.42
1:F:3:ARG:HG2	1:F:4:GLU:CG	2.43	0.42
1:E:294:PHE:CZ	1:E:298:HIS:ND1	2.87	0.42
1:E:287:ASP:HA	1:E:288:PRO:HD3	1.85	0.42
1:A:10:PHE:CA	1:A:106:ALA:HB2	2.49	0.42
1:A:417:LEU:O	1:A:421:PHE:HB2	2.19	0.42
1:B:370:ASP:OD1	1:B:371:LEU:N	2.52	0.42
1:B:381:SER:O	1:B:384:GLU:N	2.52	0.42
1:A:409:LEU:C	1:B:406:ASN:C	2.78	0.42
1:A:418:GLU:HG2	1:B:429:PRO:C	2.40	0.42
1:A:428:ILE:HG13	1:B:429:PRO:C	2.38	0.42
1:C:273:VAL:HG12	1:C:301:ILE:HD13	2.02	0.42
1:E:281:TRP:O	1:E:307:ALA:HA	2.19	0.42
1:B:246:THR:HA	1:B:269:LYS:O	2.20	0.42
1:B:322:LEU:HD22	1:B:339:VAL:HG11	2.01	0.42
1:A:272:THR:CG2	1:A:317:VAL:HG11	2.49	0.42
1:B:63:PHE:O	1:B:75:ILE:HD13	2.19	0.42
1:C:148:PHE:CZ	1:C:152:LEU:HD11	2.53	0.42
1:D:110:LEU:O	1:D:111:MET:C	2.57	0.42
1:D:120:VAL:HA	1:D:121:PRO:HD2	1.80	0.42
1:D:159:GLY:O	1:D:160:PRO:C	2.56	0.42
1:A:94:ARG:HG2	1:A:99:VAL:HG11	2.01	0.42
1:F:417:LEU:HB3	1:F:428:ILE:CD1	2.49	0.42
1:B:196:ALA:HB2	1:B:388:ASN:HB2	2.01	0.42
1:B:158:ILE:HG22	1:B:158:ILE:O	2.19	0.42
1:A:409:LEU:HD12	1:B:402:GLU:CA	2.49	0.42
1:C:475:LEU:HD23	1:C:475:LEU:HA	1.77	0.42
1:E:90:LYS:CE	1:E:199:THR:OG1	2.67	0.42
1:E:220:PHE:CE1	1:E:266:PHE:CB	3.01	0.42
1:A:356:ALA:O	1:A:360:PHE:CD2	2.72	0.42
1:D:337:PRO:HA	1:D:359:ILE:HG21	2.00	0.42
1:C:346:GLU:HG2	1:C:351:PRO:HG2	2.00	0.42
1:D:180:ALA:HB2	1:D:198:VAL:CG1	2.49	0.42
1:B:212:ILE:HD11	1:B:258:HIS:CE1	2.53	0.42
1:B:86:ARG:HD2	1:B:121:PRO:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LYS:HG3	1:A:127:ALA:N	2.31	0.42
1:E:372:TYR:CE1	1:E:461:ALA:N	2.87	0.42
1:B:250:GLN:NE2	3:B:552:NDP:H2A	2.33	0.42
1:E:16:PHE:N	1:E:16:PHE:CD2	2.86	0.42
1:D:406:ASN:C	1:D:408:HIS:H	2.22	0.42
1:A:351:PRO:HG2	1:A:352:THR:CG2	2.47	0.42
1:C:260:MET:SD	1:C:288:PRO:HA	2.59	0.42
1:C:423:LYS:C	1:C:425:GLY:H	2.23	0.42
1:A:410:LEU:CA	1:B:436:PHE:HE2	2.31	0.42
1:E:373:LEU:HA	1:E:373:LEU:HD23	1.70	0.42
1:C:181:ASP:O	1:C:184:ALA:N	2.52	0.42
1:C:353:THR:O	1:C:357:ASP:HB2	2.20	0.42
1:D:378:VAL:HA	2:D:502:GLU:OE1	2.19	0.42
1:F:272:THR:HB	1:F:281:TRP:HA	2.01	0.42
1:B:280:ILE:HG12	1:B:301:ILE:HD12	2.02	0.42
1:B:92:GLY:O	1:B:126:LYS:HD2	2.19	0.42
1:E:9:PHE:O	1:E:10:PHE:C	2.57	0.42
1:F:88:PRO:HA	1:F:162:VAL:O	2.20	0.42
1:D:37:THR:HB	1:D:38:GLU:H	1.71	0.42
1:E:477:LEU:HD23	1:E:477:LEU:HA	1.63	0.42
1:F:239:THR:HA	1:F:240:PRO:HD3	1.93	0.42
1:B:162:VAL:HG23	1:B:163:ASP:N	2.35	0.42
1:A:134:LYS:HB3	1:A:134:LYS:HE2	1.80	0.42
1:A:420:LYS:C	1:A:421:PHE:CD2	2.90	0.42
1:B:379:THR:O	1:B:380:VAL:C	2.56	0.42
1:B:413:VAL:HG13	1:C:413:VAL:HG11	1.93	0.42
1:A:213:SER:HA	1:A:258:HIS:ND1	2.34	0.42
1:E:90:LYS:HD3	1:E:122:PHE:CD1	2.53	0.42
1:A:337:PRO:HA	1:A:359:ILE:HG21	2.00	0.42
1:D:112:THR:HB	1:D:124:GLY:H	1.84	0.42
1:D:374:ASN:HD22	3:D:552:NDP:H6N	1.85	0.42
1:A:95:TYR:HB3	1:A:133:PRO:HG3	2.01	0.42
1:D:462:ARG:O	1:D:465:MET:N	2.53	0.42
1:B:326:ALA:HB1	3:B:552:NDP:C4A	2.49	0.42
1:E:234:SER:C	1:E:236:LEU:N	2.73	0.42
1:C:446:LYS:H	1:C:446:LYS:CD	2.32	0.42
1:A:157:PHE:CE1	1:D:155:LYS:HD2	2.55	0.42
1:F:490:PHE:C	1:F:492:VAL:H	2.23	0.42
1:B:256:GLY:O	1:B:259:SER:N	2.53	0.42
1:A:437:GLN:HA	1:A:440:ILE:HB	2.01	0.42
1:A:404:ASP:C	1:B:439:ARG:HG3	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:TYR:O	1:B:486:ILE:HG13	2.18	0.42
1:C:248:VAL:CG2	1:C:314:ILE:HD11	2.48	0.42
1:E:230:ALA:O	1:E:231:SER:C	2.57	0.42
1:A:227:ILE:CD1	1:A:343:ILE:CD1	2.98	0.42
1:A:339:VAL:HG21	1:A:360:PHE:CZ	2.54	0.42
1:D:108:ALA:O	1:D:112:THR:HG22	2.19	0.42
1:F:56:ASN:HD22	1:F:84:GLN:NE2	2.18	0.42
1:C:458:GLU:C	1:C:460:SER:N	2.72	0.42
1:A:131:ILE:HB	1:A:136:TYR:CE2	2.55	0.42
1:E:372:TYR:HE1	1:E:461:ALA:N	2.15	0.42
1:D:396:ARG:CD	1:D:396:ARG:C	2.88	0.42
1:B:152:LEU:HD23	1:B:157:PHE:CB	2.47	0.42
1:E:417:LEU:HD13	1:F:417:LEU:HD21	2.00	0.42
3:B:552:NDP:H8A	3:B:552:NDP:H2B	1.87	0.42
1:A:37:THR:O	1:A:38:GLU:CB	2.64	0.42
1:A:211:ARG:HA	1:A:380:VAL:HG11	2.01	0.42
1:C:282:ASN:HB2	1:C:306:LYS:O	2.19	0.42
1:D:142:GLU:O	1:D:146:ARG:HG3	2.19	0.42
1:E:330:GLN:HA	1:E:330:GLN:HE21	1.80	0.42
1:D:470:LYS:HB3	1:D:471:TYR:CD2	2.54	0.42
1:F:27:LYS:HG3	1:F:31:ASP:HB2	2.02	0.42
1:B:378:VAL:HA	1:B:381:SER:HB2	2.00	0.42
1:B:394:TYR:CE2	1:B:443:ALA:CB	3.00	0.42
1:B:416:SER:HA	1:B:419:ARG:NH1	2.35	0.42
1:A:408:HIS:CG	1:B:440:ILE:HA	2.54	0.42
1:A:439:ARG:NH1	1:C:404:ASP:HB2	2.34	0.42
1:C:316:GLU:O	1:C:317:VAL:C	2.57	0.42
1:C:227:ILE:HD13	1:C:343:ILE:CD1	2.50	0.42
1:E:165:PRO:CD	1:E:197:CYS:O	2.68	0.42
1:E:281:TRP:HB2	1:E:310:TYR:CB	2.45	0.42
1:D:331:LEU:N	1:D:331:LEU:HD12	2.34	0.42
1:E:29:VAL:HG22	1:E:30:GLU:N	2.35	0.42
1:E:370:ASP:OD1	1:E:371:LEU:N	2.42	0.42
1:E:460:SER:O	1:E:461:ALA:C	2.57	0.42
1:F:174:ARG:O	1:F:175:GLU:C	2.58	0.42
1:F:16:PHE:CE2	1:F:354:PRO:HB3	2.50	0.42
1:F:356:ALA:O	1:F:360:PHE:CD2	2.73	0.42
1:D:147:ARG:HH11	1:D:147:ARG:HG2	1.85	0.42
1:B:150:MET:O	1:B:154:LYS:HG3	2.20	0.42
1:B:187:ILE:H	1:B:187:ILE:HG12	1.47	0.42
1:C:78:TYR:HE1	1:C:99:VAL:O	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:59:LEU:HB2	1:F:157:PHE:CZ	2.54	0.42
1:F:403:ARG:HB2	1:F:441:SER:OG	2.20	0.42
1:C:208:ILE:HG13	1:C:445:GLU:CD	2.40	0.42
1:C:246:THR:N	1:C:320:ASP:OD1	2.50	0.42
1:F:362:GLU:C	1:F:364:ASN:N	2.73	0.42
1:B:423:LYS:N	1:B:423:LYS:HD2	2.33	0.42
1:A:428:ILE:HG12	1:B:428:ILE:C	2.34	0.42
1:A:372:TYR:HE1	1:A:461:ALA:N	2.18	0.42
1:B:336:ALA:N	1:B:337:PRO:CD	2.81	0.42
1:A:250:GLN:N	1:A:323:ILE:O	2.45	0.42
1:C:94:ARG:NH2	1:C:169:MET:HG3	2.31	0.42
1:E:118:VAL:HA	1:E:460:SER:OG	2.20	0.42
1:F:247:PHE:O	1:F:270:CYS:HA	2.20	0.42
1:A:236:LEU:C	1:A:236:LEU:HD23	2.40	0.42
1:F:402:GLU:O	1:F:403:ARG:C	2.58	0.42
1:C:261:ARG:HG3	1:C:288:PRO:HB3	2.01	0.42
1:A:9:PHE:CE1	1:A:328:GLU:CG	3.02	0.42
1:D:174:ARG:HB3	1:D:174:ARG:HE	1.68	0.42
1:E:322:LEU:O	1:E:324:PRO:HD3	2.18	0.42
1:D:8:ASN:C	1:D:8:ASN:OD1	2.58	0.42
1:A:397:LEU:O	1:B:448:ILE:HG13	2.20	0.42
1:A:430:ILE:CD1	1:B:410:LEU:CG	2.95	0.42
1:A:372:TYR:HB2	1:A:464:ILE:HD11	2.01	0.42
1:A:490:PHE:O	1:A:492:VAL:N	2.44	0.42
1:B:110:LEU:HA	1:B:110:LEU:HD12	1.82	0.42
1:A:272:THR:OG1	1:A:273:VAL:N	2.53	0.42
1:C:181:ASP:O	1:C:182:THR:C	2.58	0.42
1:C:324:PRO:HB2	1:C:351:PRO:HB2	2.01	0.42
1:C:223:ILE:HD13	1:C:345:ALA:HB2	2.02	0.42
1:C:380:VAL:HA	1:C:383:PHE:CD2	2.55	0.42
1:D:218:GLY:O	1:D:219:VAL:C	2.58	0.42
1:F:68:ASP:HB2	1:F:140:GLU:OE1	2.19	0.42
1:C:479:THR:O	1:C:483:VAL:CG2	2.65	0.42
1:D:421:PHE:O	1:D:422:GLY:C	2.59	0.42
1:D:147:ARG:O	1:D:151:GLU:HG2	2.20	0.42
1:C:238:MET:HG2	1:C:245:LYS:NZ	2.34	0.42
1:B:183:TYR:O	1:B:183:TYR:CD2	2.72	0.42
1:A:413:VAL:CG2	1:B:408:HIS:N	2.83	0.42
1:E:172:GLY:H	1:E:175:GLU:CG	2.33	0.42
1:E:381:SER:OG	2:E:502:GLU:OE2	2.33	0.42
1:E:90:LYS:CE	2:E:502:GLU:OE1	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:LYS:HG3	1:A:359:ILE:H	1.83	0.42
1:D:114:LYS:HA	1:D:371:LEU:HD23	2.00	0.42
1:A:146:ARG:HH21	1:A:182:THR:HG22	1.82	0.42
1:E:45:VAL:HG12	1:E:49:LEU:HD22	2.01	0.42
1:F:458:GLU:O	1:F:461:ALA:N	2.53	0.42
1:E:372:TYR:CE1	1:E:461:ALA:CB	2.95	0.42
1:D:383:PHE:O	1:D:384:GLU:C	2.56	0.42
1:D:93:ILE:HA	1:D:127:ALA:O	2.19	0.42
1:F:58:VAL:HA	1:F:80:ALA:HA	2.02	0.42
1:A:394:TYR:CE2	1:A:443:ALA:HB3	2.53	0.42
1:E:473:LEU:HB3	1:E:476:ASP:HB3	2.02	0.42
1:E:234:SER:O	1:E:236:LEU:N	2.53	0.42
1:F:66:ARG:C	1:F:67:ARG:O	2.58	0.42
1:A:89:CYS:HA	1:A:123:GLY:O	2.19	0.42
1:E:333:LYS:HB2	1:E:355:GLU:CG	2.47	0.42
1:D:202:PRO:HB2	1:D:205:GLN:HG2	2.02	0.42
1:E:295:LYS:O	1:E:295:LYS:HG3	2.20	0.42
1:A:417:LEU:CD1	1:B:411:MET:HA	2.50	0.41
1:A:436:PHE:HE2	1:B:409:LEU:HD13	1.85	0.41
1:C:414:GLN:O	1:C:415:GLU:C	2.59	0.41
1:A:111:MET:HE1	2:A:502:GLU:HG3	2.01	0.41
1:E:94:ARG:HE	1:E:169:MET:HG3	1.84	0.41
1:E:220:PHE:HE1	1:E:266:PHE:CB	2.28	0.41
1:D:359:ILE:O	1:D:361:LEU:N	2.53	0.41
1:B:21:ALA:O	1:B:25:GLU:HB2	2.20	0.41
1:D:226:PHE:CE2	1:D:465:MET:HG2	2.55	0.41
1:E:39:GLU:HG2	1:E:39:GLU:O	2.19	0.41
1:E:114:LYS:O	1:E:118:VAL:HG13	2.20	0.41
1:F:117:VAL:HG12	1:F:118:VAL:CG1	2.50	0.41
1:F:94:ARG:NH2	1:F:168:ASP:OD1	2.51	0.41
1:F:219:VAL:HG11	1:F:259:SER:HB3	2.02	0.41
1:F:280:ILE:HB	1:F:307:ALA:HB3	1.99	0.41
1:F:277:ASP:O	1:F:302:LEU:HD11	2.20	0.41
1:B:169:MET:HA	3:B:552:NDP:O2A	2.20	0.41
1:A:40:GLN:HG2	1:A:40:GLN:H	1.22	0.41
1:D:58:VAL:HG22	1:D:80:ALA:HB2	2.01	0.41
1:A:428:ILE:CG1	1:B:428:ILE:CA	2.92	0.41
1:E:150:MET:HE1	1:E:187:ILE:CD1	2.41	0.41
1:E:92:GLY:HA2	1:E:166:ALA:O	2.20	0.41
1:B:337:PRO:HB3	1:B:359:ILE:HD13	2.02	0.41
1:D:91:GLY:HA2	1:D:111:MET:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:458:GLU:O	1:C:459:ARG:C	2.58	0.41
1:F:64:PRO:O	1:F:65:ILE:HD13	2.19	0.41
1:E:173:GLU:HG2	1:E:202:PRO:CA	2.50	0.41
1:F:277:ASP:OD2	1:F:300:THR:HG23	2.19	0.41
1:F:374:ASN:HD22	3:F:552:NDP:H6N	1.85	0.41
1:F:163:ASP:OD2	1:F:164:VAL:N	2.53	0.41
1:F:260:MET:CG	1:F:288:PRO:HG3	2.49	0.41
1:C:18:ASP:O	1:C:21:ALA:HB3	2.19	0.41
1:B:122:PHE:HZ	1:B:385:TRP:CE3	2.38	0.41
1:A:411:MET:CG	1:B:436:PHE:HD2	2.32	0.41
1:C:331:LEU:HD12	1:C:331:LEU:N	2.35	0.41
1:E:174:ARG:CD	1:E:178:TRP:CH2	3.02	0.41
1:D:336:ALA:N	1:D:337:PRO:CD	2.84	0.41
1:B:40:GLN:HG2	1:B:40:GLN:H	1.51	0.41
1:D:396:ARG:HH11	1:D:396:ARG:CG	2.33	0.41
1:D:457:MET:HA	1:D:457:MET:HE1	2.01	0.41
1:F:142:GLU:O	1:F:145:THR:HG23	2.21	0.41
1:E:414:GLN:O	1:E:417:LEU:N	2.47	0.41
1:D:357:ASP:O	1:D:358:LYS:C	2.58	0.41
1:F:392:VAL:HG11	1:F:397:LEU:HD11	2.03	0.41
1:F:399:PHE:HA	1:F:441:SER:O	2.19	0.41
1:E:111:MET:CE	1:E:378:VAL:HG13	2.50	0.41
1:F:490:PHE:C	1:F:492:VAL:N	2.74	0.41
1:E:235:ILE:O	1:E:235:ILE:HG22	2.21	0.41
1:A:423:LYS:C	1:A:425:GLY:N	2.74	0.41
1:A:430:ILE:CG2	1:B:413:VAL:CG2	2.88	0.41
1:A:402:GLU:CB	1:A:441:SER:O	2.66	0.41
1:B:199:THR:HG21	1:B:381:SER:O	2.21	0.41
1:A:414:GLN:CB	1:B:431:VAL:HA	2.39	0.41
1:B:90:LYS:HG3	1:B:91:GLY:H	1.85	0.41
1:A:169:MET:HA	3:A:552:NDP:O2A	2.20	0.41
1:C:310:TYR:CZ	1:C:317:VAL:HG22	2.55	0.41
1:E:142:GLU:O	1:E:145:THR:HG23	2.19	0.41
1:E:345:ALA:O	1:E:347:GLY:N	2.54	0.41
1:D:247:PHE:CD1	1:D:247:PHE:C	2.92	0.41
1:D:315:LEU:HA	1:D:322:LEU:HD11	2.03	0.41
1:D:316:GLU:O	1:D:340:LYS:HE2	2.20	0.41
1:A:494:ASN:O	1:A:495:GLU:CB	2.67	0.41
1:C:92:GLY:HA2	1:C:166:ALA:O	2.21	0.41
1:C:9:PHE:CE2	1:C:12:MET:CE	3.03	0.41
1:D:51:ILE:O	1:D:54:PRO:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:VAL:HG11	1:C:372:TYR:HA	2.02	0.41
1:A:167:PRO:HB3	1:A:172:GLY:HA2	2.03	0.41
1:D:223:ILE:H	1:D:223:ILE:HG12	1.47	0.41
1:F:75:ILE:HG21	1:F:144:ILE:CD1	2.51	0.41
1:E:173:GLU:HG2	1:E:202:PRO:HA	2.03	0.41
1:F:115:CYS:HB3	1:F:120:VAL:O	2.20	0.41
1:C:27:LYS:O	1:C:29:VAL:N	2.53	0.41
1:C:85:HIS:CD2	1:C:86:ARG:CG	3.03	0.41
1:F:449:VAL:O	1:F:453:LEU:HB3	2.20	0.41
1:B:462:ARG:CG	1:B:466:ARG:HH22	2.29	0.41
1:A:155:LYS:O	1:D:155:LYS:HA	2.20	0.41
1:A:294:PHE:C	1:A:296:LEU:N	2.73	0.41
1:A:467:THR:CG2	1:A:483:VAL:HG11	2.50	0.41
1:A:363:ARG:HG2	1:A:363:ARG:O	2.20	0.41
1:A:405:SER:OG	1:B:442:GLY:CA	2.68	0.41
1:A:414:GLN:O	1:A:417:LEU:N	2.45	0.41
1:B:117:VAL:HG12	1:B:118:VAL:HG13	2.03	0.41
1:A:47:SER:CB	1:D:72:TRP:HB2	2.51	0.41
1:A:249:VAL:HA	1:A:323:ILE:HB	2.01	0.41
1:C:324:PRO:O	1:C:326:ALA:N	2.40	0.41
1:D:86:ARG:HB3	1:D:121:PRO:O	2.21	0.41
1:F:55:CYS:HA	1:F:82:HIS:HA	2.03	0.41
1:C:93:ILE:HG12	1:C:93:ILE:O	2.20	0.41
1:C:478:ARG:HG2	1:C:482:TYR:CE1	2.55	0.41
1:A:60:SER:HA	1:A:78:TYR:HD2	1.85	0.41
1:B:45:VAL:O	1:B:46:ARG:C	2.59	0.41
1:F:11:LYS:O	1:F:12:MET:C	2.59	0.41
1:D:214:ALA:CB	1:D:380:VAL:HG21	2.51	0.41
1:D:16:PHE:CE2	1:D:354:PRO:HB3	2.48	0.41
1:F:59:LEU:HD22	1:F:157:PHE:CE1	2.55	0.41
1:E:456:THR:HG21	1:F:396:ARG:HH21	1.85	0.41
1:F:446:LYS:H	1:F:446:LYS:CD	2.34	0.41
1:A:162:VAL:HG23	1:A:163:ASP:N	2.35	0.41
1:C:65:ILE:HD13	1:C:65:ILE:HA	1.63	0.41
1:A:427:THR:N	1:B:429:PRO:HD2	2.36	0.41
1:B:192:ILE:HG23	1:B:193:ASN:N	2.36	0.41
1:B:117:VAL:HG21	1:B:371:LEU:HD22	2.03	0.41
1:B:208:ILE:HD13	1:B:383:PHE:HB2	2.03	0.41
1:B:413:VAL:HG23	1:B:413:VAL:H	1.49	0.41
1:B:451:SER:O	1:B:454:ALA:N	2.54	0.41
1:C:405:SER:O	1:C:408:HIS:CA	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LYS:HG2	1:A:378:VAL:HG12	2.03	0.41
1:D:276:SER:HG	3:D:552:NDP:P2B	2.43	0.41
1:D:371:LEU:HD13	1:D:481:ALA:HB1	2.02	0.41
1:F:169:MET:HG2	3:F:552:NDP:C5D	2.47	0.41
1:F:219:VAL:HA	1:F:373:LEU:HD22	2.01	0.41
1:F:374:ASN:C	1:F:376:GLY:N	2.74	0.41
1:C:45:VAL:C	1:C:47:SER:H	2.24	0.41
1:C:494:ASN:C	1:C:495:GLU:HG2	2.40	0.41
1:E:13:VAL:HG11	1:E:110:LEU:HD13	2.03	0.41
1:B:30:GLU:HG2	1:B:31:ASP:H	1.84	0.41
1:B:94:ARG:NH2	1:B:169:MET:HG3	2.29	0.41
1:D:96:SER:O	1:D:99:VAL:HG22	2.20	0.41
1:F:399:PHE:C	1:F:401:TYR:H	2.24	0.41
1:E:24:VAL:HG23	1:E:28:LEU:CD2	2.48	0.41
1:D:172:GLY:O	1:D:176:MET:HE2	2.21	0.41
1:E:374:ASN:C	1:E:376:GLY:H	2.23	0.41
1:F:257:LEU:HG	1:F:257:LEU:O	2.20	0.41
1:B:66:ARG:O	1:B:67:ARG:O	2.38	0.41
1:E:134:LYS:HB3	1:E:134:LYS:HE2	1.78	0.41
1:A:399:PHE:CA	1:A:441:SER:HB3	2.50	0.41
1:A:276:SER:OG	3:A:552:NDP:O3X	2.32	0.41
1:C:363:ARG:O	1:C:365:ILE:HG12	2.20	0.41
1:A:331:LEU:HD23	1:A:360:PHE:CZ	2.56	0.41
1:D:281:TRP:HB2	1:D:310:TYR:HB2	2.01	0.41
1:C:211:ARG:O	1:C:214:ALA:HB3	2.21	0.41
1:C:332:THR:HG22	1:C:353:THR:CG2	2.46	0.41
1:D:234:SER:C	1:D:236:LEU:H	2.24	0.41
1:C:461:ALA:O	1:C:465:MET:HG3	2.20	0.41
1:B:212:ILE:HD11	1:B:258:HIS:HE1	1.85	0.41
1:A:78:TYR:O	1:A:127:ALA:HB1	2.21	0.41
1:A:93:ILE:HD11	1:A:95:TYR:CE1	2.53	0.41
1:D:451:SER:C	1:D:453:LEU:H	2.24	0.41
1:F:175:GLU:HA	1:F:178:TRP:CE3	2.55	0.41
1:F:294:PHE:HD1	1:F:300:THR:O	2.03	0.41
1:C:35:ARG:HG2	1:C:36:GLU:HG3	2.01	0.41
1:E:107:LEU:HD23	1:E:126:LYS:HG2	2.02	0.41
1:D:414:GLN:O	1:D:418:GLU:HG3	2.20	0.41
1:D:196:ALA:HB2	1:D:388:ASN:CB	2.50	0.41
1:F:467:THR:HG21	1:F:483:VAL:HG12	2.02	0.41
1:B:60:SER:HA	1:B:78:TYR:CD2	2.52	0.41
1:D:65:ILE:HA	1:D:65:ILE:HD13	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:429:PRO:HD2	1:F:420:LYS:HD3	2.02	0.41
1:A:275:GLU:HB2	1:A:301:ILE:CD1	2.50	0.41
1:E:19:ARG:HG2	1:E:19:ARG:NH1	2.31	0.41
1:E:294:PHE:CE2	1:E:298:HIS:HE1	2.37	0.41
1:B:103:GLU:O	1:B:106:ALA:HB3	2.20	0.41
1:E:235:ILE:HD12	1:E:235:ILE:N	2.36	0.41
1:A:390:ASN:O	1:A:392:VAL:HG23	2.20	0.41
1:B:408:HIS:C	1:B:410:LEU:N	2.74	0.41
1:A:121:PRO:O	1:A:122:PHE:CD2	2.72	0.41
1:C:247:PHE:CE2	1:C:263:LEU:CB	3.04	0.41
1:E:174:ARG:HG2	1:E:178:TRP:CZ3	2.55	0.41
1:D:291:LEU:O	1:D:294:PHE:N	2.40	0.41
1:D:322:LEU:O	1:D:324:PRO:HD3	2.20	0.41
1:D:328:GLU:HA	1:D:351:PRO:HA	2.03	0.41
1:D:169:MET:HA	3:D:552:NDP:O2A	2.21	0.41
1:D:111:MET:HE1	2:D:502:GLU:HG3	2.02	0.41
1:A:166:ALA:HA	1:A:199:THR:O	2.21	0.41
1:B:29:VAL:HG21	1:B:42:ARG:HE	1.86	0.41
1:A:73:GLU:OE2	1:A:75:ILE:HG22	2.21	0.41
1:E:21:ALA:O	1:E:25:GLU:HB2	2.21	0.41
1:E:372:TYR:CG	1:E:372:TYR:O	2.73	0.41
1:F:353:THR:O	1:F:357:ASP:N	2.53	0.41
1:C:47:SER:CB	1:F:72:TRP:HB2	2.47	0.41
1:A:238:MET:HG2	1:A:245:LYS:NZ	2.34	0.41
1:F:412:SER:C	1:F:414:GLN:N	2.74	0.41
1:B:201:LYS:HA	1:B:202:PRO:HD3	1.90	0.41
1:D:65:ILE:HG13	1:D:144:ILE:CD1	2.44	0.41
1:D:35:ARG:N	1:D:35:ARG:HD2	2.24	0.41
1:F:330:GLN:HE21	1:F:330:GLN:HA	1.84	0.41
1:D:177:SER:HB2	1:D:202:PRO:HG2	2.02	0.41
1:B:207:GLY:HA2	1:B:384:GLU:HG3	2.03	0.41
1:B:399:PHE:HD2	1:B:399:PHE:H	1.68	0.41
1:A:408:HIS:HD2	1:B:440:ILE:HB	1.86	0.41
1:A:412:SER:O	1:A:414:GLN:C	2.59	0.41
1:A:413:VAL:N	1:B:407:TYR:CD2	2.89	0.41
1:C:366:MET:HG3	1:C:475:LEU:CD2	2.50	0.41
1:E:89:CYS:HB3	1:E:125:ALA:CB	2.51	0.41
1:E:90:LYS:CD	1:E:122:PHE:CE1	2.95	0.41
1:E:175:GLU:CA	1:E:178:TRP:CE3	2.91	0.41
1:E:92:GLY:CA	1:E:166:ALA:O	2.69	0.41
1:E:242:PHE:CE1	1:E:263:LEU:HD22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:LEU:HD12	1:B:335:ASN:ND2	2.36	0.41
1:A:281:TRP:H	1:A:307:ALA:HB1	1.86	0.41
1:F:342:LYS:CA	1:F:365:ILE:HG23	2.49	0.41
1:F:232:TYR:CZ	1:F:477:LEU:HD21	2.56	0.41
1:D:339:VAL:O	1:D:340:LYS:HB2	2.20	0.41
1:C:325:ALA:HA	1:C:348:ALA:N	2.36	0.41
1:D:149:THR:O	1:D:150:MET:C	2.59	0.41
1:D:325:ALA:HA	1:D:348:ALA:N	2.36	0.41
1:D:374:ASN:C	1:D:376:GLY:N	2.73	0.41
1:D:234:SER:C	1:D:236:LEU:N	2.73	0.41
1:A:94:ARG:O	1:A:128:GLY:CA	2.65	0.41
1:A:142:GLU:O	1:A:146:ARG:HG3	2.21	0.41
1:A:148:PHE:CD2	1:A:152:LEU:CD1	3.04	0.41
1:E:112:THR:N	1:E:124:GLY:HA3	2.36	0.41
1:D:466:ARG:NH1	1:D:466:ARG:HB2	2.36	0.41
1:D:448:ILE:HD13	1:D:448:ILE:HA	1.79	0.41
1:F:321:ILE:HG23	1:F:343:ILE:HB	2.03	0.41
1:F:383:PHE:O	1:F:384:GLU:C	2.58	0.41
1:C:35:ARG:CG	1:C:36:GLU:H	2.12	0.41
1:B:141:LEU:O	1:B:145:THR:HG22	2.20	0.41
1:C:36:GLU:H	1:C:36:GLU:HG3	1.51	0.41
1:E:107:LEU:O	1:E:110:LEU:CB	2.69	0.41
1:E:398:THR:O	1:E:399:PHE:C	2.59	0.41
1:E:406:ASN:O	1:E:408:HIS:N	2.54	0.41
1:D:201:LYS:NZ	1:D:388:ASN:ND2	2.63	0.41
1:B:281:TRP:O	1:B:307:ALA:HA	2.21	0.41
1:F:61:LEU:HD21	1:F:151:GLU:HB3	2.03	0.41
1:D:136:TYR:HA	1:D:140:GLU:OE2	2.21	0.41
1:D:68:ASP:OD1	1:D:137:THR:CG2	2.68	0.41
1:F:150:MET:HE1	1:F:187:ILE:CD1	2.46	0.41
1:A:458:GLU:O	1:A:460:SER:N	2.53	0.41
1:C:59:LEU:CD1	1:F:157:PHE:HZ	2.34	0.41
1:E:385:TRP:CE3	1:E:386:LEU:HD13	2.55	0.41
1:F:448:ILE:O	1:F:452:GLY:N	2.51	0.41
1:E:48:ILE:HD13	1:E:494:ASN:HB3	2.02	0.41
1:E:304:PHE:CE2	1:E:306:LYS:HB2	2.56	0.41
1:B:396:ARG:CG	1:B:396:ARG:NH1	2.83	0.41
1:E:252:PHE:HB2	1:E:275:GLU:OE1	2.20	0.41
1:B:9:PHE:CD2	1:B:106:ALA:CB	3.04	0.41
1:A:23:ILE:HG22	1:A:471:TYR:HD1	1.83	0.41
1:F:291:LEU:O	1:F:292:GLU:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2:ASP:HB3	1:B:4:GLU:H	1.85	0.41
1:A:401:TYR:HA	1:A:404:ASP:CB	2.51	0.41
1:C:413:VAL:HB	1:C:430:ILE:HD13	2.03	0.41
1:A:118:VAL:CG1	1:A:375:ALA:HB1	2.47	0.41
1:C:343:ILE:HG23	1:C:366:MET:O	2.20	0.41
1:C:344:ILE:CB	1:C:367:VAL:HG12	2.40	0.41
1:E:248:VAL:HG11	1:E:317:VAL:CG1	2.51	0.41
1:D:292:GLU:O	1:D:296:LEU:HB2	2.21	0.41
1:D:101:VAL:HG22	1:D:102:ASP:N	2.34	0.41
1:E:35:ARG:HG2	1:E:36:GLU:N	2.25	0.41
1:E:372:TYR:HB2	1:E:464:ILE:HD11	2.03	0.41
1:F:223:ILE:H	1:F:223:ILE:HG12	1.36	0.41
1:B:19:ARG:HH11	1:B:19:ARG:CG	2.32	0.41
1:A:445:GLU:O	1:A:446:LYS:C	2.58	0.41
1:F:58:VAL:HG22	1:F:80:ALA:CB	2.51	0.41
1:F:445:GLU:O	1:F:449:VAL:HG23	2.22	0.41
1:B:366:MET:HG3	1:B:475:LEU:HD22	2.02	0.41
1:F:110:LEU:HD12	1:F:110:LEU:HA	1.90	0.41
1:A:404:ASP:HB3	1:B:439:ARG:HB2	2.03	0.40
1:A:412:SER:OG	1:B:440:ILE:CD1	2.66	0.40
1:A:418:GLU:O	1:A:422:GLY:HA2	2.21	0.40
1:B:417:LEU:HD23	1:B:417:LEU:HA	1.86	0.40
1:E:222:GLY:HA3	1:E:373:LEU:HD21	2.02	0.40
1:C:79:ARG:NH2	1:C:125:ALA:HB3	2.35	0.40
1:C:167:PRO:O	1:C:168:ASP:HB2	2.20	0.40
1:C:211:ARG:HD3	1:C:380:VAL:CG1	2.51	0.40
1:D:77:GLY:HA3	1:D:129:VAL:HA	2.01	0.40
1:D:13:VAL:HG11	1:D:110:LEU:HD13	2.04	0.40
1:D:245:LYS:HG3	1:D:245:LYS:HZ3	1.66	0.40
1:A:93:ILE:HA	1:A:127:ALA:O	2.20	0.40
1:A:166:ALA:HB1	1:A:167:PRO:HD2	2.03	0.40
1:C:126:LYS:HD3	1:C:126:LYS:HA	1.74	0.40
1:D:226:PHE:CD1	1:D:368:ILE:HD13	2.56	0.40
1:F:346:GLU:OE2	1:F:369:PRO:HA	2.21	0.40
1:C:37:THR:CB	1:C:41:LYS:HG3	2.50	0.40
1:A:239:THR:HA	1:A:240:PRO:HD3	1.94	0.40
1:E:398:THR:O	1:E:401:TYR:N	2.50	0.40
1:B:203:ILE:CG2	1:B:204:SER:N	2.84	0.40
1:B:458:GLU:O	1:B:459:ARG:C	2.58	0.40
1:C:23:ILE:HG13	1:C:23:ILE:H	1.67	0.40
1:A:89:CYS:O	1:A:163:ASP:HA	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:ILE:CG2	1:A:204:SER:N	2.83	0.40
1:F:27:LYS:O	1:F:28:LEU:C	2.60	0.40
1:A:399:PHE:C	1:A:441:SER:HB3	2.41	0.40
1:A:108:ALA:C	1:A:110:LEU:N	2.74	0.40
1:C:396:ARG:CD	1:C:396:ARG:C	2.89	0.40
1:A:219:VAL:HA	1:A:373:LEU:CD2	2.50	0.40
1:A:315:LEU:HD13	1:A:331:LEU:CD1	2.50	0.40
1:D:296:LEU:HD22	1:D:296:LEU:HA	1.53	0.40
1:B:391:HIS:HB3	1:C:385:TRP:CZ3	2.56	0.40
1:C:348:ALA:HA	3:C:552:NDP:C1D	2.49	0.40
1:D:91:GLY:CA	1:D:111:MET:HE2	2.52	0.40
1:F:263:LEU:O	1:F:264:HIS:C	2.60	0.40
1:D:420:LYS:CG	1:D:421:PHE:CE2	3.04	0.40
1:C:56:ASN:ND2	1:C:83:SER:HA	2.35	0.40
1:E:258:HIS:CD2	1:E:261:ARG:HH12	2.37	0.40
1:F:397:LEU:H	1:F:397:LEU:CD1	2.26	0.40
1:D:118:VAL:HG11	1:D:375:ALA:HB3	1.98	0.40
1:B:372:TYR:HB2	1:B:464:ILE:HD11	2.03	0.40
1:B:374:ASN:C	1:B:376:GLY:N	2.72	0.40
1:B:399:PHE:C	1:B:401:TYR:N	2.74	0.40
1:A:408:HIS:CG	1:B:439:ARG:C	2.94	0.40
1:A:326:ALA:HB1	3:A:552:NDP:C4A	2.51	0.40
1:A:52:ILE:O	1:A:82:HIS:CE1	2.74	0.40
1:C:272:THR:OG1	1:C:314:ILE:CD1	2.65	0.40
1:E:146:ARG:HA	1:E:182:THR:HG21	2.02	0.40
1:C:9:PHE:CE2	1:C:106:ALA:HB1	2.54	0.40
1:C:449:VAL:HG12	1:C:450:HIS:N	2.36	0.40
1:C:3:ARG:NE	1:C:4:GLU:HG3	2.36	0.40
1:C:141:LEU:O	1:C:145:THR:CG2	2.70	0.40
1:B:36:GLU:H	1:B:36:GLU:HG3	1.37	0.40
1:A:73:GLU:HG2	1:A:74:VAL:N	2.36	0.40
1:E:36:GLU:HG3	1:E:36:GLU:H	1.60	0.40
1:E:49:LEU:HD12	1:E:49:LEU:HA	1.99	0.40
1:E:370:ASP:O	1:E:371:LEU:C	2.59	0.40
1:E:482:TYR:HA	1:E:485:ALA:HB3	2.03	0.40
1:F:111:MET:HE1	1:F:378:VAL:HG13	2.02	0.40
1:F:12:MET:O	1:F:13:VAL:C	2.60	0.40
1:C:24:VAL:HG13	1:C:483:VAL:HG22	2.03	0.40
1:A:245:LYS:N	1:A:245:LYS:HD2	2.36	0.40
1:E:421:PHE:O	1:E:422:GLY:C	2.60	0.40
1:F:433:THR:C	1:F:435:GLU:H	2.25	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:85:HIS:HB3	1:D:493:TYR:CE1	2.57	0.40
1:A:292:GLU:O	1:A:296:LEU:HB2	2.21	0.40
1:F:269:LYS:HD3	1:F:284:ASP:O	2.21	0.40
1:B:214:ALA:HB1	1:B:380:VAL:CG2	2.49	0.40
1:B:394:TYR:CD2	1:B:395:GLY:N	2.90	0.40
1:C:405:SER:HB3	1:C:406:ASN:H	1.54	0.40
1:A:484:ASN:O	1:A:485:ALA:C	2.58	0.40
1:C:224:GLU:O	1:C:228:ASN:HB2	2.21	0.40
1:E:254:ASN:N	3:E:552:NDP:O2N	2.53	0.40
1:E:227:ILE:HG22	1:E:228:ASN:H	1.86	0.40
1:C:169:MET:CG	3:C:552:NDP:H52N	2.47	0.40
1:B:373:LEU:O	1:B:373:LEU:HD22	2.22	0.40
1:C:154:LYS:C	1:C:156:GLY:H	2.24	0.40
1:A:138:ASP:O	1:A:142:GLU:N	2.45	0.40
1:A:79:ARG:CB	1:A:127:ALA:HB2	2.52	0.40
1:D:463:GLN:HA	1:D:466:ARG:HB3	2.03	0.40
1:F:117:VAL:HG12	1:F:118:VAL:HG12	2.02	0.40
1:F:337:PRO:HA	1:F:359:ILE:HG21	2.04	0.40
1:F:216:GLY:O	1:F:217:ARG:C	2.60	0.40
1:C:59:LEU:O	1:C:78:TYR:HA	2.22	0.40
1:B:23:ILE:H	1:B:23:ILE:HG13	1.53	0.40
1:A:294:PHE:CZ	1:A:298:HIS:ND1	2.90	0.40
1:A:294:PHE:O	1:A:295:LYS:C	2.60	0.40
1:D:32:LEU:HD21	1:D:44:ARG:NH1	2.36	0.40
1:A:397:LEU:O	1:B:448:ILE:CD1	2.70	0.40
1:A:414:GLN:HE21	1:B:431:VAL:CA	2.35	0.40
1:B:385:TRP:CZ2	1:B:389:LEU:HD11	2.56	0.40
1:A:411:MET:CB	1:B:436:PHE:O	2.68	0.40
1:A:382:TYR:O	1:A:386:LEU:CD2	2.69	0.40
1:A:53:LYS:HB3	1:A:54:PRO:HD3	2.03	0.40
1:C:321:ILE:N	1:C:321:ILE:HD13	2.37	0.40
1:E:348:ALA:O	1:E:351:PRO:HD3	2.22	0.40
1:F:232:TYR:O	1:F:233:MET:C	2.59	0.40
1:A:146:ARG:HB3	1:A:182:THR:CG2	2.35	0.40
1:E:40:GLN:H	1:E:40:GLN:HG2	1.44	0.40
1:D:392:VAL:O	1:D:393:SER:C	2.59	0.40
1:F:255:VAL:O	1:F:255:VAL:HG22	2.22	0.40
1:F:302:LEU:HD23	1:F:302:LEU:HA	1.89	0.40
1:F:382:TYR:CZ	1:F:386:LEU:HD21	2.57	0.40
1:E:408:HIS:O	1:E:409:LEU:C	2.59	0.40
1:A:40:GLN:HA	1:A:43:ASN:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:PHE:CE2	1:D:12:MET:CE	3.05	0.40
1:A:458:GLU:HG3	1:A:459:ARG:H	1.77	0.40
1:F:394:TYR:CD2	1:F:448:ILE:HG13	2.57	0.40
1:D:489:VAL:O	1:D:490:PHE:C	2.59	0.40
1:D:28:LEU:HG	1:D:490:PHE:CD2	2.57	0.40
1:C:287:ASP:HA	1:C:288:PRO:HD3	1.87	0.40
1:D:89:CYS:HA	1:D:123:GLY:O	2.21	0.40
1:E:396:ARG:HH11	1:E:396:ARG:CG	2.35	0.40

There are no symmetry-related clashes.

## 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	493/501 (98%)	349 (71%)	100 (20%)	44 (9%)	1	5
1	B	493/501 (98%)	347 (70%)	105 (21%)	41 (8%)	1	6
1	C	493/501 (98%)	344 (70%)	103 (21%)	46 (9%)	1	5
1	D	493/501 (98%)	347 (70%)	102 (21%)	44 (9%)	1	5
1	E	493/501 (98%)	345 (70%)	102 (21%)	46 (9%)	1	5
1	F	493/501 (98%)	348 (71%)	98 (20%)	47 (10%)	1	5
All	All	2958/3006 (98%)	2080 (70%)	610 (21%)	268 (9%)	1	5

All (268) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	ARG
1	A	38	GLU
1	A	99	VAL
1	A	214	ALA

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Mol	Chain	Res	Type
1	A	235	ILE
1	A	410	LEU
1	A	412	SER
1	A	434	ALA
1	A	439	ARG
1	A	447	ASP
1	B	35	ARG
1	B	38	GLU
1	B	99	VAL
1	B	110	LEU
1	B	111	MET
1	B	189	HIS
1	B	214	ALA
1	B	268	ALA
1	B	413	VAL
1	B	422	GLY
1	B	429	PRO
1	C	5	ASP
1	C	35	ARG
1	C	38	GLU
1	C	89	CYS
1	C	99	VAL
1	C	214	ALA
1	C	317	VAL
1	C	371	LEU
1	C	405	SER
1	C	414	GLN
1	C	422	GLY
1	C	494	ASN
1	D	35	ARG
1	D	38	GLU
1	D	99	VAL
1	D	187	ILE
1	D	214	ALA
1	D	268	ALA
1	D	348	ALA
1	D	371	LEU
1	D	391	HIS
1	D	400	LYS
1	D	422	GLY
1	D	446	LYS
1	D	462	ARG

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Mol	Chain	Res	Type
1	E	35	ARG
1	E	38	GLU
1	E	99	VAL
1	E	189	HIS
1	E	214	ALA
1	E	317	VAL
1	E	391	HIS
1	E	422	GLY
1	E	474	GLY
1	F	2	ASP
1	F	35	ARG
1	F	38	GLU
1	F	67	ARG
1	F	99	VAL
1	F	179	ILE
1	F	189	HIS
1	F	371	LEU
1	F	415	GLU
1	F	422	GLY
1	A	67	ARG
1	A	186	THR
1	A	317	VAL
1	A	333	LYS
1	A	346	GLU
1	A	393	SER
1	A	413	VAL
1	A	414	GLN
1	A	422	GLY
1	A	424	HIS
1	A	474	GLY
1	B	67	ARG
1	B	186	THR
1	B	235	ILE
1	B	275	GLU
1	B	317	VAL
1	B	333	LYS
1	B	361	LEU
1	B	399	PHE
1	B	400	LYS
1	B	411	MET
1	B	412	SER
1	B	451	SER

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Mol	Chain	Res	Type
1	C	2	ASP
1	C	43	ASN
1	C	179	ILE
1	C	268	ALA
1	C	325	ALA
1	C	396	ARG
1	C	399	PHE
1	C	415	GLU
1	C	424	HIS
1	D	79	ARG
1	D	111	MET
1	D	237	GLY
1	D	384	GLU
1	D	393	SER
1	D	463	GLN
1	E	19	ARG
1	E	158	ILE
1	E	222	GLY
1	E	231	SER
1	E	235	ILE
1	E	346	GLU
1	E	399	PHE
1	E	400	LYS
1	E	415	GLU
1	E	446	LYS
1	E	462	ARG
1	E	478	ARG
1	F	45	VAL
1	F	52	ILE
1	F	144	ILE
1	F	310	TYR
1	F	359	ILE
1	F	370	ASP
1	F	413	VAL
1	F	424	HIS
1	A	18	ASP
1	A	310	TYR
1	A	363	ARG
1	A	371	LEU
1	A	394	TYR
1	A	494	ASN
1	B	69	ASP

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Mol	Chain	Res	Type
1	B	70	GLY
1	B	168	ASP
1	B	293	ASP
1	B	310	TYR
1	B	346	GLU
1	B	409	LEU
1	C	3	ARG
1	C	4	GLU
1	C	44	ARG
1	C	121	PRO
1	C	148	PHE
1	C	155	LYS
1	C	220	PHE
1	C	237	GLY
1	C	310	TYR
1	C	333	LYS
1	C	346	GLU
1	C	363	ARG
1	C	370	ASP
1	C	459	ARG
1	D	4	GLU
1	D	43	ASN
1	D	235	ILE
1	D	257	LEU
1	D	310	TYR
1	D	346	GLU
1	D	360	PHE
1	D	447	ASP
1	E	61	LEU
1	E	85	HIS
1	E	110	LEU
1	E	143	LYS
1	E	275	GLU
1	E	310	TYR
1	E	325	ALA
1	E	371	LEU
1	F	174	ARG
1	F	180	ALA
1	F	214	ALA
1	F	220	PHE
1	F	231	SER
1	F	268	ALA

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Mol	Chain	Res	Type
1	F	319	CYS
1	F	340	LYS
1	F	346	GLU
1	F	399	PHE
1	F	403	ARG
1	F	414	GLN
1	F	491	ARG
1	A	165	PRO
1	A	268	ALA
1	A	293	ASP
1	A	340	LYS
1	A	375	ALA
1	A	398	THR
1	A	411	MET
1	A	462	ARG
1	B	55	CYS
1	B	149	THR
1	B	222	GLY
1	B	257	LEU
1	B	325	ALA
1	B	491	ARG
1	C	319	CYS
1	C	379	THR
1	C	449	VAL
1	D	67	ARG
1	D	266	PHE
1	D	293	ASP
1	D	313	SER
1	D	329	LYS
1	D	334	SER
1	D	359	ILE
1	D	474	GLY
1	E	28	LEU
1	E	67	ARG
1	E	144	ILE
1	E	348	ALA
1	E	359	ILE
1	E	360	PHE
1	E	450	HIS
1	E	479	THR
1	F	111	MET
1	F	396	ARG

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Mol	Chain	Res	Type
1	A	237	GLY
1	A	485	ALA
1	B	446	LYS
1	C	106	ALA
1	C	448	ILE
1	D	110	LEU
1	D	265	ARG
1	D	476	ASP
1	E	5	ASP
1	E	27	LYS
1	E	237	GLY
1	F	46	ARG
1	F	155	LYS
1	F	361	LEU
1	F	446	LYS
1	A	29	VAL
1	A	116	ALA
1	A	180	ALA
1	A	359	ILE
1	A	432	PRO
1	B	28	LEU
1	C	27	LYS
1	C	144	ILE
1	C	168	ASP
1	C	235	ILE
1	D	150	MET
1	E	53	LYS
1	E	398	THR
1	E	454	ALA
1	E	485	ALA
1	F	43	ASN
1	F	117	VAL
1	F	235	ILE
1	F	237	GLY
1	F	462	ARG
1	B	237	GLY
1	D	179	ILE
1	F	253	GLY
1	D	219	VAL
1	D	317	VAL
1	E	20	GLY
1	E	449	VAL

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Mol	Chain	Res	Type
1	F	166	ALA
1	A	449	VAL
1	A	486	ILE
1	B	158	ILE
1	C	52	ILE
1	D	53	LYS
1	D	392	VAL
1	F	29	VAL
1	B	309	ILE
1	C	222	GLY
1	F	432	PRO
1	F	486	ILE

### 5.3.2 Protein sidechains ⓘ

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	416/420 (99%)	323 (78%)	93 (22%)	1	5
1	B	416/420 (99%)	325 (78%)	91 (22%)	1	6
1	C	416/420 (99%)	323 (78%)	93 (22%)	1	5
1	D	416/420 (99%)	323 (78%)	93 (22%)	1	5
1	E	416/420 (99%)	324 (78%)	92 (22%)	1	5
1	F	416/420 (99%)	324 (78%)	92 (22%)	1	5
All	All	2496/2520 (99%)	1942 (78%)	554 (22%)	1	5

All (554) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	9	PHE
1	A	10	PHE
1	A	28	LEU
1	A	35	ARG
1	A	36	GLU

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Mol	Chain	Res	Type
1	A	37	THR
1	A	39	GLU
1	A	40	GLN
1	A	43	ASN
1	A	60	SER
1	A	61	LEU
1	A	65	ILE
1	A	67	ARG
1	A	68	ASP
1	A	75	ILE
1	A	78	TYR
1	A	84	GLN
1	A	87	THR
1	A	93	ILE
1	A	94	ARG
1	A	98	ASP
1	A	101	VAL
1	A	107	LEU
1	A	110	LEU
1	A	112	THR
1	A	118	VAL
1	A	126	LYS
1	A	134	LYS
1	A	137	THR
1	A	145	THR
1	A	158	ILE
1	A	168	ASP
1	A	175	GLU
1	A	176	MET
1	A	182	THR
1	A	185	SER
1	A	190	TYR
1	A	198	VAL
1	A	212	ILE
1	A	219	VAL
1	A	223	ILE
1	A	224	GLU
1	A	225	ASN
1	A	239	THR
1	A	244	ASP
1	A	249	VAL
1	A	255	VAL

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Mol	Chain	Res	Type
1	A	272	THR
1	A	289	LYS
1	A	291	LEU
1	A	296	LEU
1	A	306	LYS
1	A	316	GLU
1	A	321	ILE
1	A	328	GLU
1	A	338	ARG
1	A	342	LYS
1	A	344	ILE
1	A	352	THR
1	A	365	ILE
1	A	367	VAL
1	A	368	ILE
1	A	371	LEU
1	A	372	TYR
1	A	373	LEU
1	A	378	VAL
1	A	379	THR
1	A	386	LEU
1	A	393	SER
1	A	396	ARG
1	A	397	LEU
1	A	402	GLU
1	A	405	SER
1	A	406	ASN
1	A	407	TYR
1	A	408	HIS
1	A	409	LEU
1	A	411	MET
1	A	413	VAL
1	A	423	LYS
1	A	427	THR
1	A	428	ILE
1	A	430	ILE
1	A	433	THR
1	A	437	GLN
1	A	439	ARG
1	A	446	LYS
1	A	456	THR
1	A	458	GLU

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Mol	Chain	Res	Type
1	A	463	GLN
1	A	479	THR
1	A	491	ARG
1	B	3	ARG
1	B	9	PHE
1	B	28	LEU
1	B	35	ARG
1	B	36	GLU
1	B	37	THR
1	B	39	GLU
1	B	40	GLN
1	B	49	LEU
1	B	61	LEU
1	B	65	ILE
1	B	67	ARG
1	B	68	ASP
1	B	75	ILE
1	B	78	TYR
1	B	84	GLN
1	B	87	THR
1	B	93	ILE
1	B	94	ARG
1	B	101	VAL
1	B	102	ASP
1	B	107	LEU
1	B	110	LEU
1	B	112	THR
1	B	126	LYS
1	B	134	LYS
1	B	137	THR
1	B	144	ILE
1	B	145	THR
1	B	150	MET
1	B	152	LEU
1	B	158	ILE
1	B	182	THR
1	B	187	ILE
1	B	189	HIS
1	B	190	TYR
1	B	212	ILE
1	B	217	ARG
1	B	223	ILE

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Mol	Chain	Res	Type
1	B	224	GLU
1	B	225	ASN
1	B	244	ASP
1	B	252	PHE
1	B	255	VAL
1	B	271	ILE
1	B	272	THR
1	B	289	LYS
1	B	291	LEU
1	B	296	LEU
1	B	297	GLN
1	B	306	LYS
1	B	311	GLU
1	B	313	SER
1	B	321	ILE
1	B	330	GLN
1	B	342	LYS
1	B	344	ILE
1	B	346	GLU
1	B	352	THR
1	B	357	ASP
1	B	358	LYS
1	B	361	LEU
1	B	365	ILE
1	B	367	VAL
1	B	368	ILE
1	B	373	LEU
1	B	378	VAL
1	B	379	THR
1	B	386	LEU
1	B	394	TYR
1	B	396	ARG
1	B	397	LEU
1	B	406	ASN
1	B	407	TYR
1	B	410	LEU
1	B	421	PHE
1	B	423	LYS
1	B	427	THR
1	B	428	ILE
1	B	437	GLN
1	B	440	ILE

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Mol	Chain	Res	Type
1	B	446	LYS
1	B	448	ILE
1	B	456	THR
1	B	457	MET
1	B	458	GLU
1	B	463	GLN
1	B	479	THR
1	B	487	GLU
1	B	491	ARG
1	B	494	ASN
1	C	3	ARG
1	C	9	PHE
1	C	19	ARG
1	C	28	LEU
1	C	35	ARG
1	C	36	GLU
1	C	37	THR
1	C	39	GLU
1	C	40	GLN
1	C	49	LEU
1	C	60	SER
1	C	61	LEU
1	C	62	SER
1	C	65	ILE
1	C	67	ARG
1	C	68	ASP
1	C	75	ILE
1	C	78	TYR
1	C	79	ARG
1	C	84	GLN
1	C	87	THR
1	C	93	ILE
1	C	94	ARG
1	C	101	VAL
1	C	107	LEU
1	C	110	LEU
1	C	112	THR
1	C	118	VAL
1	C	119	ASP
1	C	134	LYS
1	C	137	THR
1	C	145	THR

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Mol	Chain	Res	Type
1	C	158	ILE
1	C	168	ASP
1	C	169	MET
1	C	173	GLU
1	C	176	MET
1	C	182	THR
1	C	183	TYR
1	C	185	SER
1	C	187	ILE
1	C	190	TYR
1	C	212	ILE
1	C	223	ILE
1	C	225	ASN
1	C	239	THR
1	C	242	PHE
1	C	255	VAL
1	C	270	CYS
1	C	272	THR
1	C	289	LYS
1	C	291	LEU
1	C	296	LEU
1	C	306	LYS
1	C	311	GLU
1	C	316	GLU
1	C	321	ILE
1	C	328	GLU
1	C	342	LYS
1	C	344	ILE
1	C	352	THR
1	C	365	ILE
1	C	366	MET
1	C	367	VAL
1	C	371	LEU
1	C	373	LEU
1	C	378	VAL
1	C	379	THR
1	C	386	LEU
1	C	396	ARG
1	C	397	LEU
1	C	403	ARG
1	C	405	SER
1	C	406	ASN

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Mol	Chain	Res	Type
1	C	408	HIS
1	C	410	LEU
1	C	412	SER
1	C	413	VAL
1	C	421	PHE
1	C	423	LYS
1	C	427	THR
1	C	428	ILE
1	C	431	VAL
1	C	445	GLU
1	C	446	LYS
1	C	448	ILE
1	C	456	THR
1	C	458	GLU
1	C	463	GLN
1	C	467	THR
1	C	479	THR
1	C	490	PHE
1	C	495	GLU
1	D	2	ASP
1	D	3	ARG
1	D	8	ASN
1	D	9	PHE
1	D	19	ARG
1	D	23	ILE
1	D	28	LEU
1	D	35	ARG
1	D	36	GLU
1	D	37	THR
1	D	39	GLU
1	D	40	GLN
1	D	43	ASN
1	D	60	SER
1	D	61	LEU
1	D	67	ARG
1	D	68	ASP
1	D	71	SER
1	D	75	ILE
1	D	78	TYR
1	D	84	GLN
1	D	87	THR
1	D	93	ILE

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Mol	Chain	Res	Type
1	D	94	ARG
1	D	101	VAL
1	D	110	LEU
1	D	112	THR
1	D	119	ASP
1	D	126	LYS
1	D	134	LYS
1	D	137	THR
1	D	145	THR
1	D	154	LYS
1	D	158	ILE
1	D	176	MET
1	D	182	THR
1	D	189	HIS
1	D	190	TYR
1	D	212	ILE
1	D	219	VAL
1	D	223	ILE
1	D	224	GLU
1	D	225	ASN
1	D	239	THR
1	D	242	PHE
1	D	248	VAL
1	D	263	LEU
1	D	272	THR
1	D	275	GLU
1	D	289	LYS
1	D	291	LEU
1	D	296	LEU
1	D	297	GLN
1	D	306	LYS
1	D	311	GLU
1	D	313	SER
1	D	316	GLU
1	D	321	ILE
1	D	328	GLU
1	D	342	LYS
1	D	344	ILE
1	D	352	THR
1	D	353	THR
1	D	357	ASP
1	D	365	ILE

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Mol	Chain	Res	Type
1	D	367	VAL
1	D	368	ILE
1	D	371	LEU
1	D	372	TYR
1	D	373	LEU
1	D	378	VAL
1	D	379	THR
1	D	386	LEU
1	D	396	ARG
1	D	397	LEU
1	D	403	ARG
1	D	405	SER
1	D	407	TYR
1	D	408	HIS
1	D	409	LEU
1	D	410	LEU
1	D	412	SER
1	D	413	VAL
1	D	421	PHE
1	D	423	LYS
1	D	427	THR
1	D	446	LYS
1	D	456	THR
1	D	458	GLU
1	D	463	GLN
1	D	479	THR
1	D	490	PHE
1	D	495	GLU
1	E	3	ARG
1	E	9	PHE
1	E	19	ARG
1	E	28	LEU
1	E	29	VAL
1	E	33	LYS
1	E	35	ARG
1	E	37	THR
1	E	39	GLU
1	E	40	GLN
1	E	49	LEU
1	E	60	SER
1	E	61	LEU
1	E	65	ILE

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Mol	Chain	Res	Type
1	E	68	ASP
1	E	75	ILE
1	E	78	TYR
1	E	79	ARG
1	E	86	ARG
1	E	87	THR
1	E	93	ILE
1	E	94	ARG
1	E	98	ASP
1	E	101	VAL
1	E	110	LEU
1	E	118	VAL
1	E	126	LYS
1	E	134	LYS
1	E	137	THR
1	E	144	ILE
1	E	145	THR
1	E	150	MET
1	E	152	LEU
1	E	158	ILE
1	E	168	ASP
1	E	173	GLU
1	E	175	GLU
1	E	176	MET
1	E	182	THR
1	E	186	THR
1	E	187	ILE
1	E	189	HIS
1	E	190	TYR
1	E	198	VAL
1	E	212	ILE
1	E	223	ILE
1	E	239	THR
1	E	252	PHE
1	E	272	THR
1	E	275	GLU
1	E	279	SER
1	E	289	LYS
1	E	291	LEU
1	E	296	LEU
1	E	302	LEU
1	E	306	LYS

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Mol	Chain	Res	Type
1	E	311	GLU
1	E	316	GLU
1	E	321	ILE
1	E	342	LYS
1	E	344	ILE
1	E	352	THR
1	E	357	ASP
1	E	367	VAL
1	E	368	ILE
1	E	372	TYR
1	E	373	LEU
1	E	378	VAL
1	E	379	THR
1	E	386	LEU
1	E	396	ARG
1	E	397	LEU
1	E	403	ARG
1	E	407	TYR
1	E	408	HIS
1	E	413	VAL
1	E	416	SER
1	E	421	PHE
1	E	423	LYS
1	E	427	THR
1	E	428	ILE
1	E	431	VAL
1	E	446	LYS
1	E	451	SER
1	E	456	THR
1	E	458	GLU
1	E	463	GLN
1	E	469	MET
1	E	479	THR
1	E	492	VAL
1	E	493	TYR
1	E	495	GLU
1	F	9	PHE
1	F	10	PHE
1	F	33	LYS
1	F	35	ARG
1	F	36	GLU
1	F	37	THR

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Mol	Chain	Res	Type
1	F	39	GLU
1	F	40	GLN
1	F	60	SER
1	F	61	LEU
1	F	65	ILE
1	F	66	ARG
1	F	67	ARG
1	F	68	ASP
1	F	71	SER
1	F	75	ILE
1	F	76	GLU
1	F	78	TYR
1	F	84	GLN
1	F	87	THR
1	F	93	ILE
1	F	94	ARG
1	F	101	VAL
1	F	107	LEU
1	F	110	LEU
1	F	112	THR
1	F	119	ASP
1	F	126	LYS
1	F	134	LYS
1	F	137	THR
1	F	145	THR
1	F	150	MET
1	F	158	ILE
1	F	176	MET
1	F	182	THR
1	F	189	HIS
1	F	190	TYR
1	F	212	ILE
1	F	217	ARG
1	F	219	VAL
1	F	223	ILE
1	F	224	GLU
1	F	225	ASN
1	F	239	THR
1	F	242	PHE
1	F	245	LYS
1	F	248	VAL
1	F	249	VAL

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Mol	Chain	Res	Type
1	F	252	PHE
1	F	272	THR
1	F	275	GLU
1	F	289	LYS
1	F	291	LEU
1	F	296	LEU
1	F	306	LYS
1	F	311	GLU
1	F	313	SER
1	F	316	GLU
1	F	321	ILE
1	F	328	GLU
1	F	338	ARG
1	F	342	LYS
1	F	344	ILE
1	F	352	THR
1	F	357	ASP
1	F	361	LEU
1	F	365	ILE
1	F	367	VAL
1	F	368	ILE
1	F	371	LEU
1	F	373	LEU
1	F	378	VAL
1	F	386	LEU
1	F	396	ARG
1	F	397	LEU
1	F	408	HIS
1	F	412	SER
1	F	413	VAL
1	F	421	PHE
1	F	423	LYS
1	F	427	THR
1	F	428	ILE
1	F	431	VAL
1	F	446	LYS
1	F	456	THR
1	F	458	GLU
1	F	463	GLN
1	F	469	MET
1	F	487	GLU
1	F	491	ARG

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Mol	Chain	Res	Type
1	F	494	ASN
1	F	495	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	HIS
1	A	85	HIS
1	A	135	ASN
1	A	189	HIS
1	A	209	HIS
1	A	225	ASN
1	A	258	HIS
1	A	388	ASN
1	A	390	ASN
1	A	414	GLN
1	A	424	HIS
1	A	484	ASN
1	B	40	GLN
1	B	57	HIS
1	B	82	HIS
1	B	84	GLN
1	B	135	ASN
1	B	195	HIS
1	B	209	HIS
1	B	221	HIS
1	B	225	ASN
1	B	258	HIS
1	B	330	GLN
1	B	388	ASN
1	B	450	HIS
1	C	57	HIS
1	C	82	HIS
1	C	84	GLN
1	C	135	ASN
1	C	209	HIS
1	C	225	ASN
1	C	258	HIS
1	C	388	ASN
1	C	391	HIS
1	C	406	ASN
1	C	450	HIS

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Mol	Chain	Res	Type
1	C	484	ASN
1	D	57	HIS
1	D	82	HIS
1	D	84	GLN
1	D	135	ASN
1	D	189	HIS
1	D	205	GLN
1	D	209	HIS
1	D	221	HIS
1	D	225	ASN
1	D	258	HIS
1	D	349	ASN
1	D	388	ASN
1	D	414	GLN
1	D	424	HIS
1	D	494	ASN
1	E	82	HIS
1	E	84	GLN
1	E	135	ASN
1	E	189	HIS
1	E	209	HIS
1	E	225	ASN
1	E	388	ASN
1	E	406	ASN
1	F	56	ASN
1	F	57	HIS
1	F	82	HIS
1	F	135	ASN
1	F	209	HIS
1	F	221	HIS
1	F	388	ASN
1	F	391	HIS
1	F	406	ASN
1	F	424	HIS
1	F	494	ASN

### 5.3.3 RNA ⓘ

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](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GLU	A	502	-	3,9,9	0.51	0	2,11,11	0.23	0
3	NDP	A	552	-	42,52,52	1.55	5 (11%)	55,80,80	2.06	7 (12%)
2	GLU	B	502	-	3,9,9	0.38	0	2,11,11	0.17	0
3	NDP	B	552	-	42,52,52	1.50	6 (14%)	55,80,80	2.13	9 (16%)
2	GLU	C	502	-	3,9,9	0.49	0	2,11,11	0.17	0
3	NDP	C	552	-	42,52,52	1.52	5 (11%)	55,80,80	1.92	6 (10%)
2	GLU	D	502	-	3,9,9	0.32	0	2,11,11	0.42	0
3	NDP	D	552	-	42,52,52	1.57	5 (11%)	55,80,80	2.10	7 (12%)
2	GLU	E	502	-	3,9,9	0.34	0	2,11,11	0.35	0
3	NDP	E	552	-	42,52,52	1.55	5 (11%)	55,80,80	1.90	5 (9%)
2	GLU	F	502	-	3,9,9	0.35	0	2,11,11	0.19	0
3	NDP	F	552	-	42,52,52	1.63	6 (14%)	55,80,80	1.89	5 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLU	A	502	-	-	0/3/9/9	0/0/0/0
3	NDP	A	552	-	-	0/30/77/77	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLU	B	502	-	-	0/3/9/9	0/0/0/0
3	NDP	B	552	-	-	0/30/77/77	0/5/5/5
2	GLU	C	502	-	-	0/3/9/9	0/0/0/0
3	NDP	C	552	-	-	0/30/77/77	0/5/5/5
2	GLU	D	502	-	-	0/3/9/9	0/0/0/0
3	NDP	D	552	-	-	0/30/77/77	0/5/5/5
2	GLU	E	502	-	-	0/3/9/9	0/0/0/0
3	NDP	E	552	-	-	0/30/77/77	0/5/5/5
2	GLU	F	502	-	-	0/3/9/9	0/0/0/0
3	NDP	F	552	-	-	0/30/77/77	0/5/5/5

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	552	NDP	O4D-C4D	-2.21	1.39	1.45
3	B	552	NDP	O4D-C4D	-2.14	1.40	1.45
3	F	552	NDP	PN-O2N	-2.00	1.46	1.54
3	A	552	NDP	C2A-N1A	2.06	1.37	1.33
3	C	552	NDP	C2A-N1A	2.11	1.37	1.33
3	C	552	NDP	C2N-C3N	2.12	1.39	1.34
3	B	552	NDP	C2N-C3N	2.23	1.40	1.34
3	E	552	NDP	C2N-C3N	2.38	1.40	1.34
3	A	552	NDP	C6N-C5N	2.39	1.37	1.33
3	F	552	NDP	C2A-N1A	2.41	1.38	1.33
3	A	552	NDP	C2N-C3N	2.47	1.40	1.34
3	F	552	NDP	C6N-C5N	2.52	1.38	1.33
3	E	552	NDP	C6N-C5N	2.56	1.38	1.33
3	B	552	NDP	C2A-N1A	2.58	1.38	1.33
3	F	552	NDP	C2N-C3N	2.61	1.41	1.34
3	E	552	NDP	C2A-N1A	2.62	1.38	1.33
3	B	552	NDP	C6N-C5N	2.63	1.38	1.33
3	D	552	NDP	C2N-C3N	2.66	1.41	1.34
3	C	552	NDP	C6N-C5N	2.73	1.38	1.33
3	D	552	NDP	C6N-C5N	3.07	1.39	1.33
3	D	552	NDP	C2A-N3A	3.17	1.37	1.32
3	A	552	NDP	C2A-N3A	3.29	1.38	1.32
3	E	552	NDP	C2A-N3A	3.43	1.38	1.32
3	B	552	NDP	C2A-N3A	3.46	1.38	1.32
3	C	552	NDP	C2A-N3A	3.53	1.38	1.32
3	F	552	NDP	C2A-N3A	3.87	1.39	1.32
3	B	552	NDP	O7N-C7N	6.14	1.39	1.24
3	D	552	NDP	O7N-C7N	6.62	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	552	NDP	O7N-C7N	6.81	1.41	1.24
3	C	552	NDP	O7N-C7N	6.82	1.41	1.24
3	A	552	NDP	O7N-C7N	6.82	1.41	1.24
3	E	552	NDP	O7N-C7N	7.01	1.42	1.24

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	552	NDP	N3A-C2A-N1A	-12.17	119.58	128.89
3	A	552	NDP	N3A-C2A-N1A	-11.98	119.72	128.89
3	C	552	NDP	N3A-C2A-N1A	-11.48	120.11	128.89
3	B	552	NDP	N3A-C2A-N1A	-11.25	120.28	128.89
3	F	552	NDP	N3A-C2A-N1A	-10.93	120.52	128.89
3	E	552	NDP	N3A-C2A-N1A	-10.19	121.09	128.89
3	E	552	NDP	PN-O3-PA	-4.82	119.19	132.73
3	B	552	NDP	P2B-O2B-C2B	-4.00	111.98	121.56
3	D	552	NDP	C1D-N1N-C6N	-3.82	112.25	120.81
3	D	552	NDP	PN-O3-PA	-3.63	122.53	132.73
3	B	552	NDP	PN-O3-PA	-3.33	123.37	132.73
3	E	552	NDP	C1D-N1N-C6N	-3.29	113.45	120.81
3	A	552	NDP	C1D-N1N-C6N	-3.25	113.53	120.81
3	F	552	NDP	C1D-N1N-C6N	-3.23	113.59	120.81
3	A	552	NDP	PN-O3-PA	-3.19	123.77	132.73
3	C	552	NDP	PN-O3-PA	-2.88	124.65	132.73
3	B	552	NDP	C1D-N1N-C6N	-2.80	114.53	120.81
3	D	552	NDP	P2B-O2B-C2B	-2.61	115.31	121.56
3	C	552	NDP	C1D-N1N-C2N	-2.56	116.44	120.91
3	D	552	NDP	C4A-C5A-N7A	-2.51	107.17	109.48
3	B	552	NDP	C2D-C1D-N1N	-2.40	106.86	113.34
3	A	552	NDP	O3D-C3D-C4D	-2.33	104.05	111.05
3	C	552	NDP	C2D-C1D-N1N	-2.25	107.26	113.34
3	B	552	NDP	C3N-C2N-N1N	-2.07	120.17	123.14
3	C	552	NDP	C4A-C5A-N7A	-2.01	107.63	109.48
3	D	552	NDP	O2A-PA-O3	2.12	114.70	105.09
3	A	552	NDP	C1D-N1N-C2N	2.18	124.70	120.91
3	B	552	NDP	C3B-C2B-C1B	2.25	107.08	102.73
3	E	552	NDP	O4B-C1B-N9A	2.40	113.11	108.10
3	A	552	NDP	O4D-C1D-N1N	2.54	113.43	108.07
3	A	552	NDP	O2B-P2B-O1X	2.57	113.53	107.11
3	C	552	NDP	O4B-C1B-N9A	2.63	113.61	108.10
3	F	552	NDP	O2A-PA-O3	2.65	117.12	105.09
3	F	552	NDP	C1D-N1N-C2N	2.89	125.93	120.91

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	E	552	NDP	O4D-C1D-N1N	3.22	114.87	108.07
3	B	552	NDP	C4B-O4B-C1B	3.46	113.52	109.72
3	F	552	NDP	O4D-C1D-N1N	3.52	115.50	108.07
3	D	552	NDP	O4D-C1D-N1N	4.11	116.74	108.07
3	B	552	NDP	O4D-C1D-N1N	4.21	116.95	108.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 108 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	GLU	5	0
3	A	552	NDP	15	0
2	B	502	GLU	3	0
3	B	552	NDP	15	0
2	C	502	GLU	12	0
3	C	552	NDP	19	0
2	D	502	GLU	9	0
3	D	552	NDP	15	0
2	E	502	GLU	6	0
3	E	552	NDP	10	0
2	F	502	GLU	6	0
3	F	552	NDP	13	0

## 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(Å <sup>2</sup> )	Q<0.9
1	A	495/501 (98%)	0.45	46 (9%)	11 7	6, 32, 70, 126	0
1	B	495/501 (98%)	0.12	27 (5%)	29 18	6, 32, 73, 124	0
1	C	495/501 (98%)	0.33	45 (9%)	11 7	6, 38, 76, 128	0
1	D	495/501 (98%)	0.03	14 (2%)	56 44	6, 32, 68, 131	0
1	E	495/501 (98%)	0.13	25 (5%)	32 21	8, 35, 71, 120	0
1	F	495/501 (98%)	-0.06	12 (2%)	62 50	4, 31, 71, 132	0
All	All	2970/3006 (98%)	0.17	169 (5%)	27 17	4, 33, 72, 132	0

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	431	VAL	13.2
1	A	405	SER	11.7
1	A	430	ILE	11.6
1	A	429	PRO	11.2
1	A	412	SER	11.0
1	A	422	GLY	11.0
1	A	432	PRO	9.8
1	A	410	LEU	8.3
1	A	413	VAL	7.1
1	A	424	HIS	7.0
1	E	424	HIS	6.9
1	E	319	CYS	6.6
1	A	427	THR	6.4
1	A	418	GLU	6.3
1	A	411	MET	6.1
1	A	417	LEU	6.1
1	A	423	LYS	5.9
1	A	416	SER	5.7
1	A	404	ASP	5.6

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Mol	Chain	Res	Type	RSRZ
1	A	421	PHE	5.6
1	C	319	CYS	5.6
1	A	409	LEU	5.3
1	A	285	GLY	5.2
1	A	426	GLY	5.1
1	A	436	PHE	5.0
1	E	318	ASP	4.9
1	B	428	ILE	4.9
1	B	431	VAL	4.6
1	A	428	ILE	4.6
1	E	342	LYS	4.5
1	E	72	TRP	4.4
1	C	337	PRO	4.2
1	B	298	HIS	4.2
1	A	437	GLN	4.1
1	B	72	TRP	4.1
1	C	334	SER	4.0
1	D	413	VAL	4.0
1	C	365	ILE	4.0
1	A	420	LYS	4.0
1	B	427	THR	3.9
1	E	286	ILE	3.9
1	C	422	GLY	3.9
1	B	223	ILE	3.9
1	B	429	PRO	3.8
1	C	313	SER	3.7
1	A	425	GLY	3.5
1	C	272	THR	3.5
1	A	440	ILE	3.5
1	C	308	LYS	3.5
1	A	419	ARG	3.4
1	C	360	PHE	3.4
1	B	413	VAL	3.3
1	B	432	PRO	3.2
1	B	303	GLY	3.2
1	A	414	GLN	3.2
1	B	440	ILE	3.2
1	A	442	GLY	3.1
1	C	249	VAL	3.1
1	C	339	VAL	3.1
1	C	285	GLY	3.1
1	C	250	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	226	PHE	3.1
1	C	355	GLU	3.1
1	D	36	GLU	3.0
1	A	415	GLU	3.0
1	D	268	ALA	2.9
1	B	42	ARG	2.9
1	E	365	ILE	2.9
1	E	423	LYS	2.9
1	C	315	LEU	2.9
1	E	285	GLY	2.9
1	E	37	THR	2.9
1	A	408	HIS	2.8
1	F	242	PHE	2.8
1	F	416	SER	2.8
1	C	336	ALA	2.8
1	C	252	PHE	2.8
1	B	71	SER	2.7
1	A	401	TYR	2.7
1	F	426	GLY	2.7
1	B	304	PHE	2.7
1	A	286	ILE	2.7
1	A	33	LYS	2.6
1	A	36	GLU	2.6
1	E	270	CYS	2.6
1	C	321	ILE	2.6
1	B	232	TYR	2.6
1	B	407	TYR	2.6
1	C	344	ILE	2.6
1	C	35	ARG	2.6
1	F	34	THR	2.6
1	C	341	ALA	2.6
1	A	433	THR	2.6
1	E	227	ILE	2.5
1	A	441	SER	2.5
1	C	353	THR	2.5
1	A	390	ASN	2.5
1	A	34	THR	2.5
1	D	72	TRP	2.5
1	A	406	ASN	2.5
1	F	427	THR	2.5
1	F	431	VAL	2.5
1	B	434	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	465	MET	2.4
1	B	235	ILE	2.4
1	C	312	GLY	2.4
1	D	428	ILE	2.4
1	C	31	ASP	2.4
1	C	318	ASP	2.4
1	B	66	ARG	2.4
1	F	36	GLU	2.4
1	B	424	HIS	2.4
1	C	429	PRO	2.4
1	D	223	ILE	2.4
1	D	227	ILE	2.4
1	E	68	ASP	2.3
1	B	270	CYS	2.3
1	C	364	ASN	2.3
1	B	250	GLN	2.3
1	E	360	PHE	2.3
1	E	427	THR	2.3
1	C	224	GLU	2.3
1	E	139	ASN	2.3
1	A	272	THR	2.3
1	D	37	THR	2.3
1	F	420	LYS	2.3
1	E	302	LEU	2.3
1	C	303	GLY	2.3
1	B	412	SER	2.3
1	B	441	SER	2.3
1	E	413	VAL	2.3
1	A	435	GLU	2.2
1	E	313	SER	2.2
1	B	70	GLY	2.2
1	A	227	ILE	2.2
1	B	419	ARG	2.2
1	C	335	ASN	2.2
1	B	426	GLY	2.2
1	C	407	TYR	2.2
1	D	320	ASP	2.2
1	E	341	ALA	2.2
1	C	237	GLY	2.2
1	D	431	VAL	2.2
1	F	474	GLY	2.2
1	C	244	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	297	GLN	2.1
1	C	223	ILE	2.1
1	F	419	ARG	2.1
1	C	271	ILE	2.1
1	C	477	LEU	2.1
1	D	278	GLY	2.1
1	D	1	ALA	2.1
1	C	36	GLU	2.1
1	E	298	HIS	2.1
1	C	320	ASP	2.1
1	A	362	GLU	2.1
1	C	311	GLU	2.1
1	E	466	ARG	2.1
1	F	425	GLY	2.1
1	E	443	ALA	2.1
1	C	329	LYS	2.0
1	D	279	SER	2.0
1	A	300	THR	2.0
1	C	298	HIS	2.0
1	E	329	LYS	2.0
1	C	232	TYR	2.0
1	F	33	LYS	2.0
1	C	302	LEU	2.0
1	C	246	THR	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLU	D	502	10/10	0.94	0.20	0.72	11,13,16,17	0
2	GLU	C	502	10/10	0.93	0.24	0.70	16,22,28,30	0
2	GLU	A	502	10/10	0.97	0.17	0.04	9,11,14,15	0
3	NDP	A	552	48/48	0.93	0.18	-0.28	12,22,53,68	0
3	NDP	F	552	48/48	0.94	0.17	-0.32	7,18,40,52	0
3	NDP	D	552	48/48	0.94	0.18	-0.41	13,26,35,41	0
3	NDP	C	552	48/48	0.91	0.20	-0.51	23,37,50,62	0
3	NDP	B	552	48/48	0.93	0.16	-0.58	12,26,39,49	0
3	NDP	E	552	48/48	0.95	0.14	-0.95	18,34,58,77	0
2	GLU	B	502	10/10	0.96	0.14	-1.02	8,11,13,15	0
2	GLU	F	502	10/10	0.96	0.13	-1.04	6,8,11,13	0
2	GLU	E	502	10/10	0.95	0.14	-1.17	14,17,21,23	0
4	EU3	A	503	1/1	0.91	0.07	-2.08	67,67,67,67	0
4	EU3	D	503	1/1	0.99	0.09	-	65,65,65,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.