



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:04 AM GMT

PDB ID : 3KLF
Title : Crystal structure of wild-type HIV-1 Reverse Transcriptase crosslinked to a DSDNA with a bound excision product, AZTPPPPA
Authors : Tu, X.; Das, K.; Sarafianos, S.G.; Arnold, E.
Deposited on : 2009-11-07
Resolution : 3.15 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

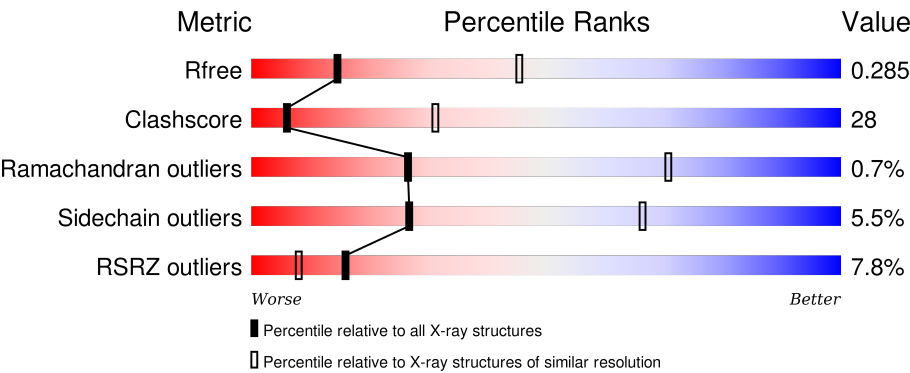
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	1112 (3.20-3.12)
Clashscore	102246	1249 (3.20-3.12)
Ramachandran outliers	100387	1222 (3.20-3.12)
Sidechain outliers	100360	1221 (3.20-3.12)
RSRZ outliers	91569	1117 (3.20-3.12)

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 >=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 <=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	557	<div><div></div><div><div></div><div>48%</div><div></div><div>46%</div><div>5%</div><div></div></div></div>
1	E	557	<div><div></div><div><div></div><div>50%</div><div></div><div>45%</div><div></div></div></div>
1	I	557	<div><div>5%</div><div><div></div><div>50%</div><div></div><div>45%</div><div></div></div></div>
1	M	557	<div><div>25%</div><div><div></div><div>48%</div><div></div><div>47%</div><div></div></div></div>
2	B	444	<div><div>3%</div><div><div></div><div>55%</div><div></div><div>36%</div><div>7%</div><div></div></div></div>

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Mol	Chain	Length	Quality of chain
2	F	444	
2	J	444	
2	N	444	
3	C	27	
3	G	27	
3	K	27	
3	O	27	
4	D	21	
4	H	21	
4	L	21	
4	P	21	

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
7	GOL	B	429	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 35440 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	0	0
			4499	2912	748	831	8			
1	E	553	Total	C	N	O	S	0	0	0
			4499	2912	748	831	8			
1	I	553	Total	C	N	O	S	0	0	0
			4499	2912	748	831	8			
1	M	553	Total	C	N	O	S	0	0	0
			4499	2912	748	831	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP P03366
A	0	VAL	-	EXPRESSION TAG	UNP P03366
A	258	CYS	GLN	ENGINEERED	UNP P03366
A	280	SER	CYS	ENGINEERED	UNP P03366
E	-1	MET	-	EXPRESSION TAG	UNP P03366
E	0	VAL	-	EXPRESSION TAG	UNP P03366
E	258	CYS	GLN	ENGINEERED	UNP P03366
E	280	SER	CYS	ENGINEERED	UNP P03366
I	-1	MET	-	EXPRESSION TAG	UNP P03366
I	0	VAL	-	EXPRESSION TAG	UNP P03366
I	258	CYS	GLN	ENGINEERED	UNP P03366
I	280	SER	CYS	ENGINEERED	UNP P03366
M	-1	MET	-	EXPRESSION TAG	UNP P03366
M	0	VAL	-	EXPRESSION TAG	UNP P03366
M	258	CYS	GLN	ENGINEERED	UNP P03366
M	280	SER	CYS	ENGINEERED	UNP P03366

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	413	Total	C	N	O	S	0	0	0
			3405	2215	564	620	6			
2	F	413	Total	C	N	O	S	0	0	0
			3405	2215	564	620	6			
2	J	413	Total	C	N	O	S	0	0	0
			3405	2215	564	620	6			
2	N	413	Total	C	N	O	S	0	0	0
			3405	2215	564	620	6			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	EXPRESSION TAG	UNP P03366
B	-14	ALA	-	EXPRESSION TAG	UNP P03366
B	-13	HIS	-	EXPRESSION TAG	UNP P03366
B	-12	HIS	-	EXPRESSION TAG	UNP P03366
B	-11	HIS	-	EXPRESSION TAG	UNP P03366
B	-10	HIS	-	EXPRESSION TAG	UNP P03366
B	-9	HIS	-	EXPRESSION TAG	UNP P03366
B	-8	HIS	-	EXPRESSION TAG	UNP P03366
B	-7	ALA	-	EXPRESSION TAG	UNP P03366
B	-6	LEU	-	EXPRESSION TAG	UNP P03366
B	-5	GLU	-	EXPRESSION TAG	UNP P03366
B	-4	VAL	-	EXPRESSION TAG	UNP P03366
B	-3	LEU	-	EXPRESSION TAG	UNP P03366
B	-2	PHE	-	EXPRESSION TAG	UNP P03366
B	-1	GLN	-	EXPRESSION TAG	UNP P03366
B	0	GLY	-	EXPRESSION TAG	UNP P03366
B	280	SER	CYS	ENGINEERED	UNP P03366
F	-15	MET	-	EXPRESSION TAG	UNP P03366
F	-14	ALA	-	EXPRESSION TAG	UNP P03366
F	-13	HIS	-	EXPRESSION TAG	UNP P03366
F	-12	HIS	-	EXPRESSION TAG	UNP P03366
F	-11	HIS	-	EXPRESSION TAG	UNP P03366
F	-10	HIS	-	EXPRESSION TAG	UNP P03366
F	-9	HIS	-	EXPRESSION TAG	UNP P03366
F	-8	HIS	-	EXPRESSION TAG	UNP P03366
F	-7	ALA	-	EXPRESSION TAG	UNP P03366
F	-6	LEU	-	EXPRESSION TAG	UNP P03366
F	-5	GLU	-	EXPRESSION TAG	UNP P03366
F	-4	VAL	-	EXPRESSION TAG	UNP P03366
F	-3	LEU	-	EXPRESSION TAG	UNP P03366
F	-2	PHE	-	EXPRESSION TAG	UNP P03366

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLN	-	EXPRESSION TAG	UNP P03366
F	0	GLY	-	EXPRESSION TAG	UNP P03366
F	280	SER	CYS	ENGINEERED	UNP P03366
J	-15	MET	-	EXPRESSION TAG	UNP P03366
J	-14	ALA	-	EXPRESSION TAG	UNP P03366
J	-13	HIS	-	EXPRESSION TAG	UNP P03366
J	-12	HIS	-	EXPRESSION TAG	UNP P03366
J	-11	HIS	-	EXPRESSION TAG	UNP P03366
J	-10	HIS	-	EXPRESSION TAG	UNP P03366
J	-9	HIS	-	EXPRESSION TAG	UNP P03366
J	-8	HIS	-	EXPRESSION TAG	UNP P03366
J	-7	ALA	-	EXPRESSION TAG	UNP P03366
J	-6	LEU	-	EXPRESSION TAG	UNP P03366
J	-5	GLU	-	EXPRESSION TAG	UNP P03366
J	-4	VAL	-	EXPRESSION TAG	UNP P03366
J	-3	LEU	-	EXPRESSION TAG	UNP P03366
J	-2	PHE	-	EXPRESSION TAG	UNP P03366
J	-1	GLN	-	EXPRESSION TAG	UNP P03366
J	0	GLY	-	EXPRESSION TAG	UNP P03366
J	280	SER	CYS	ENGINEERED	UNP P03366
N	-15	MET	-	EXPRESSION TAG	UNP P03366
N	-14	ALA	-	EXPRESSION TAG	UNP P03366
N	-13	HIS	-	EXPRESSION TAG	UNP P03366
N	-12	HIS	-	EXPRESSION TAG	UNP P03366
N	-11	HIS	-	EXPRESSION TAG	UNP P03366
N	-10	HIS	-	EXPRESSION TAG	UNP P03366
N	-9	HIS	-	EXPRESSION TAG	UNP P03366
N	-8	HIS	-	EXPRESSION TAG	UNP P03366
N	-7	ALA	-	EXPRESSION TAG	UNP P03366
N	-6	LEU	-	EXPRESSION TAG	UNP P03366
N	-5	GLU	-	EXPRESSION TAG	UNP P03366
N	-4	VAL	-	EXPRESSION TAG	UNP P03366
N	-3	LEU	-	EXPRESSION TAG	UNP P03366
N	-2	PHE	-	EXPRESSION TAG	UNP P03366
N	-1	GLN	-	EXPRESSION TAG	UNP P03366
N	0	GLY	-	EXPRESSION TAG	UNP P03366
N	280	SER	CYS	ENGINEERED	UNP P03366

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*C
P*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	23	Total	C	N	O	P	0	0	0
			473	223	95	133	22			
3	G	23	Total	C	N	O	P	0	0	0
			473	223	95	133	22			
3	K	23	Total	C	N	O	P	0	0	0
			473	223	95	133	22			
3	O	23	Total	C	N	O	P	0	0	0
			473	223	95	133	22			

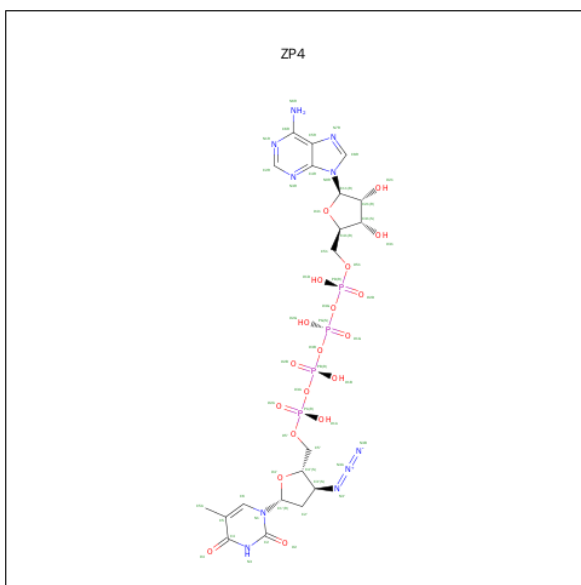
- Molecule 4 is a DNA chain called DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(2DA))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	20	Total	C	N	O	P	S	0	0	0
			406	195	72	119	19	1			
4	H	20	Total	C	N	O	P	S	0	0	0
			406	195	72	119	19	1			
4	L	20	Total	C	N	O	P	S	0	0	0
			406	195	72	119	19	1			
4	P	20	Total	C	N	O	P	S	0	0	0
			406	195	72	119	19	1			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

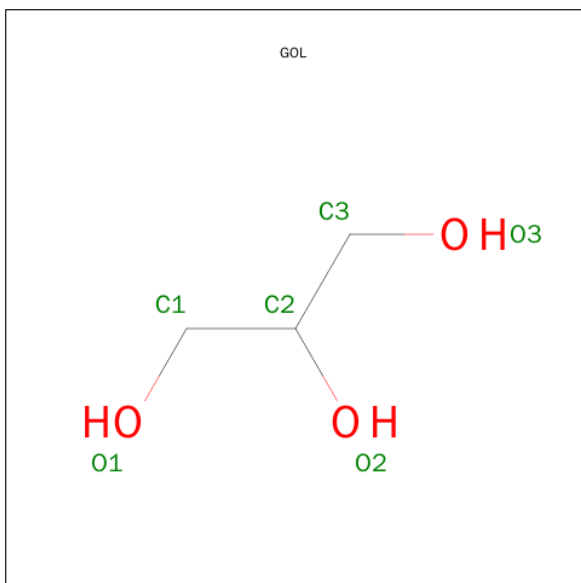
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	2	Total	Mg	0	0
			2	2		
5	A	2	Total	Mg	0	0
			2	2		
5	M	2	Total	Mg	0	0
			2	2		
5	E	2	Total	Mg	0	0
			2	2		

- Molecule 6 is [|(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL|METHOXY-HYDROXY-PHOSPHORYL|OXY-HYDROXY-PHOSPHORYL|OXY-HYDROXY-PHOSPHORYL|[(2S,3S,5R)-3-AZIDO-5-(5-METHYL-2,4-DIOXO-PYRIMIDIN-1-YL)OXOLAN-2-YL|METHYL HYDROGEN PHOSPHATE (three-letter code: ZP4) (formula: C₂₀H₂₈N₁₀O₁₉P₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	A	1	Total 53	C 20	N 10	O 19	P 4	0	0
6	E	1	Total 53	C 20	N 10	O 19	P 4	0	0
6	I	1	Total 53	C 20	N 10	O 19	P 4	0	0
6	M	1	Total 53	C 20	N 10	O 19	P 4	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			6	3	3		
7	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	12	Total	O	0	0
			12	12		
8	B	9	Total	O	0	0
			9	9		
8	E	11	Total	O	0	0
			11	11		
8	F	12	Total	O	0	0
			12	12		
8	I	10	Total	O	0	0
			10	10		
8	J	5	Total	O	0	0
			5	5		
8	M	3	Total	O	0	0
			3	3		
8	N	5	Total	O	0	0
			5	5		
8	C	1	Total	O	0	0
			1	1		
8	G	3	Total	O	0	0
			3	3		
8	K	1	Total	O	0	0
			1	1		
8	L	2	Total	O	0	0
			2	2		
8	O	2	Total	O	0	0
			2	2		

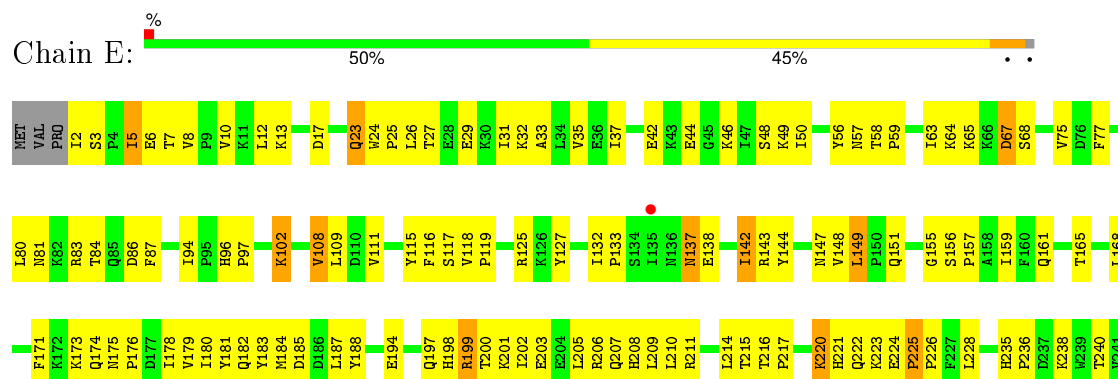
3 Residue-property plots

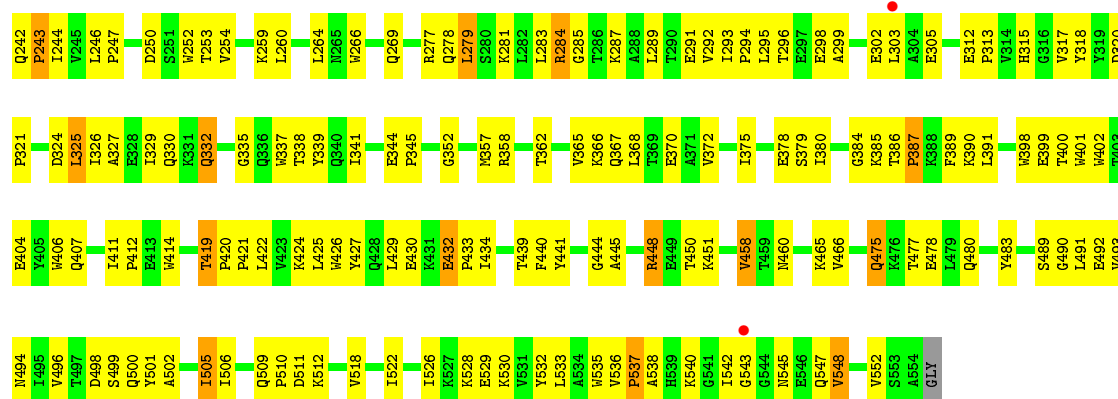
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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: Reverse transcriptase/ribonuclease H

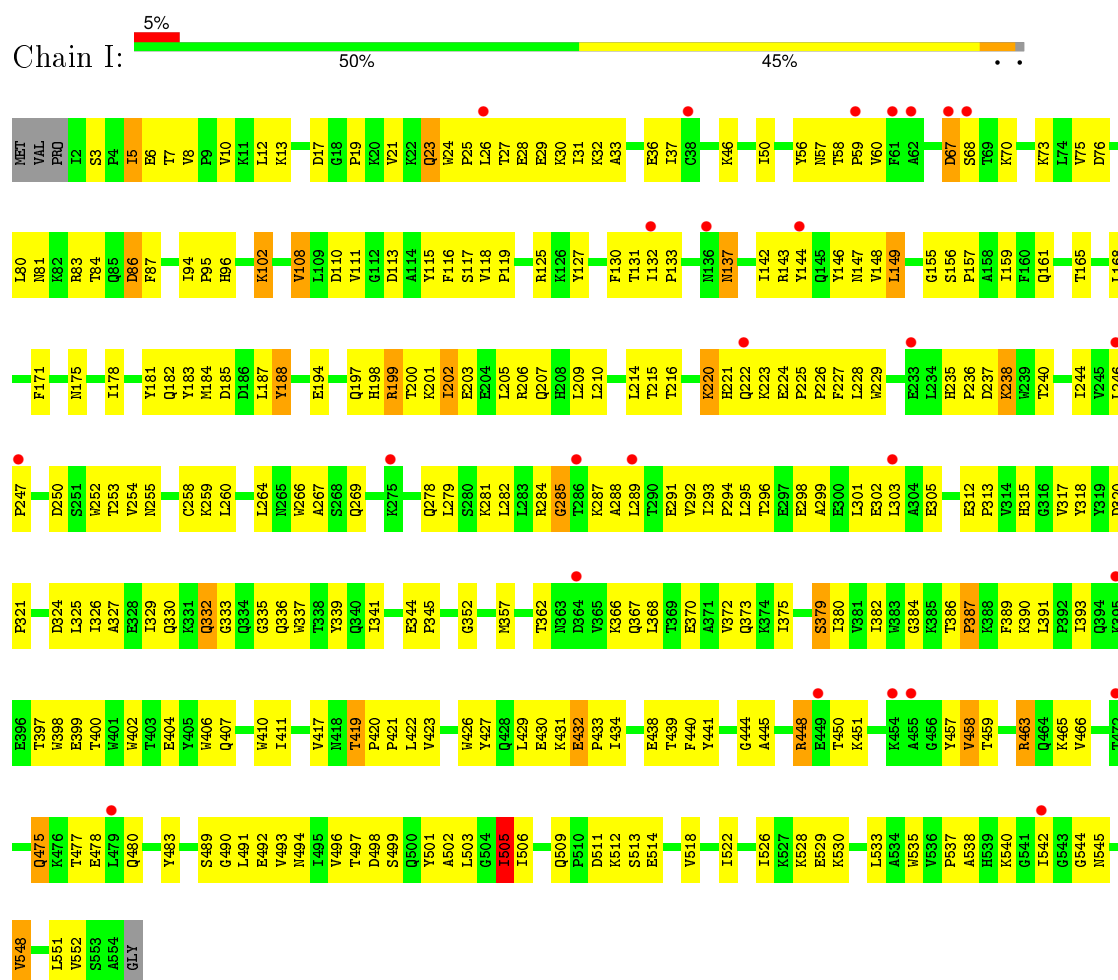


• Molecule 1: Reverse transcriptase/ribonuclease H

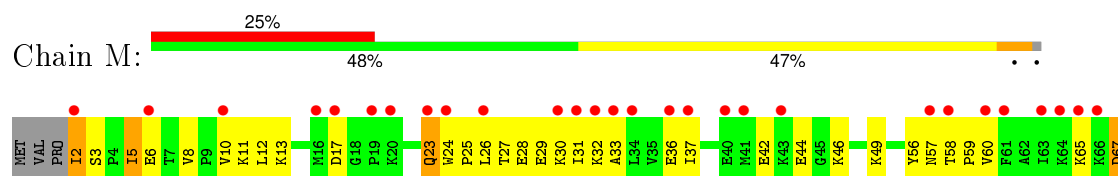


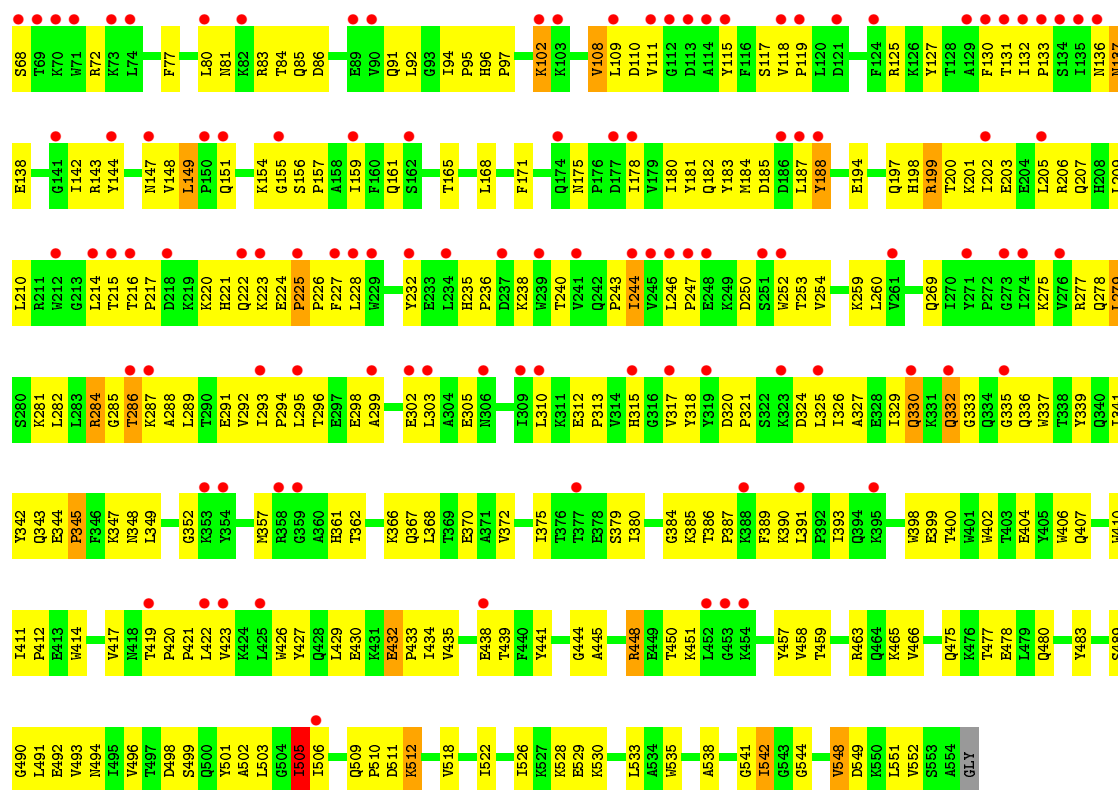


• Molecule 1: Reverse transcriptase/ribonuclease H

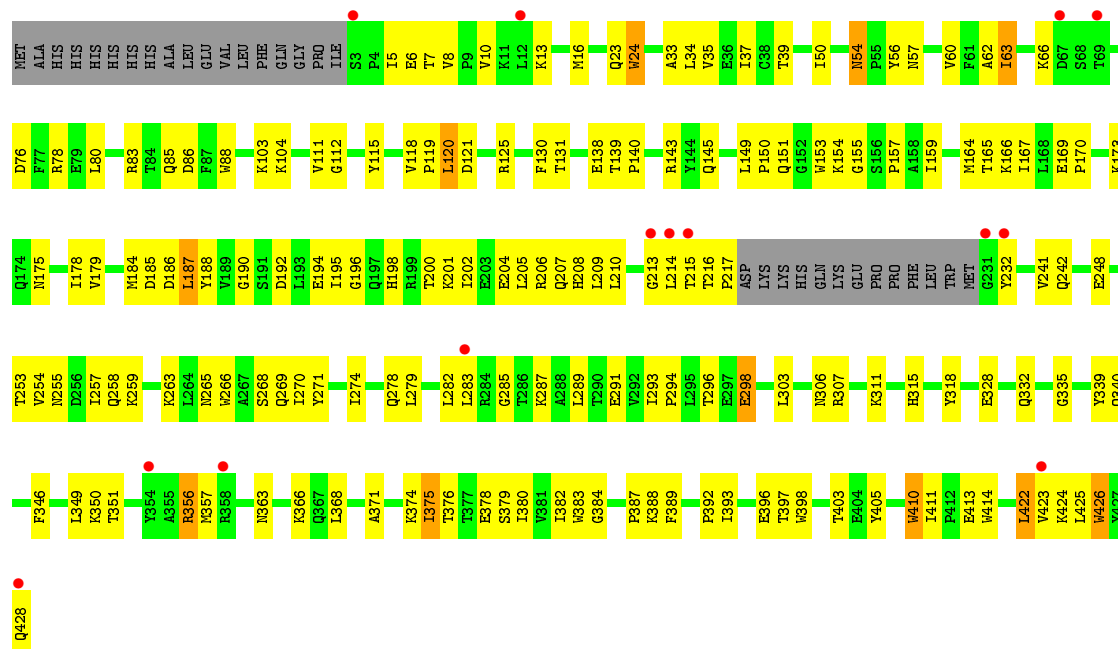


• Molecule 1: Reverse transcriptase/ribonuclease H



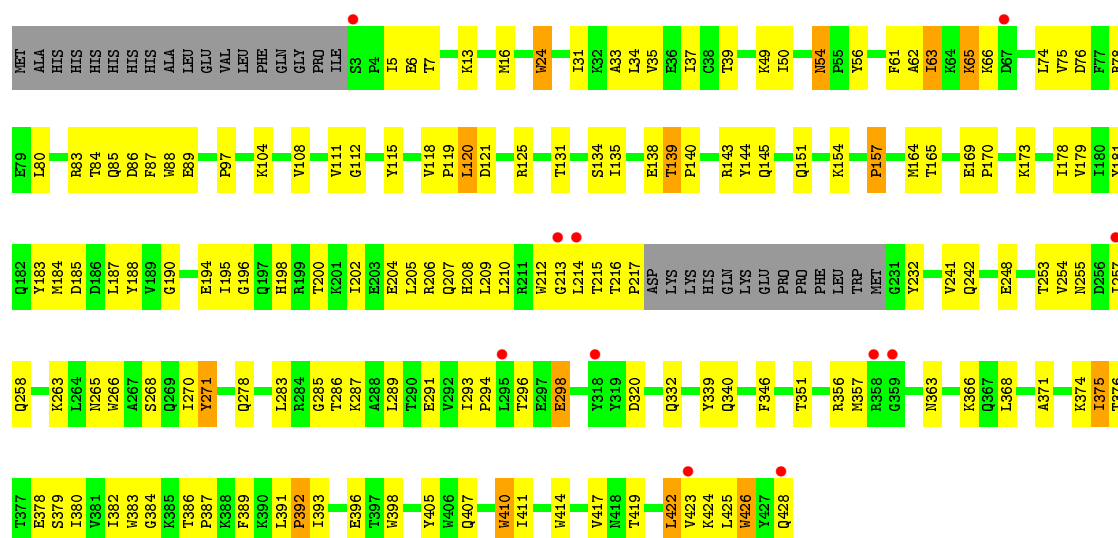


• Molecule 2: p51 RT

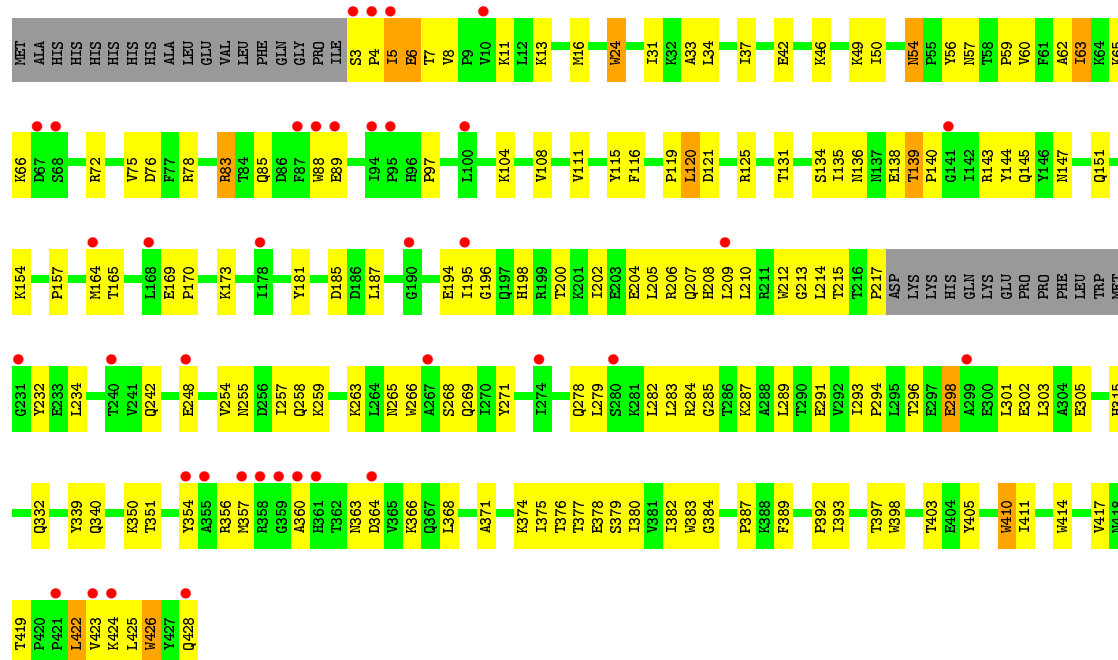


• Molecule 2: p51 RT

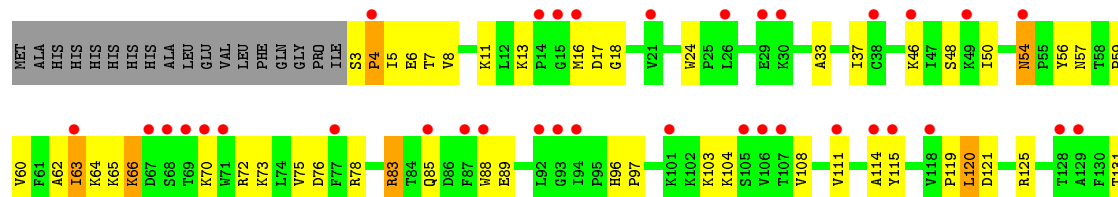


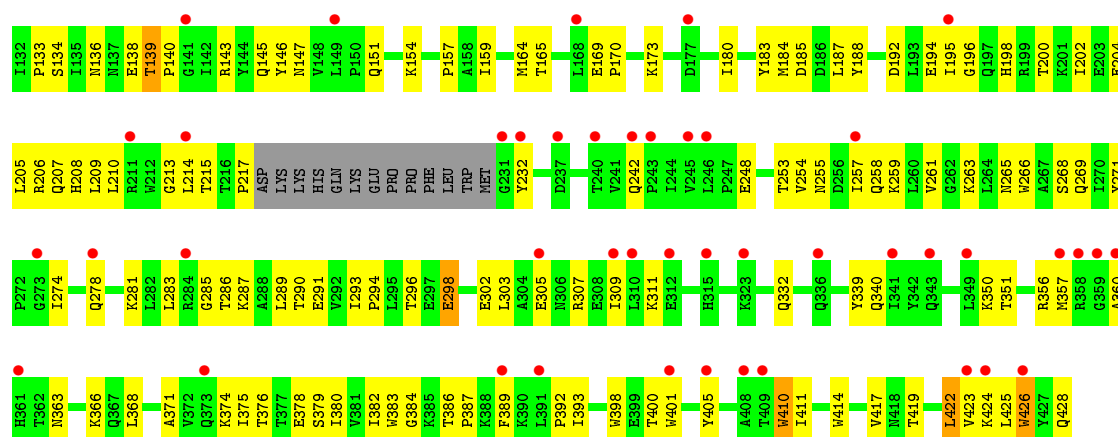


• Molecule 2: p51 RT

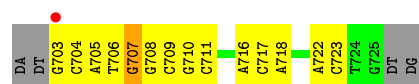


• Molecule 2: p51 RT

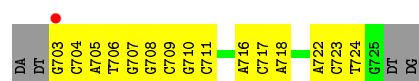




• Molecule 3: DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')



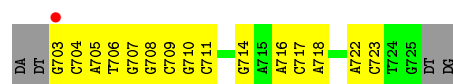
• Molecule 3: DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')



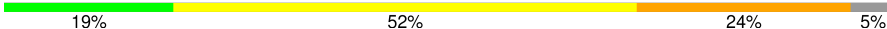
• Molecule 3: DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')



• Molecule 3: DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')




• Molecule 4: DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MR G)P*CP*GP*CP*CP*(2DA))-3')

Chain D: 



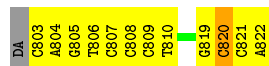
- Molecule 4: DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(2DA))-3')

Chain H: 



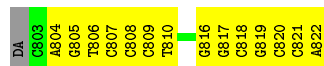
- Molecule 4: DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(2DA))-3')

Chain L: 



- Molecule 4: DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(2DA))-3')

Chain P: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.53Å 274.81Å 152.37Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	24.83 – 3.15 24.83 – 3.14	Depositor EDS
% Data completeness (in resolution range)	88.6 (24.83-3.15) 88.2 (24.83-3.14)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 3.17Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.264 , 0.288 0.260 , 0.285	Depositor DCC
R_{free} test set	1978 reflections (2.01%)	DCC
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 17.2	EDS
Estimated twinning fraction	0.359 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 98375 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	35440	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, MG, MRG, 2DA, ZP4

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	0.60	0/4616	0.69	0/6271
1	E	0.57	1/4616 (0.0%)	0.66	2/6271 (0.0%)
1	I	0.44	0/4616	0.61	0/6271
1	M	0.40	0/4616	0.60	1/6271 (0.0%)
2	B	0.67	0/3502	0.75	2/4760 (0.0%)
2	F	0.66	0/3502	0.74	1/4760 (0.0%)
2	J	0.47	0/3502	0.66	1/4760 (0.0%)
2	N	0.42	0/3502	0.64	0/4760
3	C	0.78	0/532	0.79	0/820
3	G	0.78	0/532	0.78	0/820
3	K	0.49	0/532	0.72	0/820
3	O	0.46	0/532	0.74	0/820
4	D	0.91	0/400	0.97	1/612 (0.2%)
4	H	0.90	0/400	0.87	0/612
4	L	0.59	0/400	0.78	0/612
4	P	0.50	0/400	0.77	0/612
All	All	0.55	1/36200 (0.0%)	0.68	8/49852 (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
3	C	0	1
4	D	0	5
4	H	0	2
4	L	0	1
All	All	0	9

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	378	GLU	CG-CD	5.04	1.59	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	M	286	THR	N-CA-C	5.71	126.42	111.00
2	J	65	LYS	CB-CA-C	-5.67	99.06	110.40
4	D	821	DC	O5'-P-OP1	-5.45	100.80	105.70
2	B	349	LEU	CB-CA-C	5.36	120.38	110.20
1	E	284	ARG	CB-CA-C	-5.35	99.71	110.40
2	F	65	LYS	CB-CA-C	-5.14	100.12	110.40
2	B	187	LEU	N-CA-C	-5.09	97.25	111.00
1	E	285	GLY	N-CA-C	-5.03	100.53	113.10

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	707	DG	Sidechain
4	D	810	DT	Sidechain
4	D	811	DG	Sidechain
4	D	816	DG	Sidechain
4	D	818	DC	Sidechain
4	D	820	DC	Sidechain
4	H	811	DG	Sidechain
4	H	820	DC	Sidechain
4	L	820	DC	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4499	0	4556	312	0
1	E	4499	0	4556	310	0
1	I	4499	0	4556	275	0
1	M	4499	0	4556	308	0
2	B	3405	0	3437	163	0
2	F	3405	0	3437	156	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	3405	0	3437	164	0
2	N	3405	0	3437	175	0
3	C	473	0	257	29	0
3	G	473	0	257	24	0
3	K	473	0	257	22	0
3	O	473	0	257	26	0
4	D	406	0	231	32	0
4	H	406	0	231	34	0
4	L	406	0	231	20	0
4	P	406	0	231	26	0
5	A	2	0	0	0	0
5	E	2	0	0	0	0
5	I	2	0	0	0	0
5	M	2	0	0	0	0
6	A	53	0	24	4	0
6	E	53	0	24	6	0
6	I	53	0	24	6	0
6	M	53	0	24	3	0
7	B	6	0	8	0	0
7	F	6	0	8	0	0
8	A	12	0	0	3	0
8	B	9	0	0	3	0
8	C	1	0	0	0	0
8	E	11	0	0	5	0
8	F	12	0	0	4	0
8	G	3	0	0	0	0
8	I	10	0	0	5	0
8	J	5	0	0	0	0
8	K	1	0	0	0	0
8	L	2	0	0	0	0
8	M	3	0	0	0	0
8	N	5	0	0	3	0
8	O	2	0	0	0	0
All	All	35440	0	34036	1972	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 28.

All (1972) 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:M:339:TYR:CZ	1:M:352:GLY:HA3	1.77	1.19
1:E:511:ASP:OD1	1:E:512:LYS:HG2	1.42	1.19
1:M:511:ASP:OD1	1:M:512:LYS:HG2	1.38	1.18
1:A:175:ASN:HB3	1:A:178:ILE:HD13	1.19	1.18
2:N:66:LYS:NZ	2:N:66:LYS:HB3	1.40	1.18
1:M:108:VAL:HG22	1:M:221:HIS:HB2	1.17	1.14
1:A:317:VAL:HG12	1:A:348:ASN:O	1.47	1.14
1:A:511:ASP:OD1	1:A:512:LYS:HG2	1.47	1.13
1:I:102:LYS:HD2	1:I:102:LYS:H	1.09	1.12
1:E:537:PRO:HB2	1:E:540:LYS:HB2	1.33	1.10
1:M:102:LYS:HD2	1:M:102:LYS:H	1.16	1.10
1:I:108:VAL:HG22	1:I:221:HIS:HB2	1.35	1.08
1:M:343:GLN:HG3	1:M:349:LEU:HD11	1.32	1.08
1:I:431:LYS:HA	8:I:559:HOH:O	1.53	1.07
1:A:102:LYS:HD2	1:A:102:LYS:H	1.10	1.06
1:E:175:ASN:HB3	1:E:178:ILE:HD13	1.31	1.06
1:E:102:LYS:HD2	1:E:102:LYS:H	1.18	1.06
1:M:286:THR:HG22	1:M:286:THR:O	1.46	1.06
1:A:344:GLU:HB3	1:A:345:PRO:HD2	1.34	1.05
1:I:175:ASN:HB3	1:I:178:ILE:HD13	1.34	1.04
1:M:175:ASN:HB3	1:M:178:ILE:HD13	1.34	1.04
1:E:108:VAL:HG22	1:E:221:HIS:HB2	1.07	1.03
1:I:253:THR:HG22	1:I:292:VAL:HG22	1.39	1.03
2:J:5:ILE:CG2	2:J:119:PRO:HG3	1.87	1.02
1:A:108:VAL:HG22	1:A:221:HIS:HB2	1.37	1.02
4:P:807:DC:H2''	4:P:808:DC:H5'	1.42	1.01
2:J:5:ILE:HG23	2:J:119:PRO:HG3	1.40	1.00
1:M:344:GLU:HB3	1:M:345:PRO:HD2	1.43	1.00
1:A:344:GLU:HB3	1:A:345:PRO:CD	1.91	0.99
2:N:66:LYS:HZ3	2:N:66:LYS:HB3	1.17	0.98
1:I:511:ASP:OD1	1:I:512:LYS:HG2	1.63	0.98
1:M:253:THR:HG22	1:M:292:VAL:HG22	1.45	0.97
2:N:66:LYS:CB	2:N:66:LYS:NZ	2.30	0.94
4:H:807:DC:H2''	4:H:808:DC:H5'	1.49	0.94
1:I:235:HIS:HB3	1:I:236:PRO:HD2	1.48	0.94
1:M:344:GLU:HB2	1:M:347:LYS:HB2	1.46	0.94
1:M:344:GLU:HB3	1:M:345:PRO:CD	1.96	0.94
1:E:235:HIS:HB3	1:E:236:PRO:HD2	1.49	0.94
1:E:439:THR:HG21	2:F:289:LEU:HD13	1.46	0.94
1:E:532:TYR:HA	8:E:564:HOH:O	1.66	0.93
3:G:707:DG:H2''	3:G:708:DG:H5'	1.51	0.92
1:M:342:TYR:CD2	1:M:344:GLU:O	2.23	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:THR:HG21	2:B:289:LEU:HD13	1.49	0.92
3:C:707:DG:H2"	3:C:708:DG:H5'	1.52	0.91
1:E:537:PRO:CB	1:E:540:LYS:HB2	1.99	0.91
1:E:174:GLN:HB2	8:E:563:HOH:O	1.70	0.91
1:M:434:ILE:HD12	1:M:530:LYS:HE2	1.53	0.90
1:A:518:VAL:O	1:A:522:ILE:HG12	1.71	0.90
2:J:13:LYS:HB2	2:J:16:MET:HG3	1.52	0.90
1:E:430:GLU:HG3	1:E:434:ILE:HD11	1.54	0.90
1:E:108:VAL:HG22	1:E:221:HIS:CB	2.00	0.90
2:N:66:LYS:HZ2	2:N:66:LYS:HB3	1.18	0.89
4:D:806:DT:H2"	4:D:807:DC:C5'	2.01	0.89
1:E:253:THR:HG22	1:E:292:VAL:HG22	1.54	0.89
1:A:235:HIS:HB3	1:A:236:PRO:HD2	1.53	0.89
1:E:317:VAL:HG22	1:E:318:TYR:H	1.38	0.89
1:A:223:LYS:O	1:A:223:LYS:HG2	1.73	0.88
4:D:806:DT:H2"	4:D:807:DC:H5"	1.55	0.88
1:I:430:GLU:HG3	1:I:434:ILE:HD11	1.56	0.88
2:N:422:LEU:HG	2:N:426:TRP:HZ2	1.39	0.88
1:E:518:VAL:O	1:E:522:ILE:HG12	1.74	0.87
4:L:807:DC:H2"	4:L:808:DC:H5'	1.54	0.87
2:J:422:LEU:HG	2:J:426:TRP:HZ2	1.39	0.87
1:M:235:HIS:HB3	1:M:236:PRO:HD2	1.54	0.87
1:A:317:VAL:HG13	1:A:349:LEU:HG	1.57	0.87
1:A:430:GLU:HG3	1:A:434:ILE:HD11	1.55	0.87
1:I:518:VAL:O	1:I:522:ILE:HG12	1.74	0.87
2:B:422:LEU:HG	2:B:426:TRP:HZ2	1.39	0.86
1:E:458:VAL:CG1	1:E:548:VAL:HG22	2.05	0.86
1:E:108:VAL:CG2	1:E:221:HIS:HB2	2.01	0.86
1:A:458:VAL:CG1	1:A:548:VAL:HG22	2.06	0.86
1:M:430:GLU:HG3	1:M:434:ILE:HD11	1.58	0.86
1:A:317:VAL:O	1:A:349:LEU:HD23	1.75	0.86
3:K:707:DG:H2"	3:K:708:DG:H5'	1.58	0.86
1:M:343:GLN:HG3	1:M:349:LEU:CD1	2.04	0.85
2:F:169:GLU:HG3	2:F:173:LYS:HE2	1.55	0.85
3:G:705:DA:H2"	3:G:706:DT:H5'	1.58	0.85
2:B:33:ALA:O	2:B:37:ILE:HG12	1.75	0.85
1:M:511:ASP:OD1	1:M:512:LYS:CG	2.24	0.85
4:D:807:DC:H2"	4:D:808:DC:H5'	1.56	0.85
2:B:76:ASP:OD1	2:B:78:ARG:HB2	1.75	0.85
1:E:420:PRO:HA	1:E:422:LEU:HD22	1.59	0.84
3:C:705:DA:H2"	3:C:706:DT:H5'	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:TYR:CD2	1:A:344:GLU:O	2.30	0.84
3:O:707:DG:H2''	3:O:708:DG:H5'	1.59	0.84
1:M:518:VAL:O	1:M:522:ILE:HG12	1.77	0.84
1:E:157:PRO:O	1:E:161:GLN:HG3	1.77	0.84
2:N:76:ASP:OD1	2:N:78:ARG:HB2	1.78	0.84
1:I:102:LYS:HD2	1:I:102:LYS:N	1.90	0.84
3:O:705:DA:H2''	3:O:706:DT:H5'	1.60	0.84
2:F:33:ALA:O	2:F:37:ILE:HG12	1.78	0.84
2:N:33:ALA:O	2:N:37:ILE:HG12	1.77	0.83
1:E:429:LEU:HD13	1:E:533:LEU:HD13	1.59	0.83
3:G:710:DG:H2''	3:G:711:DC:H5'	1.59	0.83
1:E:537:PRO:HB2	1:E:540:LYS:CB	2.08	0.83
1:E:174:GLN:CB	8:E:563:HOH:O	2.25	0.83
1:M:223:LYS:HG2	1:M:223:LYS:O	1.78	0.83
1:E:223:LYS:HG2	1:E:223:LYS:O	1.79	0.82
2:J:33:ALA:O	2:J:37:ILE:HG12	1.78	0.82
2:F:422:LEU:HG	2:F:426:TRP:HZ2	1.44	0.82
1:I:31:ILE:HD12	1:I:133:PRO:HG2	1.61	0.82
1:A:441:TYR:CD2	1:A:544:GLY:HA3	2.14	0.82
1:M:108:VAL:HG22	1:M:221:HIS:CB	2.06	0.82
1:M:286:THR:CG2	1:M:286:THR:O	2.22	0.82
2:B:169:GLU:HG3	2:B:173:LYS:HE2	1.61	0.82
1:M:478:GLU:HG2	1:M:499:SER:HB2	1.60	0.82
3:K:705:DA:H2''	3:K:706:DT:H5'	1.61	0.81
1:M:501:TYR:CE1	1:M:505:ILE:HD11	2.15	0.81
1:A:344:GLU:HB2	1:A:347:LYS:HB2	1.61	0.81
4:H:820:DC:H2''	4:H:821:DC:H5'	1.61	0.81
2:J:76:ASP:OD1	2:J:78:ARG:HB2	1.80	0.81
2:N:254:VAL:HG22	2:N:293:ILE:HD11	1.62	0.81
3:C:708:DG:H2'	3:C:709:DC:C6	2.16	0.81
2:N:13:LYS:HB2	2:N:16:MET:HG3	1.63	0.81
1:M:108:VAL:HG21	1:M:221:HIS:HD2	1.45	0.81
1:A:317:VAL:HG22	1:A:318:TYR:H	1.46	0.81
1:M:65:LYS:HD3	6:M:823:ZP4:O2D	1.81	0.80
2:N:111:VAL:HG11	2:N:187:LEU:HD12	1.64	0.80
1:I:441:TYR:CD2	1:I:544:GLY:HA3	2.16	0.80
2:J:6:GLU:O	2:J:6:GLU:HG3	1.81	0.80
2:F:151:GLN:HB3	2:F:185:ASP:OD2	1.82	0.80
2:F:50:ILE:HD13	2:F:145:GLN:HB3	1.63	0.80
2:B:54:ASN:C	2:B:54:ASN:HD22	1.86	0.80
3:O:708:DG:H2'	3:O:709:DC:C6	2.17	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:819:DG:H2'	4:L:820:DC:H6	1.47	0.80
1:M:317:VAL:HG13	1:M:349:LEU:HD23	1.63	0.79
1:E:458:VAL:HG12	1:E:548:VAL:HG22	1.63	0.79
2:B:13:LYS:HD3	2:B:86:ASP:HB2	1.64	0.79
1:E:215:THR:HG22	1:E:217:PRO:HD3	1.63	0.79
2:J:332:GLN:HG3	2:J:428:GLN:HG3	1.65	0.79
1:I:253:THR:HA	1:I:292:VAL:HA	1.64	0.79
1:E:434:ILE:HD12	1:E:530:LYS:HE2	1.63	0.79
2:N:371:ALA:O	2:N:375:ILE:HG12	1.83	0.79
1:A:137:ASN:N	1:A:137:ASN:HD22	1.79	0.79
1:A:429:LEU:HD13	1:A:533:LEU:HD13	1.63	0.79
1:M:31:ILE:HD12	1:M:133:PRO:HG2	1.63	0.79
1:M:293:ILE:HG13	1:M:294:PRO:HD2	1.65	0.79
1:E:109:LEU:CD2	1:E:220:LYS:HD3	2.13	0.78
1:A:253:THR:HG22	1:A:292:VAL:HG22	1.63	0.78
3:G:708:DG:H2'	3:G:709:DC:C6	2.19	0.78
1:A:215:THR:HG22	1:A:217:PRO:HD3	1.66	0.78
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.66	0.78
1:I:157:PRO:O	1:I:161:GLN:HG3	1.83	0.78
1:I:362:THR:HG22	1:I:366:LYS:HE2	1.66	0.78
2:B:332:GLN:HE22	2:B:425:LEU:HD13	1.47	0.78
2:J:169:GLU:HG3	2:J:173:LYS:HE2	1.64	0.78
2:B:194:GLU:OE2	2:B:195:ILE:HG22	1.84	0.78
1:A:109:LEU:N	1:A:109:LEU:HD12	1.99	0.77
1:E:109:LEU:CD2	1:E:220:LYS:CD	2.62	0.77
1:M:157:PRO:O	1:M:161:GLN:HG3	1.84	0.77
2:B:13:LYS:HB2	2:B:16:MET:HG3	1.66	0.77
3:C:710:DG:H2''	3:C:711:DC:H5'	1.66	0.77
1:E:24:TRP:CZ2	3:G:704:DC:H5'	2.20	0.77
1:I:5:ILE:HD12	1:I:6:GLU:N	1.99	0.77
1:I:439:THR:HG21	2:J:289:LEU:HD13	1.65	0.77
1:E:137:ASN:HD22	1:E:137:ASN:N	1.80	0.77
2:B:54:ASN:ND2	2:B:56:TYR:H	1.82	0.77
3:G:709:DC:H2'	3:G:710:DG:H8	1.50	0.76
4:D:806:DT:C2'	4:D:807:DC:H5''	2.15	0.76
3:O:710:DG:H2''	3:O:711:DC:H5'	1.67	0.76
2:J:265:ASN:O	2:J:268:SER:HB3	1.84	0.76
1:A:317:VAL:HG22	1:A:318:TYR:N	2.00	0.76
1:A:458:VAL:HG12	1:A:548:VAL:HG22	1.67	0.76
2:F:13:LYS:HB2	2:F:16:MET:HG3	1.68	0.76
2:F:332:GLN:HG3	2:F:428:GLN:HG3	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:368:LEU:HD11	2:F:392:PRO:HD2	1.67	0.76
1:E:317:VAL:HG22	1:E:318:TYR:N	1.99	0.76
1:A:157:PRO:O	1:A:161:GLN:HG3	1.86	0.75
1:M:317:VAL:HG22	1:M:318:TYR:H	1.49	0.75
1:A:102:LYS:HD2	1:A:102:LYS:N	1.95	0.75
1:A:96:HIS:HE2	1:A:269:GLN:HE21	1.34	0.75
1:A:7:THR:HG22	1:A:119:PRO:HB2	1.67	0.75
2:N:169:GLU:HG3	2:N:173:LYS:HE2	1.66	0.75
4:H:819:DG:H2'	4:H:820:DC:H6	1.52	0.75
4:H:806:DT:H2''	4:H:807:DC:C5'	2.16	0.75
1:I:102:LYS:CD	1:I:102:LYS:H	1.96	0.74
1:I:434:ILE:HD12	1:I:530:LYS:HE2	1.67	0.74
2:N:111:VAL:HG11	2:N:187:LEU:CD1	2.17	0.74
1:M:125:ARG:HD3	1:M:147:ASN:HA	1.68	0.74
2:N:254:VAL:HG23	2:N:291:GLU:O	1.87	0.74
2:F:76:ASP:OD1	2:F:78:ARG:HB2	1.87	0.74
2:J:5:ILE:HG21	2:J:119:PRO:HG3	1.69	0.74
3:O:709:DC:H2'	3:O:710:DG:H8	1.53	0.74
2:J:254:VAL:HG23	2:J:291:GLU:O	1.88	0.74
1:A:165:THR:HG21	2:B:140:PRO:HG2	1.70	0.74
1:E:478:GLU:HG2	1:E:499:SER:HB2	1.70	0.74
1:I:429:LEU:HD13	1:I:533:LEU:HD13	1.69	0.74
2:N:378:GLU:O	2:N:382:ILE:HG12	1.87	0.74
3:K:710:DG:H2''	3:K:711:DC:H5'	1.69	0.74
1:A:125:ARG:NH1	1:A:147:ASN:HB3	2.03	0.74
1:M:420:PRO:HA	1:M:422:LEU:HD22	1.70	0.73
1:A:293:ILE:HG13	1:A:294:PRO:HD2	1.68	0.73
3:K:708:DG:H2'	3:K:709:DC:C6	2.23	0.73
2:B:54:ASN:HD22	2:B:56:TYR:H	1.34	0.73
4:L:819:DG:H2'	4:L:820:DC:C6	2.24	0.73
2:J:371:ALA:O	2:J:375:ILE:HG12	1.88	0.73
2:F:371:ALA:O	2:F:375:ILE:HG12	1.89	0.73
1:M:165:THR:HG22	1:M:182:GLN:NE2	2.02	0.73
2:J:54:ASN:C	2:J:54:ASN:HD22	1.91	0.73
1:E:253:THR:HA	1:E:292:VAL:HA	1.70	0.73
1:E:548:VAL:O	1:E:552:VAL:HG22	1.88	0.73
2:B:254:VAL:HG23	2:B:291:GLU:O	1.88	0.73
1:A:318:TYR:C	1:A:349:LEU:HD21	2.09	0.73
1:E:475:GLN:HE21	4:H:809:DC:H5''	1.53	0.73
4:P:806:DT:H2''	4:P:807:DC:C5'	2.18	0.73
2:F:54:ASN:HD22	2:F:54:ASN:C	1.91	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:289:LEU:H	1:I:289:LEU:HD12	1.53	0.73
1:M:137:ASN:HD22	1:M:137:ASN:N	1.87	0.73
1:M:362:THR:HG22	1:M:366:LYS:HE2	1.69	0.73
1:E:109:LEU:HD23	1:E:220:LYS:HD3	1.69	0.73
2:J:378:GLU:O	2:J:382:ILE:HG12	1.89	0.73
1:E:108:VAL:HG21	1:E:221:HIS:HD2	1.52	0.72
2:J:254:VAL:HG22	2:J:293:ILE:HD11	1.70	0.72
1:I:317:VAL:HG22	1:I:318:TYR:H	1.54	0.72
1:M:429:LEU:HD13	1:M:533:LEU:HD13	1.72	0.72
1:I:165:THR:HG21	2:J:140:PRO:HG2	1.70	0.72
1:A:420:PRO:HA	1:A:422:LEU:HD22	1.70	0.72
1:M:296:THR:HG23	1:M:299:ALA:H	1.53	0.72
2:F:378:GLU:O	2:F:382:ILE:HG12	1.90	0.72
2:J:7:THR:HG22	2:J:119:PRO:HG2	1.72	0.71
1:I:223:LYS:HG2	1:I:223:LYS:O	1.89	0.71
1:E:296:THR:HG23	1:E:299:ALA:H	1.54	0.71
2:F:13:LYS:HD3	2:F:86:ASP:HB2	1.71	0.71
2:F:254:VAL:HG22	2:F:293:ILE:HD11	1.73	0.71
1:M:463:ARG:HH11	1:M:463:ARG:HG2	1.55	0.71
2:B:332:GLN:NE2	2:B:425:LEU:HD13	2.04	0.71
2:N:54:ASN:HD22	2:N:56:TYR:H	1.38	0.71
2:J:104:LYS:HD3	2:J:104:LYS:O	1.89	0.71
3:K:709:DC:H2'	3:K:710:DG:H8	1.56	0.71
2:F:254:VAL:O	2:F:258:GLN:HG3	1.90	0.71
1:A:327:ALA:HB2	1:A:341:ILE:HG13	1.72	0.71
1:A:426:TRP:HB3	1:A:526:ILE:HD12	1.71	0.71
2:N:265:ASN:O	2:N:268:SER:HB3	1.90	0.71
1:I:137:ASN:N	1:I:137:ASN:HD22	1.88	0.71
2:N:5:ILE:CG2	2:N:119:PRO:HG3	2.21	0.71
1:I:125:ARG:HD3	1:I:147:ASN:HA	1.72	0.71
2:F:7:THR:HG22	2:F:119:PRO:HG2	1.71	0.71
1:A:432:GLU:HG3	1:A:433:PRO:HD2	1.73	0.71
2:B:200:THR:O	2:B:204:GLU:HG3	1.91	0.71
2:F:194:GLU:OE2	2:F:195:ILE:HG22	1.91	0.70
2:B:378:GLU:O	2:B:382:ILE:HG12	1.90	0.70
1:M:108:VAL:HG21	1:M:221:HIS:CD2	2.26	0.70
1:A:445:ALA:N	1:A:477:THR:HG21	2.06	0.70
1:A:24:TRP:CH2	3:C:704:DC:H5'	2.26	0.70
1:I:246:LEU:HD12	1:I:246:LEU:H	1.56	0.70
2:N:66:LYS:HZ3	2:N:66:LYS:CB	2.00	0.70
4:H:806:DT:H2''	4:H:807:DC:H5''	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:165:THR:HG22	1:I:182:GLN:NE2	2.05	0.70
2:B:265:ASN:O	2:B:268:SER:HB3	1.92	0.70
2:F:254:VAL:HG23	2:F:291:GLU:O	1.91	0.70
1:E:165:THR:HG21	2:F:140:PRO:HG2	1.72	0.70
4:L:806:DT:H2''	4:L:807:DC:H5'	1.74	0.70
2:F:265:ASN:O	2:F:268:SER:HB3	1.92	0.70
1:E:260:LEU:O	1:E:264:LEU:HG	1.91	0.69
4:L:809:DC:H1'	4:L:810:DT:H5'	1.74	0.69
1:E:165:THR:HG22	1:E:182:GLN:NE2	2.07	0.69
1:I:420:PRO:HA	1:I:422:LEU:HD22	1.74	0.69
1:M:339:TYR:CE1	1:M:352:GLY:HA3	2.26	0.69
1:A:24:TRP:CZ2	3:C:704:DC:H5'	2.26	0.69
2:J:60:VAL:HG12	2:J:75:VAL:HG22	1.75	0.69
1:I:181:TYR:CD2	2:J:138:GLU:HA	2.27	0.69
3:G:709:DC:H2'	3:G:710:DG:C8	2.28	0.69
1:E:339:TYR:CZ	1:E:352:GLY:HA3	2.28	0.69
1:I:296:THR:HG23	1:I:299:ALA:H	1.56	0.69
1:E:108:VAL:HG21	1:E:221:HIS:CD2	2.28	0.69
1:I:445:ALA:N	1:I:477:THR:HG21	2.07	0.69
1:I:458:VAL:CG1	1:I:548:VAL:HG22	2.23	0.69
1:A:492:GLU:OE2	1:A:530:LYS:HD3	1.93	0.69
3:O:709:DC:H2'	3:O:710:DG:C8	2.28	0.69
1:A:244:ILE:O	1:A:244:ILE:HG13	1.92	0.69
1:A:289:LEU:HD12	1:A:289:LEU:H	1.58	0.69
1:A:94:ILE:CD1	3:C:708:DG:H21	2.06	0.69
4:L:806:DT:H2''	4:L:807:DC:C5'	2.23	0.69
1:M:458:VAL:HG12	1:M:548:VAL:HG22	1.74	0.69
1:E:125:ARG:HD3	1:E:147:ASN:HA	1.75	0.69
1:E:125:ARG:NH1	1:E:147:ASN:HB3	2.08	0.69
2:N:104:LYS:HD3	2:N:104:LYS:O	1.92	0.69
1:M:240:THR:HG22	1:M:315:HIS:HA	1.74	0.69
1:I:492:GLU:OE2	1:I:530:LYS:HD3	1.93	0.68
1:A:434:ILE:HD12	1:A:530:LYS:HE2	1.74	0.68
2:N:50:ILE:HD13	2:N:145:GLN:HB3	1.75	0.68
1:I:7:THR:HG22	1:I:119:PRO:HB2	1.74	0.68
1:A:287:LYS:NZ	1:A:293:ILE:HD12	2.08	0.68
1:A:25:PRO:HD2	3:C:703:DG:N2	2.08	0.68
2:N:151:GLN:HB3	2:N:185:ASP:OD2	1.93	0.68
1:I:339:TYR:CZ	1:I:352:GLY:HA3	2.28	0.68
1:E:132:ILE:HD11	1:E:142:ILE:CD1	2.24	0.68
3:C:709:DC:H2'	3:C:710:DG:H8	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:806:DT:H5'	4:D:806:DT:H6	1.58	0.68
1:A:548:VAL:O	1:A:552:VAL:HG22	1.92	0.68
4:P:806:DT:H2''	4:P:807:DC:H5''	1.75	0.68
1:I:206:ARG:HG3	1:I:216:THR:HG21	1.75	0.68
1:I:426:TRP:HB3	1:I:526:ILE:HD12	1.75	0.68
1:A:246:LEU:H	1:A:246:LEU:HD12	1.58	0.68
1:A:94:ILE:HD11	3:C:708:DG:H21	1.58	0.68
2:B:206:ARG:O	2:B:210:LEU:HD13	1.93	0.68
2:B:151:GLN:HB3	2:B:185:ASP:OD2	1.94	0.68
1:A:24:TRP:CE3	3:C:703:DG:H1'	2.28	0.67
2:B:85:GLN:HA	2:B:88:TRP:CE2	2.29	0.67
1:M:286:THR:OG1	3:O:714:DG:H4'	1.93	0.67
3:C:706:DT:H2'	3:C:707:DG:C8	2.29	0.67
1:M:56:TYR:O	1:M:143:ARG:NH2	2.27	0.67
2:B:371:ALA:O	2:B:375:ILE:HG12	1.94	0.67
1:E:108:VAL:O	1:E:108:VAL:CG2	2.43	0.67
2:F:332:GLN:HE22	2:F:425:LEU:HD13	1.59	0.67
1:I:207:GLN:HA	1:I:210:LEU:HD12	1.76	0.67
1:E:439:THR:HG21	2:F:289:LEU:CD1	2.24	0.67
2:F:54:ASN:HD22	2:F:56:TYR:H	1.43	0.67
1:M:445:ALA:N	1:M:477:THR:HG21	2.10	0.67
2:B:209:LEU:HD22	2:B:214:LEU:HD12	1.77	0.67
1:I:96:HIS:HE2	1:I:269:GLN:HE21	1.43	0.67
4:H:819:DG:H2'	4:H:820:DC:C6	2.29	0.67
2:N:254:VAL:O	2:N:258:GLN:HG3	1.95	0.67
1:E:493:VAL:HG12	1:E:494:ASN:N	2.10	0.67
4:D:806:DT:H2''	4:D:807:DC:H5'	1.74	0.66
2:N:215:THR:HG22	2:N:217:PRO:HD3	1.77	0.66
4:D:818:DC:H2''	4:D:819:DG:H5'	1.77	0.66
2:F:108:VAL:N	2:F:232:TYR:OH	2.28	0.66
1:M:207:GLN:HA	1:M:210:LEU:HD12	1.77	0.66
1:M:246:LEU:HD12	1:M:246:LEU:H	1.60	0.66
1:I:115:TYR:CD2	6:I:823:ZP4:H2'A	2.30	0.66
1:A:25:PRO:HD2	3:C:703:DG:C2	2.30	0.66
2:B:318:TYR:HB3	8:B:438:HOH:O	1.95	0.66
1:E:102:LYS:H	1:E:102:LYS:CD	2.00	0.66
4:P:807:DC:H2''	4:P:808:DC:C5'	2.23	0.66
2:F:54:ASN:ND2	2:F:56:TYR:H	1.94	0.66
1:M:492:GLU:OE2	1:M:530:LYS:HD3	1.95	0.66
4:P:820:DC:H2''	4:P:821:DC:H5'	1.78	0.66
1:M:317:VAL:HG13	1:M:349:LEU:CD2	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:54:ASN:HD22	2:N:54:ASN:C	1.98	0.66
1:A:326:ILE:HG21	1:A:390:LYS:HE2	1.77	0.66
2:B:263:LYS:HB2	2:B:423:VAL:HG11	1.77	0.66
2:N:332:GLN:HG3	2:N:428:GLN:HG3	1.76	0.66
1:A:357:MET:HG2	1:A:367:GLN:NE2	2.11	0.66
1:M:253:THR:HA	1:M:292:VAL:HA	1.76	0.66
2:J:170:PRO:HG2	2:J:208:HIS:CE1	2.31	0.66
1:A:296:THR:HG23	1:A:299:ALA:H	1.58	0.66
1:E:439:THR:CG2	2:F:289:LEU:HD13	2.24	0.66
3:K:709:DC:H2'	3:K:710:DG:C8	2.31	0.66
1:I:228:LEU:HD12	6:I:823:ZP4:N1R	2.10	0.66
1:A:108:VAL:O	1:A:108:VAL:CG2	2.44	0.66
2:J:54:ASN:HD22	2:J:56:TYR:H	1.44	0.66
2:F:206:ARG:O	2:F:210:LEU:HD13	1.96	0.66
1:E:246:LEU:H	1:E:246:LEU:HD12	1.59	0.66
1:A:406:TRP:HD1	1:A:407:GLN:HE21	1.45	0.66
1:M:317:VAL:HG22	1:M:318:TYR:N	2.10	0.65
1:I:229:TRP:HA	8:I:563:HOH:O	1.95	0.65
1:A:541:GLY:O	1:A:542:ILE:O	2.13	0.65
2:B:254:VAL:HG22	2:B:293:ILE:HD11	1.77	0.65
2:J:423:VAL:HB	2:J:426:TRP:CD1	2.31	0.65
2:J:254:VAL:O	2:J:258:GLN:HG3	1.97	0.65
1:A:181:TYR:CD2	2:B:138:GLU:HA	2.32	0.65
1:E:432:GLU:HG3	1:E:433:PRO:HD2	1.79	0.65
1:M:94:ILE:CD1	3:O:708:DG:H21	2.09	0.65
1:A:12:LEU:HD11	1:A:127:TYR:CZ	2.32	0.65
1:M:125:ARG:NH1	1:M:147:ASN:HB3	2.11	0.65
1:I:501:TYR:CE1	1:I:505:ILE:HD11	2.32	0.65
1:I:115:TYR:CE2	6:I:823:ZP4:H2'A	2.32	0.65
1:E:7:THR:HG22	1:E:119:PRO:HB2	1.79	0.65
2:F:215:THR:HG22	2:F:217:PRO:HD3	1.77	0.65
2:B:63:ILE:H	2:B:63:ILE:HD13	1.60	0.65
2:F:154:LYS:O	2:F:157:PRO:HD2	1.97	0.65
4:P:818:DC:H2''	4:P:819:DG:H5'	1.78	0.65
1:M:17:ASP:O	1:M:83:ARG:HD3	1.96	0.65
2:N:206:ARG:O	2:N:210:LEU:HD13	1.95	0.65
2:J:257:ILE:HG23	2:J:283:LEU:HD21	1.78	0.65
2:J:13:LYS:CB	2:J:16:MET:HG3	2.25	0.65
2:J:423:VAL:HB	2:J:426:TRP:NE1	2.12	0.65
2:J:215:THR:HG22	2:J:217:PRO:HD3	1.78	0.65
2:F:423:VAL:HB	2:F:426:TRP:NE1	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:206:ARG:HG3	1:M:216:THR:HG21	1.79	0.65
1:E:501:TYR:CE1	1:E:505:ILE:HD11	2.32	0.65
3:C:709:DC:H2'	3:C:710:DG:C8	2.32	0.64
3:K:716:DA:H1'	3:K:717:DC:H5'	1.79	0.64
1:A:102:LYS:CD	1:A:102:LYS:H	1.92	0.64
1:E:109:LEU:CD2	1:E:220:LYS:CG	2.75	0.64
1:A:5:ILE:HD12	1:A:6:GLU:N	2.13	0.64
2:B:340:GLN:HG3	2:B:351:THR:HG22	1.78	0.64
1:E:108:VAL:O	1:E:108:VAL:HG23	1.97	0.64
2:F:332:GLN:NE2	2:F:425:LEU:HD13	2.11	0.64
2:N:54:ASN:ND2	2:N:56:TYR:H	1.95	0.64
1:M:5:ILE:HD12	1:M:6:GLU:N	2.13	0.64
2:J:340:GLN:HG3	2:J:351:THR:HG22	1.79	0.64
2:N:209:LEU:HD22	2:N:214:LEU:HD12	1.80	0.64
1:M:335:GLY:HA2	1:M:367:GLN:HE22	1.62	0.64
1:A:500:GLN:NE2	2:B:422:LEU:HD13	2.12	0.64
3:K:706:DT:H2'	3:K:707:DG:C8	2.33	0.64
1:I:209:LEU:HB3	1:I:214:LEU:HB2	1.80	0.64
1:A:498:ASP:HB2	1:A:538:ALA:HA	1.79	0.64
1:E:289:LEU:HD12	1:E:289:LEU:H	1.63	0.64
1:I:458:VAL:HG12	1:I:548:VAL:HG22	1.79	0.64
2:F:85:GLN:HA	2:F:88:TRP:CE2	2.32	0.64
2:J:375:ILE:HB	2:J:389:PHE:HZ	1.63	0.64
2:J:54:ASN:ND2	2:J:56:TYR:H	1.95	0.64
3:G:716:DA:H1'	3:G:717:DC:H5'	1.79	0.64
1:I:252:TRP:NE1	1:I:295:LEU:HD22	2.12	0.64
1:E:244:ILE:HG23	1:E:244:ILE:O	1.96	0.64
2:F:423:VAL:HB	2:F:426:TRP:CD1	2.33	0.64
1:E:24:TRP:CE3	3:G:703:DG:H1'	2.32	0.64
1:E:132:ILE:CG1	1:E:142:ILE:HG13	2.27	0.64
1:E:132:ILE:HG13	1:E:142:ILE:HG13	1.79	0.64
4:P:806:DT:C2'	4:P:807:DC:H5''	2.28	0.63
3:O:706:DT:H2'	3:O:707:DG:C8	2.33	0.63
1:A:444:GLY:HA3	1:A:477:THR:HG22	1.80	0.63
1:M:441:TYR:CD2	1:M:544:GLY:HA3	2.33	0.63
1:E:199:ARG:O	1:E:202:ILE:HG22	1.99	0.63
2:B:368:LEU:HD11	2:B:392:PRO:HD2	1.80	0.63
1:M:108:VAL:CG2	1:M:108:VAL:O	2.46	0.63
4:H:806:DT:C2'	4:H:807:DC:H5''	2.28	0.63
1:E:529:GLU:O	1:E:530:LYS:HG3	1.98	0.63
1:M:501:TYR:HE1	1:M:505:ILE:HD11	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:375:ILE:HB	2:N:389:PHE:HZ	1.63	0.63
1:E:109:LEU:HD22	1:E:220:LYS:HG2	1.79	0.63
1:A:325:LEU:HD13	1:A:385:LYS:HE2	1.80	0.63
2:J:206:ARG:O	2:J:210:LEU:HD13	1.98	0.63
1:E:209:LEU:HB3	1:E:214:LEU:HB2	1.80	0.63
3:C:706:DT:H2'	3:C:707:DG:H8	1.63	0.63
1:A:458:VAL:HG11	1:A:548:VAL:HG22	1.79	0.63
2:N:131:THR:OG1	2:N:143:ARG:HD2	1.98	0.63
1:A:26:LEU:HB2	1:A:31:ILE:CD1	2.28	0.63
1:M:326:ILE:HG21	1:M:390:LYS:HE2	1.80	0.63
1:A:31:ILE:O	1:A:35:VAL:HG22	1.99	0.63
1:A:207:GLN:HA	1:A:210:LEU:HD12	1.79	0.63
2:B:104:LYS:O	2:B:104:LYS:HD3	1.98	0.63
1:M:94:ILE:HD11	3:O:708:DG:H21	1.61	0.63
1:A:253:THR:HA	1:A:292:VAL:HA	1.80	0.63
1:E:25:PRO:HD2	3:G:703:DG:C2	2.33	0.63
2:F:393:ILE:HD13	2:F:398:TRP:HB2	1.81	0.63
1:A:331:LYS:HE3	8:A:564:HOH:O	1.98	0.63
1:E:102:LYS:HD2	1:E:102:LYS:N	2.02	0.63
1:M:199:ARG:O	1:M:202:ILE:HG22	1.99	0.63
1:I:491:LEU:N	1:I:491:LEU:HD12	2.14	0.63
2:N:13:LYS:O	2:N:16:MET:HB2	1.99	0.63
1:A:199:ARG:O	1:A:202:ILE:HG22	1.99	0.63
1:M:215:THR:HG22	1:M:217:PRO:HD3	1.81	0.63
1:M:209:LEU:HB3	1:M:214:LEU:HB2	1.81	0.63
2:B:278:GLN:HG2	2:B:298:GLU:O	1.98	0.63
1:A:178:ILE:N	1:A:178:ILE:HD12	2.14	0.62
1:E:206:ARG:HG3	1:E:216:THR:HG21	1.80	0.62
2:N:7:THR:HG22	2:N:119:PRO:HG2	1.80	0.62
1:A:26:LEU:HB2	1:A:31:ILE:HD11	1.81	0.62
1:E:335:GLY:HA2	1:E:367:GLN:HE22	1.64	0.62
2:F:170:PRO:HG2	2:F:208:HIS:CE1	2.33	0.62
2:N:374:LYS:O	2:N:378:GLU:HG3	1.99	0.62
2:N:376:THR:O	2:N:380:ILE:HG13	1.98	0.62
2:B:170:PRO:HG2	2:B:208:HIS:CE1	2.33	0.62
2:N:332:GLN:HE22	2:N:425:LEU:HD13	1.65	0.62
1:A:132:ILE:HD11	1:A:142:ILE:CD1	2.29	0.62
1:A:137:ASN:H	1:A:137:ASN:HD22	1.48	0.62
1:I:439:THR:CG2	2:J:289:LEU:HD13	2.29	0.62
1:M:427:TYR:OH	1:M:509:GLN:HA	2.00	0.62
1:I:238:LYS:HD2	1:I:315:HIS:ND1	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:155:GLY:O	1:I:159:ILE:HG12	1.99	0.62
1:M:498:ASP:HB2	1:M:538:ALA:HA	1.80	0.62
2:B:423:VAL:HB	2:B:426:TRP:NE1	2.14	0.62
1:E:181:TYR:CD2	2:F:138:GLU:HA	2.34	0.62
2:J:151:GLN:HB3	2:J:185:ASP:OD2	1.99	0.62
1:A:317:VAL:O	1:A:349:LEU:CD2	2.46	0.62
1:E:235:HIS:HB3	1:E:236:PRO:CD	2.27	0.62
1:I:317:VAL:HG22	1:I:318:TYR:N	2.13	0.62
1:I:8:VAL:O	1:I:10:VAL:HG23	2.00	0.62
2:B:376:THR:O	2:B:380:ILE:HG13	2.00	0.62
1:E:542:ILE:HB	1:E:545:ASN:HB3	1.82	0.62
1:I:178:ILE:N	1:I:178:ILE:HD12	2.15	0.62
2:J:376:THR:O	2:J:380:ILE:HG13	1.99	0.62
1:E:498:ASP:HB2	1:E:538:ALA:HA	1.81	0.62
2:N:278:GLN:HG2	2:N:298:GLU:O	1.99	0.62
2:N:66:LYS:HZ2	2:N:66:LYS:CB	2.01	0.62
1:E:207:GLN:HA	1:E:210:LEU:HD12	1.81	0.61
2:B:154:LYS:O	2:B:157:PRO:HD2	2.00	0.61
1:M:111:VAL:HB	1:M:185:ASP:HB2	1.82	0.61
3:C:716:DA:H1'	3:C:717:DC:H5'	1.82	0.61
2:F:209:LEU:HD22	2:F:214:LEU:HD12	1.83	0.61
1:M:102:LYS:H	1:M:102:LYS:CD	2.00	0.61
2:B:263:LYS:CA	2:B:423:VAL:HG11	2.30	0.61
1:I:80:LEU:O	1:I:84:THR:HG22	1.99	0.61
1:I:59:PRO:HG2	1:I:76:ASP:HB3	1.81	0.61
2:F:278:GLN:HG2	2:F:298:GLU:O	2.00	0.61
1:E:80:LEU:O	1:E:80:LEU:HD12	2.01	0.61
2:J:85:GLN:HA	2:J:88:TRP:CE2	2.35	0.61
1:E:252:TRP:NE1	1:E:295:LEU:HD22	2.16	0.61
1:I:33:ALA:O	1:I:37:ILE:HG12	2.00	0.61
4:L:806:DT:H1'	4:L:807:DC:H5''	1.83	0.61
1:M:252:TRP:NE1	1:M:295:LEU:HD22	2.16	0.61
1:M:57:ASN:ND2	1:M:131:THR:OG1	2.33	0.61
2:N:60:VAL:HG12	2:N:75:VAL:HG22	1.83	0.61
2:B:379:SER:OG	2:B:387:PRO:HD3	2.01	0.61
1:A:501:TYR:CE1	1:A:505:ILE:HD11	2.36	0.61
1:E:24:TRP:CH2	3:G:704:DC:H5'	2.34	0.61
2:N:170:PRO:HG2	2:N:208:HIS:CE1	2.36	0.61
4:D:818:DC:H2'	4:D:819:DG:H8	1.65	0.61
2:N:88:TRP:CZ2	2:N:154:LYS:HD3	2.35	0.61
1:M:155:GLY:O	1:M:159:ILE:HG12	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:706:DT:H2'	3:K:707:DG:H8	1.66	0.61
2:N:108:VAL:HG22	2:N:188:TYR:CD2	2.36	0.61
1:E:111:VAL:HB	1:E:185:ASP:HB2	1.82	0.61
1:A:342:TYR:HB2	1:A:347:LYS:O	2.00	0.61
1:A:441:TYR:CE2	1:A:544:GLY:HA3	2.35	0.61
1:I:366:LYS:O	1:I:370:GLU:HG3	2.01	0.61
1:E:327:ALA:HB2	1:E:341:ILE:HG13	1.83	0.61
1:A:137:ASN:N	1:A:137:ASN:ND2	2.49	0.60
2:B:423:VAL:HB	2:B:426:TRP:CD1	2.36	0.60
2:B:254:VAL:O	2:B:258:GLN:HG3	2.01	0.60
2:B:241:VAL:HG13	2:B:351:THR:H	1.66	0.60
1:M:439:THR:HG21	2:N:289:LEU:HD13	1.83	0.60
1:E:65:LYS:HD3	6:E:823:ZP4:O2D	2.01	0.60
1:A:235:HIS:HB3	1:A:236:PRO:CD	2.29	0.60
1:M:478:GLU:CG	1:M:499:SER:HB2	2.30	0.60
1:E:137:ASN:H	1:E:137:ASN:HD22	1.50	0.60
1:M:96:HIS:HE2	1:M:269:GLN:HE21	1.48	0.60
1:I:228:LEU:HB2	6:I:823:ZP4:H2R	1.82	0.60
1:M:287:LYS:NZ	1:M:293:ILE:HD12	2.17	0.60
1:E:109:LEU:HD23	1:E:220:LYS:CD	2.29	0.60
1:A:206:ARG:HG3	1:A:216:THR:HG21	1.82	0.60
1:M:3:SER:HB2	1:M:119:PRO:HD3	1.82	0.60
2:J:209:LEU:HD22	2:J:214:LEU:HD12	1.83	0.60
1:M:289:LEU:HD12	1:M:289:LEU:H	1.65	0.60
1:I:108:VAL:O	1:I:108:VAL:CG2	2.49	0.60
1:E:109:LEU:HD21	1:E:220:LYS:CE	2.32	0.60
1:E:137:ASN:N	1:E:137:ASN:ND2	2.50	0.60
1:I:125:ARG:NH1	1:I:147:ASN:HB3	2.15	0.60
3:G:722:DA:H1'	3:G:723:DC:H5'	1.83	0.60
2:N:423:VAL:HB	2:N:426:TRP:CD1	2.36	0.60
4:D:818:DC:H2'	4:D:819:DG:C8	2.36	0.60
2:F:340:GLN:HG3	2:F:351:THR:HG22	1.84	0.60
1:I:17:ASP:O	1:I:83:ARG:HD3	2.02	0.60
1:I:285:GLY:N	3:K:714:DG:OP1	2.35	0.60
2:F:206:ARG:CB	2:F:206:ARG:HH11	2.15	0.60
1:E:372:VAL:HG13	1:E:389:PHE:CZ	2.37	0.60
1:I:441:TYR:CE2	1:I:544:GLY:HA3	2.36	0.59
2:N:332:GLN:NE2	2:N:425:LEU:HD13	2.16	0.59
1:I:379:SER:OG	1:I:387:PRO:HD3	2.02	0.59
2:J:278:GLN:HG2	2:J:298:GLU:O	2.01	0.59
1:I:254:VAL:HG23	1:I:291:GLU:O	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:TYR:CE1	1:E:184:MET:HE1	2.37	0.59
1:M:26:LEU:HB2	1:M:31:ILE:HD11	1.83	0.59
1:I:439:THR:HG21	2:J:289:LEU:CD1	2.32	0.59
2:F:425:LEU:CA	8:F:438:HOH:O	2.51	0.59
1:I:335:GLY:HA2	1:I:367:GLN:HE22	1.67	0.59
1:E:109:LEU:CD2	1:E:220:LYS:HG2	2.32	0.59
1:I:498:ASP:HB2	1:I:538:ALA:HA	1.84	0.59
3:G:706:DT:H2'	3:G:707:DG:C8	2.37	0.59
1:A:379:SER:OG	1:A:387:PRO:HD3	2.02	0.59
1:A:398:TRP:CZ2	1:A:411:ILE:HG12	2.37	0.59
1:M:286:THR:OG1	3:O:714:DG:C5'	2.50	0.59
1:E:151:GLN:NE2	6:E:823:ZP4:N3B	2.50	0.59
1:M:366:LYS:O	1:M:370:GLU:HG3	2.03	0.59
1:M:438:GLU:CD	1:M:463:ARG:HD2	2.23	0.59
1:I:199:ARG:O	1:I:202:ILE:HG22	2.02	0.59
1:A:493:VAL:HG12	1:A:494:ASN:N	2.16	0.59
1:M:339:TYR:CG	1:M:375:ILE:HD11	2.37	0.59
3:O:716:DA:H1'	3:O:717:DC:H5'	1.85	0.59
1:M:108:VAL:HG23	1:M:108:VAL:O	2.02	0.59
1:A:529:GLU:O	1:A:530:LYS:HG3	2.03	0.59
1:E:25:PRO:HD2	3:G:703:DG:N2	2.17	0.59
2:F:13:LYS:HE3	2:F:86:ASP:H	1.67	0.59
2:N:257:ILE:HG23	2:N:283:LEU:HD21	1.84	0.59
1:E:406:TRP:HD1	1:E:407:GLN:HE21	1.50	0.59
1:E:222:GLN:O	1:E:224:GLU:HG3	2.02	0.59
3:C:722:DA:H1'	3:C:723:DC:H5'	1.84	0.59
1:M:400:THR:O	1:M:404:GLU:HG2	2.02	0.59
1:E:5:ILE:HD12	1:E:6:GLU:N	2.17	0.59
1:A:29:GLU:O	1:A:32:LYS:HB3	2.02	0.59
2:N:340:GLN:HG3	2:N:351:THR:HG22	1.84	0.59
1:I:478:GLU:CD	1:I:499:SER:HB2	2.23	0.59
1:I:94:ILE:CD1	3:K:708:DG:H21	2.15	0.59
1:E:429:LEU:HD13	1:E:533:LEU:CD1	2.32	0.59
1:A:351:THR:HB	8:A:556:HOH:O	2.03	0.59
1:A:372:VAL:HG13	1:A:389:PHE:CZ	2.38	0.59
1:E:183:TYR:O	1:E:184:MET:HB2	2.03	0.58
2:F:425:LEU:HB3	8:F:438:HOH:O	2.02	0.58
1:I:237:ASP:C	1:I:238:LYS:HG2	2.22	0.58
1:E:178:ILE:N	1:E:178:ILE:HD12	2.18	0.58
1:M:491:LEU:HD12	1:M:491:LEU:N	2.19	0.58
3:O:706:DT:H2'	3:O:707:DG:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:33:ALA:O	1:M:37:ILE:HG12	2.03	0.58
1:A:445:ALA:H	1:A:477:THR:HG21	1.68	0.58
1:A:439:THR:CG2	2:B:289:LEU:HD13	2.29	0.58
2:F:368:LEU:HD22	2:F:398:TRP:CZ3	2.38	0.58
2:F:374:LYS:O	2:F:378:GLU:HG3	2.04	0.58
1:A:24:TRP:HE3	3:C:703:DG:H1'	1.69	0.58
1:A:31:ILE:HD12	1:A:133:PRO:HG2	1.84	0.58
2:N:85:GLN:HA	2:N:88:TRP:CE2	2.38	0.58
2:B:215:THR:HG22	2:B:217:PRO:HD3	1.85	0.58
1:E:33:ALA:O	1:E:37:ILE:HG12	2.04	0.58
1:M:8:VAL:O	1:M:10:VAL:HG23	2.04	0.58
1:M:281:LYS:HG3	1:M:284:ARG:NH1	2.19	0.58
2:B:263:LYS:CB	2:B:423:VAL:HG11	2.34	0.58
1:A:165:THR:HG21	2:B:140:PRO:CG	2.32	0.58
1:A:183:TYR:O	1:A:184:MET:HB2	2.02	0.58
2:B:13:LYS:O	2:B:16:MET:HB2	2.02	0.58
2:J:131:THR:OG1	2:J:143:ARG:HD2	2.04	0.58
2:J:194:GLU:OE2	2:J:195:ILE:HG22	2.03	0.58
2:J:200:THR:O	2:J:204:GLU:HG3	2.03	0.58
1:E:535:TRP:O	1:E:536:VAL:CG1	2.52	0.58
2:F:263:LYS:HB2	2:F:423:VAL:HG11	1.86	0.58
1:I:327:ALA:HB2	1:I:341:ILE:HG13	1.85	0.58
1:E:13:LYS:HE3	1:E:84:THR:O	2.03	0.58
1:I:235:HIS:HB3	1:I:236:PRO:CD	2.28	0.58
2:N:169:GLU:N	2:N:170:PRO:HD2	2.19	0.58
2:J:206:ARG:HH11	2:J:206:ARG:CB	2.17	0.58
3:O:722:DA:H1'	3:O:723:DC:H5'	1.86	0.58
1:E:221:HIS:CE1	6:E:823:ZP4:HN6A	2.21	0.58
1:I:429:LEU:HD23	1:I:429:LEU:N	2.18	0.58
2:B:374:LYS:O	2:B:378:GLU:HG3	2.04	0.58
2:F:206:ARG:NH1	2:F:206:ARG:HB3	2.19	0.58
1:A:27:THR:O	1:A:31:ILE:HG12	2.04	0.58
1:M:426:TRP:HB3	1:M:526:ILE:HD12	1.85	0.58
1:E:26:LEU:HB2	1:E:31:ILE:HD11	1.86	0.58
1:A:439:THR:HG21	2:B:289:LEU:CD1	2.28	0.57
1:E:109:LEU:HD21	1:E:220:LYS:CD	2.34	0.57
1:M:23:GLN:HG3	1:M:131:THR:O	2.04	0.57
2:F:104:LYS:O	2:F:104:LYS:HD3	2.04	0.57
2:B:376:THR:HG21	2:B:410:TRP:CZ3	2.39	0.57
1:A:33:ALA:O	1:A:37:ILE:HG12	2.05	0.57
4:H:808:DC:H1'	4:H:809:DC:H5'	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:422:LEU:N	1:E:422:LEU:HD22	2.19	0.57
1:I:444:GLY:HA3	1:I:477:THR:HG22	1.86	0.57
1:I:252:TRP:CD1	1:I:295:LEU:HD22	2.40	0.57
1:E:326:ILE:HG21	1:E:390:LYS:HE2	1.86	0.57
1:I:326:ILE:HG21	1:I:390:LYS:HE2	1.85	0.57
1:M:108:VAL:CG2	1:M:221:HIS:CD2	2.86	0.57
1:E:109:LEU:HD23	1:E:220:LYS:CG	2.34	0.57
2:N:114:ALA:HB2	2:N:214:LEU:HD13	1.86	0.57
1:I:260:LEU:O	1:I:264:LEU:CD1	2.52	0.57
2:B:332:GLN:HG3	2:B:428:GLN:HG3	1.86	0.57
1:M:429:LEU:HD23	1:M:429:LEU:N	2.19	0.57
1:A:132:ILE:CG1	1:A:142:ILE:HG13	2.35	0.57
1:M:344:GLU:CB	1:M:345:PRO:CD	2.73	0.57
1:M:529:GLU:O	1:M:530:LYS:HG3	2.04	0.57
2:J:108:VAL:N	2:J:232:TYR:OH	2.38	0.57
2:B:131:THR:OG1	2:B:143:ARG:HD2	2.04	0.57
1:A:44:GLU:OE1	1:A:46:LYS:HE2	2.04	0.57
2:J:66:LYS:HB3	2:J:66:LYS:NZ	2.19	0.57
1:M:317:VAL:CG1	1:M:349:LEU:HD23	2.33	0.57
4:H:806:DT:H2''	4:H:807:DC:H5'	1.87	0.57
2:J:169:GLU:N	2:J:170:PRO:HD2	2.19	0.57
1:E:379:SER:OG	1:E:387:PRO:HD3	2.04	0.57
1:E:27:THR:O	1:E:31:ILE:HG12	2.04	0.57
1:E:444:GLY:HA3	1:E:477:THR:HG22	1.84	0.57
1:M:465:LYS:HG3	1:M:466:VAL:N	2.20	0.57
1:M:60:VAL:HG11	1:M:130:PHE:CD2	2.40	0.57
1:I:438:GLU:CD	1:I:463:ARG:HD2	2.25	0.57
1:M:244:ILE:C	1:M:244:ILE:HD13	2.24	0.57
1:E:12:LEU:HD11	1:E:127:TYR:CZ	2.39	0.57
1:E:109:LEU:HD21	1:E:220:LYS:HD3	1.86	0.57
2:N:278:GLN:CG	2:N:298:GLU:HB3	2.35	0.57
1:E:252:TRP:CD1	1:E:295:LEU:HD22	2.40	0.57
1:A:209:LEU:HB3	1:A:214:LEU:HB2	1.87	0.57
1:E:492:GLU:OE2	1:E:530:LYS:HD3	2.05	0.57
2:N:423:VAL:HB	2:N:426:TRP:NE1	2.20	0.57
1:M:12:LEU:HD11	1:M:127:TYR:CZ	2.40	0.57
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.85	0.57
1:I:389:PHE:HB3	1:I:391:LEU:HD21	1.87	0.57
1:A:221:HIS:HB3	1:A:227:PHE:CD1	2.40	0.56
2:B:422:LEU:HG	2:B:426:TRP:CZ2	2.31	0.56
1:I:3:SER:HB3	1:I:5:ILE:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:463:ARG:HG2	1:M:463:ARG:NH1	2.19	0.56
1:E:260:LEU:HD23	1:E:279:LEU:HD22	1.87	0.56
1:M:444:GLY:HA3	1:M:477:THR:HG22	1.86	0.56
1:E:50:ILE:HG13	1:E:143:ARG:CB	2.34	0.56
2:J:13:LYS:O	2:J:16:MET:HB2	2.06	0.56
1:I:337:TRP:CZ3	1:I:368:LEU:HD13	2.40	0.56
2:J:357:MET:HE3	2:J:360:ALA:HB2	1.85	0.56
2:B:7:THR:HG22	2:B:119:PRO:HG2	1.87	0.56
1:M:165:THR:HA	1:M:182:GLN:HE22	1.69	0.56
1:M:337:TRP:CZ3	1:M:368:LEU:HD13	2.41	0.56
1:M:168:LEU:HD11	1:M:187:LEU:HD21	1.87	0.56
1:I:344:GLU:HB3	1:I:345:PRO:CD	2.34	0.56
2:J:285:GLY:O	2:J:287:LYS:HG3	2.06	0.56
1:A:362:THR:HG22	1:A:366:LYS:HE2	1.87	0.56
2:N:360:ALA:HB1	8:N:430:HOH:O	2.04	0.56
1:A:108:VAL:O	1:A:108:VAL:HG23	2.05	0.56
3:C:707:DG:C2'	3:C:708:DG:H5'	2.33	0.56
2:N:263:LYS:N	2:N:423:VAL:HG11	2.20	0.56
1:M:118:VAL:O	1:M:148:VAL:HG23	2.06	0.56
2:B:63:ILE:N	2:B:63:ILE:HD13	2.20	0.56
1:E:81:ASN:HA	1:E:84:THR:HG22	1.87	0.56
1:I:432:GLU:HG3	1:I:433:PRO:HD2	1.87	0.56
1:E:116:PHE:HA	1:E:148:VAL:HG21	1.88	0.56
2:J:63:ILE:H	2:J:63:ILE:HD13	1.70	0.56
1:E:475:GLN:NE2	4:H:809:DC:C5'	2.69	0.56
2:N:263:LYS:CA	2:N:423:VAL:HG11	2.36	0.56
1:A:287:LYS:HZ3	1:A:293:ILE:HD12	1.70	0.56
1:I:137:ASN:H	1:I:137:ASN:HD22	1.53	0.56
1:M:183:TYR:O	1:M:184:MET:HB2	2.05	0.56
1:E:362:THR:HG22	1:E:366:LYS:HE2	1.86	0.56
1:M:108:VAL:CG2	1:M:221:HIS:HD2	2.17	0.56
1:M:438:GLU:OE2	1:M:463:ARG:HD2	2.05	0.56
1:A:491:LEU:HD12	1:A:491:LEU:N	2.20	0.56
1:A:199:ARG:O	1:A:203:GLU:HG3	2.06	0.56
2:B:206:ARG:CB	2:B:206:ARG:HH11	2.18	0.56
2:J:206:ARG:HB3	2:J:206:ARG:NH1	2.20	0.56
1:E:326:ILE:HD12	1:E:326:ILE:N	2.21	0.56
2:B:215:THR:O	2:B:217:PRO:HD3	2.06	0.56
1:M:503:LEU:HD22	1:M:535:TRP:HB2	1.88	0.56
1:M:181:TYR:CD2	2:N:138:GLU:HA	2.41	0.56
1:E:96:HIS:HE2	1:E:269:GLN:HE21	1.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:GLN:HE22	4:D:808:DC:C4'	2.18	0.56
2:F:263:LYS:CA	2:F:423:VAL:HG11	2.35	0.56
2:B:375:ILE:HB	2:B:389:PHE:HZ	1.71	0.56
2:J:278:GLN:CG	2:J:298:GLU:HB3	2.36	0.56
1:M:29:GLU:O	1:M:32:LYS:HB3	2.06	0.56
1:E:344:GLU:HB3	1:E:345:PRO:CD	2.35	0.56
1:E:429:LEU:HD23	1:E:429:LEU:N	2.20	0.56
1:A:165:THR:HA	1:A:182:GLN:HE22	1.70	0.56
1:M:3:SER:HB3	1:M:5:ILE:HG22	1.87	0.56
2:F:339:TYR:C	2:F:340:GLN:NE2	2.59	0.56
1:I:260:LEU:HD23	1:I:279:LEU:HD22	1.88	0.56
1:I:24:TRP:CE3	3:K:703:DG:H1'	2.40	0.56
1:M:341:ILE:HD12	1:M:341:ILE:N	2.20	0.56
1:M:13:LYS:HE2	1:M:86:ASP:OD1	2.06	0.56
1:E:337:TRP:CZ3	1:E:368:LEU:HD13	2.41	0.56
1:I:183:TYR:O	1:I:184:MET:HB2	2.06	0.55
2:F:131:THR:OG1	2:F:143:ARG:HD2	2.06	0.55
1:M:81:ASN:HA	1:M:84:THR:HG22	1.87	0.55
2:J:422:LEU:HD23	2:J:422:LEU:H	1.71	0.55
1:M:67:ASP:O	1:M:68:SER:HB2	2.06	0.55
1:M:178:ILE:N	1:M:178:ILE:HD12	2.21	0.55
1:I:3:SER:HB2	1:I:119:PRO:HD3	1.88	0.55
2:F:215:THR:O	2:F:217:PRO:HD3	2.06	0.55
2:F:257:ILE:CG2	2:F:283:LEU:HD21	2.36	0.55
1:M:137:ASN:HD22	1:M:137:ASN:H	1.53	0.55
2:J:213:GLY:C	2:J:214:LEU:HD23	2.27	0.55
2:J:213:GLY:O	2:J:214:LEU:HD23	2.07	0.55
1:E:116:PHE:C	1:E:148:VAL:HG21	2.26	0.55
1:M:225:PRO:HB2	1:M:226:PRO:HD3	1.87	0.55
1:A:32:LYS:O	1:A:36:GLU:HG3	2.07	0.55
1:M:197:GLN:O	1:M:200:THR:HB	2.06	0.55
1:E:317:VAL:CG2	1:E:318:TYR:H	2.16	0.55
1:I:181:TYR:CE2	2:J:138:GLU:HA	2.41	0.55
1:A:115:TYR:O	1:A:148:VAL:HG22	2.07	0.55
1:E:165:THR:HA	1:E:182:GLN:HE22	1.72	0.55
1:E:50:ILE:HG13	1:E:143:ARG:HB2	1.87	0.55
1:A:284:ARG:HG3	1:A:284:ARG:HH11	1.71	0.55
4:P:806:DT:H2''	4:P:807:DC:H5'	1.88	0.55
4:H:809:DC:H1'	4:H:810:DT:H5''	1.89	0.55
1:E:174:GLN:HB3	8:E:563:HOH:O	2.00	0.55
4:L:820:DC:H2''	4:L:821:DC:H5'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:206:ARG:NH1	2:B:206:ARG:HB3	2.21	0.55
2:B:213:GLY:C	2:B:214:LEU:HD23	2.27	0.55
1:A:12:LEU:HD11	1:A:127:TYR:CE2	2.41	0.55
1:M:379:SER:OG	1:M:387:PRO:HD3	2.06	0.55
1:E:445:ALA:H	1:E:477:THR:HG21	1.72	0.55
2:J:354:TYR:OH	2:J:357:MET:HB2	2.05	0.55
2:N:368:LEU:HD11	2:N:392:PRO:HD2	1.89	0.55
1:I:490:GLY:O	1:I:528:LYS:HD2	2.07	0.55
1:E:426:TRP:HB3	1:E:526:ILE:HD12	1.89	0.55
1:E:108:VAL:CG2	1:E:221:HIS:CD2	2.90	0.55
2:B:54:ASN:HD21	2:B:56:TYR:HB2	1.72	0.55
1:E:284:ARG:HH11	1:E:284:ARG:HG3	1.72	0.55
2:N:200:THR:O	2:N:204:GLU:HG3	2.06	0.55
2:J:375:ILE:HB	2:J:389:PHE:CZ	2.41	0.55
2:B:35:VAL:O	2:B:39:THR:HG23	2.06	0.55
1:M:46:LYS:O	1:M:147:ASN:HB2	2.07	0.54
2:N:206:ARG:CB	2:N:206:ARG:HH11	2.20	0.54
1:I:67:ASP:O	1:I:68:SER:HB2	2.06	0.54
1:A:8:VAL:O	1:A:10:VAL:HG23	2.07	0.54
1:E:412:PRO:HB2	8:E:557:HOH:O	2.07	0.54
2:B:5:ILE:HG22	2:B:6:GLU:N	2.22	0.54
1:E:115:TYR:CE2	6:E:823:ZP4:H2'A	2.43	0.54
1:E:427:TYR:OH	1:E:509:GLN:HA	2.07	0.54
2:F:255:ASN:O	2:F:258:GLN:HB2	2.07	0.54
2:N:215:THR:O	2:N:217:PRO:HD3	2.06	0.54
1:E:57:ASN:OD1	1:E:58:THR:N	2.41	0.54
1:I:293:ILE:HG13	1:I:294:PRO:HD2	1.89	0.54
1:M:361:HIS:CD2	1:M:505:ILE:HG23	2.42	0.54
1:M:91:GLN:HG3	1:M:161:GLN:HE22	1.72	0.54
1:A:151:GLN:NE2	6:A:823:ZP4:N3B	2.56	0.54
2:J:257:ILE:CG2	2:J:283:LEU:HD21	2.37	0.54
1:M:252:TRP:CD1	1:M:295:LEU:HD22	2.43	0.54
2:J:279:LEU:HA	2:J:282:LEU:HD13	1.89	0.54
3:K:722:DA:H1'	3:K:723:DC:H5'	1.89	0.54
2:B:393:ILE:HD13	2:B:398:TRP:HB2	1.89	0.54
1:I:503:LEU:HD22	1:I:535:TRP:HB2	1.89	0.54
1:A:204:GLU:HG2	2:N:4:PRO:HG3	1.90	0.54
4:L:808:DC:H1'	4:L:809:DC:H5'	1.90	0.54
1:M:26:LEU:HB2	1:M:31:ILE:CD1	2.37	0.54
1:I:137:ASN:N	1:I:137:ASN:ND2	2.55	0.54
2:F:206:ARG:CB	2:F:206:ARG:NH1	2.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:56:TYR:O	1:I:143:ARG:NH2	2.40	0.54
1:E:138:GLU:OE2	1:E:138:GLU:N	2.40	0.54
1:M:23:GLN:HG2	1:M:59:PRO:HA	1.90	0.54
2:F:241:VAL:HG13	2:F:351:THR:H	1.73	0.54
2:F:257:ILE:HG23	2:F:283:LEU:HD21	1.89	0.54
1:A:400:THR:O	1:A:404:GLU:HG2	2.07	0.54
1:M:318:TYR:O	1:M:349:LEU:HD21	2.07	0.54
1:A:148:VAL:O	1:A:150:PRO:HD3	2.08	0.54
2:N:285:GLY:O	2:N:287:LYS:HG3	2.08	0.54
1:A:94:ILE:HD11	3:C:708:DG:N2	2.22	0.54
1:E:278:GLN:HB2	1:E:302:GLU:CD	2.27	0.54
2:F:376:THR:O	2:F:380:ILE:HG13	2.07	0.54
1:A:429:LEU:HD23	1:A:429:LEU:N	2.22	0.54
1:M:57:ASN:HD21	1:M:131:THR:CB	2.21	0.54
1:A:252:TRP:CD1	1:A:295:LEU:HD22	2.43	0.54
1:I:406:TRP:CD1	1:I:407:GLN:HG2	2.43	0.54
1:E:399:GLU:HA	1:E:402:TRP:CD1	2.43	0.54
1:A:303:LEU:O	1:A:303:LEU:HD22	2.08	0.54
2:B:257:ILE:HG23	2:B:283:LEU:HD21	1.90	0.54
1:M:493:VAL:HG12	1:M:494:ASN:N	2.22	0.54
1:M:235:HIS:HB3	1:M:236:PRO:CD	2.32	0.54
1:A:441:TYR:HA	1:A:496:VAL:HG22	1.90	0.54
2:J:379:SER:OG	2:J:387:PRO:HD3	2.08	0.54
1:I:548:VAL:O	1:I:552:VAL:HG22	2.08	0.54
1:I:287:LYS:NZ	1:I:293:ILE:HD12	2.23	0.54
1:I:542:ILE:HB	1:I:545:ASN:HB3	1.90	0.54
2:N:65:LYS:HG2	2:N:66:LYS:H	1.73	0.53
1:A:109:LEU:N	1:A:109:LEU:CD1	2.71	0.53
4:P:818:DC:H2'	4:P:819:DG:H8	1.72	0.53
2:F:206:ARG:HB2	2:F:206:ARG:HH11	1.73	0.53
1:I:21:VAL:HG23	1:I:59:PRO:HD3	1.91	0.53
2:F:278:GLN:CG	2:F:298:GLU:HB3	2.39	0.53
1:M:32:LYS:O	1:M:36:GLU:HG3	2.07	0.53
2:N:422:LEU:HG	2:N:426:TRP:CZ2	2.31	0.53
2:N:213:GLY:O	2:N:214:LEU:HD23	2.09	0.53
1:A:132:ILE:HD11	1:A:142:ILE:HD11	1.89	0.53
1:E:118:VAL:O	1:E:148:VAL:HG23	2.08	0.53
1:A:339:TYR:CG	1:A:375:ILE:HD11	2.43	0.53
1:E:197:GLN:O	1:E:200:THR:HB	2.08	0.53
1:M:24:TRP:CZ2	3:O:704:DC:H5'	2.43	0.53
1:M:450:THR:O	1:M:451:LYS:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:450:THR:O	1:I:451:LYS:HB2	2.08	0.53
1:M:344:GLU:OE1	1:M:347:LYS:HG3	2.09	0.53
1:E:475:GLN:HE21	4:H:809:DC:C5'	2.19	0.53
1:M:95:PRO:HA	2:N:136:ASN:O	2.07	0.53
2:B:13:LYS:HE3	2:B:86:ASP:H	1.73	0.53
1:M:254:VAL:HG23	1:M:291:GLU:O	2.09	0.53
1:M:222:GLN:O	1:M:224:GLU:HG3	2.09	0.53
1:A:252:TRP:NE1	1:A:295:LEU:HD22	2.24	0.53
1:M:339:TYR:OH	1:M:352:GLY:HA3	2.04	0.53
4:H:810:DT:H2''	4:H:811:DG:C8	2.44	0.53
1:I:445:ALA:H	1:I:477:THR:HG21	1.72	0.53
1:M:548:VAL:O	1:M:552:VAL:HG22	2.08	0.53
2:N:206:ARG:HB3	2:N:206:ARG:NH1	2.23	0.53
2:B:34:LEU:HD13	2:B:62:ALA:HB2	1.89	0.53
2:F:66:LYS:HB3	2:F:66:LYS:NZ	2.24	0.53
1:M:342:TYR:HD2	1:M:344:GLU:O	1.86	0.53
1:I:165:THR:HA	1:I:182:GLN:HE22	1.72	0.53
1:M:438:GLU:OE1	1:M:463:ARG:HD2	2.09	0.53
1:A:326:ILE:N	1:A:326:ILE:HD12	2.24	0.53
2:B:397:THR:HG21	8:B:432:HOH:O	2.09	0.53
1:A:222:GLN:O	1:A:224:GLU:HG3	2.09	0.53
1:M:342:TYR:CE2	1:M:344:GLU:O	2.62	0.53
1:E:441:TYR:HA	1:E:496:VAL:HG22	1.91	0.53
2:N:375:ILE:HB	2:N:389:PHE:CZ	2.44	0.53
1:M:42:GLU:OE1	1:M:49:LYS:HG3	2.09	0.53
2:F:34:LEU:HD13	2:F:62:ALA:HB2	1.91	0.53
1:E:8:VAL:O	1:E:10:VAL:HG23	2.09	0.53
1:I:5:ILE:HD12	1:I:6:GLU:H	1.71	0.53
2:N:213:GLY:C	2:N:214:LEU:HD23	2.29	0.53
2:J:115:TYR:OH	2:J:157:PRO:HB3	2.08	0.53
1:A:389:PHE:HB3	1:A:391:LEU:HD21	1.91	0.53
1:E:358:ARG:HH12	2:F:396:GLU:CD	2.12	0.53
1:M:406:TRP:HD1	1:M:407:GLN:HE21	1.56	0.53
1:E:168:LEU:HD11	1:E:187:LEU:HD21	1.90	0.53
4:H:806:DT:H1'	4:H:807:DC:H5''	1.90	0.53
1:I:58:THR:CG2	1:I:59:PRO:HD2	2.38	0.53
2:B:196:GLY:O	2:B:200:THR:HG23	2.09	0.53
4:P:819:DG:H2'	4:P:820:DC:C6	2.43	0.53
2:J:380:ILE:O	2:J:384:GLY:HA2	2.09	0.53
1:I:357:MET:HG2	1:I:367:GLN:OE1	2.09	0.53
1:E:155:GLY:O	1:E:159:ILE:HG12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:705:DA:H2"	3:C:706:DT:C5'	2.35	0.53
1:I:260:LEU:HD21	1:I:303:LEU:HD23	1.90	0.53
2:B:50:ILE:HD13	2:B:145:GLN:HB3	1.90	0.53
1:I:32:LYS:O	1:I:36:GLU:HG3	2.09	0.53
1:E:115:TYR:CD2	6:E:823:ZP4:H2'A	2.43	0.52
1:M:137:ASN:ND2	1:M:137:ASN:N	2.56	0.52
2:N:393:ILE:HD13	2:N:398:TRP:HB2	1.91	0.52
2:J:3:SER:OG	2:J:4:PRO:HD2	2.09	0.52
1:E:293:ILE:HG13	1:E:294:PRO:HD2	1.89	0.52
1:M:342:TYR:HB3	1:M:348:ASN:HA	1.91	0.52
1:I:94:ILE:HD11	3:K:708:DG:H21	1.72	0.52
3:K:717:DC:H2"	3:K:718:DA:OP2	2.09	0.52
1:M:84:THR:CG2	1:M:154:LYS:HD3	2.39	0.52
1:I:393:ILE:HB	1:I:423:VAL:HB	1.89	0.52
1:M:102:LYS:HD2	1:M:102:LYS:N	2.01	0.52
1:I:27:THR:O	1:I:31:ILE:HG12	2.09	0.52
1:I:441:TYR:HA	1:I:496:VAL:HG22	1.90	0.52
1:E:132:ILE:HD11	1:E:144:TYR:HE2	1.74	0.52
1:A:545:ASN:O	1:A:546:GLU:C	2.48	0.52
1:M:399:GLU:HA	1:M:402:TRP:CD1	2.44	0.52
3:G:707:DG:H2"	3:G:708:DG:C5'	2.34	0.52
1:M:156:SER:HB2	1:M:157:PRO:CD	2.39	0.52
2:F:425:LEU:C	8:F:438:HOH:O	2.48	0.52
1:A:282:LEU:HD21	1:A:296:THR:HG22	1.92	0.52
1:M:25:PRO:HD2	3:O:703:DG:C2	2.45	0.52
1:I:197:GLN:O	1:I:200:THR:HB	2.09	0.52
2:N:194:GLU:OE2	2:N:195:ILE:HG22	2.08	0.52
1:M:285:GLY:N	3:O:714:DG:OP1	2.42	0.52
2:N:422:LEU:HD23	2:N:422:LEU:H	1.73	0.52
1:A:115:TYR:CE2	6:A:823:ZP4:H2'A	2.45	0.52
2:N:72:ARG:NH2	2:N:151:GLN:NE2	2.58	0.52
4:D:819:DG:H2'	4:D:820:DC:H6	1.74	0.52
2:N:257:ILE:CG2	2:N:283:LEU:HD21	2.40	0.52
2:N:73:LYS:NZ	2:N:146:TYR:OH	2.37	0.52
2:N:115:TYR:OH	2:N:157:PRO:HB3	2.09	0.52
1:E:475:GLN:NE2	4:H:809:DC:H5"	2.24	0.52
2:F:375:ILE:HB	2:F:389:PHE:HZ	1.74	0.52
2:B:278:GLN:CG	2:B:298:GLU:HB3	2.40	0.52
1:A:48:SER:O	1:A:144:TYR:HA	2.10	0.52
2:F:410:TRP:O	2:F:411:ILE:HD13	2.10	0.52
1:A:197:GLN:O	1:A:200:THR:HB	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:HIS:O	1:A:200:THR:N	2.43	0.52
2:J:8:VAL:O	2:J:8:VAL:HG23	2.09	0.52
1:E:94:ILE:CD1	3:G:708:DG:H21	2.23	0.52
2:N:13:LYS:HB2	2:N:16:MET:CG	2.37	0.52
2:B:13:LYS:CD	2:B:86:ASP:HB2	2.38	0.52
1:E:215:THR:HG22	1:E:216:THR:N	2.25	0.52
1:M:109:LEU:HD23	1:M:216:THR:HG21	1.91	0.52
2:J:66:LYS:HZ2	2:J:66:LYS:HB3	1.75	0.52
1:E:148:VAL:HG22	1:E:149:LEU:N	2.25	0.52
1:I:493:VAL:HG12	1:I:494:ASN:N	2.24	0.52
1:E:491:LEU:HD12	1:E:491:LEU:N	2.25	0.52
1:A:221:HIS:HB3	1:A:227:PHE:HD1	1.73	0.52
1:M:254:VAL:HB	1:M:288:ALA:O	2.10	0.52
2:J:374:LYS:O	2:J:378:GLU:HG3	2.09	0.52
1:M:333:GLY:H	1:M:336:GLN:HB2	1.74	0.52
2:B:257:ILE:CG2	2:B:283:LEU:HD21	2.40	0.52
2:B:422:LEU:HD23	2:B:422:LEU:H	1.75	0.52
4:H:821:DC:H2'	4:H:822:2DA:H8	1.91	0.52
1:I:240:THR:HG22	1:I:315:HIS:HA	1.91	0.52
1:I:57:ASN:ND2	1:I:131:THR:OG1	2.43	0.52
1:I:29:GLU:O	1:I:32:LYS:HB3	2.10	0.52
2:F:97:PRO:HD2	2:F:181:TYR:CD1	2.45	0.52
1:A:155:GLY:O	1:A:159:ILE:HG12	2.09	0.52
1:I:31:ILE:CD1	1:I:133:PRO:HG2	2.36	0.52
2:J:170:PRO:HG2	2:J:208:HIS:NE2	2.25	0.52
1:I:225:PRO:HB2	1:I:226:PRO:HD3	1.91	0.52
2:F:293:ILE:HG23	2:F:294:PRO:HD2	1.92	0.52
2:N:266:TRP:CD1	2:N:269:GLN:NE2	2.78	0.52
2:J:88:TRP:CZ2	2:J:154:LYS:HD3	2.45	0.52
1:E:389:PHE:HB3	1:E:391:LEU:HD21	1.92	0.52
2:N:400:THR:HG22	2:N:401:TRP:CD2	2.45	0.52
1:A:317:VAL:HG12	1:A:348:ASN:C	2.26	0.51
3:G:706:DT:H2'	3:G:707:DG:H8	1.75	0.51
1:E:420:PRO:HA	1:E:422:LEU:CD2	2.36	0.51
1:A:427:TYR:OH	1:A:509:GLN:HA	2.10	0.51
2:F:13:LYS:O	2:F:16:MET:HB2	2.09	0.51
2:J:293:ILE:HG23	2:J:294:PRO:HD2	1.92	0.51
2:B:88:TRP:CZ2	2:B:154:LYS:HD3	2.45	0.51
1:I:168:LEU:HD11	1:I:187:LEU:HD21	1.92	0.51
1:A:317:VAL:CG2	1:A:318:TYR:H	2.19	0.51
1:I:246:LEU:HD12	1:I:246:LEU:N	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:260:LEU:HD21	1:E:303:LEU:HD23	1.93	0.51
1:I:260:LEU:O	1:I:264:LEU:HD13	2.10	0.51
1:I:406:TRP:HD1	1:I:407:GLN:HE21	1.57	0.51
2:B:285:GLY:O	2:B:287:LYS:HG3	2.10	0.51
1:E:535:TRP:C	1:E:536:VAL:HG13	2.30	0.51
4:L:806:DT:C2'	4:L:807:DC:H5''	2.40	0.51
3:K:707:DG:H2''	3:K:708:DG:C5'	2.36	0.51
1:A:109:LEU:H	1:A:109:LEU:HD12	1.74	0.51
1:M:445:ALA:H	1:M:477:THR:HG21	1.74	0.51
2:F:202:ILE:O	2:F:206:ARG:HG3	2.09	0.51
1:I:81:ASN:HA	1:I:84:THR:HG22	1.92	0.51
2:N:88:TRP:CE2	2:N:154:LYS:HD3	2.45	0.51
1:M:108:VAL:CG2	1:M:221:HIS:HB2	2.11	0.51
4:P:806:DT:H5'	4:P:806:DT:H6	1.75	0.51
4:H:821:DC:H2''	4:H:822:2DA:H5'	1.92	0.51
1:M:72:ARG:HG3	1:M:151:GLN:HE22	1.74	0.51
1:A:165:THR:HG22	1:A:182:GLN:NE2	2.26	0.51
2:N:54:ASN:HD21	2:N:56:TYR:HB2	1.75	0.51
2:B:410:TRP:O	2:B:411:ILE:HD13	2.11	0.51
2:J:278:GLN:HG3	2:J:298:GLU:HB3	1.93	0.51
1:M:81:ASN:HA	1:M:84:THR:CG2	2.40	0.51
1:E:281:LYS:HG3	1:E:284:ARG:NH1	2.26	0.51
2:F:376:THR:HG21	2:F:410:TRP:CZ3	2.45	0.51
1:I:480:GLN:O	1:I:483:TYR:HB3	2.10	0.51
2:B:356:ARG:NE	8:B:436:HOH:O	2.43	0.51
1:E:298:GLU:OE1	1:E:298:GLU:N	2.43	0.51
1:A:298:GLU:OE1	1:A:298:GLU:N	2.43	0.51
1:A:116:PHE:HA	1:A:148:VAL:HG21	1.91	0.51
1:E:287:LYS:NZ	1:E:293:ILE:HD12	2.25	0.51
1:I:198:HIS:O	1:I:201:LYS:N	2.44	0.51
1:M:490:GLY:O	1:M:528:LYS:HD2	2.11	0.51
1:I:116:PHE:C	1:I:148:VAL:HG21	2.31	0.51
1:E:536:VAL:O	1:E:537:PRO:C	2.48	0.51
2:B:213:GLY:O	2:B:214:LEU:HD23	2.10	0.51
1:M:184:MET:HG3	4:P:822:2DA:H1'	1.93	0.51
1:I:400:THR:O	1:I:404:GLU:HG2	2.10	0.51
1:I:399:GLU:HA	1:I:402:TRP:CD1	2.45	0.51
1:A:419:THR:O	1:A:419:THR:HG23	2.10	0.51
2:F:63:ILE:HD13	2:F:63:ILE:H	1.75	0.51
1:A:318:TYR:CA	1:A:349:LEU:HD21	2.41	0.51
1:E:445:ALA:N	1:E:477:THR:HG21	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.46	0.51
1:A:250:ASP:OD1	1:A:250:ASP:N	2.43	0.51
1:I:465:LYS:HG3	1:I:466:VAL:N	2.26	0.51
1:I:223:LYS:O	1:I:225:PRO:HD3	2.11	0.51
2:F:88:TRP:CZ2	2:F:154:LYS:HD3	2.45	0.51
2:N:368:LEU:HD22	2:N:398:TRP:CZ3	2.45	0.51
2:J:97:PRO:HD2	2:J:181:TYR:CD1	2.46	0.51
2:N:202:ILE:O	2:N:206:ARG:HG3	2.11	0.51
1:I:438:GLU:OE2	1:I:463:ARG:HD2	2.11	0.51
2:B:66:LYS:NZ	2:B:66:LYS:HB3	2.26	0.51
1:I:220:LYS:O	1:I:220:LYS:HD2	2.11	0.51
2:B:242:GLN:NE2	2:B:242:GLN:O	2.44	0.51
1:E:537:PRO:CB	1:E:540:LYS:CB	2.77	0.51
4:L:807:DC:C4	4:L:808:DC:N4	2.79	0.51
1:E:165:THR:HG21	2:F:140:PRO:CG	2.41	0.51
1:M:432:GLU:HG3	1:M:433:PRO:HD2	1.92	0.51
1:M:341:ILE:N	1:M:341:ILE:CD1	2.74	0.51
1:E:400:THR:O	1:E:404:GLU:HG2	2.11	0.51
2:J:5:ILE:O	2:J:7:THR:HG23	2.11	0.50
2:J:422:LEU:HG	2:J:426:TRP:CZ2	2.31	0.50
4:D:817:MRG:H2''	4:D:818:DC:C6	2.45	0.50
1:M:24:TRP:CH2	3:O:704:DC:H5'	2.46	0.50
1:M:303:LEU:HD22	1:M:303:LEU:O	2.11	0.50
2:J:120:LEU:HD23	2:J:121:ASP:H	1.77	0.50
2:F:285:GLY:O	2:F:287:LYS:HG3	2.11	0.50
1:E:537:PRO:HG2	1:E:542:ILE:HD11	1.91	0.50
1:M:91:GLN:HG3	1:M:161:GLN:NE2	2.26	0.50
1:M:44:GLU:HB3	1:M:46:LYS:HE2	1.92	0.50
1:M:459:THR:CG2	1:M:463:ARG:HB2	2.42	0.50
2:J:215:THR:O	2:J:217:PRO:HD3	2.10	0.50
1:M:489:SER:HB2	1:M:493:VAL:HG22	1.92	0.50
1:A:450:THR:O	1:A:451:LYS:HB2	2.11	0.50
1:A:367:GLN:NE2	1:A:512:LYS:HE3	2.25	0.50
4:H:809:DC:H2''	4:H:810:DT:OP2	2.11	0.50
1:A:109:LEU:HD11	1:A:202:ILE:HD11	1.94	0.50
2:N:54:ASN:O	2:N:143:ARG:NH2	2.44	0.50
2:F:88:TRP:CZ3	2:F:89:GLU:HB2	2.46	0.50
2:J:206:ARG:CB	2:J:206:ARG:NH1	2.74	0.50
2:B:120:LEU:HD23	2:B:121:ASP:H	1.76	0.50
1:E:156:SER:O	1:E:157:PRO:C	2.47	0.50
2:F:422:LEU:HG	2:F:426:TRP:CZ2	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:LYS:HD3	6:A:823:ZP4:O2D	2.11	0.50
1:M:337:TRP:HE1	1:M:367:GLN:NE2	2.10	0.50
2:N:380:ILE:O	2:N:384:GLY:HA2	2.11	0.50
1:I:326:ILE:O	1:I:341:ILE:HA	2.11	0.50
1:M:410:TRP:CE2	2:N:363:ASN:ND2	2.80	0.50
1:A:198:HIS:O	1:A:201:LYS:N	2.44	0.50
1:A:168:LEU:HD11	1:A:187:LEU:HD21	1.93	0.50
1:E:535:TRP:O	1:E:536:VAL:HG12	2.11	0.50
1:I:108:VAL:O	1:I:108:VAL:HG23	2.10	0.50
4:H:810:DT:H2''	4:H:811:DG:H8	1.75	0.50
1:E:458:VAL:HG11	1:E:548:VAL:HG22	1.87	0.50
2:F:213:GLY:C	2:F:214:LEU:HD23	2.32	0.50
2:F:270:ILE:HD13	2:F:346:PHE:HB3	1.94	0.50
2:B:263:LYS:HB2	2:B:423:VAL:CG1	2.41	0.50
2:F:169:GLU:N	2:F:170:PRO:HD2	2.27	0.50
1:E:225:PRO:HB2	1:E:226:PRO:HD3	1.93	0.50
2:B:115:TYR:OH	2:B:184:MET:O	2.29	0.50
2:F:108:VAL:O	2:F:232:TYR:OH	2.25	0.50
2:N:206:ARG:NH1	2:N:206:ARG:CB	2.75	0.50
1:A:281:LYS:HG3	1:A:284:ARG:NH1	2.26	0.50
1:A:358:ARG:HH12	2:B:396:GLU:CD	2.14	0.50
1:I:115:TYR:CE1	1:I:184:MET:HE3	2.47	0.50
1:A:108:VAL:HG21	1:A:221:HIS:HD2	1.75	0.50
1:I:282:LEU:HD21	1:I:296:THR:CG2	2.42	0.50
1:A:489:SER:HB2	1:A:493:VAL:HG22	1.93	0.50
1:A:17:ASP:O	1:A:83:ARG:HD3	2.12	0.50
2:F:425:LEU:CB	8:F:438:HOH:O	2.59	0.50
1:I:458:VAL:HG13	1:I:458:VAL:O	2.11	0.50
1:E:489:SER:HB2	1:E:493:VAL:HG22	1.93	0.50
1:A:541:GLY:O	1:A:542:ILE:C	2.50	0.50
1:A:542:ILE:HG22	1:A:543:GLY:N	2.27	0.50
2:N:278:GLN:HG3	2:N:298:GLU:HB3	1.94	0.50
1:E:344:GLU:CB	1:E:345:PRO:CD	2.90	0.50
1:A:237:ASP:O	1:A:238:LYS:HD3	2.12	0.50
2:N:8:VAL:HG21	2:N:159:ILE:HG12	1.94	0.50
2:N:6:GLU:HG3	2:N:6:GLU:O	2.12	0.50
1:E:132:ILE:HD11	1:E:142:ILE:HD11	1.94	0.49
1:A:246:LEU:N	1:A:246:LEU:HD12	2.26	0.49
1:I:132:ILE:HD11	1:I:142:ILE:CD1	2.41	0.49
3:O:707:DG:H2''	3:O:708:DG:C5'	2.38	0.49
2:N:13:LYS:CB	2:N:16:MET:HG3	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:26:LEU:HB2	1:E:31:ILE:CD1	2.42	0.49
1:E:366:LYS:O	1:E:370:GLU:HG3	2.12	0.49
1:I:29:GLU:HG3	1:I:30:LYS:N	2.27	0.49
1:A:138:GLU:OE2	1:A:138:GLU:N	2.44	0.49
1:E:94:ILE:HD11	3:G:708:DG:H21	1.77	0.49
1:A:115:TYR:CD2	6:A:823:ZP4:H2'A	2.47	0.49
2:N:5:ILE:HG23	2:N:119:PRO:HG3	1.94	0.49
4:P:818:DC:H2''	4:P:819:DG:C5'	2.42	0.49
2:N:366:LYS:HA	2:N:405:TYR:CD2	2.47	0.49
1:I:427:TYR:OH	1:I:509:GLN:HA	2.12	0.49
1:A:110:ASP:OD1	1:A:110:ASP:C	2.50	0.49
1:A:175:ASN:HB3	1:A:178:ILE:CD1	2.14	0.49
2:J:263:LYS:N	2:J:423:VAL:HG11	2.27	0.49
2:B:169:GLU:O	2:B:173:LYS:HG3	2.11	0.49
2:B:54:ASN:C	2:B:54:ASN:ND2	2.59	0.49
1:E:338:THR:HG22	1:E:339:TYR:N	2.28	0.49
2:N:207:GLN:O	2:N:210:LEU:HB2	2.13	0.49
2:B:241:VAL:HG22	2:B:350:LYS:HG3	1.94	0.49
2:J:50:ILE:HD13	2:J:145:GLN:HB3	1.93	0.49
1:M:459:THR:OG1	1:M:463:ARG:HB2	2.12	0.49
2:B:207:GLN:O	2:B:210:LEU:HB2	2.12	0.49
4:P:818:DC:H2'	4:P:819:DG:C8	2.47	0.49
1:I:81:ASN:HA	1:I:84:THR:CG2	2.42	0.49
1:E:194:GLU:HB2	1:E:197:GLN:HG3	1.94	0.49
2:N:134:SER:CB	2:N:139:THR:HG23	2.42	0.49
1:A:50:ILE:HG13	1:A:143:ARG:CB	2.42	0.49
2:J:24:TRP:CH2	2:J:403:THR:HG21	2.48	0.49
4:P:806:DT:H1'	4:P:807:DC:H5''	1.93	0.49
1:I:529:GLU:HG2	1:I:530:LYS:HG3	1.94	0.49
2:J:255:ASN:O	2:J:258:GLN:HB2	2.12	0.49
2:J:54:ASN:C	2:J:54:ASN:ND2	2.64	0.49
1:I:282:LEU:HD21	1:I:296:THR:HG22	1.95	0.49
1:M:326:ILE:HD12	1:M:326:ILE:N	2.27	0.49
1:I:58:THR:HG23	1:I:59:PRO:HD2	1.94	0.49
1:E:326:ILE:O	1:E:341:ILE:HA	2.13	0.49
1:I:478:GLU:CG	1:I:499:SER:HB2	2.42	0.49
2:B:335:GLY:HA3	2:B:356:ARG:HG2	1.94	0.49
1:I:132:ILE:CG1	1:I:142:ILE:HG13	2.43	0.49
1:M:298:GLU:N	1:M:298:GLU:OE1	2.45	0.49
1:I:373:GLN:NE2	2:J:397:THR:HG23	2.27	0.49
1:A:317:VAL:CG2	1:A:318:TYR:N	2.71	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:343:GLN:CG	1:M:349:LEU:HD11	2.24	0.49
2:F:13:LYS:CD	2:F:86:ASP:HB2	2.40	0.49
1:A:341:ILE:HD12	1:A:341:ILE:N	2.28	0.49
1:E:493:VAL:HG12	1:E:494:ASN:H	1.77	0.49
2:J:207:GLN:O	2:J:210:LEU:HB2	2.13	0.49
1:I:344:GLU:CB	1:I:345:PRO:CD	2.90	0.49
1:A:270:ILE:HD12	1:A:270:ILE:O	2.12	0.49
2:N:281:LYS:CE	8:N:432:HOH:O	2.60	0.49
2:F:118:VAL:HG12	2:F:119:PRO:O	2.13	0.49
1:E:339:TYR:CD1	1:E:375:ILE:HD11	2.48	0.49
1:E:48:SER:O	1:E:144:TYR:HA	2.13	0.49
1:M:199:ARG:O	1:M:203:GLU:HG3	2.13	0.49
1:I:372:VAL:HG13	1:I:389:PHE:CZ	2.47	0.49
1:M:406:TRP:CD1	1:M:407:GLN:HG2	2.47	0.49
4:L:806:DT:C1'	4:L:807:DC:H5''	2.43	0.49
2:J:266:TRP:CD1	2:J:269:GLN:NE2	2.81	0.49
4:P:821:DC:H2'	4:P:822:2DA:H8	1.95	0.49
1:A:325:LEU:C	1:A:326:ILE:HD12	2.33	0.49
1:E:357:MET:HG2	1:E:367:GLN:OE1	2.13	0.49
2:B:380:ILE:O	2:B:384:GLY:HA2	2.13	0.49
1:E:3:SER:HB3	1:E:5:ILE:HG22	1.95	0.49
1:M:457:TYR:CE2	1:M:465:LYS:HB3	2.47	0.49
1:A:366:LYS:O	1:A:370:GLU:HG3	2.12	0.49
2:F:65:LYS:HA	2:F:407:GLN:OE1	2.12	0.49
1:E:250:ASP:OD1	1:E:250:ASP:N	2.45	0.49
2:J:205:LEU:HD23	2:J:205:LEU:O	2.11	0.49
1:E:536:VAL:O	1:E:537:PRO:O	2.30	0.49
1:I:108:VAL:HG21	1:I:221:HIS:HD2	1.78	0.49
1:M:96:HIS:N	2:N:136:ASN:OD1	2.46	0.49
1:M:151:GLN:OE1	6:M:823:ZP4:N3B	2.46	0.49
1:I:339:TYR:CG	1:I:375:ILE:HD11	2.48	0.49
2:F:207:GLN:O	2:F:210:LEU:HB2	2.13	0.49
2:F:213:GLY:O	2:F:214:LEU:HD23	2.12	0.49
1:I:132:ILE:HD11	1:I:142:ILE:HD11	1.94	0.49
1:E:533:LEU:HD12	1:E:533:LEU:N	2.28	0.48
2:F:54:ASN:ND2	2:F:54:ASN:C	2.64	0.48
1:A:184:MET:HG3	4:D:822:2DA:H1'	1.94	0.48
1:I:199:ARG:O	1:I:203:GLU:HG3	2.13	0.48
1:E:198:HIS:O	1:E:200:THR:N	2.46	0.48
1:M:24:TRP:CE3	3:O:703:DG:H1'	2.47	0.48
1:A:337:TRP:CZ3	1:A:368:LEU:HD13	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:480:GLN:O	1:M:483:TYR:HB3	2.13	0.48
1:M:339:TYR:CZ	1:M:352:GLY:CA	2.72	0.48
4:P:805:DG:C2'	4:P:806:DT:H71	2.43	0.48
1:A:272:PRO:HA	8:A:556:HOH:O	2.13	0.48
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.48	0.48
2:B:24:TRP:CH2	2:B:403:THR:HG21	2.47	0.48
4:L:804:DA:H2''	4:L:805:DG:OP2	2.13	0.48
1:A:458:VAL:HG13	1:A:458:VAL:O	2.13	0.48
2:F:263:LYS:CB	2:F:423:VAL:HG11	2.43	0.48
1:E:283:LEU:CD1	4:H:817:MRG:H231	2.42	0.48
1:I:489:SER:HB2	1:I:493:VAL:HG22	1.94	0.48
1:E:425:LEU:HD22	1:E:509:GLN:NE2	2.28	0.48
2:B:169:GLU:N	2:B:170:PRO:HD2	2.29	0.48
2:J:88:TRP:CE2	2:J:154:LYS:HD3	2.48	0.48
3:O:717:DC:H2''	3:O:718:DA:OP2	2.13	0.48
1:I:326:ILE:HD12	1:I:326:ILE:N	2.28	0.48
1:I:344:GLU:HB3	1:I:345:PRO:HD2	1.93	0.48
1:M:502:ALA:O	1:M:506:ILE:HG12	2.13	0.48
1:M:286:THR:OG1	3:O:714:DG:C4'	2.62	0.48
1:M:357:MET:HG2	1:M:367:GLN:OE1	2.13	0.48
1:M:198:HIS:O	1:M:201:LYS:N	2.46	0.48
1:I:198:HIS:O	1:I:200:THR:N	2.46	0.48
2:J:42:GLU:OE2	2:J:49:LYS:HG3	2.13	0.48
1:E:480:GLN:O	1:E:483:TYR:HB3	2.14	0.48
1:A:480:GLN:O	1:A:483:TYR:HB3	2.13	0.48
1:M:2:ILE:C	1:M:2:ILE:HD13	2.33	0.48
2:F:125:ARG:HB3	2:F:145:GLN:HE21	1.77	0.48
1:I:156:SER:O	1:I:157:PRO:C	2.52	0.48
2:B:255:ASN:O	2:B:258:GLN:HB2	2.14	0.48
1:I:148:VAL:HG22	1:I:149:LEU:N	2.28	0.48
1:E:460:ASN:HB3	2:F:287:LYS:O	2.13	0.48
1:E:242:GLN:O	1:E:243:PRO:C	2.51	0.48
1:I:380:ILE:O	1:I:384:GLY:HA2	2.13	0.48
1:M:27:THR:O	1:M:31:ILE:HG12	2.14	0.48
2:B:206:ARG:CB	2:B:206:ARG:NH1	2.75	0.48
2:B:340:GLN:CG	2:B:351:THR:HG22	2.44	0.48
2:J:85:GLN:HA	2:J:88:TRP:NE1	2.28	0.48
1:I:24:TRP:CZ2	3:K:704:DC:H5'	2.48	0.48
1:A:50:ILE:HG13	1:A:143:ARG:HB2	1.95	0.48
2:F:196:GLY:O	2:F:200:THR:HG23	2.13	0.48
1:E:67:ASP:O	1:E:68:SER:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:GLN:OE1	2:N:3:SER:O	2.32	0.48
1:M:286:THR:OG1	3:O:714:DG:H5''	2.12	0.48
1:A:223:LYS:O	1:A:225:PRO:HD3	2.14	0.48
1:M:287:LYS:HZ3	1:M:293:ILE:HD12	1.79	0.48
1:E:478:GLU:CG	1:E:499:SER:HB2	2.42	0.48
1:I:325:LEU:C	1:I:326:ILE:HD12	2.33	0.48
1:E:31:ILE:O	1:E:35:VAL:HG22	2.14	0.48
1:I:264:LEU:O	1:I:267:ALA:HB3	2.14	0.48
2:N:8:VAL:HG23	2:N:8:VAL:O	2.14	0.48
2:N:417:VAL:HG22	2:N:419:THR:HG23	1.95	0.48
2:J:111:VAL:HG11	2:J:187:LEU:HD12	1.96	0.48
1:A:156:SER:O	1:A:157:PRO:C	2.50	0.48
4:D:805:DG:H2''	4:D:806:DT:H71	1.95	0.48
4:D:809:DC:H2''	4:D:810:DT:H5'	1.94	0.48
3:K:705:DA:H2''	3:K:706:DT:C5'	2.40	0.48
1:M:115:TYR:O	1:M:148:VAL:HG22	2.14	0.48
2:B:332:GLN:HE22	2:B:425:LEU:CD1	2.20	0.48
1:I:501:TYR:HE1	1:I:505:ILE:HD11	1.78	0.48
2:F:115:TYR:OH	2:F:157:PRO:HB3	2.13	0.48
1:I:13:LYS:HE3	1:I:84:THR:O	2.13	0.48
1:A:339:TYR:CD1	1:A:375:ILE:HD11	2.48	0.48
1:I:333:GLY:H	1:I:336:GLN:HB2	1.79	0.48
1:A:221:HIS:NE2	1:A:228:LEU:HB2	2.29	0.48
1:I:529:GLU:O	1:I:530:LYS:HG3	2.13	0.48
2:J:332:GLN:NE2	2:J:425:LEU:HD13	2.29	0.48
1:M:31:ILE:CD1	1:M:133:PRO:HG2	2.40	0.48
1:I:156:SER:HB2	1:I:157:PRO:CD	2.44	0.48
2:N:125:ARG:HB3	2:N:145:GLN:HE21	1.78	0.48
2:F:157:PRO:HG3	2:F:184:MET:HA	1.94	0.48
1:I:238:LYS:HD2	1:I:315:HIS:CE1	2.48	0.48
1:E:188:TYR:CD1	1:E:188:TYR:C	2.87	0.48
4:H:809:DC:H1'	4:H:810:DT:C5'	2.44	0.47
1:E:420:PRO:HA	1:E:421:PRO:C	2.34	0.47
1:E:500:GLN:NE2	2:F:422:LEU:HD13	2.29	0.47
1:E:325:LEU:C	1:E:326:ILE:HD12	2.34	0.47
1:I:260:LEU:O	1:I:264:LEU:HD12	2.13	0.47
2:J:125:ARG:HB3	2:J:145:GLN:HE21	1.78	0.47
2:B:103:LYS:HG3	2:B:192:ASP:OD2	2.13	0.47
1:A:205:LEU:O	1:A:208:HIS:N	2.38	0.47
2:J:303:LEU:HD23	2:J:303:LEU:O	2.14	0.47
1:I:444:GLY:HA3	1:I:477:THR:CG2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:206:ARG:HH11	2:N:206:ARG:HB2	1.78	0.47
1:M:336:GLN:C	1:M:337:TRP:CD1	2.88	0.47
1:A:132:ILE:HD11	1:A:144:TYR:HE2	1.79	0.47
2:B:5:ILE:CG2	2:B:6:GLU:N	2.77	0.47
1:I:502:ALA:O	1:I:506:ILE:HG12	2.14	0.47
4:P:809:DC:H1'	4:P:810:DT:H5'	1.97	0.47
1:E:109:LEU:HD23	1:E:220:LYS:HB2	1.95	0.47
1:M:156:SER:O	1:M:157:PRO:C	2.53	0.47
1:A:420:PRO:HA	1:A:421:PRO:C	2.35	0.47
2:J:202:ILE:O	2:J:206:ARG:HG3	2.15	0.47
1:M:198:HIS:O	1:M:200:THR:N	2.47	0.47
4:H:804:DA:H2''	4:H:805:DG:OP2	2.14	0.47
4:D:806:DT:C6	4:D:806:DT:H5'	2.44	0.47
1:A:475:GLN:HE22	4:D:808:DC:H4'	1.80	0.47
2:F:382:ILE:HB	2:F:383:TRP:CE3	2.50	0.47
1:M:246:LEU:HD12	1:M:246:LEU:N	2.27	0.47
1:E:148:VAL:HG22	1:E:149:LEU:H	1.78	0.47
1:A:393:ILE:HB	1:A:423:VAL:HB	1.96	0.47
2:F:74:LEU:HD12	2:F:75:VAL:N	2.29	0.47
2:N:205:LEU:O	2:N:205:LEU:HD23	2.13	0.47
2:F:242:GLN:O	2:F:242:GLN:NE2	2.47	0.47
1:A:332:GLN:OE1	1:A:332:GLN:HA	2.15	0.47
1:E:246:LEU:N	1:E:246:LEU:HD12	2.29	0.47
2:F:380:ILE:O	2:F:384:GLY:HA2	2.15	0.47
1:E:490:GLY:O	1:E:528:LYS:HD2	2.14	0.47
1:E:529:GLU:HG2	1:E:530:LYS:HG3	1.97	0.47
1:M:57:ASN:HD21	1:M:131:THR:HB	1.78	0.47
2:F:340:GLN:HG3	2:F:351:THR:CG2	2.44	0.47
1:A:278:GLN:HB2	1:A:302:GLU:OE1	2.13	0.47
1:A:338:THR:HG22	1:A:339:TYR:N	2.30	0.47
1:A:13:LYS:HE3	1:A:84:THR:O	2.14	0.47
1:A:318:TYR:O	1:A:349:LEU:HD11	2.15	0.47
1:A:157:PRO:HG3	3:C:707:DG:O4'	2.14	0.47
1:A:475:GLN:NE2	4:D:808:DC:O3'	2.48	0.47
4:D:810:DT:H2''	4:D:811:DG:H8	1.80	0.47
2:J:263:LYS:CA	2:J:423:VAL:HG11	2.45	0.47
1:A:125:ARG:NH1	1:A:147:ASN:CB	2.76	0.47
2:F:13:LYS:CB	2:F:16:MET:HG3	2.42	0.47
2:J:382:ILE:HB	2:J:383:TRP:CE3	2.50	0.47
2:B:382:ILE:HB	2:B:383:TRP:CE3	2.50	0.47
1:M:444:GLY:HA3	1:M:477:THR:CG2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:3:SER:HB2	1:M:119:PRO:CD	2.43	0.47
2:J:206:ARG:HH11	2:J:206:ARG:HB2	1.79	0.47
2:J:72:ARG:NH2	2:J:151:GLN:NE2	2.63	0.47
1:M:77:PHE:CD1	1:M:80:LEU:HD23	2.50	0.47
1:A:502:ALA:O	1:A:506:ILE:HG12	2.15	0.47
1:I:410:TRP:CE2	2:J:363:ASN:ND2	2.83	0.47
2:J:422:LEU:N	2:J:422:LEU:HD23	2.29	0.47
1:M:433:PRO:HB3	2:N:289:LEU:HD23	1.95	0.47
2:N:157:PRO:HG3	2:N:184:MET:HA	1.97	0.47
1:I:116:PHE:HA	1:I:148:VAL:HG21	1.96	0.47
1:E:450:THR:O	1:E:451:LYS:HB2	2.15	0.47
2:B:422:LEU:O	2:B:424:LYS:O	2.33	0.47
2:J:332:GLN:HE22	2:J:425:LEU:HD13	1.80	0.47
1:A:96:HIS:ND1	1:A:97:PRO:HD2	2.30	0.47
2:F:54:ASN:HD21	2:F:56:TYR:HB2	1.79	0.47
1:A:320:ASP:HA	1:A:321:PRO:HD3	1.70	0.47
1:A:242:GLN:O	1:A:243:PRO:C	2.52	0.47
2:J:368:LEU:HD22	2:J:398:TRP:CZ3	2.49	0.47
2:N:76:ASP:C	2:N:78:ARG:H	2.18	0.47
4:D:817:MRG:H2"	4:D:818:DC:H6	1.80	0.47
1:E:81:ASN:HA	1:E:84:THR:CG2	2.44	0.47
1:I:132:ILE:HD11	1:I:144:TYR:HE2	1.80	0.47
1:I:281:LYS:HG3	1:I:284:ARG:NH1	2.30	0.47
1:A:260:LEU:HD23	1:A:279:LEU:HD22	1.97	0.47
1:A:500:GLN:HE22	2:B:422:LEU:HD13	1.79	0.46
1:A:3:SER:HB3	1:A:5:ILE:HG22	1.97	0.46
1:E:49:LYS:HG2	1:E:144:TYR:CE1	2.50	0.46
2:N:363:ASN:ND2	2:N:405:TYR:OH	2.48	0.46
1:A:270:ILE:HG13	1:A:314:VAL:CG2	2.44	0.46
2:B:274:ILE:HA	2:B:306:ASN:OD1	2.15	0.46
2:F:164:MET:O	2:F:165:THR:C	2.52	0.46
2:F:120:LEU:HD23	2:F:121:ASP:H	1.80	0.46
1:E:535:TRP:C	1:E:536:VAL:CG1	2.84	0.46
4:D:806:DT:C1'	4:D:807:DC:H5"	2.46	0.46
1:E:109:LEU:HD23	1:E:220:LYS:CB	2.46	0.46
1:E:303:LEU:O	1:E:303:LEU:HD22	2.15	0.46
2:N:410:TRP:O	2:N:411:ILE:HD13	2.15	0.46
2:F:340:GLN:CG	2:F:351:THR:HG22	2.45	0.46
2:N:340:GLN:CG	2:N:351:THR:HG22	2.44	0.46
1:I:325:LEU:N	1:I:325:LEU:HD12	2.30	0.46
1:M:244:ILE:HD12	1:M:310:LEU:HD23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:VAL:HG21	2:B:159:ILE:HG12	1.97	0.46
1:M:372:VAL:HG13	1:M:389:PHE:CZ	2.50	0.46
2:B:205:LEU:O	2:B:205:LEU:HD23	2.15	0.46
1:E:448:ARG:NH1	1:E:448:ARG:HG2	2.31	0.46
1:I:188:TYR:C	1:I:188:TYR:CD1	2.88	0.46
1:I:27:THR:HG22	1:I:28:GLU:N	2.31	0.46
4:H:820:DC:C2'	4:H:821:DC:H5'	2.40	0.46
1:I:339:TYR:CD1	1:I:375:ILE:HD11	2.50	0.46
3:G:717:DC:H2''	3:G:718:DA:OP2	2.15	0.46
2:J:154:LYS:O	2:J:157:PRO:HD2	2.14	0.46
1:M:389:PHE:HB3	1:M:391:LEU:HD21	1.97	0.46
2:F:379:SER:OG	2:F:387:PRO:HD3	2.16	0.46
4:H:806:DT:C1'	4:H:807:DC:H5''	2.46	0.46
4:H:807:DC:H2''	4:H:808:DC:C5'	2.32	0.46
1:A:97:PRO:HG3	1:A:232:TYR:CD1	2.50	0.46
2:B:266:TRP:CD1	2:B:269:GLN:NE2	2.84	0.46
1:A:372:VAL:HG13	1:A:389:PHE:CE1	2.51	0.46
1:A:324:ASP:OD2	1:A:388:LYS:NZ	2.44	0.46
2:B:307:ARG:HG2	2:B:311:LYS:NZ	2.30	0.46
2:F:417:VAL:O	2:F:417:VAL:HG13	2.15	0.46
1:E:171:PHE:CD2	1:E:205:LEU:HD23	2.51	0.46
1:A:215:THR:HG22	1:A:216:THR:N	2.31	0.46
1:A:282:LEU:HD21	1:A:296:THR:CG2	2.45	0.46
1:M:199:ARG:NH2	1:M:222:GLN:NE2	2.63	0.46
1:A:132:ILE:HG13	1:A:142:ILE:HG13	1.97	0.46
1:E:198:HIS:O	1:E:201:LYS:N	2.48	0.46
2:F:200:THR:O	2:F:204:GLU:HG3	2.15	0.46
1:M:398:TRP:CZ2	1:M:411:ILE:HG12	2.50	0.46
1:E:398:TRP:CZ2	1:E:411:ILE:HG12	2.51	0.46
2:J:242:GLN:O	2:J:242:GLN:NE2	2.49	0.46
1:E:441:TYR:O	1:E:548:VAL:HG21	2.15	0.46
1:M:94:ILE:HD11	3:O:708:DG:N2	2.30	0.46
1:M:115:TYR:HB3	1:M:149:LEU:O	2.16	0.46
1:M:148:VAL:HG22	1:M:149:LEU:N	2.31	0.46
2:N:111:VAL:HG11	2:N:187:LEU:HD13	1.96	0.46
2:J:169:GLU:O	2:J:173:LYS:HG3	2.16	0.46
1:A:3:SER:HB3	1:A:5:ILE:CG2	2.45	0.46
1:M:44:GLU:HB2	1:M:46:LYS:HD3	1.98	0.46
1:M:533:LEU:HD12	1:M:533:LEU:N	2.31	0.46
1:M:548:VAL:O	1:M:551:LEU:HB2	2.15	0.46
2:N:48:SER:HB2	2:N:147:ASN:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:406:TRP:CD1	1:E:407:GLN:HG2	2.51	0.46
1:M:327:ALA:HB2	1:M:341:ILE:HG13	1.97	0.46
1:A:63:ILE:HG21	1:A:74:LEU:HD11	1.97	0.46
1:I:171:PHE:CD2	1:I:205:LEU:HD23	2.51	0.46
1:I:398:TRP:CZ2	1:I:411:ILE:HG12	2.51	0.46
1:A:490:GLY:O	1:A:528:LYS:HD2	2.15	0.46
1:E:536:VAL:HB	1:E:537:PRO:HD2	1.98	0.46
1:M:223:LYS:O	1:M:225:PRO:HD3	2.15	0.46
1:A:24:TRP:CH2	3:C:704:DC:C5'	2.96	0.46
1:M:57:ASN:OD1	1:M:58:THR:N	2.48	0.46
2:B:118:VAL:HB	2:B:149:LEU:HG	1.97	0.46
1:E:116:PHE:CA	1:E:148:VAL:HG21	2.45	0.46
2:B:178:ILE:HG23	2:B:190:GLY:O	2.16	0.46
1:M:171:PHE:CD2	1:M:205:LEU:HD23	2.51	0.46
1:E:223:LYS:O	1:E:225:PRO:HD3	2.16	0.46
2:F:332:GLN:HE22	2:F:425:LEU:CD1	2.28	0.46
1:M:439:THR:HG21	2:N:289:LEU:CD1	2.46	0.46
2:J:303:LEU:HD23	2:J:303:LEU:C	2.36	0.46
4:P:805:DG:H2''	4:P:806:DT:H71	1.98	0.46
4:P:821:DC:H2''	4:P:822:2DA:H5'	1.98	0.46
1:I:438:GLU:OE1	1:I:463:ARG:HD2	2.15	0.46
1:A:259:LYS:HG2	1:A:259:LYS:O	2.16	0.46
1:I:188:TYR:HD1	1:I:188:TYR:O	1.99	0.46
2:N:120:LEU:HD23	2:N:121:ASP:H	1.80	0.46
2:B:388:LYS:HG3	2:B:413:GLU:O	2.16	0.46
2:F:366:LYS:HA	2:F:405:TYR:CD2	2.51	0.46
1:I:250:ASP:OD1	1:I:250:ASP:N	2.45	0.46
1:I:26:LEU:HB2	1:I:31:ILE:HD11	1.96	0.46
1:E:215:THR:CG2	1:E:216:THR:N	2.78	0.46
1:E:132:ILE:CD1	1:E:144:TYR:HE2	2.29	0.46
1:A:478:GLU:HG2	1:A:499:SER:HB2	1.97	0.46
1:I:298:GLU:N	1:I:298:GLU:OE1	2.49	0.46
1:E:475:GLN:NE2	4:H:809:DC:H5'	2.30	0.45
1:E:510:PRO:HG2	1:E:522:ILE:CD1	2.46	0.45
1:M:46:LYS:N	1:M:46:LYS:HD2	2.30	0.45
2:B:85:GLN:HA	2:B:88:TRP:NE1	2.31	0.45
1:E:31:ILE:HD12	1:E:133:PRO:HG2	1.97	0.45
1:E:118:VAL:HB	1:E:149:LEU:HD22	1.98	0.45
2:F:422:LEU:HD23	2:F:422:LEU:H	1.81	0.45
1:I:26:LEU:HB2	1:I:31:ILE:CD1	2.46	0.45
2:N:255:ASN:O	2:N:258:GLN:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:46:LYS:O	2:N:147:ASN:HB2	2.17	0.45
2:B:154:LYS:C	2:B:157:PRO:HD2	2.37	0.45
1:M:325:LEU:HD13	1:M:385:LYS:HE2	1.97	0.45
1:M:11:LYS:O	1:M:85:GLN:HB3	2.16	0.45
1:A:349:LEU:O	1:A:350:LYS:HB2	2.17	0.45
1:M:529:GLU:HG2	1:M:530:LYS:HG3	1.98	0.45
1:M:148:VAL:HG22	1:M:149:LEU:H	1.81	0.45
2:J:6:GLU:CG	2:J:6:GLU:O	2.54	0.45
1:A:107:THR:OG1	1:A:202:ILE:CD1	2.65	0.45
1:A:148:VAL:HG22	1:A:149:LEU:H	1.81	0.45
2:B:112:GLY:C	2:B:151:GLN:HE21	2.19	0.45
1:I:475:GLN:HB3	1:I:501:TYR:CE2	2.52	0.45
2:J:88:TRP:CZ3	2:J:89:GLU:HB2	2.51	0.45
1:M:80:LEU:O	1:M:84:THR:HG22	2.16	0.45
2:B:413:GLU:OE1	2:B:413:GLU:HA	2.16	0.45
1:I:111:VAL:HB	1:I:185:ASP:HB2	1.99	0.45
2:F:212:TRP:N	2:F:212:TRP:CD1	2.84	0.45
1:A:344:GLU:OE1	1:A:347:LYS:HG3	2.15	0.45
4:L:821:DC:H2'	4:L:822:2DA:H8	1.99	0.45
1:A:125:ARG:O	1:A:128:THR:OG1	2.28	0.45
1:E:44:GLU:HB2	1:E:46:LYS:HD3	1.98	0.45
1:A:546:GLU:O	1:A:549:ASP:HB3	2.15	0.45
1:I:148:VAL:HG22	1:I:149:LEU:H	1.81	0.45
1:A:465:LYS:HG3	1:A:466:VAL:N	2.31	0.45
2:F:24:TRP:CH2	2:F:61:PHE:HB3	2.51	0.45
1:E:247:PRO:HB3	1:E:259:LYS:CE	2.47	0.45
2:N:215:THR:C	2:N:217:PRO:HD3	2.36	0.45
1:I:491:LEU:N	1:I:491:LEU:CD1	2.79	0.45
2:J:120:LEU:HD23	2:J:121:ASP:N	2.32	0.45
1:E:365:VAL:HG11	1:E:401:TRP:CD1	2.52	0.45
1:A:475:GLN:HB3	1:A:501:TYR:CD2	2.51	0.45
2:B:422:LEU:N	2:B:422:LEU:HD23	2.32	0.45
2:J:266:TRP:C	2:J:268:SER:H	2.20	0.45
1:A:406:TRP:CD1	1:A:407:GLN:HG2	2.52	0.45
1:M:325:LEU:C	1:M:326:ILE:HD12	2.36	0.45
1:I:13:LYS:HE2	1:I:86:ASP:OD1	2.16	0.45
2:N:350:LYS:HG2	2:N:351:THR:N	2.32	0.45
1:E:171:PHE:CG	1:E:205:LEU:HD23	2.52	0.45
1:M:393:ILE:HB	1:M:423:VAL:HB	1.97	0.45
1:A:87:PHE:CD1	1:A:87:PHE:N	2.84	0.45
1:M:132:ILE:HD11	1:M:142:ILE:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:3:SER:HB3	1:I:5:ILE:CG2	2.46	0.45
2:J:387:PRO:HG2	2:J:389:PHE:CE1	2.52	0.45
1:M:459:THR:OG1	1:M:463:ARG:N	2.49	0.45
2:B:340:GLN:HG3	2:B:351:THR:CG2	2.47	0.45
1:M:441:TYR:CE2	1:M:544:GLY:HA3	2.51	0.45
2:N:103:LYS:HG3	2:N:192:ASP:OD2	2.17	0.45
1:I:382:ILE:O	2:J:136:ASN:HB2	2.16	0.45
3:K:707:DG:H2'	3:K:708:DG:H8	1.82	0.45
1:A:202:ILE:HD12	1:A:202:ILE:HA	1.83	0.45
1:A:232:TYR:CE1	1:A:269:GLN:NE2	2.85	0.45
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.51	0.45
2:N:169:GLU:O	2:N:173:LYS:HG3	2.16	0.45
1:E:493:VAL:CG1	1:E:494:ASN:N	2.79	0.45
2:F:376:THR:HB	2:F:410:TRP:CH2	2.52	0.45
1:A:278:GLN:HB2	1:A:302:GLU:CD	2.36	0.45
1:I:284:ARG:HG3	1:I:284:ARG:HH11	1.81	0.45
2:N:164:MET:O	2:N:165:THR:C	2.55	0.45
2:J:234:LEU:HD21	2:J:377:THR:CG2	2.47	0.45
1:M:92:LEU:CD1	2:N:133:PRO:HA	2.47	0.45
3:G:705:DA:H2''	3:G:706:DT:C5'	2.39	0.45
4:L:803:DC:H2''	4:L:804:DA:C8	2.51	0.45
1:A:148:VAL:HG22	1:A:149:LEU:N	2.32	0.45
2:B:88:TRP:CE2	2:B:154:LYS:HD3	2.52	0.45
2:F:215:THR:C	2:F:217:PRO:HD3	2.38	0.45
1:M:544:GLY:HA2	2:N:286:THR:HG22	1.99	0.45
1:E:29:GLU:O	1:E:32:LYS:HB3	2.16	0.45
1:I:287:LYS:HZ3	1:I:293:ILE:HD12	1.81	0.45
1:A:397:THR:O	1:A:400:THR:HB	2.17	0.45
1:I:402:TRP:CE3	2:J:364:ASP:OD2	2.70	0.45
2:J:34:LEU:HD13	2:J:62:ALA:HB2	1.99	0.45
1:E:312:GLU:HA	1:E:313:PRO:HD2	1.76	0.45
2:F:271:TYR:CD1	2:F:271:TYR:N	2.85	0.45
1:M:221:HIS:HB3	1:M:227:PHE:CD1	2.52	0.45
4:D:806:DT:H1'	4:D:807:DC:H5''	1.98	0.45
2:N:422:LEU:O	2:N:424:LYS:O	2.35	0.45
4:L:807:DC:H2''	4:L:808:DC:C5'	2.38	0.45
2:B:293:ILE:HG23	2:B:294:PRO:HD2	1.99	0.45
1:E:75:VAL:HG11	1:E:77:PHE:CE2	2.52	0.45
1:E:188:TYR:O	1:E:188:TYR:HD1	2.00	0.45
1:E:448:ARG:HH11	1:E:448:ARG:HG2	1.81	0.45
1:A:380:ILE:O	1:A:384:GLY:HA2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:320:ASP:HA	1:E:321:PRO:HD3	1.71	0.45
2:N:375:ILE:H	2:N:375:ILE:HG12	1.60	0.44
2:N:196:GLY:O	2:N:200:THR:HG23	2.17	0.44
1:A:180:ILE:CG2	1:A:187:LEU:HD22	2.46	0.44
1:A:56:TYR:O	1:A:143:ARG:NH2	2.50	0.44
1:M:171:PHE:CE2	1:M:205:LEU:HD23	2.52	0.44
2:B:10:VAL:HG21	2:B:153:TRP:HH2	1.82	0.44
2:B:175:ASN:ND2	2:B:201:LYS:HE2	2.32	0.44
1:E:240:THR:HG22	1:E:315:HIS:HA	1.98	0.44
2:J:13:LYS:HB2	2:J:16:MET:CG	2.36	0.44
2:F:88:TRP:CE2	2:F:154:LYS:HD3	2.53	0.44
2:N:340:GLN:HG3	2:N:351:THR:CG2	2.47	0.44
1:E:23:GLN:HG2	1:E:59:PRO:HA	1.99	0.44
1:I:12:LEU:HD11	1:I:127:TYR:CZ	2.52	0.44
2:F:5:ILE:HG13	2:F:6:GLU:N	2.31	0.44
1:I:448:ARG:NH1	1:I:448:ARG:HG2	2.32	0.44
1:E:24:TRP:CH2	3:G:704:DC:C5'	3.00	0.44
1:A:232:TYR:HE1	1:A:269:GLN:NE2	2.15	0.44
1:A:422:LEU:N	1:A:422:LEU:HD22	2.33	0.44
2:N:266:TRP:O	2:N:269:GLN:HG3	2.17	0.44
1:M:207:GLN:NE2	1:M:210:LEU:HD13	2.31	0.44
2:B:278:GLN:HG3	2:B:298:GLU:HB3	1.99	0.44
2:F:278:GLN:HG3	2:F:298:GLU:HB3	2.00	0.44
1:M:244:ILE:HD13	1:M:244:ILE:O	2.17	0.44
1:I:397:THR:O	1:I:400:THR:HB	2.17	0.44
1:M:541:GLY:O	1:M:542:ILE:C	2.56	0.44
2:J:164:MET:O	2:J:165:THR:C	2.54	0.44
1:E:132:ILE:HD11	1:E:142:ILE:HD12	1.99	0.44
1:E:181:TYR:CE2	2:F:138:GLU:HA	2.52	0.44
1:I:344:GLU:O	1:I:345:PRO:C	2.55	0.44
1:A:358:ARG:HE	1:A:358:ARG:HB2	1.65	0.44
1:I:448:ARG:HH11	1:I:448:ARG:HG2	1.83	0.44
2:J:46:LYS:HD2	2:J:116:PHE:HB3	1.99	0.44
1:I:320:ASP:HA	1:I:321:PRO:HD3	1.73	0.44
1:M:278:GLN:HB2	1:M:302:GLU:CD	2.37	0.44
1:M:380:ILE:O	1:M:384:GLY:HA2	2.17	0.44
1:E:502:ALA:O	1:E:506:ILE:HG12	2.17	0.44
1:M:238:LYS:HD2	1:M:315:HIS:ND1	2.32	0.44
1:I:206:ARG:HG3	1:I:216:THR:CG2	2.47	0.44
2:N:332:GLN:HE22	2:N:425:LEU:CD1	2.29	0.44
2:B:350:LYS:HG2	2:B:351:THR:N	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:417:VAL:HG22	2:F:419:THR:HG23	1.98	0.44
1:A:333:GLY:H	1:A:336:GLN:HB2	1.82	0.44
1:E:63:ILE:HG12	1:E:64:LYS:N	2.32	0.44
2:B:363:ASN:ND2	2:B:405:TYR:OH	2.50	0.44
1:M:188:TYR:C	1:M:188:TYR:CD1	2.90	0.44
1:M:317:VAL:HG12	1:M:348:ASN:O	2.17	0.44
1:A:91:GLN:HG2	1:A:161:GLN:NE2	2.33	0.44
2:J:266:TRP:C	2:J:268:SER:N	2.71	0.44
2:B:157:PRO:HG3	2:B:184:MET:HA	1.98	0.44
1:I:463:ARG:HG2	1:I:463:ARG:NH1	2.32	0.44
1:I:24:TRP:CH2	3:K:704:DC:H5'	2.53	0.44
1:I:25:PRO:HD2	3:K:703:DG:C2	2.53	0.44
1:M:320:ASP:HA	1:M:321:PRO:HD3	1.73	0.44
1:A:77:PHE:CD1	1:A:80:LEU:HD23	2.52	0.44
2:F:31:ILE:HD12	2:F:135:ILE:HG12	2.00	0.44
2:J:11:LYS:HG2	2:J:11:LYS:H	1.57	0.44
1:A:98:ALA:O	1:A:349:LEU:HD22	2.18	0.44
1:I:113:ASP:HA	6:I:823:ZP4:N3B	2.33	0.44
2:B:258:GLN:O	2:B:259:LYS:C	2.56	0.44
1:I:289:LEU:CD1	1:I:289:LEU:H	2.28	0.44
1:A:444:GLY:HA3	1:A:477:THR:CG2	2.45	0.44
2:F:266:TRP:C	2:F:268:SER:H	2.21	0.44
4:D:819:DG:H2'	4:D:820:DC:C6	2.51	0.44
1:E:56:TYR:O	1:E:143:ARG:NH2	2.50	0.44
1:A:281:LYS:CG	1:A:284:ARG:NH1	2.80	0.44
1:M:278:GLN:HB2	1:M:302:GLU:OE1	2.18	0.44
1:E:254:VAL:HG23	1:E:291:GLU:O	2.17	0.44
4:D:812:DT:H2''	4:D:813:DT:OP2	2.17	0.44
1:A:511:ASP:C	1:A:511:ASP:OD1	2.56	0.44
1:M:510:PRO:HG2	1:M:522:ILE:CD1	2.48	0.44
1:A:3:SER:HB2	1:A:119:PRO:HD3	1.99	0.44
1:I:458:VAL:HG11	1:I:548:VAL:HG22	2.00	0.44
1:I:57:ASN:HD21	1:I:131:THR:HB	1.83	0.44
1:I:254:VAL:HB	1:I:288:ALA:O	2.18	0.44
1:A:339:TYR:O	1:A:352:GLY:N	2.51	0.44
1:M:2:ILE:HG23	1:M:2:ILE:O	2.18	0.44
1:A:448:ARG:HG2	1:A:448:ARG:NH1	2.32	0.44
1:E:221:HIS:NE2	6:E:823:ZP4:N1R	2.66	0.44
4:P:806:DT:C1'	4:P:807:DC:H5''	2.48	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.52	0.44
1:A:458:VAL:HG12	1:A:548:VAL:CG2	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:94:ILE:HA	1:M:95:PRO:HD3	1.87	0.44
1:M:287:LYS:HZ2	1:M:293:ILE:HD12	1.83	0.44
2:F:115:TYR:OH	2:F:184:MET:O	2.34	0.44
2:B:57:ASN:OD1	2:B:143:ARG:NH1	2.50	0.44
2:J:63:ILE:HD13	2:J:63:ILE:N	2.32	0.44
1:E:412:PRO:O	1:E:414:TRP:HD1	2.01	0.44
1:E:205:LEU:O	1:E:208:HIS:N	2.34	0.44
1:M:132:ILE:CG1	1:M:142:ILE:HG13	2.48	0.44
1:A:513:SER:OG	1:A:514:GLU:N	2.51	0.44
2:N:62:ALA:O	2:N:63:ILE:HG22	2.17	0.44
2:N:379:SER:OG	2:N:387:PRO:HD3	2.18	0.44
4:P:807:DC:H5'	4:P:807:DC:H6	1.83	0.43
3:G:707:DG:C2'	3:G:708:DG:H5'	2.35	0.43
1:A:91:GLN:CG	1:A:161:GLN:NE2	2.81	0.43
2:J:422:LEU:O	2:J:424:LYS:O	2.36	0.43
1:E:109:LEU:CD2	1:E:220:LYS:CE	2.94	0.43
1:E:440:PHE:N	1:E:494:ASN:O	2.45	0.43
4:D:820:DC:H2''	4:D:821:DC:H5'	1.99	0.43
2:F:198:HIS:O	2:F:202:ILE:HG12	2.18	0.43
1:M:194:GLU:HB2	1:M:197:GLN:HG3	1.98	0.43
1:A:457:TYR:CE2	1:A:465:LYS:HB3	2.53	0.43
1:A:188:TYR:C	1:A:188:TYR:CD1	2.92	0.43
1:M:317:VAL:CG2	1:M:318:TYR:H	2.25	0.43
1:A:111:VAL:HG13	1:A:215:THR:O	2.18	0.43
2:J:57:ASN:OD1	2:J:143:ARG:NH1	2.51	0.43
1:E:42:GLU:OE1	1:E:49:LYS:HG3	2.19	0.43
1:E:50:ILE:HG13	1:E:143:ARG:HB3	2.00	0.43
1:E:96:HIS:ND1	1:E:97:PRO:HD2	2.34	0.43
1:A:169:GLU:HB3	1:A:170:PRO:HD3	1.98	0.43
1:M:312:GLU:HA	1:M:313:PRO:HD2	1.79	0.43
1:E:475:GLN:NE2	4:H:808:DC:O3'	2.52	0.43
3:C:707:DG:H2''	3:C:708:DG:C5'	2.36	0.43
1:A:529:GLU:HG2	1:A:530:LYS:HG3	2.00	0.43
1:E:427:TYR:HE2	1:E:429:LEU:HD21	1.84	0.43
2:N:180:ILE:HG23	2:N:187:LEU:HD21	1.99	0.43
2:N:125:ARG:HB3	2:N:145:GLN:NE2	2.34	0.43
1:A:27:THR:HG22	1:A:28:GLU:N	2.33	0.43
1:M:325:LEU:HB2	1:M:387:PRO:HB3	2.00	0.43
2:N:88:TRP:CZ3	2:N:89:GLU:HB2	2.53	0.43
1:E:325:LEU:N	1:E:325:LEU:HD12	2.33	0.43
2:J:368:LEU:HD11	2:J:392:PRO:HD2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:412:PRO:O	1:M:414:TRP:HD1	2.02	0.43
1:M:448:ARG:NH1	1:M:448:ARG:HG2	2.33	0.43
1:M:339:TYR:CE2	1:M:352:GLY:HA3	2.42	0.43
1:A:342:TYR:HD2	1:A:344:GLU:O	1.96	0.43
2:N:422:LEU:HD23	2:N:422:LEU:N	2.32	0.43
4:L:805:DG:H2''	4:L:806:DT:H71	2.00	0.43
1:I:165:THR:HG21	2:J:140:PRO:CG	2.42	0.43
2:B:339:TYR:C	2:B:340:GLN:NE2	2.72	0.43
2:B:368:LEU:C	2:B:368:LEU:HD23	2.38	0.43
1:A:207:GLN:NE2	1:A:210:LEU:HD13	2.33	0.43
2:N:108:VAL:O	2:N:232:TYR:OH	2.27	0.43
1:I:50:ILE:HG13	1:I:143:ARG:HB2	2.01	0.43
1:I:440:PHE:N	1:I:494:ASN:O	2.46	0.43
1:M:260:LEU:HD21	1:M:303:LEU:HD23	1.99	0.43
1:I:434:ILE:HG21	1:I:492:GLU:HB3	2.00	0.43
4:L:807:DC:H5'	4:L:807:DC:H6	1.84	0.43
4:H:817:MRG:H2''	4:H:818:DC:H6	1.83	0.43
1:E:125:ARG:NH1	1:E:147:ASN:CB	2.81	0.43
1:E:44:GLU:HB3	1:E:46:LYS:HE2	2.00	0.43
1:E:505:ILE:HG12	1:E:505:ILE:H	1.53	0.43
1:I:457:TYR:CE2	1:I:465:LYS:HB3	2.54	0.43
2:B:23:GLN:HG3	2:B:24:TRP:N	2.32	0.43
2:J:366:LYS:HA	2:J:405:TYR:CD2	2.54	0.43
2:J:31:ILE:HD12	2:J:135:ILE:HG12	2.00	0.43
1:A:178:ILE:N	1:A:178:ILE:CD1	2.82	0.43
4:H:806:DT:H6	4:H:806:DT:H5'	1.82	0.43
4:D:807:DC:C2'	4:D:808:DC:H5'	2.40	0.43
1:A:441:TYR:CD2	1:A:544:GLY:CA	2.95	0.43
2:J:76:ASP:C	2:J:78:ARG:H	2.20	0.43
2:N:169:GLU:N	2:N:170:PRO:CD	2.82	0.43
2:J:54:ASN:HD21	2:J:56:TYR:HB2	1.84	0.43
2:N:57:ASN:OD1	2:N:143:ARG:NH1	2.51	0.43
2:J:104:LYS:C	2:J:104:LYS:HD3	2.38	0.43
2:J:196:GLY:O	2:J:200:THR:HG23	2.18	0.43
2:N:366:LYS:HD3	8:N:430:HOH:O	2.17	0.43
2:J:125:ARG:HD3	2:J:147:ASN:HD22	1.83	0.43
1:E:171:PHE:CE2	1:E:205:LEU:HD23	2.54	0.43
1:E:380:ILE:O	1:E:384:GLY:HA2	2.18	0.43
1:A:118:VAL:HA	1:A:119:PRO:HD3	1.85	0.43
2:B:375:ILE:HB	2:B:389:PHE:CZ	2.52	0.43
4:D:821:DC:H2''	4:D:822:2DA:H5'	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:340:GLN:CG	2:J:351:THR:HG22	2.47	0.43
1:M:325:LEU:HD12	1:M:325:LEU:N	2.34	0.43
1:E:325:LEU:HB2	1:E:387:PRO:HB3	2.01	0.43
1:E:180:ILE:CG2	1:E:187:LEU:HD22	2.49	0.43
1:I:118:VAL:HB	1:I:149:LEU:HD22	2.00	0.43
1:A:171:PHE:CD2	1:A:205:LEU:HD23	2.54	0.43
1:I:171:PHE:CG	1:I:205:LEU:HD23	2.53	0.43
2:B:279:LEU:HA	2:B:282:LEU:HD13	2.01	0.43
1:E:277:ARG:HG2	1:E:277:ARG:HH11	1.84	0.43
2:B:206:ARG:HB2	2:B:206:ARG:HH11	1.82	0.43
1:I:73:LYS:HD2	1:I:146:TYR:OH	2.19	0.43
2:J:410:TRP:O	2:J:411:ILE:HD13	2.19	0.43
1:M:332:GLN:OE1	1:M:332:GLN:HA	2.19	0.43
2:F:188:TYR:CD1	2:F:188:TYR:N	2.87	0.43
1:A:475:GLN:HE21	4:D:809:DC:H5''	1.84	0.43
4:L:805:DG:C2'	4:L:806:DT:H71	2.49	0.43
2:J:254:VAL:HG22	2:J:293:ILE:CD1	2.44	0.43
1:E:46:LYS:O	1:E:147:ASN:HB2	2.18	0.43
2:B:202:ILE:O	2:B:206:ARG:HG3	2.19	0.43
1:E:208:HIS:HA	1:E:211:ARG:CZ	2.48	0.43
1:M:448:ARG:HH11	1:M:448:ARG:HG2	1.84	0.43
4:P:816:DG:C6	4:P:817:MRG:C6	3.02	0.43
2:F:35:VAL:O	2:F:39:THR:HG23	2.18	0.43
1:I:247:PRO:HB3	1:I:259:LYS:CE	2.49	0.43
1:I:537:PRO:HB2	1:I:540:LYS:HB2	2.01	0.43
2:N:303:LEU:C	2:N:303:LEU:HD23	2.39	0.43
1:E:332:GLN:HA	1:E:332:GLN:OE1	2.18	0.43
1:E:115:TYR:C	1:E:117:SER:H	2.21	0.43
1:E:458:VAL:HG13	1:E:458:VAL:O	2.18	0.43
2:F:112:GLY:C	2:F:151:GLN:HE21	2.22	0.43
2:N:54:ASN:C	2:N:54:ASN:ND2	2.71	0.43
1:I:95:PRO:HB2	1:I:229:TRP:CH2	2.54	0.43
2:F:154:LYS:C	2:F:157:PRO:HD2	2.39	0.43
1:M:5:ILE:HD12	1:M:6:GLU:H	1.82	0.43
1:A:198:HIS:C	1:A:200:THR:N	2.72	0.43
1:A:23:GLN:HG2	1:A:59:PRO:HA	2.00	0.43
1:I:332:GLN:HA	1:I:332:GLN:OE1	2.18	0.43
1:I:3:SER:OG	1:I:117:SER:O	2.33	0.42
2:F:375:ILE:HB	2:F:389:PHE:CZ	2.53	0.42
1:I:420:PRO:HA	1:I:421:PRO:C	2.38	0.42
1:A:26:LEU:HB2	1:A:31:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:77:PHE:CD1	1:E:80:LEU:HD23	2.54	0.42
2:N:108:VAL:N	2:N:232:TYR:OH	2.52	0.42
1:M:289:LEU:HD12	1:M:289:LEU:N	2.32	0.42
1:A:448:ARG:HG2	1:A:448:ARG:HH11	1.84	0.42
2:F:178:ILE:HG23	2:F:190:GLY:O	2.19	0.42
1:M:435:VAL:HG22	2:N:290:THR:HG21	2.01	0.42
1:A:417:VAL:O	1:A:417:VAL:HG13	2.19	0.42
1:M:27:THR:HG22	1:M:28:GLU:N	2.35	0.42
2:F:389:PHE:HB3	2:F:391:LEU:CD2	2.49	0.42
2:N:266:TRP:C	2:N:268:SER:H	2.23	0.42
1:I:303:LEU:HD22	1:I:303:LEU:O	2.19	0.42
2:F:63:ILE:HD13	2:F:63:ILE:N	2.33	0.42
1:I:171:PHE:CD1	1:I:205:LEU:HD23	2.54	0.42
1:M:132:ILE:HD11	1:M:142:ILE:HD11	2.01	0.42
1:I:46:LYS:N	1:I:46:LYS:HD2	2.34	0.42
2:F:320:ASP:C	2:F:320:ASP:OD1	2.58	0.42
1:M:511:ASP:C	1:M:511:ASP:OD1	2.57	0.42
4:D:805:DG:C2'	4:D:806:DT:H71	2.48	0.42
4:D:805:DG:H2''	4:D:806:DT:OP2	2.19	0.42
1:I:266:TRP:CE2	4:L:820:DC:H4'	2.55	0.42
2:B:425:LEU:HD23	2:B:425:LEU:HA	1.76	0.42
2:F:425:LEU:HD23	2:F:425:LEU:HA	1.78	0.42
2:J:258:GLN:O	2:J:259:LYS:C	2.58	0.42
1:E:260:LEU:HD23	1:E:279:LEU:CD2	2.49	0.42
2:N:104:LYS:C	2:N:104:LYS:HD3	2.38	0.42
3:C:717:DC:H2''	3:C:718:DA:OP2	2.19	0.42
1:E:171:PHE:CD1	1:E:205:LEU:HD23	2.53	0.42
1:I:312:GLU:HA	1:I:313:PRO:HD2	1.82	0.42
1:E:179:VAL:HG23	1:E:179:VAL:O	2.18	0.42
1:M:250:ASP:OD1	1:M:250:ASP:N	2.46	0.42
1:A:179:VAL:O	1:A:179:VAL:HG23	2.19	0.42
1:E:422:LEU:N	1:E:422:LEU:CD2	2.82	0.42
1:M:215:THR:HG22	1:M:216:THR:N	2.34	0.42
1:E:244:ILE:CG2	1:E:244:ILE:O	2.65	0.42
1:I:57:ASN:OD1	1:I:58:THR:N	2.52	0.42
1:M:439:THR:CG2	2:N:289:LEU:HD13	2.48	0.42
2:F:363:ASN:HB3	2:F:366:LYS:HB3	2.00	0.42
2:N:70:LYS:HD3	2:N:70:LYS:HA	1.80	0.42
1:I:417:VAL:O	1:I:417:VAL:HG13	2.19	0.42
1:A:94:ILE:HD12	3:C:709:DC:H1'	2.00	0.42
1:E:156:SER:HB2	1:E:157:PRO:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:57:ASN:HD21	1:I:131:THR:CB	2.31	0.42
1:A:302:GLU:O	1:A:303:LEU:C	2.58	0.42
1:I:118:VAL:O	1:I:148:VAL:HG23	2.20	0.42
2:J:363:ASN:ND2	2:J:405:TYR:OH	2.52	0.42
1:I:171:PHE:CE2	1:I:205:LEU:HD23	2.54	0.42
1:M:171:PHE:CG	1:M:205:LEU:HD23	2.54	0.42
2:N:386:THR:HG23	2:N:387:PRO:HD2	2.00	0.42
1:E:465:LYS:HG3	1:E:466:VAL:N	2.34	0.42
2:B:111:VAL:HG11	2:B:187:LEU:HD12	2.02	0.42
1:I:87:PHE:N	1:I:87:PHE:CD1	2.87	0.42
2:B:76:ASP:C	2:B:78:ARG:H	2.23	0.42
2:N:59:PRO:HG2	2:N:76:ASP:HB3	2.02	0.42
1:M:44:GLU:OE1	1:M:46:LYS:HE2	2.20	0.42
1:M:459:THR:HG21	1:M:463:ARG:HB2	2.01	0.42
1:I:548:VAL:O	1:I:551:LEU:HB2	2.20	0.42
2:N:183:TYR:CD2	2:N:380:ILE:HD13	2.54	0.42
2:N:368:LEU:HD23	2:N:368:LEU:C	2.40	0.42
2:B:270:ILE:CD1	2:B:346:PHE:HD1	2.33	0.42
1:A:463:ARG:NH1	1:A:463:ARG:HG2	2.34	0.42
1:I:419:THR:O	1:I:419:THR:HG23	2.20	0.42
2:F:422:LEU:O	2:F:424:LYS:O	2.38	0.42
1:M:254:VAL:HG21	1:M:287:LYS:HB2	2.02	0.42
1:A:287:LYS:HZ2	1:A:293:ILE:HD12	1.81	0.42
1:A:327:ALA:CB	1:A:341:ILE:HG13	2.47	0.42
1:A:25:PRO:CD	3:C:703:DG:N2	2.81	0.42
1:I:341:ILE:N	1:I:341:ILE:HD12	2.34	0.42
2:J:111:VAL:HG11	2:J:187:LEU:CD1	2.49	0.42
2:N:62:ALA:C	2:N:63:ILE:CG2	2.87	0.42
1:I:222:GLN:O	1:I:224:GLU:HG3	2.20	0.42
1:E:529:GLU:O	1:E:530:LYS:CG	2.67	0.42
1:A:165:THR:CG2	2:B:140:PRO:CG	2.97	0.42
4:P:819:DG:H2'	4:P:820:DC:H6	1.84	0.42
2:J:215:THR:C	2:J:217:PRO:HD3	2.40	0.42
1:M:92:LEU:HD12	2:N:133:PRO:HA	2.01	0.42
2:N:17:ASP:O	2:N:83:ARG:NH1	2.53	0.42
1:A:57:ASN:OD1	1:A:58:THR:N	2.53	0.42
1:M:275:LYS:HB2	1:M:275:LYS:HE3	1.88	0.42
1:E:529:GLU:C	1:E:530:LYS:HG3	2.39	0.42
1:I:94:ILE:HD13	3:K:708:DG:H21	1.84	0.42
4:H:817:MRG:H2''	4:H:818:DC:C6	2.55	0.42
2:J:169:GLU:N	2:J:170:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:182:GLN:HG3	1:E:182:GLN:O	2.20	0.42
1:M:444:GLY:HA2	1:M:552:VAL:HG11	2.01	0.42
1:M:458:VAL:CG1	1:M:548:VAL:HG22	2.47	0.42
2:N:339:TYR:C	2:N:340:GLN:NE2	2.72	0.42
1:I:497:THR:OG1	1:I:499:SER:HB3	2.20	0.42
1:I:459:THR:CG2	1:I:463:ARG:HB2	2.50	0.42
1:M:29:GLU:HG3	1:M:30:LYS:N	2.35	0.42
1:E:424:LYS:NZ	1:E:426:TRP:CZ3	2.87	0.42
1:M:97:PRO:HG3	1:M:232:TYR:CD1	2.54	0.42
1:I:60:VAL:HG12	1:I:75:VAL:HG13	2.02	0.42
2:J:301:LEU:O	2:J:305:GLU:HB2	2.20	0.42
1:A:67:ASP:O	1:A:68:SER:HB2	2.19	0.42
2:B:80:LEU:O	2:B:80:LEU:HD22	2.20	0.42
1:A:552:VAL:HG22	1:A:552:VAL:H	1.65	0.42
2:N:376:THR:HB	2:N:410:TRP:CH2	2.55	0.42
2:B:118:VAL:HG12	2:B:119:PRO:O	2.20	0.42
2:B:166:LYS:O	2:B:167:ILE:C	2.57	0.42
2:N:242:GLN:O	2:N:242:GLN:NE2	2.53	0.42
1:I:221:HIS:NE2	1:I:228:LEU:HB2	2.35	0.41
2:N:258:GLN:O	2:N:259:LYS:C	2.59	0.41
2:N:382:ILE:HB	2:N:383:TRP:CE3	2.55	0.41
1:I:422:LEU:HD22	1:I:422:LEU:N	2.35	0.41
1:I:80:LEU:O	1:I:80:LEU:HD12	2.20	0.41
1:A:247:PRO:HB3	1:A:259:LYS:CE	2.50	0.41
1:I:194:GLU:HB2	1:I:197:GLN:HG3	2.01	0.41
1:A:438:GLU:CD	1:A:463:ARG:HD2	2.39	0.41
4:P:808:DC:H1'	4:P:809:DC:H5'	2.02	0.41
2:N:125:ARG:HD3	2:N:147:ASN:HD22	1.84	0.41
1:M:277:ARG:HB2	1:M:336:GLN:CD	2.41	0.41
2:B:376:THR:HB	2:B:410:TRP:CH2	2.55	0.41
2:F:339:TYR:O	2:F:340:GLN:NE2	2.53	0.41
1:E:32:LYS:O	1:E:35:VAL:CG2	2.69	0.41
2:J:49:LYS:HG2	2:J:144:TYR:CE1	2.54	0.41
2:B:366:LYS:HA	2:B:405:TYR:CD2	2.55	0.41
1:M:188:TYR:O	1:M:188:TYR:HD1	2.02	0.41
2:F:216:THR:HG22	2:F:216:THR:O	2.18	0.41
1:E:537:PRO:HB3	1:E:540:LYS:HB2	1.92	0.41
4:P:804:DA:H2''	4:P:805:DG:OP2	2.20	0.41
4:D:810:DT:H2''	4:D:811:DG:C8	2.54	0.41
2:F:170:PRO:HG2	2:F:208:HIS:NE2	2.35	0.41
2:N:254:VAL:HG22	2:N:293:ILE:CD1	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:422:LEU:HD22	1:M:422:LEU:N	2.35	0.41
1:I:182:GLN:HG3	1:I:182:GLN:O	2.19	0.41
2:B:266:TRP:C	2:B:268:SER:H	2.24	0.41
2:J:339:TYR:C	2:J:340:GLN:NE2	2.73	0.41
1:M:441:TYR:HA	1:M:496:VAL:HG22	2.01	0.41
1:M:260:LEU:HD23	1:M:279:LEU:HD22	2.02	0.41
2:J:363:ASN:HB3	2:J:366:LYS:HB3	2.01	0.41
1:E:87:PHE:N	1:E:87:PHE:CD1	2.87	0.41
1:M:115:TYR:CZ	6:M:823:ZP4:H2'A	2.56	0.41
1:A:217:PRO:C	1:A:219:LYS:H	2.23	0.41
2:F:13:LYS:HE3	2:F:86:ASP:N	2.33	0.41
2:N:170:PRO:HG2	2:N:208:HIS:NE2	2.35	0.41
2:B:198:HIS:O	2:B:202:ILE:HG12	2.20	0.41
2:B:184:MET:HB3	2:B:185:ASP:H	1.47	0.41
2:B:328:GLU:O	2:B:339:TYR:HA	2.21	0.41
1:A:31:ILE:HG12	1:A:31:ILE:H	1.65	0.41
1:E:75:VAL:HG11	1:E:77:PHE:CZ	2.55	0.41
1:A:270:ILE:HG13	1:A:314:VAL:HG21	2.02	0.41
1:E:188:TYR:O	1:E:188:TYR:CD1	2.73	0.41
2:F:386:THR:HG23	2:F:387:PRO:HD2	2.02	0.41
2:B:178:ILE:HG22	2:B:179:VAL:N	2.35	0.41
2:J:302:GLU:HA	2:J:305:GLU:CB	2.49	0.41
6:I:823:ZP4:O21	8:I:564:HOH:O	2.22	0.41
3:O:708:DG:H2'	3:O:709:DC:H6	1.81	0.41
2:F:422:LEU:N	2:F:422:LEU:HD23	2.35	0.41
2:J:59:PRO:HG2	2:J:76:ASP:HB3	2.03	0.41
2:B:13:LYS:HB2	2:B:16:MET:CG	2.45	0.41
1:A:215:THR:CG2	1:A:216:THR:N	2.83	0.41
1:I:255:ASN:HB3	8:I:558:HOH:O	2.20	0.41
2:J:198:HIS:O	2:J:202:ILE:HG12	2.20	0.41
1:E:344:GLU:HB3	1:E:345:PRO:HD3	2.02	0.41
2:F:111:VAL:HG11	2:F:187:LEU:HD12	2.03	0.41
2:B:186:ASP:HB3	2:B:188:TYR:CE1	2.55	0.41
1:E:17:ASP:O	1:E:83:ARG:HD3	2.20	0.41
3:C:705:DA:C2'	3:C:706:DT:H5'	2.40	0.41
1:A:505:ILE:H	1:A:505:ILE:HG12	1.56	0.41
1:M:115:TYR:C	1:M:117:SER:H	2.23	0.41
2:F:118:VAL:HG12	2:F:119:PRO:N	2.35	0.41
2:B:125:ARG:HB3	2:B:145:GLN:HE21	1.86	0.41
2:F:178:ILE:HG22	2:F:179:VAL:N	2.35	0.41
2:B:270:ILE:HD11	2:B:346:PHE:HD1	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:205:LEU:O	2:F:205:LEU:HD23	2.21	0.41
1:E:419:THR:HG23	1:E:419:THR:O	2.21	0.41
2:N:302:GLU:HA	2:N:305:GLU:HB3	2.02	0.41
1:E:221:HIS:NE2	1:E:228:LEU:HB2	2.36	0.41
1:A:529:GLU:C	1:A:530:LYS:HG3	2.40	0.41
4:H:821:DC:H2''	4:H:822:2DA:C5'	2.50	0.41
1:I:23:GLN:HG2	1:I:59:PRO:HA	2.02	0.41
1:E:116:PHE:HA	1:E:148:VAL:CG2	2.50	0.41
1:E:278:GLN:HB2	1:E:302:GLU:OE1	2.20	0.41
2:F:183:TYR:CD2	2:F:380:ILE:HD13	2.56	0.41
1:A:81:ASN:HA	1:A:84:THR:HG22	2.02	0.41
1:E:451:LYS:HD3	1:E:451:LYS:HA	1.85	0.41
2:J:393:ILE:HD13	2:J:398:TRP:HB2	2.02	0.41
2:J:302:GLU:HA	2:J:305:GLU:HB3	2.02	0.41
2:B:164:MET:O	2:B:165:THR:C	2.57	0.41
2:F:80:LEU:HD13	2:F:80:LEU:O	2.20	0.41
1:M:529:GLU:C	1:M:530:LYS:HG3	2.40	0.41
4:D:808:DC:H1'	4:D:809:DC:H5'	2.03	0.41
2:B:13:LYS:HE3	2:B:86:ASP:N	2.36	0.41
1:I:255:ASN:HB2	1:I:289:LEU:HB3	2.03	0.41
2:F:266:TRP:C	2:F:268:SER:N	2.73	0.41
1:I:202:ILE:HD12	1:I:202:ILE:HA	1.66	0.41
2:N:257:ILE:O	2:N:261:VAL:HG23	2.21	0.41
1:I:478:GLU:HG2	1:I:499:SER:HB2	2.01	0.41
1:M:180:ILE:CG2	1:M:187:LEU:HD22	2.51	0.41
1:A:171:PHE:CE2	1:A:205:LEU:HD23	2.55	0.41
2:B:8:VAL:O	2:B:8:VAL:HG23	2.20	0.41
2:N:307:ARG:HG2	2:N:311:LYS:NZ	2.36	0.41
1:E:543:GLY:O	1:E:547:GLN:NE2	2.53	0.41
2:F:49:LYS:HG2	2:F:144:TYR:CE1	2.55	0.41
1:M:417:VAL:O	1:M:417:VAL:HG13	2.20	0.41
1:M:330:GLN:HE21	1:M:330:GLN:HB2	1.74	0.41
2:N:11:LYS:HG2	2:N:11:LYS:H	1.61	0.41
1:M:286:THR:HG1	3:O:714:DG:H4'	1.84	0.41
1:I:178:ILE:N	1:I:178:ILE:CD1	2.83	0.41
1:I:511:ASP:OD1	1:I:511:ASP:C	2.59	0.41
2:J:16:MET:SD	2:J:83:ARG:HB3	2.61	0.41
1:M:510:PRO:O	1:M:522:ILE:HD12	2.20	0.41
1:M:91:GLN:CG	1:M:161:GLN:NE2	2.84	0.41
2:N:266:TRP:C	2:N:268:SER:N	2.74	0.41
3:G:723:DC:H2''	3:G:724:DT:OP2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:VAL:CG1	1:A:494:ASN:N	2.84	0.41
1:M:281:LYS:CG	1:M:284:ARG:NH1	2.84	0.41
1:I:302:GLU:O	1:I:303:LEU:C	2.59	0.41
1:E:198:HIS:C	1:E:200:THR:N	2.74	0.41
1:M:171:PHE:CZ	1:M:205:LEU:HD23	2.56	0.41
1:M:132:ILE:HD11	1:M:144:TYR:HE2	1.86	0.41
2:N:62:ALA:O	2:N:63:ILE:CG2	2.68	0.41
1:A:188:TYR:O	1:A:188:TYR:HD1	2.04	0.41
2:B:303:LEU:HD23	2:B:303:LEU:C	2.41	0.41
1:I:513:SER:OG	1:I:514:GLU:N	2.54	0.41
2:F:84:THR:O	2:F:87:PHE:HB3	2.21	0.41
1:A:130:PHE:N	1:A:130:PHE:CD1	2.89	0.41
2:B:216:THR:HG22	2:B:216:THR:O	2.21	0.41
1:M:136:ASN:OD1	1:M:138:GLU:HB3	2.20	0.41
2:J:266:TRP:O	2:J:269:GLN:HG3	2.21	0.41
2:N:198:HIS:O	2:N:202:ILE:HG12	2.21	0.41
2:J:350:LYS:HG2	2:J:351:THR:N	2.36	0.41
1:I:278:GLN:HB2	1:I:302:GLU:CD	2.42	0.41
1:E:344:GLU:O	1:E:345:PRO:C	2.59	0.41
8:I:562:HOH:O	2:J:50:ILE:C	2.58	0.41
2:N:274:ILE:HD11	2:N:309:ILE:HB	2.03	0.41
2:B:60:VAL:HG11	2:B:130:PHE:CD2	2.55	0.41
2:F:134:SER:CB	2:F:139:THR:HG23	2.51	0.41
1:A:310:LEU:HD12	1:A:310:LEU:N	2.36	0.41
2:J:212:TRP:CD1	2:J:212:TRP:N	2.89	0.41
1:M:221:HIS:HB3	1:M:227:PHE:HD1	1.86	0.40
1:I:221:HIS:HB3	1:I:227:PHE:CD1	2.56	0.40
1:I:522:ILE:H	1:I:522:ILE:HG12	1.76	0.40
1:E:427:TYR:CE2	1:E:429:LEU:HD21	2.56	0.40
2:N:293:ILE:HG23	2:N:294:PRO:HD2	2.03	0.40
2:N:187:LEU:HD23	2:N:187:LEU:C	2.42	0.40
2:B:266:TRP:C	2:B:268:SER:N	2.73	0.40
1:E:358:ARG:NH1	2:F:396:GLU:OE2	2.55	0.40
2:J:125:ARG:HB3	2:J:145:GLN:NE2	2.35	0.40
2:N:96:HIS:HA	2:N:97:PRO:HD2	1.98	0.40
1:M:247:PRO:HB3	1:M:259:LYS:CE	2.51	0.40
3:G:705:DA:C2'	3:G:706:DT:H5'	2.40	0.40
2:B:263:LYS:HA	2:B:423:VAL:HG11	2.00	0.40
1:M:282:LEU:HD21	1:M:296:THR:HG22	2.04	0.40
2:F:254:VAL:HG22	2:F:293:ILE:CD1	2.45	0.40
2:J:283:LEU:O	2:J:284:ARG:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ILE:CD1	1:A:144:TYR:HE2	2.34	0.40
1:E:56:TYR:O	1:E:57:ASN:HB2	2.21	0.40
2:N:363:ASN:HB3	2:N:366:LYS:HB3	2.02	0.40
1:I:198:HIS:C	1:I:200:THR:N	2.73	0.40
1:I:130:PHE:CE1	1:I:144:TYR:HB2	2.56	0.40
1:A:533:LEU:N	1:A:533:LEU:HD12	2.36	0.40
1:M:420:PRO:HA	1:M:421:PRO:C	2.41	0.40
1:E:202:ILE:HD12	1:E:202:ILE:HA	1.81	0.40
1:M:491:LEU:CD1	1:M:491:LEU:N	2.83	0.40
2:B:215:THR:C	2:B:217:PRO:HD3	2.42	0.40
1:A:194:GLU:HB2	1:A:197:GLN:HG3	2.04	0.40
1:E:171:PHE:CE1	1:E:205:LEU:HD23	2.56	0.40
1:M:171:PHE:CD1	1:M:205:LEU:HD23	2.56	0.40
1:M:72:ARG:CG	1:M:151:GLN:HE22	2.34	0.40
1:M:165:THR:HG21	2:N:140:PRO:HG2	2.03	0.40
2:J:54:ASN:O	2:J:143:ARG:NH2	2.54	0.40
1:I:317:VAL:CG2	1:I:318:TYR:H	2.28	0.40
2:B:155:GLY:C	2:B:157:PRO:HD2	2.42	0.40
1:I:19:PRO:HD3	1:I:80:LEU:HD13	2.03	0.40
2:J:154:LYS:C	2:J:157:PRO:HD2	2.41	0.40
1:I:278:GLN:HB2	1:I:302:GLU:OE1	2.21	0.40
1:I:463:ARG:HH11	1:I:463:ARG:HG2	1.86	0.40
2:J:368:LEU:HD23	2:J:368:LEU:C	2.41	0.40
2:N:62:ALA:C	2:N:63:ILE:HG23	2.40	0.40
2:J:417:VAL:HG22	2:J:419:THR:HG23	2.03	0.40
1:M:221:HIS:NE2	1:M:228:LEU:HB2	2.37	0.40
1:E:115:TYR:HE1	1:E:184:MET:HE1	1.85	0.40
1:E:317:VAL:CG2	1:E:318:TYR:N	2.71	0.40
2:J:263:LYS:HE3	2:J:263:LYS:HB2	1.86	0.40
1:E:266:TRP:CE2	4:H:820:DC:H4'	2.56	0.40
4:H:818:DC:H2'	4:H:819:DG:C8	2.56	0.40
1:A:427:TYR:HE2	1:A:429:LEU:HD21	1.87	0.40
1:A:118:VAL:O	1:A:148:VAL:HG23	2.21	0.40
1:A:432:GLU:CG	1:A:433:PRO:HD2	2.49	0.40
1:A:25:PRO:CG	3:C:703:DG:H22	2.35	0.40
1:E:199:ARG:O	1:E:203:GLU:HG3	2.22	0.40
1:M:202:ILE:HD12	1:M:202:ILE:HA	1.87	0.40
1:E:325:LEU:HD13	1:E:385:LYS:HE2	2.03	0.40
1:I:459:THR:OG1	1:I:463:ARG:HB2	2.20	0.40
1:A:247:PRO:O	1:A:252:TRP:HH2	2.04	0.40
2:B:34:LEU:HD12	2:B:34:LEU:HA	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:173:LYS:O	1:E:176:PRO:HD3	2.22	0.40
1:A:173:LYS:O	1:A:176:PRO:HD3	2.22	0.40
2:J:134:SER:CB	2:J:139:THR:HG23	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	551/557 (99%)	487 (88%)	55 (10%)	9 (2%)	12	52
1	E	551/557 (99%)	491 (89%)	56 (10%)	4 (1%)	26	71
1	I	551/557 (99%)	486 (88%)	60 (11%)	5 (1%)	21	65
1	M	551/557 (99%)	494 (90%)	51 (9%)	6 (1%)	17	61
2	B	409/444 (92%)	367 (90%)	42 (10%)	0	100	100
2	F	409/444 (92%)	363 (89%)	45 (11%)	1 (0%)	52	88
2	J	409/444 (92%)	366 (90%)	42 (10%)	1 (0%)	52	88
2	N	409/444 (92%)	364 (89%)	43 (10%)	2 (0%)	34	76
All	All	3840/4004 (96%)	3418 (89%)	394 (10%)	28 (1%)	26	71

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	542	ILE
1	A	199	ARG
1	E	199	ARG
1	E	537	PRO
2	J	6	GLU
1	M	199	ARG
1	I	199	ARG

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Mol	Chain	Res	Type
2	N	4	PRO
1	A	546	GLU
1	I	463	ARG
1	M	345	PRO
1	A	345	PRO
1	A	350	LYS
1	A	458	VAL
1	I	458	VAL
1	M	243	PRO
1	M	549	ASP
1	A	284	ARG
1	A	463	ARG
1	E	458	VAL
2	F	286	THR
1	I	285	GLY
2	N	18	GLY
1	E	243	PRO
1	I	505	ILE
1	A	243	PRO
1	M	505	ILE
1	M	542	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	494/497 (99%)	467 (94%)	27 (6%)	27	66
1	E	494/497 (99%)	466 (94%)	28 (6%)	25	65
1	I	494/497 (99%)	462 (94%)	32 (6%)	21	60
1	M	494/497 (99%)	466 (94%)	28 (6%)	25	65
2	B	375/403 (93%)	354 (94%)	21 (6%)	26	66
2	F	375/403 (93%)	355 (95%)	20 (5%)	28	67
2	J	375/403 (93%)	358 (96%)	17 (4%)	34	73
2	N	375/403 (93%)	356 (95%)	19 (5%)	29	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3476/3600 (97%)	3284 (94%)	192 (6%)	27 66

All (192) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	5	ILE
1	A	23	GLN
1	A	102	LYS
1	A	108	VAL
1	A	109	LEU
1	A	110	ASP
1	A	137	ASN
1	A	149	LEU
1	A	188	TYR
1	A	220	LYS
1	A	225	PRO
1	A	279	LEU
1	A	305	GLU
1	A	324	ASP
1	A	329	ILE
1	A	330	GLN
1	A	332	GLN
1	A	349	LEU
1	A	386	THR
1	A	387	PRO
1	A	419	THR
1	A	432	GLU
1	A	448	ARG
1	A	475	GLN
1	A	505	ILE
1	A	548	VAL
2	B	24	TRP
2	B	54	ASN
2	B	63	ILE
2	B	83	ARG
2	B	120	LEU
2	B	139	THR
2	B	150	PRO
2	B	232	TYR
2	B	248	GLU
2	B	253	THR

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Mol	Chain	Res	Type
2	B	271	TYR
2	B	296	THR
2	B	298	GLU
2	B	315	HIS
2	B	356	ARG
2	B	357	MET
2	B	375	ILE
2	B	410	TRP
2	B	414	TRP
2	B	422	LEU
2	B	426	TRP
1	E	2	ILE
1	E	5	ILE
1	E	23	GLN
1	E	67	ASP
1	E	86	ASP
1	E	102	LYS
1	E	108	VAL
1	E	137	ASN
1	E	142	ILE
1	E	149	LEU
1	E	220	LYS
1	E	225	PRO
1	E	238	LYS
1	E	279	LEU
1	E	305	GLU
1	E	324	ASP
1	E	325	LEU
1	E	329	ILE
1	E	330	GLN
1	E	332	GLN
1	E	386	THR
1	E	387	PRO
1	E	419	THR
1	E	432	GLU
1	E	448	ARG
1	E	475	GLN
1	E	505	ILE
1	E	548	VAL
2	F	24	TRP
2	F	54	ASN
2	F	63	ILE

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Mol	Chain	Res	Type
2	F	83	ARG
2	F	120	LEU
2	F	139	THR
2	F	157	PRO
2	F	248	GLU
2	F	253	THR
2	F	271	TYR
2	F	296	THR
2	F	298	GLU
2	F	356	ARG
2	F	357	MET
2	F	375	ILE
2	F	392	PRO
2	F	410	TRP
2	F	414	TRP
2	F	422	LEU
2	F	426	TRP
1	I	5	ILE
1	I	23	GLN
1	I	67	ASP
1	I	70	LYS
1	I	86	ASP
1	I	102	LYS
1	I	108	VAL
1	I	110	ASP
1	I	137	ASN
1	I	149	LEU
1	I	188	TYR
1	I	202	ILE
1	I	215	THR
1	I	220	LYS
1	I	238	LYS
1	I	244	ILE
1	I	258	CYS
1	I	301	LEU
1	I	305	GLU
1	I	324	ASP
1	I	329	ILE
1	I	330	GLN
1	I	332	GLN
1	I	379	SER
1	I	386	THR

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Mol	Chain	Res	Type
1	I	387	PRO
1	I	419	THR
1	I	432	GLU
1	I	448	ARG
1	I	475	GLN
1	I	505	ILE
1	I	548	VAL
2	J	5	ILE
2	J	24	TRP
2	J	54	ASN
2	J	63	ILE
2	J	83	ARG
2	J	120	LEU
2	J	139	THR
2	J	248	GLU
2	J	271	TYR
2	J	296	THR
2	J	298	GLU
2	J	315	HIS
2	J	356	ARG
2	J	410	TRP
2	J	414	TRP
2	J	422	LEU
2	J	426	TRP
1	M	2	ILE
1	M	5	ILE
1	M	23	GLN
1	M	67	ASP
1	M	102	LYS
1	M	108	VAL
1	M	110	ASP
1	M	137	ASN
1	M	149	LEU
1	M	188	TYR
1	M	220	LYS
1	M	225	PRO
1	M	244	ILE
1	M	279	LEU
1	M	284	ARG
1	M	305	GLU
1	M	324	ASP
1	M	329	ILE

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Mol	Chain	Res	Type
1	M	330	GLN
1	M	332	GLN
1	M	386	THR
1	M	419	THR
1	M	432	GLU
1	M	448	ARG
1	M	475	GLN
1	M	505	ILE
1	M	512	LYS
1	M	548	VAL
2	N	24	TRP
2	N	54	ASN
2	N	63	ILE
2	N	64	LYS
2	N	66	LYS
2	N	83	ARG
2	N	120	LEU
2	N	139	THR
2	N	248	GLU
2	N	253	THR
2	N	271	TYR
2	N	296	THR
2	N	298	GLU
2	N	356	ARG
2	N	357	MET
2	N	410	TRP
2	N	414	TRP
2	N	422	LEU
2	N	426	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	57	ASN
1	A	91	GLN
1	A	137	ASN
1	A	161	GLN
1	A	174	GLN
1	A	182	GLN
1	A	207	GLN
1	A	222	GLN

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Mol	Chain	Res	Type
1	A	330	GLN
1	A	373	GLN
1	A	407	GLN
1	A	428	GLN
1	A	447	ASN
1	A	475	GLN
1	A	500	GLN
1	A	509	GLN
1	A	524	GLN
2	B	54	ASN
2	B	147	ASN
2	B	151	GLN
2	B	161	GLN
2	B	175	ASN
2	B	182	GLN
2	B	207	GLN
2	B	242	GLN
2	B	269	GLN
2	B	332	GLN
2	B	336	GLN
2	B	363	ASN
1	E	23	GLN
1	E	57	ASN
1	E	91	GLN
1	E	137	ASN
1	E	161	GLN
1	E	182	GLN
1	E	207	GLN
1	E	222	GLN
1	E	330	GLN
1	E	367	GLN
1	E	407	GLN
1	E	428	GLN
1	E	447	ASN
1	E	475	GLN
1	E	500	GLN
1	E	509	GLN
1	E	520	GLN
1	E	524	GLN
1	E	547	GLN
2	F	54	ASN
2	F	147	ASN

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Mol	Chain	Res	Type
2	F	151	GLN
2	F	161	GLN
2	F	175	ASN
2	F	182	GLN
2	F	207	GLN
2	F	242	GLN
2	F	269	GLN
2	F	332	GLN
2	F	336	GLN
2	F	363	ASN
1	I	57	ASN
1	I	91	GLN
1	I	137	ASN
1	I	151	GLN
1	I	182	GLN
1	I	207	GLN
1	I	222	GLN
1	I	269	GLN
1	I	330	GLN
1	I	367	GLN
1	I	373	GLN
1	I	407	GLN
1	I	428	GLN
1	I	447	ASN
1	I	475	GLN
1	I	500	GLN
1	I	509	GLN
2	J	54	ASN
2	J	151	GLN
2	J	161	GLN
2	J	175	ASN
2	J	182	GLN
2	J	207	GLN
2	J	242	GLN
2	J	332	GLN
2	J	336	GLN
2	J	363	ASN
1	M	57	ASN
1	M	91	GLN
1	M	137	ASN
1	M	151	GLN
1	M	161	GLN

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Mol	Chain	Res	Type
1	M	182	GLN
1	M	207	GLN
1	M	222	GLN
1	M	330	GLN
1	M	367	GLN
1	M	373	GLN
1	M	407	GLN
1	M	428	GLN
1	M	447	ASN
1	M	475	GLN
1	M	509	GLN
1	M	520	GLN
1	M	524	GLN
2	N	54	ASN
2	N	151	GLN
2	N	161	GLN
2	N	175	ASN
2	N	207	GLN
2	N	242	GLN
2	N	332	GLN
2	N	336	GLN
2	N	363	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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
4	MRG	D	817	1,3,4	20,28,29	1.74	3 (15%)	25,39,42	3.71	6 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	2DA	D	822	3,4	14,22,23	0.66	0	13,31,34	0.91	0
4	MRG	H	817	1,3,4	20,28,29	1.57	3 (15%)	25,39,42	3.82	8 (32%)
4	2DA	H	822	3,4	14,22,23	0.67	0	13,31,34	1.07	0
4	MRG	L	817	1,3,4	20,28,29	1.51	3 (15%)	25,39,42	3.67	9 (36%)
4	2DA	L	822	3,4	14,22,23	0.64	0	13,31,34	0.93	0
4	MRG	P	817	1,3,4	20,28,29	1.47	2 (10%)	25,39,42	3.68	8 (32%)
4	2DA	P	822	3,4	14,22,23	0.57	0	13,31,34	0.93	0

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
4	MRG	D	817	1,3,4	-	0/8/26/27	0/3/3/3
4	2DA	D	822	3,4	-	0/3/18/19	0/3/3/3
4	MRG	H	817	1,3,4	-	0/8/26/27	0/3/3/3
4	2DA	H	822	3,4	-	0/3/18/19	0/3/3/3
4	MRG	L	817	1,3,4	-	0/8/26/27	0/3/3/3
4	2DA	L	822	3,4	-	0/3/18/19	0/3/3/3
4	MRG	P	817	1,3,4	-	0/8/26/27	0/3/3/3
4	2DA	P	822	3,4	-	0/3/18/19	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	817	MRG	C21-N2	-5.54	1.33	1.46
4	L	817	MRG	C21-N2	-5.16	1.34	1.46
4	H	817	MRG	C21-N2	-4.83	1.34	1.46
4	P	817	MRG	C21-N2	-4.78	1.34	1.46
4	D	817	MRG	C8-N7	-2.26	1.30	1.34
4	H	817	MRG	C8-N7	-2.20	1.30	1.34
4	L	817	MRG	C8-N7	-2.20	1.30	1.34
4	D	817	MRG	C6-N1	3.04	1.38	1.33
4	L	817	MRG	C6-N1	3.13	1.38	1.33
4	P	817	MRG	C6-N1	3.48	1.39	1.33
4	H	817	MRG	C6-N1	3.51	1.39	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	817	MRG	C21-N2-C2	-13.25	98.74	123.80
4	P	817	MRG	C21-N2-C2	-12.69	99.79	123.80
4	L	817	MRG	C21-N2-C2	-12.49	100.18	123.80
4	D	817	MRG	C21-N2-C2	-12.18	100.76	123.80
4	D	817	MRG	C5-C6-N1	-9.09	111.16	123.59
4	H	817	MRG	C5-C6-N1	-8.95	111.36	123.59
4	P	817	MRG	C5-C6-N1	-8.72	111.66	123.59
4	L	817	MRG	C5-C6-N1	-8.67	111.73	123.59
4	D	817	MRG	C23-C22-C21	-4.40	98.59	113.12
4	H	817	MRG	C23-C22-C21	-4.26	99.07	113.12
4	P	817	MRG	C23-C22-C21	-4.19	99.28	113.12
4	L	817	MRG	C23-C22-C21	-4.19	99.28	113.12
4	H	817	MRG	C2'-C1'-N9	-3.46	105.76	114.16
4	D	817	MRG	C2-N3-C4	-3.20	111.24	115.09
4	D	817	MRG	C2'-C1'-N9	-3.14	106.52	114.16
4	L	817	MRG	C2-N3-C4	-2.91	111.58	115.09
4	P	817	MRG	C2-N3-C4	-2.78	111.74	115.09
4	H	817	MRG	C2-N3-C4	-2.76	111.76	115.09
4	L	817	MRG	C2'-C1'-N9	-2.62	107.79	114.16
4	P	817	MRG	C2'-C1'-N9	-2.41	108.30	114.16
4	L	817	MRG	N2-C2-N3	2.05	121.06	117.22
4	L	817	MRG	C22-C21-N2	2.06	117.04	111.46
4	P	817	MRG	C22-C23-S24	2.09	119.78	112.45
4	L	817	MRG	C22-C23-S24	2.14	119.99	112.45
4	H	817	MRG	C22-C23-S24	2.19	120.14	112.45
4	P	817	MRG	C22-C21-N2	2.27	117.60	111.46
4	H	817	MRG	C22-C21-N2	2.44	118.07	111.46
4	H	817	MRG	C6-N1-C2	6.64	124.96	115.31
4	L	817	MRG	C6-N1-C2	6.69	125.03	115.31
4	P	817	MRG	C6-N1-C2	6.75	125.13	115.31
4	D	817	MRG	C6-N1-C2	6.93	125.38	115.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	817	MRG	2	0
4	D	822	2DA	2	0
4	H	817	MRG	3	0
4	H	822	2DA	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	822	2DA	1	0
4	P	817	MRG	1	0
4	P	822	2DA	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	$\# Z > 2$
6	ZP4	A	823	5	40,57,57	1.44	5 (12%)	52,88,88	2.88	9 (17%)
7	GOL	B	429	-	5,5,5	0.69	0	5,5,5	0.60	0
6	ZP4	E	823	5	40,57,57	1.48	7 (17%)	52,88,88	2.85	9 (17%)
7	GOL	F	429	-	5,5,5	0.73	0	5,5,5	0.82	0
6	ZP4	I	823	5	40,57,57	1.50	6 (15%)	52,88,88	2.87	9 (17%)
6	ZP4	M	823	5	40,57,57	1.44	6 (15%)	52,88,88	2.81	8 (15%)

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
6	ZP4	A	823	5	-	0/33/69/69	0/5/5/5
7	GOL	B	429	-	-	0/4/4/4	0/0/0/0
6	ZP4	E	823	5	-	0/33/69/69	0/5/5/5
7	GOL	F	429	-	-	0/4/4/4	0/0/0/0
6	ZP4	I	823	5	-	0/33/69/69	0/5/5/5
6	ZP4	M	823	5	-	0/33/69/69	0/5/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	823	ZP4	C6-C5	-2.51	1.33	1.40
6	I	823	ZP4	C6-C5	-2.08	1.34	1.40
6	A	823	ZP4	C6-N1	2.11	1.38	1.35
6	E	823	ZP4	C2R-N1R	2.13	1.38	1.33
6	M	823	ZP4	C4R-N3R	2.15	1.38	1.35
6	M	823	ZP4	C6-N1	2.35	1.38	1.35
6	I	823	ZP4	C6-N1	2.35	1.38	1.35
6	E	823	ZP4	C4-N3	2.45	1.37	1.33
6	I	823	ZP4	C2R-N3R	2.50	1.36	1.32
6	A	823	ZP4	C2R-N3R	2.68	1.36	1.32
6	M	823	ZP4	C2R-N3R	2.70	1.37	1.32
6	E	823	ZP4	C2R-N3R	2.84	1.37	1.32
6	M	823	ZP4	C4-N3	2.85	1.38	1.33
6	E	823	ZP4	C4R-N3R	3.05	1.40	1.35
6	A	823	ZP4	C4-N3	3.19	1.39	1.33
6	I	823	ZP4	C4-N3	3.33	1.39	1.33
6	A	823	ZP4	O41-C11	3.77	1.46	1.41
6	E	823	ZP4	O41-C11	3.92	1.46	1.41
6	M	823	ZP4	O41-C11	4.13	1.46	1.41
6	E	823	ZP4	C5R-C4R	4.20	1.50	1.40
6	I	823	ZP4	C5R-C4R	4.29	1.50	1.40
6	M	823	ZP4	C5R-C4R	4.38	1.50	1.40
6	A	823	ZP4	C5R-C4R	4.48	1.50	1.40
6	I	823	ZP4	O41-C11	4.73	1.47	1.41

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	823	ZP4	C5-C4-N3	-9.70	114.34	125.14
6	E	823	ZP4	N3R-C2R-N1R	-9.22	121.83	128.89
6	E	823	ZP4	C5-C4-N3	-9.10	115.01	125.14
6	I	823	ZP4	C5-C4-N3	-9.03	115.09	125.14
6	M	823	ZP4	C5-C4-N3	-8.90	115.23	125.14
6	M	823	ZP4	N3R-C2R-N1R	-8.54	122.36	128.89
6	A	823	ZP4	N3R-C2R-N1R	-8.52	122.37	128.89
6	I	823	ZP4	N3R-C2R-N1R	-8.45	122.43	128.89
6	I	823	ZP4	C4R-C5R-N7R	-2.81	106.89	109.48
6	I	823	ZP4	PG-O3B-PB	-2.78	124.92	132.73
6	A	823	ZP4	C4R-C5R-N7R	-2.69	107.00	109.48
6	E	823	ZP4	C4R-C5R-N7R	-2.52	107.16	109.48
6	M	823	ZP4	C4R-C5R-N7R	-2.48	107.20	109.48
6	M	823	ZP4	PG-O3B-PB	-2.35	126.13	132.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	823	ZP4	PB-O3A-PA	-2.34	126.17	132.73
6	A	823	ZP4	PD-O3G-PG	-2.32	126.20	132.73
6	A	823	ZP4	PB-O3A-PA	-2.29	126.29	132.73
6	E	823	ZP4	PD-O3G-PG	-2.26	126.40	132.73
6	I	823	ZP4	O3G-PD-O51	-2.10	97.36	102.94
6	A	823	ZP4	PG-O3B-PB	-2.07	126.90	132.73
6	E	823	ZP4	PG-O3B-PB	-2.04	127.00	132.73
6	E	823	ZP4	O31-C31-C41	-2.00	105.05	111.05
6	E	823	ZP4	C5A-C5-C6	2.01	122.66	118.62
6	M	823	ZP4	C2R-N1R-C6R	2.03	122.39	118.77
6	A	823	ZP4	C2R-N1R-C6R	2.10	122.52	118.77
6	I	823	ZP4	C2R-N1R-C6R	2.14	122.59	118.77
6	M	823	ZP4	C5A-C5-C6	2.17	122.98	118.62
6	E	823	ZP4	C2R-N1R-C6R	2.20	122.70	118.77
6	A	823	ZP4	C5A-C5-C6	2.25	123.14	118.62
6	I	823	ZP4	C5A-C5-C6	2.32	123.30	118.62
6	I	823	ZP4	C2'-C1'-N1	2.73	120.81	114.16
6	E	823	ZP4	C4-N3-C2	13.85	127.22	115.25
6	M	823	ZP4	C4-N3-C2	13.89	127.25	115.25
6	A	823	ZP4	C4-N3-C2	13.95	127.31	115.25
6	I	823	ZP4	C4-N3-C2	14.01	127.36	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	823	ZP4	4	0
6	E	823	ZP4	6	0
6	I	823	ZP4	6	0
6	M	823	ZP4	3	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, 95th 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 ²)	Q<0.9
1	A	553/557 (99%)	0.26	4 (0%) 89 82	14, 49, 75, 100	0
1	E	553/557 (99%)	0.20	3 (0%) 91 87	17, 54, 80, 100	0
1	I	553/557 (99%)	0.50	26 (4%) 35 20	41, 84, 110, 118	0
1	M	553/557 (99%)	1.26	137 (24%) 1 1	51, 108, 126, 135	0
2	B	413/444 (93%)	0.33	14 (3%) 49 32	12, 40, 96, 107	0
2	F	413/444 (93%)	0.30	11 (2%) 58 42	16, 44, 95, 111	0
2	J	413/444 (93%)	0.74	38 (9%) 11 5	35, 88, 117, 126	0
2	N	413/444 (93%)	1.07	79 (19%) 2 1	71, 98, 121, 130	0
3	C	23/27 (85%)	0.12	1 (4%) 39 23	20, 40, 68, 106	0
3	G	23/27 (85%)	-0.05	1 (4%) 39 23	20, 47, 76, 106	0
3	K	23/27 (85%)	0.04	1 (4%) 39 23	47, 95, 120, 131	0
3	O	23/27 (85%)	0.23	1 (4%) 39 23	79, 108, 131, 144	0
4	D	18/21 (85%)	-0.06	0 100 100	18, 44, 77, 103	0
4	H	18/21 (85%)	-0.31	0 100 100	34, 52, 91, 111	0
4	L	18/21 (85%)	-0.17	0 100 100	55, 82, 133, 139	0
4	P	18/21 (85%)	0.01	0 100 100	88, 105, 137, 139	0
All	All	4028/4196 (95%)	0.55	316 (7%) 16 8	12, 73, 118, 144	0

All (316) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	359	GLY	9.1
2	J	67	ASP	8.1
1	M	114	ALA	8.0
1	M	244	ILE	7.2
1	M	247	PRO	6.8

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Mol	Chain	Res	Type	RSRZ
2	N	423	VAL	6.7
1	M	306	ASN	6.7
1	M	19	PRO	6.6
2	N	87	PHE	6.4
1	M	135	ILE	6.3
1	M	134	SER	6.3
2	J	360	ALA	6.2
1	M	65	LYS	6.0
1	M	133	PRO	5.9
1	M	132	ILE	5.7
2	N	88	TRP	5.3
2	J	88	TRP	5.3
1	M	252	TRP	5.3
2	N	141	GLY	5.2
1	M	215	THR	5.1
2	N	231	GLY	5.1
1	M	30	LYS	5.1
1	M	271	TYR	5.1
1	M	34	LEU	5.0
2	J	354	TYR	5.0
1	M	111	VAL	5.0
2	N	4	PRO	4.9
3	K	703	DG	4.9
1	M	251	SER	4.9
1	M	144	TYR	4.9
1	M	17	ASP	4.8
2	N	237	ASP	4.8
1	M	20	LYS	4.7
1	M	229	TRP	4.6
2	N	105	SER	4.6
1	M	354	TYR	4.6
1	M	136	ASN	4.6
2	F	359	GLY	4.4
2	F	3	SER	4.4
2	F	214	LEU	4.4
1	M	6	GLU	4.4
1	M	293	ILE	4.3
1	M	222	GLN	4.3
2	B	232	TYR	4.3
1	I	62	ALA	4.2
2	F	67	ASP	4.2
2	F	358	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
1	M	2	ILE	4.2
2	B	231	GLY	4.2
1	M	80	LEU	4.1
2	N	361	HIS	4.1
2	N	273	GLY	4.1
2	N	115	TYR	4.1
2	B	67	ASP	4.1
3	O	703	DG	4.0
1	M	33	ALA	4.0
1	M	302	GLU	4.0
1	M	178	ILE	4.0
2	N	243	PRO	4.0
1	M	232	TYR	3.9
1	M	388	LYS	3.9
1	M	102	LYS	3.9
1	I	61	PHE	3.9
2	J	94	ILE	3.9
2	B	214	LEU	3.9
1	M	225	PRO	3.9
1	M	69	THR	3.9
1	I	222	GLN	3.8
2	N	360	ALA	3.8
1	M	115	TYR	3.8
2	N	107	THR	3.8
1	M	423	VAL	3.7
1	M	124	PHE	3.7
2	N	67	ASP	3.7
2	N	128	THR	3.7
1	M	36	GLU	3.7
1	M	422	LEU	3.7
1	M	299	ALA	3.6
2	N	389	PHE	3.6
1	M	310	LEU	3.6
1	M	66	LYS	3.6
2	J	95	PRO	3.6
1	I	455	ALA	3.6
2	J	274	ILE	3.6
1	M	150	PRO	3.5
2	N	106	VAL	3.5
2	N	424	LYS	3.5
1	I	247	PRO	3.5
1	M	58	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	M	246	LEU	3.4
1	A	207	GLN	3.4
2	N	240	THR	3.4
2	N	323	LYS	3.4
2	N	214	LEU	3.4
1	M	323	LYS	3.4
1	M	186	ASP	3.4
1	I	454	LYS	3.4
2	N	357	MET	3.3
2	N	177	ASP	3.3
1	M	248	GLU	3.3
2	N	246	LEU	3.3
1	M	63	ILE	3.3
1	M	64	LYS	3.3
2	B	423	VAL	3.3
2	B	3	SER	3.3
1	M	391	LEU	3.3
2	J	280	SER	3.3
3	G	703	DG	3.3
1	M	73	LYS	3.3
1	M	286	THR	3.3
2	N	54	ASN	3.2
1	M	205	LEU	3.2
1	M	174	GLN	3.2
2	J	68	SER	3.2
3	C	703	DG	3.2
2	J	100	LEU	3.2
1	M	237	ASP	3.2
1	M	131	THR	3.2
1	I	67	ASP	3.2
1	A	68	SER	3.2
2	N	93	GLY	3.2
1	I	68	SER	3.1
2	J	164	MET	3.1
2	J	355	ALA	3.1
2	N	242	GLN	3.1
2	N	38	CYS	3.0
1	M	16	MET	3.0
2	J	5	ILE	3.0
1	M	23	GLN	3.0
1	M	37	ILE	3.0
1	I	136	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
2	N	373	GLN	2.9
2	B	213	GLY	2.9
2	N	15	GLY	2.9
2	J	361	HIS	2.9
2	N	71	TRP	2.9
2	N	312	GLU	2.9
1	I	395	LYS	2.9
1	M	40	GLU	2.9
2	N	426	TRP	2.9
1	M	216	THR	2.9
2	J	4	PRO	2.9
1	M	188	TYR	2.9
2	N	85	GLN	2.9
1	M	121	ASP	2.9
2	N	232	TYR	2.8
2	J	267	ALA	2.8
1	M	24	TRP	2.8
1	M	147	ASN	2.8
1	M	239	TRP	2.8
2	F	318	TYR	2.8
2	J	87	PHE	2.8
1	M	438	GLU	2.8
2	N	114	ALA	2.8
2	J	364	ASP	2.8
1	M	309	ILE	2.8
1	M	227	PHE	2.8
2	N	69	THR	2.8
1	M	202	ILE	2.7
1	M	214	LEU	2.7
2	J	248	GLU	2.7
1	M	61	PHE	2.7
2	N	92	LEU	2.7
1	I	246	LEU	2.7
2	N	168	LEU	2.7
1	M	245	VAL	2.7
1	M	130	PHE	2.7
2	J	357	MET	2.7
2	N	391	LEU	2.7
1	M	330	GLN	2.7
2	N	21	VAL	2.7
1	M	159	ILE	2.7
2	N	46	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	M	212	TRP	2.7
1	M	358	ARG	2.7
2	N	211	ARG	2.7
2	F	423	VAL	2.7
2	N	309	ILE	2.6
1	M	118	VAL	2.6
1	I	144	TYR	2.6
1	M	109	LEU	2.6
2	N	70	LYS	2.6
2	N	245	VAL	2.6
2	N	14	PRO	2.6
1	M	377	THR	2.6
2	J	10	VAL	2.6
1	M	454	LYS	2.6
2	N	111	VAL	2.6
2	N	310	LEU	2.6
1	M	112	GLY	2.6
1	M	395	LYS	2.6
2	N	349	LEU	2.5
2	N	16	MET	2.5
1	M	31	ILE	2.5
1	M	315	HIS	2.5
2	N	405	TYR	2.5
1	M	71	TRP	2.5
1	I	479	LEU	2.5
1	M	26	LEU	2.5
1	M	218	ASP	2.5
1	E	135	ILE	2.5
1	I	59	PRO	2.5
1	M	57	ASN	2.5
2	N	30	LYS	2.5
1	I	364	ASP	2.5
1	M	325	LEU	2.5
2	J	423	VAL	2.5
2	N	68	SER	2.4
2	N	343	GLN	2.4
2	N	149	LEU	2.4
1	M	89	GLU	2.4
1	M	506	ILE	2.4
2	N	101	LYS	2.4
1	M	276	VAL	2.4
2	F	295	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	I	286	THR	2.4
1	M	177	ASP	2.4
2	N	129	ALA	2.4
1	M	43	LYS	2.4
2	J	231	GLY	2.4
1	I	472	THR	2.4
1	M	68	SER	2.4
1	M	295	LEU	2.4
2	J	195	ILE	2.4
1	A	67	ASP	2.3
1	I	233	GLU	2.3
1	M	74	LEU	2.3
1	M	119	PRO	2.3
1	M	353	LYS	2.3
2	N	195	ILE	2.3
2	N	341	ILE	2.3
2	N	401	TRP	2.3
2	J	89	GLU	2.3
2	J	141	GLY	2.3
2	N	118	VAL	2.3
1	I	449	GLU	2.3
1	A	357	MET	2.3
1	M	151	GLN	2.3
1	M	317	VAL	2.3
2	J	178	ILE	2.3
2	N	358	ARG	2.3
1	M	452	LEU	2.3
2	N	257	ILE	2.3
1	I	26	LEU	2.3
2	F	213	GLY	2.3
1	M	129	ALA	2.2
2	B	69	THR	2.2
1	M	273	GLY	2.2
1	I	132	ILE	2.2
2	B	283	LEU	2.2
2	J	168	LEU	2.2
2	N	77	PHE	2.2
1	I	303	LEU	2.2
1	M	141	GLY	2.2
1	M	187	LEU	2.2
1	M	359	GLY	2.2
1	I	542	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	319	TYR	2.2
1	M	32	LYS	2.2
1	M	287	LYS	2.2
1	I	38	CYS	2.2
1	M	332	GLN	2.2
1	M	103	LYS	2.2
1	M	261	VAL	2.2
2	N	284	ARG	2.2
2	J	428	GLN	2.2
1	E	543	GLY	2.2
2	B	428	GLN	2.1
2	N	278	GLN	2.1
1	M	155	GLY	2.1
1	M	274	ILE	2.1
2	J	424	LYS	2.1
1	M	41	MET	2.1
2	J	190	GLY	2.1
2	J	421	PRO	2.1
2	J	299	ALA	2.1
2	B	215	THR	2.1
1	M	82	LYS	2.1
1	M	241	VAL	2.1
2	J	3	SER	2.1
1	M	234	LEU	2.1
2	N	408	ALA	2.1
1	M	10	VAL	2.1
2	N	94	ILE	2.1
1	M	70	LYS	2.1
2	F	428	GLN	2.1
1	I	275	LYS	2.1
2	N	409	THR	2.1
2	N	305	GLU	2.1
1	M	335	GLY	2.1
1	M	223	LYS	2.1
2	N	63	ILE	2.1
1	M	228	LEU	2.1
2	J	209	LEU	2.1
1	M	453	GLY	2.1
2	N	29	GLU	2.1
2	N	359	GLY	2.1
1	M	90	VAL	2.1
2	N	315	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
2	N	336	GLN	2.0
1	E	303	LEU	2.0
1	I	289	LEU	2.0
1	M	425	LEU	2.0
2	B	12	LEU	2.0
2	B	358	ARG	2.0
2	N	49	LYS	2.0
2	B	354	TYR	2.0
2	F	257	ILE	2.0
2	J	358	ARG	2.0
1	M	303	LEU	2.0
1	M	60	VAL	2.0
1	M	113	ASP	2.0
1	M	162	SER	2.0
2	J	240	THR	2.0
2	N	26	LEU	2.0
1	M	419	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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(Å ²)	Q<0.9
4	MRG	P	817	26/27	0.81	0.20	-	116,119,127,127	0
4	2DA	H	822	20/21	0.97	0.23	-	33,37,39,41	0
4	MRG	D	817	26/27	0.95	0.22	-	32,35,49,54	0
4	MRG	L	817	26/27	0.86	0.21	-	86,88,98,99	0
4	2DA	L	822	20/21	0.96	0.23	-	64,70,72,72	0
4	2DA	D	822	20/21	0.97	0.23	-	28,29,32,32	0
4	MRG	H	817	26/27	0.95	0.17	-	42,46,55,58	0
4	2DA	P	822	20/21	0.82	0.32	-	106,114,116,116	0

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, 95th 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(Å ²)	Q<0.9
7	GOL	B	429	6/6	0.86	0.34	3.52	41,45,47,47	0
7	GOL	F	429	6/6	0.81	0.26	1.28	33,36,38,41	0
6	ZP4	A	823	53/53	0.92	0.29	0.75	36,54,95,96	0
5	MG	E	602	1/1	0.96	0.25	0.55	64,64,64,64	0
5	MG	A	602	1/1	0.94	0.22	0.40	38,38,38,38	0
6	ZP4	E	823	53/53	0.93	0.26	0.13	38,56,96,97	0
5	MG	I	602	1/1	0.95	0.21	-0.02	56,56,56,56	0
5	MG	E	600	1/1	0.96	0.16	-0.80	5,5,5,5	0
5	MG	M	602	1/1	0.84	0.16	-0.83	65,65,65,65	0
6	ZP4	M	823	53/53	0.87	0.22	-0.99	120,127,133,133	0
6	ZP4	I	823	53/53	0.90	0.22	-1.10	65,87,99,99	0
5	MG	M	600	1/1	0.91	0.13	-1.31	43,43,43,43	0
5	MG	A	600	1/1	0.95	0.11	-1.43	4,4,4,4	0
5	MG	I	600	1/1	0.90	0.06	-4.34	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.