



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 1, 2026 – 12:13 PM EDT

PDB ID : 9PVW / pdb_00009pvw
Title : RNA polymerase II elongation complex with dA at +1 site, 8-oxo-GMP added in Syn-conformation
Authors : Hou, P.; Oh, J.; Wang, D.
Deposited on : 2025-08-03
Resolution : 3.56 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

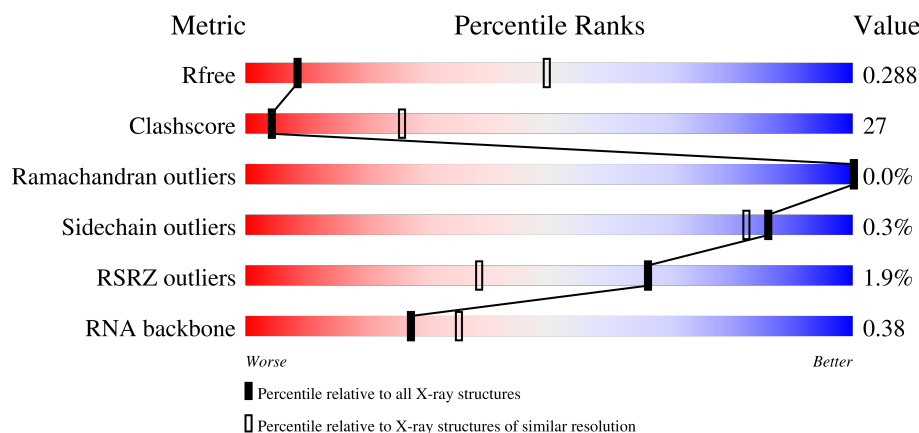
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.56 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}	180053	1410 (3.62-3.50)
Clashscore	190562	1480 (3.62-3.50)
Ramachandran outliers	187476	1440 (3.62-3.50)
Sidechain outliers	187428	1441 (3.62-3.50)
RSRZ outliers	180081	1409 (3.62-3.50)
RNA backbone	3983	1006 (4.02-3.06)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	R	10	
2	T	29	
3	N	18	
4	A	1733	

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Mol	Chain	Length	Quality of chain
5	B	1224	<div><div><div></div><div></div><div></div></div><div>2%51%41%8%</div></div>
6	C	318	<div><div><div></div><div></div><div></div></div><div>%44%40%16%</div></div>
7	E	215	<div><div><div></div><div></div><div></div></div><div>4%44%55%. .</div></div>
8	F	155	<div><div><div></div><div></div><div></div></div><div>28%27%45%</div></div>
9	H	146	<div><div><div></div><div></div><div></div></div><div>%42%49%9%</div></div>
10	I	122	<div><div><div></div><div></div><div></div></div><div>47%49%. .</div></div>
11	J	70	<div><div><div></div><div></div><div></div></div><div>4%39%53%. 7%</div></div>
12	K	120	<div><div><div></div><div></div><div></div></div><div>2%48%47%5%</div></div>
13	L	70	<div><div><div></div><div></div><div></div></div><div>4%23%37%. 39%</div></div>

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 29080 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 RNA chain called RNA with 8-oxo-guanine added to 3' end. Syn-conformation..

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	10	Total	C	N	O	P	0	0	0
			219	98	45	67	9			

- Molecule 2 is a DNA chain called Template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	26	Total	C	N	O	P	0	0	0
			519	250	80	163	26			

- Molecule 3 is a DNA chain called Non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	15	Total	C	N	O	P	0	0	0
			317	148	71	83	15			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	1384	Total	C	N	O	S	0	0	0
			10828	6831	1896	2041	60			

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1123	Total	C	N	O	S	0	0	0
			8859	5607	1552	1647	53			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	267	Total	C	N	O	S	0	0	0
			2101	1320	349	419	13			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	212	Total	C	N	O	S	0	0	0
			1731	1100	305	315	11			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	86	Total	C	N	O	S	0	0	0
			684	437	115	129	3			

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	133	Total	C	N	O	S	0	0	0
			1064	670	179	211	4			

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	118	Total	C	N	O	S	0	0	0
			952	585	173	184	10			

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	43	Total	C	N	O	S	0	0	0
			337	208	66	59	4			

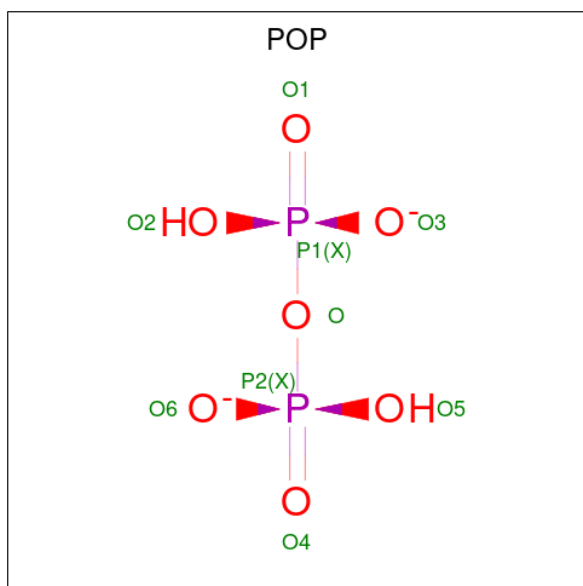
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	2	Total 2	Zn 2	0	0
14	B	1	Total 1	Zn 1	0	0
14	C	1	Total 1	Zn 1	0	0
14	I	2	Total 2	Zn 2	0	0
14	J	1	Total 1	Zn 1	0	0
14	L	1	Total 1	Zn 1	0	0

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total 1	Mg 1	0	0

- Molecule 16 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



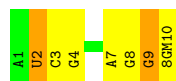
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	B	1	Total 9	O 7	P 2	0	0

3 Residue-property plots

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

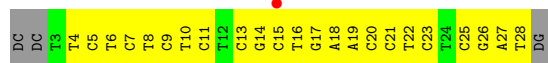
- Molecule 1: RNA with 8-oxo-guanine added to 3' end. Syn-conformation.

Chain R: 



- Molecule 2: Template strand DNA

Chain T: 

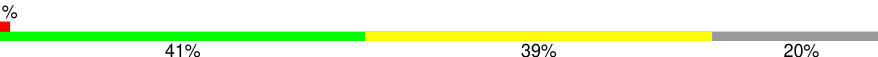


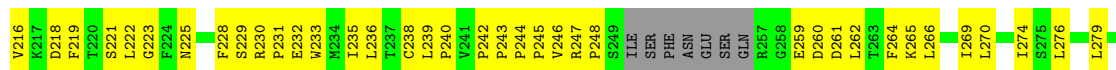
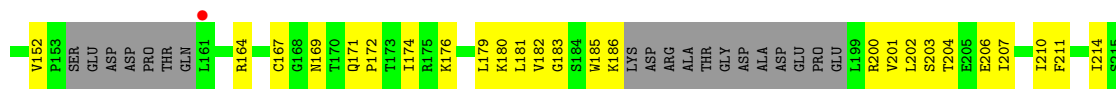
- Molecule 3: Non-template strand DNA

Chain N: 

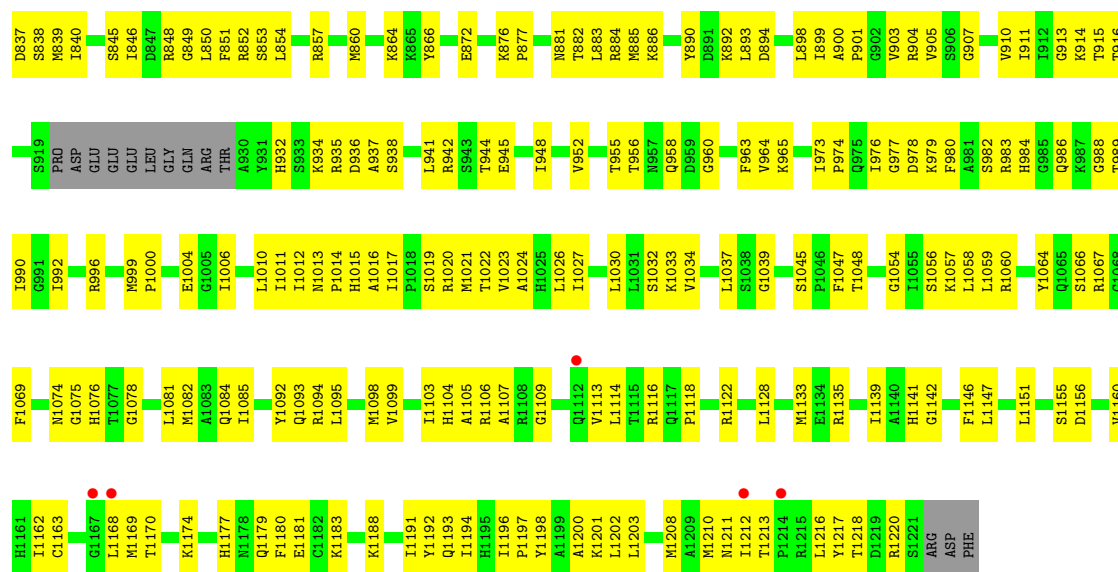


- Molecule 4: DNA-directed RNA polymerase II subunit RPB1

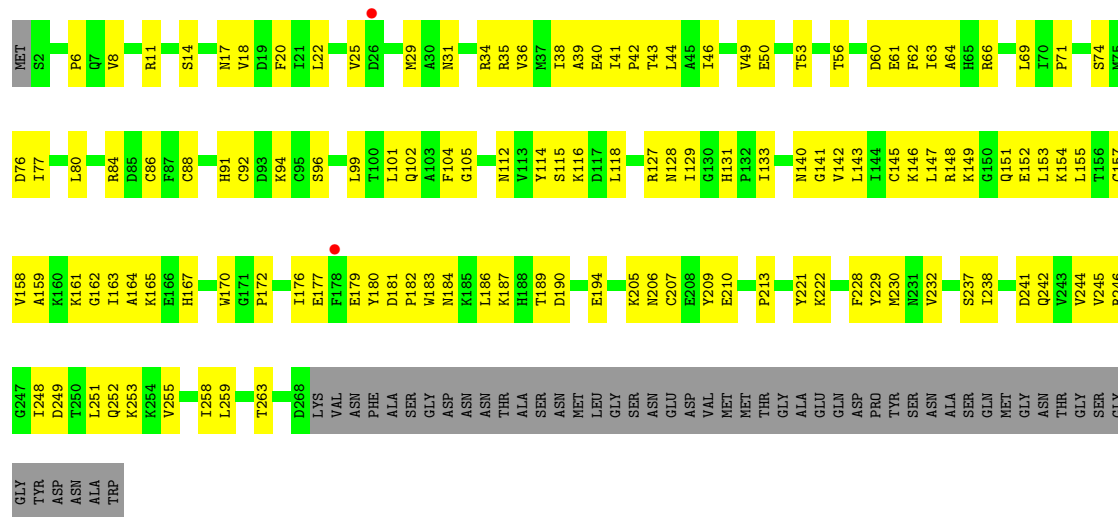
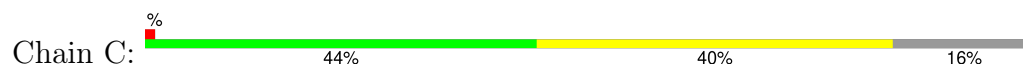
Chain A: 



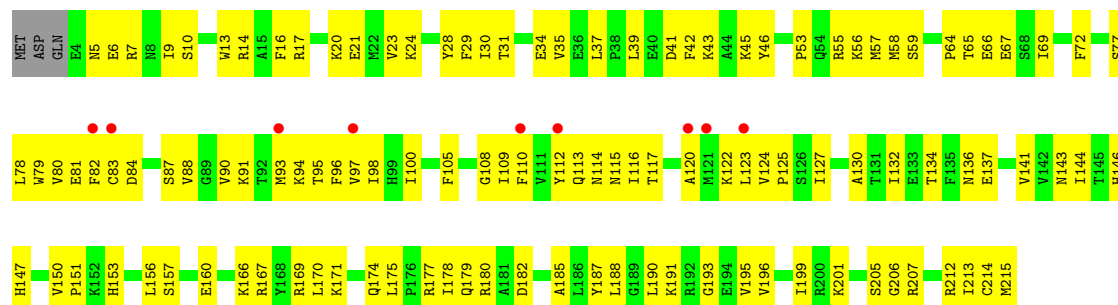
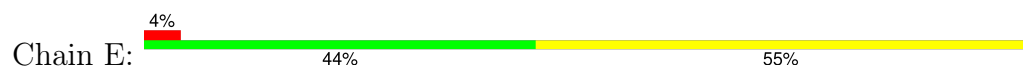
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• Molecule 6: DNA-directed RNA polymerase II subunit RPB3



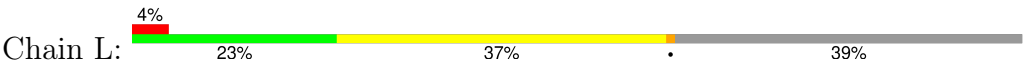
• Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| M1 | N2 | A3 | P4 | F7 | E8 | L9 | F10 | L11 | L12 | K18 | L19 | K20 | I21 | P28 | N29 | A30 | V31 | K37 | H40 | T41 | L42 | L44 | L45 | E49 | L50 | L51 | L57 | F58 | A59 | A60 | Y61 | K62 | V63 | P66 | F67 | F68 | F71 | R74 | L75 | Q76 | T77 | Y81 | A86 | L87 | A90 | C91 |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



● Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC4



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.05Å 223.24Å 192.76Å 90.00° 100.48° 90.00°	Depositor
Resolution (Å)	49.37 – 3.56 49.37 – 3.56	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.37-3.56) 99.7 (49.37-3.56)	Depositor EDS
R_{merge}	0.54	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 3.57Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.247 , 0.288 0.247 , 0.288	Depositor DCC
R_{free} test set	2000 reflections (2.42%)	wwPDB-VP
Wilson B-factor (Å ²)	103.6	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 124.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	29080	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: ZN, MG, POP, 8GM

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	R	0.15	0/219	0.33	0/341
2	T	0.23	0/576	0.43	0/884
3	N	0.23	0/359	0.39	0/553
4	A	0.23	0/11020	0.44	0/14907
5	B	0.24	1/9030 (0.0%)	0.41	0/12186
6	C	0.20	0/2139	0.39	0/2899
7	E	0.22	0/1767	0.43	0/2378
8	F	0.22	0/696	0.42	0/943
9	H	0.23	0/1082	0.49	0/1466
10	I	0.25	0/970	0.45	0/1308
11	J	0.21	0/541	0.36	0/727
12	K	0.21	0/937	0.41	0/1265
13	L	0.39	0/339	0.59	0/450
All	All	0.23	1/29675 (0.0%)	0.43	0/40307

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	729	ILE	CG1-CD1	10.89	1.94	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	219	0	99	6	0
2	T	519	0	297	26	0
3	N	317	0	166	19	0
4	A	10828	0	10876	692	0
5	B	8859	0	8816	466	0
6	C	2101	0	2056	115	0
7	E	1731	0	1758	116	0
8	F	684	0	692	41	0
9	H	1064	0	1029	89	0
10	I	952	0	897	54	0
11	J	532	0	542	37	0
12	K	919	0	929	69	0
13	L	337	0	352	41	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
16	B	9	0	0	0	0
All	All	29080	0	28509	1547	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 27.

All (1547) 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)
5:B:729:ILE:CD1	5:B:729:ILE:CG1	1.94	1.45
4:A:1224:LEU:HD21	4:A:1240:CYS:HB3	1.32	1.09
4:A:339:ASN:O	4:A:343:LYS:HG2	1.54	1.07
4:A:1128:GLN:HG2	4:A:1304:TRP:NE1	1.68	1.06
6:C:56:THR:HG22	6:C:147:LEU:HD21	1.36	1.03
4:A:463:ILE:HD13	4:A:469:ARG:HG2	1.39	1.01
4:A:613:ILE:HG21	9:H:102:TYR:HB3	1.40	1.01
9:H:38:LEU:HB3	9:H:125:LEU:HD13	1.45	0.98
4:A:42:ASP:HA	4:A:50:ILE:HG23	1.42	0.98
12:K:61:TYR:HB2	12:K:71:PHE:HE1	1.31	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1056:SER:HB3	5:B:1066:SER:HB2	1.48	0.94
6:C:61:GLU:HG2	13:L:67:PHE:HE1	1.31	0.93
13:L:40:LEU:HD13	13:L:44:ASP:CG	1.94	0.93
4:A:81:PHE:HE1	4:A:240:PRO:HB2	1.33	0.92
4:A:111:GLY:HA3	4:A:214:ILE:HA	1.50	0.92
6:C:39:ALA:HA	6:C:164:ALA:HB3	1.52	0.92
4:A:1128:GLN:HG2	4:A:1304:TRP:HE1	1.35	0.92
4:A:1282:VAL:HG22	4:A:1308:THR:HG22	1.52	0.90
4:A:1027:ALA:HB3	4:A:1030:ARG:HB2	1.51	0.90
4:A:795:GLU:HG2	5:B:731:VAL:HG11	1.54	0.89
4:A:37:PHE:HB2	4:A:52:GLY:HA3	1.53	0.89
4:A:801:GLU:CD	5:B:729:ILE:HD12	1.99	0.88
4:A:1278:ASN:HB2	4:A:1312:ASN:HB2	1.55	0.87
4:A:81:PHE:CE1	4:A:240:PRO:HB2	2.09	0.87
5:B:979:LYS:HG2	5:B:1095:LEU:HD12	1.56	0.87
13:L:40:LEU:HD13	13:L:44:ASP:CB	2.06	0.85
5:B:1162:ILE:HG22	5:B:1192:TYR:HB2	1.59	0.85
4:A:179:LEU:HD22	4:A:297:GLN:HG2	1.56	0.85
4:A:392:VAL:HG13	4:A:415:LEU:HD11	1.57	0.84
12:K:61:TYR:HB2	12:K:71:PHE:CE1	2.12	0.84
4:A:801:GLU:CD	5:B:729:ILE:CD1	2.51	0.83
10:I:50:THR:HG22	10:I:52:ILE:H	1.42	0.83
10:I:106:CYS:HB2	10:I:108:HIS:HD2	1.42	0.83
4:A:857:ARG:HH21	7:E:170:LEU:CD2	1.91	0.83
4:A:540:PHE:HB3	4:A:571:LEU:HD12	1.59	0.82
13:L:38:LEU:HD21	13:L:48:CYS:HA	1.60	0.82
4:A:877:HIS:CE1	4:A:1056:SER:HA	2.14	0.81
5:B:59:LEU:HG	5:B:95:ILE:HD13	1.62	0.81
5:B:121:ASN:HA	5:B:207:GLY:HA3	1.63	0.81
6:C:258:ILE:HD12	12:K:19:LEU:HD21	1.63	0.81
4:A:683:ILE:HG21	4:A:801:GLU:HG3	1.61	0.80
4:A:1013:ASP:HB3	7:E:207:ARG:HB2	1.63	0.80
5:B:1174:LYS:HG3	5:B:1177:HIS:HB2	1.63	0.80
4:A:975:HIS:HD2	4:A:1036:ARG:H	1.29	0.80
4:A:786:HIS:HE1	5:B:742:GLU:HG3	1.46	0.80
7:E:169:ARG:HB3	8:F:140:ASP:HB3	1.65	0.79
4:A:1192:LEU:HD22	4:A:1239:ARG:HH21	1.47	0.79
9:H:102:TYR:CZ	9:H:115:TYR:HB3	2.17	0.79
3:N:9:DA:H2"	3:N:10:DG:H5'	1.61	0.79
4:A:881:GLN:HA	4:A:961:ARG:HH21	1.47	0.79
4:A:336:ILE:HD11	5:B:1203:LEU:HD13	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:40:LEU:HD13	13:L:44:ASP:OD2	1.83	0.79
4:A:857:ARG:HH21	7:E:170:LEU:HD23	1.47	0.78
5:B:803:LEU:HD13	5:B:1032:SER:HB3	1.64	0.78
4:A:1225:PHE:CZ	4:A:1227:ILE:HG23	2.19	0.78
4:A:801:GLU:HB3	5:B:729:ILE:HD11	1.65	0.78
4:A:464:PRO:HB2	12:K:4:PRO:HD3	1.64	0.77
13:L:40:LEU:HD13	13:L:44:ASP:HB2	1.65	0.77
7:E:20:LYS:HD2	7:E:35:VAL:HA	1.65	0.77
4:A:308:ILE:HG13	4:A:312:PRO:HD2	1.65	0.77
7:E:77:SER:HB2	7:E:105:PHE:HA	1.66	0.77
4:A:801:GLU:CG	5:B:729:ILE:HD11	2.14	0.76
5:B:903:VAL:HG23	13:L:61:THR:HG21	1.67	0.76
4:A:57:ARG:HA	4:A:68:GLN:HG2	1.66	0.76
4:A:131:SER:HB3	4:A:223:GLY:HA3	1.65	0.76
7:E:83:CYS:HB2	7:E:110:PHE:HE1	1.50	0.76
5:B:115:GLN:HG2	5:B:193:LYS:HE3	1.66	0.76
10:I:10:CYS:HB3	10:I:32:CYS:HB3	1.67	0.76
4:A:339:ASN:O	4:A:343:LYS:CG	2.34	0.75
4:A:1116:LEU:HB3	4:A:1308:THR:OG1	1.85	0.75
4:A:392:VAL:HG11	4:A:424:ILE:HD11	1.67	0.75
4:A:767:GLN:HA	4:A:799:PHE:HA	1.69	0.75
5:B:258:LEU:HB2	5:B:385:LEU:HD21	1.66	0.75
6:C:102:GLN:HB3	6:C:154:LYS:HG3	1.69	0.75
5:B:25:ILE:HG12	5:B:651:LEU:HD11	1.67	0.75
4:A:997:LEU:HD21	4:A:1050:GLU:HA	1.69	0.75
6:C:25:VAL:HG23	6:C:228:PHE:CE2	2.22	0.75
7:E:188:LEU:HB2	7:E:190:LEU:CD2	2.16	0.75
6:C:36:VAL:HG23	6:C:40:GLU:HB2	1.69	0.75
4:A:550:LEU:HD22	4:A:577:ILE:CD1	2.17	0.74
6:C:69:LEU:HD12	11:J:6:ARG:HD2	1.69	0.74
4:A:239:LEU:HD12	4:A:240:PRO:HD2	1.70	0.74
8:F:119:ARG:HA	8:F:122:MET:HE2	1.70	0.74
4:A:1286:LYS:HE2	4:A:1302:PRO:HB3	1.69	0.74
4:A:550:LEU:HD22	4:A:577:ILE:HD13	1.70	0.74
5:B:1135:ARG:HG3	5:B:1147:LEU:HD11	1.70	0.74
3:N:9:DA:H2'	3:N:10:DG:C8	2.23	0.73
5:B:999:MET:HG3	5:B:1000:PRO:HD2	1.71	0.73
4:A:111:GLY:CA	4:A:214:ILE:HA	2.19	0.73
4:A:907:THR:HG21	4:A:920:LEU:HG	1.70	0.73
4:A:329:LEU:HD23	4:A:335:ARG:HD2	1.69	0.72
4:A:126:LEU:HA	4:A:134:ARG:HD3	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:26:LEU:HD12	10:I:35:VAL:HG11	1.70	0.72
6:C:61:GLU:HG2	13:L:67:PHE:CE1	2.19	0.72
5:B:661:LEU:HG	5:B:679:TYR:CD2	2.25	0.72
4:A:801:GLU:CB	5:B:729:ILE:HD11	2.20	0.71
4:A:987:VAL:HG12	4:A:991:LYS:HE2	1.71	0.71
5:B:642:ASP:HA	5:B:649:LYS:HA	1.71	0.71
4:A:302:THR:HG21	4:A:314:ALA:HB3	1.71	0.71
4:A:946:VAL:HG13	7:E:201:LYS:HB3	1.71	0.71
4:A:1386:ARG:HB3	4:A:1403:GLU:OE1	1.90	0.71
4:A:881:GLN:HB2	4:A:956:LEU:HD12	1.72	0.71
6:C:165:LYS:HB3	12:K:9:LEU:HD11	1.72	0.71
5:B:778:MET:HE2	5:B:1094:ARG:HB3	1.72	0.71
10:I:103:CYS:HB3	10:I:106:CYS:SG	2.31	0.71
4:A:446:ARG:HG3	4:A:448:PRO:HD2	1.71	0.71
5:B:603:LEU:HB2	5:B:609:ILE:HG12	1.71	0.71
12:K:61:TYR:CB	12:K:71:PHE:HE1	2.03	0.71
4:A:821:ARG:HH21	5:B:534:GLY:HA2	1.56	0.71
4:A:711:ARG:HD3	10:I:97:MET:HE2	1.72	0.71
8:F:127:GLU:HB3	8:F:129:LYS:HG2	1.72	0.71
4:A:597:LEU:HB3	9:H:102:TYR:HE2	1.55	0.70
5:B:29:ASP:HB3	5:B:658:ILE:HG21	1.73	0.70
5:B:570:VAL:HG23	5:B:573:GLN:HB2	1.73	0.70
5:B:829:CYS:HA	5:B:834:ASN:HD21	1.56	0.70
8:F:93:ILE:HG23	8:F:132:LEU:HD12	1.73	0.70
12:K:21:ILE:HG23	12:K:31:VAL:HG21	1.73	0.70
4:A:586:ILE:HD13	4:A:633:VAL:HG22	1.72	0.70
4:A:1227:ILE:HD11	4:A:1239:ARG:HD3	1.73	0.70
9:H:101:ALA:HA	9:H:116:TYR:HA	1.71	0.70
13:L:31:CYS:HB3	13:L:34:CYS:SG	2.31	0.70
4:A:179:LEU:HD22	4:A:297:GLN:CG	2.22	0.70
13:L:40:LEU:CD1	13:L:44:ASP:HB2	2.23	0.69
4:A:247:ARG:HD3	4:A:262:LEU:HD11	1.75	0.69
4:A:1118:VAL:HB	4:A:1306:LEU:HB2	1.74	0.69
4:A:444:PHE:CD2	4:A:487:MET:HE1	2.27	0.69
4:A:801:GLU:CG	5:B:729:ILE:CD1	2.70	0.69
9:H:116:TYR:HB2	9:H:123:MET:HE2	1.75	0.69
4:A:202:LEU:HB3	4:A:207:ILE:HD11	1.73	0.69
4:A:172:PRO:HG2	4:A:174:ILE:HD11	1.75	0.69
4:A:444:PHE:CE2	4:A:487:MET:CE	2.76	0.69
4:A:1329:THR:H	4:A:1335:ILE:HD11	1.56	0.69
5:B:900:ALA:HB3	13:L:61:THR:HG22	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1114:LEU:HG	5:B:1202:LEU:HD11	1.75	0.69
7:E:112:TYR:HE1	7:E:134:THR:HA	1.57	0.69
4:A:96:ILE:HD11	4:A:181:LEU:HD11	1.74	0.69
4:A:214:ILE:HB	4:A:219:PHE:CE1	2.28	0.68
4:A:18:GLN:HB2	4:A:1418:LEU:HD12	1.74	0.68
4:A:526:ASP:H	5:B:835:GLN:HE21	1.40	0.68
4:A:1229:SER:HB3	4:A:1237:ILE:H	1.59	0.68
5:B:840:ILE:HG12	5:B:992:ILE:HG22	1.73	0.68
6:C:76:ASP:HB2	6:C:129:ILE:HG12	1.74	0.68
13:L:64:LEU:HD22	13:L:66:GLN:HE21	1.58	0.68
4:A:857:ARG:HH11	8:F:139:PRO:HG2	1.58	0.68
6:C:242:GLN:HB3	6:C:246:ARG:HE	1.58	0.68
6:C:249:ASP:CG	6:C:253:LYS:HZ1	2.02	0.68
4:A:22:PHE:CD2	5:B:1213:THR:HG22	2.28	0.68
5:B:188:ASP:HA	5:B:191:LYS:HD2	1.76	0.68
5:B:365:THR:HG21	5:B:370:PHE:HB2	1.76	0.68
5:B:977:GLY:HA2	5:B:989:THR:HG22	1.76	0.68
4:A:370:ILE:HD13	5:B:1105:ALA:HB2	1.75	0.68
10:I:74:GLU:OE1	10:I:79:HIS:HA	1.93	0.68
4:A:81:PHE:CD2	4:A:243:PRO:HD3	2.29	0.67
4:A:1111:MET:HB2	4:A:1114:PRO:HG3	1.75	0.67
5:B:877:PRO:HB2	5:B:882:THR:OG1	1.95	0.67
4:A:58:LEU:HB3	4:A:244:PRO:HG2	1.76	0.67
9:H:40:LEU:HB2	9:H:123:MET:HG3	1.77	0.67
4:A:1128:GLN:HG2	4:A:1304:TRP:CE2	2.30	0.67
4:A:857:ARG:NH1	8:F:139:PRO:HG2	2.09	0.67
5:B:494:HIS:HA	5:B:497:ARG:HE	1.59	0.67
4:A:702:LEU:HD13	4:A:710:LEU:HG	1.77	0.66
4:A:815:PHE:HA	4:A:818:MET:HE3	1.77	0.66
7:E:93:MET:HE3	7:E:97:VAL:HG23	1.76	0.66
7:E:199:ILE:HG21	7:E:207:ARG:HH21	1.58	0.66
4:A:549:MET:HE1	4:A:656:TRP:HD1	1.60	0.66
4:A:899:VAL:HG13	4:A:929:LEU:HD13	1.78	0.66
7:E:66:GLU:O	7:E:69:ILE:HG12	1.96	0.66
11:J:31:ASP:HB3	11:J:34:THR:HG23	1.77	0.66
6:C:34:ARG:HB2	6:C:176:ILE:HG21	1.78	0.66
6:C:50:GLU:HB3	13:L:64:LEU:HD21	1.78	0.66
6:C:88:CYS:HB3	6:C:92:CYS:HB3	1.78	0.66
4:A:34:LYS:HA	4:A:83:HIS:O	1.97	0.65
6:C:116:LYS:HD3	6:C:140:ASN:HA	1.76	0.65
12:K:29:ASN:O	12:K:76:GLN:HA	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:702:LEU:HD22	4:A:710:LEU:HD11	1.77	0.65
5:B:293:PRO:HB2	5:B:296:GLU:HB2	1.78	0.65
5:B:886:LYS:H	5:B:886:LYS:HD2	1.62	0.65
11:J:28:ASP:HB2	11:J:30:LEU:HG	1.79	0.65
13:L:34:CYS:HB3	13:L:51:CYS:HB3	1.77	0.65
4:A:444:PHE:CD2	4:A:487:MET:CE	2.79	0.65
13:L:64:LEU:HD23	13:L:65:VAL:N	2.11	0.65
4:A:860:LEU:HD11	4:A:1394:THR:HG22	1.79	0.65
4:A:913:LEU:HD21	4:A:1032:LEU:HD22	1.78	0.65
5:B:1160:VAL:HG23	5:B:1194:ILE:HG13	1.79	0.65
7:E:24:LYS:HB2	7:E:30:ILE:HG21	1.78	0.65
5:B:1054:GLY:HA2	5:B:1057:LYS:HD2	1.78	0.65
4:A:1117:THR:O	4:A:1327:ILE:HG13	1.95	0.64
5:B:234:ILE:HD12	5:B:237:VAL:HG22	1.79	0.64
6:C:259:LEU:HD11	12:K:91:CYS:HB2	1.79	0.64
12:K:10:PHE:CD2	12:K:11:LEU:HD13	2.31	0.64
4:A:786:HIS:CE1	5:B:742:GLU:HG3	2.30	0.64
4:A:993:LEU:HD22	4:A:1046:LEU:HG	1.79	0.64
5:B:59:LEU:CG	5:B:95:ILE:HD13	2.26	0.64
5:B:1059:LEU:HD22	5:B:1064:TYR:HB2	1.78	0.64
4:A:901:LEU:HA	4:A:907:THR:HG23	1.80	0.64
5:B:866:TYR:OH	5:B:872:GLU:HG3	1.97	0.64
11:J:3:VAL:HG11	11:J:18:TRP:HB2	1.78	0.64
5:B:423:LYS:HA	5:B:426:LYS:HD3	1.78	0.64
5:B:1106:ARG:NH1	5:B:1118:PRO:HB3	2.12	0.64
7:E:83:CYS:HB2	7:E:110:PHE:CE1	2.31	0.64
4:A:1147:THR:HG22	4:A:1197:LEU:HD22	1.78	0.64
4:A:1161:THR:HG23	4:A:1167:GLU:HG2	1.80	0.64
5:B:1024:ALA:HA	5:B:1027:ILE:HD12	1.80	0.64
9:H:112:ILE:HG21	9:H:131:ASN:HB3	1.78	0.64
4:A:534:LEU:HA	4:A:539:THR:HG21	1.78	0.64
4:A:789:LYS:HG3	10:I:67:THR:HB	1.78	0.64
4:A:108:MET:H	4:A:171:GLN:HE21	1.46	0.64
5:B:606:LYS:HD2	5:B:608:ASP:HB2	1.79	0.64
7:E:46:TYR:CZ	7:E:58:MET:HB2	2.33	0.64
7:E:108:GLY:O	7:E:132:ILE:HA	1.98	0.64
4:A:1192:LEU:HD11	4:A:1239:ARG:HB3	1.78	0.63
5:B:724:ASP:HB3	5:B:727:LYS:HE2	1.79	0.63
4:A:593:GLU:HG3	4:A:601:LYS:HZ2	1.63	0.63
5:B:839:MET:HE3	5:B:988:GLY:HA3	1.80	0.63
5:B:59:LEU:CD2	5:B:95:ILE:HD13	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:21:DC:H3'	2:T:22:DT:H71	1.79	0.63
5:B:890:TYR:CD2	5:B:910:VAL:HG21	2.33	0.63
4:A:877:HIS:HE1	4:A:1056:SER:HA	1.62	0.63
4:A:1267:MET:HA	4:A:1271:ILE:HD13	1.80	0.63
5:B:661:LEU:HG	5:B:679:TYR:HD2	1.62	0.63
4:A:1217:LYS:HG2	4:A:1226:VAL:HG21	1.81	0.63
5:B:757:PRO:HD3	5:B:983:ARG:HD2	1.80	0.63
4:A:21:LEU:HB2	4:A:229:SER:HA	1.80	0.62
4:A:91:PHE:CE1	4:A:235:ILE:HD12	2.34	0.62
4:A:335:ARG:HH12	5:B:1202:LEU:HD13	1.63	0.62
4:A:683:ILE:HG21	4:A:801:GLU:CG	2.30	0.62
7:E:59:SER:HB2	7:E:80:VAL:O	1.99	0.62
9:H:17:PRO:HA	9:H:24:CYS:SG	2.40	0.62
5:B:370:PHE:HD1	5:B:373:ARG:HD3	1.64	0.62
5:B:639:ILE:HD11	5:B:691:GLU:HB2	1.82	0.62
4:A:908:LEU:HD13	4:A:913:LEU:HB2	1.80	0.62
4:A:605:MET:SD	4:A:612:ILE:HD11	2.39	0.62
5:B:350:GLN:HA	5:B:353:LYS:HD3	1.80	0.62
12:K:10:PHE:CE2	12:K:11:LEU:HD13	2.34	0.62
13:L:40:LEU:CD1	13:L:44:ASP:CB	2.77	0.62
2:T:16:DT:H2''	2:T:17:DG:C8	2.34	0.62
4:A:999:VAL:H	4:A:1011:GLN:HE21	1.48	0.62
9:H:96:VAL:HA	9:H:142:LEU:O	2.00	0.62
4:A:1105:LEU:HB3	4:A:1384:VAL:HG21	1.82	0.62
7:E:93:MET:HE1	7:E:132:ILE:HG21	1.81	0.62
4:A:182:VAL:HG12	4:A:201:VAL:HA	1.82	0.62
6:C:8:VAL:HB	6:C:22:LEU:HD12	1.82	0.62
4:A:325:ILE:HA	4:A:328:ARG:HD3	1.82	0.61
4:A:981:LEU:HG	4:A:1039:LYS:HA	1.81	0.61
9:H:125:LEU:HG	9:H:130:ARG:CZ	2.29	0.61
4:A:225:ASN:HB3	4:A:228:PHE:HB2	1.82	0.61
4:A:444:PHE:CE2	4:A:487:MET:SD	2.93	0.61
5:B:1104:HIS:HB2	5:B:1122:ARG:HG3	1.81	0.61
7:E:7:ARG:HD3	7:E:7:ARG:H	1.64	0.61
4:A:568:PRO:HB2	9:H:46:LEU:HD22	1.83	0.61
5:B:283:VAL:HG21	5:B:321:GLY:CA	2.31	0.61
4:A:630:ILE:HD12	4:A:630:ILE:H	1.65	0.61
9:H:36:CYS:SG	9:H:130:ARG:NH2	2.73	0.61
4:A:72:GLU:HB3	4:A:76:GLU:HB3	1.82	0.61
4:A:214:ILE:HB	4:A:219:PHE:HE1	1.64	0.61
4:A:298:PHE:CZ	4:A:314:ALA:HB2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:172:PRO:HB3	4:A:185:TRP:CD1	2.35	0.61
4:A:445:ASN:HB2	4:A:455:MET:HG2	1.83	0.61
5:B:599:THR:O	5:B:603:LEU:HG	2.00	0.61
6:C:77:ILE:N	6:C:129:ILE:HD11	2.16	0.61
4:A:1130:GLN:O	4:A:1134:ILE:HG12	2.00	0.61
5:B:701:ILE:HB	5:B:739:THR:OG1	2.00	0.61
4:A:243:PRO:HB2	4:A:245:PRO:HD2	1.82	0.61
5:B:95:ILE:HD11	5:B:128:LEU:HG	1.82	0.61
6:C:6:PRO:HB3	6:C:25:VAL:CG1	2.30	0.61
6:C:116:LYS:HG2	6:C:141:GLY:H	1.66	0.61
7:E:39:LEU:HD12	7:E:42:PHE:HD2	1.66	0.61
4:A:18:GLN:HB3	5:B:1217:TYR:HE2	1.65	0.61
4:A:993:LEU:HD23	4:A:1022:LEU:HD11	1.83	0.61
5:B:487:THR:HG22	5:B:489:SER:H	1.66	0.61
8:F:93:ILE:HD12	8:F:132:LEU:HD13	1.82	0.61
4:A:89:PRO:O	4:A:204:THR:HG21	2.01	0.60
4:A:1138:ILE:HA	4:A:1276:VAL:HG23	1.82	0.60
4:A:67:CYS:HB3	4:A:70:CYS:HB2	1.81	0.60
5:B:234:ILE:HD12	5:B:237:VAL:CG2	2.30	0.60
5:B:693:ILE:HG21	5:B:701:ILE:HD13	1.83	0.60
5:B:615:MET:HG2	5:B:626:ILE:HG23	1.83	0.60
5:B:980:PHE:CE1	5:B:990:ILE:HD11	2.36	0.60
4:A:666:ILE:HD11	5:B:1030:LEU:HD21	1.83	0.60
4:A:857:ARG:NH2	7:E:170:LEU:CD2	2.64	0.60
5:B:101:MET:HG2	5:B:111:ALA:HA	1.83	0.60
5:B:512:ARG:HB3	5:B:533:CYS:O	2.02	0.60
4:A:34:LYS:HE2	4:A:83:HIS:CE1	2.36	0.60
4:A:1128:GLN:CG	4:A:1304:TRP:HE1	2.11	0.60
7:E:87:SER:HA	7:E:115:ASN:HB2	1.83	0.60
3:N:6:DG:H2"	3:N:7:DA:H5"	1.84	0.60
4:A:801:GLU:HG2	5:B:729:ILE:HD11	1.84	0.60
11:J:25:LEU:HD21	11:J:32:GLU:HA	1.82	0.60
4:A:565:ILE:HG21	9:H:46:LEU:HD13	1.82	0.60
5:B:570:VAL:HG23	5:B:573:GLN:CB	2.32	0.60
4:A:997:LEU:CD2	4:A:1050:GLU:HA	2.32	0.60
4:A:1207:LEU:HG	4:A:1274:ARG:HE	1.67	0.60
5:B:102:VAL:HG22	5:B:112:LEU:HB2	1.82	0.60
6:C:133:ILE:CD1	6:C:237:SER:HA	2.32	0.60
5:B:1196:ILE:HD11	5:B:1201:LYS:HB2	1.83	0.59
10:I:44:TYR:CZ	10:I:46:HIS:HB2	2.37	0.59
13:L:28:LYS:HZ2	13:L:40:LEU:HA	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:162:GLY:HA3	6:C:170:TRP:CE2	2.38	0.59
4:A:998:LEU:HB2	4:A:1001:ARG:HH21	1.67	0.59
4:A:1325:THR:HA	7:E:147:HIS:HA	1.83	0.59
6:C:49:VAL:O	13:L:67:PHE:HB2	2.03	0.59
6:C:245:VAL:HG13	12:K:102:LYS:HD3	1.85	0.59
4:A:131:SER:CB	4:A:223:GLY:HA3	2.33	0.59
12:K:7:PHE:HA	12:K:10:PHE:CE1	2.38	0.59
5:B:597:MET:HE3	5:B:601:ARG:HH12	1.68	0.59
6:C:44:LEU:HB2	6:C:77:ILE:HD13	1.85	0.59
4:A:497:THR:HG23	5:B:1146:PHE:HA	1.85	0.59
4:A:665:GLY:HA3	5:B:1069:PHE:CE1	2.38	0.59
4:A:964:ILE:HG21	4:A:1035:TYR:CZ	2.38	0.59
6:C:259:LEU:HD11	12:K:91:CYS:CB	2.32	0.59
4:A:901:LEU:HD21	4:A:929:LEU:HD11	1.85	0.58
4:A:515:GLN:OE1	4:A:1071:SER:HA	2.03	0.58
5:B:592:ASN:ND2	5:B:595:ARG:HB3	2.17	0.58
3:N:2:DC:H2''	3:N:3:DA:O5'	2.03	0.58
4:A:902:LEU:HG	4:A:926:GLN:HG2	1.86	0.58
12:K:30:ALA:HA	12:K:75:ILE:O	2.04	0.58
4:A:1207:LEU:HD11	4:A:1273:LEU:HB2	1.85	0.58
5:B:604:ARG:NH2	5:B:614:SER:HA	2.18	0.58
7:E:17:ARG:O	7:E:21:GLU:OE1	2.22	0.58
4:A:115:LEU:HD23	4:A:142:CYS:HA	1.84	0.58
4:A:152:VAL:HG22	4:A:164:ARG:HG2	1.86	0.58
4:A:181:LEU:HB2	4:A:202:LEU:HD22	1.84	0.58
4:A:672:ASP:H	4:A:736:ASN:HD21	1.51	0.58
4:A:350:ARG:HB2	5:B:1128:LEU:HD11	1.85	0.58
5:B:1006:ILE:HD13	11:J:44:TYR:CZ	2.39	0.58
4:A:541:ILE:HD11	4:A:656:TRP:HE1	1.68	0.58
4:A:693:VAL:HG21	4:A:721:PHE:HE2	1.69	0.58
4:A:942:PHE:O	4:A:946:VAL:HG23	2.04	0.58
5:B:310:MET:HG3	5:B:386:LEU:HD13	1.85	0.58
5:B:416:LEU:HD23	5:B:457:LEU:HD23	1.86	0.58
13:L:36:SER:OG	13:L:50:ASP:OD2	2.21	0.58
4:A:548:ASN:HA	12:K:60:ALA:HB1	1.85	0.58
5:B:601:ARG:O	5:B:605:ARG:HD2	2.04	0.58
5:B:494:HIS:HA	5:B:497:ARG:NE	2.18	0.57
5:B:496:ARG:NH1	5:B:541:LEU:HA	2.19	0.57
4:A:23:SER:HB2	4:A:233:TRP:CH2	2.40	0.57
4:A:39:GLU:O	4:A:50:ILE:HD11	2.04	0.57
4:A:569:LYS:HG3	4:A:570:PRO:HD2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1135:ARG:O	5:B:1139:ILE:HG12	2.03	0.57
4:A:179:LEU:HD22	4:A:297:GLN:CD	2.29	0.57
4:A:269:ILE:HG12	4:A:299:HIS:HB3	1.85	0.57
4:A:515:GLN:O	4:A:515:GLN:HG3	2.04	0.57
4:A:901:LEU:HD22	4:A:919:ILE:HG22	1.86	0.57
5:B:806:THR:HG22	5:B:808:ALA:H	1.68	0.57
7:E:65:THR:HB	7:E:67:GLU:OE2	2.04	0.57
4:A:874:ASP:HB2	4:A:1058:VAL:HA	1.85	0.57
5:B:898:LEU:HD22	5:B:964:VAL:HG11	1.85	0.57
4:A:882:SER:H	4:A:961:ARG:NH2	2.03	0.57
4:A:1441:PHE:HB2	8:F:134:ILE:CG2	2.34	0.57
5:B:37:PHE:HB2	5:B:681:TRP:CE3	2.40	0.57
5:B:570:VAL:CG2	5:B:573:GLN:HB2	2.33	0.57
6:C:8:VAL:HG11	12:K:105:PHE:HB2	1.85	0.57
6:C:71:PRO:HB2	6:C:133:ILE:HD12	1.86	0.57
2:T:9:DC:H2''	2:T:10:DT:H5'	1.86	0.57
4:A:218:ASP:O	4:A:222:LEU:HG	2.04	0.57
4:A:614:PHE:HB3	9:H:122:LEU:HD21	1.85	0.57
4:A:676:MET:O	4:A:680:THR:HG23	2.04	0.57
4:A:915:SER:O	4:A:919:ILE:HG12	2.04	0.57
5:B:466:TRP:HE1	5:B:479:VAL:HG11	1.68	0.57
6:C:142:VAL:HG23	11:J:15:GLY:HA3	1.85	0.57
4:A:203:SER:HB3	4:A:206:GLU:HB3	1.86	0.57
5:B:308:TRP:HH2	10:I:47:GLU:HG3	1.69	0.57
12:K:28:PRO:HD2	12:K:76:GLN:HE22	1.69	0.57
4:A:303:TYR:CZ	4:A:325:ILE:HD11	2.39	0.57
9:H:100:THR:HG23	9:H:138:GLU:HA	1.86	0.57
4:A:494:SER:O	4:A:498:ARG:HG3	2.04	0.57
4:A:956:LEU:HD13	4:A:1021:LEU:HD22	1.85	0.57
4:A:1441:PHE:CZ	8:F:89:GLU:HA	2.40	0.57
5:B:435:THR:HG22	5:B:438:GLU:H	1.68	0.57
5:B:829:CYS:HA	5:B:834:ASN:ND2	2.18	0.57
7:E:39:LEU:HG	7:E:43:LYS:HD3	1.86	0.57
4:A:148:CYS:HB3	4:A:167:CYS:HB3	1.86	0.57
4:A:266:LEU:HA	4:A:269:ILE:HD12	1.87	0.57
4:A:387:ARG:O	4:A:391:LEU:HG	2.05	0.57
4:A:667:GLY:HA3	5:B:1067:ARG:HD2	1.86	0.57
2:T:25:DC:H2''	2:T:26:DG:H5'	1.85	0.56
4:A:463:ILE:HD13	4:A:469:ARG:CG	2.24	0.56
4:A:707:GLY:HA3	4:A:1281:ARG:HD2	1.86	0.56
4:A:801:GLU:OE1	5:B:729:ILE:HD12	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:898:ARG:HB2	4:A:933:TYR:CE1	2.39	0.56
5:B:757:PRO:HG2	5:B:984:HIS:CE1	2.39	0.56
5:B:1156:ASP:O	5:B:1197:PRO:HA	2.05	0.56
4:A:32:VAL:HG21	4:A:57:ARG:CB	2.35	0.56
5:B:703:ILE:HG22	5:B:740:HIS:HB2	1.87	0.56
9:H:126:GLU:C	9:H:130:ARG:HE	2.13	0.56
4:A:336:ILE:O	4:A:341:MET:HG2	2.05	0.56
4:A:482:PHE:CD2	5:B:836:GLU:HB2	2.41	0.56
5:B:308:TRP:H	5:B:308:TRP:CD1	2.23	0.56
6:C:25:VAL:HG23	6:C:228:PHE:HE2	1.68	0.56
6:C:182:PRO:HB2	6:C:207:CYS:SG	2.46	0.56
9:H:93:TYR:CG	9:H:143:LEU:HB3	2.40	0.56
11:J:7:CYS:HA	11:J:49:MET:HE3	1.86	0.56
4:A:23:SER:HB3	4:A:26:GLU:HB3	1.88	0.56
4:A:116:ASP:OD2	4:A:164:ARG:HD3	2.04	0.56
4:A:326:ARG:HG3	4:A:1406:VAL:HG11	1.85	0.56
4:A:851:HIS:CD2	8:F:139:PRO:HG3	2.40	0.56
5:B:167:ILE:O	5:B:450:ALA:HA	2.06	0.56
5:B:876:LYS:HG3	5:B:893:LEU:HB3	1.87	0.56
6:C:74:SER:HB2	6:C:238:ILE:HG13	1.86	0.56
4:A:373:THR:O	5:B:1107:ALA:HB2	2.05	0.56
4:A:800:VAL:HG13	4:A:812:GLU:CD	2.30	0.56
5:B:125:SER:HB2	5:B:169:ARG:HB3	1.88	0.56
9:H:39:THR:O	9:H:123:MET:HA	2.06	0.56
10:I:76:PRO:HD2	10:I:108:HIS:CE1	2.40	0.56
11:J:58:GLU:HA	11:J:61:LEU:HD12	1.87	0.56
4:A:913:LEU:HD21	4:A:1032:LEU:HD13	1.88	0.56
5:B:905:VAL:HB	5:B:941:LEU:HD12	1.87	0.56
4:A:204:THR:CG2	4:A:235:ILE:HD11	2.35	0.56
4:A:744:LYS:HB3	4:A:748:MET:HE2	1.87	0.56
5:B:520:GLY:HA3	5:B:635:ARG:HE	1.71	0.56
5:B:1060:ARG:HG2	5:B:1066:SER:HB3	1.87	0.56
9:H:91:ASP:OD2	9:H:96:VAL:HG21	2.06	0.56
7:E:188:LEU:HD12	7:E:190:LEU:HD21	1.87	0.56
4:A:752:LYS:HD2	5:B:1019:SER:HB3	1.86	0.56
5:B:449:ASN:HD22	5:B:452:THR:HG23	1.71	0.56
5:B:830:TYR:CE2	5:B:1000:PRO:HD3	2.40	0.56
11:J:41:LEU:HB3	11:J:46:CYS:HB2	1.88	0.56
13:L:47:ARG:NH2	13:L:54:ARG:HE	2.04	0.56
4:A:219:PHE:CE1	4:A:231:PRO:HG3	2.41	0.55
5:B:412:LEU:O	5:B:415:GLN:HG2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:10:PHE:CD2	12:K:11:LEU:CD1	2.89	0.55
4:A:353:ILE:HG21	4:A:487:MET:HG3	1.88	0.55
5:B:830:TYR:H	5:B:834:ASN:HD21	1.52	0.55
6:C:101:LEU:HB2	6:C:118:LEU:HG	1.88	0.55
7:E:124:VAL:HG22	7:E:132:ILE:HB	1.88	0.55
4:A:176:LYS:HA	4:A:181:LEU:HA	1.88	0.55
4:A:396:PRO:HD3	4:A:415:LEU:HB3	1.88	0.55
4:A:1001:ARG:HD2	8:F:83:PRO:HD3	1.87	0.55
4:A:1140:HIS:HA	4:A:1275:GLY:HA3	1.89	0.55
4:A:1428:VAL:HG13	5:B:1151:LEU:HD21	1.89	0.55
12:K:108:GLU:O	12:K:112:GLN:HG2	2.06	0.55
4:A:114:LEU:HD22	4:A:148:CYS:HB2	1.88	0.55
4:A:463:ILE:CD1	4:A:469:ARG:HG2	2.25	0.55
4:A:472:LEU:HD12	4:A:650:GLN:NE2	2.21	0.55
4:A:912:LEU:O	4:A:913:LEU:HD22	2.06	0.55
7:E:90:VAL:HA	7:E:117:THR:HG21	1.88	0.55
4:A:351:THR:HG22	5:B:1103:ILE:HG23	1.88	0.55
4:A:1106:ASN:O	4:A:1107:VAL:HG22	2.07	0.55
5:B:120:ARG:NH1	13:L:54:ARG:HD3	2.22	0.55
5:B:364:ILE:HD13	5:B:585:VAL:HG22	1.87	0.55
9:H:38:LEU:HA	9:H:124:ARG:O	2.06	0.55
4:A:96:ILE:HA	4:A:99:ILE:HB	1.87	0.55
5:B:754:SER:HB2	5:B:812:LEU:HD11	1.89	0.55
8:F:83:PRO:HA	8:F:146:TRP:CZ3	2.41	0.55
4:A:93:VAL:O	4:A:96:ILE:HG22	2.07	0.55
5:B:901:PRO:O	13:L:61:THR:HG23	2.07	0.55
8:F:89:GLU:O	8:F:93:ILE:HG12	2.07	0.55
10:I:6:PHE:HD1	10:I:13:MET:HA	1.72	0.55
4:A:598:LEU:HB3	9:H:25:ARG:HH12	1.71	0.55
4:A:848:ILE:HG21	4:A:1370:LEU:HD11	1.89	0.55
11:J:58:GLU:O	11:J:62:ARG:HG2	2.07	0.55
7:E:13:TRP:CE3	7:E:39:LEU:HB2	2.42	0.54
12:K:40:HIS:NE2	12:K:63:VAL:HG11	2.22	0.54
4:A:105:CYS:CB	4:A:142:CYS:HB3	2.37	0.54
4:A:548:ASN:ND2	12:K:61:TYR:H	2.05	0.54
4:A:550:LEU:O	4:A:553:VAL:HG22	2.07	0.54
4:A:800:VAL:HG22	4:A:812:GLU:HG2	1.89	0.54
4:A:881:GLN:HA	4:A:961:ARG:NH2	2.19	0.54
4:A:993:LEU:HD11	4:A:1050:GLU:HB2	1.90	0.54
4:A:1195:LEU:HD11	4:A:1267:MET:HE1	1.88	0.54
5:B:837:ASP:O	5:B:988:GLY:HA2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:94:LYS:HA	6:C:127:ARG:HH12	1.72	0.54
2:T:10:DT:H1'	2:T:11:DC:H5'	1.88	0.54
4:A:573:SER:HB3	4:A:576:GLN:HG3	1.89	0.54
4:A:714:PHE:CD2	10:I:97:MET:HE1	2.42	0.54
4:A:901:LEU:HG	4:A:926:GLN:OE1	2.08	0.54
4:A:1383:SER:HB2	4:A:1387:HIS:O	2.07	0.54
5:B:763:GLN:HG2	5:B:765:PRO:HD2	1.89	0.54
8:F:109:VAL:HB	8:F:124:GLU:HG2	1.90	0.54
9:H:89:LEU:HD13	9:H:91:ASP:C	2.32	0.54
4:A:53:LEU:HD21	4:A:266:LEU:HD11	1.89	0.54
4:A:134:ARG:HD2	4:A:221:SER:HA	1.89	0.54
4:A:519:PRO:O	4:A:624:SER:HB2	2.07	0.54
4:A:774:ARG:NH2	4:A:797:LYS:HG3	2.22	0.54
6:C:80:LEU:HG	6:C:94:LYS:O	2.07	0.54
7:E:23:VAL:HG13	7:E:28:TYR:HB2	1.89	0.54
5:B:219:ALA:HB2	5:B:405:ARG:HG2	1.90	0.54
5:B:827:ILE:HG12	5:B:1012:ILE:HD11	1.89	0.54
4:A:875:ALA:HB2	4:A:1366:ARG:HD2	1.90	0.54
4:A:901:LEU:HD22	4:A:919:ILE:CG2	2.37	0.54
4:A:1352:VAL:O	4:A:1356:ILE:HG12	2.08	0.54
12:K:90:ALA:O	12:K:94:ILE:HG13	2.08	0.54
4:A:96:ILE:HD13	4:A:179:LEU:CD1	2.38	0.54
4:A:407:ARG:HH11	4:A:413:ILE:HD11	1.73	0.54
4:A:845:LEU:O	4:A:1065:GLY:HA3	2.08	0.54
4:A:861:GLY:HA3	7:E:174:GLN:HE21	1.72	0.54
4:A:998:LEU:HA	4:A:1011:GLN:NE2	2.22	0.54
5:B:294:ASP:HB2	10:I:12:ASN:HA	1.90	0.54
6:C:84:ARG:HD3	12:K:11:LEU:HD21	1.90	0.54
6:C:94:LYS:HA	6:C:127:ARG:HH22	1.71	0.54
9:H:6:PHE:CZ	9:H:8:ASP:HB2	2.43	0.54
13:L:64:LEU:HD22	13:L:66:GLN:NE2	2.21	0.54
4:A:167:CYS:SG	4:A:169:ASN:HB2	2.48	0.54
4:A:727:ASP:O	4:A:731:ARG:HG2	2.08	0.54
5:B:996:ARG:HE	6:C:38:ILE:HG23	1.72	0.54
8:F:125:LEU:O	8:F:128:LYS:HD2	2.08	0.54
9:H:110:ASP:O	9:H:128:ASN:HB2	2.07	0.54
4:A:542:GLU:O	4:A:546:VAL:HG23	2.08	0.54
5:B:903:VAL:HG12	5:B:905:VAL:HG13	1.90	0.54
6:C:162:GLY:HA3	6:C:170:TRP:CD2	2.43	0.54
4:A:774:ARG:CZ	4:A:797:LYS:HG3	2.38	0.53
5:B:33:VAL:HG12	5:B:681:TRP:HZ3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:115:TYR:CE2	9:H:124:ARG:HG3	2.43	0.53
5:B:996:ARG:HH21	6:C:38:ILE:HG12	1.72	0.53
5:B:1174:LYS:HG2	5:B:1179:GLN:O	2.07	0.53
10:I:106:CYS:CB	10:I:108:HIS:HD2	2.18	0.53
4:A:868:TYR:CE1	4:A:1064:VAL:HG11	2.43	0.53
5:B:416:LEU:HD13	5:B:466:TRP:HE3	1.73	0.53
7:E:177:ARG:HB3	7:E:215:MET:HG3	1.91	0.53
8:F:82:THR:HG22	8:F:84:TYR:H	1.72	0.53
2:T:26:DG:H2''	2:T:27:DA:H5''	1.91	0.53
5:B:864:LYS:HB3	5:B:872:GLU:CD	2.34	0.53
5:B:1116:ARG:HG3	5:B:1198:TYR:CD1	2.43	0.53
4:A:30:ILE:HD12	5:B:1170:THR:HG21	1.91	0.53
4:A:200:ARG:NH2	4:A:203:SER:H	2.07	0.53
4:A:743:VAL:HG12	4:A:758:ILE:CD1	2.39	0.53
4:A:841:LEU:HD21	4:A:1105:LEU:HD13	1.91	0.53
5:B:63:ILE:O	5:B:67:SER:HB3	2.09	0.53
5:B:914:LYS:HB3	5:B:937:ALA:HB3	1.89	0.53
5:B:166:PHE:HZ	5:B:169:ARG:HG3	1.74	0.53
5:B:523:CYS:HB2	5:B:750:GLY:HA3	1.90	0.53
5:B:1106:ARG:CZ	5:B:1109:GLY:HA3	2.39	0.53
10:I:47:GLU:HB2	10:I:50:THR:OG1	2.08	0.53
4:A:30:ILE:O	5:B:1183:LYS:HD3	2.08	0.53
4:A:31:SER:HB3	4:A:83:HIS:HB3	1.91	0.53
4:A:596:THR:HB	4:A:599:SER:H	1.74	0.53
7:E:117:THR:CG2	7:E:120:ALA:HB2	2.38	0.53
4:A:666:ILE:HG23	5:B:1026:LEU:HB3	1.90	0.53
4:A:1206:ASP:HB3	4:A:1274:ARG:CZ	2.38	0.53
5:B:1168:LEU:HD23	5:B:1208:MET:HE2	1.91	0.53
6:C:62:PHE:O	6:C:66:ARG:HG3	2.09	0.53
4:A:810:PRO:HG2	5:B:705:MET:HG2	1.91	0.53
4:A:1352:VAL:O	4:A:1355:VAL:HG22	2.09	0.53
5:B:466:TRP:NE1	5:B:479:VAL:HG11	2.24	0.53
4:A:230:ARG:HB2	4:A:233:TRP:CG	2.43	0.52
4:A:629:LEU:O	4:A:633:VAL:HG23	2.09	0.52
4:A:990:VAL:HG13	4:A:1022:LEU:HD21	1.90	0.52
4:A:420:ARG:O	4:A:424:ILE:HG23	2.10	0.52
5:B:582:VAL:HA	5:B:626:ILE:O	2.09	0.52
6:C:53:THR:O	6:C:153:LEU:HD12	2.10	0.52
11:J:21:TYR:CZ	11:J:25:LEU:HD11	2.45	0.52
4:A:340:LEU:HD13	4:A:1429:ILE:HG23	1.90	0.52
4:A:528:LEU:O	4:A:531:ILE:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:67:SER:HB2	5:B:92:PHE:CD1	2.45	0.52
6:C:105:GLY:O	6:C:149:LYS:HA	2.09	0.52
6:C:205:LYS:H	6:C:205:LYS:HD2	1.74	0.52
5:B:91:SER:OG	5:B:133:LYS:HB2	2.09	0.52
5:B:311:LEU:O	5:B:315:LYS:HG3	2.10	0.52
5:B:449:ASN:ND2	5:B:452:THR:HG23	2.24	0.52
5:B:520:GLY:HA2	5:B:748:ILE:HG22	1.91	0.52
6:C:148:ARG:CZ	11:J:64:ASN:HA	2.39	0.52
6:C:251:LEU:O	6:C:255:VAL:HG23	2.10	0.52
11:J:34:THR:O	11:J:38:ARG:HG2	2.10	0.52
4:A:1287:TYR:CD2	4:A:1305:VAL:HG21	2.45	0.52
5:B:405:ARG:NH2	5:B:632:ARG:HG3	2.25	0.52
5:B:580:VAL:HG12	5:B:624:LEU:HB3	1.90	0.52
4:A:75:ASN:HA	5:B:1116:ARG:HH22	1.74	0.52
4:A:181:LEU:O	4:A:202:LEU:HB2	2.10	0.52
5:B:762:ASN:HD21	5:B:984:HIS:HB3	1.75	0.52
6:C:164:ALA:HA	6:C:167:HIS:O	2.09	0.52
2:T:4:DT:H3	3:N:15:DA:H61	1.57	0.52
5:B:205:ILE:HG13	5:B:461:LEU:HB3	1.90	0.52
5:B:827:ILE:HG23	5:B:1012:ILE:HG13	1.91	0.52
5:B:852:ARG:HD2	5:B:973:ILE:HG23	1.92	0.52
6:C:91:HIS:HB3	6:C:96:SER:OG	2.09	0.52
12:K:45:LEU:HG	12:K:94:ILE:HD13	1.92	0.52
12:K:77:THR:HB	12:K:81:TYR:HB3	1.92	0.52
4:A:354:SER:O	4:A:469:ARG:HA	2.10	0.52
4:A:443:LEU:O	4:A:489:LEU:HA	2.10	0.52
5:B:60:GLN:CD	5:B:94:LYS:HA	2.34	0.52
5:B:351:TYR:O	5:B:355:ILE:HG12	2.10	0.52
6:C:163:ILE:HD11	12:K:10:PHE:CG	2.45	0.52
9:H:24:CYS:SG	9:H:44:VAL:HG21	2.50	0.52
4:A:57:ARG:HA	4:A:68:GLN:CG	2.37	0.52
4:A:975:HIS:O	4:A:1036:ARG:HG3	2.10	0.52
6:C:96:SER:HB2	6:C:158:VAL:HG13	1.91	0.52
7:E:46:TYR:HE1	7:E:57:MET:HB3	1.74	0.52
7:E:90:VAL:CA	7:E:117:THR:HG21	2.39	0.52
10:I:34:TYR:OH	10:I:36:GLU:HB3	2.10	0.52
4:A:1348:LEU:HD22	4:A:1372:VAL:HG22	1.91	0.52
1:R:3:C:H2'	1:R:4:G:H8	1.76	0.51
5:B:751:VAL:HG23	5:B:812:LEU:HD22	1.92	0.51
5:B:1033:LYS:HG2	5:B:1059:LEU:HD21	1.91	0.51
6:C:6:PRO:HB3	6:C:25:VAL:HG12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:77:LYS:HB3	10:I:108:HIS:CD2	2.45	0.51
4:A:22:PHE:HE2	5:B:1208:MET:HA	1.75	0.51
5:B:346:GLU:HA	5:B:349:ILE:HD12	1.91	0.51
6:C:14:SER:HA	12:K:114:LEU:HD22	1.92	0.51
1:R:3:C:H2'	1:R:4:G:C8	2.46	0.51
4:A:172:PRO:HD3	4:A:185:TRP:HE1	1.73	0.51
4:A:538:ASP:CG	9:H:20:TYR:HB3	2.35	0.51
4:A:1226:VAL:HB	4:A:1228:TRP:CH2	2.45	0.51
4:A:1431:GLY:HA3	5:B:1197:PRO:HD3	1.92	0.51
5:B:639:ILE:HD12	5:B:688:GLY:O	2.10	0.51
5:B:992:ILE:HG13	12:K:67:PHE:HE1	1.75	0.51
6:C:99:LEU:HD12	6:C:118:LEU:HB3	1.91	0.51
10:I:86:PHE:CE2	10:I:89:GLN:HG2	2.45	0.51
4:A:38:PRO:O	4:A:53:LEU:HD12	2.10	0.51
4:A:804:TYR:OH	5:B:763:GLN:HG3	2.10	0.51
4:A:1031:VAL:O	4:A:1035:TYR:O	2.28	0.51
4:A:1148:ILE:HD11	4:A:1198:ASP:HA	1.93	0.51
5:B:629:ASP:N	5:B:632:ARG:HH12	2.09	0.51
6:C:183:TRP:CD2	6:C:213:PRO:HD3	2.45	0.51
9:H:127:GLY:N	9:H:130:ARG:HE	2.08	0.51
4:A:975:HIS:CD2	4:A:1036:ARG:H	2.18	0.51
6:C:183:TRP:CG	6:C:213:PRO:HD3	2.45	0.51
4:A:41:MET:HA	4:A:49:LYS:HA	1.92	0.51
4:A:1001:ARG:HB2	8:F:80:ALA:HA	1.91	0.51
4:A:1168:GLU:O	4:A:1172:LEU:HG	2.11	0.51
4:A:1436:ILE:HD12	5:B:1139:ILE:HG23	1.93	0.51
5:B:866:TYR:HH	5:B:872:GLU:HG3	1.76	0.51
4:A:248:PRO:HD3	5:B:1114:LEU:HD13	1.93	0.51
4:A:541:ILE:HD11	4:A:656:TRP:NE1	2.26	0.51
4:A:672:ASP:H	4:A:736:ASN:ND2	2.08	0.51
4:A:326:ARG:HB2	4:A:1406:VAL:HG21	1.92	0.51
8:F:83:PRO:HB2	8:F:152:ILE:HD13	1.93	0.51
9:H:6:PHE:HE2	9:H:125:LEU:HD21	1.75	0.51
12:K:51:LEU:CD1	12:K:59:ALA:HB3	2.40	0.51
4:A:206:GLU:O	4:A:210:ILE:HG13	2.11	0.51
4:A:367:PRO:HG2	4:A:370:ILE:HG13	1.92	0.51
4:A:376:TYR:CZ	4:A:498:ARG:HD2	2.46	0.51
4:A:752:LYS:HG2	5:B:1015:HIS:O	2.10	0.51
5:B:578:THR:HA	5:B:622:LYS:O	2.11	0.51
5:B:1034:VAL:HG22	5:B:1059:LEU:HG	1.93	0.51
4:A:298:PHE:HE1	4:A:312:PRO:HB2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:863:VAL:CG2	7:E:170:LEU:HD21	2.40	0.51
4:A:1109:LYS:H	4:A:1109:LYS:HD2	1.76	0.51
5:B:1118:PRO:HD3	5:B:1155:SER:HB3	1.92	0.51
7:E:127:ILE:HB	7:E:130:ALA:HB3	1.92	0.51
4:A:378:GLU:HG2	4:A:388:LEU:HD11	1.92	0.50
4:A:1138:ILE:CG2	4:A:1282:VAL:HG21	2.41	0.50
5:B:36:ALA:HA	5:B:39:ARG:HD3	1.93	0.50
9:H:97:MET:HE2	9:H:118:PHE:HB2	1.94	0.50
11:J:41:LEU:HD23	11:J:46:CYS:HB3	1.92	0.50
4:A:11:LEU:HA	5:B:1193:GLN:O	2.11	0.50
5:B:257:LYS:HB2	5:B:259:TYR:CE1	2.47	0.50
4:A:185:TRP:O	4:A:186:LYS:HG2	2.11	0.50
4:A:243:PRO:HG2	4:A:246:VAL:HG23	1.94	0.50
4:A:325:ILE:O	4:A:329:LEU:HG	2.11	0.50
4:A:449:SER:HB2	5:B:1133:MET:HE3	1.93	0.50
6:C:60:ASP:HB2	13:L:67:PHE:CZ	2.47	0.50
6:C:91:HIS:CE1	6:C:158:VAL:HG11	2.45	0.50
7:E:117:THR:HG23	7:E:120:ALA:H	1.77	0.50
4:A:55:ASP:H	4:A:58:LEU:HD22	1.76	0.50
4:A:466:SER:HB2	5:B:1103:ILE:CD1	2.41	0.50
5:B:68:THR:HA	5:B:90:ILE:O	2.11	0.50
5:B:883:LEU:HD13	5:B:932:HIS:HB3	1.94	0.50
5:B:1169:MET:HE1	5:B:1201:LYS:HG2	1.94	0.50
10:I:26:LEU:HD23	10:I:26:LEU:H	1.77	0.50
11:J:39:LEU:HB2	11:J:41:LEU:HD12	1.94	0.50
4:A:760:GLN:HG2	4:A:765:VAL:HA	1.92	0.50
4:A:1224:LEU:HD23	4:A:1226:VAL:HG13	1.92	0.50
4:A:1438:THR:HA	4:A:1441:PHE:CE2	2.45	0.50
5:B:489:SER:HA	5:B:492:LEU:HD12	1.94	0.50
5:B:846:ILE:HG23	5:B:974:PRO:HD2	1.93	0.50
5:B:1054:GLY:O	5:B:1058:LEU:HG	2.12	0.50
7:E:24:LYS:HB2	7:E:30:ILE:CG2	2.42	0.50
4:A:105:CYS:SG	4:A:114:LEU:HB2	2.52	0.50
4:A:738:LYS:HZ3	6:C:194:GLU:HA	1.76	0.50
4:A:1259:MET:HE2	4:A:1259:MET:HA	1.94	0.50
5:B:800:GLN:HB3	11:J:52:THR:HB	1.94	0.50
7:E:175:LEU:HD23	7:E:213:ILE:HB	1.93	0.50
10:I:74:GLU:HB3	10:I:81:ARG:HD2	1.94	0.50
4:A:22:PHE:CG	5:B:1213:THR:HG22	2.46	0.50
4:A:1153:TYR:CD2	10:I:42:LEU:HB2	2.47	0.50
4:A:821:ARG:NH2	5:B:534:GLY:HA2	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1004:ASN:HD21	4:A:1006:ILE:HB	1.76	0.50
4:A:1213:GLY:HA3	4:A:1228:TRP:CH2	2.47	0.50
4:A:1267:MET:O	4:A:1271:ILE:HB	2.11	0.50
5:B:193:LYS:HD2	5:B:787:VAL:HG11	1.94	0.50
7:E:169:ARG:HD2	8:F:140:ASP:CG	2.36	0.50
9:H:6:PHE:CE2	9:H:125:LEU:HD21	2.47	0.50
1:R:9:G:H3'	1:R:10:8GM:N3	2.26	0.50
4:A:114:LEU:CD2	4:A:148:CYS:HB2	2.41	0.50
4:A:801:GLU:HB3	5:B:729:ILE:CD1	2.39	0.50
5:B:127:GLY:HA2	5:B:166:PHE:HE1	1.77	0.50
5:B:308:TRP:CZ3	5:B:309:GLN:HG2	2.47	0.50
5:B:952:VAL:HB	13:L:58:LYS:HB2	1.94	0.50
10:I:63:GLY:HA3	10:I:104:LEU:HD21	1.93	0.50
11:J:8:PHE:H	11:J:49:MET:HE3	1.77	0.50
4:A:366:VAL:HG21	4:A:460:VAL:HG22	1.94	0.49
4:A:1223:ASP:O	4:A:1243:VAL:HB	2.11	0.49
5:B:367:LEU:HD11	5:B:370:PHE:HE2	1.76	0.49
5:B:806:THR:H	5:B:809:MET:HE3	1.77	0.49
4:A:492:PRO:HB3	4:A:497:THR:HG22	1.94	0.49
5:B:313:MET:HE1	5:B:390:LEU:HG	1.94	0.49
5:B:416:LEU:HD22	5:B:466:TRP:HZ3	1.76	0.49
5:B:649:LYS:O	5:B:710:LEU:HD21	2.12	0.49
7:E:91:LYS:O	7:E:95:THR:HG23	2.11	0.49
7:E:144:ILE:HD11	7:E:187:TYR:HB2	1.94	0.49
10:I:63:GLY:HA2	10:I:84:VAL:HG21	1.94	0.49
11:J:4:PRO:O	11:J:14:VAL:HG23	2.13	0.49
4:A:135:PHE:HD2	4:A:222:LEU:HA	1.76	0.49
4:A:873:MET:SD	4:A:957:PRO:HB3	2.52	0.49
5:B:378:LEU:O	5:B:382:ILE:HG13	2.12	0.49
5:B:611:PRO:HB3	5:B:685:LEU:HD11	1.93	0.49
7:E:46:TYR:OH	7:E:55:ARG:HA	2.11	0.49
7:E:46:TYR:CE2	7:E:58:MET:HB2	2.46	0.49
8:F:87:LYS:HG3	8:F:88:TYR:N	2.27	0.49
4:A:42:ASP:HA	4:A:50:ILE:CG2	2.30	0.49
4:A:452:LYS:HB2	5:B:1141:HIS:CE1	2.47	0.49
9:H:40:LEU:HD13	9:H:123:MET:HB2	1.94	0.49
12:K:49:GLU:HG3	12:K:94:ILE:HG12	1.93	0.49
4:A:464:PRO:O	12:K:2:ASN:HB3	2.13	0.49
5:B:286:PHE:HA	5:B:289:LEU:HD12	1.94	0.49
5:B:757:PRO:HG3	5:B:983:ARG:CZ	2.42	0.49
5:B:893:LEU:HD21	5:B:911:ILE:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1168:LEU:HD23	5:B:1208:MET:HG2	1.94	0.49
7:E:56:LYS:HE2	7:E:84:ASP:HB2	1.94	0.49
12:K:103:THR:O	12:K:107:THR:HG23	2.12	0.49
5:B:234:ILE:HG21	5:B:257:LYS:HB3	1.94	0.49
4:A:15:LYS:HG2	5:B:1218:THR:O	2.13	0.49
4:A:75:ASN:HA	5:B:1116:ARG:NH2	2.27	0.49
4:A:88:LYS:HD3	4:A:293:GLU:HG2	1.93	0.49
4:A:311:GLN:N	4:A:312:PRO:HD3	2.27	0.49
4:A:450:LEU:HD22	4:A:1077:THR:HG21	1.93	0.49
4:A:708:MET:HG2	4:A:713:SER:HB2	1.95	0.49
4:A:765:VAL:CG2	4:A:800:VAL:HB	2.43	0.49
4:A:793:SER:O	4:A:797:LYS:HG2	2.12	0.49
4:A:1213:GLY:HA3	4:A:1228:TRP:CZ2	2.47	0.49
5:B:313:MET:O	5:B:316:PRO:HD2	2.13	0.49
6:C:104:PHE:HD1	6:C:152:GLU:HB3	1.77	0.49
6:C:221:TYR:CE2	6:C:222:LYS:HG2	2.48	0.49
8:F:76:LYS:HE2	8:F:79:ARG:NH1	2.27	0.49
4:A:380:VAL:HG21	4:A:427:GLN:O	2.12	0.49
4:A:569:LYS:HD3	6:C:221:TYR:HB2	1.92	0.49
4:A:597:LEU:HB3	9:H:102:TYR:CE2	2.43	0.49
4:A:678:GLU:HA	4:A:681:GLU:HG3	1.95	0.49
4:A:693:VAL:HG21	4:A:721:PHE:CE2	2.48	0.49
4:A:962:ARG:HA	4:A:965:GLN:OE1	2.13	0.49
4:A:1073:GLY:O	4:A:1077:THR:HG23	2.13	0.49
4:A:1144:LYS:HG2	4:A:1268:LEU:HB3	1.95	0.49
5:B:1162:ILE:CG2	5:B:1192:TYR:HB2	2.36	0.49
9:H:22:LYS:HB3	9:H:43:ASN:HD21	1.77	0.49
4:A:176:LYS:HB2	4:A:181:LEU:HD23	1.93	0.49
4:A:1150:SER:OG	10:I:46:HIS:HB3	2.13	0.49
5:B:496:ARG:HH12	5:B:541:LEU:HA	1.78	0.49
1:R:8:G:H1	2:T:21:DC:H42	1.61	0.49
4:A:4:GLN:HG3	4:A:76:GLU:OE1	2.13	0.49
4:A:684:ALA:HA	4:A:687:LYS:HD3	1.94	0.49
5:B:177:LYS:HB3	5:B:177:LYS:HE2	1.71	0.49
6:C:60:ASP:HA	6:C:63:ILE:HD12	1.95	0.49
12:K:1:MET:HG3	12:K:2:ASN:H	1.78	0.49
4:A:658:LEU:HD21	5:B:1074:ASN:HD21	1.78	0.48
4:A:900:ASP:H	4:A:906:HIS:HB3	1.78	0.48
5:B:860:MET:HA	5:B:964:VAL:O	2.13	0.48
8:F:74:ILE:HG21	8:F:144:GLU:HG2	1.95	0.48
8:F:98:ALA:HB1	8:F:117:PRO:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:265:LYS:HZ3	4:A:314:ALA:HB1	1.78	0.48
4:A:269:ILE:CG1	4:A:299:HIS:HB3	2.42	0.48
4:A:534:LEU:HD23	4:A:578:LEU:HD22	1.94	0.48
4:A:593:GLU:HG3	4:A:601:LYS:NZ	2.27	0.48
4:A:647:GLY:O	4:A:651:LYS:HG3	2.12	0.48
5:B:451:LYS:HG2	5:B:455:SER:HB3	1.94	0.48
4:A:336:ILE:HD12	5:B:1203:LEU:HD22	1.94	0.48
4:A:896:ARG:HH12	4:A:1030:ARG:HH11	1.60	0.48
4:A:915:SER:C	4:A:919:ILE:HG12	2.37	0.48
5:B:322:PHE:CZ	10:I:30:ARG:HB2	2.48	0.48
6:C:181:ASP:OD2	6:C:186:LEU:HB2	2.13	0.48
5:B:556:THR:O	5:B:560:GLU:HG2	2.14	0.48
5:B:618:ASP:HB3	5:B:621:GLU:HB2	1.95	0.48
5:B:1082:MET:HE2	6:C:190:ASP:HB2	1.94	0.48
5:B:1106:ARG:CZ	5:B:1118:PRO:HB3	2.43	0.48
7:E:185:ALA:HB1	7:E:190:LEU:HB2	1.96	0.48
9:H:28:ALA:HB3	9:H:38:LEU:CD2	2.43	0.48
4:A:407:ARG:NH1	4:A:413:ILE:HD11	2.27	0.48
4:A:908:LEU:CD1	4:A:913:LEU:HB2	2.42	0.48
4:A:1212:VAL:HA	4:A:1273:LEU:CD2	2.43	0.48
4:A:1217:LYS:HD2	4:A:1228:TRP:HZ2	1.77	0.48
5:B:785:TYR:HE1	11:J:60:PHE:CE1	2.30	0.48
12:K:21:ILE:HG23	12:K:31:VAL:CG2	2.43	0.48
2:T:13:DC:H42	3:N:5:DC:H42	1.61	0.48
4:A:857:ARG:HH21	7:E:170:LEU:HD21	1.75	0.48
4:A:1376:THR:HG22	7:E:212:ARG:HH21	1.79	0.48
5:B:528:PRO:HG2	5:B:536:VAL:HB	1.95	0.48
5:B:944:THR:HG21	5:B:1122:ARG:HH22	1.78	0.48
7:E:178:ILE:O	7:E:214:CYS:HA	2.13	0.48
9:H:12:VAL:HG21	9:H:26:ILE:HG13	1.96	0.48
13:L:31:CYS:HB2	13:L:56:LEU:HG	1.94	0.48
4:A:204:THR:HG23	4:A:235:ILE:HD11	1.96	0.48
4:A:1368:MET:O	4:A:1372:VAL:HG23	2.14	0.48
5:B:566:LEU:HD11	5:B:586:TRP:CE2	2.48	0.48
5:B:806:THR:HG23	5:B:1045:SER:HA	1.96	0.48
7:E:28:TYR:HA	7:E:64:PRO:HA	1.95	0.48
4:A:216:VAL:HA	4:A:219:PHE:CD2	2.49	0.48
4:A:765:VAL:HG11	4:A:804:TYR:CD1	2.49	0.48
4:A:1219:THR:HG21	4:A:1271:ILE:HG13	1.96	0.48
5:B:544:CYS:HB2	5:B:634:TYR:CE2	2.49	0.48
5:B:706:GLN:HG2	5:B:708:GLU:OE1	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1081:LEU:HD13	5:B:1085:ILE:HD12	1.95	0.48
7:E:156:LEU:HD22	7:E:160:GLU:HB3	1.96	0.48
9:H:9:ILE:O	9:H:31:THR:HG22	2.13	0.48
11:J:14:VAL:HG12	11:J:41:LEU:HD21	1.95	0.48
4:A:28:ARG:HH21	4:A:238:CYS:HB3	1.78	0.48
4:A:265:LYS:HZ1	4:A:322:VAL:HG21	1.79	0.48
4:A:551:TYR:HB2	12:K:58:PHE:HZ	1.78	0.48
4:A:923:LEU:HD12	4:A:923:LEU:H	1.79	0.48
4:A:1138:ILE:HG23	4:A:1282:VAL:HG21	1.94	0.48
5:B:1078:GLY:HA3	6:C:31:ASN:HB2	1.95	0.48
5:B:1082:MET:HA	6:C:189:THR:HA	1.96	0.48
9:H:103:LYS:HD2	9:H:104:PHE:H	1.78	0.48
3:N:12:DG:H4'	3:N:13:DA:H5'	1.96	0.48
4:A:1193:LEU:HB2	4:A:1260:LEU:HD11	1.95	0.48
4:A:1331:SER:OG	4:A:1334:ASP:HB2	2.13	0.48
10:I:17:ARG:O	10:I:25:LEU:HD12	2.14	0.48
2:T:6:DT:H2''	2:T:7:DC:C5	2.49	0.47
4:A:42:ASP:OD2	4:A:46:THR:HB	2.14	0.47
4:A:72:GLU:OE1	4:A:76:GLU:HG2	2.14	0.47
4:A:81:PHE:CE2	4:A:242:PRO:HA	2.48	0.47
4:A:406:ILE:HB	4:A:431:LYS:HB2	1.95	0.47
7:E:120:ALA:HA	7:E:123:LEU:HG	1.96	0.47
8:F:75:PRO:HB2	8:F:77:ASP:OD1	2.14	0.47
8:F:99:LEU:HD23	8:F:99:LEU:HA	1.70	0.47
4:A:882:SER:HA	4:A:952:ALA:O	2.14	0.47
4:A:15:LYS:HB3	5:B:1220:ARG:HG2	1.96	0.47
4:A:96:ILE:HD13	4:A:179:LEU:HD12	1.96	0.47
4:A:355:GLY:HA3	4:A:482:PHE:CZ	2.49	0.47
4:A:478:TYR:CE2	4:A:487:MET:HE1	2.49	0.47
4:A:1356:ILE:HG22	4:A:1361:SER:O	2.14	0.47
5:B:170:LEU:HD12	5:B:171:PRO:HD2	1.97	0.47
5:B:301:ILE:HG12	5:B:382:ILE:HD12	1.96	0.47
5:B:777:ALA:HB1	5:B:1093:GLN:HB2	1.96	0.47
7:E:17:ARG:C	7:E:21:GLU:OE1	2.58	0.47
7:E:88:VAL:HG21	7:E:112:TYR:CD2	2.50	0.47
6:C:80:LEU:HD22	6:C:161:LYS:HB2	1.96	0.47
6:C:143:LEU:HD21	6:C:146:LYS:HG3	1.95	0.47
9:H:116:TYR:CE1	9:H:140:ALA:HB2	2.50	0.47
4:A:820:GLY:O	4:A:824:LEU:HG	2.14	0.47
4:A:1134:ILE:O	4:A:1138:ILE:HG22	2.14	0.47
4:A:1215:ARG:O	4:A:1218:GLN:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:129:PHE:CZ	5:B:166:PHE:HB2	2.49	0.47
5:B:361:LEU:HD21	5:B:377:PHE:CD2	2.50	0.47
6:C:163:ILE:HD12	6:C:165:LYS:HB2	1.97	0.47
8:F:85:MET:HG3	8:F:89:GLU:HG3	1.95	0.47
10:I:71:SER:HB3	10:I:83:ASN:OD1	2.14	0.47
4:A:407:ARG:HA	4:A:430:TRP:CD1	2.50	0.47
4:A:587:HIS:HA	4:A:607:ILE:O	2.15	0.47
4:A:973:ILE:HG22	4:A:975:HIS:H	1.78	0.47
4:A:1116:LEU:HB2	4:A:1311:VAL:HG22	1.97	0.47
4:A:1169:ILE:HA	4:A:1172:LEU:HD12	1.96	0.47
4:A:1286:LYS:HA	4:A:1303:GLU:O	2.14	0.47
5:B:851:PHE:CG	5:B:980:PHE:HE2	2.33	0.47
9:H:102:TYR:CE1	9:H:122:LEU:HD23	2.50	0.47
2:T:22:DT:H2'	2:T:23:DC:C6	2.49	0.47
2:T:27:DA:C8	2:T:28:DT:H72	2.49	0.47
4:A:172:PRO:HB2	4:A:183:GLY:HA3	1.97	0.47
4:A:284:ALA:HB3	4:A:289:ILE:HD11	1.97	0.47
4:A:605:MET:HE1	4:A:616:VAL:C	2.40	0.47
4:A:702:LEU:HB3	4:A:710:LEU:HD21	1.96	0.47
4:A:1030:ARG:HG2	4:A:1034:GLU:HG3	1.97	0.47
5:B:211:VAL:HG13	5:B:483:LEU:HG	1.96	0.47
5:B:884:ARG:HD3	5:B:935:ARG:HD3	1.96	0.47
5:B:1114:LEU:HD12	5:B:1114:LEU:HA	1.70	0.47
6:C:80:LEU:CD2	6:C:161:LYS:HB2	2.44	0.47
4:A:315:LEU:HA	4:A:321:PRO:HA	1.96	0.47
4:A:810:PRO:HA	5:B:1047:PHE:CE1	2.50	0.47
4:A:1158:PRO:HG3	4:A:1188:GLN:CD	2.39	0.47
5:B:283:VAL:HG21	5:B:321:GLY:HA3	1.95	0.47
5:B:457:LEU:O	5:B:461:LEU:HD23	2.14	0.47
5:B:892:LYS:NZ	5:B:905:VAL:HA	2.30	0.47
6:C:114:TYR:CE2	6:C:140:ASN:HB3	2.50	0.47
7:E:20:LYS:HE2	7:E:37:LEU:HD11	1.97	0.47
3:N:4:DG:OP1	4:A:1108:ALA:HB1	2.15	0.47
4:A:70:CYS:SG	4:A:80:HIS:CE1	3.08	0.47
4:A:230:ARG:HB3	4:A:232:GLU:CD	2.40	0.47
4:A:359:LEU:HD23	4:A:359:LEU:HA	1.82	0.47
4:A:405:VAL:HG23	4:A:415:LEU:HD21	1.97	0.47
5:B:520:GLY:HA3	5:B:635:ARG:NE	2.29	0.47
5:B:834:ASN:O	5:B:1013:ASN:HB2	2.15	0.47
5:B:1084:GLN:CD	5:B:1084:GLN:H	2.23	0.47
7:E:93:MET:HG2	7:E:120:ALA:HB1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:108:MET:CE	4:A:169:ASN:HB3	2.45	0.47
4:A:204:THR:HG22	4:A:235:ILE:HD11	1.96	0.47
4:A:537:ARG:HH12	9:H:25:ARG:HH21	1.63	0.47
5:B:393:LYS:HA	5:B:393:LYS:HD3	1.67	0.47
5:B:446:LEU:HB3	5:B:448:ILE:HD12	1.96	0.47
5:B:581:PHE:HA	5:B:585:VAL:O	2.15	0.47
5:B:883:LEU:HD12	5:B:883:LEU:HA	1.77	0.47
5:B:1168:LEU:HD12	5:B:1168:LEU:H	1.80	0.47
7:E:156:LEU:HD12	7:E:195:VAL:HB	1.97	0.47
9:H:99:GLY:HA3	9:H:118:PHE:HA	1.97	0.47
13:L:48:CYS:HB2	13:L:50:ASP:OD1	2.14	0.47
4:A:265:LYS:O	4:A:269:ILE:HG13	2.15	0.46
4:A:471:ASN:O	4:A:474:VAL:HG12	2.14	0.46
4:A:913:LEU:CD2	4:A:1032:LEU:HD13	2.44	0.46
4:A:986:ILE:HD11	4:A:1032:LEU:HD21	1.97	0.46
5:B:598:GLU:O	5:B:602:THR:HG23	2.14	0.46
6:C:43:THR:HG21	6:C:172:PRO:HB3	1.97	0.46
4:A:466:SER:HB2	5:B:1103:ILE:HD12	1.97	0.46
4:A:1213:GLY:CA	4:A:1228:TRP:CH2	2.98	0.46
5:B:424:LEU:HD11	5:B:449:ASN:H	1.80	0.46
6:C:241:ASP:HB3	12:K:109:TRP:NE1	2.29	0.46
7:E:112:TYR:CD1	7:E:116:ILE:HG12	2.50	0.46
9:H:110:ASP:O	9:H:111:LEU:HD12	2.15	0.46
4:A:708:MET:SD	4:A:712:GLU:HB3	2.55	0.46
4:A:795:GLU:HG2	5:B:731:VAL:CG1	2.37	0.46
4:A:840:ARG:HG2	4:A:1402:PHE:HE1	1.81	0.46
5:B:642:ASP:HB3	5:B:649:LYS:HE2	1.97	0.46
6:C:180:TYR:HB3	6:C:228:PHE:HD1	1.80	0.46
9:H:59:ILE:HA	9:H:141:TYR:O	2.15	0.46
9:H:142:LEU:HD22	9:H:144:ILE:HG13	1.97	0.46
4:A:541:ILE:HG22	4:A:546:VAL:HG23	1.96	0.46
4:A:665:GLY:HA3	5:B:1069:PHE:CZ	2.50	0.46
4:A:684:ALA:O	4:A:688:LYS:HG2	2.14	0.46
4:A:900:ASP:HB3	4:A:906:HIS:CB	2.45	0.46
4:A:1107:VAL:HA	4:A:1332:PHE:CZ	2.51	0.46
4:A:1116:LEU:HD13	4:A:1329:THR:OG1	2.16	0.46
5:B:881:ASN:HA	5:B:932:HIS:HA	1.98	0.46
6:C:259:LEU:O	6:C:263:THR:HG23	2.15	0.46
9:H:47:PHE:HB2	9:H:95:TYR:HD2	1.80	0.46
3:N:10:DG:H2"	3:N:11:DA:H8	1.81	0.46
4:A:31:SER:CB	4:A:83:HIS:HB3	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:526:ASP:HB3	4:A:657:LEU:CD2	2.45	0.46
5:B:361:LEU:HD21	5:B:377:PHE:HB3	1.98	0.46
5:B:392:ARG:HD3	10:I:53:GLY:HA3	1.97	0.46
12:K:12:LEU:HD21	12:K:18:LYS:HB2	1.98	0.46
12:K:49:GLU:HB2	12:K:90:ALA:HB1	1.97	0.46
4:A:148:CYS:SG	4:A:164:ARG:NH1	2.85	0.46
4:A:265:LYS:NZ	4:A:314:ALA:HB1	2.30	0.46
4:A:326:ARG:HA	4:A:329:LEU:HD12	1.98	0.46
4:A:593:GLU:HB3	4:A:603:ASN:HD22	1.80	0.46
4:A:663:SER:OG	5:B:1085:ILE:HA	2.15	0.46
4:A:845:LEU:HD12	4:A:1069:ALA:HB2	1.97	0.46
4:A:1329:THR:HB	4:A:1335:ILE:HG12	1.98	0.46
5:B:801:LYS:HB3	11:J:52:THR:O	2.16	0.46
6:C:56:THR:HB	6:C:145:CYS:SG	2.55	0.46
7:E:72:PHE:HE2	7:E:157:SER:CA	2.28	0.46
7:E:171:LYS:HB3	7:E:174:GLN:HG3	1.96	0.46
9:H:107:VAL:HG21	9:H:126:GLU:HG3	1.97	0.46
10:I:75:CYS:HB2	10:I:108:HIS:NE2	2.31	0.46
11:J:9:SER:HB2	11:J:45:CYS:HB2	1.98	0.46
12:K:50:LEU:HD21	12:K:87:LEU:HA	1.97	0.46
4:A:91:PHE:CD2	4:A:179:LEU:HD21	2.51	0.46
4:A:453:MET:HG2	4:A:520:CYS:SG	2.56	0.46
4:A:801:GLU:HG2	5:B:729:ILE:CD1	2.44	0.46
4:A:861:GLY:HA3	7:E:174:GLN:NE2	2.31	0.46
4:A:868:TYR:OH	4:A:1366:ARG:HD3	2.14	0.46
4:A:1128:GLN:CG	4:A:1304:TRP:NE1	2.59	0.46
5:B:46:GLN:HB2	5:B:408:LEU:HD11	1.97	0.46
5:B:243:ALA:HB1	5:B:249:ARG:HB2	1.96	0.46
5:B:551:PRO:O	5:B:554:ILE:HG22	2.15	0.46
5:B:552:MET:HA	5:B:555:ILE:HD12	1.97	0.46
5:B:916:THR:OG1	5:B:935:ARG:HB3	2.15	0.46
12:K:61:TYR:CB	12:K:71:PHE:CE1	2.88	0.46
12:K:95:ILE:HA	12:K:98:LEU:HD12	1.98	0.46
4:A:180:LYS:HA	4:A:180:LYS:HD3	1.73	0.46
4:A:200:ARG:HH22	4:A:203:SER:H	1.63	0.46
4:A:270:LEU:O	4:A:274:ILE:HG12	2.16	0.46
5:B:900:ALA:CB	13:L:61:THR:HG22	2.44	0.46
5:B:1037:LEU:HA	11:J:47:ARG:HH11	1.81	0.46
9:H:87:ARG:HH11	9:H:88:SER:N	2.14	0.46
13:L:38:LEU:HD22	13:L:56:LEU:HD21	1.97	0.46
4:A:779:PHE:CE2	4:A:785:PRO:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1155:ASP:OD1	4:A:1162:VAL:HG22	2.14	0.46
12:K:49:GLU:HG3	12:K:94:ILE:CG1	2.46	0.46
4:A:276:LEU:HD11	4:A:293:GLU:HG3	1.96	0.46
4:A:919:ILE:O	4:A:922:ASP:HB2	2.16	0.46
5:B:361:LEU:HD23	5:B:364:ILE:HG13	1.98	0.46
5:B:612:GLU:HG2	5:B:632:ARG:HH21	1.80	0.46
5:B:807:ARG:H	5:B:1045:SER:HG	1.62	0.46
13:L:54:ARG:H	13:L:54:ARG:HD2	1.80	0.46
4:A:57:ARG:CA	4:A:68:GLN:HG2	2.42	0.45
4:A:92:HIS:HB3	4:A:95:PHE:HB2	1.98	0.45
4:A:94:GLY:HA3	4:A:1410:PHE:HD2	1.81	0.45
4:A:700:ASN:HB3	10:I:113:ASP:OD1	2.16	0.45
4:A:777:PHE:CE1	4:A:783:THR:HG23	2.51	0.45
4:A:782:ARG:HD2	4:A:787:PHE:O	2.15	0.45
4:A:928:LEU:O	4:A:931:GLU:HG3	2.16	0.45
4:A:1129:GLU:CD	4:A:1129:GLU:H	2.23	0.45
5:B:197:PHE:CD2	5:B:817:LEU:HD11	2.51	0.45
5:B:310:MET:O	5:B:314:LEU:HG	2.16	0.45
5:B:882:THR:CG2	5:B:885:MET:HB3	2.46	0.45
5:B:1181:GLU:CD	5:B:1188:LYS:HE3	2.40	0.45
7:E:29:PHE:HD2	7:E:65:THR:HG22	1.82	0.45
7:E:156:LEU:HD23	7:E:156:LEU:HA	1.78	0.45
13:L:33:GLU:HG3	13:L:53:HIS:CE1	2.52	0.45
2:T:20:DC:H4'	5:B:1133:MET:HE2	1.98	0.45
4:A:22:PHE:HB2	5:B:1211:ASN:OD1	2.15	0.45
4:A:23:SER:HB2	4:A:233:TRP:CZ2	2.51	0.45
4:A:92:HIS:HB2	4:A:236:LEU:HD11	1.99	0.45
4:A:516:SER:OG	4:A:1362:TYR:O	2.30	0.45
4:A:1135:ARG:HA	4:A:1138:ILE:HG22	1.97	0.45
4:A:1316:VAL:O	4:A:1319:VAL:HB	2.16	0.45
5:B:244:LEU:O	5:B:249:ARG:HB3	2.17	0.45
5:B:703:ILE:HA	5:B:740:HIS:O	2.16	0.45
5:B:944:THR:HG23	5:B:945:GLU:HG3	1.98	0.45
9:H:41:ASP:HB2	9:H:121:LEU:HB3	1.99	0.45
4:A:111:GLY:HA3	4:A:214:ILE:CA	2.34	0.45
4:A:743:VAL:CG1	4:A:758:ILE:CD1	2.94	0.45
4:A:873:MET:HE3	4:A:873:MET:HB2	1.74	0.45
4:A:1210:GLY:O	4:A:1214:GLU:HG2	2.17	0.45
4:A:1215:ARG:O	4:A:1219:THR:HG23	2.16	0.45
5:B:545:ILE:HA	5:B:632:ARG:O	2.16	0.45
5:B:590:HIS:CD2	5:B:596:LEU:HD22	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:10:PHE:CE1	9:H:38:LEU:HD22	2.51	0.45
9:H:112:ILE:HG13	9:H:131:ASN:ND2	2.31	0.45
11:J:32:GLU:O	11:J:36:LEU:HG	2.16	0.45
4:A:108:MET:HE3	4:A:169:ASN:HB3	1.99	0.45
4:A:138:ILE:CD1	4:A:221:SER:HB2	2.46	0.45
5:B:25:ILE:CG1	5:B:651:LEU:HD11	2.42	0.45
9:H:87:ARG:HH11	9:H:88:SER:H	1.64	0.45
4:A:4:GLN:O	4:A:5:GLN:HB2	2.17	0.45
4:A:287:HIS:HA	4:A:290:GLU:HG3	1.99	0.45
4:A:667:GLY:CA	5:B:1067:ARG:HD2	2.46	0.45
4:A:738:LYS:HZ1	4:A:740:LEU:HD11	1.82	0.45
5:B:58:THR:O	5:B:62:ILE:HG12	2.15	0.45
5:B:778:MET:HE1	5:B:853:SER:HB3	1.99	0.45
7:E:10:SER:O	7:E:14:ARG:HG3	2.16	0.45
8:F:86:THR:O	8:F:89:GLU:HG2	2.16	0.45
2:T:15:DC:H2''	2:T:16:DT:O5'	2.15	0.45
4:A:545:GLN:HG2	4:A:549:MET:HE3	1.97	0.45
4:A:630:ILE:HG23	4:A:642:CYS:SG	2.57	0.45
4:A:1441:PHE:HE2	8:F:88:TYR:HB3	1.80	0.45
5:B:309:GLN:NE2	10:I:52:ILE:HG21	2.31	0.45
5:B:604:ARG:HH21	5:B:614:SER:HA	1.81	0.45
7:E:79:TRP:NE1	7:E:81:GLU:HB2	2.32	0.45
9:H:26:ILE:HD12	9:H:26:ILE:HA	1.86	0.45
3:N:5:DC:H4'	4:A:1391:ARG:HH12	1.81	0.45
4:A:19:PHE:HB3	4:A:1413:GLY:HA2	1.99	0.45
10:I:8:ARG:H	10:I:8:ARG:HG3	1.59	0.45
12:K:29:ASN:HB3	12:K:77:THR:OG1	2.17	0.45
4:A:399:HIS:HA	4:A:401:GLY:N	2.31	0.45
4:A:550:LEU:HD12	4:A:556:TRP:NE1	2.31	0.45
4:A:598:LEU:HD11	9:H:39:THR:HB	1.97	0.45
5:B:322:PHE:HZ	10:I:30:ARG:HB2	1.82	0.45
6:C:221:TYR:HD2	6:C:222:LYS:HE2	1.81	0.45
7:E:42:PHE:CE1	7:E:58:MET:HE2	2.52	0.45
7:E:124:VAL:HG13	7:E:132:ILE:HB	1.98	0.45
4:A:118:HIS:HE1	4:A:164:ARG:HB3	1.81	0.45
4:A:248:PRO:HD2	4:A:260:ASP:OD2	2.17	0.45
4:A:997:LEU:HD23	4:A:1050:GLU:HG3	1.99	0.45
4:A:1207:LEU:HG	4:A:1274:ARG:NE	2.29	0.45
5:B:520:GLY:HA3	5:B:635:ARG:HH21	1.80	0.45
7:E:16:PHE:CE2	7:E:20:LYS:HE3	2.52	0.45
4:A:185:TRP:CH2	4:A:200:ARG:HD3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:547:LEU:HD22	12:K:58:PHE:HD1	1.82	0.45
5:B:405:ARG:HD2	5:B:405:ARG:HA	1.84	0.45
5:B:551:PRO:O	5:B:555:ILE:HG13	2.16	0.45
5:B:1142:GLY:HA3	8:F:88:TYR:HE1	1.82	0.45
6:C:184:ASN:O	6:C:187:LYS:HG3	2.17	0.45
7:E:96:PHE:O	7:E:100:ILE:HG12	2.16	0.45
7:E:153:HIS:CD2	7:E:196:VAL:HG11	2.51	0.45
7:E:190:LEU:HD11	7:E:196:VAL:HG22	1.99	0.45
8:F:76:LYS:HB2	8:F:76:LYS:HE3	1.84	0.45
8:F:114:GLU:HB2	8:F:120:ILE:HD11	1.99	0.45
10:I:56:ALA:HB3	10:I:89:GLN:HG3	1.98	0.45
13:L:55:ILE:O	13:L:56:LEU:HD12	2.17	0.45
4:A:101:LYS:HD3	4:A:139:TRP:CE2	2.51	0.44
6:C:177:GLU:O	6:C:230:MET:HA	2.17	0.44
7:E:55:ARG:HB2	7:E:82:PHE:HB2	1.99	0.44
7:E:178:ILE:HD11	7:E:182:ASP:CG	2.41	0.44
10:I:34:TYR:CZ	10:I:36:GLU:HB3	2.52	0.44
12:K:94:ILE:HA	12:K:97:LYS:HD2	1.97	0.44
4:A:185:TRP:CZ3	4:A:200:ARG:HD3	2.52	0.44
4:A:340:LEU:HD21	5:B:1200:ALA:N	2.32	0.44
4:A:514:PRO:O	4:A:875:ALA:HB1	2.17	0.44
4:A:1003:LYS:HE3	4:A:1003:LYS:HB2	1.71	0.44
5:B:62:ILE:HG23	5:B:418:LYS:HG2	1.99	0.44
5:B:358:LYS:HA	5:B:366:GLN:OE1	2.18	0.44
5:B:387:LEU:HD23	5:B:387:LEU:HA	1.82	0.44
5:B:632:ARG:HD2	5:B:694:ASP:HB2	1.99	0.44
4:A:1121:GLU:HB3	4:A:1321:GLY:C	2.42	0.44
5:B:849:GLY:C	5:B:852:ARG:HG3	2.42	0.44
5:B:952:VAL:O	13:L:57:LEU:HA	2.18	0.44
5:B:976:ILE:HG23	5:B:990:ILE:O	2.17	0.44
6:C:128:ASN:HA	6:C:131:HIS:CE1	2.53	0.44
7:E:166:LYS:HE3	7:E:167:ARG:HE	1.81	0.44
12:K:99:GLY:O	12:K:103:THR:HG23	2.17	0.44
1:R:9:G:H5''	1:R:10:8GM:N2	2.32	0.44
2:T:22:DT:H2'	2:T:23:DC:H6	1.83	0.44
4:A:122:MET:HE1	4:A:138:ILE:HA	2.00	0.44
4:A:446:ARG:HH12	4:A:480:ALA:N	2.15	0.44
4:A:482:PHE:HB2	5:B:838:SER:HB3	1.99	0.44
4:A:1386:ARG:HD2	4:A:1404:GLU:OE2	2.18	0.44
5:B:262:GLU:HA	5:B:267:ARG:CZ	2.48	0.44
5:B:282:ILE:HD13	5:B:301:ILE:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:464:GLY:HA2	5:B:480:SER:HB3	1.99	0.44
5:B:698:GLU:HG3	5:B:701:ILE:HD11	1.99	0.44
7:E:180:ARG:HG3	7:E:215:MET:OXT	2.17	0.44
2:T:17:DG:H2'	2:T:18:DA:C8	2.52	0.44
4:A:122:MET:O	4:A:126:LEU:HG	2.16	0.44
4:A:679:ILE:HG23	4:A:729:ALA:HB1	2.00	0.44
4:A:737:LEU:HB3	4:A:744:LYS:HD2	2.00	0.44
4:A:857:ARG:HD3	4:A:861:GLY:HA2	1.99	0.44
4:A:975:HIS:HA	4:A:1036:ARG:HB2	1.98	0.44
4:A:1143:LEU:HB3	4:A:1268:LEU:HA	1.98	0.44
4:A:1196:GLU:C	4:A:1197:LEU:HD23	2.43	0.44
4:A:1315:GLU:O	4:A:1319:VAL:HG23	2.18	0.44
5:B:653:VAL:O	5:B:654:ARG:HD3	2.16	0.44
5:B:796:LEU:HB3	5:B:799:PRO:HG3	1.99	0.44
5:B:850:LEU:HB2	11:J:8:PHE:CD2	2.53	0.44
5:B:978:ASP:OD1	5:B:1099:VAL:HG22	2.17	0.44
7:E:190:LEU:HD11	7:E:196:VAL:CG2	2.47	0.44
3:N:9:DA:H2'	3:N:10:DG:H8	1.77	0.44
4:A:517:ASN:HB2	4:A:878:ILE:O	2.17	0.44
5:B:212:LEU:HA	5:B:479:VAL:O	2.17	0.44
5:B:603:LEU:CB	5:B:609:ILE:HG12	2.42	0.44
5:B:784:ASN:CG	5:B:788:ARG:HD2	2.43	0.44
5:B:806:THR:O	5:B:809:MET:HB2	2.18	0.44
5:B:1045:SER:HB2	5:B:1048:THR:HG21	1.99	0.44
6:C:17:ASN:HA	6:C:232:VAL:O	2.18	0.44
6:C:258:ILE:HG23	12:K:19:LEU:HD11	1.99	0.44
7:E:122:LYS:O	7:E:125:PRO:HD2	2.17	0.44
10:I:12:ASN:ND2	10:I:31:THR:HG21	2.33	0.44
10:I:19:ASP:HB3	10:I:24:ARG:CG	2.48	0.44
12:K:40:HIS:CD2	12:K:63:VAL:HG11	2.52	0.44
4:A:100:LYS:O	4:A:104:GLU:N	2.51	0.44
4:A:377:PRO:HD3	4:A:493:GLN:OE1	2.18	0.44
4:A:532:ARG:O	4:A:536:LEU:HG	2.18	0.44
4:A:591:PHE:HD2	4:A:595:THR:HB	1.81	0.44
4:A:678:GLU:O	4:A:681:GLU:HG3	2.17	0.44
5:B:370:PHE:CD1	5:B:373:ARG:HD3	2.49	0.44
5:B:698:GLU:O	5:B:701:ILE:HG12	2.18	0.44
6:C:76:ASP:C	6:C:129:ILE:HD11	2.43	0.44
9:H:58:THR:HB	9:H:143:LEU:HB2	2.00	0.44
9:H:102:TYR:CE2	9:H:115:TYR:HB3	2.52	0.44
4:A:465:TYR:CD2	5:B:976:ILE:HD12	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:538:ASP:OD1	9:H:20:TYR:HB3	2.18	0.44
4:A:546:VAL:CG1	4:A:550:LEU:HD23	2.48	0.44
4:A:836:TYR:OH	4:A:1403:GLU:OE2	2.33	0.44
5:B:128:LEU:HB3	5:B:167:ILE:HD11	1.99	0.44
5:B:541:LEU:CD2	5:B:812:LEU:HD21	2.47	0.44
5:B:789:MET:HE3	5:B:965:LYS:HB3	2.00	0.44
5:B:808:ALA:O	5:B:812:LEU:HG	2.17	0.44
5:B:839:MET:SD	5:B:980:PHE:HB2	2.58	0.44
6:C:11:ARG:HH12	6:C:229:TYR:HD2	1.66	0.44
8:F:97:ARG:NH2	8:F:107:VAL:HA	2.32	0.44
9:H:26:ILE:O	9:H:39:THR:HA	2.18	0.44
9:H:106:GLU:OE2	9:H:109:LYS:HA	2.17	0.44
10:I:109:ILE:HD12	10:I:109:ILE:H	1.83	0.44
4:A:265:LYS:HG3	4:A:303:TYR:HB2	1.99	0.44
4:A:526:ASP:N	5:B:835:GLN:HE21	2.10	0.44
4:A:981:LEU:HD21	4:A:1042:PHE:HB3	1.99	0.44
4:A:1212:VAL:O	4:A:1216:ILE:HG13	2.18	0.44
5:B:372:SER:OG	5:B:567:GLU:HG3	2.18	0.44
5:B:376:PHE:HB3	5:B:586:TRP:CZ3	2.53	0.44
5:B:520:GLY:HA3	5:B:635:ARG:NH2	2.33	0.44
5:B:592:ASN:HD21	5:B:595:ARG:HE	1.65	0.44
5:B:904:ARG:NH2	5:B:948:ILE:HD11	2.33	0.44
6:C:29:MET:HB2	12:K:45:LEU:HD11	2.00	0.44
9:H:101:ALA:HB2	9:H:116:TYR:CE1	2.53	0.44
4:A:54:ASN:HA	4:A:58:LEU:CD2	2.47	0.43
4:A:101:LYS:HD3	4:A:139:TRP:NE1	2.33	0.43
4:A:464:PRO:HD3	12:K:68:PHE:HZ	1.83	0.43
4:A:738:LYS:NZ	4:A:740:LEU:HD11	2.33	0.43
4:A:880:LYS:HA	4:A:955:PRO:HA	1.99	0.43
4:A:1147:THR:HG22	4:A:1197:LEU:CD2	2.47	0.43
5:B:112:LEU:HD23	5:B:124:TYR:HA	1.99	0.43
5:B:190:TYR:CZ	5:B:196:PRO:HG2	2.54	0.43
5:B:815:ARG:H	5:B:815:ARG:HG3	1.53	0.43
5:B:963:PHE:HZ	5:B:965:LYS:HE3	1.82	0.43
5:B:1183:LYS:HE2	5:B:1183:LYS:HB3	1.76	0.43
6:C:244:VAL:O	6:C:248:ILE:HG13	2.18	0.43
9:H:12:VAL:HG21	9:H:26:ILE:CD1	2.48	0.43
10:I:5:ARG:HB2	10:I:14:LEU:HD12	1.99	0.43
4:A:57:ARG:HA	4:A:68:GLN:CB	2.49	0.43
4:A:606:LEU:HD11	4:A:608:ILE:HD11	2.00	0.43
4:A:804:TYR:HB3	5:B:1023:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:807:ARG:O	5:B:810:GLU:HG2	2.17	0.43
9:H:26:ILE:HD11	9:H:49:VAL:HG11	2.00	0.43
11:J:35:ALA:O	11:J:39:LEU:HG	2.18	0.43
12:K:81:TYR:CE2	12:K:86:ALA:HB2	2.53	0.43
4:A:105:CYS:HB3	4:A:142:CYS:HB3	2.00	0.43
4:A:108:MET:O	4:A:210:ILE:HG12	2.18	0.43
4:A:367:PRO:HD3	4:A:468:PHE:CD1	2.53	0.43
4:A:368:LYS:HB2	4:A:368:LYS:HE3	1.69	0.43
4:A:500:GLU:OE2	4:A:1438:THR:HG21	2.18	0.43
4:A:564:ALA:O	9:H:97:MET:HA	2.18	0.43
4:A:859:SER:HB2	4:A:1422:ARG:HB2	2.00	0.43
4:A:1051:ALA:O	4:A:1055:ARG:HG3	2.18	0.43
4:A:1415:SER:HB2	4:A:1417:GLU:HG2	2.00	0.43
5:B:745:PRO:HB2	5:B:1047:PHE:CD2	2.53	0.43
9:H:132:LEU:HD12	9:H:132:LEU:HA	1.88	0.43
13:L:28:LYS:C	13:L:29:TYR:HD1	2.26	0.43
1:R:2:U:H2'	1:R:3:C:C6	2.53	0.43
4:A:68:GLN:H	4:A:68:GLN:HG3	1.39	0.43
4:A:91:PHE:HD2	4:A:179:LEU:HD21	1.83	0.43
4:A:123:ARG:HA	4:A:126:LEU:HD12	1.99	0.43
4:A:306:ASN:N	4:A:324:SER:HB3	2.33	0.43
4:A:523:ILE:HG23	4:A:527:THR:HB	2.01	0.43
4:A:540:PHE:CD1	4:A:573:SER:HA	2.53	0.43
4:A:705:LYS:HG2	4:A:708:MET:HB3	2.01	0.43
5:B:23:ALA:O	5:B:654:ARG:HG3	2.17	0.43
5:B:986:GLN:NE2	5:B:1017:ILE:HD13	2.33	0.43
6:C:241:ASP:HB3	12:K:109:TRP:CE2	2.54	0.43
10:I:88:SER:OG	10:I:95:THR:HG21	2.18	0.43
12:K:31:VAL:O	12:K:74:ARG:HA	2.18	0.43
4:A:210:ILE:O	4:A:214:ILE:HG13	2.19	0.43
4:A:343:LYS:HD3	5:B:1156:ASP:OD2	2.19	0.43
4:A:414:ASP:O	4:A:418:SER:HB2	2.19	0.43
4:A:605:MET:HE1	4:A:616:VAL:O	2.19	0.43
4:A:857:ARG:NH2	7:E:170:LEU:HD23	2.23	0.43
4:A:940:ARG:O	4:A:944:ARG:HG2	2.18	0.43
5:B:173:MET:O	5:B:176:SER:HB3	2.19	0.43
5:B:749:LEU:HD23	5:B:749:LEU:HA	1.81	0.43
6:C:163:ILE:HD11	12:K:10:PHE:CD1	2.53	0.43
7:E:9:ILE:H	7:E:9:ILE:HG13	1.64	0.43
7:E:179:GLN:HG3	7:E:182:ASP:HB2	2.01	0.43
8:F:130:ILE:HG22	8:F:132:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:28:ARG:NH2	4:A:238:CYS:HB3	2.34	0.43
4:A:121:LEU:HA	4:A:124:GLN:OE1	2.19	0.43
4:A:939:ASP:O	4:A:943:LEU:HG	2.18	0.43
4:A:1445:ILE:H	4:A:1445:ILE:HG13	1.67	0.43
5:B:59:LEU:HD21	5:B:128:LEU:HD21	2.01	0.43
5:B:428:ILE:O	5:B:432:MET:HG3	2.18	0.43
5:B:429:PHE:HD1	5:B:432:MET:HE3	1.84	0.43
6:C:50:GLU:OE1	13:L:66:GLN:HA	2.19	0.43
7:E:31:THR:HB	7:E:34:GLU:HB3	2.01	0.43
7:E:43:LYS:HB2	7:E:43:LYS:HE2	1.52	0.43
9:H:104:PHE:CZ	9:H:136:LYS:HA	2.54	0.43
11:J:21:TYR:HB2	11:J:39:LEU:HD11	2.00	0.43
3:N:2:DC:H4'	3:N:3:DA:OP1	2.19	0.43
4:A:22:PHE:HD2	5:B:1211:ASN:HA	1.82	0.43
4:A:70:CYS:O	4:A:72:GLU:HG2	2.19	0.43
4:A:120:GLU:O	4:A:124:GLN:HG3	2.19	0.43
4:A:683:ILE:HG21	4:A:801:GLU:CD	2.43	0.43
4:A:1227:ILE:CG1	4:A:1239:ARG:HB2	2.49	0.43
4:A:1405:THR:O	4:A:1409:LEU:HG	2.18	0.43
5:B:245:GLU:HA	5:B:249:ARG:NH1	2.34	0.43
5:B:345:LYS:N	5:B:348:ARG:HB2	2.34	0.43
5:B:408:LEU:O	5:B:412:LEU:HG	2.18	0.43
5:B:999:MET:SD	5:B:1011:ILE:HD11	2.59	0.43
5:B:1021:MET:HE2	5:B:1021:MET:HB2	1.93	0.43
6:C:206:ASN:HA	6:C:209:TYR:HD1	1.83	0.43
7:E:28:TYR:CZ	7:E:78:LEU:HB2	2.53	0.43
7:E:41:ASP:C	7:E:45:LYS:HZ2	2.26	0.43
7:E:195:VAL:HA	7:E:212:ARG:O	2.19	0.43
10:I:5:ARG:O	10:I:14:LEU:HB2	2.18	0.43
4:A:106:VAL:HG21	4:A:214:ILE:HG12	2.01	0.43
4:A:598:LEU:HD23	4:A:598:LEU:HA	1.74	0.43
4:A:666:ILE:CD1	5:B:1030:LEU:HD21	2.48	0.43
4:A:690:VAL:HG22	4:A:718:VAL:HG13	2.01	0.43
4:A:741:ASN:O	4:A:745:GLN:HG3	2.19	0.43
4:A:1014:ALA:O	7:E:205:SER:HB2	2.18	0.43
5:B:1020:ARG:HB3	5:B:1022:THR:HG23	2.01	0.43
6:C:46:ILE:HG12	6:C:157:CYS:HB3	2.00	0.43
6:C:115:SER:HA	6:C:118:LEU:HD13	2.00	0.43
9:H:125:LEU:HG	9:H:130:ARG:NH1	2.34	0.43
4:A:550:LEU:CD2	4:A:577:ILE:HD13	2.45	0.43
4:A:666:ILE:HG13	4:A:667:GLY:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:836:TYR:O	4:A:840:ARG:HG3	2.17	0.43
4:A:1120:LEU:HD12	4:A:1120:LEU:HA	1.80	0.43
4:A:1143:LEU:HG	4:A:1268:LEU:HD23	2.01	0.43
5:B:312:GLU:HG2	10:I:44:TYR:HE1	1.84	0.43
7:E:185:ALA:HA	7:E:190:LEU:HD23	2.01	0.43
2:T:21:DC:H2'	2:T:22:DT:O4'	2.19	0.43
3:N:3:DA:H1'	3:N:4:DG:C8	2.54	0.43
4:A:59:GLY:HA2	4:A:67:CYS:SG	2.58	0.43
4:A:896:ARG:HH22	4:A:1030:ARG:HH11	1.67	0.43
4:A:1075:PRO:O	4:A:1079:MET:HG3	2.19	0.43
4:A:1291:VAL:HG22	4:A:1292:PRO:HD2	2.01	0.43
5:B:124:TYR:O	5:B:171:PRO:HA	2.18	0.43
5:B:166:PHE:CZ	5:B:169:ARG:HG3	2.54	0.43
5:B:189:LEU:HA	5:B:192:LEU:HB2	2.00	0.43
5:B:400:HIS:HB3	5:B:403:LYS:HG2	2.00	0.43
5:B:429:PHE:HA	5:B:432:MET:HE2	2.00	0.43
5:B:913:GLY:HA2	5:B:938:SER:OG	2.17	0.43
9:H:113:ALA:HA	9:H:126:GLU:HA	2.00	0.43
12:K:8:GLU:O	12:K:37:LYS:HE3	2.19	0.43
13:L:64:LEU:HD23	13:L:64:LEU:C	2.44	0.43
3:N:5:DC:H2''	3:N:6:DG:C8	2.54	0.42
4:A:22:PHE:CE2	5:B:1213:THR:HG22	2.53	0.42
4:A:452:LYS:HG3	4:A:453:MET:SD	2.59	0.42
4:A:464:PRO:HD3	12:K:68:PHE:CZ	2.54	0.42
4:A:549:MET:HE1	4:A:656:TRP:CD1	2.49	0.42
4:A:556:TRP:CG	4:A:558:GLY:H	2.37	0.42
4:A:646:PHE:O	4:A:650:GLN:HG3	2.19	0.42
4:A:837:ILE:O	4:A:841:LEU:HG	2.18	0.42
4:A:848:ILE:CD1	4:A:864:ILE:HG13	2.49	0.42
5:B:367:LEU:HD12	5:B:368:GLU:O	2.18	0.42
5:B:597:MET:HE3	5:B:601:ARG:NH1	2.33	0.42
5:B:900:ALA:HB2	13:L:58:LYS:HE2	2.01	0.42
5:B:907:GLY:O	5:B:941:LEU:HB3	2.18	0.42
6:C:46:ILE:HA	6:C:159:ALA:HA	2.00	0.42
7:E:65:THR:O	7:E:69:ILE:HG23	2.19	0.42
7:E:143:ASN:HB3	7:E:146:HIS:CG	2.54	0.42
8:F:97:ARG:HD3	8:F:130:ILE:HG23	2.00	0.42
9:H:10:PHE:CD1	9:H:38:LEU:HD22	2.54	0.42
11:J:44:TYR:O	11:J:48:ARG:HG2	2.19	0.42
12:K:7:PHE:HA	12:K:10:PHE:CZ	2.54	0.42
12:K:40:HIS:HE2	12:K:63:VAL:HG11	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:743:VAL:CG1	4:A:758:ILE:HD12	2.49	0.42
5:B:809:MET:HE1	5:B:983:ARG:NH1	2.33	0.42
5:B:839:MET:HE2	5:B:1010:LEU:HD21	2.00	0.42
5:B:1039:GLY:HA3	11:J:33:GLY:N	2.34	0.42
6:C:180:TYR:CB	6:C:228:PHE:HD1	2.32	0.42
4:A:348:SER:HB2	5:B:1128:LEU:HB2	2.00	0.42
4:A:353:ILE:HD11	4:A:480:ALA:HB1	2.02	0.42
4:A:357:PRO:HG2	5:B:831:SER:O	2.19	0.42
4:A:883:LEU:HD12	4:A:952:ALA:O	2.18	0.42
4:A:1161:THR:HG21	4:A:1166:ASP:HB2	2.01	0.42
5:B:286:PHE:CE1	5:B:375:ALA:HB1	2.54	0.42
5:B:352:ALA:O	5:B:356:LEU:HG	2.20	0.42
5:B:1113:VAL:O	5:B:1116:ARG:HG2	2.19	0.42
7:E:95:THR:HA	7:E:98:ILE:HD12	2.01	0.42
7:E:169:ARG:HB3	8:F:140:ASP:CB	2.44	0.42
4:A:247:ARG:HB3	4:A:262:LEU:HD21	2.01	0.42
4:A:343:LYS:HE3	5:B:1151:LEU:HG	2.01	0.42
4:A:487:MET:HE2	4:A:487:MET:HB3	1.86	0.42
4:A:818:MET:HG3	5:B:514:LEU:HD23	2.01	0.42
4:A:1170:ILE:HD11	4:A:1239:ARG:NH1	2.34	0.42
4:A:1410:PHE:HZ	5:B:1210:MET:HE3	1.84	0.42
5:B:30:SER:O	5:B:34:ILE:HG13	2.19	0.42
5:B:127:GLY:CA	5:B:166:PHE:HE1	2.32	0.42
6:C:8:VAL:O	12:K:108:GLU:HG3	2.19	0.42
6:C:31:ASN:O	6:C:34:ARG:HG2	2.19	0.42
6:C:165:LYS:CB	12:K:9:LEU:HD11	2.44	0.42
10:I:44:TYR:OH	10:I:46:HIS:HB2	2.19	0.42
4:A:91:PHE:CG	4:A:96:ILE:HD12	2.55	0.42
4:A:298:PHE:HZ	4:A:314:ALA:HB2	1.83	0.42
5:B:639:ILE:CD1	5:B:691:GLU:HB2	2.48	0.42
5:B:992:ILE:HD11	12:K:66:PRO:HB2	2.02	0.42
5:B:1075:GLY:HA2	6:C:34:ARG:NH2	2.34	0.42
5:B:1168:LEU:CD2	5:B:1208:MET:HG2	2.49	0.42
7:E:90:VAL:O	7:E:94:LYS:HG3	2.20	0.42
4:A:22:PHE:HB2	5:B:1211:ASN:CG	2.44	0.42
4:A:368:LYS:O	4:A:372:LYS:HG3	2.19	0.42
4:A:441:PRO:HD2	4:A:498:ARG:NH2	2.35	0.42
4:A:1213:GLY:O	4:A:1217:LYS:HG3	2.20	0.42
5:B:123:THR:HG23	5:B:205:ILE:HA	2.00	0.42
5:B:876:LYS:HB2	5:B:894:ASP:O	2.19	0.42
5:B:914:LYS:HE3	5:B:937:ALA:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:44:LEU:HD22	6:C:129:ILE:HG23	2.02	0.42
6:C:251:LEU:HD12	6:C:251:LEU:HA	1.81	0.42
7:E:80:VAL:HG23	7:E:109:ILE:HG22	2.02	0.42
9:H:36:CYS:HA	9:H:126:GLU:O	2.20	0.42
9:H:50:ALA:HB3	9:H:53:ASP:CG	2.45	0.42
10:I:85:PHE:HB3	10:I:101:PHE:CD2	2.55	0.42
2:T:7:DC:H1'	2:T:8:DT:C6	2.55	0.42
4:A:99:ILE:HG23	4:A:211:PHE:CZ	2.54	0.42
4:A:527:THR:O	4:A:653:VAL:HG11	2.20	0.42
4:A:1375:MET:H	4:A:1375:MET:HG3	1.66	0.42
4:A:1441:PHE:HB2	8:F:134:ILE:HG23	2.01	0.42
5:B:681:TRP:CZ2	5:B:690:VAL:HG11	2.55	0.42
5:B:797:TYR:HB3	5:B:798:TYR:CD2	2.54	0.42
6:C:147:LEU:HD23	6:C:147:LEU:HA	1.58	0.42
8:F:123:LYS:HD2	8:F:123:LYS:HA	1.77	0.42
9:H:56:THR:O	9:H:144:ILE:HA	2.20	0.42
9:H:112:ILE:HG13	9:H:131:ASN:HD22	1.83	0.42
2:T:4:DT:H3	3:N:15:DA:N6	2.17	0.42
4:A:17:VAL:HG13	5:B:1216:LEU:HG	2.01	0.42
4:A:147:VAL:HG23	4:A:169:ASN:C	2.45	0.42
4:A:547:LEU:HD13	12:K:58:PHE:HA	2.02	0.42
4:A:746:MET:HG2	5:B:1015:HIS:CE1	2.54	0.42
4:A:1143:LEU:O	4:A:1147:THR:HG23	2.20	0.42
4:A:1282:VAL:CG2	4:A:1308:THR:HG22	2.38	0.42
5:B:211:VAL:CG1	5:B:483:LEU:HG	2.49	0.42
5:B:365:THR:HG22	5:B:374:LYS:HE3	2.01	0.42
5:B:485:ARG:NH1	5:B:491:THR:HG21	2.35	0.42
5:B:899:ILE:O	5:B:952:VAL:HG21	2.20	0.42
6:C:41:ILE:HA	6:C:42:PRO:HD3	1.86	0.42
4:A:455:MET:HE2	4:A:455:MET:HB3	1.85	0.42
4:A:602:ASP:HB3	4:A:616:VAL:HG23	2.01	0.42
4:A:1217:LYS:CG	4:A:1226:VAL:HG21	2.50	0.42
5:B:31:TRP:HA	5:B:34:ILE:HD12	2.02	0.42
5:B:791:THR:O	5:B:857:ARG:HA	2.19	0.42
5:B:831:SER:OG	5:B:833:TYR:HD2	2.02	0.42
7:E:199:ILE:HG12	7:E:207:ARG:HH21	1.83	0.42
10:I:15:TYR:CE1	10:I:30:ARG:HG2	2.54	0.42
10:I:28:GLU:HB2	10:I:35:VAL:HG13	2.02	0.42
2:T:15:DC:H2'	2:T:16:DT:C5	2.55	0.42
2:T:15:DC:H2'	2:T:16:DT:C6	2.55	0.42
4:A:139:TRP:HA	4:A:142:CYS:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:279:LEU:HD22	4:A:284:ALA:HB2	2.01	0.42
4:A:331:GLY:C	4:A:334:GLY:H	2.28	0.42
4:A:387:ARG:HG3	4:A:388:LEU:N	2.34	0.42
4:A:437:MET:HB2	4:A:437:MET:HE3	1.81	0.42
4:A:666:ILE:HG12	5:B:1030:LEU:HD11	2.02	0.42
4:A:731:ARG:HA	4:A:731:ARG:HD3	1.93	0.42
4:A:821:ARG:HH21	5:B:534:GLY:CA	2.28	0.42
4:A:932:GLU:O	4:A:936:LEU:HG	2.19	0.42
5:B:459:TYR:CZ	5:B:463:THR:HG21	2.55	0.42
5:B:1098:MET:HE3	5:B:1098:MET:HB2	1.92	0.42
7:E:93:MET:CE	7:E:132:ILE:HG21	2.48	0.42
10:I:19:ASP:HB3	10:I:24:ARG:HG3	2.02	0.42
4:A:107:CYS:HB2	4:A:167:CYS:HB2	2.02	0.41
4:A:849:MET:HE3	4:A:1061:GLY:HA2	2.01	0.41
4:A:861:GLY:O	7:E:174:GLN:HB3	2.20	0.41
4:A:1101:LEU:O	4:A:1105:LEU:HG	2.20	0.41
4:A:1141:THR:HB	4:A:1273:LEU:O	2.19	0.41
5:B:25:ILE:HA	5:B:655:LYS:HD3	2.02	0.41
5:B:941:LEU:HD23	5:B:942:ARG:N	2.35	0.41
5:B:955:THR:HA	13:L:46:VAL:HG11	2.01	0.41
6:C:112:ASN:HB3	6:C:143:LEU:HD12	2.02	0.41
7:E:6:GLU:HA	7:E:9:ILE:HD12	2.02	0.41
8:F:85:MET:SD	8:F:90:ARG:HB2	2.59	0.41
4:A:12:ARG:HB2	5:B:1218:THR:HB	2.02	0.41
4:A:261:ASP:HA	4:A:264:PHE:CD2	2.55	0.41
4:A:597:LEU:HD13	4:A:597:LEU:HA	1.86	0.41
4:A:1436:ILE:HG22	4:A:1437:GLY:H	1.84	0.41
5:B:48:LEU:HD23	5:B:173:MET:SD	2.59	0.41
5:B:227:LYS:H	5:B:395:GLN:CD	2.28	0.41
5:B:467:GLY:HA3	5:B:474:SER:HB3	2.02	0.41
5:B:797:TYR:HE1	5:B:854:LEU:HG	1.84	0.41
5:B:860:MET:HE3	5:B:860:MET:HB3	1.90	0.41
6:C:210:GLU:HG2	6:C:229:TYR:OH	2.19	0.41
7:E:46:TYR:CD2	7:E:53:PRO:HB2	2.55	0.41
7:E:72:PHE:HE2	7:E:157:SER:HA	1.86	0.41
12:K:57:LEU:HD12	12:K:76:GLN:HG2	2.02	0.41
4:A:113:LEU:HD23	4:A:113:LEU:H	1.84	0.41
4:A:988:LEU:HA	4:A:991:LYS:HD2	2.02	0.41
5:B:193:LYS:HE3	5:B:193:LYS:HB2	1.82	0.41
5:B:197:PHE:CE2	11:J:59:LYS:HE3	2.55	0.41
5:B:956:THR:OG1	5:B:960:GLY:HA2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:46:TYR:CE1	7:E:57:MET:HB3	2.55	0.41
9:H:40:LEU:HA	9:H:123:MET:HA	2.01	0.41
9:H:41:ASP:HB2	9:H:122:LEU:H	1.85	0.41
3:N:12:DG:H1'	3:N:13:DA:C4	2.55	0.41
4:A:18:GLN:HG2	4:A:228:PHE:CZ	2.56	0.41
4:A:54:ASN:HD22	4:A:61:ILE:HD11	1.85	0.41
4:A:760:GLN:HA	4:A:764:CYS:O	2.20	0.41
4:A:1341:ILE:HG13	4:A:1376:THR:HG23	2.02	0.41
4:A:1390:ASN:ND2	4:A:1402:PHE:HB3	2.36	0.41
5:B:654:ARG:O	5:B:658:ILE:HG12	2.20	0.41
5:B:982:SER:HB3	5:B:1092:TYR:CZ	2.55	0.41
7:E:113:GLN:HG3	7:E:114:ASN:ND2	2.35	0.41
9:H:12:VAL:CG2	9:H:26:ILE:HG13	2.50	0.41
9:H:118:PHE:CE1	9:H:142:LEU:HD12	2.55	0.41
4:A:464:PRO:HG2	4:A:465:TYR:CD1	2.56	0.41
4:A:481:ASP:OD1	5:B:837:ASP:HB2	2.19	0.41
5:B:209:GLU:O	5:B:482:VAL:HA	2.21	0.41
5:B:291:ILE:HD12	5:B:291:ILE:N	2.35	0.41
5:B:882:THR:HG21	5:B:885:MET:HB3	2.03	0.41
9:H:93:TYR:H	9:H:93:TYR:HD1	1.69	0.41
10:I:86:PHE:HE2	10:I:89:GLN:HG2	1.83	0.41
11:J:17:LYS:HG2	11:J:39:LEU:HB3	2.02	0.41
4:A:372:LYS:HA	4:A:435:HIS:CD2	2.55	0.41
4:A:444:PHE:CD2	4:A:487:MET:HE2	2.55	0.41
4:A:590:ARG:HG2	4:A:604:GLY:HA2	2.02	0.41
4:A:876:ALA:C	4:A:877:HIS:CG	2.98	0.41
5:B:122:LEU:HD21	5:B:958:GLN:H	1.86	0.41
5:B:901:PRO:HD2	13:L:59:ALA:O	2.19	0.41
7:E:100:ILE:HD13	7:E:100:ILE:HA	1.92	0.41
9:H:36:CYS:SG	9:H:125:LEU:HD11	2.61	0.41
2:T:17:DG:O5'	4:A:1403:GLU:HG2	2.20	0.41
2:T:25:DC:H5''	5:B:792:MET:HE3	2.02	0.41
3:N:7:DA:H5''	3:N:7:DA:H8	1.86	0.41
4:A:589:GLN:HG3	4:A:606:LEU:HD13	2.01	0.41
4:A:618:GLU:OE2	4:A:621:THR:HG23	2.20	0.41
4:A:619:LYS:HE3	4:A:750:GLY:HA3	2.02	0.41
4:A:694:THR:O	4:A:698:GLN:HG3	2.20	0.41
4:A:824:LEU:HD21	5:B:765:PRO:HB3	2.02	0.41
4:A:942:PHE:HZ	7:E:206:GLY:CA	2.34	0.41
4:A:964:ILE:HG12	4:A:1035:TYR:CE2	2.56	0.41
5:B:90:ILE:HD12	5:B:90:ILE:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:391:ASP:HB3	10:I:91:ARG:O	2.21	0.41
7:E:193:GLY:HA2	7:E:213:ILE:HD11	2.01	0.41
9:H:102:TYR:CE1	9:H:115:TYR:HB3	2.53	0.41
4:A:15:LYS:CB	5:B:1220:ARG:HG2	2.50	0.41
4:A:525:GLN:HA	5:B:1015:HIS:HD2	1.85	0.41
4:A:813:PHE:HZ	5:B:767:ASN:ND2	2.19	0.41
4:A:1166:ASP:O	4:A:1170:ILE:HG12	2.20	0.41
4:A:1413:GLY:HA3	5:B:1212:ILE:HG23	2.03	0.41
4:A:1434:ALA:HB3	4:A:1436:ILE:HG12	2.02	0.41
5:B:845:SER:HB3	11:J:8:PHE:HB3	2.03	0.41
5:B:915:THR:HG21	5:B:934:LYS:HD3	2.03	0.41
5:B:1004:GLU:HB2	5:B:1006:ILE:HD12	2.02	0.41
5:B:1075:GLY:HA2	6:C:34:ARG:HH21	1.85	0.41
6:C:248:ILE:HG23	12:K:98:LEU:HB3	2.02	0.41
7:E:180:ARG:HG2	7:E:214:CYS:SG	2.60	0.41
9:H:138:GLU:H	9:H:138:GLU:HG3	1.69	0.41
11:J:2:ILE:HD12	11:J:2:ILE:HA	1.92	0.41
4:A:538:ASP:OD1	9:H:22:LYS:HB2	2.20	0.41
4:A:550:LEU:HD11	4:A:580:VAL:HG21	2.02	0.41
4:A:598:LEU:HB3	9:H:25:ARG:NH1	2.34	0.41
4:A:664:THR:OG1	5:B:1014:PRO:HB3	2.21	0.41
4:A:1059:HIS:ND1	8:F:86:THR:HA	2.36	0.41
5:B:63:ILE:HA	5:B:421:PHE:CE2	2.56	0.41
5:B:314:LEU:HD21	5:B:386:LEU:HD11	2.03	0.41
5:B:522:VAL:HG11	5:B:537:LYS:HB3	2.03	0.41
5:B:566:LEU:O	5:B:569:TYR:HB3	2.21	0.41
6:C:101:LEU:HB3	6:C:155:LEU:HD11	2.03	0.41
7:E:112:TYR:O	7:E:136:ASN:HA	2.21	0.41
7:E:179:GLN:H	7:E:179:GLN:HG2	1.59	0.41
8:F:96:THR:O	8:F:100:GLN:HG2	2.21	0.41
8:F:97:ARG:HE	8:F:124:GLU:CD	2.29	0.41
9:H:47:PHE:HB2	9:H:95:TYR:CD2	2.56	0.41
9:H:89:LEU:HD13	9:H:91:ASP:O	2.21	0.41
10:I:59:VAL:HG12	10:I:61:ASP:H	1.85	0.41
12:K:42:LEU:HD12	12:K:42:LEU:HA	1.84	0.41
4:A:136:ALA:O	4:A:140:THR:HG23	2.21	0.41
4:A:349:ALA:HB1	4:A:370:ILE:HD12	2.03	0.41
4:A:353:ILE:HD13	4:A:487:MET:HG3	2.03	0.41
4:A:591:PHE:HA	4:A:595:THR:HG21	2.03	0.41
4:A:961:ARG:HE	4:A:1025:ARG:HH21	1.69	0.41
4:A:974:ASP:HB3	9:H:136:LYS:HE3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:998:LEU:HB2	4:A:1001:ARG:NH2	2.36	0.41
5:B:104:GLU:HG2	5:B:110:HIS:CE1	2.55	0.41
5:B:781:PHE:HE1	5:B:793:ALA:HB1	1.86	0.41
6:C:64:ALA:HB1	13:L:69:ALA:HA	2.02	0.41
6:C:252:GLN:HG3	12:K:95:ILE:HG23	2.03	0.41
7:E:150:VAL:HA	7:E:151:PRO:HD3	1.89	0.41
2:T:5:DC:H1'	2:T:6:DT:H5'	2.02	0.40
3:N:14:DG:C6	3:N:15:DA:C6	3.09	0.40
4:A:56:PRO:O	4:A:58:LEU:HD13	2.21	0.40
4:A:822:GLU:HA	4:A:825:ILE:HD12	2.03	0.40
4:A:863:VAL:HG21	7:E:170:LEU:HD21	2.03	0.40
4:A:912:LEU:HD22	4:A:1036:ARG:NH2	2.36	0.40
5:B:46:GLN:O	5:B:408:LEU:HD13	2.20	0.40
5:B:885:MET:HA	5:B:936:ASP:HB2	2.03	0.40
5:B:1180:PHE:HD2	5:B:1191:ILE:HD13	1.86	0.40
7:E:5:ASN:HA	7:E:7:ARG:CZ	2.51	0.40
2:T:13:DC:C4	2:T:14:DG:C6	3.09	0.40
4:A:259:GLU:HB3	4:A:264:PHE:CZ	2.55	0.40
4:A:306:ASN:OD1	4:A:323:LYS:HA	2.21	0.40
4:A:350:ARG:NE	4:A:486:GLU:HB3	2.36	0.40
4:A:535:THR:HG21	4:A:617:VAL:HG23	2.03	0.40
4:A:667:GLY:HA2	4:A:670:ILE:HD12	2.02	0.40
4:A:728:LYS:O	4:A:732:LEU:HG	2.20	0.40
4:A:1290:LYS:HA	4:A:1300:LYS:HA	2.03	0.40
4:A:1397:LEU:HG	4:A:1419:ASP:OD2	2.22	0.40
7:E:147:HIS:HB3	7:E:150:VAL:HG23	2.03	0.40
10:I:20:LYS:H	10:I:20:LYS:HG2	1.66	0.40
13:L:55:ILE:O	13:L:55:ILE:HG13	2.21	0.40
2:T:19:DA:H3'	2:T:20:DC:C6	2.56	0.40
4:A:21:LEU:HD23	4:A:21:LEU:HA	1.77	0.40
4:A:55:ASP:N	4:A:58:LEU:HD22	2.37	0.40
4:A:363:GLN:HA	4:A:459:ARG:O	2.21	0.40
4:A:403:LYS:O	4:A:415:LEU:HB2	2.20	0.40
4:A:765:VAL:HG11	4:A:804:TYR:CE1	2.56	0.40
5:B:732:SER:HB3	5:B:734:HIS:NE2	2.37	0.40
5:B:899:ILE:HD12	5:B:899:ILE:HA	1.97	0.40
6:C:179:GLU:HG2	6:C:206:ASN:HB2	2.04	0.40
7:E:137:GLU:O	7:E:141:VAL:HG23	2.21	0.40
9:H:130:ARG:HA	9:H:133:ASN:OD1	2.21	0.40
11:J:6:ARG:HG2	11:J:13:VAL:HA	2.03	0.40
11:J:36:LEU:HA	11:J:39:LEU:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:956:LEU:HA	4:A:957:PRO:HD3	1.91	0.40
4:A:996:ASN:HB3	4:A:1050:GLU:OE2	2.21	0.40
5:B:364:ILE:H	5:B:364:ILE:HG12	1.67	0.40
5:B:414:ALA:O	5:B:418:LYS:HG3	2.21	0.40
5:B:1016:ALA:O	5:B:1020:ARG:HG2	2.22	0.40
6:C:18:VAL:HG12	6:C:20:PHE:HD1	1.85	0.40
3:N:5:DC:H2"	3:N:6:DG:OP2	2.21	0.40
4:A:84:ILE:CD1	4:A:270:LEU:HG	2.52	0.40
4:A:528:LEU:HD23	4:A:751:SER:HA	2.03	0.40
5:B:485:ARG:NH1	5:B:782:LEU:HD11	2.37	0.40
5:B:778:MET:HE2	5:B:778:MET:HB2	1.85	0.40
5:B:848:ARG:HD2	11:J:8:PHE:HA	2.03	0.40
5:B:1076:HIS:CG	12:K:40:HIS:ND1	2.90	0.40
6:C:35:ARG:HD3	12:K:41:THR:OG1	2.21	0.40
6:C:148:ARG:HB3	6:C:151:GLN:CD	2.47	0.40
7:E:191:LYS:O	7:E:214:CYS:HB3	2.22	0.40
9:H:28:ALA:HB3	9:H:38:LEU:HD21	2.03	0.40
9:H:93:TYR:HB3	9:H:144:ILE:O	2.21	0.40
10:I:90:GLN:NE2	10:I:92:ARG:HD3	2.37	0.40
10:I:101:PHE:HE1	10:I:112:SER:HB3	1.87	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	
4	A	1370/1733 (79%)	1343 (98%)	26 (2%)	1 (0%)	48	79
5	B	1103/1224 (90%)	1092 (99%)	11 (1%)	0	100	100
6	C	265/318 (83%)	264 (100%)	1 (0%)	0	100	100
7	E	210/215 (98%)	207 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	F	84/155 (54%)	81 (96%)	3 (4%)	0	100	100
9	H	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
10	I	116/122 (95%)	115 (99%)	1 (1%)	0	100	100
11	J	63/70 (90%)	63 (100%)	0	0	100	100
12	K	112/120 (93%)	110 (98%)	2 (2%)	0	100	100
13	L	41/70 (59%)	40 (98%)	1 (2%)	0	100	100
All	All	3493/4173 (84%)	3442 (98%)	50 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	55	ASP

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	
4	A	1194/1520 (79%)	1192 (100%)	2 (0%)	87	85
5	B	955/1061 (90%)	954 (100%)	1 (0%)	88	87
6	C	235/274 (86%)	234 (100%)	1 (0%)	84	80
7	E	193/197 (98%)	193 (100%)	0	100	100
8	F	73/137 (53%)	73 (100%)	0	100	100
9	H	116/128 (91%)	116 (100%)	0	100	100
10	I	110/116 (95%)	107 (97%)	3 (3%)	39	61
11	J	60/65 (92%)	59 (98%)	1 (2%)	53	69
12	K	99/102 (97%)	99 (100%)	0	100	100
13	L	37/57 (65%)	36 (97%)	1 (3%)	39	61
All	All	3072/3657 (84%)	3063 (100%)	9 (0%)	86	82

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	68	GLN
4	A	110	CYS
5	B	1163	CYS
6	C	86	CYS
10	I	7	CYS
10	I	29	CYS
10	I	32	CYS
11	J	46	CYS
13	L	51	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	54	ASN
4	A	169	ASN
4	A	171	GLN
4	A	358	ASN
4	A	427	GLN
4	A	548	ASN
4	A	851	HIS
4	A	953	ASN
4	A	975	HIS
4	A	1004	ASN
4	A	1011	GLN
4	A	1033	GLN
4	A	1106	ASN
4	A	1171	GLN
4	A	1211	GLN
4	A	1265	ASN
4	A	1393	ASN
4	A	1427	ASN
5	B	206	ASN
5	B	278	GLN
5	B	309	GLN
5	B	350	GLN
5	B	395	GLN
5	B	465	ASN
5	B	592	ASN
5	B	657	HIS
5	B	835	GLN
5	B	1161	HIS
5	B	1178	ASN
5	B	1193	GLN

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Mol	Chain	Res	Type
6	C	206	ASN
7	E	99	HIS
7	E	146	HIS
10	I	60	GLN
10	I	90	GLN
10	I	108	HIS
11	J	64	ASN
12	K	76	GLN
13	L	66	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	8/10 (80%)	3 (37%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	2	U
1	R	7	A
1	R	9	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 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	$\# Z > 2$
16	POP	B	1302	-	6,8,8	0.74	0	12,13,13	0.97	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
16	POP	B	1302	-	-	0/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	R	9/10 (90%)	0.14	0 100 100	106, 122, 174, 191	0
2	T	26/29 (89%)	0.35	1 (3%) 44 24	131, 170, 243, 266	0
3	N	15/18 (83%)	0.33	0 100 100	192, 217, 255, 271	0
4	A	1384/1733 (79%)	0.23	24 (1%) 69 40	56, 118, 199, 291	0
5	B	1123/1224 (91%)	0.27	22 (1%) 65 37	50, 102, 175, 269	0
6	C	267/318 (83%)	0.15	2 (0%) 84 61	57, 105, 150, 202	0
7	E	212/215 (98%)	0.28	9 (4%) 40 21	93, 153, 234, 278	0
8	F	86/155 (55%)	-0.03	0 100 100	81, 117, 167, 191	0
9	H	133/146 (91%)	0.23	2 (1%) 72 44	97, 141, 198, 302	0
10	I	118/122 (96%)	0.15	0 100 100	71, 130, 176, 198	0
11	J	65/70 (92%)	0.28	3 (4%) 37 20	60, 93, 141, 194	0
12	K	114/120 (95%)	0.23	3 (2%) 57 32	70, 112, 157, 240	0
13	L	43/70 (61%)	0.50	3 (6%) 22 14	92, 186, 307, 371	0
All	All	3595/4230 (84%)	0.24	69 (1%) 66 38	50, 115, 197, 371	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	B	775	LYS	4.9
5	B	525	ALA	4.3
7	E	93	MET	4.1
13	L	32	ALA	4.0
7	E	112	TYR	3.8
7	E	110	PHE	3.7
4	A	1328	TYR	3.6
5	B	779	GLY	3.6
4	A	1434	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
5	B	751	VAL	3.4
4	A	355	GLY	3.3
5	B	416	LEU	3.3
5	B	533	CYS	3.2
4	A	135	PHE	3.1
11	J	65	PRO	3.0
4	A	798	GLY	3.0
5	B	753	ALA	3.0
4	A	1035	TYR	3.0
13	L	65	VAL	2.9
13	L	66	GLN	2.8
9	H	23	VAL	2.8
5	B	823	ALA	2.8
5	B	162	SER	2.7
5	B	1168	LEU	2.7
4	A	3	GLY	2.7
4	A	776	ALA	2.7
5	B	819	ALA	2.7
7	E	123	LEU	2.7
5	B	1214	PRO	2.7
5	B	386	LEU	2.7
12	K	61	TYR	2.6
4	A	1332	PHE	2.6
4	A	1061	GLY	2.6
5	B	681	TRP	2.5
4	A	1257	ASP	2.5
4	A	1228	TRP	2.5
4	A	642	CYS	2.5
7	E	82	PHE	2.5
7	E	120	ALA	2.5
5	B	811	TYR	2.5
5	B	1212	ILE	2.5
12	K	57	LEU	2.5
11	J	54	VAL	2.5
4	A	161	LEU	2.4
7	E	121	MET	2.4
12	K	42	LEU	2.4
4	A	957	PRO	2.4
7	E	97	VAL	2.3
5	B	473	MET	2.3
4	A	698	GLN	2.3
5	B	420	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
6	C	178	PHE	2.2
4	A	590	ARG	2.2
4	A	801	GLU	2.2
4	A	997	LEU	2.2
6	C	26	ASP	2.2
7	E	83	CYS	2.2
9	H	91	ASP	2.2
4	A	1002	GLY	2.2
2	T	15	DC	2.1
4	A	666	ILE	2.1
5	B	1167	GLY	2.1
4	A	1081	LEU	2.1
4	A	1396	ALA	2.1
4	A	591	PHE	2.1
5	B	1112	GLN	2.1
5	B	381	MET	2.1
11	J	44	TYR	2.0
5	B	509	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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	B-factors(\AA^2)	Q<0.9
16	POP	B	1302	9/9	0.59	0.10	125,155,169,176	0
14	ZN	L	101	1/1	0.84	0.10	300,300,300,300	0
15	MG	A	1803	1/1	0.92	0.17	160,160,160,160	0
14	ZN	A	1801	1/1	0.93	0.07	269,269,269,269	0
14	ZN	I	202	1/1	0.95	0.07	163,163,163,163	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
14	ZN	B	1301	1/1	0.97	0.05	200,200,200,200	0
14	ZN	I	201	1/1	0.97	0.06	144,144,144,144	0
14	ZN	A	1802	1/1	0.99	0.03	160,160,160,160	0
14	ZN	C	401	1/1	0.99	0.05	145,145,145,145	0
14	ZN	J	101	1/1	0.99	0.04	97,97,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.