



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2025 – 02:07 AM EDT

PDB ID : 2ED6 / pdb_00002ed6
Title : Crystal Structure of Envelope Protein VP28 from White Spot Syndrome Virus (WSSV)
Authors : Hew, C.L.; Sivaraman, J.; Tang, X.H.
Deposited on : 2007-02-14
Resolution : 2.00 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	:	4.02b-467
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

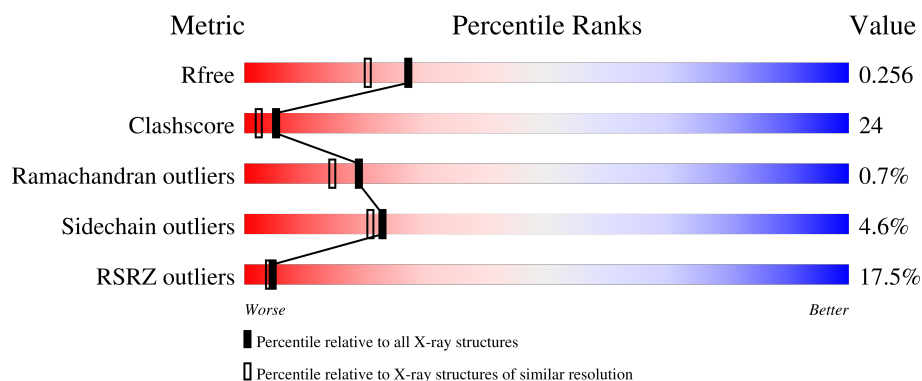
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.







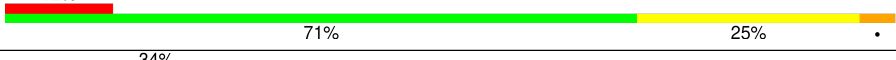
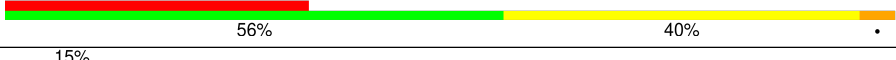

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	A	170	<div> <div>18%</div> <div>68%</div> <div>28%</div> <div>.</div> </div>
1	B	170	<div> <div>14%</div> <div>68%</div> <div>28%</div> <div>.</div> </div>
1	C	170	<div> <div>14%</div> <div>67%</div> <div>29%</div> <div>.</div> </div>
1	D	170	<div> <div>14%</div> <div>66%</div> <div>29%</div> <div>5%</div> </div>
1	E	170	<div> <div>16%</div> <div>65%</div> <div>31%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	170	
1	G	170	
1	H	170	
1	I	170	
1	J	170	
1	K	170	
1	L	170	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 16843 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 25kDa structural protein VP25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	B	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	C	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	D	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	E	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	F	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	G	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	H	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	I	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	J	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	K	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			
1	L	170	Total	C	N	O	S	0	0	0
			1288	803	211	267	7			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	107	Total	O	0	0
			107	107		
2	B	133	Total	O	0	0
			133	133		

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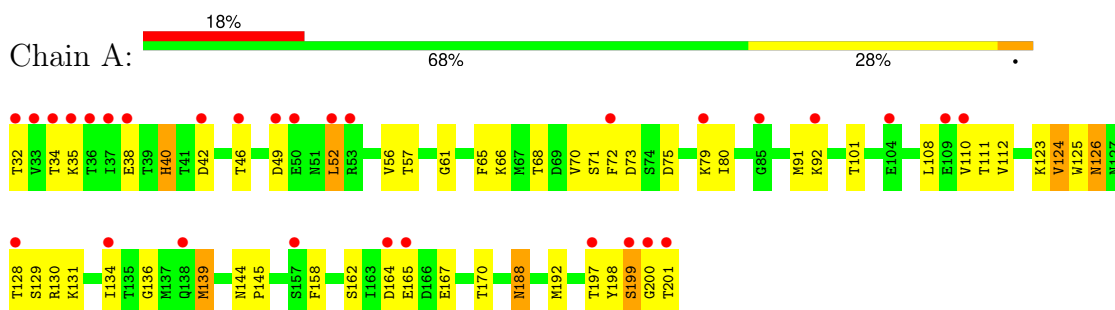
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	124	Total 124	O 124	0	0
2	D	112	Total 112	O 112	0	0
2	E	138	Total 138	O 138	0	0
2	F	154	Total 154	O 154	0	0
2	G	136	Total 136	O 136	0	0
2	H	122	Total 122	O 122	0	0
2	I	125	Total 125	O 125	0	0
2	J	102	Total 102	O 102	0	0
2	K	53	Total 53	O 53	0	0
2	L	81	Total 81	O 81	0	0

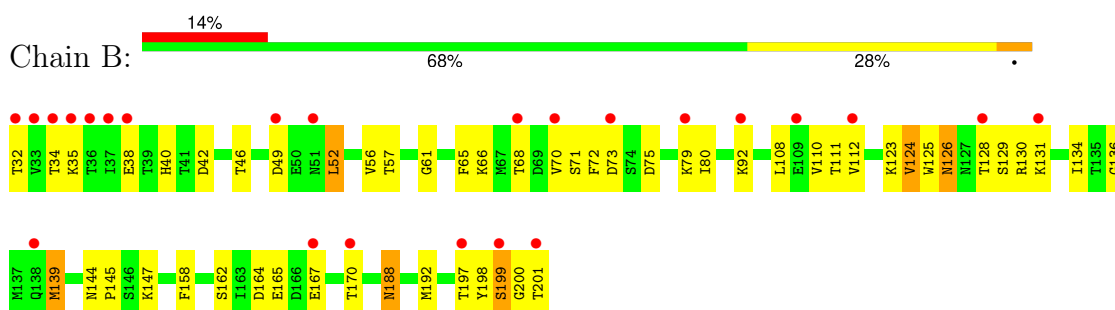
3 Residue-property plots [i](#)

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.

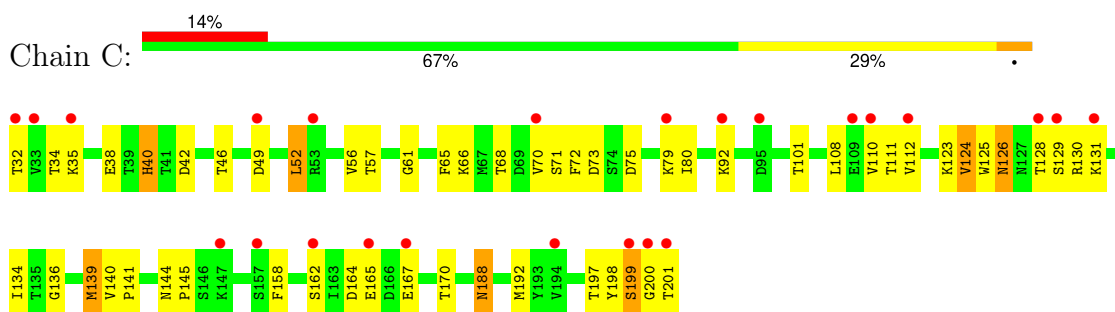
- Molecule 1: 25kDa structural protein VP25



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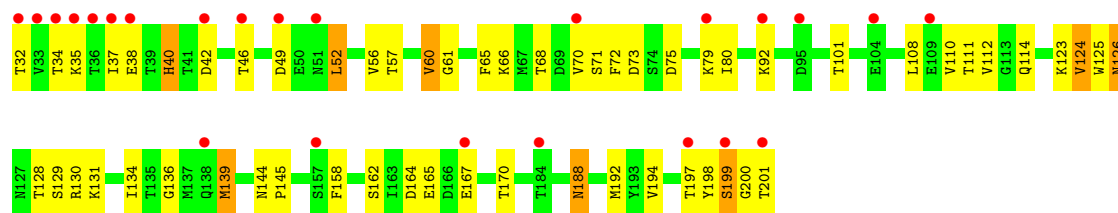


- Molecule 1: 25kDa structural protein VP25

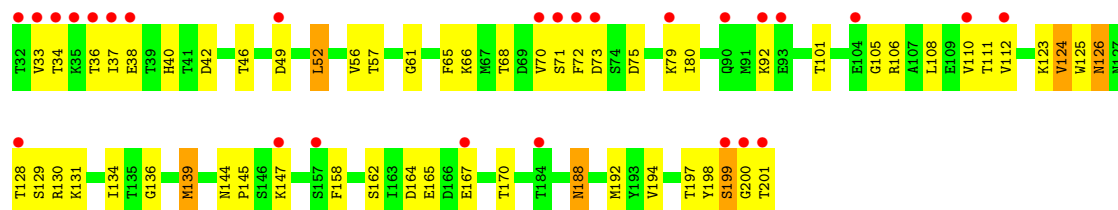


- Molecule 1: 25kDa structural protein VP25

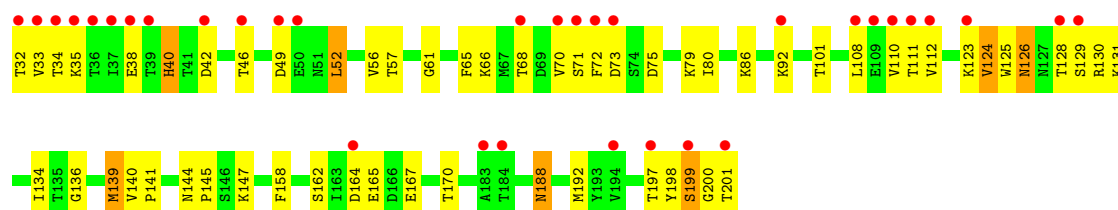




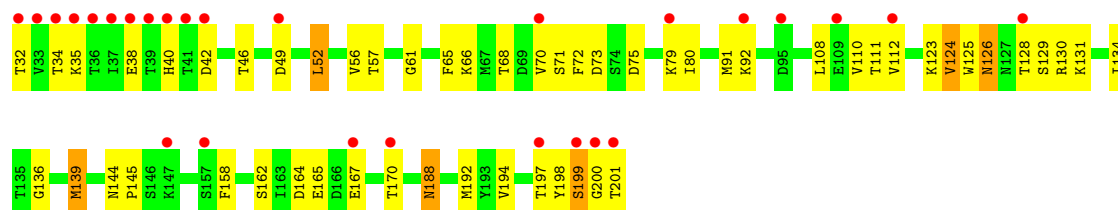
• Molecule 1: 25kDa structural protein VP25



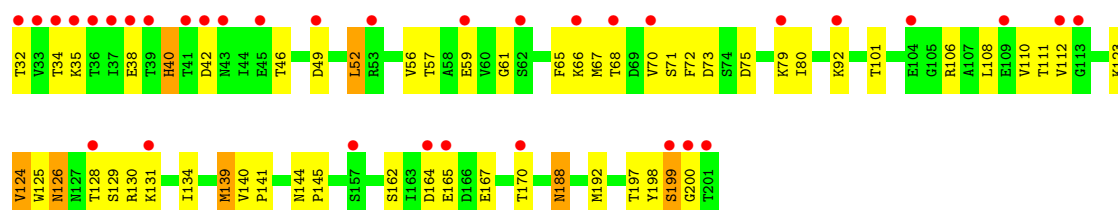
• Molecule 1: 25kDa structural protein VP25



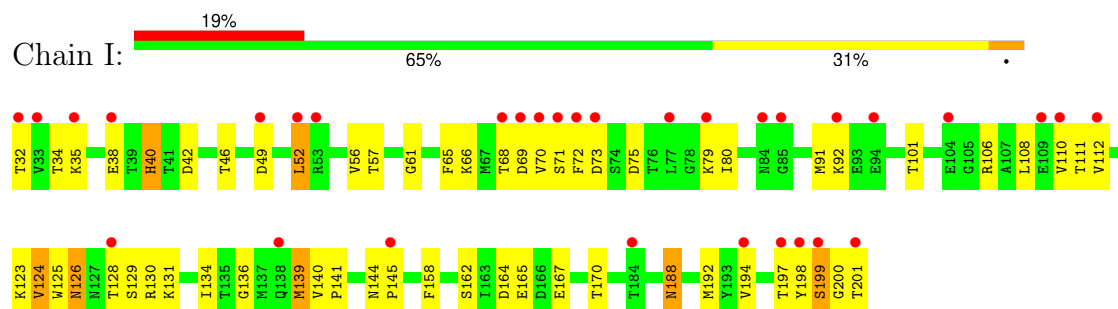
• Molecule 1: 25kDa structural protein VP25



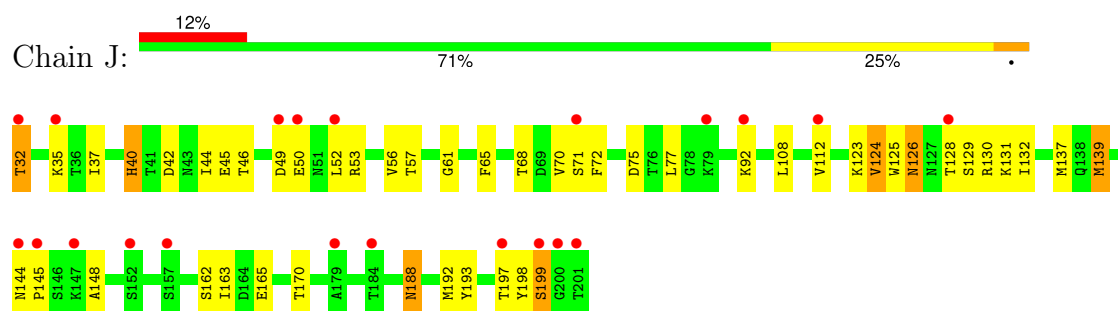
• Molecule 1: 25kDa structural protein VP25



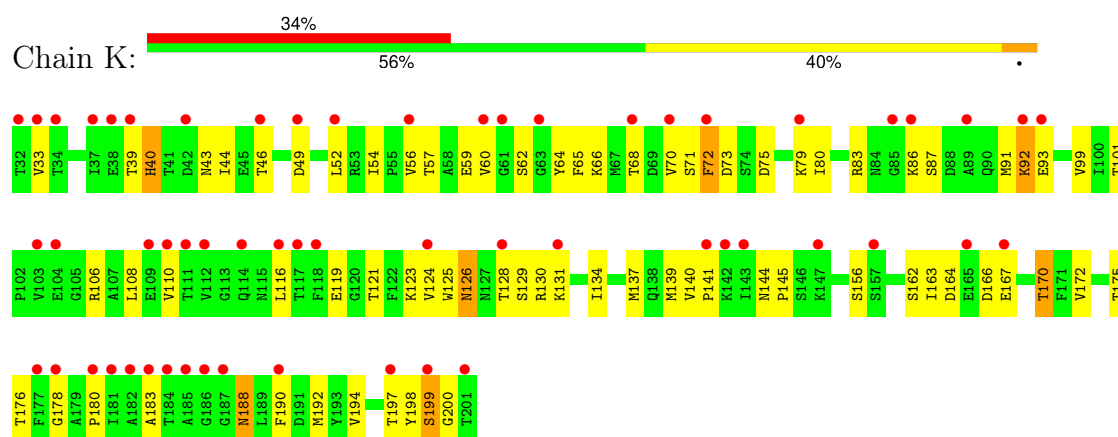
- Molecule 1: 25kDa structural protein VP25



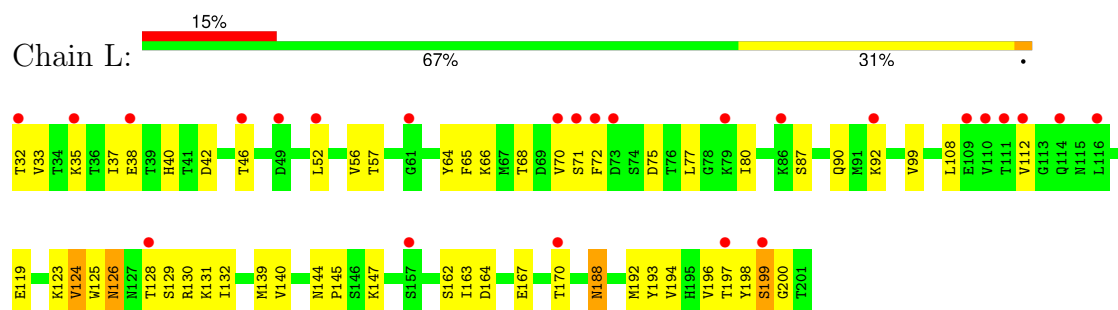
- Molecule 1: 25kDa structural protein VP25



- Molecule 1: 25kDa structural protein VP25



- Molecule 1: 25kDa structural protein VP25



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.33Å 106.71Å 200.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.00 45.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (45.00-2.00) 99.8 (45.00-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.63 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.248 , 0.281 0.252 , 0.256	Depositor DCC
R_{free} test set	7649 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.020 for k,h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	16843	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	0/1309	0.61	0/1775
1	B	0.35	0/1309	0.61	0/1775
1	C	0.34	0/1309	0.61	0/1775
1	D	0.41	1/1309 (0.1%)	0.62	0/1775
1	E	0.35	0/1309	0.61	0/1775
1	F	0.37	0/1309	0.62	0/1775
1	G	0.37	0/1309	0.62	0/1775
1	H	0.37	0/1309	0.61	0/1775
1	I	0.34	0/1309	0.61	0/1775
1	J	0.37	0/1309	0.64	0/1775
1	K	0.32	0/1309	0.57	0/1775
1	L	0.33	0/1309	0.58	0/1775
All	All	0.36	1/15708 (0.0%)	0.61	0/21300

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	60	VAL	CB-CG1	-7.91	1.36	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1288	0	1256	59	0
1	B	1288	0	1256	63	0
1	C	1288	0	1256	62	0
1	D	1288	0	1256	64	1
1	E	1288	0	1256	71	0
1	F	1288	0	1256	62	0
1	G	1288	0	1256	62	0
1	H	1288	0	1256	63	1
1	I	1288	0	1256	73	0
1	J	1288	0	1256	65	0
1	K	1288	0	1256	71	0
1	L	1288	0	1256	54	0
2	A	107	0	0	5	0
2	B	133	0	0	5	0
2	C	124	0	0	8	0
2	D	112	0	0	8	0
2	E	138	0	0	5	0
2	F	154	0	0	5	0
2	G	136	0	0	3	0
2	H	122	0	0	7	0
2	I	125	0	0	6	0
2	J	102	0	0	5	0
2	K	53	0	0	2	0
2	L	81	0	0	2	0
All	All	16843	0	15072	732	1

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 24.

All (732) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:56:VAL:HG11	1:F:65:PHE:HB3	1.28	1.14
1:B:56:VAL:HG11	1:B:65:PHE:HB3	1.29	1.13
1:D:56:VAL:HG11	1:D:65:PHE:HB3	1.30	1.13
1:A:56:VAL:HG11	1:A:65:PHE:HB3	1.29	1.12
1:G:56:VAL:HG11	1:G:65:PHE:HB3	1.27	1.10
1:E:56:VAL:HG11	1:E:65:PHE:HB3	1.29	1.09
1:C:56:VAL:HG11	1:C:65:PHE:HB3	1.30	1.09
1:H:56:VAL:HG11	1:H:65:PHE:HB3	1.29	1.08
1:I:56:VAL:HG11	1:I:65:PHE:HB3	1.31	1.07
1:H:46:THR:HG22	1:H:130:ARG:HH22	1.19	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:THR:HG22	1:D:199:SER:H	1.22	1.04
1:G:46:THR:HG22	1:G:130:ARG:HH22	1.23	1.04
1:A:197:THR:HG22	1:A:199:SER:H	1.23	1.03
1:L:46:THR:HG22	1:L:130:ARG:HH22	1.23	1.03
1:L:56:VAL:HG11	1:L:65:PHE:HB3	1.38	1.03
1:I:46:THR:HG22	1:I:130:ARG:HH22	1.21	1.03
1:F:197:THR:HG22	1:F:199:SER:H	1.22	1.03
1:C:46:THR:HG22	1:C:130:ARG:HH22	1.23	1.03
1:B:46:THR:HG22	1:B:130:ARG:HH22	1.22	1.02
1:B:197:THR:HG22	1:B:199:SER:H	1.22	1.02
1:E:46:THR:HG22	1:E:130:ARG:HH22	1.24	1.02
1:K:197:THR:HG22	1:K:199:SER:H	1.17	1.02
1:A:46:THR:HG22	1:A:130:ARG:HH22	1.22	1.01
1:C:197:THR:HG22	1:C:199:SER:H	1.24	1.01
1:D:46:THR:HG22	1:D:130:ARG:HH22	1.21	1.01
1:H:197:THR:HG22	1:H:199:SER:H	1.23	1.00
1:E:197:THR:HG22	1:E:199:SER:H	1.24	1.00
1:F:46:THR:HG22	1:F:130:ARG:HH22	1.21	0.99
1:I:197:THR:HG22	1:I:199:SER:H	1.23	0.99
1:G:197:THR:HG22	1:G:199:SER:H	1.22	0.99
1:K:139:MET:HE1	1:K:190:PHE:HB2	1.44	0.98
1:J:197:THR:HG22	1:J:199:SER:H	1.28	0.97
1:D:126:ASN:HD21	1:D:128:THR:HB	1.34	0.91
1:A:126:ASN:HD21	1:A:128:THR:HB	1.36	0.91
1:I:126:ASN:HD21	1:I:128:THR:HB	1.36	0.91
1:E:126:ASN:HD21	1:E:128:THR:HB	1.36	0.90
1:H:126:ASN:HD21	1:H:128:THR:HB	1.36	0.90
1:C:126:ASN:HD21	1:C:128:THR:HB	1.36	0.90
1:J:126:ASN:HD21	1:J:128:THR:HB	1.36	0.89
1:J:46:THR:HG22	1:J:130:ARG:HH22	1.38	0.89
1:B:126:ASN:HD21	1:B:128:THR:HB	1.37	0.89
1:F:126:ASN:HD21	1:F:128:THR:HB	1.35	0.89
1:J:56:VAL:HG11	1:J:65:PHE:HB3	1.54	0.89
1:E:49:ASP:HB2	2:F:1516:HOH:O	1.73	0.89
1:G:126:ASN:HD21	1:G:128:THR:HB	1.35	0.88
1:K:39:THR:HG22	1:K:43:ASN:HD21	1.38	0.88
1:K:56:VAL:HG11	1:K:65:PHE:HB3	1.55	0.88
1:H:46:THR:HG22	1:H:130:ARG:NH2	1.90	0.86
1:L:126:ASN:HD21	1:L:128:THR:HB	1.41	0.86
1:F:46:THR:HG22	1:F:130:ARG:NH2	1.90	0.86
1:I:46:THR:HG22	1:I:130:ARG:NH2	1.91	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:197:THR:HG22	1:L:199:SER:H	1.41	0.85
1:B:46:THR:HG22	1:B:130:ARG:NH2	1.91	0.85
1:G:46:THR:HG22	1:G:130:ARG:NH2	1.91	0.85
1:K:46:THR:HG22	1:K:130:ARG:HH22	1.39	0.85
1:A:46:THR:HG22	1:A:130:ARG:NH2	1.91	0.84
1:C:46:THR:HG22	1:C:130:ARG:NH2	1.92	0.84
1:D:46:THR:HG22	1:D:130:ARG:NH2	1.90	0.84
1:E:46:THR:HG22	1:E:130:ARG:NH2	1.92	0.83
1:L:46:THR:HG22	1:L:130:ARG:NH2	1.93	0.82
1:B:49:ASP:HB2	2:C:1518:HOH:O	1.79	0.82
1:J:188:ASN:HD22	1:J:188:ASN:H	1.27	0.81
1:D:49:ASP:HB2	2:D:1519:HOH:O	1.81	0.81
1:L:188:ASN:HD22	1:L:188:ASN:H	1.29	0.81
1:J:46:THR:HG22	1:J:130:ARG:NH2	1.96	0.80
1:K:141:PRO:HA	1:K:190:PHE:HD1	1.46	0.80
1:G:49:ASP:HB2	2:I:1515:HOH:O	1.80	0.79
1:F:131:LYS:HE2	1:F:162:SER:HB2	1.63	0.79
1:D:131:LYS:HE2	1:D:162:SER:HB2	1.64	0.79
1:K:124:VAL:HG11	1:K:134:ILE:HD11	1.65	0.78
1:H:131:LYS:HE2	1:H:162:SER:HB2	1.63	0.78
1:I:131:LYS:HE2	1:I:162:SER:HB2	1.64	0.78
1:E:147:LYS:HE3	2:F:2214:HOH:O	1.82	0.78
1:A:131:LYS:HE2	1:A:162:SER:HB2	1.65	0.77
1:E:131:LYS:HE2	1:E:162:SER:HB2	1.65	0.77
1:G:131:LYS:HE2	1:G:162:SER:HB2	1.66	0.76
1:B:131:LYS:HE2	1:B:162:SER:HB2	1.66	0.76
1:F:188:ASN:H	1:F:188:ASN:HD22	1.30	0.76
1:F:139:MET:HE3	1:F:192:MET:HA	1.68	0.75
1:I:188:ASN:H	1:I:188:ASN:HD22	1.34	0.75
1:C:131:LYS:HE2	1:C:162:SER:HB2	1.67	0.75
2:H:2339:HOH:O	1:I:49:ASP:HB2	1.87	0.75
1:E:139:MET:HE3	1:E:192:MET:HA	1.69	0.75
1:H:139:MET:HE3	1:H:192:MET:HA	1.67	0.75
1:B:188:ASN:HD22	1:B:188:ASN:H	1.35	0.74
1:A:188:ASN:H	1:A:188:ASN:HD22	1.35	0.74
1:L:128:THR:HG21	1:L:198:TYR:OH	1.88	0.74
1:J:68:THR:O	1:J:70:VAL:HG23	1.88	0.74
1:H:188:ASN:H	1:H:188:ASN:HD22	1.32	0.74
1:K:126:ASN:HD21	1:K:128:THR:HB	1.52	0.73
1:C:139:MET:HE3	1:C:192:MET:HA	1.68	0.73
1:A:139:MET:HE3	1:A:192:MET:HA	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:188:ASN:HD22	1:C:188:ASN:H	1.35	0.73
1:G:56:VAL:CG1	1:G:65:PHE:HB3	2.15	0.73
1:I:139:MET:HE3	1:I:192:MET:HA	1.68	0.73
1:G:188:ASN:HD22	1:G:188:ASN:H	1.35	0.73
1:L:68:THR:O	1:L:70:VAL:HG23	1.89	0.73
2:G:1517:HOH:O	1:H:49:ASP:HB2	1.87	0.73
1:J:144:ASN:HD21	1:J:148:ALA:HB3	1.54	0.72
1:E:188:ASN:HD22	1:E:188:ASN:H	1.37	0.72
1:D:188:ASN:H	1:D:188:ASN:HD22	1.36	0.72
1:K:164:ASP:HB2	1:K:167:GLU:OE1	1.90	0.72
1:B:139:MET:HE3	1:B:192:MET:HA	1.70	0.71
1:B:139:MET:HE3	1:B:139:MET:HA	1.72	0.71
1:D:139:MET:HE3	1:D:139:MET:HA	1.71	0.71
1:D:139:MET:HE3	1:D:192:MET:HA	1.73	0.71
1:J:52:LEU:HD11	1:J:72:PHE:CE1	2.25	0.71
1:G:139:MET:HE3	1:G:192:MET:HA	1.71	0.70
1:E:106:ARG:HB3	1:I:68:THR:CG2	2.21	0.70
1:K:139:MET:CE	1:K:190:PHE:HB2	2.20	0.70
1:L:139:MET:HE2	1:L:192:MET:HB2	1.74	0.70
1:B:139:MET:HA	1:B:139:MET:CE	2.22	0.70
1:H:199:SER:O	1:I:75:ASP:OD2	2.09	0.70
1:F:56:VAL:CG1	1:F:65:PHE:HB3	2.16	0.69
1:J:75:ASP:OD2	1:K:199:SER:O	2.10	0.69
1:L:52:LEU:HD11	1:L:77:LEU:HD12	1.73	0.69
1:G:199:SER:O	1:H:75:ASP:OD2	2.11	0.69
1:D:139:MET:HA	1:D:139:MET:CE	2.22	0.69
1:I:139:MET:HA	1:I:139:MET:CE	2.23	0.69
1:J:139:MET:HE3	1:J:192:MET:HA	1.74	0.69
1:F:139:MET:CE	1:F:139:MET:HA	2.23	0.69
1:K:197:THR:HG22	1:K:199:SER:N	2.00	0.68
1:J:52:LEU:HD11	1:J:72:PHE:HE1	1.59	0.68
1:A:139:MET:CE	1:A:139:MET:HA	2.24	0.68
1:C:139:MET:HA	1:C:139:MET:CE	2.23	0.68
1:K:197:THR:CG2	1:K:199:SER:H	1.99	0.68
1:J:199:SER:O	1:L:75:ASP:OD2	2.12	0.68
1:G:128:THR:HG21	1:G:198:TYR:OH	1.94	0.68
1:H:139:MET:HA	1:H:139:MET:CE	2.24	0.68
1:L:131:LYS:HE2	1:L:162:SER:HB2	1.76	0.67
1:B:92:LYS:HG3	1:B:125:TRP:CZ2	2.29	0.67
1:G:92:LYS:HG3	1:G:125:TRP:CZ2	2.29	0.67
1:J:131:LYS:HE2	1:J:162:SER:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:92:LYS:HG3	1:L:125:TRP:CZ2	2.27	0.67
1:A:56:VAL:CG1	1:A:65:PHE:HB3	2.17	0.67
1:F:197:THR:HG21	2:F:1083:HOH:O	1.93	0.67
1:G:197:THR:HG21	2:G:1088:HOH:O	1.94	0.67
1:G:139:MET:HA	1:G:139:MET:CE	2.24	0.67
1:K:188:ASN:H	1:K:188:ASN:HD22	1.41	0.67
1:D:49:ASP:OD2	1:E:49:ASP:OD2	2.13	0.67
1:E:106:ARG:HG2	1:I:69:ASP:O	1.94	0.67
1:G:68:THR:O	1:G:70:VAL:HG23	1.95	0.67
1:E:139:MET:HA	1:E:139:MET:CE	2.24	0.67
1:I:92:LYS:HG3	1:I:125:TRP:CZ2	2.30	0.67
1:I:139:MET:HE3	1:I:139:MET:HA	1.77	0.67
1:E:56:VAL:CG1	1:E:65:PHE:HB3	2.17	0.66
1:F:92:LYS:HG3	1:F:125:TRP:CZ2	2.30	0.66
1:D:56:VAL:CG1	1:D:65:PHE:HB3	2.18	0.66
1:H:92:LYS:HG3	1:H:125:TRP:CZ2	2.30	0.66
1:K:39:THR:HG22	1:K:43:ASN:ND2	2.09	0.66
1:G:139:MET:HE3	1:G:139:MET:HA	1.77	0.66
1:K:46:THR:HG22	1:K:130:ARG:NH2	2.09	0.66
1:C:92:LYS:HG3	1:C:125:TRP:CZ2	2.31	0.66
1:A:75:ASP:OD2	1:B:199:SER:O	2.13	0.65
1:A:199:SER:O	1:C:75:ASP:OD2	2.14	0.65
1:L:42:ASP:O	1:L:46:THR:HG23	1.95	0.65
1:L:87:SER:OG	1:L:90:GLN:HG3	1.96	0.65
1:C:128:THR:HG21	1:C:198:TYR:OH	1.97	0.65
1:D:49:ASP:OD2	1:F:49:ASP:OD2	2.15	0.65
1:J:124:VAL:HG22	1:J:163:ILE:CD1	2.25	0.65
1:A:92:LYS:HG3	1:A:125:TRP:CZ2	2.31	0.65
1:C:68:THR:O	1:C:70:VAL:HG23	1.96	0.64
1:D:92:LYS:HG3	1:D:125:TRP:CZ2	2.32	0.64
1:E:92:LYS:HG3	1:E:125:TRP:CZ2	2.31	0.64
1:D:75:ASP:OD2	1:E:199:SER:O	2.15	0.64
1:L:52:LEU:HD11	1:L:77:LEU:CD1	2.27	0.64
1:A:139:MET:HE3	1:A:139:MET:HA	1.80	0.64
1:A:128:THR:HG21	1:A:198:TYR:OH	1.98	0.64
1:I:128:THR:HG21	1:I:198:TYR:OH	1.98	0.64
1:J:139:MET:HA	1:J:139:MET:CE	2.28	0.64
1:F:128:THR:HG21	1:F:198:TYR:OH	1.97	0.64
1:I:68:THR:O	1:I:70:VAL:HG23	1.98	0.64
1:K:131:LYS:HE2	1:K:162:SER:HB2	1.80	0.63
1:F:170:THR:HG23	2:F:1304:HOH:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:126:ASN:ND2	1:F:128:THR:HB	2.12	0.63
1:D:128:THR:HG21	1:D:198:TYR:OH	1.99	0.63
1:J:126:ASN:ND2	1:J:128:THR:HB	2.10	0.63
1:B:56:VAL:CG1	1:B:65:PHE:HB3	2.18	0.63
1:C:197:THR:HG21	2:C:1084:HOH:O	1.98	0.63
1:E:128:THR:HG21	1:E:198:TYR:OH	1.99	0.63
1:B:128:THR:HG21	1:B:198:TYR:OH	1.99	0.62
1:D:197:THR:HG21	2:D:1918:HOH:O	1.97	0.62
1:K:75:ASP:OD2	1:L:199:SER:O	2.15	0.62
1:G:170:THR:HG23	2:G:2286:HOH:O	1.99	0.62
1:H:67:MET:HE3	2:H:2129:HOH:O	1.99	0.62
1:K:72:PHE:CE1	1:K:80:ILE:HB	2.34	0.62
1:H:56:VAL:CG1	1:H:65:PHE:HB3	2.17	0.62
1:L:124:VAL:HG22	1:L:163:ILE:CD1	2.29	0.62
1:B:68:THR:O	1:B:70:VAL:HG23	1.98	0.62
1:C:32:THR:HG23	2:C:2063:HOH:O	1.99	0.62
1:D:126:ASN:ND2	1:D:128:THR:HB	2.12	0.62
1:E:139:MET:HE3	1:E:139:MET:HA	1.80	0.62
1:A:40:HIS:HD2	2:A:1254:HOH:O	1.84	0.61
1:E:49:ASP:OD2	1:F:49:ASP:OD2	2.19	0.61
1:G:126:ASN:ND2	1:G:128:THR:HB	2.12	0.61
1:F:139:MET:HE3	1:F:139:MET:HA	1.81	0.61
1:C:56:VAL:CG1	1:C:65:PHE:HB3	2.18	0.61
1:C:126:ASN:ND2	1:C:128:THR:HB	2.13	0.61
1:B:70:VAL:HG21	2:B:1802:HOH:O	1.99	0.61
1:D:68:THR:O	1:D:70:VAL:HG23	2.01	0.61
1:J:37:ILE:CD1	1:K:33:VAL:HG13	2.31	0.61
1:A:126:ASN:ND2	1:A:128:THR:HB	2.13	0.61
1:C:139:MET:HE3	1:C:139:MET:HA	1.81	0.60
1:A:49:ASP:OD2	1:B:49:ASP:OD2	2.20	0.60
1:A:68:THR:O	1:A:70:VAL:HG23	2.01	0.60
1:H:128:THR:HG21	1:H:198:TYR:OH	2.00	0.60
1:J:128:THR:HG21	1:J:198:TYR:OH	2.02	0.60
1:K:123:LYS:HA	1:K:170:THR:HA	1.83	0.60
1:J:188:ASN:H	1:J:188:ASN:ND2	1.99	0.59
1:C:56:VAL:HG12	1:C:57:THR:N	2.17	0.59
1:I:56:VAL:CG1	1:I:65:PHE:HB3	2.19	0.59
1:L:144:ASN:HB2	1:L:145:PRO:CD	2.32	0.59
1:B:126:ASN:ND2	1:B:128:THR:HB	2.14	0.59
1:G:56:VAL:HG12	1:G:57:THR:N	2.18	0.59
1:H:40:HIS:HD2	2:H:1104:HOH:O	1.86	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:68:THR:O	1:H:70:VAL:HG23	2.02	0.59
1:J:70:VAL:HG12	1:J:71:SER:N	2.17	0.59
1:E:56:VAL:HG11	1:E:65:PHE:CB	2.20	0.59
1:H:139:MET:HE3	1:H:139:MET:HA	1.83	0.59
1:J:56:VAL:CG1	1:J:65:PHE:HB3	2.31	0.59
1:A:56:VAL:HG12	1:A:57:THR:N	2.18	0.59
1:E:68:THR:O	1:E:70:VAL:HG23	2.03	0.58
1:I:56:VAL:HG12	1:I:57:THR:N	2.18	0.58
1:J:45:GLU:HG3	1:J:130:ARG:HH11	1.68	0.58
1:K:137:MET:HG3	1:K:192:MET:HE2	1.85	0.58
1:I:126:ASN:ND2	1:I:128:THR:HB	2.14	0.58
1:D:37:ILE:CD1	1:E:33:VAL:HG13	2.34	0.58
1:F:56:VAL:HG12	1:F:57:THR:N	2.19	0.58
1:H:56:VAL:HG12	1:H:57:THR:N	2.18	0.58
1:J:45:GLU:HG3	1:J:130:ARG:NH1	2.19	0.58
1:B:56:VAL:HG12	1:B:57:THR:N	2.19	0.58
1:K:49:ASP:OD1	1:K:197:THR:HG23	2.03	0.58
1:E:75:ASP:OD2	1:F:199:SER:O	2.22	0.58
1:K:70:VAL:HG12	1:K:71:SER:N	2.17	0.58
1:E:126:ASN:ND2	1:E:128:THR:HB	2.13	0.57
1:G:188:ASN:HD22	1:G:188:ASN:N	2.01	0.57
1:E:92:LYS:HB2	2:E:1525:HOH:O	2.04	0.57
1:A:49:ASP:OD2	1:C:49:ASP:OD2	2.22	0.57
1:B:123:LYS:HB3	1:B:170:THR:HG22	1.86	0.57
1:H:126:ASN:ND2	1:H:128:THR:HB	2.14	0.57
1:K:124:VAL:HG13	1:K:163:ILE:CD1	2.34	0.57
1:L:188:ASN:H	1:L:188:ASN:ND2	2.00	0.57
1:A:197:THR:HG21	2:C:2012:HOH:O	2.03	0.57
1:E:46:THR:CG2	1:E:130:ARG:HH12	2.18	0.57
1:C:52:LEU:HD21	1:C:80:ILE:HD13	1.87	0.57
1:J:37:ILE:HD11	1:K:33:VAL:HG13	1.87	0.57
1:E:56:VAL:HG12	1:E:57:THR:N	2.20	0.57
1:I:123:LYS:HB3	1:I:170:THR:HG22	1.87	0.56
1:J:126:ASN:ND2	1:J:128:THR:H	2.02	0.56
1:H:56:VAL:HG11	1:H:65:PHE:CB	2.20	0.56
1:K:73:ASP:OD1	1:K:79:LYS:HG3	2.04	0.56
1:B:52:LEU:HD21	1:B:80:ILE:HD13	1.87	0.56
1:B:56:VAL:HG11	1:B:65:PHE:CB	2.19	0.56
1:C:123:LYS:HB3	1:C:170:THR:HG22	1.87	0.56
1:D:199:SER:O	1:F:75:ASP:OD2	2.24	0.56
1:F:56:VAL:HG11	1:F:65:PHE:CB	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:32:THR:HG23	2:I:1412:HOH:O	2.05	0.56
1:A:123:LYS:HB3	1:A:170:THR:HG22	1.87	0.56
1:B:170:THR:HG23	2:B:2148:HOH:O	2.05	0.56
1:E:170:THR:HG23	2:E:2491:HOH:O	2.04	0.56
1:E:52:LEU:HD21	1:E:80:ILE:HD13	1.87	0.56
1:E:70:VAL:HG12	1:E:71:SER:N	2.21	0.56
1:H:123:LYS:HB3	1:H:170:THR:HG22	1.88	0.56
1:G:123:LYS:HB3	1:G:170:THR:HG22	1.87	0.56
1:I:68:THR:HG23	2:I:1306:HOH:O	2.06	0.56
1:L:52:LEU:HB2	1:L:194:VAL:CG2	2.36	0.56
1:C:46:THR:HG21	2:C:1470:HOH:O	2.05	0.56
1:D:56:VAL:HG12	1:D:57:THR:N	2.20	0.56
1:E:46:THR:HG21	2:E:1404:HOH:O	2.05	0.56
1:F:123:LYS:HB3	1:F:170:THR:HG22	1.87	0.56
1:H:110:VAL:HG11	2:H:1380:HOH:O	2.05	0.55
1:J:129:SER:HA	1:J:165:GLU:OE2	2.06	0.55
1:A:56:VAL:HG11	1:A:65:PHE:CB	2.20	0.55
1:D:52:LEU:HD21	1:D:80:ILE:HD13	1.87	0.55
1:D:123:LYS:HB3	1:D:170:THR:HG22	1.87	0.55
1:G:124:VAL:HG11	1:G:134:ILE:HD11	1.87	0.55
1:E:123:LYS:HB3	1:E:170:THR:HG22	1.87	0.55
1:B:46:THR:CG2	1:B:130:ARG:HH12	2.19	0.55
1:A:52:LEU:HD21	1:A:80:ILE:HD13	1.89	0.55
1:H:52:LEU:HD21	1:H:80:ILE:HD13	1.88	0.55
2:D:1588:HOH:O	1:F:147:LYS:HE3	2.07	0.55
1:F:70:VAL:HG12	1:F:71:SER:N	2.22	0.55
1:B:75:ASP:OD2	1:C:199:SER:O	2.24	0.55
1:F:52:LEU:HD21	1:F:80:ILE:HD13	1.88	0.55
1:I:124:VAL:HG11	1:I:134:ILE:HD11	1.88	0.55
1:I:188:ASN:HD22	1:I:188:ASN:N	2.00	0.55
1:J:46:THR:CG2	1:J:130:ARG:HH12	2.20	0.55
1:D:46:THR:CG2	1:D:130:ARG:HH12	2.20	0.54
1:D:73:ASP:OD1	1:D:79:LYS:HG2	2.08	0.54
1:K:197:THR:HG21	2:K:1095:HOH:O	2.06	0.54
1:B:70:VAL:HG12	1:B:71:SER:N	2.23	0.54
1:D:124:VAL:HG11	1:D:134:ILE:HD11	1.89	0.54
1:H:70:VAL:HG12	1:H:71:SER:N	2.22	0.54
1:G:46:THR:CG2	1:G:130:ARG:HH12	2.21	0.54
1:I:73:ASP:OD1	1:I:79:LYS:HG2	2.08	0.54
1:J:188:ASN:HD22	1:J:188:ASN:N	1.92	0.54
1:F:46:THR:CG2	1:F:130:ARG:HH12	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:92:LYS:HG3	1:J:125:TRP:CZ2	2.43	0.54
1:K:108:LEU:O	1:K:110:VAL:HG23	2.06	0.54
1:J:123:LYS:HB3	1:J:170:THR:HG22	1.90	0.54
1:L:139:MET:CE	1:L:192:MET:HB2	2.37	0.54
1:G:73:ASP:OD1	1:G:79:LYS:HG2	2.08	0.54
1:I:52:LEU:HD21	1:I:80:ILE:HD13	1.90	0.54
1:K:64:TYR:CD2	1:K:119:GLU:HB3	2.43	0.54
1:A:46:THR:CG2	1:A:130:ARG:HH12	2.21	0.54
1:E:106:ARG:HB3	1:I:68:THR:HG22	1.88	0.54
1:H:73:ASP:OD1	1:H:79:LYS:HG2	2.08	0.54
1:K:56:VAL:HG12	1:K:57:THR:N	2.23	0.54
1:K:92:LYS:HE3	1:K:166:ASP:OD2	2.08	0.53
1:B:73:ASP:OD1	1:B:79:LYS:HG2	2.09	0.53
1:D:70:VAL:HG12	1:D:71:SER:N	2.23	0.53
1:G:49:ASP:OD2	1:H:49:ASP:OD2	2.25	0.53
1:G:52:LEU:HD21	1:G:80:ILE:HD13	1.90	0.53
1:G:70:VAL:HG12	1:G:71:SER:N	2.23	0.53
1:A:73:ASP:OD1	1:A:79:LYS:HG2	2.08	0.53
1:C:70:VAL:HG12	1:C:71:SER:N	2.23	0.53
1:G:56:VAL:HG11	1:G:65:PHE:CB	2.18	0.53
1:A:70:VAL:HG12	1:A:71:SER:N	2.23	0.53
1:H:124:VAL:HG11	1:H:134:ILE:HD11	1.91	0.53
1:J:170:THR:HG23	2:J:1246:HOH:O	2.09	0.53
1:K:99:VAL:O	1:K:124:VAL:HA	2.08	0.53
1:C:73:ASP:OD1	1:C:79:LYS:HG2	2.08	0.53
1:F:73:ASP:OD1	1:F:79:LYS:HG2	2.08	0.53
1:I:46:THR:CG2	1:I:130:ARG:HH12	2.22	0.53
1:I:70:VAL:HG12	1:I:71:SER:N	2.24	0.52
1:K:83:ARG:HB3	1:K:86:LYS:HD2	1.91	0.52
1:K:101:THR:CG2	1:K:123:LYS:HZ2	2.23	0.52
1:E:105:GLY:O	1:I:68:THR:HG23	2.10	0.52
1:F:124:VAL:HG11	1:F:134:ILE:HD11	1.91	0.52
1:C:164:ASP:HB2	1:C:167:GLU:CD	2.30	0.52
1:L:123:LYS:HB3	1:L:170:THR:HG22	1.92	0.52
1:E:73:ASP:OD1	1:E:79:LYS:HG2	2.08	0.52
1:D:164:ASP:HB2	1:D:167:GLU:CD	2.30	0.52
1:B:164:ASP:HB2	1:B:167:GLU:CD	2.30	0.52
1:L:56:VAL:HG12	1:L:57:THR:N	2.25	0.52
1:L:126:ASN:ND2	1:L:128:THR:HB	2.18	0.52
1:A:124:VAL:HG11	1:A:134:ILE:HD11	1.91	0.52
1:G:75:ASP:OD2	1:I:199:SER:O	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:70:VAL:HG12	1:J:71:SER:H	1.75	0.52
1:J:131:LYS:CE	1:J:162:SER:HB2	2.40	0.52
1:C:56:VAL:HG11	1:C:65:PHE:CB	2.21	0.52
1:L:46:THR:CG2	1:L:130:ARG:HH12	2.23	0.52
1:K:139:MET:CE	1:K:190:PHE:CB	2.88	0.52
1:L:70:VAL:HG12	1:L:71:SER:N	2.25	0.52
1:C:46:THR:CG2	1:C:130:ARG:HH12	2.22	0.51
1:C:124:VAL:HG11	1:C:134:ILE:HD11	1.91	0.51
1:E:124:VAL:HG11	1:E:134:ILE:HD11	1.91	0.51
1:F:68:THR:O	1:F:70:VAL:HG23	2.09	0.51
1:J:42:ASP:O	1:J:46:THR:HG23	2.11	0.51
1:J:46:THR:HG22	1:J:130:ARG:CZ	2.40	0.51
1:I:164:ASP:HB2	1:I:167:GLU:CD	2.30	0.51
1:D:56:VAL:HG13	1:D:66:LYS:O	2.11	0.51
1:H:56:VAL:HG13	1:H:66:LYS:O	2.10	0.51
1:K:46:THR:CG2	1:K:130:ARG:HH12	2.24	0.51
1:A:46:THR:HG21	2:A:1673:HOH:O	2.10	0.51
1:A:164:ASP:HB2	1:A:167:GLU:CD	2.31	0.51
1:L:46:THR:HG21	2:L:2137:HOH:O	2.11	0.51
1:D:56:VAL:HG11	1:D:65:PHE:CB	2.22	0.51
1:K:54:ILE:O	1:K:56:VAL:HG23	2.10	0.51
1:K:106:ARG:HA	1:K:106:ARG:NE	2.26	0.51
1:K:60:VAL:HG21	1:K:183:ALA:H	1.74	0.51
1:B:124:VAL:HG11	1:B:134:ILE:HD11	1.93	0.51
1:H:188:ASN:HD22	1:H:188:ASN:N	2.00	0.51
1:E:164:ASP:HB2	1:E:167:GLU:CD	2.30	0.51
1:F:86:LYS:HE2	2:F:2344:HOH:O	2.09	0.51
1:L:46:THR:HG22	1:L:130:ARG:HH12	1.75	0.51
1:B:46:THR:HG21	2:B:1396:HOH:O	2.11	0.50
1:C:56:VAL:HG13	1:C:66:LYS:O	2.12	0.50
1:K:56:VAL:HG13	1:K:66:LYS:O	2.12	0.50
1:K:178:GLY:HA3	2:K:2471:HOH:O	2.12	0.50
1:E:92:LYS:HD2	2:E:1525:HOH:O	2.11	0.50
1:K:144:ASN:HB2	1:K:145:PRO:CD	2.42	0.50
1:L:144:ASN:HB2	1:L:145:PRO:HD2	1.92	0.50
1:C:56:VAL:CG1	1:C:57:THR:N	2.74	0.50
2:J:1397:HOH:O	1:L:147:LYS:HE3	2.12	0.50
1:D:46:THR:HG21	2:D:1566:HOH:O	2.11	0.50
2:D:1346:HOH:O	1:F:72:PHE:HB2	2.11	0.50
1:G:128:THR:HG22	1:G:129:SER:N	2.26	0.50
1:J:45:GLU:CG	1:J:130:ARG:HH11	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:132:ILE:HD11	1:L:196:VAL:HG11	1.94	0.50
1:E:188:ASN:HD22	1:E:188:ASN:N	2.03	0.49
1:J:128:THR:HG22	1:J:129:SER:N	2.26	0.49
1:H:56:VAL:CG1	1:H:57:THR:N	2.75	0.49
1:H:128:THR:HG22	1:H:129:SER:N	2.27	0.49
1:A:56:VAL:CG1	1:A:57:THR:N	2.75	0.49
1:G:56:VAL:CG1	1:G:57:THR:N	2.75	0.49
1:K:137:MET:HE3	1:K:156:SER:HB3	1.94	0.49
1:H:131:LYS:HE2	1:H:162:SER:CB	2.40	0.49
2:H:1104:HOH:O	1:I:40:HIS:HD2	1.95	0.49
1:I:56:VAL:CG1	1:I:57:THR:N	2.75	0.49
1:G:164:ASP:HB2	1:G:167:GLU:CD	2.32	0.49
1:B:56:VAL:HG13	1:B:66:LYS:O	2.13	0.49
1:I:128:THR:HG22	1:I:129:SER:N	2.26	0.49
1:B:56:VAL:CG1	1:B:57:THR:N	2.76	0.49
1:E:37:ILE:CD1	1:F:33:VAL:HG13	2.42	0.49
1:H:164:ASP:HB2	1:H:167:GLU:CD	2.32	0.49
1:I:144:ASN:HB2	1:I:145:PRO:CD	2.43	0.49
1:K:199:SER:OG	1:K:200:GLY:N	2.43	0.49
1:D:128:THR:HG22	1:D:129:SER:N	2.28	0.49
1:E:128:THR:HG22	1:E:129:SER:N	2.28	0.49
1:F:56:VAL:CG1	1:F:57:THR:N	2.76	0.49
1:F:128:THR:HG22	1:F:129:SER:N	2.28	0.49
1:I:188:ASN:H	1:I:188:ASN:ND2	2.08	0.49
1:J:139:MET:CE	1:J:192:MET:HA	2.42	0.49
1:L:128:THR:HG22	1:L:129:SER:N	2.27	0.49
1:E:56:VAL:CG1	1:E:57:THR:N	2.76	0.48
1:A:56:VAL:HG13	1:A:66:LYS:O	2.13	0.48
1:C:34:THR:O	1:C:38:GLU:HG3	2.13	0.48
1:D:56:VAL:CG1	1:D:57:THR:N	2.76	0.48
1:H:46:THR:CG2	1:H:130:ARG:HH12	2.25	0.48
1:J:139:MET:HE3	1:J:192:MET:CA	2.43	0.48
1:F:34:THR:O	1:F:38:GLU:HG3	2.14	0.48
1:L:164:ASP:HB2	1:L:167:GLU:OE1	2.13	0.48
1:L:46:THR:HG22	1:L:130:ARG:CZ	2.43	0.48
1:L:132:ILE:HD11	1:L:196:VAL:CG1	2.43	0.48
1:B:128:THR:HG22	1:B:129:SER:N	2.27	0.48
1:C:128:THR:HG22	1:C:129:SER:N	2.28	0.48
1:D:34:THR:O	1:D:38:GLU:HG3	2.14	0.48
1:E:56:VAL:HG13	1:E:66:LYS:O	2.13	0.48
1:K:128:THR:HG22	1:K:129:SER:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:188:ASN:HD22	1:K:188:ASN:N	2.07	0.48
1:F:46:THR:HG23	1:F:130:ARG:HH12	1.77	0.48
1:F:164:ASP:HB2	1:F:167:GLU:CD	2.33	0.48
1:G:49:ASP:OD2	1:I:49:ASP:OD2	2.32	0.48
1:C:188:ASN:HD22	1:C:188:ASN:N	2.01	0.48
1:G:46:THR:HG22	1:G:130:ARG:CZ	2.44	0.48
1:E:101:THR:HB	1:E:123:LYS:HZ2	1.78	0.48
1:G:197:THR:HG22	1:G:199:SER:N	2.07	0.48
1:H:34:THR:O	1:H:38:GLU:HG3	2.13	0.48
1:K:52:LEU:HD11	1:K:72:PHE:CE1	2.48	0.48
1:F:56:VAL:HG13	1:F:66:LYS:O	2.14	0.48
1:D:37:ILE:HD11	1:E:33:VAL:HG13	1.96	0.47
1:D:201:THR:HG23	1:F:73:ASP:O	2.14	0.47
1:E:46:THR:HG22	1:E:130:ARG:CZ	2.43	0.47
1:K:49:ASP:OD1	1:K:197:THR:CG2	2.62	0.47
1:L:32:THR:HG22	1:L:35:LYS:H	1.79	0.47
1:A:110:VAL:HG11	2:A:1543:HOH:O	2.14	0.47
1:A:128:THR:HG22	1:A:129:SER:N	2.28	0.47
1:D:188:ASN:HD22	1:D:188:ASN:N	2.02	0.47
1:E:34:THR:O	1:E:38:GLU:HG3	2.12	0.47
1:J:49:ASP:HB2	1:K:49:ASP:OD2	2.14	0.47
1:A:34:THR:O	1:A:38:GLU:HG3	2.14	0.47
1:B:46:THR:HG22	1:B:130:ARG:CZ	2.44	0.47
1:D:46:THR:HG22	1:D:130:ARG:CZ	2.44	0.47
1:G:61:GLY:O	1:G:112:VAL:CG1	2.62	0.47
1:D:42:ASP:O	1:D:46:THR:HG23	2.15	0.47
1:F:139:MET:HE3	1:F:192:MET:CA	2.41	0.47
1:F:101:THR:HB	1:F:123:LYS:HZ2	1.79	0.47
1:B:34:THR:O	1:B:38:GLU:HG3	2.15	0.47
2:E:1568:HOH:O	1:I:70:VAL:HG22	2.14	0.47
1:B:49:ASP:OD2	1:C:49:ASP:OD2	2.33	0.47
1:C:110:VAL:HG11	2:C:1316:HOH:O	2.15	0.47
1:C:139:MET:HE3	1:C:192:MET:CA	2.41	0.47
1:I:34:THR:O	1:I:38:GLU:HG3	2.14	0.47
1:J:50:GLU:HG2	1:J:77:LEU:CD1	2.45	0.47
2:A:1254:HOH:O	1:C:40:HIS:HD2	1.98	0.47
1:K:140:VAL:O	1:K:190:PHE:HB3	2.15	0.47
1:F:131:LYS:HE2	1:F:162:SER:CB	2.41	0.47
1:H:61:GLY:O	1:H:112:VAL:CG1	2.62	0.47
1:J:32:THR:HG23	1:J:35:LYS:H	1.80	0.47
1:J:61:GLY:O	1:J:112:VAL:CG1	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:99:VAL:O	1:L:124:VAL:HA	2.15	0.47
1:D:61:GLY:O	1:D:112:VAL:CG1	2.64	0.46
1:D:114:GLN:HG2	2:D:1203:HOH:O	2.15	0.46
1:G:34:THR:O	1:G:38:GLU:HG3	2.14	0.46
1:A:79:LYS:HB3	2:A:2075:HOH:O	2.14	0.46
1:E:131:LYS:HE2	1:E:162:SER:CB	2.42	0.46
1:B:164:ASP:HB2	1:B:167:GLU:OE1	2.15	0.46
1:G:56:VAL:HG13	1:G:66:LYS:O	2.15	0.46
1:J:139:MET:HA	1:J:139:MET:HE2	1.96	0.46
1:K:124:VAL:HG11	1:K:134:ILE:CD1	2.41	0.46
1:L:46:THR:HG22	1:L:130:ARG:NH1	2.30	0.46
1:E:106:ARG:CB	1:I:68:THR:CG2	2.91	0.46
1:I:46:THR:HG23	1:I:130:ARG:HH12	1.81	0.46
1:L:64:TYR:CD2	1:L:119:GLU:HB3	2.50	0.46
1:A:46:THR:HG22	1:A:130:ARG:CZ	2.45	0.46
1:H:101:THR:HB	1:H:123:LYS:HZ2	1.81	0.46
1:H:197:THR:HG23	2:H:1253:HOH:O	2.15	0.46
1:I:56:VAL:HG13	1:I:66:LYS:O	2.15	0.46
1:C:42:ASP:O	1:C:46:THR:HG23	2.15	0.46
1:C:188:ASN:H	1:C:188:ASN:ND2	2.11	0.46
1:F:72:PHE:CE1	1:F:80:ILE:HD12	2.51	0.46
1:G:144:ASN:HB2	1:G:145:PRO:CD	2.45	0.46
1:I:164:ASP:HB2	1:I:167:GLU:OE1	2.16	0.46
1:J:197:THR:HG23	2:J:1534:HOH:O	2.15	0.46
1:K:59:GLU:HB3	1:K:62:SER:OG	2.16	0.46
1:L:198:TYR:O	1:L:199:SER:O	2.33	0.46
1:C:46:THR:HG22	1:C:130:ARG:CZ	2.45	0.46
1:C:61:GLY:O	1:C:112:VAL:CG1	2.64	0.46
1:F:46:THR:HG22	1:F:130:ARG:CZ	2.44	0.46
1:J:46:THR:HG22	1:J:130:ARG:NH1	2.30	0.46
1:J:128:THR:HG22	1:J:130:ARG:H	1.80	0.46
1:A:46:THR:HG23	1:A:130:ARG:HH12	1.80	0.46
1:B:72:PHE:CE1	1:B:80:ILE:HD12	2.51	0.46
1:C:101:THR:HB	1:C:123:LYS:HZ2	1.80	0.46
1:E:46:THR:HG23	1:E:130:ARG:HH12	1.80	0.46
1:D:144:ASN:HB2	1:D:145:PRO:CD	2.46	0.46
1:C:170:THR:HG23	2:C:2423:HOH:O	2.16	0.45
1:J:137:MET:HA	1:J:193:TYR:O	2.15	0.45
1:C:32:THR:HG22	1:C:35:LYS:H	1.81	0.45
1:E:188:ASN:H	1:E:188:ASN:ND2	2.11	0.45
1:G:61:GLY:O	1:G:112:VAL:HG13	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:139:MET:HE3	1:I:192:MET:CA	2.43	0.45
1:J:128:THR:CG2	1:J:129:SER:N	2.78	0.45
1:C:131:LYS:HE2	1:C:162:SER:CB	2.43	0.45
1:D:40:HIS:HD2	2:D:1558:HOH:O	1.99	0.45
1:G:201:THR:CG2	1:H:72:PHE:CD1	2.99	0.45
1:A:61:GLY:O	1:A:112:VAL:CG1	2.64	0.45
1:B:199:SER:OG	1:B:200:GLY:N	2.49	0.45
1:E:46:THR:HG22	1:E:130:ARG:HH12	1.81	0.45
1:E:144:ASN:HB2	1:E:145:PRO:CD	2.47	0.45
1:G:128:THR:CG2	1:G:129:SER:N	2.80	0.45
1:H:46:THR:HG23	1:H:130:ARG:HH12	1.82	0.45
1:J:124:VAL:HG22	1:J:163:ILE:HD12	1.94	0.45
1:J:139:MET:HE3	1:J:139:MET:HA	1.98	0.45
1:L:197:THR:HG22	1:L:199:SER:N	2.21	0.45
1:D:128:THR:O	1:D:165:GLU:HG2	2.16	0.45
1:E:42:ASP:O	1:E:46:THR:HG23	2.17	0.45
1:L:188:ASN:HD22	1:L:188:ASN:N	1.95	0.45
1:A:139:MET:HE3	1:A:192:MET:CA	2.42	0.45
1:G:91:MET:SD	1:G:123:LYS:NZ	2.81	0.45
1:I:128:THR:CG2	1:I:129:SER:N	2.79	0.45
1:L:56:VAL:CG1	1:L:57:THR:N	2.79	0.45
1:A:128:THR:O	1:A:165:GLU:HG2	2.17	0.45
1:B:46:THR:HG23	1:B:130:ARG:HH12	1.79	0.45
1:G:136:GLY:HA2	1:G:158:PHE:CZ	2.52	0.45
1:H:197:THR:HG21	2:I:1092:HOH:O	2.17	0.45
1:B:144:ASN:HB2	1:B:145:PRO:CD	2.47	0.45
1:C:128:THR:O	1:C:165:GLU:HG2	2.16	0.45
1:L:139:MET:HE2	1:L:192:MET:CB	2.46	0.45
1:B:188:ASN:HD22	1:B:188:ASN:N	2.01	0.45
1:E:128:THR:CG2	1:E:129:SER:N	2.80	0.45
1:F:140:VAL:HA	1:F:141:PRO:HD3	1.89	0.45
1:H:139:MET:HE3	1:H:192:MET:CA	2.40	0.45
1:I:56:VAL:HG11	1:I:65:PHE:CB	2.23	0.45
1:B:42:ASP:O	1:B:46:THR:HG23	2.17	0.44
1:E:139:MET:HE3	1:E:192:MET:CA	2.43	0.44
1:G:46:THR:HG23	1:G:130:ARG:HH12	1.82	0.44
1:H:61:GLY:O	1:H:112:VAL:HG13	2.17	0.44
1:H:128:THR:CG2	1:H:129:SER:N	2.80	0.44
1:L:52:LEU:HB2	1:L:194:VAL:HG22	1.98	0.44
1:L:56:VAL:HG13	1:L:66:LYS:O	2.16	0.44
1:A:144:ASN:HB2	1:A:145:PRO:CD	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:SER:OG	1:D:200:GLY:N	2.50	0.44
1:G:188:ASN:H	1:G:188:ASN:ND2	2.10	0.44
1:J:53:ARG:HG3	1:J:193:TYR:CE1	2.52	0.44
1:K:46:THR:HG23	1:K:130:ARG:HH12	1.82	0.44
1:D:46:THR:HG23	1:D:130:ARG:HH12	1.81	0.44
1:E:164:ASP:HB2	1:E:167:GLU:OE1	2.17	0.44
1:I:42:ASP:O	1:I:46:THR:HG23	2.18	0.44
1:I:61:GLY:O	1:I:112:VAL:CG1	2.66	0.44
1:K:121:THR:HG23	1:K:172:VAL:HA	2.00	0.44
1:A:42:ASP:O	1:A:46:THR:HG23	2.18	0.44
1:D:61:GLY:O	1:D:112:VAL:HG13	2.18	0.44
1:D:128:THR:CG2	1:D:129:SER:N	2.80	0.44
1:F:188:ASN:HD22	1:F:188:ASN:N	1.98	0.44
1:G:201:THR:O	1:G:201:THR:HG22	2.17	0.44
1:I:32:THR:HG22	1:I:35:LYS:H	1.82	0.44
1:I:110:VAL:HG11	2:I:1192:HOH:O	2.17	0.44
1:A:72:PHE:CE1	1:A:80:ILE:HD12	2.52	0.44
1:A:128:THR:CG2	1:A:129:SER:N	2.80	0.44
1:A:188:ASN:HD22	1:A:188:ASN:N	2.02	0.44
1:B:92:LYS:HD2	2:B:2227:HOH:O	2.17	0.44
1:B:128:THR:CG2	1:B:129:SER:N	2.80	0.44
1:G:128:THR:O	1:G:165:GLU:HG2	2.17	0.44
1:H:72:PHE:CE1	1:H:80:ILE:HD12	2.52	0.44
1:I:144:ASN:HB2	1:I:145:PRO:HD2	2.00	0.44
1:J:46:THR:HG22	1:J:130:ARG:HH12	1.83	0.44
1:K:87:SER:O	1:K:91:MET:HG3	2.17	0.44
1:J:46:THR:HG23	1:J:130:ARG:HH12	1.83	0.44
1:H:140:VAL:HA	1:H:141:PRO:HD3	1.89	0.44
1:I:46:THR:HG22	1:I:130:ARG:CZ	2.46	0.44
1:B:128:THR:O	1:B:165:GLU:HG2	2.18	0.44
1:E:199:SER:OG	1:E:200:GLY:N	2.50	0.44
1:H:144:ASN:HB2	1:H:145:PRO:CD	2.48	0.44
1:A:164:ASP:HB2	1:A:167:GLU:OE1	2.18	0.43
1:B:61:GLY:O	1:B:112:VAL:CG1	2.66	0.43
1:I:131:LYS:HE2	1:I:162:SER:CB	2.41	0.43
1:J:144:ASN:HB2	1:J:145:PRO:CD	2.48	0.43
1:D:72:PHE:CE1	1:D:80:ILE:HD12	2.53	0.43
1:E:46:THR:HG22	1:E:130:ARG:NH1	2.33	0.43
1:E:61:GLY:O	1:E:112:VAL:CG1	2.66	0.43
1:F:128:THR:CG2	1:F:129:SER:N	2.81	0.43
1:H:199:SER:OG	1:H:200:GLY:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:91:MET:SD	1:I:123:LYS:NZ	2.85	0.43
1:K:175:THR:HG22	1:K:176:THR:N	2.34	0.43
1:C:128:THR:CG2	1:C:129:SER:N	2.81	0.43
1:C:164:ASP:HB2	1:C:167:GLU:OE1	2.17	0.43
1:D:37:ILE:HG21	1:E:36:THR:HG21	2.00	0.43
1:E:194:VAL:O	1:E:194:VAL:HG23	2.17	0.43
1:G:164:ASP:HB2	1:G:167:GLU:OE1	2.18	0.43
1:G:199:SER:OG	1:G:200:GLY:N	2.50	0.43
1:J:32:THR:CG2	1:J:35:LYS:H	2.31	0.43
1:J:45:GLU:OE1	1:J:130:ARG:HD2	2.18	0.43
1:K:116:LEU:HD23	1:K:180:PRO:HA	2.01	0.43
1:A:61:GLY:O	1:A:112:VAL:HG13	2.18	0.43
1:I:199:SER:OG	1:I:200:GLY:N	2.49	0.43
1:E:72:PHE:CE1	1:E:80:ILE:HD12	2.53	0.43
1:F:128:THR:O	1:F:165:GLU:HG2	2.19	0.43
1:I:197:THR:HG21	2:I:1086:HOH:O	2.18	0.43
1:D:164:ASP:HB2	1:D:167:GLU:OE1	2.18	0.43
1:J:56:VAL:HG11	1:J:65:PHE:CB	2.38	0.43
1:C:46:THR:HG23	1:C:130:ARG:HH12	1.84	0.43
1:C:61:GLY:O	1:C:112:VAL:HG13	2.19	0.43
1:C:144:ASN:HB2	1:C:145:PRO:CD	2.48	0.43
1:G:42:ASP:O	1:G:46:THR:HG23	2.19	0.43
1:A:101:THR:HB	1:A:123:LYS:HZ2	1.84	0.43
1:I:128:THR:O	1:I:165:GLU:HG2	2.18	0.43
1:A:32:THR:HG22	1:A:35:LYS:H	1.84	0.43
1:E:105:GLY:O	1:I:68:THR:CG2	2.67	0.43
1:E:128:THR:O	1:E:165:GLU:HG2	2.19	0.43
1:K:40:HIS:O	1:K:44:ILE:HG13	2.18	0.43
1:L:33:VAL:HG12	1:L:37:ILE:HG13	2.01	0.43
1:F:144:ASN:HB2	1:F:145:PRO:CD	2.48	0.43
1:G:72:PHE:CE1	1:G:80:ILE:HD12	2.53	0.43
1:I:194:VAL:HG23	1:I:194:VAL:O	2.19	0.43
1:D:124:VAL:HG11	1:D:134:ILE:CD1	2.49	0.42
1:J:132:ILE:HD12	1:J:198:TYR:CZ	2.54	0.42
1:K:68:THR:O	1:K:70:VAL:HG23	2.19	0.42
1:G:46:THR:HG22	1:G:130:ARG:HH12	1.83	0.42
1:J:40:HIS:O	1:J:44:ILE:HG13	2.20	0.42
1:B:46:THR:HG22	1:B:130:ARG:NH1	2.34	0.42
1:C:136:GLY:HA2	1:C:158:PHE:CZ	2.54	0.42
1:F:136:GLY:HA2	1:F:158:PHE:CZ	2.54	0.42
1:I:72:PHE:CE1	1:I:80:ILE:HD12	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:VAL:HG23	1:D:194:VAL:O	2.19	0.42
1:D:201:THR:HG22	1:D:201:THR:O	2.20	0.42
1:F:32:THR:HG22	1:F:35:LYS:H	1.84	0.42
1:G:144:ASN:HB2	1:G:145:PRO:HD2	2.00	0.42
1:I:140:VAL:HA	1:I:141:PRO:HD3	1.90	0.42
1:K:52:LEU:HB3	1:K:194:VAL:HG22	2.02	0.42
1:L:72:PHE:CE1	1:L:80:ILE:HB	2.54	0.42
1:A:199:SER:OG	1:A:200:GLY:N	2.50	0.42
1:B:139:MET:CE	1:B:139:MET:CA	2.96	0.42
1:B:147:LYS:HE3	2:C:1887:HOH:O	2.19	0.42
1:D:46:THR:HG22	1:D:130:ARG:HH12	1.84	0.42
1:D:110:VAL:HG12	1:D:111:THR:N	2.34	0.42
1:G:124:VAL:HG11	1:G:134:ILE:CD1	2.50	0.42
1:A:91:MET:SD	1:A:123:LYS:NZ	2.88	0.42
1:B:32:THR:HG22	1:B:35:LYS:H	1.84	0.42
1:H:197:THR:HG22	1:H:199:SER:N	2.09	0.42
1:E:144:ASN:HB2	1:E:145:PRO:HD2	2.02	0.42
1:F:72:PHE:HE1	1:F:80:ILE:HD12	1.85	0.42
1:F:42:ASP:O	1:F:46:THR:HG23	2.20	0.42
1:H:42:ASP:O	1:H:46:THR:HG23	2.19	0.42
1:I:136:GLY:HA2	1:I:158:PHE:CZ	2.55	0.42
1:J:53:ARG:HG3	1:J:193:TYR:CZ	2.55	0.42
1:K:56:VAL:CG1	1:K:57:THR:N	2.83	0.42
1:F:199:SER:OG	1:F:200:GLY:N	2.52	0.42
1:H:128:THR:O	1:H:165:GLU:HG2	2.19	0.42
1:K:70:VAL:CG1	1:K:71:SER:N	2.82	0.42
1:K:141:PRO:HA	1:K:190:PHE:CD1	2.38	0.42
1:A:110:VAL:HG12	1:A:111:THR:N	2.35	0.41
1:A:136:GLY:HA2	1:A:158:PHE:CZ	2.55	0.41
1:B:46:THR:HG22	1:B:130:ARG:HH12	1.83	0.41
1:D:136:GLY:HA2	1:D:158:PHE:CZ	2.54	0.41
2:D:1558:HOH:O	1:F:40:HIS:HD2	2.03	0.41
1:E:201:THR:O	1:E:201:THR:HG22	2.20	0.41
1:G:110:VAL:HG12	1:G:111:THR:N	2.35	0.41
1:H:106:ARG:HA	1:H:106:ARG:NE	2.34	0.41
1:L:128:THR:CG2	1:L:129:SER:N	2.83	0.41
1:A:131:LYS:HE2	1:A:162:SER:CB	2.42	0.41
1:A:201:THR:HG22	1:A:201:THR:O	2.20	0.41
1:B:131:LYS:HE2	1:B:162:SER:CB	2.43	0.41
1:C:110:VAL:HG12	1:C:111:THR:N	2.35	0.41
1:C:201:THR:O	1:C:201:THR:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:61:GLY:C	1:H:112:VAL:HG13	2.40	0.41
1:C:140:VAL:HA	1:C:141:PRO:HD3	1.88	0.41
2:J:2246:HOH:O	1:L:140:VAL:HG22	2.20	0.41
1:K:92:LYS:HG3	1:K:125:TRP:CZ2	2.55	0.41
1:B:61:GLY:O	1:B:112:VAL:HG13	2.20	0.41
1:B:197:THR:HG22	1:B:199:SER:N	2.07	0.41
1:C:46:THR:HG22	1:C:130:ARG:HH12	1.84	0.41
1:D:144:ASN:HB2	1:D:145:PRO:HD2	2.02	0.41
1:F:110:VAL:HG12	1:F:111:THR:N	2.34	0.41
1:G:32:THR:HG22	1:G:35:LYS:H	1.86	0.41
1:G:194:VAL:O	1:G:194:VAL:HG23	2.21	0.41
1:J:56:VAL:CG1	1:J:57:THR:N	2.82	0.41
1:D:101:THR:HB	1:D:123:LYS:HZ2	1.85	0.41
1:F:61:GLY:O	1:F:112:VAL:CG1	2.68	0.41
1:F:139:MET:HA	1:F:139:MET:HE2	2.01	0.41
1:G:131:LYS:HE2	1:G:162:SER:CB	2.43	0.41
1:I:124:VAL:HG11	1:I:134:ILE:CD1	2.50	0.41
1:K:59:GLU:OE1	1:K:66:LYS:HE3	2.21	0.41
1:K:144:ASN:HB2	1:K:145:PRO:HD2	2.01	0.41
1:D:61:GLY:C	1:D:112:VAL:HG13	2.41	0.41
1:D:197:THR:HG22	1:D:198:TYR:N	2.36	0.41
1:G:46:THR:HG22	1:G:130:ARG:NH1	2.35	0.41
1:H:32:THR:HG22	1:H:35:LYS:H	1.86	0.41
1:H:164:ASP:HB2	1:H:167:GLU:OE1	2.19	0.41
1:L:52:LEU:O	1:L:193:TYR:HA	2.20	0.41
1:C:72:PHE:CE1	1:C:80:ILE:HD12	2.55	0.41
1:C:199:SER:OG	1:C:200:GLY:N	2.50	0.41
1:D:32:THR:HG22	1:D:35:LYS:H	1.85	0.41
1:F:201:THR:HG22	1:F:201:THR:O	2.20	0.41
1:L:197:THR:HG23	2:L:1350:HOH:O	2.20	0.41
1:L:199:SER:OG	1:L:200:GLY:N	2.50	0.41
1:E:37:ILE:HD11	1:F:33:VAL:HG13	2.03	0.41
1:H:139:MET:HA	1:H:139:MET:HE2	2.01	0.41
1:I:106:ARG:NE	1:I:106:ARG:HA	2.36	0.41
1:I:110:VAL:HG12	1:I:111:THR:N	2.34	0.41
1:K:91:MET:C	1:K:93:GLU:H	2.22	0.41
1:A:144:ASN:HB2	1:A:145:PRO:HD2	2.02	0.41
1:I:61:GLY:C	1:I:112:VAL:HG13	2.41	0.41
1:J:92:LYS:HG2	2:J:1873:HOH:O	2.21	0.41
1:K:124:VAL:HG13	1:K:163:ILE:HD12	2.03	0.41
1:F:188:ASN:H	1:F:188:ASN:ND2	2.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:PHE:HE1	1:B:80:ILE:HD12	1.86	0.40
1:B:110:VAL:HG12	1:B:111:THR:N	2.35	0.40
1:A:46:THR:HG22	1:A:130:ARG:HH12	1.86	0.40
1:B:70:VAL:HG22	2:B:1302:HOH:O	2.20	0.40
1:B:201:THR:HG22	1:B:201:THR:O	2.20	0.40
1:G:139:MET:HE3	1:G:192:MET:CA	2.46	0.40
1:H:46:THR:HG22	1:H:130:ARG:CZ	2.48	0.40
1:H:49:ASP:OD2	1:I:49:ASP:OD2	2.40	0.40
1:H:144:ASN:HB2	1:H:145:PRO:HD2	2.04	0.40
1:I:61:GLY:O	1:I:112:VAL:HG13	2.21	0.40
1:B:139:MET:HE3	1:B:192:MET:CA	2.45	0.40
1:B:144:ASN:HB2	1:B:145:PRO:HD2	2.02	0.40
1:C:46:THR:HG22	1:C:130:ARG:NH1	2.36	0.40
1:I:201:THR:HG22	1:I:201:THR:O	2.21	0.40
1:B:136:GLY:HA2	1:B:158:PHE:CZ	2.56	0.40
1:E:136:GLY:HA2	1:E:158:PHE:CZ	2.56	0.40
1:H:110:VAL:HG12	1:H:111:THR:N	2.35	0.40
1:H:141:PRO:HG3	2:H:1283:HOH:O	2.21	0.40
1:I:139:MET:CE	1:I:139:MET:CA	2.97	0.40
1:K:92:LYS:O	1:K:92:LYS:HG2	2.21	0.40
1:C:61:GLY:C	1:C:112:VAL:HG13	2.42	0.40
1:E:110:VAL:HG12	1:E:111:THR:N	2.36	0.40
1:I:101:THR:HB	1:I:123:LYS:HZ2	1.86	0.40
1:J:126:ASN:C	1:J:126:ASN:HD22	2.25	0.40
1:K:198:TYR:O	1:K:199:SER:O	2.39	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:VAL:CG1	1:H:59:GLU:OE2[3_656]	1.92	0.28

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	B	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	C	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	D	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	E	168/170 (99%)	162 (96%)	5 (3%)	1 (1%)	22	17
1	F	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	G	168/170 (99%)	162 (96%)	5 (3%)	1 (1%)	22	17
1	H	168/170 (99%)	163 (97%)	4 (2%)	1 (1%)	22	17
1	I	168/170 (99%)	162 (96%)	5 (3%)	1 (1%)	22	17
1	J	168/170 (99%)	159 (95%)	8 (5%)	1 (1%)	22	17
1	K	168/170 (99%)	158 (94%)	8 (5%)	2 (1%)	11	6
1	L	168/170 (99%)	163 (97%)	3 (2%)	2 (1%)	11	6
All	All	2016/2040 (99%)	1944 (96%)	58 (3%)	14 (1%)	19	14

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	SER
1	B	199	SER
1	C	199	SER
1	D	199	SER
1	E	199	SER
1	F	199	SER
1	G	199	SER
1	H	199	SER
1	I	199	SER
1	K	199	SER
1	L	199	SER
1	J	199	SER
1	L	112	VAL
1	K	92	LYS

5.3.2 Protein sidechains ⓘ

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	B	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	C	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	D	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	E	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	F	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	G	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	H	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	I	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	J	146/146 (100%)	139 (95%)	7 (5%)	21	19
1	K	146/146 (100%)	141 (97%)	5 (3%)	32	32
1	L	146/146 (100%)	140 (96%)	6 (4%)	26	25
All	All	1752/1752 (100%)	1671 (95%)	81 (5%)	23	21

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	52	LEU
1	A	108	LEU
1	A	124	VAL
1	A	126	ASN
1	A	139	MET
1	A	188	ASN
1	B	40	HIS
1	B	52	LEU
1	B	108	LEU
1	B	124	VAL
1	B	126	ASN
1	B	139	MET
1	B	188	ASN
1	C	40	HIS
1	C	52	LEU
1	C	108	LEU
1	C	124	VAL

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Mol	Chain	Res	Type
1	C	126	ASN
1	C	139	MET
1	C	188	ASN
1	D	40	HIS
1	D	52	LEU
1	D	108	LEU
1	D	124	VAL
1	D	126	ASN
1	D	139	MET
1	D	188	ASN
1	E	40	HIS
1	E	52	LEU
1	E	108	LEU
1	E	124	VAL
1	E	126	ASN
1	E	139	MET
1	E	188	ASN
1	F	40	HIS
1	F	52	LEU
1	F	108	LEU
1	F	124	VAL
1	F	126	ASN
1	F	139	MET
1	F	188	ASN
1	G	40	HIS
1	G	52	LEU
1	G	108	LEU
1	G	124	VAL
1	G	126	ASN
1	G	139	MET
1	G	188	ASN
1	H	40	HIS
1	H	52	LEU
1	H	108	LEU
1	H	124	VAL
1	H	126	ASN
1	H	139	MET
1	H	188	ASN
1	I	40	HIS
1	I	52	LEU
1	I	108	LEU
1	I	124	VAL

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Mol	Chain	Res	Type
1	I	126	ASN
1	I	139	MET
1	I	188	ASN
1	J	32	THR
1	J	40	HIS
1	J	108	LEU
1	J	124	VAL
1	J	126	ASN
1	J	139	MET
1	J	188	ASN
1	K	40	HIS
1	K	72	PHE
1	K	126	ASN
1	K	170	THR
1	K	188	ASN
1	L	38	GLU
1	L	40	HIS
1	L	108	LEU
1	L	124	VAL
1	L	126	ASN
1	L	188	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	126	ASN
1	A	127	ASN
1	A	188	ASN
1	B	126	ASN
1	B	127	ASN
1	B	188	ASN
1	C	40	HIS
1	C	126	ASN
1	C	127	ASN
1	C	188	ASN
1	D	40	HIS
1	D	126	ASN
1	D	127	ASN
1	D	188	ASN
1	E	40	HIS
1	E	126	ASN

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Mol	Chain	Res	Type
1	E	127	ASN
1	E	188	ASN
1	F	40	HIS
1	F	126	ASN
1	F	127	ASN
1	F	188	ASN
1	G	40	HIS
1	G	126	ASN
1	G	127	ASN
1	G	188	ASN
1	H	40	HIS
1	H	126	ASN
1	H	127	ASN
1	H	188	ASN
1	I	40	HIS
1	I	126	ASN
1	I	127	ASN
1	I	188	ASN
1	J	40	HIS
1	J	126	ASN
1	J	127	ASN
1	J	188	ASN
1	K	40	HIS
1	K	43	ASN
1	K	126	ASN
1	K	127	ASN
1	K	188	ASN
1	L	126	ASN
1	L	127	ASN
1	L	138	GLN
1	L	188	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	170/170 (100%)	0.83	30 (17%) 4 4	8, 17, 47, 74	0
1	B	170/170 (100%)	0.76	24 (14%) 7 6	6, 14, 40, 110	0
1	C	170/170 (100%)	0.64	24 (14%) 7 6	7, 15, 38, 67	0
1	D	170/170 (100%)	0.86	24 (14%) 7 6	6, 16, 39, 87	0
1	E	170/170 (100%)	0.77	27 (15%) 6 5	7, 13, 39, 84	0
1	F	170/170 (100%)	1.09	33 (19%) 4 3	4, 13, 38, 66	0
1	G	170/170 (100%)	1.04	27 (15%) 6 5	5, 13, 48, 124	0
1	H	170/170 (100%)	1.28	34 (20%) 3 3	6, 17, 53, 88	0
1	I	170/170 (100%)	0.90	32 (18%) 4 3	6, 16, 37, 60	0
1	J	170/170 (100%)	0.59	21 (12%) 9 8	7, 17, 38, 56	0
1	K	170/170 (100%)	1.61	57 (33%) 1 1	12, 29, 51, 68	0
1	L	170/170 (100%)	0.85	25 (14%) 7 6	10, 21, 41, 66	0
All	All	2040/2040 (100%)	0.93	358 (17%) 5 4	4, 17, 45, 124	0

All (358) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	32	THR	15.8
1	G	36	THR	14.1
1	G	34	THR	13.8
1	G	37	ILE	13.7
1	B	32	THR	13.5
1	G	33	VAL	13.1
1	F	33	VAL	11.2
1	H	33	VAL	10.7
1	H	37	ILE	10.0
1	F	32	THR	9.9
1	G	38	GLU	9.1

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Mol	Chain	Res	Type	RSRZ
1	B	35	LYS	8.4
1	H	36	THR	8.2
1	F	36	THR	8.2
1	L	199	SER	8.1
1	H	35	LYS	8.0
1	D	199	SER	7.8
1	D	201	THR	7.8
1	G	39	THR	7.8
1	G	35	LYS	7.7
1	F	34	THR	7.5
1	B	38	GLU	7.5
1	F	39	THR	7.4
1	B	33	VAL	7.3
1	I	199	SER	7.2
1	D	35	LYS	7.2
1	E	201	THR	7.0
1	H	59	GLU	6.9
1	E	33	VAL	6.8
1	H	199	SER	6.8
1	B	199	SER	6.8
1	F	72	PHE	6.7
1	F	35	LYS	6.5
1	G	199	SER	6.5
1	H	34	THR	6.5
1	H	42	ASP	6.5
1	G	92	LYS	6.4
1	A	34	THR	6.4
1	D	32	THR	6.4
1	A	199	SER	6.4
1	C	199	SER	6.4
1	B	201	THR	6.3
1	E	32	THR	6.3
1	E	199	SER	6.3
1	H	32	THR	6.3
1	E	38	GLU	6.2
1	H	38	GLU	6.2
1	D	34	THR	6.1
1	A	35	LYS	6.1
1	D	33	VAL	6.1
1	F	112	VAL	6.1
1	F	71	SER	6.0
1	H	45	GLU	5.9

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Mol	Chain	Res	Type	RSRZ
1	D	37	ILE	5.8
1	K	199	SER	5.7
1	E	79	LYS	5.6
1	F	110	VAL	5.4
1	B	36	THR	5.4
1	C	92	LYS	5.4
1	E	36	THR	5.3
1	D	36	THR	5.3
1	I	70	VAL	5.3
1	I	32	THR	5.2
1	F	201	THR	5.2
1	E	73	ASP	5.2
1	K	32	THR	5.2
1	J	157	SER	5.2
1	B	109	GLU	5.1
1	A	33	VAL	5.1
1	H	201	THR	5.1
1	L	38	GLU	5.1
1	B	34	THR	5.1
1	I	68	THR	5.1
1	F	199	SER	5.0
1	L	72	PHE	4.9
1	C	167	GLU	4.9
1	E	34	THR	4.9
1	L	49	ASP	4.8
1	E	72	PHE	4.8
1	I	69	ASP	4.8
1	J	92	LYS	4.8
1	H	112	VAL	4.8
1	H	39	THR	4.7
1	B	92	LYS	4.7
1	K	185	ALA	4.7
1	C	35	LYS	4.7
1	A	32	THR	4.7
1	F	111	THR	4.6
1	F	184	THR	4.6
1	H	92	LYS	4.6
1	K	190	PHE	4.6
1	G	79	LYS	4.5
1	D	70	VAL	4.5
1	K	61	GLY	4.5
1	L	32	THR	4.4

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Mol	Chain	Res	Type	RSRZ
1	H	66	LYS	4.4
1	A	92	LYS	4.4
1	A	37	ILE	4.4
1	B	79	LYS	4.4
1	G	201	THR	4.3
1	I	73	ASP	4.3
1	K	49	ASP	4.2
1	B	37	ILE	4.2
1	I	92	LYS	4.1
1	F	73	ASP	4.1
1	L	92	LYS	4.1
1	K	186	GLY	4.1
1	C	109	GLU	4.1
1	F	37	ILE	4.1
1	K	92	LYS	4.0
1	A	109	GLU	4.0
1	I	109	GLU	4.0
1	E	92	LYS	4.0
1	G	95	ASP	4.0
1	E	90	GLN	4.0
1	K	85	GLY	4.0
1	F	49	ASP	3.9
1	J	35	LYS	3.9
1	I	184	THR	3.9
1	I	201	THR	3.9
1	H	109	GLU	3.9
1	A	38	GLU	3.9
1	L	110	VAL	3.8
1	L	157	SER	3.8
1	A	200	GLY	3.8
1	G	200	GLY	3.8
1	D	38	GLU	3.8
1	K	128	THR	3.7
1	G	42	ASP	3.7
1	K	38	GLU	3.7
1	C	162	SER	3.7
1	C	32	THR	3.7
1	K	180	PRO	3.7
1	E	71	SER	3.6
1	C	201	THR	3.6
1	H	41	THR	3.6
1	H	49	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	49	ASP	3.6
1	K	184	THR	3.6
1	K	63	GLY	3.5
1	H	170	THR	3.5
1	C	129	SER	3.5
1	G	40	HIS	3.5
1	G	49	ASP	3.5
1	H	62	SER	3.5
1	A	42	ASP	3.5
1	I	35	LYS	3.5
1	C	79	LYS	3.4
1	D	92	LYS	3.4
1	C	165	GLU	3.4
1	A	46	THR	3.4
1	A	104	GLU	3.4
1	E	49	ASP	3.4
1	B	70	VAL	3.3
1	F	109	GLU	3.3
1	G	167	GLU	3.3
1	B	49	ASP	3.3
1	D	167	GLU	3.3
1	G	70	VAL	3.3
1	H	70	VAL	3.3
1	I	49	ASP	3.3
1	K	70	VAL	3.3
1	D	197	THR	3.3
1	E	184	THR	3.3
1	H	165	GLU	3.3
1	K	182	ALA	3.2
1	K	114	GLN	3.2
1	J	147	LYS	3.2
1	K	165	GLU	3.2
1	L	112	VAL	3.2
1	H	128	THR	3.2
1	I	72	PHE	3.2
1	B	73	ASP	3.2
1	C	95	ASP	3.2
1	C	131	LYS	3.2
1	K	86	LYS	3.2
1	A	165	GLU	3.2
1	K	56	VAL	3.1
1	K	103	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	J	199	SER	3.1
1	K	52	LEU	3.1
1	D	49	ASP	3.1
1	K	93	GLU	3.1
1	K	181	ILE	3.1
1	A	157	SER	3.1
1	I	38	GLU	3.1
1	C	49	ASP	3.1
1	G	128	THR	3.1
1	J	128	THR	3.1
1	K	109	GLU	3.1
1	K	33	VAL	3.1
1	G	109	GLU	3.0
1	F	70	VAL	3.0
1	L	61	GLY	3.0
1	H	53	ARG	3.0
1	J	201	THR	3.0
1	K	178	GLY	3.0
1	A	79	LYS	3.0
1	D	79	LYS	2.9
1	B	128	THR	2.9
1	B	138	GLN	2.9
1	L	109	GLU	2.9
1	G	112	VAL	2.9
1	L	52	LEU	2.9
1	H	200	GLY	2.9
1	F	92	LYS	2.9
1	B	197	THR	2.8
1	I	85	GLY	2.8
1	J	79	LYS	2.8
1	K	39	THR	2.8
1	K	116	LEU	2.8
1	F	129	SER	2.8
1	E	37	ILE	2.8
1	G	197	THR	2.8
1	K	111	THR	2.8
1	L	197	THR	2.8
1	F	42	ASP	2.8
1	L	70	VAL	2.8
1	G	157	SER	2.8
1	L	86	LYS	2.8
1	D	184	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	167	GLU	2.8
1	F	50	GLU	2.8
1	K	104	GLU	2.8
1	F	197	THR	2.7
1	K	143	ILE	2.7
1	I	112	VAL	2.7
1	K	157	SER	2.7
1	A	201	THR	2.7
1	E	93	GLU	2.7
1	E	35	LYS	2.7
1	C	128	THR	2.7
1	J	32	THR	2.7
1	A	164	ASP	2.7
1	E	157	SER	2.7
1	H	113	GLY	2.7
1	K	177	PHE	2.7
1	B	170	THR	2.7
1	K	183	ALA	2.6
1	J	197	THR	2.6
1	K	42	ASP	2.6
1	I	53	ARG	2.6
1	I	110	VAL	2.6
1	D	157	SER	2.6
1	C	200	GLY	2.6
1	E	70	VAL	2.6
1	F	46	THR	2.6
1	K	72	PHE	2.6
1	G	147	LYS	2.5
1	K	79	LYS	2.5
1	K	112	VAL	2.5
1	L	170	THR	2.5
1	K	118	PHE	2.5
1	I	145	PRO	2.5
1	H	157	SER	2.5
1	D	104	GLU	2.5
1	A	72	PHE	2.5
1	K	89	ALA	2.5
1	C	110	VAL	2.5
1	C	194	VAL	2.5
1	F	128	THR	2.5
1	I	33	VAL	2.5
1	H	43	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	197	THR	2.5
1	C	70	VAL	2.5
1	J	144	ASN	2.5
1	I	71	SER	2.4
1	I	77	LEU	2.4
1	G	170	THR	2.4
1	K	197	THR	2.4
1	K	201	THR	2.4
1	C	33	VAL	2.4
1	J	200	GLY	2.4
1	L	114	GLN	2.4
1	D	109	GLU	2.4
1	I	104	GLU	2.4
1	F	183	ALA	2.4
1	H	68	THR	2.4
1	H	79	LYS	2.4
1	K	131	LYS	2.4
1	J	52	LEU	2.3
1	L	35	LYS	2.3
1	L	128	THR	2.3
1	K	110	VAL	2.3
1	A	138	GLN	2.3
1	D	42	ASP	2.3
1	K	187	GLY	2.3
1	E	104	GLU	2.3
1	I	52	LEU	2.3
1	K	142	LYS	2.3
1	F	68	THR	2.3
1	K	117	THR	2.3
1	F	164	ASP	2.3
1	H	164	ASP	2.3
1	L	71	SER	2.3
1	F	38	GLU	2.3
1	J	50	GLU	2.3
1	L	79	LYS	2.3
1	A	52	LEU	2.3
1	J	184	THR	2.3
1	K	46	THR	2.3
1	L	46	THR	2.3
1	C	157	SER	2.3
1	J	71	SER	2.3
1	J	152	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	167	GLU	2.2
1	A	53	ARG	2.2
1	A	36	THR	2.2
1	G	41	THR	2.2
1	J	49	ASP	2.2
1	E	200	GLY	2.2
1	B	112	VAL	2.2
1	D	51	ASN	2.2
1	E	128	THR	2.2
1	I	128	THR	2.2
1	B	131	LYS	2.2
1	K	167	GLU	2.2
1	F	108	LEU	2.2
1	E	147	LYS	2.2
1	I	84	ASN	2.2
1	C	112	VAL	2.2
1	F	194	VAL	2.2
1	I	94	GLU	2.1
1	A	134	ILE	2.1
1	A	128	THR	2.1
1	I	197	THR	2.1
1	K	37	ILE	2.1
1	D	95	ASP	2.1
1	K	68	THR	2.1
1	K	141	PRO	2.1
1	I	138	GLN	2.1
1	A	110	VAL	2.1
1	I	194	VAL	2.1
1	K	147	LYS	2.1
1	B	68	THR	2.1
1	L	73	ASP	2.1
1	J	179	ALA	2.1
1	A	85	GLY	2.1
1	J	145	PRO	2.1
1	F	123	LYS	2.1
1	H	131	LYS	2.1
1	L	116	LEU	2.1
1	D	46	THR	2.1
1	K	34	THR	2.1
1	B	51	ASN	2.0
1	H	104	GLU	2.0
1	C	53	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	147	LYS	2.0
1	I	79	LYS	2.0
1	K	124	VAL	2.0
1	D	138	GLN	2.0
1	L	111	THR	2.0
1	A	50	GLU	2.0
1	I	198	TYR	2.0
1	E	110	VAL	2.0
1	E	112	VAL	2.0
1	J	112	VAL	2.0
1	K	60	VAL	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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.