



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 11:36 am GMT

PDB ID : 2ZF5
Title : Crystal Structure of highly thermostable glycerol kinase from a hyperthermophilic archaeon
Authors : Koga, Y.; Katsumi, R.; You, D.-J.; Matsumura, H.; Takano, K.; Kanaya, S.
Deposited on : 2007-12-20
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

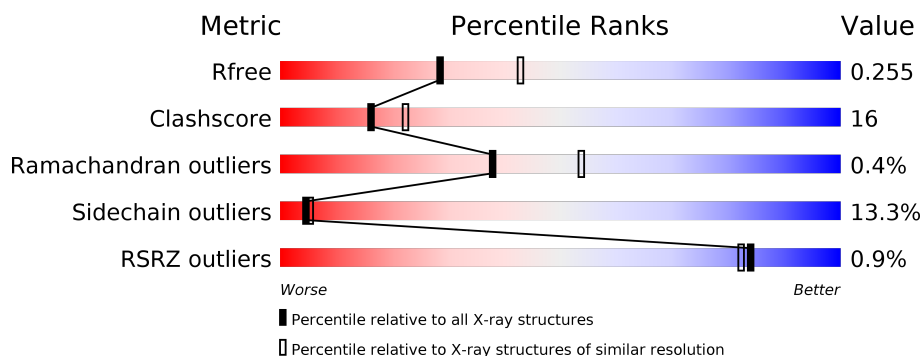
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	O	497	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>30%</div> <div>7%</div> <div>..</div> </div> </div>
1	Y	497	<div> <div>%</div> <div> <div></div> <div>57%</div> <div>33%</div> <div>8%</div> <div>..</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7975 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 Glycerol kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	494	Total	C	N	O	S	0	0	0
			3921	2505	663	741	12			
1	Y	494	Total	C	N	O	S	0	0	0
			3921	2505	663	741	12			

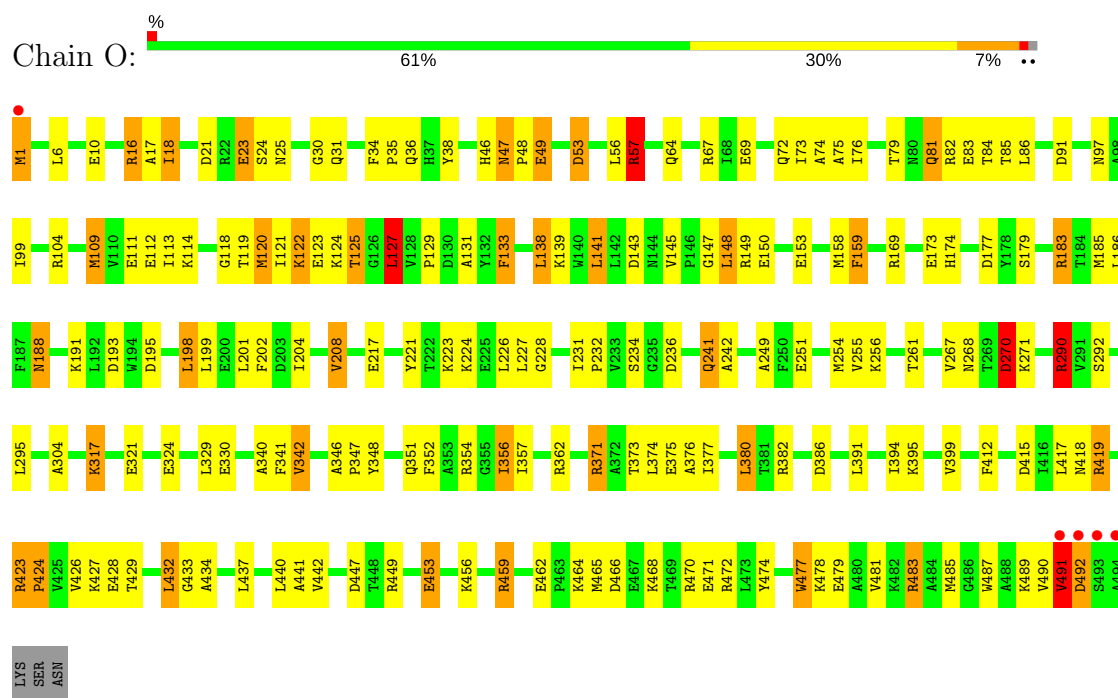
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	O	68	Total	O	0	0
			68	68		
2	Y	65	Total	O	0	0
			65	65		

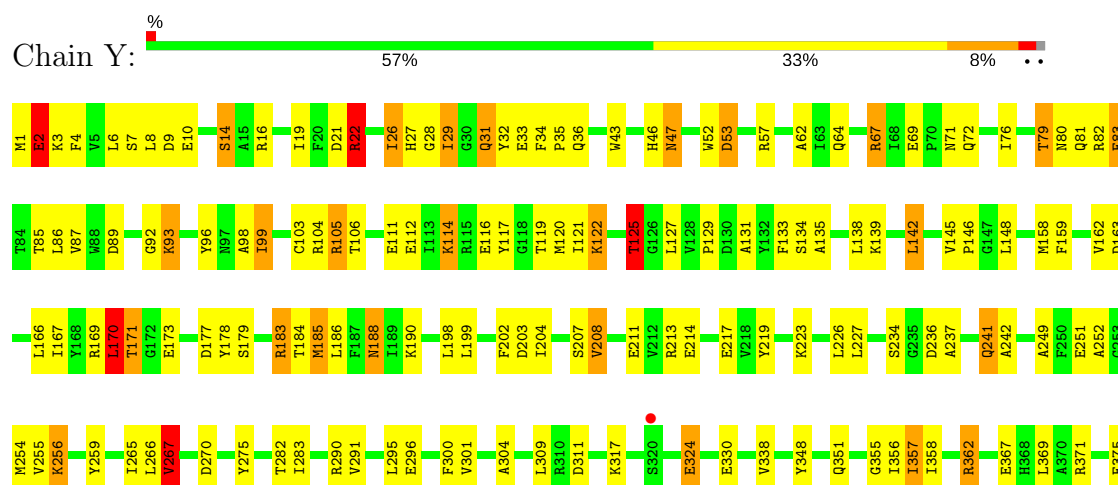
3 Residue-property plots

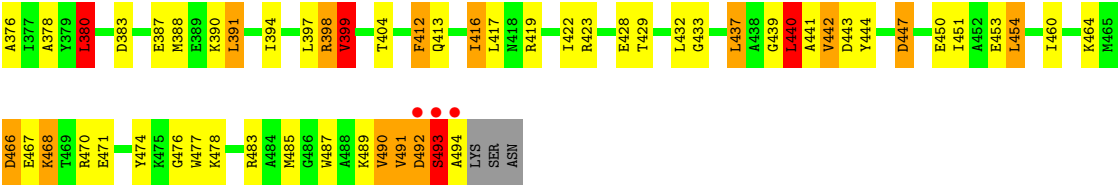
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Glycerol kinase



• Molecule 1: Glycerol kinase





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	217.48Å 217.48Å 66.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.10 – 2.40 41.10 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.2 (41.10-2.40) 98.2 (41.10-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.174 , 0.255 0.173 , 0.255	Depositor DCC
R_{free} test set	2271 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7975	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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	O	1.48	25/4003 (0.6%)	1.31	41/5422 (0.8%)
1	Y	1.41	24/4003 (0.6%)	1.28	42/5422 (0.8%)
All	All	1.45	49/8006 (0.6%)	1.30	83/10844 (0.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	1	2
1	Y	1	2
All	All	2	4

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Y	494	ALA	CA-CB	9.88	1.73	1.52
1	Y	494	ALA	N-CA	8.54	1.63	1.46
1	O	23	GLU	CD-OE1	7.63	1.34	1.25
1	Y	324	GLU	CB-CG	7.57	1.66	1.52
1	O	477	TRP	CZ3-CH2	7.43	1.51	1.40
1	Y	324	GLU	CG-CD	7.32	1.62	1.51
1	O	111	GLU	CG-CD	7.25	1.62	1.51
1	Y	471	GLU	CG-CD	7.13	1.62	1.51
1	O	38	TYR	CD2-CE2	7.04	1.50	1.39
1	O	49	GLU	CG-CD	6.87	1.62	1.51
1	O	342	VAL	CB-CG1	6.85	1.67	1.52
1	O	342	VAL	CB-CG2	6.82	1.67	1.52
1	O	479	GLU	CB-CG	6.58	1.64	1.52
1	Y	203	ASP	CB-CG	6.51	1.65	1.51
1	O	471	GLU	CG-CD	6.50	1.61	1.51
1	O	399	VAL	CB-CG2	6.36	1.66	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	453	GLU	CG-CD	6.16	1.61	1.51
1	O	49	GLU	CB-CG	6.12	1.63	1.52
1	O	324	GLU	CD-OE1	6.11	1.32	1.25
1	Y	251	GLU	CG-CD	6.07	1.61	1.51
1	Y	275	TYR	CG-CD1	5.92	1.46	1.39
1	Y	467	GLU	CG-CD	5.88	1.60	1.51
1	O	348	TYR	CE2-CZ	5.83	1.46	1.38
1	Y	96	TYR	CE2-CZ	5.81	1.46	1.38
1	Y	291	VAL	CB-CG2	5.80	1.65	1.52
1	O	362	ARG	CZ-NH2	5.79	1.40	1.33
1	O	412	PHE	CG-CD1	5.61	1.47	1.38
1	Y	71	ASN	CB-CG	5.55	1.63	1.51
1	Y	447	ASP	CB-CG	-5.53	1.40	1.51
1	Y	211	GLU	CG-CD	5.50	1.60	1.51
1	Y	252	ALA	CA-CB	-5.49	1.41	1.52
1	O	133	PHE	CG-CD1	5.45	1.47	1.38
1	Y	412	PHE	CG-CD1	5.44	1.47	1.38
1	Y	357	ILE	CB-CG2	5.32	1.69	1.52
1	Y	133	PHE	CE1-CZ	5.29	1.47	1.37
1	O	173	GLU	CG-CD	5.29	1.59	1.51
1	O	159	PHE	CE2-CZ	5.28	1.47	1.37
1	Y	300	PHE	CE1-CZ	5.27	1.47	1.37
1	Y	2	GLU	CD-OE2	5.23	1.31	1.25
1	O	221	TYR	CG-CD2	5.22	1.46	1.39
1	Y	53	ASP	CB-CG	5.18	1.62	1.51
1	O	57	ARG	CG-CD	5.17	1.64	1.51
1	Y	83	GLU	CG-CD	5.17	1.59	1.51
1	O	221	TYR	CE2-CZ	5.16	1.45	1.38
1	Y	2	GLU	CG-CD	5.14	1.59	1.51
1	O	133	PHE	CE1-CZ	5.12	1.47	1.37
1	Y	375	GLU	CG-CD	5.12	1.59	1.51
1	O	481	VAL	CB-CG1	-5.11	1.42	1.52
1	O	330	GLU	CG-CD	5.07	1.59	1.51

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	82	ARG	C-N-CA	-11.09	93.98	121.70
1	O	419	ARG	NE-CZ-NH2	-10.00	115.30	120.30
1	Y	398	ARG	NE-CZ-NH1	9.77	125.18	120.30
1	Y	440	LEU	CA-CB-CG	9.68	137.56	115.30
1	O	362	ARG	NE-CZ-NH1	-9.54	115.53	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	183	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	Y	398	ARG	NE-CZ-NH2	-9.06	115.77	120.30
1	Y	270	ASP	CB-CA-C	8.78	127.95	110.40
1	Y	391	LEU	CA-CB-CG	7.95	133.58	115.30
1	O	354	ARG	NE-CZ-NH1	7.83	124.21	120.30
1	O	183	ARG	NE-CZ-NH2	-7.66	116.47	120.30
1	O	354	ARG	NE-CZ-NH2	-7.61	116.50	120.30
1	O	82	ARG	O-C-N	-7.60	110.53	122.70
1	Y	82	ARG	C-N-CA	-7.42	103.14	121.70
1	Y	371	ARG	NE-CZ-NH1	-7.24	116.68	120.30
1	Y	470	ARG	NE-CZ-NH2	-7.23	116.69	120.30
1	Y	466	ASP	CB-CG-OD2	7.22	124.80	118.30
1	O	183	ARG	CB-CG-CD	-7.22	92.83	111.60
1	Y	169	ARG	NE-CZ-NH2	-7.12	116.74	120.30
1	O	423	ARG	NE-CZ-NH2	-7.12	116.74	120.30
1	Y	185	MET	CG-SD-CE	-7.10	88.84	100.20
1	Y	267	VAL	CB-CA-C	-7.09	97.92	111.40
1	Y	419	ARG	NE-CZ-NH1	-7.04	116.78	120.30
1	O	356	ILE	CG1-CB-CG2	-7.00	96.01	111.40
1	O	419	ARG	NE-CZ-NH1	6.99	123.80	120.30
1	O	362	ARG	NE-CZ-NH2	6.93	123.77	120.30
1	O	423	ARG	NE-CZ-NH1	6.93	123.76	120.30
1	Y	170	LEU	CA-CB-CG	6.90	131.17	115.30
1	Y	9	ASP	CB-CG-OD1	6.74	124.36	118.30
1	O	236	ASP	CB-CG-OD2	6.57	124.21	118.30
1	Y	309	LEU	CB-CG-CD1	-6.55	99.87	111.00
1	Y	125	THR	N-CA-CB	-6.54	97.87	110.30
1	Y	236	ASP	CB-CG-OD1	6.51	124.16	118.30
1	Y	493	SER	N-CA-C	-6.39	93.74	111.00
1	O	270	ASP	CB-CG-OD1	-6.37	112.57	118.30
1	O	415	ASP	CB-CG-OD1	6.30	123.97	118.30
1	Y	290	ARG	NE-CZ-NH2	-6.21	117.19	120.30
1	Y	447	ASP	CB-CA-C	-6.19	98.01	110.40
1	O	485	MET	CA-CB-CG	-6.02	103.07	113.30
1	Y	183	ARG	CB-CG-CD	-6.02	95.95	111.60
1	Y	22	ARG	NE-CZ-NH1	-5.99	117.30	120.30
1	O	290	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	O	183	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	O	386	ASP	CB-CG-OD2	-5.92	112.98	118.30
1	Y	369	LEU	CB-CG-CD1	-5.89	100.99	111.00
1	Y	104	ARG	NE-CZ-NH2	-5.83	117.39	120.30
1	O	371	ARG	NE-CZ-NH2	-5.80	117.40	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	104	ARG	NE-CZ-NH1	-5.75	117.43	120.30
1	Y	398	ARG	CD-NE-CZ	5.75	131.64	123.60
1	Y	311	ASP	CB-CG-OD1	5.74	123.47	118.30
1	O	492	ASP	N-CA-C	5.67	126.31	111.00
1	O	148	LEU	CA-CB-CG	5.66	128.31	115.30
1	Y	397	LEU	CA-CB-CG	5.65	128.30	115.30
1	O	459	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	Y	399	VAL	CG1-CB-CG2	5.62	119.89	110.90
1	Y	29	ILE	CB-CA-C	-5.58	100.44	111.60
1	O	472	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	O	459	ARG	NE-CZ-NH2	5.45	123.03	120.30
1	O	18	ILE	CG1-CB-CG2	-5.44	99.43	111.40
1	Y	437	LEU	CA-CB-CG	5.44	127.81	115.30
1	Y	380	LEU	CA-CB-CG	5.42	127.78	115.30
1	O	295	LEU	CA-CB-CG	5.41	127.75	115.30
1	O	193	ASP	CB-CG-OD1	5.38	123.14	118.30
1	Y	493	SER	N-CA-CB	5.37	118.55	110.50
1	O	483	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	Y	82	ARG	O-C-N	-5.29	114.23	122.70
1	O	267	VAL	CB-CA-C	-5.29	101.35	111.40
1	O	342	VAL	CG1-CB-CG2	5.29	119.36	110.90
1	Y	295	LEU	CA-CB-CG	5.24	127.35	115.30
1	Y	142	LEU	CB-CG-CD2	5.24	119.90	111.00
1	Y	2	GLU	CB-CA-C	5.21	120.82	110.40
1	O	143	ASP	CB-CG-OD1	5.19	122.97	118.30
1	O	441	ALA	N-CA-C	5.18	124.99	111.00
1	Y	22	ARG	NE-CZ-NH2	5.18	122.89	120.30
1	O	127	LEU	CB-CG-CD1	5.17	119.78	111.00
1	O	30	GLY	N-CA-C	-5.14	100.25	113.10
1	O	382	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	O	491	VAL	C-N-CA	5.11	134.48	121.70
1	Y	437	LEU	CB-CG-CD1	5.10	119.68	111.00
1	O	1	MET	CG-SD-CE	5.10	108.35	100.20
1	Y	493	SER	C-N-CA	-5.06	109.04	121.70
1	O	271	LYS	CD-CE-NZ	5.03	123.27	111.70
1	Y	82	ARG	NE-CZ-NH1	-5.01	117.79	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	O	270	ASP	CA
1	Y	270	ASP	CA

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	491	VAL	Peptide
1	O	492	ASP	Peptide
1	Y	492	ASP	Peptide
1	Y	493	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	3921	0	3897	118	0
1	Y	3921	0	3897	139	0
2	O	68	0	0	2	0
2	Y	65	0	0	1	0
All	All	7975	0	7794	251	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 16.

All (251) 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:Y:183:ARG:HH21	1:Y:282:THR:HG21	1.10	1.09
1:Y:159:PHE:HB3	1:Y:208:VAL:HG13	1.32	1.06
1:Y:489:LYS:HG3	1:Y:489:LYS:O	1.55	1.05
1:Y:125:THR:HG22	1:Y:127:LEU:H	1.22	1.05
1:Y:26:ILE:HD12	1:Y:28:GLY:H	1.21	1.04
1:Y:171:THR:HG22	1:Y:173:GLU:H	1.28	0.95
1:O:57:ARG:HH11	1:O:57:ARG:HG3	1.30	0.94
1:Y:255:VAL:HG22	1:Y:267:VAL:HG13	1.50	0.93
1:O:16:ARG:NH1	1:O:428:GLU:OE1	2.01	0.93
1:Y:121:ILE:O	1:Y:125:THR:HB	1.70	0.91
1:Y:142:LEU:HD23	1:Y:148:LEU:HD23	1.54	0.89
1:Y:183:ARG:NH2	1:Y:282:THR:HG21	1.85	0.89
1:Y:26:ILE:HD12	1:Y:28:GLY:N	1.90	0.87
1:Y:159:PHE:CB	1:Y:208:VAL:HG13	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:159:PHE:HB3	1:Y:208:VAL:CG1	2.07	0.84
1:Y:183:ARG:HH21	1:Y:282:THR:CG2	1.91	0.84
1:O:125:THR:CG2	1:O:127:LEU:HB2	2.09	0.82
1:Y:362:ARG:NH2	2:Y:537:HOH:O	2.08	0.80
1:Y:16:ARG:HG2	1:Y:31:GLN:HB3	1.62	0.80
1:O:224:LYS:O	1:O:228:GLY:N	2.14	0.80
1:O:120:MET:O	1:O:124:LYS:HG3	1.82	0.79
1:O:188:ASN:ND2	1:O:191:LYS:H	1.81	0.79
1:Y:1:MET:CE	1:Y:3:LYS:HE3	2.12	0.79
1:Y:213:ARG:HD2	1:Y:217:GLU:OE2	1.82	0.78
1:Y:1:MET:HE2	1:Y:3:LYS:HE3	1.66	0.76
1:Y:67:ARG:HG3	1:Y:67:ARG:HH11	1.52	0.74
1:O:270:ASP:HB2	1:O:292:SER:OG	1.90	0.72
1:Y:19:ILE:HD13	1:Y:62:ALA:HB1	1.72	0.72
1:O:121:ILE:O	1:O:125:THR:HB	1.89	0.71
1:O:125:THR:HG23	1:O:127:LEU:HD22	1.72	0.71
1:O:255:VAL:HG21	1:O:394:ILE:HG23	1.71	0.71
1:Y:125:THR:CG2	1:Y:127:LEU:HB2	2.21	0.71
1:O:69:GLU:H	1:O:72:GLN:NE2	1.90	0.70
1:Y:301:VAL:HG13	1:Y:304:ALA:HB3	1.71	0.70
1:Y:22:ARG:HD3	1:Y:444:TYR:O	1.91	0.70
1:O:487:TRP:CZ2	1:O:491:VAL:HG21	2.27	0.70
1:Y:489:LYS:CG	1:Y:489:LYS:O	2.37	0.70
1:O:109:MET:CE	1:O:113:ILE:HD12	2.21	0.70
1:Y:47:ASN:HD22	1:Y:47:ASN:C	1.94	0.69
1:Y:234:SER:HB2	1:Y:441:ALA:HB3	1.73	0.69
1:Y:69:GLU:H	1:Y:72:GLN:HE21	1.41	0.68
1:Y:103:CYS:SG	1:Y:105:ARG:HD2	2.35	0.67
1:Y:16:ARG:NH1	1:Y:428:GLU:OE1	2.28	0.67
1:Y:188:ASN:HD22	1:Y:190:LYS:H	1.42	0.67
1:Y:26:ILE:HG13	1:Y:26:ILE:O	1.95	0.67
1:O:125:THR:HG23	1:O:127:LEU:HB2	1.76	0.66
1:O:447:ASP:OD2	1:O:449:ARG:HB3	1.94	0.66
1:O:109:MET:HE2	1:O:113:ILE:HD12	1.77	0.66
1:Y:21:ASP:OD2	1:Y:27:HIS:NE2	2.24	0.66
1:Y:79:THR:HG22	1:Y:237:ALA:O	1.96	0.65
1:Y:6:LEU:HD23	1:Y:76:ILE:HG12	1.79	0.65
1:O:159:PHE:HB3	1:O:208:VAL:HG13	1.80	0.64
1:O:380:LEU:HD13	1:O:477:TRP:HZ2	1.64	0.63
1:O:16:ARG:HG3	1:O:31:GLN:HB3	1.81	0.63
1:O:53:ASP:OD2	1:O:57:ARG:NH1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:69:GLU:H	1:O:72:GLN:HE21	1.45	0.63
1:O:57:ARG:CG	1:O:57:ARG:HH11	2.10	0.63
1:Y:125:THR:HG22	1:Y:127:LEU:N	2.04	0.63
1:O:47:ASN:HD22	1:O:47:ASN:C	2.02	0.62
1:O:290:ARG:HH11	1:O:290:ARG:HB2	1.64	0.61
1:O:47:ASN:ND2	1:O:49:GLU:H	1.99	0.61
1:Y:142:LEU:HD23	1:Y:148:LEU:CD2	2.26	0.61
1:O:147:GLY:HA2	1:O:150:GLU:OE1	2.00	0.60
1:O:394:ILE:O	1:O:419:ARG:HD3	2.01	0.60
1:O:118:GLY:HA2	1:O:129:PRO:HG2	1.83	0.60
1:O:36:GLN:OE1	1:O:46:HIS:HE1	1.84	0.60
1:O:356:ILE:HG22	1:Y:358:ILE:HG13	1.84	0.59
1:O:109:MET:CE	1:O:113:ILE:CD1	2.81	0.59
1:O:6:LEU:HD23	1:O:76:ILE:HG12	1.84	0.59
1:O:138:LEU:HD13	1:O:204:ILE:HG12	1.85	0.59
1:Y:259:TYR:HE1	1:Y:399:VAL:HG22	1.68	0.59
1:O:109:MET:HE1	1:O:113:ILE:CD1	2.33	0.58
1:O:122:LYS:HG2	1:O:127:LEU:O	2.03	0.58
1:O:149:ARG:O	1:O:153:GLU:HG3	2.03	0.58
1:O:158:MET:HE1	1:O:174:HIS:HB2	1.86	0.58
1:Y:491:VAL:O	1:Y:491:VAL:CG1	2.51	0.58
1:O:133:PHE:CD2	1:O:185:MET:CE	2.87	0.57
1:O:79:THR:HB	1:O:434:ALA:HB2	1.87	0.57
1:Y:134:SER:HB2	1:Y:184:THR:HA	1.85	0.57
1:Y:26:ILE:CD1	1:Y:28:GLY:N	2.65	0.57
1:Y:114:LYS:HG2	1:Y:129:PRO:HB2	1.86	0.57
1:Y:214:GLU:O	1:Y:219:TYR:OH	2.17	0.57
1:O:186:LEU:HD21	1:O:204:ILE:HD13	1.86	0.57
1:Y:1:MET:HE3	1:Y:3:LYS:HE3	1.85	0.57
1:Y:422:ILE:HG12	1:Y:460:ILE:HG12	1.86	0.57
1:Y:487:TRP:O	1:Y:490:VAL:HG12	2.05	0.56
1:O:179:SER:HB2	1:O:241:GLN:HG3	1.88	0.56
1:O:356:ILE:HA	1:Y:357:ILE:O	2.05	0.56
1:Y:171:THR:CG2	1:Y:173:GLU:H	2.10	0.55
1:Y:67:ARG:NH1	1:Y:67:ARG:HG3	2.21	0.55
1:O:133:PHE:CD2	1:O:185:MET:HE3	2.42	0.55
1:O:21:ASP:OD1	1:O:23:GLU:N	2.38	0.55
1:Y:442:VAL:HG13	1:Y:442:VAL:O	2.07	0.54
1:Y:86:LEU:N	1:Y:86:LEU:HD12	2.22	0.54
1:O:224:LYS:O	1:O:228:GLY:CA	2.55	0.54
1:Y:179:SER:HB2	1:Y:241:GLN:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:188:ASN:ND2	1:Y:190:LYS:H	2.06	0.54
1:O:125:THR:HG22	1:O:127:LEU:H	1.74	0.53
1:O:491:VAL:HG22	1:Y:476:GLY:HA2	1.90	0.53
1:O:109:MET:HE1	1:O:113:ILE:HD12	1.90	0.53
1:Y:26:ILE:CD1	1:Y:28:GLY:H	2.08	0.53
1:O:83:GLU:OE2	1:O:183:ARG:HD2	2.09	0.53
1:Y:177:ASP:HA	1:Y:213:ARG:O	2.07	0.53
1:O:226:LEU:HB3	1:O:227:LEU:HD22	1.90	0.53
1:Y:491:VAL:O	1:Y:491:VAL:HG12	2.08	0.53
1:O:424:PRO:HG2	1:O:426:VAL:O	2.09	0.52
1:O:133:PHE:HD2	1:O:185:MET:HE1	1.74	0.52
1:Y:256:LYS:O	1:Y:265:ILE:HA	2.10	0.52
1:Y:367:GLU:CD	1:Y:367:GLU:H	2.13	0.52
1:Y:348:TYR:OH	1:Y:383:ASP:OD2	2.24	0.52
1:Y:388:MET:HB3	1:Y:394:ILE:HD11	1.91	0.52
1:Y:105:ARG:HG2	1:Y:106:THR:HG23	1.92	0.51
1:Y:47:ASN:ND2	1:Y:47:ASN:C	2.62	0.51
1:O:17:ALA:C	1:O:18:ILE:HD12	2.30	0.51
1:O:109:MET:HE3	1:O:139:LYS:HD3	1.93	0.51
1:O:141:LEU:O	1:O:145:VAL:HG23	2.09	0.51
1:Y:171:THR:HG22	1:Y:173:GLU:N	2.11	0.51
1:O:86:LEU:N	1:O:86:LEU:HD12	2.26	0.51
1:Y:6:LEU:HD13	1:Y:19:ILE:HD11	1.92	0.51
1:Y:442:VAL:O	1:Y:442:VAL:CG1	2.59	0.50
1:O:487:TRP:CH2	1:O:491:VAL:HG21	2.47	0.50
1:Y:19:ILE:HD13	1:Y:62:ALA:CB	2.39	0.50
1:Y:178:TYR:HB3	1:Y:283:ILE:HG21	1.93	0.50
1:O:158:MET:CE	1:O:174:HIS:HB2	2.41	0.50
1:Y:242:ALA:O	1:Y:433:GLY:HA3	2.12	0.50
1:O:380:LEU:HD13	1:O:477:TRP:CZ2	2.46	0.50
1:Y:131:ALA:H	1:Y:351:GLN:NE2	2.09	0.49
1:O:21:ASP:OD2	1:O:25:ASN:HB2	2.12	0.49
1:O:73:ILE:HG22	1:O:231:ILE:HG21	1.95	0.49
1:Y:125:THR:CG2	1:Y:127:LEU:CB	2.90	0.49
1:O:129:PRO:HA	1:O:185:MET:HE2	1.94	0.49
1:O:217:GLU:O	1:O:234:SER:HA	2.12	0.49
1:O:85:THR:C	1:O:86:LEU:HD12	2.32	0.49
1:Y:83:GLU:OE2	1:Y:183:ARG:HD2	2.12	0.49
1:O:21:ASP:C	1:O:21:ASP:OD1	2.50	0.49
1:O:47:ASN:HD22	1:O:49:GLU:N	2.11	0.49
1:Y:378:ALA:HB1	1:Y:416:ILE:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:32:TYR:CE2	1:Y:57:ARG:NH1	2.81	0.49
1:O:352:PHE:CD2	1:O:489:LYS:HD3	2.49	0.48
1:Y:404:THR:O	1:Y:423:ARG:NH1	2.45	0.48
1:Y:85:THR:HG23	1:Y:159:PHE:HE1	1.77	0.48
1:O:47:ASN:ND2	1:O:47:ASN:C	2.67	0.48
1:O:133:PHE:HD2	1:O:185:MET:CE	2.25	0.48
1:O:202:PHE:HB2	1:O:204:ILE:HD12	1.95	0.48
1:Y:186:LEU:HD11	1:Y:204:ILE:HD13	1.96	0.48
1:Y:378:ALA:HA	1:Y:413:GLN:NE2	2.29	0.48
1:Y:387:GLU:HA	1:Y:390:LYS:HD3	1.96	0.48
1:Y:79:THR:HG21	1:Y:242:ALA:HB3	1.96	0.47
1:O:24:SER:HB2	1:O:432:LEU:HD21	1.96	0.47
1:Y:255:VAL:HG21	1:Y:394:ILE:HG23	1.96	0.47
1:Y:85:THR:HG23	1:Y:159:PHE:CE1	2.48	0.47
1:Y:116:GLU:HB2	1:Y:117:TYR:CD2	2.50	0.47
1:Y:125:THR:HG23	1:Y:127:LEU:CG	2.45	0.47
1:Y:129:PRO:HA	1:Y:185:MET:HE1	1.97	0.47
1:Y:217:GLU:O	1:Y:234:SER:HA	2.14	0.47
1:Y:122:LYS:HG2	1:Y:127:LEU:O	2.15	0.47
1:Y:412:PHE:O	1:Y:416:ILE:HG13	2.15	0.47
1:O:270:ASP:CB	1:O:292:SER:OG	2.60	0.47
1:Y:2:GLU:HG3	1:Y:4:PHE:CZ	2.50	0.47
1:O:47:ASN:ND2	1:O:49:GLU:N	2.62	0.46
1:Y:466:ASP:OD1	1:Y:468:LYS:HE3	2.15	0.46
1:Y:81:GLN:O	1:Y:81:GLN:HG3	2.16	0.46
1:O:47:ASN:HD22	1:O:49:GLU:H	1.64	0.46
1:Y:162:VAL:O	1:Y:166:LEU:HG	2.15	0.46
1:Y:324:GLU:CD	1:Y:324:GLU:H	2.18	0.46
1:Y:99:ILE:HD13	1:Y:105:ARG:CZ	2.45	0.46
1:Y:256:LYS:C	1:Y:256:LYS:HD2	2.36	0.46
1:O:357:ILE:O	1:Y:356:ILE:HA	2.15	0.46
1:O:251:GLU:O	1:O:254:MET:HB2	2.16	0.46
1:Y:265:ILE:C	1:Y:266:LEU:HD12	2.36	0.46
1:Y:416:ILE:H	1:Y:416:ILE:HG13	1.58	0.46
1:Y:46:HIS:HB2	1:Y:98:ALA:HB3	1.98	0.46
1:Y:439:GLY:O	1:Y:440:LEU:C	2.46	0.45
1:O:465:MET:O	1:O:470:ARG:NH1	2.46	0.45
1:O:131:ALA:H	1:O:351:GLN:NE2	2.15	0.45
1:O:159:PHE:CB	1:O:208:VAL:HG13	2.46	0.45
1:O:183:ARG:HA	1:O:183:ARG:HD3	1.72	0.45
1:O:329:LEU:HD12	1:O:371:ARG:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:87:VAL:HA	1:Y:158:MET:O	2.16	0.45
1:O:186:LEU:CD2	1:O:204:ILE:HD13	2.45	0.45
1:O:426:VAL:HG23	2:O:515:HOH:O	2.17	0.45
1:Y:89:ASP:O	1:Y:92:GLY:N	2.43	0.45
1:Y:22:ARG:HB2	1:Y:22:ARG:HE	1.41	0.44
1:Y:451:ILE:HA	1:Y:454:LEU:HD22	1.99	0.44
1:O:474:TYR:CD2	1:O:478:LYS:HD2	2.52	0.44
1:O:223:LYS:H	1:O:223:LYS:HG2	1.54	0.44
1:Y:129:PRO:HA	1:Y:185:MET:CE	2.47	0.44
1:Y:79:THR:CG2	1:Y:237:ALA:O	2.65	0.44
1:Y:388:MET:CB	1:Y:394:ILE:HD11	2.46	0.44
1:Y:121:ILE:HG21	1:Y:185:MET:HE1	1.98	0.44
1:Y:183:ARG:NH2	1:Y:282:THR:CG2	2.65	0.44
1:Y:139:LYS:HG3	1:Y:202:PHE:O	2.17	0.44
1:Y:14:SER:HA	1:Y:33:GLU:HA	2.00	0.44
1:O:317:LYS:HB2	1:O:321:GLU:OE2	2.18	0.43
1:O:483:ARG:O	1:Y:483:ARG:NH1	2.49	0.43
1:Y:167:ILE:O	1:Y:171:THR:HB	2.18	0.43
1:Y:249:ALA:HB1	1:Y:254:MET:HB2	2.00	0.43
1:O:371:ARG:O	1:O:375:GLU:HG3	2.18	0.43
1:Y:80:ASN:ND2	1:Y:163:ASP:HB3	2.32	0.43
1:Y:36:GLN:OE1	1:Y:46:HIS:HE1	2.02	0.43
1:O:466:ASP:N	1:O:466:ASP:OD1	2.49	0.43
1:O:81:GLN:NE2	1:O:84:THR:OG1	2.51	0.43
1:O:86:LEU:CD1	1:O:86:LEU:N	2.82	0.43
1:Y:145:VAL:HA	1:Y:146:PRO:HD3	1.74	0.43
1:Y:121:ILE:HG21	1:Y:185:MET:CE	2.48	0.43
1:Y:93:LYS:HE2	1:Y:93:LYS:HB3	1.64	0.43
1:O:188:ASN:HD22	1:O:191:LYS:H	1.62	0.43
1:O:456:LYS:N	2:O:561:HOH:O	2.08	0.43
1:O:74:ALA:O	1:O:232:PRO:HG2	2.19	0.43
1:Y:266:LEU:HD12	1:Y:266:LEU:N	2.34	0.43
1:Y:159:PHE:CB	1:Y:208:VAL:CG1	2.84	0.43
1:O:195:ASP:HB3	1:O:198:LEU:HD22	2.00	0.42
1:O:231:ILE:HG23	1:O:232:PRO:HD2	2.00	0.42
1:O:99:ILE:HD11	1:O:141:LEU:HD13	2.02	0.42
1:O:373:THR:O	1:O:377:ILE:HG13	2.19	0.42
1:Y:490:VAL:HG22	1:Y:490:VAL:O	2.19	0.42
1:O:109:MET:HE2	1:O:113:ILE:CD1	2.45	0.42
1:Y:52:TRP:HH2	1:Y:170:LEU:HD13	1.85	0.42
1:Y:34:PHE:HA	1:Y:35:PRO:HD3	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:249:ALA:HA	1:O:254:MET:HE2	2.00	0.42
1:Y:338:VAL:O	1:Y:355:GLY:HA2	2.20	0.42
1:Y:447:ASP:CB	1:Y:450:GLU:H	2.33	0.42
1:Y:380:LEU:HD13	1:Y:477:TRP:HZ2	1.84	0.42
1:O:131:ALA:H	1:O:351:GLN:HE22	1.68	0.42
1:O:75:ALA:HB2	1:O:442:VAL:HG21	2.02	0.42
1:O:376:ALA:O	1:O:380:LEU:HD22	2.19	0.42
1:O:459:ARG:HD3	1:O:459:ARG:HH11	1.68	0.42
1:O:270:ASP:OD1	1:O:292:SER:OG	2.38	0.41
1:O:427:LYS:HA	1:O:427:LYS:HD3	1.67	0.41
1:O:114:LYS:HG3	1:O:129:PRO:HB2	2.02	0.41
1:Y:474:TYR:O	1:Y:478:LYS:HG3	2.20	0.41
1:Y:179:SER:CB	1:Y:241:GLN:HG3	2.50	0.41
1:Y:376:ALA:O	1:Y:380:LEU:HD22	2.19	0.41
1:O:34:PHE:HA	1:O:35:PRO:HD3	1.85	0.41
1:O:356:ILE:HG22	1:Y:358:ILE:CG1	2.48	0.41
1:Y:188:ASN:HD22	1:Y:190:LYS:N	2.15	0.41
1:Y:79:THR:HG21	1:Y:242:ALA:CB	2.51	0.41
1:O:242:ALA:O	1:O:433:GLY:HA3	2.21	0.41
1:O:48:PRO:HD3	1:O:97:ASN:HA	2.03	0.41
1:O:202:PHE:HB2	1:O:204:ILE:CD1	2.50	0.41
1:O:374:LEU:HD23	1:O:374:LEU:HA	1.85	0.41
1:Y:43:TRP:CE2	1:Y:105:ARG:HB2	2.55	0.41
1:Y:317:LYS:HB2	1:Y:317:LYS:HE2	1.88	0.40
1:O:261:THR:HG23	1:O:304:ALA:HB2	2.03	0.40
1:O:346:ALA:HA	1:O:347:PRO:HA	1.81	0.40
1:O:340:ALA:O	1:O:341:PHE:C	2.60	0.40
1:Y:183:ARG:NH2	1:Y:296:GLU:OE1	2.55	0.40
1:Y:447:ASP:HB3	1:Y:450:GLU:H	1.86	0.40
1:O:268:ASN:OD1	1:O:270:ASP:HB3	2.21	0.40
1:O:36:GLN:OE1	1:O:46:HIS:CE1	2.70	0.40
1:Y:134:SER:O	1:Y:135:ALA:C	2.59	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	492/497 (99%)	460 (94%)	31 (6%)	1 (0%)	51	67
1	Y	492/497 (99%)	463 (94%)	26 (5%)	3 (1%)	28	41
All	All	984/994 (99%)	923 (94%)	57 (6%)	4 (0%)	38	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Y	490	VAL
1	Y	114	LYS
1	Y	111	GLU
1	O	169	ARG

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	O	406/409 (99%)	356 (88%)	50 (12%)	5	7
1	Y	406/409 (99%)	348 (86%)	58 (14%)	4	4
All	All	812/818 (99%)	704 (87%)	108 (13%)	4	5

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	1	MET
1	O	10	GLU
1	O	16	ARG
1	O	47	ASN
1	O	53	ASP
1	O	56	LEU
1	O	57	ARG
1	O	64	GLN

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Mol	Chain	Res	Type
1	O	67	ARG
1	O	81	GLN
1	O	91	ASP
1	O	109	MET
1	O	112	GLU
1	O	119	THR
1	O	120	MET
1	O	122	LYS
1	O	123	GLU
1	O	125	THR
1	O	127	LEU
1	O	138	LEU
1	O	141	LEU
1	O	148	LEU
1	O	177	ASP
1	O	188	ASN
1	O	198	LEU
1	O	199	LEU
1	O	201	LEU
1	O	208	VAL
1	O	241	GLN
1	O	256	LYS
1	O	270	ASP
1	O	290	ARG
1	O	317	LYS
1	O	342	VAL
1	O	380	LEU
1	O	391	LEU
1	O	395	LYS
1	O	417	LEU
1	O	418	ASN
1	O	423	ARG
1	O	424	PRO
1	O	429	THR
1	O	432	LEU
1	O	437	LEU
1	O	440	LEU
1	O	453	GLU
1	O	462	GLU
1	O	464	LYS
1	O	468	LYS
1	O	490	VAL

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Mol	Chain	Res	Type
1	Y	2	GLU
1	Y	7	SER
1	Y	8	LEU
1	Y	10	GLU
1	Y	14	SER
1	Y	22	ARG
1	Y	26	ILE
1	Y	29	ILE
1	Y	31	GLN
1	Y	47	ASN
1	Y	53	ASP
1	Y	64	GLN
1	Y	67	ARG
1	Y	79	THR
1	Y	93	LYS
1	Y	99	ILE
1	Y	105	ARG
1	Y	112	GLU
1	Y	119	THR
1	Y	120	MET
1	Y	122	LYS
1	Y	125	THR
1	Y	138	LEU
1	Y	170	LEU
1	Y	171	THR
1	Y	188	ASN
1	Y	198	LEU
1	Y	199	LEU
1	Y	207	SER
1	Y	208	VAL
1	Y	223	LYS
1	Y	226	LEU
1	Y	227	LEU
1	Y	241	GLN
1	Y	256	LYS
1	Y	267	VAL
1	Y	330	GLU
1	Y	362	ARG
1	Y	380	LEU
1	Y	391	LEU
1	Y	398	ARG
1	Y	399	VAL

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Mol	Chain	Res	Type
1	Y	416	ILE
1	Y	417	LEU
1	Y	429	THR
1	Y	432	LEU
1	Y	437	LEU
1	Y	440	LEU
1	Y	442	VAL
1	Y	443	ASP
1	Y	453	GLU
1	Y	454	LEU
1	Y	464	LYS
1	Y	468	LYS
1	Y	485	MET
1	Y	491	VAL
1	Y	492	ASP
1	Y	493	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	O	37	HIS
1	O	46	HIS
1	O	47	ASN
1	O	55	GLN
1	O	64	GLN
1	O	72	GLN
1	O	80	ASN
1	O	81	GLN
1	O	144	ASN
1	O	174	HIS
1	O	180	ASN
1	O	188	ASN
1	O	307	GLN
1	O	351	GLN
1	O	413	GLN
1	O	418	ASN
1	Y	31	GLN
1	Y	37	HIS
1	Y	46	HIS
1	Y	47	ASN
1	Y	55	GLN
1	Y	72	GLN

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Mol	Chain	Res	Type
1	Y	80	ASN
1	Y	174	HIS
1	Y	180	ASN
1	Y	188	ASN
1	Y	278	ASN
1	Y	351	GLN
1	Y	413	GLN
1	Y	418	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	O	494/497 (99%)	-0.43	5 (1%) 82 80	24, 43, 68, 98	0
1	Y	494/497 (99%)	-0.35	4 (0%) 86 84	25, 46, 69, 99	0
All	All	988/994 (99%)	-0.39	9 (0%) 84 82	24, 45, 68, 99	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	493	SER	6.7
1	Y	493	SER	4.9
1	Y	492	ASP	3.8
1	O	494	ALA	3.0
1	O	491	VAL	2.8
1	Y	494	ALA	2.7
1	O	492	ASP	2.6
1	Y	320	SER	2.3
1	O	1	MET	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.