



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:41 AM UTC

PDB ID : 1XI8 / pdb_00001xi8
Title : Molybdenum cofactor biosynthesis protein from *Pyrococcus furiosus* Pfu-1657500-001
Authors : Zhou, W.; Zhao, M.; Chang, J.C.; Liu, Z.-J.; Chen, L.; Horanyi, P.; Xu, H.; Yang, H.; Habel, J.E.; Lee, D.; Chang, S.-H.; Rose, J.P.; Wang, B.-C.; Southeast Collaboratory for Structural Genomics (SECSG)
Deposited on : 2004-09-21
Resolution : 2.50 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
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

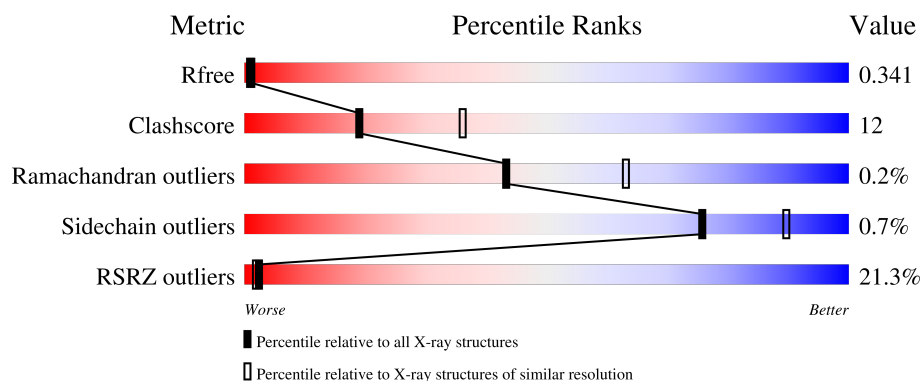
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	403	
1	B	403	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4034 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 Molybdenum cofactor biosynthesis protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2027	1321	321	381	4			
1	B	265	Total	C	N	O	S	0	0	0
			2007	1301	326	376	4			

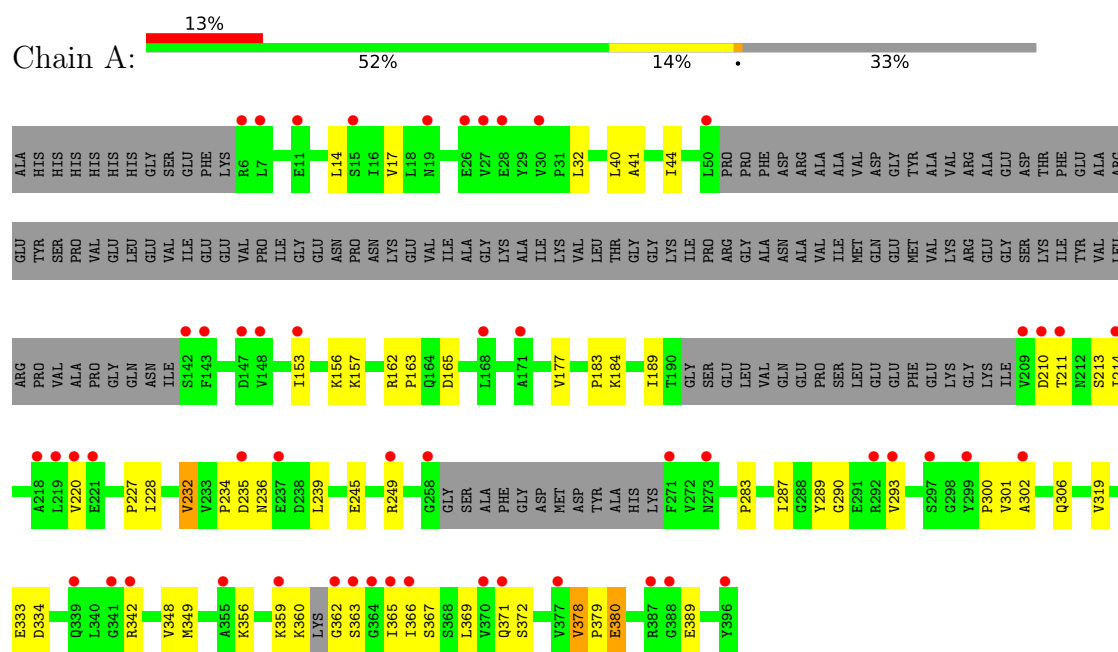
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ALA	-	expression tag	UNP Q8U034
A	-5	HIS	-	expression tag	UNP Q8U034
A	-4	HIS	-	expression tag	UNP Q8U034
A	-3	HIS	-	expression tag	UNP Q8U034
A	-2	HIS	-	expression tag	UNP Q8U034
A	-1	HIS	-	expression tag	UNP Q8U034
A	0	HIS	-	expression tag	UNP Q8U034
A	1	GLY	-	expression tag	UNP Q8U034
A	2	SER	-	expression tag	UNP Q8U034
B	-6	ALA	-	expression tag	UNP Q8U034
B	-5	HIS	-	expression tag	UNP Q8U034
B	-4	HIS	-	expression tag	UNP Q8U034
B	-3	HIS	-	expression tag	UNP Q8U034
B	-2	HIS	-	expression tag	UNP Q8U034
B	-1	HIS	-	expression tag	UNP Q8U034
B	0	HIS	-	expression tag	UNP Q8U034
B	1	GLY	-	expression tag	UNP Q8U034
B	2	SER	-	expression tag	UNP Q8U034

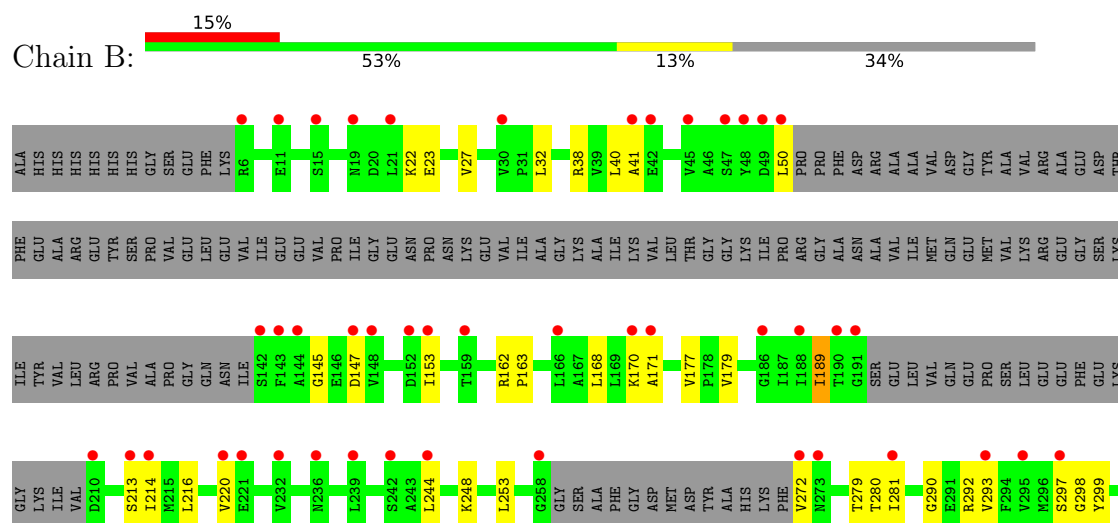
3 Residue-property plots

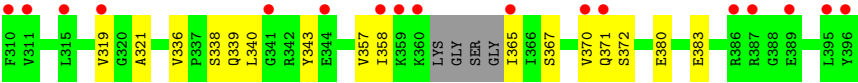
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: Molybdenum cofactor biosynthesis protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.55Å 116.60Å 147.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.95 – 2.50 42.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.2 (42.95-2.50) 96.1 (42.95-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.65 (at 2.51Å)	Xtriage
Refinement program	REFMAC refmac_5.2.0005	Depositor
R, R_{free}	0.306 , 0.343 0.304 , 0.341	Depositor DCC
R_{free} test set	1875 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	55.5	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 20.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4034	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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](#)

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	0.58	0/2061	0.89	2/2804 (0.1%)
1	B	0.58	0/2039	0.90	4/2772 (0.1%)
All	All	0.58	0/4100	0.90	6/5576 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	145	GLY	N-CA-C	-7.71	104.07	115.72
1	A	378	VAL	CA-C-N	7.09	128.71	119.84
1	A	378	VAL	C-N-CA	7.09	128.71	119.84
1	B	299	TYR	CA-C-N	6.45	125.94	119.24
1	B	299	TYR	C-N-CA	6.45	125.94	119.24
1	B	189	ILE	N-CA-C	5.72	116.23	107.77

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	A	2027	0	2017	64	0
1	B	2007	0	2003	40	0
All	All	4034	0	4020	95	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 12.

All (95) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:ILE:HG21	1:A:210:ASP:OD2	1.59	1.00
1:A:302:ALA:HB2	1:A:362:GLY:HA3	1.56	0.85
1:A:301:VAL:HG11	1:A:363:SER:HB3	1.59	0.84
1:B:358:ILE:HD11	1:B:371:GLN:O	1.82	0.80
1:A:379:PRO:O	1:A:380:GLU:HG2	1.82	0.78
1:A:301:VAL:HG23	1:A:369:LEU:HD21	1.66	0.77
1:B:367:SER:HA	1:B:370:VAL:HG12	1.67	0.77
1:A:302:ALA:HB2	1:A:362:GLY:CA	2.15	0.76
1:A:189:ILE:CD1	1:A:213:SER:HB2	2.18	0.72
1:A:234:PRO:HG2	1:A:239:LEU:CD1	2.20	0.72
1:B:279:THR:HG23	1:B:281:ILE:H	1.55	0.71
1:A:283:PRO:HB2	1:A:362:GLY:HA2	1.72	0.71
1:A:234:PRO:HG2	1:A:239:LEU:HD12	1.75	0.68
1:A:300:PRO:CB	1:A:366:ILE:HG22	2.24	0.67
1:A:366:ILE:HD11	1:B:168:LEU:HA	1.78	0.65
1:A:301:VAL:HG12	1:A:363:SER:H	1.62	0.64
1:A:234:PRO:C	1:A:236:ASN:H	2.06	0.63
1:B:358:ILE:HD12	1:B:372:SER:HB3	1.83	0.61
1:B:367:SER:HA	1:B:370:VAL:CG1	2.31	0.59
1:B:50:LEU:HB2	1:B:147:ASP:HB3	1.84	0.59
1:A:189:ILE:HD13	1:A:210:ASP:OD2	2.02	0.59
1:A:189:ILE:HD11	1:A:213:SER:HB2	1.85	0.58
1:B:216:LEU:O	1:B:220:VAL:HG12	2.04	0.57
1:A:283:PRO:CB	1:A:362:GLY:HA2	2.35	0.57
1:A:287:ILE:HB	1:A:306:GLN:NE2	2.19	0.57
1:A:14:LEU:O	1:A:17:VAL:HG22	2.05	0.57
1:A:333:GLU:OE2	1:A:356:LYS:HB2	2.05	0.56
1:A:349:MET:HE2	1:A:371:GLN:O	2.04	0.56
1:A:301:VAL:HG12	1:A:363:SER:N	2.20	0.56
1:A:32:LEU:HD23	1:A:177:VAL:CG2	2.36	0.56
1:B:189:ILE:HD12	1:B:213:SER:HB2	1.87	0.56
1:A:300:PRO:HB2	1:A:366:ILE:HG22	1.86	0.55
1:B:272:VAL:HG11	1:B:293:VAL:HG11	1.89	0.55
1:A:32:LEU:HB3	1:B:214:ILE:CD1	2.36	0.55
1:A:153:ILE:O	1:A:153:ILE:HG13	2.07	0.55
1:A:153:ILE:HD12	1:A:156:LYS:HG2	1.90	0.53
1:A:300:PRO:HB3	1:A:366:ILE:HG22	1.90	0.53
1:B:244:LEU:O	1:B:248:LYS:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:ARG:HD3	1:B:179:VAL:HG21	1.91	0.53
1:A:366:ILE:CD1	1:B:168:LEU:HA	2.40	0.52
1:A:333:GLU:OE2	1:A:356:LYS:HD3	2.09	0.52
1:A:220:VAL:HG11	1:A:227:PRO:HB3	1.92	0.52
1:A:234:PRO:HG2	1:A:239:LEU:HD13	1.91	0.51
1:A:334:ASP:OD2	1:A:356:LYS:HD2	2.11	0.51
1:B:162:ARG:HB3	1:B:163:PRO:HD2	1.93	0.50
1:A:245:GLU:O	1:A:249:ARG:HG3	2.13	0.49
1:A:189:ILE:O	1:A:232:VAL:HA	2.12	0.49
1:B:336:VAL:HG22	1:B:357:VAL:HG21	1.93	0.49
1:A:359:LYS:O	1:A:360:LYS:CB	2.61	0.49
1:B:27:VAL:HG12	1:B:41:ALA:HB1	1.94	0.49
1:B:253:LEU:HD12	1:B:292:ARG:O	2.12	0.49
1:A:287:ILE:HD12	1:A:306:GLN:HB3	1.95	0.47
1:B:338:SER:HB3	1:B:383:GLU:O	2.13	0.47
1:B:297:SER:OG	1:B:298:GLY:N	2.46	0.47
1:A:234:PRO:C	1:A:236:ASN:N	2.73	0.46
1:B:153:ILE:O	1:B:153:ILE:HG13	2.15	0.46
1:A:342:ARG:HG3	1:A:342:ARG:HH11	1.79	0.46
1:A:234:PRO:CG	1:A:239:LEU:CD1	2.94	0.46
1:A:342:ARG:HG3	1:A:342:ARG:NH1	2.30	0.45
1:A:301:VAL:HG12	1:A:363:SER:O	2.16	0.45
1:A:378:VAL:HA	1:A:379:PRO:HD3	1.65	0.45
1:B:162:ARG:HB3	1:B:163:PRO:CD	2.47	0.45
1:B:365:ILE:HG22	1:B:365:ILE:O	2.16	0.45
1:B:290:GLY:O	1:B:293:VAL:HG12	2.17	0.45
1:A:162:ARG:HB3	1:A:163:PRO:HD2	1.98	0.45
1:A:32:LEU:HD23	1:A:177:VAL:HG21	1.99	0.44
1:A:214:ILE:CD1	1:B:170:LYS:HB2	2.48	0.44
1:A:365:ILE:HG23	1:B:147:ASP:HA	2.00	0.44
1:A:165:ASP:OD2	1:B:370:VAL:HG23	2.17	0.44
1:B:32:LEU:HD23	1:B:177:VAL:CG2	2.48	0.44
1:B:280:THR:OG1	1:B:380:GLU:OE2	2.30	0.44
1:A:32:LEU:HB3	1:B:214:ILE:HD13	2.00	0.43
1:B:339:GLN:HG2	1:B:340:LEU:O	2.19	0.43
1:A:301:VAL:CG1	1:A:363:SER:N	2.81	0.43
1:A:40:LEU:HD11	1:A:44:ILE:HD12	2.01	0.43
1:A:183:PRO:HD3	1:A:319:VAL:HG12	2.00	0.42
1:B:281:ILE:HA	1:B:343:TYR:O	2.20	0.42
1:A:289:TYR:CG	1:A:290:GLY:N	2.88	0.42
1:A:162:ARG:HB3	1:A:163:PRO:CD	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:VAL:HG23	1:B:321:ALA:H	1.84	0.42
1:A:184:LYS:HB3	1:A:228:ILE:HD12	2.02	0.42
1:A:211:THR:HG21	1:B:171:ALA:HB2	2.01	0.42
1:B:22:LYS:O	1:B:23:GLU:C	2.63	0.42
1:A:367:SER:HB3	1:B:147:ASP:OD1	2.21	0.41
1:B:40:LEU:HD12	1:B:40:LEU:HA	1.78	0.41
1:A:41:ALA:C	1:A:157:LYS:HG3	2.45	0.41
1:B:358:ILE:HD11	1:B:371:GLN:C	2.43	0.41
1:B:290:GLY:O	1:B:293:VAL:CG1	2.68	0.41
1:A:234:PRO:CG	1:A:239:LEU:HD13	2.51	0.41
1:A:348:VAL:O	1:A:372:SER:HB2	2.20	0.41
1:B:358:ILE:CD1	1:B:371:GLN:C	2.94	0.41
1:A:220:VAL:CG1	1:A:227:PRO:HB3	2.51	0.40
1:A:301:VAL:CG1	1:A:363:SER:HB3	2.40	0.40
1:A:290:GLY:O	1:A:293:VAL:HG12	2.21	0.40
1:A:234:PRO:O	1:A:236:ASN:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	259/403 (64%)	242 (93%)	16 (6%)	1 (0%)	30	49
1	B	255/403 (63%)	240 (94%)	15 (6%)	0	100	100
All	All	514/806 (64%)	482 (94%)	31 (6%)	1 (0%)	43	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	235	ASP

5.3.2 Protein sidechains [i](#)

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	211/338 (62%)	208 (99%)	3 (1%)	59	81
1	B	209/338 (62%)	209 (100%)	0	100	100
All	All	420/676 (62%)	417 (99%)	3 (1%)	76	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	232	VAL
1	A	380	GLU
1	A	389	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 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	269/403 (66%)	1.42	52 (19%) 3 2	55, 55, 55, 55	0
1	B	265/403 (65%)	1.49	62 (23%) 2 1	55, 55, 55, 55	0
All	All	534/806 (66%)	1.46	114 (21%) 2 2	55, 55, 55, 55	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	143	PHE	6.2
1	A	235	ASP	6.1
1	A	362	GLY	5.6
1	A	364	GLY	5.0
1	A	148	VAL	4.6
1	A	341	GLY	4.6
1	A	209	VAL	4.5
1	A	214	ILE	4.4
1	B	50	LEU	4.3
1	A	6	ARG	4.2
1	B	273	ASN	4.2
1	A	143	PHE	4.1
1	A	363	SER	4.1
1	A	210	ASP	4.0
1	A	142	SER	4.0
1	B	144	ALA	3.9
1	B	171	ALA	3.8
1	B	272	VAL	3.7
1	B	191	GLY	3.7
1	A	50	LEU	3.7
1	B	310	PHE	3.6
1	B	371	GLN	3.6
1	B	42	GLU	3.6
1	B	359	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	388	GLY	3.5
1	B	344	GLU	3.4
1	B	295	VAL	3.4
1	B	370	VAL	3.3
1	A	258	GLY	3.3
1	A	342	ARG	3.3
1	B	41	ALA	3.3
1	A	366	ILE	3.3
1	A	271	PHE	3.2
1	A	153	ILE	3.2
1	A	220	VAL	3.1
1	B	387	ARG	3.1
1	A	396	TYR	3.0
1	A	339	GLN	3.0
1	B	242	SER	3.0
1	A	365	ILE	2.9
1	B	15	SER	2.9
1	B	188	ILE	2.9
1	A	26	GLU	2.9
1	A	359	LYS	2.8
1	B	170	LYS	2.8
1	B	220	VAL	2.8
1	B	186	GLY	2.8
1	B	365	ILE	2.8
1	B	30	VAL	2.8
1	B	214	ILE	2.7
1	B	281	ILE	2.7
1	B	147	ASP	2.7
1	A	292	ARG	2.7
1	B	152	ASP	2.6
1	B	239	LEU	2.6
1	A	168	LEU	2.5
1	B	159	THR	2.5
1	B	153	ILE	2.5
1	B	232	VAL	2.5
1	B	213	SER	2.5
1	A	171	ALA	2.5
1	B	142	SER	2.5
1	A	237	GLU	2.5
1	A	219	LEU	2.5
1	B	244	LEU	2.5
1	A	27	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	311	VAL	2.5
1	A	11	GLU	2.4
1	B	210	ASP	2.4
1	B	360	LYS	2.4
1	A	147	ASP	2.3
1	A	377	VAL	2.3
1	A	273	ASN	2.3
1	A	387	ARG	2.3
1	B	358	ILE	2.3
1	B	45	VAL	2.3
1	A	371	GLN	2.3
1	B	395	LEU	2.3
1	B	48	TYR	2.3
1	B	190	THR	2.3
1	B	258	GLY	2.3
1	B	389	GLU	2.3
1	B	319	VAL	2.3
1	A	19	ASN	2.2
1	A	218	ALA	2.2
1	B	221	GLU	2.2
1	B	293	VAL	2.2
1	A	7	LEU	2.2
1	A	297	SER	2.2
1	A	249	ARG	2.2
1	B	148	VAL	2.2
1	B	396	TYR	2.2
1	A	15	SER	2.2
1	B	236	ASN	2.2
1	A	211	THR	2.2
1	B	297	SER	2.2
1	B	11	GLU	2.2
1	B	6	ARG	2.1
1	A	370	VAL	2.1
1	A	299	TYR	2.1
1	B	166	LEU	2.1
1	B	315	LEU	2.1
1	B	49	ASP	2.1
1	A	293	VAL	2.1
1	B	21	LEU	2.1
1	B	341	GLY	2.1
1	A	28	GLU	2.1
1	A	30	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	302	ALA	2.0
1	B	19	ASN	2.0
1	B	386	ARG	2.0
1	A	355	ALA	2.0
1	A	221	GLU	2.0
1	B	47	SER	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.