



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:54 AM UTC

PDB ID : 1ZEE / pdb_00001zee
Title : X-Ray Crystal Structure of Protein SO4414 from *Shewanella oneidensis*.
Northeast Structural Genomics Consortium Target SoR52.
Authors : Forouhar, F.; Abashidze, M.; Vorobiev, S.M.; Conover, K.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2005-04-18
Resolution : 2.31 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

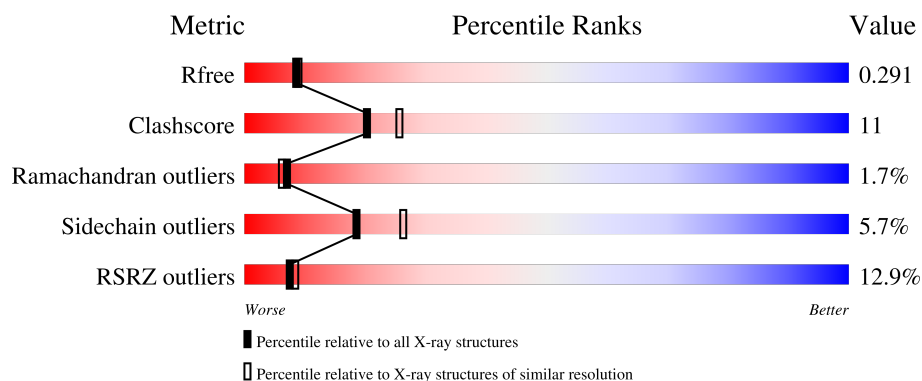
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	13% 62% 26% 10%
1	B	403	10% 67% 20% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6215 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 hypothetical protein SO4414.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	Se	0	0	0
			2953	1863	523	554	6	7			
1	B	363	Total	C	N	O	S	Se	0	0	0
			2953	1863	523	554	6	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q8E972
A	85	MSE	MET	modified residue	UNP Q8E972
A	112	MSE	MET	modified residue	UNP Q8E972
A	262	MSE	MET	modified residue	UNP Q8E972
A	270	MSE	MET	modified residue	UNP Q8E972
A	271	MSE	MET	modified residue	UNP Q8E972
A	282	MSE	MET	modified residue	UNP Q8E972
A	288	MSE	MET	modified residue	UNP Q8E972
A	340	MSE	MET	modified residue	UNP Q8E972
A	393	LEU	-	cloning artifact	UNP Q8E972
A	394	GLU	-	cloning artifact	UNP Q8E972
A	395	ALA	-	cloning artifact	UNP Q8E972
A	396	ALA	-	cloning artifact	UNP Q8E972
A	397	ALA	-	cloning artifact	UNP Q8E972
A	398	HIS	-	expression tag	UNP Q8E972
A	399	HIS	-	expression tag	UNP Q8E972
A	400	HIS	-	expression tag	UNP Q8E972
A	401	HIS	-	expression tag	UNP Q8E972
A	402	HIS	-	expression tag	UNP Q8E972
A	403	HIS	-	expression tag	UNP Q8E972
B	1	MSE	MET	modified residue	UNP Q8E972
B	85	MSE	MET	modified residue	UNP Q8E972
B	112	MSE	MET	modified residue	UNP Q8E972
B	262	MSE	MET	modified residue	UNP Q8E972
B	270	MSE	MET	modified residue	UNP Q8E972

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Chain	Residue	Modelled	Actual	Comment	Reference
B	271	MSE	MET	modified residue	UNP Q8E972
B	282	MSE	MET	modified residue	UNP Q8E972
B	288	MSE	MET	modified residue	UNP Q8E972
B	340	MSE	MET	modified residue	UNP Q8E972
B	393	LEU	-	cloning artifact	UNP Q8E972
B	394	GLU	-	cloning artifact	UNP Q8E972
B	395	ALA	-	cloning artifact	UNP Q8E972
B	396	ALA	-	cloning artifact	UNP Q8E972
B	397	ALA	-	cloning artifact	UNP Q8E972
B	398	HIS	-	expression tag	UNP Q8E972
B	399	HIS	-	expression tag	UNP Q8E972
B	400	HIS	-	expression tag	UNP Q8E972
B	401	HIS	-	expression tag	UNP Q8E972
B	402	HIS	-	expression tag	UNP Q8E972
B	403	HIS	-	expression tag	UNP Q8E972

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	164	Total O 164 164	0	0
2	B	145	Total O 145 145	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	138.08Å 68.02Å 90.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.50 – 2.31 27.50 – 2.31	Depositor EDS
% Data completeness (in resolution range)	87.1 (27.50-2.31) 93.1 (27.50-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.57 (at 2.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.234 , 0.275 0.252 , 0.291	Depositor DCC
R_{free} test set	6936 reflections (9.90%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6215	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.45 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3632e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.42	0/3003	0.80	4/4047 (0.1%)
1	B	0.44	0/3003	0.80	3/4047 (0.1%)
All	All	0.43	0/6006	0.80	7/8094 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	93	ILE	N-CA-C	-6.80	104.16	113.00
1	A	93	ILE	N-CA-C	-6.59	104.43	113.00
1	A	100	THR	N-CA-C	-6.05	106.51	114.31
1	B	100	THR	N-CA-C	-5.86	106.47	113.97
1	A	149	GLU	N-CA-C	-5.46	105.41	111.36
1	A	156	ASN	N-CA-C	-5.10	105.63	111.14
1	B	149	GLU	N-CA-C	-5.03	105.88	111.36

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	2953	0	2908	71	0
1	B	2953	0	2908	61	0
2	A	164	0	0	8	0
2	B	145	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6215	0	5816	132	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 11.

All (132) 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:B:180:HIS:HD2	1:B:182:ILE:H	1.26	0.83
1:A:180:HIS:HD2	1:A:182:ILE:H	1.26	0.81
1:B:33:GLN:HG3	1:B:36:ARG:H	1.44	0.80
1:A:33:GLN:HG3	1:A:36:ARG:H	1.45	0.80
1:A:359:LEU:O	1:A:363:GLU:HG3	1.87	0.75
1:A:368:ARG:HH11	1:A:368:ARG:HG3	1.53	0.73
1:A:95:GLU:HB3	1:A:98:ARG:HB3	1.75	0.68
1:B:108:SER:HB3	1:B:112:MSE:CE	2.24	0.67
1:A:372:VAL:O	1:A:379:THR:HG21	1.96	0.66
1:B:95:GLU:HB3	1:B:98:ARG:HB3	1.77	0.66
1:A:108:SER:HB3	1:A:112:MSE:CE	2.26	0.65
1:B:106:GLU:HG2	2:B:505:HOH:O	1.96	0.65
1:B:218:ARG:HB3	1:B:218:ARG:NH1	2.12	0.65
1:B:246:ASP:OD1	1:B:317:HIS:HE1	1.81	0.64
1:A:298:ILE:HD13	1:A:390:SER:HB3	1.80	0.64
1:A:218:ARG:HB3	1:A:218:ARG:NH1	2.13	0.64
1:B:108:SER:HB3	1:B:112:MSE:HE2	1.78	0.63
1:A:246:ASP:OD1	1:A:317:HIS:HE1	1.81	0.63
1:A:178:ILE:HD13	1:A:290:ASP:HB3	1.80	0.62
1:B:178:ILE:HD13	1:B:290:ASP:HB3	1.81	0.62
1:B:301:ASP:HB2	2:B:486:HOH:O	1.98	0.62
1:A:108:SER:HB3	1:A:112:MSE:HE2	1.83	0.59
1:B:361:SER:HA	1:B:364:ARG:HE	1.66	0.59
1:A:240:ALA:HB2	1:A:274:ASP:HB3	1.84	0.59
1:A:368:ARG:HG3	1:A:368:ARG:NH1	2.16	0.59
1:B:218:ARG:N	1:B:219:PRO:HD2	2.18	0.59
1:B:64:GLU:HG3	2:B:435:HOH:O	2.02	0.59
1:A:303:TYR:O	1:A:307:LEU:HB2	2.02	0.59
1:A:218:ARG:N	1:A:219:PRO:HD2	2.18	0.58
1:A:329:VAL:HG11	1:A:362:LEU:HD23	1.86	0.58
1:B:292:LEU:HD23	1:B:387:LEU:HD21	1.84	0.58
1:B:298:ILE:HD11	1:B:390:SER:O	2.03	0.58
1:A:42:VAL:HG13	1:A:43:GLY:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:303:TYR:O	1:B:307:LEU:HB2	2.04	0.57
1:B:240:ALA:HB2	1:B:274:ASP:HB3	1.86	0.57
1:A:279:ARG:NH2	2:A:549:HOH:O	2.31	0.57
1:B:42:VAL:HG13	1:B:43:GLY:H	1.67	0.57
1:B:218:ARG:HB3	1:B:218:ARG:HH11	1.70	0.56
1:A:296:GLY:HA3	2:A:439:HOH:O	2.06	0.56
1:A:191:LYS:O	1:A:195:GLN:HG3	2.06	0.55
1:A:318:GLY:HA3	1:A:370:ALA:HA	1.89	0.55
1:B:312:GLU:O	1:B:316:LEU:HB2	2.06	0.54
1:A:312:GLU:O	1:A:316:LEU:HB2	2.07	0.54
1:A:218:ARG:HB3	1:A:218:ARG:HH11	1.72	0.54
1:B:368:ARG:HH11	1:B:368:ARG:HG3	1.73	0.53
1:A:201:ASN:HB3	1:A:205:PHE:CE2	2.43	0.52
1:B:30:TYR:O	1:B:33:GLN:HG2	2.09	0.52
1:B:201:ASN:HB3	1:B:205:PHE:CE2	2.44	0.52
1:A:379:THR:HG22	1:A:381:TYR:H	1.74	0.52
1:A:30:TYR:O	1:A:33:GLN:HG2	2.09	0.51
1:A:374:ARG:HD3	1:A:376:ASP:OD1	2.10	0.51
1:B:42:VAL:HG13	1:B:43:GLY:N	2.24	0.51
1:A:39:VAL:O	1:A:42:VAL:HG12	2.11	0.51
1:B:318:GLY:HA3	1:B:370:ALA:HA	1.92	0.51
1:B:39:VAL:O	1:B:42:VAL:HG12	2.10	0.51
1:B:191:LYS:O	1:B:195:GLN:HG3	2.11	0.50
1:A:23:ASN:O	1:A:27:GLU:HG2	2.12	0.50
1:A:42:VAL:HG13	1:A:43:GLY:N	2.25	0.50
1:B:23:ASN:O	1:B:27:GLU:HG2	2.12	0.50
1:B:177:GLY:HA2	2:B:448:HOH:O	2.12	0.49
1:A:132:HIS:NE2	1:A:271:MSE:HE2	2.28	0.49
1:A:391:LEU:O	1:A:392:ARG:HB2	2.12	0.49
1:A:153:VAL:HG21	2:A:420:HOH:O	2.12	0.49
1:B:61:LEU:C	1:B:63:ASP:H	2.21	0.49
1:B:134:ARG:NH2	2:B:490:HOH:O	2.46	0.49
1:A:108:SER:C	1:A:112:MSE:HE3	2.38	0.49
1:B:108:SER:C	1:B:112:MSE:HE3	2.38	0.48
1:B:8:THR:HA	1:B:61:LEU:HD21	1.96	0.48
1:B:132:HIS:NE2	1:B:271:MSE:HE2	2.29	0.48
1:A:61:LEU:C	1:A:63:ASP:H	2.21	0.48
1:B:180:HIS:CD2	1:B:182:ILE:H	2.18	0.47
1:A:296:GLY:C	1:A:298:ILE:H	2.22	0.47
1:B:325:HIS:O	1:B:329:VAL:HB	2.15	0.47
1:A:308:LYS:O	1:A:312:GLU:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:THR:HA	1:A:61:LEU:HD21	1.96	0.46
1:A:325:HIS:O	1:A:329:VAL:HB	2.15	0.46
1:A:297:CYS:HB3	1:A:300:GLN:HG3	1.97	0.46
1:B:296:GLY:C	1:B:298:ILE:H	2.23	0.46
1:B:298:ILE:HD13	1:B:390:SER:HB3	1.97	0.46
1:B:308:LYS:O	1:B:312:GLU:HG3	2.16	0.46
1:B:187:LEU:HD12	1:B:187:LEU:HA	1.85	0.46
1:A:26:LEU:HD13	1:A:91:HIS:CE1	2.52	0.45
1:B:39:VAL:HG12	1:B:47:LYS:NZ	2.31	0.45
1:B:297:CYS:HB3	1:B:300:GLN:HG3	1.98	0.45
1:B:39:VAL:HG12	1:B:47:LYS:HZ1	1.81	0.45
1:A:180:HIS:CD2	1:A:182:ILE:H	2.18	0.45
1:B:218:ARG:HD3	2:B:464:HOH:O	2.16	0.45
1:B:295:LYS:HD2	2:B:536:HOH:O	2.17	0.45
1:A:65:GLY:C	2:A:485:HOH:O	2.59	0.45
1:A:209:ASP:HB3	1:A:212:ARG:HB2	1.99	0.44
1:A:146:LEU:HB3	2:A:515:HOH:O	2.16	0.44
2:A:567:HOH:O	1:B:297:CYS:SG	2.62	0.44
1:B:360:ALA:O	1:B:364:ARG:HG3	2.17	0.44
1:A:322:ILE:HG12	1:A:366:ARG:HD3	2.00	0.43
1:A:240:ALA:HB2	1:A:274:ASP:CB	2.48	0.43
1:A:311:ILE:HD13	1:A:388:LYS:CG	2.48	0.43
1:A:298:ILE:HA	1:A:303:TYR:CD2	2.54	0.43
1:A:309:LEU:HD12	1:A:309:LEU:HA	1.88	0.43
1:B:209:ASP:HB3	1:B:212:ARG:HB2	2.00	0.43
1:B:374:ARG:HD2	1:B:377:ILE:HG12	2.00	0.43
1:A:324:HIS:CE1	1:A:328:LEU:HD22	2.53	0.43
1:B:324:HIS:CE1	1:B:328:LEU:HD22	2.54	0.43
1:A:172:LYS:HG3	2:A:446:HOH:O	2.18	0.42
1:A:249:LEU:O	1:A:288:MSE:HB2	2.19	0.42
1:A:113:HIS:O	1:A:117:SER:HB2	2.19	0.42
1:A:367:ASP:HB3	1:A:372:VAL:HG22	2.01	0.42
1:A:283:ARG:O	1:A:284:ARG:HD2	2.19	0.42
1:B:113:HIS:O	1:B:117:SER:HB2	2.19	0.42
1:B:240:ALA:HB2	1:B:274:ASP:CB	2.49	0.42
1:B:249:LEU:O	1:B:288:MSE:HB2	2.20	0.42
1:A:39:VAL:HG12	1:A:47:LYS:NZ	2.33	0.42
1:A:17:SER:OG	1:A:18:ARG:N	2.50	0.42
1:B:85:MSE:HE3	1:B:224:TYR:HE1	1.85	0.41
1:A:154:ASP:O	1:A:158:LYS:HG3	2.20	0.41
1:A:108:SER:O	1:A:112:MSE:HE3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:TYR:CE2	1:A:307:LEU:HD12	2.55	0.41
1:B:146:LEU:HB3	2:B:517:HOH:O	2.20	0.41
1:A:370:ALA:O	1:A:371:ALA:C	2.64	0.41
1:A:187:LEU:HD12	1:A:187:LEU:HA	1.83	0.41
1:B:298:ILE:HA	1:B:303:TYR:CD2	2.56	0.41
1:B:309:LEU:HD12	1:B:309:LEU:HA	1.87	0.41
1:A:99:GLU:CD	1:A:103:PRO:HD3	2.46	0.41
1:A:195:GLN:HG2	2:A:536:HOH:O	2.21	0.41
1:A:173:ILE:HD11	1:A:187:LEU:HD13	2.03	0.41
1:A:118:ILE:HG13	1:A:120:VAL:HG22	2.03	0.40
1:A:242:ILE:HD11	1:A:369:ARG:NH1	2.36	0.40
1:A:311:ILE:HD13	1:A:388:LYS:HG2	2.02	0.40
1:B:303:TYR:CE2	1:B:307:LEU:HD12	2.56	0.40
1:B:386:LYS:HB2	1:B:386:LYS:HE3	1.84	0.40
1:A:85:MSE:HE3	1:A:224:TYR:CE1	2.57	0.40
1:B:85:MSE:HE3	1:B:224:TYR:CE1	2.57	0.40
1:B:26:LEU:HD13	1:B:91:HIS:CE1	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	359/403 (89%)	337 (94%)	16 (4%)	6 (2%)	7	6
1	B	359/403 (89%)	336 (94%)	17 (5%)	6 (2%)	7	6
All	All	718/806 (89%)	673 (94%)	33 (5%)	12 (2%)	7	6

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	VAL

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Mol	Chain	Res	Type
1	B	42	VAL
1	A	41	GLU
1	B	41	GLU
1	A	96	PRO
1	B	96	PRO
1	A	33	GLN
1	A	68	ASP
1	A	241	GLY
1	B	68	ASP
1	B	33	GLN
1	B	241	GLY

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	318/341 (93%)	300 (94%)	18 (6%)	18	26
1	B	318/341 (93%)	300 (94%)	18 (6%)	18	26
All	All	636/682 (93%)	600 (94%)	36 (6%)	18	26

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	45	GLU
1	A	62	LEU
1	A	64	GLU
1	A	83	LEU
1	A	106	GLU
1	A	108	SER
1	A	117	SER
1	A	170	LEU
1	A	187	LEU
1	A	194	LEU
1	A	218	ARG

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Mol	Chain	Res	Type
1	A	247	LEU
1	A	278	LEU
1	A	284	ARG
1	A	293	GLN
1	A	307	LEU
1	A	316	LEU
1	B	36	ARG
1	B	45	GLU
1	B	62	LEU
1	B	64	GLU
1	B	83	LEU
1	B	106	GLU
1	B	108	SER
1	B	117	SER
1	B	170	LEU
1	B	187	LEU
1	B	194	LEU
1	B	218	ARG
1	B	247	LEU
1	B	278	LEU
1	B	284	ARG
1	B	293	GLN
1	B	307	LEU
1	B	316	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	33	GLN
1	A	66	ASN
1	A	156	ASN
1	A	180	HIS
1	A	192	GLN
1	A	206	ASN
1	A	235	ASN
1	A	300	GLN
1	A	317	HIS
1	A	324	HIS
1	A	325	HIS
1	B	32	GLN
1	B	33	GLN

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Mol	Chain	Res	Type
1	B	66	ASN
1	B	136	HIS
1	B	156	ASN
1	B	180	HIS
1	B	192	GLN
1	B	203	GLN
1	B	206	ASN
1	B	235	ASN
1	B	300	GLN
1	B	317	HIS
1	B	324	HIS
1	B	325	HIS

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	356/403 (88%)	0.87	51 (14%) 6 7	19, 40, 72, 80	0
1	B	356/403 (88%)	0.73	41 (11%) 9 11	17, 37, 70, 77	0
All	All	712/806 (88%)	0.80	92 (12%) 7 8	17, 39, 71, 80	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	6	TYR	6.0
1	A	65	GLY	5.8
1	A	357	VAL	5.5
1	B	43	GLY	4.7
1	B	326	ASN	4.4
1	B	296	GLY	4.3
1	B	42	VAL	4.0
1	B	63	ASP	4.0
1	B	206	ASN	4.0
1	B	67	THR	3.9
1	B	64	GLU	3.9
1	A	42	VAL	3.9
1	B	376	ASP	3.7
1	B	61	LEU	3.7
1	B	357	VAL	3.6
1	B	218	ARG	3.5
1	A	43	GLY	3.5
1	A	358	LEU	3.4
1	A	332	TYR	3.4
1	A	97	THR	3.4
1	A	60	ALA	3.4
1	B	205	PHE	3.3
1	A	320	THR	3.3
1	A	64	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	39	VAL	3.2
1	A	328	LEU	3.2
1	B	65	GLY	3.2
1	A	48	HIS	3.2
1	A	258	SER	3.1
1	A	6	TYR	3.0
1	B	66	ASN	3.0
1	A	392	ARG	2.9
1	B	39	VAL	2.9
1	A	31	TYR	2.9
1	A	391	LEU	2.9
1	A	44	THR	2.9
1	B	361	SER	2.8
1	B	99	GLU	2.8
1	A	323	GLN	2.8
1	B	392	ARG	2.8
1	A	382	TYR	2.8
1	B	320	THR	2.8
1	A	63	ASP	2.8
1	B	300	GLN	2.7
1	B	62	LEU	2.7
1	B	360	ALA	2.7
1	A	327	GLU	2.7
1	B	379	THR	2.7
1	B	328	LEU	2.7
1	B	358	LEU	2.7
1	A	360	ALA	2.7
1	A	61	LEU	2.6
1	A	296	GLY	2.6
1	B	44	THR	2.6
1	A	298	ILE	2.6
1	A	206	ASN	2.6
1	A	379	THR	2.6
1	A	326	ASN	2.5
1	A	40	GLN	2.5
1	A	105	LEU	2.5
1	A	54	GLY	2.5
1	A	375	ASP	2.4
1	B	390	SER	2.4
1	A	294	ALA	2.4
1	A	34	THR	2.4
1	B	293	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	7	ASN	2.4
1	A	67	THR	2.4
1	A	390	SER	2.4
1	B	34	THR	2.3
1	A	35	ASP	2.3
1	B	330	THR	2.3
1	A	29	LEU	2.3
1	A	66	ASN	2.3
1	A	377	ILE	2.3
1	B	295	LYS	2.3
1	A	52	SER	2.3
1	B	100	THR	2.2
1	A	218	ARG	2.2
1	B	297	CYS	2.2
1	A	376	ASP	2.2
1	A	292	LEU	2.1
1	A	38	ASN	2.1
1	A	297	CYS	2.1
1	B	49	THR	2.1
1	B	97	THR	2.1
1	B	382	TYR	2.1
1	A	359	LEU	2.1
1	B	208	LEU	2.1
1	B	359	LEU	2.1
1	A	318	GLY	2.0
1	A	295	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.