



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:05 AM UTC

PDB ID : 6E9C / pdb_00006e9c
Title : Selenomethionine Derivative Structure of A Bacterial Homolog to Human Lysosomal Transporter, Spinster
Authors : Zhou, F.; Yao, D.; Rao, B.; Zhang, L.; Cao, Y.
Deposited on : 2018-07-31
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

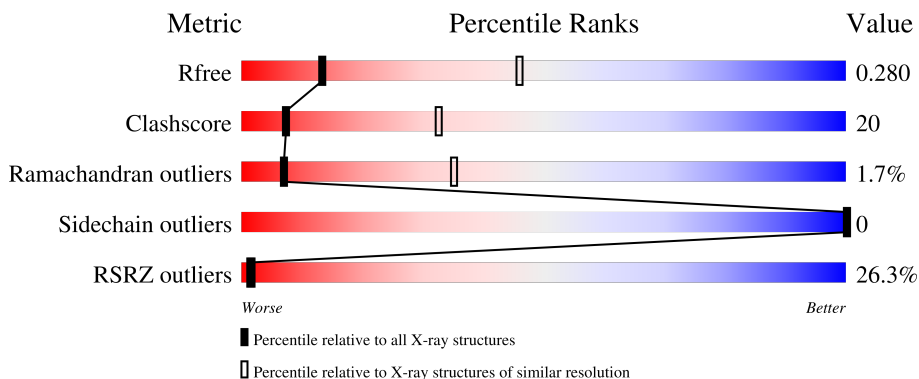
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	508	24% 61% 31% 6%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3628 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 Major facilitator family transporter.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	Se	0	0	0
			3628	2412	582	614	5	15			

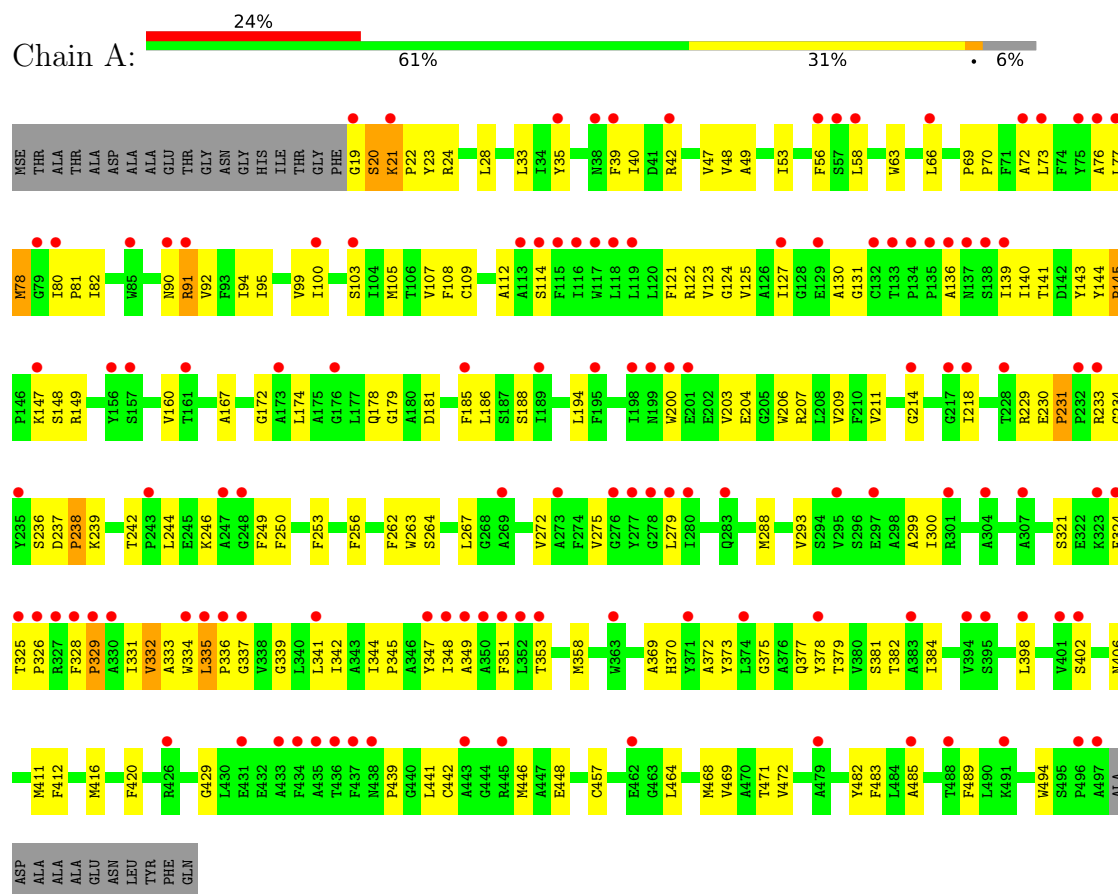
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	500	ALA	-	expression tag	UNP Q0C3L7
A	501	ALA	-	expression tag	UNP Q0C3L7
A	502	ALA	-	expression tag	UNP Q0C3L7
A	503	GLU	-	expression tag	UNP Q0C3L7
A	504	ASN	-	expression tag	UNP Q0C3L7
A	505	LEU	-	expression tag	UNP Q0C3L7
A	506	TYR	-	expression tag	UNP Q0C3L7
A	507	PHE	-	expression tag	UNP Q0C3L7
A	508	GLN	-	expression tag	UNP Q0C3L7

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: Major facilitator family transporter



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.59Å 87.33Å 122.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 3.20 29.98 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.98-3.20) 99.7 (29.98-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 3.18Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.277 , 0.284 0.280 , 0.280	Depositor DCC
R_{free} test set	776 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	101.3	Xtriage
Anisotropy	0.717	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.033 for k,h,-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3628	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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	0.35	2/3720 (0.1%)	0.66	2/5050 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	231	PRO	CA-C	-5.89	1.48	1.52
1	A	145	PRO	CA-C	5.05	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	ARG	CG-CD-NE	6.77	126.89	112.00
1	A	231	PRO	O-C-N	-5.30	118.66	121.15

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	3628	0	3688	150	1
All	All	3628	0	3688	150	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 20.

All (150) 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:332:VAL:HG21	1:A:337:GLY:HA2	1.45	0.95
1:A:335:LEU:HB2	1:A:336:PRO:CD	2.08	0.83
1:A:91:ARG:HH11	1:A:233:ARG:HD3	1.47	0.79
1:A:21:LYS:HE2	1:A:22:PRO:HD3	1.66	0.78
1:A:24:ARG:NH2	1:A:143:TYR:O	2.17	0.78
1:A:112:ALA:H	1:A:207:ARG:HH22	1.32	0.77
1:A:91:ARG:HD3	1:A:230:GLU:OE2	1.87	0.75
1:A:91:ARG:HH11	1:A:233:ARG:CD	2.03	0.71
1:A:105:MSE:HE3	1:A:124:GLY:HA3	1.72	0.70
1:A:20:SER:O	1:A:24:ARG:NE	2.17	0.70
1:A:77:LEU:O	1:A:81:PRO:HD2	1.91	0.69
1:A:441:LEU:H	1:A:441:LEU:HD23	1.57	0.69
1:A:92:VAL:HG23	1:A:230:GLU:OE1	1.94	0.68
1:A:324:PHE:HB3	1:A:331:ILE:HD12	1.75	0.67
1:A:20:SER:OG	1:A:21:LYS:N	2.21	0.67
1:A:91:ARG:HE	1:A:233:ARG:HD2	1.59	0.67
1:A:144:TYR:O	1:A:149:ARG:NH2	2.27	0.66
1:A:139:ILE:O	1:A:143:TYR:HB2	1.95	0.66
1:A:349:ALA:O	1:A:353:THR:OG1	2.13	0.66
1:A:42:ARG:O	1:A:122:ARG:NH2	2.26	0.65
1:A:335:LEU:HB2	1:A:336:PRO:HD2	1.77	0.64
1:A:40:ILE:HA	1:A:167:ALA:HB2	1.80	0.63
1:A:341:LEU:O	1:A:345:PRO:HD3	1.98	0.63
1:A:78:MSE:HE3	1:A:82:ILE:HG12	1.81	0.62
1:A:80:ILE:HB	1:A:81:PRO:HD3	1.81	0.62
1:A:373:TYR:O	1:A:377:GLN:HG3	2.00	0.62
1:A:91:ARG:NE	1:A:233:ARG:HD2	2.15	0.62
1:A:90:ASN:O	1:A:94:ILE:HG13	1.99	0.61
1:A:24:ARG:NH2	1:A:145:PRO:HD3	2.17	0.59
1:A:324:PHE:CD1	1:A:328:PHE:HB2	2.37	0.59
1:A:253:PHE:HA	1:A:256:PHE:CE2	2.38	0.58
1:A:66:LEU:O	1:A:70:PRO:HG2	2.03	0.58
1:A:141:THR:O	1:A:149:ARG:NH2	2.38	0.57
1:A:186:LEU:HD13	1:A:194:LEU:HD12	1.87	0.56
1:A:369:ALA:O	1:A:372:ALA:HB3	2.04	0.56
1:A:141:THR:HA	1:A:149:ARG:HD3	1.87	0.56
1:A:353:THR:HG21	1:A:358:MSE:HB3	1.88	0.56
1:A:103:SER:HB3	1:A:214:GLY:O	2.05	0.56
1:A:91:ARG:NH1	1:A:233:ARG:CD	2.69	0.55
1:A:262:PHE:HB2	1:A:384:ILE:HD11	1.88	0.55
1:A:35:TYR:HE2	1:A:160:VAL:HG23	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ARG:HH21	1:A:144:TYR:HA	1.71	0.55
1:A:204:GLU:N	1:A:204:GLU:OE1	2.37	0.55
1:A:77:LEU:HD12	1:A:78:MSE:SE	2.57	0.55
1:A:91:ARG:HD3	1:A:230:GLU:CD	2.32	0.55
1:A:379:THR:O	1:A:382:THR:OG1	2.26	0.54
1:A:272:VAL:HG13	1:A:370:HIS:CD2	2.42	0.54
1:A:324:PHE:HB3	1:A:331:ILE:CD1	2.37	0.54
1:A:172:GLY:HA3	1:A:300:ILE:HG13	1.89	0.54
1:A:78:MSE:HB3	1:A:130:ALA:HB3	1.90	0.53
1:A:378:TYR:O	1:A:381:SER:OG	2.24	0.53
1:A:53:ILE:HG23	1:A:58:LEU:HB2	1.91	0.53
1:A:108:PHE:HB3	1:A:121:PHE:CE2	2.44	0.53
1:A:336:PRO:HB3	1:A:483:PHE:CD2	2.44	0.53
1:A:464:LEU:O	1:A:468:MSE:HG2	2.09	0.53
1:A:253:PHE:HA	1:A:256:PHE:CZ	2.44	0.53
1:A:72:ALA:O	1:A:76:ALA:HB2	2.09	0.52
1:A:348:ILE:HG12	1:A:469:VAL:HG13	1.91	0.52
1:A:332:VAL:CG2	1:A:337:GLY:HA2	2.29	0.52
1:A:174:LEU:HB2	1:A:209:VAL:HG22	1.91	0.52
1:A:35:TYR:CE2	1:A:160:VAL:HG23	2.44	0.52
1:A:234:GLY:C	1:A:236:SER:H	2.17	0.52
1:A:77:LEU:CD1	1:A:78:MSE:SE	3.08	0.52
1:A:91:ARG:NH1	1:A:233:ARG:HD3	2.21	0.52
1:A:91:ARG:O	1:A:95:ILE:HD12	2.10	0.52
1:A:49:ALA:O	1:A:53:ILE:HG13	2.11	0.51
1:A:100:ILE:HD13	1:A:218:ILE:HA	1.93	0.51
1:A:329:PRO:HG2	1:A:489:PHE:CE2	2.46	0.51
1:A:19:GLY:O	1:A:24:ARG:NH1	2.44	0.50
1:A:108:PHE:HB3	1:A:121:PHE:CZ	2.46	0.50
1:A:200:TRP:O	1:A:203:VAL:HG22	2.12	0.50
1:A:288:MSE:HG2	1:A:293:VAL:O	2.12	0.50
1:A:333:ALA:O	1:A:334:TRP:HD1	1.94	0.50
1:A:91:ARG:HB3	1:A:139:ILE:HD11	1.94	0.49
1:A:246:LYS:HE3	1:A:249:PHE:CE1	2.48	0.49
1:A:336:PRO:HB3	1:A:483:PHE:HD2	1.76	0.49
1:A:412:PHE:CE1	1:A:416:MSE:HG3	2.48	0.49
1:A:73:LEU:HA	1:A:76:ALA:HB3	1.95	0.49
1:A:147:LYS:HD3	1:A:148:SER:HB3	1.94	0.49
1:A:324:PHE:CE1	1:A:328:PHE:HB2	2.47	0.49
1:A:82:ILE:HG21	1:A:131:GLY:HA2	1.95	0.48
1:A:143:TYR:HE1	1:A:231:PRO:HD3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ILE:O	1:A:99:VAL:HG23	2.14	0.48
1:A:91:ARG:HB2	1:A:230:GLU:CD	2.39	0.47
1:A:325:THR:N	1:A:326:PRO:HD2	2.29	0.47
1:A:91:ARG:NH1	1:A:233:ARG:HD2	2.30	0.47
1:A:339:GLY:HA3	1:A:373:TYR:CE1	2.50	0.47
1:A:107:VAL:HG12	1:A:211:VAL:HA	1.97	0.47
1:A:23:TYR:HH	1:A:229:ARG:H	1.59	0.46
1:A:412:PHE:CD1	1:A:471:THR:HG22	2.50	0.46
1:A:412:PHE:HD1	1:A:471:THR:HG22	1.79	0.46
1:A:143:TYR:OH	1:A:229:ARG:O	2.28	0.46
1:A:275:VAL:O	1:A:279:LEU:HD23	2.16	0.46
1:A:73:LEU:HD13	1:A:123:VAL:CG1	2.46	0.46
1:A:123:VAL:O	1:A:127:ILE:HG12	2.16	0.46
1:A:242:THR:OG1	1:A:244:LEU:HD12	2.16	0.46
1:A:20:SER:OG	1:A:22:PRO:HD2	2.15	0.46
1:A:69:PRO:O	1:A:72:ALA:HB3	2.16	0.46
1:A:238:PRO:HG2	1:A:239:LYS:H	1.79	0.46
1:A:328:PHE:HA	1:A:329:PRO:HD3	1.70	0.46
1:A:56:PHE:HE2	1:A:114:SER:C	2.23	0.46
1:A:246:LYS:HE3	1:A:249:PHE:CZ	2.51	0.46
1:A:446:MSE:HE1	1:A:457:CYS:SG	2.56	0.46
1:A:402:SER:O	1:A:406:ASN:HB2	2.15	0.46
1:A:78:MSE:HG3	1:A:127:ILE:O	2.16	0.45
1:A:49:ALA:HA	1:A:63:TRP:CZ2	2.51	0.45
1:A:63:TRP:CZ3	1:A:66:LEU:HD23	2.52	0.45
1:A:249:PHE:CG	1:A:250:PHE:N	2.85	0.45
1:A:448:GLU:O	1:A:448:GLU:HG3	2.17	0.45
1:A:178:GLN:HB2	1:A:181:ASP:CG	2.42	0.45
1:A:179:GLY:O	1:A:200:TRP:HB3	2.17	0.45
1:A:342:ILE:O	1:A:345:PRO:HD2	2.16	0.45
1:A:263:TRP:O	1:A:267:LEU:HD23	2.18	0.44
1:A:439:PRO:O	1:A:442:CYS:HB2	2.17	0.44
1:A:91:ARG:CZ	1:A:233:ARG:HD2	2.47	0.44
1:A:344:ILE:HB	1:A:345:PRO:HD3	1.98	0.44
1:A:69:PRO:HG3	1:A:411:MSE:HE2	2.00	0.44
1:A:335:LEU:HB2	1:A:336:PRO:HD3	1.91	0.43
1:A:373:TYR:HE2	1:A:482:TYR:HE2	1.65	0.43
1:A:109:CYS:SG	1:A:121:PHE:HB3	2.58	0.43
1:A:39:PHE:CE1	1:A:160:VAL:HG22	2.53	0.43
1:A:234:GLY:C	1:A:236:SER:N	2.76	0.43
1:A:91:ARG:CD	1:A:230:GLU:OE2	2.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:SER:HB2	1:A:485:ALA:HB2	2.01	0.43
1:A:375:GLY:O	1:A:378:TYR:HB3	2.19	0.43
1:A:334:TRP:O	1:A:336:PRO:HD2	2.18	0.42
1:A:279:LEU:HD11	1:A:351:PHE:HZ	1.85	0.42
1:A:332:VAL:HG22	1:A:333:ALA:H	1.85	0.42
1:A:21:LYS:HE2	1:A:21:LYS:HB3	1.82	0.42
1:A:78:MSE:O	1:A:82:ILE:HB	2.19	0.42
1:A:48:VAL:HB	1:A:206:TRP:HB3	2.02	0.42
1:A:143:TYR:CD1	1:A:231:PRO:HB3	2.55	0.42
1:A:237:ASP:OD1	1:A:238:PRO:HD2	2.20	0.42
1:A:347:TYR:HB3	1:A:472:VAL:HG11	2.02	0.41
1:A:82:ILE:HD13	1:A:82:ILE:HA	1.90	0.41
1:A:21:LYS:H	1:A:22:PRO:HD2	1.86	0.41
1:A:112:ALA:H	1:A:207:ARG:NH2	2.09	0.41
1:A:47:VAL:HG13	1:A:299:ALA:HB2	2.02	0.41
1:A:77:LEU:C	1:A:81:PRO:HD2	2.46	0.41
1:A:105:MSE:HB3	1:A:125:VAL:HG23	2.03	0.41
1:A:28:LEU:HD13	1:A:140:ILE:HD12	2.02	0.41
1:A:185:PHE:O	1:A:188:SER:OG	2.33	0.41
1:A:329:PRO:HG2	1:A:489:PHE:HE2	1.85	0.41
1:A:33:LEU:HD12	1:A:33:LEU:HA	1.74	0.41
1:A:136:ALA:O	1:A:140:ILE:HG12	2.21	0.41
1:A:321:SER:HB2	1:A:379:THR:HG21	2.03	0.40
1:A:321:SER:O	1:A:325:THR:OG1	2.37	0.40
1:A:398:LEU:HD23	1:A:398:LEU:HA	1.93	0.40
1:A:69:PRO:N	1:A:70:PRO:CD	2.84	0.40
1:A:416:MSE:O	1:A:420:PHE:HD1	2.05	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:A:448:GLU:OE1	1:A:494:TRP:NE1[2_455]	2.01	0.19

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	477/508 (94%)	427 (90%)	42 (9%)	8 (2%)	7	35

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	PRO
1	A	335	LEU
1	A	21	LYS
1	A	238	PRO
1	A	20	SER
1	A	78	MSE
1	A	429	GLY
1	A	332	VAL

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	366/368 (100%)	366 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	ASN

5.3.3 RNA ⓘ

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	464/508 (91%)	1.54	122 (26%) 1 2	66, 98, 136, 164	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	326	PRO	23.3
1	A	328	PHE	16.2
1	A	327	ARG	12.6
1	A	325	THR	11.7
1	A	431	GLU	10.1
1	A	324	PHE	8.1
1	A	497	ALA	8.0
1	A	117	TRP	6.6
1	A	398	LEU	6.5
1	A	113	ALA	6.4
1	A	57	SER	6.3
1	A	195	PHE	6.1
1	A	329	PRO	6.1
1	A	133	THR	6.0
1	A	378	TYR	6.0
1	A	136	ALA	6.0
1	A	276	GLY	5.8
1	A	114	SER	5.6
1	A	437	PHE	5.6
1	A	435	ALA	5.4
1	A	434	PHE	5.3
1	A	438	ASN	5.3
1	A	137	ASN	5.2
1	A	273	ALA	5.1
1	A	436	THR	5.0
1	A	402	SER	5.0
1	A	138	SER	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	132	CYS	4.6
1	A	135	PRO	4.6
1	A	462	GLU	4.5
1	A	75	TYR	4.4
1	A	243	PRO	4.4
1	A	247	ALA	4.3
1	A	56	PHE	4.2
1	A	496	PRO	4.2
1	A	491	LYS	4.2
1	A	330	ALA	4.1
1	A	91	ARG	4.1
1	A	352	LEU	4.1
1	A	301	ARG	4.0
1	A	277	TYR	4.0
1	A	323	LYS	4.0
1	A	19	GLY	3.8
1	A	147	LYS	3.8
1	A	199	ASN	3.7
1	A	21	LYS	3.7
1	A	374	LEU	3.7
1	A	443	ALA	3.7
1	A	100	ILE	3.7
1	A	198	ILE	3.7
1	A	176	GLY	3.6
1	A	156	TYR	3.6
1	A	73	LEU	3.6
1	A	77	LEU	3.5
1	A	351	PHE	3.5
1	A	119	LEU	3.4
1	A	80	ILE	3.4
1	A	279	LEU	3.3
1	A	348	ILE	3.3
1	A	35	TYR	3.2
1	A	395	SER	3.2
1	A	189	ILE	3.2
1	A	233	ARG	3.2
1	A	350	ALA	3.2
1	A	334	TRP	3.2
1	A	118	LEU	3.2
1	A	278	GLY	3.1
1	A	269	ALA	3.1
1	A	383	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	349	ALA	3.0
1	A	426	ARG	2.9
1	A	307	ALA	2.9
1	A	371	TYR	2.9
1	A	295	VAL	2.9
1	A	445	ARG	2.9
1	A	58	LEU	2.8
1	A	232	PRO	2.8
1	A	115	PHE	2.8
1	A	79	GLY	2.8
1	A	394	VAL	2.7
1	A	134	PRO	2.7
1	A	90	ASN	2.7
1	A	297	GLU	2.7
1	A	353	THR	2.7
1	A	433	ALA	2.6
1	A	116	ILE	2.6
1	A	185	PHE	2.5
1	A	363	TRP	2.5
1	A	129	GLU	2.5
1	A	235	TYR	2.5
1	A	42	ARG	2.5
1	A	347	TYR	2.5
1	A	72	ALA	2.5
1	A	200	TRP	2.5
1	A	201	GLU	2.4
1	A	341	LEU	2.4
1	A	161	THR	2.4
1	A	39	PHE	2.4
1	A	139	ILE	2.3
1	A	218	ILE	2.3
1	A	127	ILE	2.3
1	A	280	ILE	2.3
1	A	66	LEU	2.3
1	A	401	VAL	2.2
1	A	335	LEU	2.2
1	A	157	SER	2.2
1	A	485	ALA	2.2
1	A	488	THR	2.2
1	A	214	GLY	2.2
1	A	304	ALA	2.2
1	A	336	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	228	THR	2.1
1	A	76	ALA	2.1
1	A	85	TRP	2.1
1	A	283	GLN	2.1
1	A	173	ALA	2.1
1	A	103	SER	2.0
1	A	479	ALA	2.0
1	A	248	GLY	2.0
1	A	337	GLY	2.0
1	A	38	ASN	2.0
1	A	217	GLY	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.