



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:52 PM UTC

PDB ID : 1YFM / pdb_00001yfm
Title : RECOMBINANT YEAST FUMARASE
Authors : Weaver, T.M.; Lees, M.R.; Banaszak, L.J.
Deposited on : 1998-01-07
Resolution : 2.60 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

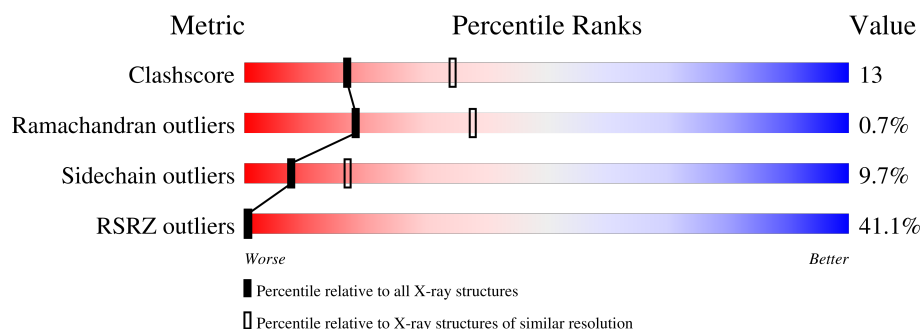
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	488	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3439 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 FUMARASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	0	0
			3439	2166	602	656	15			

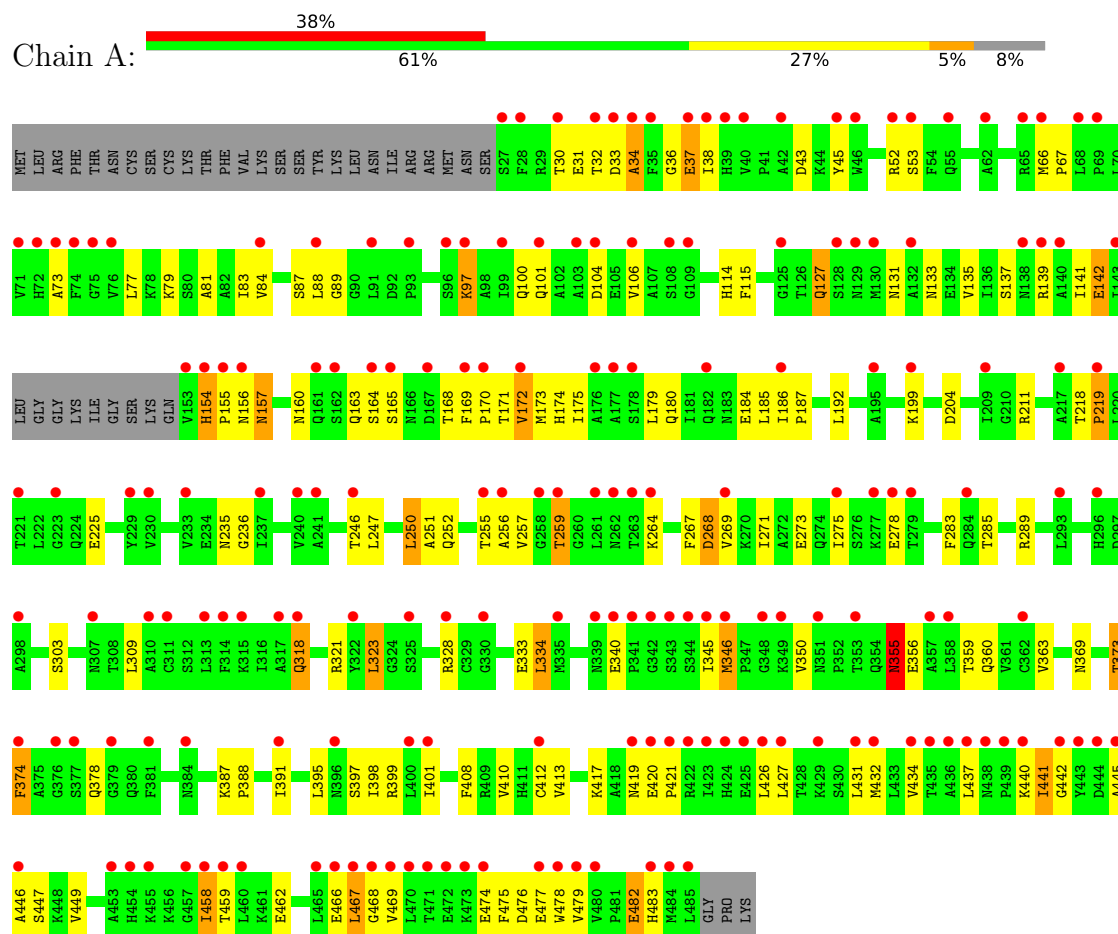
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ARG	LYS	engineered mutation	UNP P08417

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: FUMARASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	95.19Å 95.19Å 100.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	60.0 (30.00-2.60) 88.2 (30.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.95 (at 2.61Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.196 , 0.315 0.309 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	3439	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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	6/3502 (0.2%)	1.11	18/4741 (0.4%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	468	GLY	C-N	10.12	1.47	1.33
1	A	426	LEU	C-N	8.64	1.45	1.33
1	A	285	THR	C-N	-6.98	1.20	1.33
1	A	446	ALA	C-N	-6.50	1.24	1.33
1	A	355	ASN	C-N	-5.57	1.25	1.33
1	A	31	GLU	C-N	5.30	1.41	1.33

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	VAL	N-CA-C	-9.13	101.97	110.82
1	A	427	LEU	CA-C-N	-7.77	107.55	121.14
1	A	427	LEU	C-N-CA	-7.77	107.55	121.14
1	A	427	LEU	O-C-N	7.66	130.88	122.15
1	A	426	LEU	O-C-N	-7.62	112.90	122.27
1	A	219	PRO	N-CA-C	6.45	121.09	111.41
1	A	255	THR	N-CA-C	6.25	117.80	108.31
1	A	474	GLU	N-CA-C	-6.14	107.62	114.62
1	A	256	ALA	N-CA-C	6.07	118.86	111.82
1	A	255	THR	CB-CA-C	-5.63	110.06	116.54
1	A	378	GLN	N-CA-C	5.61	119.21	112.93
1	A	426	LEU	CA-C-N	5.46	128.05	120.29
1	A	426	LEU	C-N-CA	5.46	128.05	120.29
1	A	154	HIS	N-CA-C	5.41	116.75	109.24
1	A	165	SER	N-CA-C	-5.37	106.68	113.18
1	A	157	ASN	N-CA-C	5.33	118.01	111.82
1	A	410	VAL	N-CA-C	5.30	115.51	110.42
1	A	43	ASP	N-CA-C	5.08	119.32	113.18

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	3439	0	3441	87	0
All	All	3439	0	3441	87	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 13.

All (87) 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:77:LEU:HD21	1:A:168:THR:HG23	1.39	1.05
1:A:345:ILE:HG23	1:A:346:MET:HG2	1.60	0.83
1:A:139:ARG:NH1	1:A:142:GLU:HG2	2.00	0.77
1:A:139:ARG:HH11	1:A:142:GLU:HG2	1.52	0.74
1:A:33:ASP:HB3	1:A:52:ARG:HH22	1.54	0.72
1:A:173:MET:HE3	1:A:391:ILE:HB	1.71	0.72
1:A:38:ILE:HD12	1:A:52:ARG:HG2	1.75	0.69
1:A:133:ASN:ND2	1:A:160:ASN:HB2	2.08	0.69
1:A:37:GLU:H	1:A:37:GLU:CD	2.01	0.68
1:A:269:VAL:O	1:A:273:GLU:HB2	1.97	0.65
1:A:387:LYS:HB2	1:A:388:PRO:HD3	1.76	0.65
1:A:84:VAL:HG21	1:A:271:ILE:HA	1.77	0.65
1:A:73:ALA:HB3	1:A:172:VAL:HG22	1.81	0.62
1:A:137:SER:O	1:A:141:ILE:HG12	2.00	0.61
1:A:257:VAL:HG23	1:A:259:THR:HB	1.82	0.61
1:A:479:VAL:HG13	1:A:479:VAL:O	2.00	0.60
1:A:115:PHE:HA	1:A:131:ASN:HD21	1.66	0.60
1:A:356:GLU:O	1:A:360:GLN:HG3	2.02	0.60
1:A:397:SER:O	1:A:401:ILE:HG13	2.03	0.58
1:A:440:LYS:HD3	1:A:478:TRP:CE2	2.38	0.58
1:A:180:GLN:O	1:A:184:GLU:HB2	2.03	0.58
1:A:458:ILE:HG13	1:A:462:GLU:OE1	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:SER:HB2	1:A:127:GLN:NE2	2.20	0.57
1:A:267:PHE:O	1:A:271:ILE:HG22	2.05	0.56
1:A:374:PHE:CD1	1:A:374:PHE:N	2.75	0.54
1:A:466:GLU:HG3	1:A:467:LEU:HD13	1.89	0.54
1:A:437:LEU:O	1:A:441:ILE:HG22	2.08	0.53
1:A:169:PHE:O	1:A:172:VAL:HG12	2.09	0.53
1:A:441:ILE:HD11	1:A:469:VAL:CG1	2.39	0.53
1:A:225:GLU:OE1	1:A:323:LEU:HD21	2.09	0.52
1:A:369:ASN:O	1:A:373:THR:HG23	2.09	0.52
1:A:475:PHE:O	1:A:479:VAL:HG12	2.10	0.52
1:A:445:ALA:O	1:A:449:VAL:HG23	2.09	0.51
1:A:88:LEU:HD13	1:A:264:LYS:HB2	1.93	0.51
1:A:81:ALA:HB1	1:A:163:GLN:HE22	1.75	0.51
1:A:66:MET:SD	1:A:67:PRO:HD2	2.51	0.51
1:A:32:THR:HG22	1:A:33:ASP:N	2.26	0.51
1:A:133:ASN:HD21	1:A:160:ASN:HB2	1.75	0.51
1:A:97:LYS:NZ	1:A:101:GLN:HE21	2.10	0.50
1:A:160:ASN:O	1:A:163:GLN:HG2	2.12	0.50
1:A:355:ASN:HD22	1:A:355:ASN:N	2.09	0.50
1:A:271:ILE:O	1:A:275:ILE:HG13	2.12	0.50
1:A:303:SER:OG	1:A:369:ASN:ND2	2.45	0.50
1:A:482:GLU:H	1:A:482:GLU:CD	2.21	0.49
1:A:83:ILE:HG12	1:A:100:GLN:NE2	2.28	0.49
1:A:441:ILE:HD11	1:A:469:VAL:HG13	1.94	0.49
1:A:441:ILE:HG23	1:A:442:GLY:N	2.28	0.49
1:A:419:ASN:HD22	1:A:421:PRO:HD2	1.78	0.48
1:A:458:ILE:HG23	1:A:462:GLU:HB2	1.94	0.48
1:A:211:ARG:HH22	1:A:333:GLU:CD	2.21	0.48
1:A:97:LYS:HZ2	1:A:101:GLN:HE21	1.62	0.48
1:A:175:ILE:O	1:A:179:LEU:HG	2.14	0.48
1:A:268:ASP:OD1	1:A:269:VAL:HG23	2.14	0.47
1:A:154:HIS:HD2	1:A:157:ASN:CG	2.21	0.47
1:A:318:GLN:NE2	1:A:321:ARG:HH21	2.14	0.46
1:A:170:PRO:HA	1:A:173:MET:SD	2.56	0.46
1:A:186:ILE:HB	1:A:187:PRO:HD3	1.97	0.46
1:A:475:PHE:CE2	1:A:479:VAL:HG11	2.49	0.46
1:A:180:GLN:HB3	1:A:398:ILE:HG21	1.98	0.45
1:A:34:ALA:C	1:A:36:GLY:H	2.25	0.45
1:A:251:ALA:O	1:A:252:GLN:C	2.59	0.45
1:A:236:GLY:HA3	1:A:309:LEU:HD13	1.98	0.44
1:A:359:THR:O	1:A:363:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:ASN:N	1:A:355:ASN:ND2	2.65	0.44
1:A:441:ILE:CG2	1:A:442:GLY:N	2.80	0.44
1:A:250:LEU:HD22	1:A:283:PHE:HB3	1.99	0.43
1:A:420:GLU:HB2	1:A:421:PRO:HD3	2.00	0.43
1:A:154:HIS:HA	1:A:155:PRO:HD3	1.88	0.43
1:A:417:LYS:HE2	1:A:417:LYS:HB3	1.79	0.43
1:A:437:LEU:HB3	1:A:441:ILE:HG21	2.00	0.43
1:A:408:PHE:O	1:A:412:CYS:HB3	2.18	0.43
1:A:432:MET:C	1:A:434:VAL:H	2.27	0.43
1:A:437:LEU:C	1:A:441:ILE:HG22	2.44	0.42
1:A:154:HIS:CD2	1:A:157:ASN:H	2.37	0.42
1:A:164:SER:O	1:A:168:THR:HB	2.20	0.42
1:A:199:LYS:HE3	1:A:413:VAL:O	2.18	0.42
1:A:419:ASN:HD22	1:A:419:ASN:C	2.28	0.42
1:A:45:TYR:H	1:A:114:HIS:CD2	2.38	0.42
1:A:171:THR:O	1:A:175:ILE:HG13	2.19	0.42
1:A:235:ASN:HD22	1:A:235:ASN:N	2.17	0.42
1:A:459:THR:HG23	1:A:462:GLU:H	1.85	0.42
1:A:77:LEU:CD2	1:A:168:THR:HG23	2.28	0.41
1:A:174:HIS:ND1	1:A:247:LEU:HA	2.35	0.41
1:A:79:LYS:HD2	1:A:104:ASP:HB2	2.02	0.41
1:A:87:SER:C	1:A:89:GLY:H	2.27	0.41
1:A:323:LEU:HB3	1:A:334:LEU:HD22	2.03	0.41
1:A:218:THR:HB	1:A:219:PRO:HD2	2.03	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	446/488 (91%)	402 (90%)	41 (9%)	3 (1%)	18 38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	ILE
1	A	34	ALA
1	A	185	LEU

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	373/407 (92%)	337 (90%)	36 (10%)	8 17

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

Mol	Chain	Res	Type
1	A	30	THR
1	A	37	GLU
1	A	97	LYS
1	A	127	GLN
1	A	135	VAL
1	A	142	GLU
1	A	156	ASN
1	A	172	VAL
1	A	192	LEU
1	A	204	ASP
1	A	246	THR
1	A	250	LEU
1	A	259	THR
1	A	268	ASP
1	A	278	GLU
1	A	289	ARG
1	A	318	GLN
1	A	323	LEU
1	A	328	ARG
1	A	334	LEU
1	A	340	GLU
1	A	346	MET

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Mol	Chain	Res	Type
1	A	350	VAL
1	A	355	ASN
1	A	373	THR
1	A	374	PHE
1	A	395	LEU
1	A	399	ARG
1	A	431	LEU
1	A	447	SER
1	A	458	ILE
1	A	467	LEU
1	A	476	ASP
1	A	477	GLU
1	A	482	GLU
1	A	483	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	72	HIS
1	A	85	ASN
1	A	101	GLN
1	A	114	HIS
1	A	131	ASN
1	A	138	ASN
1	A	154	HIS
1	A	183	ASN
1	A	191	ASN
1	A	235	ASN
1	A	262	ASN
1	A	274	GLN
1	A	318	GLN
1	A	351	ASN
1	A	354	GLN
1	A	355	ASN
1	A	369	ASN
1	A	393	ASN
1	A	419	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	285:THR	C	286:ALA	N	1.20

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	450/488 (92%)	1.99	185 (41%) 0 0	4, 23, 54, 100	0

All (185) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	468	GLY	7.0
1	A	342	GLY	6.8
1	A	317	ALA	6.1
1	A	348	GLY	5.4
1	A	310	ALA	5.3
1	A	374	PHE	5.2
1	A	33	ASP	5.2
1	A	477	GLU	5.0
1	A	465	LEU	4.9
1	A	344	SER	4.8
1	A	471	THR	4.7
1	A	71	VAL	4.7
1	A	436	ALA	4.7
1	A	466	GLU	4.5
1	A	219	PRO	4.5
1	A	483	HIS	4.5
1	A	421	PRO	4.4
1	A	426	LEU	4.3
1	A	443	TYR	4.3
1	A	358	LEU	4.3
1	A	470	LEU	4.2
1	A	438	ASN	4.2
1	A	439	PRO	4.2
1	A	345	ILE	4.1
1	A	458	ILE	4.0
1	A	165	SER	4.0
1	A	444	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	339	ASN	4.0
1	A	138	ASN	3.9
1	A	128	SER	3.9
1	A	172	VAL	3.9
1	A	330	GLY	3.8
1	A	176	ALA	3.8
1	A	256	ALA	3.8
1	A	341	PRO	3.7
1	A	129	ASN	3.6
1	A	478	TRP	3.6
1	A	101	GLN	3.6
1	A	340	GLU	3.6
1	A	454	HIS	3.6
1	A	32	THR	3.6
1	A	132	ALA	3.6
1	A	53	SER	3.6
1	A	30	THR	3.5
1	A	437	LEU	3.5
1	A	479	VAL	3.5
1	A	258	GLY	3.5
1	A	442	GLY	3.5
1	A	278	GLU	3.5
1	A	357	ALA	3.4
1	A	28	PHE	3.4
1	A	419	ASN	3.4
1	A	424	HIS	3.4
1	A	480	VAL	3.4
1	A	427	LEU	3.4
1	A	230	VAL	3.4
1	A	473	LYS	3.3
1	A	72	HIS	3.3
1	A	37	GLU	3.3
1	A	284	GLN	3.2
1	A	293	LEU	3.2
1	A	485	LEU	3.2
1	A	445	ALA	3.2
1	A	349	LYS	3.2
1	A	65	ARG	3.1
1	A	263	THR	3.1
1	A	434	VAL	3.1
1	A	459	THR	3.1
1	A	313	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	125	GLY	3.1
1	A	376	GLY	3.0
1	A	343	SER	3.0
1	A	262	ASN	3.0
1	A	195	ALA	3.0
1	A	412	CYS	3.0
1	A	209	ILE	3.0
1	A	169	PHE	3.0
1	A	39	HIS	2.9
1	A	106	VAL	2.9
1	A	55	GLN	2.9
1	A	68	LEU	2.9
1	A	97	LYS	2.9
1	A	130	MET	2.9
1	A	199	LYS	2.9
1	A	35	PHE	2.9
1	A	88	LEU	2.8
1	A	318	GLN	2.8
1	A	277	LYS	2.8
1	A	423	ILE	2.8
1	A	153	VAL	2.8
1	A	469	VAL	2.8
1	A	45	TYR	2.8
1	A	435	THR	2.7
1	A	453	ALA	2.7
1	A	381	PHE	2.7
1	A	69	PRO	2.7
1	A	315	LYS	2.7
1	A	240	VAL	2.7
1	A	422	ARG	2.7
1	A	46	TRP	2.7
1	A	167	ASP	2.7
1	A	170	PRO	2.7
1	A	346	MET	2.6
1	A	431	LEU	2.6
1	A	425	GLU	2.6
1	A	140	ALA	2.6
1	A	467	LEU	2.6
1	A	429	LYS	2.6
1	A	99	ILE	2.5
1	A	440	LYS	2.5
1	A	108	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	155	PRO	2.5
1	A	42	ALA	2.5
1	A	298	ALA	2.5
1	A	255	THR	2.5
1	A	109	GLY	2.5
1	A	241	ALA	2.5
1	A	420	GLU	2.5
1	A	457	GLY	2.5
1	A	379	GLY	2.4
1	A	161	GLN	2.4
1	A	143	ILE	2.4
1	A	76	VAL	2.4
1	A	314	PHE	2.4
1	A	177	ALA	2.4
1	A	40	VAL	2.4
1	A	246	THR	2.3
1	A	154	HIS	2.3
1	A	275	ILE	2.3
1	A	279	THR	2.3
1	A	66	MET	2.3
1	A	484	MET	2.3
1	A	96	SER	2.3
1	A	178	SER	2.3
1	A	75	GLY	2.3
1	A	34	ALA	2.3
1	A	237	ILE	2.3
1	A	325	SER	2.3
1	A	52	ARG	2.3
1	A	269	VAL	2.3
1	A	223	GLY	2.3
1	A	91	LEU	2.3
1	A	261	LEU	2.3
1	A	186	ILE	2.2
1	A	362	CYS	2.2
1	A	391	ILE	2.2
1	A	384	ASN	2.2
1	A	396	ASN	2.2
1	A	264	LYS	2.2
1	A	455	LYS	2.2
1	A	311	CYS	2.2
1	A	221	THR	2.2
1	A	27	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	322	TYR	2.2
1	A	93	PRO	2.2
1	A	38	ILE	2.2
1	A	296	HIS	2.2
1	A	217	ALA	2.2
1	A	353	THR	2.2
1	A	351	ASN	2.2
1	A	74	PHE	2.2
1	A	73	ALA	2.1
1	A	446	ALA	2.1
1	A	474	GLU	2.1
1	A	139	ARG	2.1
1	A	259	THR	2.1
1	A	307	ASN	2.1
1	A	103	ALA	2.1
1	A	84	VAL	2.1
1	A	472	GLU	2.1
1	A	335	MET	2.1
1	A	156	ASN	2.1
1	A	233	VAL	2.1
1	A	104	ASP	2.1
1	A	162	SER	2.1
1	A	229	TYR	2.1
1	A	62	ALA	2.0
1	A	377	SER	2.0
1	A	432	MET	2.0
1	A	460	LEU	2.0
1	A	401	ILE	2.0
1	A	328	ARG	2.0
1	A	164	SER	2.0
1	A	182	GLN	2.0
1	A	400	LEU	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.