



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:28 AM UTC

PDB ID : 5EYV / pdb_00005eyv
Title : Crystal Structure of Adenylosuccinate lyase from Schistosoma mansoni in APO form.
Authors : Romanello, L.; Torini, J.R.; Bird, L.E.; Nettleship, J.E.; Owens, R.J.; Reddivari, Y.; Brandao-Neto, J.; Pereira, H.M.
Deposited on : 2015-11-25
Resolution : 2.14 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

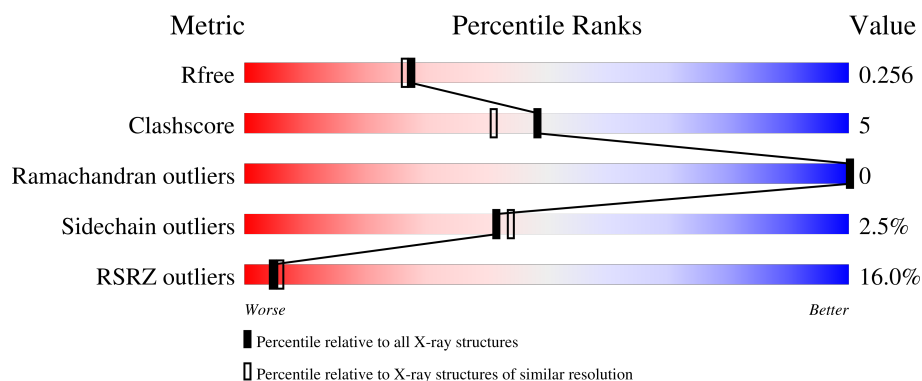
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	497	
1	B	497	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7268 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 Adenylosuccinate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	466	Total	C	N	O	S	0	0	0
			3602	2282	635	658	27			
1	B	420	Total	C	N	O	S	0	0	0
			3269	2076	573	595	25			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	initiating methionine	UNP G4VQX9
A	-15	ALA	-	expression tag	UNP G4VQX9
A	-14	HIS	-	expression tag	UNP G4VQX9
A	-13	HIS	-	expression tag	UNP G4VQX9
A	-12	HIS	-	expression tag	UNP G4VQX9
A	-11	HIS	-	expression tag	UNP G4VQX9
A	-10	HIS	-	expression tag	UNP G4VQX9
A	-9	HIS	-	expression tag	UNP G4VQX9
A	-8	SER	-	expression tag	UNP G4VQX9
A	-7	SER	-	expression tag	UNP G4VQX9
A	-6	GLY	-	expression tag	UNP G4VQX9
A	-5	LEU	-	expression tag	UNP G4VQX9
A	-4	GLU	-	expression tag	UNP G4VQX9
A	-3	VAL	-	expression tag	UNP G4VQX9
A	-2	LEU	-	expression tag	UNP G4VQX9
A	-1	PHE	-	expression tag	UNP G4VQX9
A	0	GLN	-	expression tag	UNP G4VQX9
B	-16	MET	-	initiating methionine	UNP G4VQX9
B	-15	ALA	-	expression tag	UNP G4VQX9
B	-14	HIS	-	expression tag	UNP G4VQX9
B	-13	HIS	-	expression tag	UNP G4VQX9
B	-12	HIS	-	expression tag	UNP G4VQX9
B	-11	HIS	-	expression tag	UNP G4VQX9
B	-10	HIS	-	expression tag	UNP G4VQX9
B	-9	HIS	-	expression tag	UNP G4VQX9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	SER	-	expression tag	UNP G4VQX9
B	-7	SER	-	expression tag	UNP G4VQX9
B	-6	GLY	-	expression tag	UNP G4VQX9
B	-5	LEU	-	expression tag	UNP G4VQX9
B	-4	GLU	-	expression tag	UNP G4VQX9
B	-3	VAL	-	expression tag	UNP G4VQX9
B	-2	LEU	-	expression tag	UNP G4VQX9
B	-1	PHE	-	expression tag	UNP G4VQX9
B	0	GLN	-	expression tag	UNP G4VQX9

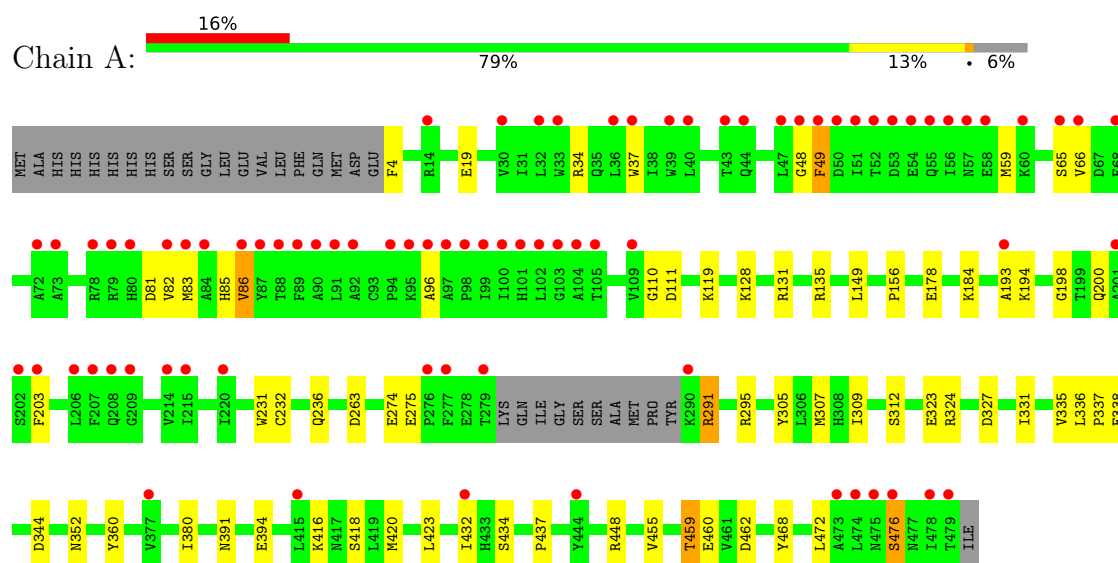
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	174	Total O 174 174	0	0
2	B	223	Total O 223 223	0	0

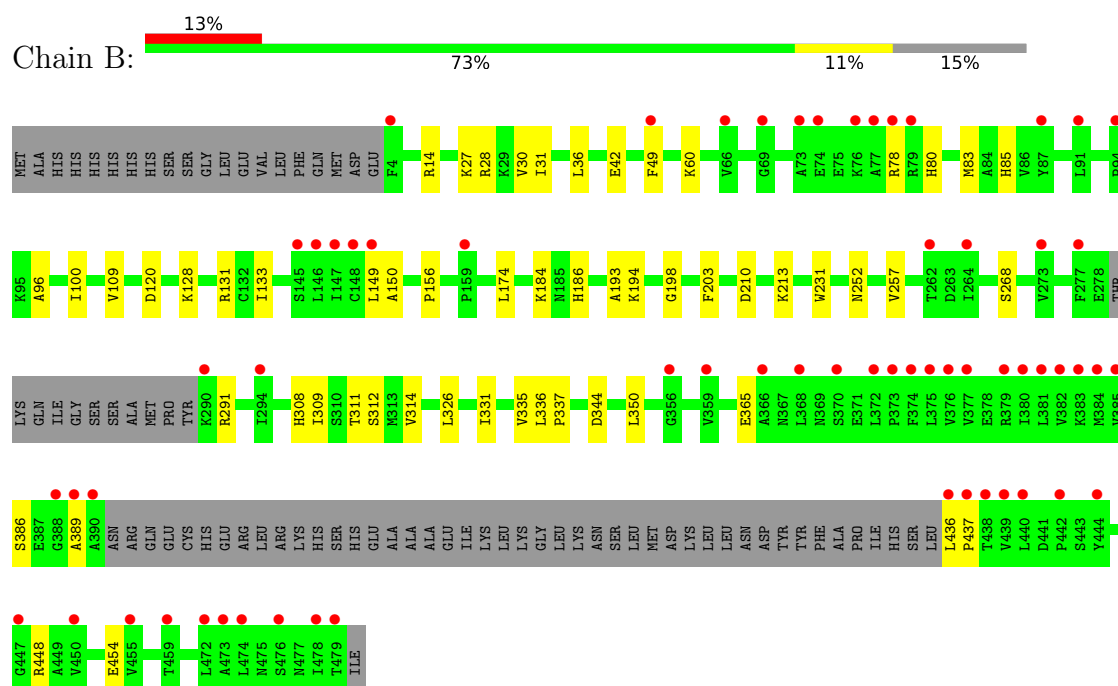
3 Residue-property plots [i](#)

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: Adenylosuccinate lyase



• Molecule 1: Adenylosuccinate lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	76.16Å 82.63Å 163.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.16 – 2.14 58.16 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.8 (58.16-2.14) 99.8 (58.16-2.14)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.14Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.222 , 0.256 0.224 , 0.256	Depositor DCC
R_{free} test set	2903 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7268	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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	0.13	0/3666	0.31	0/4971
1	B	0.10	0/3327	0.31	1/4510 (0.0%)
All	All	0.12	0/6993	0.31	1/9481 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	389	ALA	CB-CA-C	-6.20	109.44	116.63

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	3602	0	3581	48	0
1	B	3269	0	3281	31	0
2	A	174	0	0	17	1
2	B	223	0	0	9	1
All	All	7268	0	6862	75	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 5.

All (75) 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:416:LYS:O	2:A:502:HOH:O	1.86	0.93
1:A:48:GLY:O	2:A:501:HOH:O	1.86	0.92
1:B:85:HIS:O	2:B:501:HOH:O	1.92	0.87
1:B:194:LYS:NZ	1:B:231:TRP:O	2.13	0.80
1:A:448:ARG:NH1	2:A:508:HOH:O	2.14	0.79
1:B:436:LEU:N	2:B:504:HOH:O	2.15	0.79
1:A:110:GLY:O	2:A:503:HOH:O	2.00	0.79
1:A:263:ASP:OD1	2:A:504:HOH:O	2.02	0.77
1:B:268:SER:OG	2:B:502:HOH:O	2.02	0.77
1:A:462:ASP:OD1	2:A:505:HOH:O	2.03	0.74
1:B:42:GLU:O	2:B:503:HOH:O	2.04	0.74
1:A:295:ARG:NH1	1:A:352:ASN:OD1	2.22	0.72
1:A:275:GLU:O	2:A:506:HOH:O	2.08	0.71
1:A:232:CYS:SG	2:A:645:HOH:O	2.52	0.68
1:A:85:HIS:O	2:A:507:HOH:O	2.12	0.66
1:A:459:THR:HG22	1:A:460:GLU:HG3	1.78	0.65
1:A:4:PHE:N	2:A:516:HOH:O	2.30	0.65
1:A:194:LYS:HB3	1:A:198:GLY:HA2	1.83	0.61
1:B:128:LYS:NZ	1:B:344:ASP:OD1	2.28	0.61
1:A:476:SER:O	2:A:509:HOH:O	2.15	0.60
1:A:178:GLU:OE2	1:B:186:HIS:NE2	2.32	0.58
1:A:309:ILE:HG12	1:A:335:VAL:HG13	1.86	0.58
1:B:386:SER:O	2:B:505:HOH:O	2.18	0.57
1:A:34:ARG:NH1	1:A:65:SER:O	2.38	0.56
1:A:420:MET:HE1	1:A:437:PRO:HA	1.87	0.56
1:B:149:LEU:HD21	1:B:156:PRO:HB3	1.86	0.55
1:B:28:ARG:NH1	2:B:517:HOH:O	2.39	0.55
1:A:149:LEU:HD21	1:A:156:PRO:HB3	1.89	0.55
1:B:42:GLU:OE2	1:B:60:LYS:NZ	2.37	0.55
1:A:307:MET:HE3	1:B:314:VAL:HG22	1.89	0.54
1:A:391:ASN:HB3	1:A:394:GLU:HB2	1.90	0.54
1:A:200:GLN:OE1	1:B:448:ARG:NH1	2.41	0.53
1:A:418:SER:N	2:A:502:HOH:O	2.42	0.53
1:A:312:SER:HB3	1:A:331:ILE:HD11	1.91	0.52
1:B:309:ILE:HG12	1:B:335:VAL:HG13	1.90	0.51
1:A:59:MET:HE3	1:A:96:ALA:HB1	1.92	0.50
1:A:434:SER:HB3	2:A:579:HOH:O	2.11	0.50
1:A:305:TYR:OH	1:A:338:GLU:OE1	2.29	0.50
1:A:455:VAL:O	1:A:459:THR:HB	2.13	0.49
1:A:380:ILE:HG23	1:A:432:ILE:CD1	2.43	0.48
1:A:327:ASP:OD1	1:A:327:ASP:N	2.46	0.48
1:B:193:ALA:HB1	1:B:203:PHE:CE2	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:PHE:HD1	1:A:49:PHE:HA	1.61	0.48
1:B:27:LYS:O	1:B:31:ILE:HG12	2.13	0.48
1:A:119:LYS:NZ	1:A:184:LYS:O	2.36	0.47
1:B:437:PRO:HD2	2:B:504:HOH:O	2.14	0.47
1:A:83:MET:HA	1:A:86:VAL:HG22	1.98	0.46
1:A:274:GLU:HB2	1:A:360:TYR:HE2	1.79	0.46
1:A:110:GLY:HA2	2:A:503:HOH:O	2.15	0.46
1:A:274:GLU:OE2	2:A:511:HOH:O	2.21	0.46
1:A:336:LEU:HB2	1:A:337:PRO:HD3	1.96	0.46
1:B:96:ALA:O	1:B:100:ILE:HG13	2.16	0.45
1:B:312:SER:HB2	1:B:331:ILE:HD11	1.99	0.45
1:A:37:TRP:CZ2	1:A:86:VAL:HG12	2.51	0.45
1:A:236:GLN:HG2	1:A:324:ARG:HD2	1.99	0.45
1:B:194:LYS:HB3	1:B:198:GLY:HA2	1.99	0.44
1:A:291:ARG:NH1	2:A:527:HOH:O	2.49	0.44
1:B:257:VAL:HG22	1:B:350:LEU:HD22	2.00	0.44
1:B:184:LYS:NZ	2:B:520:HOH:O	2.44	0.44
1:A:231:TRP:HB3	2:A:572:HOH:O	2.17	0.44
1:B:210:ASP:CG	1:B:213:LYS:HD3	2.43	0.44
1:A:81:ASP:OD1	1:A:82:VAL:N	2.50	0.43
1:B:80:HIS:ND1	1:B:83:MET:HG2	2.33	0.43
1:B:133:ILE:HD13	1:B:174:LEU:HD23	2.00	0.43
1:B:36:LEU:HD13	1:B:109:VAL:HA	1.99	0.43
1:A:34:ARG:HA	1:A:37:TRP:CE3	2.54	0.43
1:A:128:LYS:NZ	1:A:344:ASP:OD1	2.40	0.43
1:B:308:HIS:O	1:B:311:THR:HG22	2.20	0.42
1:A:193:ALA:HB1	1:A:203:PHE:CE2	2.54	0.42
1:B:28:ARG:NH2	1:B:120:ASP:OD2	2.47	0.42
1:B:131:ARG:NH2	2:B:526:HOH:O	2.53	0.41
1:B:336:LEU:HB2	1:B:337:PRO:HD3	2.02	0.41
1:A:131:ARG:O	1:A:135:ARG:HG2	2.20	0.41
1:A:323:GLU:HG2	1:B:150:ALA:HB1	2.01	0.41
1:A:468:TYR:O	1:A:472:LEU:HG	2.21	0.41

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)
2:A:672:HOH:O	2:B:684:HOH:O[3_454]	2.16	0.04

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	462/497 (93%)	447 (97%)	15 (3%)	0	100	100
1	B	414/497 (83%)	400 (97%)	14 (3%)	0	100	100
All	All	876/994 (88%)	847 (97%)	29 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	381/434 (88%)	372 (98%)	9 (2%)	43	45
1	B	351/434 (81%)	342 (97%)	9 (3%)	40	42
All	All	732/868 (84%)	714 (98%)	18 (2%)	42	44

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	49	PHE
1	A	66	VAL
1	A	86	VAL
1	A	111	ASP
1	A	291	ARG
1	A	423	LEU
1	A	459	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	476	SER
1	B	14	ARG
1	B	30	VAL
1	B	49	PHE
1	B	78	ARG
1	B	252	ASN
1	B	291	ARG
1	B	326	LEU
1	B	365	GLU
1	B	454	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	GLN
1	A	475	ASN
1	A	477	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 ⓘ

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	466/497 (93%)	0.78	79 (16%) 4 5	18, 44, 98, 129	0
1	B	420/497 (84%)	0.87	63 (15%) 5 6	20, 50, 93, 122	0
All	All	886/994 (89%)	0.82	142 (16%) 5 6	18, 46, 95, 129	0

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	436	LEU	7.2
1	B	390	ALA	5.6
1	A	474	LEU	4.8
1	A	52	THR	4.6
1	A	99	ILE	4.4
1	A	50	ASP	4.4
1	B	479	THR	4.3
1	A	66	VAL	4.3
1	A	86	VAL	4.3
1	B	478	ILE	4.2
1	B	438	THR	4.1
1	A	87	TYR	4.1
1	B	385	VAL	4.0
1	B	381	LEU	3.9
1	B	440	LEU	3.9
1	B	439	VAL	3.9
1	B	49	PHE	3.9
1	B	149	LEU	3.7
1	B	377	VAL	3.7
1	A	56	ILE	3.6
1	A	95	LYS	3.6
1	B	389	ALA	3.6
1	B	374	PHE	3.6
1	A	100	ILE	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	444	TYR	3.5
1	A	479	THR	3.5
1	A	201	ALA	3.5
1	A	206	LEU	3.4
1	A	49	PHE	3.4
1	A	102	LEU	3.4
1	A	103	GLY	3.3
1	A	54	GLU	3.3
1	A	90	ALA	3.3
1	B	290	LYS	3.3
1	A	51	ILE	3.2
1	A	89	PHE	3.2
1	A	55	GLN	3.2
1	A	91	LEU	3.2
1	A	83	MET	3.2
1	B	77	ALA	3.2
1	A	478	ILE	3.2
1	B	437	PRO	3.2
1	A	65	SER	3.1
1	B	382	VAL	3.1
1	A	37	TRP	3.1
1	A	47	LEU	3.1
1	B	294	ILE	3.1
1	A	36	LEU	3.0
1	A	202	SER	3.0
1	A	276	PRO	3.0
1	A	80	HIS	3.0
1	B	384	MET	3.0
1	A	33	TRP	3.0
1	A	207	PHE	2.8
1	A	58	GLU	2.8
1	B	376	VAL	2.8
1	B	145	SER	2.8
1	A	73	ALA	2.8
1	A	97	ALA	2.8
1	A	214	VAL	2.8
1	B	146	LEU	2.7
1	B	380	ILE	2.7
1	A	68	PHE	2.7
1	A	92	ALA	2.7
1	B	368	LEU	2.7
1	A	105	THR	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	109	VAL	2.6
1	A	43	THR	2.6
1	A	30	VAL	2.6
1	A	377	VAL	2.6
1	A	104	ALA	2.6
1	B	73	ALA	2.6
1	B	442	PRO	2.6
1	B	473	ALA	2.5
1	B	370	SER	2.5
1	A	94	PRO	2.5
1	A	32	LEU	2.5
1	B	474	LEU	2.5
1	B	147	ILE	2.5
1	B	375	LEU	2.5
1	A	101	HIS	2.5
1	B	459	THR	2.4
1	A	98	PRO	2.4
1	A	96	ALA	2.4
1	A	79	ARG	2.4
1	B	78	ARG	2.4
1	A	39	TRP	2.4
1	A	57	ASN	2.4
1	A	277	PHE	2.4
1	B	87	TYR	2.4
1	A	44	GLN	2.4
1	A	475	ASN	2.4
1	B	388	GLY	2.4
1	B	76	LYS	2.4
1	B	91	LEU	2.3
1	A	476	SER	2.3
1	A	193	ALA	2.3
1	B	79	ARG	2.3
1	B	4	PHE	2.3
1	A	208	GLN	2.3
1	A	444	TYR	2.3
1	B	69	GLY	2.3
1	B	476	SER	2.3
1	B	447	GLY	2.3
1	A	279	THR	2.2
1	A	72	ALA	2.2
1	A	209	GLY	2.2
1	B	366	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	215	ILE	2.2
1	B	264	ILE	2.2
1	B	359	VAL	2.2
1	B	373	PRO	2.2
1	A	84	ALA	2.2
1	A	415	LEU	2.2
1	A	88	THR	2.2
1	B	372	LEU	2.2
1	A	14	ARG	2.2
1	A	60	LYS	2.2
1	B	262	THR	2.2
1	A	203	PHE	2.1
1	B	148	CYS	2.1
1	B	472	LEU	2.1
1	B	383	LYS	2.1
1	A	220	ILE	2.1
1	A	82	VAL	2.1
1	B	66	VAL	2.1
1	A	40	LEU	2.1
1	B	74	GLU	2.1
1	B	94	PRO	2.1
1	A	432	ILE	2.1
1	B	379	ARG	2.1
1	A	473	ALA	2.1
1	A	290	LYS	2.1
1	B	277	PHE	2.1
1	B	450	VAL	2.1
1	B	455	VAL	2.1
1	A	78	ARG	2.0
1	B	356	GLY	2.0
1	B	273	VAL	2.0
1	A	53	ASP	2.0
1	B	159	PRO	2.0
1	A	48	GLY	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 [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.