



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 02:58 PM GMT

PDB ID : 2CVY
Title : Structures of Yeast Ribonucleotide Reductase I
Authors : Xu, H.; Faber, C.; Uchiki, T.; Fairman, J.W.; Racca, J.; Dealwis, C.
Deposited on : 2005-06-14
Resolution : 2.40 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

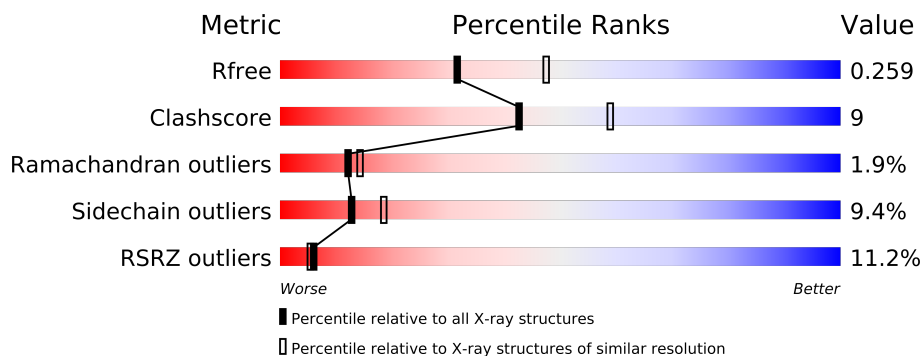
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	888	
2	B	9	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	2001	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5298 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Ribonucleoside-diphosphatereductase large chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	640	Total	C	N	O	S	0	0	0
			5128	3272	865	960	31			

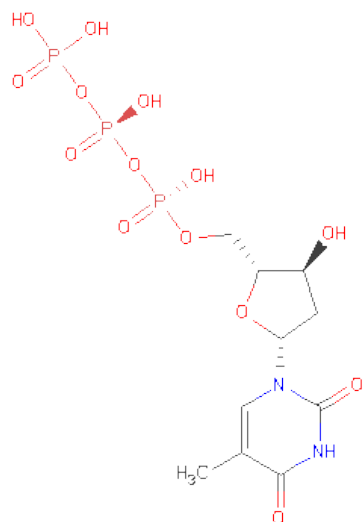
- Molecule 2 is a protein called 9-per peptide from Ribonucleoside-diphosphatereductase small chain 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	0	0	0
			66	44	8	14			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

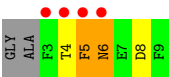
- Molecule 4 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: C₁₀H₁₇N₂O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	29	10	2	14	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	74	Total	O	0	0
			74	74		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	108.06Å 117.59Å 64.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 49.10 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.9 (50.00-2.40) 97.9 (49.10-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.218 , 0.263 0.216 , 0.259	Depositor DCC
R_{free} test set	3222 reflections (11.12%)	DCC
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 36.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 32194 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5298	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, TTP

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	0.67	0/5247	0.86	16/7103 (0.2%)
2	B	0.63	0/68	0.93	1/89 (1.1%)
All	All	0.67	0/5315	0.87	17/7192 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	503	ARG	NE-CZ-NH2	-9.20	115.70	120.30
1	A	365	ASP	CB-CG-OD2	7.61	125.14	118.30
1	A	233	ASP	CB-CG-OD2	7.20	124.78	118.30
1	A	226	ASP	CB-CG-OD2	7.16	124.74	118.30
1	A	100	ASP	CB-CG-OD2	7.10	124.69	118.30
1	A	336	ASP	CB-CG-OD2	6.62	124.25	118.30
1	A	707	ASP	CB-CG-OD2	6.13	123.82	118.30
1	A	138	ASP	CB-CG-OD2	5.97	123.67	118.30
2	B	8	ASP	CB-CG-OD2	5.92	123.63	118.30
1	A	438	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	648	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	140	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	118	ASP	CB-CG-OD2	5.21	122.98	118.30
1	A	182	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	701	ASP	CB-CG-OD2	5.08	122.87	118.30
1	A	503	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	A	119	ASP	CB-CG-OD2	5.02	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5128	0	5057	90	0
2	B	66	0	49	2	0
3	A	1	0	0	0	0
4	A	29	0	13	1	0
5	A	74	0	0	3	0
All	All	5298	0	5119	92	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (92) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:159:ILE:HG23	1:A:160:ASN:H	1.35	0.91
1:A:270:ASN:HB3	1:A:274:PRO:HG2	1.54	0.89
2:B:5:PHE:O	2:B:6:ASN:HB2	1.82	0.78
1:A:251:HIS:HD2	5:A:2014:HOH:O	1.65	0.78
1:A:170:LEU:HD22	1:A:173:ARG:NH2	1.99	0.77
1:A:263:ALA:HB3	4:A:1001:TTP:O1G	1.85	0.74
1:A:213:PRO:HD2	1:A:489:TYR:HB2	1.69	0.74
1:A:109:THR:HG23	1:A:111:LYS:H	1.53	0.73
1:A:334:ILE:HD12	1:A:404:VAL:HG13	1.73	0.71
1:A:210:THR:HB	1:A:211:PRO:HD2	1.75	0.69
1:A:273:ILE:HD12	1:A:314:ILE:HD11	1.76	0.67
1:A:296:ALA:HB3	1:A:427:LEU:HD21	1.79	0.65
1:A:486:ASP:CG	1:A:503:ARG:HH22	2.01	0.64
1:A:318:HIS:O	1:A:324:ARG:NH1	2.30	0.64
1:A:317:ASN:HA	1:A:326:ARG:NH2	2.14	0.63
1:A:445:LEU:HD23	1:A:506:ALA:HB3	1.81	0.61
1:A:486:ASP:OD2	1:A:503:ARG:NH2	2.33	0.61
1:A:127:ASN:HB2	1:A:131:LEU:HD22	1.82	0.61
1:A:481:LEU:HB3	1:A:505:ILE:HD12	1.82	0.61
1:A:606:MET:HE2	5:A:2017:HOH:O	2.00	0.60
1:A:538:THR:HB	1:A:583:TRP:NE1	2.16	0.60
1:A:92:LYS:HB2	1:A:166:ARG:HH22	1.67	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:159:ILE:HG23	1:A:160:ASN:N	2.13	0.59
1:A:280:ASN:HB2	1:A:328:LEU:HD11	1.84	0.58
1:A:438:ASP:OD1	1:A:497:LYS:NZ	2.34	0.58
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.38	0.58
1:A:92:LYS:HB2	1:A:166:ARG:NH2	2.19	0.57
1:A:332:LEU:HD11	1:A:392:ILE:HD12	1.87	0.57
1:A:456:THR:HA	1:A:463:SER:HA	1.88	0.56
1:A:212:LYS:HD2	1:A:489:TYR:CE1	2.41	0.56
1:A:318:HIS:H	1:A:318:HIS:CD2	2.23	0.56
1:A:317:ASN:HA	1:A:326:ARG:HH21	1.71	0.55
1:A:510:GLN:HB3	1:A:608:THR:HG21	1.87	0.55
1:A:401:THR:HB	1:A:402:PRO:HA	1.90	0.54
1:A:444:ASN:HD21	1:A:499:ASN:HD21	1.56	0.53
1:A:625:THR:HA	1:A:687:VAL:HG12	1.91	0.53
1:A:92:LYS:HD2	1:A:166:ARG:HH12	1.74	0.52
1:A:508:GLY:HA3	1:A:606:MET:CE	2.40	0.52
1:A:388:LEU:O	1:A:392:ILE:HG12	2.10	0.52
1:A:484:VAL:O	1:A:488:ASN:HB2	2.10	0.52
1:A:506:ALA:HB1	1:A:604:ALA:HB3	1.93	0.51
1:A:106:ASN:OD1	1:A:109:THR:HG22	2.11	0.51
1:A:101:LEU:HB3	1:A:115:MET:HB3	1.93	0.51
1:A:383:ILE:CG1	1:A:384:LYS:H	2.23	0.51
1:A:409:ALA:HB2	5:A:2019:HOH:O	2.11	0.51
1:A:316:LYS:HD3	1:A:318:HIS:CE1	2.47	0.50
1:A:508:GLY:HA3	1:A:606:MET:HE1	1.94	0.49
1:A:217:SER:OG	1:A:445:LEU:HD12	2.13	0.48
1:A:93:GLN:O	1:A:97:VAL:HG13	2.14	0.48
1:A:455:GLU:O	1:A:464:THR:N	2.39	0.48
1:A:159:ILE:CG2	1:A:160:ASN:H	2.18	0.48
1:A:602:THR:N	1:A:707:ASP:OD2	2.47	0.47
1:A:745:THR:O	1:A:746:GLN:HB2	2.14	0.46
1:A:413:LYS:HE3	1:A:575:TRP:CE2	2.50	0.46
1:A:266:ASN:H	1:A:266:ASN:ND2	2.12	0.46
1:A:273:ILE:HB	1:A:274:PRO:HD3	1.97	0.46
1:A:220:LEU:HD21	1:A:426:ASN:HB3	1.96	0.46
1:A:217:SER:CB	1:A:445:LEU:HD12	2.46	0.46
1:A:282:THR:O	1:A:286:VAL:HG22	2.16	0.46
1:A:326:ARG:O	1:A:327:ASP:HB2	2.15	0.45
1:A:203:PRO:HG2	1:A:217:SER:HA	1.98	0.45
1:A:170:LEU:HD22	1:A:173:ARG:HH22	1.75	0.45
1:A:713:ASN:ND2	1:A:742:TYR:H	2.14	0.44
1:A:273:ILE:HG21	1:A:323:ILE:HA	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:534:GLN:O	1:A:538:THR:HG23	2.16	0.44
1:A:713:ASN:HD22	1:A:742:TYR:H	1.65	0.44
1:A:195:LEU:O	1:A:196:LYS:HB2	2.17	0.44
1:A:675:ASN:ND2	1:A:675:ASN:O	2.47	0.44
1:A:383:ILE:HG13	1:A:384:LYS:H	1.82	0.44
1:A:280:ASN:CB	1:A:328:LEU:HD11	2.48	0.43
1:A:120:VAL:O	1:A:124:VAL:HG23	2.19	0.43
1:A:475:LYS:HD2	1:A:546:ALA:HB2	2.00	0.43
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.46	0.43
1:A:135:ILE:HG23	1:A:168:GLN:HB3	2.00	0.43
1:A:431:ILE:HG13	1:A:443:CYS:SG	2.59	0.43
1:A:351:PHE:HE1	1:A:371:TYR:CE1	2.37	0.42
1:A:472:GLU:O	1:A:475:LYS:HB2	2.19	0.42
1:A:450:LEU:N	1:A:451:PRO:CD	2.82	0.42
2:B:5:PHE:O	2:B:6:ASN:CB	2.59	0.42
1:A:172:MET:O	1:A:176:LEU:HD22	2.20	0.42
1:A:641:VAL:HG13	1:A:646:LEU:HD22	2.02	0.41
1:A:328:LEU:HD12	1:A:328:LEU:H	1.85	0.41
1:A:627:ASN:HB3	1:A:645:LEU:HD22	2.02	0.41
1:A:481:LEU:CD1	1:A:505:ILE:HG23	2.50	0.41
1:A:300:TYR:OH	1:A:425:SER:HB3	2.21	0.41
1:A:621:PHE:HZ	1:A:711:SER:O	2.02	0.41
1:A:724:LEU:HD22	1:A:728:HIS:CD2	2.55	0.41
1:A:109:THR:OG1	1:A:111:LYS:HG3	2.21	0.40
1:A:124:VAL:HA	1:A:131:LEU:HD23	2.02	0.40
1:A:490:TYR:HA	1:A:491:PRO:HD2	1.91	0.40
1:A:483:ARG:NH2	1:A:487:ARG:HD2	2.36	0.40
1:A:364:GLY:O	1:A:368:GLU:HG3	2.21	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	634/888 (71%)	589 (93%)	34 (5%)	11 (2%)	14 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	5/9 (56%)	4 (80%)	0	1 (20%)	0	0
All	All	639/897 (71%)	593 (93%)	34 (5%)	12 (2%)	12	14

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	6	ASN
1	A	245	ALA
1	A	327	ASP
1	A	458	GLU
1	A	659	MET
1	A	664	ILE
1	A	93	GLN
1	A	159	ILE
1	A	320	LYS
1	A	639	GLN
1	A	666	GLN
1	A	196	LYS

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	557/761 (73%)	506 (91%)	51 (9%)	13	19
2	B	7/7 (100%)	5 (71%)	2 (29%)	0	0
All	All	564/768 (73%)	511 (91%)	53 (9%)	13	18

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	THR
1	A	97	VAL
1	A	131	LEU
1	A	142	GLN
1	A	154	SER
1	A	170	LEU

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Mol	Chain	Res	Type
1	A	176	LEU
1	A	214	GLN
1	A	244	THR
1	A	266	ASN
1	A	284	ARG
1	A	297	PHE
1	A	301	LEU
1	A	314	ILE
1	A	317	ASN
1	A	321	GLU
1	A	322	GLU
1	A	326	ARG
1	A	327	ASP
1	A	328	LEU
1	A	337	LEU
1	A	359	LEU
1	A	383	ILE
1	A	388	LEU
1	A	427	LEU
1	A	462	THR
1	A	469	LYS
1	A	505	ILE
1	A	507	LEU
1	A	512	LEU
1	A	518	LEU
1	A	524	ASP
1	A	530	LEU
1	A	538	THR
1	A	594	LYS
1	A	597	VAL
1	A	606	MET
1	A	610	SER
1	A	628	MET
1	A	638	PHE
1	A	659	MET
1	A	663	LEU
1	A	675	ASN
1	A	686	THR
1	A	707	ASP
1	A	711	SER
1	A	712	LEU
1	A	714	LEU

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Mol	Chain	Res	Type
1	A	721	MET
1	A	724	LEU
1	A	726	SER
2	B	4	THR
2	B	5	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	142	GLN
1	A	168	GLN
1	A	251	HIS
1	A	266	ASN
1	A	317	ASN
1	A	444	ASN
1	A	613	GLN
1	A	618	ASN
1	A	692	GLN
1	A	713	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	TTP	A	1001	3	30,30,30	1.19	2 (6%)	42,47,47	1.44	4 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TTP	A	1001	3	-	0/19/34/34	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1001	TTP	C2-N1	3.53	1.42	1.38
4	A	1001	TTP	C4-C5	3.34	1.50	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001	TTP	N3-C2-N1	5.14	120.26	115.97
4	A	1001	TTP	PB-O3A-PA	-3.33	121.92	131.68
4	A	1001	TTP	PB-O3B-PG	-2.84	123.35	131.68
4	A	1001	TTP	C4-N3-C2	-2.28	120.72	125.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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	640/888 (72%)	0.56	69 (10%) 6 6	28, 43, 82, 93	0
2	B	7/9 (77%)	2.56	4 (57%) 0 0	75, 84, 86, 87	0
All	All	647/897 (72%)	0.59	73 (11%) 6 5	28, 43, 84, 93	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	460	GLY	8.7
1	A	630	SER	7.6
1	A	638	PHE	7.5
1	A	323	ILE	7.3
1	A	639	GLN	6.9
1	A	664	ILE	6.1
1	A	321	GLU	5.9
1	A	325	ALA	5.5
1	A	320	LYS	5.5
1	A	319	GLY	5.3
2	B	4	THR	5.3
1	A	91	THR	5.3
1	A	145	TYR	5.2
1	A	646	LEU	4.9
1	A	647	ARG	4.8
1	A	456	THR	4.7
2	B	3	PHE	4.7
1	A	660	LYS	4.5
1	A	326	ARG	4.5
1	A	146	PHE	4.5
1	A	459	ASP	4.4
1	A	457	SER	4.4
1	A	661	GLN	4.3
1	A	322	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	461	LYS	4.2
1	A	318	HIS	4.2
1	A	429	CYS	4.1
1	A	667	ASN	4.0
1	A	390	TYR	4.0
1	A	159	ILE	3.9
1	A	462	THR	3.9
1	A	431	ILE	3.7
1	A	432	VAL	3.4
1	A	746	GLN	3.3
1	A	675	ASN	3.3
1	A	657	GLU	3.3
1	A	141	PHE	3.3
1	A	655	TRP	3.2
1	A	628	MET	3.2
1	A	153	ARG	3.2
1	A	663	LEU	3.2
1	A	150	THR	3.1
1	A	629	TYR	2.9
1	A	317	ASN	2.9
1	A	428	CYS	2.9
1	A	266	ASN	2.9
1	A	650	VAL	2.9
1	A	115	MET	2.9
2	B	6	ASN	2.9
2	B	5	PHE	2.8
1	A	142	GLN	2.8
1	A	154	SER	2.7
1	A	410	CYS	2.7
1	A	133	SER	2.7
1	A	613	GLN	2.7
1	A	653	GLY	2.6
1	A	121	TYR	2.6
1	A	651	ASP	2.5
1	A	162	GLN	2.4
1	A	409	ALA	2.4
1	A	426	ASN	2.4
1	A	130	LYS	2.4
1	A	102	TYR	2.3
1	A	717	ARG	2.3
1	A	96	LYS	2.3
1	A	738	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	324	ARG	2.3
1	A	425	SER	2.3
1	A	298	ALA	2.2
1	A	605	PRO	2.1
1	A	447	SER	2.1
1	A	430	GLU	2.1
1	A	509	VAL	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 carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MG	A	2001	1/1	0.29	22.37	48,48,48,48	0
4	TTP	A	1001	29/29	0.14	-0.65	43,50,59,63	0

6.5 Other polymers ⓘ

There are no such residues in this entry.