



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:09 PM UTC

PDB ID : 3FQD / pdb_00003fqd
Title : Crystal Structure of the S. pombe Rat1-Rai1 Complex
Authors : Xiang, S.; Tong, L.
Deposited on : 2009-01-07
Resolution : 2.20 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

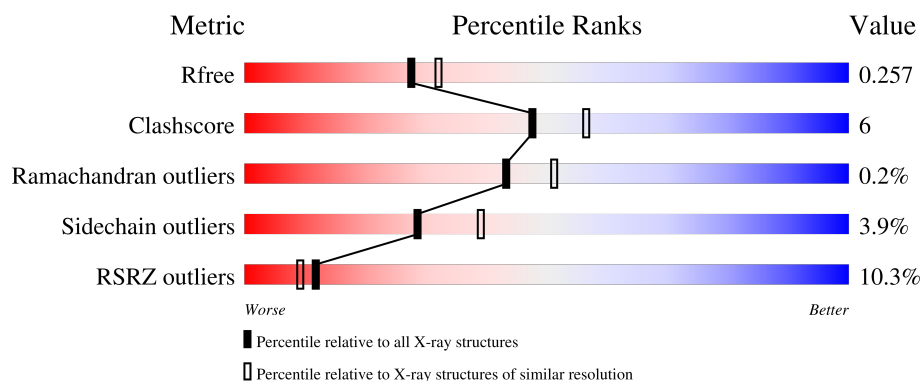
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	899	 10% 65% 10% • 24%
2	B	352	 4% 79% 14% • 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8926 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 5'-3' exoribonuclease 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	682	Total	C	N	O	S	Se	0	0	0
			5550	3553	946	1029	7	15			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	expression tag	UNP P40848
A	0	ALA	-	expression tag	UNP P40848
A	0A	SER	-	expression tag	UNP P40848
A	886	ALA	-	expression tag	UNP P40848
A	887	ALA	-	expression tag	UNP P40848
A	888	ALA	-	expression tag	UNP P40848
A	889	LEU	-	expression tag	UNP P40848
A	890	GLU	-	expression tag	UNP P40848
A	891	HIS	-	expression tag	UNP P40848
A	892	HIS	-	expression tag	UNP P40848
A	893	HIS	-	expression tag	UNP P40848
A	894	HIS	-	expression tag	UNP P40848
A	895	HIS	-	expression tag	UNP P40848
A	896	HIS	-	expression tag	UNP P40848

- Molecule 2 is a protein called Protein din1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	332	Total	C	N	O	S	Se	0	0	0
			2721	1755	452	496	7	11			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

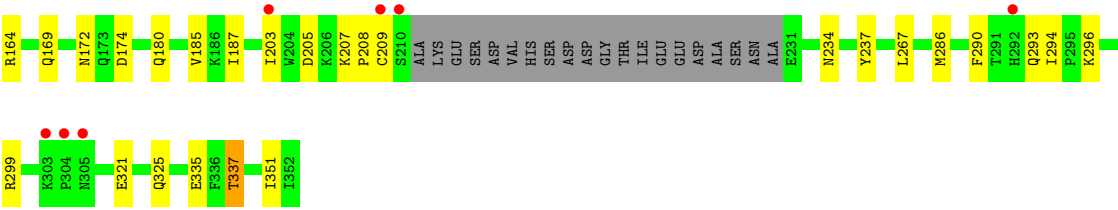
- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	387	Total	O	0	0
			387	387		
5	B	261	Total	O	0	0
			261	261		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	96.69Å 190.87Å 84.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.3 (30.00-2.20) 94.2 (30.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.218 , 0.258 0.217 , 0.257	Depositor DCC
R_{free} test set	3924 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8926	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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](#)

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

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	0.48	2/5675 (0.0%)	0.85	2/7669 (0.0%)
2	B	0.49	1/2787 (0.0%)	0.82	0/3767
All	All	0.49	3/8462 (0.0%)	0.84	2/11436 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	406	ASN	C-O	6.66	1.36	1.23
1	A	31	ASP	C-N	5.47	1.41	1.33
2	B	294	ILE	CA-CB	5.33	1.57	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ASP	O-C-N	6.50	130.26	122.26
1	A	328	PHE	N-CA-C	5.13	116.73	111.03

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	5550	0	5479	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2721	0	2715	30	0
3	B	1	0	0	0	0
4	B	6	0	8	0	0
5	A	387	0	0	3	0
5	B	261	0	0	3	0
All	All	8926	0	8202	93	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 6.

All (93) 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:194:ARG:HD3	1:A:766:MSE:HE1	1.27	1.10
1:A:194:ARG:HD3	1:A:766:MSE:CE	2.05	0.86
1:A:194:ARG:CD	1:A:766:MSE:HE1	2.06	0.83
1:A:863:THR:HG22	1:A:864:PRO:HD2	1.62	0.81
1:A:857:MSE:HA	1:A:857:MSE:HE3	1.63	0.79
2:B:86:MSE:HE1	2:B:91:LEU:HD22	1.65	0.78
1:A:857:MSE:HA	1:A:857:MSE:CE	2.15	0.76
1:A:855:VAL:HG13	1:A:857:MSE:HE1	1.67	0.76
1:A:78:MSE:HG3	1:A:79:MSE:HE3	1.67	0.76
1:A:681:LYS:HD2	1:A:693:THR:HG21	1.70	0.74
2:B:23:GLU:HB2	2:B:234:ASN:HD21	1.52	0.74
2:B:203:ILE:HG22	2:B:237:TYR:HD2	1.56	0.71
1:A:855:VAL:HG13	1:A:857:MSE:CE	2.20	0.71
2:B:44:TYR:CE2	2:B:203:ILE:HD11	2.26	0.70
2:B:42:LEU:HD11	2:B:203:ILE:HG23	1.75	0.68
1:A:78:MSE:HG3	1:A:79:MSE:CE	2.23	0.68
1:A:692:MSE:HE3	1:A:703:TYR:CE2	2.30	0.66
1:A:27:GLU:HB2	1:A:35:ILE:HB	1.80	0.64
1:A:370:THR:CG2	5:A:906:HOH:O	2.45	0.63
1:A:119:ARG:NH2	1:A:163:THR:OG1	2.32	0.63
1:A:365:MSE:HG2	1:A:379:ARG:HG2	1.80	0.62
2:B:94:ARG:NH2	5:B:1234:HOH:O	2.27	0.62
2:B:203:ILE:HG22	2:B:237:TYR:CD2	2.34	0.62
1:A:79:MSE:HA	1:A:79:MSE:HE2	1.84	0.60
1:A:764:HIS:CE1	1:A:766:MSE:HE2	2.37	0.60
2:B:42:LEU:HD11	2:B:203:ILE:CG2	2.32	0.59
1:A:620:GLY:HA2	1:A:637:TRP:CH2	2.38	0.59
1:A:1:MSE:SE	1:A:6:LEU:HB2	2.52	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ILE:O	1:A:333:VAL:HG22	2.05	0.57
1:A:240:MSE:HE1	1:A:326:TRP:HZ3	1.70	0.57
1:A:857:MSE:HE3	1:A:857:MSE:CA	2.34	0.57
2:B:127:GLU:OE2	2:B:129:ARG:HD2	2.05	0.56
1:A:162:ILE:HA	1:A:169:MSE:HE3	1.88	0.55
2:B:296:LYS:HG2	2:B:299:ARG:HH12	1.71	0.55
1:A:779:ARG:HH11	1:A:781:GLY:HA3	1.71	0.55
2:B:82:LYS:HZ2	2:B:84:ILE:HD11	1.72	0.55
1:A:583:THR:HB	1:A:598:GLN:HE22	1.71	0.55
2:B:115:LEU:HG	2:B:126:MSE:HG3	1.90	0.54
1:A:676:LEU:O	1:A:692:MSE:HE1	2.08	0.53
1:A:692:MSE:HE3	1:A:703:TYR:CD2	2.45	0.52
2:B:337:THR:HG22	5:B:900:HOH:O	2.08	0.52
2:B:82:LYS:HE3	5:B:1059:HOH:O	2.10	0.51
1:A:245:THR:HG22	1:A:247:GLU:H	1.76	0.51
1:A:134:GLN:HE22	1:A:153:LYS:HE2	1.77	0.50
1:A:592:ARG:HD3	1:A:646:PHE:CD1	2.46	0.50
2:B:142:MSE:HG2	2:B:145:TRP:CZ3	2.46	0.50
1:A:248:PRO:HG3	1:A:857:MSE:HE1	1.94	0.50
2:B:28:SER:HB3	2:B:41:LYS:HG2	1.94	0.50
1:A:863:THR:CG2	1:A:864:PRO:HD2	2.37	0.49
1:A:240:MSE:HE1	1:A:326:TRP:CZ3	2.47	0.48
2:B:169:GLN:NE2	2:B:172:ASN:HD22	2.11	0.48
1:A:64:SER:HA	1:A:78:MSE:HE1	1.95	0.48
2:B:21:PRO:HG3	2:B:187:ILE:HD12	1.94	0.48
1:A:181:ILE:HG22	1:A:828:ILE:HD13	1.96	0.48
1:A:399:LYS:HG3	1:A:587:TYR:CD2	2.48	0.47
1:A:583:THR:HB	1:A:598:GLN:NE2	2.29	0.47
1:A:3:VAL:HB	1:A:4:PRO:HD3	1.96	0.47
1:A:716:PHE:HD2	1:A:718:TRP:HD1	1.63	0.47
1:A:61:HIS:HB2	1:A:62:PRO:HD3	1.97	0.47
2:B:149:PHE:HZ	2:B:286:MSE:HE3	1.79	0.47
1:A:698:GLU:HG3	5:A:967:HOH:O	2.14	0.47
1:A:248:PRO:HG3	1:A:857:MSE:CE	2.45	0.47
2:B:149:PHE:CZ	2:B:286:MSE:HE3	2.50	0.47
1:A:762:GLU:HG2	1:A:767:PHE:CZ	2.51	0.46
1:A:112:MSE:HE1	5:A:1529:HOH:O	2.14	0.46
2:B:135:SER:O	2:B:138:ASN:HB2	2.16	0.45
1:A:188:PRO:HA	1:A:191:ARG:HD3	1.98	0.45
2:B:335:GLU:HB3	2:B:351:ILE:HD12	1.99	0.45
1:A:245:THR:CG2	1:A:247:GLU:H	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:63:HIS:HE1	2:B:174:ASP:OD2	2.00	0.44
1:A:338:LEU:HD21	1:A:620:GLY:HA3	1.99	0.43
2:B:138:ASN:HD22	2:B:138:ASN:HA	1.60	0.43
1:A:268:LYS:HA	1:A:271:ARG:HE	1.83	0.43
2:B:6:SER:HB3	2:B:9:ASP:HB2	2.01	0.43
2:B:29:LEU:HD12	2:B:180:GLN:HG3	2.01	0.43
2:B:58:PHE:HA	2:B:59:PRO:HA	1.71	0.43
1:A:716:PHE:HB3	1:A:718:TRP:CD1	2.54	0.43
1:A:7:PHE:HE2	1:A:293:ILE:HD11	1.83	0.42
1:A:639:TYR:HA	1:A:640:PRO:HD3	1.91	0.42
1:A:29:LEU:HD23	1:A:29:LEU:N	2.34	0.42
2:B:207:LYS:HA	2:B:208:PRO:HD2	1.92	0.42
1:A:812:CYS:HA	1:A:813:PRO:HD3	1.82	0.42
1:A:103:ILE:HD11	1:A:176:LEU:HD12	2.02	0.42
1:A:325:ASP:OD1	1:A:370:THR:HB	2.20	0.42
1:A:302:GLU:OE2	1:A:860:ARG:HG3	2.20	0.41
2:B:321:GLU:HG3	2:B:325:GLN:HE21	1.85	0.41
1:A:805:ILE:HA	1:A:806:PRO:HD3	1.94	0.41
1:A:686:GLU:H	1:A:686:GLU:CD	2.28	0.41
1:A:715:LYS:HG2	1:A:719:GLN:HG3	2.01	0.41
1:A:134:GLN:O	1:A:138:GLU:HG2	2.20	0.41
1:A:71:ALA:HA	1:A:72:PRO:HD2	1.96	0.40
1:A:620:GLY:CA	1:A:637:TRP:CH2	3.04	0.40
2:B:290:PHE:O	2:B:293:GLN:HB2	2.20	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	674/899 (75%)	650 (96%)	23 (3%)	1 (0%)	48 57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	328/352 (93%)	323 (98%)	4 (1%)	1 (0%)	36	42
All	All	1002/1251 (80%)	973 (97%)	27 (3%)	2 (0%)	43	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	209	CYS
1	A	715	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	613/791 (78%)	588 (96%)	25 (4%)	27	37
2	B	309/314 (98%)	298 (96%)	11 (4%)	31	42
All	All	922/1105 (83%)	886 (96%)	36 (4%)	28	39

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

Mol	Chain	Res	Type
1	A	17	VAL
1	A	19	THR
1	A	29	LEU
1	A	182	ASN
1	A	219	VAL
1	A	237	ASP
1	A	245	THR
1	A	251	ARG
1	A	347	ARG
1	A	370	THR
1	A	402	GLU
1	A	405	ARG
1	A	583	THR
1	A	597	GLU

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Mol	Chain	Res	Type
1	A	611	ARG
1	A	661	GLU
1	A	675	VAL
1	A	686	GLU
1	A	766	MSE
1	A	811	GLN
1	A	837	VAL
1	A	855	VAL
1	A	857	MSE
1	A	860	ARG
1	A	863	THR
2	B	1	MSE
2	B	94	ARG
2	B	108	ARG
2	B	129	ARG
2	B	130	THR
2	B	138	ASN
2	B	164	ARG
2	B	185	VAL
2	B	205	ASP
2	B	267	LEU
2	B	337	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	A	65	HIS
1	A	134	GLN
1	A	182	ASN
1	A	598	GLN
1	A	682	ASN
2	B	63	HIS
2	B	87	ASN
2	B	138	ASN
2	B	169	GLN
2	B	173	GLN
2	B	180	GLN
2	B	234	ASN
2	B	292	HIS
2	B	318	HIS
2	B	325	GLN

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Mol	Chain	Res	Type
2	B	350	GLN

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](#)

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	GOL	B	1001	-	5,5,5	0.41	0	5,5,5	0.13	0

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	GOL	B	1001	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1001	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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	667/899 (74%)	0.72	87 (13%) 7 5	22, 45, 85, 119	0
2	B	321/352 (91%)	0.05	15 (4%) 36 33	20, 31, 54, 66	0
All	All	988/1251 (78%)	0.50	102 (10%) 12 9	20, 39, 81, 119	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	808	VAL	7.2
1	A	806	PRO	6.8
1	A	780	GLN	6.2
1	A	30	PRO	5.8
1	A	716	PHE	5.7
1	A	0	ALA	5.6
1	A	805	ILE	5.6
1	A	714	LYS	5.4
1	A	719	GLN	5.2
1	A	406	ASN	4.9
1	A	68	ASP	4.6
1	A	3	VAL	4.6
1	A	0(A)	SER	4.6
1	A	32	GLY	4.5
2	B	130	THR	4.4
2	B	210	SER	4.4
1	A	713	GLY	4.3
1	A	2	GLY	4.1
1	A	715	LYS	3.9
1	A	718	TRP	3.9
1	A	278	ASP	3.7
1	A	807	ASN	3.7
1	A	821	ALA	3.6
1	A	31	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	209	CYS	3.5
1	A	268	LYS	3.5
1	A	779	ARG	3.4
1	A	781	GLY	3.4
1	A	605	ASP	3.4
1	A	863	THR	3.3
1	A	279	ASP	3.3
1	A	33	THR	3.3
1	A	69	ARG	3.2
1	A	585	ARG	3.2
1	A	290	LYS	3.2
1	A	867	ILE	3.2
1	A	871	ARG	3.2
1	A	29	LEU	3.2
2	B	304	PRO	3.2
1	A	145	ILE	3.2
1	A	592	ARG	3.2
1	A	777	LYS	3.1
1	A	804	VAL	3.1
1	A	4	PRO	3.1
2	B	8	TYR	3.0
1	A	70	PRO	3.0
1	A	277	LEU	2.9
1	A	35	ILE	2.8
1	A	144	GLY	2.8
1	A	155	LYS	2.8
1	A	816	VAL	2.8
1	A	398	LEU	2.7
1	A	274	ILE	2.7
1	A	258	PHE	2.6
1	A	822	LEU	2.6
2	B	9	ASP	2.6
1	A	404	ARG	2.6
1	A	819	ALA	2.6
1	A	820	ASP	2.6
1	A	582	ASP	2.5
2	B	138	ASN	2.5
2	B	305	ASN	2.5
1	A	778	LYS	2.5
1	A	872	ALA	2.5
1	A	139	GLU	2.5
1	A	273	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	150	ASN	2.5
1	A	143	GLN	2.5
2	B	106	ASP	2.4
1	A	397	ARG	2.4
1	A	584	VAL	2.4
1	A	868	ASN	2.4
2	B	292	HIS	2.4
1	A	802	ASP	2.4
1	A	140	ALA	2.4
1	A	142	GLN	2.4
1	A	370	THR	2.3
1	A	809	SER	2.3
1	A	405	ARG	2.3
1	A	125	GLU	2.3
1	A	401	GLN	2.3
1	A	608	GLU	2.3
1	A	154	LYS	2.3
2	B	87	ASN	2.3
1	A	818	SER	2.3
1	A	67	GLU	2.3
2	B	14	HIS	2.3
1	A	237	ASP	2.2
1	A	865	GLU	2.2
2	B	203	ILE	2.2
1	A	275	LYS	2.2
1	A	817	THR	2.2
1	A	711	LEU	2.2
1	A	746	GLU	2.1
2	B	88	SER	2.1
1	A	5	ALA	2.1
1	A	151	ALA	2.0
1	A	870	VAL	2.0
2	B	303	LYS	2.0
1	A	6	LEU	2.0
1	A	8	ARG	2.0
1	A	864	PRO	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](#)

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. 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	B	1001	6/6	0.85	0.17	59,59,60,60	0
3	MG	B	1000	1/1	0.98	0.05	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.