



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 07:52 am BST

PDB ID : 2A71
Title : Crystal structure of Emp47p carbohydrate recognition domain (CRD), orthorhombic crystal form
Authors : Satoh, T.; Sato, K.; Kanoh, A.; Yamashita, K.; Kato, R.; Nakano, A.; Wakatsuki, S.
Deposited on : 2005-07-04
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

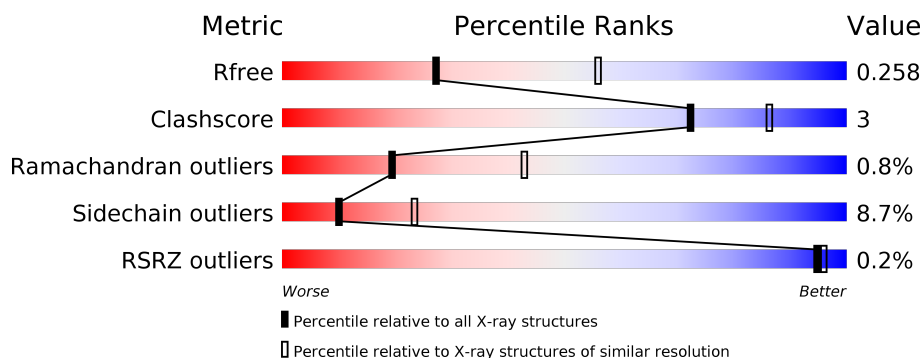
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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	222	
1	B	222	
1	C	222	
1	D	222	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7082 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 Emp47p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1719	1080	295	339	5			
1	B	219	Total	C	N	O	S	0	0	0
			1730	1086	297	342	5			
1	C	217	Total	C	N	O	S	0	0	0
			1719	1080	295	339	5			
1	D	216	Total	C	N	O	S	0	0	0
			1710	1074	293	338	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	GLY	-	CLONING ARTIFACT	GB 854516
B	6	GLY	-	CLONING ARTIFACT	GB 854516
C	6	GLY	-	CLONING ARTIFACT	GB 854516
D	6	GLY	-	CLONING ARTIFACT	GB 854516

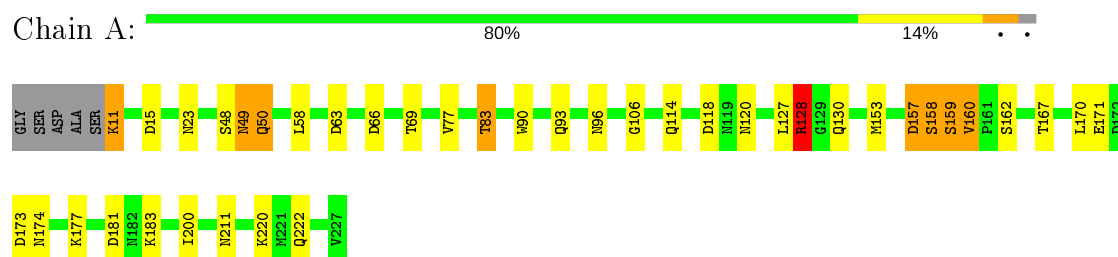
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	65	Total	O	0	0
			65	65		
2	B	66	Total	O	0	0
			66	66		
2	C	21	Total	O	0	0
			21	21		
2	D	52	Total	O	0	0
			52	52		

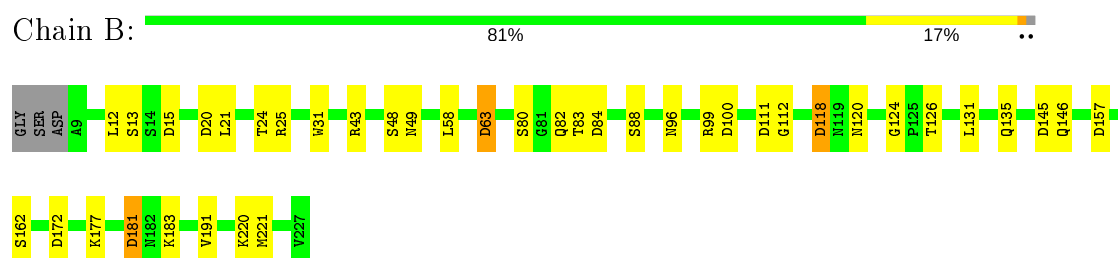
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

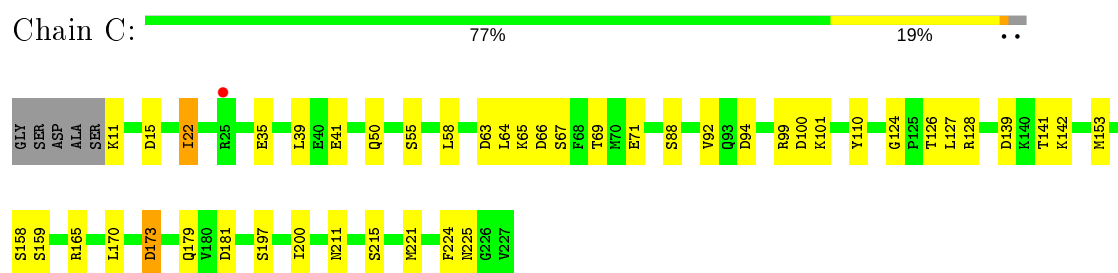
• Molecule 1: Emp47p



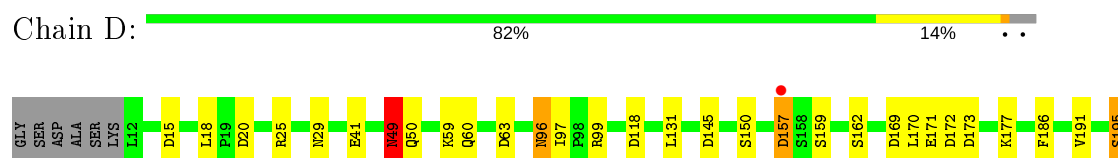
• Molecule 1: Emp47p



• Molecule 1: Emp47p



• Molecule 1: Emp47p





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.59Å 129.62Å 170.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 42.72 – 2.69	Depositor EDS
% Data completeness (in resolution range)	87.8 (20.00-2.70) 87.6 (42.72-2.69)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.76 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.198 , 0.258 0.203 , 0.258	Depositor DCC
R_{free} test set	1132 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7082	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.95% 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

5.1 Standard geometry

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	0.61	0/1755	0.85	7/2376 (0.3%)
1	B	0.61	0/1766	0.85	11/2391 (0.5%)
1	C	0.56	0/1755	0.78	6/2376 (0.3%)
1	D	0.63	0/1746	0.87	8/2365 (0.3%)
All	All	0.60	0/7022	0.84	32/9508 (0.3%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	145	ASP	CB-CG-OD2	7.88	125.39	118.30
1	D	172	ASP	CB-CG-OD2	7.30	124.87	118.30
1	A	66	ASP	CB-CG-OD2	7.17	124.75	118.30
1	D	63	ASP	CB-CG-OD2	7.05	124.65	118.30
1	B	181	ASP	CB-CG-OD2	6.80	124.42	118.30
1	D	157	ASP	CB-CG-OD2	6.76	124.38	118.30
1	A	63	ASP	CB-CG-OD2	6.62	124.26	118.30
1	D	15	ASP	CB-CG-OD2	6.47	124.13	118.30
1	A	157	ASP	CB-CG-OD2	6.41	124.07	118.30
1	B	145	ASP	CB-CG-OD2	6.30	123.97	118.30
1	B	15	ASP	CB-CG-OD2	6.20	123.88	118.30
1	A	15	ASP	CB-CG-OD2	6.15	123.83	118.30
1	B	100	ASP	CB-CG-OD2	6.05	123.74	118.30
1	C	63	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	173	ASP	CB-CG-OD2	5.81	123.53	118.30
1	D	173	ASP	CB-CG-OD2	5.71	123.44	118.30
1	B	157	ASP	CB-CG-OD2	5.56	123.30	118.30
1	C	173	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	128	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	C	181	ASP	CB-CG-OD2	5.25	123.03	118.30
1	D	49	ASN	CB-CA-C	5.24	120.87	110.40
1	B	111	ASP	CB-CG-OD2	5.21	122.99	118.30
1	C	15	ASP	CB-CG-OD2	5.19	122.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	20	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	84	ASP	CB-CG-OD1	5.18	122.96	118.30
1	B	172	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	100	ASP	CB-CG-OD2	5.08	122.87	118.30
1	B	63	ASP	CB-CG-OD2	5.07	122.86	118.30
1	B	118	ASP	CB-CG-OD2	5.04	122.83	118.30
1	C	66	ASP	CB-CG-OD2	5.04	122.83	118.30
1	B	20	ASP	CB-CG-OD2	5.03	122.82	118.30
1	A	181	ASP	CB-CG-OD2	5.00	122.80	118.30

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	1719	0	1656	16	0
1	B	1730	0	1666	9	0
1	C	1719	0	1656	14	0
1	D	1710	0	1643	9	0
2	A	65	0	0	2	0
2	B	66	0	0	1	0
2	C	21	0	0	0	0
2	D	52	0	0	0	0
All	All	7082	0	6621	46	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 3.

All (46) 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:B:82:GLN:HE21	1:B:120:ASN:HA	1.41	0.85
1:C:58:LEU:HD12	1:C:200:ILE:HB	1.74	0.69
1:A:58:LEU:HD12	1:A:200:ILE:HB	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:ASP:HB2	2:B:261:HOH:O	1.99	0.62
1:A:11:LYS:N	2:A:273:HOH:O	2.33	0.61
1:D:49:ASN:ND2	1:D:50:GLN:N	2.53	0.56
1:D:29:ASN:O	1:D:59:LYS:NZ	2.34	0.55
1:B:131:LEU:HD11	1:B:191:VAL:HG22	1.90	0.52
1:C:139:ASP:OD1	1:C:141:THR:OG1	2.26	0.52
1:A:127:LEU:HD23	1:A:127:LEU:C	2.31	0.50
1:B:83:THR:O	1:B:120:ASN:HB2	2.13	0.48
1:D:131:LEU:HD11	1:D:191:VAL:HG22	1.95	0.48
1:A:127:LEU:HD23	1:A:128:ARG:N	2.28	0.48
1:D:18:LEU:HB2	1:D:221:MET:HB3	1.96	0.47
1:A:157:ASP:HB3	1:C:22:ILE:HG12	1.96	0.47
1:D:169:ASP:OD2	1:D:227:VAL:HG21	2.14	0.47
1:C:126:THR:HG21	1:C:128:ARG:HH21	1.81	0.46
1:C:69:THR:HB	1:C:224:PHE:HB2	1.99	0.45
1:B:183:LYS:HB3	1:B:183:LYS:NZ	2.32	0.44
1:A:83:THR:O	1:A:120:ASN:HB2	2.18	0.44
1:A:49:ASN:N	1:A:49:ASN:OD1	2.51	0.44
1:D:49:ASN:ND2	1:D:50:GLN:H	2.14	0.44
1:C:124:GLY:O	1:C:126:THR:HG23	2.18	0.44
1:B:31:TRP:CE2	1:B:58:LEU:HD21	2.53	0.43
1:C:165:ARG:HB3	1:C:179:GLN:HB2	1.99	0.43
1:C:35:GLU:OE1	1:C:55:SER:HB3	2.19	0.43
1:D:96:ASN:O	1:D:97:ILE:C	2.57	0.43
1:A:127:LEU:CD2	1:A:127:LEU:C	2.87	0.43
1:A:50:GLN:NE2	1:A:211:ASN:HB3	2.34	0.43
1:B:124:GLY:O	1:B:126:THR:HG23	2.19	0.43
1:B:112:GLY:O	1:B:131:LEU:HD23	2.18	0.42
1:A:158:SER:O	1:A:160:VAL:N	2.53	0.42
1:A:220:LYS:CE	1:A:222:GLN:NE2	2.83	0.42
1:A:158:SER:O	1:A:159:SER:C	2.56	0.42
1:A:153:MET:HG3	2:A:253:HOH:O	2.20	0.42
1:C:127:LEU:HD23	1:C:127:LEU:C	2.40	0.42
1:C:71:GLU:O	1:C:221:MET:HA	2.20	0.42
1:C:173:ASP:OD1	1:D:177:LYS:NZ	2.34	0.41
1:D:186:PHE:C	1:D:186:PHE:CD1	2.92	0.41
1:B:21:LEU:O	1:B:24:THR:HB	2.19	0.41
1:A:90:TRP:CZ2	1:A:106:GLY:HA3	2.56	0.41
1:A:114:GLN:HB3	1:A:130:GLN:HB2	2.04	0.40
1:A:220:LYS:HE2	1:A:222:GLN:NE2	2.36	0.40
1:C:92:VAL:HG11	1:C:110:TYR:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ARG:O	1:C:101:LYS:HG2	2.20	0.40
1:C:50:GLN:HE21	1:C:211:ASN:HB3	1.86	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	215/222 (97%)	194 (90%)	18 (8%)	3 (1%)	11	28
1	B	217/222 (98%)	201 (93%)	15 (7%)	1 (0%)	29	54
1	C	215/222 (97%)	197 (92%)	17 (8%)	1 (0%)	29	54
1	D	214/222 (96%)	194 (91%)	18 (8%)	2 (1%)	17	40
All	All	861/888 (97%)	786 (91%)	68 (8%)	7 (1%)	19	43

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	67	SER
1	D	41	GLU
1	A	48	SER
1	A	159	SER
1	B	135	GLN
1	A	158	SER
1	D	195	SER

5.3.2 Protein sidechains [i](#)

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	193/196 (98%)	174 (90%)	19 (10%)	8	18
1	B	194/196 (99%)	177 (91%)	17 (9%)	10	23
1	C	193/196 (98%)	177 (92%)	16 (8%)	11	25
1	D	192/196 (98%)	177 (92%)	15 (8%)	12	29
All	All	772/784 (98%)	705 (91%)	67 (9%)	10	23

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	23	ASN
1	A	49	ASN
1	A	50	GLN
1	A	69	THR
1	A	77	VAL
1	A	83	THR
1	A	93	GLN
1	A	96	ASN
1	A	118	ASP
1	A	128	ARG
1	A	160	VAL
1	A	162	SER
1	A	167	THR
1	A	170	LEU
1	A	171	GLU
1	A	174	ASN
1	A	177	LYS
1	A	183	LYS
1	B	12	LEU
1	B	13	SER
1	B	25	ARG
1	B	43	ARG
1	B	48	SER
1	B	49	ASN
1	B	80	SER
1	B	88	SER
1	B	96	ASN
1	B	99	ARG
1	B	118	ASP

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Mol	Chain	Res	Type
1	B	146	GLN
1	B	162	SER
1	B	177	LYS
1	B	181	ASP
1	B	220	LYS
1	B	221	MET
1	C	11	LYS
1	C	22	ILE
1	C	39	LEU
1	C	41	GLU
1	C	64	LEU
1	C	65	LYS
1	C	88	SER
1	C	94	ASP
1	C	142	LYS
1	C	153	MET
1	C	158	SER
1	C	159	SER
1	C	170	LEU
1	C	197	SER
1	C	215	SER
1	C	225	ASN
1	D	25	ARG
1	D	49	ASN
1	D	60	GLN
1	D	96	ASN
1	D	99	ARG
1	D	118	ASP
1	D	150	SER
1	D	157	ASP
1	D	159	SER
1	D	162	SER
1	D	170	LEU
1	D	171	GLU
1	D	195	SER
1	D	210	ASN
1	D	220	LYS

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

Mol	Chain	Res	Type
1	A	50	GLN

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Mol	Chain	Res	Type
1	A	51	ASN
1	A	109	ASN
1	A	135	GLN
1	A	210	ASN
1	A	222	GLN
1	B	29	ASN
1	B	82	GLN
1	B	102	GLN
1	C	36	GLN
1	C	50	GLN
1	C	114	GLN
1	C	135	GLN
1	C	225	ASN
1	D	32	GLN
1	D	49	ASN
1	D	114	GLN
1	D	179	GLN
1	D	210	ASN
1	D	225	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	217/222 (97%)	-0.70	0 100 100	14, 28, 44, 52	0
1	B	219/222 (98%)	-0.54	0 100 100	14, 33, 56, 67	0
1	C	217/222 (97%)	-0.36	1 (0%) 91 92	21, 45, 62, 71	0
1	D	216/222 (97%)	-0.64	1 (0%) 91 92	13, 29, 46, 54	0
All	All	869/888 (97%)	-0.56	2 (0%) 95 96	13, 32, 55, 71	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	157	ASP	2.3
1	C	25	ARG	2.1

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 carbohydrates 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.