



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:42 AM UTC

PDB ID : 2IX2 / pdb_00002ix2
Title : Crystal structure of the heterotrimeric PCNA from *Sulfolobus solfataricus*
Authors : Williams, G.J.; Johnson, K.; McMahon, S.A.; Carter, L.; Oke, M.; Liu, H.;
Taylor, G.L.; White, M.F.; Naismith, J.H.
Deposited on : 2006-07-05
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
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

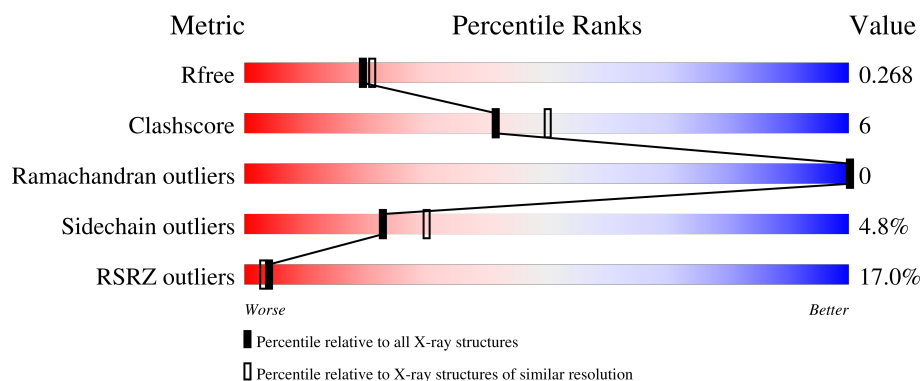
1 Overall quality at a glance

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	249	14% 73% 17% 9%
2	B	245	9% 84% 16% •
3	C	259	24% 77% 13% • 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5701 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 DNA POLYMERASE SLIDING CLAMP B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1738	1115	277	338	8			

- Molecule 2 is a protein called DNA POLYMERASE SLIDING CLAMP C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	245	Total	C	N	O	S	0	0	0
			1926	1238	301	383	4			

- Molecule 3 is a protein called DNA POLYMERASE SLIDING CLAMP A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1917	1224	310	379	4			

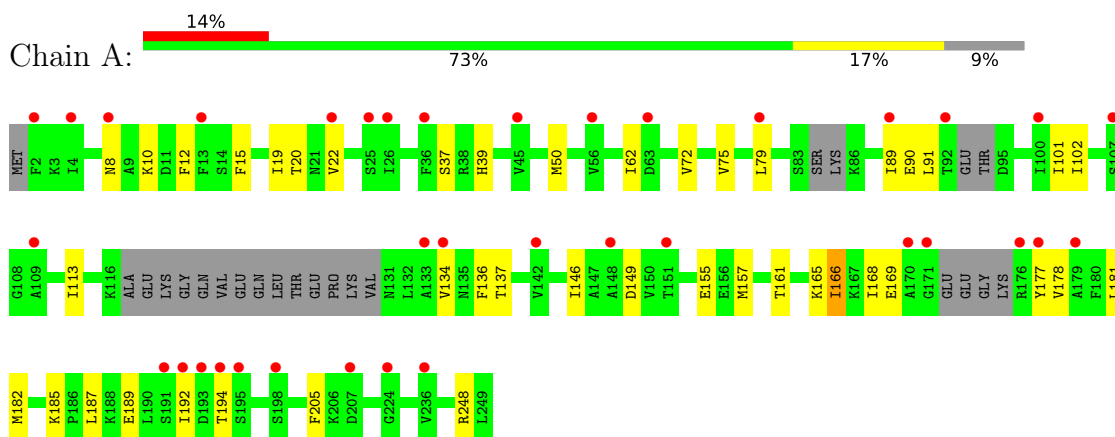
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	45	Total	O	0	0
			45	45		
4	C	67	Total	O	0	0
			67	67		

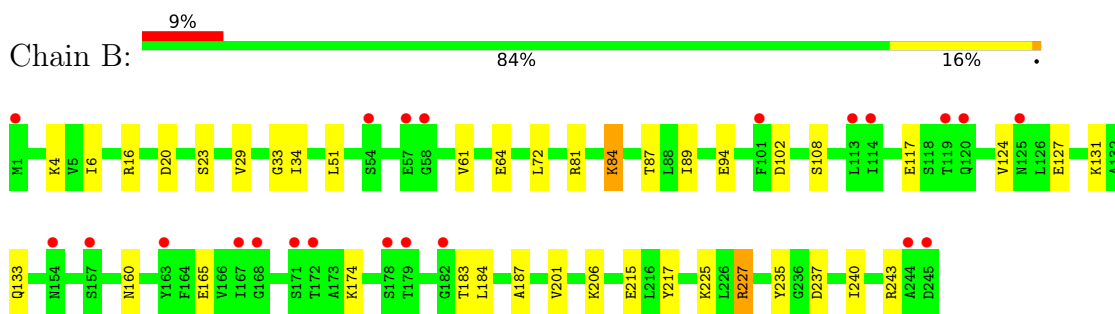
3 Residue-property plots

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.

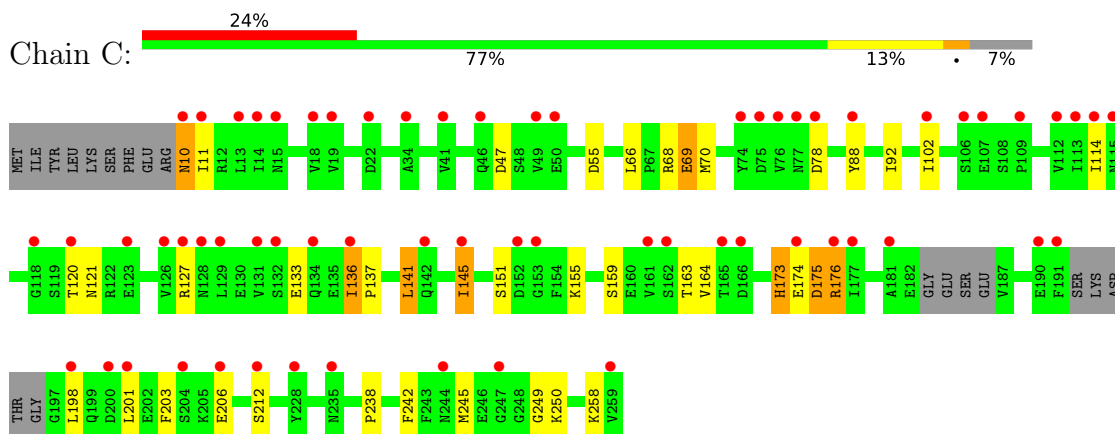
• Molecule 1: DNA POLYMERASE SLIDING CLAMP B



• Molecule 2: DNA POLYMERASE SLIDING CLAMP C



• Molecule 3: DNA POLYMERASE SLIDING CLAMP A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.81Å 78.80Å 125.61Å 90.00° 100.51° 90.00°	Depositor
Resolution (Å)	48.62 – 2.20 48.62 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.2 (48.62-2.20) 91.3 (48.62-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.217 , 0.273 0.217 , 0.268	Depositor DCC
R_{free} test set	2026 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	47.7	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5701	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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	0.53	0/1761	0.78	0/2370
2	B	0.77	2/1961 (0.1%)	0.90	2/2653 (0.1%)
3	C	1.06	7/1941 (0.4%)	1.00	4/2615 (0.2%)
All	All	0.82	9/5663 (0.2%)	0.90	6/7638 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	176	ARG	NE-CZ	17.93	1.52	1.33
3	C	175	ASP	CG-OD1	16.79	1.57	1.25
3	C	173	HIS	CE1-NE2	11.99	1.44	1.32
2	B	84	LYS	CE-NZ	10.99	1.82	1.49
3	C	176	ARG	CD-NE	8.51	1.58	1.46
3	C	176	ARG	CZ-NH2	8.00	1.43	1.33
2	B	84	LYS	CD-CE	7.49	1.75	1.52
3	C	173	HIS	CG-CD2	7.41	1.44	1.35
3	C	69	GLU	CD-OE1	7.39	1.39	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	176	ARG	NE-CZ-NH2	-13.07	107.44	119.20
3	C	176	ARG	CD-NE-CZ	-10.07	110.31	124.40
3	C	176	ARG	NH1-CZ-NH2	7.16	128.61	119.30
2	B	84	LYS	CD-CE-NZ	-5.92	92.96	111.90
3	C	258	LYS	N-CA-C	-5.40	104.94	112.45
2	B	33	GLY	N-CA-C	5.22	117.07	110.38

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	1738	0	1769	25	0
2	B	1926	0	1904	28	0
3	C	1917	0	1935	25	0
4	A	8	0	0	0	0
4	B	45	0	0	2	0
4	C	67	0	0	1	0
All	All	5701	0	5608	71	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 (71) 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)
2:B:84:LYS:CD	2:B:84:LYS:CE	1.74	1.54
2:B:84:LYS:CE	2:B:84:LYS:NZ	1.82	1.42
1:A:20:THR:HG21	1:A:72:VAL:HG11	1.53	0.88
2:B:183:THR:HG21	3:C:120:THR:HG23	1.56	0.87
2:B:183:THR:HG21	3:C:120:THR:CG2	2.09	0.82
2:B:84:LYS:CE	2:B:84:LYS:CG	2.59	0.81
3:C:155:LYS:NZ	4:C:2055:HOH:O	2.23	0.72
2:B:133:GLN:HG2	2:B:215:GLU:HG2	1.74	0.70
2:B:227:ARG:HD3	2:B:237:ASP:OD1	1.92	0.69
1:A:37:SER:HB3	1:A:50:MET:HG2	1.75	0.69
3:C:141:LEU:HD11	3:C:238:PRO:HD2	1.75	0.68
1:A:169:GLU:HG2	1:A:178:VAL:HG12	1.76	0.67
1:A:8:ASN:HD21	1:A:10:LYS:HB3	1.59	0.67
2:B:84:LYS:CD	2:B:84:LYS:NZ	2.58	0.67
3:C:10:ASN:N	3:C:10:ASN:OD1	2.28	0.66
2:B:183:THR:CG2	3:C:120:THR:HG23	2.25	0.66
1:A:157:MET:HE1	1:A:205:PHE:CG	2.32	0.65
1:A:149:ASP:OD1	2:B:81:ARG:HD3	1.97	0.64
1:A:20:THR:HG21	1:A:72:VAL:CG1	2.28	0.62
1:A:75:VAL:HG23	1:A:113:ILE:HD13	1.80	0.62
1:A:161:THR:HG23	1:A:192:ILE:HD13	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:173:HIS:HA	3:C:206:GLU:HG2	1.81	0.61
2:B:227:ARG:CD	2:B:237:ASP:OD1	2.48	0.61
2:B:16:ARG:HD2	2:B:206:LYS:HD3	1.83	0.59
3:C:245:MET:HE3	3:C:249:GLY:HA3	1.84	0.58
2:B:201:VAL:HG22	2:B:240:ILE:HD12	1.85	0.57
1:A:137:THR:HB	1:A:189:GLU:HB3	1.85	0.57
1:A:12:PHE:HD2	1:A:89:ILE:HD13	1.69	0.56
3:C:198:LEU:HD21	3:C:201:LEU:HD13	1.88	0.55
3:C:66:LEU:HD22	3:C:70:MET:HE1	1.89	0.54
3:C:88:TYR:CE2	3:C:92:ILE:HD11	2.43	0.53
1:A:90:GLU:HB2	1:A:101:ILE:HB	1.89	0.52
1:A:79:LEU:HD13	1:A:102:ILE:HD13	1.91	0.52
2:B:183:THR:CG2	3:C:120:THR:CG2	2.86	0.51
2:B:183:THR:HG21	3:C:120:THR:HG21	1.90	0.50
2:B:131:LYS:HG2	2:B:217:TYR:CD1	2.46	0.50
2:B:160:ASN:ND2	4:B:2024:HOH:O	2.47	0.48
2:B:243:ARG:NH1	4:B:2043:HOH:O	2.45	0.48
1:A:136:PHE:CD1	1:A:166:ILE:HD12	2.48	0.47
2:B:184:LEU:HD13	2:B:187:ALA:HB2	1.97	0.47
1:A:134:VAL:HG13	1:A:192:ILE:HG12	1.95	0.47
3:C:175:ASP:OD2	3:C:176:ARG:HD3	2.14	0.47
1:A:161:THR:HG21	1:A:192:ILE:HG21	1.95	0.47
3:C:249:GLY:O	3:C:250:LYS:HD3	2.15	0.46
2:B:29:VAL:HG22	2:B:34:ILE:HG12	1.99	0.45
3:C:242:PHE:HE1	3:C:250:LYS:HB3	1.82	0.45
2:B:127:GLU:OE1	2:B:127:GLU:HA	2.16	0.45
2:B:20:ASP:OD2	2:B:206:LYS:NZ	2.34	0.45
1:A:157:MET:HE3	1:A:157:MET:HB3	1.69	0.44
2:B:227:ARG:HD2	2:B:235:TYR:HB2	2.00	0.44
3:C:136:ILE:HA	3:C:137:PRO:HD3	1.88	0.43
2:B:165:GLU:OE2	2:B:174:LYS:NZ	2.40	0.43
3:C:47:ASP:HA	3:C:68:ARG:HD2	2.00	0.43
3:C:159:SER:O	3:C:163:THR:HG23	2.18	0.42
1:A:182:MET:HG3	1:A:185:LYS:HB3	2.00	0.42
2:B:131:LYS:HG2	2:B:217:TYR:HD1	1.83	0.42
3:C:69:GLU:H	3:C:69:GLU:CD	2.27	0.42
1:A:165:LYS:HB3	1:A:182:MET:HB3	2.02	0.42
1:A:181:LEU:HD23	1:A:187:LEU:HD21	2.01	0.42
1:A:146:ILE:HG21	1:A:168:ILE:HD13	2.02	0.42
1:A:22:VAL:HB	1:A:39:HIS:CE1	2.55	0.41
3:C:145:ILE:HD11	3:C:201:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:121:ASN:N	3:C:121:ASN:HD22	2.17	0.41
3:C:102:ILE:HD11	3:C:114:ILE:CG2	2.50	0.41
2:B:4:LYS:HG2	2:B:89:ILE:HG12	2.03	0.41
1:A:15:PHE:O	1:A:19:ILE:HG12	2.21	0.41
3:C:174:GLU:O	3:C:201:LEU:HD22	2.21	0.41
3:C:203:PHE:CZ	3:C:206:GLU:HG3	2.56	0.41
1:A:8:ASN:ND2	1:A:10:LYS:HB3	2.31	0.40
1:A:177:TYR:HA	2:B:108:SER:O	2.22	0.40
2:B:217:TYR:HB2	2:B:225:LYS:HB3	2.04	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	216/249 (87%)	209 (97%)	7 (3%)	0	100	100
2	B	243/245 (99%)	234 (96%)	9 (4%)	0	100	100
3	C	235/259 (91%)	230 (98%)	5 (2%)	0	100	100
All	All	694/753 (92%)	673 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	195/220 (89%)	189 (97%)	6 (3%)	35	48
2	B	215/219 (98%)	203 (94%)	12 (6%)	19	24
3	C	218/235 (93%)	206 (94%)	12 (6%)	19	24
All	All	628/674 (93%)	598 (95%)	30 (5%)	23	30

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	A	91	LEU
1	A	155	GLU
1	A	166	ILE
1	A	194	THR
1	A	248	ARG
2	B	6	ILE
2	B	23	SER
2	B	51	LEU
2	B	61	VAL
2	B	64	GLU
2	B	72	LEU
2	B	87	THR
2	B	94	GLU
2	B	102	ASP
2	B	117	GLU
2	B	124	VAL
2	B	227	ARG
3	C	10	ASN
3	C	11	ILE
3	C	55	ASP
3	C	78	ASP
3	C	127	ARG
3	C	133	GLU
3	C	136	ILE
3	C	141	LEU
3	C	145	ILE
3	C	151	SER
3	C	164	VAL
3	C	212	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	17	ASN
1	A	29	ASN
1	A	39	HIS
1	A	135	ASN
2	B	125	ASN
2	B	203	ASN
3	C	10	ASN
3	C	31	GLN
3	C	121	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](#)

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	226/249 (90%)	1.20	36 (15%) 5 3	46, 55, 63, 69	0
2	B	245/245 (100%)	1.11	22 (8%) 15 12	43, 54, 62, 66	1 (0%)
3	C	241/259 (93%)	1.49	63 (26%) 1 1	44, 54, 65, 69	0
All	All	712/753 (94%)	1.27	121 (16%) 4 3	43, 54, 64, 69	1 (0%)

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	78	ASP	4.2
3	C	118	GLY	4.0
2	B	168	GLY	3.8
2	B	154	ASN	3.7
3	C	112	VAL	3.6
1	A	36	PHE	3.6
3	C	128	ASN	3.5
3	C	22	ASP	3.5
3	C	13	LEU	3.4
1	A	133	ALA	3.3
1	A	107	SER	3.3
3	C	113	ILE	3.3
3	C	115	ASN	3.2
3	C	114	ILE	3.2
2	B	57	GLU	3.2
3	C	247	GLY	3.1
3	C	129	LEU	3.1
3	C	181	ALA	3.1
3	C	76	VAL	3.1
3	C	198	LEU	3.1
3	C	109	PRO	3.1
3	C	259	VAL	3.1
3	C	11	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
3	C	120	THR	3.0
3	C	88	TYR	3.0
2	B	171	SER	2.9
1	A	2	PHE	2.9
3	C	14	ILE	2.9
1	A	151	THR	2.9
3	C	244	ASN	2.9
3	C	161	VAL	2.8
3	C	50	GLU	2.8
3	C	174	GLU	2.8
1	A	13	PHE	2.8
1	A	142	VAL	2.8
1	A	176	ARG	2.8
1	A	92	THR	2.8
1	A	25	SER	2.8
1	A	148	ALA	2.8
3	C	235	ASN	2.7
1	A	236	VAL	2.7
1	A	109	ALA	2.7
3	C	152	ASP	2.7
3	C	34	ALA	2.6
1	A	22	VAL	2.6
3	C	75	ASP	2.6
1	A	4	ILE	2.6
1	A	171	GLY	2.6
3	C	177	ILE	2.6
3	C	166	ASP	2.6
2	B	1	MET	2.6
2	B	172	THR	2.6
1	A	193	ASP	2.6
3	C	200	ASP	2.6
1	A	134	VAL	2.6
2	B	120	GLN	2.5
3	C	127	ARG	2.5
1	A	45	VAL	2.5
3	C	132	SER	2.5
3	C	228	TYR	2.5
2	B	178	SER	2.5
3	C	212	SER	2.5
3	C	126	VAL	2.5
3	C	145	ILE	2.5
1	A	8	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	77	ASN	2.5
3	C	165	THR	2.4
2	B	58	GLY	2.4
3	C	191	PHE	2.4
2	B	245	ASP	2.4
2	B	179	THR	2.4
3	C	74	TYR	2.4
3	C	106	SER	2.4
3	C	204	SER	2.4
1	A	89	ILE	2.4
2	B	167	ILE	2.4
3	C	142	GLN	2.4
2	B	125	ASN	2.3
1	A	179	ALA	2.3
3	C	102	ILE	2.3
3	C	15	ASN	2.3
3	C	153	GLY	2.3
2	B	114	ILE	2.3
3	C	41	VAL	2.3
3	C	46	GLN	2.3
2	B	119	THR	2.3
1	A	195	SER	2.3
3	C	176	ARG	2.3
3	C	206	GLU	2.3
1	A	192	ILE	2.3
3	C	10	ASN	2.3
1	A	194	THR	2.3
1	A	198	SER	2.3
3	C	49	VAL	2.3
1	A	63	ASP	2.2
1	A	224	GLY	2.2
2	B	157	SER	2.2
1	A	100	ILE	2.2
1	A	79	LEU	2.2
3	C	18	VAL	2.2
3	C	19	VAL	2.2
2	B	182	GLY	2.2
1	A	56	VAL	2.2
1	A	170	ALA	2.2
3	C	162	SER	2.2
1	A	207	ASP	2.2
2	B	54	SER	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	131	VAL	2.1
3	C	134	GLN	2.1
2	B	101	PHE	2.1
3	C	107	GLU	2.1
3	C	123	GLU	2.1
3	C	201	LEU	2.1
2	B	163	TYR	2.1
2	B	244	ALA	2.0
2	B	113	LEU	2.0
1	A	177	TYR	2.0
1	A	191	SER	2.0
3	C	190	GLU	2.0
1	A	26	ILE	2.0
3	C	136	ILE	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 oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.