



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:41 PM UTC

PDB ID : 3LX2 / pdb_00003lx2
Title : Crystal Structure analysis of PCNA from Thermococcus kodakaraensis tk0582
Authors : Ladner, J.E.; Kelman, Z.; Pan, M.
Deposited on : 2010-02-24
Resolution : 2.40 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

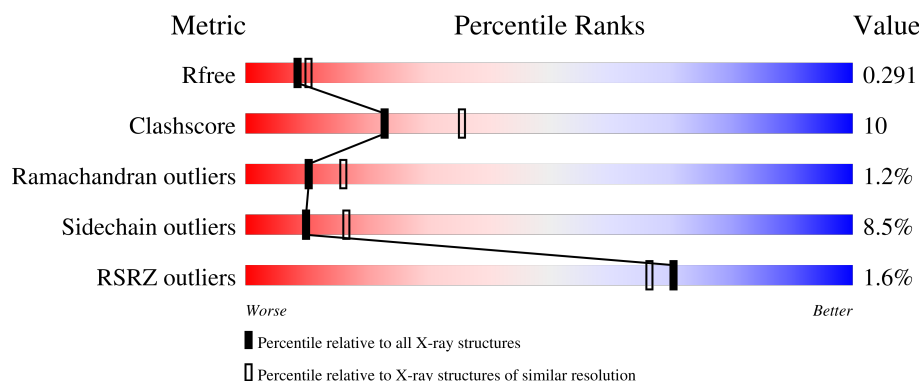
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (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 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	259	2% 74% 20% • 5%
1	B	259	2% 66% 25% • 5%
1	C	259	% 64% 27% • 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5952 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 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	0	0	0
			1955	1268	315	365	7			
1	B	246	Total	C	N	O	S	0	0	0
			1948	1263	314	364	7			
1	C	246	Total	C	N	O	S	0	0	0
			1948	1263	314	364	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	254	HIS	-	expression tag	UNP Q5JFD3
A	255	HIS	-	expression tag	UNP Q5JFD3
A	256	HIS	-	expression tag	UNP Q5JFD3
A	257	HIS	-	expression tag	UNP Q5JFD3
A	258	HIS	-	expression tag	UNP Q5JFD3
A	259	HIS	-	expression tag	UNP Q5JFD3
B	254	HIS	-	expression tag	UNP Q5JFD3
B	255	HIS	-	expression tag	UNP Q5JFD3
B	256	HIS	-	expression tag	UNP Q5JFD3
B	257	HIS	-	expression tag	UNP Q5JFD3
B	258	HIS	-	expression tag	UNP Q5JFD3
B	259	HIS	-	expression tag	UNP Q5JFD3
C	254	HIS	-	expression tag	UNP Q5JFD3
C	255	HIS	-	expression tag	UNP Q5JFD3
C	256	HIS	-	expression tag	UNP Q5JFD3
C	257	HIS	-	expression tag	UNP Q5JFD3
C	258	HIS	-	expression tag	UNP Q5JFD3
C	259	HIS	-	expression tag	UNP Q5JFD3

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	28	Total	O	0	0
			28	28		
3	B	20	Total	O	0	0
			20	20		
3	C	23	Total	O	0	0
			23	23		

- Molecule 1: DNA polymerase sliding clamp 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	120.48Å 136.27Å 123.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.63 – 2.40 29.63 – 2.40	Depositor EDS
% Data completeness (in resolution range)	89.5 (29.63-2.40) 89.4 (29.63-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.39Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.243 , 0.305 0.235 , 0.291	Depositor DCC
R_{free} test set	1798 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	61.7	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.6	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	5952	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.11	2/1990 (0.1%)	1.17	3/2691 (0.1%)
1	B	1.03	0/1983	1.17	10/2681 (0.4%)
1	C	1.00	0/1983	1.12	6/2681 (0.2%)
All	All	1.05	2/5956 (0.0%)	1.15	19/8053 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	ALA	CA-CB	-5.74	1.44	1.53
1	A	15	SER	N-CA	-5.03	1.39	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	200	TYR	N-CA-C	8.25	121.43	109.14
1	B	163	LYS	N-CA-C	8.08	121.67	108.99
1	C	169	GLU	N-CA-C	7.97	119.74	108.74
1	B	119	ASN	N-CA-C	7.59	122.94	107.69
1	B	225	ASP	N-CA-C	7.24	121.39	111.39
1	A	222	PHE	N-CA-C	7.24	117.80	108.24
1	C	53	LEU	CA-C-N	6.14	126.10	119.78
1	C	53	LEU	C-N-CA	6.14	126.10	119.78
1	A	178	VAL	N-CA-C	6.01	116.66	107.77
1	B	66	GLU	N-CA-C	5.86	117.59	109.15
1	B	237	ALA	N-CA-C	5.54	118.51	111.69
1	C	108	ASN	N-CA-C	5.43	117.37	108.52
1	B	127	SER	N-CA-C	-5.42	102.37	110.23
1	B	134	ALA	N-CA-C	5.36	117.40	108.99
1	C	163	LYS	N-CA-C	5.30	117.25	109.24
1	C	192	LYS	N-CA-C	-5.19	106.79	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	VAL	CB-CA-C	-5.11	103.06	110.63
1	B	118	ALA	CA-C-N	-5.02	115.56	123.13
1	B	118	ALA	C-N-CA	-5.02	115.56	123.13

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	1955	0	2006	29	0
1	B	1948	0	1997	46	0
1	C	1948	0	1997	52	0
2	A	15	0	0	1	0
2	B	10	0	0	1	0
2	C	5	0	0	0	0
3	A	28	0	0	4	0
3	B	20	0	0	2	0
3	C	23	0	0	3	0
All	All	5952	0	6000	123	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 10.

All (123) 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:155:ILE:HD11	1:B:166:PHE:HB3	1.57	0.86
1:C:155:ILE:HD11	1:C:166:PHE:HB3	1.60	0.83
1:B:33:MET:HE2	1:B:66:GLU:HG3	1.68	0.73
1:C:57:LEU:HD21	1:C:237:ALA:HB3	1.70	0.72
1:C:161:PRO:HA	1:C:191:HIS:NE2	2.06	0.71
1:C:93:LYS:NZ	1:C:115:LEU:CD1	2.54	0.71
1:A:225:ASP:O	1:A:226:ILE:HD12	1.90	0.71
1:C:200:TYR:CZ	1:C:228:LEU:HB2	2.26	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:SER:O	2:B:261:SO4:O4	2.10	0.70
1:C:41:ILE:HG13	1:C:123:ILE:HD13	1.75	0.68
1:B:48:LEU:HD22	1:B:243:LEU:HD12	1.79	0.64
1:A:192:LYS:O	1:A:193:MET:HB2	1.97	0.64
1:C:93:LYS:HZ2	1:C:115:LEU:CD1	2.12	0.63
1:B:226:ILE:HG23	1:B:227:PRO:HD2	1.81	0.62
1:B:8:ASP:CG	1:B:235:ARG:HH12	2.07	0.62
1:B:170:GLY:O	1:B:171:ASN:OD1	2.18	0.62
1:A:122:GLU:HA	1:A:122:GLU:OE1	2.01	0.60
1:C:63:VAL:O	1:C:63:VAL:HG22	2.01	0.60
1:B:158:MET:SD	1:B:167:LYS:HE2	2.42	0.60
1:A:22:LYS:HE3	3:A:275:HOH:O	2.01	0.60
1:B:220:ILE:HG22	1:B:230:LEU:CD2	2.32	0.60
1:C:3:PHE:O	1:C:3:PHE:CD1	2.55	0.60
1:C:85:SER:HB2	1:C:86:ARG:HD3	1.84	0.60
1:C:209:LEU:HA	1:C:212:LEU:HD12	1.84	0.59
1:A:143:ARG:HD2	1:C:109:THR:OG1	2.03	0.58
1:C:160:THR:HB	1:C:161:PRO:HD2	1.84	0.58
1:C:96:GLU:HB3	1:C:98:PHE:CE2	2.38	0.58
1:B:220:ILE:HG22	1:B:230:LEU:HD22	1.86	0.57
1:A:48:LEU:C	1:A:48:LEU:HD23	2.29	0.57
1:C:231:LYS:HB2	1:C:241:SER:HB3	1.86	0.57
1:B:133:LYS:HE3	1:B:190:GLU:OE1	2.04	0.56
1:C:93:LYS:HZ3	1:C:115:LEU:CD1	2.18	0.56
1:B:207:ASP:OD1	1:B:210:ARG:NH1	2.38	0.56
1:A:192:LYS:HG3	3:A:288:HOH:O	2.07	0.55
1:B:228:LEU:HD23	1:B:244:ILE:HD13	1.88	0.55
1:A:178:VAL:HG13	3:C:276:HOH:O	2.07	0.55
1:B:2:THR:N	3:B:279:HOH:O	2.39	0.55
1:B:132:VAL:HG21	1:B:196:ALA:CB	2.36	0.55
1:B:221:ARG:HD2	1:B:229:LEU:HD23	1.87	0.55
1:B:26:GLU:OE1	1:B:116:ILE:HD12	2.07	0.54
1:A:225:ASP:C	1:A:226:ILE:HD12	2.33	0.53
1:C:172:ASP:N	1:C:172:ASP:OD1	2.40	0.53
1:A:178:VAL:CG1	3:C:276:HOH:O	2.56	0.53
1:C:200:TYR:CE2	1:C:228:LEU:HB2	2.43	0.53
1:C:93:LYS:HZ3	1:C:115:LEU:HD13	1.74	0.53
1:B:234:VAL:HB	1:B:238:GLY:HA3	1.91	0.53
1:C:8:ASP:HB2	3:C:277:HOH:O	2.09	0.52
1:A:130:TRP:CE3	1:A:221:ARG:HD3	2.45	0.51
1:B:133:LYS:HG3	1:B:221:ARG:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:LYS:HB2	1:C:174:GLU:HG2	1.91	0.51
1:C:3:PHE:CD1	1:C:3:PHE:C	2.89	0.51
1:B:8:ASP:HB2	1:B:235:ARG:HH22	1.74	0.51
1:C:131:THR:HB	1:C:193:MET:HB2	1.92	0.50
1:B:207:ASP:HA	1:B:210:ARG:HD2	1.92	0.50
1:C:96:GLU:CB	1:C:98:PHE:CE2	2.94	0.50
1:B:200:TYR:CZ	1:B:228:LEU:HB2	2.48	0.49
1:B:8:ASP:OD2	1:B:8:ASP:N	2.45	0.49
1:C:234:VAL:O	1:C:235:ARG:C	2.55	0.49
1:A:239:GLU:HB3	3:A:276:HOH:O	2.13	0.48
1:C:39:ARG:O	1:C:40:ALA:HB2	2.13	0.48
1:A:224:PHE:O	1:A:226:ILE:HD13	2.14	0.48
1:C:93:LYS:HZ2	1:C:115:LEU:HD12	1.76	0.48
1:C:171:ASN:HB3	1:C:172:ASP:OD1	2.14	0.48
1:C:130:TRP:CD2	1:C:221:ARG:HD2	2.50	0.47
1:B:76:PHE:O	1:B:79:VAL:HB	2.13	0.47
1:C:16:LEU:O	1:C:17:ILE:C	2.56	0.47
1:A:228:LEU:HD23	1:A:244:ILE:HD13	1.97	0.47
1:A:234:VAL:HG13	1:A:238:GLY:HA3	1.97	0.46
1:B:98:PHE:HE1	1:C:172:ASP:O	1.97	0.46
1:C:42:ASP:OD1	1:C:44:SER:OG	2.25	0.46
1:B:226:ILE:CG2	1:B:227:PRO:HD2	2.45	0.46
1:B:37:GLN:HA	1:B:51:LEU:O	2.15	0.46
1:B:235:ARG:O	1:B:236:ASP:HB2	2.16	0.46
1:A:33:MET:HB3	1:A:33:MET:HE3	1.80	0.46
1:A:136:VAL:HG21	1:A:141:LEU:HG	1.97	0.46
1:B:33:MET:HG2	1:B:66:GLU:OE2	2.16	0.46
1:B:133:LYS:HB3	1:B:190:GLU:HB3	1.96	0.46
1:C:170:GLY:O	1:C:171:ASN:C	2.59	0.46
1:A:167:LYS:HA	1:A:175:VAL:O	2.16	0.46
1:B:39:ARG:NE	1:B:50:ASP:OD1	2.49	0.45
1:B:181:MET:HE2	1:B:181:MET:HB2	1.82	0.45
1:C:93:LYS:HE3	1:C:94:GLY:O	2.15	0.45
1:A:200:TYR:CZ	1:A:228:LEU:HB2	2.52	0.45
1:B:172:ASP:OD1	1:B:172:ASP:N	2.50	0.45
1:A:84:ARG:NH1	3:A:266:HOH:O	2.50	0.45
1:C:87:ASP:HA	1:C:104:LEU:O	2.18	0.44
1:A:142:LYS:O	1:A:146:LYS:HB2	2.17	0.44
1:B:110:TRP:O	1:C:175:VAL:HA	2.17	0.44
1:B:132:VAL:HG21	1:B:196:ALA:HB3	2.00	0.44
1:C:90:VAL:CG2	1:C:104:LEU:HD22	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:VAL:HB	1:C:60:LYS:HB3	2.00	0.44
1:C:40:ALA:O	1:C:49:VAL:HG12	2.18	0.43
1:C:74:LYS:HZ2	1:C:78:LYS:HE3	1.83	0.43
1:B:33:MET:HA	1:B:63:VAL:HG21	2.00	0.43
1:C:28:VAL:HG21	1:C:120:THR:HB	2.00	0.43
1:B:92:ARG:HB3	1:B:100:GLU:HB3	2.00	0.43
1:B:165:THR:HG21	3:B:273:HOH:O	2.19	0.43
1:A:48:LEU:O	1:A:242:PHE:HA	2.18	0.43
1:B:234:VAL:O	1:B:235:ARG:C	2.61	0.43
1:C:93:LYS:NZ	1:C:115:LEU:HD13	2.30	0.43
1:A:103:LEU:C	1:A:104:LEU:HD23	2.44	0.43
1:C:158:MET:HB2	1:C:165:THR:HB	1.99	0.43
1:B:152:SER:OG	1:B:153:ASP:N	2.51	0.42
1:C:226:ILE:C	1:C:246:PRO:HG3	2.44	0.42
1:A:9:SER:OG	2:A:261:SO4:O1	2.32	0.42
1:A:22:LYS:HD3	1:A:22:LYS:HA	1.85	0.42
1:C:175:VAL:HG13	1:C:175:VAL:O	2.19	0.42
1:A:148:ALA:HB2	1:A:155:ILE:HD12	2.02	0.42
1:A:149:LYS:HB2	1:A:202:VAL:HG11	2.02	0.42
1:B:17:ILE:HD13	1:B:17:ILE:HA	1.88	0.42
1:C:130:TRP:CE2	1:C:221:ARG:HD2	2.55	0.42
1:C:202:VAL:HG12	1:C:203:ALA:N	2.33	0.42
1:A:39:ARG:HA	1:A:49:VAL:O	2.20	0.41
1:B:153:ASP:O	1:B:202:VAL:HB	2.19	0.41
1:C:198:SER:HB2	1:C:200:TYR:CE1	2.55	0.41
1:C:143:ARG:O	1:C:144:ALA:C	2.63	0.41
1:C:152:SER:OG	1:C:153:ASP:N	2.54	0.41
1:B:142:LYS:O	1:B:146:LYS:HB2	2.21	0.41
1:A:159:ALA:HA	1:A:163:LYS:O	2.22	0.40
1:B:132:VAL:CG2	1:B:196:ALA:HB2	2.50	0.40
1:B:227:PRO:HA	1:B:244:ILE:O	2.22	0.40
1:C:142:LYS:NZ	1:C:212:LEU:O	2.45	0.40
1:C:228:LEU:O	1:C:243:LEU:HA	2.22	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	245/259 (95%)	230 (94%)	13 (5%)	2 (1%)	16	25
1	B	244/259 (94%)	230 (94%)	11 (4%)	3 (1%)	10	16
1	C	244/259 (94%)	218 (89%)	22 (9%)	4 (2%)	7	11
All	All	733/777 (94%)	678 (92%)	46 (6%)	9 (1%)	10	16

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	MET
1	B	235	ARG
1	C	172	ASP
1	A	237	ALA
1	B	56	MET
1	B	171	ASN
1	C	63	VAL
1	C	246	PRO
1	C	43	PRO

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	213/224 (95%)	197 (92%)	16 (8%)	12	21
1	B	212/224 (95%)	193 (91%)	19 (9%)	9	15
1	C	212/224 (95%)	193 (91%)	19 (9%)	9	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	637/672 (95%)	583 (92%)	54 (8%)	10	16

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ARG
1	A	15	SER
1	A	59	SER
1	A	62	SER
1	A	64	GLU
1	A	75	ARG
1	A	96	GLU
1	A	120	THR
1	A	127	SER
1	A	150	LEU
1	A	182	GLU
1	A	194	THR
1	A	226	ILE
1	A	234	VAL
1	A	236	ASP
1	A	248	VAL
1	B	8	ASP
1	B	42	ASP
1	B	56	MET
1	B	60	LYS
1	B	63	VAL
1	B	100	GLU
1	B	113	LEU
1	B	120	THR
1	B	150	LEU
1	B	151	VAL
1	B	154	SER
1	B	162	GLU
1	B	165	THR
1	B	181	MET
1	B	182	GLU
1	B	198	SER
1	B	208	ILE
1	B	212	LEU
1	B	247	ARG
1	C	43	PRO
1	C	46	VAL

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Mol	Chain	Res	Type
1	C	55	GLU
1	C	59	SER
1	C	63	VAL
1	C	64	GLU
1	C	80	LEU
1	C	85	SER
1	C	86	ARG
1	C	88	THR
1	C	104	LEU
1	C	107	GLU
1	C	124	GLU
1	C	153	ASP
1	C	169	GLU
1	C	171	ASN
1	C	202	VAL
1	C	239	GLU
1	C	241	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	B	30	GLN
1	B	32	ASN
1	B	108	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	B	260	-	4,4,4	0.25	0	6,6,6	0.44	0
2	SO4	A	261	-	4,4,4	0.23	0	6,6,6	0.66	0
2	SO4	B	261	-	4,4,4	0.23	0	6,6,6	0.69	0
2	SO4	C	260	-	4,4,4	0.39	0	6,6,6	0.74	0
2	SO4	A	260	-	4,4,4	0.25	0	6,6,6	0.60	0
2	SO4	A	262	-	4,4,4	0.25	0	6,6,6	0.32	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	261	SO4	1	0
2	B	261	SO4	1	0

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 [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	247/259 (95%)	0.06	6 (2%) 59 55	35, 50, 80, 91	0
1	B	246/259 (94%)	0.20	4 (1%) 70 66	34, 56, 76, 87	0
1	C	246/259 (94%)	0.30	2 (0%) 82 80	42, 59, 76, 88	0
All	All	739/777 (95%)	0.19	12 (1%) 70 66	34, 55, 77, 91	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	ILE	3.1
1	C	118	ALA	2.7
1	B	118	ALA	2.6
1	C	125	ILE	2.6
1	B	98	PHE	2.5
1	B	95	GLY	2.2
1	A	119	ASN	2.1
1	A	193	MET	2.1
1	A	194	THR	2.1
1	A	248	VAL	2.1
1	A	123	ILE	2.1
1	B	8	ASP	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 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(Å ²)	Q<0.9
2	SO4	A	260	5/5	0.84	0.11	80,81,82,83	0
2	SO4	A	262	5/5	0.84	0.21	64,66,67,67	5
2	SO4	B	261	5/5	0.91	0.10	47,48,49,49	5
2	SO4	B	260	5/5	0.92	0.09	75,76,78,78	0
2	SO4	A	261	5/5	0.94	0.14	53,54,56,59	0
2	SO4	C	260	5/5	0.94	0.09	37,38,40,42	5

6.5 Other polymers [i](#)

There are no such residues in this entry.