



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:48 PM UTC

PDB ID : 4LIY / pdb_00004liy
Title : Structure of the adenovirus 3 knob domain K217E and F224S mutant
Authors : Zubieta, C.; Fender, P.
Deposited on : 2013-07-04
Resolution : 2.10 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

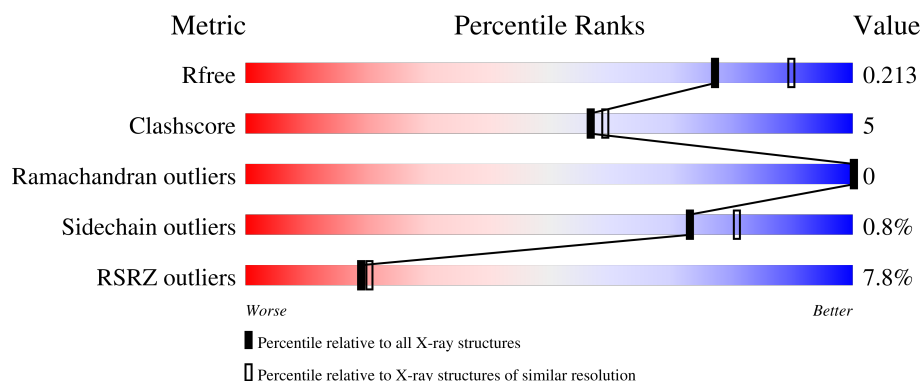
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	257	5% 66% 6% 28%
1	B	257	5% 62% 8% 30%
1	C	257	7% 67% 5% 28%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4587 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 Fiber protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	186	Total	C	N	O	S	0	0	0
			1442	923	230	283	6			
1	B	181	Total	C	N	O	S	0	0	0
			1417	909	225	277	6			
1	C	186	Total	C	N	O	S	0	1	0
			1451	928	231	286	6			

There are 186 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MET	-	expression tag	UNP P04501
A	64	ARG	-	expression tag	UNP P04501
A	65	GLY	-	expression tag	UNP P04501
A	66	SER	-	expression tag	UNP P04501
A	67	HIS	-	expression tag	UNP P04501
A	68	HIS	-	expression tag	UNP P04501
A	69	HIS	-	expression tag	UNP P04501
A	70	HIS	-	expression tag	UNP P04501
A	71	HIS	-	expression tag	UNP P04501
A	72	HIS	-	expression tag	UNP P04501
A	73	GLY	-	expression tag	UNP P04501
A	74	SER	-	expression tag	UNP P04501
A	75	LYS	-	expression tag	UNP P04501
A	76	VAL	-	expression tag	UNP P04501
A	77	SER	-	expression tag	UNP P04501
A	78	ALA	-	expression tag	UNP P04501
A	79	LEU	-	expression tag	UNP P04501
A	80	LYS	-	expression tag	UNP P04501
A	81	GLU	-	expression tag	UNP P04501
A	82	LYS	-	expression tag	UNP P04501
A	83	VAL	-	expression tag	UNP P04501
A	84	SER	-	expression tag	UNP P04501
A	85	ALA	-	expression tag	UNP P04501

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Chain	Residue	Modelled	Actual	Comment	Reference
A	86	LEU	-	expression tag	UNP P04501
A	87	LYS	-	expression tag	UNP P04501
A	88	GLU	-	expression tag	UNP P04501
A	89	LYS	-	expression tag	UNP P04501
A	90	VAL	-	expression tag	UNP P04501
A	91	SER	-	expression tag	UNP P04501
A	92	ALA	-	expression tag	UNP P04501
A	93	LEU	-	expression tag	UNP P04501
A	94	LYS	-	expression tag	UNP P04501
A	95	GLU	-	expression tag	UNP P04501
A	96	LYS	-	expression tag	UNP P04501
A	97	VAL	-	expression tag	UNP P04501
A	98	SER	-	expression tag	UNP P04501
A	99	ALA	-	expression tag	UNP P04501
A	100	LEU	-	expression tag	UNP P04501
A	101	LYS	-	expression tag	UNP P04501
A	102	GLU	-	expression tag	UNP P04501
A	103	LYS	-	expression tag	UNP P04501
A	104	VAL	-	expression tag	UNP P04501
A	105	SER	-	expression tag	UNP P04501
A	106	ALA	-	expression tag	UNP P04501
A	107	LEU	-	expression tag	UNP P04501
A	108	LYS	-	expression tag	UNP P04501
A	109	GLU	-	expression tag	UNP P04501
A	110	GLY	-	expression tag	UNP P04501
A	111	SER	-	expression tag	UNP P04501
A	112	GLY	-	expression tag	UNP P04501
A	113	GLY	-	expression tag	UNP P04501
A	114	GLY	-	expression tag	UNP P04501
A	115	SER	-	expression tag	UNP P04501
A	116	GLY	-	expression tag	UNP P04501
A	117	GLY	-	expression tag	UNP P04501
A	118	GLY	-	expression tag	UNP P04501
A	119	SER	-	expression tag	UNP P04501
A	120	GLY	-	expression tag	UNP P04501
A	121	GLY	-	expression tag	UNP P04501
A	122	GLY	-	expression tag	UNP P04501
A	217	GLU	LYS	engineered mutation	UNP P04501
A	224	SER	PHE	engineered mutation	UNP P04501
B	63	MET	-	expression tag	UNP P04501
B	64	ARG	-	expression tag	UNP P04501
B	65	GLY	-	expression tag	UNP P04501

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Chain	Residue	Modelled	Actual	Comment	Reference
B	66	SER	-	expression tag	UNP P04501
B	67	HIS	-	expression tag	UNP P04501
B	68	HIS	-	expression tag	UNP P04501
B	69	HIS	-	expression tag	UNP P04501
B	70	HIS	-	expression tag	UNP P04501
B	71	HIS	-	expression tag	UNP P04501
B	72	HIS	-	expression tag	UNP P04501
B	73	GLY	-	expression tag	UNP P04501
B	74	SER	-	expression tag	UNP P04501
B	75	LYS	-	expression tag	UNP P04501
B	76	VAL	-	expression tag	UNP P04501
B	77	SER	-	expression tag	UNP P04501
B	78	ALA	-	expression tag	UNP P04501
B	79	LEU	-	expression tag	UNP P04501
B	80	LYS	-	expression tag	UNP P04501
B	81	GLU	-	expression tag	UNP P04501
B	82	LYS	-	expression tag	UNP P04501
B	83	VAL	-	expression tag	UNP P04501
B	84	SER	-	expression tag	UNP P04501
B	85	ALA	-	expression tag	UNP P04501
B	86	LEU	-	expression tag	UNP P04501
B	87	LYS	-	expression tag	UNP P04501
B	88	GLU	-	expression tag	UNP P04501
B	89	LYS	-	expression tag	UNP P04501
B	90	VAL	-	expression tag	UNP P04501
B	91	SER	-	expression tag	UNP P04501
B	92	ALA	-	expression tag	UNP P04501
B	93	LEU	-	expression tag	UNP P04501
B	94	LYS	-	expression tag	UNP P04501
B	95	GLU	-	expression tag	UNP P04501
B	96	LYS	-	expression tag	UNP P04501
B	97	VAL	-	expression tag	UNP P04501
B	98	SER	-	expression tag	UNP P04501
B	99	ALA	-	expression tag	UNP P04501
B	100	LEU	-	expression tag	UNP P04501
B	101	LYS	-	expression tag	UNP P04501
B	102	GLU	-	expression tag	UNP P04501
B	103	LYS	-	expression tag	UNP P04501
B	104	VAL	-	expression tag	UNP P04501
B	105	SER	-	expression tag	UNP P04501
B	106	ALA	-	expression tag	UNP P04501
B	107	LEU	-	expression tag	UNP P04501

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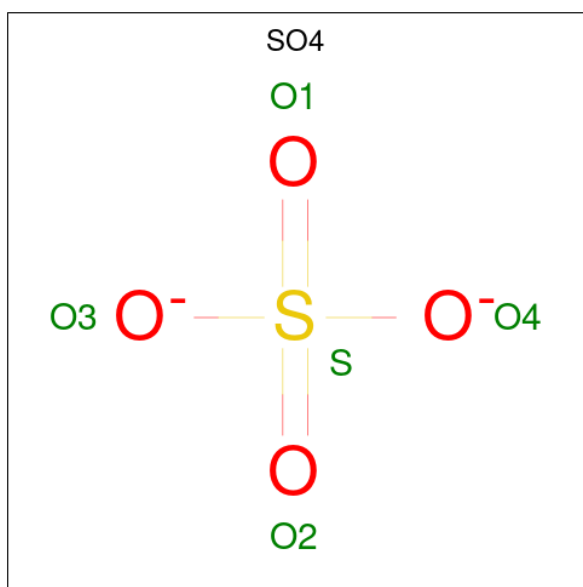
Chain	Residue	Modelled	Actual	Comment	Reference
B	108	LYS	-	expression tag	UNP P04501
B	109	GLU	-	expression tag	UNP P04501
B	110	GLY	-	expression tag	UNP P04501
B	111	SER	-	expression tag	UNP P04501
B	112	GLY	-	expression tag	UNP P04501
B	113	GLY	-	expression tag	UNP P04501
B	114	GLY	-	expression tag	UNP P04501
B	115	SER	-	expression tag	UNP P04501
B	116	GLY	-	expression tag	UNP P04501
B	117	GLY	-	expression tag	UNP P04501
B	118	GLY	-	expression tag	UNP P04501
B	119	SER	-	expression tag	UNP P04501
B	120	GLY	-	expression tag	UNP P04501
B	121	GLY	-	expression tag	UNP P04501
B	122	GLY	-	expression tag	UNP P04501
B	217	GLU	LYS	engineered mutation	UNP P04501
B	224	SER	PHE	engineered mutation	UNP P04501
C	63	MET	-	expression tag	UNP P04501
C	64	ARG	-	expression tag	UNP P04501
C	65	GLY	-	expression tag	UNP P04501
C	66	SER	-	expression tag	UNP P04501
C	67	HIS	-	expression tag	UNP P04501
C	68	HIS	-	expression tag	UNP P04501
C	69	HIS	-	expression tag	UNP P04501
C	70	HIS	-	expression tag	UNP P04501
C	71	HIS	-	expression tag	UNP P04501
C	72	HIS	-	expression tag	UNP P04501
C	73	GLY	-	expression tag	UNP P04501
C	74	SER	-	expression tag	UNP P04501
C	75	LYS	-	expression tag	UNP P04501
C	76	VAL	-	expression tag	UNP P04501
C	77	SER	-	expression tag	UNP P04501
C	78	ALA	-	expression tag	UNP P04501
C	79	LEU	-	expression tag	UNP P04501
C	80	LYS	-	expression tag	UNP P04501
C	81	GLU	-	expression tag	UNP P04501
C	82	LYS	-	expression tag	UNP P04501
C	83	VAL	-	expression tag	UNP P04501
C	84	SER	-	expression tag	UNP P04501
C	85	ALA	-	expression tag	UNP P04501
C	86	LEU	-	expression tag	UNP P04501
C	87	LYS	-	expression tag	UNP P04501

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Chain	Residue	Modelled	Actual	Comment	Reference
C	88	GLU	-	expression tag	UNP P04501
C	89	LYS	-	expression tag	UNP P04501
C	90	VAL	-	expression tag	UNP P04501
C	91	SER	-	expression tag	UNP P04501
C	92	ALA	-	expression tag	UNP P04501
C	93	LEU	-	expression tag	UNP P04501
C	94	LYS	-	expression tag	UNP P04501
C	95	GLU	-	expression tag	UNP P04501
C	96	LYS	-	expression tag	UNP P04501
C	97	VAL	-	expression tag	UNP P04501
C	98	SER	-	expression tag	UNP P04501
C	99	ALA	-	expression tag	UNP P04501
C	100	LEU	-	expression tag	UNP P04501
C	101	LYS	-	expression tag	UNP P04501
C	102	GLU	-	expression tag	UNP P04501
C	103	LYS	-	expression tag	UNP P04501
C	104	VAL	-	expression tag	UNP P04501
C	105	SER	-	expression tag	UNP P04501
C	106	ALA	-	expression tag	UNP P04501
C	107	LEU	-	expression tag	UNP P04501
C	108	LYS	-	expression tag	UNP P04501
C	109	GLU	-	expression tag	UNP P04501
C	110	GLY	-	expression tag	UNP P04501
C	111	SER	-	expression tag	UNP P04501
C	112	GLY	-	expression tag	UNP P04501
C	113	GLY	-	expression tag	UNP P04501
C	114	GLY	-	expression tag	UNP P04501
C	115	SER	-	expression tag	UNP P04501
C	116	GLY	-	expression tag	UNP P04501
C	117	GLY	-	expression tag	UNP P04501
C	118	GLY	-	expression tag	UNP P04501
C	119	SER	-	expression tag	UNP P04501
C	120	GLY	-	expression tag	UNP P04501
C	121	GLY	-	expression tag	UNP P04501
C	122	GLY	-	expression tag	UNP P04501
C	217	GLU	LYS	engineered mutation	UNP P04501
C	224	SER	PHE	engineered mutation	UNP P04501

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



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	104	Total	O	0	0
			104	104		
3	C	97	Total	O	0	0
			97	97		

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.66Å 96.66Å 156.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.33 – 2.10 48.33 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.33-2.10) 99.6 (48.33-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1391)	Depositor
R, R_{free}	0.176 , 0.201 0.189 , 0.213	Depositor DCC
R_{free} test set	2528 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.436	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4587	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% 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	0.59	0/1476	0.76	1/2011 (0.0%)
1	B	0.65	0/1450	0.84	3/1974 (0.2%)
1	C	0.66	2/1488 (0.1%)	0.90	9/2027 (0.4%)
All	All	0.63	2/4414 (0.0%)	0.84	13/6012 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	297	ALA	CA-CB	6.27	1.64	1.53
1	C	297	ALA	CA-C	-5.53	1.45	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	295	GLY	N-CA-C	-8.19	101.58	113.86
1	C	296	LEU	N-CA-C	8.02	122.63	109.24
1	C	296	LEU	CA-C-N	7.93	135.06	121.35
1	C	296	LEU	C-N-CA	7.93	135.06	121.35
1	B	297	ALA	N-CA-C	-6.63	101.16	110.31
1	B	295	GLY	N-CA-C	-6.22	104.80	112.77
1	A	134	TRP	N-CA-C	6.07	117.46	108.60
1	B	296	LEU	N-CA-C	5.90	118.37	109.41
1	C	240	LEU	CA-C-N	5.74	127.01	119.84
1	C	240	LEU	C-N-CA	5.74	127.01	119.84
1	C	136	GLY	CA-C-N	5.32	125.01	119.64
1	C	136	GLY	C-N-CA	5.32	125.01	119.64
1	C	134	TRP	N-CA-C	5.12	116.07	108.60

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	1442	0	1400	12	0
1	B	1417	0	1382	26	0
1	C	1451	0	1410	6	0
2	C	5	0	0	0	0
3	A	71	0	0	4	0
3	B	104	0	0	4	0
3	C	97	0	0	1	0
All	All	4587	0	4192	39	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 5.

All (39) 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)
3:A:461:HOH:O	1:B:174:MET:SD	2.16	1.01
1:C:163:ASN:OD1	3:C:590:HOH:O	2.04	0.76
1:B:187:LYS:HE2	1:B:297:ALA:HB2	1.68	0.74
1:B:140:GLU:OE1	3:B:460:HOH:O	2.11	0.69
1:B:187:LYS:HE2	1:B:297:ALA:CB	2.24	0.67
1:B:187:LYS:HZ3	1:B:296:LEU:HG	1.59	0.66
1:A:217:GLU:OE1	3:A:456:HOH:O	2.14	0.66
1:B:317:GLU:OE2	3:B:404:HOH:O	2.13	0.65
1:B:187:LYS:HD2	1:B:296:LEU:C	2.22	0.64
1:B:187:LYS:HD3	1:B:297:ALA:HB2	1.85	0.58
1:A:186:ASN:OD1	1:A:187:LYS:N	2.37	0.57
1:B:134:TRP:NE1	1:B:217:GLU:OE1	2.38	0.57
1:B:187:LYS:HD2	1:B:297:ALA:N	2.21	0.56
1:B:187:LYS:CE	1:B:297:ALA:HB2	2.34	0.55
1:C:144:ILE:HD12	1:C:211:LYS:HE3	1.91	0.53
1:A:304:THR:O	3:A:438:HOH:O	2.19	0.53
1:B:187:LYS:NZ	1:B:296:LEU:HD12	2.25	0.51
1:A:276:ARG:NH1	3:A:464:HOH:O	2.45	0.50
1:A:149:LYS:HG3	1:A:150:GLN:H	1.77	0.49
1:A:227:ARG:NH2	1:A:319:ASP:OXT	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LYS:CD	1:B:297:ALA:HB2	2.42	0.49
1:A:247:ASN:OD1	1:B:258:LYS:HB3	2.12	0.49
1:B:150:GLN:HG2	1:B:151:ASN:ND2	2.29	0.48
1:A:258:LYS:HE3	1:C:252:PHE:CZ	2.49	0.47
1:B:188:ASN:OD1	1:B:293:ASN:ND2	2.45	0.47
1:A:258:LYS:HE3	1:C:252:PHE:HZ	1.80	0.47
1:C:239:VAL:HG11	1:C:246:HIS:CG	2.51	0.46
1:B:239:VAL:HG11	1:B:246:HIS:NE2	2.31	0.46
1:B:187:LYS:CD	1:B:297:ALA:N	2.81	0.44
1:B:131:ASN:ND2	3:B:503:HOH:O	2.51	0.43
1:A:130:ASN:N	1:A:218:TYR:H	2.16	0.43
1:B:245:THR:O	1:B:245:THR:CG2	2.66	0.43
1:B:187:LYS:NZ	1:B:296:LEU:HA	2.34	0.42
1:A:174:MET:HE1	1:C:248:GLU:OE1	2.19	0.42
1:B:192:ASN:OD1	3:B:448:HOH:O	2.22	0.41
1:B:239:VAL:HG11	1:B:246:HIS:CD2	2.56	0.41
1:B:259:ALA:HB2	1:B:298:PRO:HB3	2.03	0.41
1:A:247:ASN:HB2	1:B:306:ILE:HD12	2.02	0.41
1:B:187:LYS:HZ3	1:B:296:LEU:CG	2.31	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	182/257 (71%)	177 (97%)	5 (3%)	0	100	100
1	B	175/257 (68%)	167 (95%)	8 (5%)	0	100	100
1	C	183/257 (71%)	174 (95%)	9 (5%)	0	100	100
All	All	540/771 (70%)	518 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	160/215 (74%)	159 (99%)	1 (1%)	78	86
1	B	159/215 (74%)	158 (99%)	1 (1%)	78	86
1	C	162/215 (75%)	159 (98%)	3 (2%)	50	58
All	All	481/645 (75%)	476 (99%)	5 (1%)	73	76

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	248	GLU
1	B	296	LEU
1	C	217[A]	GLU
1	C	217[B]	GLU
1	C	248	GLU

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

Mol	Chain	Res	Type
1	B	151	ASN
1	B	247	ASN
1	B	254	GLN
1	C	188	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	C	401	-	4,4,4	0.21	0	6,6,6	0.24	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.

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	186/257 (72%)	0.44	13 (6%) 22 24	31, 52, 84, 107	0
1	B	181/257 (70%)	0.13	12 (6%) 24 26	27, 43, 72, 87	0
1	C	186/257 (72%)	0.33	18 (9%) 13 14	31, 45, 77, 108	1 (0%)
All	All	553/771 (71%)	0.30	43 (7%) 19 20	27, 46, 80, 108	1 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	296	LEU	8.6
1	B	218	TYR	6.6
1	A	130	ASN	6.4
1	B	241	PRO	5.1
1	B	130	ASN	4.6
1	C	218	TYR	4.3
1	C	149	LYS	4.3
1	C	129	LYS	4.0
1	B	187	LYS	3.9
1	A	296	LEU	3.8
1	B	297	ALA	3.7
1	C	241	PRO	3.7
1	A	245	THR	3.7
1	B	296	LEU	3.7
1	A	224	SER	3.7
1	C	130	ASN	3.6
1	B	245	THR	3.6
1	C	187	LYS	3.6
1	A	225	SER	3.4
1	B	217	GLU	3.2
1	C	216	LEU	3.2
1	A	218	TYR	3.0
1	C	246	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	150	GLN	2.8
1	A	219	LYS	2.7
1	C	242	ASN	2.7
1	C	224	SER	2.7
1	C	319	ASP	2.7
1	C	276	ARG	2.6
1	C	262	GLY	2.4
1	B	319	ASP	2.4
1	A	186	ASN	2.3
1	C	217[A]	GLU	2.2
1	B	301	THR	2.2
1	C	297	ALA	2.2
1	A	188	ASN	2.2
1	C	147	TYR	2.2
1	A	293	ASN	2.2
1	A	192	ASN	2.1
1	B	150	GLN	2.1
1	A	277	LEU	2.0
1	B	246	HIS	2.0
1	A	136	GLY	2.0

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($\text{\AA}^2$)	Q<0.9
2	SO4	C	401	5/5	0.67	0.30	119,125,128,133	0

6.5 Other polymers [i](#)

There are no such residues in this entry.