



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:56 AM UTC

PDB ID : 2V0R / pdb_00002v0r
Title : crystal structure of a hairpin exchange variant (LTx) of the targeting LINE-1 retrotransposon endonuclease
Authors : Repanas, K.; Zingler, N.; Layer, L.E.; Schumann, G.G.; Perrakis, A.; Weichenrieder, O.
Deposited on : 2007-05-17
Resolution : 2.30 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

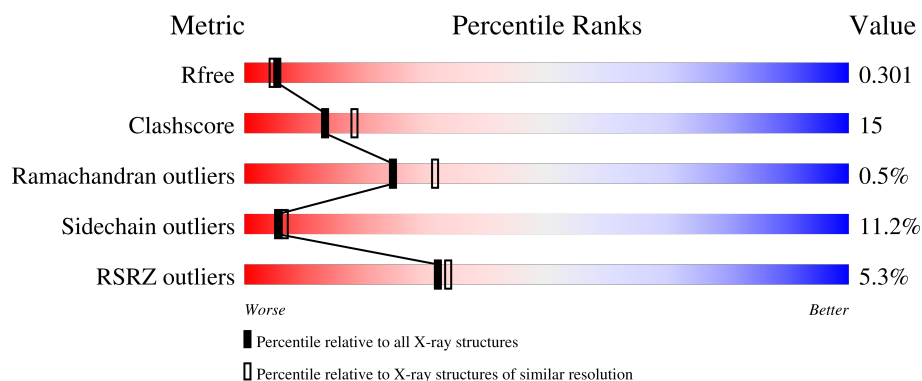
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	240	3% 72% 22% • •
1	B	240	8% 67% 25% 5% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3952 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 LTX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	0	0
			1885	1180	349	350	6			
1	B	234	Total	C	N	O	S	0	1	0
			1882	1179	348	349	6			

- 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	A	1	Total	O	S	0	0
			5	4	1		

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

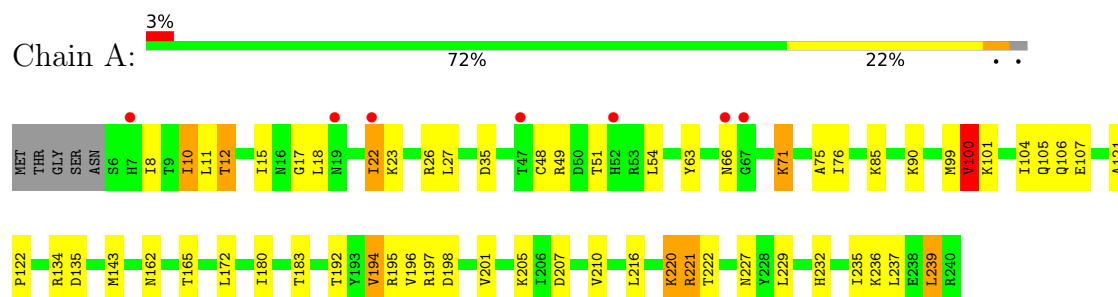
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	79	Total	O	0	0
			79	79		
3	B	76	Total	O	0	0
			76	76		

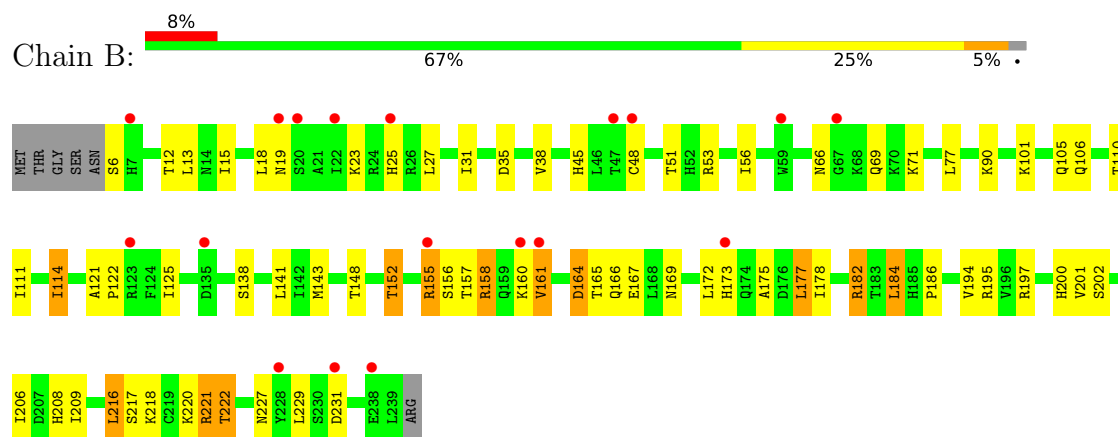
3 Residue-property plots [i](#)

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: LTX



• Molecule 1: LTX



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.73Å 70.14Å 130.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.53 – 2.30 19.53 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.53-2.30) 98.9 (19.53-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.272 (Not available) , 0.301	Depositor DCC
R_{free} test set	1156 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.9	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	3952	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 67.46 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.1251e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	1.19	5/1915 (0.3%)	1.07	2/2581 (0.1%)
1	B	1.13	1/1915 (0.1%)	1.07	2/2581 (0.1%)
All	All	1.16	6/3830 (0.2%)	1.07	4/5162 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	35	ASP	C-O	-8.76	1.19	1.23
1	A	100	VAL	CA-CB	7.06	1.63	1.54
1	A	180	ILE	CA-CB	6.98	1.63	1.54
1	A	12	THR	CA-CB	5.89	1.64	1.53
1	A	35	ASP	CA-CB	5.71	1.56	1.52
1	A	194	VAL	CA-C	5.28	1.59	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	ARG	N-CA-C	8.00	121.82	110.23
1	B	31	ILE	N-CA-C	5.97	116.71	110.62
1	B	222	THR	N-CA-C	5.27	118.15	109.72
1	A	85	LYS	CB-CA-C	5.01	115.74	110.17

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	220	LYS	Peptide
1	B	221	ARG	Peptide

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	1885	0	1948	54	0
1	B	1882	0	1948	63	0
2	A	20	0	0	0	0
2	B	10	0	0	0	0
3	A	79	0	0	3	0
3	B	76	0	0	10	0
All	All	3952	0	3896	114	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 15.

All (114) 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[B]:ARG:NH2	3:B:2041:HOH:O	1.75	1.18
1:B:155[B]:ARG:CZ	3:B:2041:HOH:O	1.93	1.12
1:A:12:THR:HB	1:A:143:MET:HE2	1.33	1.11
1:B:161:VAL:HG13	1:B:165:THR:HB	1.51	0.91
1:B:25:HIS:HB3	3:B:2001:HOH:O	1.71	0.91
1:A:90:LYS:HG3	1:A:99:MET:HE2	1.52	0.91
1:B:182:ARG:HG2	1:B:182:ARG:HH11	1.36	0.91
1:B:12:THR:HB	1:B:143:MET:HE2	1.53	0.89
1:A:76:ILE:HD12	1:A:100:VAL:HG13	1.59	0.83
1:A:22:ILE:HD11	1:A:26:ARG:NH1	1.95	0.81
1:B:155[B]:ARG:NH1	3:B:2041:HOH:O	2.03	0.80
1:A:162:ASN:OD1	1:A:165:THR:HG23	1.82	0.78
1:A:195:ARG:HH21	1:A:197:ARG:HE	1.33	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ARG:NH2	1:A:197:ARG:HE	1.85	0.75
1:B:175:ALA:HB3	1:B:177:LEU:HD22	1.69	0.74
1:B:48:CYS:HA	1:B:51:THR:HG23	1.69	0.73
1:A:18:LEU:HD21	1:A:27:LEU:HD22	1.70	0.73
1:A:207:ASP:OD2	1:A:232:HIS:HD2	1.71	0.72
1:A:18:LEU:HD13	1:A:54:LEU:HD13	1.72	0.72
1:B:15:ILE:HD11	1:B:229:LEU:HD13	1.74	0.70
1:B:182:ARG:HH11	1:B:182:ARG:CG	2.05	0.68
1:A:22:ILE:HD11	1:A:26:ARG:HH11	1.59	0.68
1:A:90:LYS:HG3	1:A:99:MET:CE	2.24	0.67
1:A:51:THR:HG22	1:A:66:ASN:OD1	1.94	0.66
1:B:227:ASN:HD22	1:B:229:LEU:H	1.44	0.65
1:A:101:LYS:NZ	1:A:135:ASP:O	2.32	0.62
1:A:48:CYS:HA	1:A:51:THR:HG23	1.83	0.61
1:B:90:LYS:NZ	3:B:2024:HOH:O	2.33	0.61
1:B:155[B]:ARG:HH11	1:B:155[B]:ARG:HG3	1.66	0.60
1:A:227:ASN:HD22	1:A:229:LEU:H	1.50	0.60
1:A:195:ARG:HH21	1:A:197:ARG:NE	2.01	0.59
1:A:8:ILE:HD13	1:A:104:ILE:HD12	1.84	0.58
1:A:71:LYS:NZ	3:A:2023:HOH:O	2.36	0.58
1:A:134:ARG:HG2	1:A:134:ARG:NH1	2.18	0.58
1:B:175:ALA:CB	1:B:177:LEU:HD22	2.34	0.57
1:B:19:ASN:ND2	1:B:45:HIS:O	2.37	0.56
1:B:18:LEU:HD21	1:B:27:LEU:HD22	1.88	0.55
1:B:56:ILE:HD12	1:B:77:LEU:CD2	2.37	0.55
1:A:17:GLY:O	1:A:23:LYS:NZ	2.39	0.55
1:B:161:VAL:HG13	1:B:165:THR:CB	2.29	0.55
1:B:227:ASN:ND2	1:B:229:LEU:HG	2.22	0.55
1:A:227:ASN:ND2	1:A:229:LEU:HB2	2.21	0.54
1:B:155[B]:ARG:HH11	1:B:155[B]:ARG:CG	2.19	0.54
1:A:227:ASN:HD22	1:A:229:LEU:HB2	1.71	0.54
1:B:178:ILE:HD13	1:B:216:LEU:HD21	1.90	0.54
1:A:134:ARG:HH11	1:A:134:ARG:CG	2.20	0.53
1:B:164:ASP:O	1:B:167:GLU:HB2	2.08	0.53
1:B:143:MET:HE3	1:B:209:ILE:CD1	2.38	0.53
1:A:192:THR:HG23	1:A:205:LYS:HD2	1.91	0.51
1:A:197:ARG:HG2	1:A:198:ASP:OD1	2.11	0.51
1:B:182:ARG:HD2	1:B:186:PRO:O	2.11	0.51
1:A:194:VAL:CG1	1:B:201:VAL:HG11	2.41	0.51
1:A:201:VAL:HG21	1:B:231:ASP:CG	2.36	0.50
1:A:15:ILE:HD11	1:A:27:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:GLN:O	1:B:106:GLN:HB2	2.10	0.50
1:B:15:ILE:HD12	1:B:23:LYS:HZ3	1.77	0.50
1:B:169:ASN:O	1:B:173:HIS:ND1	2.45	0.50
1:B:13:LEU:HD21	1:B:229:LEU:HD11	1.94	0.49
1:B:12:THR:CB	1:B:143:MET:HE2	2.34	0.49
1:A:22:ILE:HG23	1:A:23:LYS:N	2.26	0.49
1:A:105:GLN:O	1:A:106:GLN:HB2	2.11	0.49
1:A:222:THR:CG2	1:A:236:LYS:O	2.61	0.48
1:B:15:ILE:HD11	1:B:229:LEU:CD1	2.41	0.48
1:A:134:ARG:HG2	1:A:134:ARG:HH11	1.77	0.48
1:B:178:ILE:HD11	1:B:216:LEU:CD1	2.43	0.48
1:A:237:LEU:HG	1:A:239:LEU:HD23	1.95	0.48
1:B:15:ILE:HD12	1:B:23:LYS:NZ	2.29	0.48
1:A:10:ILE:CD1	1:A:239:LEU:HD21	2.43	0.48
1:B:178:ILE:HD11	1:B:216:LEU:HD13	1.96	0.48
1:B:56:ILE:HD12	1:B:77:LEU:HD21	1.95	0.47
1:A:134:ARG:NH1	1:A:134:ARG:CG	2.76	0.47
1:B:152:THR:HG22	3:B:2037:HOH:O	2.14	0.47
1:B:155[A]:ARG:HD2	1:B:157:THR:H	1.80	0.47
1:A:18:LEU:HD13	1:A:54:LEU:CD1	2.42	0.46
1:A:172:LEU:HD22	1:A:210:VAL:HG11	1.97	0.46
1:A:162:ASN:OD1	1:A:165:THR:CG2	2.58	0.46
1:A:196:VAL:HG21	1:B:200:HIS:HA	1.97	0.46
1:B:15:ILE:CD1	1:B:229:LEU:CD1	2.94	0.46
1:A:17:GLY:O	1:A:23:LYS:HG2	2.16	0.46
1:B:155[B]:ARG:NH1	3:B:2040:HOH:O	2.49	0.46
1:B:114:ILE:HD13	1:B:125:ILE:HG12	1.98	0.46
1:A:121:ALA:HB3	1:A:122:PRO:HD3	1.97	0.45
1:B:101:LYS:HG2	1:B:110:THR:HG23	1.97	0.45
1:B:161:VAL:HG12	1:B:166:GLN:HG2	1.98	0.45
1:A:11:LEU:C	1:A:11:LEU:HD23	2.42	0.45
1:B:51:THR:HG22	1:B:66:ASN:OD1	2.17	0.44
1:B:184:LEU:HD23	1:B:222:THR:HG22	1.99	0.44
1:B:227:ASN:HD22	1:B:229:LEU:HG	1.82	0.44
1:A:183:THR:HG21	1:A:216:LEU:HD11	1.98	0.44
1:B:206:ILE:HD13	1:B:206:ILE:HG21	1.83	0.44
1:A:71:LYS:CE	3:A:2023:HOH:O	2.65	0.43
1:B:18:LEU:HD21	1:B:27:LEU:CD2	2.47	0.43
1:B:38:VAL:HG11	1:B:111:ILE:HD13	2.00	0.43
1:B:69:GLN:HG3	1:B:71:LYS:HE2	2.00	0.43
1:A:195:ARG:NH2	1:A:197:ARG:NE	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ILE:CD1	1:A:27:LEU:HD13	2.48	0.43
1:A:71:LYS:HE3	3:A:2023:HOH:O	2.20	0.42
1:A:222:THR:HG22	1:A:236:LYS:O	2.19	0.42
1:B:121:ALA:HB3	1:B:122:PRO:HD3	2.01	0.42
1:A:99:MET:HE2	1:A:99:MET:HB3	1.95	0.41
1:A:122:PRO:HG3	1:A:165:THR:HG22	2.03	0.41
1:A:220:LYS:HB3	1:A:221:ARG:H	1.78	0.41
1:B:173:HIS:HB3	3:B:2046:HOH:O	2.20	0.41
1:B:195:ARG:NH2	1:B:197:ARG:HD2	2.35	0.41
1:A:221:ARG:H	1:A:221:ARG:HG2	1.66	0.41
1:B:148:THR:O	1:B:208:HIS:HE1	2.04	0.41
1:B:182:ARG:CG	1:B:182:ARG:NH1	2.75	0.41
1:B:15:ILE:HD13	1:B:15:ILE:O	2.21	0.41
1:B:53:ARG:CB	3:B:2011:HOH:O	2.68	0.41
1:B:178:ILE:HD13	1:B:216:LEU:CD2	2.50	0.40
1:B:172:LEU:HD23	1:B:177:LEU:HD23	2.04	0.40
1:B:182:ARG:CD	1:B:186:PRO:O	2.69	0.40
1:B:158:ARG:NH2	3:B:2043:HOH:O	2.54	0.40
1:A:63:TYR:O	1:A:75:ALA:HA	2.21	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	184/240 (77%)	178 (97%)	5 (3%)	1 (0%)	24	31
1	B	233/240 (97%)	222 (95%)	10 (4%)	1 (0%)	30	38
All	All	417/480 (87%)	400 (96%)	15 (4%)	2 (0%)	24	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	221	ARG
1	A	220	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	102/218 (47%)	94 (92%)	8 (8%)	11	16
1	B	139/218 (64%)	119 (86%)	20 (14%)	3	3
All	All	241/436 (55%)	213 (88%)	28 (12%)	5	6

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ILE
1	A	22	ILE
1	A	49	ARG
1	A	71	LYS
1	A	100	VAL
1	A	107	GLU
1	A	235	ILE
1	A	239	LEU
1	B	6	SER
1	B	114	ILE
1	B	138	SER
1	B	141	LEU
1	B	152	THR
1	B	155[A]	ARG
1	B	155[B]	ARG
1	B	156	SER
1	B	158	ARG
1	B	160	LYS
1	B	161	VAL
1	B	164	ASP
1	B	177	LEU
1	B	182	ARG

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Mol	Chain	Res	Type
1	B	184	LEU
1	B	194	VAL
1	B	202	SER
1	B	216	LEU
1	B	217	SER
1	B	218	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	42	GLN
1	A	69	GLN
1	A	96	HIS
1	A	105	GLN
1	A	232	HIS
1	B	208	HIS
1	B	227	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 ⓘ

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	A	1241	-	4,4,4	0.29	0	6,6,6	0.64	0
2	SO4	B	1241	-	4,4,4	0.21	0	6,6,6	0.66	0
2	SO4	A	1244	-	4,4,4	0.27	0	6,6,6	0.34	0
2	SO4	A	1243	-	4,4,4	0.33	0	6,6,6	0.36	0
2	SO4	A	1242	-	4,4,4	0.18	0	6,6,6	0.47	0
2	SO4	B	1240	-	4,4,4	0.24	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	235/240 (97%)	0.45	7 (2%) 52 54	15, 35, 50, 63	0
1	B	234/240 (97%)	0.73	18 (7%) 19 21	16, 35, 50, 64	1 (0%)
All	All	469/480 (97%)	0.59	25 (5%) 32 34	15, 35, 50, 64	1 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	HIS	3.8
1	B	155[A]	ARG	3.6
1	B	123	ARG	3.5
1	B	7	HIS	3.3
1	A	67	GLY	3.2
1	B	67	GLY	3.2
1	B	238	GLU	2.8
1	B	173	HIS	2.6
1	B	135	ASP	2.6
1	B	25	HIS	2.6
1	B	48	CYS	2.4
1	A	47	THR	2.4
1	B	22	ILE	2.4
1	B	47	THR	2.4
1	A	22	ILE	2.4
1	B	228	TYR	2.3
1	B	20	SER	2.3
1	B	161	VAL	2.3
1	B	19	ASN	2.3
1	B	59	TRP	2.3
1	A	19	ASN	2.2
1	A	66	ASN	2.1
1	A	52	HIS	2.1
1	B	231	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	160	LYS	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	A	1242	5/5	0.66	0.23	82,84,84,86	0
2	SO4	A	1243	5/5	0.71	0.21	94,96,97,97	0
2	SO4	A	1241	5/5	0.74	0.19	70,71,72,73	0
2	SO4	B	1240	5/5	0.77	0.15	90,90,90,91	0
2	SO4	B	1241	5/5	0.81	0.13	65,67,69,69	0
2	SO4	A	1244	5/5	0.92	0.14	57,58,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.