



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:34 am GMT

PDB ID : 4OJO
Title : Crystal Structure of Putative Tailspike Protein (TSP1, orf210) from Escherichia coli O157:H7 Bacteriophage CBA120 in Complex with Lactose
Authors : Chen, C.; Herzberg, O.
Deposited on : 2014-01-21
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

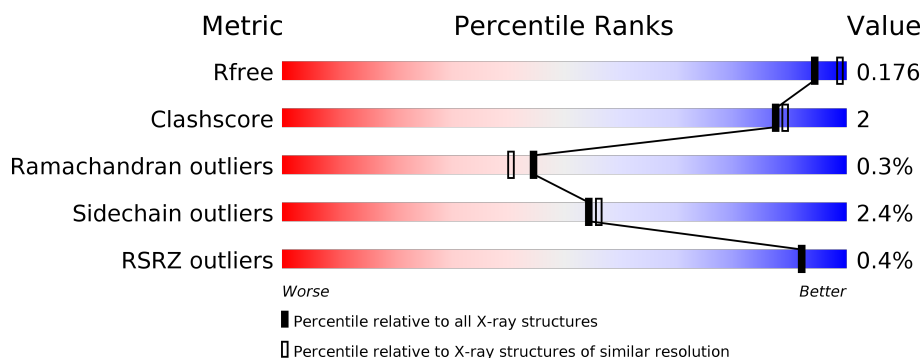
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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. 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	776	<div> <div>91%</div> <div>6% .</div> </div>
1	B	776	<div> <div>90%</div> <div>7% . .</div> </div>
1	C	776	<div> <div>92%</div> <div>5% . .</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	LBT	A	801	-	-	-	X
2	LBT	B	800	-	-	-	X
2	LBT	C	800	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19352 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.

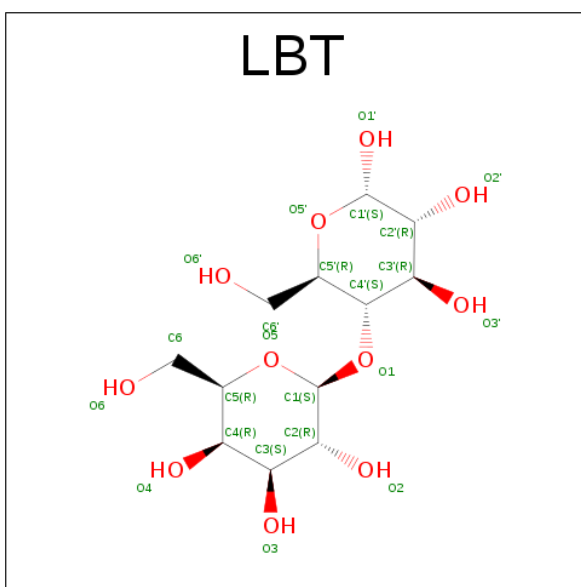
- Molecule 1 is a protein called Tailspike protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	758	Total	C	N	O	S	1	0	0
			5675	3578	955	1123	19			
1	B	756	Total	C	N	O	S	0	0	0
			5653	3568	947	1119	19			
1	C	759	Total	C	N	O	S	1	0	0
			5679	3580	958	1122	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	771	HIS	-	EXPRESSION TAG	UNP G3M189
A	772	HIS	-	EXPRESSION TAG	UNP G3M189
A	773	HIS	-	EXPRESSION TAG	UNP G3M189
A	774	HIS	-	EXPRESSION TAG	UNP G3M189
A	775	HIS	-	EXPRESSION TAG	UNP G3M189
A	776	HIS	-	EXPRESSION TAG	UNP G3M189
B	771	HIS	-	EXPRESSION TAG	UNP G3M189
B	772	HIS	-	EXPRESSION TAG	UNP G3M189
B	773	HIS	-	EXPRESSION TAG	UNP G3M189
B	774	HIS	-	EXPRESSION TAG	UNP G3M189
B	775	HIS	-	EXPRESSION TAG	UNP G3M189
B	776	HIS	-	EXPRESSION TAG	UNP G3M189
C	771	HIS	-	EXPRESSION TAG	UNP G3M189
C	772	HIS	-	EXPRESSION TAG	UNP G3M189
C	773	HIS	-	EXPRESSION TAG	UNP G3M189
C	774	HIS	-	EXPRESSION TAG	UNP G3M189
C	775	HIS	-	EXPRESSION TAG	UNP G3M189
C	776	HIS	-	EXPRESSION TAG	UNP G3M189

- Molecule 2 is SUGAR (ALPHA-LACTOSE) (three-letter code: LBT) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			23	12	11		
2	B	1	Total	C	O	0	0
			23	12	11		
2	C	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	1
			1	1		

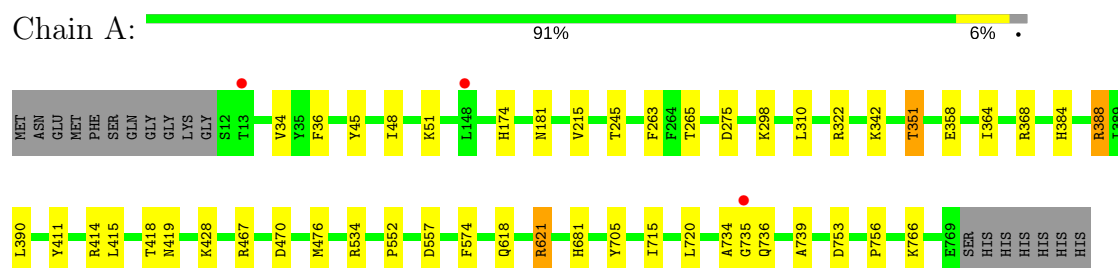
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	664	Total	O	0	0
			664	664		
4	B	820	Total	O	0	0
			820	820		
4	C	791	Total	O	0	0
			791	791		

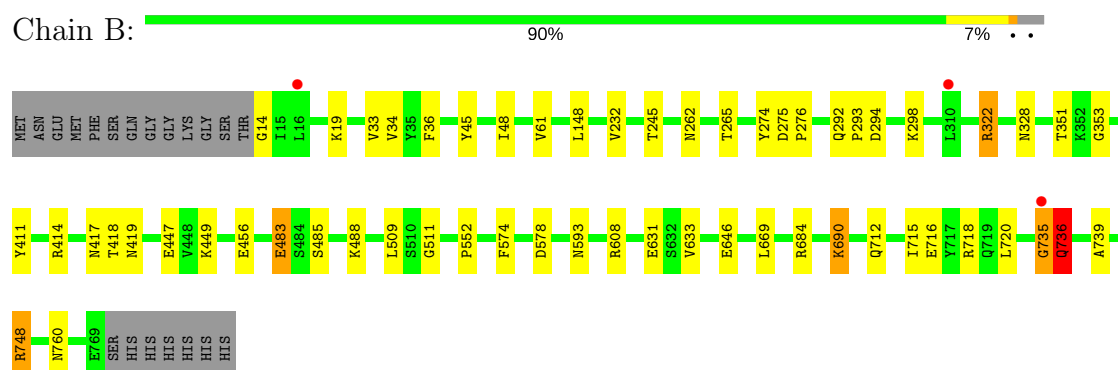
3 Residue-property plots [i](#)

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.

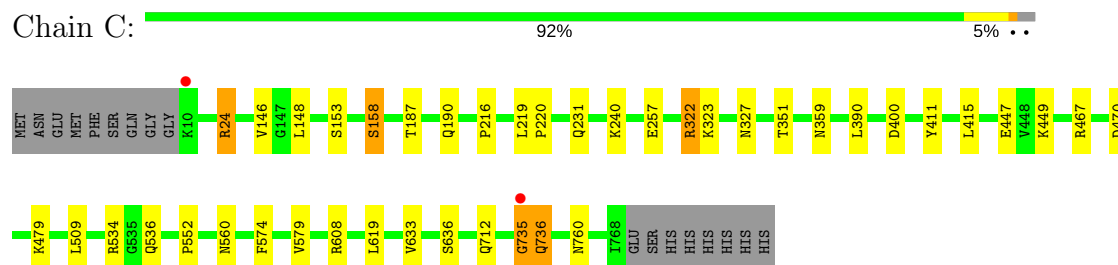
• Molecule 1: Tailspike protein



• Molecule 1: Tailspike protein



• Molecule 1: Tailspike protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	123.41Å 152.88Å 171.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.00 – 2.00 76.44 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.8 (76.00-2.00) 95.3 (76.44-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.177 , 0.214 0.174 , 0.176	Depositor DCC
R_{free} test set	10660 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.0	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	0.96	EDS
Total number of atoms	19352	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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](#)

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

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	0.36	0/5779	0.65	0/7856
1	B	0.39	0/5757	0.69	3/7828 (0.0%)
1	C	0.38	0/5783	0.66	0/7861
All	All	0.37	0/17319	0.67	3/23545 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	718	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	B	718	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	B	684	ARG	NE-CZ-NH2	-5.66	117.47	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5675	0	5638	30	0
1	B	5653	0	5600	29	0
1	C	5679	0	5641	20	0
2	A	23	0	22	3	0
2	B	23	0	22	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	23	0	22	0	0
3	A	1	0	0	0	0
4	A	664	0	0	13	0
4	B	820	0	0	11	0
4	C	791	0	0	2	0
All	All	19352	0	16945	80	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 2.

All (80) 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:A:801:LBT:C6'	4:A:1530:HOH:O	1.91	1.16
2:A:801:LBT:H6'1	4:A:1530:HOH:O	1.51	1.00
1:A:534:ARG:CZ	4:A:1558:HOH:O	2.20	0.88
1:A:681:HIS:HD2	1:A:705:TYR:H	1.26	0.83
1:B:414:ARG:NH2	1:B:418:THR:O	2.18	0.75
1:C:187:THR:HG22	1:C:190:GLN:HG3	1.73	0.70
1:C:216:PRO:HG2	1:C:219:LEU:HD21	1.75	0.68
1:B:449:LYS:NZ	4:B:1282:HOH:O	2.27	0.66
1:A:735:GLY:O	4:A:929:HOH:O	2.12	0.66
1:B:14:GLY:N	4:B:1688:HOH:O	2.30	0.65
1:B:322:ARG:NH1	4:B:1074:HOH:O	2.30	0.64
1:A:364:ILE:HG13	1:A:415:LEU:HB3	1.80	0.63
1:A:414:ARG:NH2	1:A:418:THR:O	2.34	0.61
1:A:181:ASN:O	1:C:187:THR:HG21	2.00	0.61
1:C:24:ARG:NH2	4:C:1027:HOH:O	2.34	0.61
1:A:351:THR:HG22	1:A:384:HIS:HA	1.83	0.60
1:A:358:GLU:OE1	1:A:368:ARG:HD3	2.03	0.59
1:B:14:GLY:N	4:B:1280:HOH:O	2.35	0.59
1:B:417:ASN:HB3	1:B:488:LYS:HD3	1.85	0.58
2:A:801:LBT:O6'	4:A:1530:HOH:O	1.84	0.58
1:B:593:ASN:ND2	4:B:1631:HOH:O	2.35	0.57
1:A:388:ARG:NH2	4:A:1039:HOH:O	2.33	0.57
1:A:681:HIS:CD2	1:A:705:TYR:H	2.16	0.56
1:A:263:PHE:H	1:A:265:THR:HG23	1.70	0.56
1:A:467:ARG:HD2	1:A:470:ASP:OD1	2.05	0.55
1:B:578:ASP:CB	4:B:1702:HOH:O	2.54	0.55
1:C:736:GLN:HA	1:C:760:ASN:O	2.07	0.54
1:B:19:LYS:HE3	1:B:33:VAL:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:ASP:O	1:A:766:LYS:NZ	2.40	0.53
1:C:449:LYS:NZ	4:C:902:HOH:O	2.42	0.52
1:C:712:GLN:HG2	1:C:735:GLY:O	2.10	0.51
1:C:153:SER:OG	1:C:158:SER:HB3	2.12	0.50
1:C:467:ARG:HD2	1:C:470:ASP:OD1	2.12	0.49
1:B:712:GLN:HG2	1:B:735:GLY:O	2.12	0.49
1:B:328:ASN:HD22	1:B:353:GLY:HA3	1.78	0.49
1:B:690:LYS:NZ	1:B:716:GLU:OE2	2.44	0.48
1:B:736:GLN:HA	1:B:760:ASN:O	2.12	0.48
2:B:800:LBT:O1'	4:B:1614:HOH:O	2.20	0.48
1:A:715:ILE:O	1:A:739:ALA:HA	2.13	0.48
1:B:417:ASN:ND2	1:B:485:SER:O	2.46	0.47
1:A:476:MET:SD	1:C:479:LYS:HD3	2.54	0.47
1:C:322:ARG:HG3	1:C:323:LYS:HG3	1.97	0.46
1:C:257:GLU:HA	1:C:327:ASN:O	2.14	0.46
1:A:298:LYS:HE2	4:A:1557:HOH:O	2.15	0.46
1:A:618:GLN:OE1	4:A:1530:HOH:O	2.20	0.46
1:B:262:ASN:HB2	1:B:265:THR:CG2	2.47	0.45
1:A:534:ARG:NH1	4:A:1558:HOH:O	2.41	0.45
1:A:756:PRO:HG3	1:A:766:LYS:HD2	1.98	0.45
1:B:298:LYS:NZ	4:B:1466:HOH:O	2.42	0.45
1:C:536:GLN:HA	1:C:560:ASN:HB3	1.99	0.45
1:A:621:ARG:HD2	1:A:621:ARG:N	2.32	0.44
1:B:265:THR:HG21	1:C:323:LYS:HD3	2.00	0.44
1:C:552:PRO:HB3	1:C:574:PHE:O	2.16	0.44
1:B:245:THR:HG22	1:B:275:ASP:O	2.17	0.44
4:A:1558:HOH:O	1:C:534:ARG:CZ	2.65	0.44
1:A:342:LYS:HB3	1:A:342:LYS:HE2	1.77	0.44
1:C:219:LEU:HA	1:C:220:PRO:HD3	1.84	0.44
1:B:36:PHE:HB2	1:B:48:ILE:HD11	2.00	0.43
1:C:579:VAL:HG23	1:C:619:LEU:HD22	2.01	0.43
1:C:359:ASN:OD1	1:C:415:LEU:HD11	2.18	0.43
1:A:534:ARG:NH1	4:A:1517:HOH:O	2.52	0.43
1:A:419:ASN:HB2	4:A:1499:HOH:O	2.19	0.42
1:C:24:ARG:HA	1:C:24:ARG:HD3	1.58	0.42
1:A:322:ARG:NH2	4:A:1269:HOH:O	2.37	0.42
1:B:715:ILE:O	1:B:739:ALA:HA	2.19	0.42
1:B:748:ARG:NH2	4:B:1640:HOH:O	2.52	0.42
1:A:36:PHE:HB2	1:A:48:ILE:HD11	2.00	0.42
1:A:34:VAL:HB	1:A:45:TYR:CD1	2.55	0.42
1:B:552:PRO:HB3	1:B:574:PHE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:552:PRO:HB3	1:A:574:PHE:O	2.19	0.41
1:B:292:GLN:HB3	1:B:293:PRO:HD2	2.01	0.41
1:B:488:LYS:NZ	4:B:1496:HOH:O	2.52	0.41
1:B:456:GLU:HA	1:B:483:GLU:O	2.21	0.41
1:B:274:TYR:CE2	1:B:276:PRO:HG3	2.56	0.41
1:B:34:VAL:HB	1:B:45:TYR:CD1	2.55	0.41
1:A:34:VAL:HB	1:A:45:TYR:CG	2.56	0.41
1:A:245:THR:HG22	1:A:275:ASP:O	2.20	0.41
1:B:631:GLU:HG2	1:B:633:VAL:HG12	2.03	0.41
1:A:534:ARG:HG2	1:A:557:ASP:HB3	2.02	0.40
1:B:419:ASN:ND2	4:B:1381:HOH:O	2.55	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	756/776 (97%)	729 (96%)	25 (3%)	2 (0%)	44	40
1	B	754/776 (97%)	726 (96%)	25 (3%)	3 (0%)	38	33
1	C	757/776 (98%)	729 (96%)	26 (3%)	2 (0%)	44	40
All	All	2267/2328 (97%)	2184 (96%)	76 (3%)	7 (0%)	44	40

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	736	GLN
1	B	736	GLN
1	C	736	GLN
1	B	735	GLY
1	C	735	GLY
1	A	734	ALA

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Mol	Chain	Res	Type
1	B	511	GLY

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	621/637 (98%)	610 (98%)	11 (2%)	64	68
1	B	615/637 (96%)	598 (97%)	17 (3%)	49	49
1	C	620/637 (97%)	604 (97%)	16 (3%)	51	52
All	All	1856/1911 (97%)	1812 (98%)	44 (2%)	54	56

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	174	HIS
1	A	215	VAL
1	A	310	LEU
1	A	351	THR
1	A	388	ARG
1	A	390	LEU
1	A	411	TYR
1	A	428	LYS
1	A	621	ARG
1	A	720	LEU
1	B	61	VAL
1	B	148	LEU
1	B	232	VAL
1	B	294	ASP
1	B	322	ARG
1	B	351	THR
1	B	411	TYR
1	B	447	GLU
1	B	483	GLU
1	B	509	LEU

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Mol	Chain	Res	Type
1	B	608	ARG
1	B	646	GLU
1	B	669	LEU
1	B	690	LYS
1	B	720	LEU
1	B	736	GLN
1	B	748	ARG
1	C	24	ARG
1	C	146	VAL
1	C	148	LEU
1	C	158	SER
1	C	231	GLN
1	C	240	LYS
1	C	322	ARG
1	C	351	THR
1	C	390	LEU
1	C	400	ASP
1	C	411	TYR
1	C	447	GLU
1	C	509	LEU
1	C	608	ARG
1	C	633	VAL
1	C	636	SER

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

Mol	Chain	Res	Type
1	A	174	HIS
1	A	262	ASN
1	A	409	ASN
1	A	681	HIS
1	B	165	ASN
1	B	328	ASN
1	C	192	ASN
1	C	262	ASN
1	C	280	ASN
1	C	327	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 ⓘ

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	LBT	A	801	-	24,24,24	0.53	0	35,35,35	0.52	0
2	LBT	B	800	-	24,24,24	0.49	0	35,35,35	0.55	0
2	LBT	C	800	-	24,24,24	0.53	0	35,35,35	0.56	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LBT	A	801	-	-	0/8/48/48	0/2/2/2
2	LBT	B	800	-	-	0/8/48/48	0/2/2/2
2	LBT	C	800	-	-	0/8/48/48	0/2/2/2

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 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	LBT	3	0
2	B	800	LBT	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	758/776 (97%)	-0.42	3 (0%)	92 92	20, 29, 43, 63	1 (0%)
1	B	756/776 (97%)	-0.45	3 (0%)	92 92	16, 25, 39, 56	0
1	C	759/776 (97%)	-0.46	2 (0%)	93 93	18, 25, 40, 56	0
All	All	2273/2328 (97%)	-0.45	8 (0%)	92 92	16, 27, 41, 63	1 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	735	GLY	4.1
1	C	735	GLY	3.3
1	B	735	GLY	3.0
1	B	310	LEU	2.9
1	C	10	LYS	2.6
1	A	13	THR	2.4
1	A	148	LEU	2.1
1	B	16	LEU	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](#)

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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	LBT	B	800	23/23	0.77	0.28	11.50	40,48,56,59	0
2	LBT	A	801	23/23	0.80	0.27	8.05	40,51,57,63	0
2	LBT	C	800	23/23	0.81	0.24	6.83	40,48,55,56	0
3	ZN	A	802[A]	1/1	0.99	0.08	-	45,45,45,45	1

6.5 Other polymers

There are no such residues in this entry.