



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:26 PM UTC

PDB ID : 6UHT / pdb_00006uht
Title : Crystal structure of BoNT/B receptor-binding domain in complex with VHH JLI-G10
Authors : Lam, K.; Jin, R.
Deposited on : 2019-09-28
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

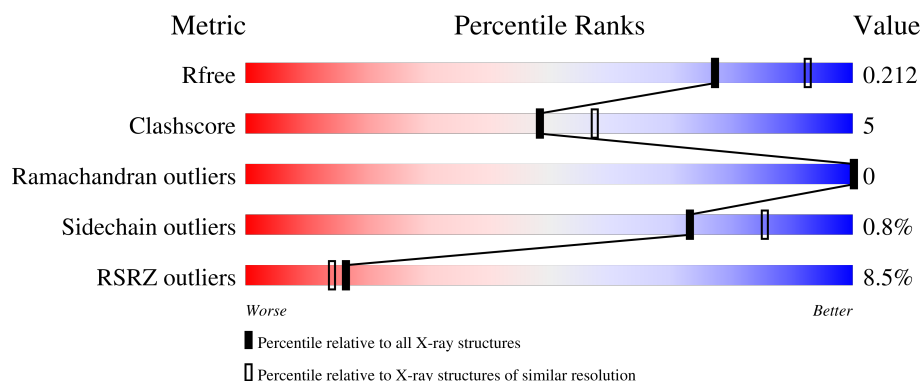
1 Overall quality at a glance

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	438	6% 85% 13% .
1	B	438	10% 87% 9% .
2	C	140	11% 72% 15% . 11%
2	D	140	8% 72% 19% . 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9563 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 Botulinum neurotoxin type B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3664	2370	598	688	8			
1	B	421	Total	C	N	O	S	0	1	0
			3560	2300	585	667	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	854	GLY	-	expression tag	UNP P10844
A	855	PRO	-	expression tag	UNP P10844
A	856	LEU	-	expression tag	UNP P10844
A	857	GLY	-	expression tag	UNP P10844
A	858	SER	-	expression tag	UNP P10844
B	854	GLY	-	expression tag	UNP P10844
B	855	PRO	-	expression tag	UNP P10844
B	856	LEU	-	expression tag	UNP P10844
B	857	GLY	-	expression tag	UNP P10844
B	858	SER	-	expression tag	UNP P10844

- Molecule 2 is a protein called JLI-G10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	124	Total	C	N	O	S	0	1	0
			942	590	160	186	6			
2	D	130	Total	C	N	O	S	0	1	0
			989	621	168	194	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total	O	0	0
			252	252		

Continued on next page...

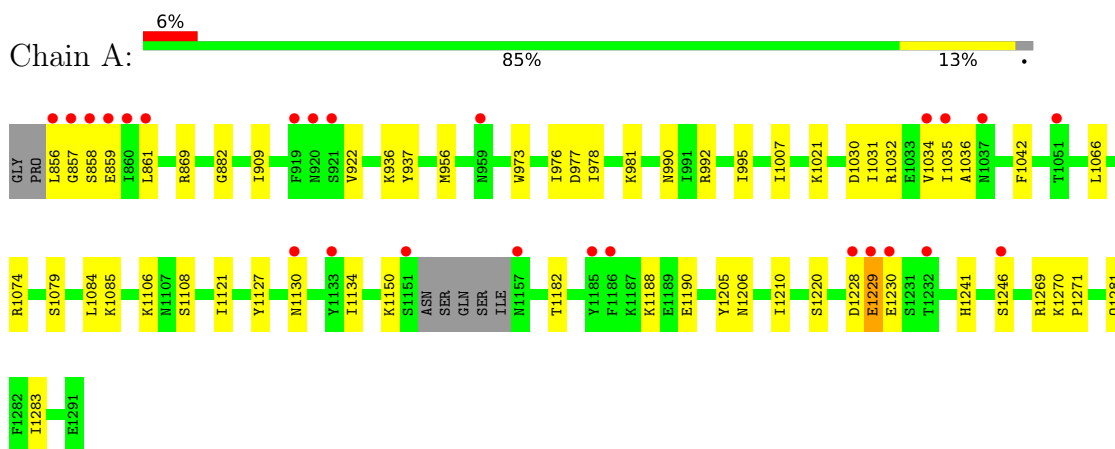
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	115	Total 115	O 115	0	0
3	C	23	Total 23	O 23	0	0
3	D	18	Total 18	O 18	0	0

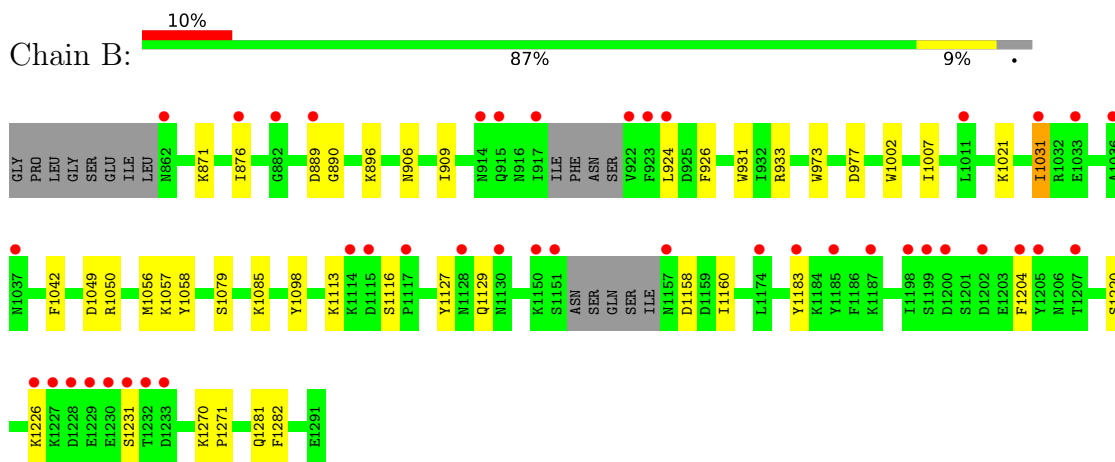
3 Residue-property plots [i](#)

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.

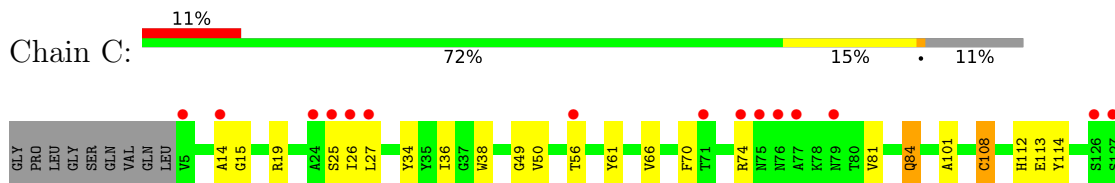
• Molecule 1: Botulinum neurotoxin type B

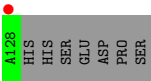


• Molecule 1: Botulinum neurotoxin type B

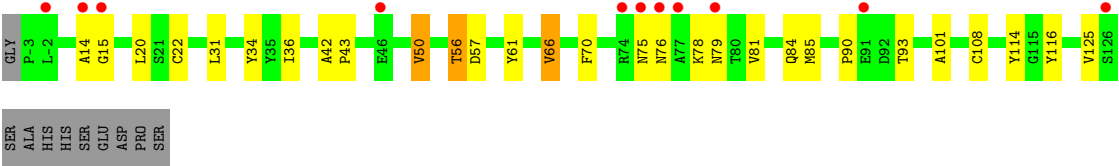


• Molecule 2: JLI-G10





● Molecule 2: JLI-G10



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	223.15Å 223.15Å 58.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	96.63 – 2.20 96.63 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (96.63-2.20) 99.0 (96.63-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.211 (Not available) , 0.212	Depositor DCC
R_{free} test set	4214 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9563	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% 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

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	0.58	0/3751	0.87	6/5057 (0.1%)
1	B	0.43	0/3645	0.75	0/4914
2	C	0.57	0/966	0.87	1/1314 (0.1%)
2	D	0.53	0/1014	0.85	0/1379
All	All	0.52	0/9376	0.82	7/12664 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	25	SER	N-CA-C	-6.95	104.62	113.23
1	A	922	VAL	N-CA-C	5.86	116.30	107.80
1	A	1130	ASN	N-CA-C	5.81	119.40	111.39
1	A	1230	GLU	N-CA-C	5.75	117.54	111.28
1	A	1229	GLU	N-CA-C	-5.56	105.22	111.28
1	A	1283	ILE	N-CA-C	5.52	113.51	107.60
1	A	1246	SER	CA-C-O	5.31	121.02	117.94

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	3664	0	3569	38	0
1	B	3560	0	3462	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	942	0	896	17	0
2	D	989	0	951	19	0
3	A	252	0	0	5	0
3	B	115	0	0	1	0
3	C	23	0	0	0	0
3	D	18	0	0	0	0
All	All	9563	0	8878	99	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 (99) 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:924:LEU:HD11	1:B:926:PHE:CE1	2.10	0.86
2:C:38:TRP:O	2:C:50:VAL:HG12	1.82	0.80
1:B:890:GLY:HA3	1:B:906:ASN:OD1	1.84	0.78
2:D:93:THR:HG22	2:D:125:VAL:H	1.50	0.75
1:B:924:LEU:HD11	1:B:926:PHE:CD1	2.24	0.73
2:D:75:ASN:O	2:D:76:ASN:HB2	1.89	0.72
1:A:978:ILE:HG22	1:A:1035:ILE:HG13	1.71	0.71
2:C:50:VAL:CG2	2:C:66:VAL:HG11	2.22	0.69
1:A:1269:ARG:CZ	2:C:56:THR:HG23	2.23	0.68
2:C:50:VAL:HG23	2:C:66:VAL:HG11	1.76	0.68
1:A:856:LEU:C	1:A:869:ARG:HE	2.01	0.67
1:A:1269:ARG:NH2	2:C:56:THR:CG2	2.58	0.67
1:A:857:GLY:HA2	1:A:869:ARG:HH21	1.58	0.67
1:B:924:LEU:HD11	1:B:926:PHE:HE1	1.60	0.66
1:B:890:GLY:CA	1:B:906:ASN:OD1	2.44	0.65
1:B:1049:ASP:OD1	1:B:1050:ARG:N	2.32	0.62
2:C:34:TYR:OH	2:C:74:ARG:NH2	2.33	0.62
1:A:1228:ASP:OD1	1:A:1229:GLU:N	2.34	0.61
2:D:66:VAL:HG13	2:D:70:PHE:HB2	1.82	0.59
1:A:856:LEU:HD12	3:A:1405:HOH:O	2.03	0.58
1:A:858:SER:CB	1:A:1074:ARG:HG3	2.34	0.56
1:A:1190:GLU:HG3	1:A:1241:HIS:CG	2.41	0.56
1:B:1113:LYS:HB3	1:B:1116:SER:HB3	1.89	0.55
1:A:1270:LYS:HA	1:A:1271:PRO:C	2.31	0.54
1:A:1079:SER:O	1:A:1085:LYS:NZ	2.41	0.54
2:D:79:ASN:OD1	2:D:79:ASN:O	2.25	0.54
2:D:90:PRO:O	2:D:93:THR:HG23	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1206:ASN:ND2	3:A:1303:HOH:O	2.27	0.53
1:B:909:ILE:HB	1:B:1042:PHE:HB2	1.89	0.53
1:A:1269:ARG:CZ	2:C:56:THR:CG2	2.86	0.53
1:B:1057:LYS:HE2	1:B:1058:TYR:CE2	2.44	0.53
1:B:1098:TYR:CG	1:B:1282:PHE:HB3	2.44	0.52
1:A:1220:SER:HA	1:A:1281:GLN:HG2	1.91	0.52
2:D:34:TYR:CE1	2:D:36:ILE:HG13	2.45	0.51
2:D:61:TYR:HB2	2:D:108[A]:CYS:SG	2.50	0.51
1:B:977:ASP:HB3	1:B:1031:ILE:HG23	1.92	0.51
2:D:93:THR:CG2	2:D:125:VAL:H	2.21	0.51
1:B:931:TRP:HB2	1:B:1057:LYS:HB3	1.93	0.50
2:D:56:THR:HG22	2:D:57:ASP:N	2.26	0.50
1:B:1127:TYR:CZ	1:B:1129:GLN:HB2	2.46	0.50
1:A:1036:ALA:HB1	3:A:1351:HOH:O	2.11	0.49
2:D:22:CYS:HB3	2:D:81:VAL:HG13	1.93	0.49
1:A:859:GLU:O	1:A:1074:ARG:NH2	2.36	0.48
2:C:19:ARG:NH1	2:C:84:GLN:HG2	2.28	0.48
2:C:61:TYR:HB2	2:C:108[A]:CYS:SG	2.54	0.48
1:A:1084:LEU:HD13	1:A:1210:ILE:HG12	1.95	0.47
1:A:857:GLY:CA	1:A:869:ARG:HH21	2.23	0.47
2:D:93:THR:HG22	2:D:125:VAL:N	2.24	0.47
1:B:889:ASP:CG	3:B:1307:HOH:O	2.57	0.47
1:A:1127:TYR:CZ	1:A:1134:ILE:HD11	2.50	0.47
1:B:1079:SER:O	1:B:1085:LYS:NZ	2.42	0.46
1:A:1108:SER:HB3	1:A:1121:ILE:CG2	2.46	0.46
2:C:36:ILE:HG21	2:C:81:VAL:HG21	1.98	0.46
2:D:20:LEU:HG	2:D:85:MET:HE2	1.99	0.45
2:D:14:ALA:HA	2:D:15:GLY:HA2	1.67	0.45
2:D:31:LEU:HD11	2:D:116:TYR:CE2	2.52	0.45
1:A:981:LYS:HG2	1:A:1031:ILE:HG22	1.99	0.45
1:B:1021:LYS:HA	1:B:1021:LYS:HD3	1.81	0.45
1:A:882:GLY:HA2	3:A:1335:HOH:O	2.16	0.45
1:A:1150:LYS:HE3	1:A:1229:GLU:OE2	2.17	0.45
1:B:1158:ASP:OD2	1:B:1160:ILE:HD12	2.17	0.45
2:D:22:CYS:HB3	2:D:81:VAL:CG1	2.48	0.44
2:C:14:ALA:HA	2:C:15:GLY:HA2	1.63	0.44
1:B:871:LYS:HD3	1:B:876:ILE:HD12	2.00	0.44
2:C:101:ALA:HB2	2:C:114:TYR:HA	1.99	0.44
1:A:995:ILE:HG13	1:A:1106:LYS:HB3	2.00	0.44
2:D:50:VAL:HG13	2:D:66:VAL:HG11	2.00	0.44
1:A:856:LEU:HG	1:A:869:ARG:HG3	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1220:SER:HA	1:B:1281:GLN:HG2	2.00	0.43
2:D:78:LYS:O	2:D:79:ASN:OD1	2.36	0.43
1:B:973:TRP:CD2	1:B:1007:ILE:HG21	2.54	0.43
1:B:896:LYS:O	1:B:1057:LYS:HE3	2.18	0.43
1:A:1066:LEU:HD13	1:A:1074:ARG:NH1	2.34	0.42
2:C:26:ILE:HG13	2:C:27:LEU:H	1.83	0.42
1:A:956:MET:HE1	1:A:976:ILE:HD12	2.01	0.42
2:C:26:ILE:HG23	2:C:27:LEU:HG	2.01	0.42
2:D:101:ALA:HB2	2:D:114:TYR:HA	2.02	0.42
1:A:1190:GLU:HG3	1:A:1241:HIS:CD2	2.54	0.42
1:A:909:ILE:HB	1:A:1042:PHE:HB2	2.02	0.42
1:A:978:ILE:HD11	1:A:1032:ARG:CZ	2.49	0.42
1:A:1021:LYS:HA	1:A:1021:LYS:HD3	1.91	0.42
2:C:50:VAL:HG21	2:C:70:PHE:CE2	2.54	0.42
1:B:924:LEU:CD1	1:B:926:PHE:CD1	3.00	0.41
1:A:973:TRP:CD2	1:A:1007:ILE:HG21	2.55	0.41
1:A:1030:ASP:OD1	1:A:1030:ASP:N	2.53	0.41
1:A:861:LEU:HD23	1:A:861:LEU:HA	1.74	0.41
1:A:990:ASN:OD1	1:A:992:ARG:N	2.48	0.41
1:B:933:ARG:HD3	1:B:1002:TRP:CD1	2.55	0.41
1:B:1183:TYR:CD1	1:B:1204:PHE:HE1	2.38	0.41
1:A:977:ASP:HA	1:A:1034:VAL:HG22	2.03	0.41
1:B:1056:MET:HE2	1:B:1056:MET:HB3	1.92	0.41
2:D:42:ALA:HB1	2:D:43:PRO:HD2	2.03	0.41
1:A:1182:THR:CG2	1:A:1205:TYR:HB2	2.51	0.41
3:A:1344:HOH:O	2:C:49:GLY:HA3	2.21	0.41
2:C:112:HIS:CE1	2:C:113:GLU:HG3	2.56	0.41
1:A:936:LYS:HG2	1:A:937:TYR:O	2.21	0.40
1:B:1226:LYS:NZ	1:B:1231:SER:O	2.54	0.40
1:B:871:LYS:HB3	1:B:876:ILE:HD12	2.03	0.40
1:B:1270:LYS:HA	1:B:1271:PRO:C	2.45	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	427/438 (98%)	409 (96%)	18 (4%)	0	100	100
1	B	416/438 (95%)	400 (96%)	16 (4%)	0	100	100
2	C	123/140 (88%)	115 (94%)	8 (6%)	0	100	100
2	D	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
All	All	1095/1156 (95%)	1044 (95%)	51 (5%)	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	403/411 (98%)	402 (100%)	1 (0%)	87	94
1	B	389/411 (95%)	388 (100%)	1 (0%)	86	93
2	C	97/110 (88%)	94 (97%)	3 (3%)	35	48
2	D	103/110 (94%)	99 (96%)	4 (4%)	28	39
All	All	992/1042 (95%)	983 (99%)	9 (1%)	73	84

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1188	LYS
1	B	1031	ILE
2	C	84	GLN
2	C	108[A]	CYS
2	C	108[B]	CYS
2	D	50	VAL
2	D	56	THR
2	D	66	VAL
2	D	84	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	943	GLN
1	A	947	HIS
1	A	954	ASN
1	A	979	ASN
1	A	1012	ASN
1	A	1052	GLN
1	B	954	ASN
1	B	958	ASN
1	B	1052	GLN
1	B	1129	GLN
2	C	41	GLN
2	D	41	GLN
2	D	75	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	431/438 (98%)	0.00	25 (5%)	29 25	20, 33, 71, 114	0
1	B	421/438 (96%)	0.62	42 (9%)	12 10	26, 51, 94, 131	1 (0%)
2	C	124/140 (88%)	0.47	16 (12%)	7 5	21, 39, 75, 101	1 (0%)
2	D	130/140 (92%)	0.55	11 (8%)	16 14	31, 44, 75, 93	1 (0%)
All	All	1106/1156 (95%)	0.35	94 (8%)	16 14	20, 42, 84, 131	3 (0%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	858	SER	9.2
1	A	860	ILE	6.8
1	B	923	PHE	6.8
1	A	856	LEU	6.5
2	C	128	ALA	5.9
1	A	861	LEU	5.8
2	C	14	ALA	5.7
1	B	924	LEU	5.7
1	A	921	SER	5.3
1	A	859	GLU	4.6
1	B	922	VAL	4.5
1	A	1228	ASP	4.4
2	D	79	ASN	4.3
2	D	126	SER	4.3
1	B	1151	SER	4.2
1	A	1185	TYR	4.2
1	B	917	ILE	3.9
1	B	1130	ASN	3.9
1	B	1185	TYR	3.8
1	B	1204	PHE	3.7
2	D	75	ASN	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	C	79	ASN	3.6
1	B	1011	LEU	3.6
2	D	14	ALA	3.5
2	D	76	ASN	3.4
1	A	919	PHE	3.4
1	A	1229	GLU	3.4
1	B	1227	LYS	3.3
2	C	127	SER	3.3
1	A	1157	ASN	3.3
1	B	1183	TYR	3.2
2	C	26	ILE	3.2
1	B	1200	ASP	3.0
1	A	1035	ILE	3.0
1	B	1150	LYS	3.0
2	D	74	ARG	2.9
1	B	1036	ALA	2.9
1	B	1228	ASP	2.9
1	A	1230	GLU	2.9
1	B	1231	SER	2.8
2	C	5	VAL	2.8
1	A	857	GLY	2.8
1	B	1207	THR	2.8
1	B	1205	TYR	2.8
1	B	876	ILE	2.8
2	C	77	ALA	2.8
1	A	959	ASN	2.7
1	B	1157	ASN	2.7
1	B	1232	THR	2.7
2	C	27	LEU	2.7
2	D	-2	LEU	2.7
1	B	1128	ASN	2.6
1	B	882	GLY	2.6
2	C	56	THR	2.6
1	A	1151	SER	2.6
2	C	75	ASN	2.6
1	A	1034	VAL	2.6
1	B	1031	ILE	2.6
1	B	1226	LYS	2.6
2	D	77	ALA	2.5
1	A	1186	PHE	2.5
2	C	25	SER	2.5
1	A	920	ASN	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1246	SER	2.5
1	B	1174	LEU	2.5
2	C	74	ARG	2.4
1	A	1037	ASN	2.4
1	B	1198	ILE	2.4
1	A	1133	TYR	2.3
1	B	889	ASP	2.3
1	B	1202	ASP	2.3
2	D	91	GLU	2.3
1	A	1232	THR	2.3
2	C	126	SER	2.3
1	B	1229	GLU	2.3
1	B	1233	ASP	2.2
2	C	76	ASN	2.2
1	B	915	GLN	2.2
2	D	46	GLU	2.2
1	B	914	ASN	2.2
2	D	15	GLY	2.2
1	B	1115	ASP	2.2
1	B	1199	SER	2.2
2	C	71	THR	2.1
1	A	1051	THR	2.1
1	B	1114	LYS	2.1
1	A	1130	ASN	2.1
1	B	862	ASN	2.1
1	B	1037	ASN	2.1
1	B	1117	PRO	2.1
1	B	1230	GLU	2.0
2	C	24	ALA	2.0
1	B	1033	GLU	2.0
1	B	1187	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.