



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 9, 2014 – 04:25 PM EDT

PDB ID : 3OBT
Title : Crystal structure of Botulinum neurotoxin serotype D ligand binding domain
in complex with N-Acetylneuraminic acid
Authors : Lee, K.K.; Zong, Y.; Jin, R.
Deposited on : 2010-08-09
Resolution : 2.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

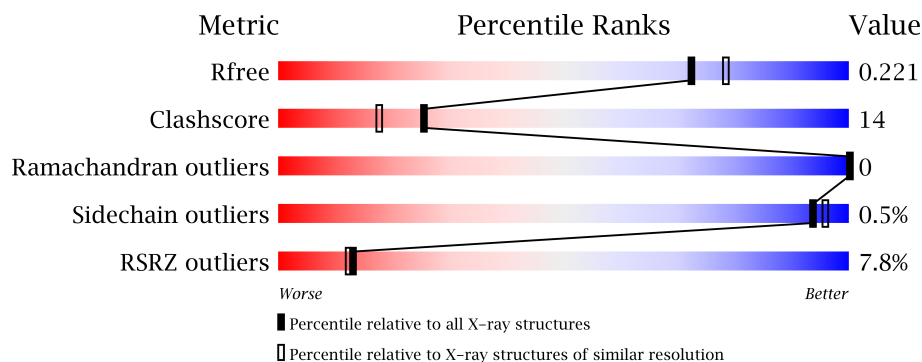
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
Xtriage (Phenix) : dev-1439
EDS : stable22978
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	434	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SLB	A	1	-	X
3	GOL	A	10	-	X
3	GOL	A	11	-	X
3	GOL	A	12	-	X
3	GOL	A	2	-	X
3	GOL	A	3	-	X
3	GOL	A	5	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	A	6	-	X
3	GOL	A	8	-	X
3	GOL	A	9	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3831 atoms, of which 36 are hydrogens and 0 are deuterium.

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.

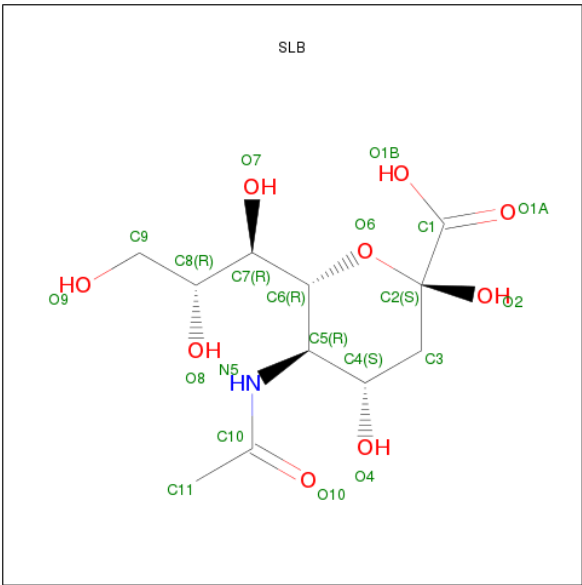
- Molecule 1 is a protein called Botulinum neurotoxin type D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	412	3427	2168	36	558	653	12	0	5	0

There are 20 discrepancies between the modelled and reference sequences:

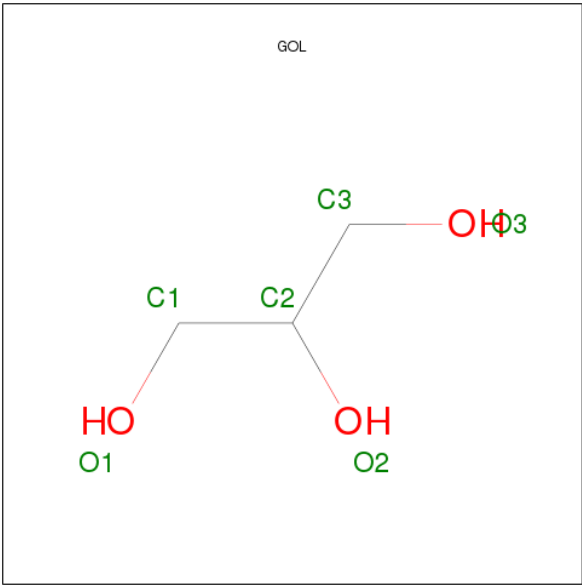
Chain	Residue	Modelled	Actual	Comment	Reference
A	856	MET	-	EXPRESSION TAG	UNP P19321
A	857	ARG	-	EXPRESSION TAG	UNP P19321
A	858	GLY	-	EXPRESSION TAG	UNP P19321
A	859	SER	-	EXPRESSION TAG	UNP P19321
A	860	ALA	-	EXPRESSION TAG	UNP P19321
A	861	MET	-	EXPRESSION TAG	UNP P19321
A	862	ALA	-	EXPRESSION TAG	UNP P19321
A	1277	PRO	-	EXPRESSION TAG	UNP P19321
A	1278	PRO	-	EXPRESSION TAG	UNP P19321
A	1279	THR	-	EXPRESSION TAG	UNP P19321
A	1280	PRO	-	EXPRESSION TAG	UNP P19321
A	1281	GLY	-	EXPRESSION TAG	UNP P19321
A	1282	TRP	-	EXPRESSION TAG	UNP P19321
A	1283	SER	-	EXPRESSION TAG	UNP P19321
A	1284	HIS	-	EXPRESSION TAG	UNP P19321
A	1285	PRO	-	EXPRESSION TAG	UNP P19321
A	1286	GLN	-	EXPRESSION TAG	UNP P19321
A	1287	PHE	-	EXPRESSION TAG	UNP P19321
A	1288	GLU	-	EXPRESSION TAG	UNP P19321
A	1289	LYS	-	EXPRESSION TAG	UNP P19321

- Molecule 2 is SUGAR (5-N-ACETYL-BETA-D-NEURAMINICACID) (three-letter code: SLB) (formula: C₁₁H₁₉NO₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0

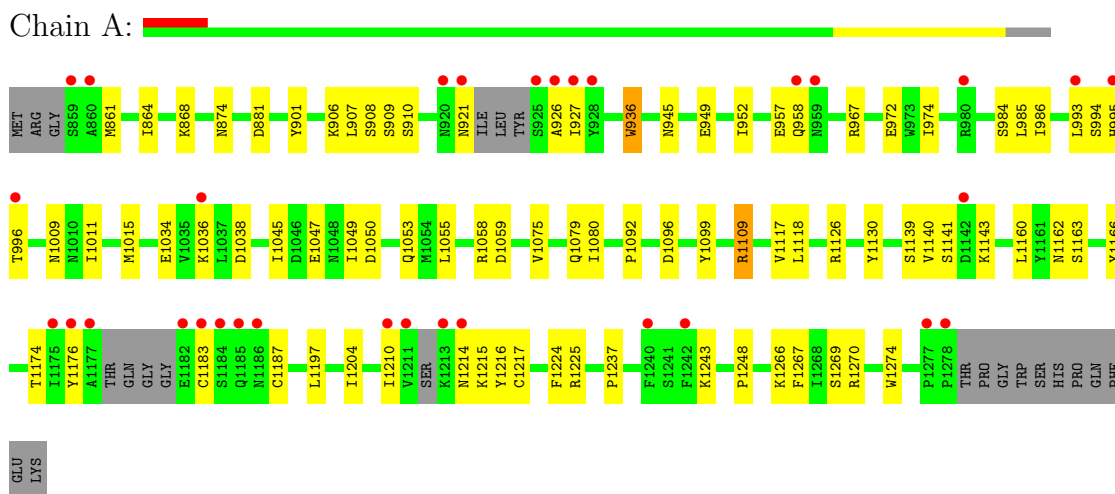
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	317	Total O 317 317	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.23Å 90.04Å 93.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 40.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (50.00-2.00) 97.5 (40.57-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.172 , 0.221 0.181 , 0.221	Depositor DCC
R_{free} test set	1736 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.5	EDS
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34444 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3831	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.88	4/3477 (0.1%)	0.82	6/4709 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1166	TYR	CD2-CE2	5.94	1.48	1.39
1	A	936	TRP	CB-CG	5.88	1.60	1.50
1	A	1274	TRP	CB-CG	5.56	1.60	1.50
1	A	1224	PHE	CE2-CZ	5.56	1.48	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1059	ASP	CB-CG-OD1	7.80	125.32	118.30
1	A	1109	ARG	NE-CZ-NH1	-6.86	116.87	120.30
1	A	1109	ARG	NE-CZ-NH2	6.52	123.56	120.30
1	A	1225	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	A	881	ASP	CB-CG-OD1	5.16	122.95	118.30
1	A	1096	ASP	CB-CG-OD1	5.03	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3391	36	3287	93	0
2	A	21	0	18	0	0
3	A	66	0	88	24	0
4	A	317	0	0	14	1
All	All	3795	36	3393	94	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 14.

All (94) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:994:SER:OG	1:A:996:THR:HG22	1.42	1.17
1:A:994:SER:CB	1:A:996:THR:HG22	1.80	1.10
1:A:1210:ILE:O	4:A:314:HOH:O	1.68	1.09
1:A:1270:ARG:HH22	3:A:7:GOL:H12	1.13	1.09
1:A:1050:ASP:OD1	1:A:1053:GLN:HG3	1.53	1.05
1:A:1217[B]:CYS:SG	1:A:1266:LYS:NZ	2.32	1.03
1:A:945:ASN:OD1	1:A:993:LEU:HD11	1.56	1.02
1:A:1210:ILE:HD11	1:A:1217[A]:CYS:SG	2.08	0.93
1:A:1270:ARG:NH2	3:A:7:GOL:H12	1.85	0.92
1:A:995:HIS:HE1	4:A:140:HOH:O	1.52	0.91
1:A:1270:ARG:HH22	3:A:7:GOL:C1	1.86	0.88
1:A:868:LYS:NZ	3:A:11:GOL:H31	1.88	0.88
1:A:1215:LYS:HB2	4:A:283:HOH:O	1.74	0.87
1:A:994:SER:HB3	1:A:996:THR:HG22	1.55	0.86
1:A:1079:GLN:HE21	3:A:11:GOL:H2	1.42	0.82
1:A:1243:LYS:HD3	3:A:6:GOL:O3	1.82	0.79
1:A:1183:CYS:SG	4:A:311:HOH:O	2.41	0.78
1:A:921:ASN:O	4:A:288:HOH:O	2.02	0.77
1:A:945:ASN:OD1	1:A:993:LEU:CD1	2.31	0.77
1:A:994:SER:OG	1:A:996:THR:CG2	2.30	0.75
1:A:1210:ILE:HA	4:A:299:HOH:O	1.88	0.74
1:A:1243:LYS:HD3	3:A:6:GOL:HO3	1.53	0.73
1:A:926:ALA:HA	1:A:1036:LYS:HA	1.70	0.73
1:A:868:LYS:HZ1	3:A:11:GOL:H31	1.56	0.70
1:A:1217[B]:CYS:SG	1:A:1266:LYS:CE	2.79	0.70
1:A:967:ARG:NH1	1:A:972:GLU:OE1	2.24	0.68
1:A:994:SER:C	1:A:996:THR:H	1.96	0.66
1:A:1217[B]:CYS:SG	1:A:1266:LYS:CG	2.83	0.66
1:A:994:SER:HB3	1:A:996:THR:CG2	2.26	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1163:SER:H	3:A:9:GOL:C3	2.11	0.63
1:A:868:LYS:HZ3	3:A:11:GOL:H31	1.63	0.63
1:A:1243:LYS:CD	3:A:6:GOL:O3	2.46	0.63
1:A:994:SER:C	1:A:996:THR:N	2.51	0.63
1:A:1109:ARG:HH11	3:A:4:GOL:H31	1.64	0.60
1:A:1109:ARG:NH1	3:A:4:GOL:H31	2.15	0.60
1:A:1217[B]:CYS:SG	1:A:1266:LYS:HG2	2.41	0.60
1:A:1215:LYS:O	1:A:1216:TYR:HB2	2.04	0.58
1:A:994:SER:CB	1:A:996:THR:CG2	2.70	0.57
1:A:985:LEU:HD11	1:A:1015:MET:HG2	1.86	0.57
1:A:949:GLU:OE1	1:A:967:ARG:NH1	2.38	0.56
1:A:974:ILE:HD13	1:A:984:SER:CB	2.36	0.56
1:A:996:THR:HG23	4:A:289:HOH:O	2.06	0.56
1:A:1117:VAL:HG11	1:A:1237:PRO:HB2	1.88	0.55
1:A:1079:GLN:NE2	3:A:11:GOL:H2	2.18	0.55
1:A:1050:ASP:OD1	1:A:1053:GLN:CG	2.43	0.55
1:A:957:GLU:HG3	1:A:957:GLU:O	2.08	0.54
1:A:1266:LYS:NZ	4:A:294:HOH:O	2.41	0.54
1:A:972:GLU:HG3	1:A:986:ILE:HG12	1.90	0.54
1:A:1162:ASN:N	3:A:9:GOL:H32	2.25	0.52
1:A:1126:ARG:HD3	4:A:198:HOH:O	2.10	0.52
1:A:927:ILE:HD12	1:A:1011:ILE:CG2	2.41	0.51
1:A:901:TYR:CZ	1:A:1092:PRO:HD3	2.46	0.51
1:A:957:GLU:O	1:A:958:GLN:HB2	2.11	0.50
1:A:936:TRP:HB2	1:A:1058:ARG:HG2	1.94	0.50
1:A:1217[B]:CYS:SG	1:A:1266:LYS:HE2	2.52	0.50
1:A:1079:GLN:HE21	3:A:11:GOL:C2	2.19	0.50
1:A:945:ASN:HD21	1:A:993:LEU:HD21	1.76	0.50
1:A:1126:ARG:NH1	4:A:198:HOH:O	2.45	0.49
1:A:1217[B]:CYS:SG	1:A:1266:LYS:HG3	2.51	0.49
1:A:1243:LYS:CE	3:A:6:GOL:O3	2.62	0.48
1:A:1080:ILE:CD1	1:A:1215:LYS:HD2	2.43	0.48
1:A:974:ILE:HD13	1:A:984:SER:HB3	1.96	0.48
1:A:1174:THR:HG22	1:A:1187:CYS:HB3	1.96	0.47
1:A:1099:TYR:CE1	1:A:1269:SER:HB3	2.50	0.47
1:A:1139:SER:OG	1:A:1141:SER:O	2.30	0.46
1:A:1160:LEU:HG	3:A:9:GOL:H31	1.98	0.46
1:A:1141:SER:OG	1:A:1143:LYS:NZ	2.34	0.46
1:A:996:THR:CG2	4:A:289:HOH:O	2.63	0.45
1:A:909:SER:C	1:A:1049:ILE:HD11	2.35	0.45
3:A:4:GOL:H12	4:A:56:HOH:O	2.16	0.45
1:A:1214:ASN:OD1	4:A:312:HOH:O	2.21	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:907:LEU:HD12	1:A:1055:LEU:HD11	1.99	0.45
1:A:874:ASN:HB2	4:A:89:HOH:O	2.16	0.45
1:A:952:ILE:HD12	1:A:1055:LEU:HD21	1.98	0.44
1:A:1139:SER:OG	1:A:1143:LYS:HD2	2.17	0.44
1:A:1075:VAL:HG13	3:A:11:GOL:H32	2.00	0.44
1:A:1130:TYR:O	3:A:7:GOL:H11	2.18	0.44
1:A:926:ALA:HB2	1:A:1034:GLU:OE2	2.18	0.43
1:A:868:LYS:HZ3	3:A:11:GOL:C1	2.31	0.43
1:A:1163:SER:H	3:A:9:GOL:H32	1.84	0.43
1:A:906:LYS:HG2	1:A:908:SER:HB3	2.00	0.43
1:A:910:SER:HB3	1:A:1047:GLU:O	2.19	0.43
1:A:927:ILE:HD12	1:A:1011:ILE:HG22	2.00	0.42
1:A:909:SER:OG	1:A:910:SER:O	2.30	0.42
1:A:1140:VAL:HG21	1:A:1204:ILE:HD12	2.02	0.42
1:A:952:ILE:HD13	1:A:1045:ILE:HG12	2.02	0.41
1:A:967:ARG:HB2	1:A:967:ARG:HH11	1.86	0.41
1:A:972:GLU:OE2	1:A:974:ILE:HD11	2.20	0.41
1:A:1038:ASP:OD2	3:A:3:GOL:O1	2.37	0.41
1:A:1118:LEU:O	1:A:1248:PRO:HD2	2.20	0.41
1:A:1267:PHE:CD1	1:A:1267:PHE:N	2.89	0.41
1:A:927:ILE:HD12	1:A:1011:ILE:HG21	2.02	0.41
1:A:861:MET:HA	1:A:864:ILE:HD12	2.03	0.41
1:A:1009:ASN:OD1	1:A:1015:MET:HG3	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:305:HOH:O	4:A:310:HOH:O[2_665]	1.86	0.34

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	409/434 (94%)	395 (97%)	14 (3%)	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	389/402 (97%)	387 (100%)	2 (0%)	94 96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1176	TYR
1	A	1197	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.8 Polymer linkage issues

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	412/434 (94%)	0.15	32 (7%) 13 12	17, 28, 56, 79	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1177	ALA	8.6
1	A	1183	CYS	6.7
1	A	1278	PRO	6.4
1	A	1214	ASN	6.1
1	A	927	ILE	5.8
1	A	926	ALA	5.7
1	A	1176	TYR	5.6
1	A	925	SER	5.0
1	A	1184	SER	5.0
1	A	860	ALA	4.6
1	A	1182	GLU	4.6
1	A	920	ASN	4.2
1	A	958	GLN	3.7
1	A	993	LEU	3.6
1	A	1242	PHE	3.6
1	A	1185	GLN	3.5
1	A	1277	PRO	3.4
1	A	859	SER	3.3
1	A	921	ASN	3.0
1	A	1142	ASP	2.9
1	A	1036	LYS	2.9
1	A	1240	PHE	2.6
1	A	1210	ILE	2.6
1	A	959	ASN	2.4
1	A	1186	ASN	2.4
1	A	1175	ILE	2.2
1	A	980	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1211	VAL	2.2
1	A	995	HIS	2.1
1	A	928	TYR	2.1
1	A	1213	LYS	2.0
1	A	996	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q < 0.9
3	GOL	A	9	6/6	0.28	16.05	45,51,54,56	0
3	GOL	A	6	6/6	0.30	5.78	116,117,117,117	0
3	GOL	A	3	6/6	0.25	3.96	56,63,64,69	0
3	GOL	A	2	6/6	0.40	3.86	93,95,96,96	0
3	GOL	A	12	6/6	0.20	3.68	72,72,73,74	0
3	GOL	A	11	6/6	0.27	3.59	58,61,62,65	0
3	GOL	A	5	6/6	0.21	2.47	57,58,58,61	0
3	GOL	A	8	6/6	0.25	2.38	74,76,78,78	0
2	SLB	A	1	21/21	0.25	2.24	28,33,41,53	0
3	GOL	A	10	6/6	0.29	2.00	57,60,63,64	0
3	GOL	A	7	6/6	0.37	1.17	42,58,60,65	0
3	GOL	A	4	6/6	0.14	0.68	39,49,51,53	0

6.5 Other polymers ⓘ

There are no such residues in this entry.