



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:14 AM GMT

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 X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

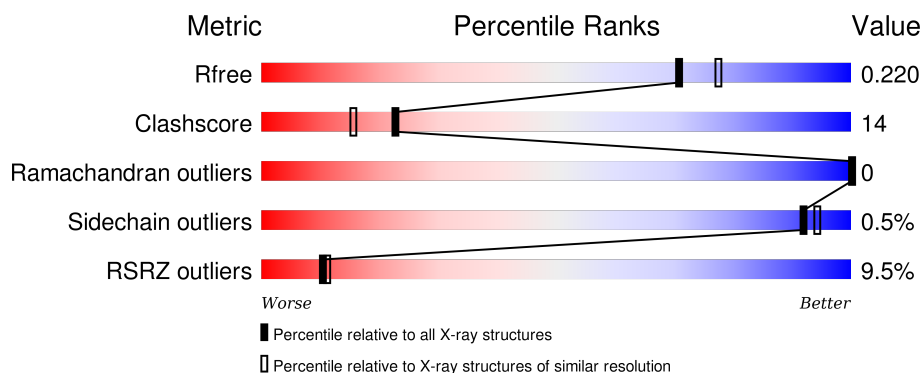
# 1 Overall quality at a glance

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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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  $\geq 3$ , 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	434	<div> <div>9%</div> <div>76%</div> <div>19%</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
3	GOL	A	11	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	12	-	-	-	X
3	GOL	A	2	-	-	-	X
3	GOL	A	3	-	-	-	X
3	GOL	A	5	-	-	-	X
3	GOL	A	6	-	-	X	-
3	GOL	A	7	-	-	X	-
3	GOL	A	9	-	-	X	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 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.

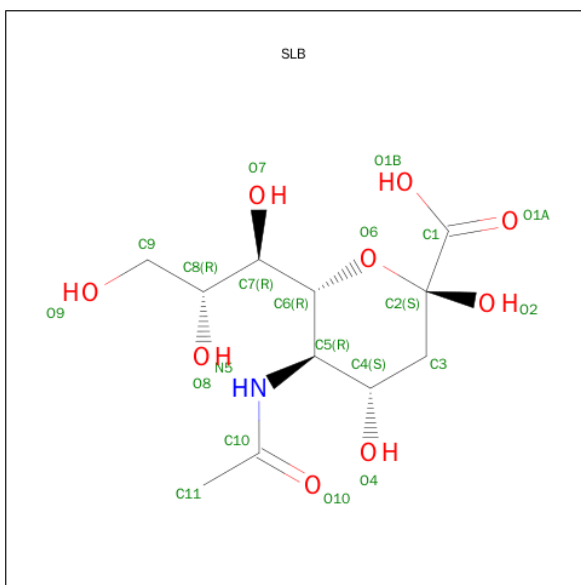
- Molecule 1 is a protein called Botulinum neurotoxin type D.

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

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-NEURAMINIC ACID) (three-letter code: SLB) (formula: C<sub>11</sub>H<sub>19</sub>NO<sub>9</sub>).



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

- 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		
			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

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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		
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		
3	A	1	Total	C	O	0	0
			6	3	3		

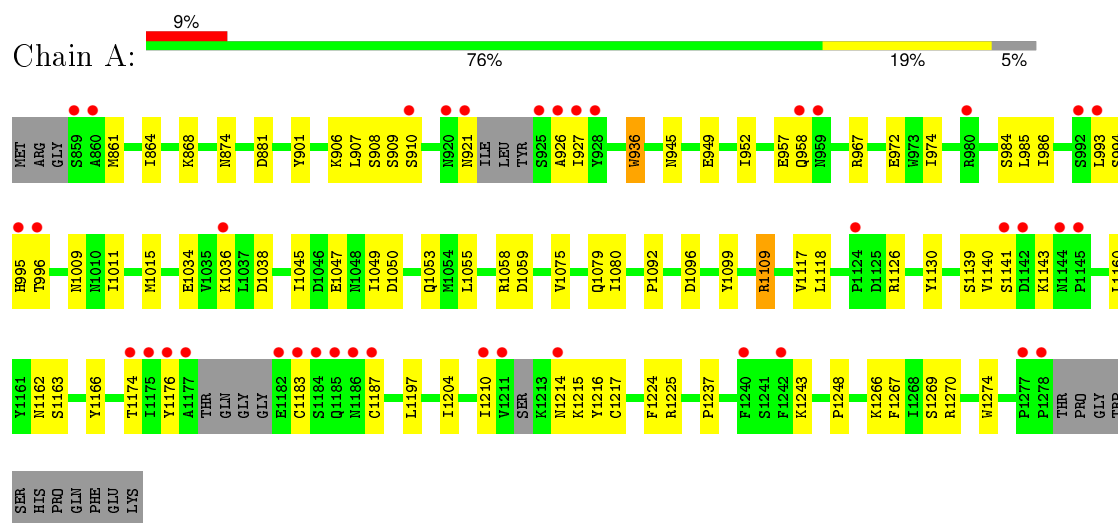
- Molecule 4 is water.

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

### 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 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, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.172 , 0.221 0.181 , 0.220	Depositor DCC
$R_{free}$ test set	1728 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.9	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.0	EDS
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	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 <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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 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	3391	36	3319	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	3425	94	1

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 14.

All (94) 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: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
1:A:1163:SER:H	3:A:9:GOL:C3	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:868:LYS:HZ3	3:A:11:GOL:H31	1.63	0.63
1:A:994:SER:C	1:A:996:THR:N	2.51	0.63
1:A:1243:LYS:CD	3:A:6:GOL:O3	2.46	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:996:THR:HG23	4:A:289:HOH:O	2.06	0.56
1:A:974:ILE:HD13	1:A:984:SER:CB	2.36	0.56
1:A:1079:GLN:NE2	3:A:11:GOL:H2	2.18	0.55
1:A:1117:VAL:HG11	1:A:1237:PRO:HB2	1.88	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:901:TYR:CZ	1:A:1092:PRO:HD3	2.46	0.51
1:A:927:ILE:HD12	1:A:1011:ILE:CG2	2.41	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:1160:LEU:HG	3:A:9:GOL:H31	1.98	0.46
1:A:1139:SER:OG	1:A:1141:SER:O	2.30	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	Interatomic distance (Å)	Clash overlap (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:1139:SER:OG	1:A:1143:LYS:HD2	2.17	0.44
1:A:952:ILE:HD12	1:A:1055:LEU:HD21	1.98	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:910:SER:HB3	1:A:1047:GLU:O	2.19	0.43
1:A:906:LYS:HG2	1:A:908:SER:HB3	2.00	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:967:ARG:HB2	1:A:967:ARG:HH11	1.86	0.41
1:A:952:ILE:HD13	1:A:1045:ILE:HG12	2.02	0.41
1:A:972:GLU:OE2	1:A:974:ILE:HD11	2.20	0.41
1:A:1118:LEU:O	1:A:1248:PRO:HD2	2.20	0.41
1:A:1038:ASP:OD2	3:A:3:GOL:O1	2.37	0.41
1:A:927:ILE:HD12	1:A:1011:ILE:HG21	2.02	0.41
1:A:1267:PHE:CD1	1:A:1267:PHE:N	2.89	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	Interatomic distance (Å)	Clash overlap (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 [i](#)

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%)	92	94

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 [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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

12 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	SLB	A	1	-	17,21,21	1.71	5 (29%)	19,31,31	2.15	10 (52%)
3	GOL	A	10	-	5,5,5	0.45	0	5,5,5	0.61	0
3	GOL	A	11	-	5,5,5	0.65	0	5,5,5	1.32	1 (20%)
3	GOL	A	12	-	5,5,5	0.56	0	5,5,5	0.69	0
3	GOL	A	2	-	5,5,5	0.36	0	5,5,5	0.32	0
3	GOL	A	3	-	5,5,5	0.37	0	5,5,5	0.44	0
3	GOL	A	4	-	5,5,5	0.31	0	5,5,5	1.04	0
3	GOL	A	5	-	5,5,5	0.49	0	5,5,5	0.69	0
3	GOL	A	6	-	5,5,5	0.57	0	5,5,5	0.52	0
3	GOL	A	7	-	5,5,5	0.60	0	5,5,5	0.95	0
3	GOL	A	8	-	5,5,5	0.33	0	5,5,5	0.46	0
3	GOL	A	9	-	5,5,5	0.65	0	5,5,5	0.28	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	SLB	A	1	-	-	0/14/38/38	0/1/1/1
3	GOL	A	10	-	-	0/4/4/4	0/0/0/0
3	GOL	A	11	-	-	0/4/4/4	0/0/0/0
3	GOL	A	12	-	-	0/4/4/4	0/0/0/0
3	GOL	A	2	-	-	0/4/4/4	0/0/0/0
3	GOL	A	3	-	-	0/4/4/4	0/0/0/0
3	GOL	A	4	-	-	0/4/4/4	0/0/0/0
3	GOL	A	5	-	-	0/4/4/4	0/0/0/0
3	GOL	A	6	-	-	0/4/4/4	0/0/0/0
3	GOL	A	7	-	-	0/4/4/4	0/0/0/0
3	GOL	A	8	-	-	0/4/4/4	0/0/0/0
3	GOL	A	9	-	-	0/4/4/4	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	SLB	O4-C4	2.05	1.48	1.43
2	A	1	SLB	O10-C10	2.18	1.28	1.23
2	A	1	SLB	O6-C2	2.72	1.45	1.42
2	A	1	SLB	O2-C2	3.49	1.43	1.40
2	A	1	SLB	C5-N5	3.74	1.52	1.45

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	SLB	O2-C2-C3	-3.51	105.02	109.41
2	A	1	SLB	C11-C10-N5	-3.46	109.48	116.11
2	A	1	SLB	O8-C8-C9	-3.09	102.00	109.22
2	A	1	SLB	O6-C6-C7	-3.00	102.71	107.26
2	A	1	SLB	C6-C5-N5	-2.20	107.23	111.07
2	A	1	SLB	O9-C9-C8	-2.18	106.36	111.10
2	A	1	SLB	C8-C7-C6	-2.14	108.70	113.01
2	A	1	SLB	O2-C2-O6	-2.10	106.80	110.22
3	A	11	GOL	C3-C2-C1	2.08	119.28	111.12
2	A	1	SLB	C9-C8-C7	2.47	118.26	112.48
2	A	1	SLB	O10-C10-N5	3.24	128.46	121.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	11	GOL	8	0
3	A	3	GOL	1	0
3	A	4	GOL	3	0
3	A	6	GOL	4	0
3	A	7	GOL	4	0
3	A	9	GOL	4	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	412/434 (94%)	0.28	39 (9%) 10 11	17, 28, 56, 79	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1177	ALA	9.3
1	A	1183	CYS	8.5
1	A	1278	PRO	6.9
1	A	1176	TYR	6.7
1	A	1214	ASN	6.4
1	A	927	ILE	6.3
1	A	860	ALA	5.9
1	A	1184	SER	5.7
1	A	926	ALA	5.6
1	A	925	SER	5.2
1	A	1182	GLU	5.0
1	A	920	ASN	4.8
1	A	958	GLN	4.5
1	A	1242	PHE	4.3
1	A	1185	GLN	4.2
1	A	993	LEU	4.2
1	A	1240	PHE	3.9
1	A	1277	PRO	3.7
1	A	1142	ASP	3.5
1	A	921	ASN	3.5
1	A	1210	ILE	3.2
1	A	859	SER	3.2
1	A	1186	ASN	3.1
1	A	1036	LYS	3.1
1	A	1141	SER	2.9
1	A	1211	VAL	2.9
1	A	980	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	1175	ILE	2.5
1	A	928	TYR	2.5
1	A	959	ASN	2.4
1	A	910	SER	2.4
1	A	1144	ASN	2.4
1	A	1187	CYS	2.4
1	A	1145	PRO	2.3
1	A	996	THR	2.2
1	A	992	SER	2.1
1	A	1174	THR	2.1
1	A	1124	PRO	2.1
1	A	995	HIS	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GOL	A	9	6/6	0.87	0.29	38.27	45,51,54,56	0
3	GOL	A	2	6/6	0.46	0.41	3.44	93,95,96,96	0
3	GOL	A	11	6/6	0.75	0.26	3.19	58,61,62,65	0
3	GOL	A	3	6/6	0.75	0.26	3.16	56,63,64,69	0
3	GOL	A	12	6/6	0.83	0.21	3.12	72,72,73,74	0
3	GOL	A	5	6/6	0.85	0.20	2.12	57,58,58,61	0
2	SLB	A	1	21/21	0.92	0.25	1.97	28,33,41,53	0
3	GOL	A	10	6/6	0.77	0.29	1.79	57,60,63,64	0
3	GOL	A	7	6/6	0.78	0.37	1.25	42,58,60,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	4	6/6	0.91	0.15	1.15	39,49,51,53	0
3	GOL	A	8	6/6	0.69	0.27	-	74,76,78,78	0
3	GOL	A	6	6/6	0.84	0.31	-	116,117,117,117	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.