



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:58 PM UTC

PDB ID : 6G5G / pdb_00006g5g
Title : Crystal structure of an engineered Botulinum Neurotoxin type B mutant E1191M/S1199Y in complex with human synaptotagmin 2
Authors : Masuyer, G.; Elliot, M.; Favre-Guilmand, C.; Liu, S.M.; Maignel, J.; Beard, M.; Carre, D.; Kalinichev, M.; Lezmi, S.; Mir, I.; Nicoleau, C.; Palan, S.; Perier, C.; Raban, E.; Dong, M.; Krupp, J.; Stenmark, P.
Deposited on : 2018-03-29
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

<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

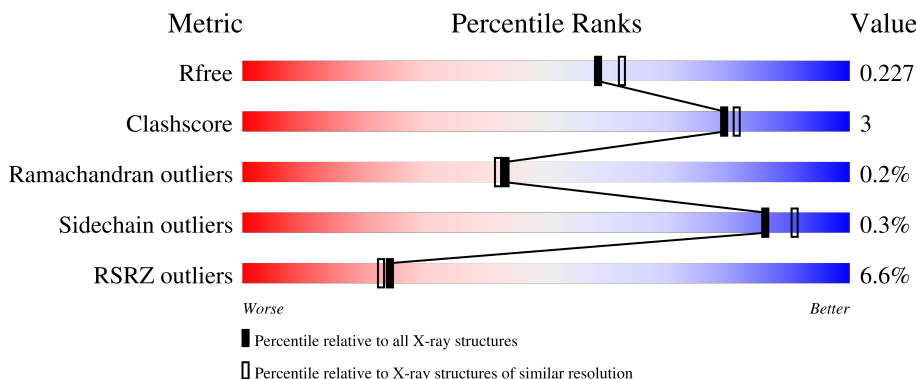
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 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	1291	2% 31% 67%
1	B	1291	5% 61% 5% 34%
2	P	21	14% 86% 14%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11548 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	426	Total	C	N	O	S	0	0	0
			3470	2236	565	654	15			
1	B	848	Total	C	N	O	S	0	3	0
			7079	4574	1125	1361	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	231	GLN	GLU	engineered mutation	UNP P10844
A	234	TYR	HIS	engineered mutation	UNP P10844
A	1191	MET	GLU	conflict	UNP P10844
A	1199	TYR	SER	conflict	UNP P10844
B	231	GLN	GLU	engineered mutation	UNP P10844
B	234	TYR	HIS	engineered mutation	UNP P10844
B	1191	MET	GLU	conflict	UNP P10844
B	1199	TYR	SER	conflict	UNP P10844

- Molecule 2 is a protein called Synaptotagmin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	18	Total	C	N	O	S	0	0	0
			156	100	25	30	1			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

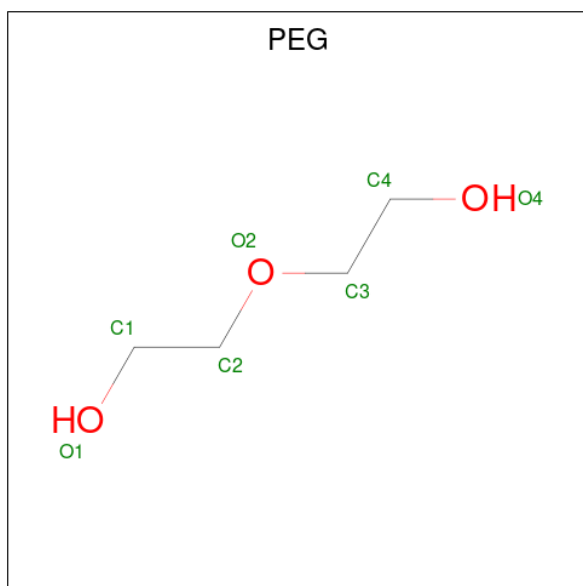
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

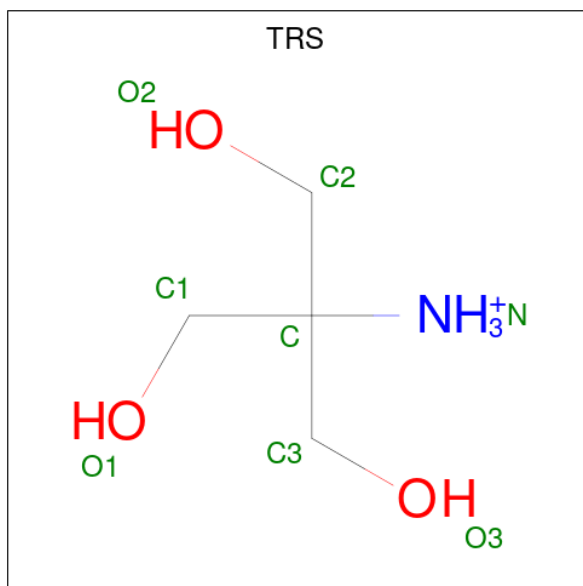
- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

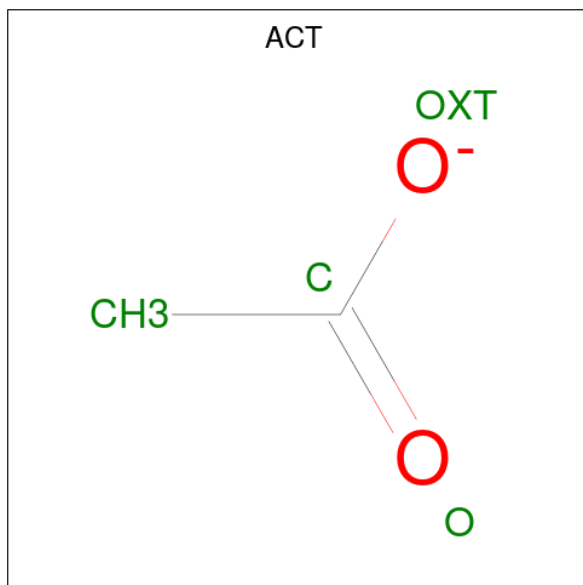
- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS)

(formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	173	Total	O	0	0
			173	173		
9	B	601	Total	O	0	0
			601	601		
9	P	14	Total	O	0	0
			14	14		

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	166.60Å 211.05Å 120.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.50 – 2.00 57.50 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (57.50-2.00) 99.9 (57.50-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.190 , 0.223 0.197 , 0.227	Depositor DCC
R_{free} test set	7218 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11548	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: EDO, TRS, ACT, GOL, PEG, MG

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	0.61	0/3548	0.79	0/4787
1	B	0.65	0/7232	0.78	1/9774 (0.0%)
2	P	0.66	0/157	0.81	0/204
All	All	0.63	0/10937	0.79	1/14765 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1134	ILE	N-CA-C	5.03	115.15	108.11

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	3470	0	3440	14	0
1	B	7079	0	6953	43	0
2	P	156	0	158	0	0
3	A	1	0	0	0	0
4	A	4	0	6	0	0
5	B	14	0	20	2	0
6	B	8	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	4	0	3	1	0
8	B	24	0	32	1	0
9	A	173	0	0	3	0
9	B	601	0	0	8	0
9	P	14	0	0	0	0
All	All	11548	0	10624	57	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 3.

All (57) 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:659:LEU:H	1:B:703:GLN:HE22	1.25	0.85
1:B:1222:GLN:HE21	1:B:1279:ASN:HD22	1.34	0.76
1:B:992[A]:ARG:NH2	9:B:1402:HOH:O	2.11	0.75
1:B:910:ARG:NE	9:B:1401:HOH:O	1.98	0.70
1:A:410:ARG:HG2	1:A:416:ILE:HD13	1.73	0.70
1:B:803:LYS:HE3	1:B:829:ASN:HD22	1.61	0.66
1:B:1222:GLN:HE21	1:B:1279:ASN:ND2	1.93	0.65
1:B:1095:ASN:HD22	1:B:1148:ARG:HH11	1.44	0.64
1:B:910:ARG:NH2	9:B:1401:HOH:O	2.27	0.64
1:B:693:TRP:CH2	1:B:835:ILE:HG23	2.36	0.60
1:A:67:ASN:HB3	9:A:1499:HOH:O	2.05	0.57
1:B:654:PHE:H	1:B:711:GLN:HE22	1.54	0.56
1:B:1226:LYS:O	9:B:1403:HOH:O	2.18	0.56
1:A:83:ASP:OD1	9:A:1401:HOH:O	2.18	0.55
1:B:1050:ARG:NH1	9:B:1413:HOH:O	2.41	0.54
1:A:417:ASN:ND2	9:A:1403:HOH:O	2.32	0.54
1:B:862:ASN:HD21	5:B:1302:PEG:C2	2.21	0.53
1:B:803:LYS:CE	1:B:829:ASN:HD22	2.20	0.53
1:B:862:ASN:HD21	5:B:1302:PEG:H22	1.74	0.53
1:A:16:ASN:ND2	1:A:142:ILE:HG23	2.24	0.52
1:B:848:ILE:HG22	1:B:852:MET:CE	2.40	0.52
1:B:916:ASN:ND2	9:B:1415:HOH:O	2.41	0.50
1:B:1242:ARG:HG2	1:B:1253:TYR:HB3	1.93	0.50
1:B:1002:TRP:HE1	1:B:1090:ASN:HD21	1.59	0.49
1:A:60:ASN:ND2	1:A:76:PRO:HG3	2.28	0.49
1:B:973:TRP:CD2	1:B:1007:ILE:HG21	2.47	0.49
1:B:1184:LYS:HE2	1:B:1205:TYR:CE1	2.50	0.47
1:B:952:ILE:HD12	1:B:1056:MET:HE1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1095:ASN:ND2	1:B:1148:ARG:HH11	2.10	0.47
1:B:860:ILE:HA	1:B:863:ASN:HD22	1.80	0.47
6:B:1303:TRS:O1	7:B:1304:ACT:H2	2.15	0.47
1:A:98:ARG:HD3	1:A:392:TYR:OH	2.15	0.46
1:A:122:ARG:NH1	1:A:180:HIS:CD2	2.83	0.46
1:B:1156:ILE:HG22	1:B:1157:ASN:N	2.31	0.46
1:B:898:GLN:HE22	1:B:1090:ASN:ND2	2.14	0.45
1:B:1248:ILE:HD12	9:B:1953:HOH:O	2.15	0.45
1:A:118:TYR:HA	1:A:324:PHE:CZ	2.52	0.45
1:B:547:PRO:HD3	8:B:1307:GOL:H32	1.98	0.45
1:A:73:TYR:CE2	1:A:199:TYR:CE2	3.05	0.44
1:B:910:ARG:HD3	1:B:1039:GLU:OE1	2.17	0.44
1:B:1015:LYS:HE2	1:B:1025:ASN:ND2	2.31	0.44
1:B:803:LYS:CE	1:B:829:ASN:ND2	2.81	0.44
1:B:1067:SER:H	1:B:1070:ASN:HD22	1.64	0.44
1:A:329:LYS:HE3	1:B:496:ASP:O	2.19	0.43
1:B:646:ALA:HB3	1:B:650:ILE:CG2	2.48	0.43
1:A:65:ILE:HG13	1:A:72:GLU:OE1	2.19	0.43
1:A:171:GLU:HB3	1:A:194:LYS:HE3	2.00	0.42
1:B:803:LYS:HE2	1:B:829:ASN:ND2	2.35	0.42
1:B:610:THR:HG23	1:B:620:ILE:HG21	2.02	0.42
1:B:1098:TYR:CG	1:B:1282:PHE:HB3	2.55	0.42
1:B:1260:SER:HB3	1:B:1263:TYR:CD2	2.55	0.41
1:B:632:ASN:HB3	9:B:1407:HOH:O	2.21	0.41
1:B:764:ILE:HG22	1:B:768:ILE:CD1	2.51	0.41
1:A:368:LYS:HB2	1:A:409:TYR:CG	2.57	0.40
1:B:658:LEU:HD11	1:B:787:MET:HG2	2.04	0.40
1:B:1002:TRP:HE1	1:B:1090:ASN:ND2	2.19	0.40
1:B:1006:THR:HG21	1:B:1071:ILE:HG12	2.03	0.40

There are no symmetry-related clashes.

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	422/1291 (33%)	411 (97%)	11 (3%)	0	100	100
1	B	849/1291 (66%)	820 (97%)	27 (3%)	2 (0%)	43	42
2	P	16/21 (76%)	16 (100%)	0	0	100	100
All	All	1287/2603 (49%)	1247 (97%)	38 (3%)	2 (0%)	43	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1156	ILE
1	B	922	VAL

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	387/1190 (32%)	386 (100%)	1 (0%)	86	91
1	B	790/1190 (66%)	788 (100%)	2 (0%)	86	91
2	P	17/19 (90%)	17 (100%)	0	100	100
All	All	1194/2399 (50%)	1191 (100%)	3 (0%)	86	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	PHE
1	B	612	ASP
1	B	1024	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	17	ASN
1	A	60	ASN

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Mol	Chain	Res	Type
1	A	178	GLN
1	A	180	HIS
1	B	599	ASN
1	B	703	GLN
1	B	709	ASN
1	B	711	GLN
1	B	726	GLN
1	B	770	ASN
1	B	773	ASN
1	B	813	ASN
1	B	829	ASN
1	B	863	ASN
1	B	944	ASN
1	B	958	ASN
1	B	1013	ASN
1	B	1070	ASN
1	B	1090	ASN
1	B	1095	ASN
1	B	1129	GLN
1	B	1216	GLN
1	B	1279	ASN
2	P	43	GLN
2	P	56	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](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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
8	GOL	B	1305	-	5,5,5	0.29	0	5,5,5	0.29	0
8	GOL	B	1306	-	5,5,5	0.31	0	5,5,5	0.26	0
4	EDO	A	1302	-	3,3,3	0.50	0	2,2,2	0.43	0
8	GOL	B	1307	-	5,5,5	0.43	0	5,5,5	0.51	0
5	PEG	B	1302	-	6,6,6	0.63	0	5,5,5	0.38	0
8	GOL	B	1308	-	5,5,5	0.26	0	5,5,5	0.49	0
7	ACT	B	1304	-	3,3,3	0.89	0	3,3,3	0.61	0
6	TRS	B	1303	-	7,7,7	0.22	0	9,9,9	0.93	0
5	PEG	B	1301	-	6,6,6	0.47	0	5,5,5	0.21	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
8	GOL	B	1305	-	-	2/4/4/4	-
8	GOL	B	1306	-	-	2/4/4/4	-
4	EDO	A	1302	-	-	1/1/1/1	-
8	GOL	B	1307	-	-	2/4/4/4	-
5	PEG	B	1302	-	-	2/4/4/4	-
8	GOL	B	1308	-	-	0/4/4/4	-
6	TRS	B	1303	-	-	3/9/9/9	-
5	PEG	B	1301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	1306	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
8	B	1306	GOL	O2-C2-C3-O3
5	B	1302	PEG	O1-C1-C2-O2
5	B	1302	PEG	O2-C3-C4-O4
8	B	1305	GOL	C1-C2-C3-O3
8	B	1307	GOL	C1-C2-C3-O3
5	B	1301	PEG	O1-C1-C2-O2
8	B	1307	GOL	O2-C2-C3-O3
8	B	1305	GOL	O2-C2-C3-O3
4	A	1302	EDO	O1-C1-C2-O2
5	B	1301	PEG	C4-C3-O2-C2
6	B	1303	TRS	C3-C-C1-O1
6	B	1303	TRS	C2-C-C3-O3
6	B	1303	TRS	N-C-C3-O3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	1307	GOL	1	0
5	B	1302	PEG	2	0
7	B	1304	ACT	1	0
6	B	1303	TRS	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 ⓘ

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	426/1291 (32%)	0.44	22 (5%)	33 31	30, 47, 81, 105	0
1	B	848/1291 (65%)	0.20	60 (7%)	22 20	12, 38, 83, 115	3 (0%)
2	P	18/21 (85%)	0.67	3 (16%)	4 4	30, 44, 92, 95	0
All	All	1292/2603 (49%)	0.29	85 (6%)	24 23	12, 42, 83, 115	3 (0%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	VAL	6.1
1	B	835	ILE	5.8
1	B	817	LEU	4.8
1	B	611	MET	4.5
1	B	610	THR	4.3
1	B	923	PHE	4.1
1	B	1249	VAL	4.0
1	B	482	ILE	3.9
1	B	815	LEU	3.9
1	A	218	ARG	3.8
1	A	205	ASN	3.7
1	B	672	ILE	3.7
1	A	310	ILE	3.6
1	B	818	ILE	3.6
2	P	43	GLN	3.6
1	B	1156	ILE	3.6
1	B	922	VAL	3.5
1	B	816	TYR	3.5
1	B	919	PHE	3.5
1	B	671	TYR	3.5
2	P	46	MET	3.4
1	A	428	HIS	3.4
1	B	1175	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	667	LEU	3.3
1	B	831	TYR	3.2
1	B	821	ALA	3.1
1	B	1174	LEU	3.1
1	B	484	ASN	3.0
1	A	416	ILE	3.0
1	A	391	ILE	2.9
1	A	426	LYS	2.9
1	A	142	ILE	2.9
1	B	612	ASP	2.8
1	B	749	ILE	2.8
1	B	675	LYS	2.8
1	A	145	PRO	2.7
1	B	1229	GLU	2.7
1	A	219	GLY	2.7
1	B	819	GLY	2.7
1	B	483	GLU	2.6
1	B	834	THR	2.6
1	A	100	LYS	2.6
1	B	814	LYS	2.6
1	B	918	ILE	2.5
1	B	1083[A]	TYR	2.5
1	B	1157	ASN	2.5
1	B	1232	THR	2.5
1	B	1155	SER	2.4
1	B	487	PRO	2.4
1	A	387	LEU	2.4
1	B	807	LEU	2.4
1	B	500	LYS	2.4
1	B	920	ASN	2.4
1	B	486	PHE	2.4
1	A	394	ILE	2.4
1	B	585	VAL	2.4
1	B	820	SER	2.4
1	A	415	ALA	2.3
1	A	146	GLY	2.3
1	B	1250	PHE	2.3
1	A	143	SER	2.3
1	A	429	LEU	2.3
1	B	614	ILE	2.2
1	B	495	THR	2.2
1	B	1152	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	668	LEU	2.2
1	B	832	LEU	2.2
1	B	607	LYS	2.2
1	B	836	MET	2.2
1	B	501	ILE	2.1
1	B	740	ILE	2.1
1	B	493	LEU	2.1
1	B	619	LEU	2.1
1	B	609	ASN	2.1
2	P	44	GLU	2.1
1	B	1200	ASP	2.1
1	B	589	LEU	2.1
1	B	753	PHE	2.1
1	A	421	TYR	2.0
1	B	613	LYS	2.0
1	B	720	TYR	2.0
1	B	678	ILE	2.0
1	A	425	SER	2.0
1	A	419	GLN	2.0
1	A	150	ARG	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(Å ²)	Q<0.9
7	ACT	B	1304	4/4	0.74	0.21	57,65,65,68	0
5	PEG	B	1302	7/7	0.86	0.19	45,55,58,59	0
5	PEG	B	1301	7/7	0.86	0.19	67,72,74,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	GOL	B	1307	6/6	0.86	0.15	51,56,57,59	0
8	GOL	B	1305	6/6	0.89	0.13	41,50,57,59	0
4	EDO	A	1302	4/4	0.89	0.16	43,52,58,63	0
8	GOL	B	1306	6/6	0.91	0.15	59,64,65,68	0
8	GOL	B	1308	6/6	0.92	0.17	70,73,74,74	0
6	TRS	B	1303	8/8	0.94	0.09	40,46,48,50	0
3	MG	A	1301	1/1	0.98	0.04	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.