



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:03 AM UTC

PDB ID : 7BY5 / pdb_00007by5
Title : Tetanus neurotoxin mutant-(H233A/E234Q/H237A/Y375F)
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Deposited on : 2020-04-21
Resolution : 2.27 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

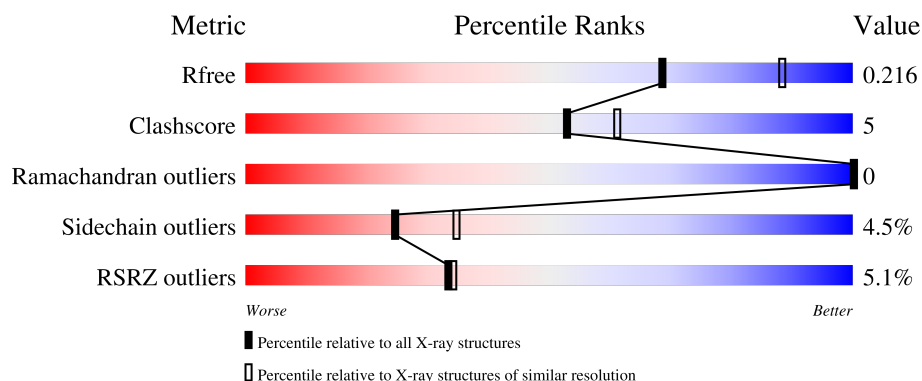
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	1322	5% 84% 11% ...

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11306 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.

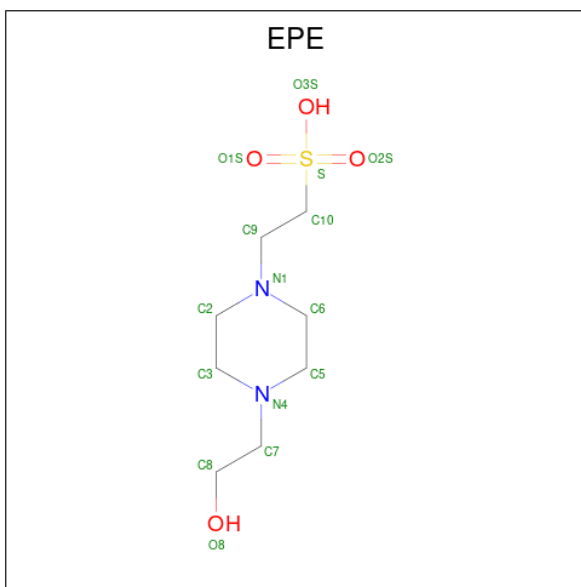
- Molecule 1 is a protein called Tetanus toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1286	Total	C	N	O	S	0	10	0
			10470	6706	1713	2017	34			

There are 12 discrepancies between the modelled and reference sequences:

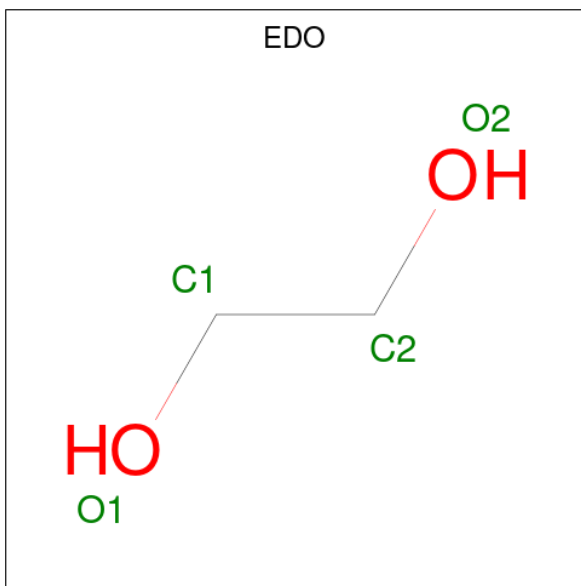
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	HIS	-	expression tag	UNP P04958
A	-5	HIS	-	expression tag	UNP P04958
A	-4	HIS	-	expression tag	UNP P04958
A	-3	HIS	-	expression tag	UNP P04958
A	-2	HIS	-	expression tag	UNP P04958
A	-1	HIS	-	expression tag	UNP P04958
A	0	HIS	-	expression tag	UNP P04958
A	1	MET	-	expression tag	UNP P04958
A	233	ALA	HIS	engineered mutation	UNP P04958
A	234	GLN	GLU	engineered mutation	UNP P04958
A	237	ALA	HIS	engineered mutation	UNP P04958
A	375	PHE	TYR	engineered mutation	UNP P04958

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Na 3 3	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0

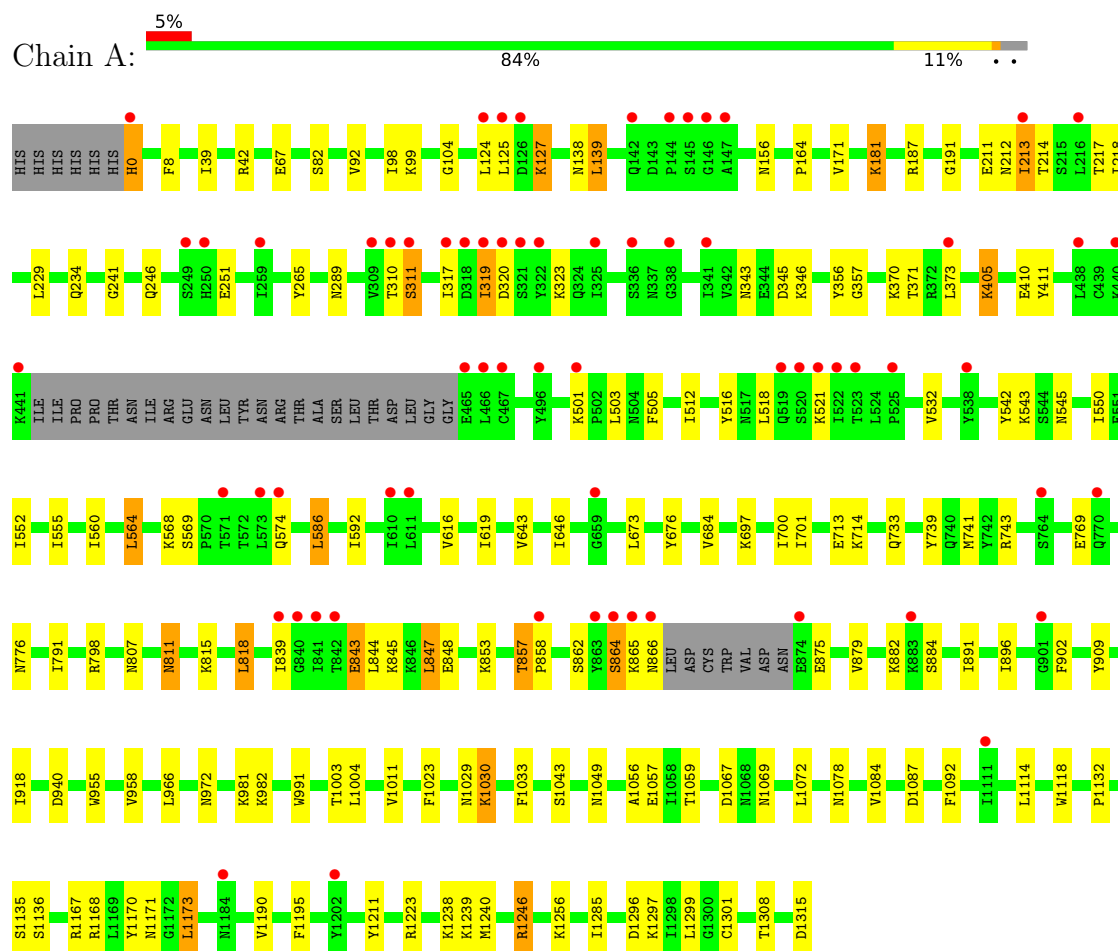
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	772	Total O 785 785	0	14

3 Residue-property plots

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: Tetanus toxin



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.54Å 145.54Å 129.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.28 – 2.27 48.28 – 2.27	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.28-2.27) 99.1 (48.28-2.27)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.186 , 0.233 (Not available) , 0.216	Depositor DCC
R_{free} test set	3663 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11306	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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, CL, NA, EPE

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	0.42	0/10702	0.88	1/14493 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	909	TYR	CB-CA-C	5.75	118.51	109.37

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	10470	0	10405	104	0
2	A	15	0	18	4	0
3	A	32	0	48	1	0
4	A	3	0	0	0	0
5	A	1	0	0	0	0
6	A	785	0	0	4	0
All	All	11306	0	10471	104	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 (104) 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:138:ASN:HD21	1:A:532:VAL:H	1.05	0.97
1:A:127:LYS:NZ	1:A:311:SER:HB2	1.84	0.91
1:A:127:LYS:HZ1	1:A:311:SER:HB2	1.38	0.89
1:A:1246:ARG:NH2	1:A:1296:ASP:O	2.07	0.85
1:A:127:LYS:HG3	1:A:311:SER:O	1.78	0.84
1:A:187:ARG:HE	1:A:246:GLN:HE21	1.28	0.82
1:A:739[B]:TYR:HD2	1:A:743[B]:ARG:HH21	1.36	0.73
1:A:807:ASN:O	1:A:811:ASN:HB2	1.91	0.69
1:A:171:VAL:HG23	1:A:234:GLN:HE21	1.58	0.69
1:A:138:ASN:HD21	1:A:532:VAL:N	1.87	0.67
1:A:229:LEU:HD21	1:A:371:THR:HG22	1.75	0.67
1:A:646:ILE:HD12	1:A:741:MET:HG3	1.77	0.67
1:A:982:LYS:NZ	1:A:1069:ASN:HD22	1.92	0.66
1:A:982:LYS:HZ3	1:A:1069:ASN:HD22	1.45	0.64
1:A:127:LYS:CG	1:A:311:SER:O	2.46	0.63
1:A:569:SER:HA	1:A:592:ILE:HD11	1.80	0.62
1:A:229:LEU:CD2	1:A:371:THR:HG22	2.30	0.61
1:A:212:ASN:OD1	1:A:798:ARG:NH1	2.34	0.60
1:A:1033:PHE:H	1:A:1049:ASN:ND2	1.99	0.60
1:A:289:ASN:HD21	1:A:501:LYS:HB3	1.67	0.60
1:A:972:ASN:HD21	1:A:1078:ASN:H	1.48	0.59
1:A:958:VAL:HG12	1:A:1084:VAL:HG12	1.84	0.58
1:A:1023:PHE:CE2	1:A:1136:SER:HB2	2.40	0.57
1:A:1168:ARG:NH2	1:A:1315:ASP:O	2.37	0.57
1:A:319:ILE:HD12	1:A:319:ILE:N	2.20	0.57
1:A:138:ASN:ND2	1:A:532:VAL:H	1.88	0.56
1:A:543:LYS:HB3	2:A:1401:EPE:H32	1.86	0.56
1:A:357:GLY:HA3	1:A:512:ILE:HD11	1.88	0.56
1:A:972:ASN:ND2	1:A:1078:ASN:H	2.05	0.55
1:A:98:ILE:O	1:A:104:GLY:HA3	2.07	0.54
1:A:127:LYS:HG3	1:A:311:SER:C	2.33	0.54
1:A:67:GLU:OE2	2:A:1401:EPE:H62	2.08	0.54
1:A:127:LYS:HZ2	1:A:311:SER:HB2	1.73	0.53
1:A:643:VAL:O	1:A:646:ILE:HG12	2.08	0.53
1:A:866:ASN:HD21	1:A:940:ASP:HB2	1.73	0.52
1:A:866:ASN:HA	1:A:902:PHE:HE1	1.76	0.51
1:A:1030:LYS:HB2	6:A:1790:HOH:O	2.10	0.51
1:A:839:ILE:HG22	1:A:843:GLU:HB3	1.93	0.51
1:A:217:THR:HG22	1:A:410:GLU:OE2	2.11	0.51
1:A:127:LYS:HA	1:A:311:SER:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:TYR:H	1:A:733:GLN:HE22	1.59	0.50
1:A:139:LEU:H	1:A:139:LEU:HD12	1.75	0.50
1:A:229:LEU:HD21	1:A:371:THR:CG2	2.41	0.50
1:A:1170:TYR:CE1	1:A:1308:THR:HA	2.47	0.50
1:A:127:LYS:NZ	1:A:311:SER:CB	2.65	0.49
1:A:1171:ASN:HB2	6:A:1569:HOH:O	2.12	0.49
1:A:501:LYS:HB2	1:A:713[B]:GLU:OE1	2.12	0.49
1:A:320:ASP:HA	1:A:323:LYS:HB2	1.94	0.49
1:A:545:ASN:OD1	2:A:1401:EPE:H61	2.12	0.49
1:A:289:ASN:ND2	1:A:501:LYS:HB3	2.26	0.49
1:A:265:TYR:CD1	2:A:1401:EPE:H21	2.49	0.48
1:A:39:ILE:HD11	1:A:92:VAL:HA	1.96	0.48
1:A:1240:MET:HA	1:A:1256:LYS:O	2.13	0.48
1:A:139:LEU:HD12	1:A:139:LEU:N	2.29	0.48
1:A:697:LYS:O	1:A:701:ILE:HG12	2.14	0.47
1:A:891:ILE:HG12	1:A:896:ILE:HG12	1.97	0.47
1:A:343:ASN:HD22	1:A:346:LYS:H	1.62	0.47
1:A:646:ILE:CD1	1:A:741:MET:HG3	2.44	0.47
1:A:991:TRP:HA	1:A:1003:THR:O	2.16	0.46
1:A:503:LEU:HD21	1:A:713[B]:GLU:HG3	1.96	0.46
1:A:884:SER:O	1:A:1092:PHE:HA	2.15	0.46
1:A:213:ILE:CG1	1:A:218:ILE:HG22	2.46	0.46
1:A:356:TYR:CE2	1:A:505:PHE:HB3	2.50	0.46
1:A:862:SER:HB3	6:A:1793:HOH:O	2.16	0.46
1:A:918:ILE:HG12	1:A:955:TRP:CD2	2.52	0.45
1:A:211:GLU:HG3	1:A:373:LEU:HD22	1.98	0.45
1:A:714:LYS:NZ	6:A:1521:HOH:O	2.50	0.45
1:A:875:GLU:HB3	1:A:879:VAL:HG21	1.99	0.45
1:A:1132:PRO:CB	3:A:1407:EDO:H21	2.47	0.44
1:A:370:LYS:HB2	1:A:411:TYR:CG	2.52	0.44
1:A:319:ILE:N	1:A:319:ILE:CD1	2.81	0.44
1:A:866:ASN:HA	1:A:902:PHE:CE1	2.53	0.44
1:A:164:PRO:HG2	1:A:542:TYR:CZ	2.53	0.44
1:A:700:ILE:HG21	1:A:839:ILE:HD11	2.00	0.44
1:A:1195:PHE:CD1	1:A:1239:LYS:HE2	2.53	0.44
1:A:0:HIS:HE1	1:A:516:TYR:O	2.00	0.43
1:A:191:GLY:HA2	1:A:241:GLY:O	2.19	0.43
1:A:847:LEU:HD12	1:A:847:LEU:HA	1.84	0.43
1:A:818:LEU:HD12	1:A:818:LEU:HA	1.89	0.43
1:A:1033:PHE:H	1:A:1049:ASN:HD21	1.65	0.43
1:A:181:LYS:HD3	1:A:181:LYS:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:LYS:HA	1:A:1067:ASP:HB2	2.01	0.42
1:A:343:ASN:HD21	1:A:345:ASP:HB2	1.83	0.42
1:A:864:SER:HA	1:A:902:PHE:O	2.19	0.42
1:A:1043:SER:HB2	1:A:1056:ALA:O	2.19	0.42
1:A:1072:LEU:HD12	1:A:1072:LEU:N	2.35	0.42
1:A:42:ARG:HD2	1:A:156:ASN:OD1	2.20	0.42
1:A:586:LEU:HD12	1:A:586:LEU:HA	1.85	0.42
1:A:1114:LEU:HD12	1:A:1190:VAL:HG12	2.02	0.42
1:A:1004:LEU:O	1:A:1011:VAL:HA	2.20	0.42
1:A:405:LYS:HB3	1:A:405:LYS:HE2	1.84	0.41
1:A:319:ILE:CD1	1:A:319:ILE:H	2.34	0.41
1:A:373:LEU:H	1:A:373:LEU:HD23	1.84	0.41
1:A:857:THR:HA	1:A:858:PRO:HD2	1.92	0.41
1:A:955:TRP:HB2	1:A:1087:ASP:HB3	2.03	0.41
1:A:213:ILE:HD13	1:A:791:ILE:HG12	2.03	0.41
1:A:1029:ASN:HB3	1:A:1118:TRP:CZ3	2.56	0.41
1:A:564:LEU:HD12	1:A:564:LEU:HA	1.86	0.41
1:A:1299:LEU:HD13	1:A:1301:CYS:SG	2.60	0.41
1:A:616:VAL:HA	1:A:619:ILE:HD12	2.02	0.40
1:A:966:LEU:HD12	1:A:966:LEU:HA	1.91	0.40
1:A:1173:LEU:HD12	1:A:1173:LEU:HA	1.85	0.40
1:A:1211:TYR:CD1	1:A:1223:ARG:HB3	2.56	0.40
1:A:1223:ARG:O	1:A:1285:ILE:HA	2.21	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	1290/1322 (98%)	1255 (97%)	35 (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	1182/1205 (98%)	1129 (96%)	53 (4%)	24	35

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	8	PHE
1	A	82	SER
1	A	99	LYS
1	A	124	LEU
1	A	125	LEU
1	A	127	LYS
1	A	139	LEU
1	A	181	LYS
1	A	213	ILE
1	A	214	THR
1	A	251	GLU
1	A	310	THR
1	A	311	SER
1	A	317	ILE
1	A	319	ILE
1	A	405	LYS
1	A	518	LEU
1	A	521	LYS
1	A	550	ILE
1	A	552	ILE
1	A	555	ILE
1	A	560	ILE
1	A	564	LEU
1	A	568	LYS
1	A	574	GLN
1	A	586	LEU
1	A	673	LEU
1	A	684	VAL
1	A	769	GLU

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Mol	Chain	Res	Type
1	A	776	ASN
1	A	811	ASN
1	A	815	LYS
1	A	818	LEU
1	A	843	GLU
1	A	844	LEU
1	A	845	LYS
1	A	847	LEU
1	A	848	GLU
1	A	853	LYS
1	A	857	THR
1	A	864	SER
1	A	865	LYS
1	A	882	LYS
1	A	1030	LYS
1	A	1057	GLU
1	A	1059	THR
1	A	1135	SER
1	A	1167	ARG
1	A	1173	LEU
1	A	1238	LYS
1	A	1246	ARG
1	A	1297	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	16	ASN
1	A	138	ASN
1	A	182	ASN
1	A	234	GLN
1	A	246	GLN
1	A	289	ASN
1	A	297	ASN
1	A	324	GLN
1	A	343	ASN
1	A	504	ASN
1	A	526	ASN
1	A	567	GLN
1	A	625	ASN
1	A	696	GLN

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Mol	Chain	Res	Type
1	A	733	GLN
1	A	777	ASN
1	A	807	ASN
1	A	826	ASN
1	A	866	ASN
1	A	972	ASN
1	A	983	HIS
1	A	998	ASN
1	A	1049	ASN
1	A	1069	ASN
1	A	1204	ASN
1	A	1207	HIS
1	A	1216	ASN
1	A	1219	ASN
1	A	1288	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 13 ligands modelled in this entry, 4 are 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
3	EDO	A	1405	-	3,3,3	0.16	0	2,2,2	0.28	0
3	EDO	A	1408	-	3,3,3	0.11	0	2,2,2	0.24	0
3	EDO	A	1403	-	3,3,3	0.07	0	2,2,2	0.12	0
2	EPE	A	1401	-	15,15,15	1.84	1 (6%)	19,20,20	1.47	4 (21%)
3	EDO	A	1407	-	3,3,3	0.09	0	2,2,2	0.23	0
3	EDO	A	1406	-	3,3,3	0.07	0	2,2,2	0.11	0
3	EDO	A	1409	-	3,3,3	0.06	0	2,2,2	0.18	0
3	EDO	A	1402	-	3,3,3	0.05	0	2,2,2	0.06	0
3	EDO	A	1404	-	3,3,3	0.08	0	2,2,2	0.06	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
3	EDO	A	1405	-	-	0/1/1/1	-
3	EDO	A	1408	-	-	0/1/1/1	-
3	EDO	A	1403	-	-	1/1/1/1	-
2	EPE	A	1401	-	-	2/9/19/19	0/1/1/1
3	EDO	A	1407	-	-	0/1/1/1	-
3	EDO	A	1406	-	-	0/1/1/1	-
3	EDO	A	1409	-	-	0/1/1/1	-
3	EDO	A	1402	-	-	0/1/1/1	-
3	EDO	A	1404	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1401	EPE	C10-S	-6.71	1.68	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1401	EPE	O1S-S-C10	3.25	111.64	106.73
2	A	1401	EPE	C3-C2-N1	2.40	115.48	110.65
2	A	1401	EPE	C9-N1-C2	-2.04	105.81	111.24
2	A	1401	EPE	C6-N1-C2	2.04	113.23	108.84

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1404	EDO	O1-C1-C2-O2
3	A	1403	EDO	O1-C1-C2-O2
2	A	1401	EPE	C8-C7-N4-C5
2	A	1401	EPE	C8-C7-N4-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1401	EPE	4	0
3	A	1407	EDO	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	1286/1322 (97%)	0.40	66 (5%) 33 34	23, 56, 85, 122	10 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	125	LEU	5.9
1	A	124	LEU	5.8
1	A	522	ILE	5.8
1	A	319	ILE	5.2
1	A	309	VAL	4.7
1	A	864	SER	4.4
1	A	144	PRO	4.4
1	A	322	TYR	4.4
1	A	317	ILE	3.9
1	A	145	SER	3.8
1	A	321	SER	3.8
1	A	866	ASN	3.7
1	A	521	LYS	3.7
1	A	310	THR	3.7
1	A	441	LYS	3.6
1	A	865	LYS	3.6
1	A	1111	ILE	3.5
1	A	0	HIS	3.5
1	A	538	TYR	3.5
1	A	496	TYR	3.2
1	A	338	GLY	3.2
1	A	520	SER	3.1
1	A	373	LEU	3.1
1	A	519	GLN	3.1
1	A	311	SER	3.0
1	A	863	TYR	3.0
1	A	146	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	126	ASP	2.8
1	A	1184	ASN	2.8
1	A	250	HIS	2.7
1	A	523	THR	2.7
1	A	325	ILE	2.6
1	A	874	GLU	2.6
1	A	840	GLY	2.6
1	A	858	PRO	2.6
1	A	320	ASP	2.6
1	A	466	LEU	2.4
1	A	611	LEU	2.4
1	A	573	LEU	2.4
1	A	770	GLN	2.4
1	A	1202	TYR	2.3
1	A	467	CYS	2.3
1	A	142	GLN	2.3
1	A	841	ILE	2.3
1	A	764	SER	2.3
1	A	571	THR	2.2
1	A	842	THR	2.2
1	A	249	SER	2.2
1	A	318	ASP	2.2
1	A	465	GLU	2.2
1	A	883	LYS	2.2
1	A	901	GLY	2.2
1	A	438	LEU	2.1
1	A	610	ILE	2.1
1	A	525	PRO	2.1
1	A	574	GLN	2.1
1	A	659	GLY	2.1
1	A	216	LEU	2.1
1	A	259	ILE	2.1
1	A	501	LYS	2.0
1	A	147	ALA	2.0
1	A	213	ILE	2.0
1	A	839	ILE	2.0
1	A	440	LYS	2.0
1	A	336	SER	2.0
1	A	341	ILE	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($\text{\AA}^2$)	Q<0.9
4	NA	A	1410	1/1	0.68	0.23	83,83,83,83	0
3	EDO	A	1404	4/4	0.86	0.18	77,85,86,87	0
3	EDO	A	1409	4/4	0.87	0.19	66,67,69,71	0
2	EPE	A	1401	15/15	0.87	0.17	74,85,101,103	0
5	CL	A	1413	1/1	0.89	0.28	90,90,90,90	0
4	NA	A	1412	1/1	0.93	0.16	79,79,79,79	0
3	EDO	A	1403	4/4	0.94	0.12	60,61,61,65	0
3	EDO	A	1402	4/4	0.94	0.13	63,67,68,73	0
3	EDO	A	1405	4/4	0.94	0.12	51,53,57,57	0
3	EDO	A	1407	4/4	0.94	0.10	52,54,56,61	0
4	NA	A	1411	1/1	0.95	0.07	64,64,64,64	0
3	EDO	A	1406	4/4	0.95	0.11	53,54,54,57	0
3	EDO	A	1408	4/4	0.95	0.09	56,56,58,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.