



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:45 PM UTC

PDB ID : 3ZUQ / pdb_00003zuq
Title : Crystal structure of an engineered botulinum neurotoxin type B - derivative,
LC-B-GS-Hn-B
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Deposited on : 2011-07-19
Resolution : 2.70 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

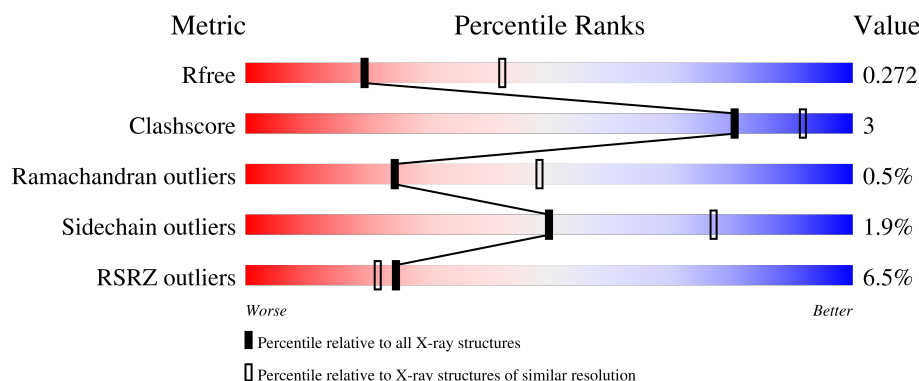
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	906	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6953 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	850	Total	C	N	O	S	0	0	0
			6908	4450	1102	1331	25			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	894	LEU	-	expression tag	UNP P10844
A	895	GLU	-	expression tag	UNP P10844
A	896	ALA	-	expression tag	UNP P10844
A	897	LEU	-	expression tag	UNP P10844
A	898	ALA	-	expression tag	UNP P10844
A	899	SER	-	expression tag	UNP P10844
A	900	GLY	-	expression tag	UNP P10844
A	901	HIS	-	expression tag	UNP P10844
A	902	HIS	-	expression tag	UNP P10844
A	903	HIS	-	expression tag	UNP P10844
A	904	HIS	-	expression tag	UNP P10844
A	905	HIS	-	expression tag	UNP P10844
A	906	HIS	-	expression tag	UNP P10844

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	44	Total	O	0	0
			44	44		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.37Å 103.79Å 114.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.03 – 2.70 77.03 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.1 (77.03-2.70) 93.1 (77.03-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.248 , 0.281 0.240 , 0.272	Depositor DCC
R_{free} test set	1417 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 25.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6953	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: ZN

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	0.43	1/7049 (0.0%)	0.75	0/9530

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	823	ILE	CA-CB	5.11	1.57	1.54

There are no bond angle outliers.

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	6908	0	6848	36	0
2	A	1	0	0	0	0
3	A	44	0	0	0	0
All	All	6953	0	6848	36	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 (36) 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:368:LYS:H	1:A:412:GLN:HE22	1.44	0.65
1:A:261:THR:HG22	1:A:262:ASP:O	1.98	0.64
1:A:437:CYS:HB3	1:A:479:LEU:HD21	1.79	0.63
1:A:492:ILE:HG23	1:A:742:THR:HG23	1.84	0.60
1:A:102:LYS:HE3	1:A:365:TYR:HA	1.85	0.57
1:A:572:ILE:HG22	1:A:663:LEU:HB3	1.85	0.57
1:A:693:LEU:HD11	1:A:822:MET:HG2	1.88	0.55
1:A:673:ASN:HD22	1:A:676:ASN:H	1.54	0.55
1:A:626:ALA:HA	1:A:786:ILE:HD11	1.89	0.53
1:A:653:SER:HB3	1:A:808:ASN:HD21	1.75	0.52
1:A:75:ASP:HB3	1:A:167:LEU:HD11	1.95	0.49
1:A:200:VAL:HG11	1:A:224:PRO:HG3	1.96	0.48
1:A:81:THR:HG22	1:A:83:ASP:H	1.78	0.48
1:A:399:ASN:HD21	1:A:412:GLN:HE21	1.61	0.48
1:A:312:ASP:HB3	1:A:315:ILE:HG12	1.95	0.47
1:A:693:LEU:HD21	1:A:822:MET:HE3	1.96	0.47
1:A:399:ASN:HB3	1:A:406:GLU:HA	1.95	0.47
1:A:273:GLY:HA3	1:A:357:THR:CG2	2.46	0.46
1:A:572:ILE:HG13	1:A:573:PHE:N	2.31	0.45
1:A:786:ILE:HG22	1:A:787:ASP:N	2.31	0.45
1:A:666:GLY:HA2	1:A:688:GLU:HA	1.99	0.44
1:A:20:ILE:HG12	1:A:44:TRP:CZ3	2.53	0.44
1:A:38:LYS:HG2	1:A:40:THR:O	2.18	0.44
1:A:691:PRO:HB3	1:A:742:THR:CG2	2.48	0.44
1:A:10:TYR:H	1:A:86:ASN:HD22	1.66	0.43
1:A:213:SER:C	1:A:215:PHE:N	2.74	0.43
1:A:357:THR:HG22	1:A:360:ASN:H	1.82	0.43
1:A:154:ILE:HA	1:A:541:GLU:O	2.18	0.43
1:A:297:ARG:HG2	1:A:340:ILE:HD12	2.01	0.43
1:A:273:GLY:HA3	1:A:357:THR:HG21	2.01	0.42
1:A:207:GLN:H	1:A:207:GLN:HE21	1.66	0.41
1:A:10:TYR:H	1:A:86:ASN:ND2	2.18	0.41
1:A:206:VAL:HG21	1:A:752:GLU:OE1	2.21	0.41
1:A:779:LYS:H	1:A:779:LYS:HG3	1.68	0.41
1:A:728:TRP:CE3	1:A:830:LEU:HD13	2.56	0.40
1:A:118:TYR:HA	1:A:324:PHE:CZ	2.56	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	844/906 (93%)	811 (96%)	29 (3%)	4 (0%)	24	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	GLY
1	A	213	SER
1	A	210	LYS
1	A	214	ILE

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	776/801 (97%)	761 (98%)	15 (2%)	50	77

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLU
1	A	65	ILE
1	A	207	GLN
1	A	216	ASN
1	A	357	THR
1	A	479	LEU
1	A	504	LYS

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Mol	Chain	Res	Type
1	A	515	ASN
1	A	564	LYS
1	A	566	PHE
1	A	621	GLU
1	A	641	ASN
1	A	779	LYS
1	A	796	ASN
1	A	885	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	180	HIS
1	A	207	GLN
1	A	259	GLN
1	A	275	GLN
1	A	294	GLN
1	A	314	ASN
1	A	399	ASN
1	A	412	GLN
1	A	435	GLN
1	A	519	ASN
1	A	559	GLN
1	A	579	GLN
1	A	641	ASN
1	A	673	ASN
1	A	676	ASN
1	A	719	ASN
1	A	761	GLN
1	A	783	ASN
1	A	808	ASN
1	A	835	ASN
1	A	843	ASN
1	A	864	ASN
1	A	889	ASN

5.3.3 RNA ⓘ

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	850/906 (93%)	0.52	55 (6%)	25 22	25, 42, 66, 80	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	VAL	5.0
1	A	146	GLY	4.9
1	A	785	ASN	4.4
1	A	212	ALA	4.4
1	A	145	PRO	4.1
1	A	784	ILE	4.1
1	A	566	PHE	4.0
1	A	652	ILE	3.6
1	A	149	GLU	3.5
1	A	213	SER	3.4
1	A	211	GLY	3.3
1	A	891	TYR	3.3
1	A	786	ILE	3.3
1	A	308	VAL	3.2
1	A	214	ILE	3.2
1	A	245	ASP	3.2
1	A	707	ILE	3.1
1	A	313	PRO	3.0
1	A	439	ASP	2.9
1	A	708	ASP	2.9
1	A	516	TYR	2.9
1	A	143	SER	2.8
1	A	477	LEU	2.8
1	A	1	MET	2.8
1	A	718	ASP	2.8
1	A	2	PRO	2.8
1	A	314	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	881	ASP	2.7
1	A	783	ASN	2.7
1	A	595	ASP	2.6
1	A	882	THR	2.6
1	A	147	GLU	2.5
1	A	742	THR	2.5
1	A	883	ILE	2.5
1	A	11	ASN	2.5
1	A	853	ILE	2.5
1	A	141	LEU	2.5
1	A	782	SER	2.4
1	A	586	ARG	2.4
1	A	568	ASP	2.4
1	A	515	ASN	2.3
1	A	524	ASN	2.3
1	A	584	ASP	2.3
1	A	517	ILE	2.3
1	A	69	ASP	2.2
1	A	121	ASP	2.2
1	A	523	ILE	2.2
1	A	892	ASN	2.1
1	A	402	ASP	2.1
1	A	152	LYS	2.1
1	A	70	VAL	2.1
1	A	870	ILE	2.1
1	A	884	LEU	2.1
1	A	610	MET	2.0
1	A	808	ASN	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
2	ZN	A	1440	1/1	0.98	0.03	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.