



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 01:33 AM GMT

PDB ID : 1XTF
Title : neurotoxin BoNT/A E224Q Y366F mutant
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Deposited on : 2004-10-21
Resolution : 2.20 Å(reported)

This is a wwPDB validation summary 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>

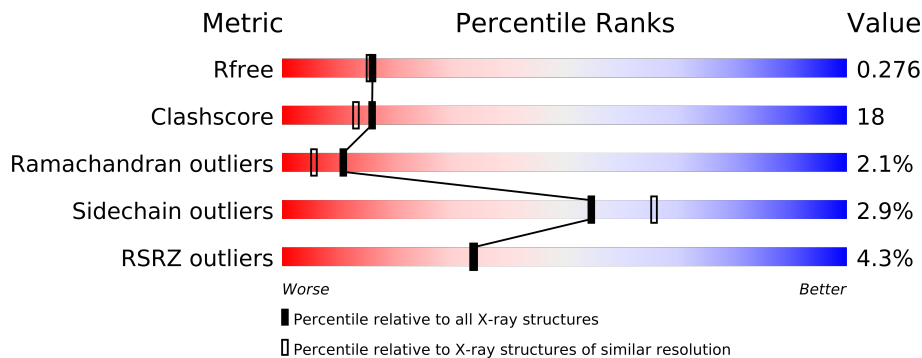
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
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)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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	427	
1	B	427	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7239 atoms, of which 0 are hydrogen 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 neurotoxin BoNT/A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	101	0	0
			3462	2230	576	648	8			
1	B	427	Total	C	N	O	S	101	0	0
			3462	2230	576	648	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	224	GLN	GLU	ENGINEERED	GB 33321098
A	366	PHE	TYR	ENGINEERED	GB 33321098
A	421	PRO	-	CLONING ARTIFACT	GB 33321098
A	422	GLY	-	CLONING ARTIFACT	GB 33321098
A	423	HIS	-	EXPRESSION TAG	GB 33321098
A	424	HIS	-	EXPRESSION TAG	GB 33321098
A	425	HIS	-	EXPRESSION TAG	GB 33321098
A	426	HIS	-	EXPRESSION TAG	GB 33321098
A	427	HIS	-	EXPRESSION TAG	GB 33321098
A	428	HIS	-	EXPRESSION TAG	GB 33321098
B	652	GLN	GLU	ENGINEERED	GB 33321098
B	794	PHE	TYR	ENGINEERED	GB 33321098
B	849	PRO	-	CLONING ARTIFACT	GB 33321098
B	850	GLY	-	CLONING ARTIFACT	GB 33321098
B	851	HIS	-	EXPRESSION TAG	GB 33321098
B	852	HIS	-	EXPRESSION TAG	GB 33321098
B	853	HIS	-	EXPRESSION TAG	GB 33321098
B	854	HIS	-	EXPRESSION TAG	GB 33321098
B	855	HIS	-	EXPRESSION TAG	GB 33321098
B	856	HIS	-	EXPRESSION TAG	GB 33321098

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is water.

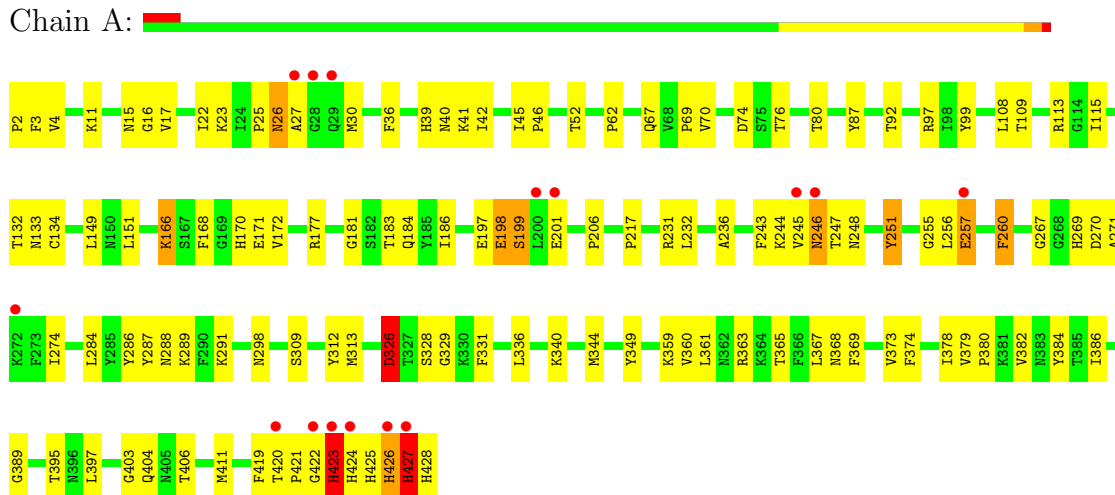
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	146	Total 146	O 146	0	0
3	B	167	Total 167	O 167	0	0

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 ($\text{RSRZ} > 2$). 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.

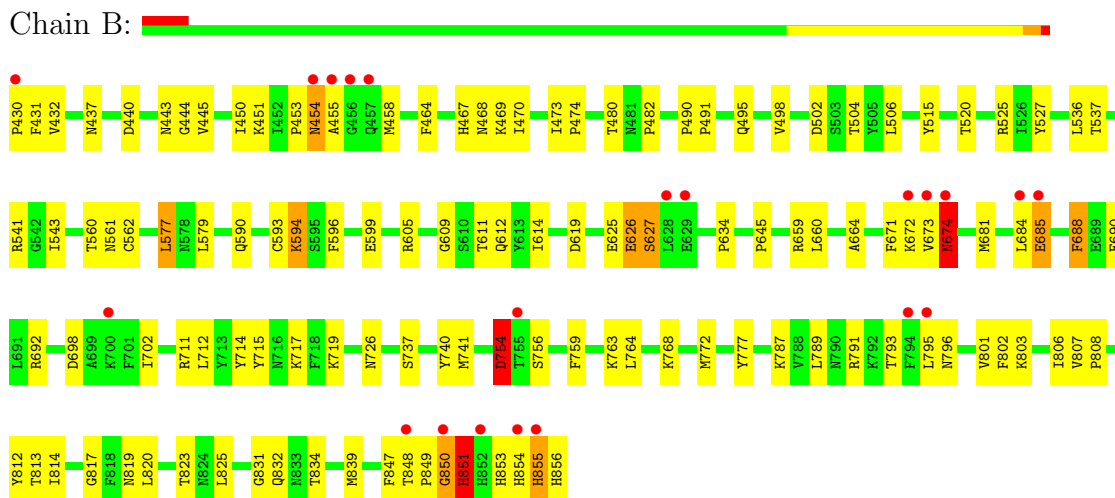
• Molecule 1: neurotoxin BoNT/A

Chain A:



• Molecule 1: neurotoxin BoNT/A

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	57.90Å 40.49Å 195.89Å 90.00° 90.25° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 49.94 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 93.2 (49.94-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.273 0.221 , 0.276	Depositor DCC
R_{free} test set	2262 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.949	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.2	EDS
Estimated twinning fraction	0.460 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 44297 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7239	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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: 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	0.55	0/3550	0.77	3/4807 (0.1%)
1	B	0.55	1/3550 (0.0%)	0.79	7/4807 (0.1%)
All	All	0.55	1/7100 (0.0%)	0.78	10/9614 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	593	CYS	CB-SG	-5.31	1.73	1.81

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	427	HIS	CA-CB-CG	-8.20	99.66	113.60
1	B	634	PRO	CA-N-CD	-7.82	100.55	111.50
1	B	674	ASN	CA-C-N	-7.41	100.89	117.20
1	B	851	HIS	N-CA-C	6.29	127.99	111.00
1	B	851	HIS	CA-C-N	-6.04	103.92	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	286	TYR	Sidechain
1	B	714	TYR	Sidechain

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	3462	0	3393	128	0
1	B	3462	0	3393	119	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	146	0	0	8	0
3	B	167	0	0	8	0
All	All	7239	0	6786	246	0

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 18.

The worst 5 of 246 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:674:ASN:HD22	1:B:674:ASN:C	1.39	1.13
1:A:421:PRO:HB2	1:A:423:HIS:NE2	1.67	1.10
1:A:365:THR:HG22	1:A:367:LEU:H	1.27	0.98
1:A:425:HIS:ND1	1:A:427:HIS:HD2	1.61	0.98
1:B:726:ASN:HD21	1:B:759:PHE:H	1.05	0.98

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	425/427 (100%)	382 (90%)	32 (8%)	11 (3%)	8	4
1	B	425/427 (100%)	387 (91%)	31 (7%)	7 (2%)	14	9
All	All	850/854 (100%)	769 (90%)	63 (7%)	18 (2%)	11	5

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	SER
1	A	247	THR
1	A	248	ASN
1	A	251	TYR
1	B	627	SER

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	382/382 (100%)	372 (97%)	10 (3%)	59	70
1	B	382/382 (100%)	370 (97%)	12 (3%)	52	63
All	All	764/764 (100%)	742 (97%)	22 (3%)	55	66

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	423	HIS
1	B	594	LYS
1	B	787	LYS
1	B	454	ASN
1	B	577	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	410	ASN
1	B	468	ASN
1	B	832	GLN

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Mol	Chain	Res	Type
1	A	424	HIS
1	A	427	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are 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.

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, 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	414/427 (96%)	0.03	15 (3%) 41 41	23, 42, 75, 101	0
1	B	414/427 (96%)	0.06	21 (5%) 27 27	21, 42, 75, 97	0
All	All	828/854 (96%)	0.04	36 (4%) 34 34	21, 42, 75, 101	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	628	LEU	8.0
1	A	422	GLY	7.6
1	A	423	HIS	7.5
1	B	850	GLY	7.2
1	A	426	HIS	5.3

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(\AA^2)	Q<0.9
2	ZN	B	857	1/1	0.12	-0.42	31,31,31,31	0
2	ZN	A	429	1/1	0.10	-1.47	30,30,30,30	0

6.5 Other polymers ⓘ

There are no such residues in this entry.