



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:12 AM UTC

PDB ID : 7EAR / pdb_00007ear
Title : A positively charged mutant Cry3Aa endotoxin
Authors : Yang, Z.; Lee, M.M.; Chan, M.K.
Deposited on : 2021-03-08
Resolution : 2.20 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
Xtrriage (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

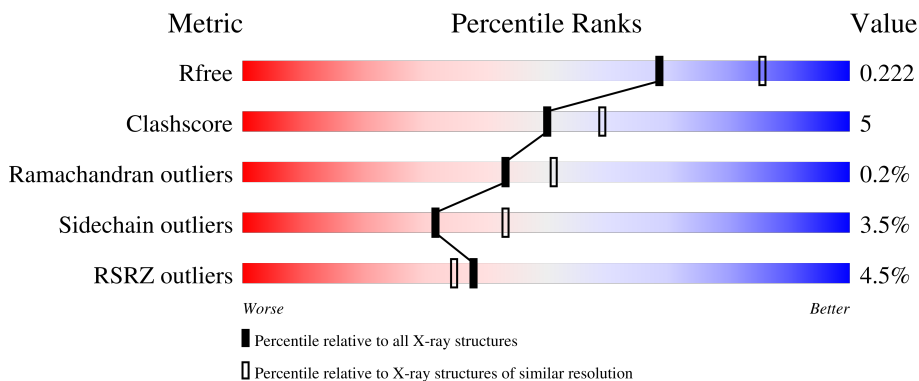
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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	644	 4% 78% 12% 9%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4914 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 Crystalline entomocidal protoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	584	4698	3018	784	886	10	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	391	LYS	ASN	engineered mutation	UNP Q9S6N9
A	395	LYS	ASN	engineered mutation	UNP Q9S6N9
A	423	LYS	GLU	engineered mutation	UNP Q9S6N9
A	430	LYS	GLN	engineered mutation	UNP Q9S6N9
A	432	LYS	ASP	engineered mutation	UNP Q9S6N9
A	433	LYS	GLU	engineered mutation	UNP Q9S6N9
A	436	LYS	THR	engineered mutation	UNP Q9S6N9
A	461	LYS	THR	engineered mutation	UNP Q9S6N9
A	462	LYS	ASP	engineered mutation	UNP Q9S6N9
A	463	LYS	GLU	engineered mutation	UNP Q9S6N9
A	466	LYS	GLU	engineered mutation	UNP Q9S6N9

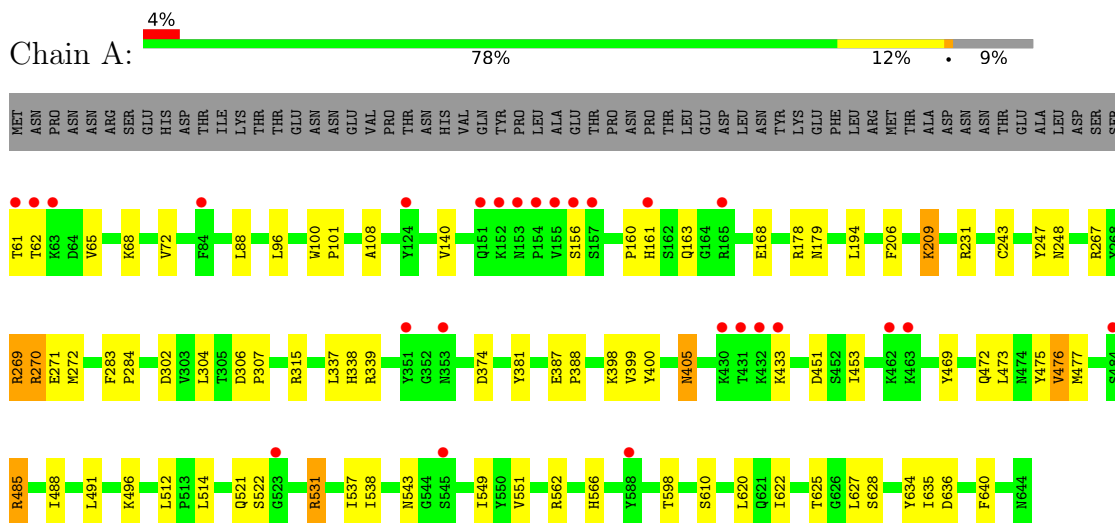
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	216	Total	O	0	0
			216	216		

3 Residue-property plots [i](#)

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: Crystalline entomocidal protoxin



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	114.84Å 132.89Å 103.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.54 – 2.20 66.54 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (66.54-2.20) 99.9 (66.54-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.180 , 0.216 0.188 , 0.222	Depositor DCC
R_{free} test set	1998 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtrriage
Anisotropy	0.079	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 31.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4914	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.77% 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](#)

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	1.07	0/4821	1.39	11/6541 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	302	ASP	CB-CA-C	6.10	119.87	109.80
1	A	622	ILE	CA-C-N	5.43	125.92	122.18
1	A	622	ILE	C-N-CA	5.43	125.92	122.18
1	A	270	ARG	NE-CZ-NH2	-5.26	114.47	119.20
1	A	522	SER	CA-C-O	-5.25	115.51	121.65
1	A	269	ARG	CA-C-O	-5.17	115.40	120.82
1	A	62	THR	CB-CA-C	5.12	117.89	109.90
1	A	179	ASN	CA-C-N	5.02	127.42	120.29
1	A	179	ASN	C-N-CA	5.02	127.42	120.29
1	A	374	ASP	CA-C-N	5.01	127.29	120.63
1	A	374	ASP	C-N-CA	5.01	127.29	120.63

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	4698	0	4597	49	0
2	A	216	0	0	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4914	0	4597	49	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 (49) 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:543:ASN:HD21	1:A:627:LEU:H	1.21	0.89
1:A:476:VAL:HG22	1:A:491:LEU:HD22	1.58	0.85
1:A:160:PRO:HA	1:A:163:GLN:HE21	1.46	0.79
1:A:194:LEU:HD23	1:A:272:MET:HE3	1.72	0.71
1:A:512:LEU:HD11	1:A:551:VAL:HG12	1.74	0.70
1:A:543:ASN:HD22	1:A:625:THR:HA	1.57	0.68
1:A:248:ASN:OD1	1:A:531:ARG:NH1	2.27	0.66
1:A:96:LEU:HD21	1:A:140:VAL:HG12	1.77	0.66
1:A:178:ARG:HD3	1:A:231:ARG:HD3	1.83	0.60
1:A:485:ARG:CG	1:A:485:ARG:HH11	2.16	0.59
1:A:485:ARG:HH11	1:A:485:ARG:HG3	1.68	0.59
1:A:475:TYR:HE2	1:A:477:MET:HE3	1.70	0.57
1:A:270:ARG:HD2	2:A:757:HOH:O	2.03	0.56
1:A:381:TYR:CZ	1:A:477:MET:HE2	2.40	0.56
1:A:543:ASN:ND2	1:A:625:THR:HA	2.20	0.56
1:A:398:LYS:HG2	1:A:472:GLN:HE22	1.71	0.55
1:A:65:VAL:CG1	1:A:108:ALA:HB1	2.36	0.54
1:A:514:LEU:HD13	1:A:635:ILE:HG22	1.92	0.51
1:A:315:ARG:NH1	2:A:704:HOH:O	2.45	0.50
1:A:566:HIS:HD2	1:A:636:ASP:OD2	1.95	0.50
1:A:399:VAL:O	1:A:472:GLN:HA	2.12	0.49
1:A:304:LEU:HD12	1:A:304:LEU:N	2.28	0.49
1:A:566:HIS:HE1	2:A:913:HOH:O	1.95	0.49
1:A:61:THR:HA	1:A:271:GLU:OE2	2.15	0.46
1:A:100:TRP:N	1:A:101:PRO:CD	2.78	0.46
1:A:194:LEU:HD11	1:A:243:CYS:HA	1.97	0.46
1:A:61:THR:HG23	1:A:267:ARG:HD3	1.98	0.46
1:A:269:ARG:HD3	2:A:805:HOH:O	2.16	0.45
1:A:206:PHE:O	1:A:209:LYS:HG3	2.17	0.43
1:A:307:PRO:HB3	1:A:488:ILE:CG2	2.48	0.43
1:A:475:TYR:CE2	1:A:477:MET:HE3	2.53	0.43
1:A:451:ASP:CG	1:A:453:ILE:HG13	2.44	0.42
1:A:433:LYS:HA	1:A:433:LYS:HD3	1.87	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:TYR:HE2	1:A:531:ARG:NH1	2.16	0.42
1:A:338:HIS:HD2	2:A:877:HOH:O	2.02	0.42
1:A:543:ASN:HD21	1:A:627:LEU:N	2.02	0.42
1:A:514:LEU:HB3	1:A:538:ILE:HG12	2.01	0.42
1:A:68:LYS:O	1:A:72:VAL:HG23	2.19	0.42
1:A:387:GLU:HB3	1:A:388:PRO:HD2	2.03	0.41
1:A:451:ASP:OD1	1:A:453:ILE:HG13	2.20	0.41
1:A:512:LEU:CD1	1:A:551:VAL:HG12	2.47	0.41
1:A:620:LEU:HD22	1:A:640:PHE:HZ	1.85	0.41
1:A:512:LEU:HD23	1:A:512:LEU:HA	1.93	0.41
1:A:398:LYS:HG2	1:A:472:GLN:NE2	2.36	0.41
1:A:400:TYR:HB2	1:A:469:TYR:CG	2.55	0.41
1:A:283:PHE:HB2	1:A:284:PRO:HD3	2.03	0.41
1:A:537:ILE:HD12	1:A:634:TYR:HB3	2.03	0.41
1:A:405:ASN:HD22	1:A:405:ASN:N	2.20	0.40
1:A:270:ARG:NH2	1:A:306:ASP:OD1	2.44	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	582/644 (90%)	565 (97%)	16 (3%)	1 (0%)	43 51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	531	ARG

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	514/571 (90%)	496 (96%)	18 (4%)	32 43

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LEU
1	A	156	SER
1	A	161	HIS
1	A	168	GLU
1	A	209	LYS
1	A	337	LEU
1	A	339	ARG
1	A	405	ASN
1	A	473	LEU
1	A	476	VAL
1	A	485	ARG
1	A	496	LYS
1	A	521	GLN
1	A	549	ILE
1	A	562	ARG
1	A	598	THR
1	A	610	SER
1	A	628	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	119	GLN
1	A	127	ASN
1	A	134	GLN
1	A	139	ASN
1	A	151	GLN
1	A	153	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	163	GLN
1	A	176	HIS
1	A	232	GLN
1	A	326	ASN
1	A	338	HIS
1	A	347	GLN
1	A	405	ASN
1	A	437	GLN
1	A	472	GLN
1	A	539	GLN
1	A	543	ASN
1	A	566	HIS
1	A	586	GLN
1	A	644	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](#)

There are no ligands in this entry.

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	584/644 (90%)	-0.03	26 (4%) 38 35	18, 29, 52, 90	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	61	THR	6.6
1	A	62	THR	5.3
1	A	155	VAL	3.7
1	A	84	PHE	3.7
1	A	588	TYR	3.6
1	A	124	TYR	3.3
1	A	156	SER	3.1
1	A	351	TYR	3.1
1	A	462	LYS	3.0
1	A	433	LYS	2.7
1	A	430	LYS	2.7
1	A	154	PRO	2.7
1	A	63	LYS	2.6
1	A	431	THR	2.4
1	A	463	LYS	2.4
1	A	165	ARG	2.4
1	A	152	LYS	2.4
1	A	523	GLY	2.3
1	A	157	SER	2.3
1	A	545	SER	2.2
1	A	153	ASN	2.2
1	A	353	ASN	2.1
1	A	432	LYS	2.1
1	A	151	GLN	2.1
1	A	161	HIS	2.1
1	A	484	SER	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.