



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:42 PM UTC

PDB ID : 6LFP / pdb_00006lfp
Title : Cry3Aa protein for enzyme entrapment
Authors : Heater, B.S.; Chan, M.K.
Deposited on : 2019-12-03
Resolution : 3.31 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

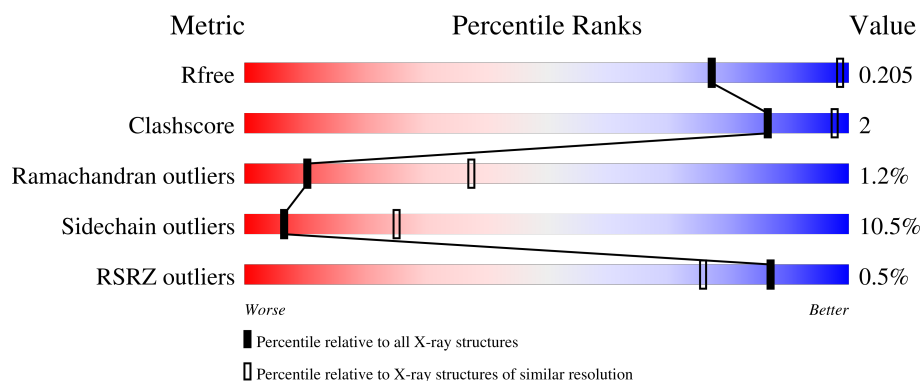
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)

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	 77% 12% • 10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4676 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.

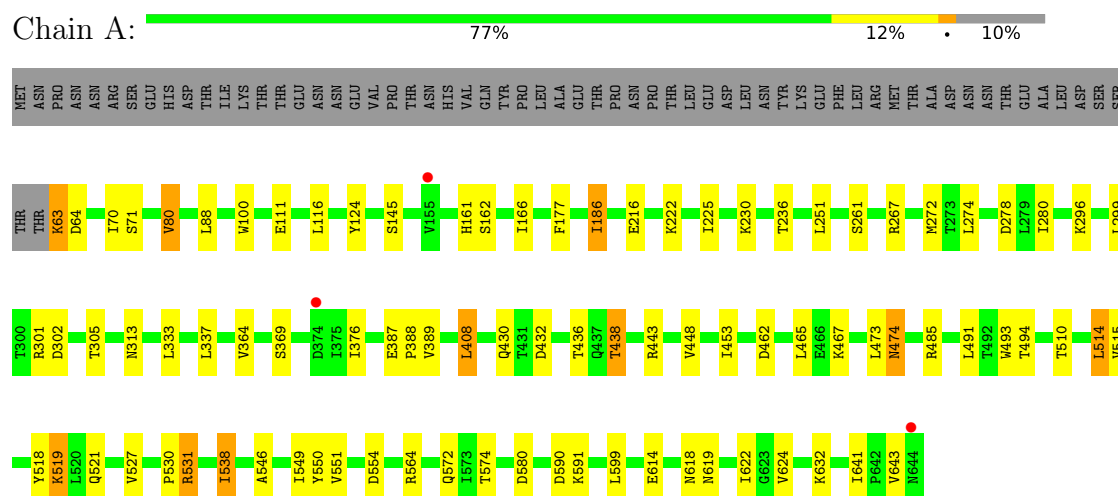
- Molecule 1 is a protein called Cry3Aa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	582	4676	2993	774	899	10	0	0	0

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: Cry3Aa protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	116.35Å 132.61Å 102.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.34 – 3.31 38.34 – 3.31	Depositor EDS
% Data completeness (in resolution range)	98.7 (38.34-3.31) 98.7 (38.34-3.31)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.93 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.157 , 0.209 0.162 , 0.205	Depositor DCC
R_{free} test set	615 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 23.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4676	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.54% 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	0.90	0/4799	1.09	8/6524 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	80	VAL	CB-CA-C	5.69	119.34	111.38
1	A	438	THR	N-CA-C	5.63	118.37	108.75
1	A	236	THR	N-CA-C	-5.50	104.67	111.33
1	A	177	PHE	N-CA-C	5.35	116.79	111.07
1	A	80	VAL	N-CA-C	-5.34	100.95	109.17
1	A	448	VAL	N-CA-CB	5.24	116.76	110.31
1	A	186	ILE	N-CA-C	-5.16	102.93	109.58
1	A	443	ARG	N-CA-C	5.12	117.14	108.02

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	4676	0	4506	19	0
All	All	4676	0	4506	19	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 2.

All (19) 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:564:ARG:HD3	1:A:641:ILE:HD11	1.75	0.68
1:A:514:LEU:HD11	1:A:622:ILE:HD13	1.90	0.54
1:A:474:ASN:HB3	1:A:494:THR:HG23	1.90	0.53
1:A:116:LEU:HD21	1:A:267:ARG:HG2	1.92	0.52
1:A:453:ILE:HD11	1:A:465:LEU:HD21	1.91	0.52
1:A:408:LEU:HD12	1:A:408:LEU:C	2.37	0.49
1:A:518:TYR:OH	1:A:619:ASN:OD1	2.24	0.48
1:A:530:PRO:O	1:A:531:ARG:HB2	2.14	0.47
1:A:514:LEU:HB3	1:A:538:ILE:HD13	1.97	0.46
1:A:453:ILE:HD11	1:A:465:LEU:HD11	1.97	0.46
1:A:296:LYS:HD3	1:A:510:THR:HG23	1.98	0.46
1:A:550:TYR:CZ	1:A:618:ASN:OD1	2.69	0.45
1:A:70:ILE:HD11	1:A:274:LEU:HD13	1.99	0.45
1:A:305:THR:HG23	1:A:493:TRP:CD1	2.54	0.42
1:A:313:ASN:C	1:A:313:ASN:OD1	2.62	0.42
1:A:63:LYS:O	1:A:64:ASP:C	2.63	0.41
1:A:278:ASP:CG	1:A:301:ARG:HE	2.29	0.41
1:A:387:GLU:HB3	1:A:388:PRO:HD2	2.03	0.40
1:A:622:ILE:HD12	1:A:622:ILE:N	2.36	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	580/644 (90%)	544 (94%)	29 (5%)	7 (1%)	10 37

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	432	ASP
1	A	531	ARG
1	A	580	ASP
1	A	462	ASP
1	A	519	LYS
1	A	546	ALA
1	A	100	TRP

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	512/571 (90%)	458 (90%)	54 (10%)	6	25

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	LYS
1	A	71	SER
1	A	80	VAL
1	A	88	LEU
1	A	111	GLU
1	A	124	TYR
1	A	145	SER
1	A	161	HIS
1	A	162	SER
1	A	166	ILE
1	A	186	ILE
1	A	216	GLU
1	A	222	LYS
1	A	225	ILE
1	A	230	LYS
1	A	251	LEU
1	A	261	SER
1	A	272	MET
1	A	280	ILE
1	A	299	LEU

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Mol	Chain	Res	Type
1	A	302	ASP
1	A	333	LEU
1	A	337	LEU
1	A	364	VAL
1	A	369	SER
1	A	376	ILE
1	A	389	VAL
1	A	408	LEU
1	A	430	GLN
1	A	436	THR
1	A	438	THR
1	A	467	LYS
1	A	473	LEU
1	A	474	ASN
1	A	485	ARG
1	A	491	LEU
1	A	514	LEU
1	A	515	VAL
1	A	519	LYS
1	A	521	GLN
1	A	527	VAL
1	A	538	ILE
1	A	549	ILE
1	A	551	VAL
1	A	554	ASP
1	A	572	GLN
1	A	574	THR
1	A	590	ASP
1	A	591	LYS
1	A	599	LEU
1	A	614	GLU
1	A	624	VAL
1	A	632	LYS
1	A	643	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	159	ASN
1	A	163	GLN
1	A	338	HIS

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Mol	Chain	Res	Type
1	A	341	GLN
1	A	343	HIS
1	A	347	GLN
1	A	362	ASN
1	A	572	GLN
1	A	602	ASN
1	A	621	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	582/644 (90%)	-0.44	3 (0%) 87 76	15, 32, 58, 87	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	374	ASP	2.8
1	A	155	VAL	2.5
1	A	644	ASN	2.1

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.