



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 09:50 AM EDT

PDB ID : 231L
Title : T4 LYSOZYME MUTANT M106K
Authors : Lipscomb, L.A.; Drew, D.L.; Gassner, N.; Baase, W.A.; Matthews, B.W.
Deposited on : 1997-10-03
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

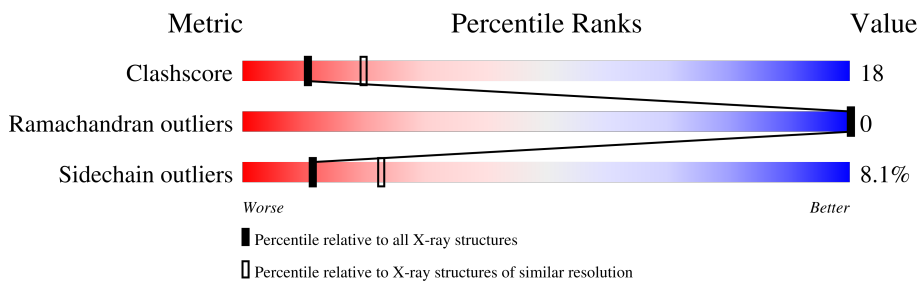
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	164	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1322 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 T4 LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	1293	815	236	238	4	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	THR	CYS	engineered mutation	UNP P00720
A	97	ALA	CYS	engineered mutation	UNP P00720
A	106	LYS	MET	engineered mutation	UNP P00720

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is water.

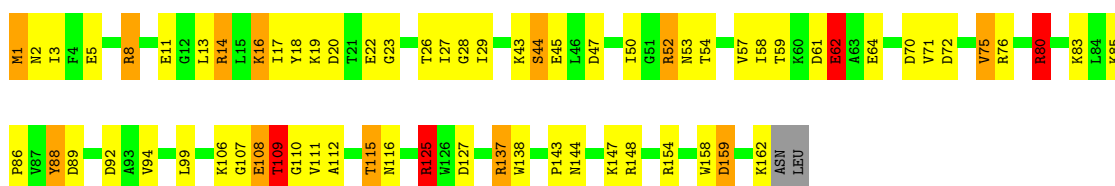
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	28	Total	O	0	0
			28	28		

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. 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. 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: T4 LYSOZYME

Chain A:  57% 32% 7% ..



4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	61.02Å 61.02Å 96.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.50 22.17 – 1.91	Depositor EDS
% Data completeness (in resolution range)	93.0 (30.00-2.50) 86.8 (22.17-1.91)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.90 (at 1.92Å)	Xtrriage
Refinement program	TNT	Depositor
R, R_{free}	0.177 , (Not available) 0.165 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	13.6	Xtrriage
Anisotropy	0.150	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 100.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.059 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1322	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.24% 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:
CL

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	1.17	6/1313 (0.5%)	1.74	33/1768 (1.9%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	62	GLU	CD-OE2	6.54	1.32	1.25
1	A	64	GLU	CD-OE2	6.20	1.32	1.25
1	A	108	GLU	CD-OE2	6.09	1.32	1.25
1	A	22	GLU	CD-OE2	5.87	1.32	1.25
1	A	11	GLU	CD-OE2	5.68	1.31	1.25
1	A	45	GLU	CD-OE2	5.02	1.31	1.25

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	ASP	CB-CG-OD2	-8.89	110.30	118.30
1	A	148	ARG	NE-CZ-NH1	8.69	124.64	120.30
1	A	70	ASP	CB-CG-OD1	8.31	125.78	118.30
1	A	89	ASP	CB-CG-OD2	-8.19	110.93	118.30
1	A	72	ASP	CB-CG-OD2	-8.08	111.03	118.30
1	A	92	ASP	CB-CG-OD1	7.99	125.49	118.30
1	A	8	ARG	NE-CZ-NH1	7.71	124.16	120.30
1	A	20	ASP	CB-CG-OD1	7.63	125.17	118.30
1	A	80	ARG	NE-CZ-NH1	7.21	123.91	120.30
1	A	127	ASP	CB-CG-OD1	7.12	124.71	118.30
1	A	76	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	A	72	ASP	CB-CG-OD1	6.99	124.59	118.30
1	A	89	ASP	CB-CG-OD1	6.87	124.48	118.30
1	A	109	THR	CA-CB-CG2	-6.84	102.83	112.40
1	A	54	THR	CA-CB-CG2	-6.50	103.30	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	ASP	CB-CG-OD1	6.45	124.10	118.30
1	A	52	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	A	125	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	A	127	ASP	CB-CG-OD2	-6.29	112.64	118.30
1	A	61	ASP	CB-CG-OD2	-6.18	112.74	118.30
1	A	61	ASP	CB-CG-OD1	6.14	123.82	118.30
1	A	70	ASP	CB-CG-OD2	-6.07	112.84	118.30
1	A	94	VAL	CG1-CB-CG2	-5.91	101.45	110.90
1	A	137	ARG	NE-CZ-NH2	-5.73	117.44	120.30
1	A	88	TYR	CB-CG-CD2	-5.72	117.57	121.00
1	A	80	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	1	MET	CG-SD-CE	-5.64	91.17	100.20
1	A	88	TYR	N-CA-CB	-5.58	100.55	110.60
1	A	159	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	A	75	VAL	CA-CB-CG2	-5.43	102.75	110.90
1	A	20	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	A	115	THR	CA-CB-CG2	-5.40	104.84	112.40
1	A	47	ASP	CB-CG-OD1	5.34	123.11	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1293	0	1323	48	0
2	A	1	0	0	1	0
3	A	28	0	0	1	0
All	All	1322	0	1323	48	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 18.

All (48) 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:159:ASP:HA	1:A:162:LYS:HE2	1.50	0.93
1:A:143:PRO:O	1:A:147:LYS:HG3	1.84	0.77
1:A:1:MET:HA	1:A:5:GLU:OE1	1.85	0.77
1:A:107:GLY:O	1:A:111:VAL:HG23	1.89	0.73
1:A:88:TYR:HD1	1:A:99:LEU:HD23	1.57	0.69
1:A:8:ARG:HG3	1:A:8:ARG:HH11	1.57	0.67
1:A:80:ARG:CB	1:A:80:ARG:HH11	2.08	0.66
1:A:80:ARG:HH11	1:A:80:ARG:HB2	1.62	0.64
1:A:1:MET:HG3	1:A:2:ASN:N	2.18	0.58
1:A:125:ARG:CG	1:A:125:ARG:HH11	2.17	0.58
1:A:1:MET:HG2	1:A:158:TRP:CE3	2.40	0.56
1:A:115:THR:HG22	1:A:116:ASN:N	2.19	0.56
1:A:159:ASP:CA	1:A:162:LYS:HE2	2.30	0.55
1:A:125:ARG:HH11	1:A:125:ARG:HG3	1.73	0.54
1:A:19:LYS:HD3	1:A:23:GLY:O	2.06	0.54
1:A:80:ARG:HB2	1:A:80:ARG:NH1	2.23	0.54
1:A:1:MET:HG2	1:A:158:TRP:CD2	2.44	0.53
1:A:144:ASN:N	1:A:144:ASN:OD1	2.36	0.53
1:A:106:LYS:HE3	1:A:138:TRP:HB2	1.91	0.53
1:A:144:ASN:HB2	2:A:173:CL:CL	2.47	0.51
1:A:159:ASP:HA	1:A:162:LYS:CE	2.33	0.51
1:A:13:LEU:C	1:A:14:ARG:HG2	2.32	0.51
1:A:159:ASP:OD1	1:A:162:LYS:NZ	2.30	0.50
1:A:8:ARG:HG3	1:A:8:ARG:NH1	2.24	0.49
1:A:27:ILE:HG13	1:A:28:GLY:H	1.77	0.49
1:A:8:ARG:HG3	1:A:8:ARG:O	2.13	0.48
1:A:13:LEU:HD12	1:A:14:ARG:N	2.28	0.48
1:A:88:TYR:CD1	1:A:99:LEU:HD23	2.45	0.48
1:A:85:LYS:N	1:A:86:PRO:CD	2.77	0.47
1:A:59:THR:H	1:A:62:GLU:HG3	1.80	0.47
1:A:108:GLU:O	1:A:112:ALA:N	2.39	0.46
1:A:43:LYS:O	1:A:44:SER:C	2.54	0.46
1:A:125:ARG:CG	1:A:125:ARG:NH1	2.79	0.46
1:A:26:THR:HG22	1:A:27:ILE:N	2.32	0.45
1:A:59:THR:N	1:A:62:GLU:HG3	2.32	0.45
1:A:109:THR:O	1:A:110:GLY:C	2.54	0.45
1:A:143:PRO:HG2	3:A:291:HOH:O	2.18	0.44
1:A:16:LYS:HG3	1:A:17:ILE:N	2.32	0.43
1:A:13:LEU:HD13	1:A:29:ILE:HG13	2.00	0.43
1:A:3:ILE:HD12	1:A:3:ILE:HA	1.73	0.42
1:A:27:ILE:CG1	1:A:28:GLY:N	2.83	0.41
1:A:85:LYS:N	1:A:86:PRO:HD2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:VAL:O	1:A:112:ALA:C	2.58	0.41
1:A:18:TYR:CZ	1:A:26:THR:HG22	2.56	0.41
1:A:52:ARG:HH11	1:A:52:ARG:HG3	1.85	0.41
1:A:57:VAL:HG12	1:A:58:ILE:N	2.36	0.41
1:A:71:VAL:O	1:A:75:VAL:HG23	2.22	0.40
1:A:137:ARG:O	1:A:137:ARG:HG2	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	160/164 (98%)	152 (95%)	8 (5%)	0	100 100

There are no Ramachandran outliers to report.

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	135/137 (98%)	124 (92%)	11 (8%)	11 23

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	16	LYS
1	A	44	SER
1	A	50	ILE
1	A	53	ASN
1	A	62	GLU
1	A	80	ARG
1	A	83	LYS
1	A	109	THR
1	A	125	ARG
1	A	154	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN

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 monosaccharides 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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.