Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 06:33 PM BST

PDB ID	:	1L66
Title	:	TOLERANCE OF T4 LYSOZYME TO MULTIPLE XAA (RIGHT ARROW) ALA SUBSTITUTIONS: A POLYALANINE ALPHA-HELIX CONTAINING TEN CONSECUTIVE ALANINES
Authors	:	Heinz, D.; Matthews, B.W.
Deposited on	:	1991-09-23
Resolution	:	1.70 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 following versions of software and data (see references ⓘ) were used in the production of this report:

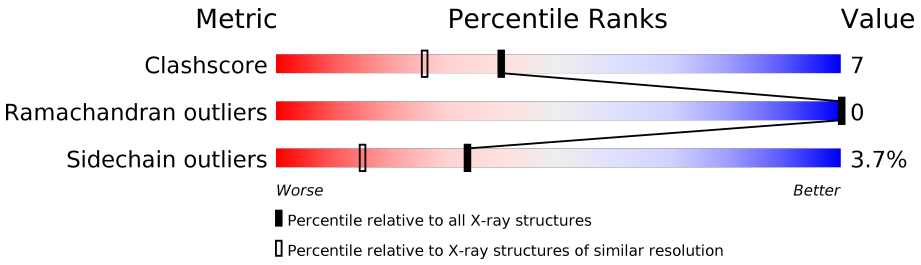
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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 on 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	164	77% 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1438 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 LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1288	811	234	238	5			

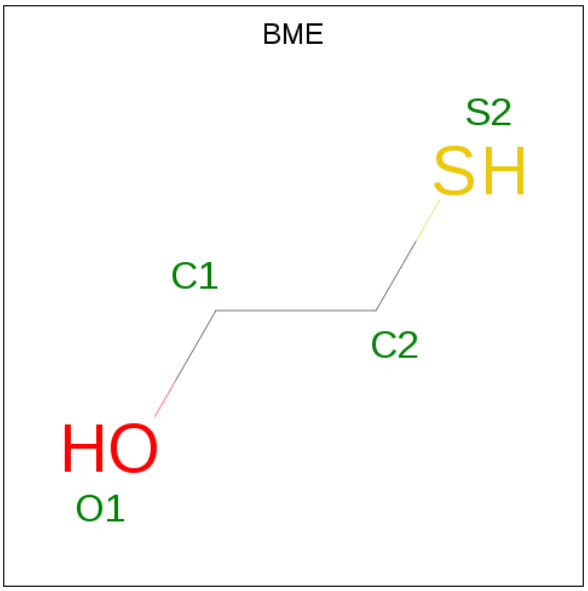
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	ALA	LYS	conflict	UNP P00720
A	54	THR	CYS	conflict	UNP P00720
A	97	ALA	CYS	conflict	UNP P00720

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

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

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O S 4 2 1 1	0	0
3	A	1	Total C O S 4 2 1 1	0	0

- Molecule 4 is water.

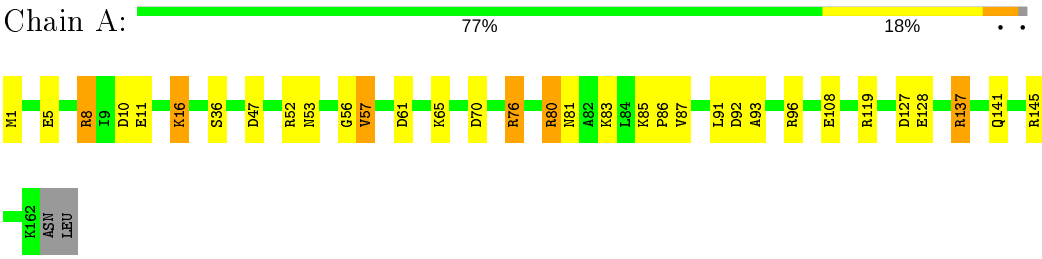
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	140	Total O 140 140	0	0

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. 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: LYSOZYME

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	60.90Å 60.90Å 97.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 1.70 52.74 – 1.62	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-1.70) 77.6 (52.74-1.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.14 (at 1.62Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.158 , (Not available) 0.209 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	15.4	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 92.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.052 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1438	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.31% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, BME

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	0.98	1/1308 (0.1%)	1.53	23/1763 (1.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	11	GLU	CD-OE2	5.93	1.32	1.25

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	127	ASP	CB-CG-OD1	11.38	128.55	118.30
1	A	47	ASP	CB-CG-OD2	-11.05	108.36	118.30
1	A	80	ARG	NE-CZ-NH2	-10.91	114.84	120.30
1	A	80	ARG	NE-CZ-NH1	10.57	125.59	120.30
1	A	8	ARG	NE-CZ-NH1	9.92	125.26	120.30
1	A	127	ASP	CB-CG-OD2	-9.31	109.92	118.30
1	A	47	ASP	CB-CG-OD1	8.58	126.03	118.30
1	A	70	ASP	CB-CG-OD1	8.26	125.73	118.30
1	A	70	ASP	CB-CG-OD2	-7.57	111.49	118.30
1	A	96	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	A	154	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	A	10	ASP	CB-CG-OD2	-6.92	112.07	118.30
1	A	96	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	A	61	ASP	CB-CG-OD2	-6.50	112.45	118.30
1	A	92	ASP	CB-CG-OD2	-6.47	112.47	118.30
1	A	8	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	A	92	ASP	CB-CG-OD1	5.99	123.69	118.30
1	A	145	ARG	CD-NE-CZ	-5.89	115.36	123.60
1	A	137	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	A	61	ASP	CB-CG-OD1	5.26	123.03	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	52	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	57	VAL	CA-CB-CG2	-5.15	103.17	110.90
1	A	119	ARG	NE-CZ-NH1	5.08	122.84	120.30

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	1288	0	1311	19	0
2	A	2	0	0	0	0
3	A	8	0	9	1	1
4	A	140	0	0	3	0
All	All	1438	0	1320	19	1

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 7.

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:16:LYS:HE3	1:A:57:VAL:HG23	1.62	0.81
1:A:65:LYS:HG3	4:A:320:HOH:O	1.81	0.77
1:A:128:GLU:HG3	4:A:311:HOH:O	1.96	0.65
1:A:1:MET:HG2	1:A:158:TRP:CE3	2.40	0.56
1:A:80:ARG:NH2	4:A:242:HOH:O	2.39	0.55
1:A:16:LYS:HE2	1:A:56:GLY:O	2.09	0.53
1:A:8:ARG:O	1:A:8:ARG:HG3	2.07	0.51
1:A:16:LYS:HD2	1:A:57:VAL:CG2	2.44	0.47
1:A:1:MET:HG2	1:A:158:TRP:CD2	2.51	0.46
1:A:85:LYS:N	1:A:86:PRO:CD	2.79	0.45
1:A:1:MET:HA	1:A:5:GLU:OE1	2.17	0.44
1:A:76:ARG:NH1	1:A:76:ARG:HB2	2.34	0.43
1:A:76:ARG:NH1	1:A:76:ARG:CB	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ARG:HH11	1:A:8:ARG:HG3	1.84	0.41
1:A:81:ASN:ND2	1:A:108:GLU:HG2	2.35	0.41
1:A:93:ALA:HB1	3:A:902:BME:H11	2.03	0.41
1:A:137:ARG:CZ	1:A:141:GLN:HG3	2.50	0.41
1:A:16:LYS:HE3	1:A:57:VAL:CG2	2.42	0.41
1:A:87:VAL:O	1:A:91:LEU:HG	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:901:BME:O1	3:A:901:BME:O1[5_555]	1.91	0.29

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%)	158 (99%)	2 (1%)	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	134/136 (98%)	129 (96%)	5 (4%)	34 15

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	36	SER
1	A	53	ASN
1	A	76	ARG
1	A	83	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	123	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	BME	A	902	3	3,3,3	1.54	1 (33%)	1,2,2	0.22	0
3	BME	A	901	3	3,3,3	1.33	0	1,2,2	0.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BME	A	902	3	-	0/1/1/1	-
3	BME	A	901	3	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	902	BME	C2-S2	-2.31	1.72	1.80

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	902	BME	1	0
3	A	901	BME	0	1

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.