

Full wwPDB X-ray Structure Validation Report (i)

Mar 4, 2021 – 04:13 PM EST

PDB ID : 1JSE

Title : FULL-MATRIX LEAST-SQUARES REFINEMENT OF TURKEY

LYSOZYME

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Deposited on : 1998-01-05

Resolution : 1.12 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.17.1

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)

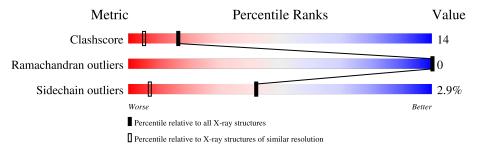
 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.17.1 \end{tabular}$

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 1.12 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)

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 <=5%

Mol	Chain	Length	Quality of chain		
1	A	129	82%	14%	••



2 Entry composition (i)

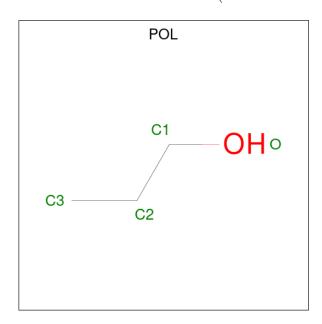
There are 3 unique types of molecules in this entry. The entry contains 1181 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	129	Total 1016	C 623	N 198	O 185	S 10	0	5	0

• Molecule 2 is N-PROPANOL (three-letter code: POL) (formula: C₃H₈O).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	A	1	Total 8	C 6	O 2	0	1

• Molecule 3 is water.

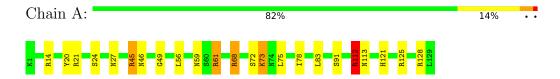
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	143	Total O 157 157	0	12



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	38.15Å 33.32Å 46.24Å	Donositor
a, b, c, α , β , γ	90.00° 110.14° 90.00°	Depositor
Resolution (Å)	22.30 - 1.12	Depositor
Resolution (A)	22.27 - 1.12	EDS
% Data completeness	86.1 (22.30-1.12)	Depositor
(in resolution range)	85.9 (22.27-1.12)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.06 (at 1.12Å)	Xtriage
Refinement program	SHELXL-93, X-PLOR	Depositor
D D.	0.104 , 0.140	Depositor
R, R_{free}	0.170 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	10.9	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.11 , 132.3	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	1181	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 16.71% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: POL

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).

Mal	Chain	Bond	lengths	Bond angles		
IVIOI	Mol Chain		RMSZ # Z > 5		# Z > 5	
1	A	0.75	0/1057	0.94	2/1426 (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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^{o})$
1	A	68	ARG	NE-CZ-NH1	-7.43	116.58	120.30
1	A	68	ARG	NE-CZ-NH2	6.44	123.52	120.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	ARG	Sidechain
1	A	125	ARG	Sidechain
1	A	14	ARG	Sidechain
1	A	45	ARG	Sidechain
1	A	61	ARG	Sidechain
1	A	68	ARG	Sidechain



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	1016	0	978	29	0
2	A	8	0	16	3	0
3	A	157	0	0	6	0
All	All	1181	0	994	29	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 14.

All (29) 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:73:LYS:O	1:A:73:LYS:HD3	` '	1.28
		1.32	
1:A:45:ARG:HH22	1:A:49:GLY:C	1.34	1.28
1:A:113:ASN:HB3	3:A:286:HOH:O	1.36	1.20
1:A:45:ARG:NH2	1:A:49:GLY:C	2.09	1.04
1:A:73:LYS:HD3	1:A:73:LYS:C	1.91	0.88
1:A:56:LEU:HD12	3:A:318:HOH:O	1.75	0.86
1:A:73:LYS:HD2	1:A:75:LEU:CD2	2.06	0.85
1:A:73:LYS:HD2	1:A:75:LEU:HG	1.70	0.72
1:A:73:LYS:O	1:A:73:LYS:CD	2.27	0.70
1:A:45:ARG:HH22	1:A:49:GLY:CA	2.07	0.68
1:A:73:LYS:HD2	1:A:75:LEU:CG	2.24	0.67
1:A:45:ARG:NH2	1:A:49:GLY:CA	2.57	0.67
1:A:46:ASN:OD1	1:A:59[B]:ASN:OD1	2.13	0.66
1:A:27:ASN:HD21	2:A:130[B]:POL:H31	1.62	0.64
1:A:72:SER:HB2	3:A:326:HOH:O	1.98	0.63
1:A:121:HIS:HB3	3:A:310:HOH:O	2.03	0.59
1:A:91:SER:HB3	3:A:318:HOH:O	2.03	0.57
1:A:112:ARG:O	1:A:112:ARG:HD3	2.04	0.57
1:A:20:TYR:CE2	1:A:21[B]:ARG:HG3	2.44	0.53
1:A:27:ASN:HD21	2:A:130[B]:POL:C3	2.22	0.53
1:A:59[B]:ASN:ND2	1:A:61:ARG:H	2.06	0.53
1:A:78:ILE:CD1	1:A:83:LEU:HD21	2.40	0.52
1:A:73:LYS:HE2	3:A:307:HOH:O	2.09	0.51
1:A:73:LYS:HD2	1:A:75:LEU:HD23	1.91	0.49

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Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{($\mathring{\mathbf{A}}$)} \end{aligned}$	Clash overlap (Å)
1:A:45:ARG:NH2	1:A:49:GLY:O	2.30	0.49
1:A:59[B]:ASN:ND2	1:A:61:ARG:HB3	2.28	0.48
1:A:24:SER:OG	2:A:130[A]:POL:H22	2.14	0.47
1:A:73:LYS:HD2	1:A:75:LEU:HD21	1.95	0.47
1:A:45:ARG:NH2	1:A:49:GLY:HA2	2.31	0.45

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			
1	A	132/129 (102%)	130 (98%)	2 (2%)	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	108/103 (105%)	104 (96%)	4 (4%)	34 4		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	LYS

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Mol	Chain	Res	Type
1	A	112	ARG
1	A	128[A]	ARG
1	A	128[B]	ARG

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

Mol	Chain	Res	Type
1	A	37	ASN
1	A	113	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

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	Trunc	Chain	Dag	Link	\mathbf{B}_{i}	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	POL	A	130[B]	-	3,3,3	0.38	0	2,2,2	0.22	0
2	POL	A	130[A]	-	3,3,3	0.71	0	2,2,2	0.79	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
2	POL	A	130[B]	-	-	0/1/1/1	-
2	POL	A	130[A]	-	-	0/1/1/1	-

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	130[B]	POL	2	0
2	A	130[A]	POL	1	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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

