



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 02:37 PM GMT

PDB ID : 2LZH
Title : THE STRUCTURES OF THE MONOCLINIC AND ORTHORHOMBIC FORMS OF HEN EGG-WHITE LYSOZYME AT 6 ANGSTROMS RESOLUTION.
Authors : Artymiuk, P.J.; Blake, C.C.F.; Rice, D.W.; Wilson, K.S.
Deposited on : 1981-06-29
Resolution : 6.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

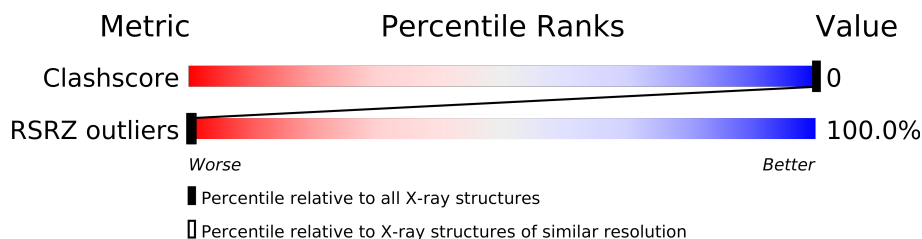
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 6.00 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	79885	1024 (8.20-3.52)
RSRZ outliers	66119	1088 (8.20-3.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	129	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 129 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

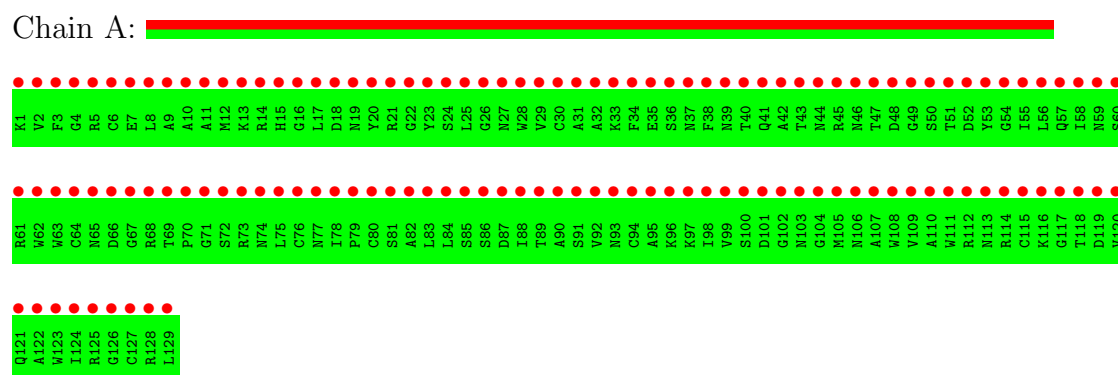
- Molecule 1 is a protein called HEN EGG WHITE LYSOZYME.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
1	A	129	Total 129	C 129	0	0	129

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: HEN EGG WHITE LYSOZYME



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.40Å 68.70Å 30.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 6.00 25.40 – 5.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-6.00) 99.5 (25.40-5.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	71.40 (at 6.02Å)	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available) 0.638 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	16.5	Xtriage
Anisotropy	4.938	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.92 , 282.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 398 reflections	Xtriage
F_o, F_c correlation	0.60	EDS
Total number of atoms	129	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	$\# Z > 5$

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	129	0	0	0	0
All	All	129	0	0	0	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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 ⓘ

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	129/129 (100%)	10.17	129 (100%) 0 0	0, 0, 0, 0	0

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	118	THR	28.7
1	A	76	CYS	25.7
1	A	119	ASP	23.3
1	A	113	ASN	20.6
1	A	15	HIS	20.2
1	A	79	PRO	18.7
1	A	73	ARG	18.7
1	A	34	PHE	18.2
1	A	114	ARG	17.6
1	A	40	THR	17.3
1	A	121	GLN	16.8
1	A	43	THR	16.3
1	A	115	CYS	15.6
1	A	35	GLU	15.5
1	A	94	CYS	15.4
1	A	20	TYR	15.2
1	A	120	VAL	14.9
1	A	45	ARG	14.2
1	A	62	TRP	14.1
1	A	42	ALA	13.3
1	A	87	ASP	13.1
1	A	32	ALA	13.0
1	A	95	ALA	12.9
1	A	77	ASN	12.9
1	A	22	GLY	12.8
1	A	96	LYS	12.8
1	A	48	ASP	12.8

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Mol	Chain	Res	Type	RSRZ
1	A	14	ARG	12.7
1	A	4	GLY	12.6
1	A	11	ALA	12.6
1	A	37	ASN	12.6
1	A	41	GLN	12.3
1	A	111	TRP	12.3
1	A	105	MET	12.3
1	A	16	GLY	12.2
1	A	51	THR	12.2
1	A	21	ARG	12.2
1	A	75	LEU	11.8
1	A	53	TYR	11.8
1	A	116	LYS	11.8
1	A	80	CYS	11.8
1	A	10	ALA	11.7
1	A	18	ASP	11.6
1	A	89	THR	11.6
1	A	27	ASN	11.6
1	A	122	ALA	11.3
1	A	78	ILE	11.2
1	A	13	LYS	11.1
1	A	28	TRP	11.1
1	A	110	ALA	11.1
1	A	129	LEU	11.0
1	A	63	TRP	10.9
1	A	9	ALA	10.9
1	A	31	ALA	10.9
1	A	17	LEU	10.6
1	A	50	SER	10.6
1	A	39	ASN	10.6
1	A	47	THR	10.5
1	A	30	CYS	10.5
1	A	98	ILE	10.5
1	A	65	ASN	10.3
1	A	3	PHE	10.3
1	A	71	GLY	10.3
1	A	44	ASN	10.1
1	A	46	ASN	10.1
1	A	88	ILE	9.8
1	A	112	ARG	9.8
1	A	72	SER	9.7
1	A	64	CYS	9.7

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Mol	Chain	Res	Type	RSRZ
1	A	61	ARG	9.7
1	A	7	GLU	9.6
1	A	123	TRP	9.6
1	A	93	ASN	9.6
1	A	59	ASN	9.4
1	A	33	LYS	9.4
1	A	117	GLY	9.2
1	A	54	GLY	9.0
1	A	125	ARG	8.9
1	A	5	ARG	8.9
1	A	24	SER	8.7
1	A	85	SER	8.6
1	A	84	LEU	8.6
1	A	12	MET	8.5
1	A	19	ASN	8.5
1	A	6	CYS	8.3
1	A	2	VAL	8.3
1	A	23	TYR	8.1
1	A	25	LEU	7.9
1	A	108	TRP	7.9
1	A	38	PHE	7.8
1	A	92	VAL	7.4
1	A	49	GLY	7.3
1	A	99	VAL	7.3
1	A	97	LYS	6.9
1	A	124	ILE	6.7
1	A	103	ASN	6.6
1	A	107	ALA	6.6
1	A	106	ASN	6.6
1	A	102	GLY	6.6
1	A	74	ASN	6.5
1	A	104	GLY	6.4
1	A	26	GLY	6.3
1	A	58	ILE	6.3
1	A	52	ASP	6.2
1	A	100	SER	6.1
1	A	127	CYS	5.9
1	A	109	VAL	5.7
1	A	82	ALA	5.7
1	A	66	ASP	5.5
1	A	70	PRO	5.4
1	A	86	SER	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	8	LEU	5.3
1	A	69	THR	5.2
1	A	36	SER	5.0
1	A	60	SER	5.0
1	A	101	ASP	4.9
1	A	57	GLN	4.6
1	A	1	LYS	4.4
1	A	126	GLY	4.3
1	A	67	GLY	4.2
1	A	68	ARG	4.2
1	A	90	ALA	4.1
1	A	29	VAL	4.0
1	A	81	SER	3.8
1	A	91	SER	3.4
1	A	83	LEU	3.0
1	A	128	ARG	2.9
1	A	55	ILE	2.3
1	A	56	LEU	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.