



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:24 AM UTC

PDB ID : 1LZH / pdb_00001lzh
Title : THE STRUCTURES OF THE MONOCLINIC AND ORTHORHOMBIC FORMS OF HEN EGG-WHITE LYSOZYME AT 6 ANGSTROMS RESOLUTION.
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Deposited on : 1981-06-29
Resolution : 6.00 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

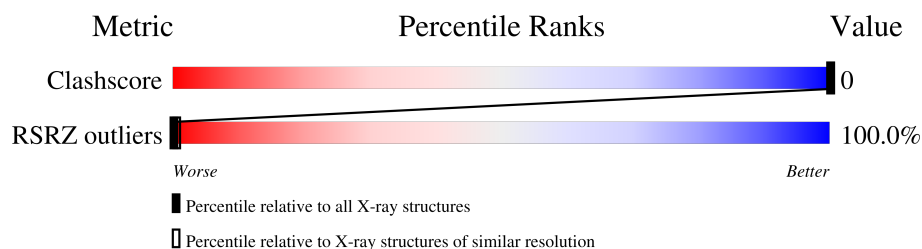
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	190562	1210 (8.00-4.00)
RSRZ outliers	180081	1136 (8.00-4.00)

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	129	
1	B	129	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 258 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.

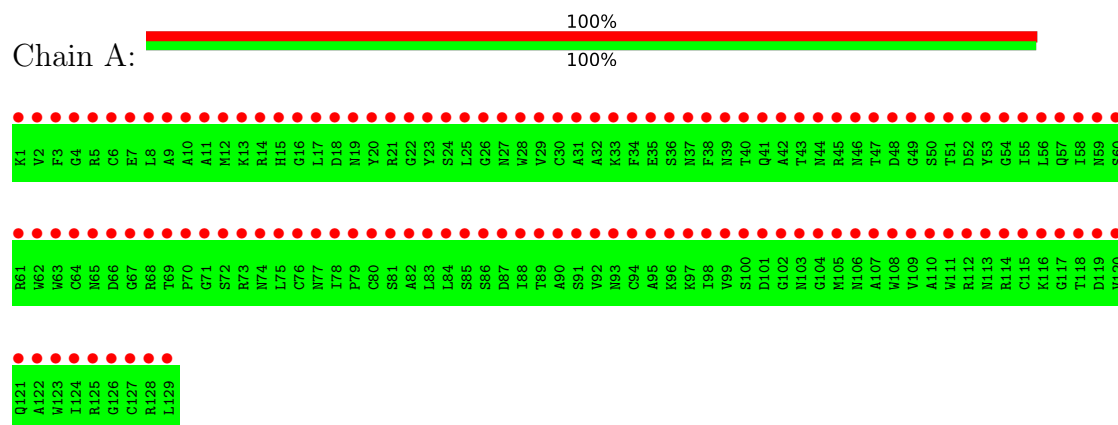
- Molecule 1 is a protein called HEN EGG WHITE LYSOZYME.

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

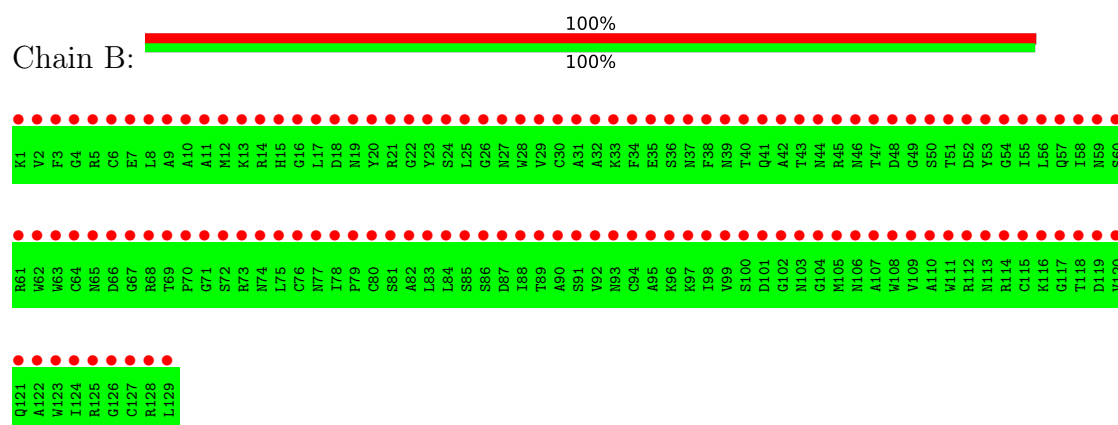
3 Residue-property plots

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: HEN EGG WHITE LYSOZYME



• Molecule 1: HEN EGG WHITE LYSOZYME



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	28.12Å 63.61Å 60.52Å 90.00° 91.05° 90.00°	Depositor
Resolution (Å)	(Not available) – 6.00 60.51 – 6.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-6.00) 98.2 (60.51-6.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	36.04 (at 6.05Å)	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available) 0.430 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	-0.1	Xtriage
Anisotropy	-30.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	7.62 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k 0.000 for -h,l,k 0.137 for h,-k,-l	Xtriage
F_o, F_c correlation	0.31	EDS
Total number of atoms	258	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 56.28 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.8009e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

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	129	0	0	0	0
1	B	129	0	0	0	0
All	All	258	0	0	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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%)	12.39	129 (100%) 0 0	0, 0, 0, 0	0
1	B	129/129 (100%)	12.00	129 (100%) 0 0	0, 0, 0, 0	0
All	All	258/258 (100%)	12.19	258 (100%) 0 0	0, 0, 0, 0	0

All (258) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	79	PRO	52.7
1	A	80	CYS	37.8
1	B	9	ALA	29.1
1	B	10	ALA	28.7
1	B	79	PRO	28.1
1	B	80	CYS	27.9
1	A	8	LEU	26.3
1	A	66	ASP	24.9
1	A	78	ILE	24.7
1	B	4	GLY	24.6
1	B	7	GLU	24.3
1	B	8	LEU	23.3
1	A	127	CYS	23.3
1	A	7	GLU	22.2
1	A	70	PRO	21.1
1	B	5	ARG	20.3
1	A	76	CYS	20.1
1	B	82	ALA	19.8
1	A	81	SER	19.4
1	B	102	GLY	18.9
1	B	120	VAL	18.9
1	B	76	CYS	18.9
1	B	81	SER	18.6
1	B	119	ASP	18.5

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Mol	Chain	Res	Type	RSRZ
1	A	121	GLN	17.6
1	A	98	ILE	17.5
1	B	37	ASN	17.3
1	A	3	PHE	17.2
1	B	12	MET	17.1
1	A	124	ILE	17.0
1	B	115	CYS	17.0
1	B	118	THR	16.9
1	B	66	ASP	16.9
1	B	78	ILE	16.8
1	A	38	PHE	16.8
1	A	119	ASP	16.4
1	A	55	ILE	16.4
1	B	83	LEU	16.3
1	B	11	ALA	16.1
1	A	120	VAL	16.1
1	B	15	HIS	16.1
1	A	77	ASN	16.0
1	B	21	ARG	15.9
1	A	101	ASP	15.9
1	B	70	PRO	15.8
1	A	67	GLY	15.8
1	A	27	ASN	15.6
1	B	86	SER	15.6
1	A	68	ARG	15.5
1	B	67	GLY	15.4
1	A	44	ASN	15.4
1	B	98	ILE	15.4
1	B	91	SER	15.4
1	B	6	CYS	15.2
1	B	87	ASP	15.2
1	B	14	ARG	15.1
1	B	92	VAL	15.0
1	A	48	ASP	15.0
1	A	32	ALA	14.9
1	A	87	ASP	14.7
1	A	43	THR	14.7
1	B	113	ASN	14.7
1	B	95	ALA	14.6
1	A	108	TRP	14.6
1	A	94	CYS	14.5
1	A	49	GLY	14.4

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Mol	Chain	Res	Type	RSRZ
1	A	47	THR	14.4
1	B	114	ARG	14.3
1	A	24	SER	14.3
1	A	58	ILE	14.3
1	A	93	ASN	14.2
1	B	122	ALA	14.1
1	A	118	THR	14.1
1	A	15	HIS	14.0
1	B	123	TRP	13.9
1	A	97	LYS	13.9
1	A	89	THR	13.8
1	A	19	ASN	13.7
1	B	89	THR	13.6
1	B	101	ASP	13.6
1	B	68	ARG	13.5
1	A	126	GLY	13.5
1	B	77	ASN	13.5
1	A	92	VAL	13.4
1	A	22	GLY	13.3
1	B	105	MET	13.3
1	B	73	ARG	13.2
1	A	18	ASP	13.2
1	A	4	GLY	13.1
1	A	56	LEU	13.1
1	B	104	GLY	13.1
1	A	11	ALA	13.0
1	B	43	THR	13.0
1	B	24	SER	12.9
1	B	20	TYR	12.8
1	A	125	ARG	12.8
1	A	86	SER	12.8
1	A	26	GLY	12.8
1	B	58	ILE	12.7
1	B	19	ASN	12.7
1	A	128	ARG	12.7
1	A	115	CYS	12.7
1	A	129	LEU	12.6
1	A	52	ASP	12.5
1	B	56	LEU	12.5
1	A	88	ILE	12.4
1	A	35	GLU	12.2
1	B	44	ASN	12.2

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Mol	Chain	Res	Type	RSRZ
1	A	113	ASN	12.2
1	A	69	THR	12.2
1	B	75	LEU	12.0
1	B	85	SER	12.0
1	A	41	GLN	12.0
1	A	46	ASN	11.9
1	A	21	ARG	11.9
1	B	18	ASP	11.8
1	B	59	ASN	11.8
1	A	91	SER	11.8
1	A	51	THR	11.8
1	B	52	ASP	11.7
1	B	16	GLY	11.6
1	A	42	ALA	11.6
1	A	20	TYR	11.5
1	B	41	GLN	11.5
1	A	16	GLY	11.4
1	A	57	GLN	11.3
1	A	105	MET	11.2
1	B	108	TRP	11.2
1	A	14	ARG	11.2
1	B	84	LEU	11.2
1	A	37	ASN	11.2
1	A	30	CYS	11.1
1	A	114	ARG	11.1
1	A	23	TYR	11.0
1	B	62	TRP	10.9
1	B	129	LEU	10.9
1	B	71	GLY	10.8
1	B	45	ARG	10.7
1	B	46	ASN	10.6
1	A	106	ASN	10.6
1	A	122	ALA	10.6
1	B	51	THR	10.6
1	B	34	PHE	10.5
1	B	47	THR	10.4
1	A	34	PHE	10.4
1	B	1	LYS	10.4
1	B	88	ILE	10.3
1	B	100	SER	10.3
1	B	90	ALA	10.2
1	A	17	LEU	10.2

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Mol	Chain	Res	Type	RSRZ
1	B	23	TYR	10.1
1	A	59	ASN	10.1
1	B	48	ASP	10.1
1	A	71	GLY	10.1
1	A	104	GLY	10.0
1	B	40	THR	10.0
1	A	36	SER	9.9
1	B	127	CYS	9.9
1	B	93	ASN	9.9
1	B	35	GLU	9.9
1	B	63	TRP	9.8
1	A	117	GLY	9.8
1	A	45	ARG	9.8
1	A	107	ALA	9.8
1	B	57	GLN	9.7
1	A	103	ASN	9.7
1	A	100	SER	9.7
1	A	65	ASN	9.6
1	A	90	ALA	9.5
1	B	22	GLY	9.5
1	B	53	TYR	9.5
1	B	117	GLY	9.4
1	A	39	ASN	9.4
1	A	95	ALA	9.4
1	B	42	ALA	9.4
1	B	110	ALA	9.3
1	B	96	LYS	9.2
1	B	94	CYS	9.2
1	B	97	LYS	9.2
1	B	103	ASN	9.2
1	A	96	LYS	9.1
1	A	28	TRP	9.1
1	A	13	LYS	9.1
1	A	54	GLY	9.0
1	B	17	LEU	8.9
1	A	62	TRP	8.9
1	B	125	ARG	8.8
1	A	85	SER	8.8
1	B	107	ALA	8.8
1	B	106	ASN	8.8
1	A	12	MET	8.7
1	B	28	TRP	8.7

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Mol	Chain	Res	Type	RSRZ
1	A	50	SER	8.7
1	A	110	ALA	8.6
1	A	102	GLY	8.6
1	B	36	SER	8.6
1	A	53	TYR	8.6
1	A	72	SER	8.5
1	B	128	ARG	8.5
1	B	109	VAL	8.4
1	A	111	TRP	8.4
1	A	112	ARG	8.4
1	A	73	ARG	8.4
1	B	30	CYS	8.3
1	A	25	LEU	8.3
1	A	109	VAL	8.2
1	A	74	ASN	8.2
1	B	2	VAL	8.1
1	A	6	CYS	8.1
1	A	123	TRP	8.0
1	B	31	ALA	8.0
1	A	40	THR	8.0
1	A	31	ALA	8.0
1	B	39	ASN	8.0
1	B	111	TRP	8.0
1	A	1	LYS	8.0
1	B	13	LYS	7.9
1	B	54	GLY	7.8
1	A	82	ALA	7.8
1	B	50	SER	7.7
1	B	99	VAL	7.5
1	B	65	ASN	7.4
1	B	121	GLN	7.4
1	A	10	ALA	7.4
1	A	116	LYS	7.4
1	B	55	ILE	7.3
1	A	60	SER	7.3
1	A	2	VAL	7.2
1	B	116	LYS	7.0
1	A	33	LYS	6.9
1	B	61	ARG	6.8
1	B	112	ARG	6.8
1	B	69	THR	6.8
1	A	75	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
1	B	3	PHE	6.7
1	B	60	SER	6.7
1	B	74	ASN	6.5
1	A	84	LEU	6.4
1	B	72	SER	6.4
1	B	126	GLY	6.4
1	B	27	ASN	6.3
1	A	64	CYS	6.0
1	A	63	TRP	6.0
1	B	49	GLY	6.0
1	A	61	ARG	5.9
1	B	32	ALA	5.9
1	A	83	LEU	5.8
1	A	29	VAL	5.7
1	B	29	VAL	5.6
1	B	64	CYS	5.5
1	B	38	PHE	5.4
1	A	9	ALA	5.2
1	B	124	ILE	5.0
1	A	5	ARG	4.4
1	B	33	LYS	4.3
1	A	99	VAL	4.3
1	B	26	GLY	4.1
1	B	25	LEU	3.2

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.