



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:42 PM UTC

PDB ID : 1LAG / pdb_00001lag
Title : STRUCTURAL BASES FOR MULTIPLE LIGAND SPECIFICITY OF THE PERIPLASMIC LYSINE-, ARGININE-, ORNITHINE-BINDING PROTEIN
Authors : Kim, S.-H.; Oh, B.-H.
Deposited on : 1993-10-06
Resolution : 2.06 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

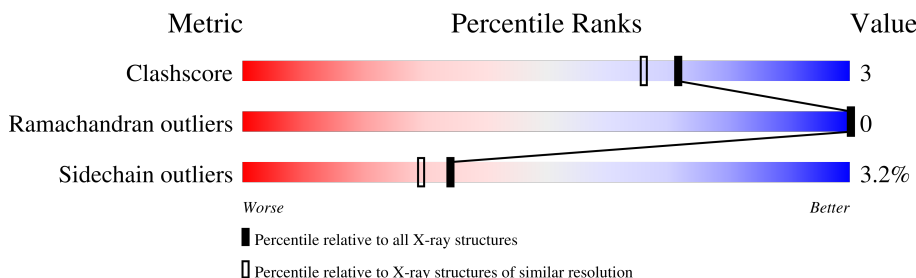
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	238	 84% 15% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1959 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.

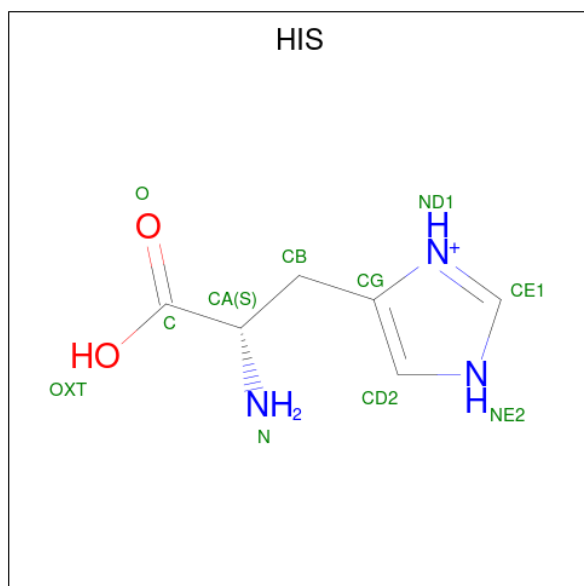
- Molecule 1 is a protein called LYSINE, ARGININE, ORNITHINE-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	238	Total	C	N	O	S	0	0	0
			1814	1145	301	363	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	102	ILE	VAL	conflict	UNP P02911

- Molecule 2 is HISTIDINE (CCD ID: HIS) (formula: C₆H₁₀N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	E	1	Total	C	N	O	0	0
			11	6	3	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	134	Total 134	O 134	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.

Note EDS was not executed.

- Molecule 1: LYSINE, ARGININE, ORNITHINE-BINDING PROTEIN

Chain E:  84% 15% .



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	37.49Å 58.19Å 117.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.06	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.06)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.162 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1959	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E	0.90	2/1846 (0.1%)	1.62	25/2493 (1.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	113	HIS	CD2-NE2	-6.06	1.31	1.37
1	E	113	HIS	CG-ND1	-5.34	1.32	1.38

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	234	ASN	OD1-CG-ND2	-11.24	111.36	122.60
1	E	234	ASN	CB-CG-ND2	10.23	131.74	116.40
1	E	127	ASN	CB-CG-ND2	7.71	127.97	116.40
1	E	26	PHE	CA-CB-CG	7.34	121.14	113.80
1	E	103	GLN	O-C-N	-6.96	116.94	121.88
1	E	113	HIS	CA-CB-CG	-6.75	107.05	113.80
1	E	238	ASP	CA-CB-CG	6.52	119.12	112.60
1	E	21	ASP	CA-CB-CG	6.49	119.09	112.60
1	E	219	GLN	OE1-CD-NE2	-6.48	116.12	122.60
1	E	42	GLN	OE1-CD-NE2	-6.43	116.17	122.60
1	E	127	ASN	OD1-CG-ND2	-6.43	116.17	122.60
1	E	176	LYS	N-CA-C	6.28	120.04	112.38
1	E	160	GLN	OE1-CD-NE2	-5.93	116.67	122.60
1	E	142	ASN	CA-CB-CG	5.39	117.99	112.60
1	E	129	ASN	OD1-CG-ND2	-5.32	117.28	122.60
1	E	130	TRP	CG-CD2-CE3	5.30	139.20	133.90
1	E	6	VAL	N-CA-C	-5.30	100.75	108.17
1	E	53	ASP	CA-CB-CG	5.20	117.80	112.60
1	E	162	GLU	N-CA-C	5.18	117.59	111.33
1	E	135	VAL	N-CA-C	-5.13	102.23	109.21
1	E	85	ASP	CA-CB-CG	5.09	117.69	112.60
1	E	79	GLN	N-CA-C	-5.03	106.65	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	107	GLU	CB-CG-CD	5.03	121.16	112.60
1	E	171	LYS	CA-CB-CG	-5.03	104.05	114.10
1	E	35	ASN	OD1-CG-ND2	-5.01	117.59	122.60

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	E	1814	0	1767	11	0
2	E	11	0	6	2	0
3	E	134	0	0	1	0
All	All	1959	0	1773	11	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 3.

All (11) 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:E:97:ALA:O	1:E:100:SER:HB2	2.03	0.58
1:E:35:ASN:HD21	1:E:47:TRP:HE1	1.56	0.53
1:E:222:THR:HG22	1:E:226:MET:HE2	1.93	0.51
1:E:35:ASN:ND2	1:E:47:TRP:HE1	2.08	0.51
1:E:12:THR:O	1:E:19:SER:HA	2.14	0.47
1:E:72:SER:HG	2:E:240:HIS:N	2.11	0.47
1:E:44:LYS:HD3	1:E:44:LYS:HA	1.80	0.46
1:E:223:TYR:HB3	3:E:456:HOH:O	2.16	0.45
1:E:70:SER:O	2:E:240:HIS:HD2	2.01	0.43
1:E:107:GLU:CD	1:E:107:GLU:H	2.27	0.43
1:E:6:VAL:O	1:E:45:CYS:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	E	236/238 (99%)	229 (97%)	7 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	E	186/191 (97%)	180 (97%)	6 (3%)	34	29

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	11	ASP
1	E	23	LYS
1	E	78	GLN
1	E	101	PRO
1	E	107	GLU
1	E	219	GLN

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

Mol	Chain	Res	Type
1	E	35	ASN
1	E	143	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HIS	E	240	-	10,11,11	1.61	3 (30%)	10,14,14	1.75	1 (10%)

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	HIS	E	240	-	-	2/8/8/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	240	HIS	OXT-C	-2.72	1.22	1.30
2	E	240	HIS	CG-ND1	-2.27	1.32	1.38
2	E	240	HIS	CD2-NE2	-2.16	1.31	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	E	240	HIS	CA-CB-CG	4.14	123.98	113.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	240	HIS	CA-CB-CG-CD2
2	E	240	HIS	CA-CB-CG-ND1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	240	HIS	2	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.