



Full wwPDB EM Validation Report ⓘ

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PDB ID : 9PSE / pdb_00009pse
Title : In situ MicroED structure of IL-5 activated human eosinophil major basic protein-1
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Deposited on : 2025-07-25
Resolution : 3.18 Å (reported)
Based on initial models : ., 1h8u

This is a Full wwPDB EM Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
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
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

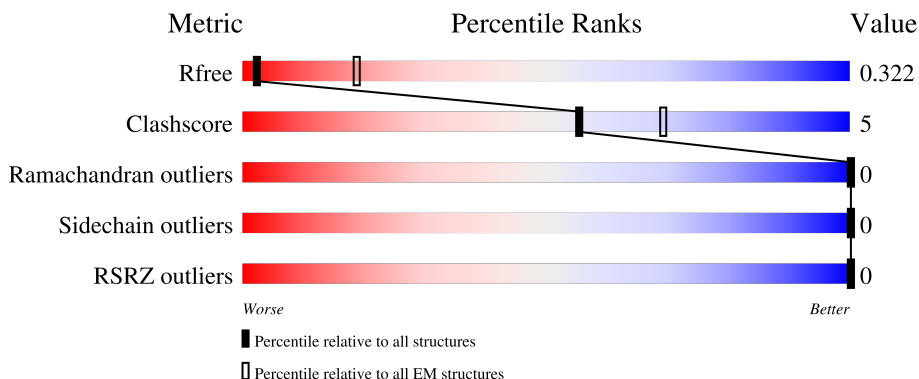
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 3.18 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)	EM structures (#Entries)
R_{free}	180332	208
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RSRZ outliers	180361	209

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	116	 81% 19%
1	B	116	 92% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3783 atoms, of which 1850 are hydrogens and 0 are deuteriums.

In the tables below, 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 Bone marrow proteoglycan.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	116	Total	C	H	N	O	S	0	0
			1889	608	925	197	150	9		
1	A	116	Total	C	H	N	O	S	0	0
			1889	608	925	197	150	9		

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total	Cl	0
			1	1	
2	A	1	Total	Cl	0
			1	1	

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	B	2	Total	O	0
			2	2	
3	A	1	Total	O	0
			1	1	

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: Bone marrow proteoglycan

Chain B:  92% 8%



- Molecule 1: Bone marrow proteoglycan

Chain A:  81% 19%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	30.20Å 57.80Å 58.60Å 90.00° 91.20° 90.00°	Depositor
Resolution (Å)	3.18 – 3.18 3.18 – 3.18	Depositor EDS
% Data completeness (in resolution range)	85.0 (3.18-3.18) 0.0 (3.18-3.18)	Depositor EDS
R_{merge}	0.66	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.278 , 0.320 0.285 , 0.322	Depositor DCC
R_{free} test set	363 reflections (8.82%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.794	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.51 , 859.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.058 for -h,l,k 0.059 for -h,-l,-k 0.287 for h,-k,-l	Xtriage
F_o, F_c correlation	0.00	EDS
Total number of atoms	3783	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.46% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

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

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	0.10	0/995	0.25	0/1344
1	B	0.10	0/995	0.24	0/1344
All	All	0.10	0/1990	0.24	0/2688

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

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	964	925	924	15	2
1	B	964	925	924	6	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
All	All	1933	1850	1848	19	2

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 5.

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:B:171:ARG:HD2	1:A:110:LEU:HD11	1.75	0.68
1:A:162:ARG:NH1	1:A:212:CYS:SG	2.73	0.60
1:A:111:LEU:HD11	1:A:152:LEU:HD11	1.84	0.58
1:B:163:ILE:O	1:B:163:ILE:HG23	2.06	0.55
1:A:188:HIS:O	1:A:193:ARG:NH1	2.44	0.51
1:A:116:GLN:OE1	1:A:124:THR:HG21	2.11	0.50
1:A:111:LEU:HD21	1:A:152:LEU:HG	1.95	0.48
1:A:186:ALA:HB2	1:A:206:HIS:HB3	1.98	0.46
1:A:134:VAL:HG21	1:A:145:ILE:HD11	1.98	0.45
1:B:154:GLN:O	1:B:202:THR:HG21	2.16	0.45
1:A:162:ARG:NH1	1:A:197:CYS:SG	2.91	0.43
1:A:189:GLN:OE1	1:A:193:ARG:NH2	2.51	0.43
1:A:200:LEU:HD23	1:A:200:LEU:O	2.18	0.42
1:B:162:ARG:HD2	1:B:175:VAL:HG12	2.01	0.42
1:A:111:LEU:CD1	1:A:152:LEU:HD11	2.48	0.42
1:B:163:ILE:HG22	1:B:196:HIS:O	2.21	0.41
1:A:186:ALA:HB3	1:A:189:GLN:HG3	2.02	0.41
1:A:214:ARG:HE	1:A:216:LEU:HD21	1.87	0.40
1:B:168:ARG:CZ	1:A:108:ARG:HD3	2.51	0.40

All (2) 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)
1:A:127:ARG:NH1	1:A:140:ASN:OD1[2_656]	2.14	0.06
1:B:184:TYR:OH	1:A:184:TYR:OH[2_656]	2.19	0.01

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 PDB entries followed by that with respect to all EM entries.

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	114/116 (98%)	102 (90%)	12 (10%)	0	100	100
1	B	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
All	All	228/232 (98%)	208 (91%)	20 (9%)	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 PDB entries followed by that with respect to all EM entries.

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	98/98 (100%)	98 (100%)	0	100	100
1	B	98/98 (100%)	98 (100%)	0	100	100
All	All	196/196 (100%)	196 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	188	HIS
1	B	189	GLN
1	B	206	HIS
1	A	120	GLN
1	A	156	GLN
1	A	196	HIS
1	A	211	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.