



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 03:19 PM UTC

PDB ID : 1BVL / pdb_00001bvl
Title : HUMANIZED ANTI-LYSOZYME FV
Authors : Holmes, M.A.; Foote, J.
Deposited on : 1998-09-16
Resolution : 2.87 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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) : **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

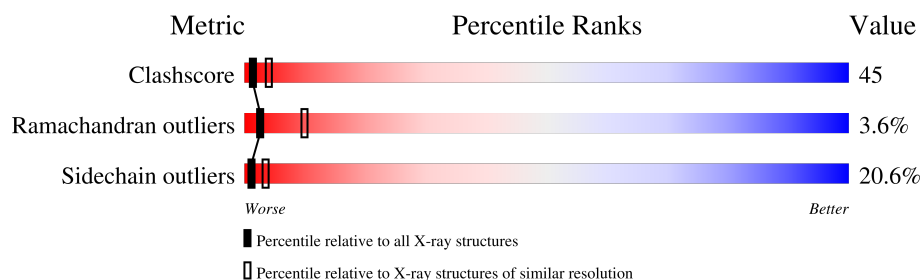
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.87 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	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)

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	A	117	
1	C	117	
2	B	108	
2	D	108	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3486 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 HULYS11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	116	Total	C	N	O	S	0	0	0
			900	563	158	175	4			
1	C	116	Total	C	N	O	S	0	0	0
			900	563	158	175	4			

- Molecule 2 is a protein called HULYS11.

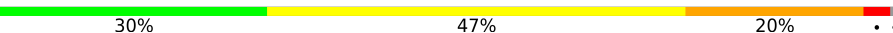
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	108	Total	C	N	O	S	0	0	0
			843	532	143	165	3			
2	D	108	Total	C	N	O	S	0	0	0
			843	532	143	165	3			

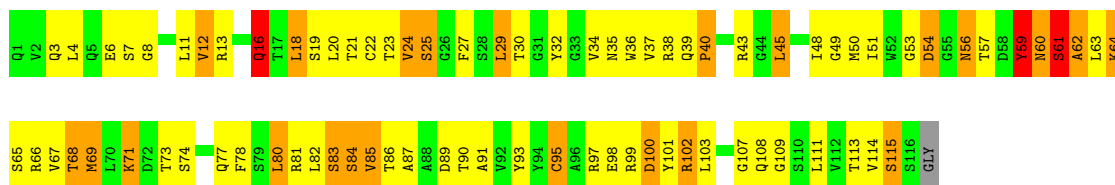
3 Residue-property plots

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. 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: HULYS11

Chain A: 



T74	I75	S76	S77	L78	Q79	P80	E81	D82	I83	A84	T85	Y86	Y87	C88	Q89	H90	F91	P95	R96	G99	Q100	G101	T102	K103	V104	E105	I106	K107	R108
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.00Å 143.00Å 72.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.87	Depositor
% Data completeness (in resolution range)	93.7 (10.00-2.87)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.220 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3486	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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	A	1.11	2/919 (0.2%)	1.47	15/1249 (1.2%)
1	C	1.25	5/919 (0.5%)	1.52	15/1249 (1.2%)
2	B	1.04	2/865 (0.2%)	1.31	10/1175 (0.9%)
2	D	1.18	6/865 (0.7%)	1.52	18/1175 (1.5%)
All	All	1.15	15/3568 (0.4%)	1.46	58/4848 (1.2%)

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 mainchain group or atoms of a sidechain that are expected to be planar.

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

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	69	MET	SD-CE	-7.96	1.59	1.79
1	C	16	GLN	CD-OE1	6.07	1.35	1.23
1	C	56	ASN	CG-OD1	6.02	1.34	1.23
2	D	4	MET	SD-CE	-5.98	1.64	1.79
2	B	3	GLN	CD-OE1	5.98	1.34	1.23

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	96	ARG	N-CA-C	-9.92	97.43	110.43
2	D	99	GLY	N-CA-C	-9.24	98.38	112.51
1	A	107	GLY	N-CA-C	-9.12	98.65	112.60
2	B	53	THR	N-CA-C	8.69	123.58	109.76
2	D	75	ILE	N-CA-C	-8.44	94.05	106.88

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	59	TYR	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	900	0	878	88	0
1	C	900	0	878	72	0
2	B	843	0	816	102	0
2	D	843	0	816	65	0
All	All	3486	0	3388	310	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 45.

The worst 5 of 310 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:71:LYS:HE2	1:A:73:THR:HG22	1.29	1.14
1:A:32:TYR:HE1	1:A:99:ARG:HG3	1.15	1.04
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.44	0.98
2:D:54:LEU:HD13	2:D:58:VAL:HB	1.46	0.95
2:B:1:ASP:HB3	2:B:95:PRO:HD2	1.51	0.93

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	Percentiles	
1	A	114/117 (97%)	97 (85%)	13 (11%)	4 (4%)	3	10
1	C	114/117 (97%)	94 (82%)	13 (11%)	7 (6%)	1	3
2	B	106/108 (98%)	92 (87%)	10 (9%)	4 (4%)	2	9
2	D	106/108 (98%)	97 (92%)	8 (8%)	1 (1%)	14	38
All	All	440/450 (98%)	380 (86%)	44 (10%)	16 (4%)	2	10

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	SER
1	A	61	SER
1	A	109	GLY
1	C	64	LYS
2	B	68	GLY

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	A	99/99 (100%)	76 (77%)	23 (23%)	1	2
1	C	99/99 (100%)	73 (74%)	26 (26%)	0	1
2	B	93/93 (100%)	76 (82%)	17 (18%)	2	5
2	D	93/93 (100%)	80 (86%)	13 (14%)	3	10
All	All	384/384 (100%)	305 (79%)	79 (21%)	1	3

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	73	THR
2	D	33	LEU
1	C	80	LEU
1	C	114	VAL

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Mol	Chain	Res	Type
2	D	103	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	31	ASN
2	D	79	GLN
2	B	31	ASN
2	B	38	GLN
2	B	79	GLN

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

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.