



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:46 AM UTC

PDB ID : 6WF1 / pdb_00006wf1
Title : Crystal Structure of Broadly Neutralizing Antibody 3I14 Bound to the Influenza A H10 Hemagglutinin
Authors : Harshbarger, W.D.; Lockbaum, G.J.; Deming, D.T.; Attatippaholkun, N.; Schiffer, C.A.; Marasco, W.A.
Deposited on : 2020-04-03
Resolution : 4.19 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

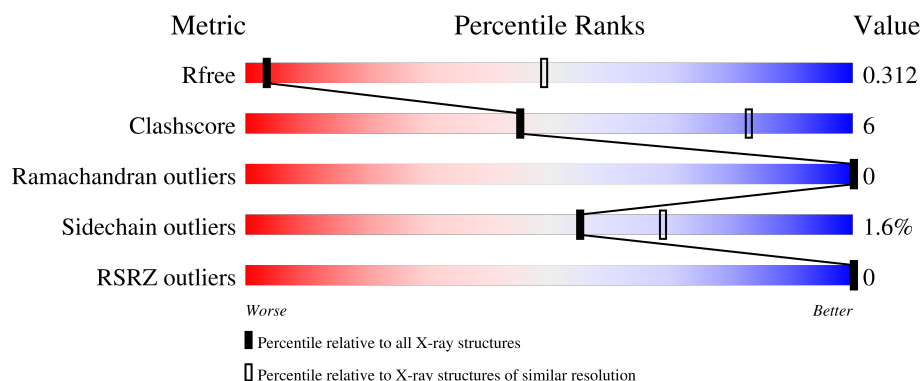
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.19 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))
R_{free}	180053	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	323	 89% 10% .
2	B	220	 66% 12% 22%
3	H	231	 77% 19% .
4	L	213	 77% 21% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6973 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2437	1506	449	465	17			

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	171	Total	C	N	O	S	0	0	0
			1382	854	239	281	8			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	175	SER	-	expression tag	UNP A0A0J9X253
B	176	GLY	-	expression tag	UNP A0A0J9X253
B	177	ARG	-	expression tag	UNP A0A0J9X253
B	178	LEU	-	expression tag	UNP A0A0J9X253
B	179	VAL	-	expression tag	UNP A0A0J9X253
B	180	PRO	-	expression tag	UNP A0A0J9X253
B	181	ARG	-	expression tag	UNP A0A0J9X253
B	182	GLY	-	expression tag	UNP A0A0J9X253
B	183	SER	-	expression tag	UNP A0A0J9X253
B	184	PRO	-	expression tag	UNP A0A0J9X253
B	185	GLY	-	expression tag	UNP A0A0J9X253
B	186	SER	-	expression tag	UNP A0A0J9X253
B	187	GLY	-	expression tag	UNP A0A0J9X253
B	188	TYR	-	expression tag	UNP A0A0J9X253
B	189	ILE	-	expression tag	UNP A0A0J9X253
B	190	PRO	-	expression tag	UNP A0A0J9X253
B	191	GLU	-	expression tag	UNP A0A0J9X253
B	192	ALA	-	expression tag	UNP A0A0J9X253
B	193	PRO	-	expression tag	UNP A0A0J9X253
B	194	ARG	-	expression tag	UNP A0A0J9X253

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Chain	Residue	Modelled	Actual	Comment	Reference
B	195	ASP	-	expression tag	UNP A0A0J9X253
B	196	GLY	-	expression tag	UNP A0A0J9X253
B	197	GLN	-	expression tag	UNP A0A0J9X253
B	198	ALA	-	expression tag	UNP A0A0J9X253
B	199	TYR	-	expression tag	UNP A0A0J9X253
B	200	VAL	-	expression tag	UNP A0A0J9X253
B	201	ARG	-	expression tag	UNP A0A0J9X253
B	202	LYS	-	expression tag	UNP A0A0J9X253
B	203	ASP	-	expression tag	UNP A0A0J9X253
B	204	GLY	-	expression tag	UNP A0A0J9X253
B	205	GLU	-	expression tag	UNP A0A0J9X253
B	206	TRP	-	expression tag	UNP A0A0J9X253
B	207	VAL	-	expression tag	UNP A0A0J9X253
B	208	LEU	-	expression tag	UNP A0A0J9X253
B	209	LEU	-	expression tag	UNP A0A0J9X253
B	210	SER	-	expression tag	UNP A0A0J9X253
B	211	THR	-	expression tag	UNP A0A0J9X253
B	212	PHE	-	expression tag	UNP A0A0J9X253
B	213	LEU	-	expression tag	UNP A0A0J9X253
B	214	GLY	-	expression tag	UNP A0A0J9X253
B	215	HIS	-	expression tag	UNP A0A0J9X253
B	216	HIS	-	expression tag	UNP A0A0J9X253
B	217	HIS	-	expression tag	UNP A0A0J9X253
B	218	HIS	-	expression tag	UNP A0A0J9X253
B	219	HIS	-	expression tag	UNP A0A0J9X253
B	220	HIS	-	expression tag	UNP A0A0J9X253

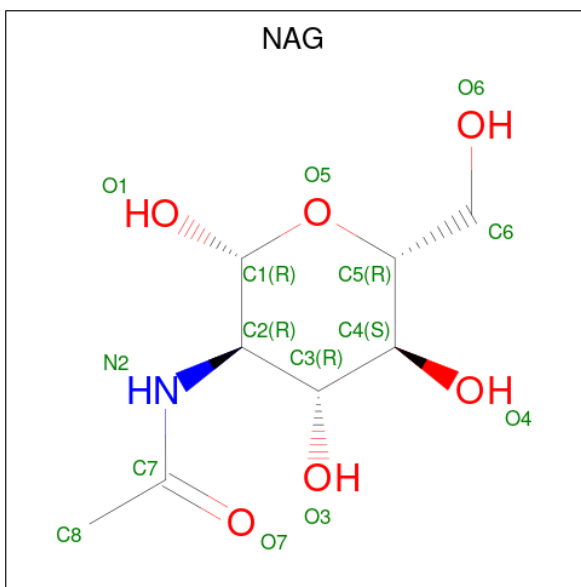
- Molecule 3 is a protein called heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	222	Total	C	N	O	S	0	0	0
			1684	1077	283	318	6			

- Molecule 4 is a protein called light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	211	Total	C	N	O	S	0	0	0
			1456	910	244	297	5			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

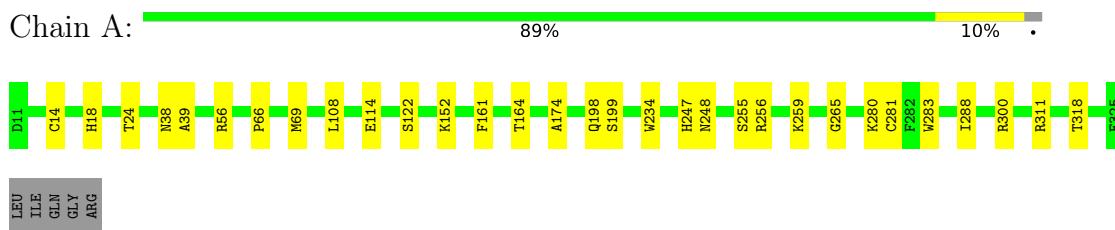


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0

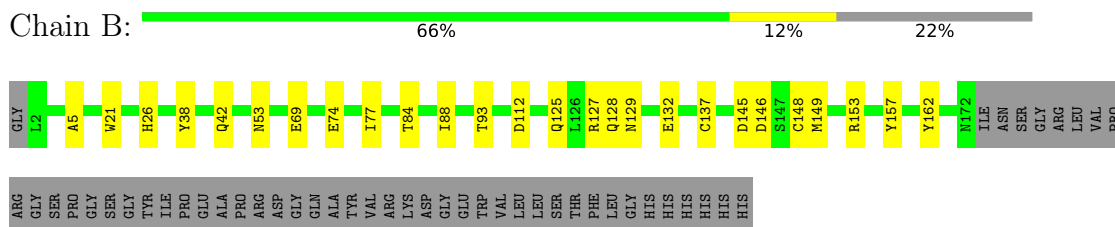
3 Residue-property plots [i](#)

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 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.

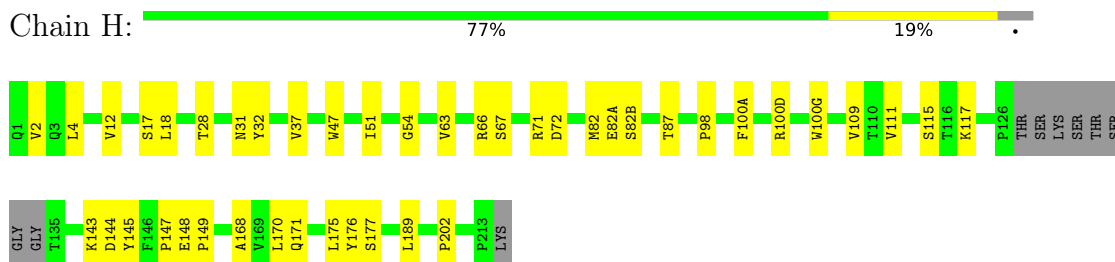
- Molecule 1: Hemagglutinin



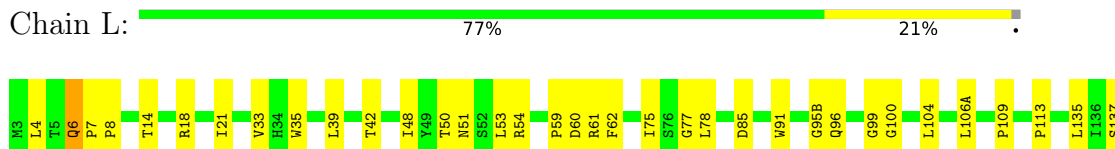
- Molecule 2: Hemagglutinin HA2 chain



- Molecule 3: heavy chain



- Molecule 4: light chain



D138	F139	P154	A157	GLY	VAL	E160	P164	S165	N170	K171	Y172	A173	A174	S175	P182	P208	G211
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4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	127.02Å 127.02Å 158.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.58 – 4.19 41.58 – 4.19	Depositor EDS
% Data completeness (in resolution range)	84.6 (41.58-4.19) 84.5 (41.58-4.19)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 4.13Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.261 , 0.308 0.261 , 0.312	Depositor DCC
R_{free} test set	962 reflections (8.50%)	wwPDB-VP
Wilson B-factor (Å ²)	175.7	Xtriage
Anisotropy	0.721	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 206.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.069 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6973	wwPDB-VP
Average B, all atoms (Å ²)	244.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.09	0/2486	0.26	0/3368
2	B	0.10	0/1407	0.27	0/1899
3	H	0.11	0/1730	0.35	0/2357
4	L	0.09	0/1485	0.27	0/2020
All	All	0.10	0/7108	0.29	0/9644

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	2437	0	2386	19	0
2	B	1382	0	1279	18	1
3	H	1684	0	1654	29	0
4	L	1456	0	1292	21	0
5	A	14	0	13	0	0
All	All	6973	0	6624	80	1

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 6.

The worst 5 of 80 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)
4:L:138:ASP:HA	4:L:171:LYS:HB2	1.73	0.68
4:L:6:GLN:HB3	4:L:100:GLY:HA3	1.79	0.65
1:A:18:HIS:HD2	2:B:21:TRP:HA	1.62	0.63
2:B:127:ARG:HG2	2:B:128:GLN:HG2	1.81	0.62
3:H:17:SER:HB3	3:H:82(A):GLU:HG2	1.80	0.62

All (1) 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)
2:B:127:ARG:NH1	2:B:132:GLU:O[3_655]	2.17	0.03

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	316/323 (98%)	310 (98%)	6 (2%)	0	100	100
2	B	169/220 (77%)	163 (96%)	6 (4%)	0	100	100
3	H	218/231 (94%)	194 (89%)	24 (11%)	0	100	100
4	L	207/213 (97%)	193 (93%)	14 (7%)	0	100	100
All	All	910/987 (92%)	860 (94%)	50 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	269/273 (98%)	269 (100%)	0	100	100
2	B	146/185 (79%)	145 (99%)	1 (1%)	76	78
3	H	187/194 (96%)	184 (98%)	3 (2%)	55	69
4	L	144/177 (81%)	136 (94%)	8 (6%)	19	42
All	All	746/829 (90%)	734 (98%)	12 (2%)	55	69

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	109	PRO
4	L	154	PRO
4	L	208	PRO
4	L	164	PRO
3	H	189	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
4	L	31	ASN
2	B	172	ASN
2	B	75	HIS
2	B	53	ASN
2	B	105	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 [i](#)

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$
5	NAG	A	601	1	14,14,15	0.26	0	17,19,21	0.40	0

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
5	NAG	A	601	1	-	0/6/23/26	0/1/1/1

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.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	318/323 (98%)	-0.71	0 100 100	154, 205, 281, 344	0
2	B	171/220 (77%)	-0.56	0 100 100	177, 295, 338, 345	0
3	H	222/231 (96%)	-0.65	0 100 100	226, 270, 297, 340	0
4	L	211/213 (99%)	-0.60	0 100 100	208, 239, 267, 281	0
All	All	922/987 (93%)	-0.64	0 100 100	154, 242, 329, 345	0

There are no RSRZ outliers to report.

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	A	601	14/15	0.88	0.06	238,255,277,281	0

6.5 Other polymers [i](#)

There are no such residues in this entry.