



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:29 AM UTC

PDB ID : 9MR0 / pdb_00009mr0
Title : Neisseria meningitidis haptoglobin-hemoglobin utilization protein A
Authors : Ng, D.; Au, N.Y.T.; Lai, C.C.; Huynh, M.S.; Moraes, T.F.
Deposited on : 2025-01-06
Resolution : 2.23 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

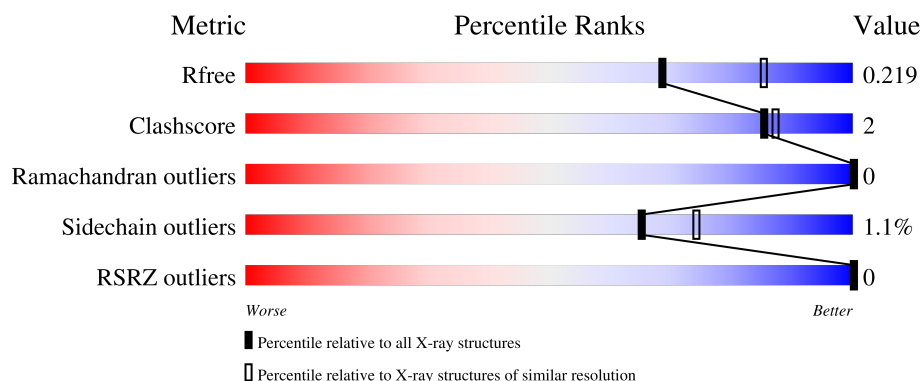
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	342	 85% 11%
1	B	342	 84% 5% 11%
1	C	342	 78% 8% 13%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7486 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 Hemoglobin-haptoglobin utilization protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2274	1427	385	459	3			
1	B	305	Total	C	N	O	S	0	0	0
			2294	1437	387	467	3			
1	C	296	Total	C	N	O	S	0	0	0
			2239	1407	381	448	3			

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	323	GLU	-	expression tag	UNP P96948
A	324	LEU	-	expression tag	UNP P96948
A	325	ALA	-	expression tag	UNP P96948
A	326	LEU	-	expression tag	UNP P96948
A	327	VAL	-	expression tag	UNP P96948
A	328	PRO	-	expression tag	UNP P96948
A	329	ARG	-	expression tag	UNP P96948
A	330	GLY	-	expression tag	UNP P96948
A	331	SER	-	expression tag	UNP P96948
A	332	SER	-	expression tag	UNP P96948
A	333	ALA	-	expression tag	UNP P96948
A	334	GLY	-	expression tag	UNP P96948
A	335	HIS	-	expression tag	UNP P96948
A	336	HIS	-	expression tag	UNP P96948
A	337	HIS	-	expression tag	UNP P96948
A	338	HIS	-	expression tag	UNP P96948
A	339	HIS	-	expression tag	UNP P96948
A	340	HIS	-	expression tag	UNP P96948
A	341	HIS	-	expression tag	UNP P96948
B	323	GLU	-	expression tag	UNP P96948
B	324	LEU	-	expression tag	UNP P96948
B	325	ALA	-	expression tag	UNP P96948
B	326	LEU	-	expression tag	UNP P96948

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	327	VAL	-	expression tag	UNP P96948
B	328	PRO	-	expression tag	UNP P96948
B	329	ARG	-	expression tag	UNP P96948
B	330	GLY	-	expression tag	UNP P96948
B	331	SER	-	expression tag	UNP P96948
B	332	SER	-	expression tag	UNP P96948
B	333	ALA	-	expression tag	UNP P96948
B	334	GLY	-	expression tag	UNP P96948
B	335	HIS	-	expression tag	UNP P96948
B	336	HIS	-	expression tag	UNP P96948
B	337	HIS	-	expression tag	UNP P96948
B	338	HIS	-	expression tag	UNP P96948
B	339	HIS	-	expression tag	UNP P96948
B	340	HIS	-	expression tag	UNP P96948
B	341	HIS	-	expression tag	UNP P96948
C	323	GLU	-	expression tag	UNP P96948
C	324	LEU	-	expression tag	UNP P96948
C	325	ALA	-	expression tag	UNP P96948
C	326	LEU	-	expression tag	UNP P96948
C	327	VAL	-	expression tag	UNP P96948
C	328	PRO	-	expression tag	UNP P96948
C	329	ARG	-	expression tag	UNP P96948
C	330	GLY	-	expression tag	UNP P96948
C	331	SER	-	expression tag	UNP P96948
C	332	SER	-	expression tag	UNP P96948
C	333	ALA	-	expression tag	UNP P96948
C	334	GLY	-	expression tag	UNP P96948
C	335	HIS	-	expression tag	UNP P96948
C	336	HIS	-	expression tag	UNP P96948
C	337	HIS	-	expression tag	UNP P96948
C	338	HIS	-	expression tag	UNP P96948
C	339	HIS	-	expression tag	UNP P96948
C	340	HIS	-	expression tag	UNP P96948
C	341	HIS	-	expression tag	UNP P96948

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	281	Total O 281 281	0	0
2	B	274	Total O 274 274	0	0

Continued on next page...

Continued from previous page...

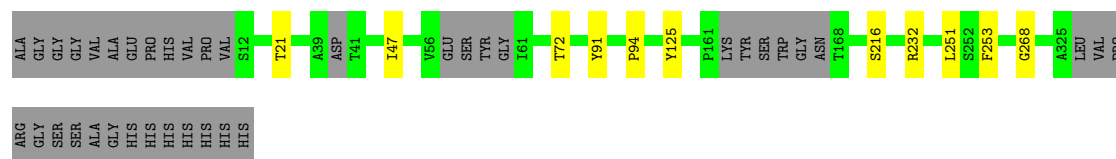
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	124	Total 124	O 124	0	0

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.

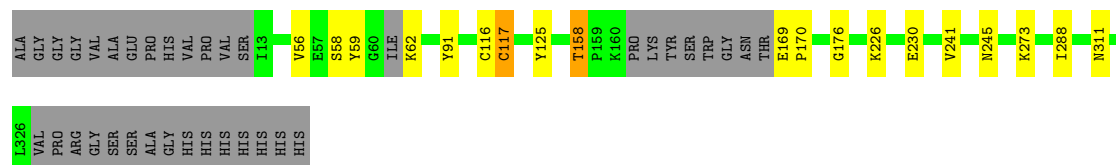
- Molecule 1: Hemoglobin-haptoglobin utilization protein A

Chain A: 



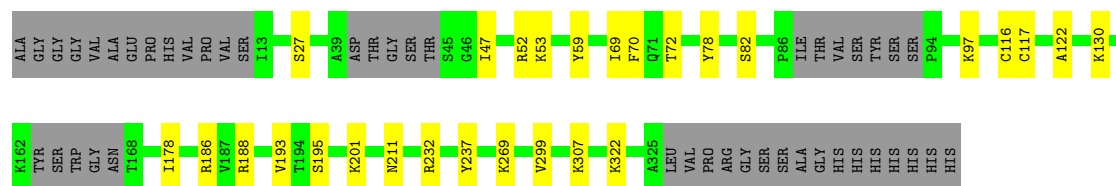
- Molecule 1: Hemoglobin-haptoglobin utilization protein A

Chain B: 



- Molecule 1: Hemoglobin-haptoglobin utilization protein A

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.75Å 94.03Å 121.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.57 – 2.23 34.57 – 2.23	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.57-2.23) 99.1 (34.57-2.23)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.21.2-5419, REFMAC 5.0	Depositor
R, R_{free}	0.173 , 0.220 0.172 , 0.219	Depositor DCC
R_{free} test set	2563 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 29.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.267 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7486	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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

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	0.30	0/2319	0.46	0/3135
1	B	0.25	0/2340	0.47	0/3164
1	C	0.25	0/2285	0.41	0/3086
All	All	0.27	0/6944	0.45	0/9385

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	2274	0	2189	5	0
1	B	2294	0	2208	12	0
1	C	2239	0	2155	13	0
2	A	281	0	0	1	0
2	B	274	0	0	0	0
2	C	124	0	0	0	0
All	All	7486	0	6552	29	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 2.

All (29) 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:C:178:ILE:HG23	1:C:307:LYS:HG2	1.77	0.66
1:C:47:ILE:HD13	1:C:72:THR:HA	1.88	0.55
1:B:58:SER:H	1:B:62:LYS:HD3	1.74	0.52
1:B:158:THR:HG21	1:B:273:LYS:HE3	1.95	0.49
1:C:27:SER:HA	1:C:53:LYS:HD3	1.96	0.48
1:B:241:VAL:HG11	1:B:288:ILE:HD13	1.95	0.47
1:B:56:VAL:HG13	1:C:59:TYR:HB3	1.95	0.47
1:C:70:PHE:CZ	1:C:78:TYR:HB2	2.50	0.47
1:C:322:LYS:HB2	1:C:322:LYS:HE2	1.66	0.47
1:C:122:ALA:O	1:C:130:LYS:HE2	2.14	0.47
1:B:59:TYR:H	1:B:62:LYS:HE2	1.81	0.46
1:B:116:CYS:HG	1:B:117:CYS:HG	1.61	0.46
1:B:116:CYS:HA	1:B:117:CYS:HA	1.82	0.46
1:B:169:GLU:N	1:B:170:PRO:HD2	2.31	0.46
1:C:201:LYS:HB3	1:C:211:ASN:CG	2.40	0.46
1:C:52:ARG:HD2	1:C:69:ILE:HG21	1.99	0.44
1:A:91:TYR:HB2	1:A:125:TYR:CZ	2.52	0.44
1:A:253:PHE:CE2	1:A:268:GLY:HA3	2.53	0.43
1:A:216:SER:OG	1:A:232:ARG:HG3	2.17	0.43
1:B:226:LYS:HD2	1:B:245:ASN:OD1	2.17	0.43
1:B:176:GLY:HA2	1:B:311:ASN:O	2.19	0.43
1:C:186:ARG:HG3	1:C:237:TYR:CE1	2.52	0.43
1:B:91:TYR:HB2	1:B:125:TYR:CZ	2.55	0.41
1:C:116:CYS:HA	1:C:117:CYS:HA	1.72	0.41
1:B:230:GLU:HG3	1:B:241:VAL:O	2.21	0.41
1:A:47:ILE:HD13	1:A:72:THR:HA	2.03	0.40
1:C:195:SER:HB2	1:C:232:ARG:O	2.21	0.40
1:C:188:ARG:HG3	1:C:193:VAL:HG21	2.02	0.40
1:A:94:PRO:HD2	2:A:549:HOH:O	2.21	0.40

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	295/342 (86%)	287 (97%)	8 (3%)	0	100	100
1	B	299/342 (87%)	289 (97%)	10 (3%)	0	100	100
1	C	288/342 (84%)	280 (97%)	8 (3%)	0	100	100
All	All	882/1026 (86%)	856 (97%)	26 (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	A	243/280 (87%)	241 (99%)	2 (1%)	73	80
1	B	246/280 (88%)	244 (99%)	2 (1%)	73	80
1	C	237/280 (85%)	233 (98%)	4 (2%)	53	63
All	All	726/840 (86%)	718 (99%)	8 (1%)	65	74

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	251	LEU
1	B	117	CYS
1	B	158	THR
1	C	82	SER
1	C	97	LYS
1	C	269	LYS
1	C	299	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	50	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	71	GLN
1	A	77	GLN
1	A	189	ASN
1	B	50	GLN
1	B	51	GLN
1	B	77	GLN
1	C	50	GLN
1	C	77	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 [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	303/342 (88%)	-1.65	0 100 100	13, 24, 54, 90	0
1	B	305/342 (89%)	-1.65	0 100 100	14, 25, 53, 73	0
1	C	296/342 (86%)	-1.45	0 100 100	29, 51, 73, 85	0
All	All	904/1026 (88%)	-1.58	0 100 100	13, 32, 68, 90	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.