



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4AYN / pdb_00004ayn
Title : Structure of the C-terminal barrel of Neisseria meningitidis FHbp Variant 2
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Deposited on : 2012-06-21
Resolution : 2.06 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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

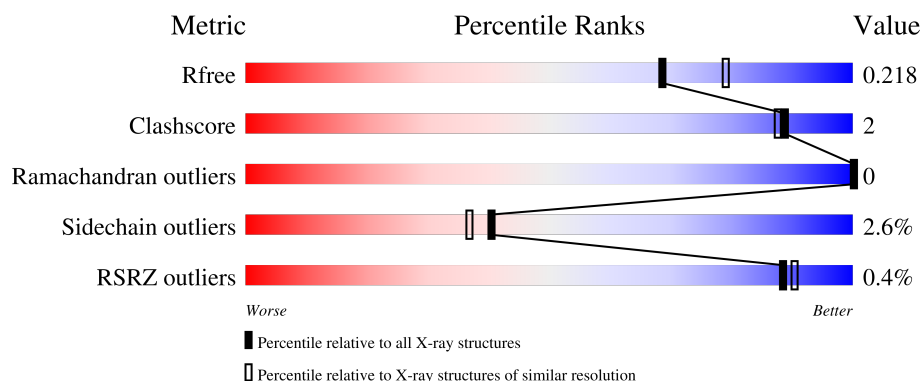
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	180053	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (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 $\leq 5\%$. 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	267	
1	B	267	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2060 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 FACTOR H-BINDING PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	125	Total	C	N	O	0	0	0
			973	605	179	189			
1	B	119	Total	C	N	O	0	0	0
			922	574	167	181			

There are 42 discrepancies between the modelled and reference sequences:

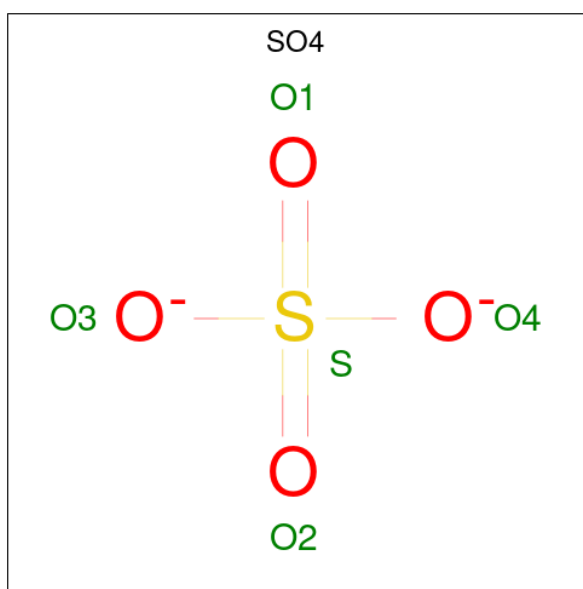
Chain	Residue	Modelled	Actual	Comment	Reference
A	61	MET	-	expression tag	UNP C6KHT4
A	62	GLY	-	expression tag	UNP C6KHT4
A	63	PRO	-	expression tag	UNP C6KHT4
A	64	ASP	-	expression tag	UNP C6KHT4
A	65	SER	-	expression tag	UNP C6KHT4
A	66	ASP	-	expression tag	UNP C6KHT4
A	67	ARG	-	expression tag	UNP C6KHT4
A	68	LEU	-	expression tag	UNP C6KHT4
A	69	GLN	-	expression tag	UNP C6KHT4
A	70	GLN	-	expression tag	UNP C6KHT4
A	71	ARG	-	expression tag	UNP C6KHT4
A	72	ARG	-	expression tag	UNP C6KHT4
A	321	LEU	-	expression tag	UNP C6KHT4
A	322	GLU	-	expression tag	UNP C6KHT4
A	323	HIS	-	expression tag	UNP C6KHT4
A	324	HIS	-	expression tag	UNP C6KHT4
A	325	HIS	-	expression tag	UNP C6KHT4
A	326	HIS	-	expression tag	UNP C6KHT4
A	327	HIS	-	expression tag	UNP C6KHT4
A	328	HIS	-	expression tag	UNP C6KHT4
A	211	SER	GLY	conflict	UNP C6KHT4
B	61	MET	-	expression tag	UNP C6KHT4
B	62	GLY	-	expression tag	UNP C6KHT4
B	63	PRO	-	expression tag	UNP C6KHT4
B	64	ASP	-	expression tag	UNP C6KHT4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	65	SER	-	expression tag	UNP C6KHT4
B	66	ASP	-	expression tag	UNP C6KHT4
B	67	ARG	-	expression tag	UNP C6KHT4
B	68	LEU	-	expression tag	UNP C6KHT4
B	69	GLN	-	expression tag	UNP C6KHT4
B	70	GLN	-	expression tag	UNP C6KHT4
B	71	ARG	-	expression tag	UNP C6KHT4
B	72	ARG	-	expression tag	UNP C6KHT4
B	321	LEU	-	expression tag	UNP C6KHT4
B	322	GLU	-	expression tag	UNP C6KHT4
B	323	HIS	-	expression tag	UNP C6KHT4
B	324	HIS	-	expression tag	UNP C6KHT4
B	325	HIS	-	expression tag	UNP C6KHT4
B	326	HIS	-	expression tag	UNP C6KHT4
B	327	HIS	-	expression tag	UNP C6KHT4
B	328	HIS	-	expression tag	UNP C6KHT4
B	211	SER	GLY	conflict	UNP C6KHT4

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	64	Total	O	0	0
			64	64		
3	B	56	Total	O	0	0
			56	56		

• Molecule 1: FACTOR H-BINDING PROTEIN

ASN	PRO	ASP	LYS	ILE	ASP	SER	SER	ILE	ASN	GLN	ARG	SER	PHE	VAL	SER	GLY	LEU	G200	G201	Q208	N228	V256	D266	R295	E298	S302	K310	E313	K319	Q320	L321	H325	HIS	HIS
ASN	PRO	ASP	LYS	ILE	ASP	SER	SER	ILE	ASN	GLN	ARG	SER	PHE	VAL	SER	GLY	LEU	G200	G201	Q208	N228	V256	D266	R295	E298	S302	K310	E313	K319	Q320	L321	H325	HIS	HIS
THR	TYR	GLY	ASN	GLY	ASP	SER	SER	LEU	ASN	THR	GLY	LYS	LEU	VAL	SER	ARG	ARG	PHE	PHE	ILE	GLN	ILE	GLU	VAL	ASP	GLY	GLN	ILE	THR	LEU	SER	GLY	ASN	
MET	PRO	GLY	ASP	SER	ASP	ARG	ARG	GLN	ARG	ARG	ARG	VAL	ALA	ALA	GLY	GLY	LEU	ALA	ASP	ALA	THR	PRO	LEU	ASP	HIS	LYS	ASP	LYS	SER	LEU	VAL	ARG	ASN	GLU

- Molecule 1: FACTOR H-BINDING PROTEIN

ASN	PRO	ASP	LYS	ILE	ASP	SER	LEU	ILE	ASN	GLN	ARG	SER	LEU	VAL	ASP	GLY	LEU	GLY	G201	G216	E217	H218	N228	V256	D266	S269	H288	E298	S302	E313	K319	Q320	LEU	GLY	HIS	HIS	HIS	HIS	HIS									
ASN	PRO	ASP	LYS	ILE	ASP	SER	LEU	ILE	ASN	GLN	ARG	SER	LEU	VAL	ASP	GLY	LEU	GLY	G201	G216	E217	H218	N228	V256	D266	S269	H288	E298	S302	E313	K319	Q320	LEU	GLY	HIS	HIS	HIS	HIS	HIS									
THR	TYR	GLY	ASN	GLY	ASP	SER	LEU	ASN	THR	GLY	LYS	LEU	ASN	VAL	LYS	VAL	ARG	PHE	ASP	ASP	ILE	GLY	ARG	GLY	THR	GLN	LEU	SER	GLY	THR	ASP	GLN	ILE	TYR	LYS	VAL	SER	ASN	LYS	GLY	ALA	ALA	LEU	GLY	ALA	LEU	GLY	THR
MET	GLY	PRO	ASP	SER	ASP	ARG	LEU	GLN	GLN	ARG	ARG	VAL	ALA	ALA	ASP	ILE	GLY	GLY	ALA	ASP	ALA	LEU	LEU	THR	ALA	ALA	PRO	LEU	ASP	HIS	LYS	ASP	GLN	SER	VAL	ARG	LYS	ASN	LYS	GLY	GLU	GLY	ALA	LEU	LEU	GLY	GLY	THR

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	74.79Å 75.95Å 40.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.06 15.00 – 2.06	Depositor EDS
% Data completeness (in resolution range)	98.6 (15.00-2.06) 98.3 (15.00-2.06)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.10 (at 2.07Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.179 , 0.213 0.182 , 0.218	Depositor DCC
R_{free} test set	746 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.411	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2060	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% 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: SO4

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	0.85	0/994	1.11	3/1334 (0.2%)
1	B	0.85	1/940 (0.1%)	1.11	4/1261 (0.3%)
All	All	0.85	1/1934 (0.1%)	1.11	7/2595 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	218	HIS	ND1-CE1	6.30	1.38	1.32

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	218	HIS	CB-CG-CD2	-7.75	121.13	131.20
1	B	228	ASN	N-CA-C	6.95	121.47	112.92
1	A	228	ASN	N-CA-C	6.83	121.32	112.92
1	A	266	ASP	CA-CB-CG	6.07	118.67	112.60
1	B	266	ASP	CA-CB-CG	5.93	118.53	112.60

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	973	0	931	3	0
1	B	922	0	890	4	0
2	A	30	0	0	0	0
2	B	15	0	0	1	0
3	A	64	0	0	0	0
3	B	56	0	0	1	0
All	All	2060	0	1821	7	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.

The worst 5 of 7 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:216:GLU:OE2	3:B:2013:HOH:O	2.13	0.67
1:B:302:SER:HB2	1:B:313:GLU:OE2	2.03	0.58
1:A:302:SER:HB2	1:A:313:GLU:OE2	2.04	0.58
1:B:288:HIS:NE2	2:B:1322:SO4:O1	2.45	0.49
1:A:298:GLU:HG2	1:A:319:LYS:HG2	1.95	0.48

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	123/267 (46%)	122 (99%)	1 (1%)	0	100	100
1	B	117/267 (44%)	116 (99%)	1 (1%)	0	100	100
All	All	240/534 (45%)	238 (99%)	2 (1%)	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	98/220 (44%)	94 (96%)	4 (4%)	27	21
1	B	93/220 (42%)	92 (99%)	1 (1%)	65	68
All	All	191/440 (43%)	186 (97%)	5 (3%)	40	37

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	208	GLN
1	A	310	LYS
1	A	320	GLN
1	A	321	LEU
1	B	269	SER

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

Mol	Chain	Res	Type
1	B	241	GLN
1	B	320	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](#)

9 ligands are 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	SO4	A	1328	-	4,4,4	0.25	0	6,6,6	0.18	0
2	SO4	B	1323	-	4,4,4	0.25	0	6,6,6	0.11	0
2	SO4	B	1322	-	4,4,4	0.23	0	6,6,6	0.34	0
2	SO4	A	1327	-	4,4,4	0.31	0	6,6,6	0.17	0
2	SO4	A	1330	-	4,4,4	0.20	0	6,6,6	0.28	0
2	SO4	A	1331	-	4,4,4	0.32	0	6,6,6	0.30	0
2	SO4	A	1326	-	4,4,4	0.27	0	6,6,6	0.22	0
2	SO4	A	1329	-	4,4,4	0.26	0	6,6,6	0.12	0
2	SO4	B	1321	-	4,4,4	0.22	0	6,6,6	0.18	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1322	SO4	1	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 [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	125/267 (46%)	-0.37	1 (0%) 82 84	16, 26, 49, 65	0
1	B	119/267 (44%)	-0.35	0 100 100	19, 27, 50, 72	0
All	All	244/534 (45%)	-0.36	1 (0%) 88 90	16, 27, 50, 72	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	GLY	2.2

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
2	SO4	B	1322	5/5	0.77	0.23	71,73,74,75	0
2	SO4	B	1323	5/5	0.79	0.11	109,109,110,110	0
2	SO4	A	1329	5/5	0.81	0.14	76,77,78,80	0
2	SO4	B	1321	5/5	0.83	0.14	76,77,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	1327	5/5	0.85	0.14	76,78,79,80	0
2	SO4	A	1331	5/5	0.87	0.10	57,59,59,60	0
2	SO4	A	1328	5/5	0.88	0.17	73,76,77,77	0
2	SO4	A	1330	5/5	0.89	0.13	59,60,62,63	0
2	SO4	A	1326	5/5	0.94	0.09	49,50,51,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.