



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 20, 2021 – 06:42 pm BST

PDB ID : 7OFZ  
Title : Nontypeable Haemophilus influenzae SapA in complex with double stranded RNA  
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Deposited on : 2021-05-05  
Resolution : 2.62 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

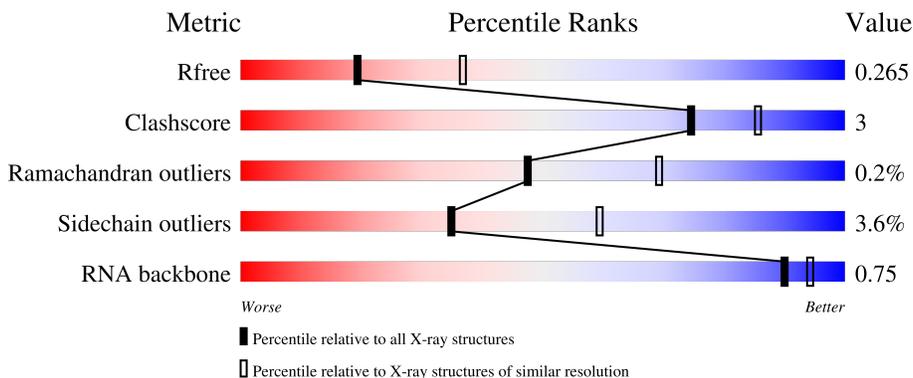
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.62 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))
$R_{free}$	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RNA backbone	3102	1062 (2.94-2.30)

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  $\geq 3$ , 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	526	 82% 12% 6%
2	C	19	 100%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4527 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 ABC-type transport system, periplasmic component, involved in antimicrobial peptide resistance.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	497	4005	2570	675	746	14	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	LYS	ARG	conflict	UNP Q4QL73

- Molecule 2 is a RNA chain called RNA (5'-R(P\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*GP\*GP\*GP\*GP\*GP\*GP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	19	407	180	75	133	19	0	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

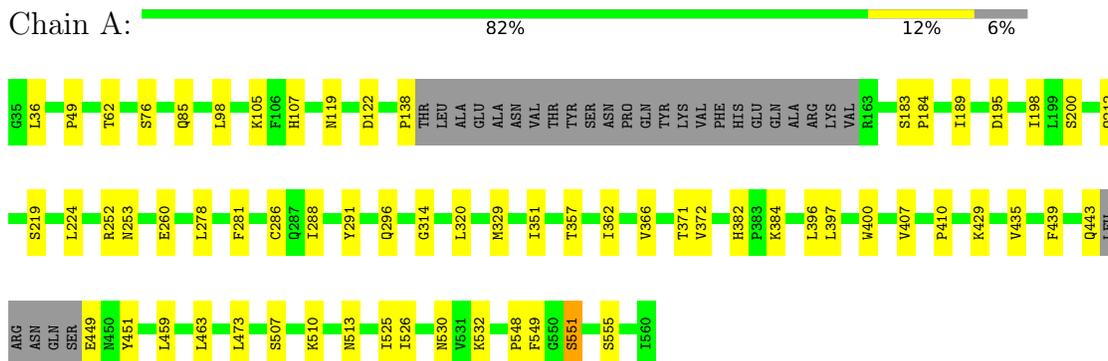
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total	O	0	0
			113	113		
4	C	1	Total	O	0	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: ABC-type transport system, periplasmic component, involved in antimicrobial peptide resistance



- Molecule 2: RNA (5'-R(P\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*GP\*GP\*GP\*GP\*GP\*GP\*GP\*GP\*GP\*G)-3')



There are no outlier residues recorded for this chain.

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.40Å 144.40Å 62.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.20 – 2.62 102.11 – 2.62	Depositor EDS
% Data completeness (in resolution range)	94.9 (72.20-2.62) 94.9 (102.11-2.62)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.62Å)	Xtrriage
Refinement program	BUSTER 2.10.3, REFMAC 7.04.09, PHENIX 2.5.6	Depositor
R, $R_{free}$	0.217 , 0.263 0.224 , 0.265	Depositor DCC
$R_{free}$ test set	940 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.0	Xtrriage
Anisotropy	0.409	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4527	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NA

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	0.50	0/4106	0.73	0/5579
2	C	1.11	0/453	0.91	0/705
All	All	0.59	0/4559	0.75	0/6284

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	4005	0	3938	27	0
2	C	407	0	210	0	0
3	A	1	0	0	0	0
4	A	113	0	0	1	0
4	C	1	0	0	0	0
All	All	4527	0	4148	27	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 3.

All (27) 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:357:THR:HB	1:A:530:ASN:HB2	1.73	0.70
1:A:314:GLY:HA2	1:A:366:VAL:HG21	1.80	0.64
1:A:371:THR:HG22	1:A:513:ASN:ND2	2.17	0.60
1:A:36:LEU:HD21	1:A:288:ILE:HD12	1.86	0.58
1:A:252:ARG:HD2	1:A:260:GLU:HG2	1.86	0.55
1:A:435:VAL:HG13	1:A:439:PHE:HD2	1.72	0.55
1:A:195:ASP:HB3	1:A:198:ILE:HG12	1.90	0.54
1:A:329:MET:HE2	1:A:397:LEU:HD22	1.89	0.54
1:A:382:HIS:CE1	1:A:384:LYS:HB2	2.44	0.53
1:A:98:LEU:HD11	1:A:189:ILE:HD11	1.91	0.53
1:A:200:SER:HB3	4:A:779:HOH:O	2.10	0.52
1:A:351:ILE:HG22	1:A:410:PRO:HD2	1.92	0.51
1:A:362:ILE:HD12	1:A:525:ILE:HD11	1.95	0.49
1:A:119:ASN:HB2	1:A:184:PRO:O	2.13	0.48
1:A:400:TRP:CD2	1:A:451:TYR:HB3	2.49	0.47
1:A:396:LEU:HD13	1:A:429:LYS:HD3	1.97	0.45
1:A:281:PHE:HA	1:A:286:CYS:HB3	1.97	0.45
1:A:122:ASP:HA	1:A:212:GLN:HB2	2.00	0.44
1:A:548:PRO:HD2	1:A:549:PHE:CE2	2.53	0.43
1:A:138:PRO:HD2	1:A:219:SER:HB3	2.01	0.43
1:A:320:LEU:HD23	1:A:526:ILE:HD12	2.00	0.43
1:A:400:TRP:CG	1:A:451:TYR:HB3	2.54	0.43
1:A:382:HIS:HE1	1:A:384:LYS:HB2	1.84	0.43
1:A:107:HIS:CE1	1:A:253:ASN:HD22	2.38	0.41
1:A:407:VAL:HG11	1:A:459:LEU:HD22	2.01	0.41
1:A:49:PRO:HD3	1:A:62:THR:HG21	2.03	0.41
1:A:278:LEU:HD12	1:A:296:GLN:HB3	2.03	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	492/526 (94%)	474 (96%)	17 (4%)	1 (0%)	47 69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	551	SER

### 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	440/466 (94%)	423 (96%)	17 (4%)	32 56

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	SER
1	A	85	GLN
1	A	105	LYS
1	A	183	SER
1	A	224	LEU
1	A	291[A]	TYR
1	A	291[B]	TYR
1	A	372	VAL
1	A	443	GLN
1	A	449	GLU
1	A	463	LEU
1	A	473	LEU
1	A	507	SER
1	A	510	LYS
1	A	532	LYS
1	A	551	SER
1	A	555	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	133	HIS
1	A	253	ASN
1	A	406	GLN
1	A	479	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	18/19 (94%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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

There are no chain breaks in this entry.

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

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.