



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2020 – 11:02 AM BST

PDB ID : 5NF4
Title : The tip fimbrial protein Mfa3 from Porphyromonas gingivalis with C-terminal truncation.
Authors : Hall, M.; Hasegawa, Y.; Yoshimura, F.; Persson, K.
Deposited on : 2017-03-13
Resolution : 1.75 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

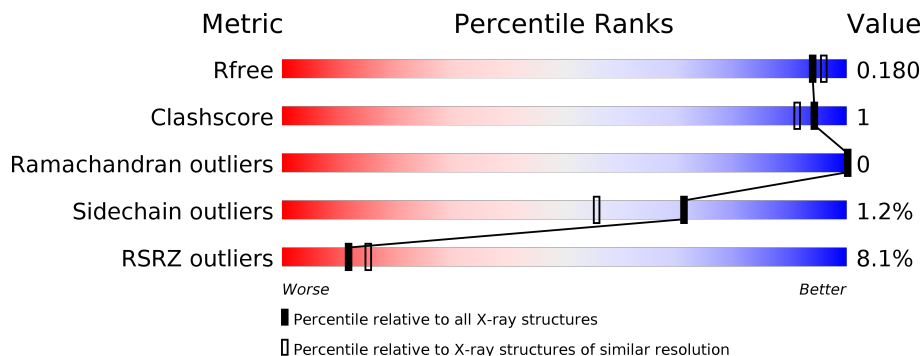
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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 on 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	451	 4% 63% 35%
1	B	451	 7% 62% 35%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9782 atoms, of which 4629 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 Minor fimbrium tip subunit Mfa3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	295	4668	1506	2312	407	433	10	0	0	0
1	B	295	4667	1506	2311	407	433	10	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

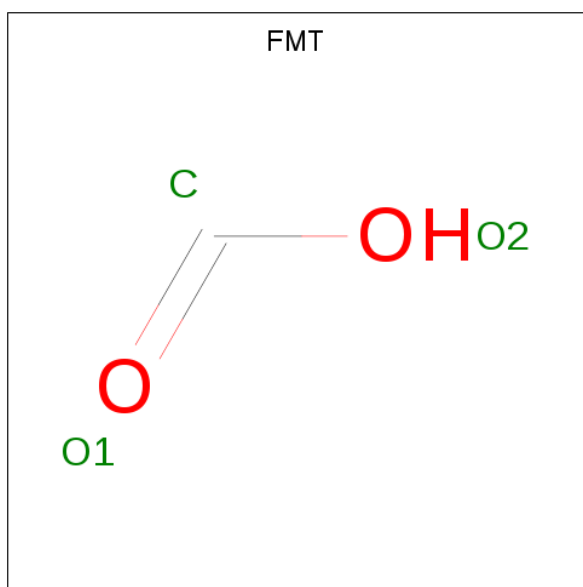
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MET	-	initiating methionine	UNP B2RHG3
A	-3	LYS	-	expression tag	UNP B2RHG3
A	-2	HIS	-	expression tag	UNP B2RHG3
A	-1	HIS	-	expression tag	UNP B2RHG3
A	0	HIS	-	expression tag	UNP B2RHG3
A	1	HIS	-	expression tag	UNP B2RHG3
A	2	HIS	-	expression tag	UNP B2RHG3
A	3	HIS	-	expression tag	UNP B2RHG3
A	4	PRO	-	expression tag	UNP B2RHG3
A	5	MET	-	expression tag	UNP B2RHG3
A	6	SER	-	expression tag	UNP B2RHG3
A	7	ASP	-	expression tag	UNP B2RHG3
A	8	TYR	-	expression tag	UNP B2RHG3
A	9	ASP	-	expression tag	UNP B2RHG3
A	10	ILE	-	expression tag	UNP B2RHG3
A	11	PRO	-	expression tag	UNP B2RHG3
A	12	THR	-	expression tag	UNP B2RHG3
A	13	THR	-	expression tag	UNP B2RHG3
A	14	GLU	-	expression tag	UNP B2RHG3
A	15	ASN	-	expression tag	UNP B2RHG3
A	16	LEU	-	expression tag	UNP B2RHG3
A	17	TYR	-	expression tag	UNP B2RHG3
A	18	PHE	-	expression tag	UNP B2RHG3
A	19	GLN	-	expression tag	UNP B2RHG3
A	20	GLY	-	expression tag	UNP B2RHG3

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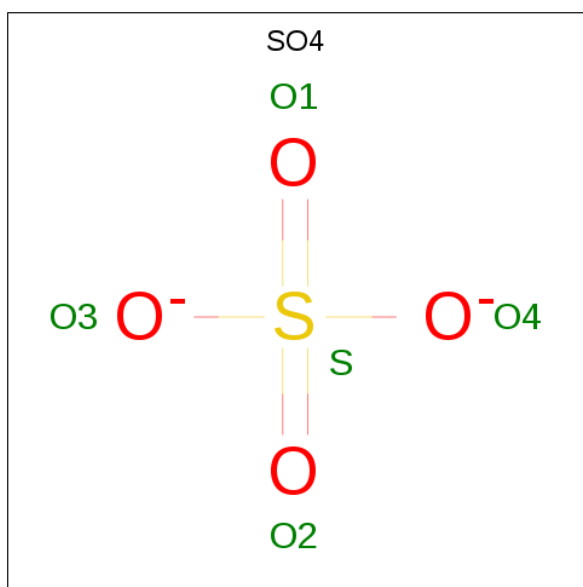
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ALA	-	expression tag	UNP B2RHG3
A	22	MET	-	expression tag	UNP B2RHG3
B	-4	MET	-	initiating methionine	UNP B2RHG3
B	-3	LYS	-	expression tag	UNP B2RHG3
B	-2	HIS	-	expression tag	UNP B2RHG3
B	-1	HIS	-	expression tag	UNP B2RHG3
B	0	HIS	-	expression tag	UNP B2RHG3
B	1	HIS	-	expression tag	UNP B2RHG3
B	2	HIS	-	expression tag	UNP B2RHG3
B	3	HIS	-	expression tag	UNP B2RHG3
B	4	PRO	-	expression tag	UNP B2RHG3
B	5	MET	-	expression tag	UNP B2RHG3
B	6	SER	-	expression tag	UNP B2RHG3
B	7	ASP	-	expression tag	UNP B2RHG3
B	8	TYR	-	expression tag	UNP B2RHG3
B	9	ASP	-	expression tag	UNP B2RHG3
B	10	ILE	-	expression tag	UNP B2RHG3
B	11	PRO	-	expression tag	UNP B2RHG3
B	12	THR	-	expression tag	UNP B2RHG3
B	13	THR	-	expression tag	UNP B2RHG3
B	14	GLU	-	expression tag	UNP B2RHG3
B	15	ASN	-	expression tag	UNP B2RHG3
B	16	LEU	-	expression tag	UNP B2RHG3
B	17	TYR	-	expression tag	UNP B2RHG3
B	18	PHE	-	expression tag	UNP B2RHG3
B	19	GLN	-	expression tag	UNP B2RHG3
B	20	GLY	-	expression tag	UNP B2RHG3
B	21	ALA	-	expression tag	UNP B2RHG3
B	22	MET	-	expression tag	UNP B2RHG3

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			5	1	2	2		
2	B	1	Total	C	H	O	0	0
			5	1	2	2		
2	B	1	Total	C	H	O	0	0
			5	1	2	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	232	Total	O	0	0
			232	232		
4	B	190	Total	O	0	0
			190	190		

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	80.18Å 80.18Å 116.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.52 – 1.75 44.52 – 1.75	Depositor EDS
% Data completeness (in resolution range)	93.2 (44.52-1.75) 93.2 (44.52-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.148 , 0.177 0.152 , 0.180	Depositor DCC
R_{free} test set	6009 reflections (7.61%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l 0.040 for h,-h-k,-l 0.022 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9782	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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: FMT, 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	0.53	0/2417	0.66	1/3285 (0.0%)
1	B	0.48	0/2417	0.61	1/3285 (0.0%)
All	All	0.51	0/4834	0.63	2/6570 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ASP	CB-CG-OD1	5.52	123.27	118.30
1	B	317	ARG	NE-CZ-NH2	-5.45	117.58	120.30

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	2356	2312	2311	7	0
1	B	2356	2311	2311	6	0
2	A	3	2	1	0	0
2	B	6	4	2	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	232	0	0	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	190	0	0	0	1
All	All	5153	4629	4625	12	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 1.

The worst 5 of 12 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:147:ASN:OD1	1:A:236:ARG:NH1	2.22	0.73
1:B:83:HIS:NE2	1:B:85:SER:OG	2.45	0.49
1:B:134:MET:HB3	1:B:220:VAL:HG13	1.97	0.47
1:A:311:PRO:HG2	1:A:313:TYR:CZ	2.48	0.47
1:A:275:LEU:HD11	1:A:325:ILE:HD13	1.97	0.46

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)
4:A:694:HOH:O	4:B:786:HOH:O[3_555]	2.07	0.13

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	291/451 (64%)	285 (98%)	6 (2%)	0	100	100
1	B	291/451 (64%)	284 (98%)	7 (2%)	0	100	100
All	All	582/902 (64%)	569 (98%)	13 (2%)	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	258/392 (66%)	257 (100%)	1 (0%)	91	86
1	B	258/392 (66%)	253 (98%)	5 (2%)	57	36
All	All	516/784 (66%)	510 (99%)	6 (1%)	71	56

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	205	LEU
1	B	324	ARG
1	B	248	MET
1	B	87	SER
1	B	278	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
3	SO4	A	502	-	4,4,4	0.13	0	6,6,6	0.11	0
2	FMT	A	501	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	501	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	502	-	0,2,2	0.00	-	0,1,1	0.00	-
3	SO4	B	503	-	4,4,4	0.17	0	6,6,6	0.05	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.

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	295/451 (65%)	0.39	16 (5%) 25 30	28, 41, 71, 120	0
1	B	295/451 (65%)	0.69	32 (10%) 5 7	28, 45, 87, 142	0
All	All	590/902 (65%)	0.54	48 (8%) 12 15	28, 43, 81, 142	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	ILE	15.6
1	B	92	THR	12.2
1	B	88	ILE	9.6
1	B	90	SER	8.8
1	B	93	SER	7.8

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 monosaccharides 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(\AA^2)	Q<0.9
3	SO4	A	502	5/5	0.92	0.14	85,85,88,89	5
2	FMT	B	502	3/3	0.94	0.21	47,54,65,69	0
3	SO4	B	503	5/5	0.94	0.10	85,87,92,96	0
2	FMT	A	501	3/3	0.97	0.18	48,53,62,64	0
2	FMT	B	501	3/3	0.97	0.07	53,71,85,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.