



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:56 AM UTC

PDB ID : 4J3O / pdb_00004j3o
Title : Crystal structure of the FimD usher traversed by the pilus tip complex assembly composed of FimC:FimF:FimG:FimH
Authors : Geibel, S.; Waksman, G.
Deposited on : 2013-02-06
Resolution : 3.80 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
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

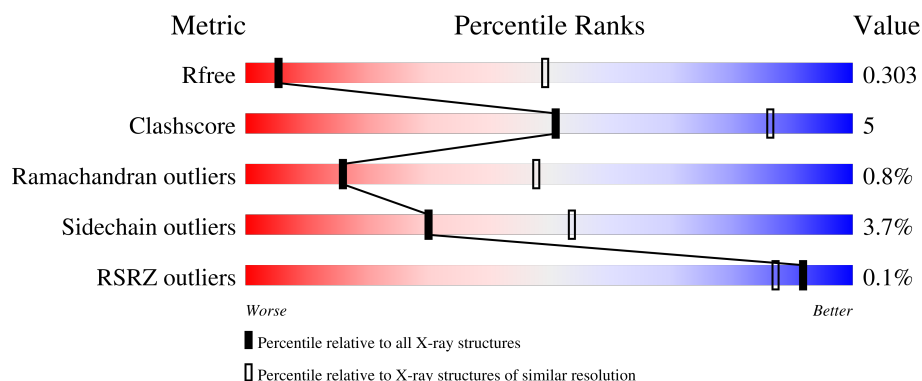
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	G	144	89% 10% .
2	H	279	82% 17% .
3	C	211	82% 11% . 6%
4	F	154	82% 16% .
5	D	843	76% 16% . 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11732 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 Protein FimG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	144	Total	C	N	O	S	0	0	0
			1043	640	176	224	3			

- Molecule 2 is a protein called Protein FimH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	279	Total	C	N	O	S	0	0	0
			2051	1297	342	408	4			

- Molecule 3 is a protein called Chaperone protein FimC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	199	Total	C	N	O	S	0	0	0
			1550	981	268	295	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	206	HIS	-	expression tag	UNP P31697
C	207	HIS	-	expression tag	UNP P31697
C	208	HIS	-	expression tag	UNP P31697
C	209	HIS	-	expression tag	UNP P31697
C	210	HIS	-	expression tag	UNP P31697
C	211	HIS	-	expression tag	UNP P31697

- Molecule 4 is a protein called Protein FimF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	154	Total	C	N	O	S	0	0	0
			1137	711	196	226	4			

- Molecule 5 is a protein called Outer membrane usher protein FimD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	778	Total	C	N	O	S	0	0	0
			5951	3714	1055	1163	19			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	348	PRO	THR	conflict	UNP P30130
D	834	SER	-	expression tag	UNP P30130
D	835	ALA	-	expression tag	UNP P30130
D	836	TRP	-	expression tag	UNP P30130
D	837	SER	-	expression tag	UNP P30130
D	838	HIS	-	expression tag	UNP P30130
D	839	PRO	-	expression tag	UNP P30130
D	840	GLN	-	expression tag	UNP P30130
D	841	PHE	-	expression tag	UNP P30130
D	842	GLU	-	expression tag	UNP P30130
D	843	LYS	-	expression tag	UNP P30130

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.

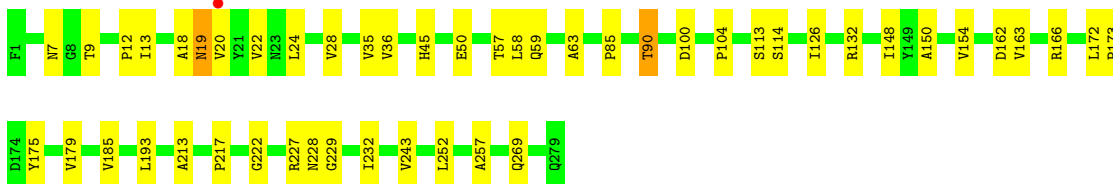
- Molecule 1: Protein FimG

Chain G:  89% 10% .



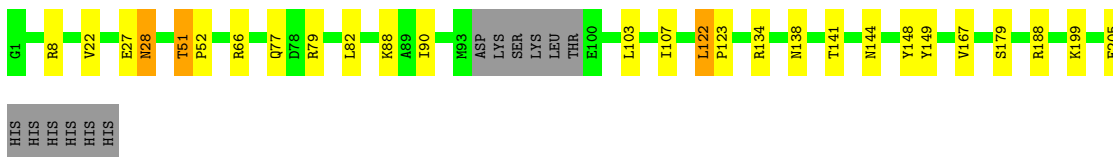
- Molecule 2: Protein FimH

Chain H:  82% 17% .



- Molecule 3: Chaperone protein FimC

Chain C:  82% 11% . 6%



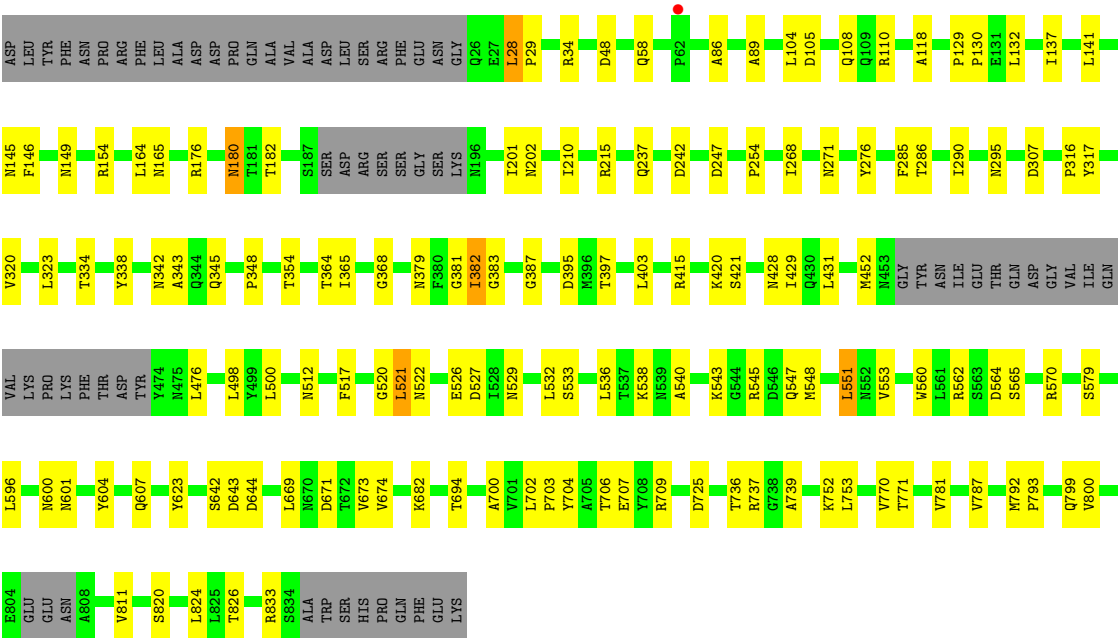
- Molecule 4: Protein FimF

Chain F:  82% 16% .



- Molecule 5: Outer membrane usher protein FimD

Chain D:  76% 16% . 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	122.36Å 122.36Å 328.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.67 – 3.80 83.67 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (83.67-3.80) 86.0 (83.67-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.43 (at 3.78Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.248 , 0.299 0.255 , 0.303	Depositor DCC
R_{free} test set	1263 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	160.2	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 151.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11732	wwPDB-VP
Average B, all atoms (Å ²)	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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](#)

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	G	0.26	0/1057	0.68	0/1445
2	H	0.26	0/2096	0.68	0/2881
3	C	0.27	0/1578	0.75	4/2146 (0.2%)
4	F	0.28	0/1157	0.69	0/1584
5	D	0.25	0/6079	0.66	0/8276
All	All	0.26	0/11967	0.68	4/16332 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	167	VAL	CA-C-N	5.32	123.54	119.66
3	C	167	VAL	C-N-CA	5.32	123.54	119.66
3	C	122	LEU	CA-C-N	5.03	123.33	119.66
3	C	122	LEU	C-N-CA	5.03	123.33	119.66

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	G	1043	0	1009	11	0
2	H	2051	0	2007	26	0
3	C	1550	0	1582	13	0
4	F	1137	0	1126	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	5951	0	5656	67	0
All	All	11732	0	11380	121	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 5.

The worst 5 of 121 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)
5:D:562:ARG:HG2	5:D:564:ASP:H	1.53	0.72
5:D:165:ASN:HA	5:D:182:THR:HG22	1.74	0.69
2:H:12:PRO:HA	2:H:18:ALA:HB2	1.75	0.68
5:D:538:LYS:HD2	5:D:545:ARG:HG2	1.76	0.68
2:H:163:VAL:HG12	2:H:185:VAL:HG22	1.76	0.67

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	G	142/144 (99%)	130 (92%)	11 (8%)	1 (1%)	18	51
2	H	277/279 (99%)	250 (90%)	23 (8%)	4 (1%)	9	37
3	C	195/211 (92%)	181 (93%)	14 (7%)	0	100	100
4	F	152/154 (99%)	135 (89%)	15 (10%)	2 (1%)	9	38
5	D	770/843 (91%)	701 (91%)	64 (8%)	5 (1%)	21	54
All	All	1536/1631 (94%)	1397 (91%)	127 (8%)	12 (1%)	16	48

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	27	VAL
2	H	228	ASN
1	G	98	THR
2	H	7	ASN
5	D	452	MET

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	G	115/115 (100%)	113 (98%)	2 (2%)	53	67
2	H	226/226 (100%)	220 (97%)	6 (3%)	39	59
3	C	170/182 (93%)	163 (96%)	7 (4%)	27	51
4	F	124/124 (100%)	118 (95%)	6 (5%)	23	47
5	D	621/694 (90%)	596 (96%)	25 (4%)	28	52
All	All	1256/1341 (94%)	1210 (96%)	46 (4%)	30	54

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	D	271	ASN
5	D	527	ASP
5	D	286	THR
5	D	500	LEU
5	D	543	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	40	ASN
5	D	688	ASN
5	D	295	ASN
5	D	799	GLN
5	D	583	ASN

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	G	144/144 (100%)	-0.65	0	100 100	119, 153, 181, 201	1 (0%)
2	H	279/279 (100%)	-0.86	1 (0%)	88 74	118, 187, 225, 290	2 (0%)
3	C	199/211 (94%)	-0.91	0	100 100	108, 202, 249, 262	1 (0%)
4	F	154/154 (100%)	-0.76	0	100 100	136, 211, 304, 331	0
5	D	778/843 (92%)	-0.70	1 (0%)	92 87	110, 180, 318, 369	2 (0%)
All	All	1554/1631 (95%)	-0.76	2 (0%)	92 87	108, 184, 288, 369	6 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	20	VAL	2.4
5	D	62	PRO	2.1

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.