



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:49 AM UTC

PDB ID : 1KLF / pdb_00001klf
Title : FIMH ADHESIN-FIMC CHAPERONE COMPLEX WITH D-MANNOSE
Authors : Hung, C.S.; Bouckaert, J.
Deposited on : 2001-12-11
Resolution : 2.79 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
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

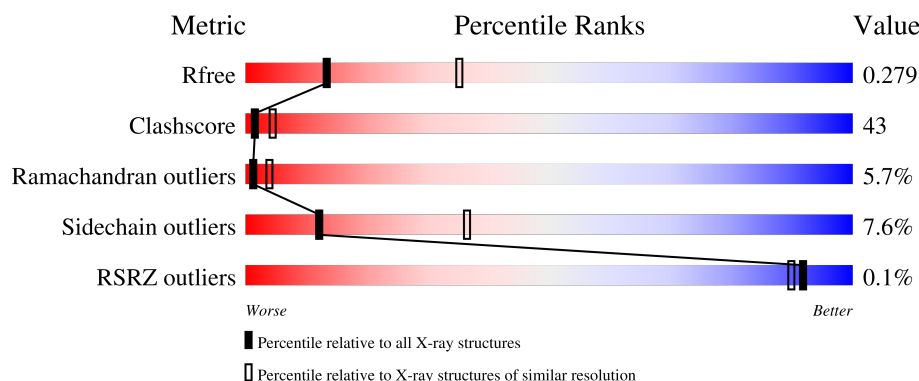
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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.



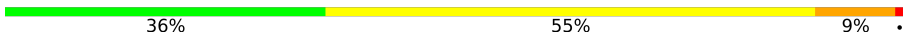
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	205	40% 48% 12%
1	C	205	41% 45% 14%
1	E	205	40% 46% 13%
1	G	205	39% 48% 13%
1	I	205	36% 54% 9%

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Mol	Chain	Length	Quality of chain
1	K	205	 37% 54% 9%
1	M	205	 36% 55% 9%
1	O	205	 36% 54% 9%
2	B	279	 53% 37% 10%
2	D	279	 55% 35% 10%
2	F	279	 54% 36% 10%
2	H	279	 53% 37% 10%
2	J	279	 32% 59% 9%
2	L	279	 31% 61% 8%
2	N	279	 32% 59% 8%
2	P	279	 31% 61% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29775 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 CHAPERONE PROTEIN FIMC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	C	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	E	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	G	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	I	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	K	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	M	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			
1	O	205	Total	C	N	O	S	0	0	0
			1596	1010	276	304	6			

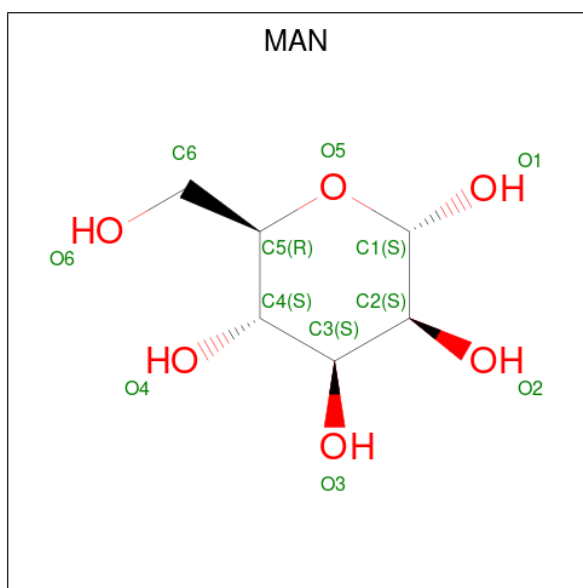
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	VAL	GLU	conflict	UNP P31697
C	18	VAL	GLU	conflict	UNP P31697
E	18	VAL	GLU	conflict	UNP P31697
G	18	VAL	GLU	conflict	UNP P31697
I	18	VAL	GLU	conflict	UNP P31697
K	18	VAL	GLU	conflict	UNP P31697
M	18	VAL	GLU	conflict	UNP P31697
O	18	VAL	GLU	conflict	UNP P31697

- Molecule 2 is a protein called FIMH PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	D	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	F	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	H	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	J	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	L	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	N	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			
2	P	279	Total	C	N	O	S	0	0	0
			2052	1297	342	409	4			

- Molecule 3 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			12	6	6		
3	D	1	Total	C	O	0	0
			12	6	6		
3	F	1	Total	C	O	0	0
			12	6	6		
3	H	1	Total	C	O	0	0
			12	6	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	J	1	Total	C	O	0	0
			12	6	6		
3	L	1	Total	C	O	0	0
			12	6	6		
3	N	1	Total	C	O	0	0
			12	6	6		
3	P	1	Total	C	O	0	0
			12	6	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	34	Total	O	0	0
			34	34		
4	B	82	Total	O	0	0
			82	82		
4	C	37	Total	O	0	0
			37	37		
4	D	69	Total	O	0	0
			69	69		
4	E	39	Total	O	0	0
			39	39		
4	F	78	Total	O	0	0
			78	78		
4	G	39	Total	O	0	0
			39	39		
4	H	73	Total	O	0	0
			73	73		
4	I	2	Total	O	0	0
			2	2		
4	J	9	Total	O	0	0
			9	9		
4	K	4	Total	O	0	0
			4	4		
4	L	8	Total	O	0	0
			8	8		
4	M	2	Total	O	0	0
			2	2		
4	N	8	Total	O	0	0
			8	8		
4	O	4	Total	O	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	7	Total	O	0	0
			7	7		

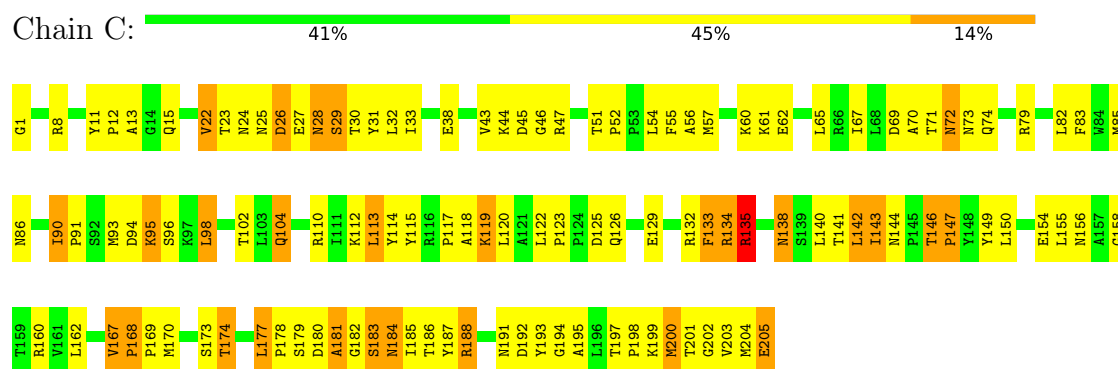
3 Residue-property plots

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: CHAPERONE PROTEIN FIMC



• Molecule 1: CHAPERONE PROTEIN FIMC



• Molecule 1: CHAPERONE PROTEIN FIMC

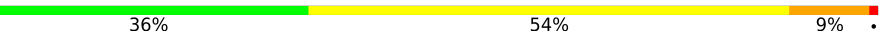


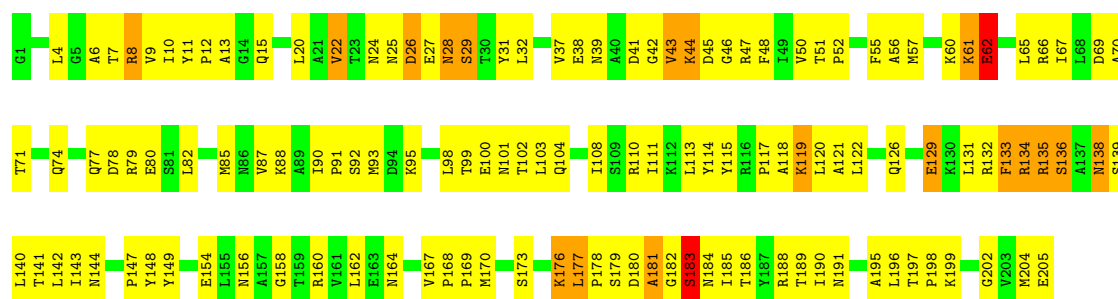
- Molecule 1: CHAPERONE PROTEIN FIMC

Chain G: 



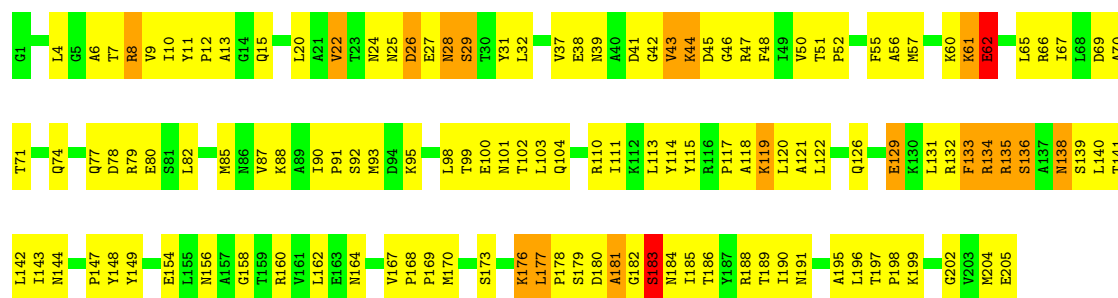
- Molecule 1: CHAPERONE PROTEIN FIMC

Chain I: 



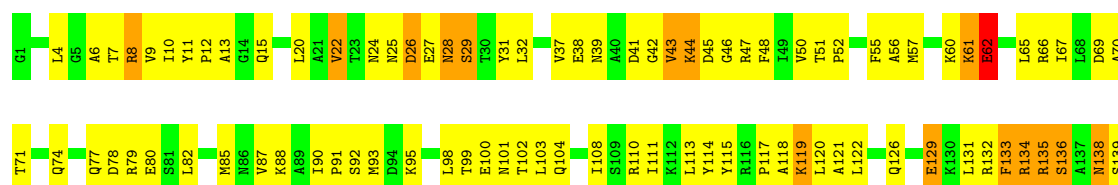
- Molecule 1: CHAPERONE PROTEIN FIMC

Chain K: 



- Molecule 1: CHAPERONE PROTEIN FIMC

Chain M: 





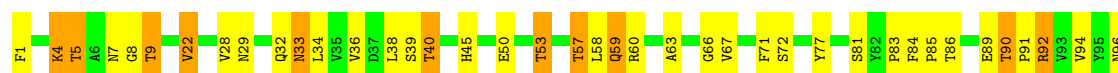
• Molecule 1: CHAPERONE PROTEIN FIMC



• Molecule 2: FIMH PROTEIN

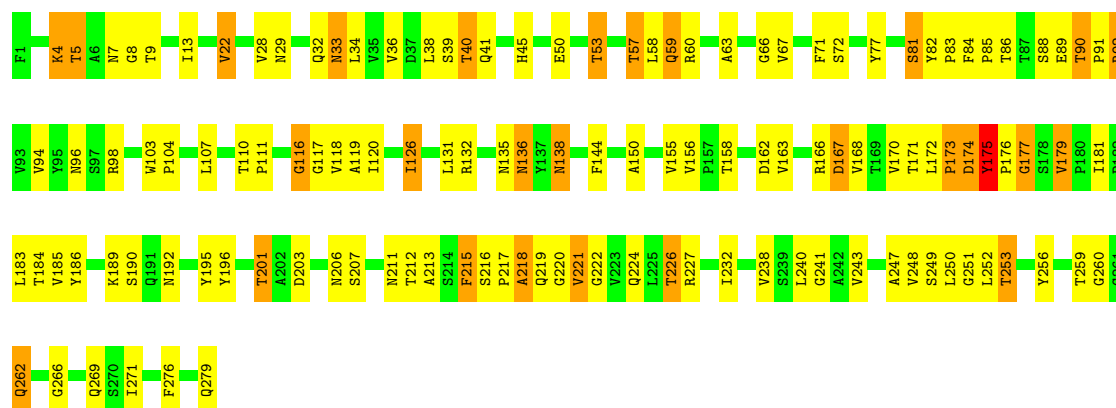


• Molecule 2: FIMH PROTEIN

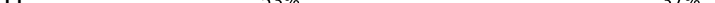


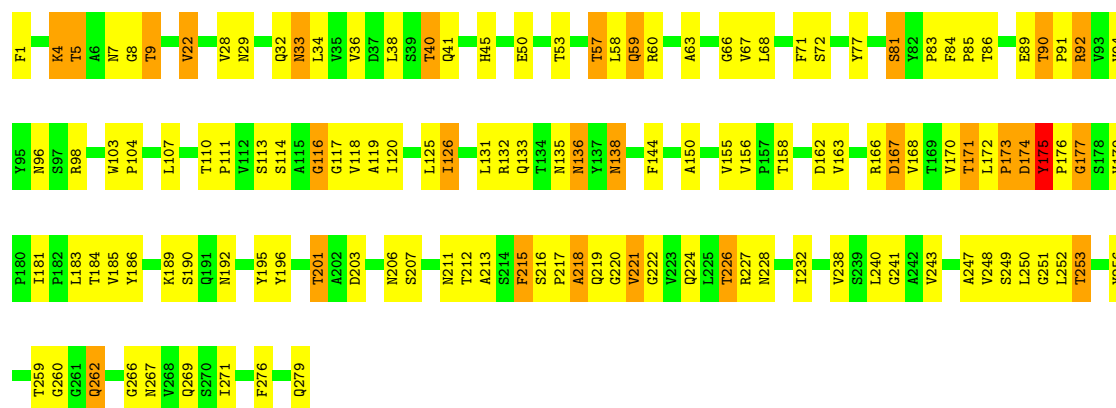
• Molecule 2: FIMH PROTEIN

Chain F: 54% 36% 10%

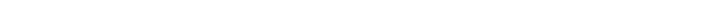


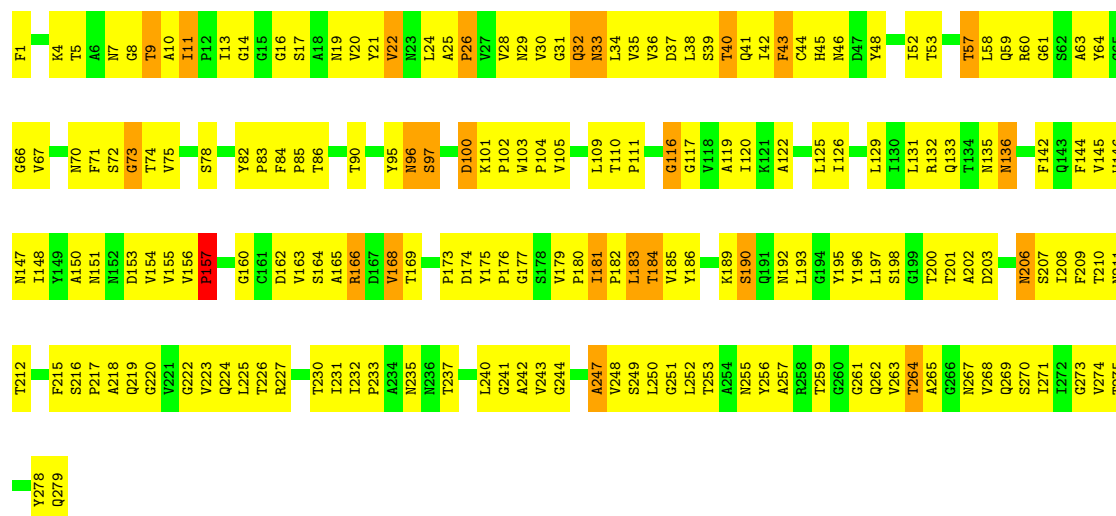
- Molecule 2: FIMH PROTEIN

Chain H:  53% 37% 10%

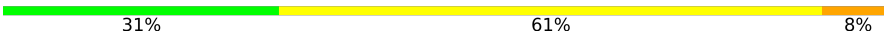


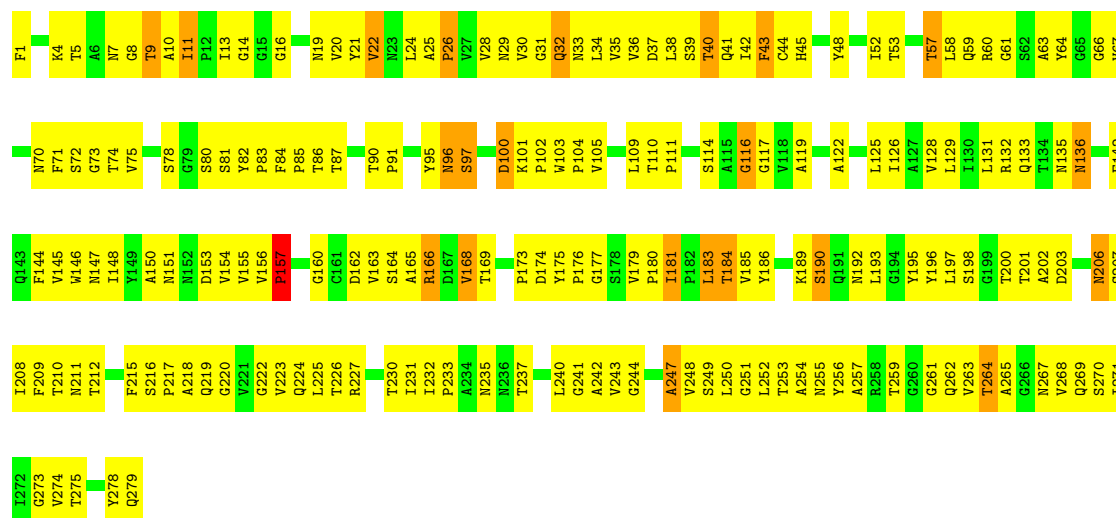
- Molecule 2: FIMH PROTEIN

Chain J:  32% 59% 9%

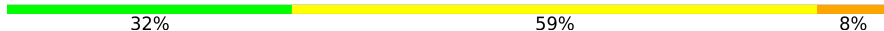


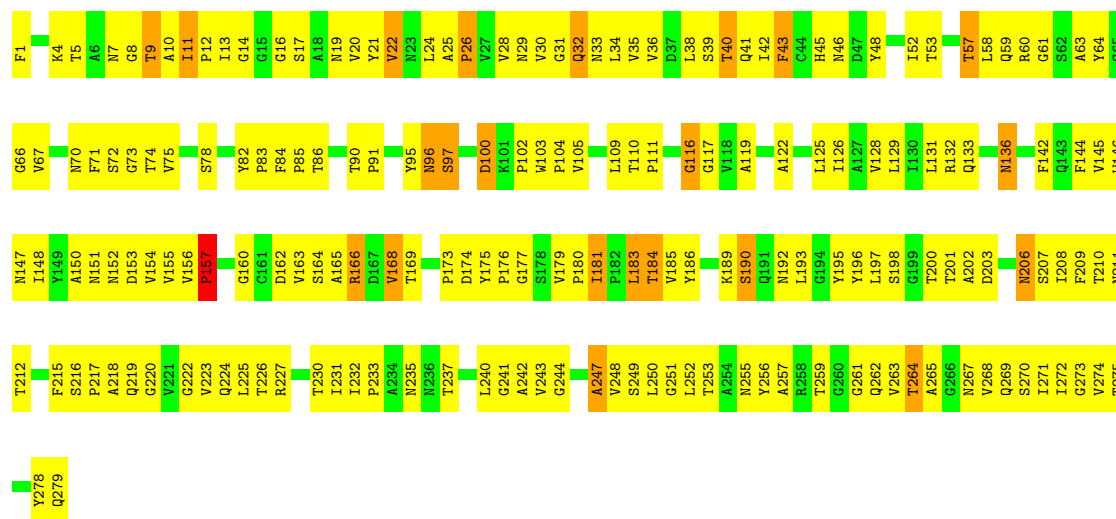
- Molecule 2: FIMH PROTEIN

Chain L: 

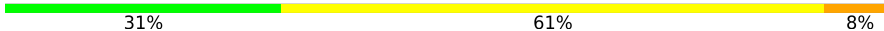


- Molecule 2: FIMH PROTEIN

Chain N: 



- Molecule 2: FIMH PROTEIN

Chain P: 





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.08Å 138.13Å 215.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.68 – 2.79 43.68 – 2.79	Depositor EDS
% Data completeness (in resolution range)	98.9 (43.68-2.79) 99.0 (43.68-2.79)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.239 , 0.280 0.240 , 0.279	Depositor DCC
R_{free} test set	9936 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	59.1	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 80.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.477 for k,h,-l 0.476 for -k,-h,-l 0.477 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	29775	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.45% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MAN

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	0.54	0/1625	1.13	15/2209 (0.7%)
1	C	0.54	0/1625	1.13	17/2209 (0.8%)
1	E	0.54	0/1625	1.13	18/2209 (0.8%)
1	G	0.54	0/1625	1.13	17/2209 (0.8%)
1	I	0.37	0/1625	0.97	6/2209 (0.3%)
1	K	0.37	0/1625	0.97	6/2209 (0.3%)
1	M	0.37	0/1625	0.97	6/2209 (0.3%)
1	O	0.38	0/1625	0.97	6/2209 (0.3%)
2	B	0.60	0/2097	1.11	13/2881 (0.5%)
2	D	0.61	0/2097	1.12	13/2881 (0.5%)
2	F	0.60	0/2097	1.11	12/2881 (0.4%)
2	H	0.60	0/2097	1.11	13/2881 (0.5%)
2	J	0.36	0/2097	0.92	7/2881 (0.2%)
2	L	0.36	0/2097	0.92	7/2881 (0.2%)
2	N	0.36	0/2097	0.92	7/2881 (0.2%)
2	P	0.36	0/2097	0.92	7/2881 (0.2%)
All	All	0.48	0/29776	1.04	170/40720 (0.4%)

There are no bond length outliers.

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	167	VAL	CA-C-N	9.17	126.35	119.66
1	E	167	VAL	C-N-CA	9.17	126.35	119.66
1	A	167	VAL	CA-C-N	8.98	126.21	119.66
1	A	167	VAL	C-N-CA	8.98	126.21	119.66
1	G	167	VAL	CA-C-N	8.87	126.13	119.66

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	1596	0	1639	144	0
1	C	1596	0	1639	154	0
1	E	1596	0	1639	137	0
1	G	1596	0	1639	143	0
1	I	1596	0	1639	156	0
1	K	1596	0	1639	156	0
1	M	1596	0	1639	158	0
1	O	1596	0	1639	158	0
2	B	2052	0	2007	146	0
2	D	2052	0	2007	146	0
2	F	2052	0	2007	140	0
2	H	2052	0	2007	146	0
2	J	2052	0	2007	206	0
2	L	2052	0	2007	212	0
2	N	2052	0	2007	211	0
2	P	2052	0	2007	214	0
3	B	12	0	12	0	0
3	D	12	0	12	0	0
3	F	12	0	12	0	0
3	H	12	0	12	0	0
3	J	12	0	12	3	0
3	L	12	0	12	2	0
3	N	12	0	12	1	0
3	P	12	0	12	2	0
4	A	34	0	0	3	0
4	B	82	0	0	3	0
4	C	37	0	0	1	0
4	D	69	0	0	4	0
4	E	39	0	0	0	0
4	F	78	0	0	4	0
4	G	39	0	0	3	0
4	H	73	0	0	4	0
4	I	2	0	0	0	0
4	J	9	0	0	1	0
4	K	4	0	0	0	0
4	L	8	0	0	1	0
4	M	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	N	8	0	0	0	0
4	O	4	0	0	0	0
4	P	7	0	0	0	0
All	All	29775	0	29264	2522	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 43.

The worst 5 of 2522 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:134:ARG:HB3	1:C:141:THR:HG22	1.26	1.14
2:F:126:ILE:HD12	2:F:150:ALA:HB2	1.33	1.10
2:P:224:GLN:HE21	2:P:231:ILE:HG21	1.16	1.10
2:H:126:ILE:HD12	2:H:150:ALA:HB2	1.34	1.09
2:D:126:ILE:HD12	2:D:150:ALA:HB2	1.33	1.09

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	203/205 (99%)	163 (80%)	29 (14%)	11 (5%)	1	4
1	C	203/205 (99%)	164 (81%)	28 (14%)	11 (5%)	1	4
1	E	203/205 (99%)	163 (80%)	29 (14%)	11 (5%)	1	4
1	G	203/205 (99%)	164 (81%)	28 (14%)	11 (5%)	1	4
1	I	203/205 (99%)	162 (80%)	29 (14%)	12 (6%)	1	3
1	K	203/205 (99%)	162 (80%)	29 (14%)	12 (6%)	1	3
1	M	203/205 (99%)	162 (80%)	29 (14%)	12 (6%)	1	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	203/205 (99%)	163 (80%)	28 (14%)	12 (6%)	1	3
2	B	277/279 (99%)	244 (88%)	24 (9%)	9 (3%)	3	11
2	D	277/279 (99%)	243 (88%)	24 (9%)	10 (4%)	2	10
2	F	277/279 (99%)	244 (88%)	23 (8%)	10 (4%)	2	10
2	H	277/279 (99%)	243 (88%)	24 (9%)	10 (4%)	2	10
2	J	277/279 (99%)	195 (70%)	60 (22%)	22 (8%)	1	1
2	L	277/279 (99%)	195 (70%)	60 (22%)	22 (8%)	1	1
2	N	277/279 (99%)	195 (70%)	60 (22%)	22 (8%)	1	1
2	P	277/279 (99%)	196 (71%)	59 (21%)	22 (8%)	1	1
All	All	3840/3872 (99%)	3058 (80%)	563 (15%)	219 (6%)	1	4

5 of 219 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	A	119	LYS
1	A	181	ALA
1	A	183	SER
2	B	175	TYR

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	176/176 (100%)	157 (89%)	19 (11%)	6	21
1	C	176/176 (100%)	157 (89%)	19 (11%)	6	21
1	E	176/176 (100%)	157 (89%)	19 (11%)	6	21
1	G	176/176 (100%)	157 (89%)	19 (11%)	6	21
1	I	176/176 (100%)	163 (93%)	13 (7%)	13	37
1	K	176/176 (100%)	163 (93%)	13 (7%)	13	37
1	M	176/176 (100%)	163 (93%)	13 (7%)	13	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	176/176 (100%)	163 (93%)	13 (7%)	13	37
2	B	226/226 (100%)	205 (91%)	21 (9%)	8	27
2	D	226/226 (100%)	204 (90%)	22 (10%)	8	25
2	F	226/226 (100%)	203 (90%)	23 (10%)	7	23
2	H	226/226 (100%)	205 (91%)	21 (9%)	8	27
2	J	226/226 (100%)	218 (96%)	8 (4%)	32	67
2	L	226/226 (100%)	218 (96%)	8 (4%)	32	67
2	N	226/226 (100%)	219 (97%)	7 (3%)	35	70
2	P	226/226 (100%)	218 (96%)	8 (4%)	32	67
All	All	3216/3216 (100%)	2970 (92%)	246 (8%)	12	36

5 of 246 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	138	ASN
2	N	136	ASN
2	H	5	THR
2	N	57	THR
1	O	183	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	96	ASN
2	L	138	ASN
2	P	191	GLN
2	J	151	ASN
1	K	72	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

8 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	MAN	H	1603	-	12,12,12	0.40	0	17,17,17	0.47	0
3	MAN	D	1601	-	12,12,12	0.35	0	17,17,17	0.49	0
3	MAN	B	1500	-	12,12,12	0.38	0	17,17,17	0.37	0
3	MAN	N	1506	-	12,12,12	0.26	0	17,17,17	0.43	0
3	MAN	P	1607	-	12,12,12	0.29	0	17,17,17	0.39	0
3	MAN	J	1605	-	12,12,12	0.29	0	17,17,17	0.35	0
3	MAN	L	1504	-	12,12,12	0.30	0	17,17,17	0.44	0
3	MAN	F	1502	-	12,12,12	0.37	0	17,17,17	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	H	1603	-	-	2/2/22/22	0/1/1/1
3	MAN	D	1601	-	-	1/2/22/22	0/1/1/1
3	MAN	B	1500	-	-	2/2/22/22	0/1/1/1
3	MAN	N	1506	-	-	0/2/22/22	0/1/1/1
3	MAN	P	1607	-	-	0/2/22/22	0/1/1/1
3	MAN	J	1605	-	-	0/2/22/22	0/1/1/1
3	MAN	L	1504	-	-	0/2/22/22	0/1/1/1
3	MAN	F	1502	-	-	1/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1603	MAN	C4-C5-C6-O6
3	B	1500	MAN	C4-C5-C6-O6
3	B	1500	MAN	O5-C5-C6-O6
3	H	1603	MAN	O5-C5-C6-O6
3	D	1601	MAN	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	N	1506	MAN	1	0
3	P	1607	MAN	2	0
3	J	1605	MAN	3	0
3	L	1504	MAN	2	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

6.1 Protein, DNA and RNA chains

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	205/205 (100%)	-1.24	0 100 100	20, 55, 108, 132	0
1	C	205/205 (100%)	-1.29	0 100 100	20, 57, 108, 130	0
1	E	205/205 (100%)	-1.25	0 100 100	20, 59, 108, 129	0
1	G	205/205 (100%)	-1.28	0 100 100	19, 58, 110, 132	0
1	I	205/205 (100%)	-0.61	0 100 100	20, 168, 190, 196	0
1	K	205/205 (100%)	-0.59	0 100 100	20, 171, 195, 198	0
1	M	205/205 (100%)	-0.53	0 100 100	20, 170, 193, 198	0
1	O	205/205 (100%)	-0.61	2 (0%) 79 72	20, 168, 193, 198	0
2	B	279/279 (100%)	-1.36	0 100 100	17, 40, 79, 114	0
2	D	279/279 (100%)	-1.36	0 100 100	18, 41, 80, 116	0
2	F	279/279 (100%)	-1.34	0 100 100	18, 41, 83, 112	0
2	H	279/279 (100%)	-1.34	0 100 100	17, 42, 83, 114	0
2	J	279/279 (100%)	-0.74	0 100 100	51, 112, 192, 200	0
2	L	279/279 (100%)	-0.70	0 100 100	56, 113, 190, 200	0
2	N	279/279 (100%)	-0.75	0 100 100	53, 115, 193, 200	0
2	P	279/279 (100%)	-0.78	0 100 100	50, 112, 191, 200	0
All	All	3872/3872 (100%)	-1.00	2 (0%) 92 90	17, 85, 186, 200	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	105	LEU	2.9
1	O	103	LEU	2.4

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($\text{\AA}^2$)	Q<0.9
3	MAN	H	1603	12/12	0.98	0.04	28,34,39,39	0
3	MAN	L	1504	12/12	0.98	0.04	96,99,103,106	0
3	MAN	N	1506	12/12	0.98	0.05	90,94,100,101	0
3	MAN	B	1500	12/12	0.99	0.04	30,35,39,39	0
3	MAN	J	1605	12/12	0.99	0.05	96,100,105,106	0
3	MAN	D	1601	12/12	0.99	0.03	28,36,41,41	0
3	MAN	F	1502	12/12	0.99	0.05	29,35,41,41	0
3	MAN	P	1607	12/12	0.99	0.04	110,112,116,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.