



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:20 AM UTC

PDB ID : 7VHP / pdb_00007vhp
EMDB ID : EMD-32002
Title : Structural insights into the membrane microdomain organization by SPFH family proteins
Authors : Ma, C.Y.; Wang, C.K.; Luo, D.Y.; Yan, L.; Yang, W.X.; Li, N.N.; Gao, N.
Deposited on : 2021-09-22
Resolution : 3.27 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

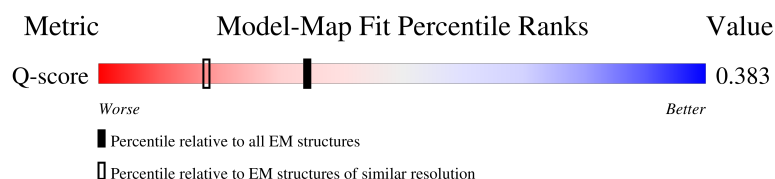
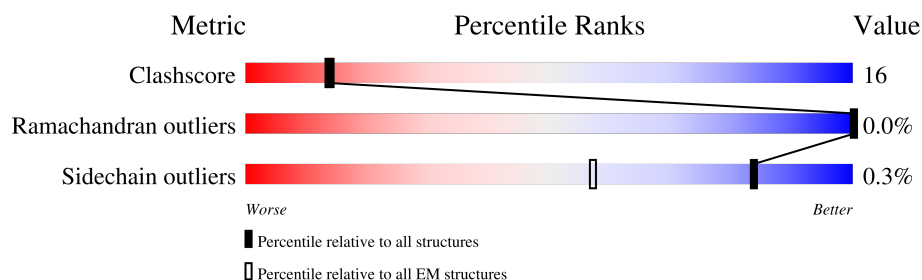
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.27 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.



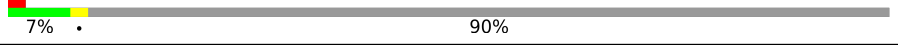
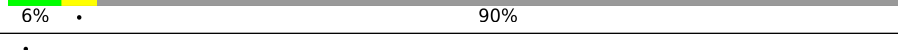
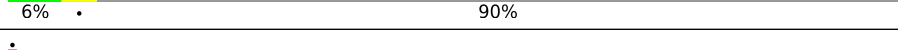
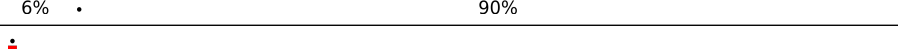
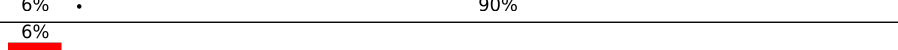
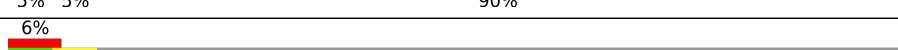
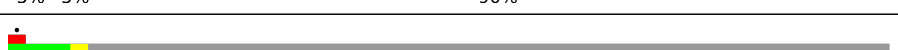
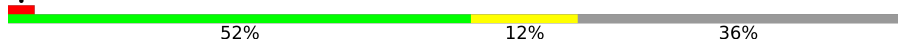
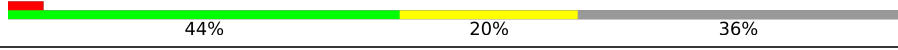
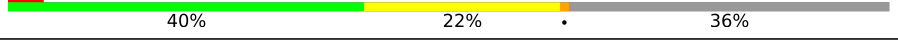
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14508 (2.77 - 3.77)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	644	 6% . 90%
1	B	644	 6% . 90%
1	C	644	 5% 5% 90%
1	D	644	 7% . 90%

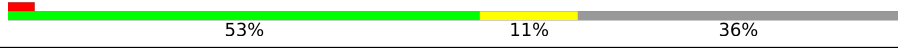
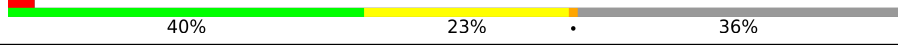
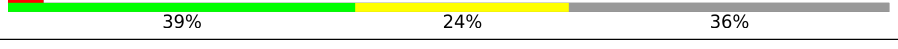
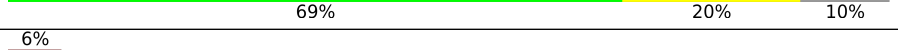
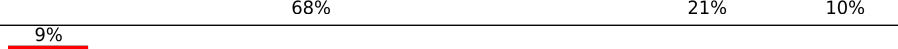
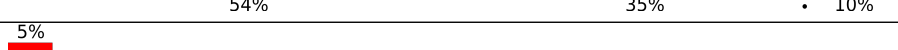
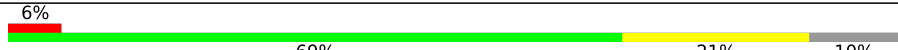
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Mol	Chain	Length	Quality of chain
1	J	644	 6% 90%
1	K	644	 6% 90%
1	L	644	 5% 5% 90%
1	M	644	 7% 90%
1	T	644	 7% 90%
1	V	644	 8% 90%
1	W	644	 6% 90%
1	X	644	 6% 90%
1	Y	644	 6% 90%
1	Z	644	 6% 90%
1	a	644	 5% 5% 90%
1	b	644	 6% 5% 90%
1	c	644	 7% 90%
1	d	644	 8% 90%
1	e	644	 7% 90%
1	f	644	 8% 90%
1	s	644	 7% 90%
1	t	644	 7% 90%
1	u	644	 8% 90%
1	v	644	 8% 90%
2	E	419	 52% 12% 36%
2	F	419	 44% 20% 36%
2	N	419	 53% 11% 36%
2	O	419	 40% 22% 36%
2	S	419	 50% 14% 36%

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Mol	Chain	Length	Quality of chain
2	U	419	
2	g	419	
2	h	419	
2	i	419	
2	j	419	
2	q	419	
2	r	419	
3	G	334	
3	H	334	
3	I	334	
3	P	334	
3	Q	334	
3	R	334	
3	k	334	
3	l	334	
3	m	334	
3	n	334	
3	o	334	
3	p	334	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 66600 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 ATP-dependent zinc metalloprotease FtsH.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	63	Total	C	N	O	0	0
			516	321	94	101		
1	B	63	Total	C	N	O	0	0
			516	321	94	101		
1	C	63	Total	C	N	O	0	0
			516	321	94	101		
1	D	63	Total	C	N	O	0	0
			516	321	94	101		
1	e	63	Total	C	N	O	0	0
			516	321	94	101		
1	f	63	Total	C	N	O	0	0
			516	321	94	101		
1	W	63	Total	C	N	O	0	0
			516	321	94	101		
1	Y	63	Total	C	N	O	0	0
			516	321	94	101		
1	a	63	Total	C	N	O	0	0
			516	321	94	101		
1	c	63	Total	C	N	O	0	0
			516	321	94	101		
1	s	63	Total	C	N	O	0	0
			516	321	94	101		
1	u	63	Total	C	N	O	0	0
			516	321	94	101		
1	X	63	Total	C	N	O	0	0
			516	321	94	101		
1	Z	63	Total	C	N	O	0	0
			516	321	94	101		
1	b	63	Total	C	N	O	0	0
			516	321	94	101		
1	d	63	Total	C	N	O	0	0
			516	321	94	101		
1	t	63	Total	C	N	O	0	0
			516	321	94	101		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	v	63	Total	C	N	O	0	0
			516	321	94	101		
1	J	63	Total	C	N	O	0	0
			516	321	94	101		
1	K	63	Total	C	N	O	0	0
			516	321	94	101		
1	L	63	Total	C	N	O	0	0
			516	321	94	101		
1	M	63	Total	C	N	O	0	0
			516	321	94	101		
1	T	63	Total	C	N	O	0	0
			516	321	94	101		
1	V	63	Total	C	N	O	0	0
			516	321	94	101		

- Molecule 2 is a protein called Protein HflK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	F	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	U	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	g	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	i	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	q	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	h	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	j	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	r	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	N	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	O	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	S	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		

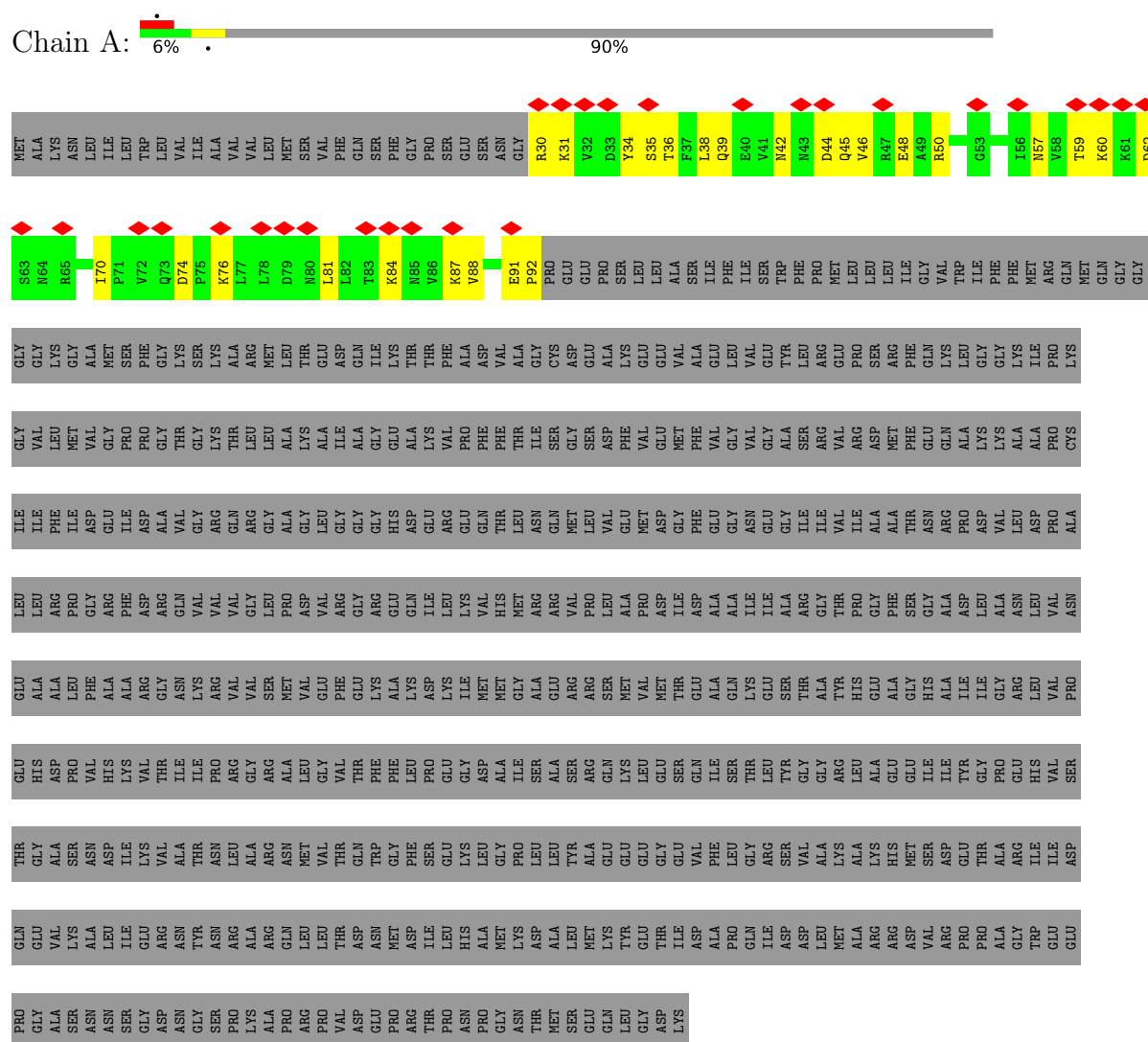
- Molecule 3 is a protein called Modulator of FtsH protease HflC.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	H	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	I	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	k	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	m	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	o	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	l	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	n	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	p	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	P	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	Q	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	R	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: ATP-dependent zinc metalloprotease FtsH



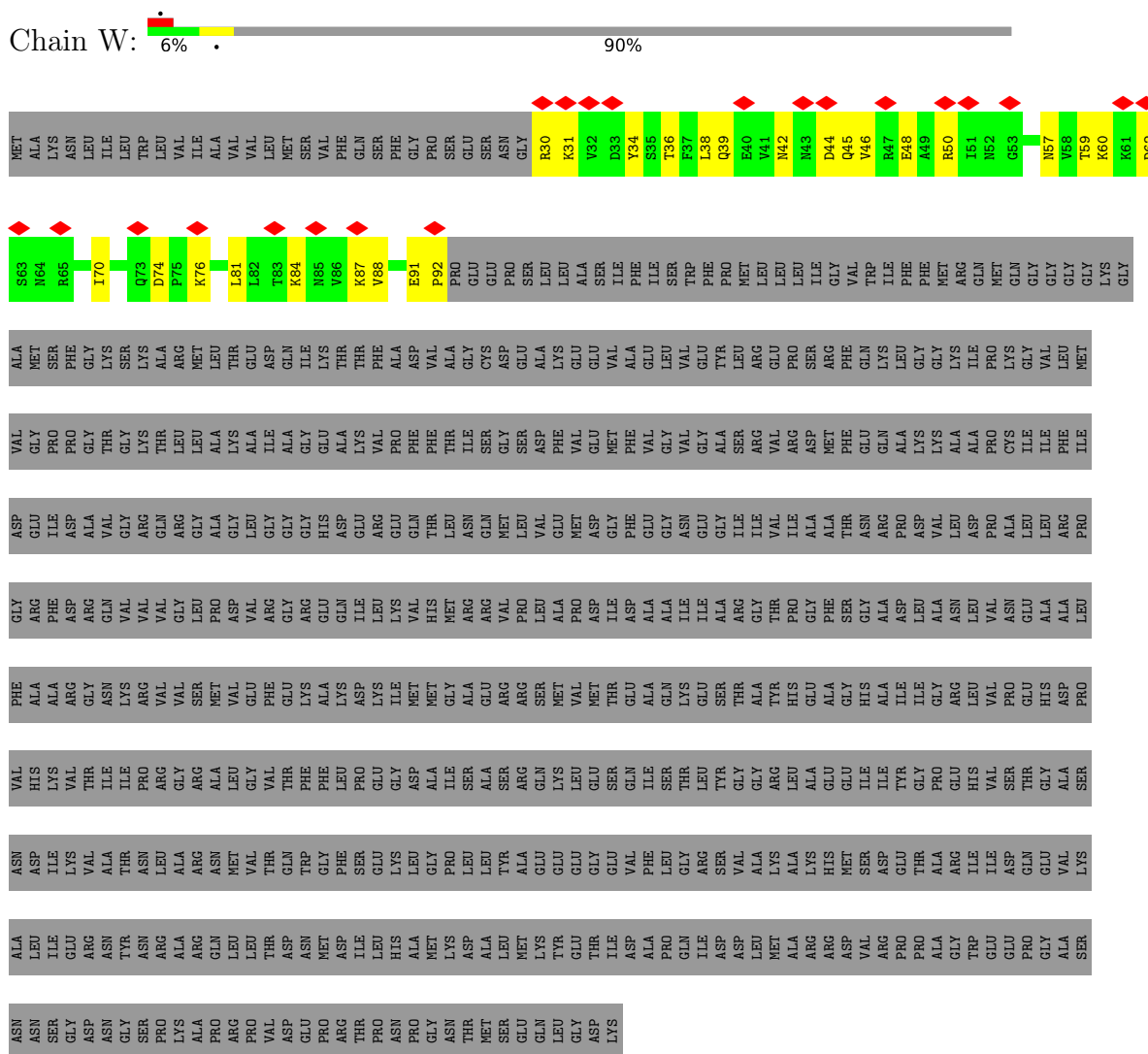
- Molecule 1: ATP-dependent zinc metalloprotease FtsH



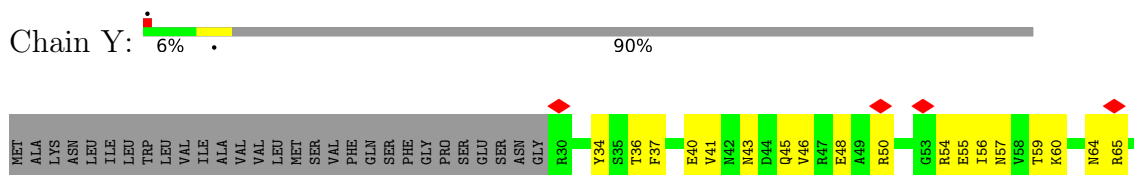


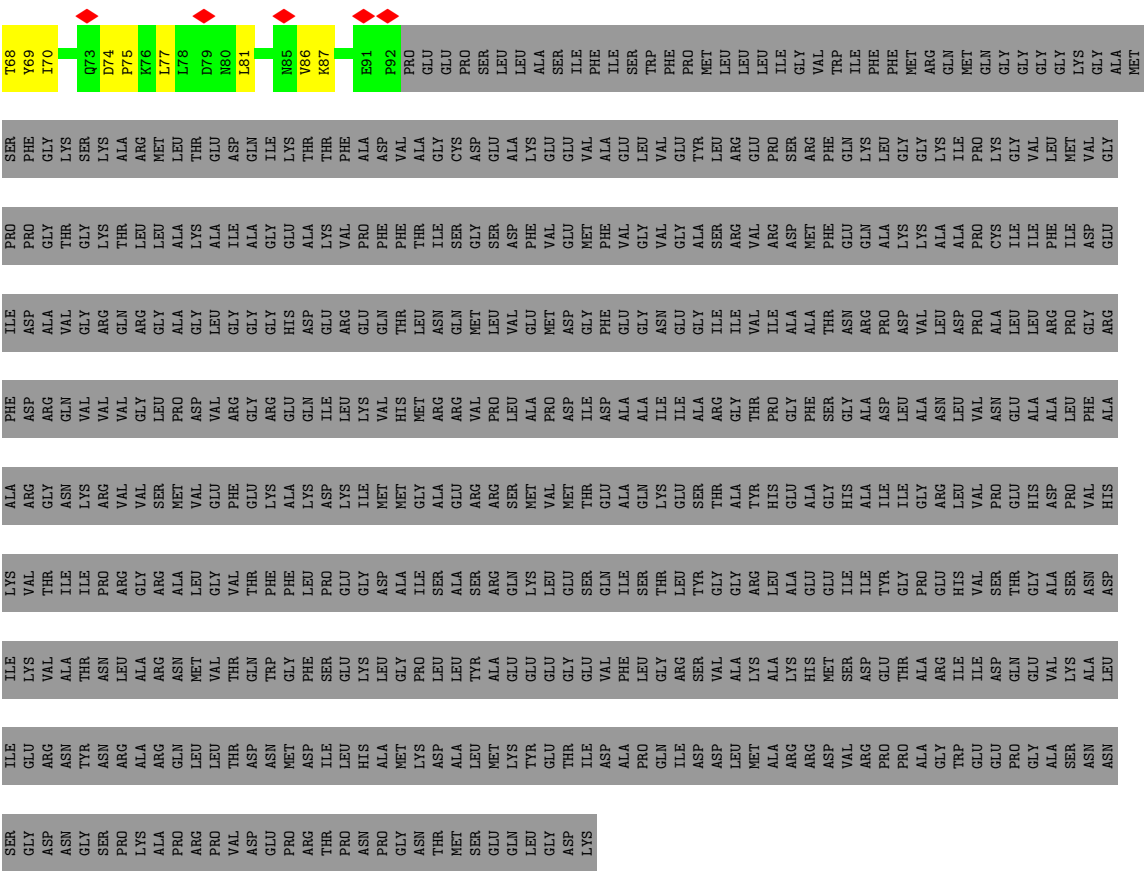
[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH



- Molecule 1: ATP-dependent zinc metalloprotease FtsH

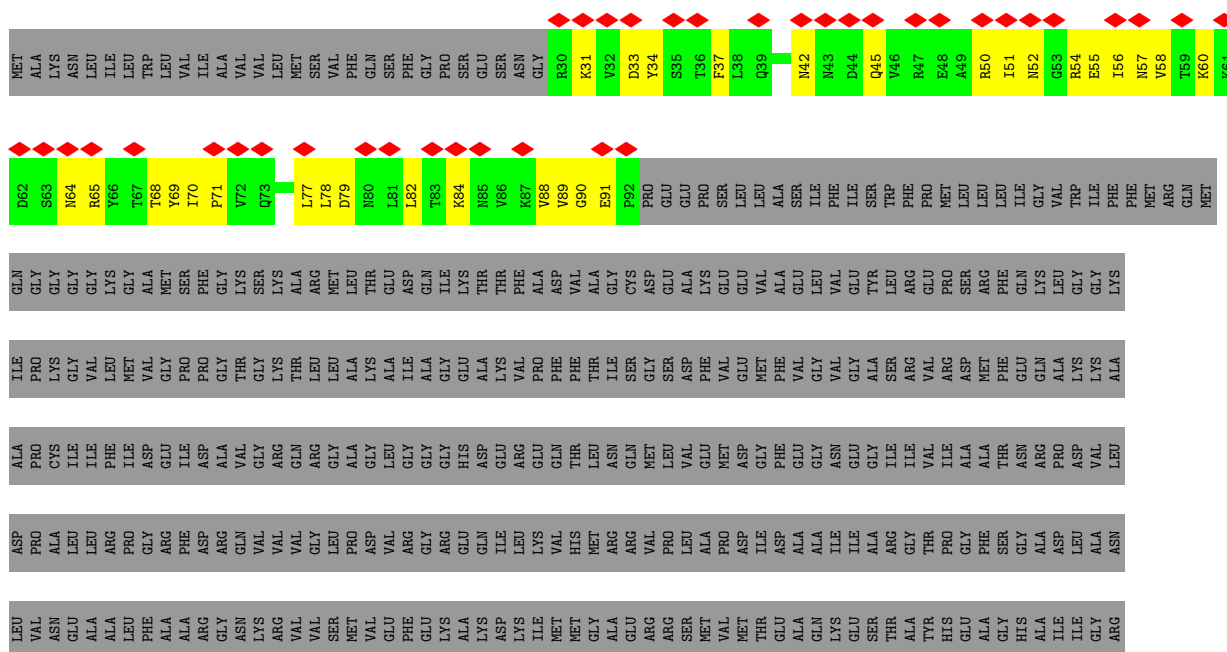




[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH

[illegible]

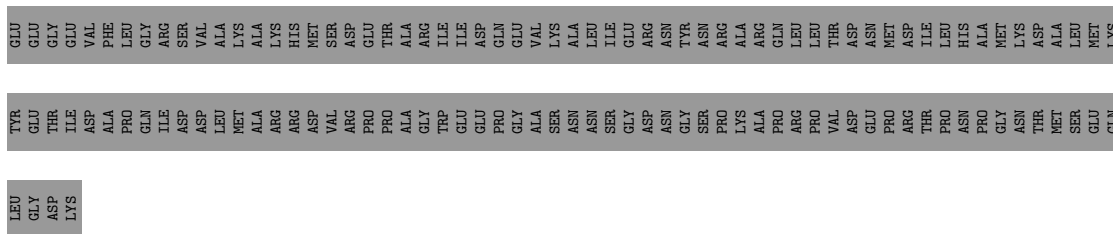


[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH

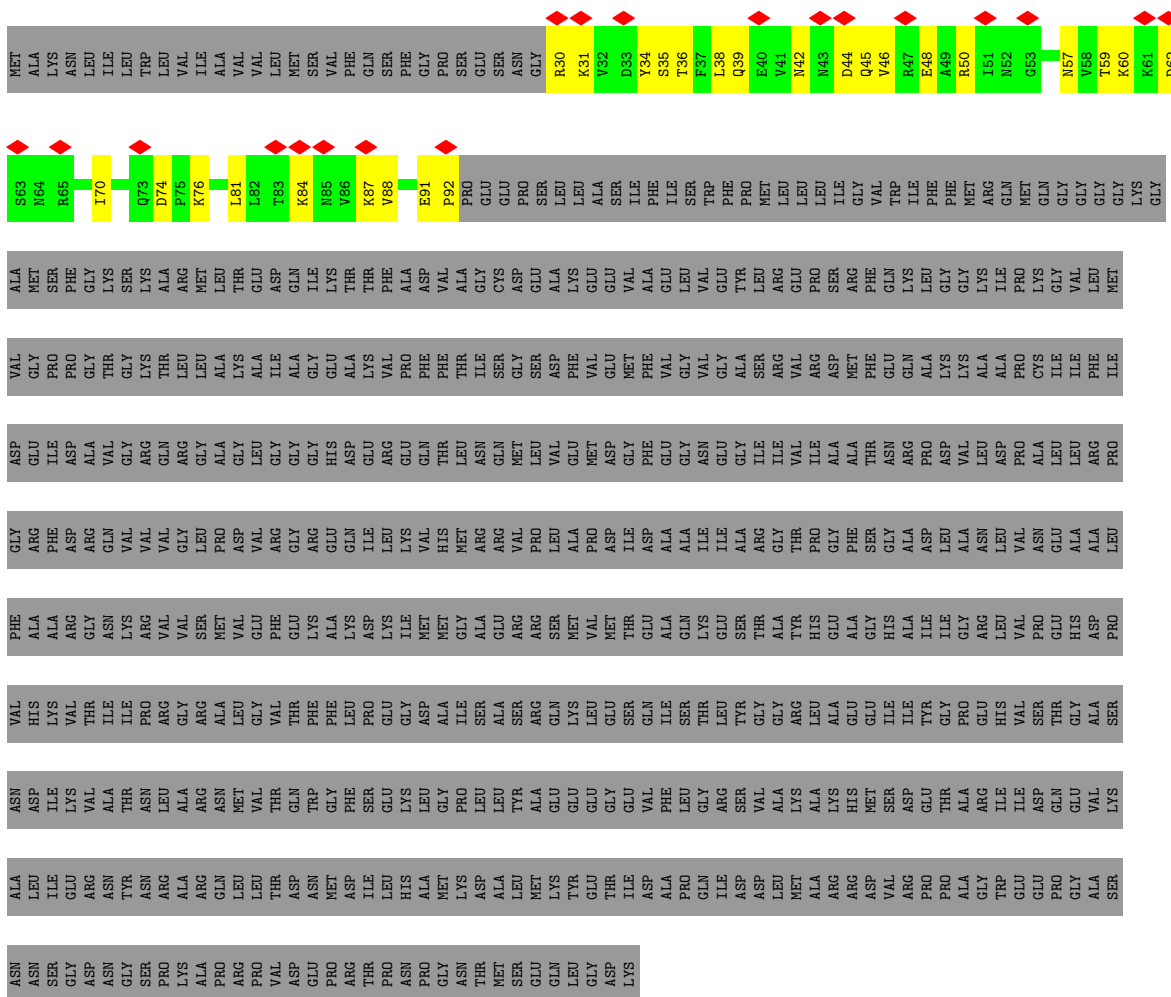
Chain v: 8% . 90%

Lys	Met	Ala	Glu	Phe	Lys	Ser
Leu	Val	Pro	Met	Val	Glu	Ile
Glu	Met	Asp	Asp	Glu	Glu	Lys
Ser	Thr	Ile	Gly	Phe	Val	Ile
Gln	Ala	Asp	Glu	Val	Ala	Leu
Ser	Gln	Ala	Gly	Gly	Leu	Trp
Thr	Lys	Ile	Asn	Val	Val	Phe
Leu	Glu	Ile	Glu	Gly	Val	Pro
Thr	Ser	Ala	Gly	Ala	Trp	Leu
Gly	Thr	Arg	Ile	Ser	Leu	Val
Gly	Ala	Gly	Ile	Arg	Leu	Ile
Arg	Tyr	Thr	Val	Val	Arg	Ala
Leu	His	Pro	Ile	Arg	Pro	Val
Ala	Glu	Gly	Ala	Asp	Ser	Val
Glu	Ala	Phe	Met	Met	Arg	Gln
Glu	Ala	Ser	Thr	Phe	Gly	Phe
Ile	His	Gly	Asn	Glu	Gln	Val
Ile	Ala	Ala	Arg	Gln	Lys	Val
Tyr	Ile	Asp	Pro	Ala	Leu	Gln
Gly	Ile	Leu	Asp	Lys	Gly	Ser
Pro	Gly	Ala	Val	Lys	Val	Glu
Glu	Arg	Asn	Leu	Ala	Leu	Asn
His	Leu	Leu	Asp	Ala	Lys	Gly
Val	Val	Val	Pro	Pro	Met	R390
Ser	Pro	Asn	Ala	Cys	Val	R390
Thr	Glu	Glu	Leu	Ile	Glu	D33
Ala	His	Ala	Leu	Ile	Phe	D33
Gly	Asp	Ala	Arg	Ala	Pro	L38
Val	Thr	Gly	Arg	Val	Pro	L38
Ala	Ile	Asn	Gln	Val	Thr	V41
Thr	Ile	Lys	Val	Val	Gly	V41
Asn	Pro	Arg	Val	Gln	Lys	V46
Leu	Arg	Val	Val	Gln	Lys	V46
Ala	Gly	Val	Val	Arg	Leu	R47
Arg	Arg	Ser	Leu	Gly	Met	R47
Asn	Ala	Met	Pro	Ala	Leu	E48
Met	Leu	Val	Asp	Gly	Ala	E48
Met	Leu	Val	Asp	Gly	Ala	A49
Met	Leu	Val	Asp	Gly	Ala	A49
Met	Leu	Val	Asp	Gly	Ala	R50
Met	Leu	Val	Asp	Gly	Ala	R50
Met	Leu	Val	Asp	Gly	Ala	T59
Met	Leu	Val	Asp	Gly	Ala	K60
Met	Leu	Val	Asp	Gly	Ala	K60
Met	Leu	Val	Asp	Gly	Ala	Q73
Met	Leu	Val	Asp	Gly	Ala	Q73
Met	Leu	Val	Asp	Gly	Ala	V89
Met	Leu	Val	Asp	Gly	Ala	V89
Met	Leu	Val	Asp	Gly	Ala	G90
Met	Leu	Val	Asp	Gly	Ala	E91
Met	Leu	Val	Asp	Gly	Ala	P92
Met	Leu	Val	Asp	Gly	Ala	P92
Met	Leu	Val	Asp	Gly	Ala	Pro
Met	Leu	Val	Asp	Gly	Ala	Glu
Met	Leu	Val	Asp	Gly	Ala	Glu
Met	Leu	Val	Asp	Gly	Ala	Pro
Met	Leu	Val	Asp	Gly	Ala	Pro
Met	Leu	Val	Asp	Gly	Ala	Ser
Met	Leu	Val	Asp	Gly	Ala	Ser
Met	Leu	Val	Asp	Gly	Ala	Leu

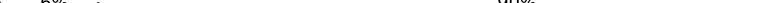


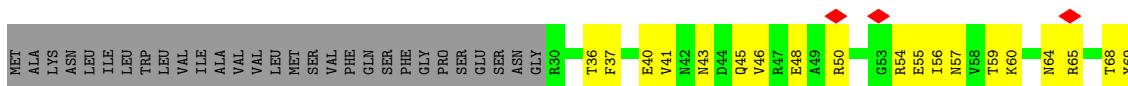
- Molecule 1: ATP-dependent zinc metalloprotease FtsH

Chain J:



- Molecule 1: ATP-dependent zinc metalloprotease FtsH

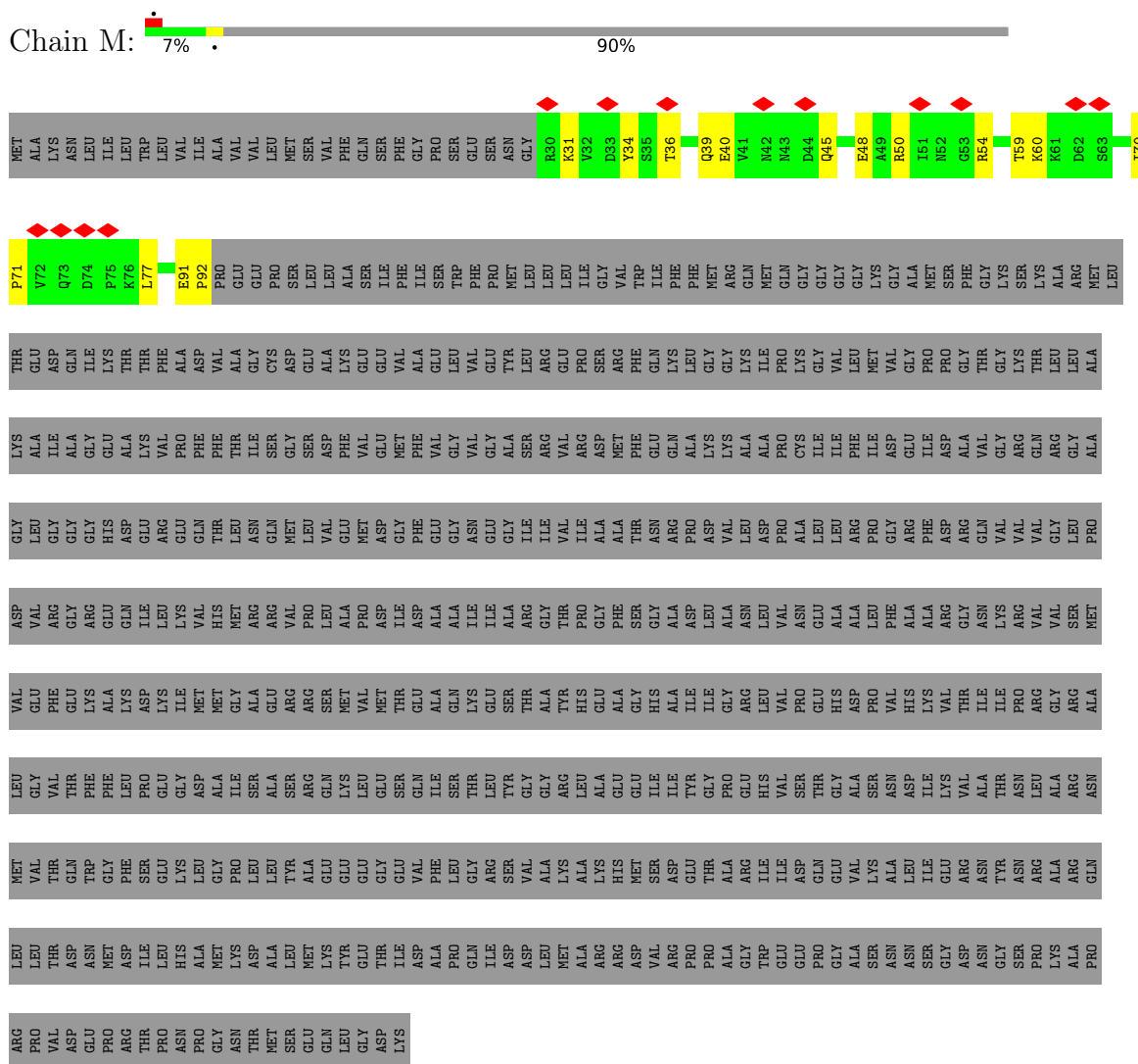
Chain K:  6% 90%



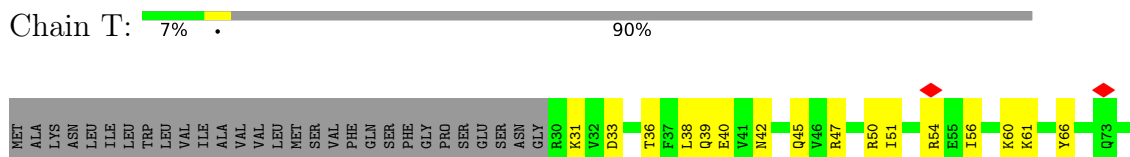


[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH

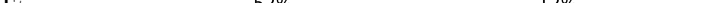


- Molecule 1: ATP-dependent zinc metalloprotease FtsH



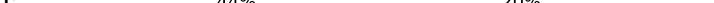
[illegible]

- Molecule 2: Protein HflK

Chain E:  52% 12% 36%

[illegible]

- Molecule 2: Protein HflK

Chain F:  44% 20% 36%

[illegible]

- Molecule 2: Protein HflK

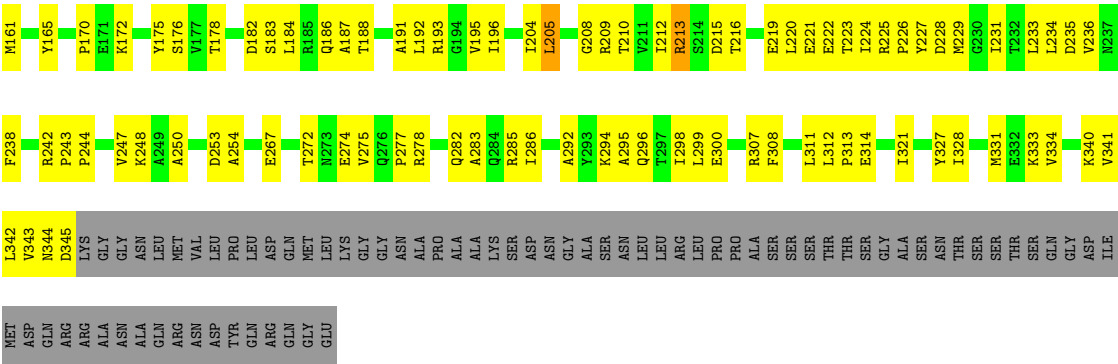
Chain U: 49% 15% 36%

- Molecule 2: Protein HflK

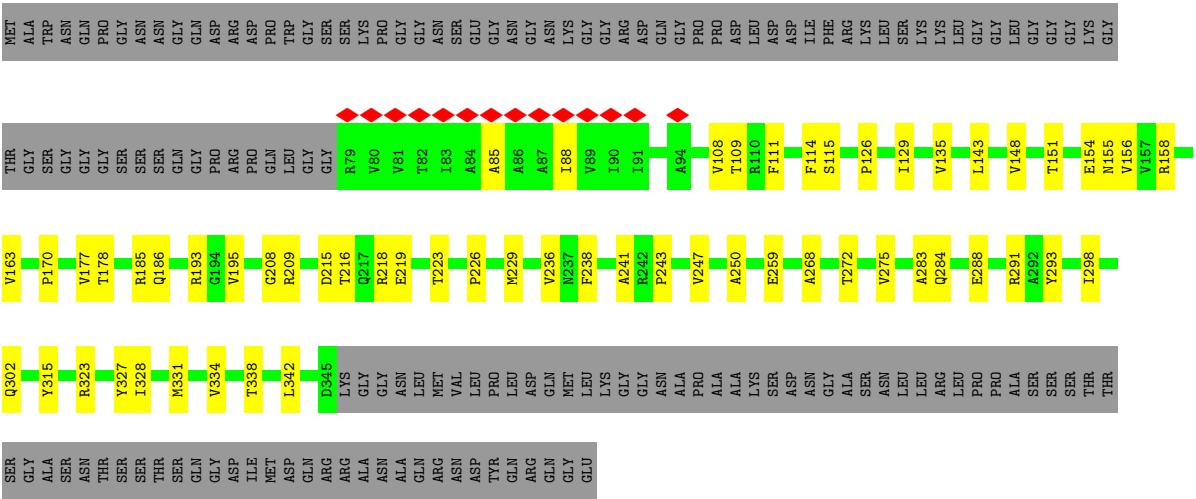
- Molecule 2: Protein HflK

- Molecule 2: Protein HflK

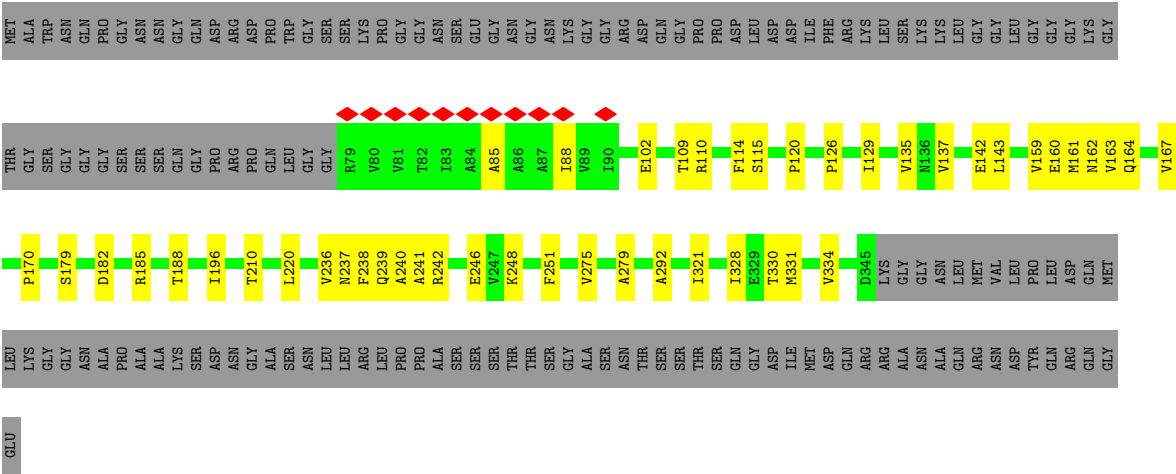
TBR
GLY
SER
GLY
GLY
GLY
SER
SER
SER
Gln
GLY
PRO
ARG
PRO
Gln
LEU
GLY
GLY
R79
V80
V81
T82
I83
A84
A85
A86
A87
T88
V89
P90
A93
A94
A103
E104
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P120
G121
L122
V135
E138
L143
V148
M149
V156



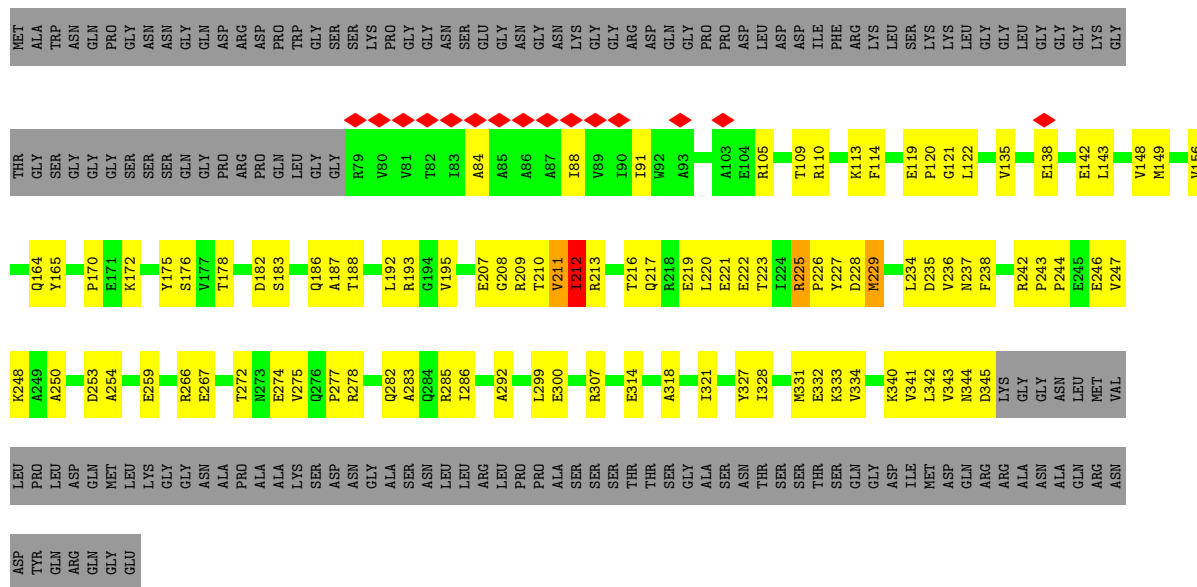
• Molecule 2: Protein HflK



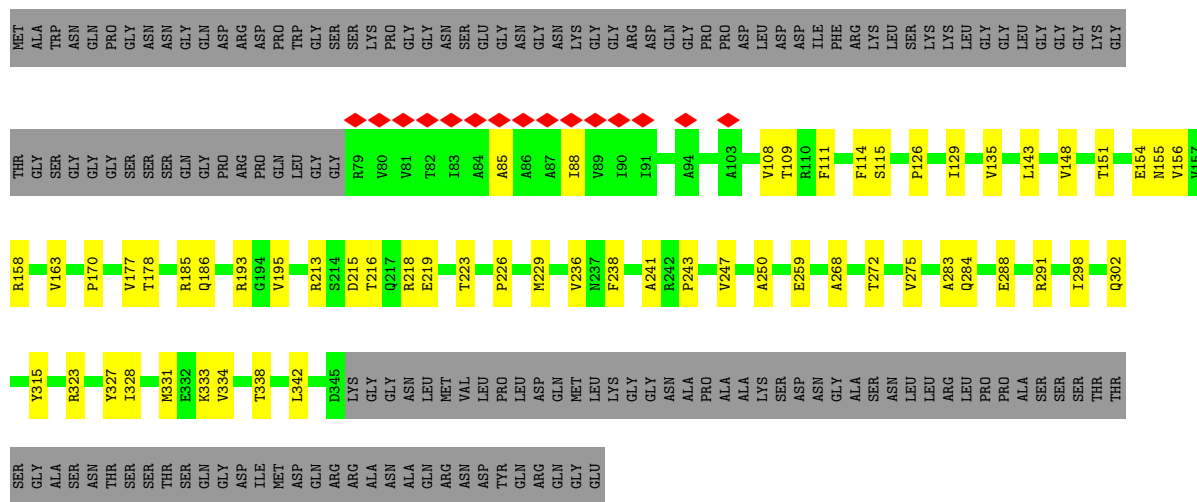
• Molecule 2: Protein HflK



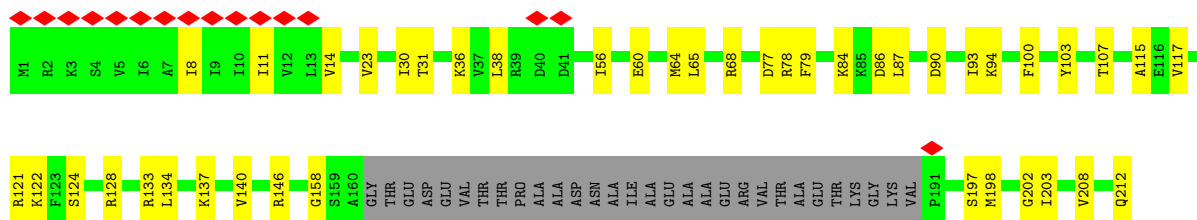
• Molecule 2: Protein HflK



• Molecule 2: Protein HflK

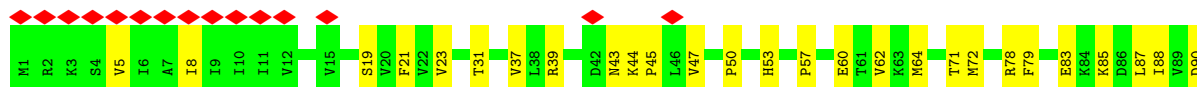


• Molecule 3: Modulator of FtsH protease HflC

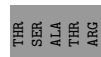
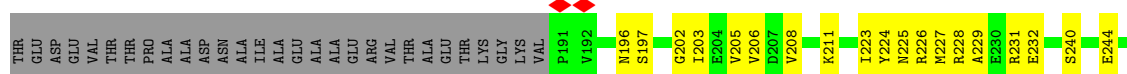
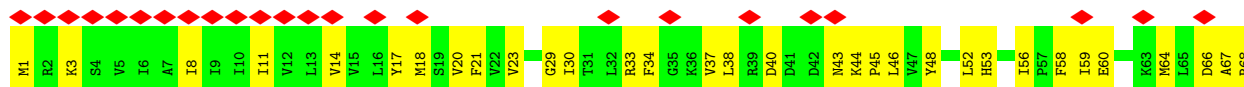




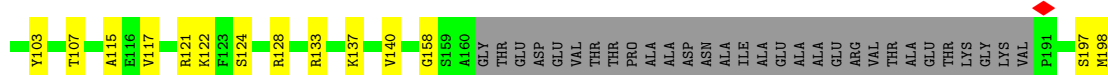
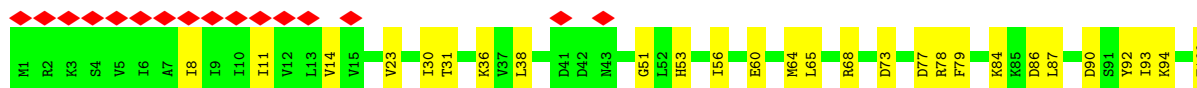
• Molecule 3: Modulator of FtsH protease HflC



• Molecule 3: Modulator of FtsH protease HflC

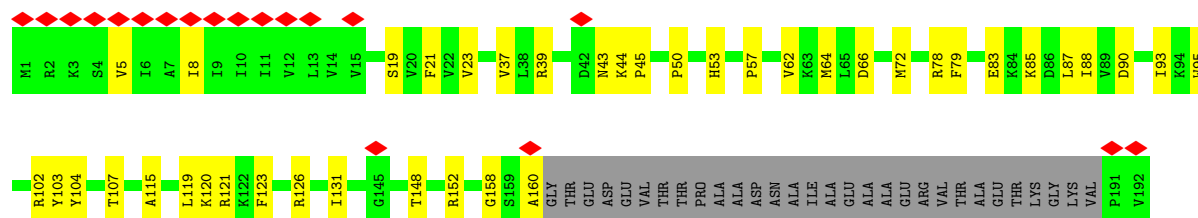


• Molecule 3: Modulator of FtsH protease HflC

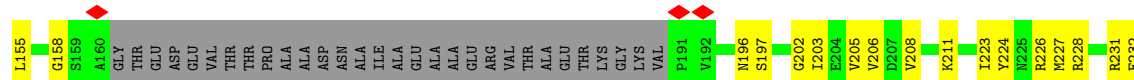
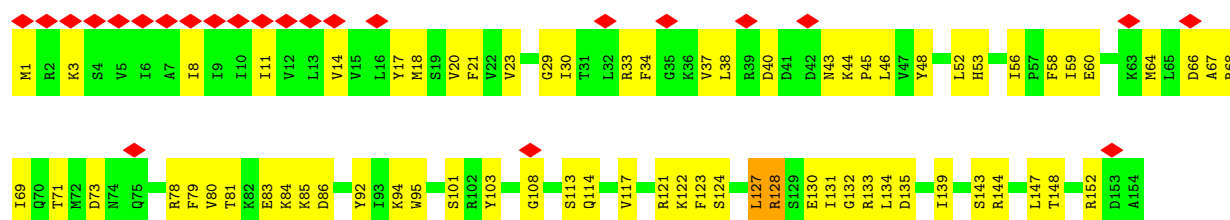




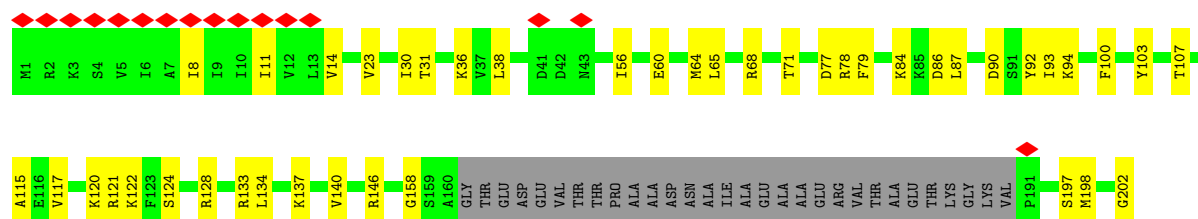
• Molecule 3: Modulator of FtsH protease HflC



• Molecule 3: Modulator of FtsH protease HflC

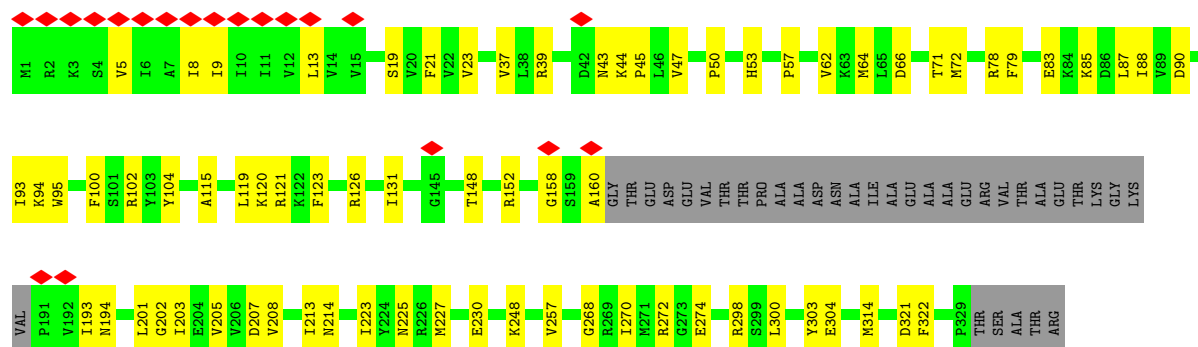


• Molecule 3: Modulator of FtsH protease HflC

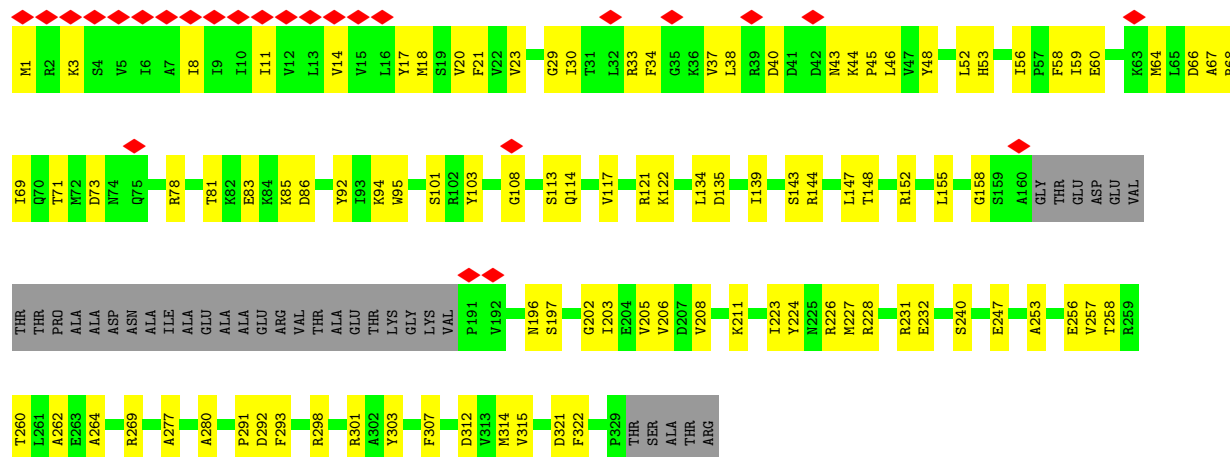


Chain n:





• Molecule 3: Modulator of FtsH protease HflC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84693	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0146	Depositor
Map size ($\text{\AA}$)	422.80002, 422.80002, 422.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.057, 1.057, 1.057	Depositor

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	A	0.17	0/522	0.50	0/706
1	B	0.14	0/522	0.37	0/706
1	C	0.18	0/522	0.52	0/706
1	D	0.17	0/522	0.45	0/706
1	J	0.17	0/522	0.50	0/706
1	K	0.14	0/522	0.37	0/706
1	L	0.19	0/522	0.52	0/706
1	M	0.17	0/522	0.45	0/706
1	T	0.18	0/522	0.54	0/706
1	V	0.14	0/522	0.29	0/706
1	W	0.17	0/522	0.50	0/706
1	X	0.17	0/522	0.50	0/706
1	Y	0.14	0/522	0.37	0/706
1	Z	0.14	0/522	0.37	0/706
1	a	0.19	0/522	0.52	0/706
1	b	0.19	0/522	0.52	0/706
1	c	0.17	0/522	0.45	0/706
1	d	0.17	0/522	0.45	0/706
1	e	0.18	0/522	0.54	0/706
1	f	0.14	0/522	0.29	0/706
1	s	0.18	0/522	0.54	0/706
1	t	0.18	0/522	0.54	0/706
1	u	0.14	0/522	0.29	0/706
1	v	0.14	0/522	0.29	0/706
2	E	0.15	0/2154	0.33	0/2921
2	F	0.23	0/2154	0.38	0/2921
2	N	0.15	0/2154	0.33	0/2921
2	O	0.18	0/2154	0.43	1/2921 (0.0%)
2	S	0.15	0/2154	0.34	0/2921
2	U	0.15	0/2154	0.34	0/2921
2	g	0.15	0/2154	0.33	0/2921
2	h	0.15	0/2154	0.33	0/2921
2	i	0.21	0/2154	0.48	1/2921 (0.0%)
2	j	0.21	0/2154	0.51	0/2921

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	q	0.15	0/2154	0.34	0/2921
2	r	0.15	0/2154	0.34	0/2921
3	G	0.15	0/2432	0.32	0/3268
3	H	0.14	0/2432	0.33	0/3268
3	I	0.20	0/2432	0.42	1/3268 (0.0%)
3	P	0.16	0/2432	0.33	0/3268
3	Q	0.14	0/2432	0.33	0/3268
3	R	0.15	0/2432	0.36	0/3268
3	k	0.16	0/2432	0.35	0/3268
3	l	0.15	0/2432	0.33	0/3268
3	m	0.14	0/2432	0.33	0/3268
3	n	0.14	0/2432	0.33	0/3268
3	o	0.19	0/2432	0.46	1/3268 (0.0%)
3	p	0.18	0/2432	0.46	1/3268 (0.0%)
All	All	0.16	0/67560	0.39	5/91212 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	212	ILE	N-CA-C	7.12	117.22	110.53
3	p	112	ILE	N-CA-C	6.88	117.64	110.62
3	o	264	ALA	N-CA-C	-5.54	98.99	110.80
2	i	224	ILE	N-CA-C	5.43	116.21	110.72
3	I	131	ILE	N-CA-C	5.09	115.86	110.72

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	516	0	525	19	0
1	B	516	0	525	17	0
1	C	516	0	525	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	516	0	525	18	0
1	J	516	0	525	19	0
1	K	516	0	525	16	0
1	L	516	0	525	24	0
1	M	516	0	525	17	0
1	T	516	0	525	15	0
1	V	516	0	525	9	0
1	W	516	0	525	18	0
1	X	516	0	525	20	0
1	Y	516	0	525	18	0
1	Z	516	0	525	16	0
1	a	516	0	525	24	0
1	b	516	0	525	25	0
1	c	516	0	525	18	0
1	d	516	0	525	17	0
1	e	516	0	525	13	0
1	f	516	0	525	8	0
1	s	516	0	525	12	0
1	t	516	0	525	15	0
1	u	516	0	525	9	0
1	v	516	0	525	9	0
2	E	2121	0	2129	42	0
2	F	2121	0	2127	118	0
2	N	2121	0	2129	37	0
2	O	2121	0	2126	201	0
2	S	2121	0	2129	44	0
2	U	2121	0	2129	53	0
2	g	2121	0	2129	38	0
2	h	2121	0	2129	37	0
2	i	2121	0	2127	216	0
2	j	2121	0	2128	187	0
2	q	2121	0	2129	75	0
2	r	2121	0	2129	72	0
3	G	2397	0	2431	84	0
3	H	2397	0	2431	51	0
3	I	2397	0	2431	188	0
3	P	2397	0	2431	93	0
3	Q	2397	0	2431	48	0
3	R	2397	0	2429	112	0
3	k	2397	0	2431	112	0
3	l	2397	0	2431	74	0
3	m	2397	0	2431	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	n	2397	0	2431	44	0
3	o	2397	0	2431	177	0
3	p	2397	0	2428	229	0
All	All	66600	0	67307	2103	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 16.

The worst 5 of 2103 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)
3:G:328:THR:HG22	2:q:327:TYR:CE2	1.20	1.67
2:i:149:MET:HE3	2:i:196:ILE:CD1	1.25	1.60
2:j:161:MET:HE3	2:j:212:ILE:CG2	1.29	1.57
2:i:149:MET:CE	2:i:196:ILE:CD1	1.87	1.50
2:F:310:LYS:NZ	3:o:274:GLU:CG	1.72	1.50

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 PDB entries followed by that with respect to all EM entries.

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	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	B	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	C	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	D	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	J	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	K	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	L	61/644 (10%)	58 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	T	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	V	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	W	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	X	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	Y	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	Z	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	a	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	b	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	c	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	d	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	e	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	f	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	s	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	t	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	u	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	v	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
2	E	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	F	265/419 (63%)	257 (97%)	8 (3%)	0	100	100
2	N	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	O	265/419 (63%)	256 (97%)	8 (3%)	1 (0%)	30	60
2	S	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	U	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	g	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	h	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	i	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	j	265/419 (63%)	257 (97%)	8 (3%)	0	100	100
2	q	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	r	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
3	G	295/334 (88%)	287 (97%)	8 (3%)	0	100	100
3	H	295/334 (88%)	286 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	295/334 (88%)	290 (98%)	5 (2%)	0	100	100
3	P	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	Q	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	R	295/334 (88%)	290 (98%)	5 (2%)	0	100	100
3	k	295/334 (88%)	287 (97%)	8 (3%)	0	100	100
3	l	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	m	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	n	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	o	295/334 (88%)	289 (98%)	5 (2%)	1 (0%)	36	66
3	p	295/334 (88%)	289 (98%)	5 (2%)	1 (0%)	36	66
All	All	8184/24492 (33%)	7925 (97%)	256 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	o	264	ALA
2	O	229	MET
3	p	132	GLY

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 PDB entries followed by that with respect to all EM entries.

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	60/527 (11%)	60 (100%)	0	100	100
1	B	60/527 (11%)	60 (100%)	0	100	100
1	C	60/527 (11%)	60 (100%)	0	100	100
1	D	60/527 (11%)	60 (100%)	0	100	100
1	J	60/527 (11%)	60 (100%)	0	100	100
1	K	60/527 (11%)	60 (100%)	0	100	100
1	L	60/527 (11%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	60/527 (11%)	60 (100%)	0	100	100
1	T	60/527 (11%)	60 (100%)	0	100	100
1	V	60/527 (11%)	60 (100%)	0	100	100
1	W	60/527 (11%)	60 (100%)	0	100	100
1	X	60/527 (11%)	60 (100%)	0	100	100
1	Y	60/527 (11%)	60 (100%)	0	100	100
1	Z	60/527 (11%)	60 (100%)	0	100	100
1	a	60/527 (11%)	60 (100%)	0	100	100
1	b	60/527 (11%)	60 (100%)	0	100	100
1	c	60/527 (11%)	60 (100%)	0	100	100
1	d	60/527 (11%)	60 (100%)	0	100	100
1	e	60/527 (11%)	60 (100%)	0	100	100
1	f	60/527 (11%)	60 (100%)	0	100	100
1	s	60/527 (11%)	60 (100%)	0	100	100
1	t	60/527 (11%)	60 (100%)	0	100	100
1	u	60/527 (11%)	60 (100%)	0	100	100
1	v	60/527 (11%)	60 (100%)	0	100	100
2	E	224/336 (67%)	224 (100%)	0	100	100
2	F	224/336 (67%)	223 (100%)	1 (0%)	84	85
2	N	224/336 (67%)	224 (100%)	0	100	100
2	O	224/336 (67%)	218 (97%)	6 (3%)	39	63
2	S	224/336 (67%)	224 (100%)	0	100	100
2	U	224/336 (67%)	224 (100%)	0	100	100
2	g	224/336 (67%)	224 (100%)	0	100	100
2	h	224/336 (67%)	224 (100%)	0	100	100
2	i	224/336 (67%)	220 (98%)	4 (2%)	51	70
2	j	224/336 (67%)	221 (99%)	3 (1%)	61	75
2	q	224/336 (67%)	224 (100%)	0	100	100
2	r	224/336 (67%)	224 (100%)	0	100	100
3	G	258/283 (91%)	258 (100%)	0	100	100
3	H	258/283 (91%)	258 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	258/283 (91%)	255 (99%)	3 (1%)	63	75
3	P	258/283 (91%)	258 (100%)	0	100	100
3	Q	258/283 (91%)	258 (100%)	0	100	100
3	R	258/283 (91%)	258 (100%)	0	100	100
3	k	258/283 (91%)	258 (100%)	0	100	100
3	l	258/283 (91%)	258 (100%)	0	100	100
3	m	258/283 (91%)	258 (100%)	0	100	100
3	n	258/283 (91%)	258 (100%)	0	100	100
3	o	258/283 (91%)	256 (99%)	2 (1%)	73	79
3	p	258/283 (91%)	255 (99%)	3 (1%)	63	75
All	All	7224/20076 (36%)	7202 (100%)	22 (0%)	84	86

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	p	131	ILE
2	O	211	VAL
2	O	210	THR
2	O	212	ILE
2	i	212	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	r	186	GLN
1	M	39	GLN
1	L	42	ASN
2	N	262	GLN
1	Y	85	ASN

5.3.3 RNA ⓘ

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.

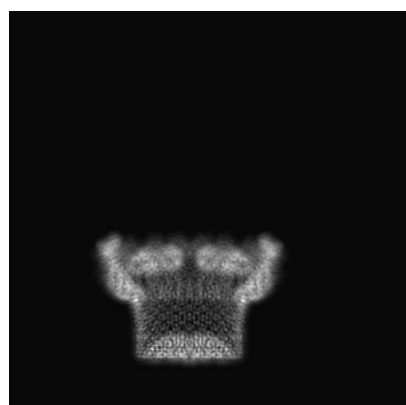
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32002. These allow visual inspection of the internal detail of the map and identification of artifacts.

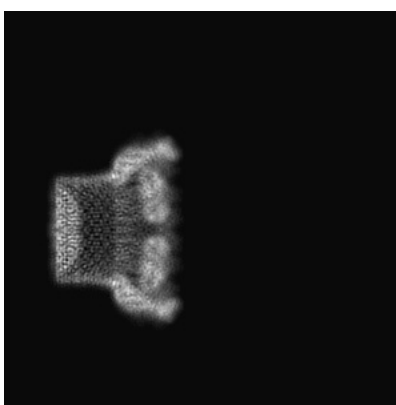
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

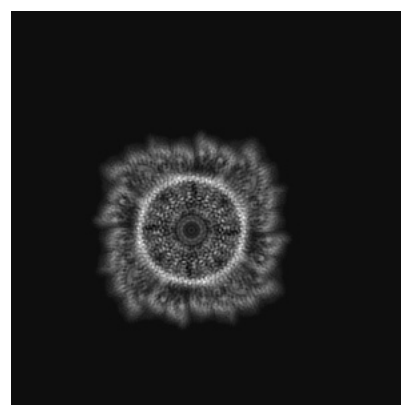
6.1.1 Primary map



X



Y



Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

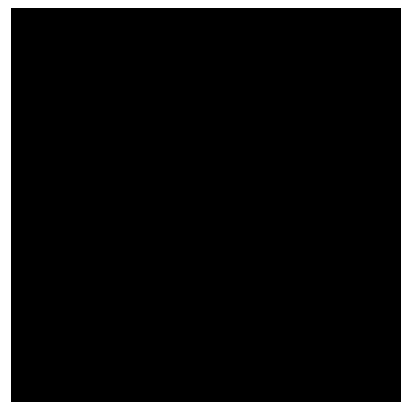
6.2.1 Primary map



X Index: 200



Y Index: 200

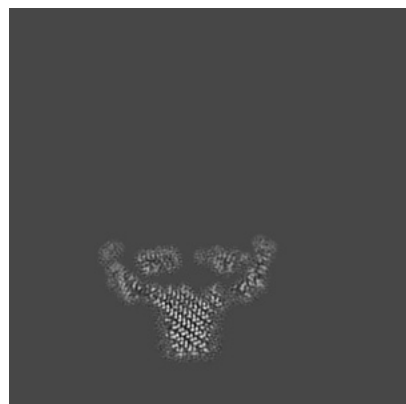


Z Index: 200

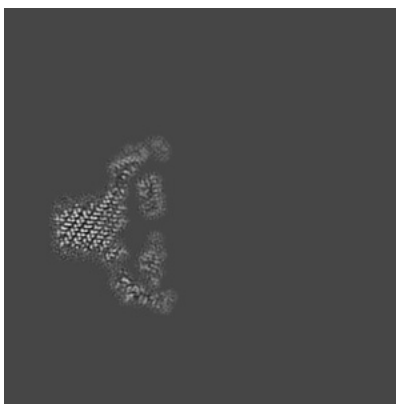
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

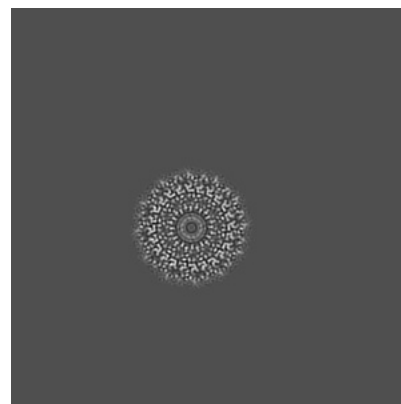
6.3.1 Primary map



X Index: 129



Y Index: 129

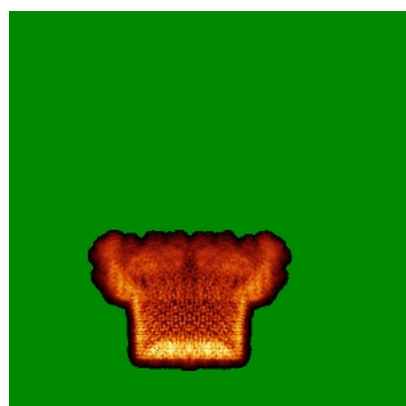


Z Index: 60

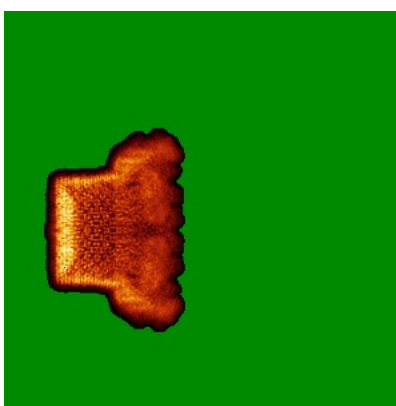
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

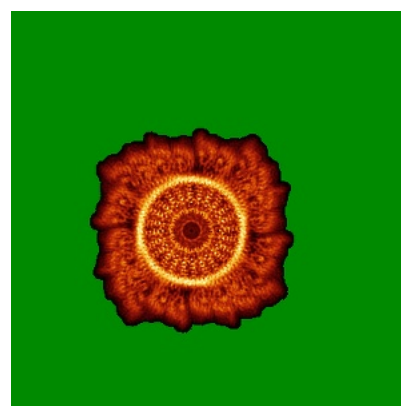
6.4.1 Primary map



X



Y

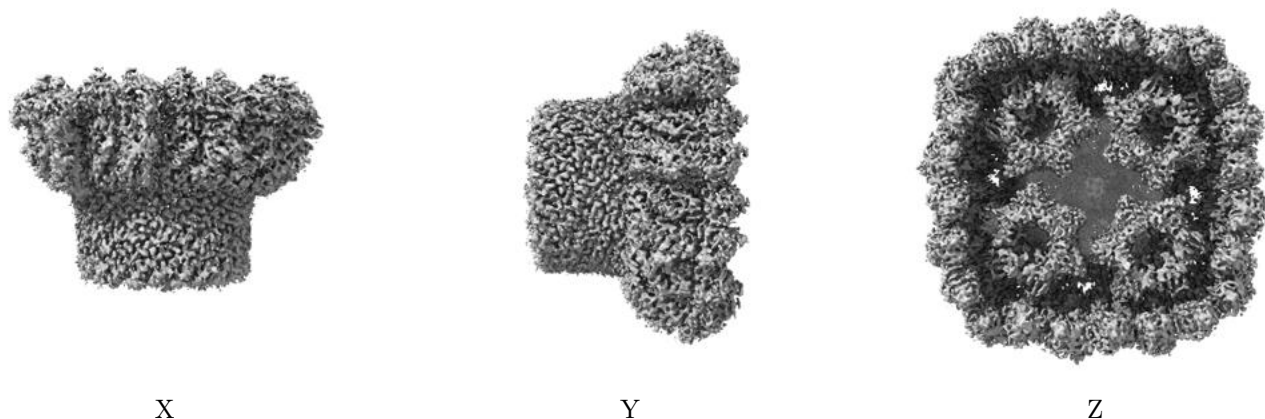


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0146. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

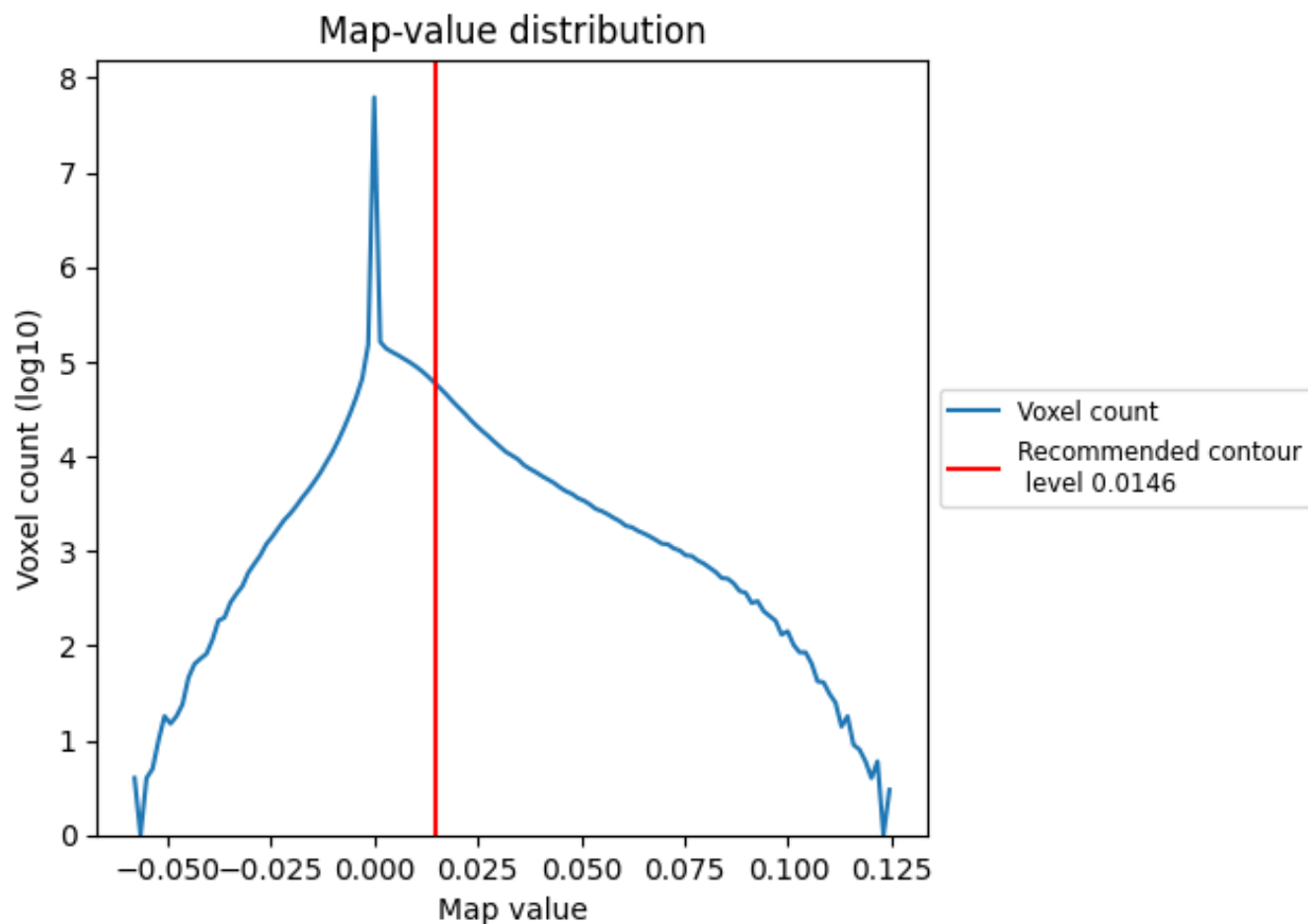
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

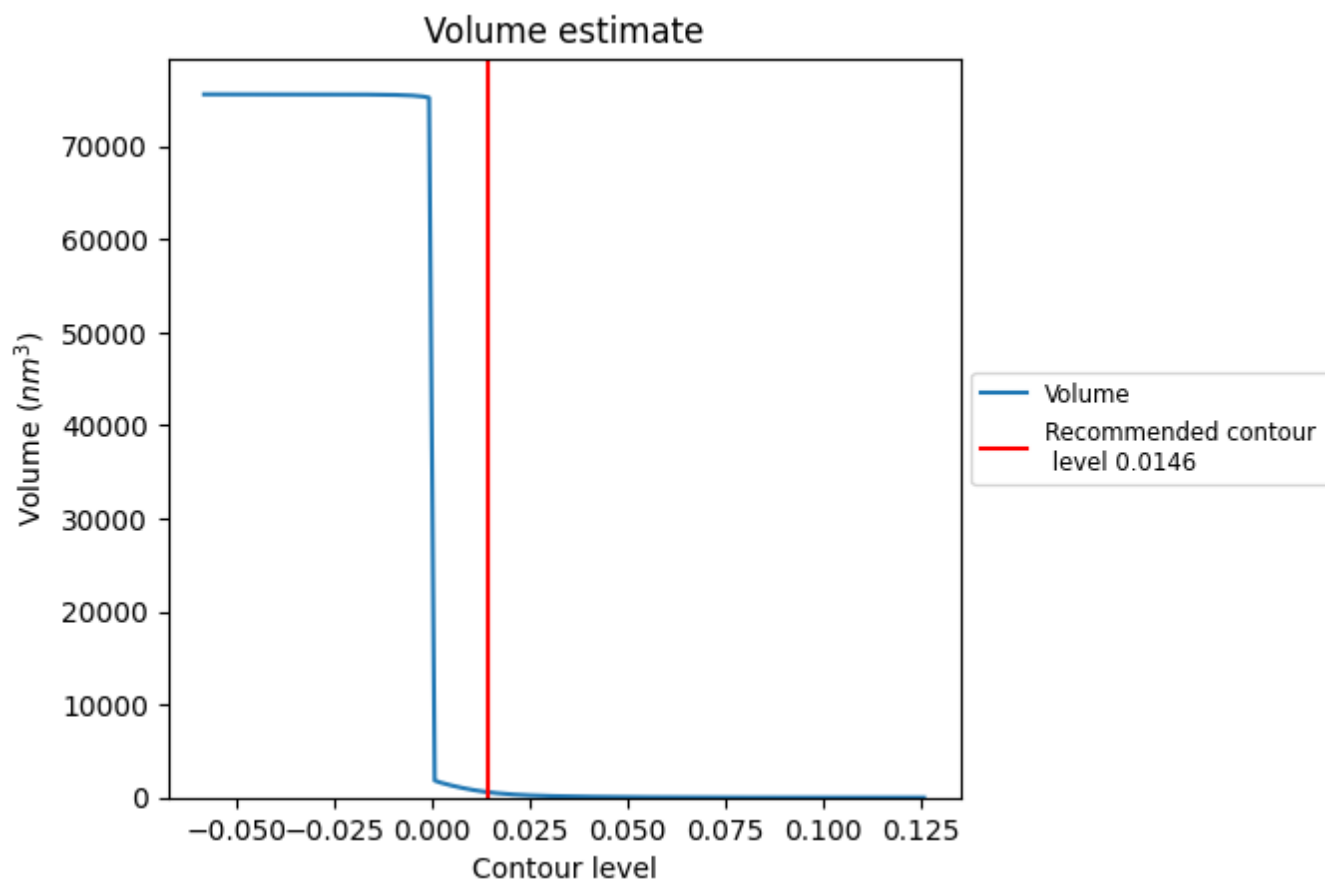
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

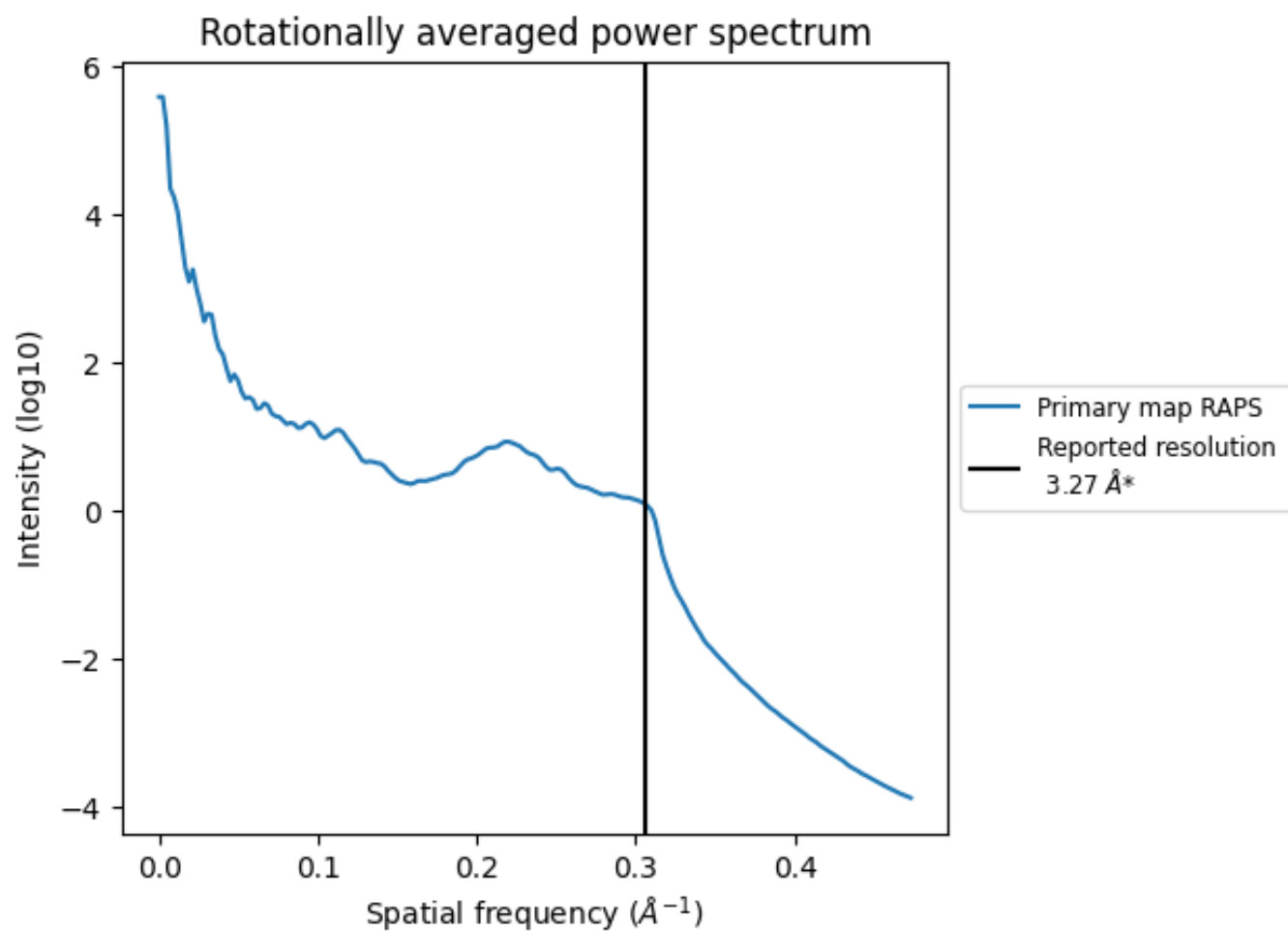
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 576 nm³; this corresponds to an approximate mass of 520 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.306 Å⁻¹

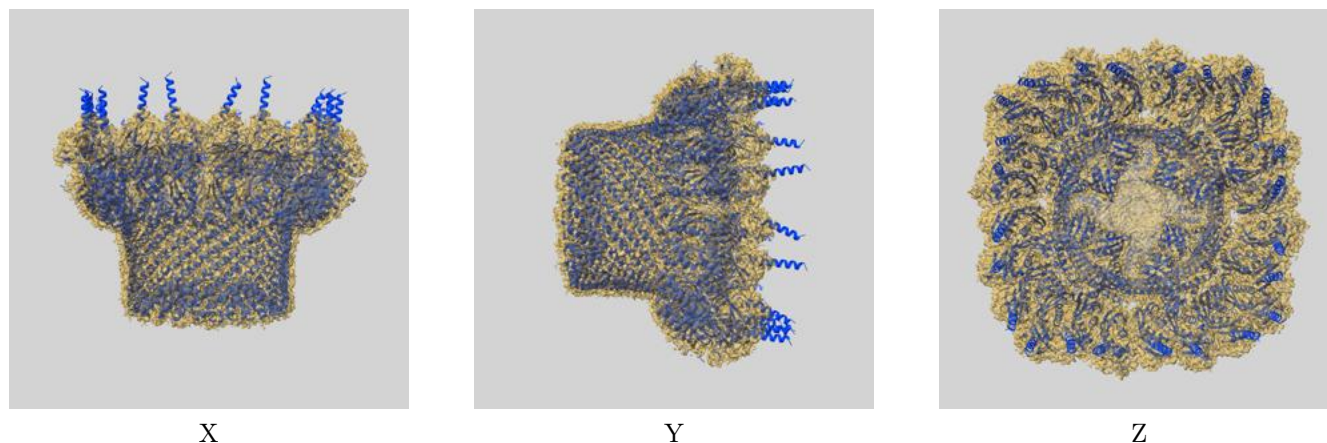
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

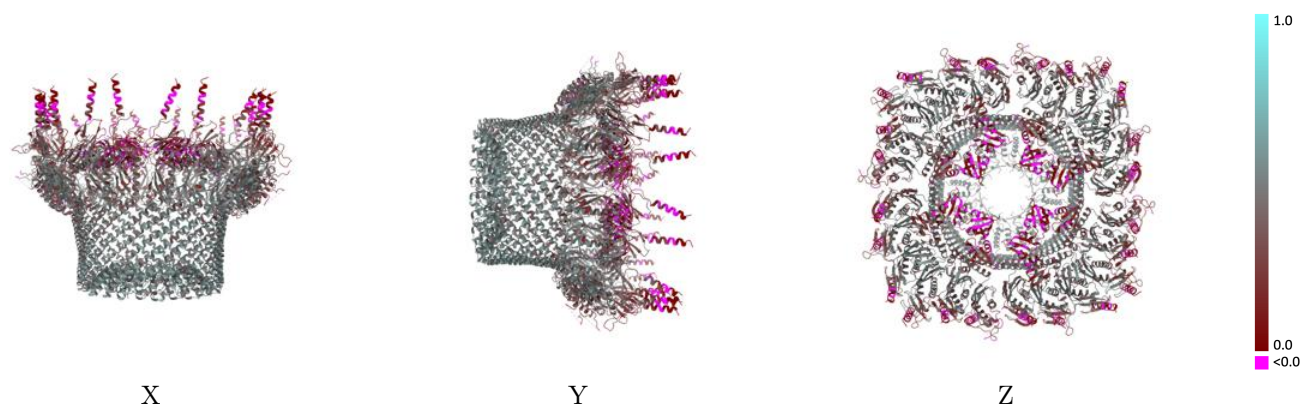
This section contains information regarding the fit between EMDB map EMD-32002 and PDB model 7VHP. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



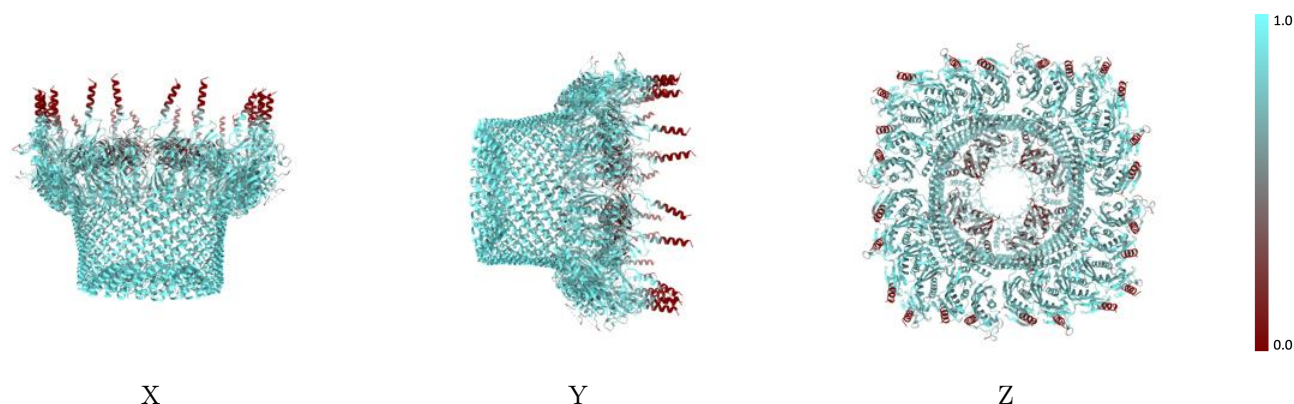
The images above show the 3D surface view of the map at the recommended contour level 0.0146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



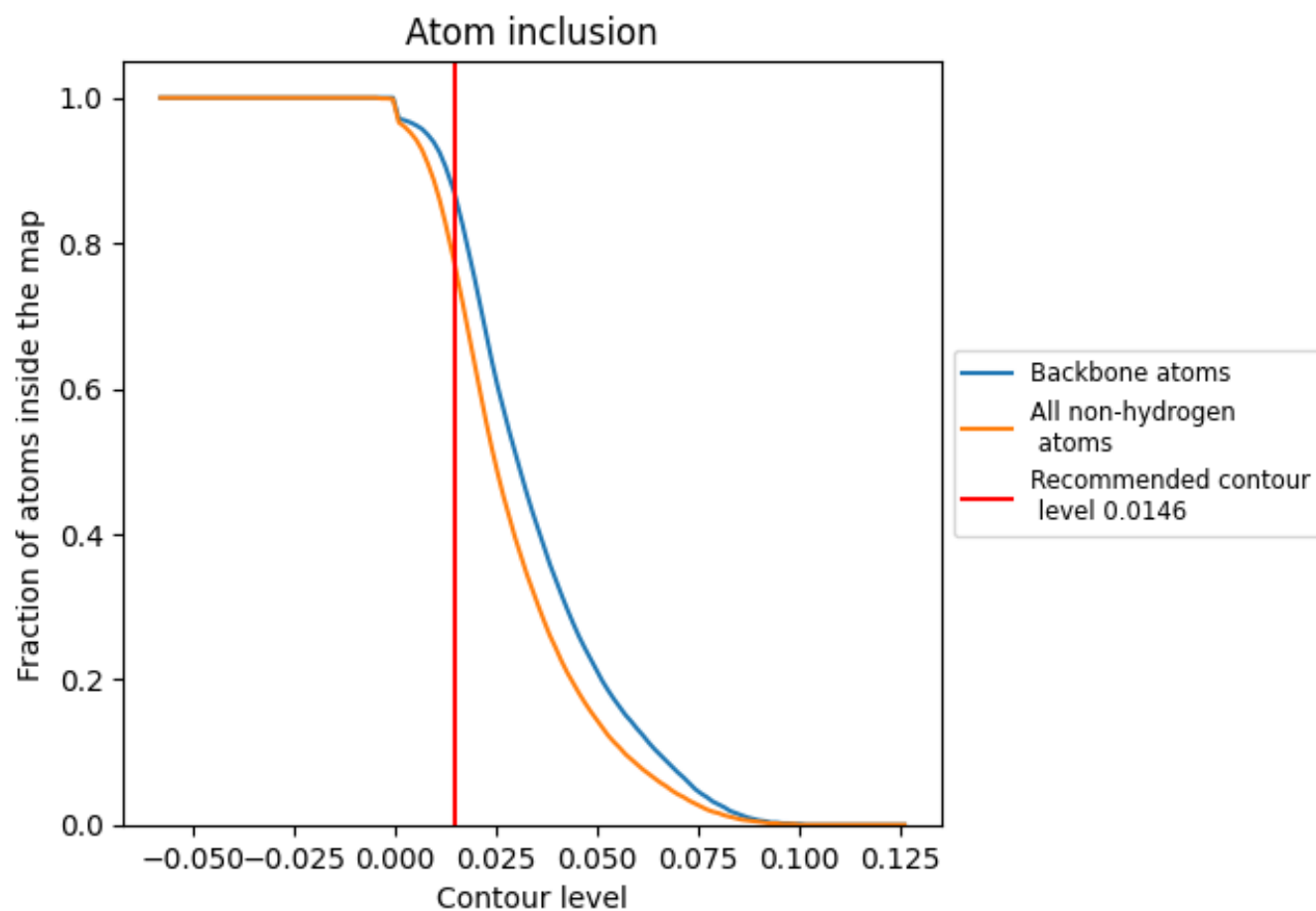
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0146).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7740	 0.3830
A	 0.4450	 0.1140
B	 0.6500	 0.2300
C	 0.3380	 0.0330
D	 0.5530	 0.1680
E	 0.8540	 0.4470
F	 0.8060	 0.4070
G	 0.8090	 0.4170
H	 0.8000	 0.4100
I	 0.7570	 0.3670
J	 0.4650	 0.1310
K	 0.6540	 0.2480
L	 0.3500	 0.0450
M	 0.5550	 0.1860
N	 0.8640	 0.4580
O	 0.8220	 0.4190
P	 0.8270	 0.4320
Q	 0.8130	 0.4210
R	 0.7730	 0.3840
S	 0.8280	 0.4250
T	 0.7510	 0.3930
U	 0.8230	 0.4140
V	 0.8030	 0.4390
W	 0.4810	 0.1270
X	 0.4470	 0.1230
Y	 0.6480	 0.2440
Z	 0.6540	 0.2480
a	 0.3680	 0.0310
b	 0.3480	 0.0310
c	 0.5450	 0.1710
d	 0.5470	 0.1740
e	 0.7510	 0.3840
f	 0.7930	 0.4270
g	 0.8690	 0.4620
h	 0.8590	 0.4520



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Chain	Atom inclusion	Q-score
i	 0.8110	 0.4050
j	 0.8040	 0.4000
k	 0.8270	 0.4320
l	 0.8170	 0.4290
m	 0.8140	 0.4240
n	 0.8120	 0.4200
o	 0.7740	 0.3790
p	 0.7720	 0.3710
q	 0.8330	 0.4270
r	 0.8290	 0.4250
s	 0.7510	 0.3880
t	 0.7610	 0.3820
u	 0.8070	 0.4450
v	 0.8010	 0.4360