



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:28 PM UTC

PDB ID : 7WI3 / pdb_00007wi3
EMDB ID : EMD-32520
Title : Cryo-EM structure of E.Coli FtsH-HflkC AAA protease complex
Authors : Qiao, Z.; Gao, Y.G.
Deposited on : 2022-01-02
Resolution : 4.00 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:

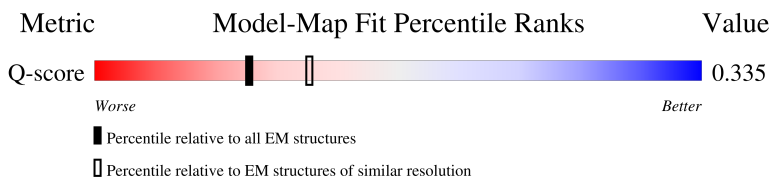
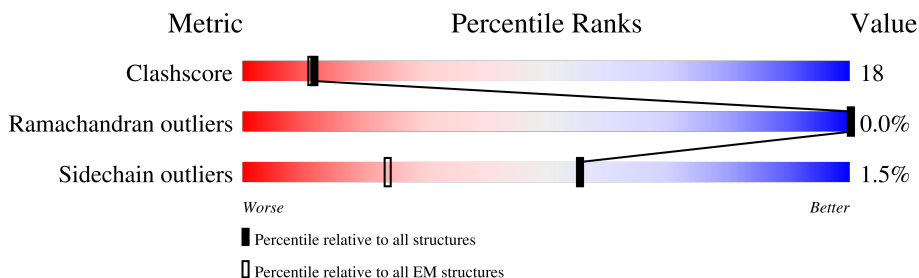
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.00 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.



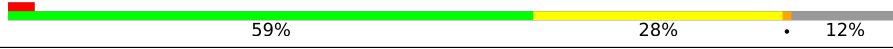
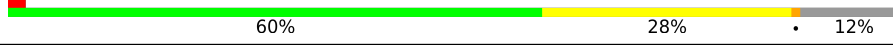
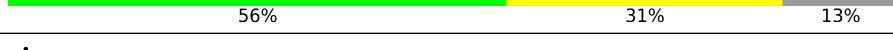
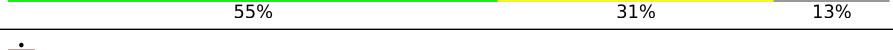
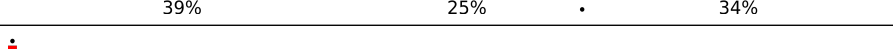
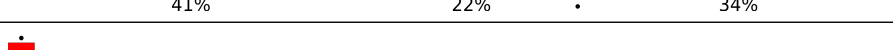
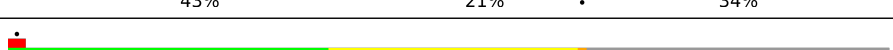
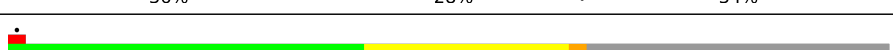
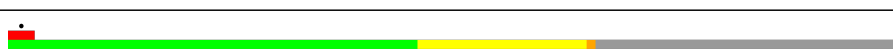
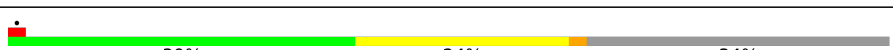
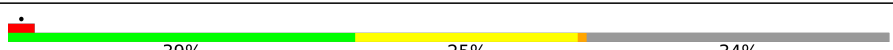
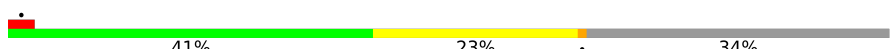
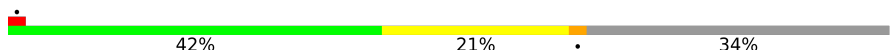
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	334	
1	C	334	
1	D	334	
1	M	334	

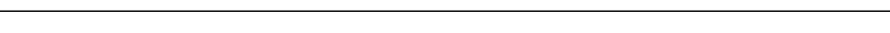
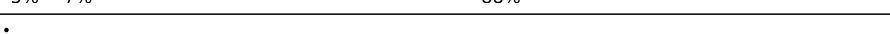
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Mol	Chain	Length	Quality of chain
1	O	334	
1	P	334	
1	Y	334	
1	Z	334	
1	c	334	
1	d	334	
1	e	334	
1	f	334	
2	B	419	
2	F	419	
2	G	419	
2	N	419	
2	R	419	
2	S	419	
2	a	419	
2	b	419	
2	i	419	
2	j	419	
2	k	419	
2	l	419	
3	E	644	
3	H	644	
3	I	644	
3	J	644	
3	K	644	

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Mol	Chain	Length	Quality of chain
3	L	644	 6% 6% 88%
3	Q	644	 9% 87%
3	T	644	 9% 87%
3	U	644	 7% 5% 88%
3	V	644	 5% 7% 88%
3	W	644	 7% 5% 88%
3	X	644	 6% 6% 88%
3	g	644	 9% 87%
3	h	644	 9% 87%
3	m	644	 9% 87%
3	n	644	 7% 5% 87%
3	o	644	 7% 5% 88%
3	p	644	 8% 88%
3	q	644	 6% 5% 88%
3	r	644	 5% 7% 88%
3	s	644	 9% 88%
3	t	644	 6% 6% 88%
3	u	644	 5% 7% 88%
3	v	644	 5% 7% 88%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 69304 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 Modulator of FtsH protease HflC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	293	Total	C	N	O	S	0	0
			2338	1472	419	437	10		
1	C	287	Total	C	N	O	S	0	0
			2290	1444	411	426	9		
1	D	290	Total	C	N	O	S	0	0
			2311	1457	414	430	10		
1	Y	293	Total	C	N	O	S	0	0
			2338	1472	419	437	10		
1	c	287	Total	C	N	O	S	0	0
			2290	1444	411	426	9		
1	e	290	Total	C	N	O	S	0	0
			2311	1457	414	430	10		
1	Z	293	Total	C	N	O	S	0	0
			2338	1472	419	437	10		
1	d	287	Total	C	N	O	S	0	0
			2290	1444	411	426	9		
1	f	290	Total	C	N	O	S	0	0
			2311	1457	414	430	10		
1	M	293	Total	C	N	O	S	0	0
			2338	1472	419	437	10		
1	O	287	Total	C	N	O	S	0	0
			2290	1444	411	426	9		
1	P	290	Total	C	N	O	S	0	0
			2311	1457	414	430	10		

- Molecule 2 is a protein called Modulator of FtsH protease HflK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	275	Total	C	N	O	S	0	0
			2169	1362	383	418	6		
2	F	275	Total	C	N	O	S	0	0
			2165	1360	383	416	6		
2	G	275	Total	C	N	O	S	0	0
			2173	1364	384	419	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	275	Total	C	N	O	S	0	0
			2169	1362	383	418	6		
2	i	275	Total	C	N	O	S	0	0
			2165	1360	383	416	6		
2	k	275	Total	C	N	O	S	0	0
			2173	1364	384	419	6		
2	b	275	Total	C	N	O	S	0	0
			2169	1362	383	418	6		
2	j	275	Total	C	N	O	S	0	0
			2165	1360	383	416	6		
2	l	275	Total	C	N	O	S	0	0
			2173	1364	384	419	6		
2	N	275	Total	C	N	O	S	0	0
			2169	1362	383	418	6		
2	R	275	Total	C	N	O	S	0	0
			2165	1360	383	416	6		
2	S	275	Total	C	N	O	S	0	0
			2173	1364	384	419	6		

- Molecule 3 is a protein called ATP-dependent zinc metalloprotease FtsH.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	81	Total	C	N	O	S	0	0
			658	418	113	126	1		
3	H	81	Total	C	N	O	S	0	0
			658	418	113	126	1		
3	I	79	Total	C	N	O		0	0
			643	408	111	124			
3	J	78	Total	C	N	O		0	0
			635	405	107	123			
3	K	79	Total	C	N	O		0	0
			643	408	111	124			
3	L	79	Total	C	N	O		0	0
			643	408	111	124			
3	g	81	Total	C	N	O	S	0	0
			658	418	113	126	1		
3	m	81	Total	C	N	O	S	0	0
			658	418	113	126	1		
3	o	79	Total	C	N	O		0	0
			643	408	111	124			
3	q	78	Total	C	N	O		0	0
			635	405	107	123			

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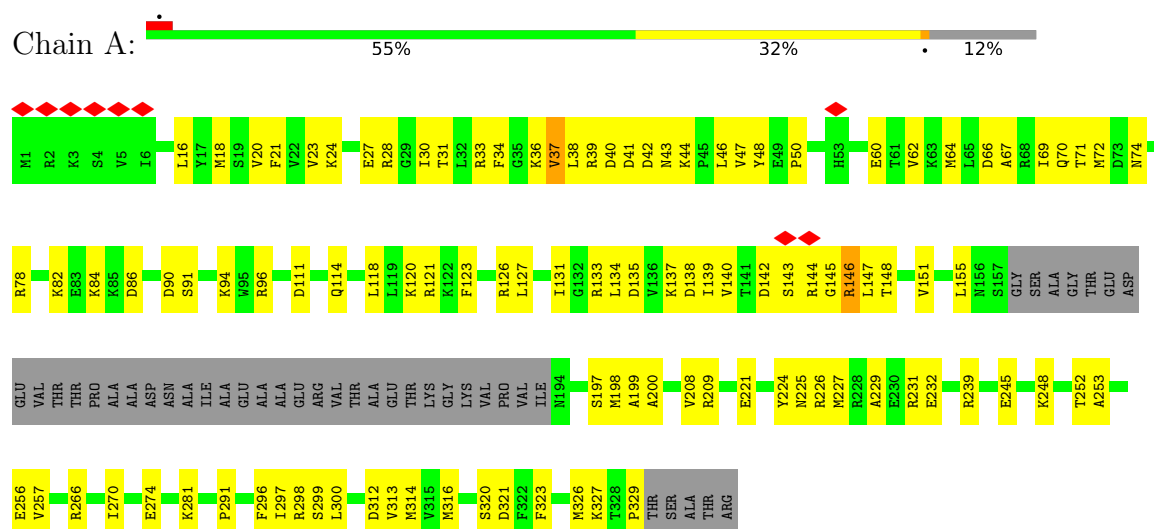
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Mol	Chain	Residues	Atoms				AltConf	Trace
3	s	79	Total 643	C 408	N 111	O 124	0	0
3	u	79	Total 643	C 408	N 111	O 124	0	0
3	h	81	Total 658	C 418	N 113	O 126	S 1	0
3	n	81	Total 658	C 418	N 113	O 126	S 1	0
3	p	79	Total 643	C 408	N 111	O 124	0	0
3	r	78	Total 635	C 405	N 107	O 123	0	0
3	t	79	Total 643	C 408	N 111	O 124	0	0
3	v	79	Total 643	C 408	N 111	O 124	0	0
3	Q	81	Total 658	C 418	N 113	O 126	S 1	0
3	T	81	Total 658	C 418	N 113	O 126	S 1	0
3	U	79	Total 643	C 408	N 111	O 124	0	0
3	V	78	Total 635	C 405	N 107	O 123	0	0
3	W	79	Total 643	C 408	N 111	O 124	0	0
3	X	79	Total 643	C 408	N 111	O 124	0	0

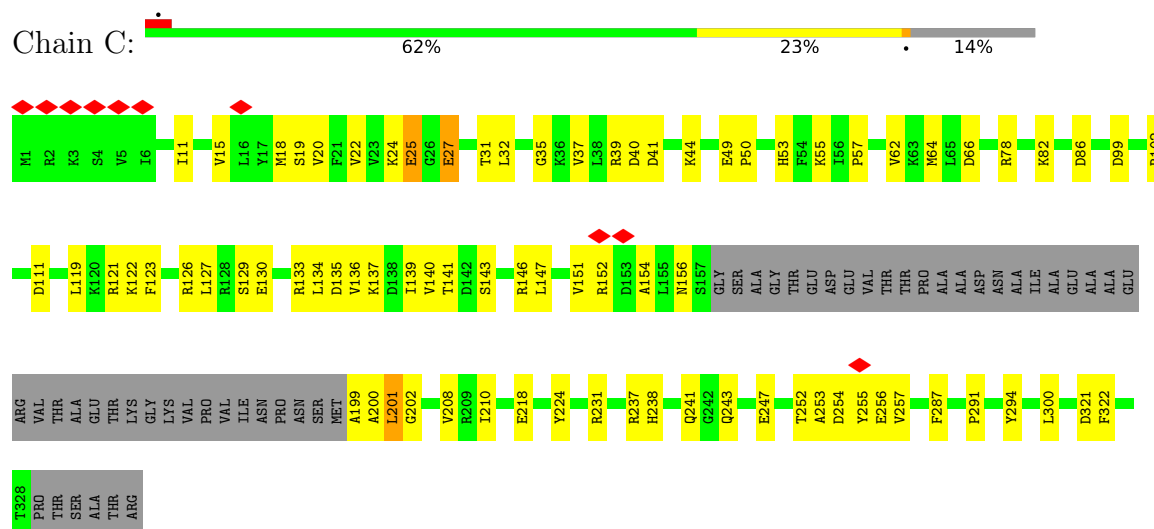
3 Residue-property plots

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.

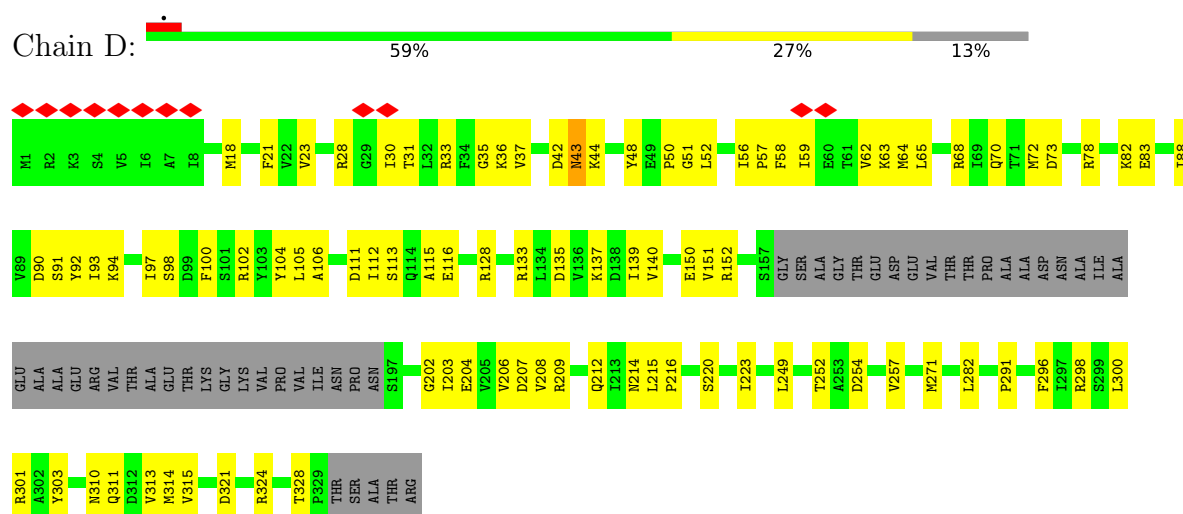
• Molecule 1: Modulator of FtsH protease HflC



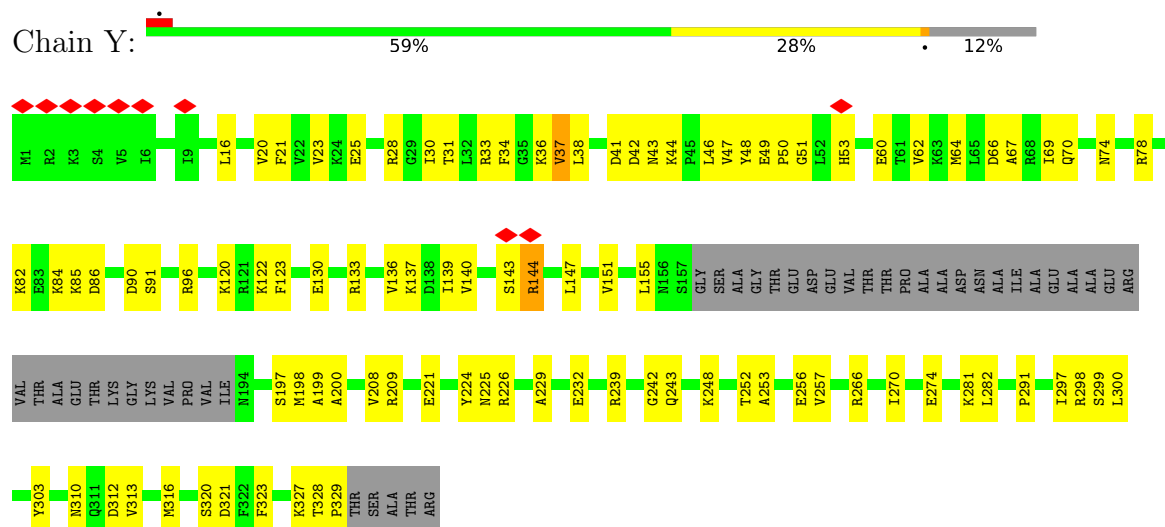
• Molecule 1: Modulator of FtsH protease HflC



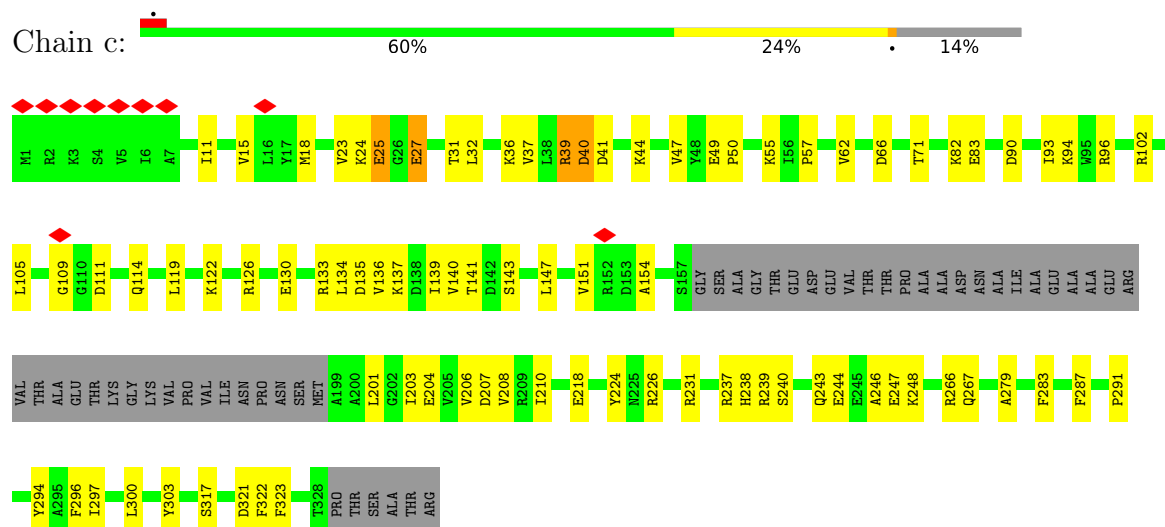
• Molecule 1: Modulator of FtsH protease HflC



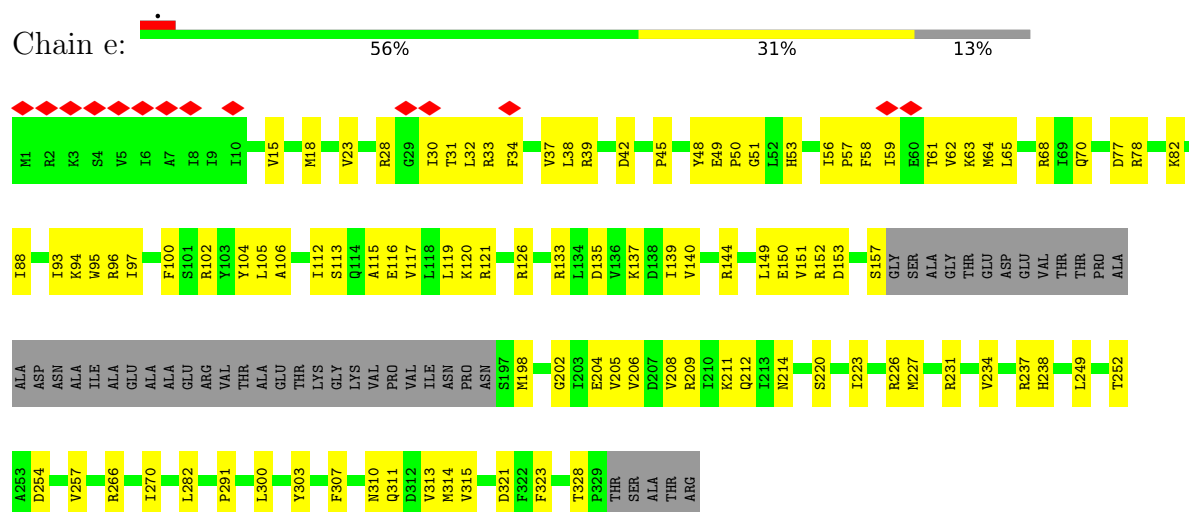
• Molecule 1: Modulator of FtsH protease HflC



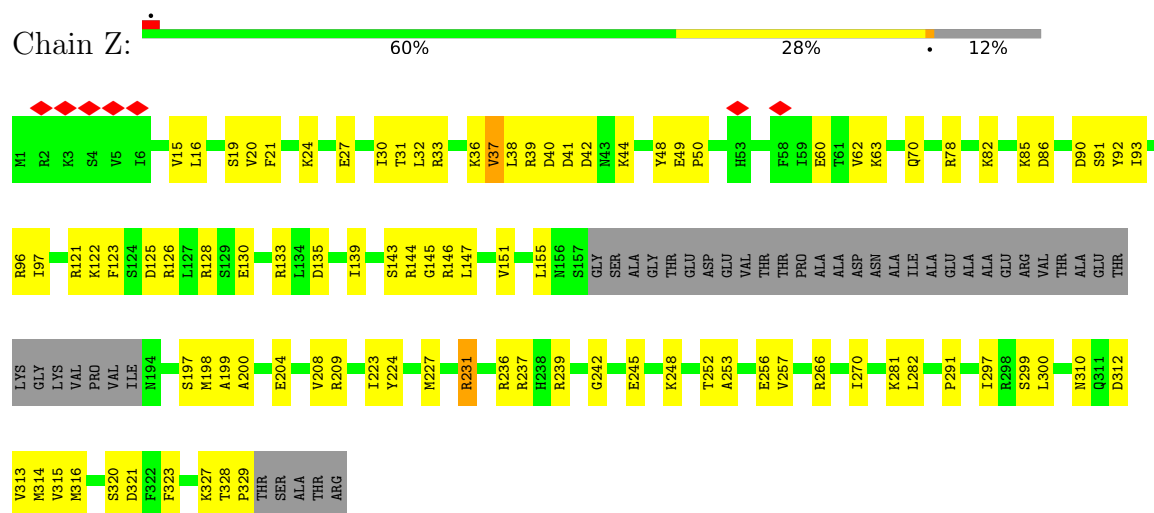
• Molecule 1: Modulator of FtsH protease HflC



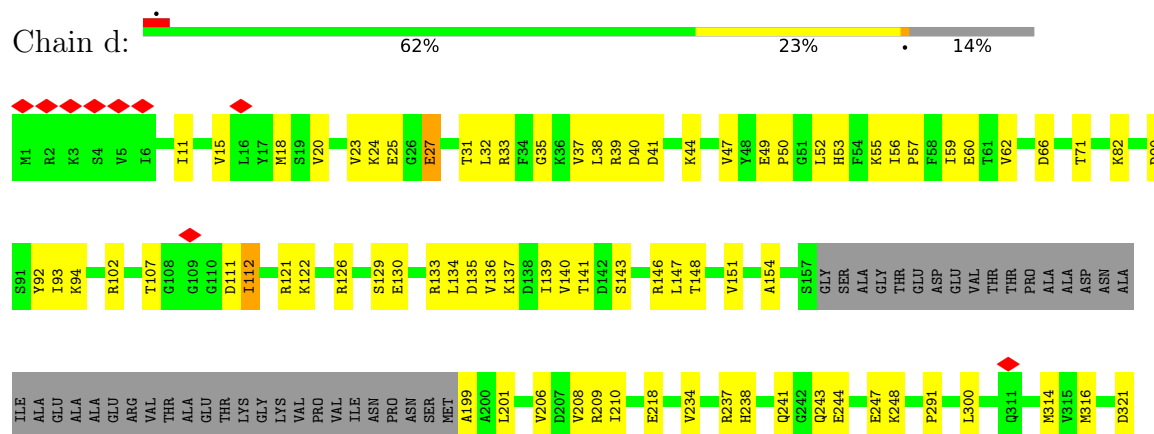
• Molecule 1: Modulator of FtsH protease HflC

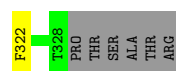


• Molecule 1: Modulator of FtsH protease HflC

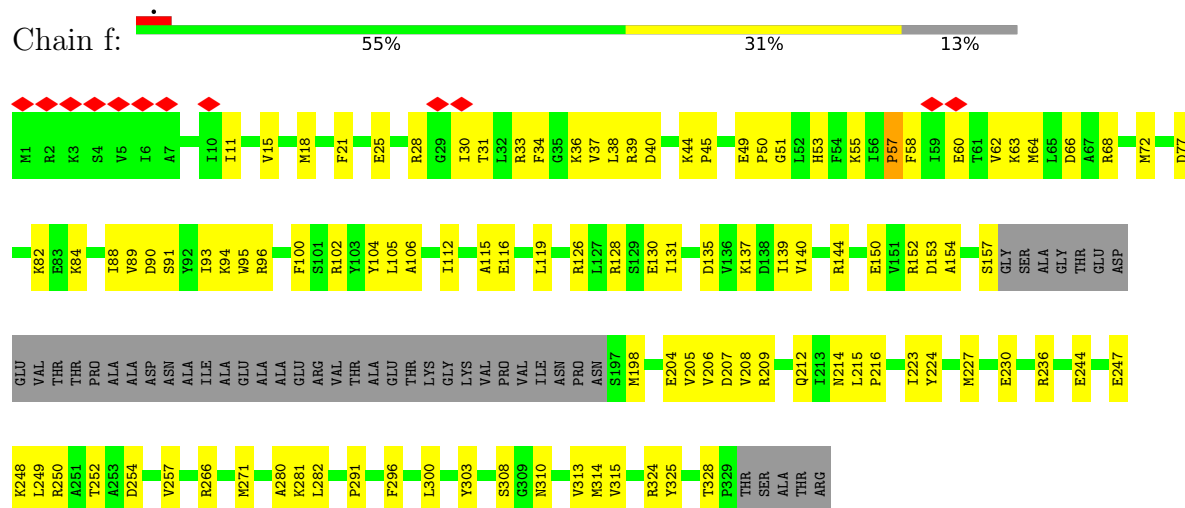


• Molecule 1: Modulator of FtsH protease HflC

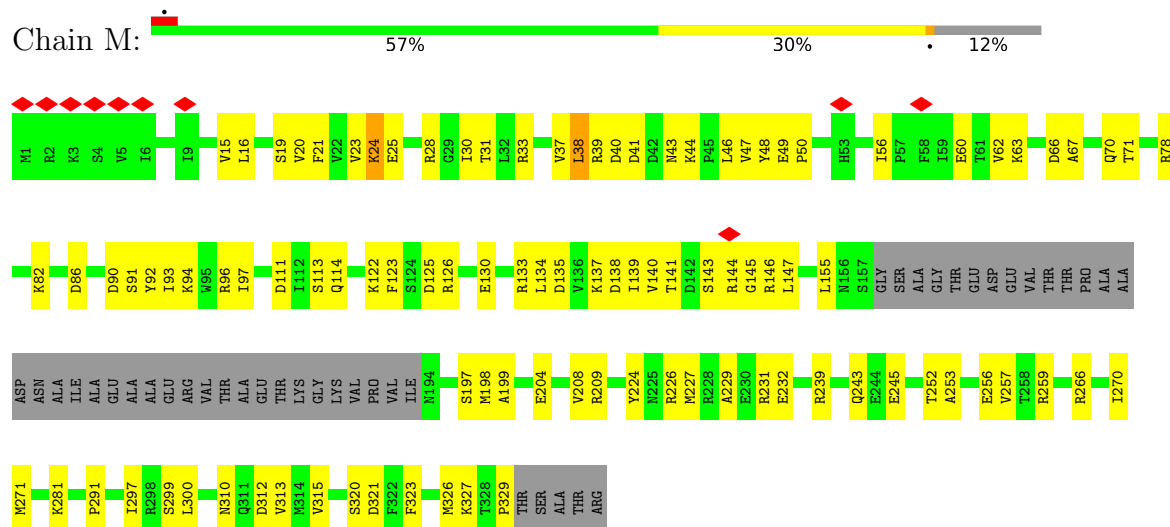




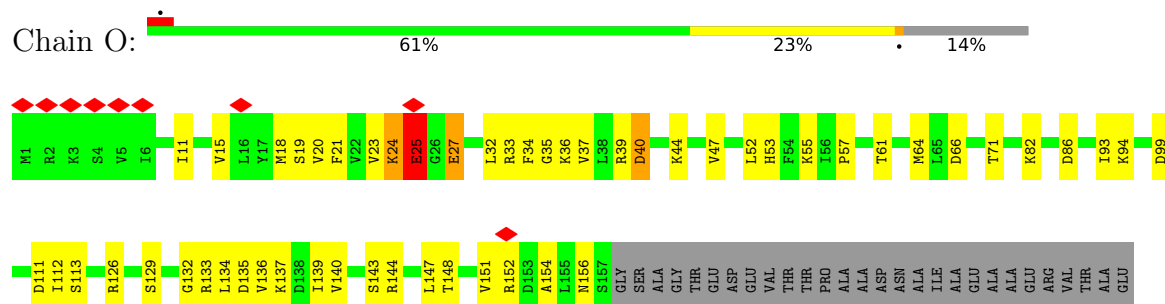
• Molecule 1: Modulator of FtsH protease HflC

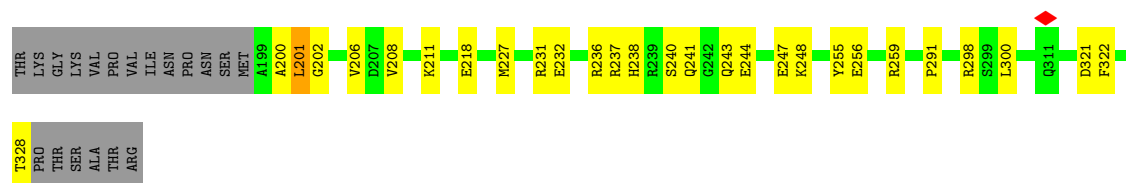


• Molecule 1: Modulator of FtsH protease HflC



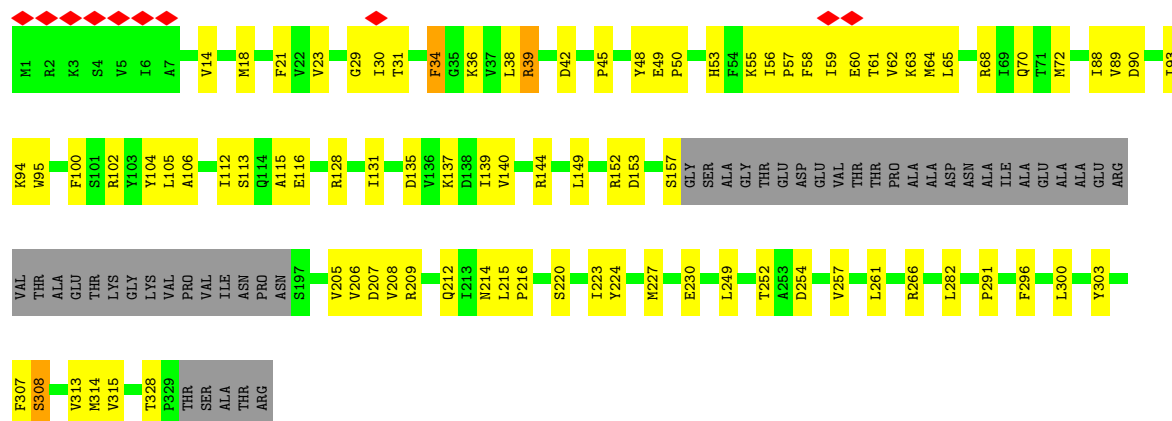
• Molecule 1: Modulator of FtsH protease HflC





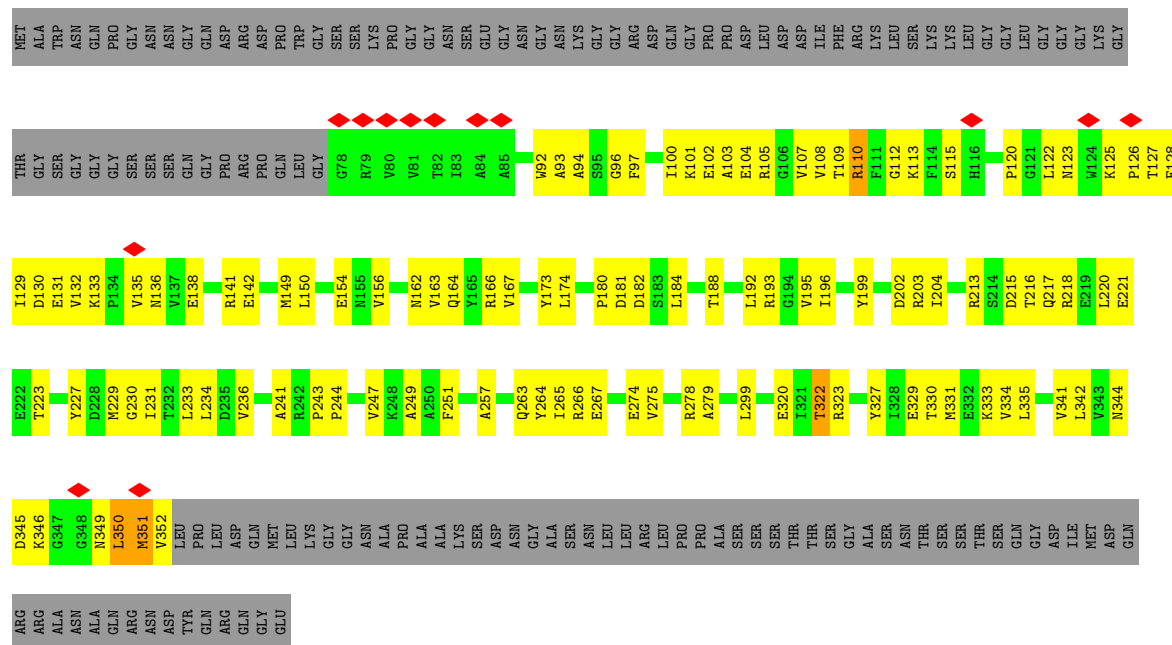
• Molecule 1: Modulator of FtsH protease HflC

Chain P: 60% 25% 13%



• Molecule 2: Modulator of FtsH protease HflK

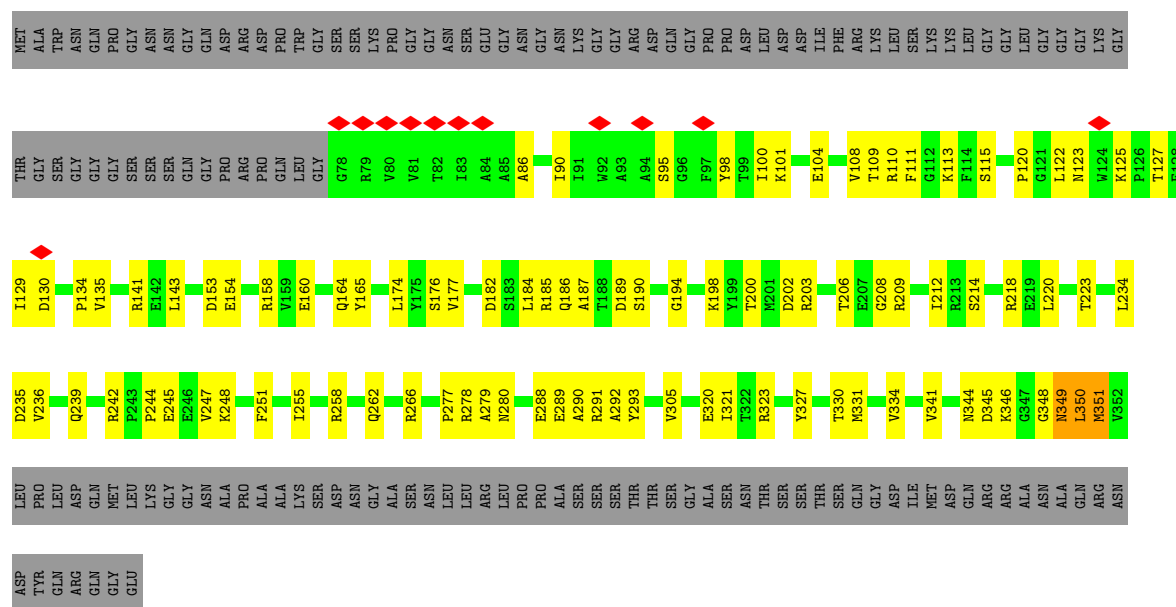
Chain B: 39% 25% 34%



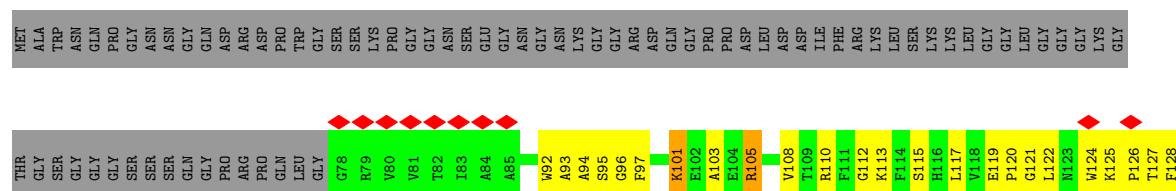
• Molecule 2: Modulator of FtsH protease HflK

Chain F: 41% 22% 34%

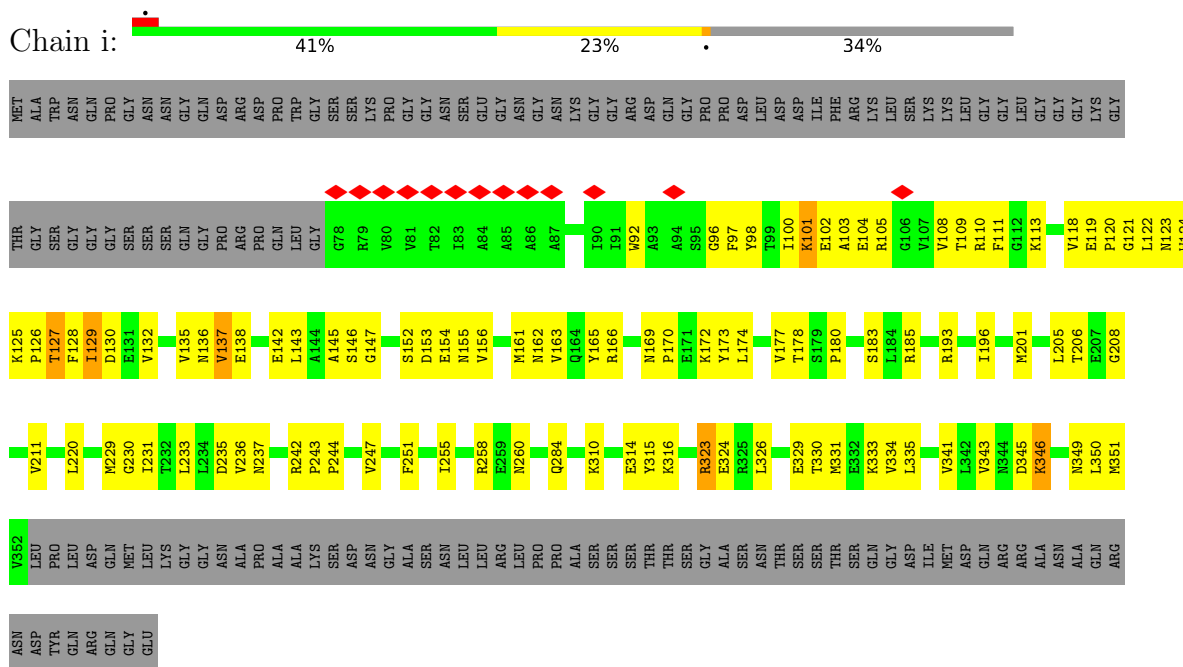
- Molecule 2: Modulator of FtsH protease HflK



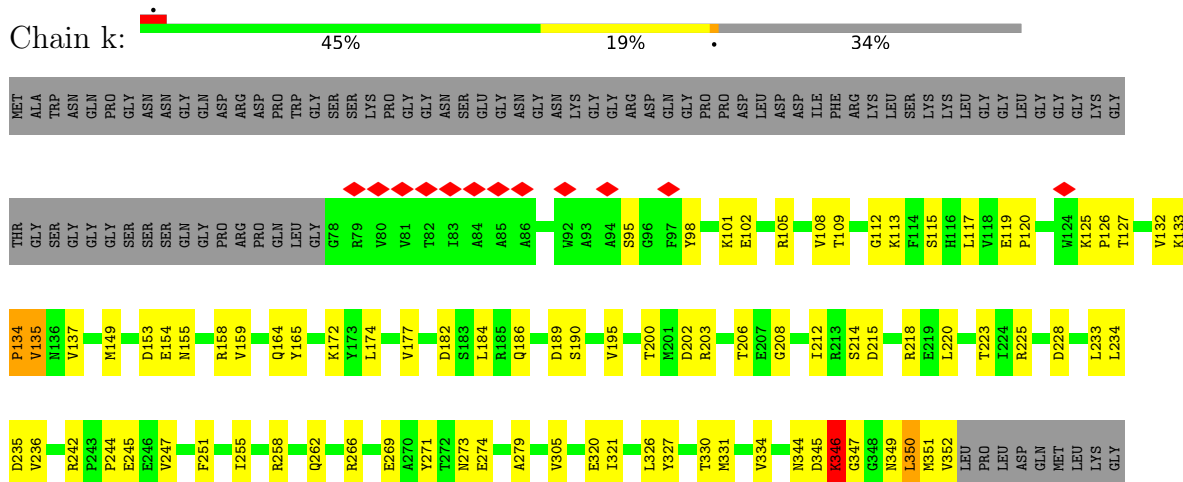
- Molecule 2: Modulator of FtsH protease HflK



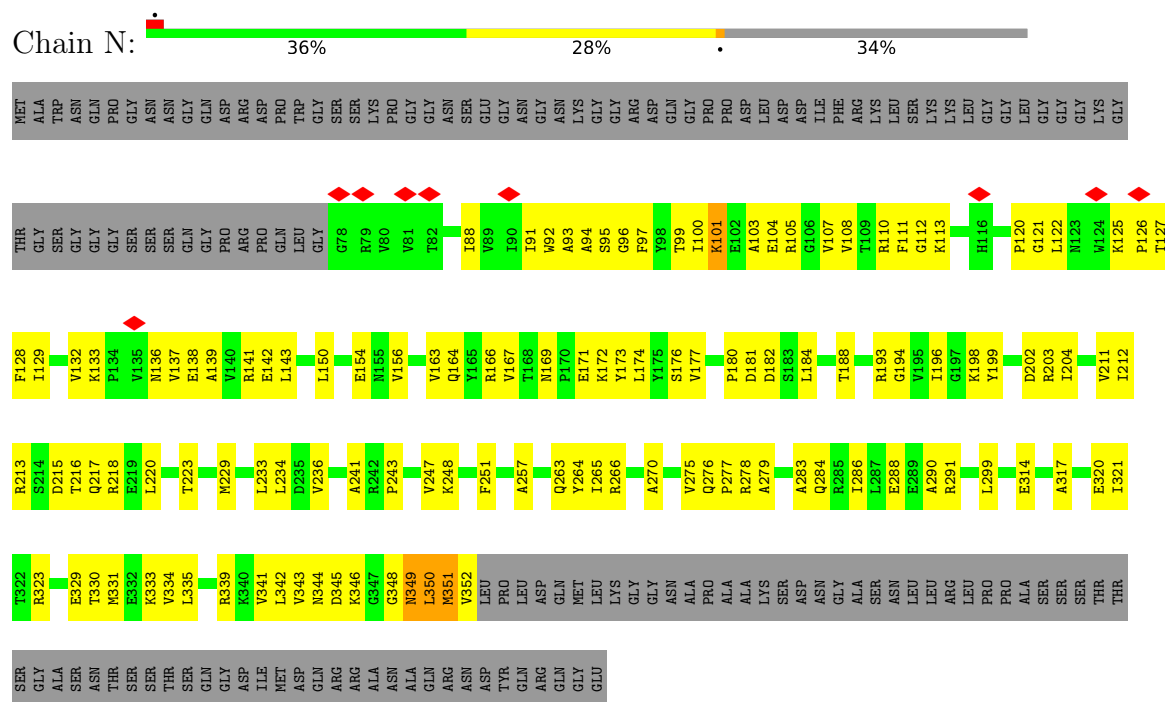
- Molecule 2: Modulator of FtsH protease HflK



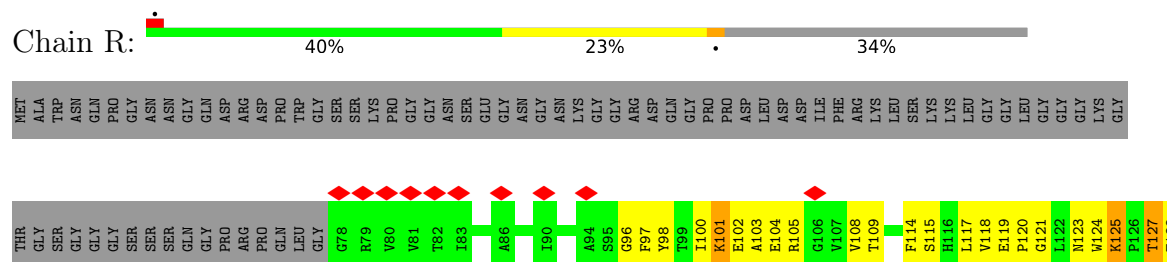
- Molecule 2: Modulator of FtsH protease HflK



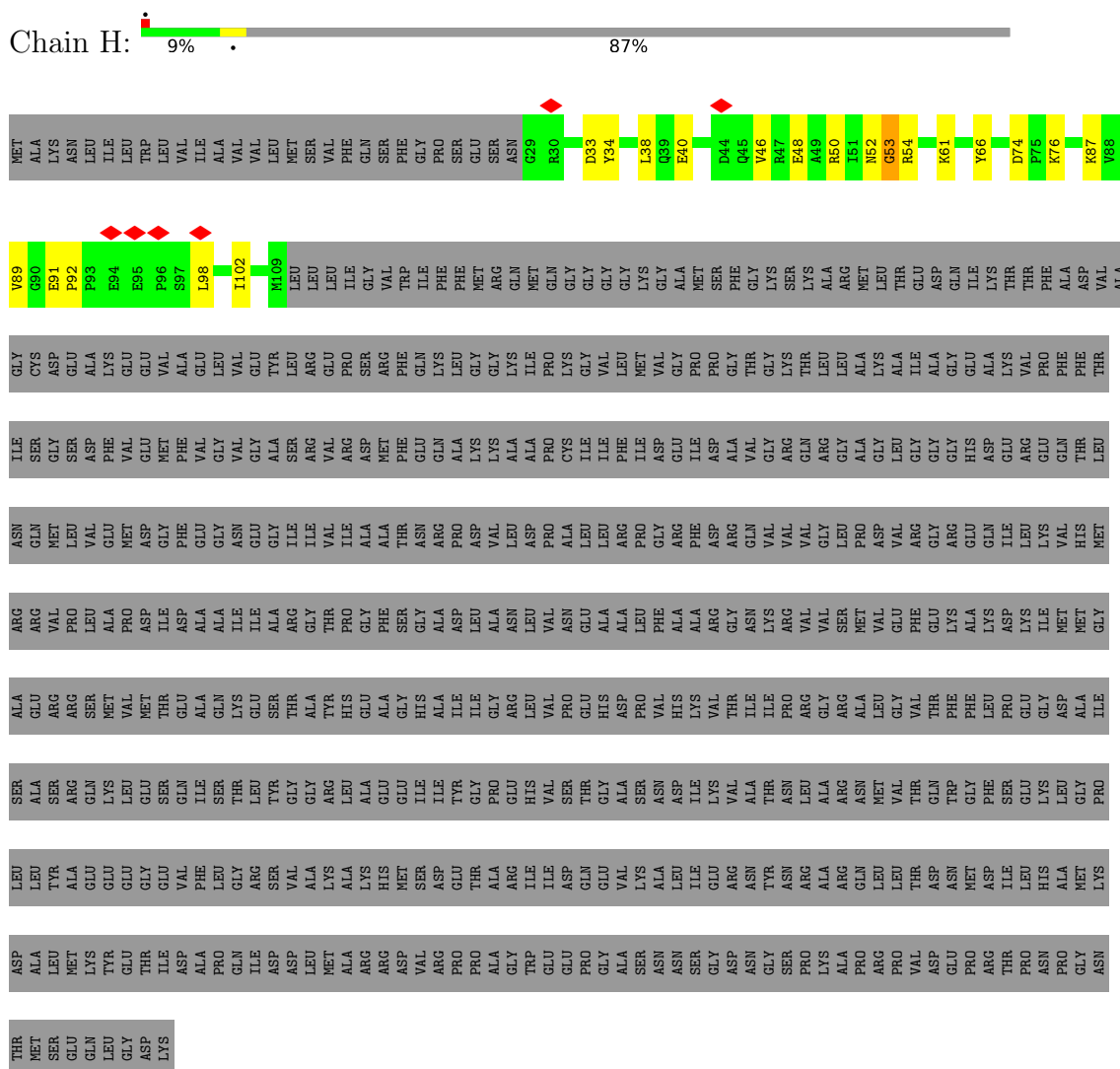
- Molecule 2: Modulator of FtsH protease HflK



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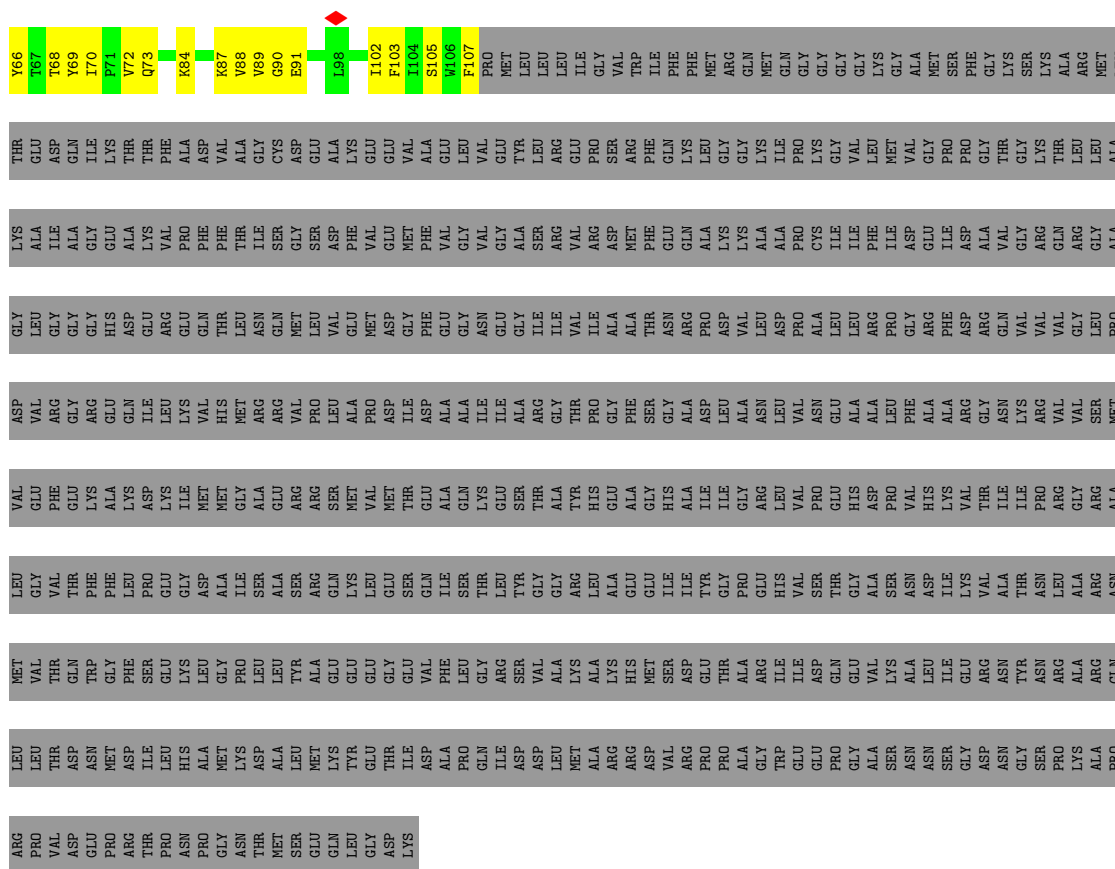
- Molecule 3: ATP-dependent zinc metalloprotease FtsH



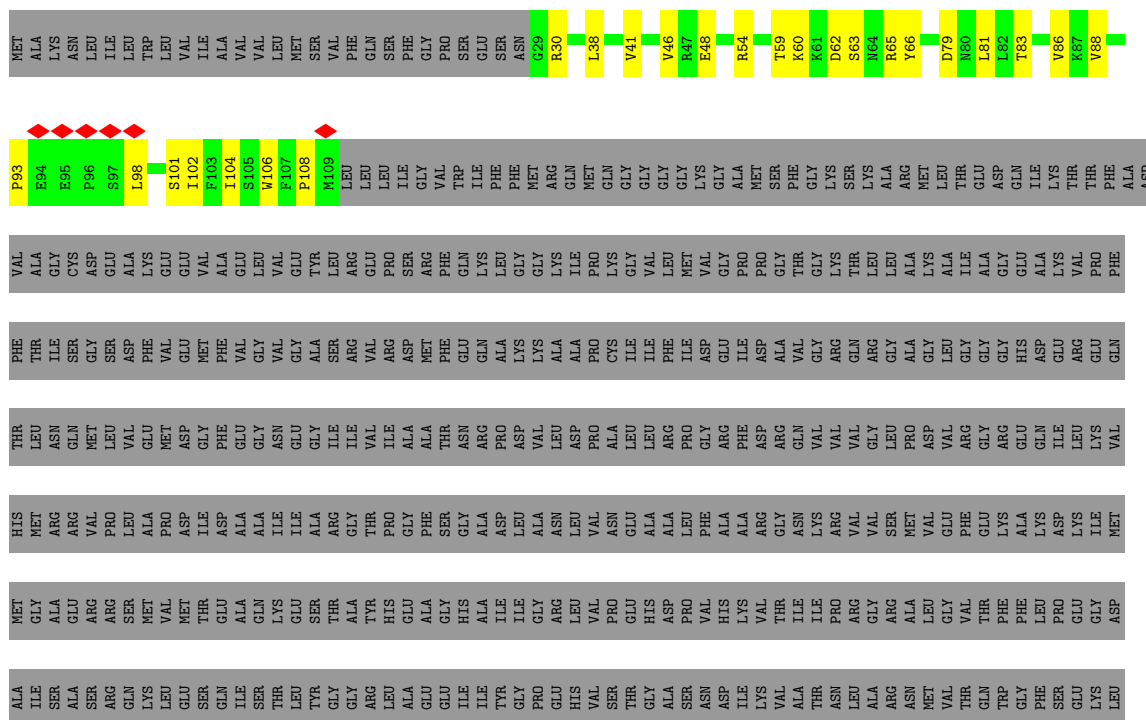
- Molecule 3: ATP-dependent zinc metalloprotease FtsH

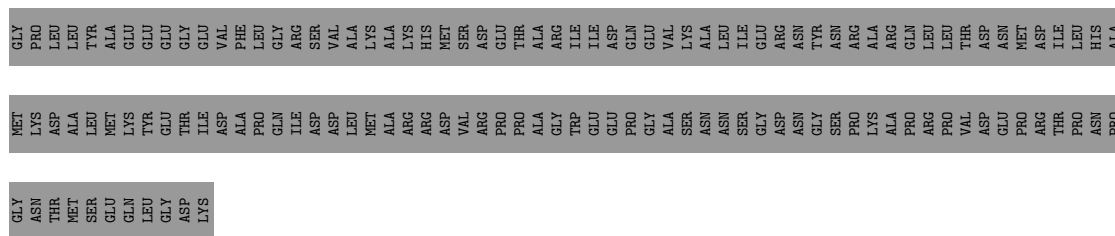






- Molecule 3: ATP-dependent zinc metalloprotease FtsH

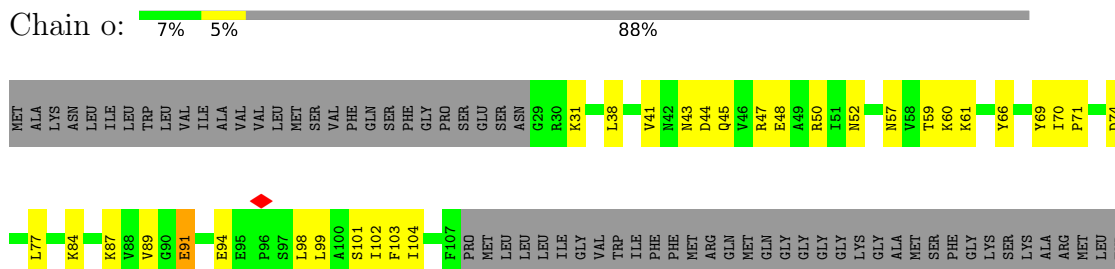




- Molecule 3: ATP-dependent zinc metalloprotease FtsH



- Molecule 3: ATP-dependent zinc metalloprotease FtsH



[illegible]

- Molecule 3: ATP-dependent zinc metalloprotease FtsH

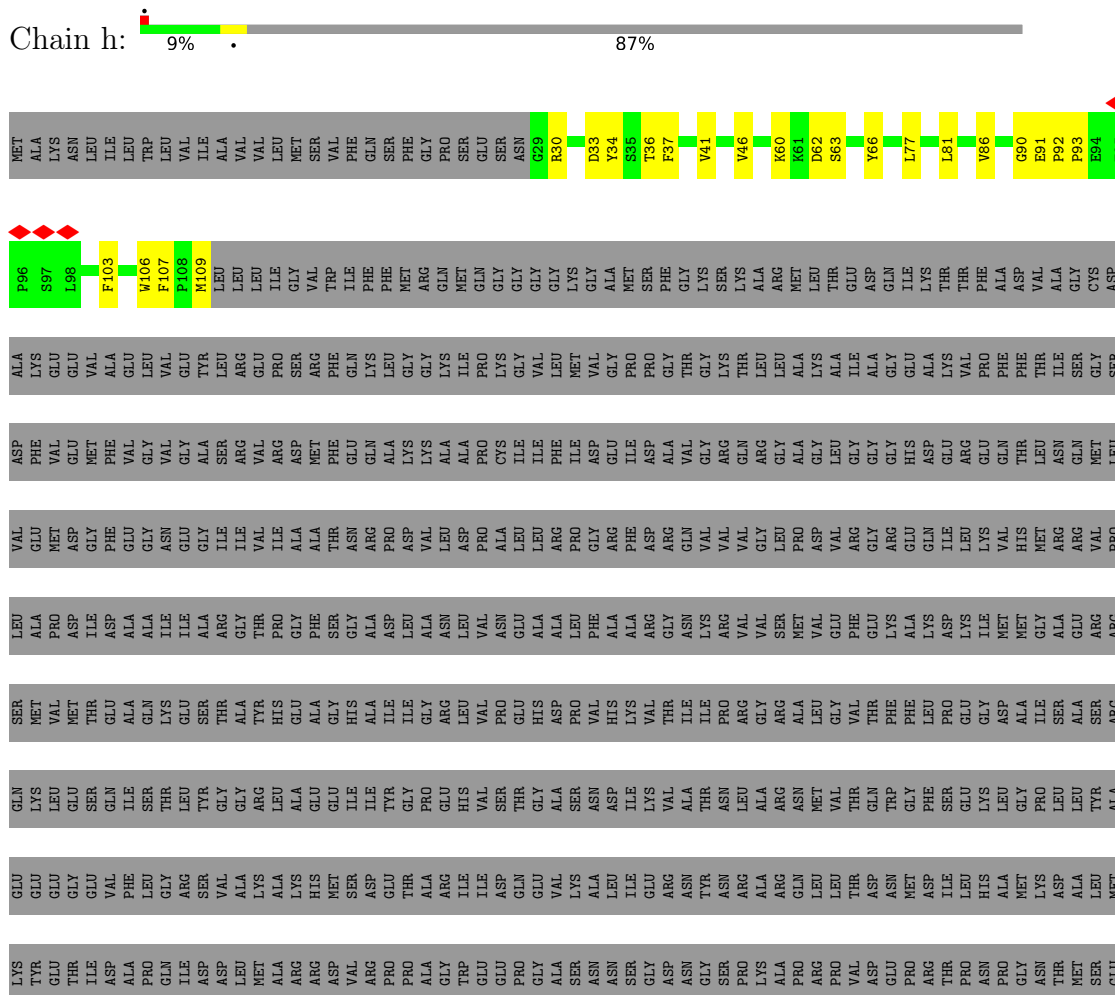
[illegible]

- Molecule 3: ATP-dependent zinc metalloprotease FtsH

[illegible]

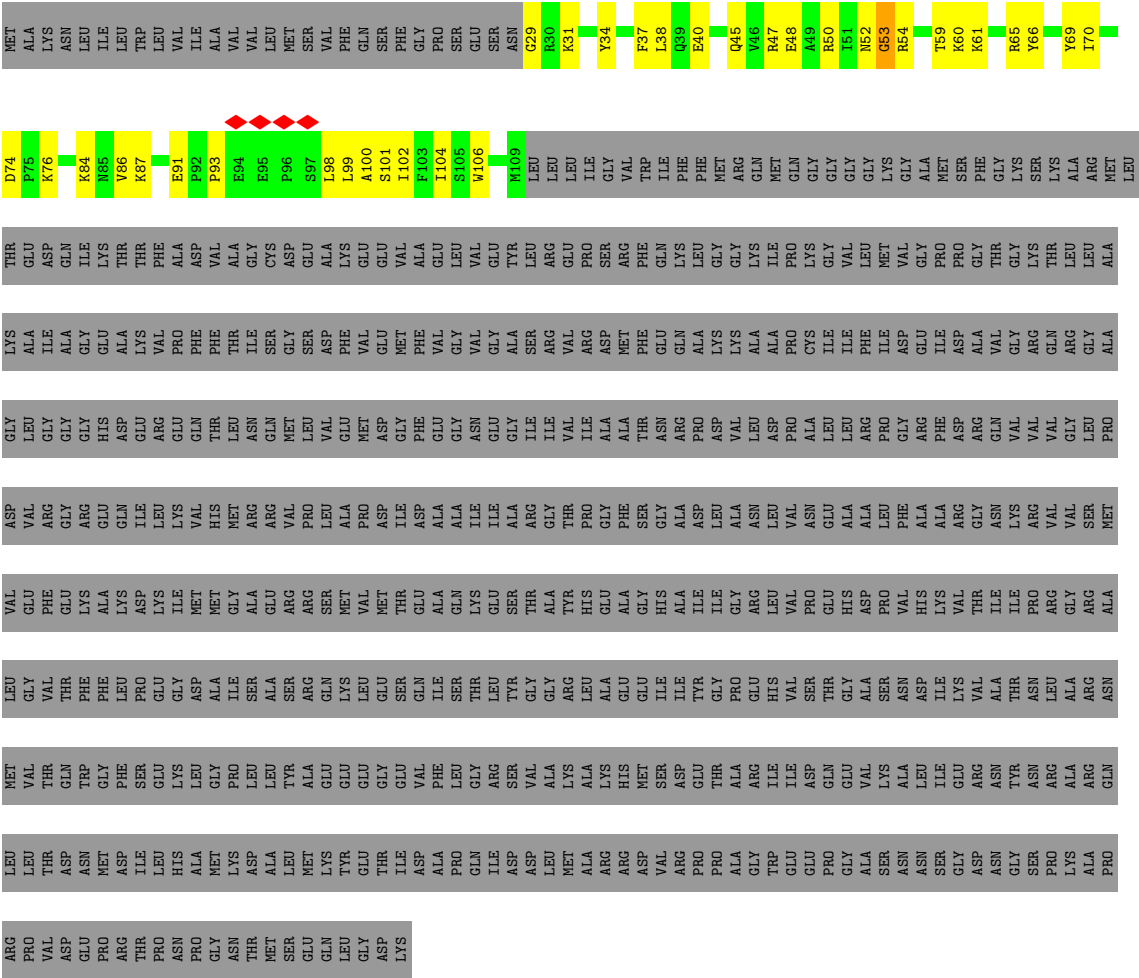
[illegible]

- Molecule 3: ATP-dependent zinc metalloprotease FtsH

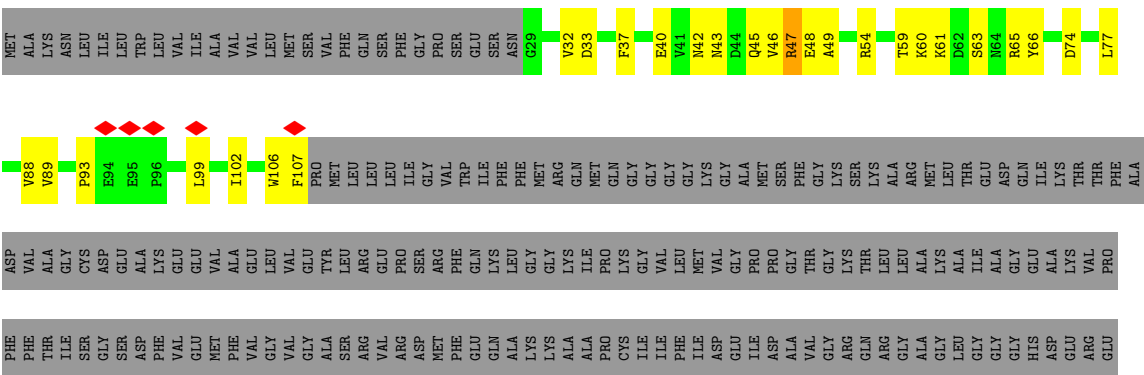


GLN
LEU
GLY
ASP
LYS

● Molecule 3: ATP-dependent zinc metalloprotease FtsH



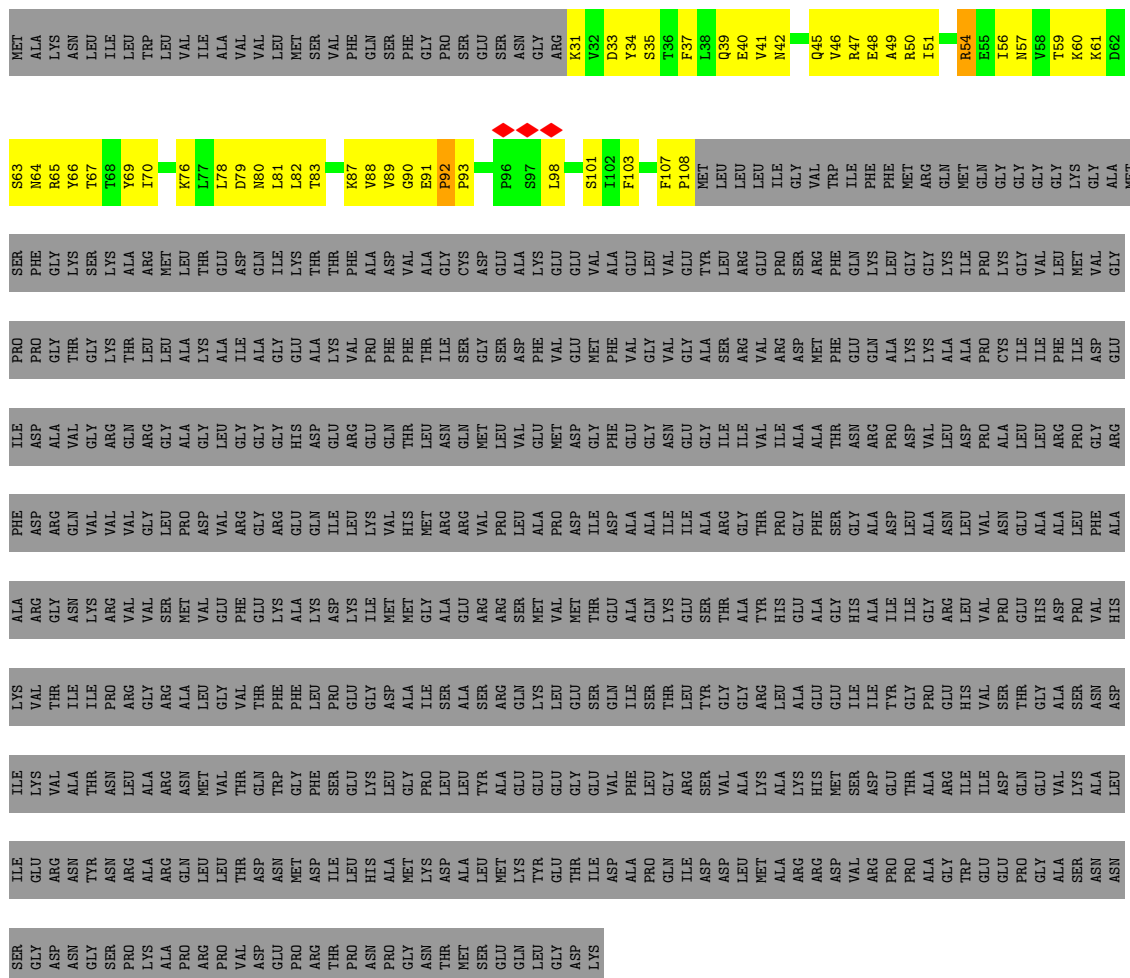
● Molecule 3: ATP-dependent zinc metalloprotease FtsH



PRO	ALA	LEU	ASP	MET	VAL	GLN
GLY	MET	GLY	ALA	MET	HIS	THR
ASN	LYS	PRO	ILE	GLY	MET	LEU
THR	ASP	LEU	SER	ALA	ARG	ASN
MET	ALA	LEU	ALA	GLU	ARG	GLN
SER	LEU	TYR	SER	ARG	VAL	MET
GLU	MET	ALA	ARG	ARG	PRO	LEU
GLN	LYS	GLU	GLN	SER	LEU	VAL
LEU	TYR	GLU	LEU	MET	ALA	GLU
GLY	GLU	GLU	LEU	VAL	PRO	MET
ASP	THR	GLY	GLU	MET	ASP	ASP
LYS	ILE	GLU	SER	THR	ILE	GLY
	ASP	VAL	GLN	GLU	ASP	PHE
	ALA	PHE	ILE	ALA	ALA	GLU
	PRO	LEU	SER	GLN	ILE	GLY
	GLN	GLY	THR	LYS	ILE	ASN
	ILE	ARG	LEU	GLU	ILE	GLU
	ASP	SER	TYR	SER	ALA	GLY
	ASP	VAL	GLY	THR	ARG	ILE
	LEU	ALA	GLY	ALA	GLY	ILE
	MET	LYS	ARG	TYR	THR	VAL
	ALA	ALA	LEU	HIS	PRO	ILE
	ARG	LYS	ALA	GLU	GLY	ALA
	ASP	HIS	GLU	ALA	PHE	ALA
	ASP	MET	GLU	GLY	SER	THR
	VAL	SER	ILE	HIS	GLY	ASN
	ARG	ASP	ILE	ASP	ALA	ASN
	PRO	GLU	TYR	ILE	ASP	PRO
	PRO	THR	GLY	ILE	LEU	ASP
	ALA	ALA	PRO	GLY	ALA	VAL
	GLY	ARG	GLU	ARG	ASN	LEU
	THR	ILE	HIS	LEU	ALA	LEU
	GLU	ILE	GLY	LEU	ALA	ARG
	SER	LYS	SER	PRO	LEU	PRO
	ASN	ALA	ASN	VAL	PHE	GLY
	GLY	GLU	ASN	THR	ALA	PHE
	ASN	ASN	VAL	LYS	ARG	ASP
	ASN	ARG	ALA	THR	GLY	ARG
	GLY	TYR	THR	ILE	LYS	VAL
	SER	ASN	ASN	PRO	ARG	VAL
	PRO	ARG	LEU	ARG	VAL	VAL
	LYS	ALA	ALA	GLY	VAL	GLY
	ALA	ARG	GLN	ALA	SER	LEU
	PRO	GLN	ASN	ILE	SER	PRO
	ARG	LEU	MET	ALA	VAL	ASP
	PRO	THR	VAL	GLY	GLU	VAL
	ASP	ASP	THR	VAL	PHE	ARG
	GLU	ASN	GLN	THR	GLU	GLY
	THR	ASP	TRP	PHE	LYS	ARG
	ARG	MET	THR	GLY	ALA	GLU
	THR	ASP	PHE	LYS	MET	GLN
	THR	ILE	SER	PRO	ASP	ILE
	PRO	LEU	SER	PRO	ASP	ILE
	ASN	HEP	GLY	GLY	LYS	THR

- Molecule 3: ATP-dependent zinc metalloprotease FtsH

Chain r: 5% 7% 88%



● Molecule 3: ATP-dependent zinc metalloprotease FtsH

Chain t:  6% 6% 88%

ALA	PRO	ARG	PRO	VAL	ASP	GLU	GLU	PRO	ARG	ASP	GLY	ASN	THR	ILE	ASP	GLY	GLU	GLY	ASN	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GL
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● Molecule 3: ATP-dependent zinc metalloprotease FtsH

Chain v:  5% 7% 88%

MET	ALA	LYS	ASN	LEU	ILE	LEU	TRP	VAL	VAL	VAL	VAL	LEU	MET	SER	VAL	PHE	GLN	SER	GLU	ASN	G29	R30	K31	V32	D33	Y34	S35	T36	F37	L38	Q39	E40	V41	N42	N43	D44	Q45	V46	R47	E48	A49	N52	G53	R54	E55	I56	N57	V58	T59	K60	K61		
D62	S63	N64	R65	T68	Y69	I70	P71	V72	Q73	N80	T83	K84	N85	V86	K87	P92	S97	L98	L99	I102	F103	I104	S105	W106	F107	PRO	MET	LEU	LEU	LEU	ILE	GLY	VAL	TRP	ILE	PHE	PHE	MET	ARG	GLN	MET	GLN	GLY	GLY	GLY	LYS	GLY	VAL	LYS	GLY	PRO	PHE	GLY
LYS	SER	ALA	ARG	MET	LEU	THR	LYS	GLU	ASP	GLN	THR	THR	PHE	ALA	ASP	VAL	ALA	CYS	GLY	GLU	VAL	VAL	GLU	LEU	VAL	GLU	TYR	ALA	ARG	GLY	PRO	SER	ARG	PHE	GLN	LYS	LEU	GLY	GLY	GLY	VAL	VAL	LYS	ILE	GLY	VAL	LYS	GLY	PRO	GLY			
THR	GLY	THR	THR	LEU	ALA	LYS	LYS	ALA	ALA	GLY	ALA	VAL	PHE	PHE	THR	ILE	SER	GLY	GLY	GLY	PHE	VAL	VAL	GLY	VAL	VAL	ALA	ARG	ILE	ARG	VAL	ARG	ASP	MET	PHE	GLN	ALA	LYS	LYS	LYS	ALA	ALA	ALA	PRO	CYS	ILE	ILE	PHE	ILE	ILE	GLY	ASP	ALA
VAL	GLY	ARG	GLN	ARG	GLY	GLY	GLY	GLY	HIS	ASP	GLU	GLU	GLU	GLN	THR	LEU	ASN	GLN	MET	GLY	ASP	GLY	GLY	GLY	ASN	GLU	GLY	ILE	ILE	ILE	ALA	ALA	THR	THR	ASN	ARG	PRO	PRO	ASP	ARG	PRO	PRO	ARG	PRO	ARG	ARG	ARG	ARG	ARG	ARG	ARG		

LEU	GLY	ASP	LYS	TYR	GLU	GLY	LYS	MET	ALA	GLU	PHE	LYS	A100	MET
GLY	THR	GLU	GLU	GLU	GLU	GLY	LEU	VAL	PRO	ASP	VAL	GLU	S101	ALA
ASP	ILE	GLU	GLU	THR	THR	SER	THR	ILE	ASP	ILE	MET	VAL	I102	LYS
ALA	ASP	VAL	PHE	ILE	GLN	ILE	ALA	ALA	ASP	PHE	PHE	ALA	F103	ASN
PRO	GLN	LEU	LEU	THR	THR	GLN	GLN	ALA	ALA	GLU	VAL	GLU	H106	ILE
ILE	ASP	ARG	GLY	THR	GLU	THR	ILE	ILE	ILE	ASN	VAL	VAL	F107	TRP
ASP	ASP	SER	GLY	TYR	GLU	GLU	ALA	PHE	ALA	GLY	ALA	TYR	P108	LEU
LEU	ASP	VAL	VAL	GLY	GLY	THR	ARG	ALA	ARG	ILE	SER	LEU	M109	VAL
MET	ALA	LYS	ALA	ARG	GLY	ALA	GLY	THR	THR	ILE	ARG	ARG	LEU	ILE
ALA	ARG	ALA	ALA	HIS	LEU	GLY	PRO	PRO	ILE	ILE	VAL	GLU	LEU	ALA
ARG	ASP	HIS	LYS	GLU	ALA	GLU	GLY	GLY	ALA	ASP	ASP	PRO	GLY	VAL
ASP	ASP	GLU	GLU	ALA	GLU	PHE	ALA	ALA	ALA	ALA	MET	SER	LEU	TRP
VAL	ASP	SER	ILE	GLY	GLY	THR	GLY	ASP	GLY	ASN	PHE	GLN	LEU	GLY
ARG	ASP	ILE	ASP	ILE	ALA	ALA	ILE	ASP	ALA	PRO	GLN	LYS	LEU	GLN
PRO	PRO	GLU	GLU	TYR	TYR	GLU	TYR	ILE	ASP	PRO	ALA	LEU	MET	ASN
PRO	ALA	ALA	ALA	GLU	PRO	GLY	GLY	ILE	LEU	VAL	LYS	GLY	GLY	SER
GLY	ALA	ALA	ALA	ARG	ALA	ARG	ALA	ALA	ALA	ASN	ASN	VAL	GLY	SER
TRP	ILE	ILE	ILE	THR	ILE	HIS	LEU	LEU	LEU	ASP	ALA	ILE	GLN	PRO
GLU	ILE	VAL	VAL	VAL	VAL	VAL	VAL	PHE	GLY	PRO	PRO	LYS	GLY	SER
GLU	ASP	ASP	ASP	PRO	THR	SER	SER	ALA	ASN	ALA	CYS	LYS	GLY	GLU
PRO	GLN	GLN	THR	THR	THR	THR	GLY	GLU	GLU	LEU	ILE	VAL	GLY	SER
GLY	GLY	ALA	ALA	HIS	ALA	ALA	ALA	ARG	LEU	LEU	PHE	LYS	GLY	ASN
ALA	ALA	VAL	VAL	ALA	ALA	ALA	ALA	ARG	ALA	ARG	PHE	LEU	LYS	GLY
SER	SER	LYS	LEU	SER	VAL	VAL	VAL	ALA	LEU	ASP	ASP	LEU	ALA	GLY
ASN	ASN	ASN	LEU	VAL	VAL	VAL	VAL	ALA	PRO	GLY	GLY	ALA	ALA	GLY
SER	SER	ILE	ILE	LYS	VAL	VAL	VAL	ALA	ARG	PHE	ILE	GLY	ALA	GLY
GLY	ASP	ARG	ARG	THR	THR	THR	THR	ARG	GLY	ARG	ALA	PRO	SER	GLY
ASN	ASN	VAL	VAL	ALA	ALA	ALA	ALA	PHE	ILE	ALA	ILE	VAL	ALA	GLY
ASN	ASN	ASN	ASN	VAL	ASN	ASN	ASN	VAL	ASN	ASN	GLY	THR	ALA	ASN
PRO	PRO	ARG	ARG	ALA	ALA	ALA	ALA	VAL	VAL	VAL	GLN	LYS	ARG	GLY
LYS	ALA	ALA	ALA	LYS	ALA	ALA	ALA	VAL	SER	GLY	GLY	LEU	ARG	GLY
ALA	PRO	GLN	ASN	ALA	ASN	ASN	ASN	MET	PRO	LEU	ALA	ALA	LEU	MET
ARG	ARG	LEU	LEU	VAL	MET	MET	VAL	VAL	VAL	ASP	GLY	LYS	THR	THR
PRO	VAL	THR	THR	VAL	GLY	GLY	GLY	GLY	GLU	VAL	GLY	ILE	GLU	GLU
ASP	ASP	ASN	ASN	THR	GLN	THR	PHE	THR	PHE	ARG	GLY	ALA	GLN	ASP
GLU	PRO	MET	ASP	THR	THR	THR	GLY	ALA	LYS	GLY	HIS	GLY	LYS	LYS
THR	ARG	ASP	ASP	THR	PHE	PHE	PHE	ALA	ASP	GLU	GLY	GLU	THR	THR
PRO	PRO	ILE	ILE	PRO	SER	SER	SER	ASP	ASP	ILE	GLU	VAL	THR	ALA
ASN	ASN	GLU	HIS	ASN	GLU	GLY	GLY	ILE	VAL	ILE	GLU	PRO	ALA	VAL
PRO	ASN	ALA	LYS	LYS	GLY	LYS	LYS	MET	MET	VAL	GLY	ASP	ASP	ASP
GLY	GLY	ALA	ALA	ASP	ALA	ALA	ALA	THR	THR	THR	GLN	THR	VAL	VAL
THR	THR	LYS	LYS	ASP	THR</									

Chain U: 7% 5% 88%

[illegible]

- Molecule 3: ATP-dependent zinc metalloprotease FtsH



- Molecule 3: ATP-dependent zinc metalloprotease FtsH



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26863	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.032	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	384.384, 384.384, 384.384	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3728, 1.3728, 1.3728	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.23	0/2371	0.80	6/3187 (0.2%)
1	C	0.31	0/2321	0.78	4/3118 (0.1%)
1	D	0.25	0/2343	0.58	1/3148 (0.0%)
1	M	0.29	0/2371	0.70	4/3187 (0.1%)
1	O	0.29	0/2321	0.74	7/3118 (0.2%)
1	P	1.40	8/2343 (0.3%)	0.79	10/3148 (0.3%)
1	Y	0.23	0/2371	0.89	5/3187 (0.2%)
1	Z	0.23	0/2371	0.76	5/3187 (0.2%)
1	c	0.28	0/2321	0.58	1/3118 (0.0%)
1	d	0.30	0/2321	0.61	1/3118 (0.0%)
1	e	0.25	0/2343	0.59	1/3148 (0.0%)
1	f	0.31	0/2343	0.68	4/3148 (0.1%)
2	B	0.31	0/2202	1.05	9/2984 (0.3%)
2	F	0.33	0/2198	0.84	8/2979 (0.3%)
2	G	0.28	0/2206	0.62	2/2989 (0.1%)
2	N	0.33	0/2202	0.73	3/2984 (0.1%)
2	R	0.32	0/2198	0.78	3/2979 (0.1%)
2	S	0.29	0/2206	0.58	2/2989 (0.1%)
2	a	0.35	0/2202	0.82	6/2984 (0.2%)
2	b	0.41	1/2202 (0.0%)	0.84	10/2984 (0.3%)
2	i	0.32	0/2198	0.98	12/2979 (0.4%)
2	j	0.33	0/2198	0.93	10/2979 (0.3%)
2	k	0.27	0/2206	0.70	3/2989 (0.1%)
2	l	0.29	0/2206	0.58	0/2989
3	E	0.26	0/671	0.52	0/911
3	H	0.25	0/671	0.60	2/911 (0.2%)
3	I	0.44	0/655	0.69	1/889 (0.1%)
3	J	0.21	0/648	0.56	0/882
3	K	0.24	0/655	0.68	0/889
3	L	0.22	0/655	0.58	0/889
3	Q	0.24	0/671	0.56	0/911
3	T	0.27	0/671	0.65	1/911 (0.1%)
3	U	0.38	0/655	0.67	1/889 (0.1%)
3	V	0.27	0/648	0.77	1/882 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	W	0.22	0/655	0.55	0/889
3	X	0.22	0/655	0.58	0/889
3	g	0.24	0/671	0.61	0/911
3	h	0.28	0/671	0.62	2/911 (0.2%)
3	m	0.29	0/671	0.55	0/911
3	n	0.26	0/671	0.63	2/911 (0.2%)
3	o	0.34	0/655	0.63	0/889
3	p	0.35	0/655	0.70	1/889 (0.1%)
3	q	0.32	0/648	0.68	2/882 (0.2%)
3	r	0.35	0/648	0.77	2/882 (0.2%)
3	s	0.27	0/655	0.60	0/889
3	t	0.21	0/655	0.52	1/889 (0.1%)
3	u	0.25	0/655	0.84	5/889 (0.6%)
3	v	0.26	0/655	0.74	1/889 (0.1%)
All	All	0.39	9/70384 (0.0%)	0.73	139/95104 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1
1	c	0	2
2	R	0	1
2	S	0	2
2	a	0	1
2	b	0	1
2	j	0	1
2	k	0	2
2	l	0	1
3	h	0	1
3	q	0	1
All	All	0	14

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	34	PHE	CE1-CZ	27.17	2.20	1.38
1	P	34	PHE	CD2-CE2	27.07	2.19	1.38
1	P	34	PHE	CD1-CE1	26.21	2.17	1.38
1	P	39	ARG	CD-NE	26.13	1.82	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	34	PHE	CE2-CZ	24.97	2.13	1.38

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	37	VAL	N-CA-C	-34.87	70.80	110.21
2	B	101	LYS	N-CA-C	34.30	148.66	111.28
1	A	37	VAL	N-CA-C	-28.11	72.42	109.80
1	C	201	LEU	N-CA-C	-26.93	74.98	110.53
1	Z	37	VAL	N-CA-C	-26.43	73.08	109.55

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	a	240	ALA	Peptide
1	c	39	ARG	Peptide
1	c	40	ASP	Peptide
2	k	134	PRO	Peptide
2	k	135	VAL	Peptide

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	2338	0	2354	93	0
1	C	2290	0	2310	75	0
1	D	2311	0	2331	77	0
1	M	2338	0	2354	88	0
1	O	2290	0	2310	71	0
1	P	2311	0	2331	106	0
1	Y	2338	0	2354	75	0
1	Z	2338	0	2354	81	0
1	c	2290	0	2310	75	0
1	d	2290	0	2310	61	0
1	e	2311	0	2331	94	0
1	f	2311	0	2331	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2169	0	2180	92	0
2	F	2165	0	2176	91	0
2	G	2173	0	2186	82	0
2	N	2169	0	2180	110	0
2	R	2165	0	2176	83	0
2	S	2173	0	2186	75	0
2	a	2169	0	2180	91	0
2	b	2169	0	2180	89	0
2	i	2165	0	2176	84	0
2	j	2165	0	2176	88	0
2	k	2173	0	2186	73	0
2	l	2173	0	2186	94	0
3	E	658	0	662	13	0
3	H	658	0	662	17	0
3	I	643	0	646	34	0
3	J	635	0	637	46	0
3	K	643	0	646	37	0
3	L	643	0	646	38	0
3	Q	658	0	662	18	0
3	T	658	0	662	18	0
3	U	643	0	646	24	0
3	V	635	0	637	58	0
3	W	643	0	646	28	0
3	X	643	0	646	48	0
3	g	658	0	662	20	0
3	h	658	0	662	13	0
3	m	658	0	662	17	0
3	n	658	0	662	30	0
3	o	643	0	646	27	0
3	p	643	0	646	28	0
3	q	635	0	637	34	0
3	r	635	0	637	49	0
3	s	643	0	646	20	0
3	t	643	0	646	37	0
3	u	643	0	646	51	0
3	v	643	0	646	50	0
All	All	69304	0	69744	2436	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 18.

The worst 5 of 2436 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:P:34:PHE:CD2	1:P:34:PHE:CG	1.78	1.68
1:P:34:PHE:CG	1:P:34:PHE:CD1	1.77	1.61
3:V:88:VAL:CG2	3:X:35:SER:HB3	1.09	1.51
1:P:39:ARG:CD	1:P:39:ARG:NE	1.82	1.42
3:V:88:VAL:HG22	3:X:35:SER:CB	1.51	1.39

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 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	289/334 (86%)	260 (90%)	29 (10%)	0	100	100
1	C	283/334 (85%)	264 (93%)	19 (7%)	0	100	100
1	D	286/334 (86%)	263 (92%)	23 (8%)	0	100	100
1	M	289/334 (86%)	262 (91%)	27 (9%)	0	100	100
1	O	283/334 (85%)	259 (92%)	24 (8%)	0	100	100
1	P	286/334 (86%)	263 (92%)	23 (8%)	0	100	100
1	Y	289/334 (86%)	266 (92%)	23 (8%)	0	100	100
1	Z	289/334 (86%)	262 (91%)	27 (9%)	0	100	100
1	c	283/334 (85%)	266 (94%)	17 (6%)	0	100	100
1	d	283/334 (85%)	268 (95%)	15 (5%)	0	100	100
1	e	286/334 (86%)	263 (92%)	23 (8%)	0	100	100
1	f	286/334 (86%)	259 (91%)	27 (9%)	0	100	100
2	B	273/419 (65%)	251 (92%)	22 (8%)	0	100	100
2	F	273/419 (65%)	246 (90%)	27 (10%)	0	100	100
2	G	273/419 (65%)	257 (94%)	16 (6%)	0	100	100
2	N	273/419 (65%)	254 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	273/419 (65%)	245 (90%)	28 (10%)	0	100	100
2	S	273/419 (65%)	252 (92%)	21 (8%)	0	100	100
2	a	273/419 (65%)	254 (93%)	18 (7%)	1 (0%)	30	65
2	b	273/419 (65%)	256 (94%)	17 (6%)	0	100	100
2	i	273/419 (65%)	243 (89%)	30 (11%)	0	100	100
2	j	273/419 (65%)	245 (90%)	28 (10%)	0	100	100
2	k	273/419 (65%)	254 (93%)	19 (7%)	0	100	100
2	l	273/419 (65%)	256 (94%)	17 (6%)	0	100	100
3	E	79/644 (12%)	72 (91%)	7 (9%)	0	100	100
3	H	79/644 (12%)	71 (90%)	8 (10%)	0	100	100
3	I	77/644 (12%)	72 (94%)	5 (6%)	0	100	100
3	J	76/644 (12%)	69 (91%)	7 (9%)	0	100	100
3	K	77/644 (12%)	70 (91%)	7 (9%)	0	100	100
3	L	77/644 (12%)	73 (95%)	4 (5%)	0	100	100
3	Q	79/644 (12%)	74 (94%)	5 (6%)	0	100	100
3	T	79/644 (12%)	73 (92%)	6 (8%)	0	100	100
3	U	77/644 (12%)	72 (94%)	5 (6%)	0	100	100
3	V	76/644 (12%)	69 (91%)	7 (9%)	0	100	100
3	W	77/644 (12%)	70 (91%)	7 (9%)	0	100	100
3	X	77/644 (12%)	73 (95%)	4 (5%)	0	100	100
3	g	79/644 (12%)	73 (92%)	6 (8%)	0	100	100
3	h	79/644 (12%)	72 (91%)	7 (9%)	0	100	100
3	m	79/644 (12%)	72 (91%)	7 (9%)	0	100	100
3	n	79/644 (12%)	71 (90%)	8 (10%)	0	100	100
3	o	77/644 (12%)	70 (91%)	7 (9%)	0	100	100
3	p	77/644 (12%)	72 (94%)	5 (6%)	0	100	100
3	q	76/644 (12%)	70 (92%)	6 (8%)	0	100	100
3	r	76/644 (12%)	70 (92%)	6 (8%)	0	100	100
3	s	77/644 (12%)	70 (91%)	7 (9%)	0	100	100
3	t	77/644 (12%)	70 (91%)	7 (9%)	0	100	100
3	u	77/644 (12%)	71 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	v	77/644 (12%)	69 (90%)	8 (10%)	0	100	100
All	All	8568/24492 (35%)	7876 (92%)	691 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a	319	PRO

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	248/283 (88%)	248 (100%)	0	100	100
1	C	241/283 (85%)	237 (98%)	4 (2%)	53	68
1	D	244/283 (86%)	243 (100%)	1 (0%)	84	84
1	M	248/283 (88%)	244 (98%)	4 (2%)	55	70
1	O	241/283 (85%)	238 (99%)	3 (1%)	63	73
1	P	244/283 (86%)	243 (100%)	1 (0%)	84	84
1	Y	248/283 (88%)	247 (100%)	1 (0%)	84	84
1	Z	248/283 (88%)	248 (100%)	0	100	100
1	c	241/283 (85%)	237 (98%)	4 (2%)	53	68
1	d	241/283 (85%)	235 (98%)	6 (2%)	42	62
1	e	244/283 (86%)	244 (100%)	0	100	100
1	f	244/283 (86%)	243 (100%)	1 (0%)	84	84
2	B	228/336 (68%)	222 (97%)	6 (3%)	40	61
2	F	227/336 (68%)	220 (97%)	7 (3%)	35	56
2	G	229/336 (68%)	226 (99%)	3 (1%)	61	72
2	N	228/336 (68%)	219 (96%)	9 (4%)	28	51
2	R	227/336 (68%)	217 (96%)	10 (4%)	25	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	S	229/336 (68%)	223 (97%)	6 (3%)	40	61
2	a	228/336 (68%)	219 (96%)	9 (4%)	28	51
2	b	228/336 (68%)	221 (97%)	7 (3%)	35	56
2	i	227/336 (68%)	221 (97%)	6 (3%)	40	61
2	j	227/336 (68%)	220 (97%)	7 (3%)	35	56
2	k	229/336 (68%)	225 (98%)	4 (2%)	53	68
2	l	229/336 (68%)	225 (98%)	4 (2%)	53	68
3	E	76/527 (14%)	76 (100%)	0	100	100
3	H	76/527 (14%)	76 (100%)	0	100	100
3	I	74/527 (14%)	73 (99%)	1 (1%)	59	71
3	J	74/527 (14%)	74 (100%)	0	100	100
3	K	74/527 (14%)	74 (100%)	0	100	100
3	L	74/527 (14%)	74 (100%)	0	100	100
3	Q	76/527 (14%)	76 (100%)	0	100	100
3	T	76/527 (14%)	76 (100%)	0	100	100
3	U	74/527 (14%)	72 (97%)	2 (3%)	39	60
3	V	74/527 (14%)	74 (100%)	0	100	100
3	W	74/527 (14%)	74 (100%)	0	100	100
3	X	74/527 (14%)	74 (100%)	0	100	100
3	g	76/527 (14%)	76 (100%)	0	100	100
3	h	76/527 (14%)	76 (100%)	0	100	100
3	m	76/527 (14%)	76 (100%)	0	100	100
3	n	76/527 (14%)	76 (100%)	0	100	100
3	o	74/527 (14%)	72 (97%)	2 (3%)	39	60
3	p	74/527 (14%)	74 (100%)	0	100	100
3	q	74/527 (14%)	74 (100%)	0	100	100
3	r	74/527 (14%)	73 (99%)	1 (1%)	59	71
3	s	74/527 (14%)	74 (100%)	0	100	100
3	t	74/527 (14%)	74 (100%)	0	100	100
3	u	74/527 (14%)	73 (99%)	1 (1%)	59	71
3	v	74/527 (14%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7460/20076 (37%)	7350 (98%)	110 (2%)	55 70

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	d	25	GLU
2	l	350	LEU
3	U	94	GLU
2	R	350	LEU
1	d	107	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	212	GLN
3	X	57	ASN
2	R	260	ASN
2	S	284	GLN
1	c	70	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

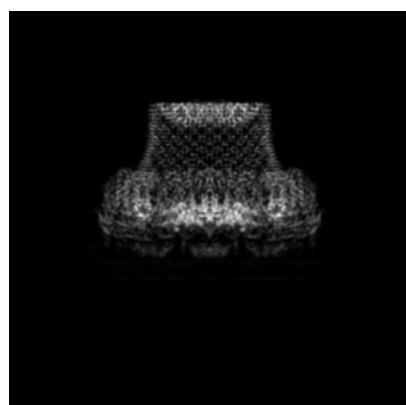
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32520. These allow visual inspection of the internal detail of the map and identification of artifacts.

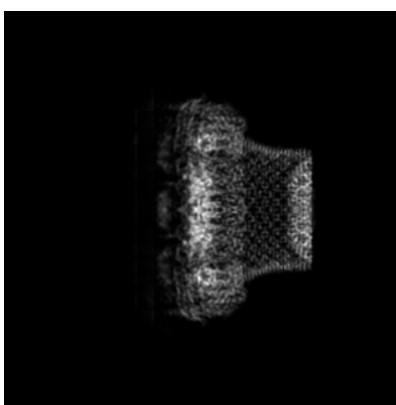
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

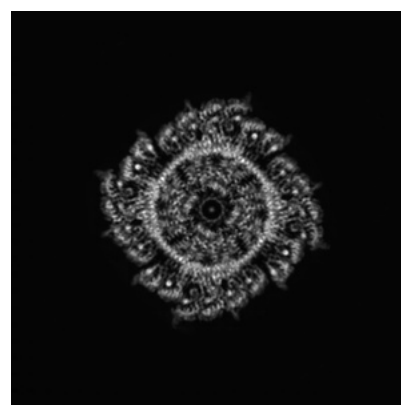
6.1.1 Primary map



X



Y

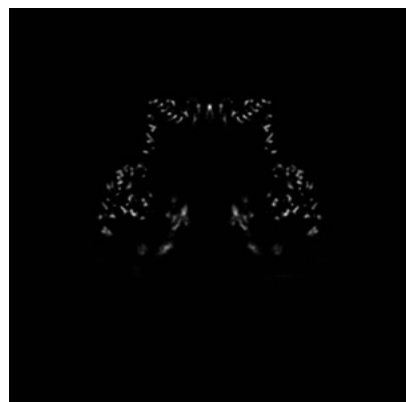


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 140



Y Index: 140

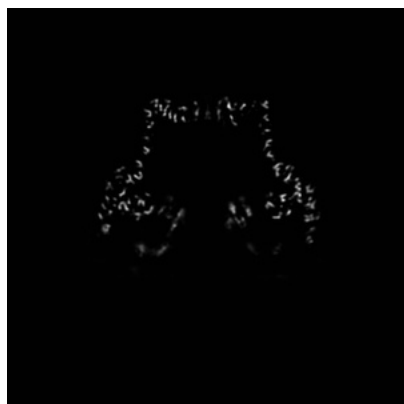


Z Index: 140

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: 142



Y Index: 142

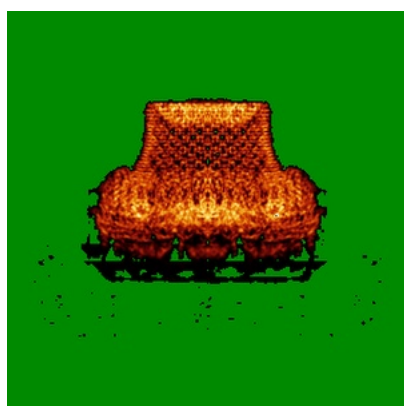


Z Index: 139

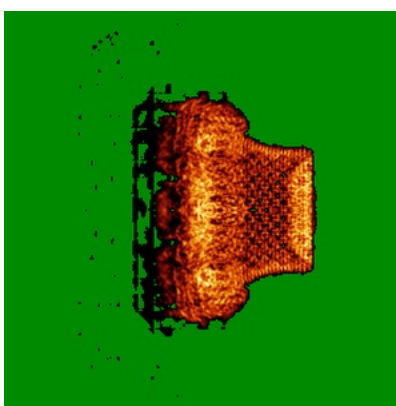
The images above show the largest variance slices of the map in three orthogonal directions.

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

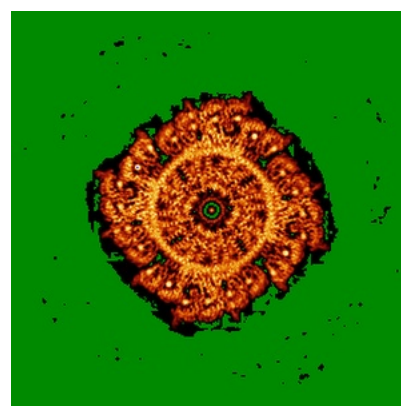
6.4.1 Primary map



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

This section was not generated.

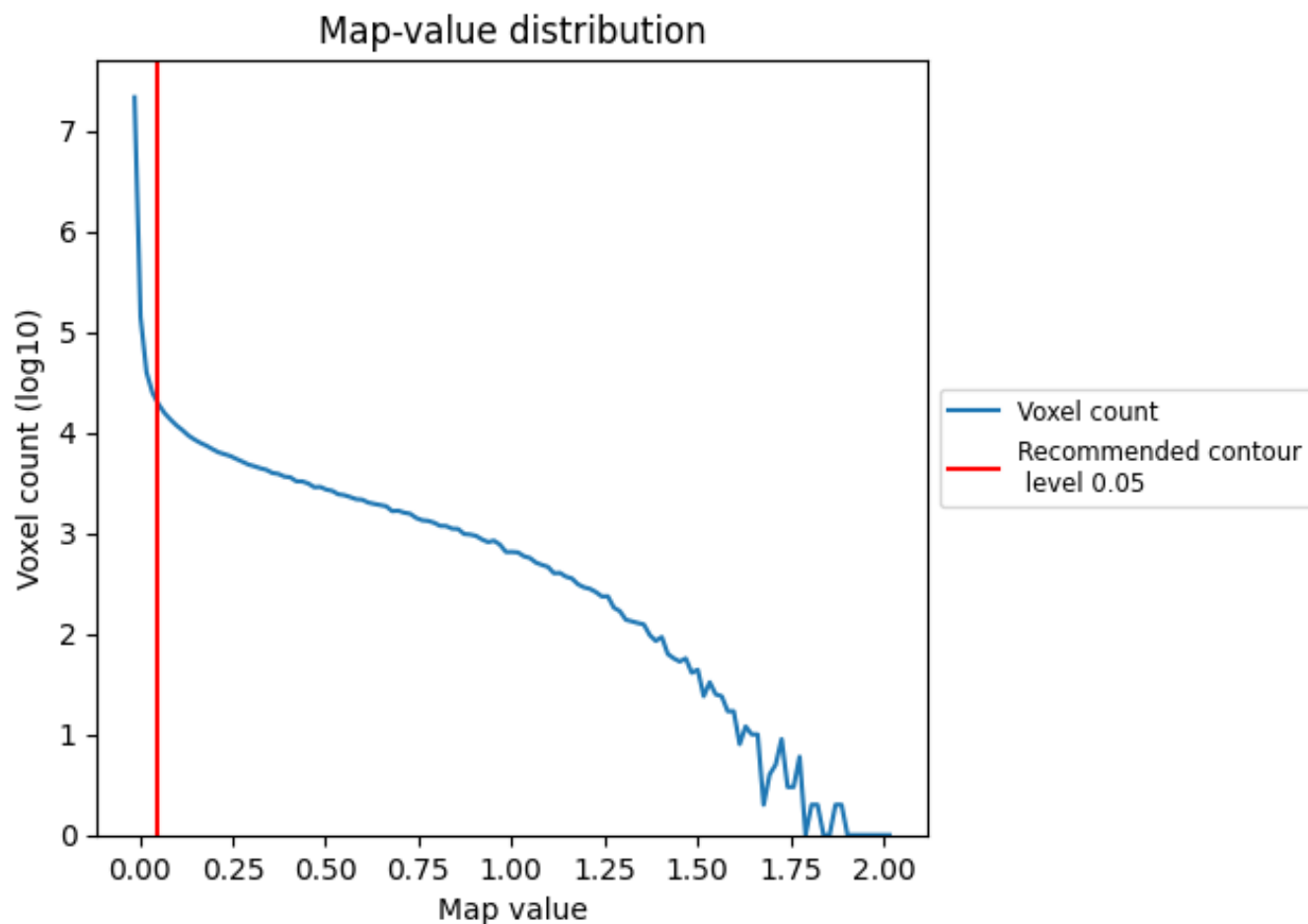
6.6 Mask visualisation

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

7 Map analysis [i](#)

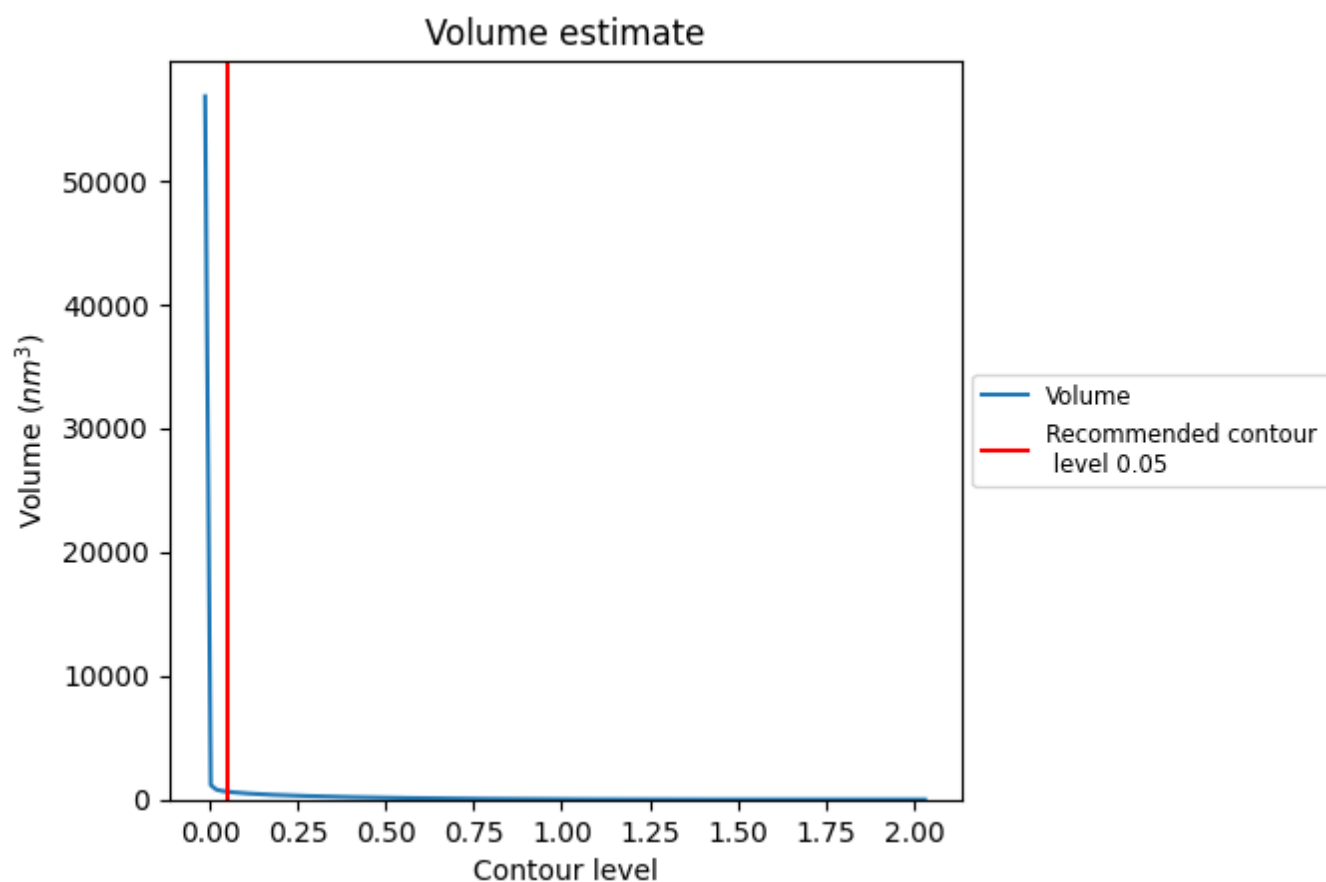
This section contains the results of statistical analysis of the map.

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.

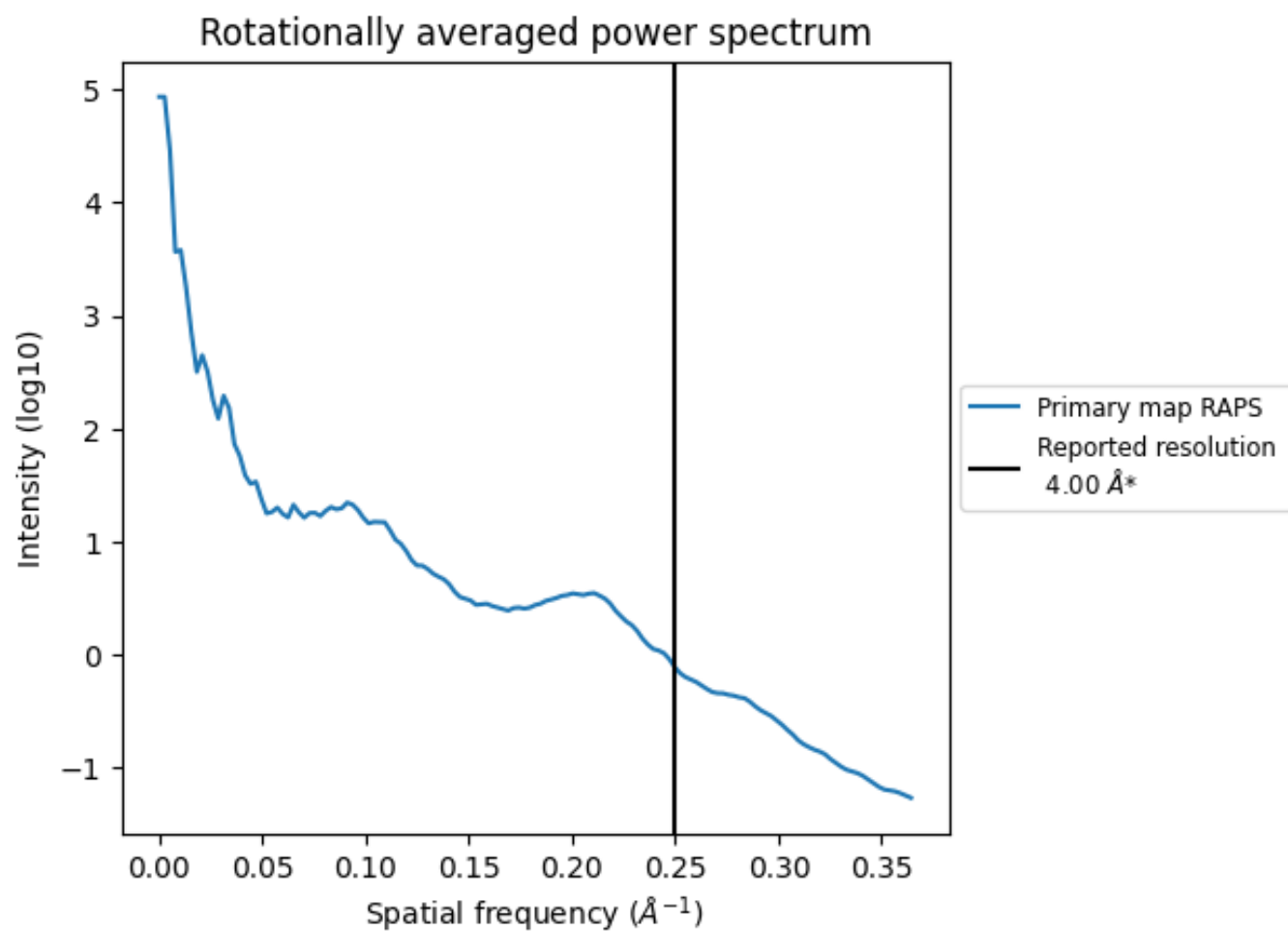
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 638 nm^3 ; this corresponds to an approximate mass of 577 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 0.250 $\text{\AA}^{-1}$

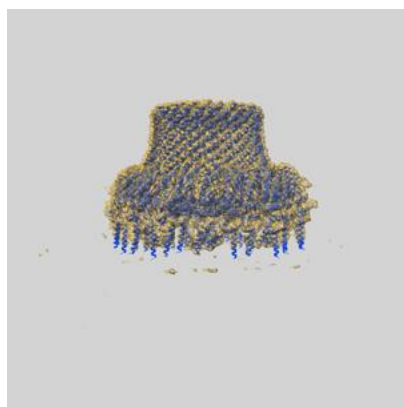
8 Fourier-Shell correlation

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

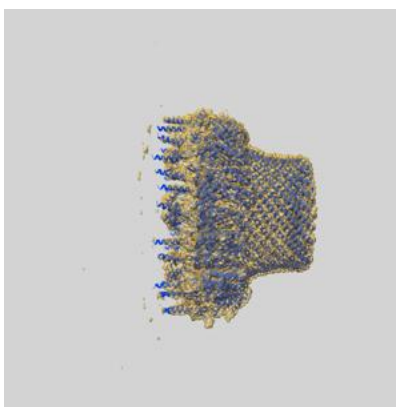
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32520 and PDB model 7WI3. Per-residue inclusion information can be found in section [3](#) on page [8](#).

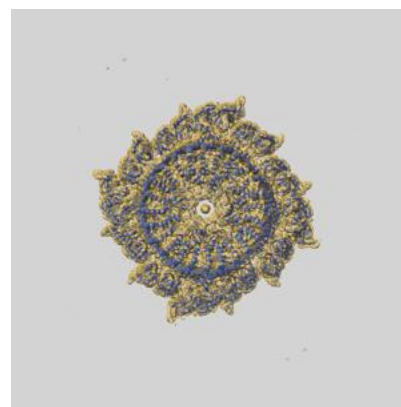
9.1 Map-model overlay [i](#)



X



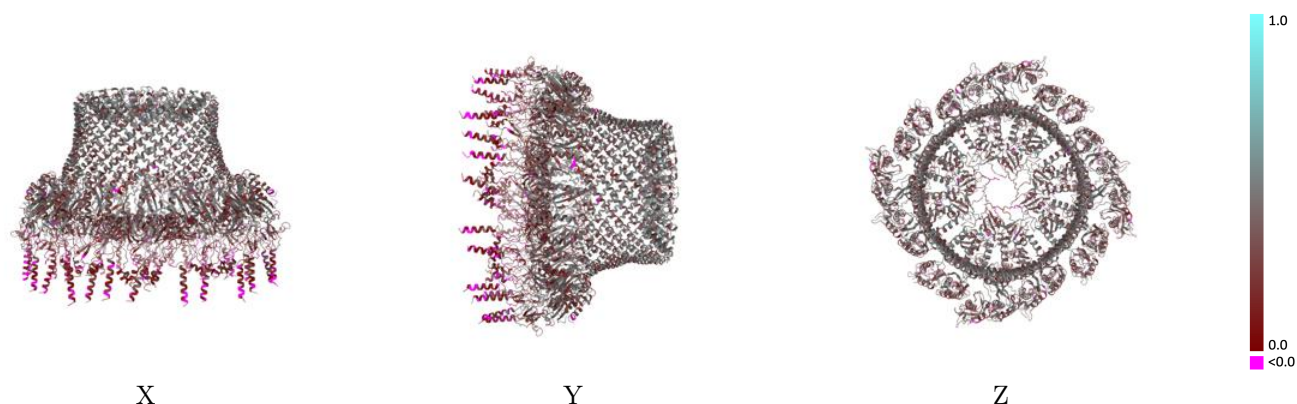
Y



Z

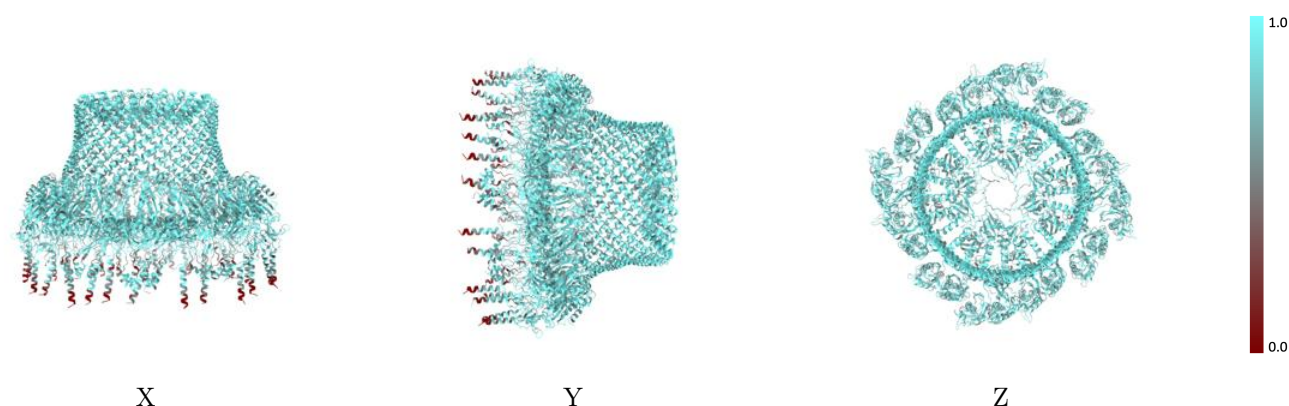
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



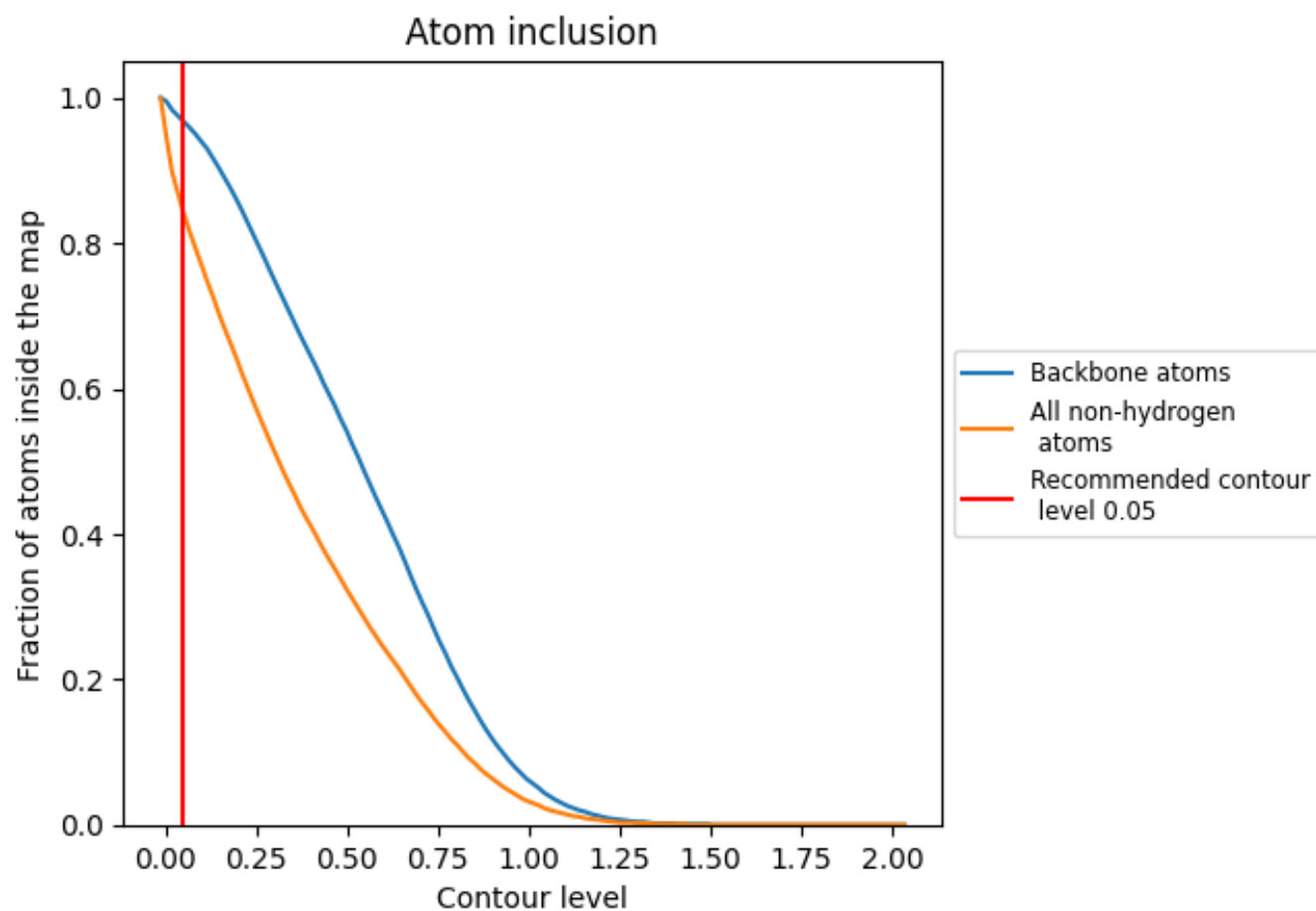
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 84% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.3350
A	 0.8590	 0.3640
B	 0.8360	 0.3420
C	 0.8300	 0.3410
D	 0.8280	 0.3310
E	 0.8250	 0.3270
F	 0.8700	 0.3760
G	 0.8430	 0.3500
H	 0.8370	 0.3540
I	 0.7900	 0.2600
J	 0.8520	 0.2250
K	 0.8300	 0.2860
L	 0.8630	 0.2260
M	 0.8580	 0.3600
N	 0.8540	 0.3470
O	 0.8360	 0.3410
P	 0.8270	 0.3310
Q	 0.8350	 0.3350
R	 0.8630	 0.3740
S	 0.8430	 0.3550
T	 0.8560	 0.3560
U	 0.7810	 0.2560
V	 0.8280	 0.2120
W	 0.8090	 0.2850
X	 0.8460	 0.2160
Y	 0.8540	 0.3620
Z	 0.8650	 0.3670
a	 0.8470	 0.3500
b	 0.8340	 0.3440
c	 0.8290	 0.3410
d	 0.8450	 0.3430
e	 0.8260	 0.3330
f	 0.8340	 0.3270
g	 0.8060	 0.3250
h	 0.8400	 0.3340



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Chain	Atom inclusion	Q-score
i	 0.8490	 0.3630
j	 0.8720	 0.3760
k	 0.8340	 0.3530
l	 0.8590	 0.3560
m	 0.8340	 0.3520
n	 0.8350	 0.3520
o	 0.8030	 0.2460
p	 0.7650	 0.2430
q	 0.8590	 0.2260
r	 0.8460	 0.2320
s	 0.8120	 0.2820
t	 0.8410	 0.2750
u	 0.8430	 0.2150
v	 0.8570	 0.2320