



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:03 PM UTC

PDB ID : 8XPM / pdb_00008xpm
EMDB ID : EMD-38556
Title : Mature virion portal of phage lambda with DNA
Authors : Wang, J.W.; Gu, Z.W.
Deposited on : 2024-01-04
Resolution : 3.90 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

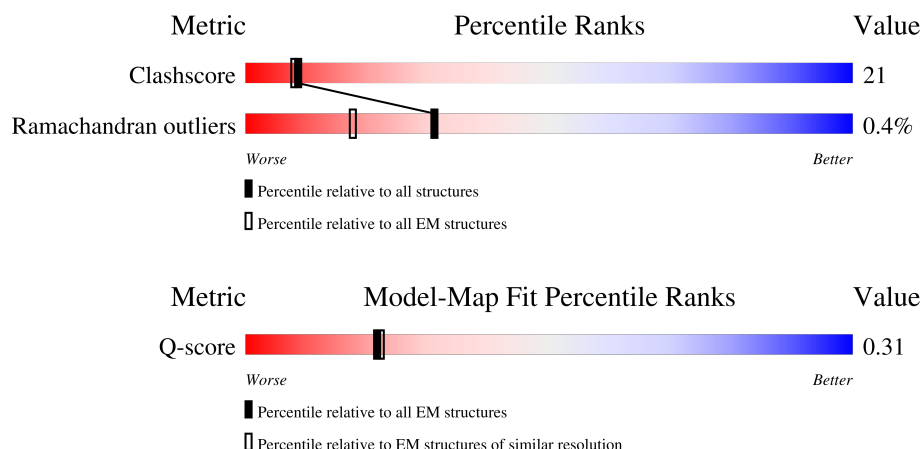
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



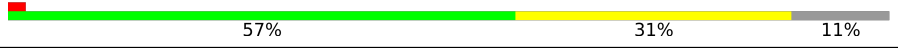
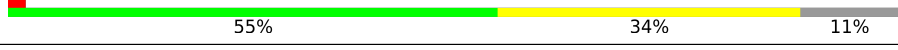
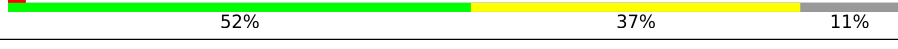
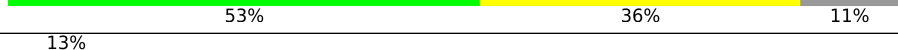
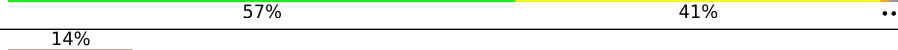
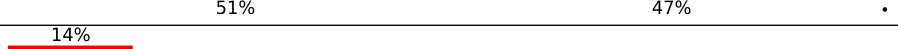
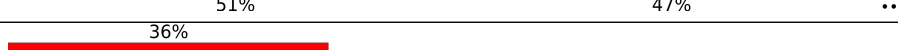
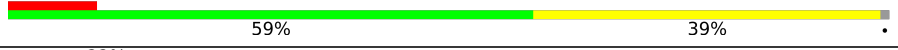
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	B	533	
1	B1	533	
1	B2	533	
1	B3	533	
1	B4	533	

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Mol	Chain	Length	Quality of chain
1	B5	533	
1	b	533	
1	b1	533	
1	b2	533	
1	b3	533	
1	b4	533	
1	b5	533	
2	O	246	
2	O1	246	
2	O2	246	
2	P	246	
2	P1	246	
2	P2	246	
2	Q	246	
2	Q1	246	
2	Q2	246	
2	R	246	
2	R1	246	
2	R2	246	
2	V	246	
2	V1	246	
2	V2	246	
2	o	246	
2	o1	246	
2	o2	246	

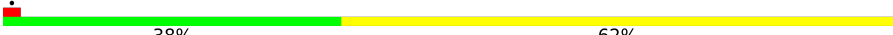
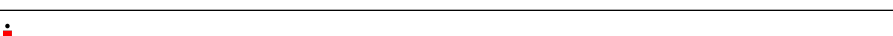
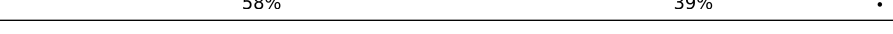
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Mol	Chain	Length	Quality of chain
2	p	246	
2	p1	246	
2	p2	246	
2	q	246	
2	q1	246	
2	q2	246	
2	r	246	
2	r1	246	
2	r2	246	
2	v	246	
2	v1	246	
2	v2	246	
3	U	131	
3	U1	131	
3	U2	131	
3	U3	131	
3	U4	131	
3	U5	131	
4	W	68	
4	W1	68	
4	W2	68	
4	W3	68	
4	W4	68	
4	W5	68	
4	w	68	

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Mol	Chain	Length	Quality of chain
4	w1	68	 59% 40% .
4	w2	68	 46% 51% ..
4	w3	68	 54% 43% ..
4	w4	68	 59% 38% ..
4	w5	68	 49% 49% ..
5	DA	104	 38% 62%
6	DB	92	 30% 70%
7	f	117	 58% 39% .
7	f1	117	 49% 49% .
7	f2	117	 50% 47% .
7	f3	117	 58% 39% .
7	f4	117	 51% 46% .
7	f5	117	 48% 50% .

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 120109 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 Portal protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		
1	B1	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b1	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		
1	B2	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b2	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		
1	B3	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b3	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		
1	B4	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b4	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		
1	B5	475	Total	C	N	O	S	0	0
			3727	2328	671	704	24		
1	b5	473	Total	C	N	O	S	0	0
			3710	2316	669	701	24		

- Molecule 2 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	P	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	Q	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	V	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	v	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	V1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	v1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	V2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	v2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	o	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	O1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	o1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	O2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	o2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	p	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	P1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	p1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	P2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	p2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	q	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	Q1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	q1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	Q2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	q2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	r	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	R1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	r1	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	R2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		
2	r2	243	Total	C	N	O	S	0	0
			1792	1119	302	366	5		

- Molecule 3 is a protein called Tail tube terminator protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		
3	U1	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		
3	U2	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		
3	U3	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		
3	U4	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		
3	U5	131	Total	C	N	O	S	0	0
			1032	655	159	213	5		

- Molecule 4 is a protein called Head completion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	W	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	w	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	W1	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	w1	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	W2	67	Total	C	N	O	S	0	0
			524	323	101	98	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	w2	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	W3	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	w3	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	W4	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	w4	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	W5	67	Total	C	N	O	S	0	0
			524	323	101	98	2		
4	w5	67	Total	C	N	O	S	0	0
			524	323	101	98	2		

- Molecule 5 is a DNA chain called DNA (104-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DA	104	Total	C	N	O	P	0	0
			2128	1010	400	614	104		

- Molecule 6 is a DNA chain called DNA (92-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	DB	92	Total	C	N	O	P	0	0
			1887	900	333	562	92		

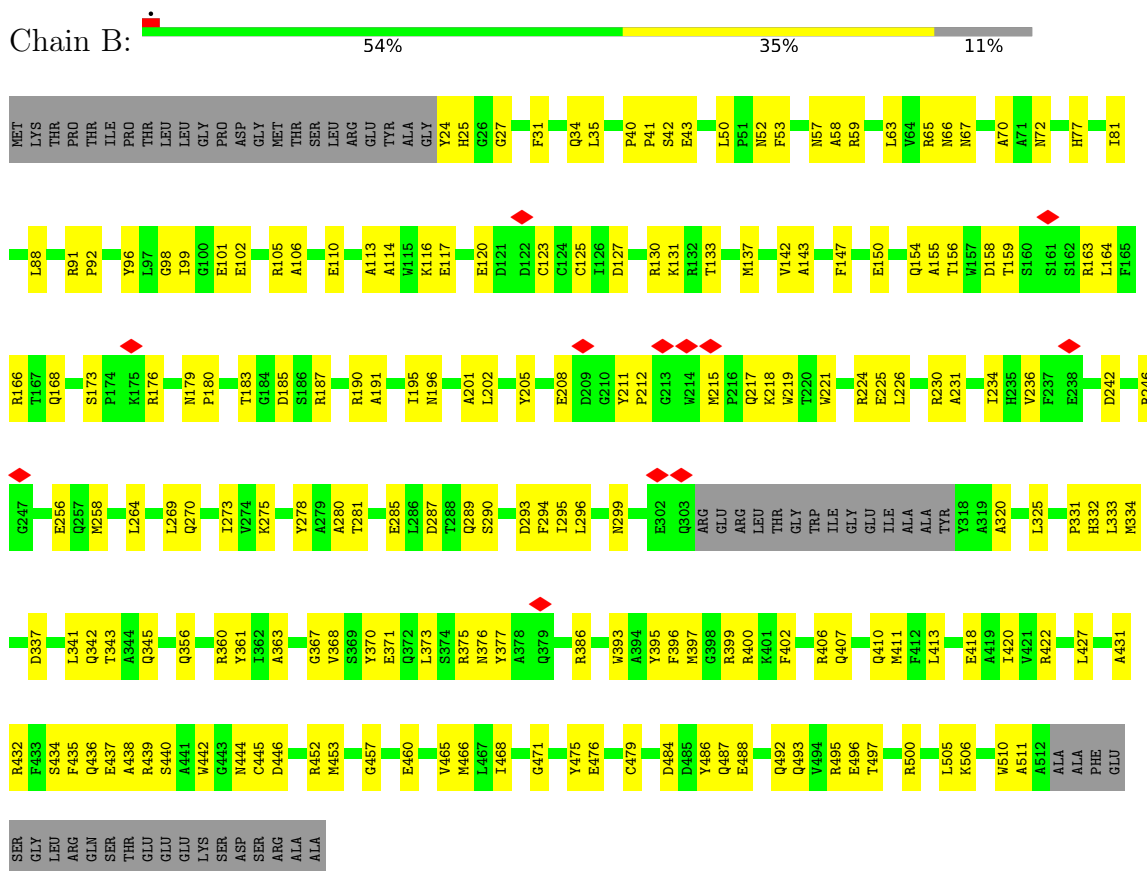
- Molecule 7 is a protein called Head-tail connector protein FII.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	114	Total	C	N	O	S	0	0
			872	535	161	174	2		
7	f1	114	Total	C	N	O	S	0	0
			872	535	161	174	2		
7	f2	114	Total	C	N	O	S	0	0
			872	535	161	174	2		
7	f3	114	Total	C	N	O	S	0	0
			872	535	161	174	2		
7	f4	114	Total	C	N	O	S	0	0
			872	535	161	174	2		
7	f5	114	Total	C	N	O	S	0	0
			872	535	161	174	2		

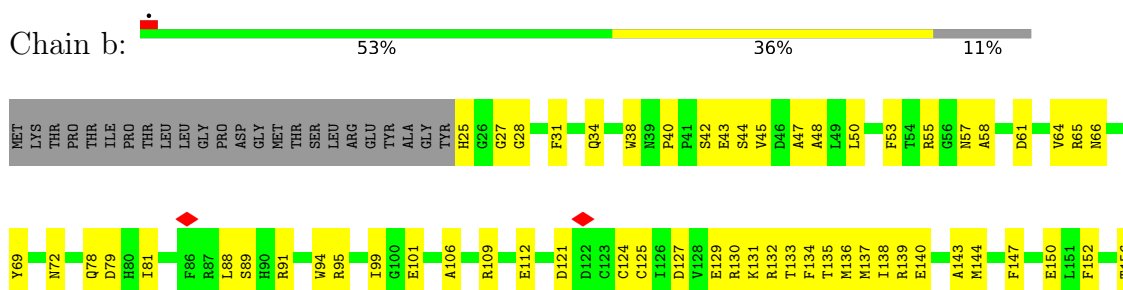
3 Residue-property plots

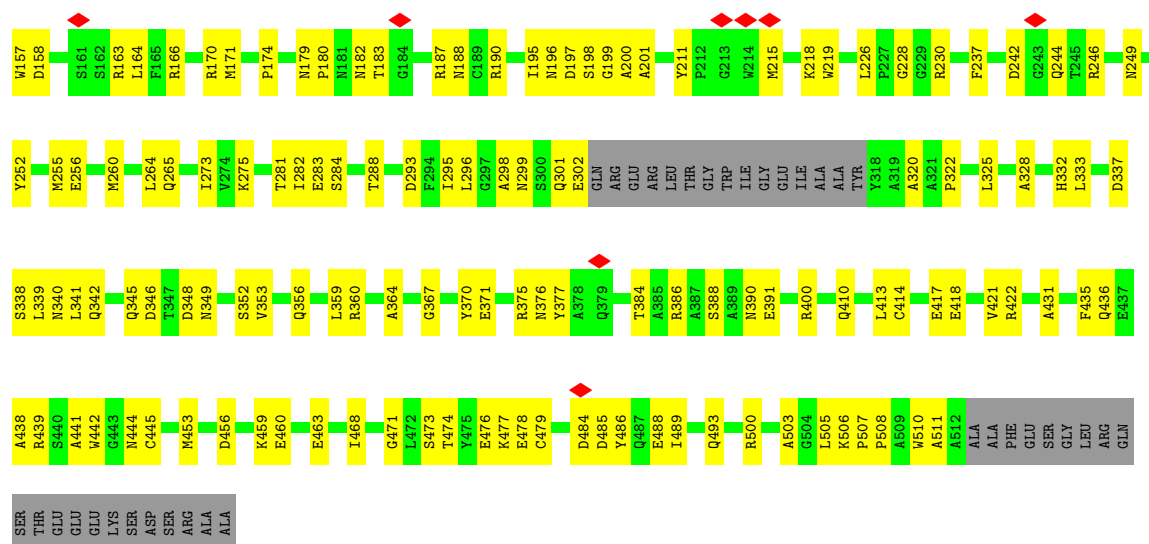
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Portal protein B

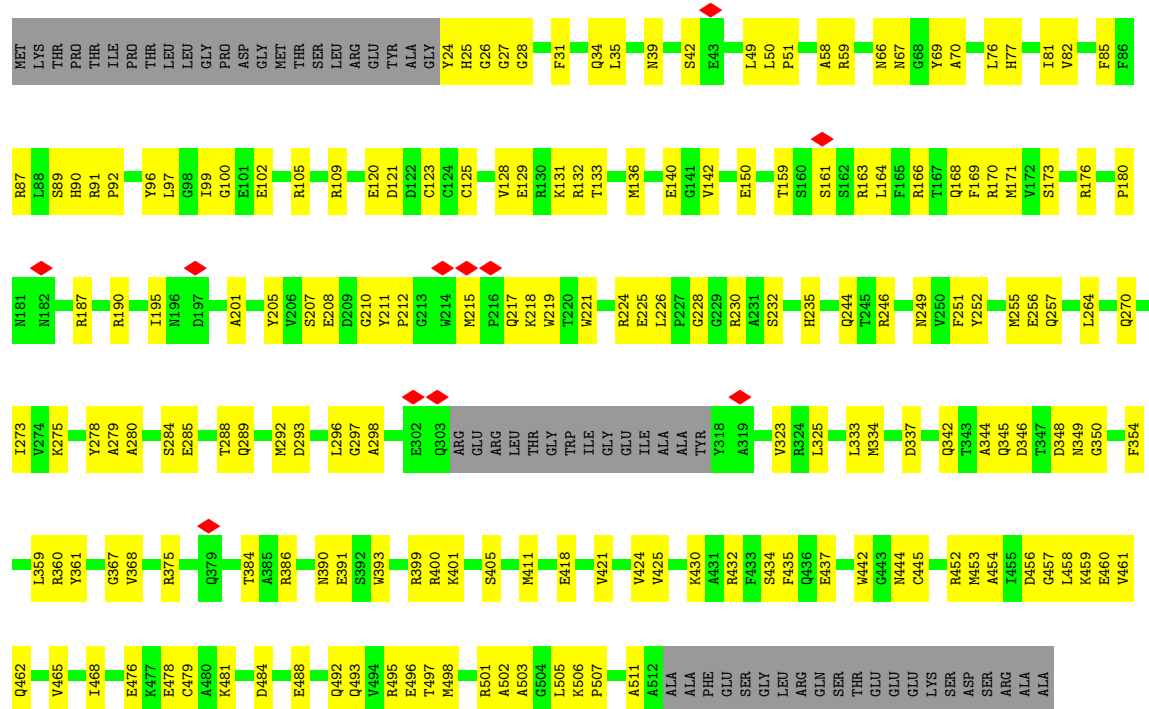


• Molecule 1: Portal protein B

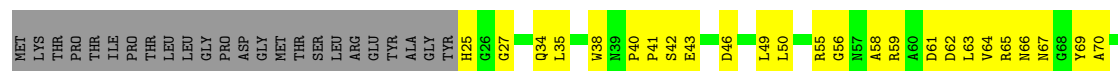




• Molecule 1: Portal protein B



• Molecule 1: Portal protein B



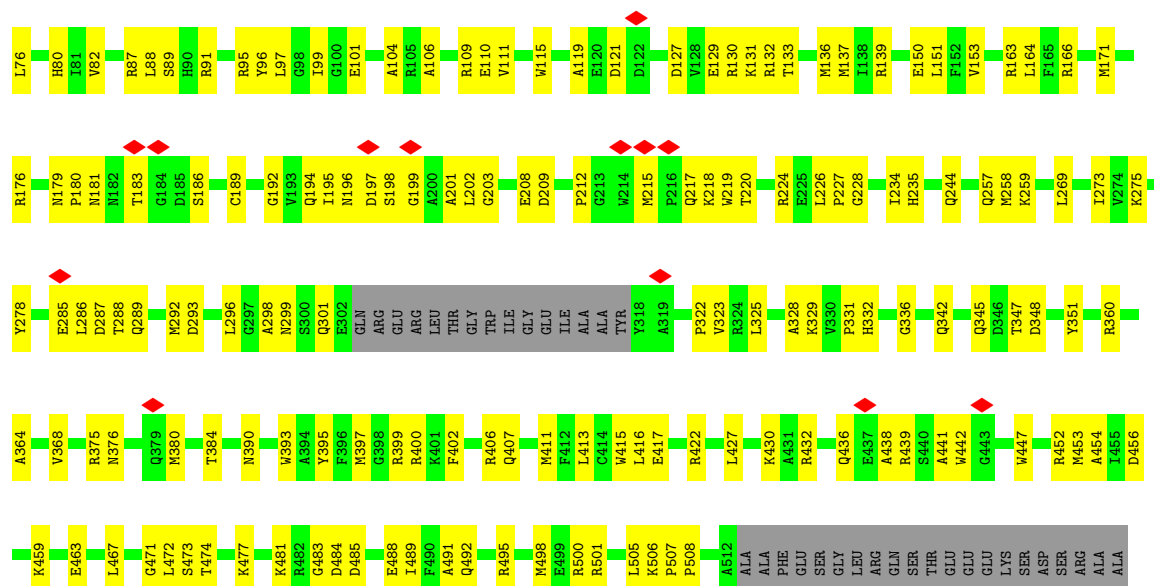


Frequency	Percentage
Daily	55%
Weekly	34%
Monthly	11%

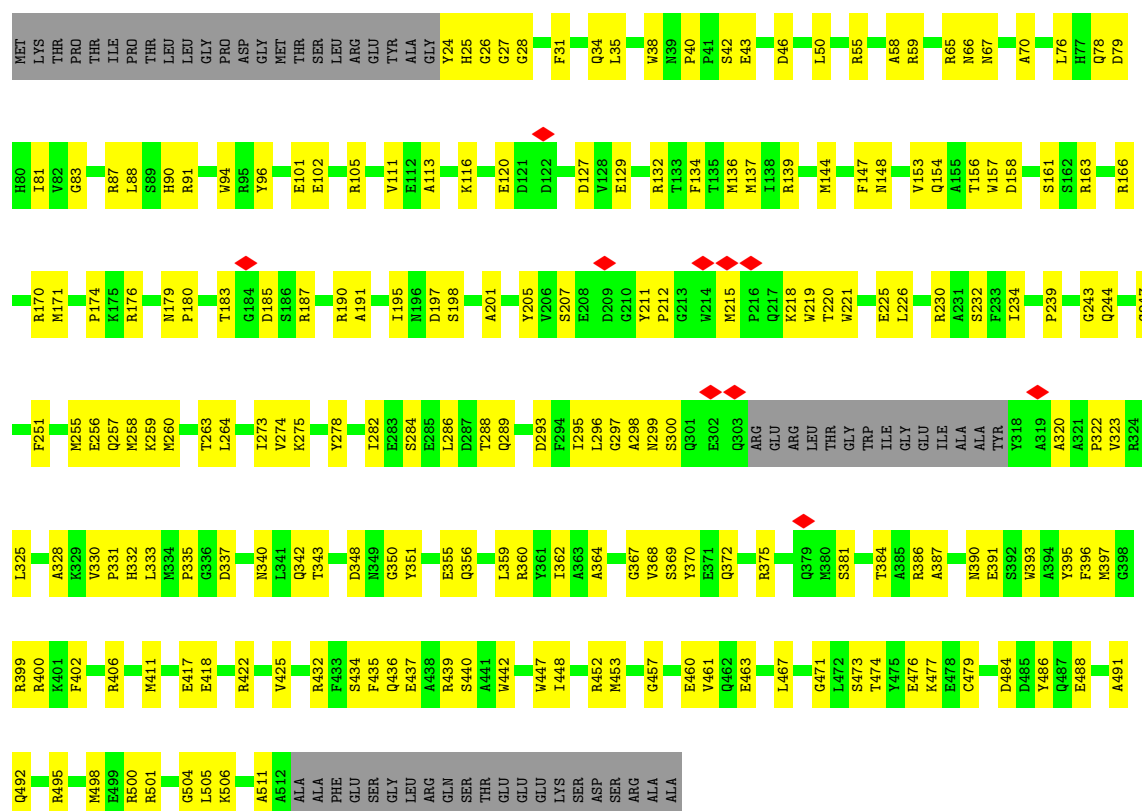


Response	Percentage
Good country	55%
Not a good country	34%
Don't know	11%



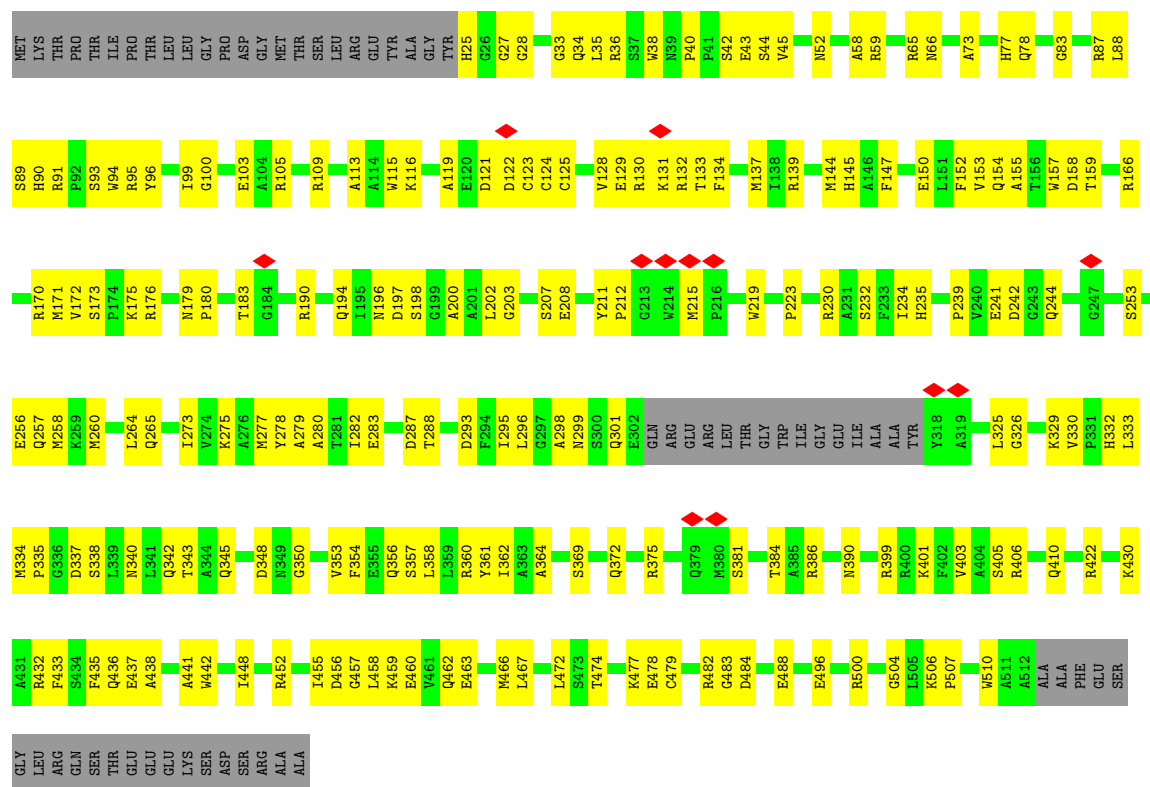


• Molecule 1: Portal protein B

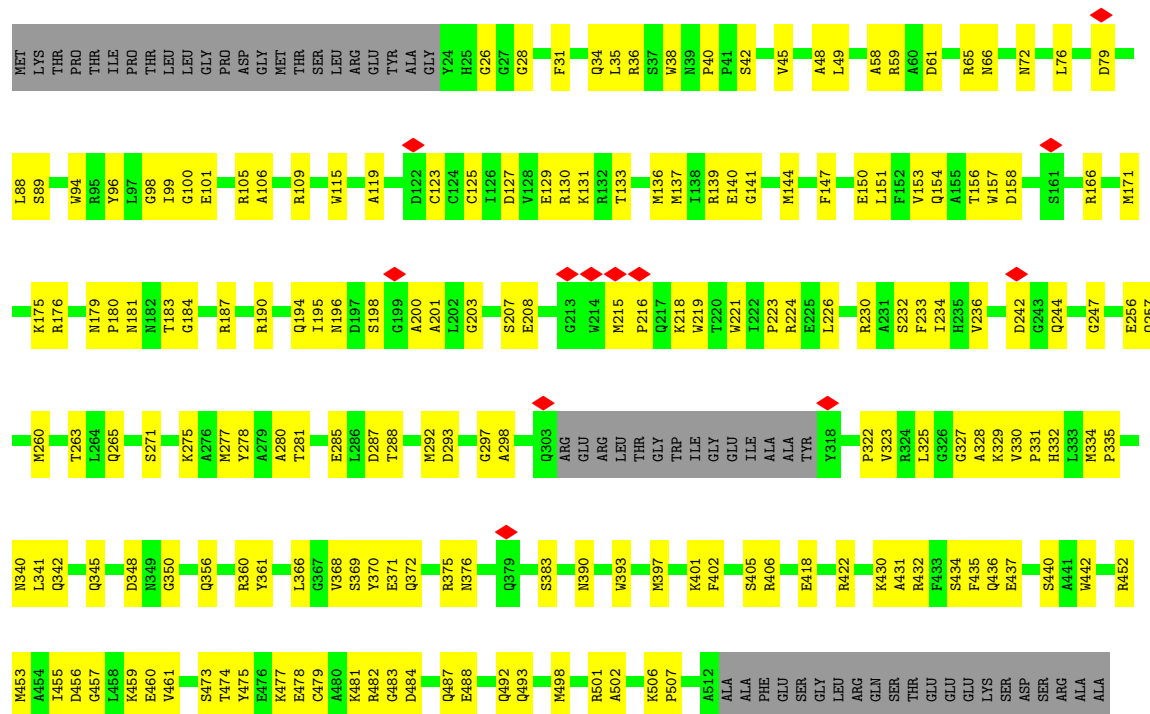


• Molecule 1: Portal protein B



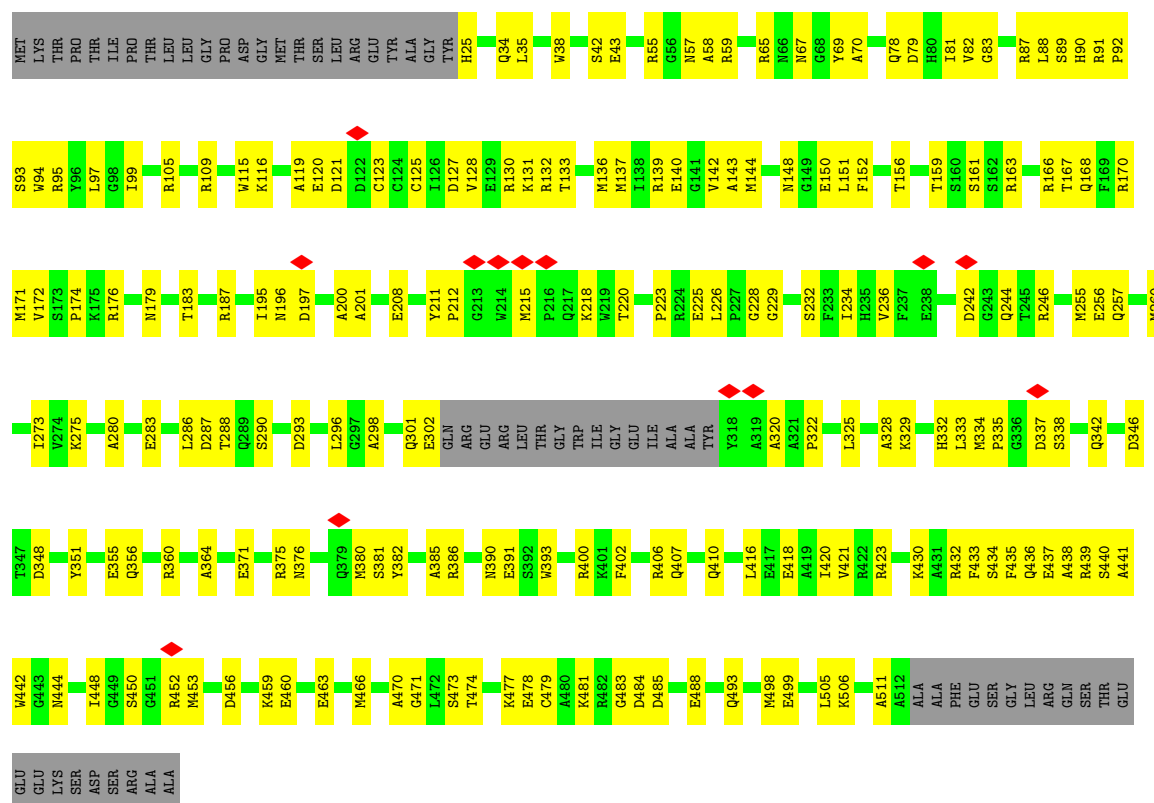


- Molecule 1: Portal protein B



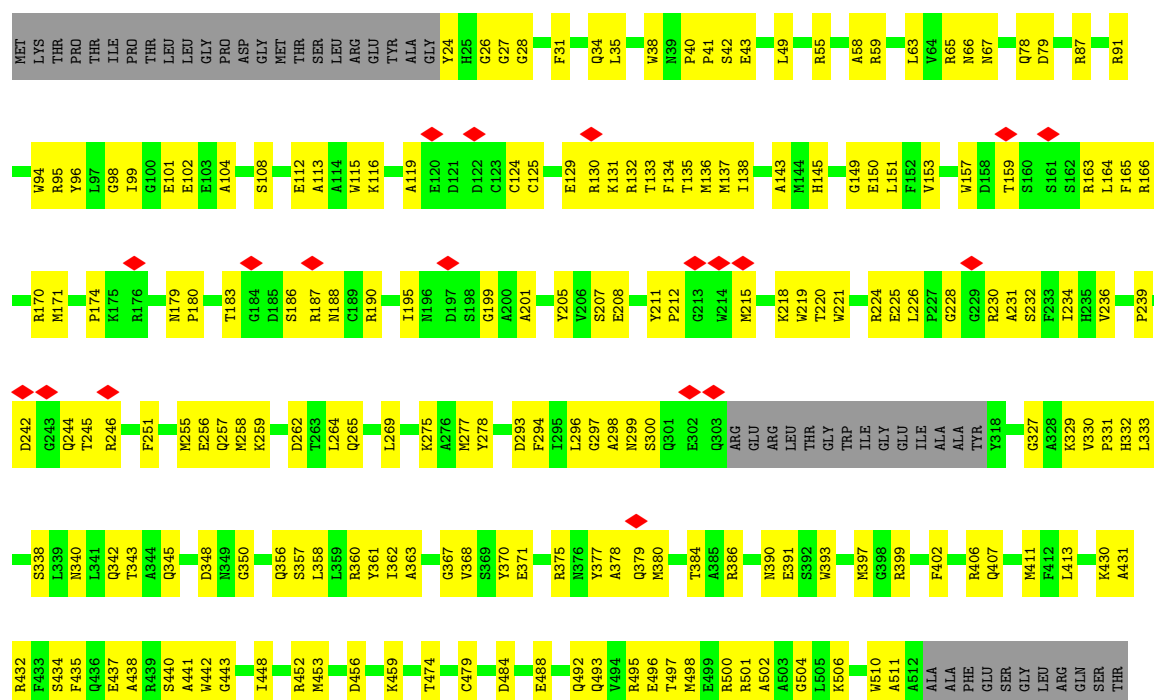
- Molecule 1: Portal protein B

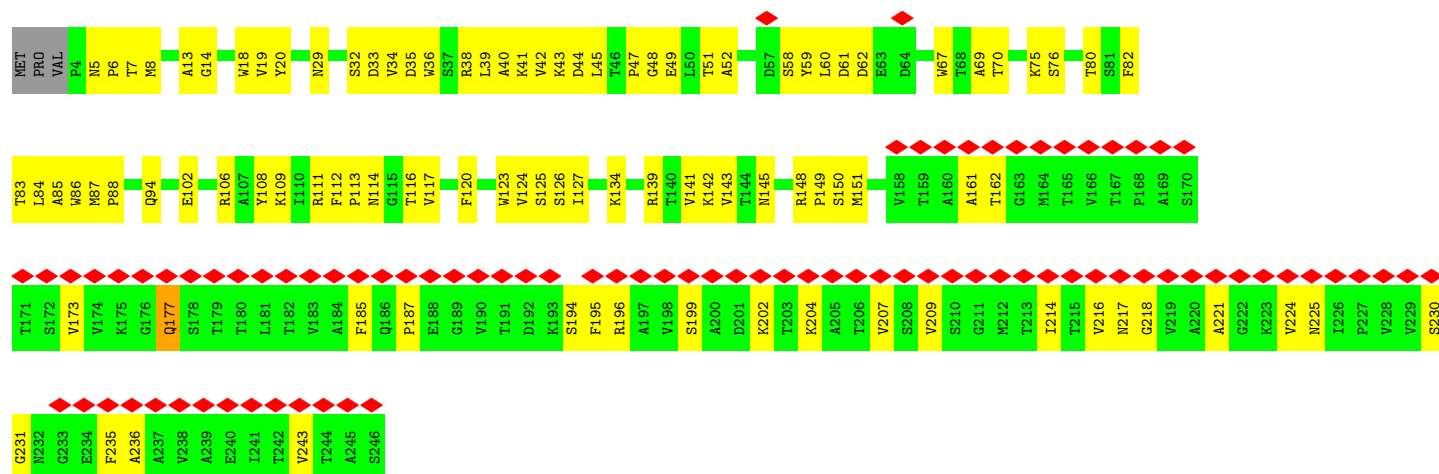
Chain b4: 



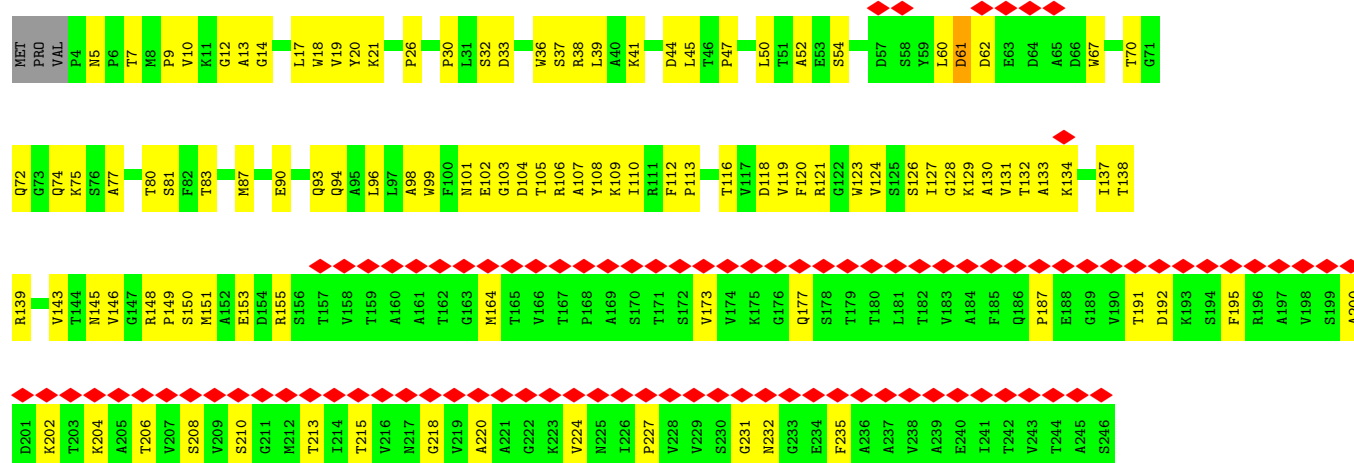
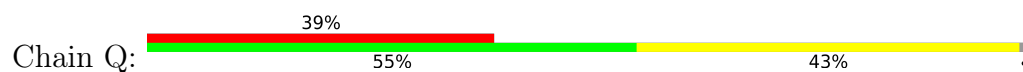
• Molecule 1: Portal protein B

Chain B5: 

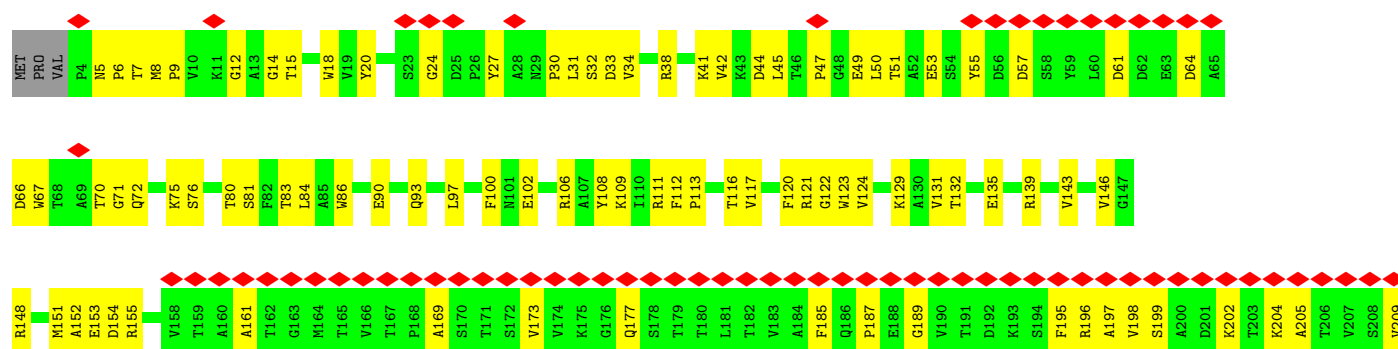




• Molecule 2: Tail tube protein

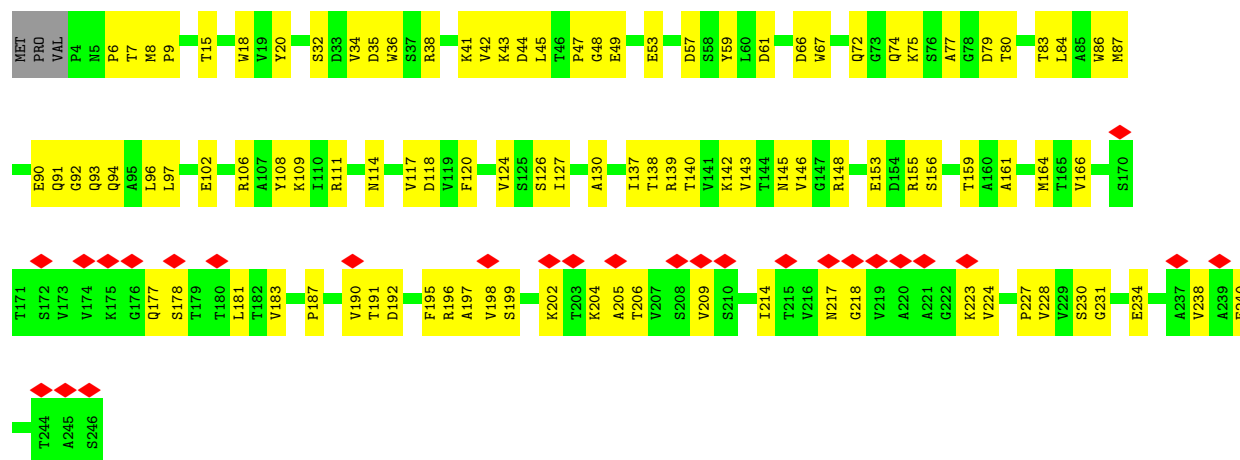


• Molecule 2: Tail tube protein

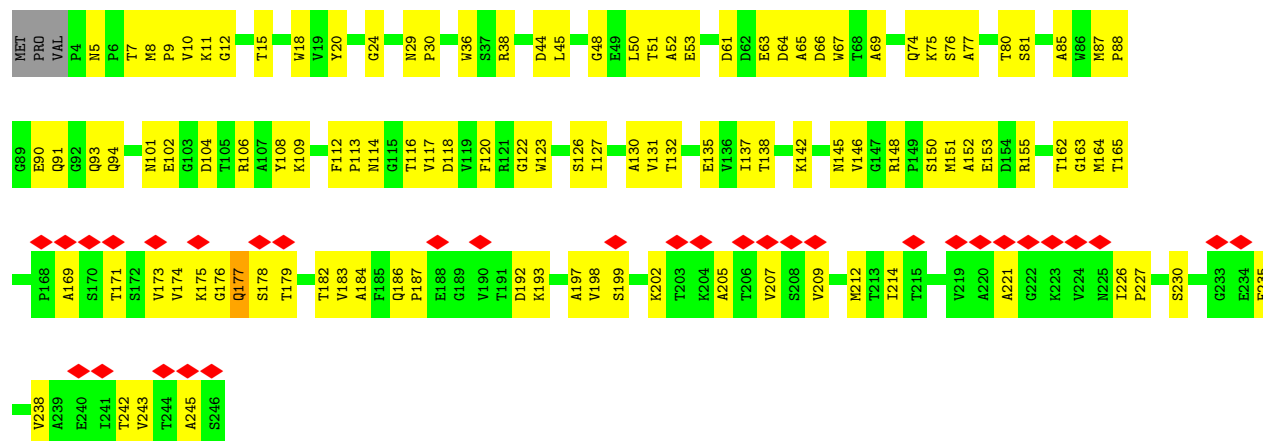




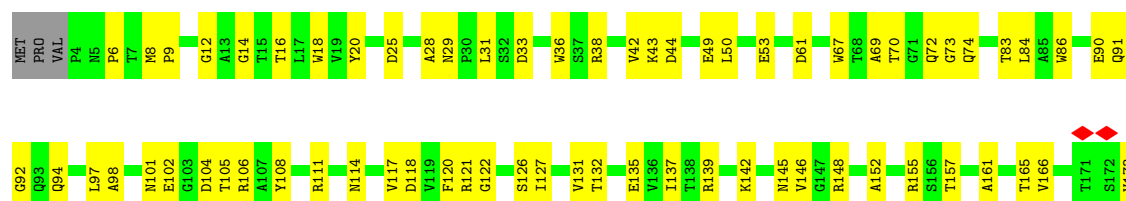
• Molecule 2: Tail tube protein

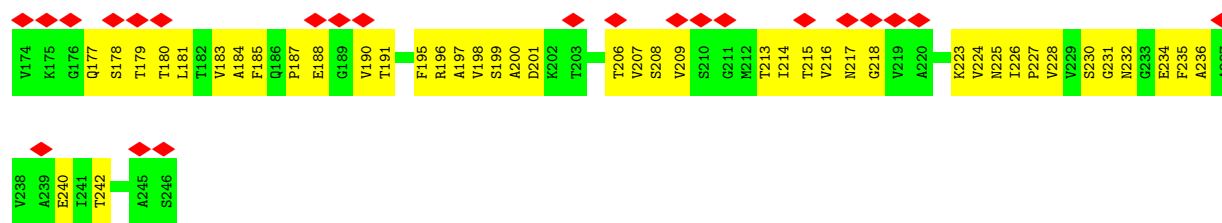


• Molecule 2: Tail tube protein

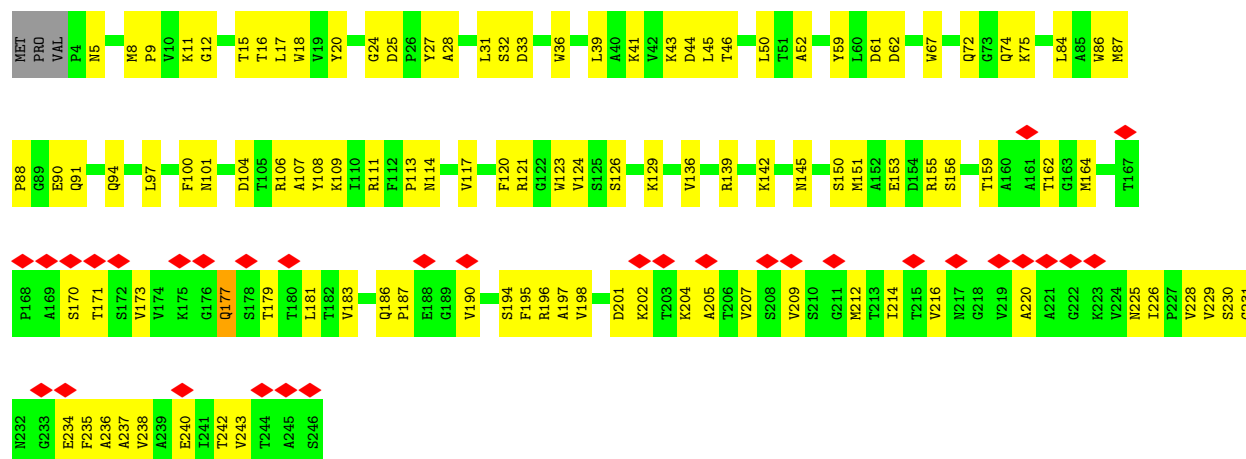


• Molecule 2: Tail tube protein

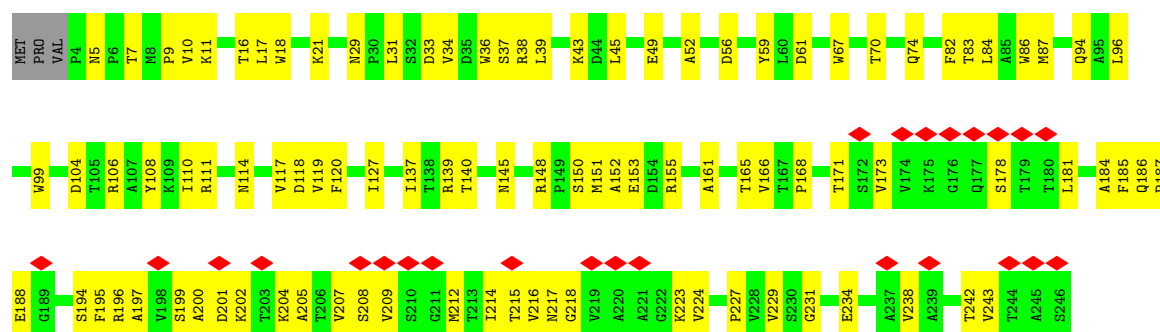




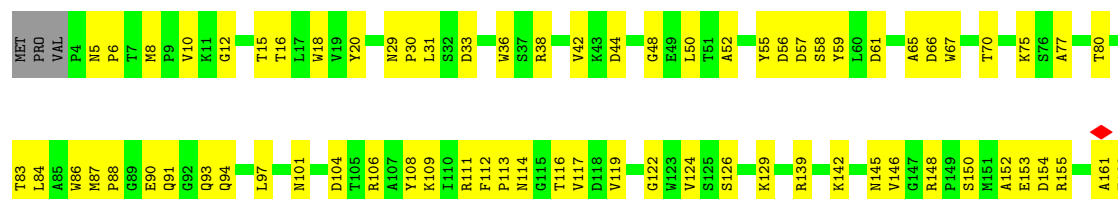
• Molecule 2: Tail tube protein

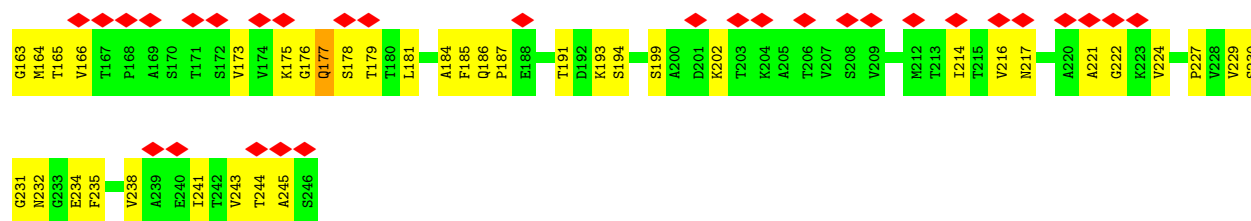


• Molecule 2: Tail tube protein

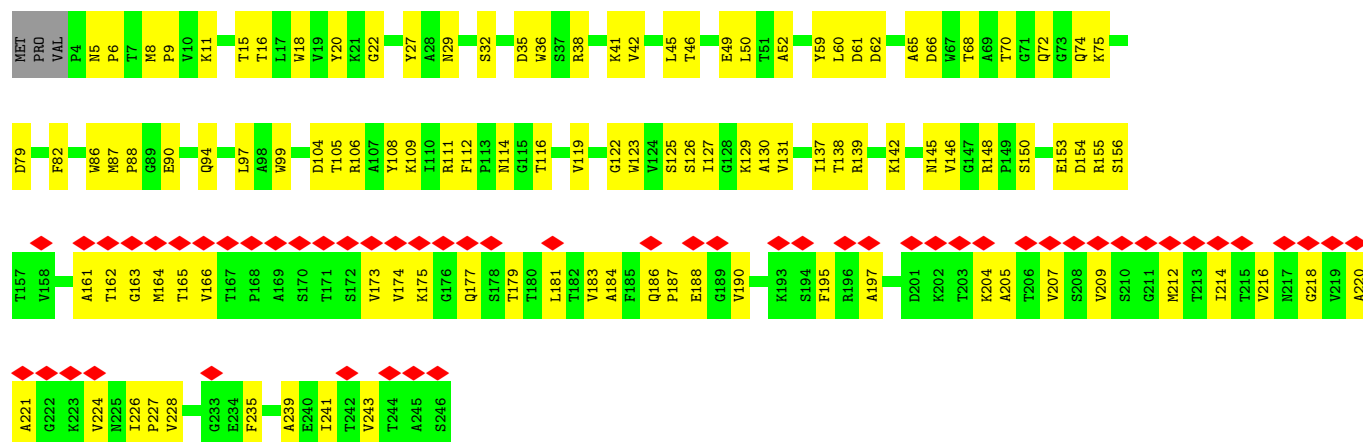


• Molecule 2: Tail tube protein

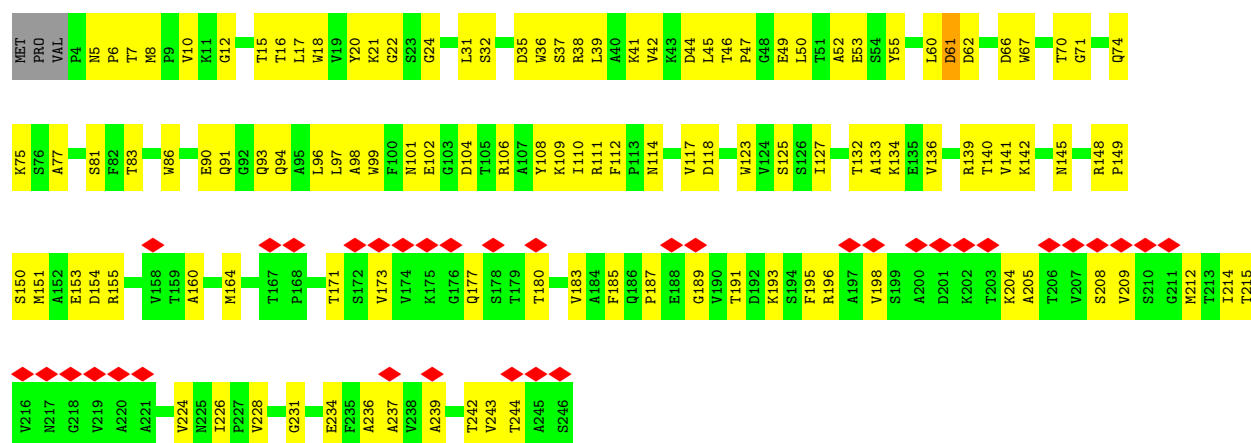




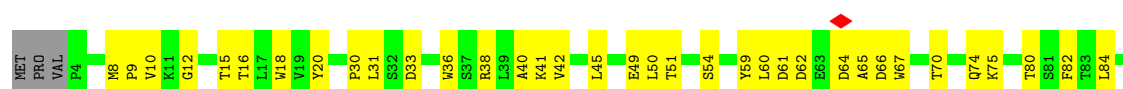
• Molecule 2: Tail tube protein

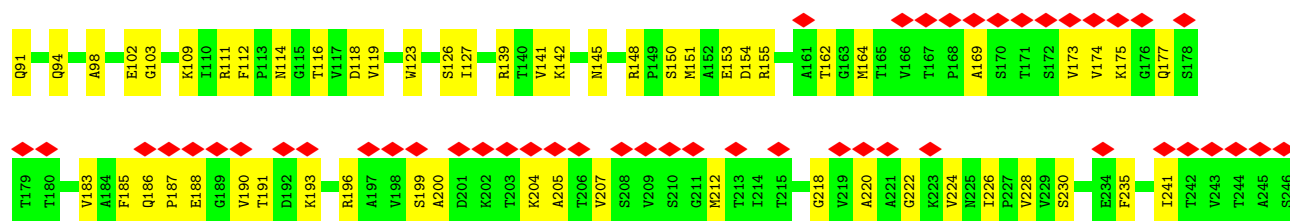


• Molecule 2: Tail tube protein

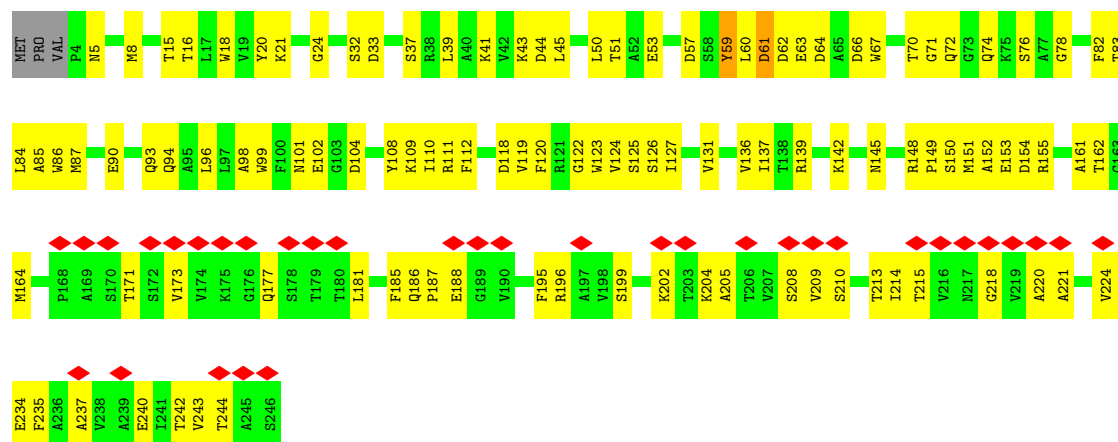


• Molecule 2: Tail tube protein

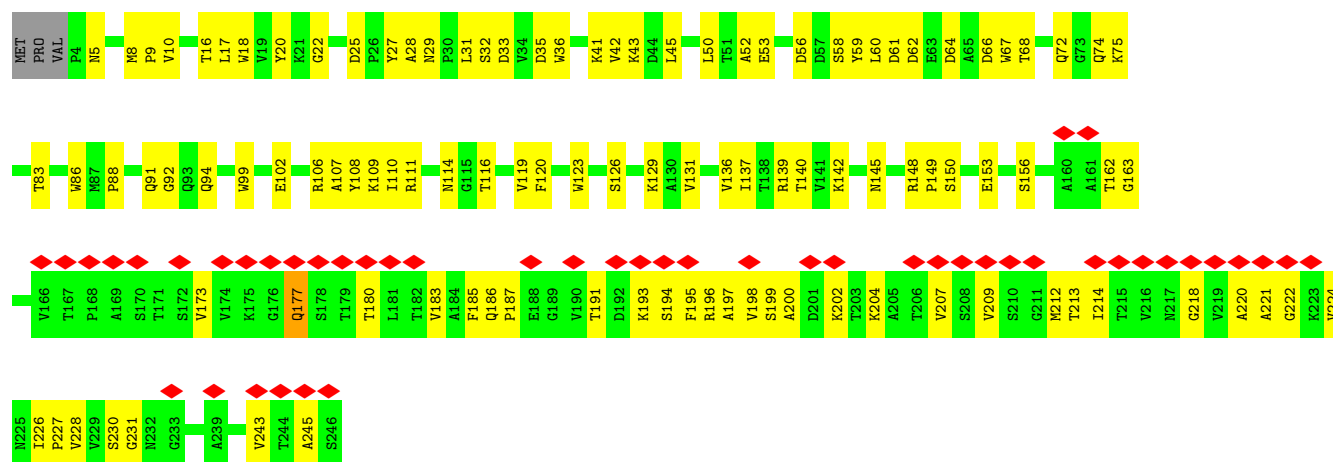




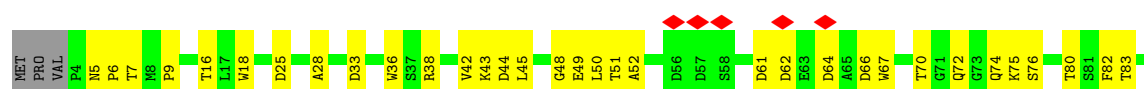
• Molecule 2: Tail tube protein

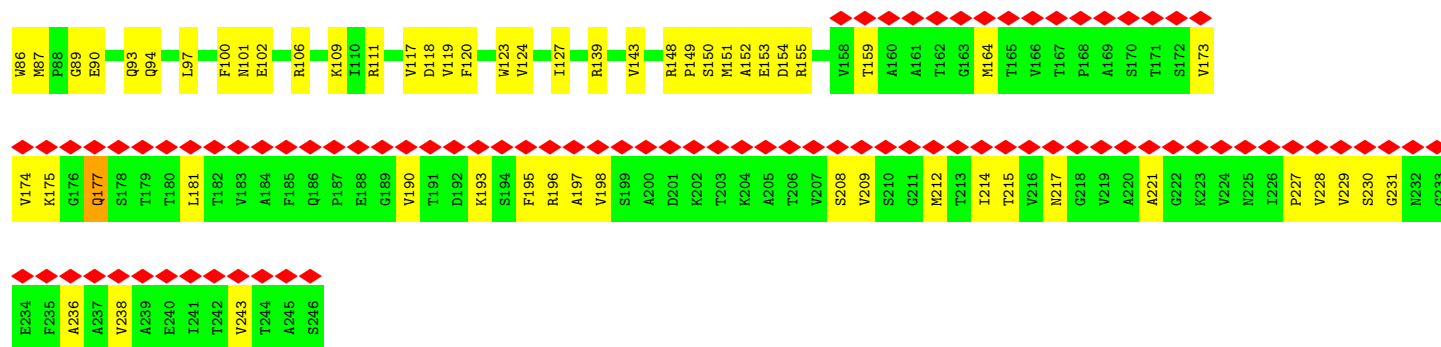


• Molecule 2: Tail tube protein

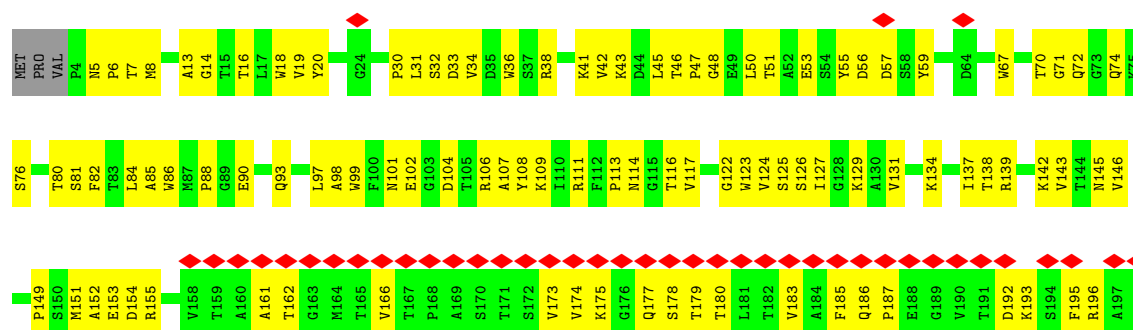


• Molecule 2: Tail tube protein

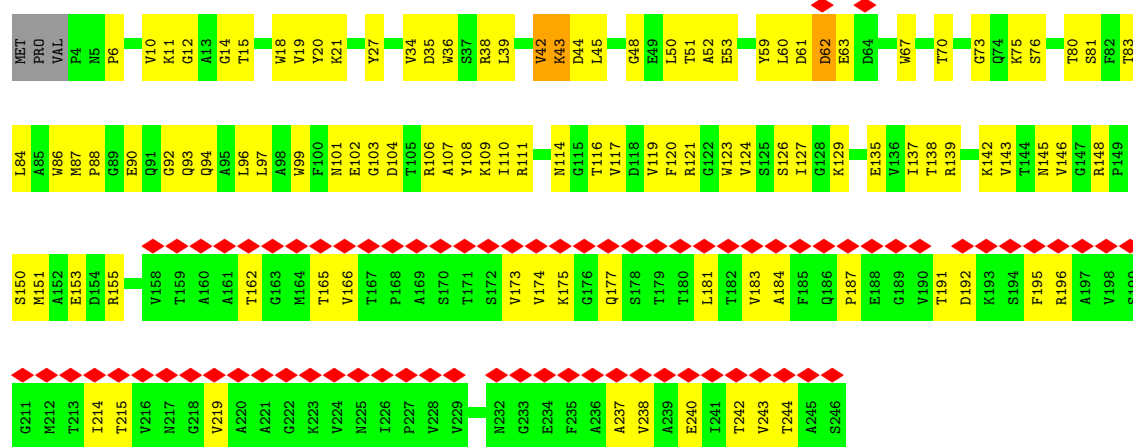




• Molecule 2: Tail tube protein

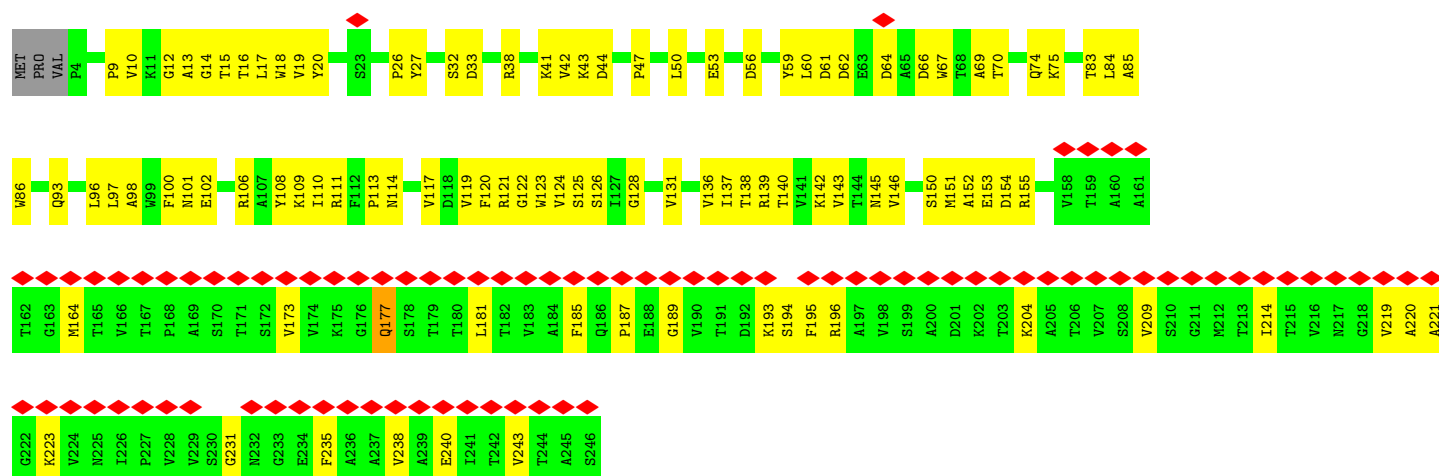


• Molecule 2: Tail tube protein

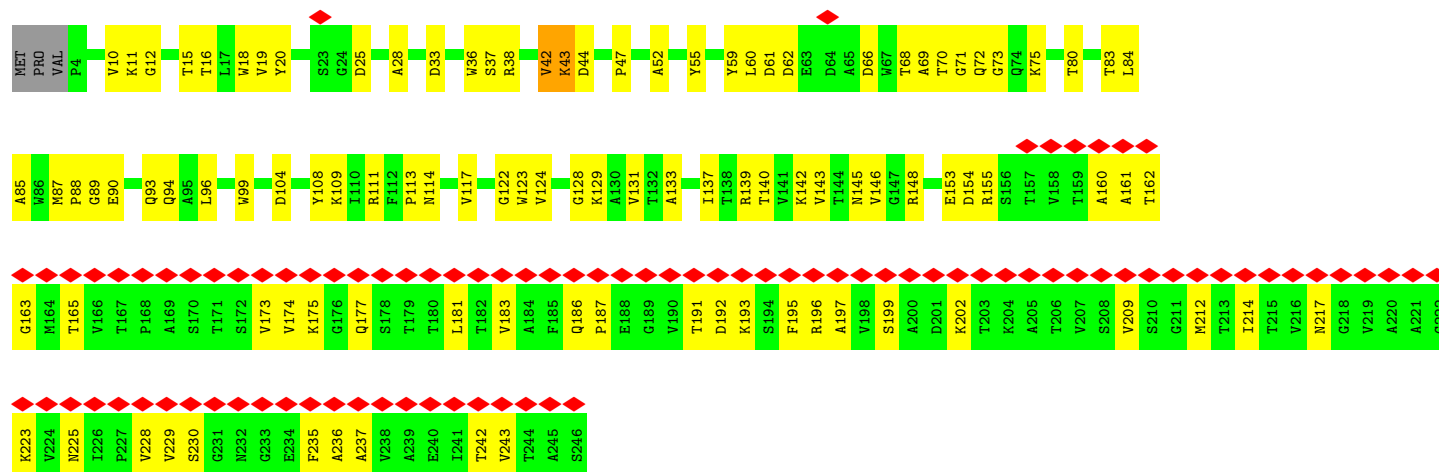
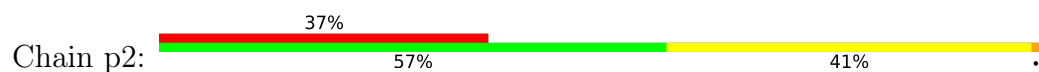


• Molecule 2: Tail tube protein

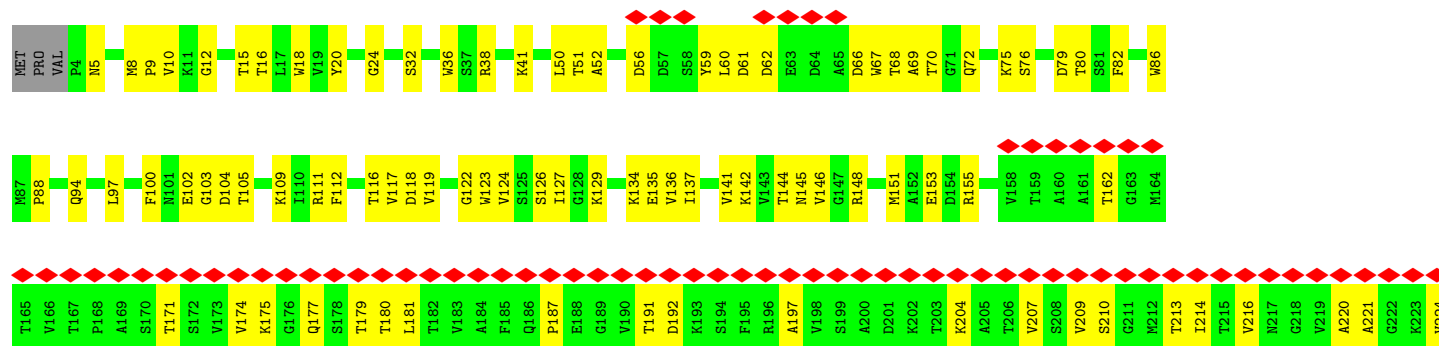


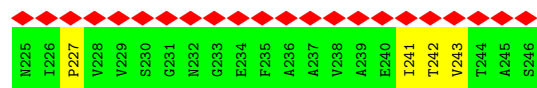


• Molecule 2: Tail tube protein

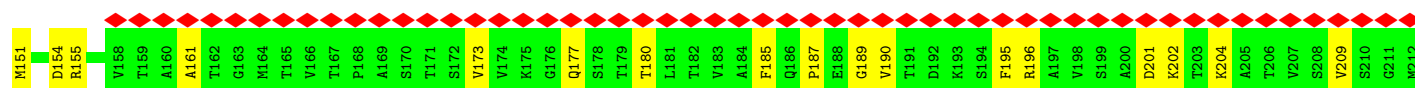
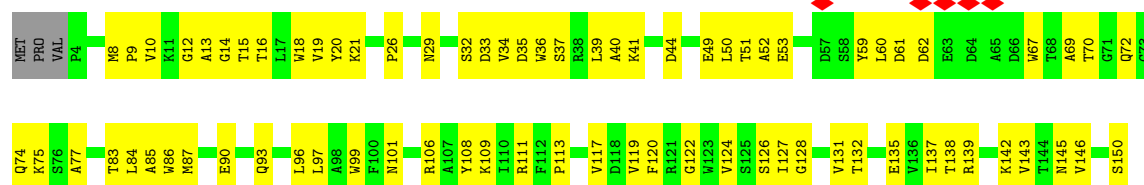
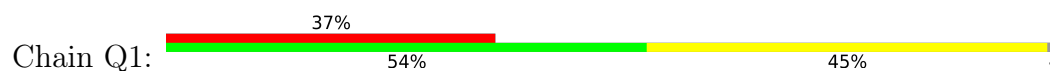


• Molecule 2: Tail tube protein

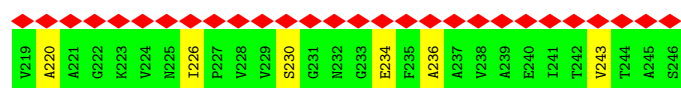
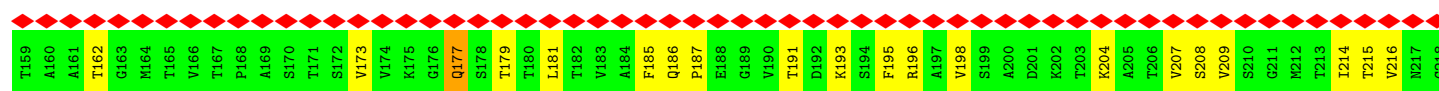
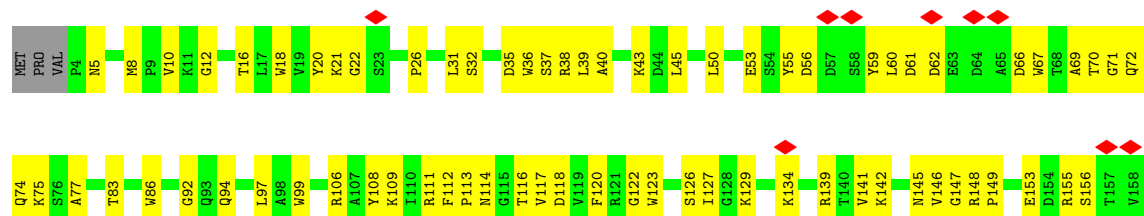
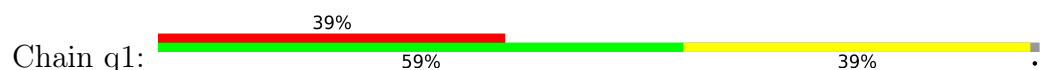




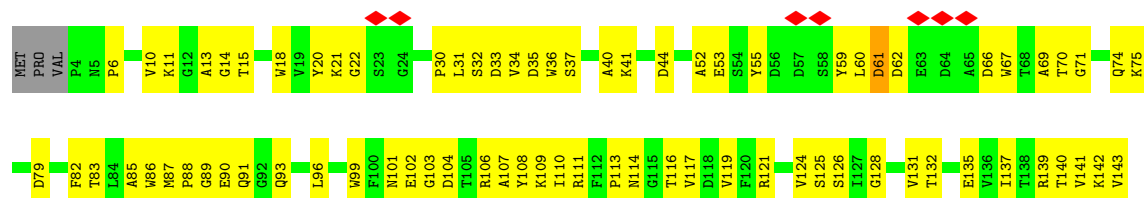
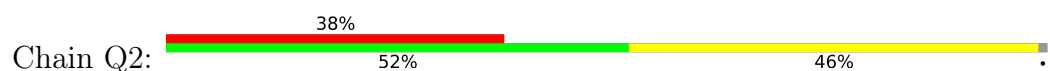
• Molecule 2: Tail tube protein



• Molecule 2: Tail tube protein

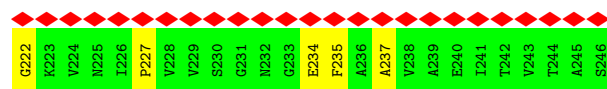
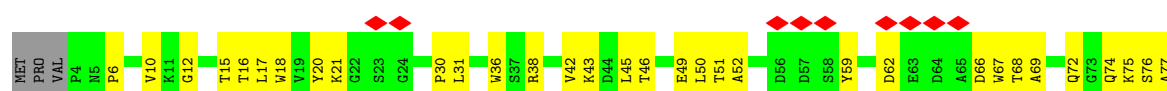
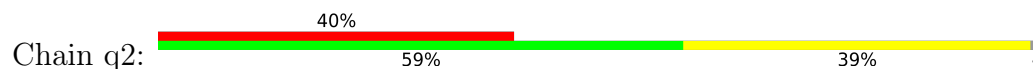


• Molecule 2: Tail tube protein

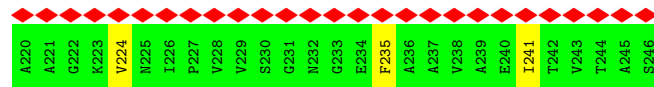
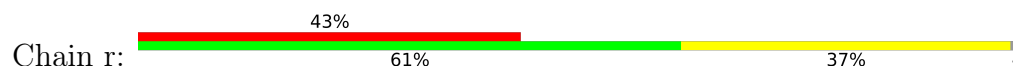




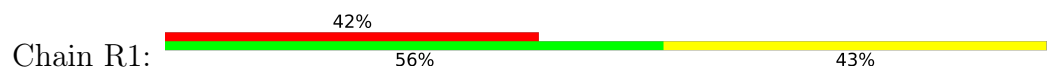
• Molecule 2: Tail tube protein

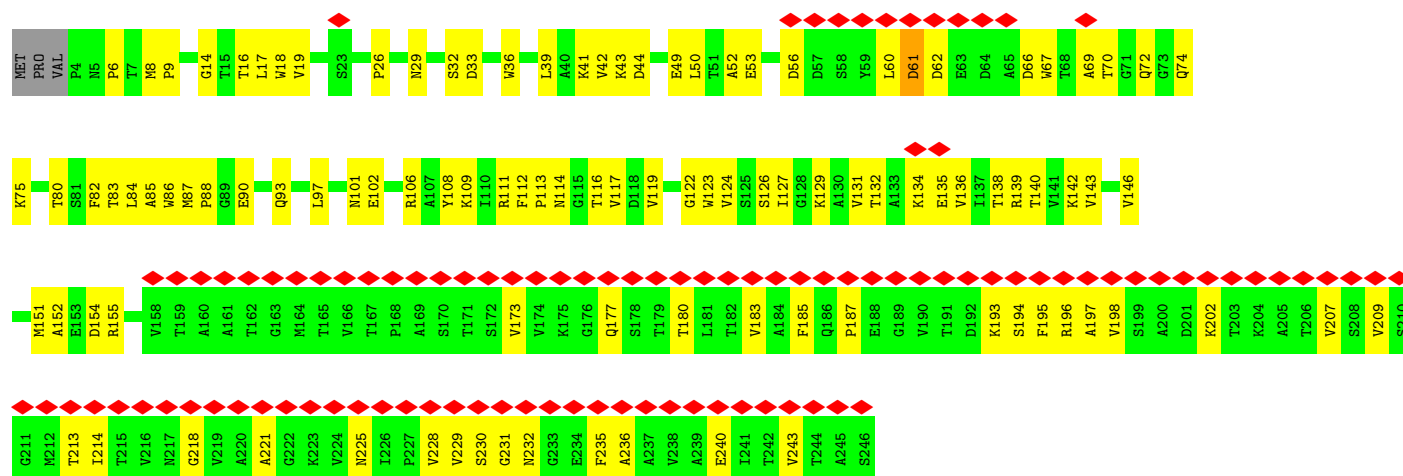


• Molecule 2: Tail tube protein

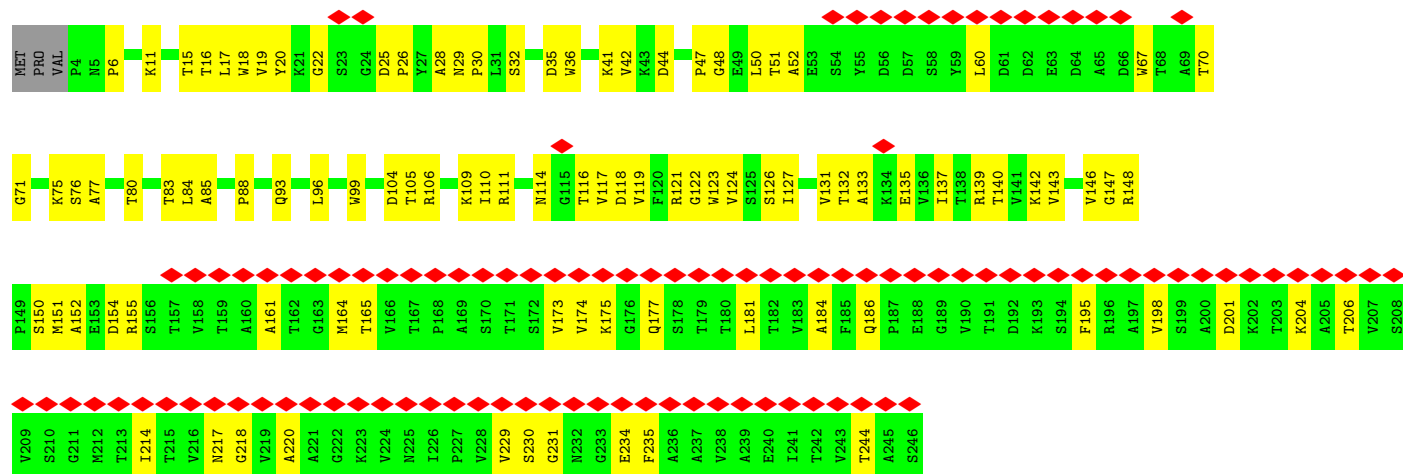
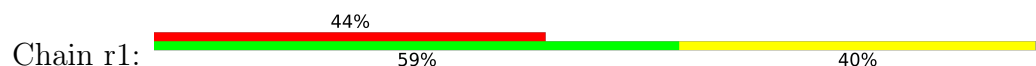


• Molecule 2: Tail tube protein

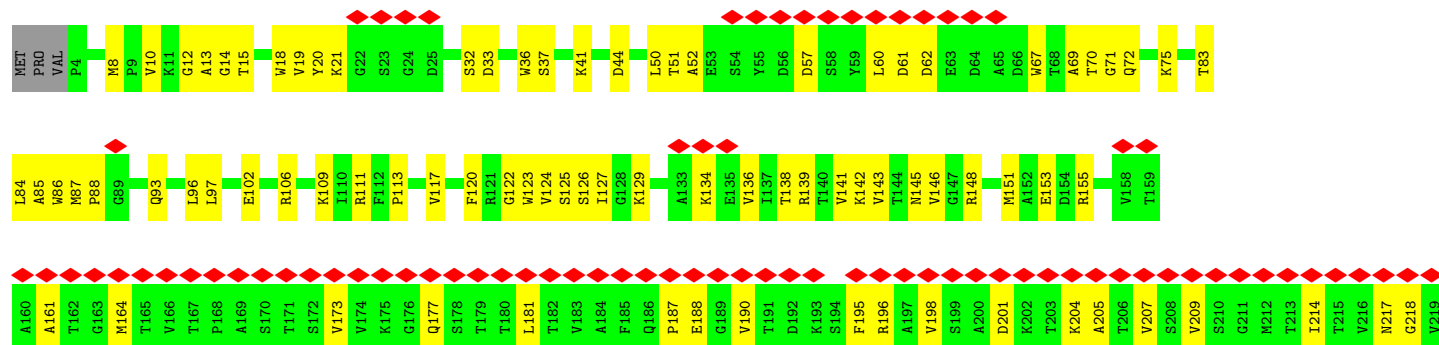


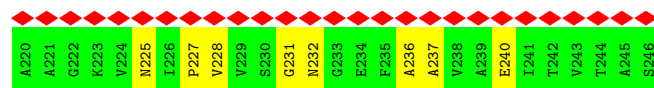


• Molecule 2: Tail tube protein

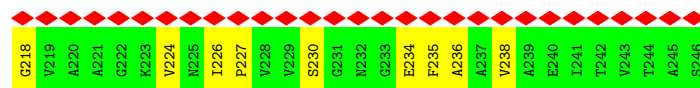
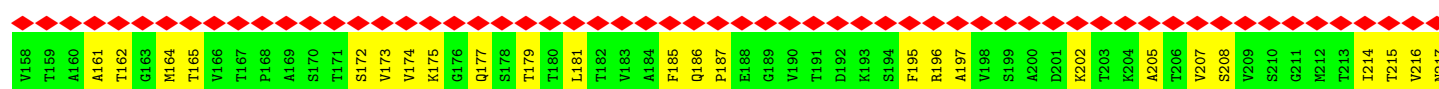
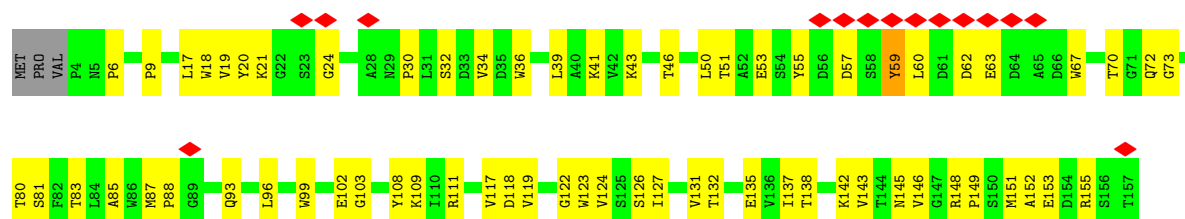
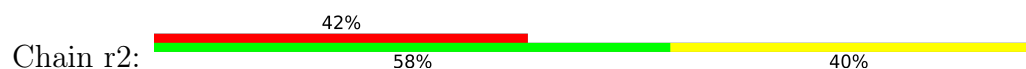


• Molecule 2: Tail tube protein

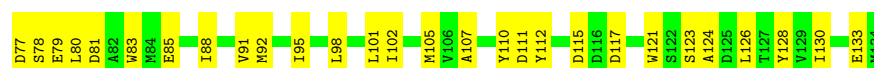
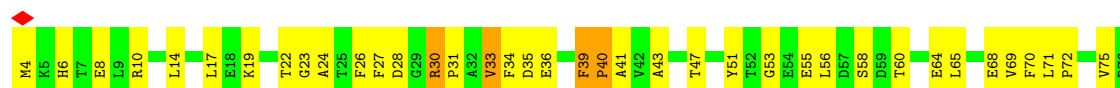




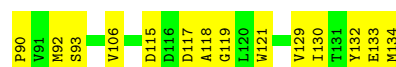
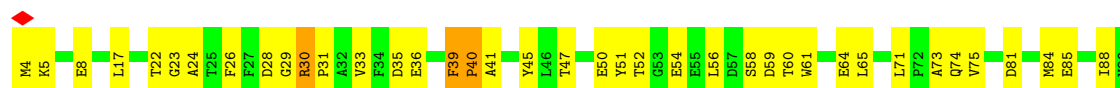
• Molecule 2: Tail tube protein



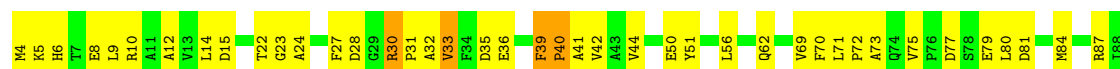
• Molecule 3: Tail tube terminator protein



• Molecule 3: Tail tube terminator protein



• Molecule 3: Tail tube terminator protein





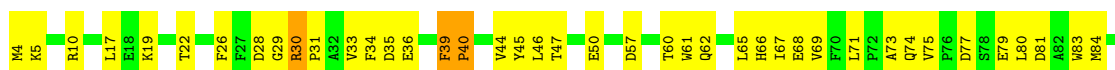
- Molecule 3: Tail tube terminator protein

Chain U3: 54% 44%



- Molecule 3: Tail tube terminator protein

Chain U4: 56% 42%



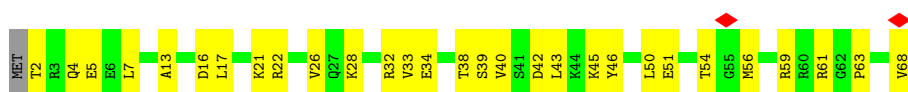
- Molecule 3: Tail tube terminator protein

Chain U5: 52% 47%



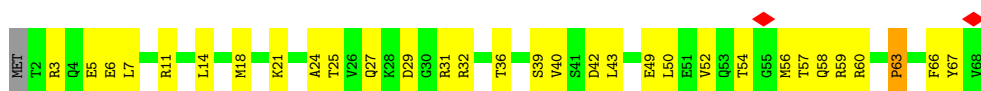
- Molecule 4: Head completion protein

Chain W: 56% 43%



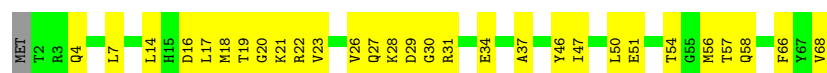
- Molecule 4: Head completion protein

Chain w: 53% 44%



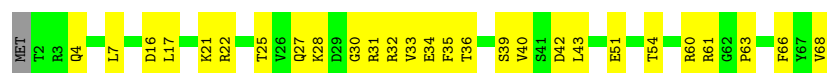
- Molecule 4: Head completion protein

Chain W1: 



- Molecule 4: Head completion protein

Chain w1: 



- Molecule 4: Head completion protein

Chain W2: 



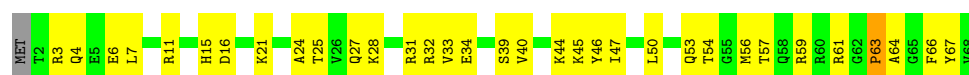
- Molecule 4: Head completion protein

Chain w2: 



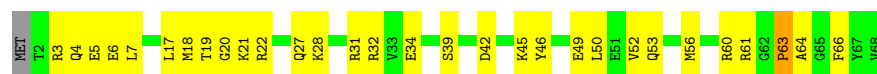
- Molecule 4: Head completion protein

Chain W3: 



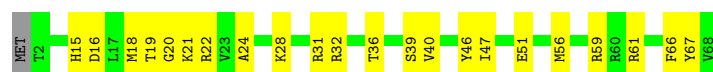
- Molecule 4: Head completion protein

Chain w3: 



- Molecule 4: Head completion protein

Chain W4: 



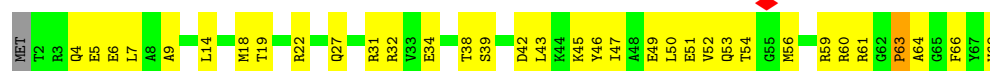
- Molecule 4: Head completion protein



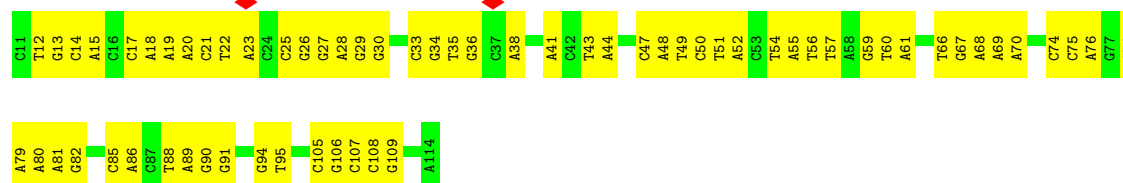
- Molecule 4: Head completion protein



- Molecule 4: Head completion protein



- Molecule 5: DNA (104-MER)



- Molecule 6: DNA (92-MER)



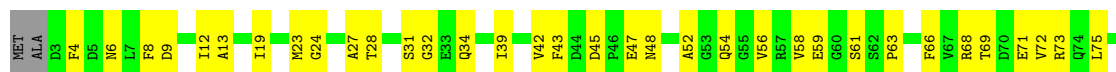
- Molecule 7: Head-tail connector protein FII





• Molecule 7: Head-tail connector protein FII

Chain f1: 49% 49%



• Molecule 7: Head-tail connector protein FII

Chain f2: 50% 47%



• Molecule 7: Head-tail connector protein FII

Chain f3: 58% 39%



• Molecule 7: Head-tail connector protein FII

Chain f4: 51% 46%



• Molecule 7: Head-tail connector protein FII

Chain f5: 48% 50%



C78	D79	T80	L81	T82	E85	E86	N87	F88	W89	V90	D91	S94	D97	H102	L103	W104	L105	G106	R107	N114	R115	R116	ARG
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19060	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.199	Depositor
Minimum map value	-1.385	Depositor
Average map value	-0.016	Depositor
Map value standard deviation	0.142	Depositor
Recommended contour level	0.52	Depositor
Map size ($\text{\AA}$)	515.616, 515.616, 515.616	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0742, 1.0742, 1.0742	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	B	0.18	0/3811	0.32	0/5151
1	B1	0.17	0/3811	0.31	0/5151
1	B2	0.17	0/3811	0.31	0/5151
1	B3	0.16	0/3811	0.30	0/5151
1	B4	0.17	0/3811	0.29	0/5151
1	B5	0.17	0/3811	0.31	1/5151 (0.0%)
1	b	0.18	0/3793	0.35	1/5126 (0.0%)
1	b1	0.17	0/3793	0.30	0/5126
1	b2	0.17	0/3793	0.30	0/5126
1	b3	0.17	0/3793	0.30	0/5126
1	b4	0.17	0/3793	0.31	1/5126 (0.0%)
1	b5	0.17	0/3793	0.30	1/5126 (0.0%)
2	O	1.46	6/1827 (0.3%)	0.35	0/2494
2	O1	0.15	0/1827	0.32	0/2494
2	O2	1.47	6/1827 (0.3%)	0.35	0/2494
2	P	0.15	0/1827	0.33	0/2494
2	P1	0.14	0/1827	0.31	0/2494
2	P2	0.14	0/1827	0.39	2/2494 (0.1%)
2	Q	0.13	0/1827	0.34	0/2494
2	Q1	0.12	0/1827	0.32	0/2494
2	Q2	0.12	0/1827	0.31	0/2494
2	R	0.12	0/1827	0.32	1/2494 (0.0%)
2	R1	0.12	0/1827	0.30	0/2494
2	R2	0.12	0/1827	0.31	0/2494
2	V	0.17	0/1827	0.35	0/2494
2	V1	0.18	0/1827	0.34	0/2494
2	V2	0.16	0/1827	0.33	0/2494
2	o	0.15	0/1827	0.35	0/2494
2	o1	0.15	0/1827	0.35	1/2494 (0.0%)
2	o2	0.15	0/1827	0.32	0/2494
2	p	0.14	0/1827	0.35	0/2494
2	p1	0.60	2/1827 (0.1%)	0.73	5/2494 (0.2%)
2	p2	0.57	2/1827 (0.1%)	0.62	4/2494 (0.2%)
2	q	0.12	0/1827	0.34	0/2494

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	q1	0.12	0/1827	0.31	0/2494
2	q2	0.12	0/1827	0.32	0/2494
2	r	0.11	0/1827	0.31	1/2494 (0.0%)
2	r1	0.12	0/1827	0.32	0/2494
2	r2	0.12	0/1827	0.33	0/2494
2	v	0.16	0/1827	0.35	1/2494 (0.0%)
2	v1	0.17	0/1827	0.34	0/2494
2	v2	0.17	0/1827	0.33	0/2494
3	U	0.20	0/1058	0.43	0/1444
3	U1	0.21	0/1058	0.39	1/1444 (0.1%)
3	U2	0.20	0/1058	0.41	0/1444
3	U3	0.20	0/1058	0.38	0/1444
3	U4	0.19	0/1058	0.42	1/1444 (0.1%)
3	U5	0.19	0/1058	0.37	0/1444
4	W	0.18	0/529	0.39	0/709
4	W1	0.18	0/529	0.34	0/709
4	W2	0.18	0/529	0.39	0/709
4	W3	0.19	0/529	0.41	0/709
4	W4	0.18	0/529	0.36	0/709
4	W5	0.20	0/529	0.45	0/709
4	w	0.21	0/529	0.42	0/709
4	w1	0.20	0/529	0.41	0/709
4	w2	0.18	0/529	0.40	0/709
4	w3	0.19	0/529	0.37	0/709
4	w4	0.19	0/529	0.39	0/709
4	w5	0.19	0/529	0.42	0/709
5	DA	0.20	0/2389	0.37	0/3682
6	DB	0.21	0/2113	0.38	0/3261
7	f	0.18	0/888	0.39	0/1204
7	f1	0.21	0/888	0.39	0/1204
7	f2	0.18	0/888	0.38	0/1204
7	f3	0.19	0/888	0.38	1/1204 (0.1%)
7	f4	0.18	0/888	0.37	0/1204
7	f5	0.18	0/888	0.37	0/1204
All	All	0.32	16/122960 (0.0%)	0.35	22/167821 (0.0%)

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
3	U	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
3	U1	0	1
3	U2	0	1
3	U3	0	1
3	U4	0	1
3	U5	0	1
All	All	0	6

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O2	59	TYR	CD1-CE1	33.31	2.38	1.38
2	O	59	TYR	CD1-CE1	32.56	2.36	1.38
2	O2	59	TYR	CD2-CE2	31.46	2.33	1.38
2	O	59	TYR	CD2-CE2	31.20	2.32	1.38
2	O	59	TYR	CE1-CZ	22.85	1.93	1.38

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	p1	42	VAL	CA-C-N	20.95	152.32	120.89
2	p1	42	VAL	C-N-CA	20.95	152.32	120.89
2	p2	42	VAL	CA-C-N	16.77	152.49	121.81
2	p2	42	VAL	C-N-CA	16.77	152.49	121.81
2	p2	42	VAL	CA-C-O	-9.44	109.62	120.66

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	U	39	PHE	Peptide
3	U1	39	PHE	Peptide
3	U2	39	PHE	Peptide
3	U3	39	PHE	Peptide
3	U4	39	PHE	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3727	0	3562	169	0
1	B1	3727	0	3562	165	0
1	B2	3727	0	3562	169	0
1	B3	3727	0	3562	185	0
1	B4	3727	0	3562	176	0
1	B5	3727	0	3562	175	0
1	b	3710	0	3551	173	0
1	b1	3710	0	3551	153	0
1	b2	3710	0	3551	157	0
1	b3	3710	0	3551	167	0
1	b4	3710	0	3551	165	0
1	b5	3710	0	3551	184	0
2	O	1792	0	1760	116	0
2	O1	1792	0	1760	103	0
2	O2	1792	0	1760	143	0
2	P	1792	0	1760	89	0
2	P1	1792	0	1760	120	0
2	P2	1792	0	1760	91	0
2	Q	1792	0	1760	98	0
2	Q1	1792	0	1760	100	0
2	Q2	1792	0	1760	102	0
2	R	1792	0	1760	83	0
2	R1	1792	0	1760	100	0
2	R2	1792	0	1760	82	0
2	V	1792	0	1760	83	0
2	V1	1792	0	1760	85	0
2	V2	1792	0	1760	84	0
2	o	1792	0	1760	103	0
2	o1	1792	0	1760	89	0
2	o2	1792	0	1760	101	0
2	p	1792	0	1760	89	0
2	p1	1792	0	1760	139	0
2	p2	1792	0	1760	121	0
2	q	1792	0	1760	86	0
2	q1	1792	0	1760	89	0
2	q2	1792	0	1760	87	0
2	r	1792	0	1760	82	0
2	r1	1792	0	1760	92	0
2	r2	1792	0	1760	88	0
2	v	1792	0	1760	105	0
2	v1	1792	0	1760	91	0
2	v2	1792	0	1760	93	0
3	U	1032	0	956	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	U1	1032	0	956	38	0
3	U2	1032	0	956	52	0
3	U3	1032	0	956	48	0
3	U4	1032	0	956	44	0
3	U5	1032	0	956	48	0
4	W	524	0	536	29	0
4	W1	524	0	536	29	0
4	W2	524	0	536	29	0
4	W3	524	0	536	31	0
4	W4	524	0	536	22	0
4	W5	524	0	536	35	0
4	w	524	0	536	26	0
4	w1	524	0	536	27	0
4	w2	524	0	536	40	0
4	w3	524	0	536	29	0
4	w4	524	0	536	26	0
4	w5	524	0	536	43	0
5	DA	2128	0	1165	52	0
6	DB	1887	0	1042	51	0
7	f	872	0	823	40	0
7	f1	872	0	823	52	0
7	f2	872	0	823	44	0
7	f3	872	0	823	44	0
7	f4	872	0	823	46	0
7	f5	872	0	823	52	0
All	All	120109	0	114791	4976	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 21.

The worst 5 of 4976 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)
2:O2:59:TYR:CD2	2:O2:59:TYR:CG	1.80	1.70
2:O:59:TYR:CD2	2:O:59:TYR:CG	1.80	1.65
2:O:59:TYR:CG	2:O:59:TYR:CD1	1.81	1.63
2:O2:59:TYR:CG	2:O2:59:TYR:CD1	1.81	1.60
2:O2:59:TYR:CE1	2:O2:59:TYR:CZ	1.92	1.58

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	B	471/533 (88%)	445 (94%)	26 (6%)	0	100	100
1	B1	471/533 (88%)	436 (93%)	35 (7%)	0	100	100
1	B2	471/533 (88%)	438 (93%)	33 (7%)	0	100	100
1	B3	471/533 (88%)	433 (92%)	37 (8%)	1 (0%)	43	74
1	B4	471/533 (88%)	434 (92%)	36 (8%)	1 (0%)	43	74
1	B5	471/533 (88%)	436 (93%)	35 (7%)	0	100	100
1	b	469/533 (88%)	446 (95%)	23 (5%)	0	100	100
1	b1	469/533 (88%)	437 (93%)	32 (7%)	0	100	100
1	b2	469/533 (88%)	441 (94%)	28 (6%)	0	100	100
1	b3	469/533 (88%)	433 (92%)	36 (8%)	0	100	100
1	b4	469/533 (88%)	443 (94%)	25 (5%)	1 (0%)	43	74
1	b5	469/533 (88%)	441 (94%)	28 (6%)	0	100	100
2	O	241/246 (98%)	220 (91%)	19 (8%)	2 (1%)	16	50
2	O1	241/246 (98%)	214 (89%)	26 (11%)	1 (0%)	30	64
2	O2	241/246 (98%)	221 (92%)	19 (8%)	1 (0%)	30	64
2	P	241/246 (98%)	218 (90%)	21 (9%)	2 (1%)	16	50
2	P1	241/246 (98%)	219 (91%)	22 (9%)	0	100	100
2	P2	241/246 (98%)	215 (89%)	25 (10%)	1 (0%)	30	64
2	Q	241/246 (98%)	216 (90%)	24 (10%)	1 (0%)	30	64
2	Q1	241/246 (98%)	219 (91%)	21 (9%)	1 (0%)	30	64
2	Q2	241/246 (98%)	222 (92%)	18 (8%)	1 (0%)	30	64
2	R	241/246 (98%)	216 (90%)	24 (10%)	1 (0%)	30	64
2	R1	241/246 (98%)	220 (91%)	20 (8%)	1 (0%)	30	64
2	R2	241/246 (98%)	217 (90%)	23 (10%)	1 (0%)	30	64
2	V	241/246 (98%)	222 (92%)	19 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V1	241/246 (98%)	218 (90%)	23 (10%)	0	100	100
2	V2	241/246 (98%)	211 (88%)	30 (12%)	0	100	100
2	o	241/246 (98%)	219 (91%)	22 (9%)	0	100	100
2	o1	241/246 (98%)	220 (91%)	21 (9%)	0	100	100
2	o2	241/246 (98%)	219 (91%)	21 (9%)	1 (0%)	30	64
2	p	241/246 (98%)	217 (90%)	23 (10%)	1 (0%)	30	64
2	p1	241/246 (98%)	217 (90%)	23 (10%)	1 (0%)	30	64
2	p2	241/246 (98%)	219 (91%)	22 (9%)	0	100	100
2	q	241/246 (98%)	221 (92%)	20 (8%)	0	100	100
2	q1	241/246 (98%)	219 (91%)	21 (9%)	1 (0%)	30	64
2	q2	241/246 (98%)	222 (92%)	18 (8%)	1 (0%)	30	64
2	r	241/246 (98%)	220 (91%)	21 (9%)	0	100	100
2	r1	241/246 (98%)	219 (91%)	22 (9%)	0	100	100
2	r2	241/246 (98%)	221 (92%)	19 (8%)	1 (0%)	30	64
2	v	241/246 (98%)	225 (93%)	15 (6%)	1 (0%)	30	64
2	v1	241/246 (98%)	220 (91%)	20 (8%)	1 (0%)	30	64
2	v2	241/246 (98%)	221 (92%)	19 (8%)	1 (0%)	30	64
3	U	129/131 (98%)	107 (83%)	19 (15%)	3 (2%)	5	30
3	U1	129/131 (98%)	102 (79%)	23 (18%)	4 (3%)	3	25
3	U2	129/131 (98%)	104 (81%)	21 (16%)	4 (3%)	3	25
3	U3	129/131 (98%)	105 (81%)	20 (16%)	4 (3%)	3	25
3	U4	129/131 (98%)	102 (79%)	24 (19%)	3 (2%)	5	30
3	U5	129/131 (98%)	111 (86%)	15 (12%)	3 (2%)	5	30
4	W	65/68 (96%)	61 (94%)	4 (6%)	0	100	100
4	W1	65/68 (96%)	61 (94%)	4 (6%)	0	100	100
4	W2	65/68 (96%)	60 (92%)	4 (6%)	1 (2%)	8	37
4	W3	65/68 (96%)	58 (89%)	6 (9%)	1 (2%)	8	37
4	W4	65/68 (96%)	59 (91%)	6 (9%)	0	100	100
4	W5	65/68 (96%)	58 (89%)	6 (9%)	1 (2%)	8	37
4	w	65/68 (96%)	60 (92%)	4 (6%)	1 (2%)	8	37
4	w1	65/68 (96%)	60 (92%)	4 (6%)	1 (2%)	8	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	w2	65/68 (96%)	57 (88%)	7 (11%)	1 (2%)	8	37
4	w3	65/68 (96%)	59 (91%)	5 (8%)	1 (2%)	8	37
4	w4	65/68 (96%)	57 (88%)	7 (11%)	1 (2%)	8	37
4	w5	65/68 (96%)	58 (89%)	6 (9%)	1 (2%)	8	37
7	f	112/117 (96%)	97 (87%)	15 (13%)	0	100	100
7	f1	112/117 (96%)	95 (85%)	17 (15%)	0	100	100
7	f2	112/117 (96%)	90 (80%)	21 (19%)	1 (1%)	14	47
7	f3	112/117 (96%)	94 (84%)	18 (16%)	0	100	100
7	f4	112/117 (96%)	92 (82%)	20 (18%)	0	100	100
7	f5	112/117 (96%)	91 (81%)	21 (19%)	0	100	100
All	All	15096/16080 (94%)	13728 (91%)	1312 (9%)	56 (0%)	31	64

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	61	ASP
2	P	61	ASP
2	Q	61	ASP
3	U	30	ARG
4	w	63	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

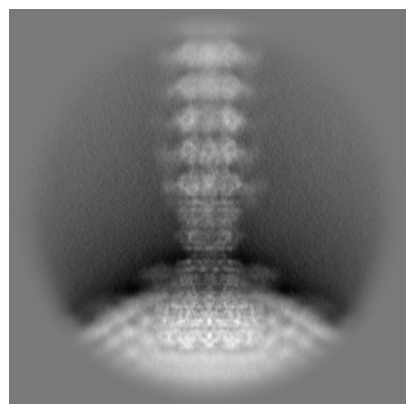
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38556. These allow visual inspection of the internal detail of the map and identification of artifacts.

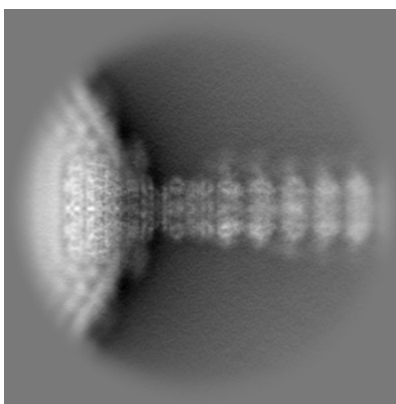
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

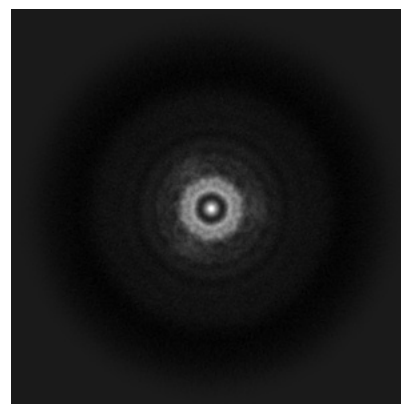
6.1.1 Primary map



X

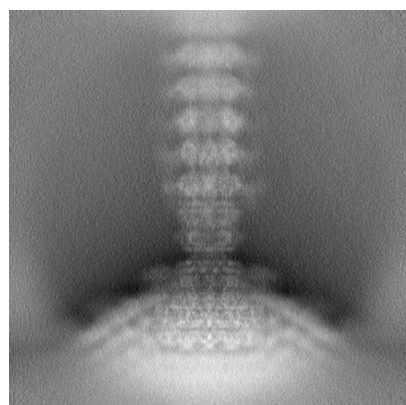


Y

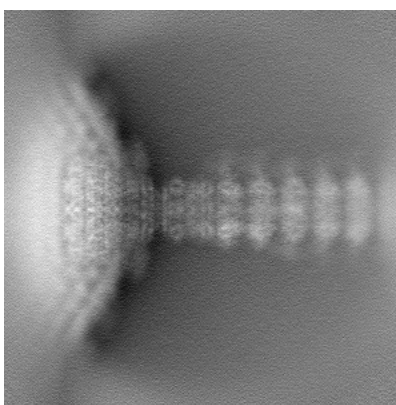


Z

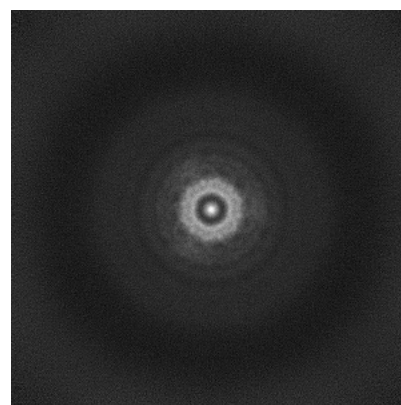
6.1.2 Raw map



X



Y

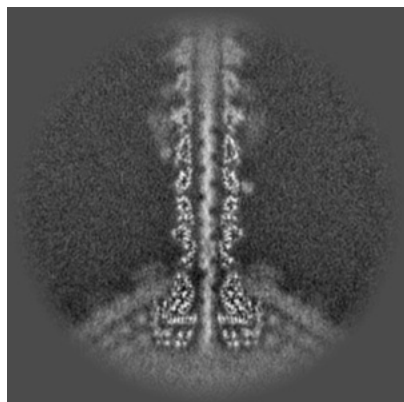


Z

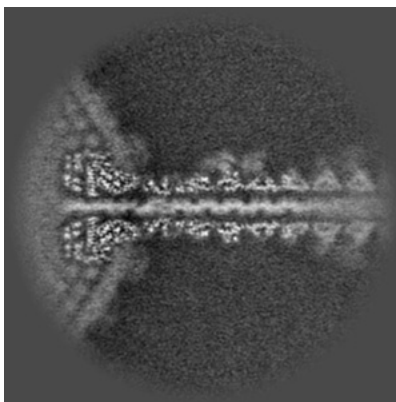
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

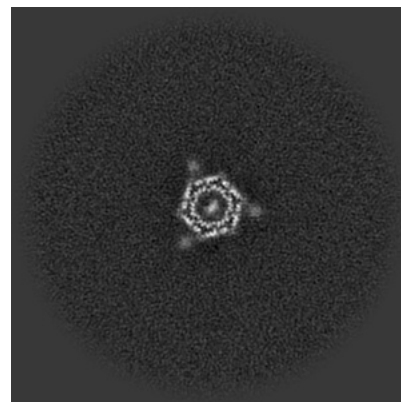
6.2.1 Primary map



X Index: 240

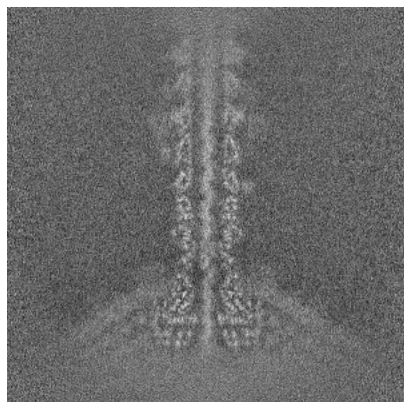


Y Index: 240

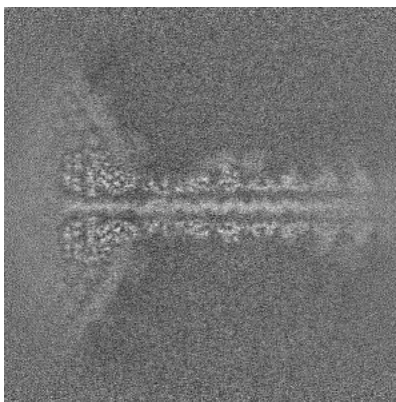


Z Index: 240

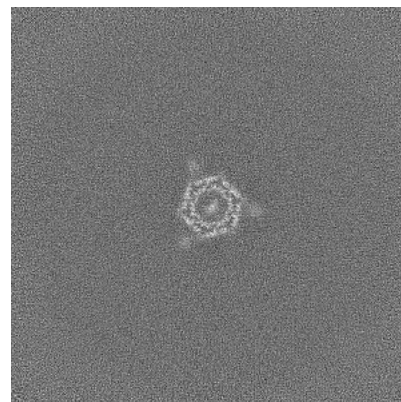
6.2.2 Raw map



X Index: 240



Y Index: 240

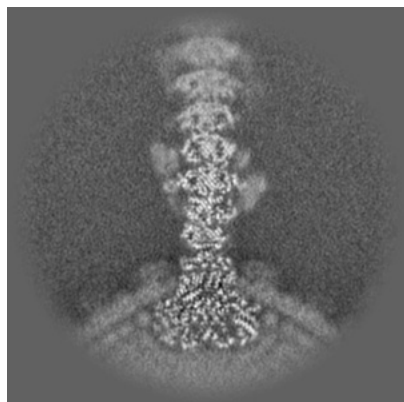


Z Index: 240

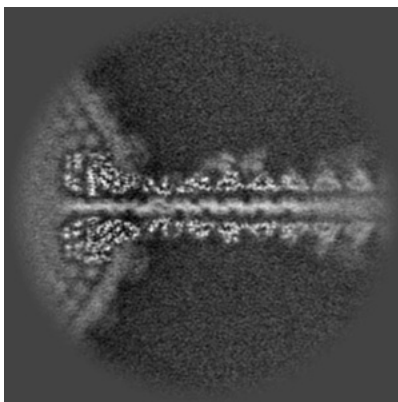
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

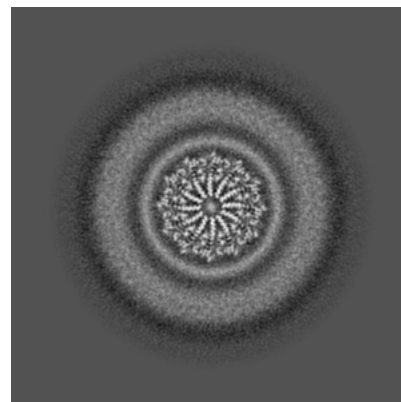
6.3.1 Primary map



X Index: 218

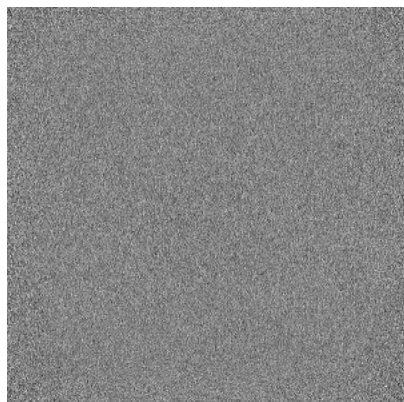


Y Index: 241

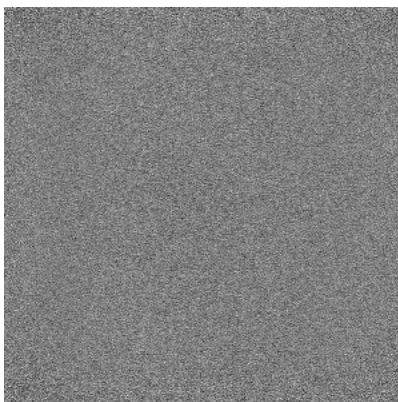


Z Index: 106

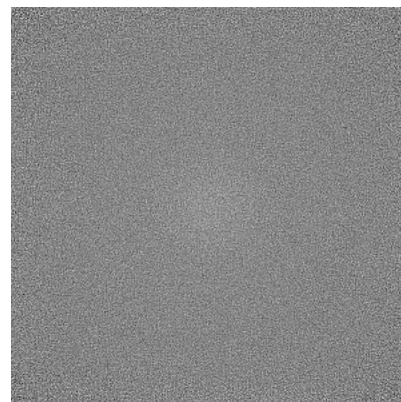
6.3.2 Raw map



X Index: 0



Y Index: 0

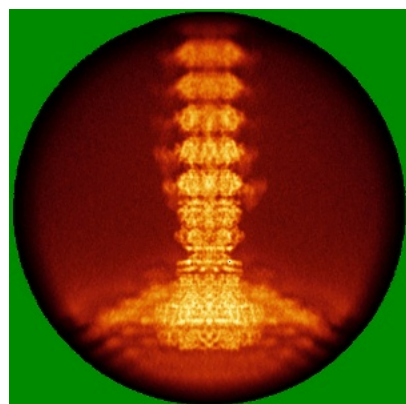


Z Index: 0

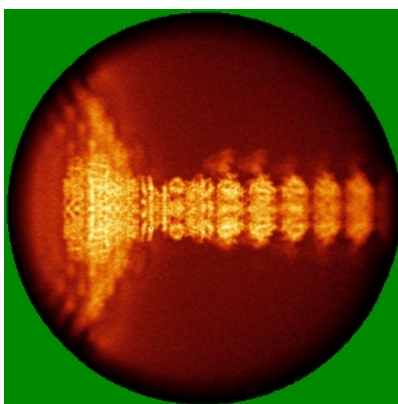
The images above show the largest variance slices of the map in three orthogonal directions.

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

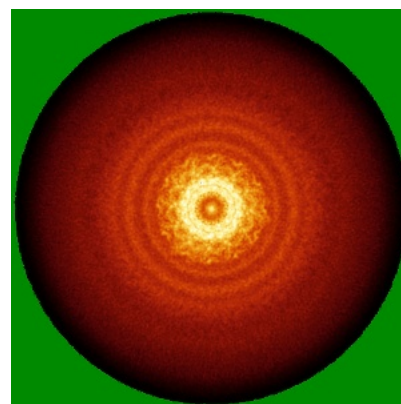
6.4.1 Primary map



X

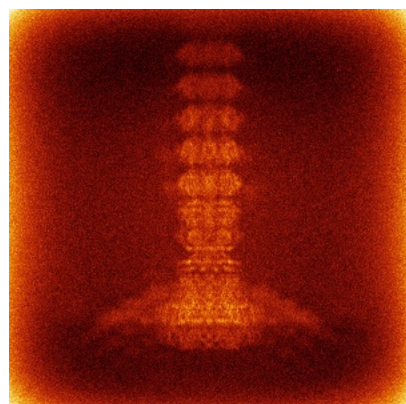


Y

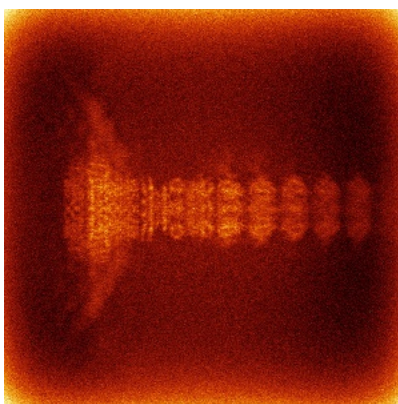


Z

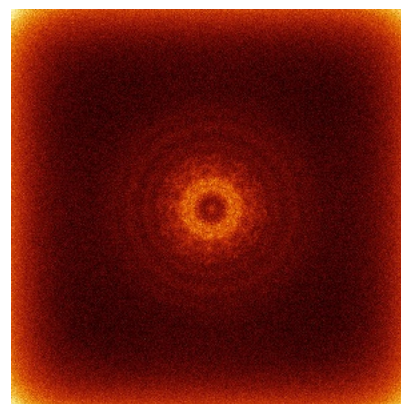
6.4.2 Raw map



X



Y

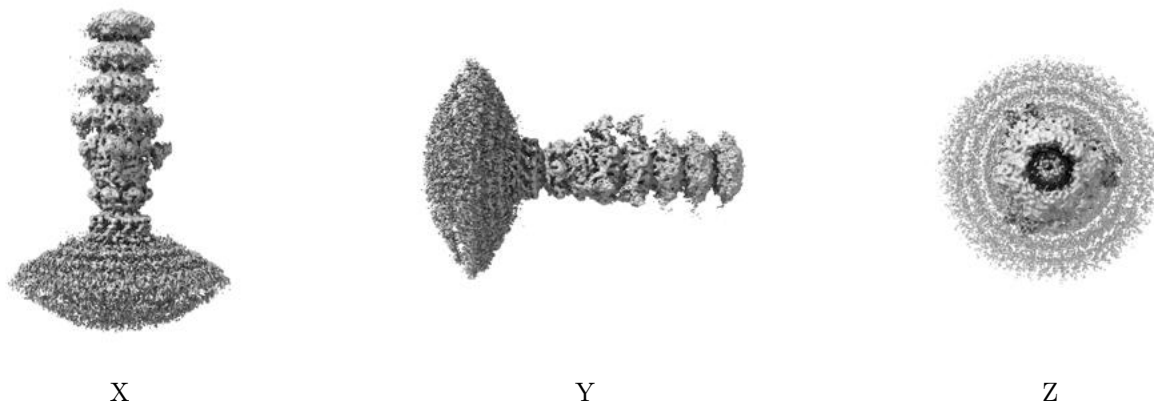


Z

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.

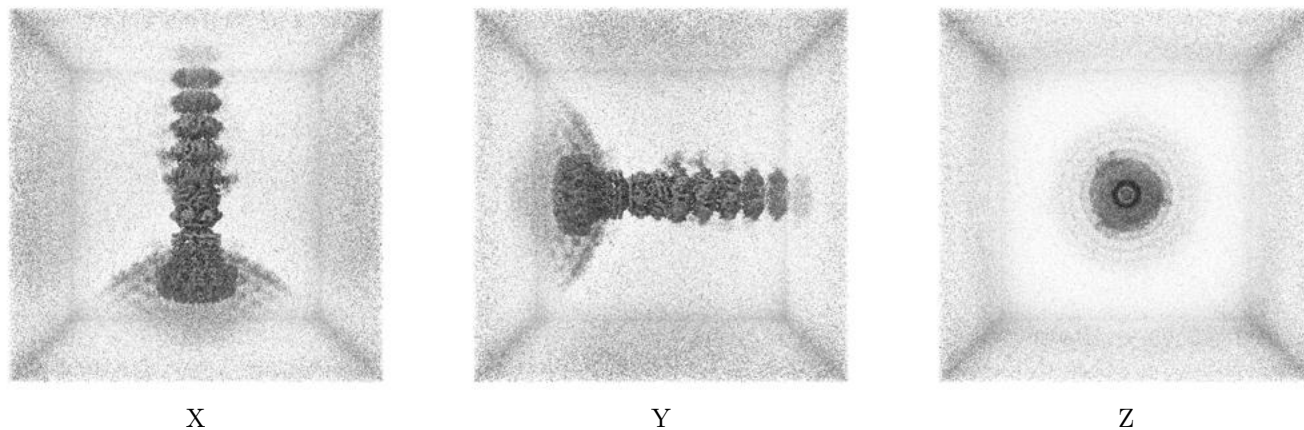
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.52. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

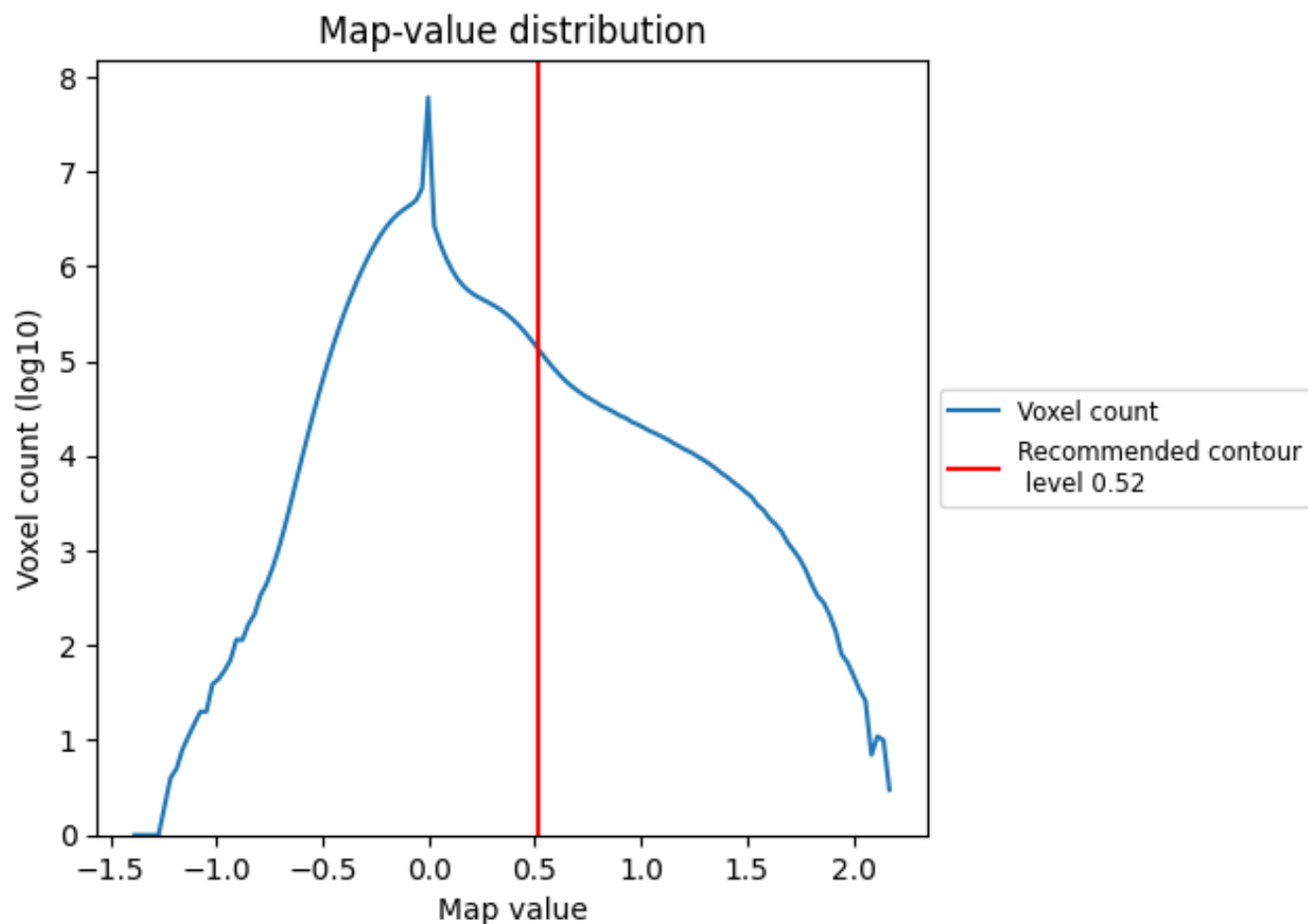
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

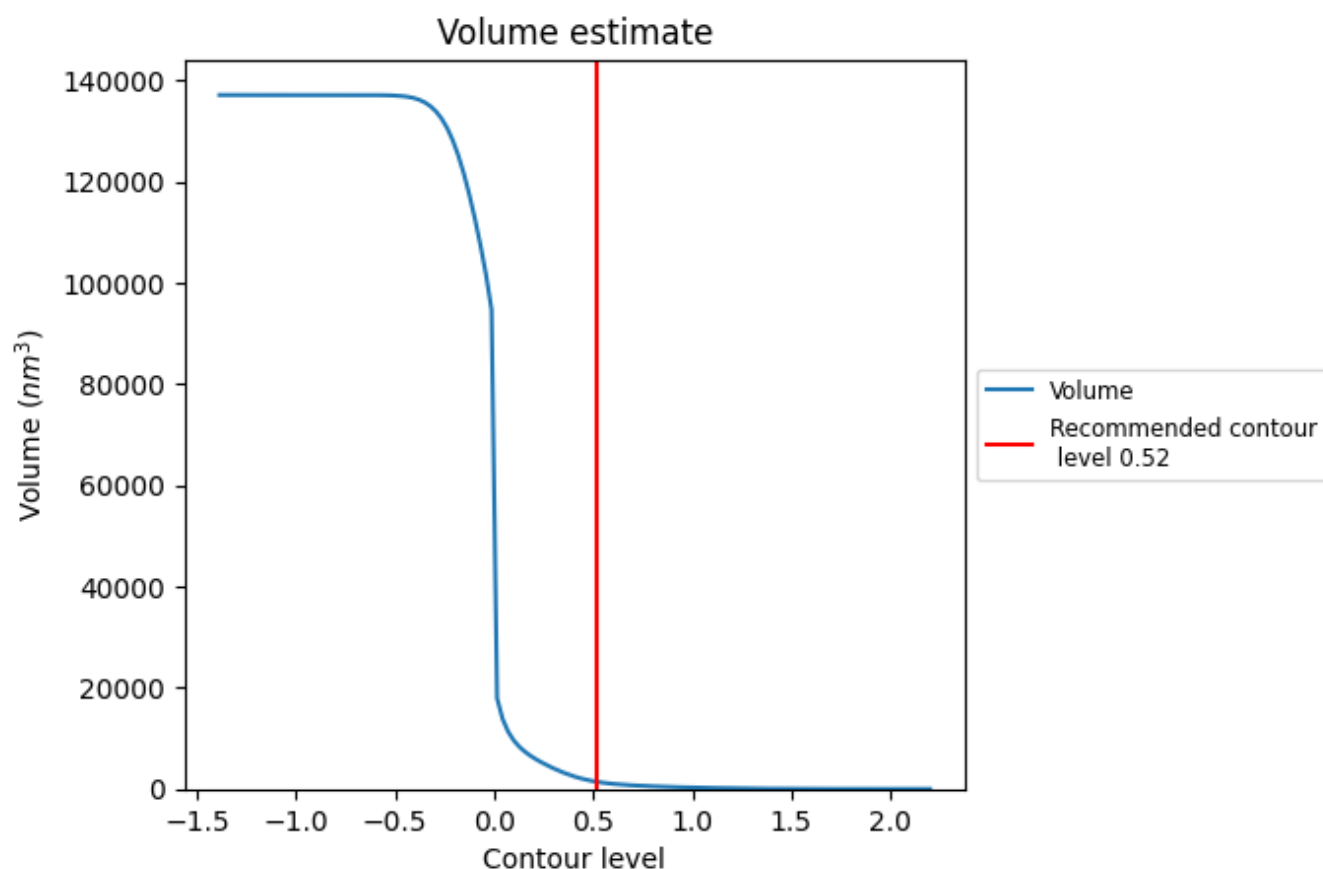
This section contains the results of statistical analysis of the map.

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.

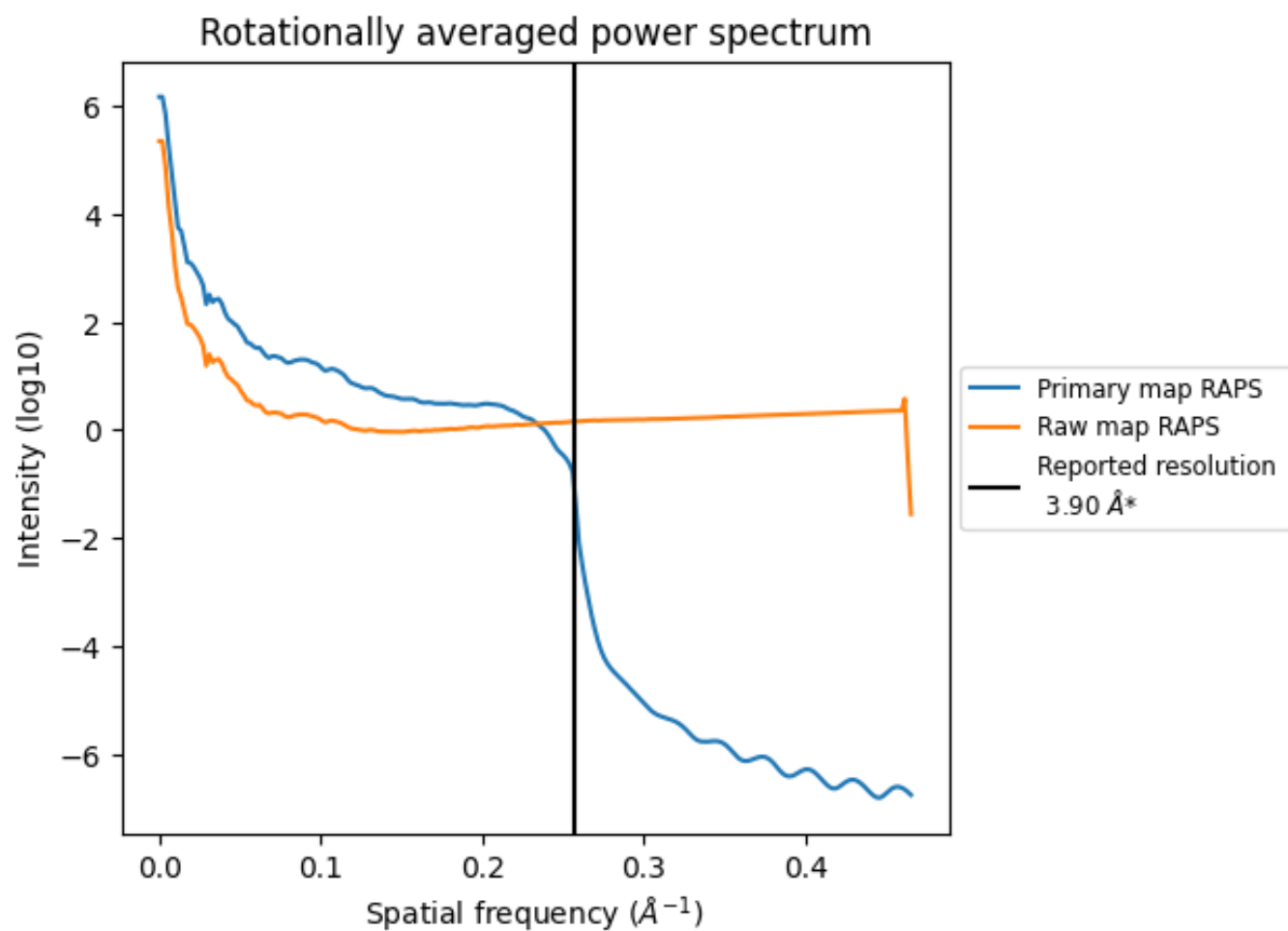
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1400 nm^3 ; this corresponds to an approximate mass of 1265 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 ⓘ

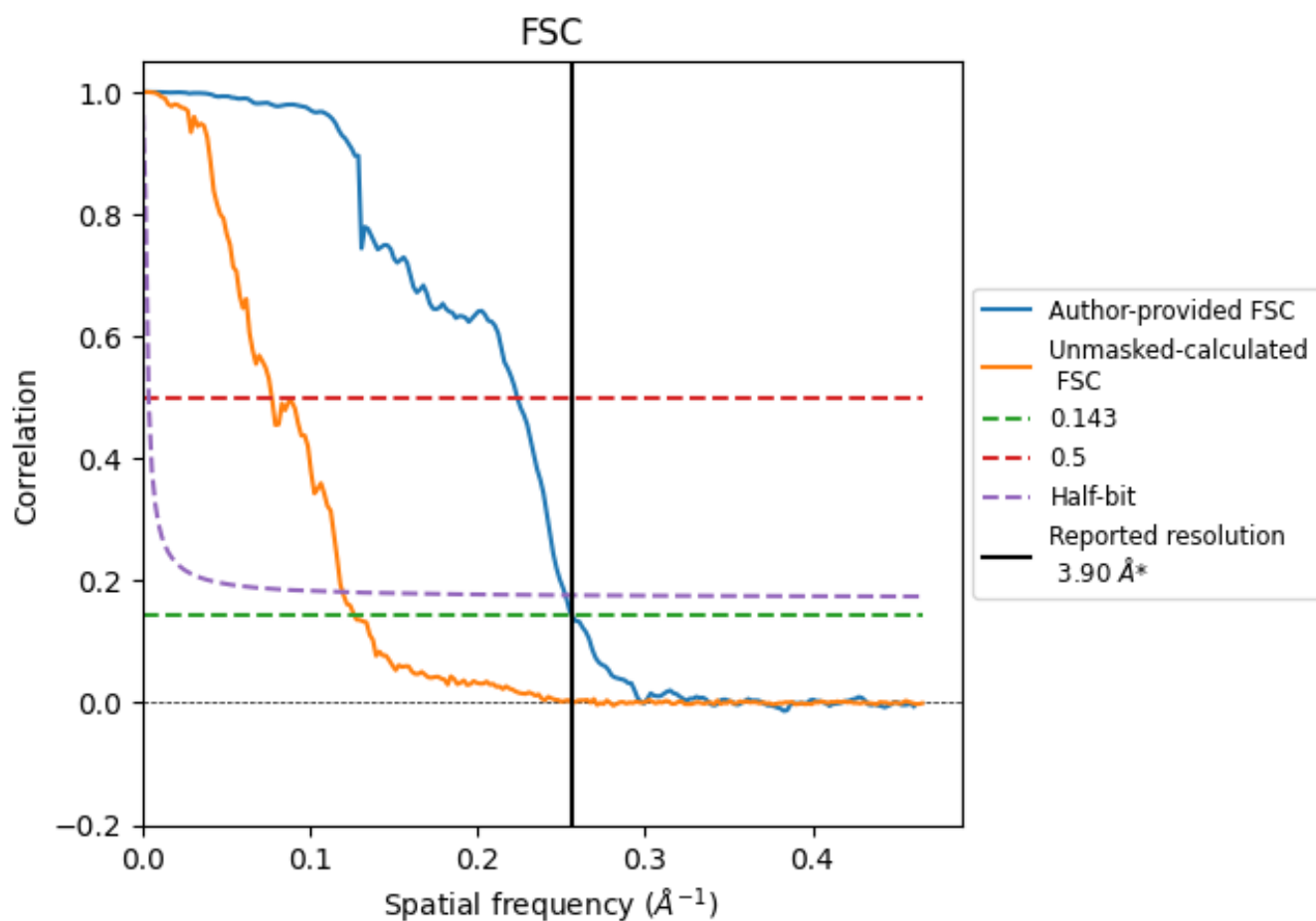


*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.90	4.47	3.96
Unmasked-calculated*	7.90	12.94	8.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.90 differs from the reported value 3.9 by more than 10 %

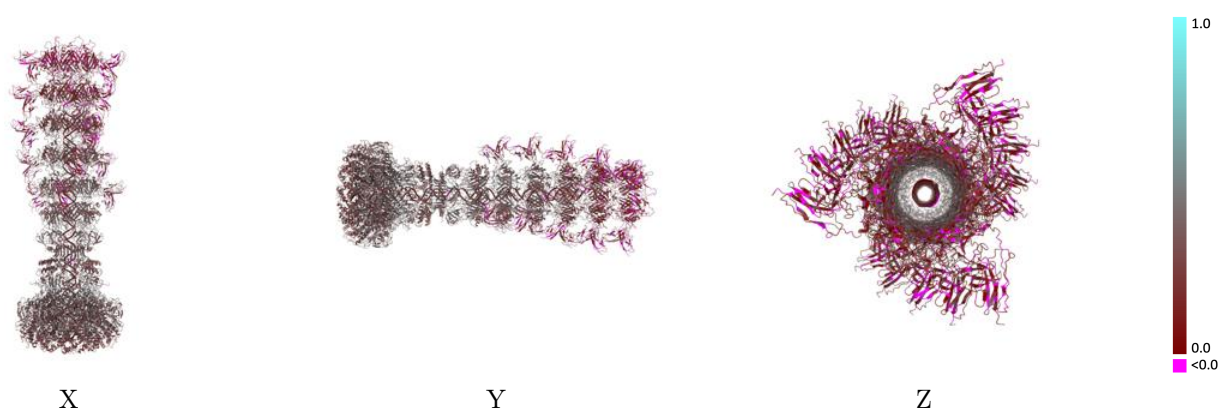
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38556 and PDB model 8XPM. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

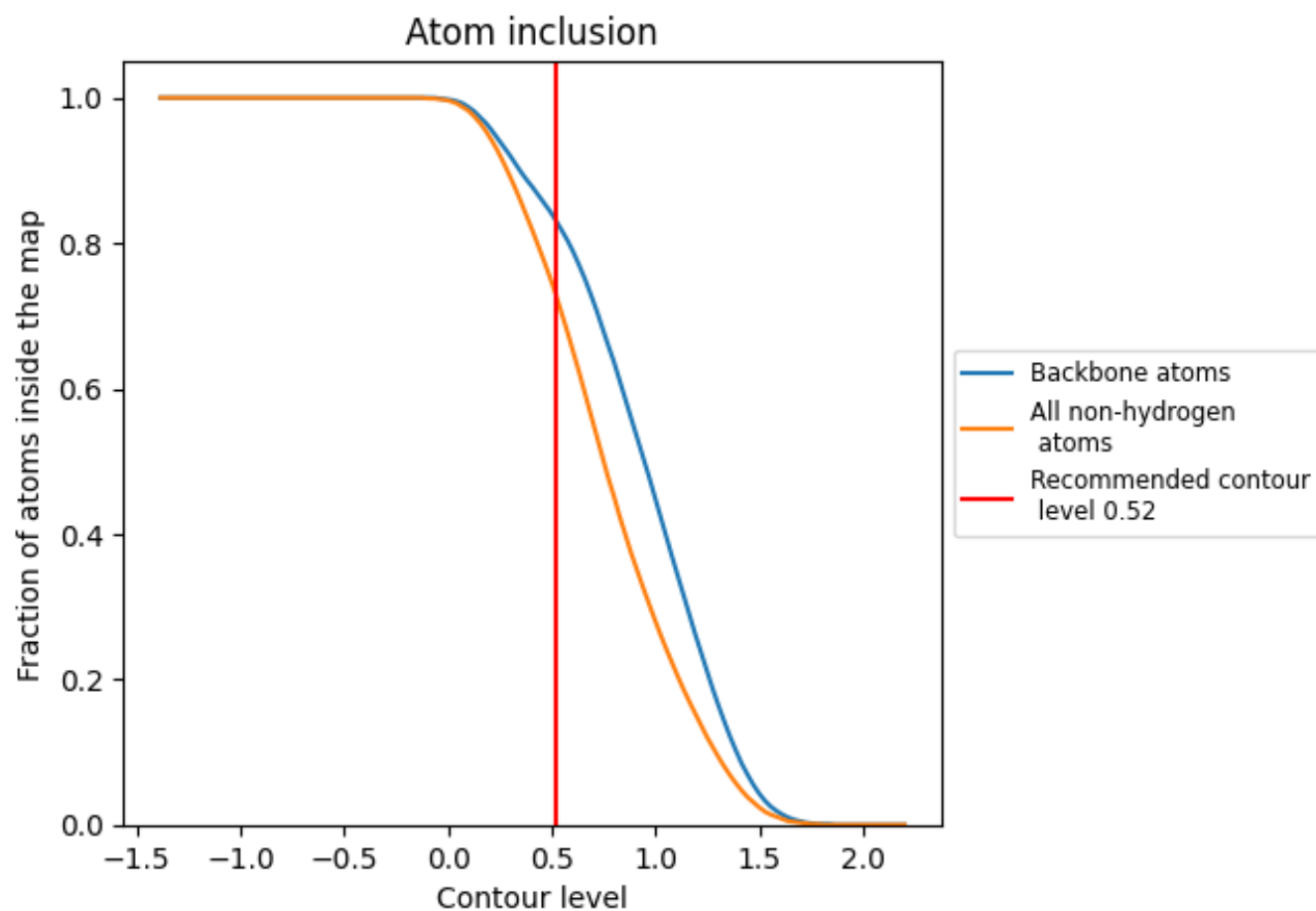


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 73% 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 (0.52) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.3100
B	 0.7540	 0.3630
B1	 0.7580	 0.3640
B2	 0.7550	 0.3690
B3	 0.7630	 0.3710
B4	 0.7660	 0.3690
B5	 0.7470	 0.3660
DA	 0.7530	 0.1910
DB	 0.7500	 0.1890
O	 0.7830	 0.3220
O1	 0.7880	 0.3060
O2	 0.7940	 0.3130
P	 0.6030	 0.2470
P1	 0.6120	 0.2430
P2	 0.6040	 0.2590
Q	 0.5860	 0.1770
Q1	 0.5980	 0.2090
Q2	 0.5900	 0.1930
R	 0.5270	 0.1480
R1	 0.5450	 0.1470
R2	 0.5380	 0.1690
U	 0.8750	 0.3730
U1	 0.8900	 0.3760
U2	 0.8870	 0.3780
U3	 0.8950	 0.3700
U4	 0.9020	 0.3780
U5	 0.8920	 0.3650
V	 0.8150	 0.3250
V1	 0.8180	 0.3320
V2	 0.8360	 0.3500
W	 0.7900	 0.3780
W1	 0.7980	 0.3780
W2	 0.8000	 0.3800
W3	 0.8120	 0.3750
W4	 0.7790	 0.3780



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Chain	Atom inclusion	Q-score
W5	 0.8060	 0.3700
b	 0.7550	 0.3660
b1	 0.7610	 0.3710
b2	 0.7620	 0.3690
b3	 0.7540	 0.3660
b4	 0.7620	 0.3690
b5	 0.7560	 0.3710
f	 0.9000	 0.3970
f1	 0.9020	 0.3940
f2	 0.9020	 0.4010
f3	 0.8910	 0.3920
f4	 0.8960	 0.3900
f5	 0.8930	 0.3850
o	 0.7290	 0.2920
o1	 0.7390	 0.3060
o2	 0.7590	 0.2930
p	 0.6020	 0.2400
p1	 0.6100	 0.2590
p2	 0.6050	 0.2350
q	 0.5810	 0.2050
q1	 0.5730	 0.1920
q2	 0.5780	 0.1960
r	 0.5360	 0.1410
r1	 0.5340	 0.1590
r2	 0.5410	 0.1560
v	 0.7860	 0.3320
v1	 0.8000	 0.3270
v2	 0.8100	 0.3330
w	 0.7770	 0.3680
w1	 0.8020	 0.3770
w2	 0.8260	 0.3740
w3	 0.7900	 0.3790
w4	 0.7980	 0.3710
w5	 0.8000	 0.3750