



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:20 PM UTC

PDB ID : 6QZF / pdb_00006qzf
EMDB ID : EMD-4685
Title : The cryo-EM structure of the collar complex and tail axis in genome emptied bacteriophage phi29
Authors : Xu, J.; Wang, D.; Gui, M.; Xiang, Y.
Deposited on : 2019-03-11
Resolution : 3.80 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:

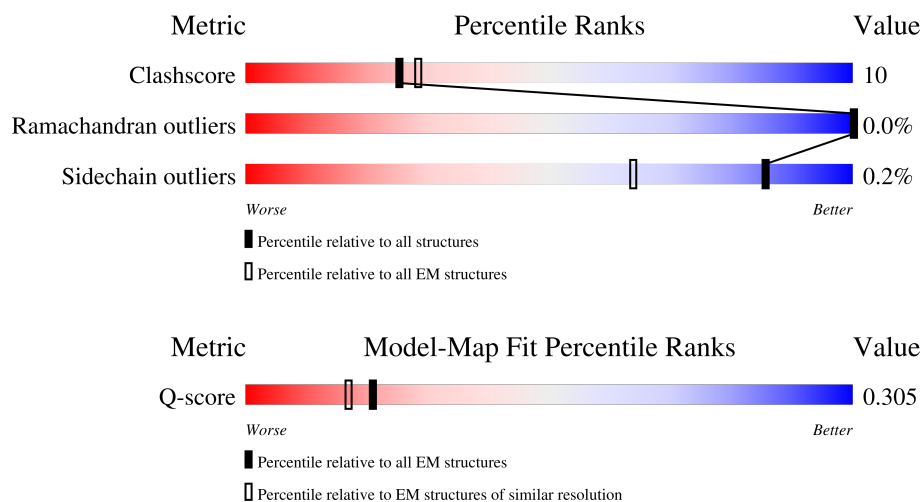
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	0a	309	74% 69% 22% 9%
1	0b	309	75% 68% 23% 9%
1	0c	309	75% 70% 21% 9%
1	0d	309	74% 69% 22% 9%

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Mol	Chain	Length	Quality of chain
1	0e	309	74% 69% 22% 9%
1	0f	309	75% 67% 24% 9%
1	0g	309	74% 67% 23% 9%
1	0h	309	75% 69% 22% 9%
1	0i	309	75% 69% 22% 9%
1	0j	309	75% 69% 22% 9%
1	0k	309	74% 68% 23% 9%
1	0l	309	75% 69% 22% 9%
2	0A	293	9% 70% 29% ..
2	0B	293	9% 67% 32% .
2	0C	293	9% 62% 37% ..
2	0D	293	9% 65% 34% ..
2	0E	293	9% 68% 31% ..
2	0F	293	9% 65% 34% ..
2	0G	293	10% 66% 33% ..
2	0H	293	10% 69% 30% ..
2	0I	293	9% 68% 31% ..
2	0J	293	9% 69% 30% ..
2	0K	293	9% 68% 30% ..
2	0L	293	9% 67% 32% ..
3	A	854	5% 5% . 94%
3	B	854	5% 5% . 93%
3	C	854	6% 6% . 93%
3	D	854	5% 5% . 94%
3	E	854	5% 5% . 93%

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Mol	Chain	Length	Quality of chain	
3	F	854	 6% .	93%
3	G	854	 5% .	94%
3	H	854	 5% .	93%
3	I	854	 6% .	93%
3	J	854	 5% .	94%
3	K	854	 5% .	93%
3	L	854	 6% .	93%
3	M	854	 5% .	94%
3	N	854	 5% .	93%
3	O	854	 6% .	93%
3	P	854	 5% .	94%
3	Q	854	 5% .	93%
3	R	854	 6% .	93%
3	S	854	 5% .	94%
3	T	854	 5% .	93%
3	U	854	 6% .	93%
3	V	854	 5% .	94%
3	W	854	 5% .	93%
3	X	854	 6% .	93%
3	Y	854	 5% .	94%
3	Z	854	 5% .	93%
3	a	854	 6% .	93%
3	b	854	 5% .	94%
3	c	854	 5% .	93%
3	d	854	 6% .	93%

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Mol	Chain	Length	Quality of chain	
3	e	854	5% 5% . 94%	
3	f	854	5% 5% . 93%	
3	g	854	6% 6% . 93%	
3	h	854	5% 5% . 94%	
3	i	854	5% 5% . 93%	
3	j	854	6% 6% . 93%	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 71628 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0a	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0b	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0c	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0d	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0e	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0f	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0g	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0h	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0i	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0j	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0k	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		
1	0l	280	Total	C	N	O	S	0	0
			2240	1429	376	428	7		

- Molecule 2 is a protein called Proximal tail tube connector protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0A	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0B	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0C	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	0D	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0E	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0F	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0G	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0H	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0I	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0J	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0K	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		
2	0L	291	Total	C	N	O	S	0	0
			2300	1416	397	479	8		

- Molecule 3 is a protein called Pre-neck appendage protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	B	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	C	61	Total	C	N	O	S	0	0
			514	334	78	98	4		
3	D	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	E	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	F	61	Total	C	N	O	S	0	0
			514	334	78	98	4		
3	G	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	H	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	I	61	Total	C	N	O	S	0	0
			514	334	78	98	4		
3	J	51	Total	C	N	O	S	0	0
			433	281	67	83	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	L	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	M	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	N	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	O	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	P	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	Q	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	R	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	S	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	T	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	U	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	V	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	W	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	X	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	Y	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	Z	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	a	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	b	51	Total 433	C 281	N 67	O 83	S 2	0	0
3	c	57	Total 482	C 312	N 74	O 92	S 4	0	0
3	d	61	Total 514	C 334	N 78	O 98	S 4	0	0
3	e	51	Total 433	C 281	N 67	O 83	S 2	0	0

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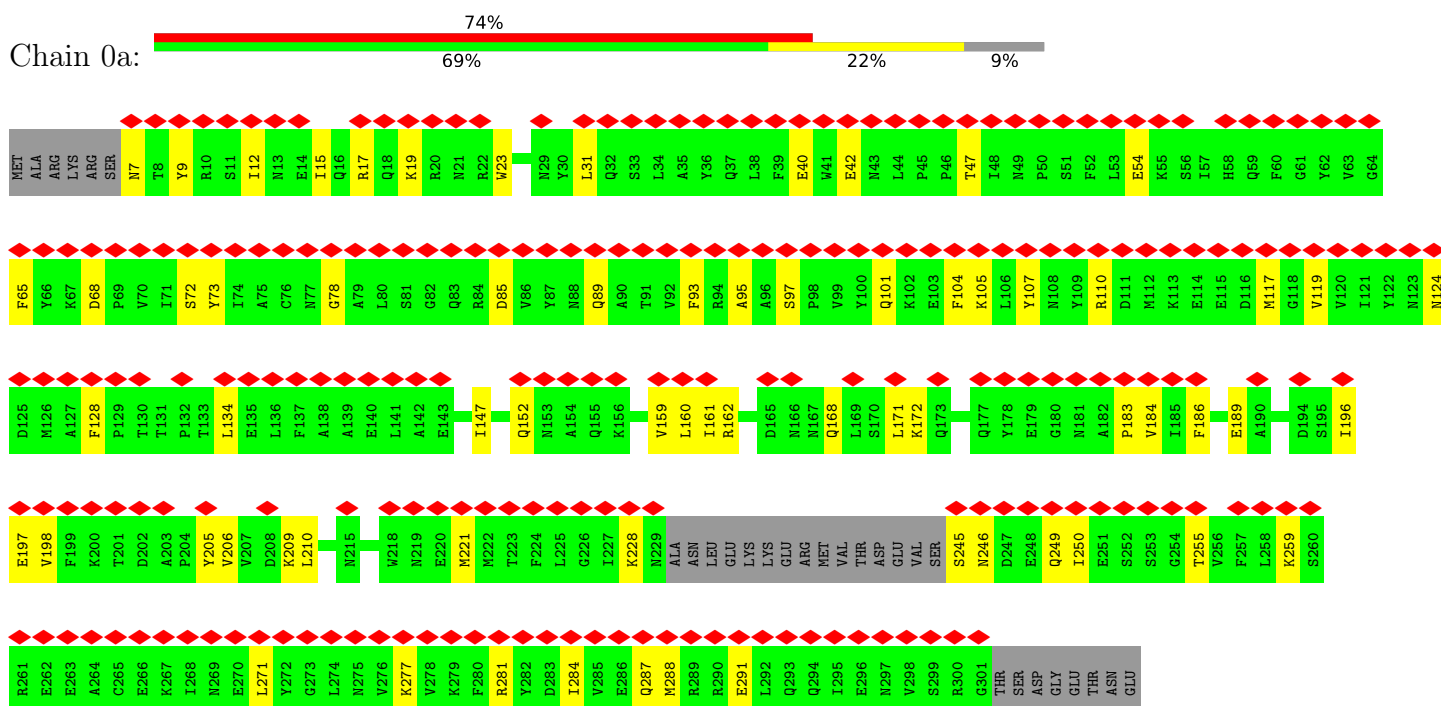
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	f	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	g	61	Total	C	N	O	S	0	0
			514	334	78	98	4		
3	h	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	i	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	j	61	Total	C	N	O	S	0	0
			514	334	78	98	4		

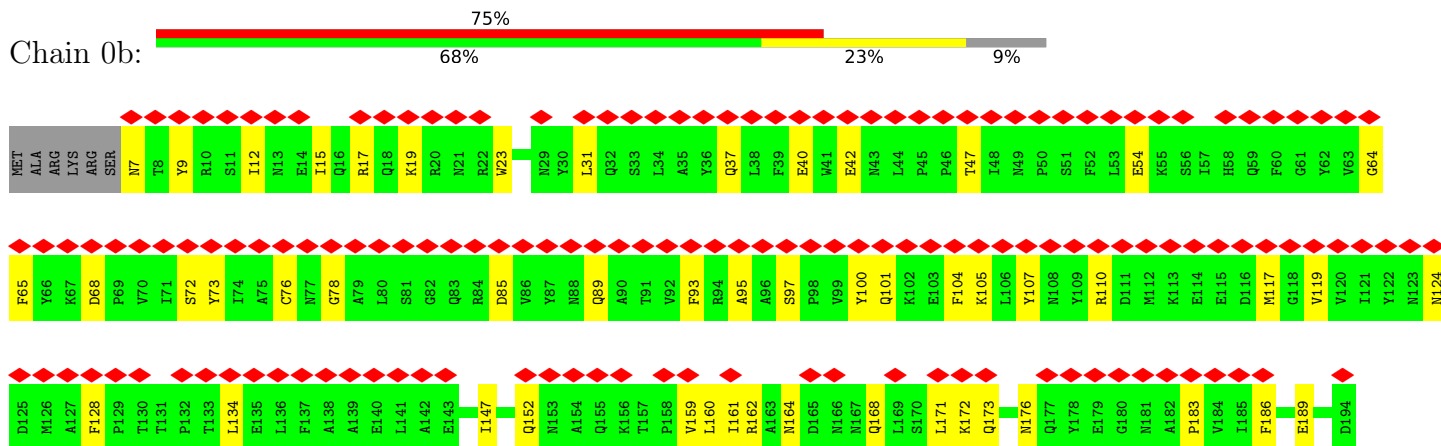
3 Residue-property plots

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

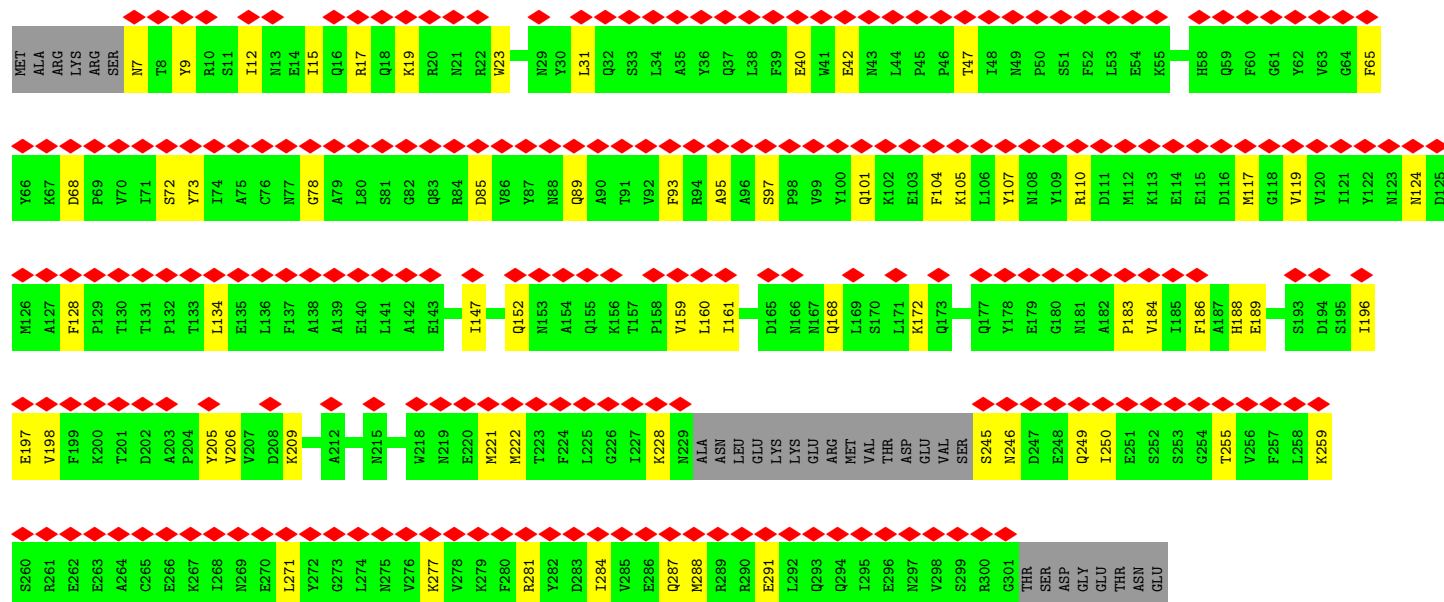
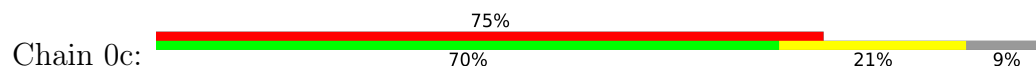


- Molecule 1: Portal protein

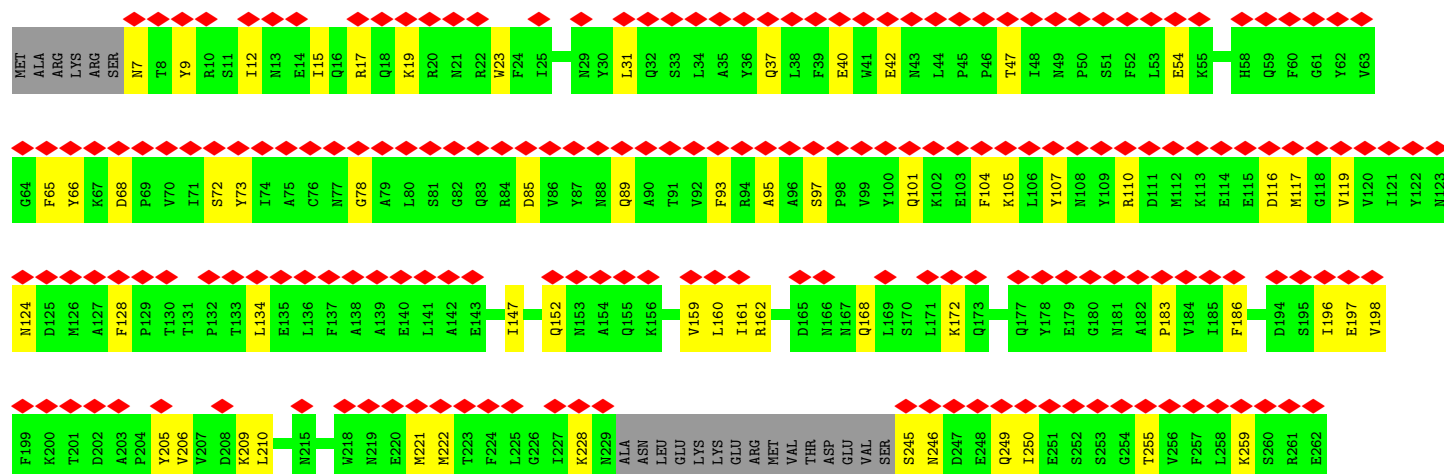
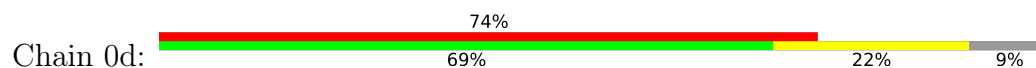




• Molecule 1: Portal protein

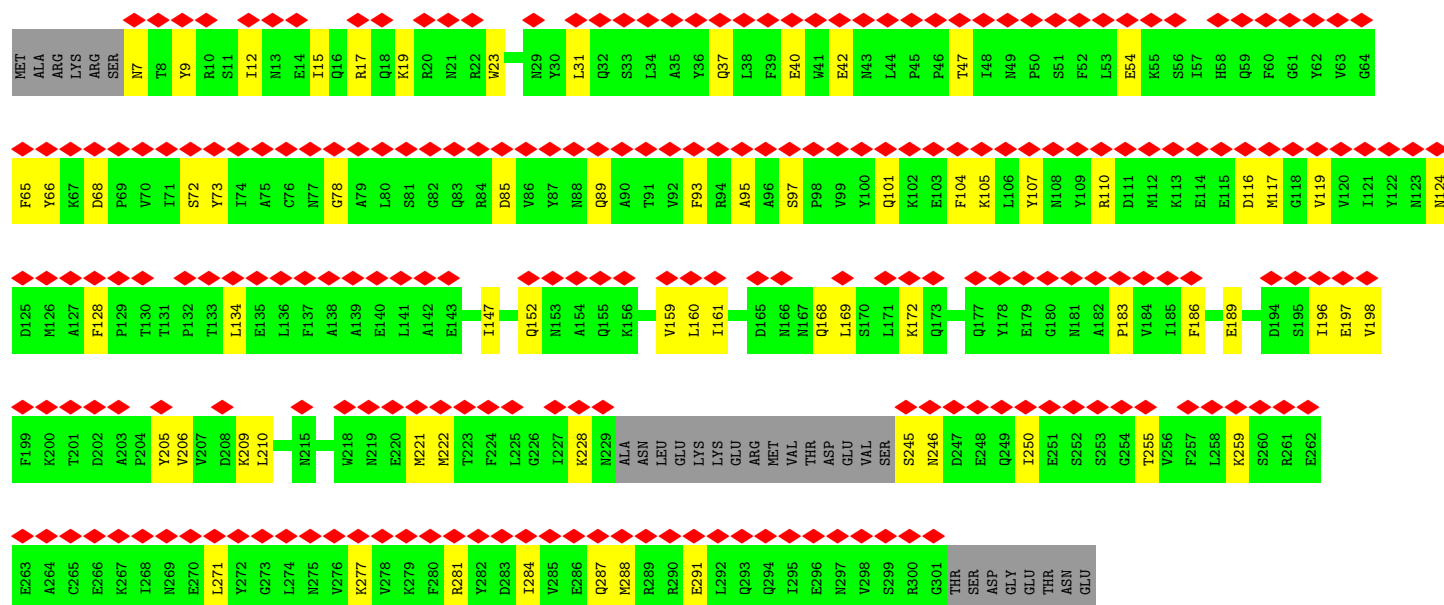
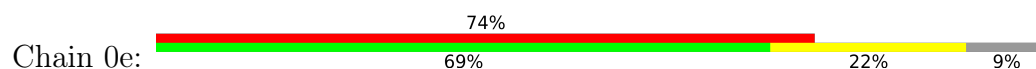


• Molecule 1: Portal protein

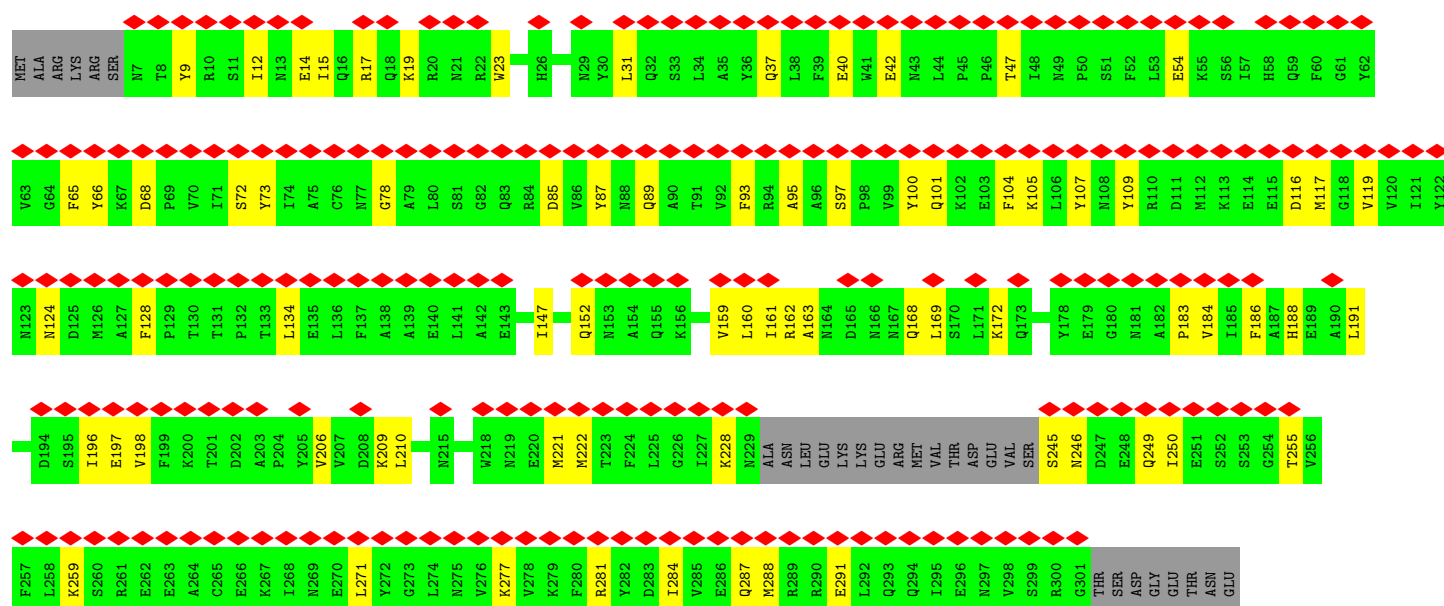
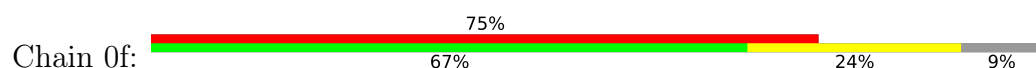




• Molecule 1: Portal protein



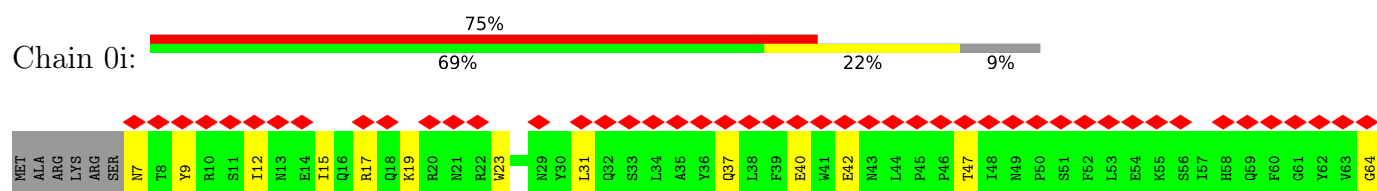
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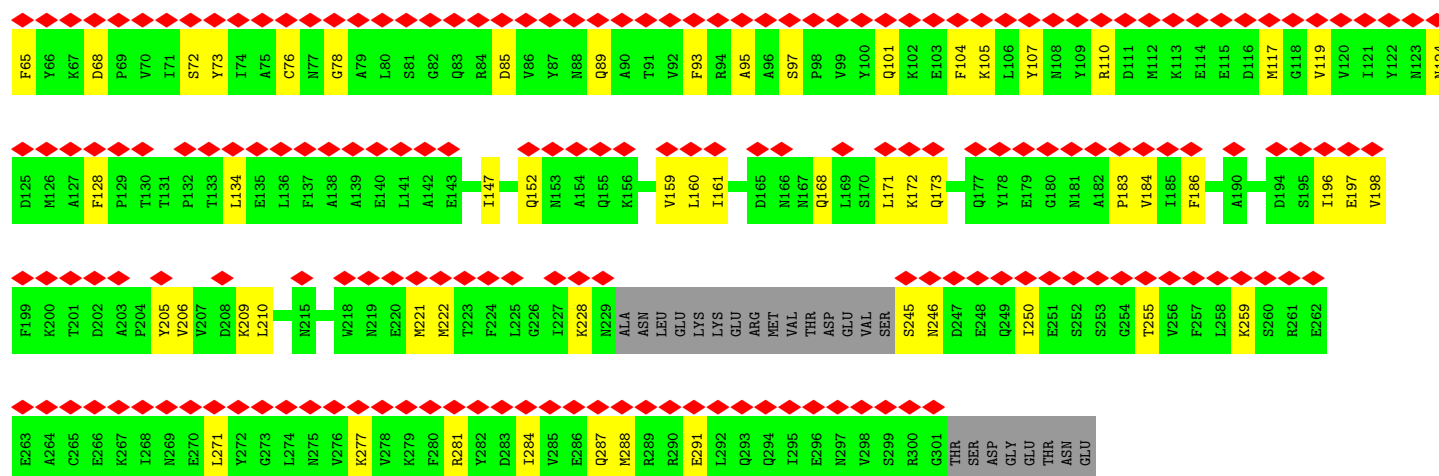


• Molecule 1: Portal protein

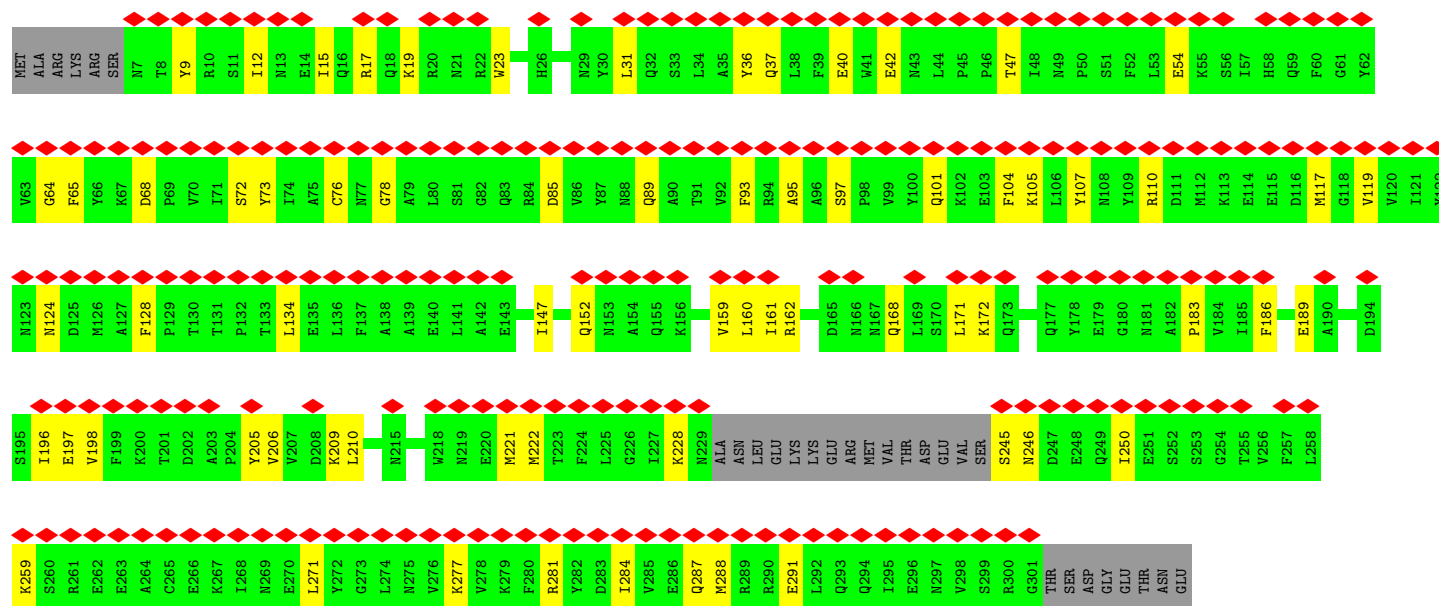
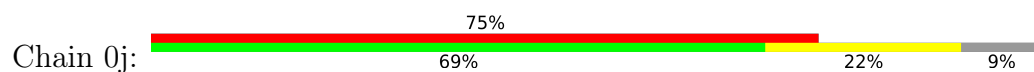
- Molecule 1: Portal protein

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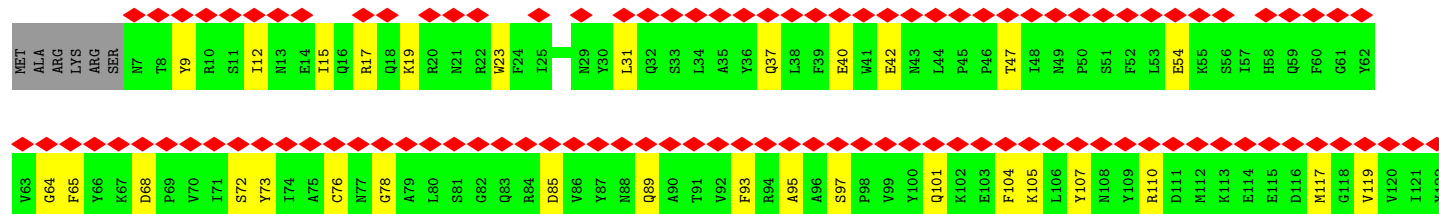
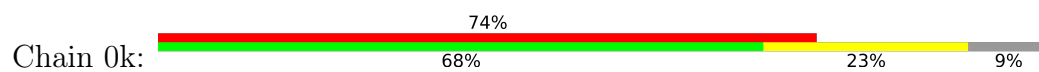


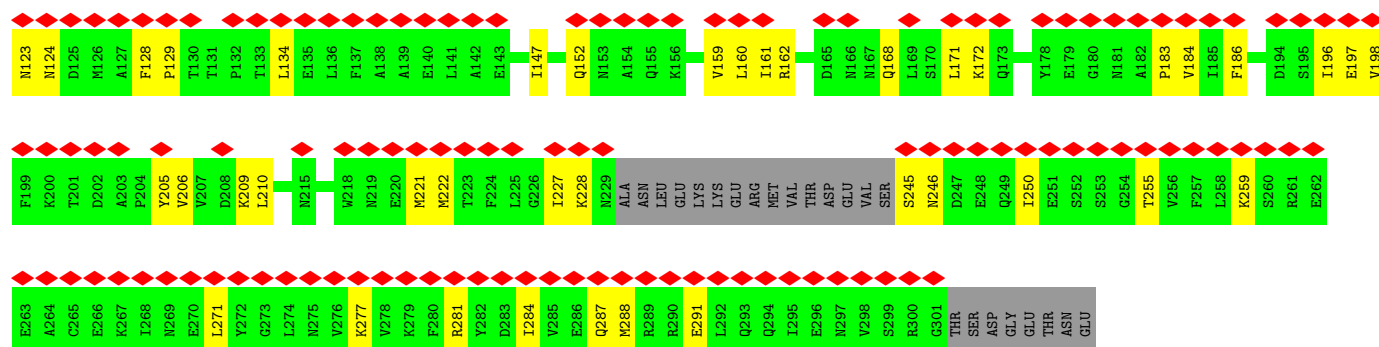


• Molecule 1: Portal protein

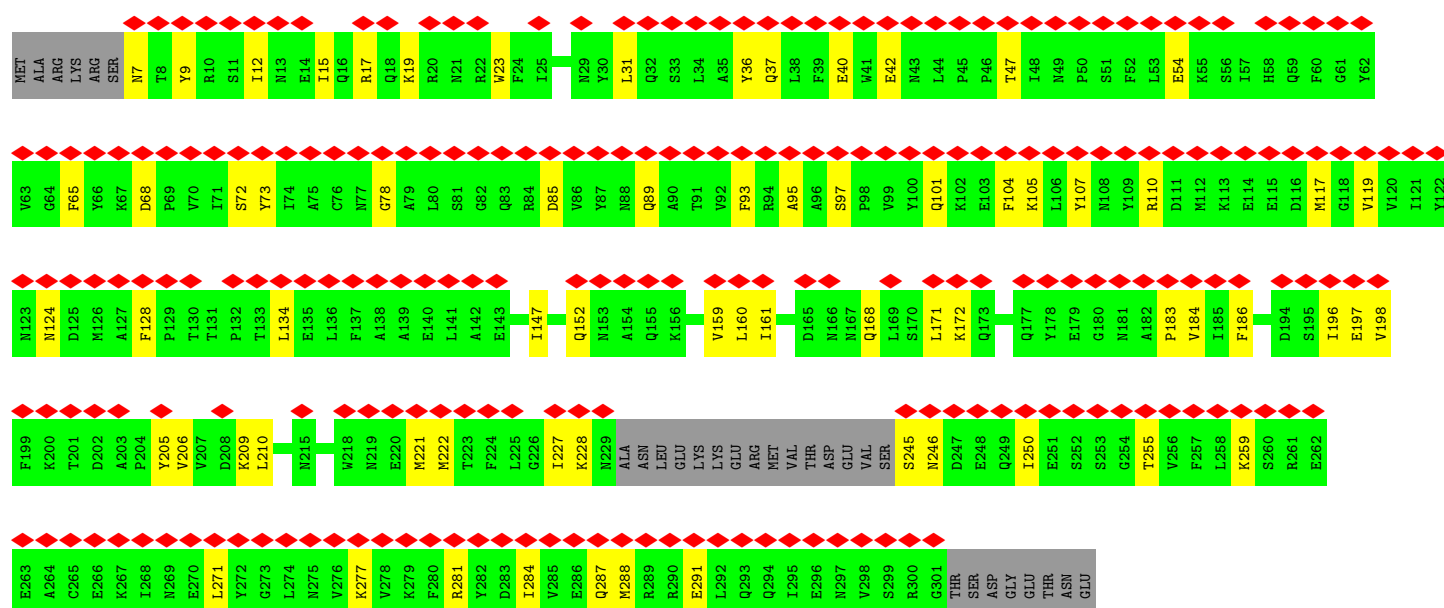
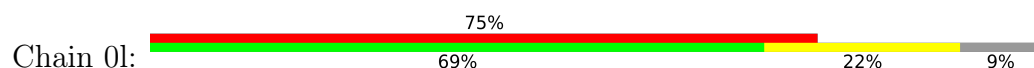


• Molecule 1: Portal protein

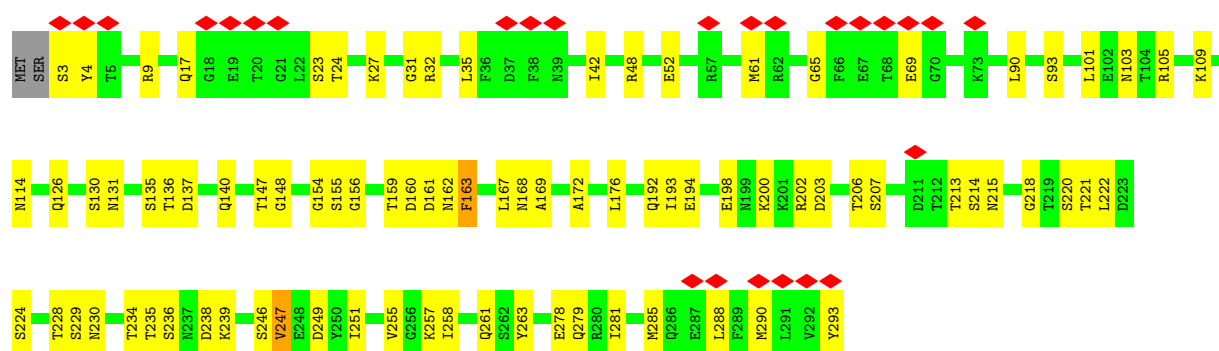




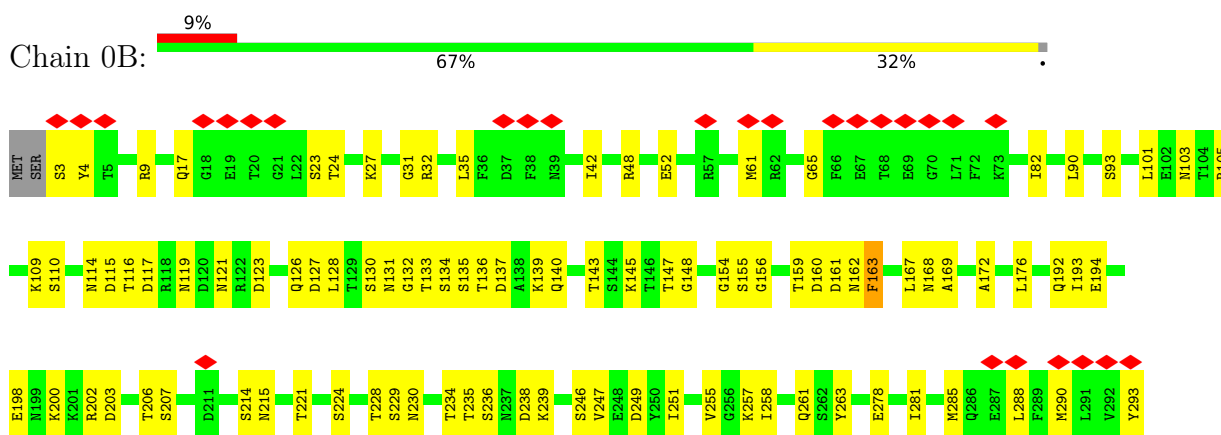
• Molecule 1: Portal protein



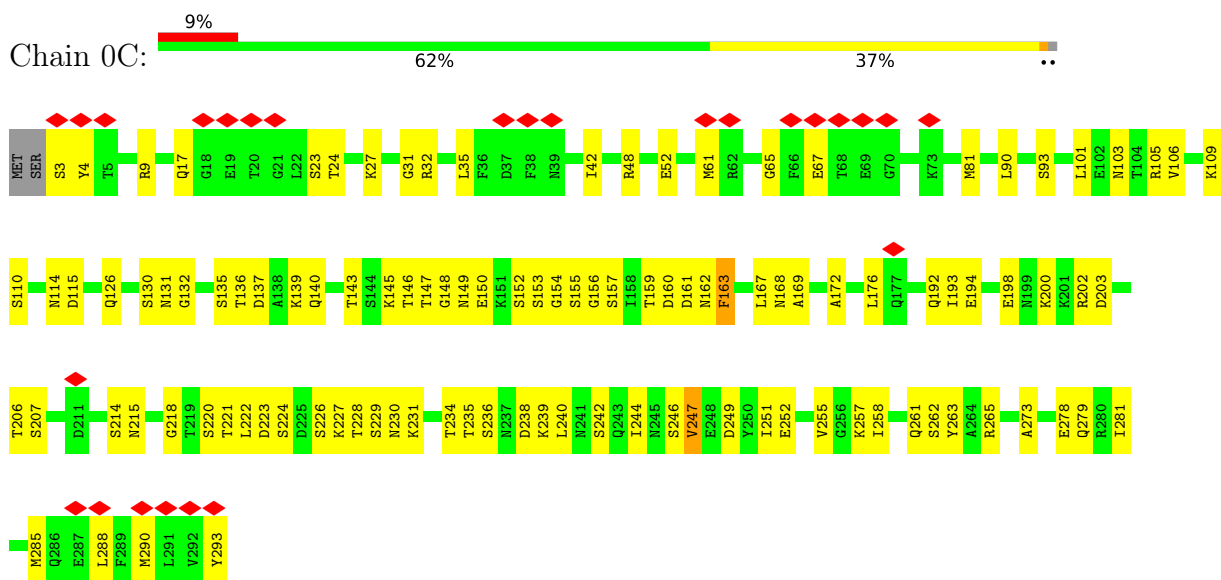
• Molecule 2: Proximal tail tube connector protein



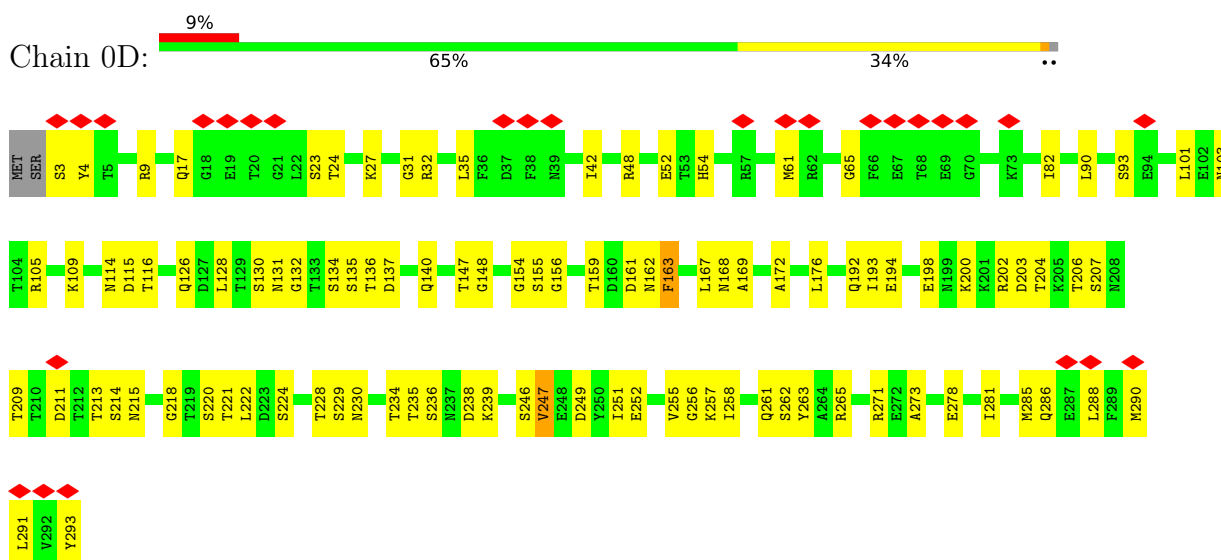
• Molecule 2: Proximal tail tube connector protein



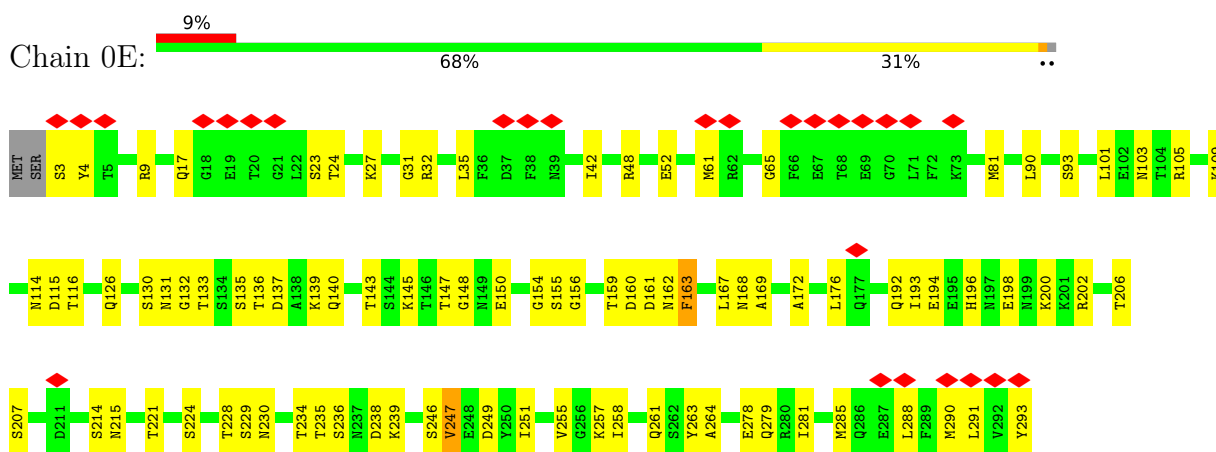
• Molecule 2: Proximal tail tube connector protein



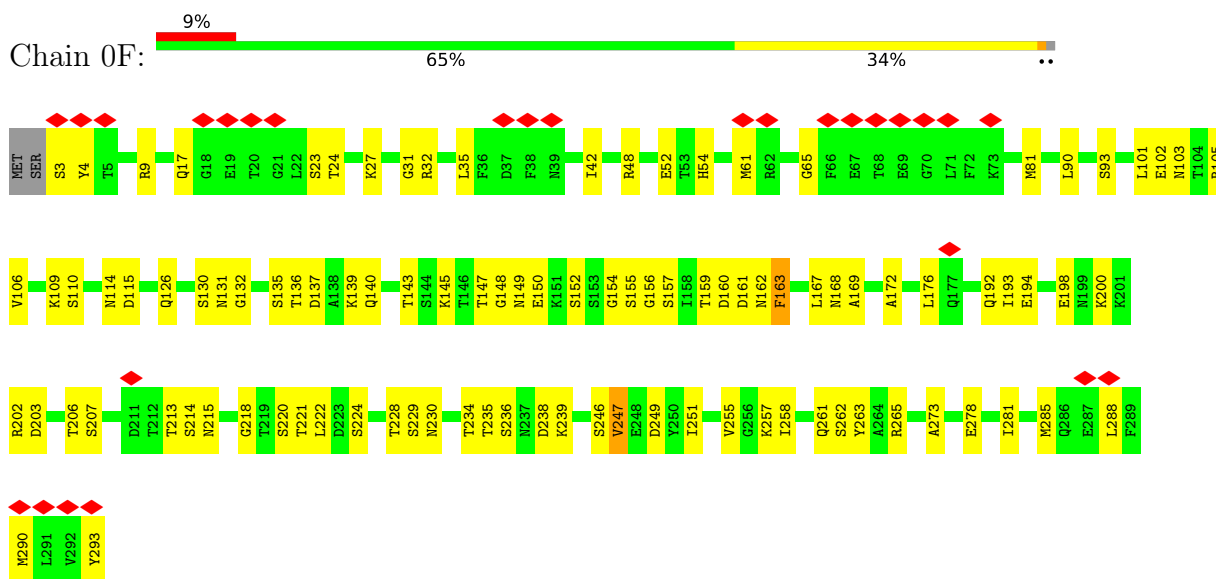
• Molecule 2: Proximal tail tube connector protein



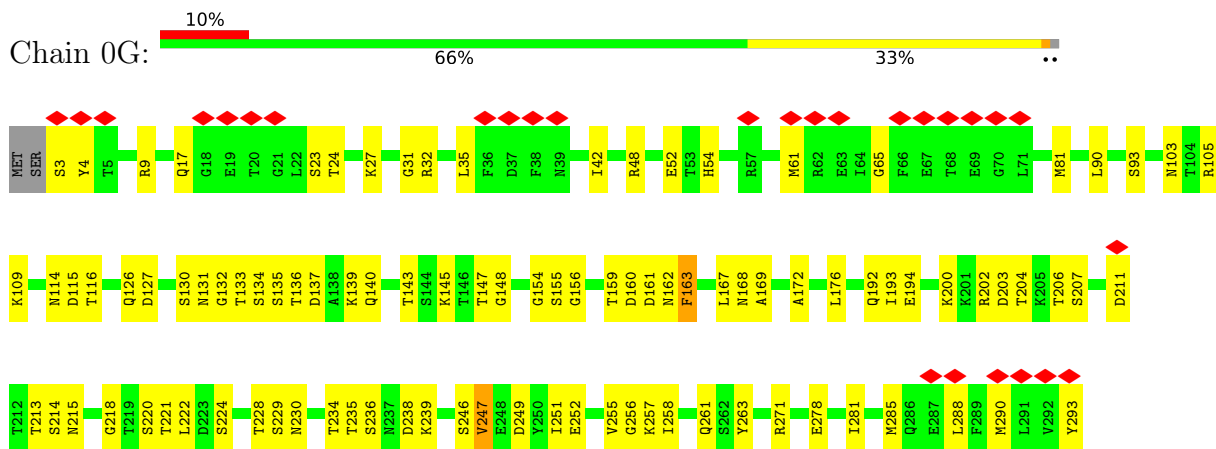
• Molecule 2: Proximal tail tube connector protein



• Molecule 2: Proximal tail tube connector protein

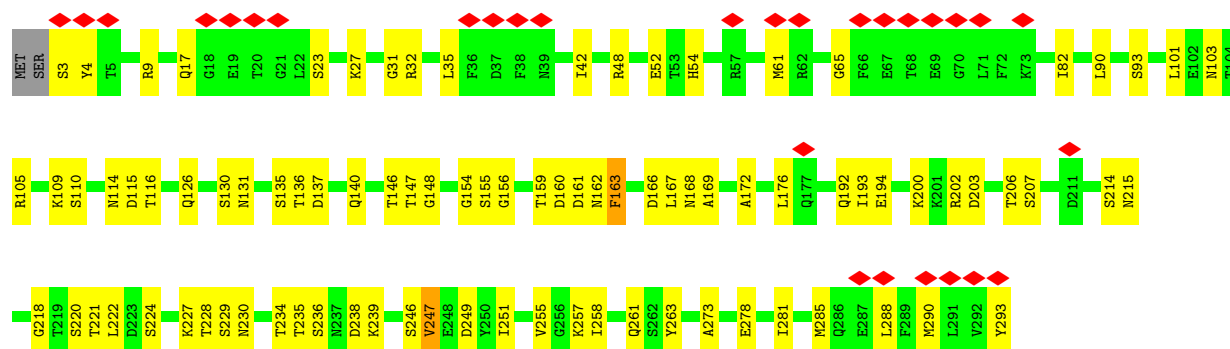


• Molecule 2: Proximal tail tube connector protein

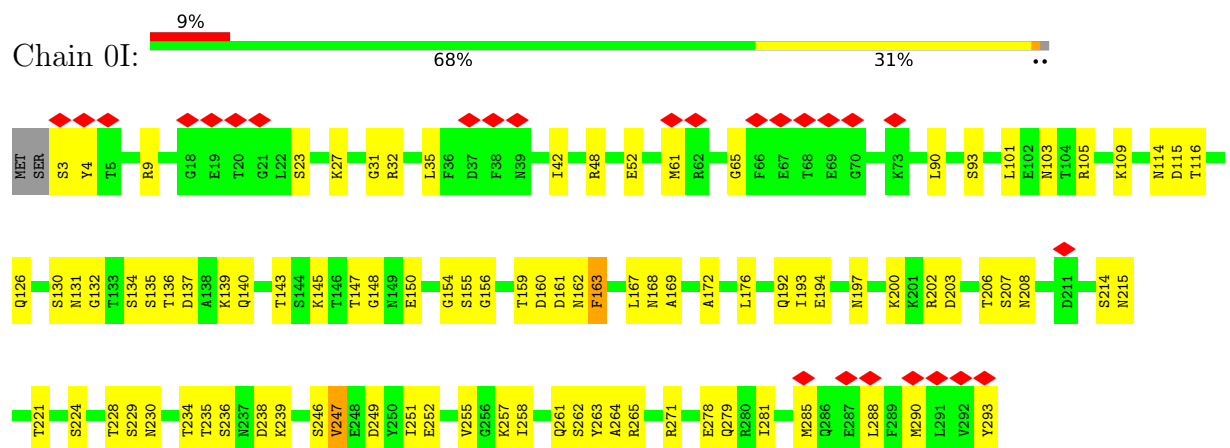


• Molecule 2: Proximal tail tube connector protein

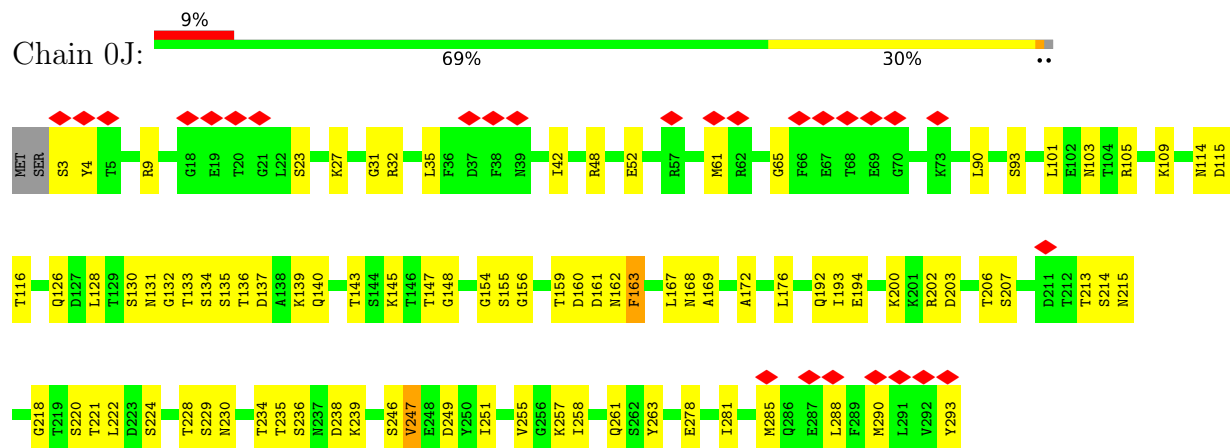




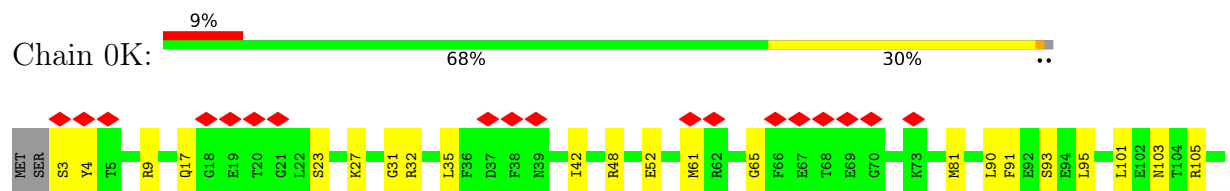
- Molecule 2: Proximal tail tube connector protein

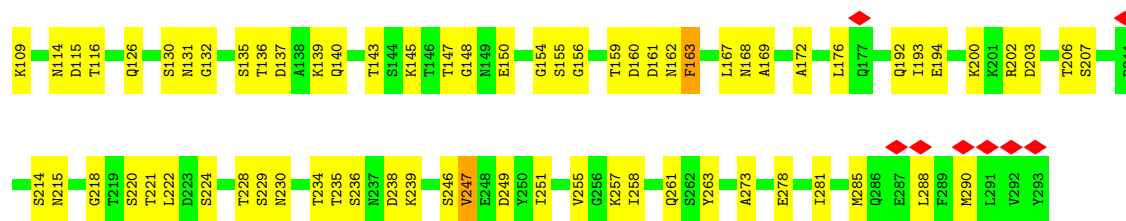


- Molecule 2: Proximal tail tube connector protein

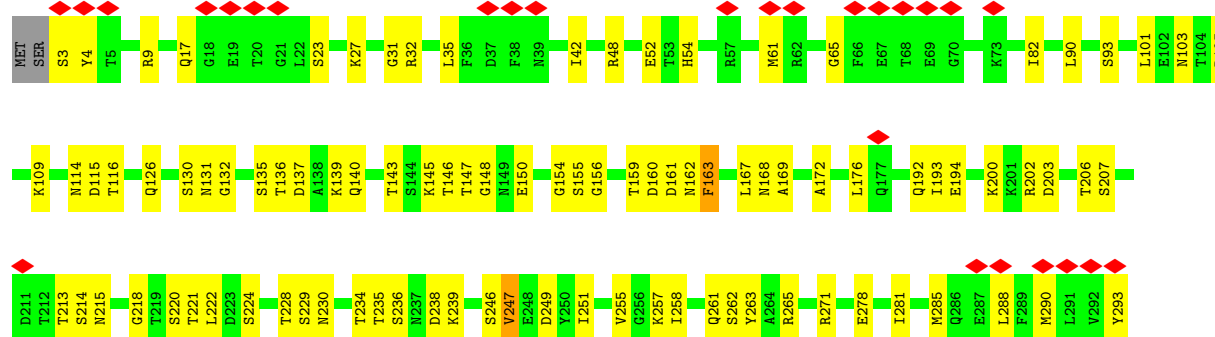


- Molecule 2: Proximal tail tube connector protein

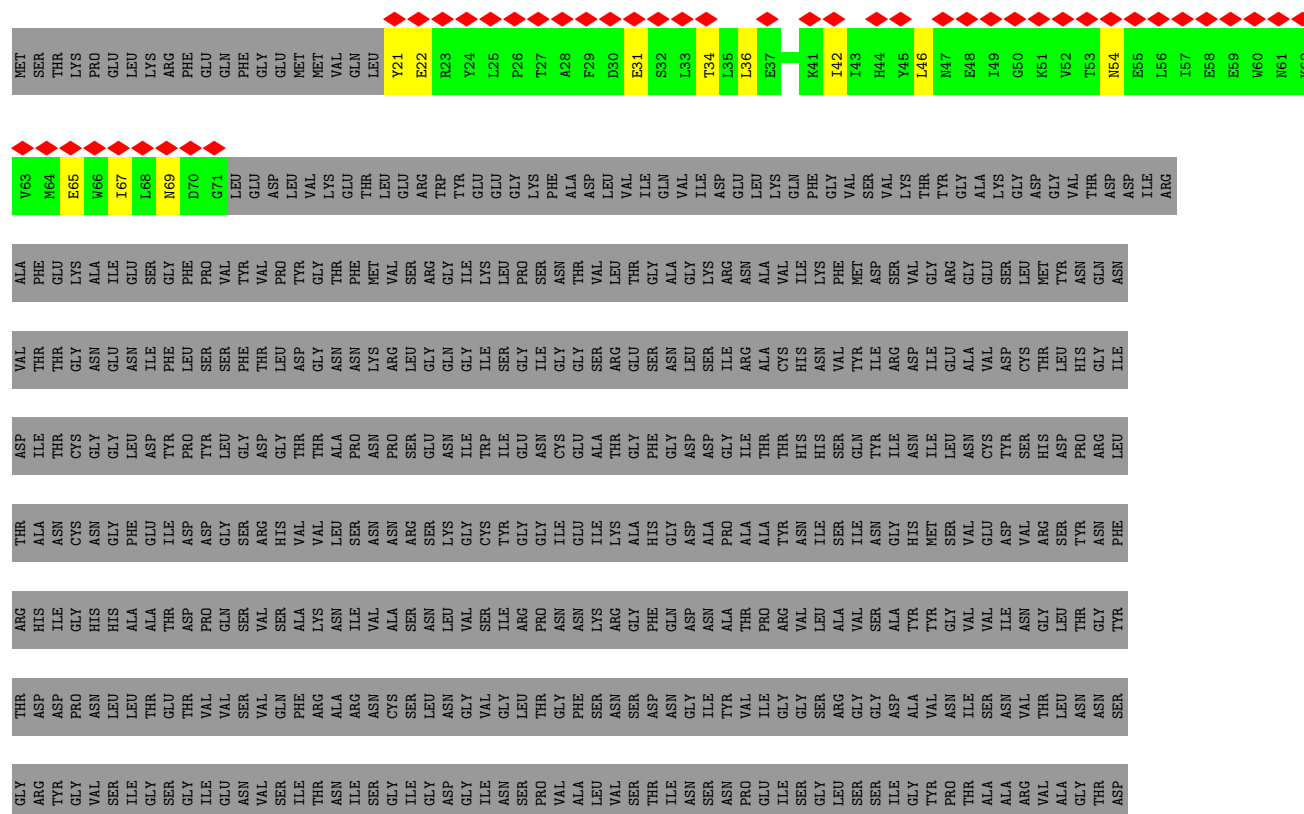


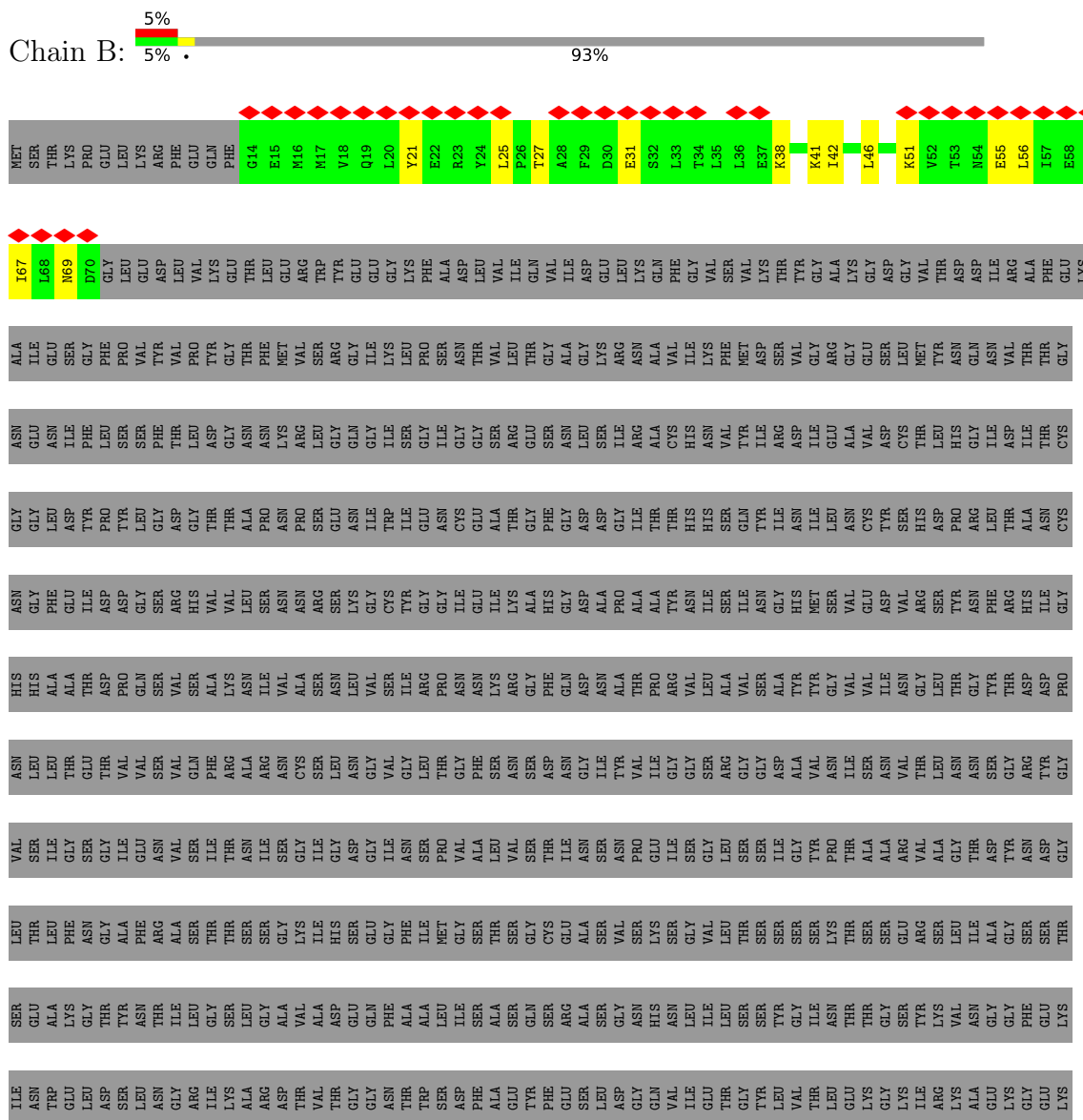


• Molecule 2: Proximal tail tube connector protein



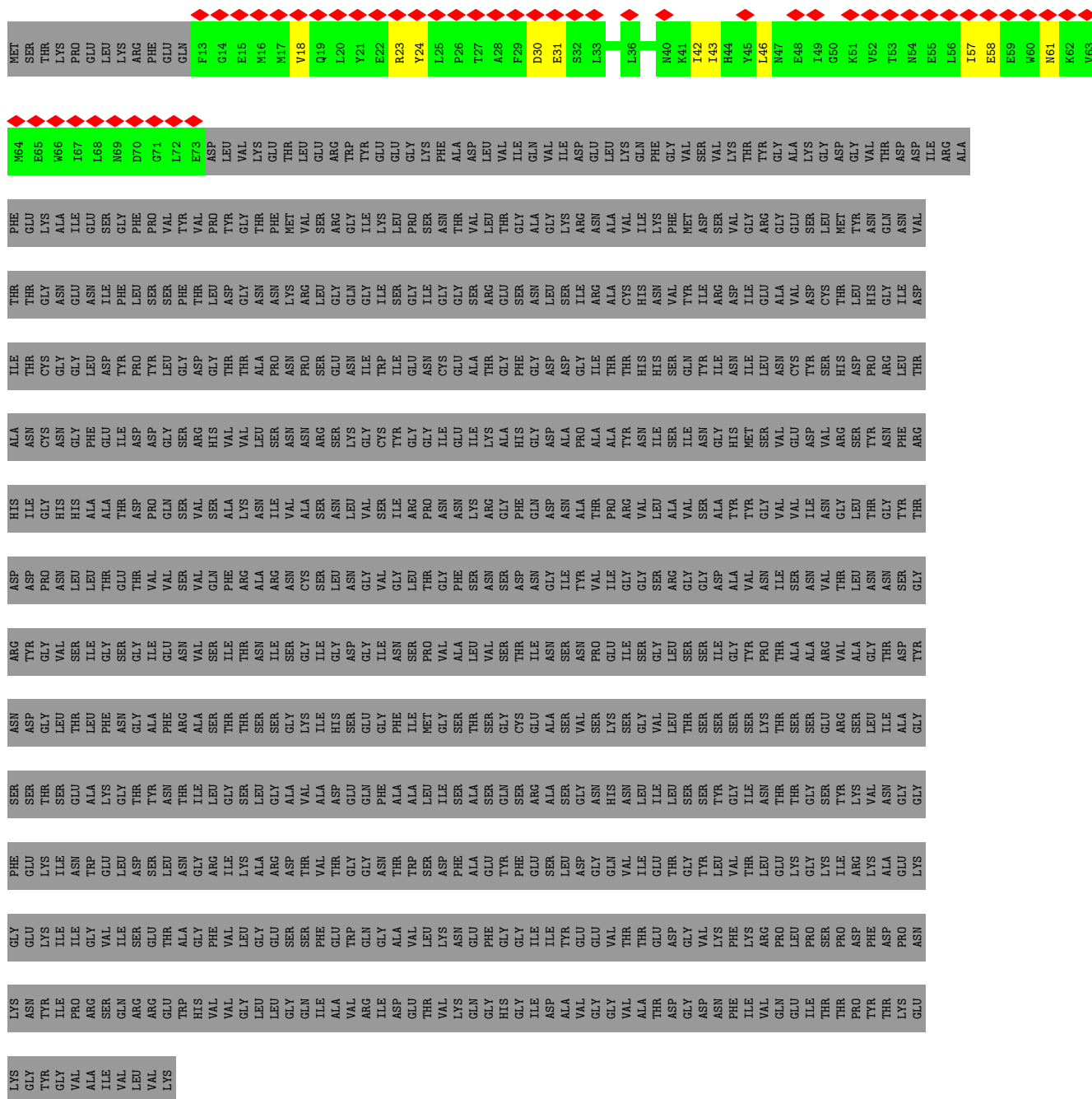
• Molecule 3: Pre-neck appendage protein



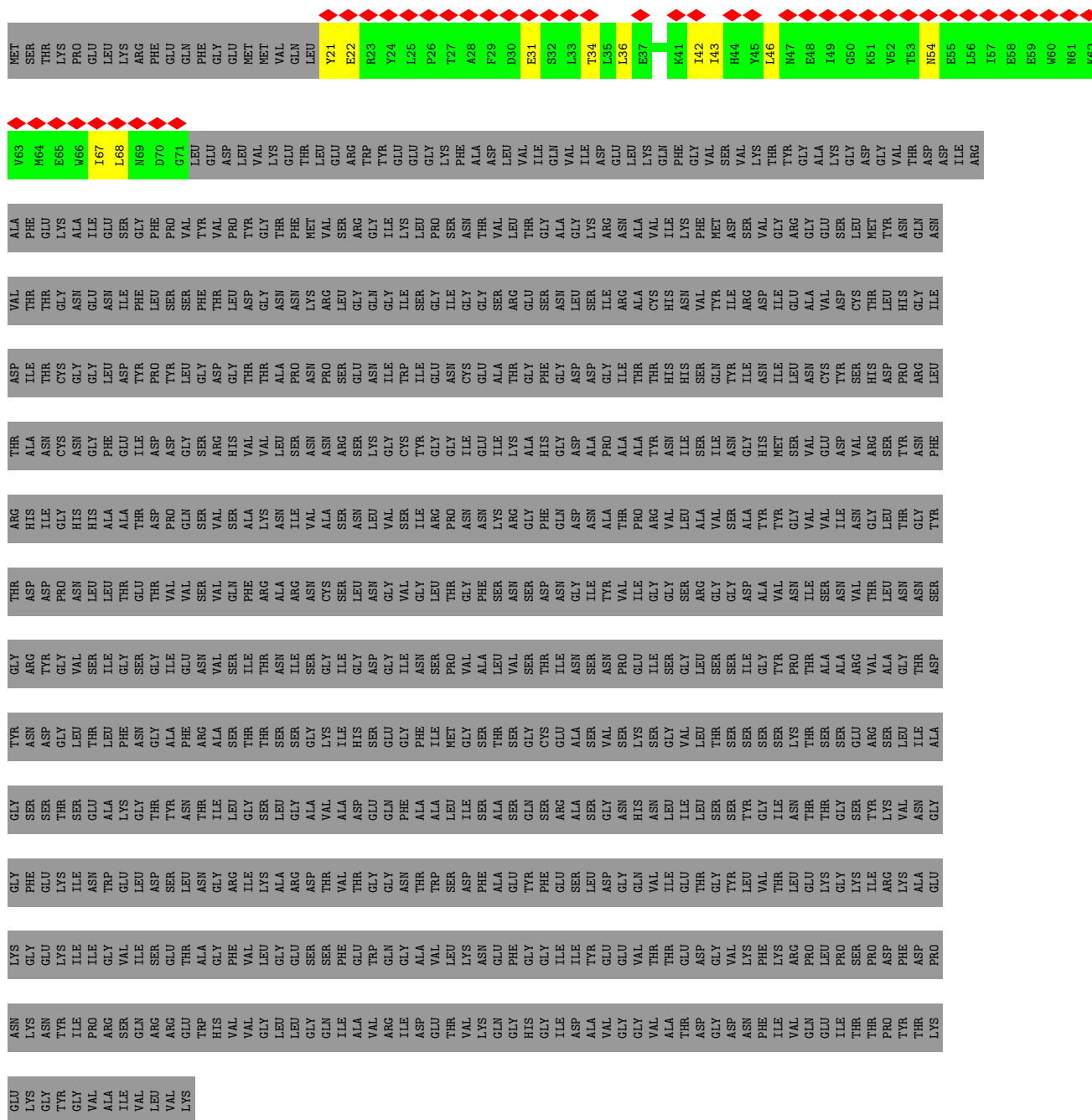


GLY
VAL
ALA
ILE
VAL
LEU
VAL
LYS

Chain C: 6% 6% 93%

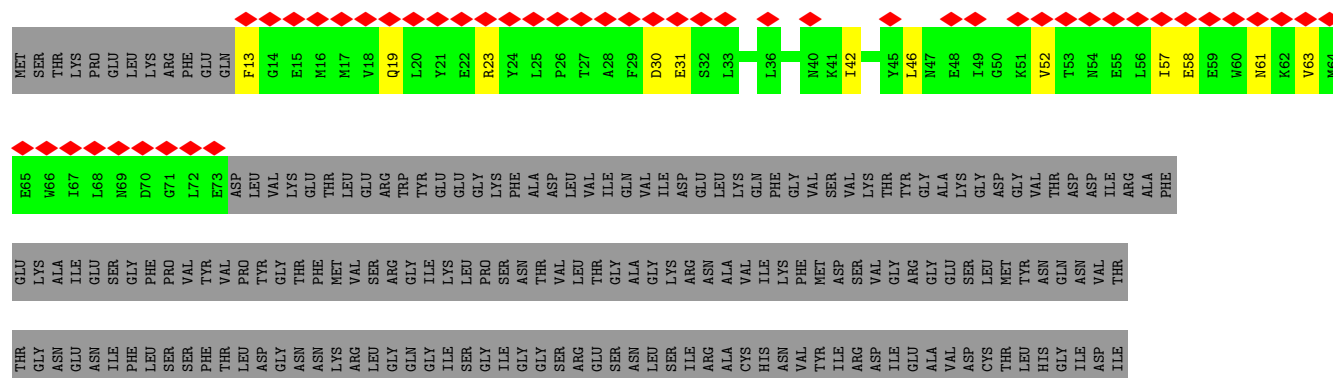


Chain D: 5% 5% 94%



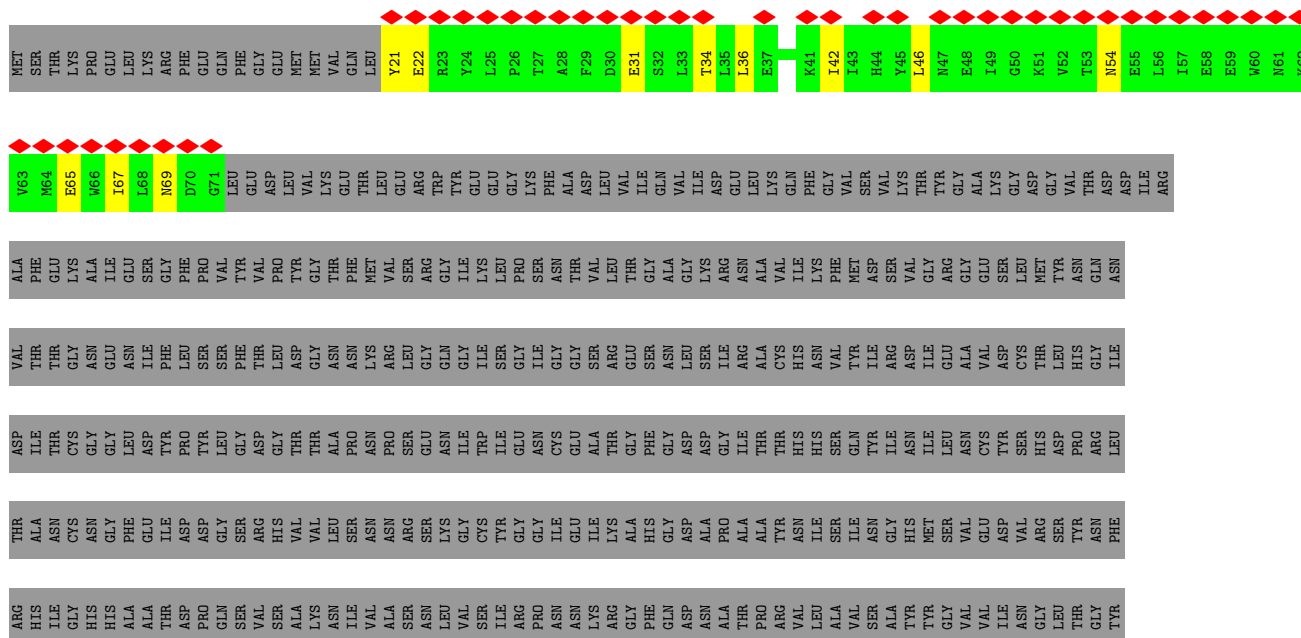
Chain E: 5% 5% 93%





[illegible]

- Molecule 3: Pre-neck appendage protein



- Molecule 3: Pre-neck appendage protein



GLU	LYS	GLY	THR	SER	ASP	TYR	ASP	THR	ASN	THR	THR	GLU	GLY	MET
LYS	ILE	LEU	SER	THR	GLY	VAL	ASN	GLY	HIS	GLY	ASN	GLY	ALA	SER
ILE	ASN	THR	GLU	GLU	THR	ILE	SER	LEU	HIS	GLY	GLY	ILE	ILE	THR
GLY	TRP	ALA	GLY	ALA	THR	ILE	LEU	ALA	ALA	PHE	LEU	ASP	GLU	PRO
VAL	GLU	LYS	GLY	GLY	PHE	SER	ASN	THR	LYS	ILE	THR	SER	GLY	GLU
ILE	LEU	GLY	GLY	THR	GLY	SER	ASN	THR	THR	ILE	ASP	PHE	LEU	LEU
SER	ASP	THR	TYR	THR	GLY	GLY	THR	ASP	ASP	PRO	LEU	PHE	LYS	LYS
GLU	SER	THR	ASN	ASN	PHE	GLU	LEU	VAL	GLN	TYR	PRO	ARG	ARG	ARG
ALA	ALA	THR	THR	THR	ALA	GLU	VAL	VAL	GLN	SER	VAL	VAL	THR	GLN
GLY	GLY	GLY	ILE	ILE	ALA	VAL	VAL	VAL	VAL	HIS	THR	THR	VAL	F13
PHE	ARG	THR	GLY	GLY	SER	ILE	PHE	ARG	LYS	VAL	THR	ASP	THR	G14
VAL	ILE	THR	SER	SER	THR	THR	THR	ARG	LYS	VAL	THR	THR	GLY	E15
LYS	LYS	THR	LEU	LEU	THR	THR	THR	ASN	ASN	ALA	THR	GLY	LYS	M16
ARG	ALA	GLY	SER	GLY	ARG	ILE	ARG	ILE	SER	PRO	PHE	THR	THR	M17
VAL	ASP	THR	VAL	VAL	CYS	ILE	CYS	ALA	ASN	PRO	ASN	VAL	LEU	V18
PHE	PHE	ALA	ALA	ILE	SER	ILE	SER	SER	ARG	GLY	LEU	SER	ARG	Q19
GLU	GLU	THR	ASP	ASP	HIS	GLY	LEU	ASN	SER	GLU	TRP	TRP	ARG	L20
TRP	GLY	TRP	GLU	GLU	SER	GLY	ASN	LYS	LYS	ASN	GLY	TYR	TYR	Y21
GLN	GLY	GLY	GLN	PHE	GLY	ILE	VAL	GLY	ILE	ILE	GLY	GLU	GLU	E22
ALA	ALA	THR	ALA	ALA	PHE	ALA	THR	ASN	TYR	ILE	GLY	PRO	GLY	R23
VAL	TRP	ALA	THR	ALA	ILE	SER	LEU	ARG	GLY	GLY	ASN	SER	LYS	Y24
SER	ASP	ILE	ILE	ILE	GLY	VAL	THR	PRO	ASN	ILE	GLY	ASN	ALA	L25
LYS	LYS	ASP	ILE	ILE	GLY	VAL	GLY	GLY	ASN	CYS	GLY	THR	THR	P26
ASN	ASN	PHE	SER	SER	PHE	ALA	SER	ASN	ILE	ALA	GLY	VAL	VAL	LEU
GLU	GLU	THR	THR	THR	THR	GLY	GLY	GLY	ALA	GLY	GLU	THR	THR	VAL
ILE	ILE	SER	THR	THR	ASN	ILE	PHE	PHE	HIS	HIS	GLY	ILE	ILE	A28
ILE	ILE	GLU	ARG	ALA	GLY	ASN	GLY	GLY	ASN	ASN	GLN	ALA	VAL	F29
ILE	TYR	LEU	SER	SER	ILE	ASN	ASP	ASP	ASN	ASP	GLY	GLY	VAL	D30
GLY	GLU	SER	GLY	GLY	VAL	ASN	ASN	ASN	ALA	SER	LYS	LYS	ILE	E31
GLU	GLU	ASP	GLY	GLY	THR	ASN	TYR	ILE	ALA	GLY	ASN	GLU	ASP	S32
VAL	VAL	GLN	ASN	HIS	LYS	ILE	PRO	ALA	ALA	THR	ALA	LEU	LEU	L33
THR	THR	VAL	ASN	ASN	SER	ILE	ARG	TYR	TYR	THR	CYS	VAL	LYS	G36
THR	ILE	SER	LEU	LEU	GLY	SER	VAL	VAL	ASN	HIS	HIS	ILE	GLN	E37
GLU	GLU	THR	ILE	ILE	VAL	GLY	LEU	VAL	ILE	HIS	ASN	ILE	PHE	L36
ASP	THR	LEU	LEU	ARG	THR	LEU	ALA	ALA	ILE	HIS	ASN	PHE	GLY	E37
GLY	GLY	THR	GLY	GLY	GLY	VAL	VAL	VAL	ILE	GLN	VAL	PHE	VAL	G37
VAL	VAL	SER	SER	SER	THR	SER	GLY	VAL	ILE	GLN	ASN	MET	SER	M40
PHE	PHE	GLY	SER	GLY	ALA	ILE	ALA	ALA	GLY	ASN	ASP	VAL	VAL	K41
LYS	LYS	THR	SER	ILE	VAL	TYR	THR	TYR	MET	ILE	ASP	GLY	THR	I42
PRO	ARG	THR	THR	PRO	ASN	PRO	ASN	ASN	SER	LEU	ARG	TYR	TYR	L46
GLU	LEU	THR	THR	THR	THR	THR	THR	THR	SER	LEU	GLU	GLY	GLY	M47
LYS	LYS	THR	THR	THR	ILE	VAL	VAL	VAL	VAL	ASN	ALA	GLY	ALA	E48
PRO	GLU	LYS	THR	ALA	SER	ALA	GLY	GLU	CYS	TYR	ASP	SER	LYS	I49
PRO	GLY	PRO	GLY	SER	ASN	ILE	ASN	ASP	TYR	ASN	VAL	LEU	CYS	G50
SER	LYS	PRO	SER	GLU	ARG	VAL	ASN	VAL	CYS	HIS	THR	MET	GLY	K51
PRO	ILE	THR	THR	THR	THR	GLY	GLY	GLY	ASP	ASP	LEU	TYR	VAL	V52
ASP	ARG	ASP	LYS	SER	LEU	ALA	SER	THR	HIS	THR	HIS	VAL	VAL	E58
PHE	PHE	VAL	VAL	VAL	ASN	THR	TYR	TYR	ARG	ARG	GLY	GLN	THR	E59
ASP	ASP	ALA	ASN	ASN	ASN	GLY	GLY	ASN	THR	THR	GLY	ASN	ASP	W60
PRO	PRO	GLU	GLY	GLY	GLY	THR	PHE	PHE	ILE	ILE	ILE	ASN	ASP	N61
ASN	LYS	LYS	GLY	GLY	THR	THR	THR	THR	THR	THR	ASP	VAL	VAL	K62
LYS	LYS	GLY	PHE	PHE	ARG	GLY	THR	THR	ALA	ALA	ARG	ARG	ALA	V63
														M64

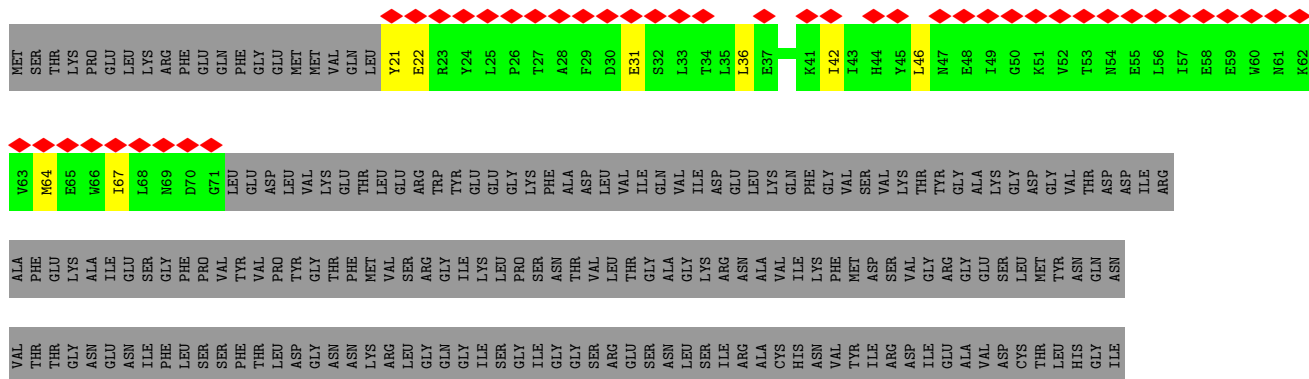
[illegible]

- Molecule 3: Pre-neck appendage protein

[illegible]

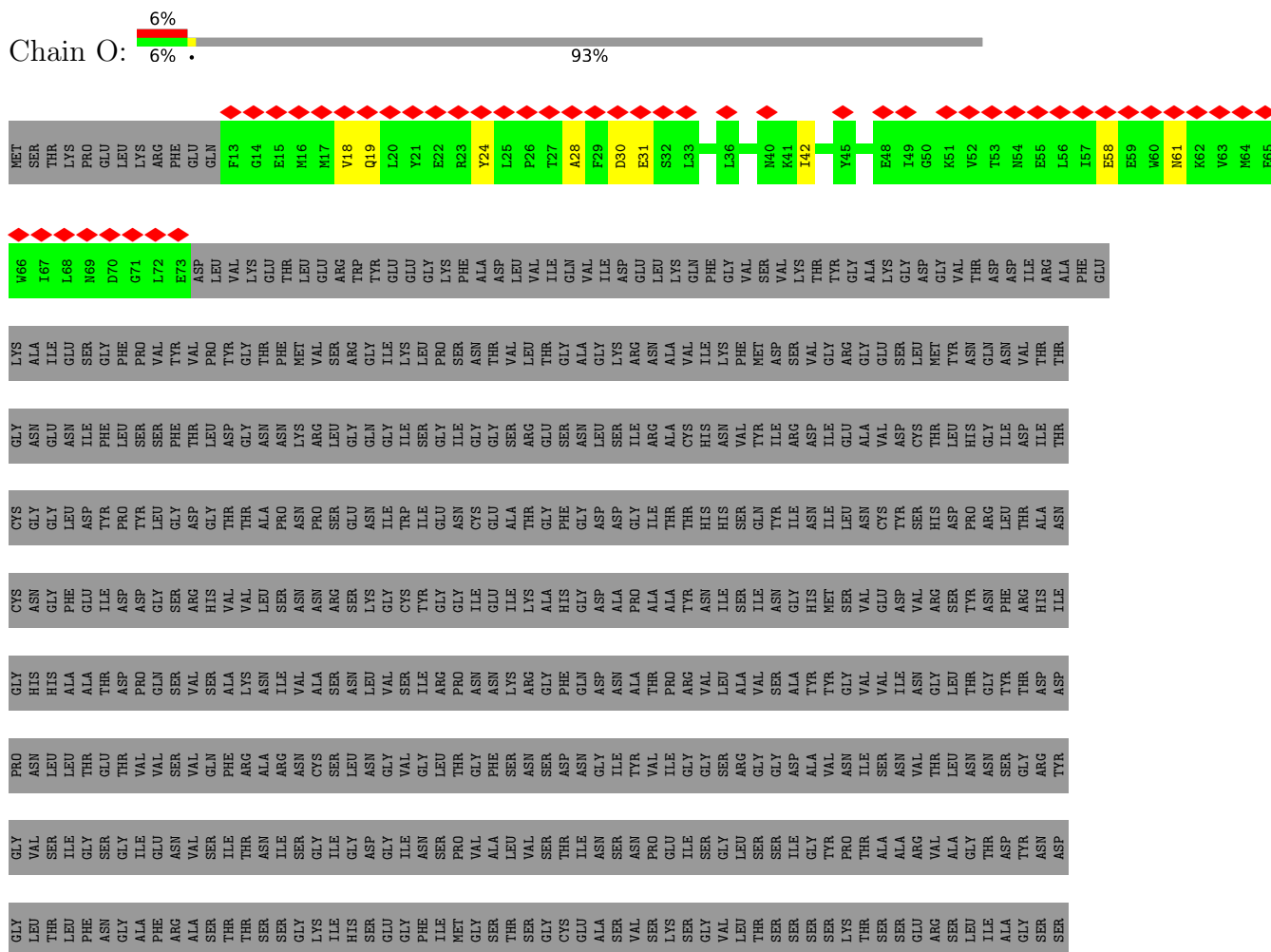
- Molecule 3: Pre-neck appendage protein

- Molecule 3: Pre-neck appendage protein

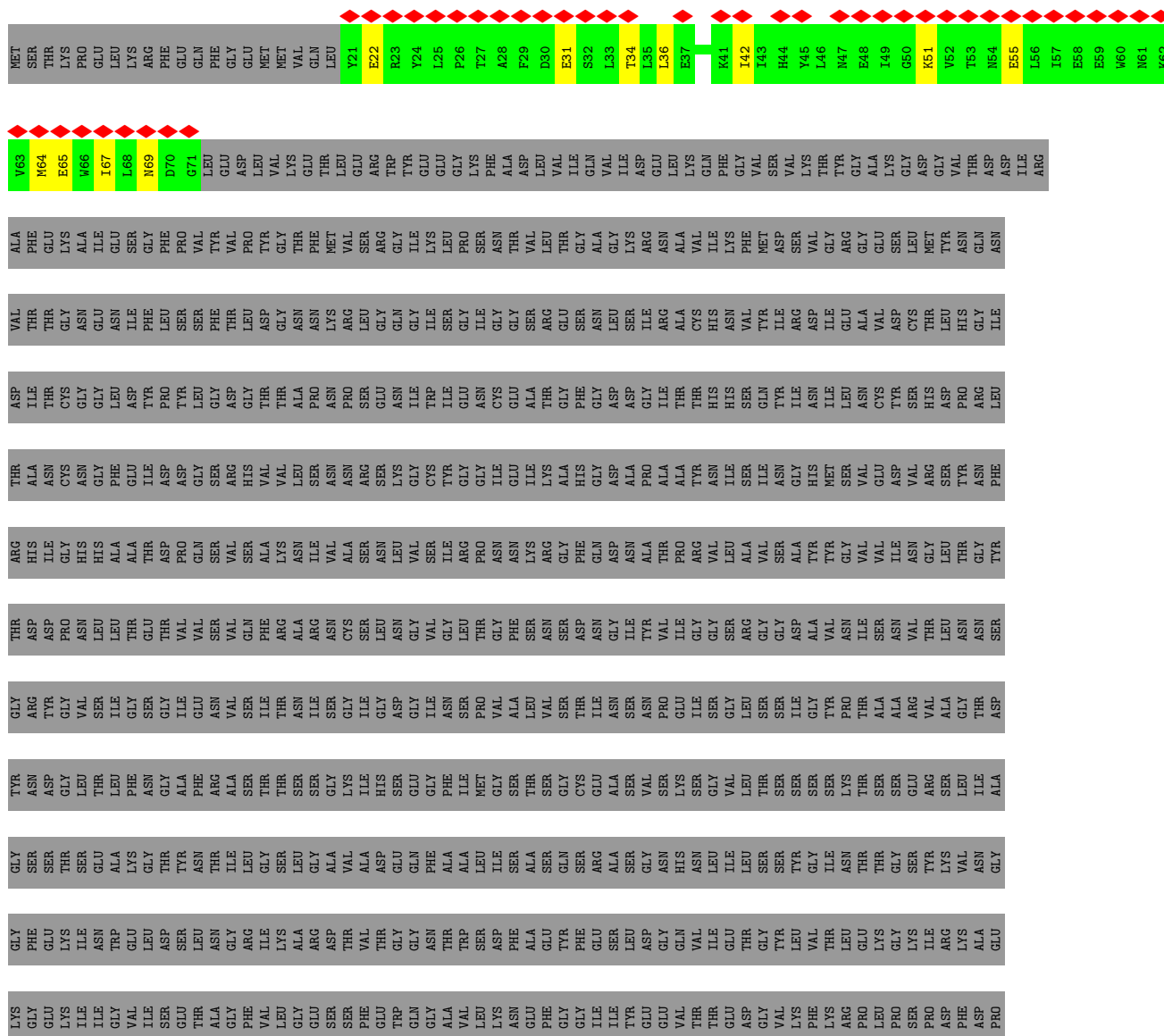


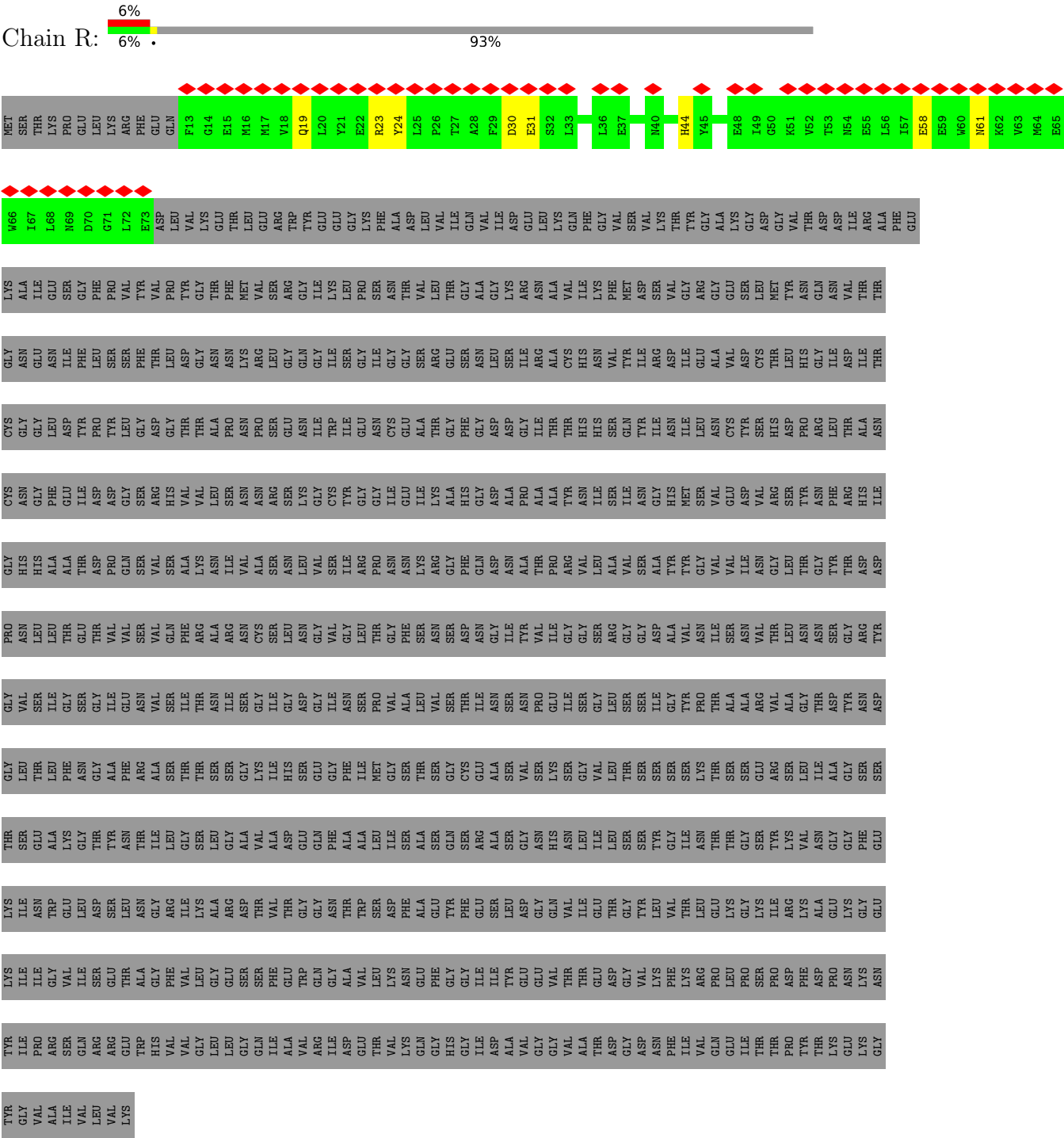
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ILE	SER	VAL	GLU	LYS	PHE	GLY	LEU
VAL	GLN	ILE	LEU	GLY	ASN	SER	GLU
VAL	ARG	SER	ASP	THR	GLY	ILE	VAL
LYS	GLU	THR	LEU	ASN	PHE	GLU	VAL
	ALA	THR	ALA	THR	ASN	ASN	SER
	TRP	ALA	GLY	ILE	ARG	VAL	SER
	HIS	PHE	GLY	ILE	ALA	VAL	GLN
	VAL	VAL	ILE	GLY	SER	ILE	PHE
	GLY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

- Molecule 3: Pre-neck appendage protein

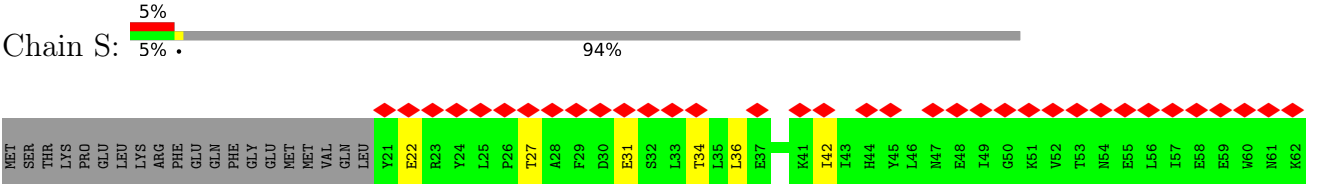


- Molecule 3: Pre-neck appendage protein

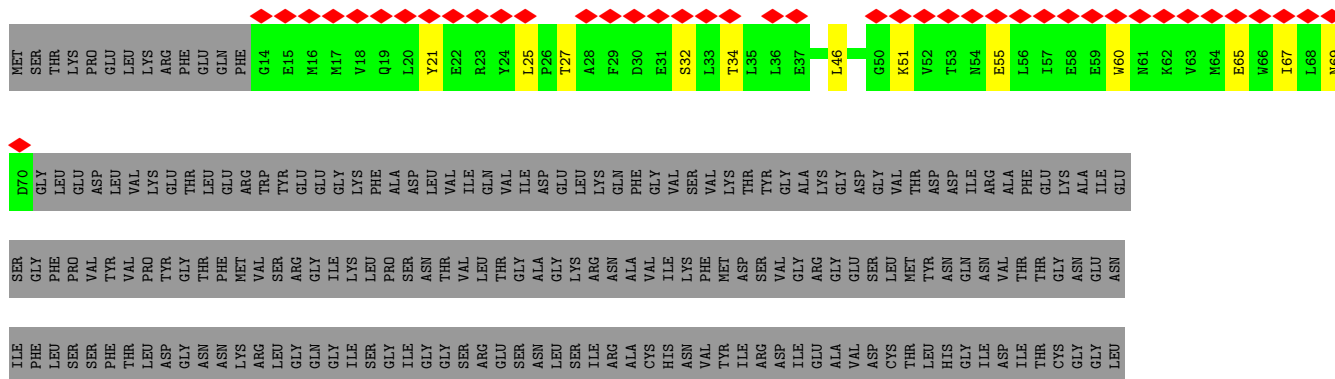




● Molecule 3: Pre-neck appendage protein

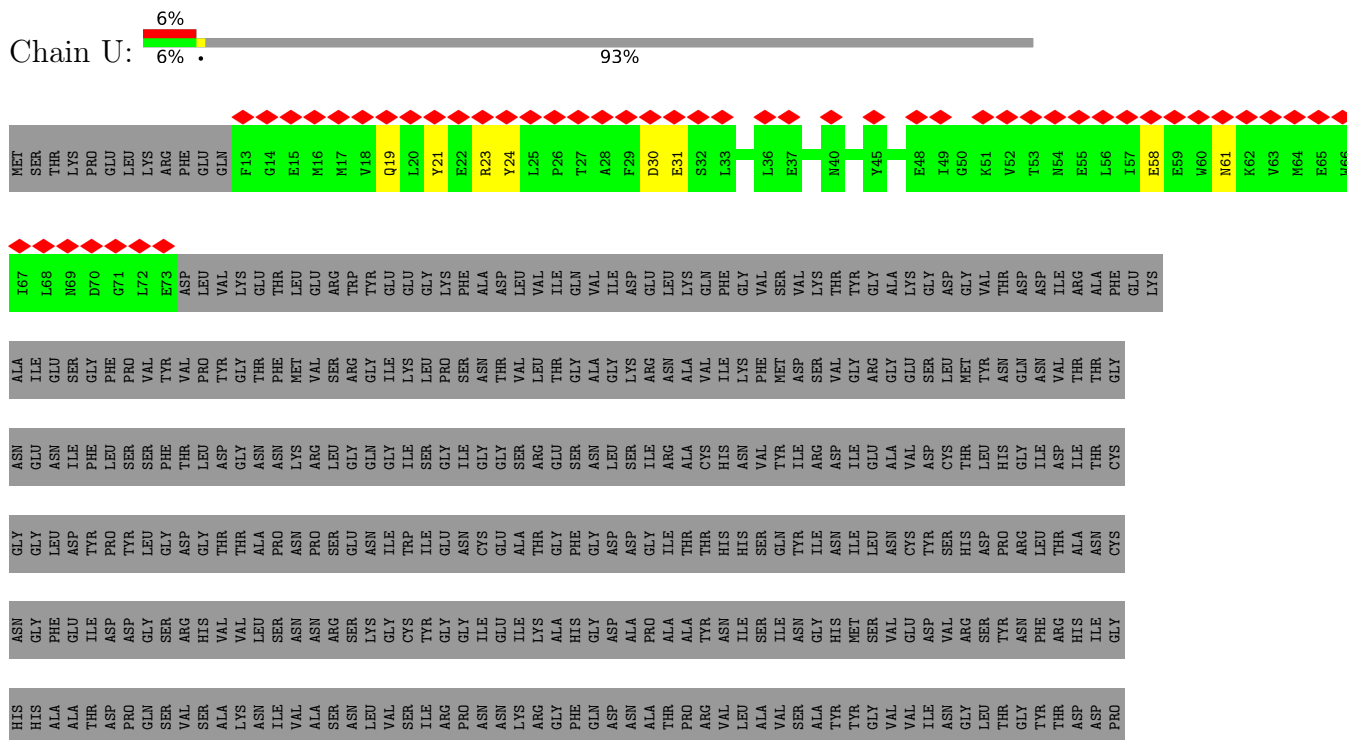


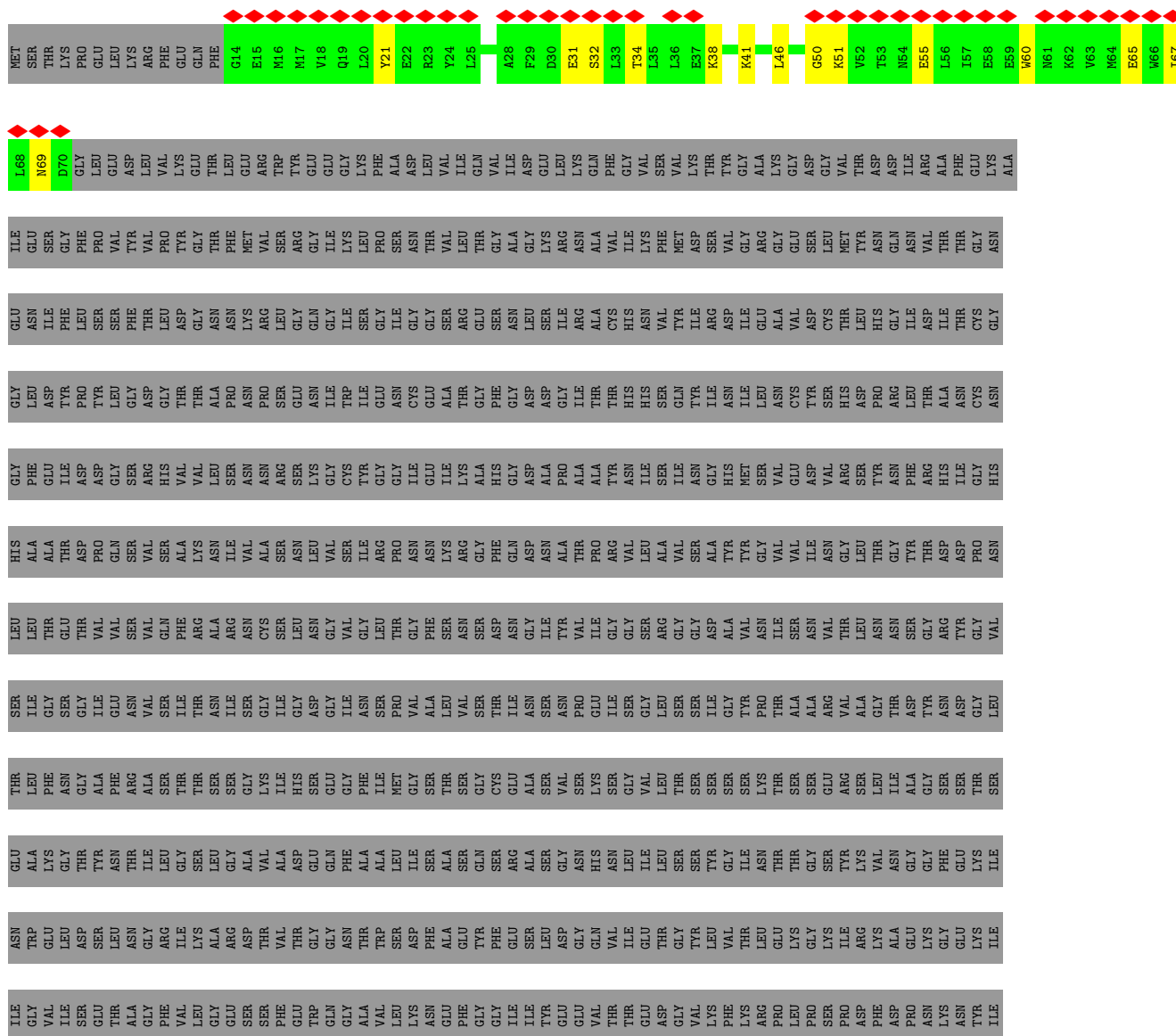
- Molecule 3: Pre-neck appendage protein



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

- Molecule 3: Pre-neck appendage protein



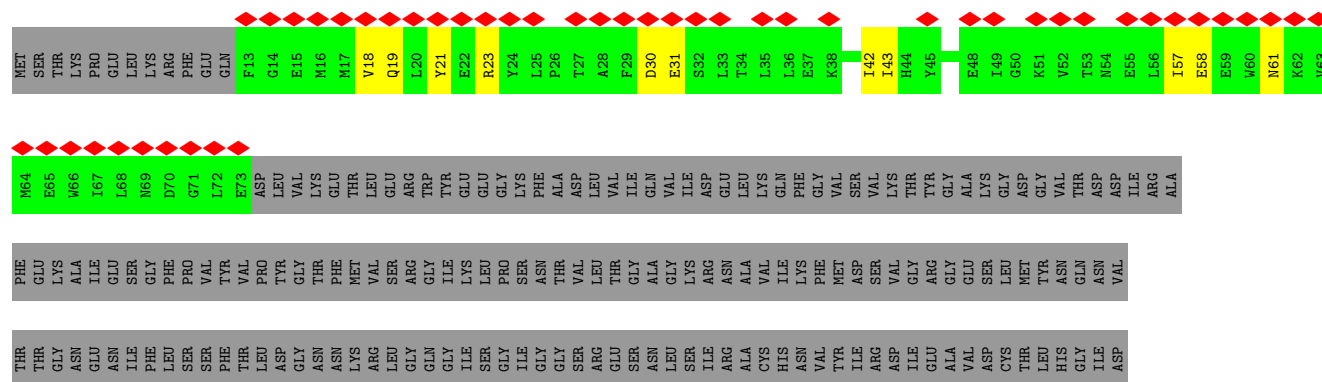


[illegible]

- Molecule 3: Pre-neck appendage protein

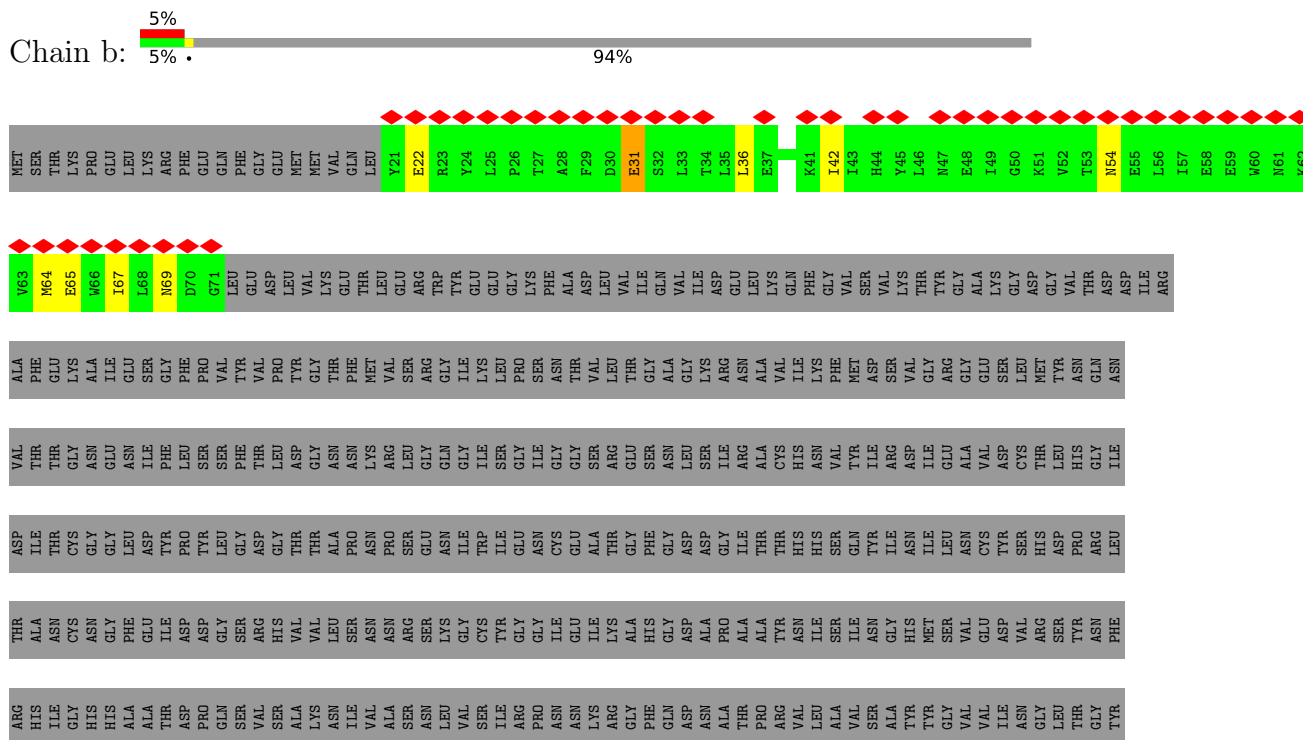
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- Molecule 3: Pre-neck appendage protein



[illegible]

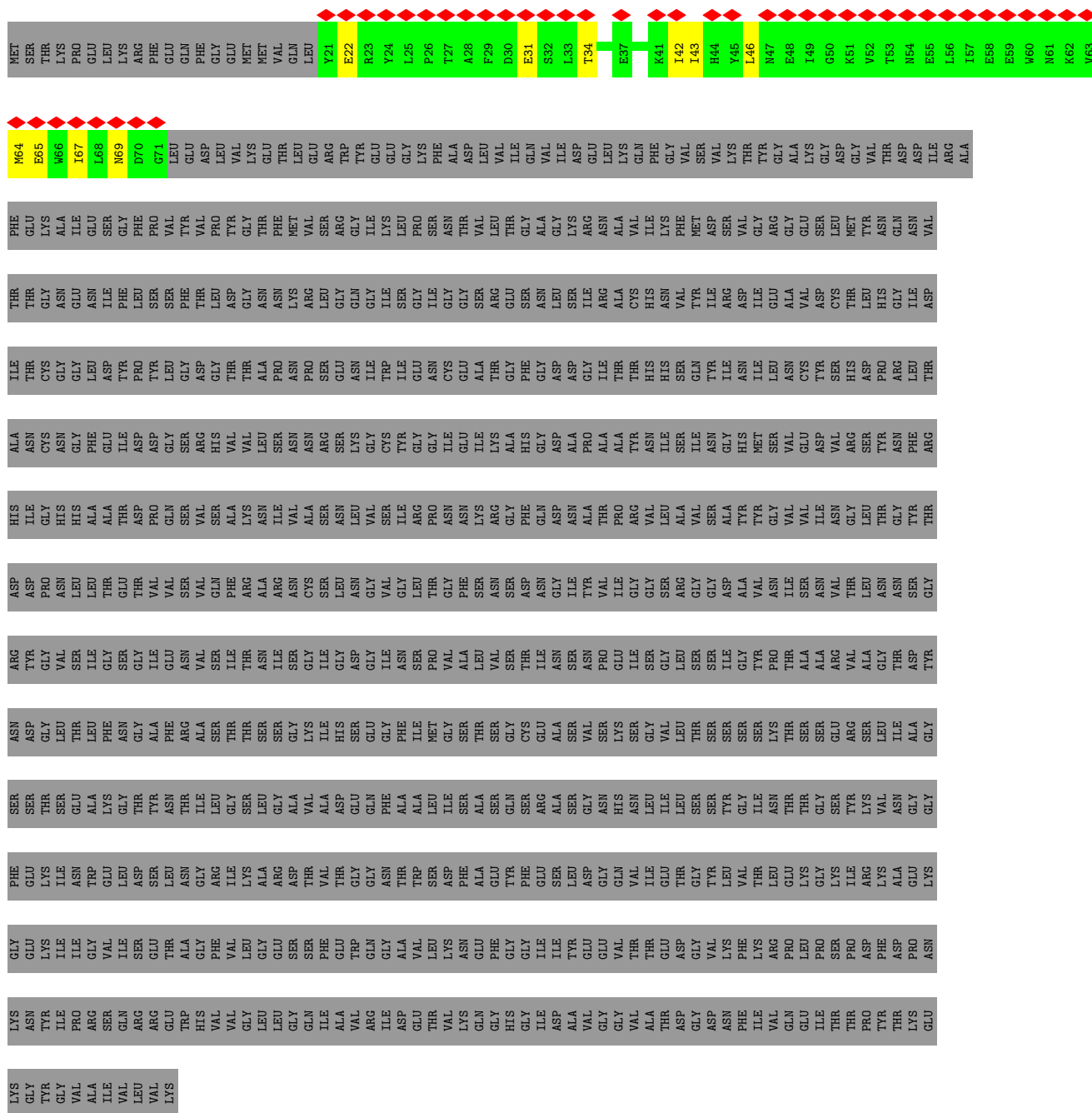
- Molecule 3: Pre-neck appendage protein



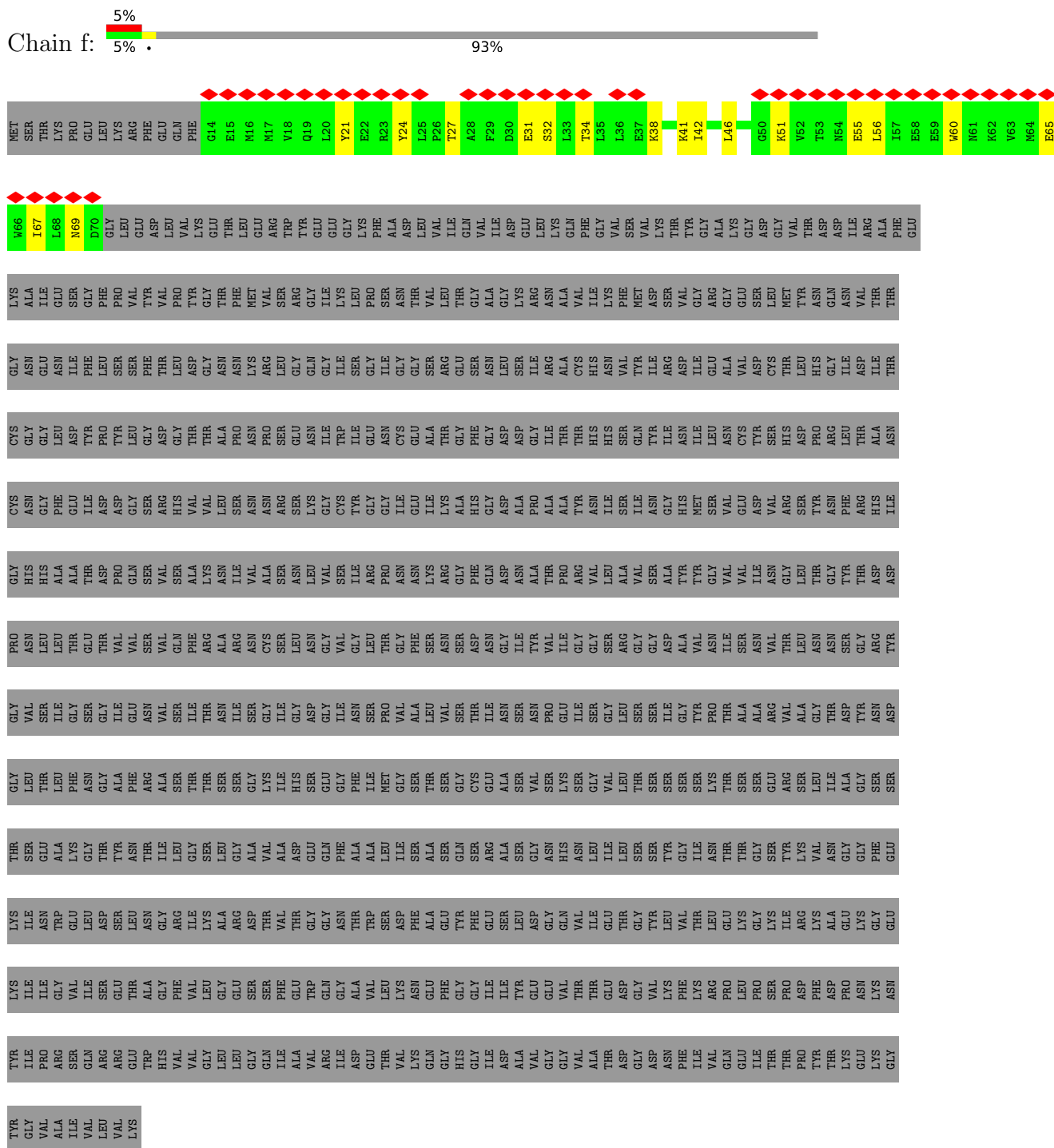
- Molecule 3: Pre-neck appendage protein

[illegible]

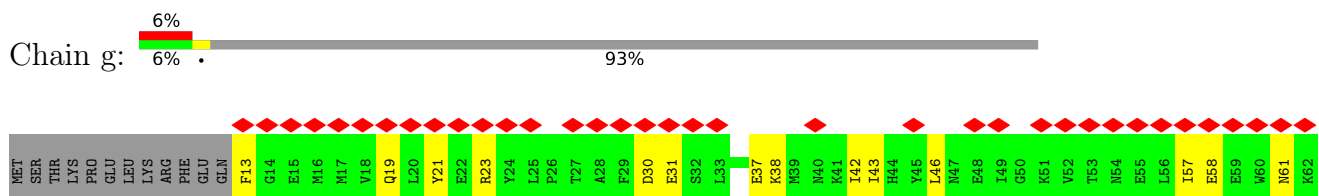
- Molecule 3: Pre-neck appendage protein



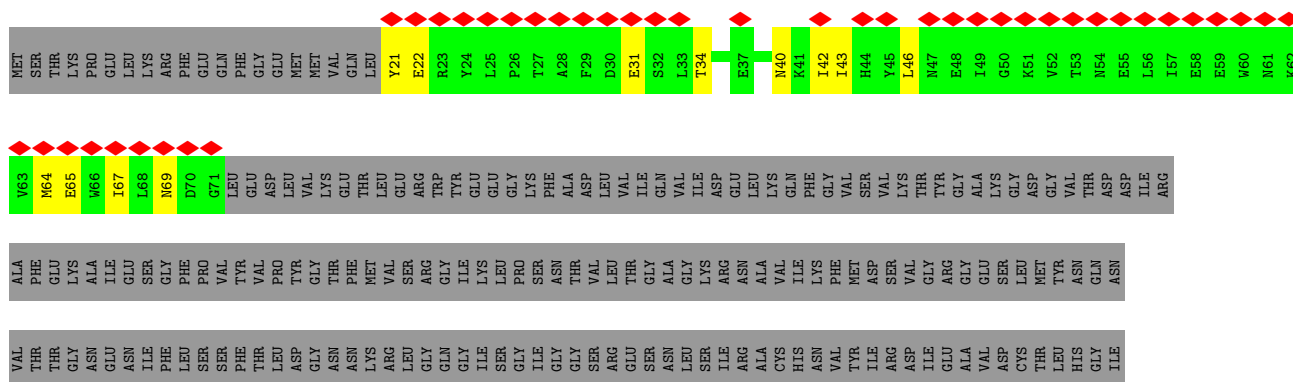
- Molecule 3: Pre-neck appendage protein



- Molecule 3: Pre-neck appendage protein

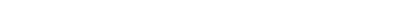


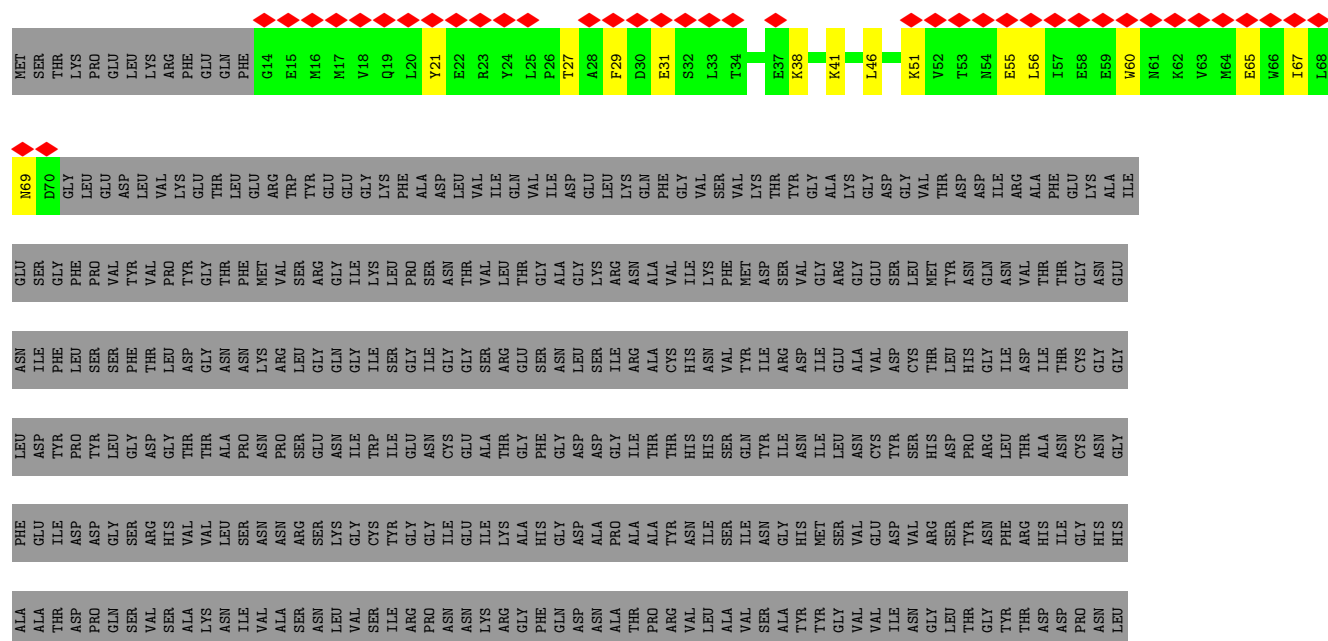
- Molecule 3: Pre-neck appendage protein



[illegible]

- Molecule 3: Pre-neck appendage protein

Chain i: 





[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31478	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	22.011	Depositor
Minimum map value	-4.860	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.233	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	734.4, 734.4, 734.4	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.36, 1.36, 1.36	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	0a	0.36	0/2288	0.52	0/3103
1	0b	0.36	0/2288	0.52	0/3103
1	0c	0.36	0/2288	0.52	0/3103
1	0d	0.36	0/2288	0.53	0/3103
1	0e	0.36	0/2288	0.53	0/3103
1	0f	0.36	0/2288	0.53	0/3103
1	0g	0.36	0/2288	0.53	0/3103
1	0h	0.36	0/2288	0.53	0/3103
1	0i	0.36	0/2288	0.52	0/3103
1	0j	0.36	0/2288	0.53	0/3103
1	0k	0.36	0/2288	0.52	0/3103
1	0l	0.36	0/2288	0.52	0/3103
2	0A	0.62	0/2335	0.75	0/3149
2	0B	0.62	0/2335	0.75	0/3149
2	0C	0.62	0/2335	0.75	0/3149
2	0D	0.62	0/2335	0.75	0/3149
2	0E	0.62	0/2335	0.75	0/3149
2	0F	0.62	0/2335	0.75	0/3149
2	0G	0.62	0/2335	0.75	0/3149
2	0H	0.62	0/2335	0.75	0/3149
2	0I	0.62	0/2335	0.75	0/3149
2	0J	0.62	0/2335	0.75	0/3149
2	0K	0.62	0/2335	0.75	0/3149
2	0L	0.62	0/2335	0.75	0/3149
3	A	0.34	0/442	0.66	0/598
3	B	0.41	0/491	0.59	0/663
3	C	0.36	0/524	0.64	0/707
3	D	0.34	0/442	0.65	0/598
3	E	0.39	0/491	0.60	0/663
3	F	0.36	0/524	0.64	0/707
3	G	0.34	0/442	0.65	0/598
3	H	0.40	0/491	0.60	0/663
3	I	0.36	0/524	0.64	0/707
3	J	0.33	0/442	0.66	0/598

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	K	0.40	0/491	0.60	0/663
3	L	0.36	0/524	0.64	0/707
3	M	0.32	0/442	0.65	0/598
3	N	0.38	0/491	0.57	0/663
3	O	0.36	0/524	0.64	0/707
3	P	0.31	0/442	0.66	0/598
3	Q	0.37	0/491	0.58	0/663
3	R	0.36	0/524	0.64	0/707
3	S	0.32	0/442	0.66	0/598
3	T	0.37	0/491	0.57	0/663
3	U	0.36	0/524	0.64	0/707
3	V	0.32	0/442	0.65	0/598
3	W	0.39	0/491	0.57	0/663
3	X	0.36	0/524	0.64	0/707
3	Y	0.33	0/442	0.65	0/598
3	Z	0.38	0/491	0.56	0/663
3	a	0.36	0/524	0.64	0/707
3	b	0.32	0/442	0.65	0/598
3	c	0.38	0/491	0.57	0/663
3	d	0.36	0/524	0.64	0/707
3	e	0.34	0/442	0.67	0/598
3	f	0.38	0/491	0.59	0/663
3	g	0.36	0/524	0.64	0/707
3	h	0.38	0/442	0.66	0/598
3	i	0.41	0/491	0.59	0/663
3	j	0.36	0/524	0.64	0/707
All	All	0.48	0/72960	0.64	0/98640

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
2	0A	0	3
2	0B	0	3
2	0C	0	3
2	0D	0	3
2	0E	0	3
2	0F	0	3
2	0G	0	3
2	0H	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	0I	0	3
2	0J	0	3
2	0K	0	3
2	0L	0	3
All	All	0	36

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	0A	163	PHE	Peptide
2	0A	172	ALA	Peptide
2	0A	176	LEU	Peptide
2	0B	163	PHE	Peptide
2	0B	172	ALA	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	0a	2240	0	2130	55	0
1	0b	2240	0	2130	61	0
1	0c	2240	0	2130	51	0
1	0d	2240	0	2130	53	0
1	0e	2240	0	2130	52	0
1	0f	2240	0	2130	65	0
1	0g	2240	0	2130	67	0
1	0h	2240	0	2130	55	0
1	0i	2240	0	2130	55	0
1	0j	2240	0	2130	51	0
1	0k	2240	0	2130	59	0
1	0l	2240	0	2130	52	0
2	0A	2300	0	2149	63	0
2	0B	2300	0	2149	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	0C	2300	0	2149	95	0
2	0D	2300	0	2149	83	0
2	0E	2300	0	2149	70	0
2	0F	2300	0	2149	83	0
2	0G	2300	0	2149	80	0
2	0H	2300	0	2149	73	0
2	0I	2300	0	2149	66	0
2	0J	2300	0	2149	66	0
2	0K	2300	0	2149	68	0
2	0L	2300	0	2149	69	0
3	A	433	0	425	11	0
3	B	482	0	477	15	0
3	C	514	0	506	11	0
3	D	433	0	425	11	0
3	E	482	0	477	13	0
3	F	514	0	506	12	0
3	G	433	0	425	11	0
3	H	482	0	477	13	0
3	I	514	0	506	13	0
3	J	433	0	425	10	0
3	K	482	0	477	13	0
3	L	514	0	506	13	0
3	M	433	0	425	9	0
3	N	482	0	477	12	0
3	O	514	0	506	8	0
3	P	433	0	425	10	0
3	Q	482	0	477	11	0
3	R	514	0	506	8	0
3	S	433	0	425	10	0
3	T	482	0	477	11	0
3	U	514	0	506	11	0
3	V	433	0	425	10	0
3	W	482	0	477	10	0
3	X	514	0	506	10	0
3	Y	433	0	425	9	0
3	Z	482	0	477	11	0
3	a	514	0	506	11	0
3	b	433	0	425	9	0
3	c	482	0	477	11	0
3	d	514	0	506	6	0
3	e	433	0	425	10	0
3	f	482	0	477	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	g	514	0	506	17	0
3	h	433	0	425	11	0
3	i	482	0	477	14	0
3	j	514	0	506	13	0
All	All	71628	0	68244	1455	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 10.

The worst 5 of 1455 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)
1:0h:17:ARG:HE	3:X:23:ARG:HB2	1.46	0.80
2:0H:160:ASP:HB2	2:0I:203:ASP:HB3	1.67	0.76
1:0k:17:ARG:HE	3:g:23:ARG:HB2	1.52	0.75
2:0B:132:GLY:HA3	2:0C:230:ASN:HA	1.68	0.74
1:0g:17:ARG:HH12	3:P:22:GLU:HB2	1.55	0.72

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	0a	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0b	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0c	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0d	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0e	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0f	276/309 (89%)	258 (94%)	18 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0g	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0h	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0i	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0j	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0k	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
1	0l	276/309 (89%)	258 (94%)	18 (6%)	0	100	100
2	0A	289/293 (99%)	248 (86%)	41 (14%)	0	100	100
2	0B	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0C	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0D	289/293 (99%)	248 (86%)	41 (14%)	0	100	100
2	0E	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0F	289/293 (99%)	248 (86%)	41 (14%)	0	100	100
2	0G	289/293 (99%)	248 (86%)	41 (14%)	0	100	100
2	0H	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0I	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0J	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
2	0K	289/293 (99%)	248 (86%)	41 (14%)	0	100	100
2	0L	289/293 (99%)	249 (86%)	40 (14%)	0	100	100
3	A	49/854 (6%)	44 (90%)	5 (10%)	0	100	100
3	B	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	C	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	D	49/854 (6%)	44 (90%)	5 (10%)	0	100	100
3	E	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	F	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	G	49/854 (6%)	43 (88%)	6 (12%)	0	100	100
3	H	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	I	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	J	49/854 (6%)	43 (88%)	5 (10%)	1 (2%)	6	32
3	K	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	L	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	M	49/854 (6%)	44 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	N	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	O	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	P	49/854 (6%)	43 (88%)	6 (12%)	0	100	100
3	Q	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	R	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	S	49/854 (6%)	43 (88%)	6 (12%)	0	100	100
3	T	55/854 (6%)	53 (96%)	2 (4%)	0	100	100
3	U	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	V	49/854 (6%)	44 (90%)	5 (10%)	0	100	100
3	W	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	X	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	Y	49/854 (6%)	43 (88%)	5 (10%)	1 (2%)	6	32
3	Z	55/854 (6%)	51 (93%)	4 (7%)	0	100	100
3	a	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	b	49/854 (6%)	44 (90%)	4 (8%)	1 (2%)	6	32
3	c	55/854 (6%)	53 (96%)	2 (4%)	0	100	100
3	d	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	e	49/854 (6%)	44 (90%)	5 (10%)	0	100	100
3	f	55/854 (6%)	51 (93%)	4 (7%)	0	100	100
3	g	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
3	h	49/854 (6%)	44 (90%)	5 (10%)	0	100	100
3	i	55/854 (6%)	52 (94%)	3 (6%)	0	100	100
3	j	59/854 (7%)	54 (92%)	5 (8%)	0	100	100
All	All	8736/37968 (23%)	7874 (90%)	859 (10%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	J	31	GLU
3	Y	31	GLU
3	b	31	GLU

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	0a	235/277 (85%)	235 (100%)	0	100	100
1	0b	235/277 (85%)	235 (100%)	0	100	100
1	0c	235/277 (85%)	235 (100%)	0	100	100
1	0d	235/277 (85%)	235 (100%)	0	100	100
1	0e	235/277 (85%)	235 (100%)	0	100	100
1	0f	235/277 (85%)	235 (100%)	0	100	100
1	0g	235/277 (85%)	235 (100%)	0	100	100
1	0h	235/277 (85%)	235 (100%)	0	100	100
1	0i	235/277 (85%)	235 (100%)	0	100	100
1	0j	235/277 (85%)	235 (100%)	0	100	100
1	0k	235/277 (85%)	235 (100%)	0	100	100
1	0l	235/277 (85%)	235 (100%)	0	100	100
2	0A	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0B	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0C	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0D	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0E	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0F	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0G	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0H	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0I	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0J	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0K	250/270 (93%)	249 (100%)	1 (0%)	84	83
2	0L	250/270 (93%)	249 (100%)	1 (0%)	84	83
3	A	48/706 (7%)	48 (100%)	0	100	100
3	B	54/706 (8%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	57/706 (8%)	57 (100%)	0	100	100
3	D	48/706 (7%)	48 (100%)	0	100	100
3	E	54/706 (8%)	54 (100%)	0	100	100
3	F	57/706 (8%)	57 (100%)	0	100	100
3	G	48/706 (7%)	48 (100%)	0	100	100
3	H	54/706 (8%)	54 (100%)	0	100	100
3	I	57/706 (8%)	57 (100%)	0	100	100
3	J	48/706 (7%)	48 (100%)	0	100	100
3	K	54/706 (8%)	54 (100%)	0	100	100
3	L	57/706 (8%)	57 (100%)	0	100	100
3	M	48/706 (7%)	48 (100%)	0	100	100
3	N	54/706 (8%)	54 (100%)	0	100	100
3	O	57/706 (8%)	57 (100%)	0	100	100
3	P	48/706 (7%)	48 (100%)	0	100	100
3	Q	54/706 (8%)	54 (100%)	0	100	100
3	R	57/706 (8%)	57 (100%)	0	100	100
3	S	48/706 (7%)	48 (100%)	0	100	100
3	T	54/706 (8%)	54 (100%)	0	100	100
3	U	57/706 (8%)	57 (100%)	0	100	100
3	V	48/706 (7%)	48 (100%)	0	100	100
3	W	54/706 (8%)	54 (100%)	0	100	100
3	X	57/706 (8%)	57 (100%)	0	100	100
3	Y	48/706 (7%)	48 (100%)	0	100	100
3	Z	54/706 (8%)	54 (100%)	0	100	100
3	a	57/706 (8%)	57 (100%)	0	100	100
3	b	48/706 (7%)	48 (100%)	0	100	100
3	c	54/706 (8%)	54 (100%)	0	100	100
3	d	57/706 (8%)	57 (100%)	0	100	100
3	e	48/706 (7%)	48 (100%)	0	100	100
3	f	54/706 (8%)	54 (100%)	0	100	100
3	g	57/706 (8%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	h	48/706 (7%)	48 (100%)	0	100	100
3	i	54/706 (8%)	54 (100%)	0	100	100
3	j	57/706 (8%)	57 (100%)	0	100	100
All	All	7728/31980 (24%)	7716 (100%)	12 (0%)	85	87

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	0H	247	VAL
2	0I	247	VAL
2	0L	247	VAL
2	0J	247	VAL
2	0D	247	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
2	0J	17	GLN
3	I	61	ASN
2	0J	192	GLN
2	0L	126	GLN
3	N	54	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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.

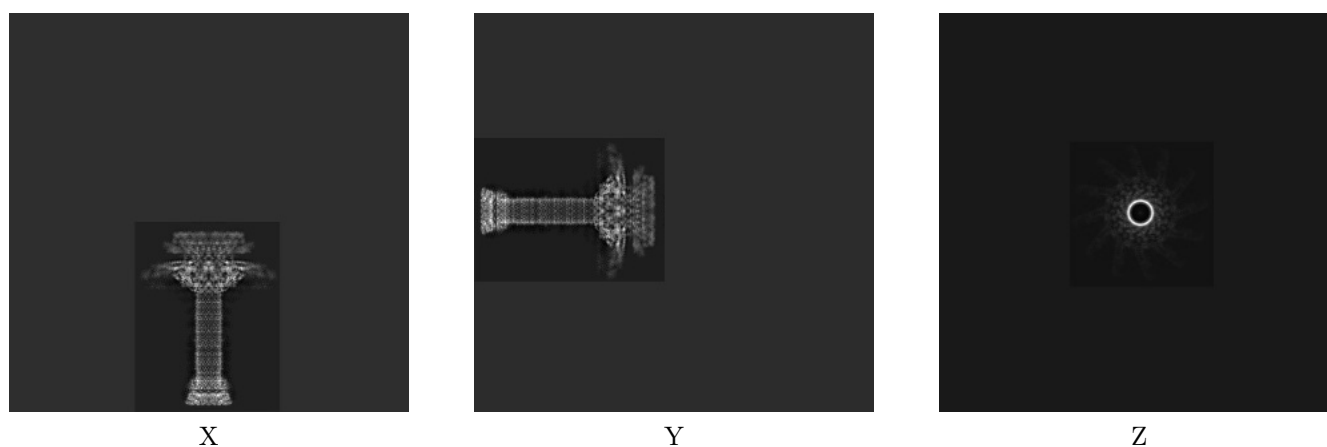
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4685. 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](#)

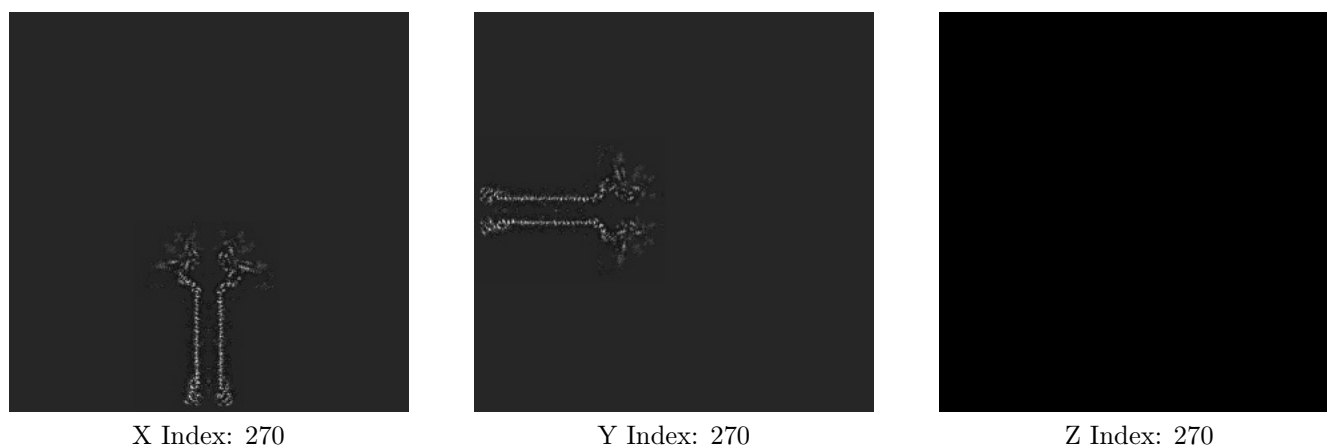
6.1.1 Primary map



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

6.2 Central slices [i](#)

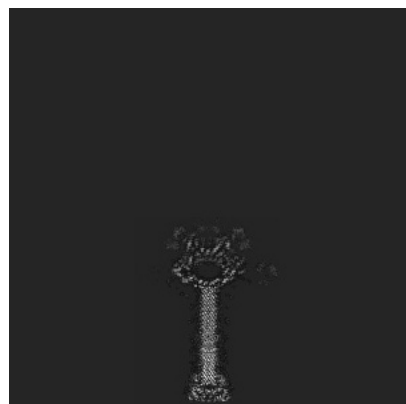
6.2.1 Primary map



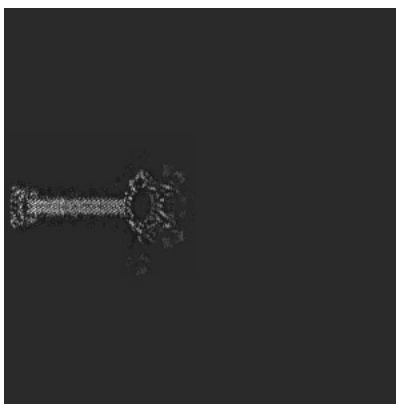
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

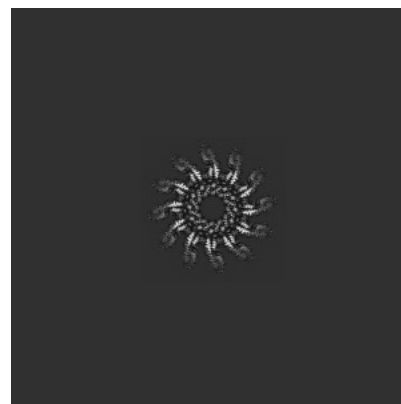
6.3.1 Primary map



X Index: 256



Y Index: 254

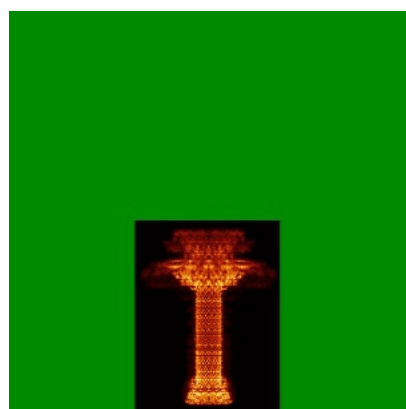


Z Index: 194

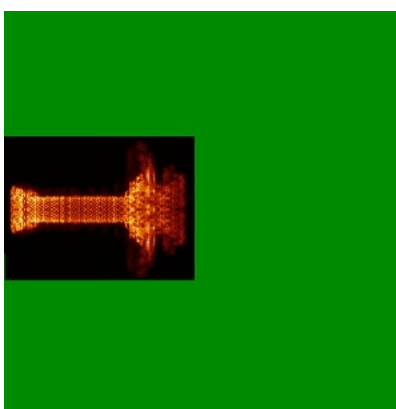
The images above show the largest variance slices of the map in three orthogonal directions.

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

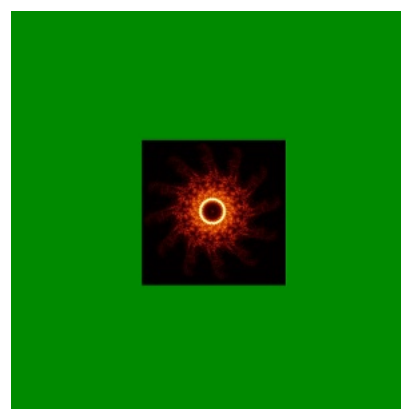
6.4.1 Primary map



X



Y

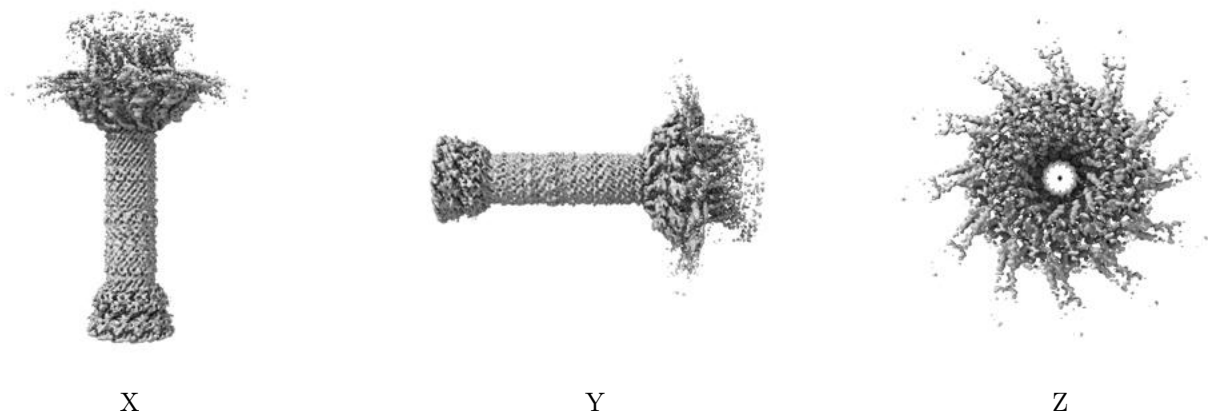


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

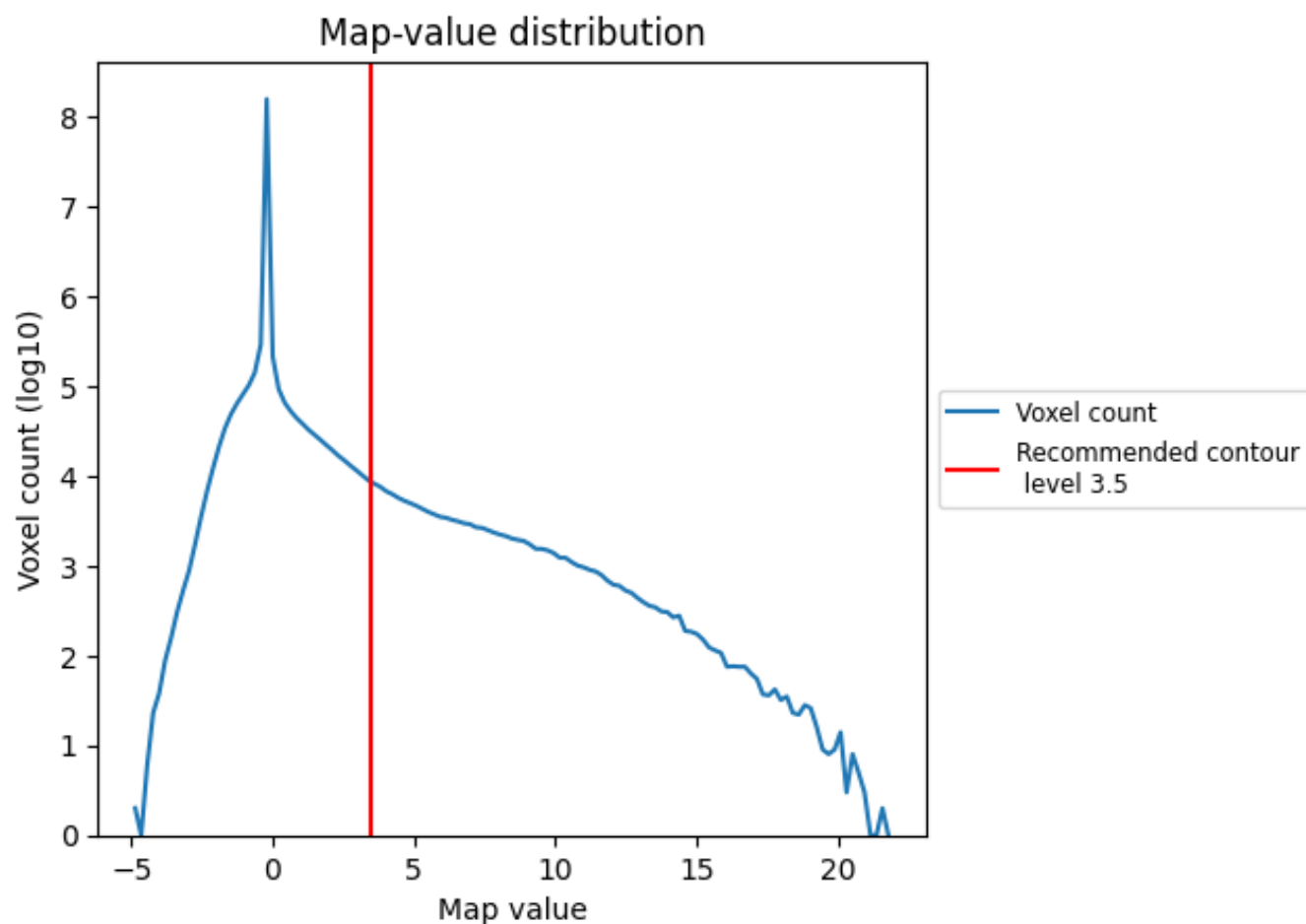
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

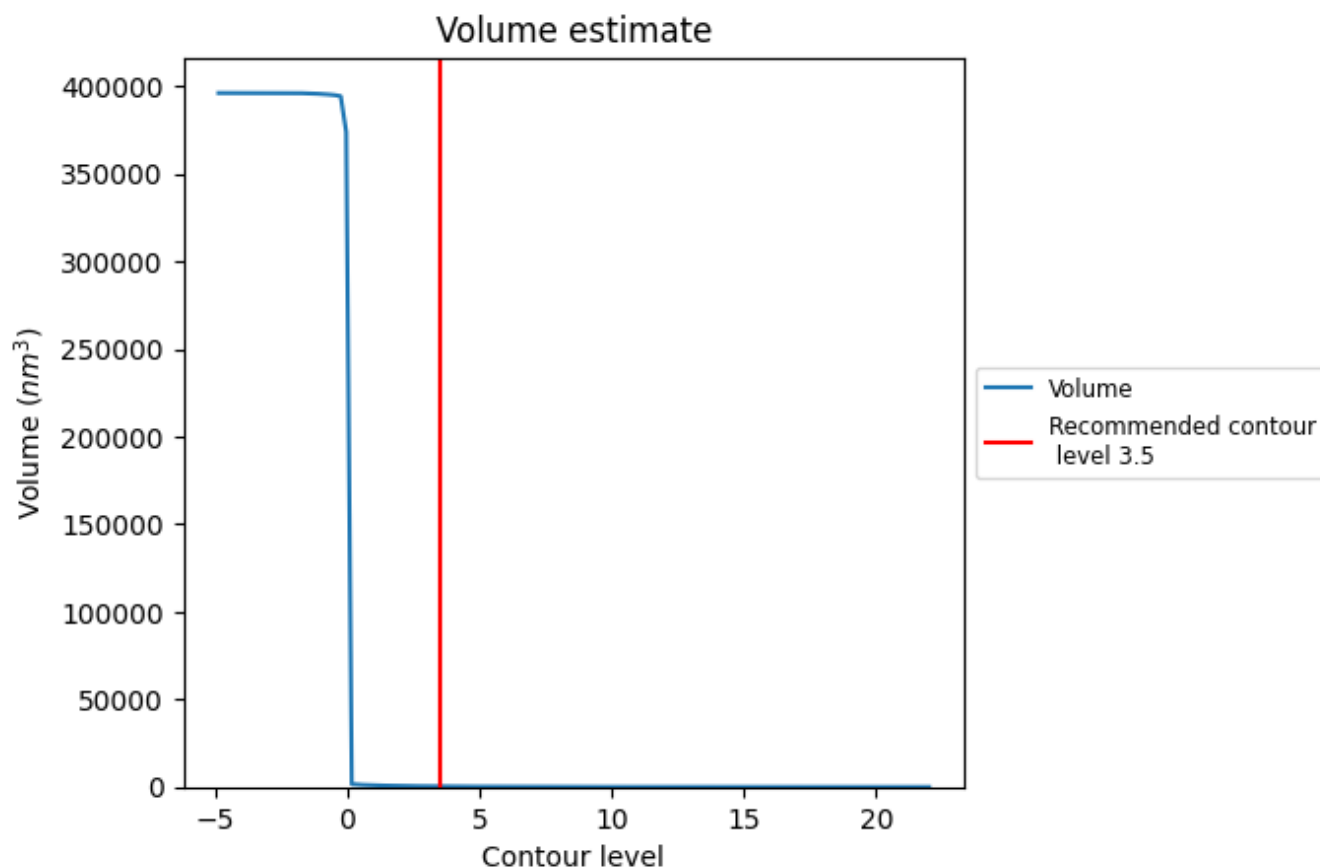
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

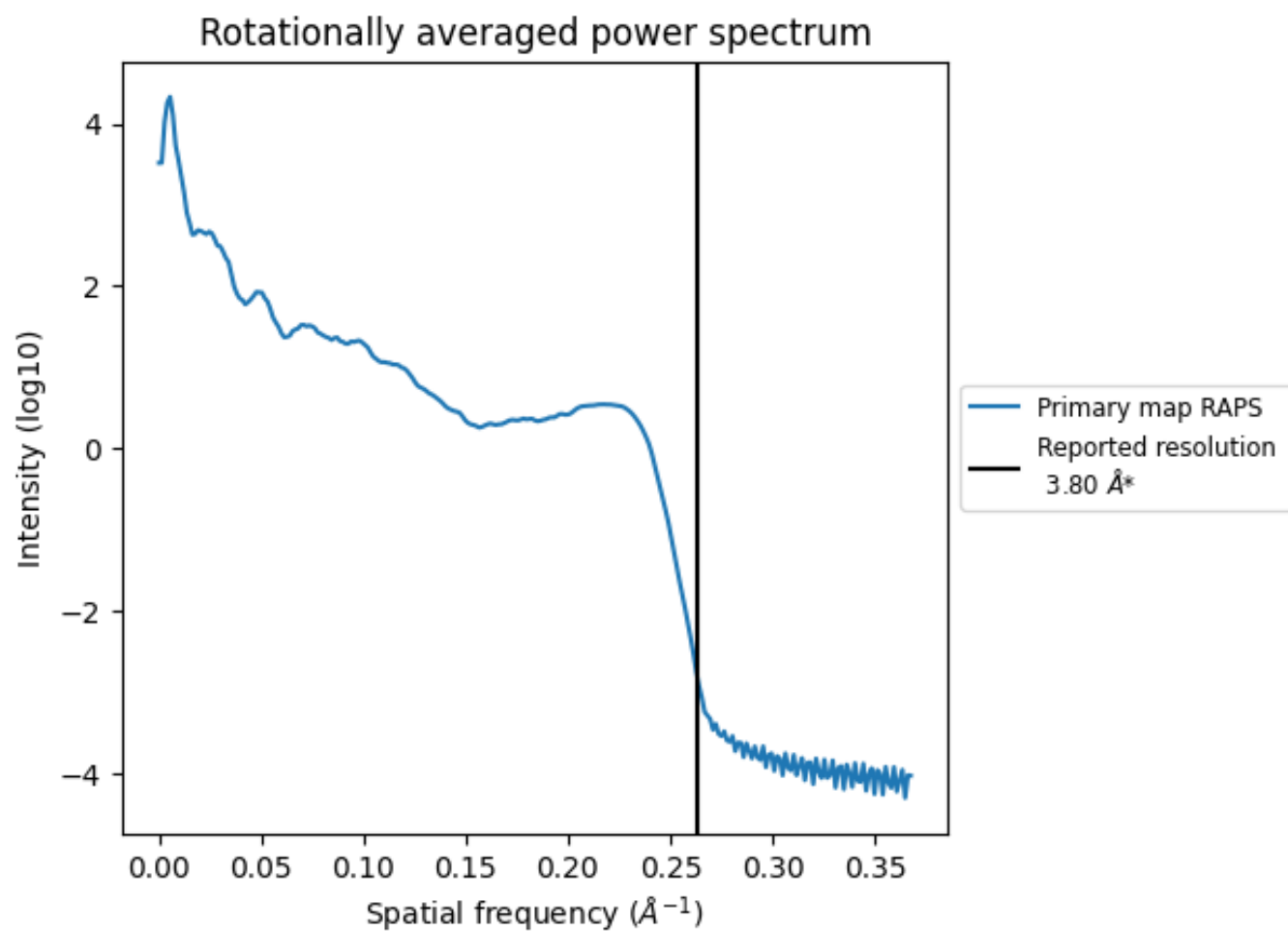
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 323 nm^3 ; this corresponds to an approximate mass of 291 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

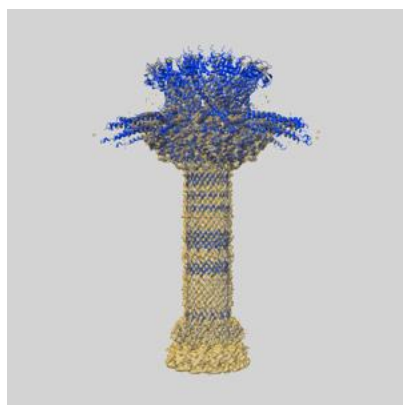
8 Fourier-Shell correlation

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

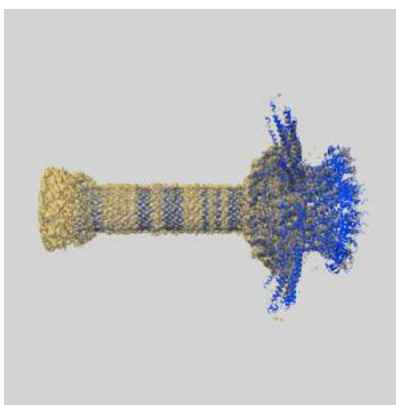
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4685 and PDB model 6QZF. Per-residue inclusion information can be found in section 3 on page 10.

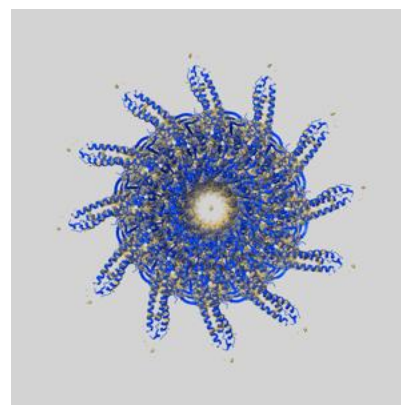
9.1 Map-model overlay [i](#)



X



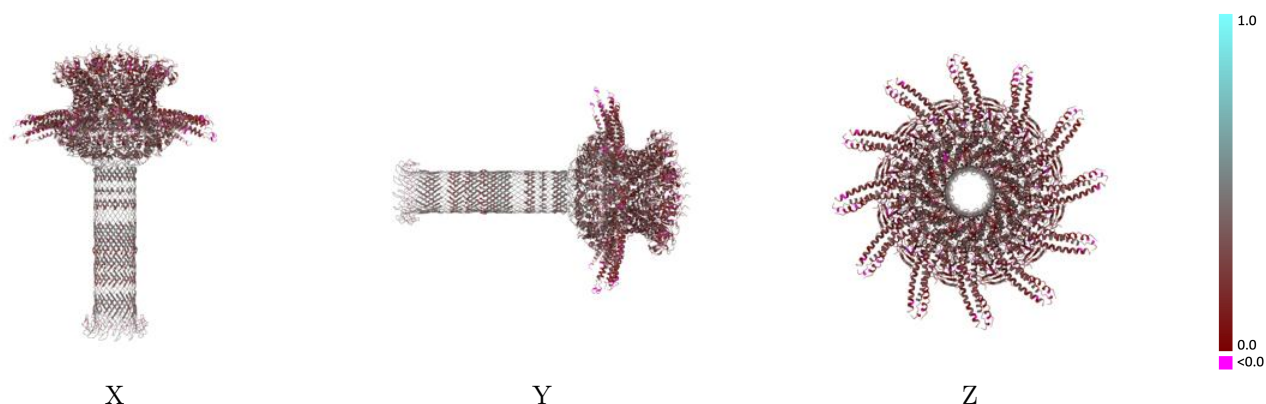
Y



Z

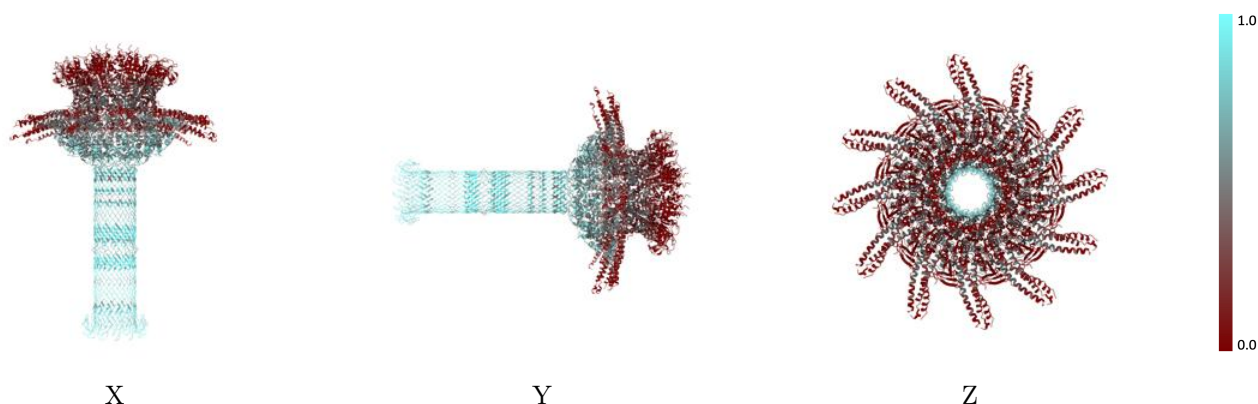
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



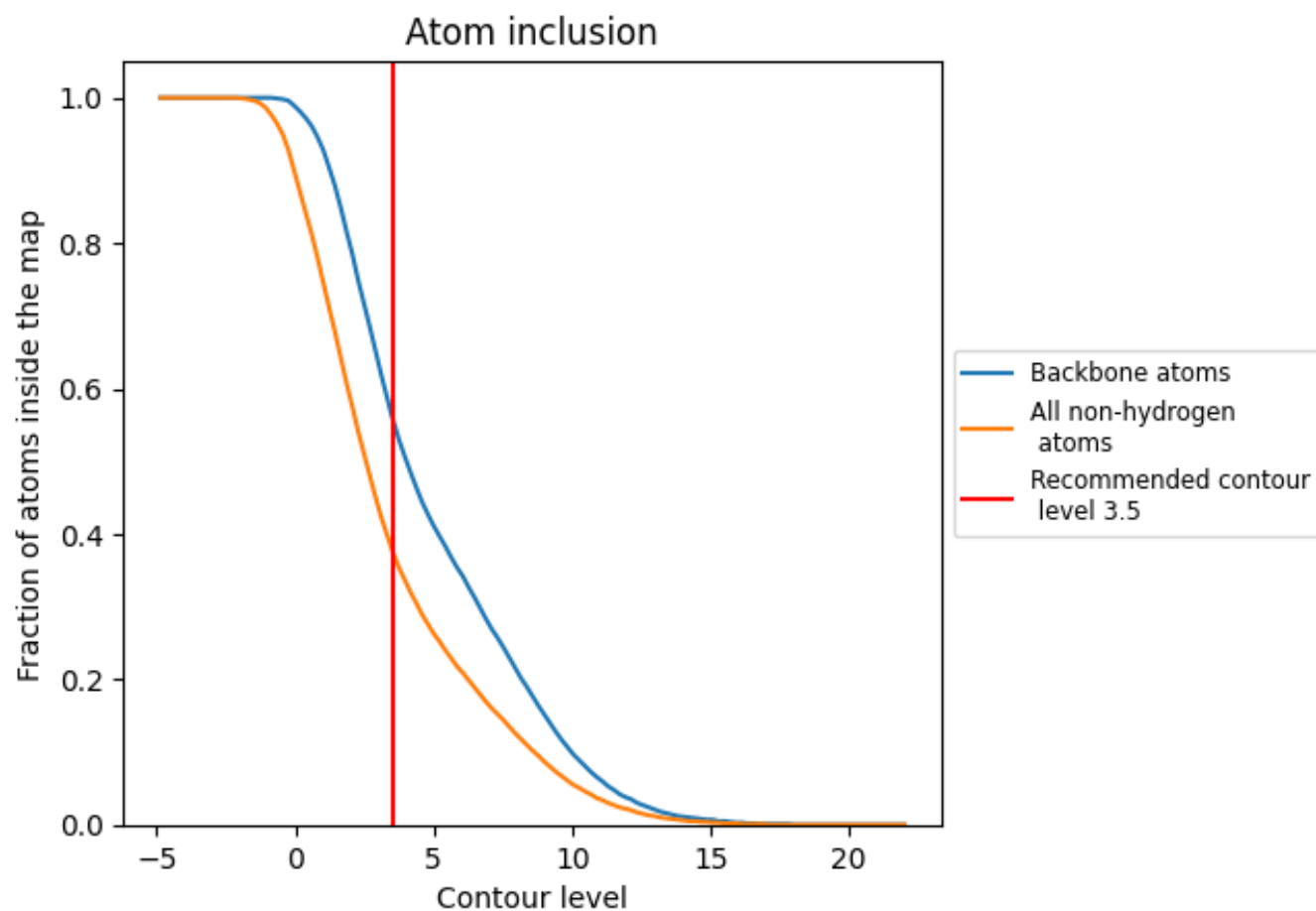
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 38% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3780	 0.3050
0A	 0.6740	 0.3690
0B	 0.6740	 0.3690
0C	 0.6760	 0.3730
0D	 0.6760	 0.3720
0E	 0.6780	 0.3720
0F	 0.6770	 0.3740
0G	 0.6740	 0.3720
0H	 0.6780	 0.3730
0I	 0.6750	 0.3730
0J	 0.6760	 0.3720
0K	 0.6770	 0.3700
0L	 0.6720	 0.3710
0a	 0.1890	 0.2840
0b	 0.1910	 0.2840
0c	 0.1910	 0.2840
0d	 0.1920	 0.2820
0e	 0.1930	 0.2860
0f	 0.1870	 0.2830
0g	 0.1880	 0.2820
0h	 0.1910	 0.2850
0i	 0.1900	 0.2850
0j	 0.1880	 0.2830
0k	 0.1870	 0.2830
0l	 0.1880	 0.2850
A	 0.1740	 0.2080
B	 0.2270	 0.2470
C	 0.1870	 0.2480
D	 0.1670	 0.2090
E	 0.2320	 0.2420
F	 0.1930	 0.2530
G	 0.1620	 0.2100
H	 0.2300	 0.2390
I	 0.1870	 0.2500
J	 0.1670	 0.2020



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Chain	Atom inclusion	Q-score
K	 0.2230	 0.2330
L	 0.1910	 0.2470
M	 0.1690	 0.2010
N	 0.2190	 0.2330
O	 0.1930	 0.2490
P	 0.1690	 0.2010
Q	 0.2190	 0.2310
R	 0.1910	 0.2420
S	 0.1710	 0.2040
T	 0.2210	 0.2340
U	 0.1870	 0.2500
V	 0.1740	 0.2080
W	 0.2190	 0.2260
X	 0.1810	 0.2400
Y	 0.1690	 0.2010
Z	 0.2210	 0.2290
a	 0.1810	 0.2430
b	 0.1670	 0.2000
c	 0.2170	 0.2290
d	 0.1930	 0.2480
e	 0.1690	 0.1960
f	 0.2210	 0.2390
g	 0.1770	 0.2390
h	 0.1710	 0.1950
i	 0.2230	 0.2390
j	 0.1890	 0.2500