



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:39 AM UTC

PDB ID : 6QZ9 / pdb_00006qz9
EMDB ID : EMD-4684
Title : The cryo-EM structure of the collar complex and tail axis in bacteriophage phi29
Authors : Xu, J.; Wang, D.; Gui, M.; Xiang, Y.
Deposited on : 2019-03-11
Resolution : 3.30 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:

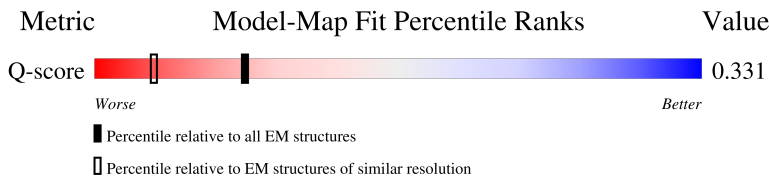
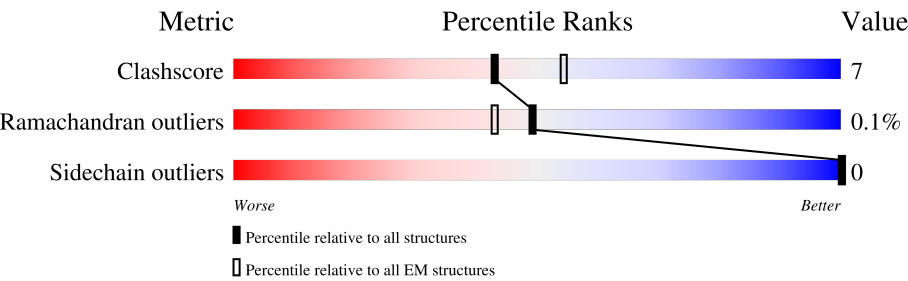
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	50% 70% 15% 15%
1	0b	309	50% 70% 16% 15%
1	0c	309	50% 70% 16% 15%
1	0d	309	50% 69% 16% 15%

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Mol	Chain	Length	Quality of chain
1	0e	309	
1	0f	309	
1	0g	309	
1	0h	309	
1	0i	309	
1	0j	309	
1	0k	309	
1	0l	309	
2	0A	293	
2	0B	293	
2	0C	293	
2	0D	293	
2	0E	293	
2	0F	293	
2	0G	293	
2	0H	293	
2	0I	293	
2	0J	293	
2	0K	293	
2	0L	293	
3	A	854	
3	B	854	
3	C	854	
3	D	854	
3	E	854	

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Mol	Chain	Length	Quality of chain	
3	F	854		92%
3	G	854		94%
3	H	854		93%
3	I	854		92%
3	J	854		94%
3	K	854		93%
3	L	854		92%
3	M	854		94%
3	N	854		93%
3	O	854		92%
3	P	854		94%
3	Q	854		93%
3	R	854		92%
3	S	854		94%
3	T	854		93%
3	U	854		92%
3	V	854		94%
3	W	854		93%
3	X	854		92%
3	Y	854		94%
3	Z	854		93%
3	a	854		92%
3	b	854		94%
3	c	854		93%
3	d	854		92%

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Mol	Chain	Length	Quality of chain	
3	e	854		94%
3	f	854		93%
3	g	854		92%
3	h	854		94%
3	i	854		93%
3	j	854		92%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 71724 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	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0b	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0c	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0d	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0e	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0f	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0g	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0h	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0i	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0j	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0k	264	Total 2163	C 1384	N 360	O 412	S 7	0	0
1	0l	264	Total 2163	C 1384	N 360	O 412	S 7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0A	291	Total 2296	C 1414	N 396	O 478	S 8	0	0
2	0B	291	Total 2296	C 1414	N 396	O 478	S 8	0	0
2	0C	291	Total 2296	C 1414	N 396	O 478	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	0D	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0E	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0F	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0G	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0H	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0I	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0J	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0K	291	Total	C	N	O	S	0	0
			2296	1414	396	478	8		
2	0L	291	Total	C	N	O	S	0	0
			2296	1414	396	478	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	71	Total	C	N	O	S	0	0
			603	391	94	114	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	71	Total	C	N	O	S	0	0
			603	391	94	114	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	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	J	51	Total	C	N	O	S	0	0
			433	281	67	83	2		

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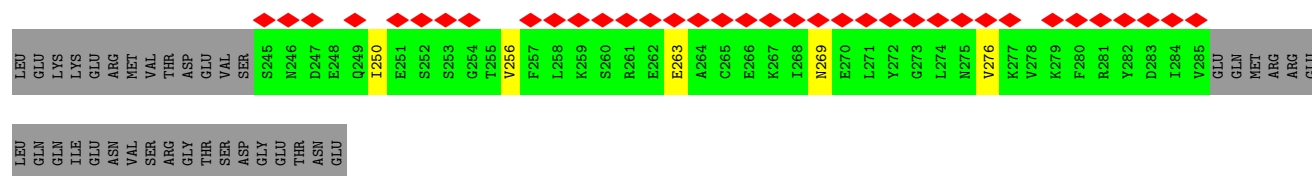
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	L	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	M	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	N	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	O	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	P	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	Q	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	R	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	S	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	T	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	U	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	V	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	W	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	X	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	Y	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	Z	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	a	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	b	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	c	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	d	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	e	51	Total	C	N	O	S	0	0
			433	281	67	83	2		

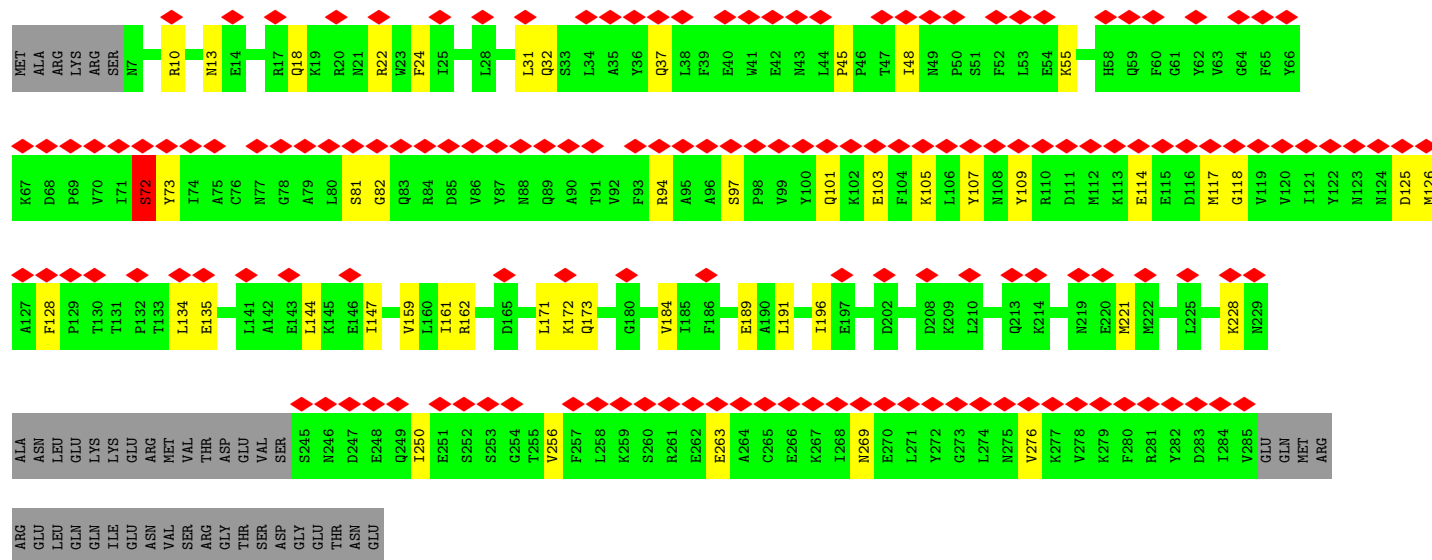
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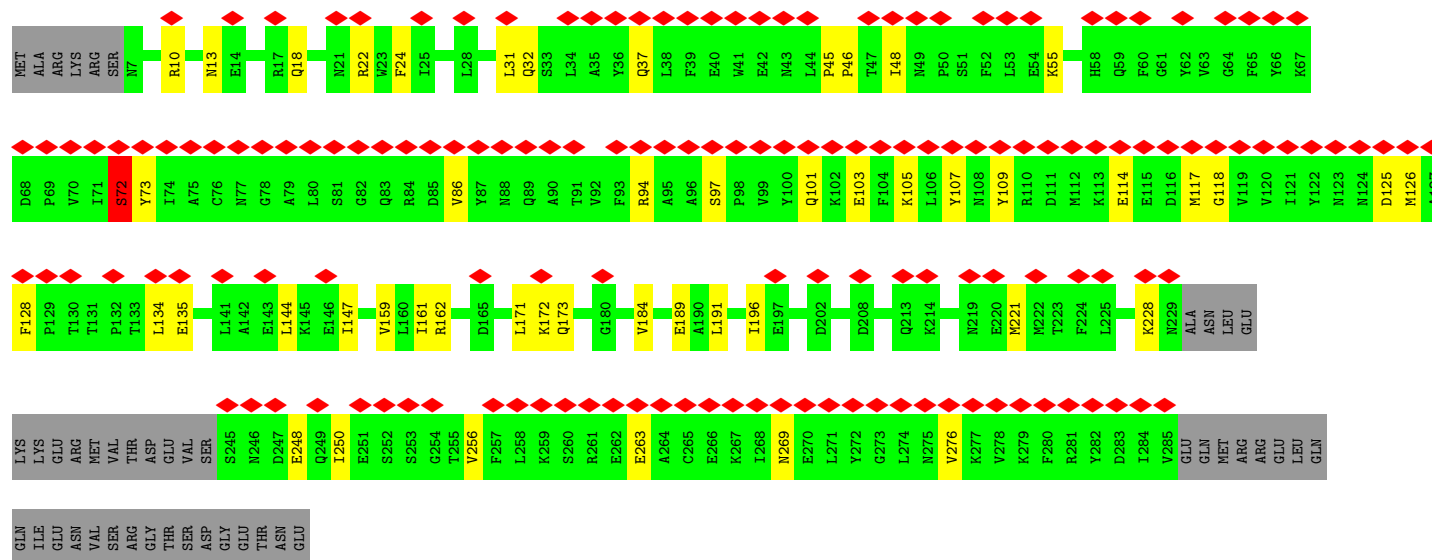
Mol	Chain	Residues	Atoms					AltConf	Trace
3	f	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	g	71	Total	C	N	O	S	0	0
			603	391	94	114	4		
3	h	51	Total	C	N	O	S	0	0
			433	281	67	83	2		
3	i	57	Total	C	N	O	S	0	0
			482	312	74	92	4		
3	j	71	Total	C	N	O	S	0	0
			603	391	94	114	4		



• Molecule 1: Portal protein

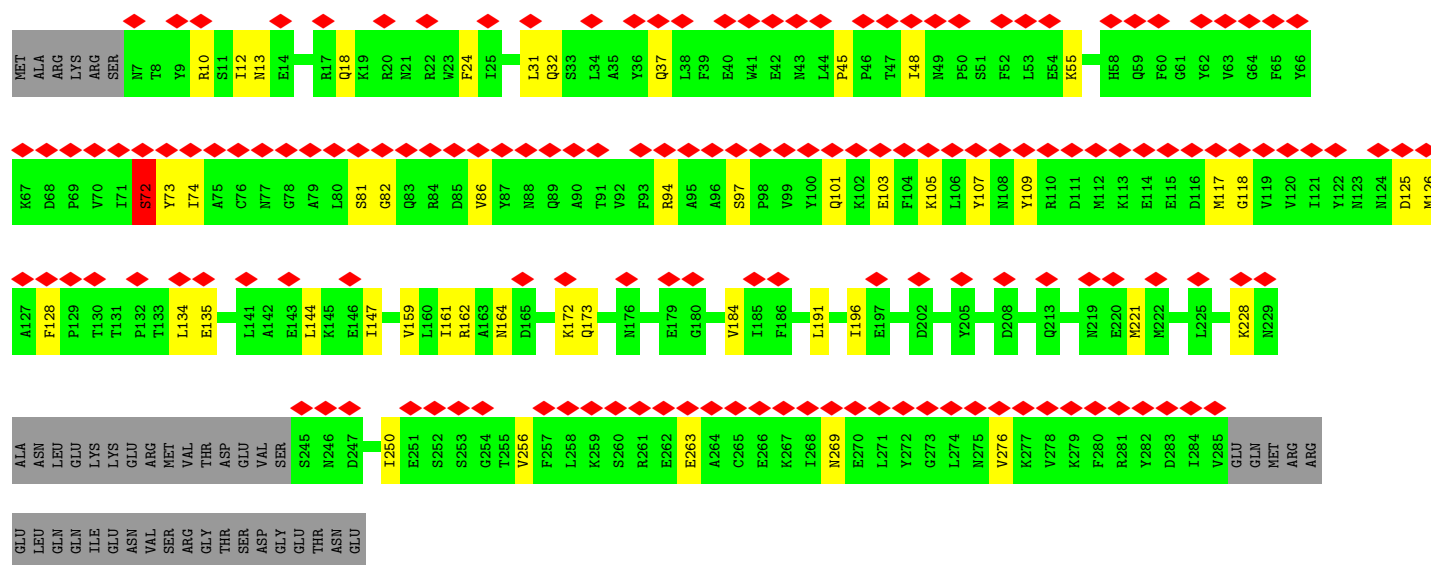


• Molecule 1: Portal protein



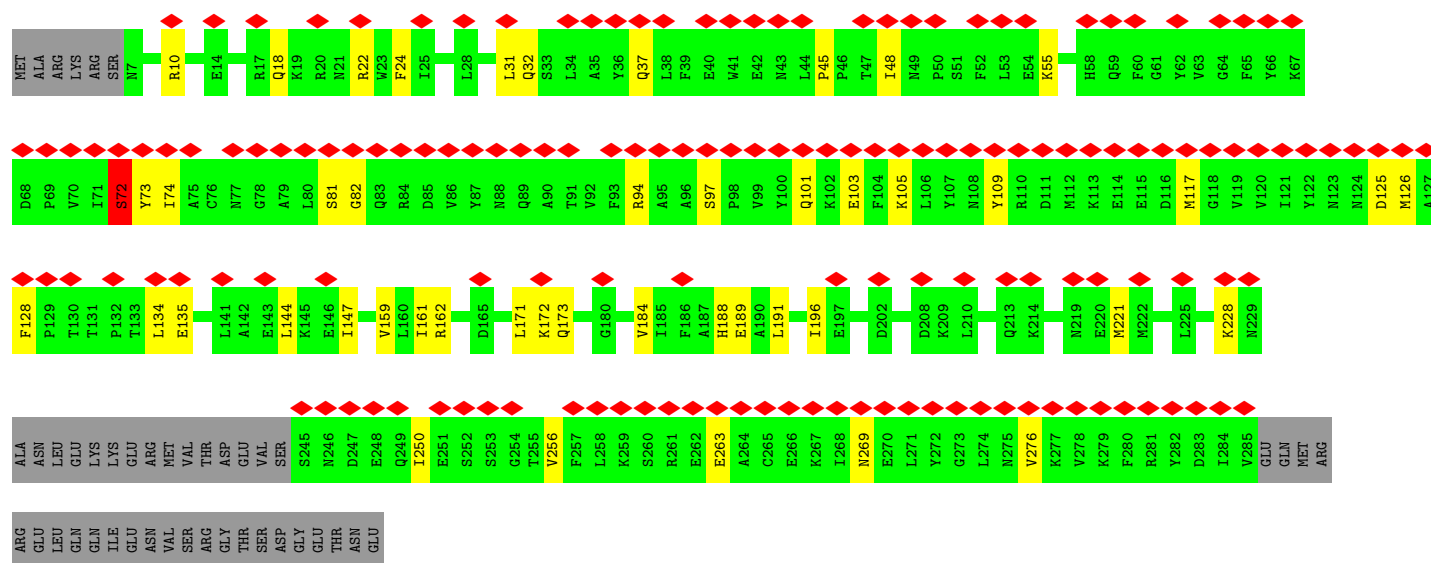
• Molecule 1: Portal protein

Chain 0e: 



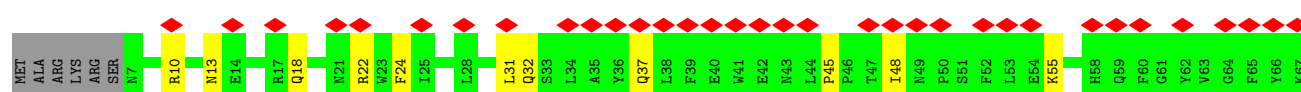
• Molecule 1: Portal protein

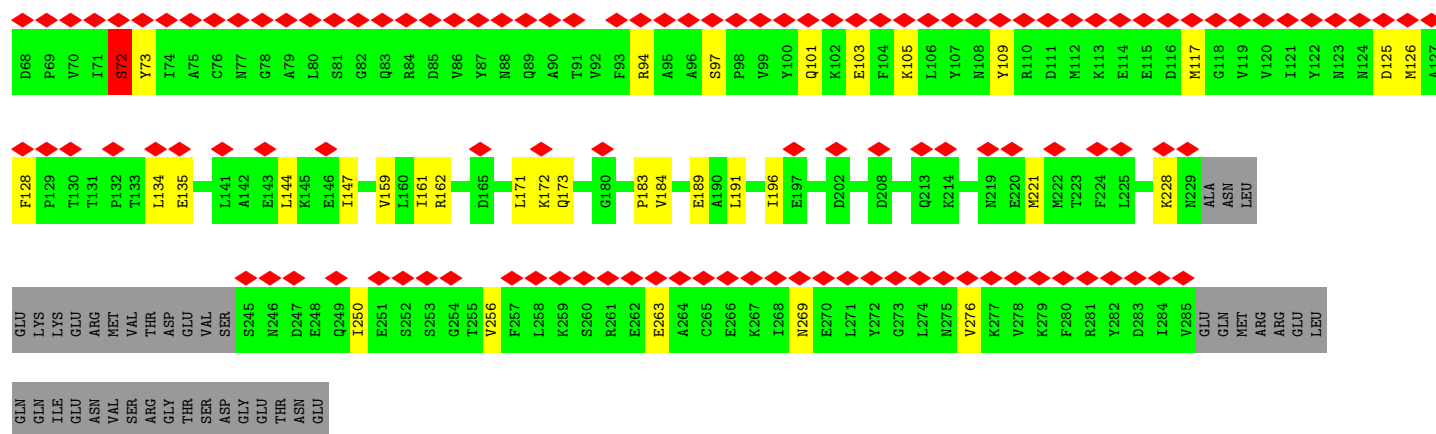
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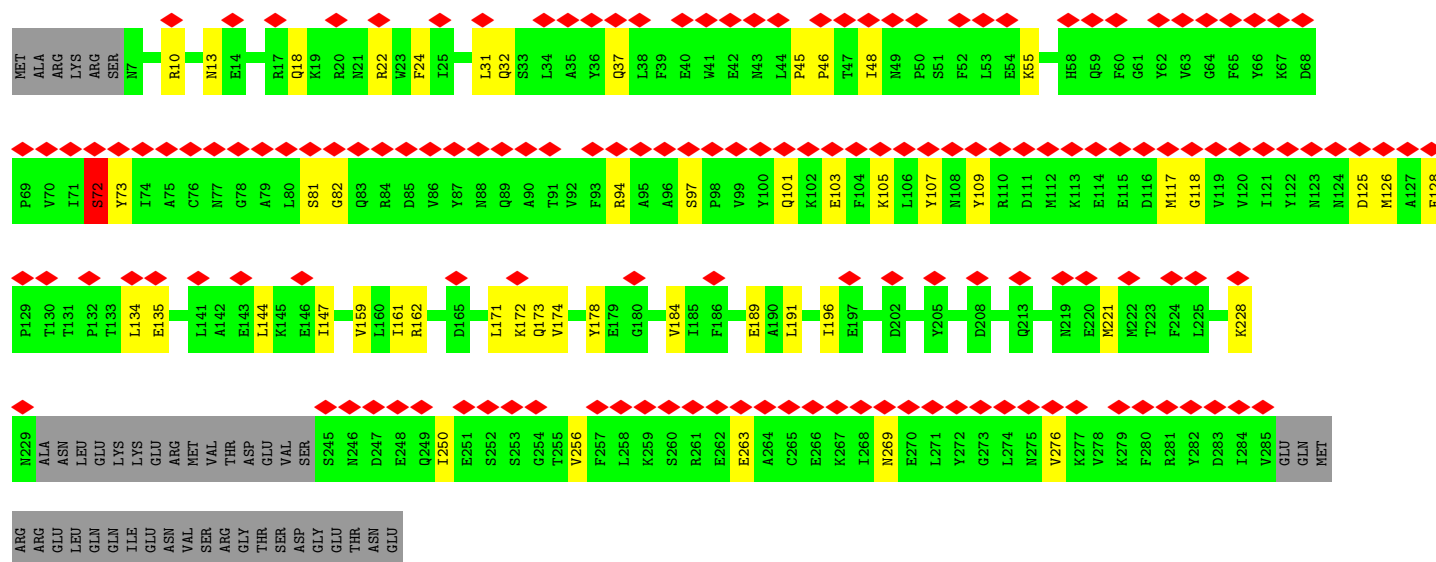
• Molecule 1: Portal protein

Chain 0g: 

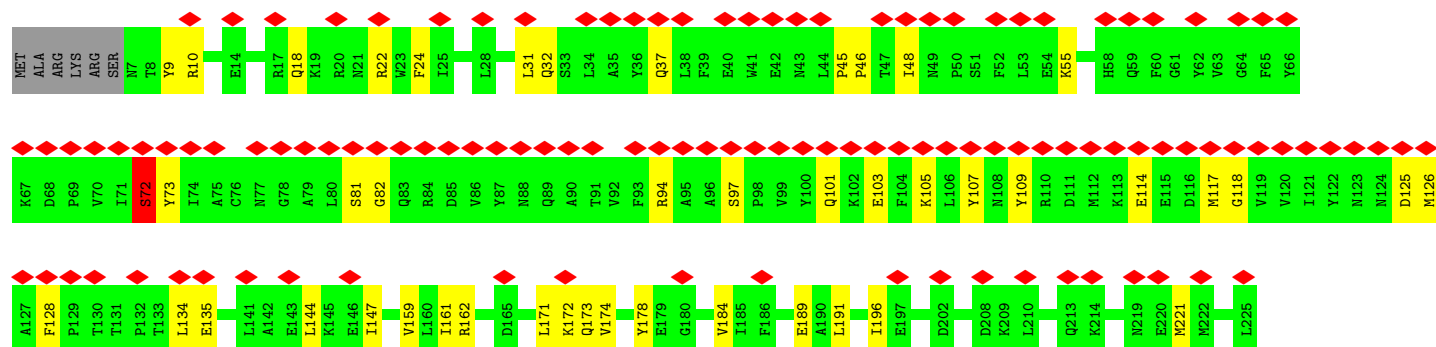


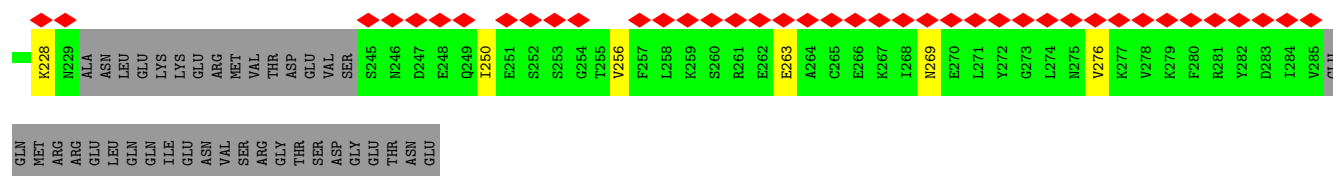


• Molecule 1: Portal protein

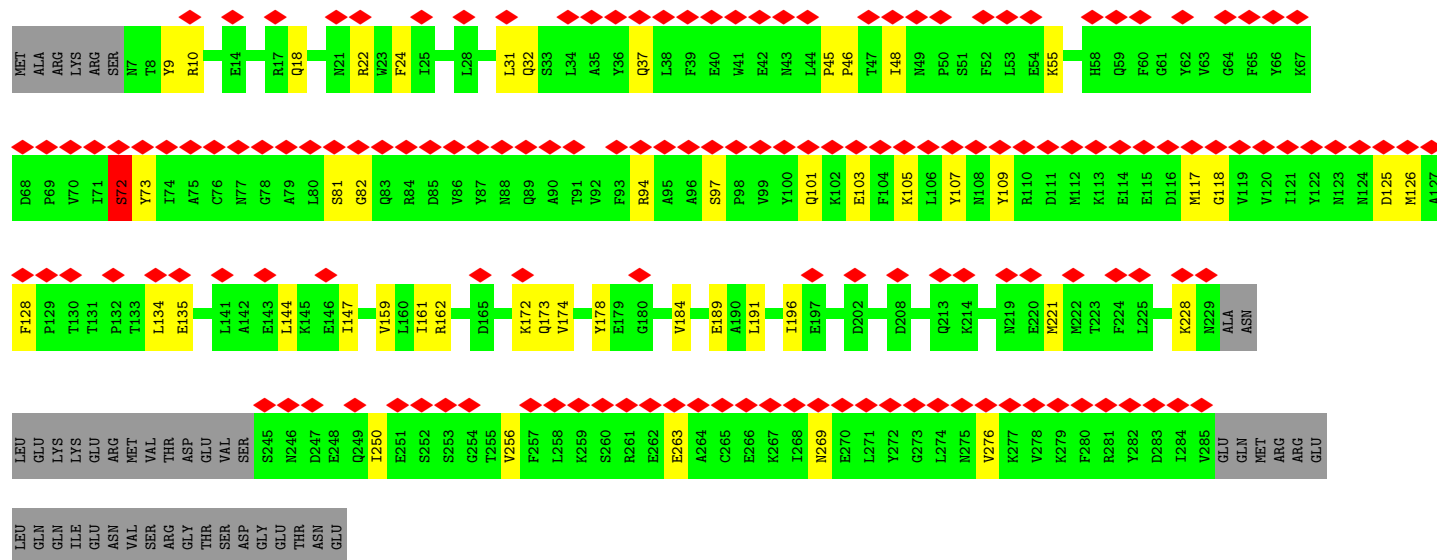


• Molecule 1: Portal protein

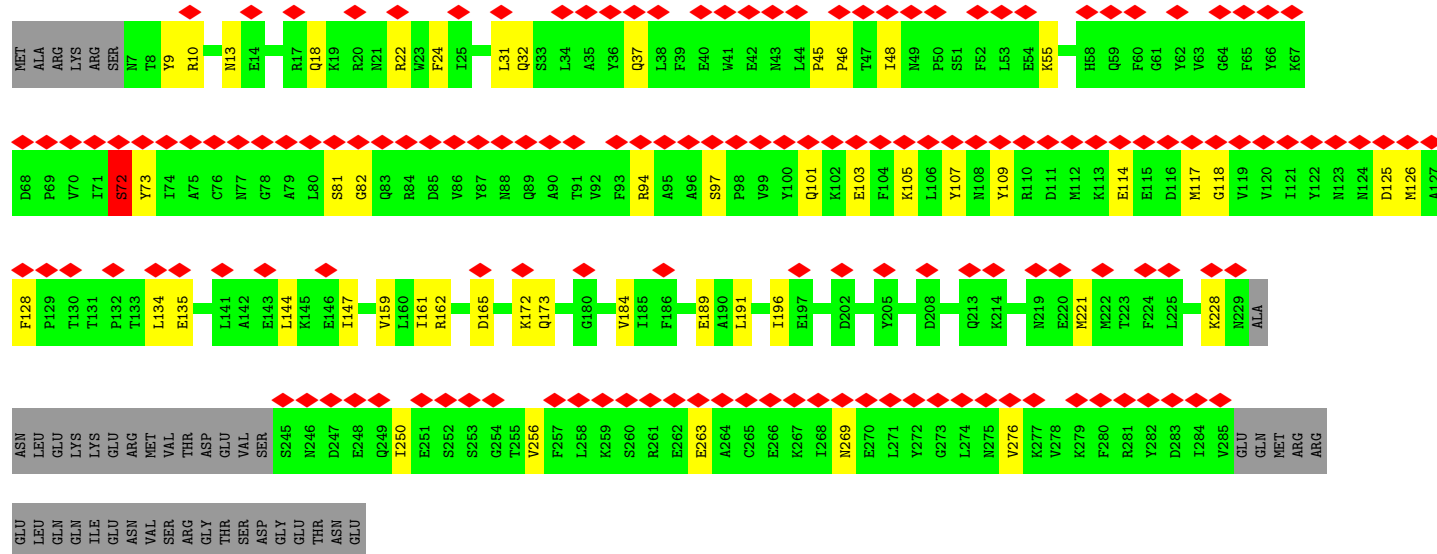




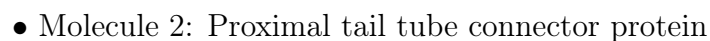
• Molecule 1: Portal protein

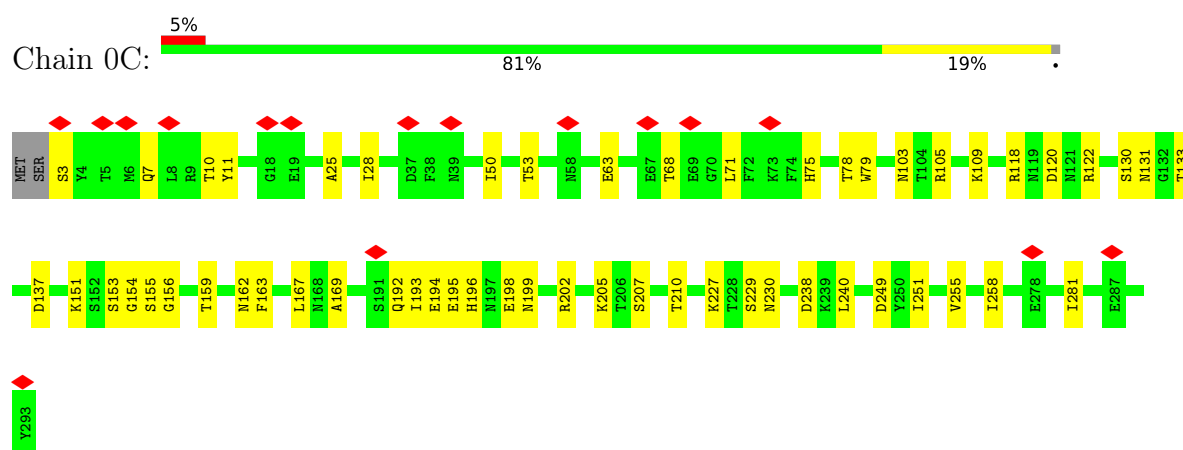


• Molecule 1: Portal protein

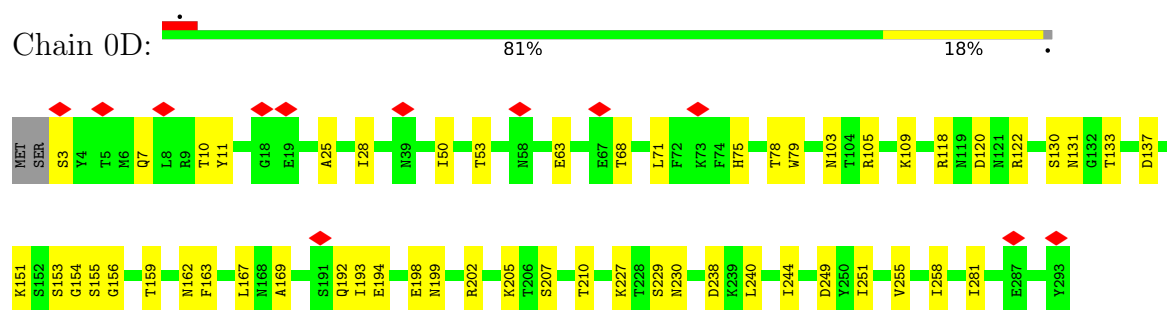


• Molecule 1: Portal protein

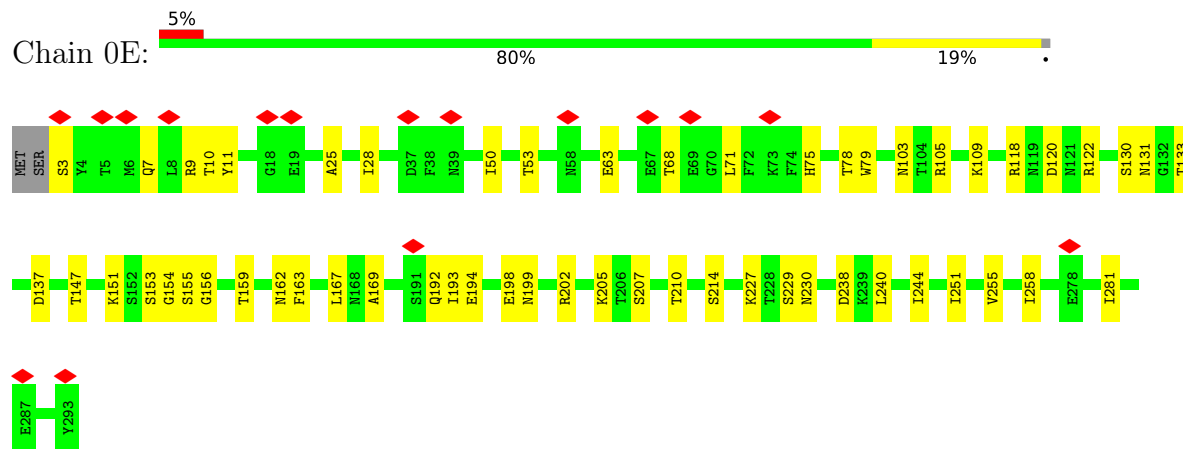




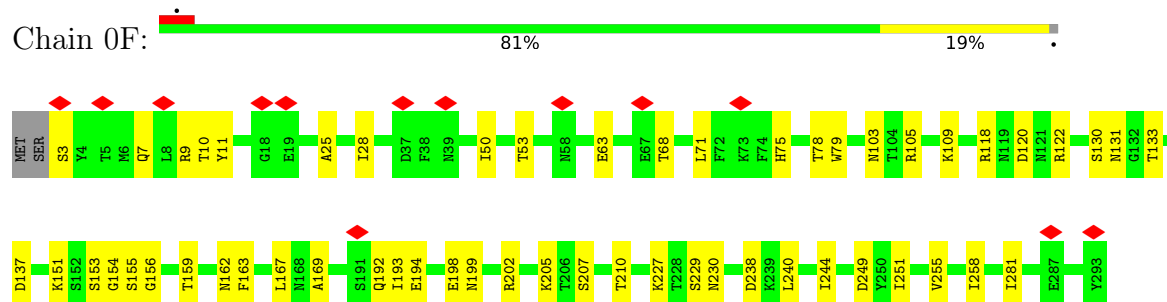
- Molecule 2: Proximal tail tube connector protein



- Molecule 2: Proximal tail tube connector protein

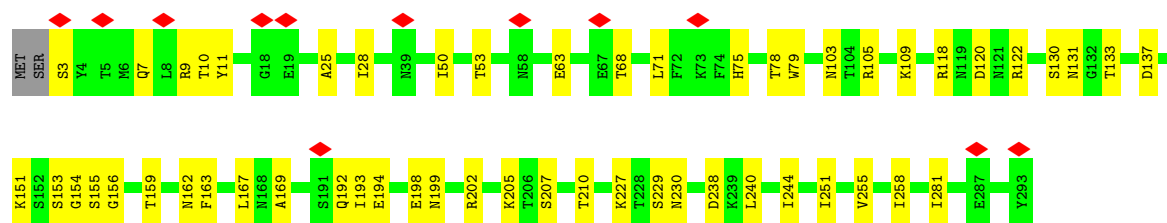


- Molecule 2: Proximal tail tube connector protein



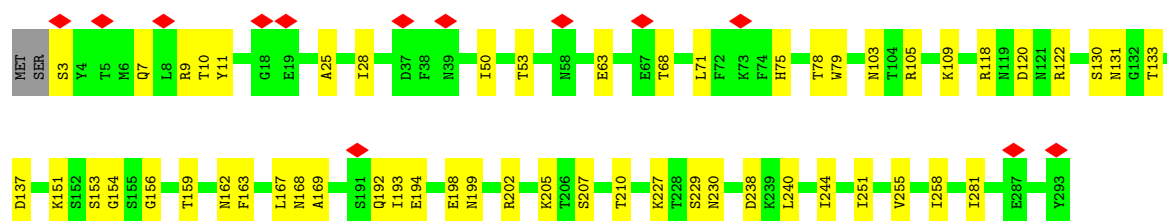
- Molecule 2: Proximal tail tube connector protein

Chain 0G:  81% 18%



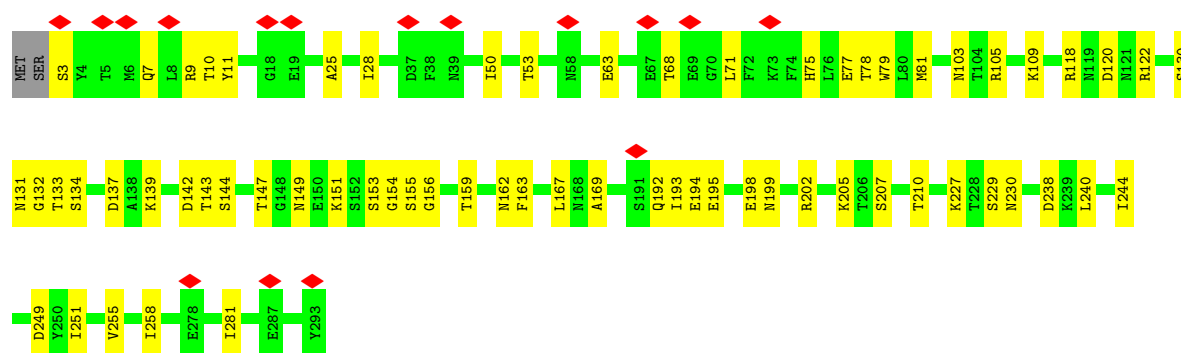
- Molecule 2: Proximal tail tube connector protein

Chain 0H:  81% 18%



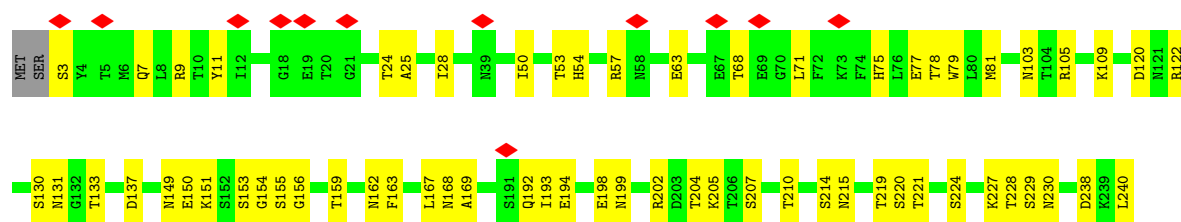
- Molecule 2: Proximal tail tube connector protein

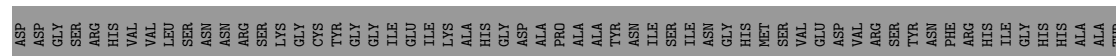
Chain 0I:  5% 77% 23%



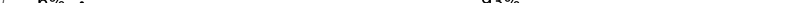
- Molecule 2: Proximal tail tube connector protein

Chain 0J:  5% 75% 24%







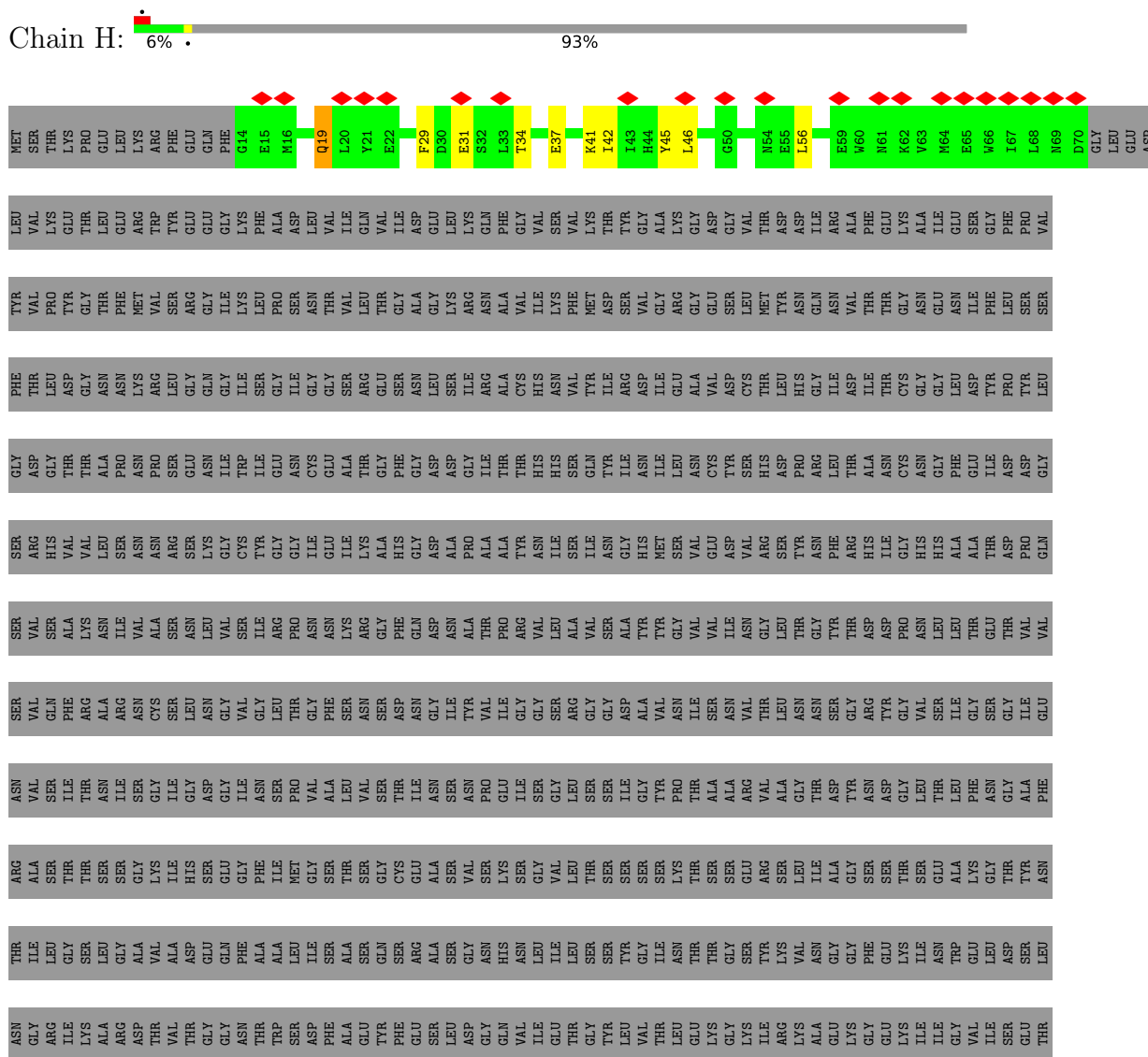
Chain E:  6% 93%



PHE										THR										LEU										MET									
THR										LEU										GLU										T3									
ASP										GLY										THR										K4									
ASN										PHE										LEU										P5									
ASN										MET										GLU										E6									
ARG										VAL										TRP										L7									
LEU										SER										GLY										K8									
GLY										ARG										GLU										R9									
GLN										GLY										GLY										F10									
ILE										LYS										LYS										E11									
SER										LEU										PHE										Q12									
GLY										PRO										ALA										F13									
ILE										SER										ASP										G14									
GLY										ASN										LEU										E15									
GLY										THR										VAL										M16									
SER										VAL										ILE										—									
ARG										LEU										GLN																			
GLU										THR										GLY										L20									
SER										ASN										ILE										Y21									
ASN										ALA										ASP										E22									
SER										GLY										GLU										R23									
LEU										LYS										LEU										Y24									
ILE										ARG										LYS										L25									
ARG										ASN										GLN										—									
ALA										PHE										GLY																			
ALA										ILE										VAL										D30									
HIS										LYS										SER										F29									
ASN										ASN										VAL										Y30									
VAL										PHE										VAL										E31									
THR										MET										LYS										S32									
VAL										ILE										THR										L33									
ARG										SER										TYR										T34									
ASP										VAL										GLY										L35									
ILE										GLY										ALA										L36									
GLU										ARG										LYS										—									
ALA										GLY										GLY																			
VAL										GLU										ASP										L46									
CYS										SER										GLY										T49									
ASP										LEU										VAL										G50									
THR										MET										THR										R51									
LEU										TYR										ASP										V52									
HIS										ASN										ASP										T53									
GLY										GLN										ILE										M54									
ILE										ASN										ARG										E55									
ASP										VAL										PHE										L56									
THR										THR										GLU										I57									
THR										THR										LYS										E58									
CYS										ASN										ALA										E59									
GLY										GLU										ILE										W60									
GLY										ASN										GLU										M61									
THR										PHE										SER										—									
ASP										GLY										GLY																			
PRO										LEU										PHE										M64									
TYR										SER										VAL										E65									
LEU										THR										PHE										W66									
SER										SER										THR										I67									
SER										SER										THR										L68									
SER										SER										THR										W69									
SER										SER										THR										D70									
SER										SER										THR										G71									
SER										SER										THR										L72									
SER										SER										THR										E73									
SER										SER										THR										A74									



- Molecule 3: Pre-neck appendage protein



[illegible]

- Molecule 3: Pre-neck appendage protein



VAL LYS	ARG	GLU	SER	TYR	ALA	ILE	VAL	PRO	ASP	TYR	SER	PRO	ASP	GLY	LEU	ASP	E73		MET
TRP	GLU	THR	LEU	ASN	PHE	GLU	VAL	GLN	GLY	GLY	SER	VAL	SER	SER	THR	LEU	VAL	T3	
HIS	VAL	GLY	GLY	ILE	ALA	VAL	VAL	VAL	ASN	ASN	THR	PRO	THR	THR	PRO	VAL	VAL	K4	
VAL	VAL	VAL	ILE	GLY	THR	ILE	PHE	ALA	VAL	VAL	HIS	VAL	ASP	ASP	TYR	LYS	GLY	P5	
GLY	LEU	GLY	LYS	SER	THR	THR	ARG	LYS	ASN	ARG	ALA	THR	GLY	THR	THR	THR	THR	E6	
LEU	LEU	GLU	ARG	GLY	SER	ILE	ARG	ILE	ALA	ALA	ASN	THR	ASN	THR	THR	THR	LEU	L7	
GLY	GLY	SER	ASP	ALA	GLY	SER	ASN	VAL	VAL	ASN	SER	PRO	LYS	ASN	PHE	MET	GLU	K8	
GLN	GLN	SER	THR	VAL	LYS	GLY	CYS	ALA	ASN	PRO	ARG	VAL	ARG	VAL	TRP	TRP	ARG	R9	
ILE	ILE	PHE	VAL	ALA	ILE	ILE	SER	SER	SER	SER	SER	SER	LEU	SER	TYR	TYR	GLU	F10	
GLU	ALA	GLU	THR	ASP	HIS	GLY	LEU	ASN	ASN	ASN	GLY	ARG	GLY	GLY	GLU	GLU	GLU	E11	
TRP	VAL	TRP	GLY	GLN	SER	GLY	ASN	VAL	LYS	ASN	LYS	ARG	GLN	GLY	ILE	GLY	GLY	Q12	
GLN	ARG	GLN	GLY	PHE	GLU	ILE	VAL	SER	THR	TRP	ILE	LYS	ILE	ILE	LYS	LYS	LYS	F13	
ILE	ASP	ALA	THR	ALA	PHE	GLY	GLY	ILE	GLY	ILE	TYR	SER	LEU	PHE	PHE	ALA	ALA	G14	
GLU	THR	VAL	TRP	ALA	ILE	ILE	LEU	ARG	GLY	GLY	GLY	PRO	GLY	PRO	ALA	ASP	ASP	E15	
LEU	GLU	LEU	SER	LEU	MET	PRO	THR	PRO	GLY	ASN	ILE	SER	ILE	SER	ASN	LEU	LEU	M16	
LYS	VAL	LYS	ASP	ILE	GLY	VAL	GLY	ASN	ILE	CYS	GLY	ASN	GLY	ASN	GLY	VAL	VAL	L20	
LYS	GLN	GLU	PHE	ALA	THR	ASN	PHE	ASN	GLY	GLU	GLY	THR	GLY	THR	GLY	GLY	GLY	Y21	
GLY	HIS	GLY	TYR	GLN	GLY	SER	SER	ARG	PHE	GLY	ALA	THR	ARG	ASN	ASN	GLN	LYS	E22	
GLY	GLY	ILE	PHE	SER	GLY	THR	ASN	ASN	GLN	GLY	GLY	ASN	SER	ASN	ALA	ASP	ASP	Y24	
ILE	ILE	ILE	GLJ	ARG	GLU	ILE	ASN	ASP	GLY	ASP	ASP	GLY	ASN	ASN	GLY	LEU	LEU	L25	
ASP	ASP	ILE	LEU	ALA	ALA	ASN	GLY	ASP	ASN	GLY	PRQ	ILE	ILE	ARG	ALA	LYS	LYS	F29	
ALA	VAL	THR	ASN	HIS	LYS	ILE	ILE	PRO	ALA	ALA	THR	THR	THR	ALA	ALA	GLN	GLY	D30	
ALA	ALA	THR	ILE	LEU	GLY	SER	GLY	VAL	ARG	TYR	ASN	THR	HIS	CYS	VAL	PHE	PHE	E31	
THR	THR	GLU	GLU	ILE	VAL	GLY	SER	VAL	VAL	ASN	ASN	ILE	HIS	ASN	LYS	VAL	VAL	S32	
ASP	ASP	ASP	THR	LEU	LEU	ARG	GLY	ALA	ALA	SER	VAL	PHE	VAL	VAL	VAL	VAL	VAL	L33	
GLY	GLY	GLY	THR	SER	THR	SER	GLY	VAL	THR	ILE	GLY	MET	LYS	LYS	LYS	THR	LYS	T34	
ASN	ASN	LYS	TYR	SER	SER	SER	GLY	SER	ASN	ASN	TYR	ASP	ASP	THR	THR	THR	THR	L35	
VAL	PHE	PHE	VAL	GLY	SER	ILE	ASP	ALA	ALA	ILE	ILE	SER	ASN	GLY	TYR	TYR	GLY	L36	
ILE	ILE	LYS	ILE	TYR	SER	GLY	ALA	TYR	THR	ASN	ASN	VAL	ARG	ASP	VAL	GLY	GLY	E37	
VAL	VAL	ARG	LEU	ASN	LYS	TYR	VAL	GLY	GLY	ILE	ILE	GLY	ILE	ILE	GLY	ARG	LYS	L38	
GLN	GLU	PRO	GLU	THR	THR	THR	ILE	VAL	VAL	ASN	ALA	GLY	ALA	ALA	GLY	GLY	GLY	K38	
ILE	ILE	PRO	GLY	GLY	SER	ALA	SER	ILE	ILE	CYS	VAL	GLY	GLY	GLY	GLY	ASP	GLY	L46	
THR	THR	SER	LYS	SER	GLU	ARG	VAL	ASN	ASP	TYR	ASP	SER	SER	GLY	LEU	THR	THR	I49	
PRO	PRO	PRO	ILE	TYR	ARG	VAL	THR	GLY	VAL	SER	CYS	LEU	VAL	VAL	VAL	VAL	VAL	G50	
ASP	ASP	ASP	ARG	LYS	SER	ALA	LEU	LEU	ARG	HIS	THR	MET	THR	THR	THR	THR	THR	K51	
THR	PHE	PHE	VAL	VAL	LEU	GLY	ASN	THR	SER	PRO	HIS	ASN	ASP	ASP	ASN	ASP	ASP	V52	
THR	THR	ASP	ALA	ASN	ILE	THR	ASN	GLY	ASN	ARG	GLY	GLN	ILE	ILE	ILE	ILE	ILE	T53	
LYS	LYS	PRO	GLU	GLY	ALA	ASP	SER	TYR	PHE	LEU	ILE	ASN	ARG	ARG	ASN	ASN	ARG	N54	
LYS	GLU	ASN	LYS	GLY	GLY	TYR	ARG	THR	ARG	THR	ASP	VAL	VAL	VAL	VAL	VAL	ALA	E55	
LYS	GLY	LYS	GLY	PHE	SER	ARG	ARG	ASN	HIS	ALA	ILE	ILE	THR	THR	THR	THR	PHE	L56	
GLY	GLY	ASN	ASN	ASN	SER	TYR	TYR	ASP	ILE	ASN	GLU	GLY	GLY	GLY	GLY	GLY	GLY	I57	
TYR	TYR	TYR	LYS	GLY	THR	GLY	GLY	PRO	GLY	CYS	ASN	GLY	CYS	GLY	GLY	GLY	LYS	E58	
GLY	VAL	ILE	ILE	ILE	SER	VAL	VAL	ASN	HIS	ASN	HIS	ASN	ASN	ALA	ALA	ALA	ALA	E59	
VAL	VAL	PRO	ILE	ASN	GLU	THR	SER	LEU	HIS	GLY	PHE	GLY	GLY	GLU	GLU	ILE	ILE	W60	
ALA	ALA	ARG	GLY	TRP	ALA	LEU	ILE	LEU	ALA	ALA	THR	LEU	LEU	ASN	ASN	ASN	GLU	W61	
ILE	ILE	SER	VAL	GLU	LYS	PHE	GLY	THR	ALA	THR	ASP	ASP	ASP	ILE	ILE	ILE	GLU	N61	
VAL	VAL	GLN	ILE	LEU	GLY	ASN	SER	GLY	THR	ILE	TYR	PHE	PHE	GLY	GLY	GLY	GLY	M64	
LEU	LEU	ARG	SER	ASP	THR	THR	GLY	THR	THR	GLY	ASP	THR	THR	THR	THR	THR	PHE	E65	
																		W66	
																		I67	
																		L68	
																		N69	
																		D70	
																		G71	
																		I72	

- Molecule 3: Pre-neck appendage protein

Chain J:  6% 94%

LEU	VAL	LYS	ARG	GLU	THR	ALA	THR	GLY	ASP	SER	THR	TYR	GLY	ALA	PHE	ARG	GLY	THR	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR
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● Molecule 3: Pre-neck appendage protein

Chain K:  6% 93%

MET	SER	THR	LYS	PRO	GLU	LEU	LYS	ARG	PHE	GLU	GLN	PHE	G14	E15	M16	Q19	L20	Y21	E22	F29	D30	E31	S32	L33	T34	E37	K41	I42	I43	L46	G50	M54	E55	L56	E59	W60	M61	K62	W63	M64	E65	W66	I67	L68	M69	D70	GLY	LEU	GLU	ASP	LEU	
VAL	LYS	GLU	THR	LEU	GLU	ARG	TRP	TYR	GLU	GLY	LYS	PHE	ALA	ASP	LEU	VAL	ILE	GLN	VAL	PHE	GLY	GLN	ASP	GLY	VAL	VAL	LYS	THR	TYR	GLY	ALA	LYS	GLY	ASP	GLY	VAL	THR	ASP	ASP	ILE	ARG	ALA	PHE	GLY	LYS	GLY	GLY	PHE	PRO	VAL	VAL	THR

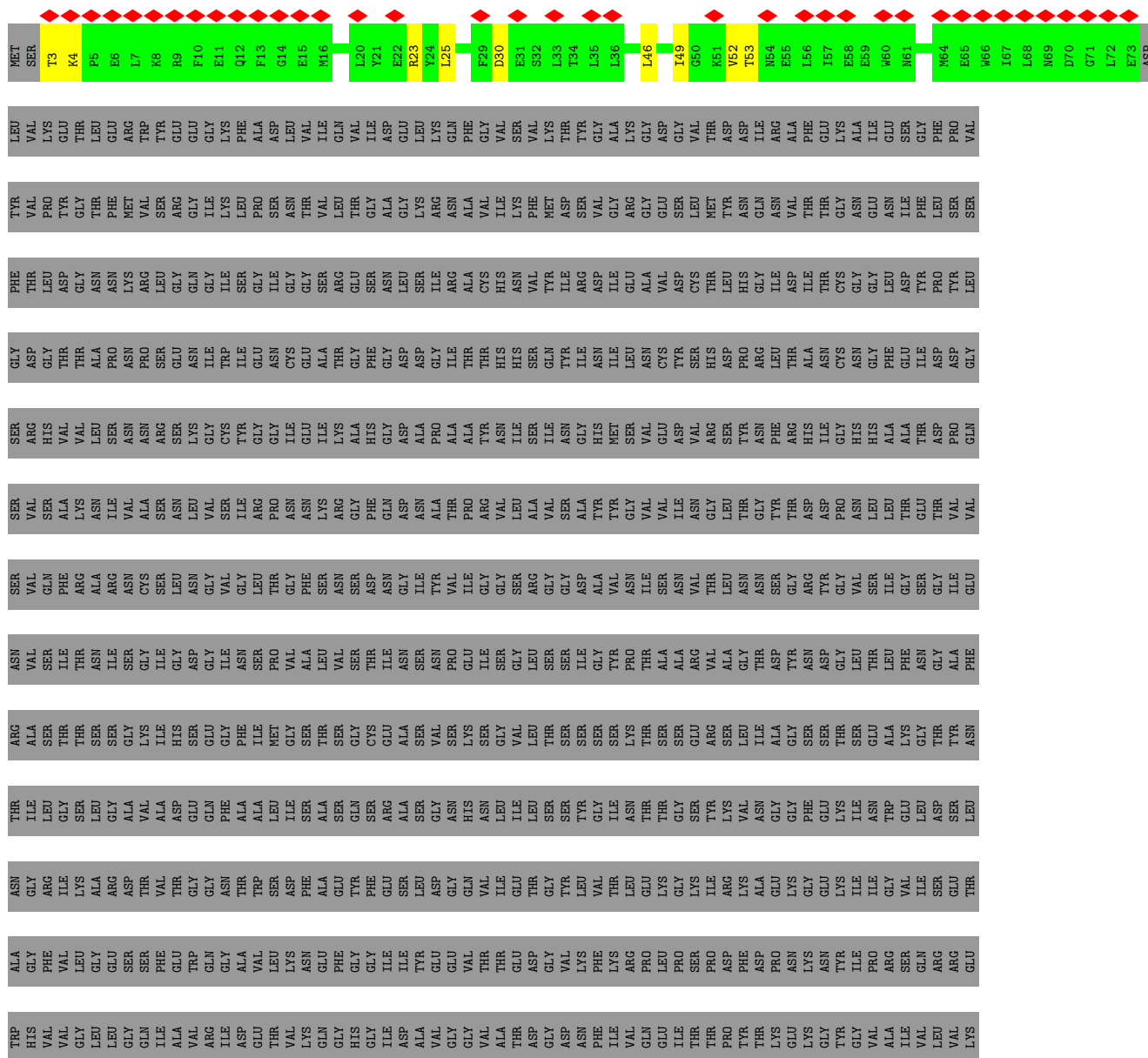




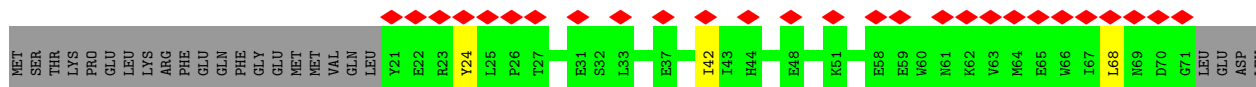
- Molecule 3: Pre-neck appendage protein

[illegible]

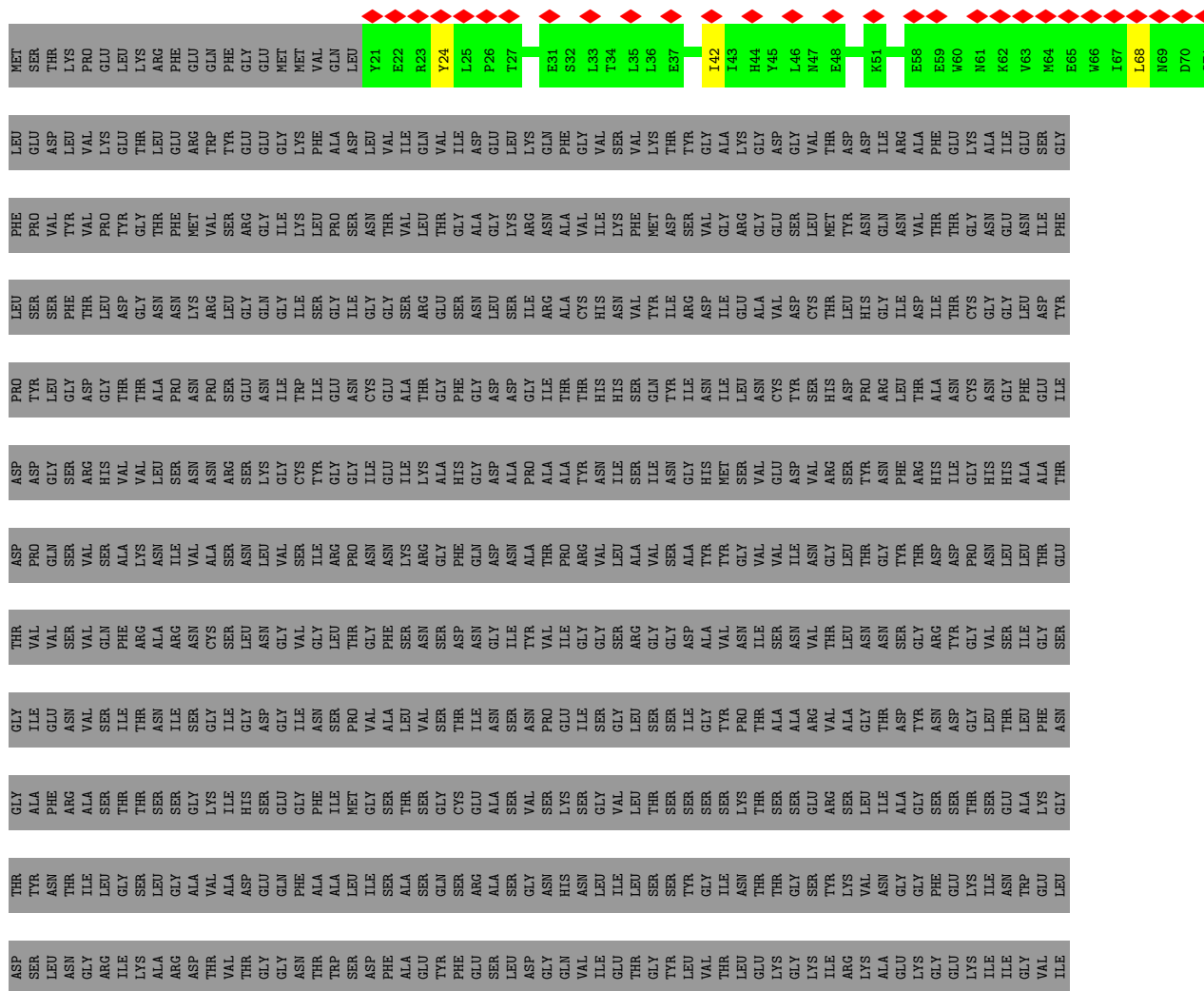
Chain 0: 7% 92%



Chain P: 6% 94%

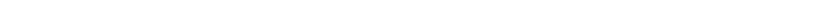






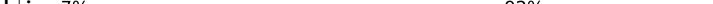
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- Molecule 3: Pre-neck appendage protein

Chain T:  5% 93%

[illegible]

- Molecule 3: Pre-neck appendage protein

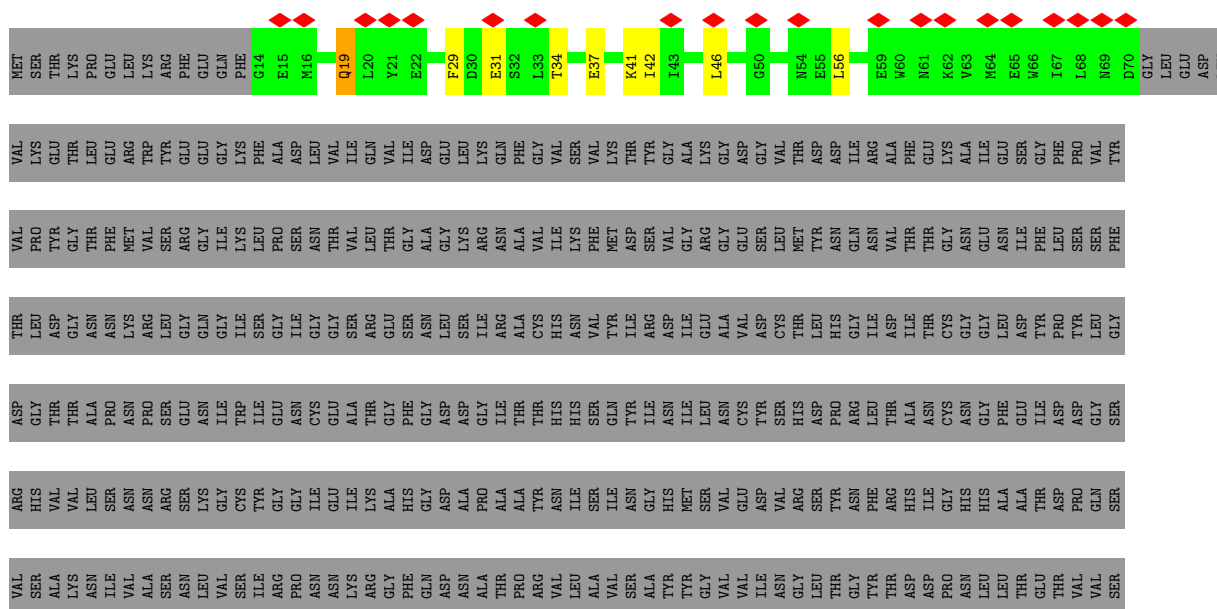
Chain U:  5% 7% 92%

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- Molecule 3: Pre-neck appendage protein

Chain W:  6% 93%





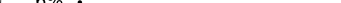
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- Molecule 3: Pre-neck appendage protein

Chain Y: 6% 94%

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- Molecule 3: Pre-neck appendage protein

Chain Z:  6% 93%

TRP	HIS	GLY	ALA	ASN	THR	ARG	THR	ILE	THR	ASN	VAL	SER	VAL	SER	VAL	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
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● Molecule 3: Pre-neck appendage protein

Chain a:  7% .  92%

MET		SER		T3		K4		P5		E6		L7		K8		R9		F10		E11		Q12		F13		G14		E15		M16		L20		Y21		E22		R23		Y24		L25		F29		D30		E31		S32		L33		T34		L35		L36		E37		K38		L46		I49		G50		N51		V52		T53		L56		I57		E58		E59		W60		N61		M64		E65		W66		I67		L68		N69		D70		G71		L72		E73	
ASP		LEU		VAL		LYS		THR		THR		LEU		GLU		TRP		TYR		GLU		GLU		LYS		PHE		ALA		ASP		LEU		ILE		GLN		VAL		PHE		GLY		VAL		GLY		SER		LYS		GLN		PHE		GLY		VAL		THR		TYR		THR		GLY		LYS		ALA		LYS		GLY		ASP		GLY		ASP		GLY		VAL		PHE		GLU		LYS		ALA		ILE		GLU		SER		GLY		PHE		PRO			
VAL		TYR		VAL		PRO		TYR		GLY		THR		PHE		VAL		VAL		ARG		ILE		LYS		LEU		PRO		SER		ASN		THR		VAL		GLY		ALA		VAL		ASN		ARG		ASN		GLY		VAL		SER		GLY		SER		MET		ASP		VAL		GLY		GLY		GLY		GLY		ASN		VAL		THR		THR		GLY		ASN		GLY		ASN		ILE		PHE		LEU		SER											
SER		PHE		THR		LEU		ASP		GLY		ASN		ASN		ARG		LEU		GLY		GLN		ILE		SER		GLY		GLY		GLY		SER		VAL		ARG		ASN		ALA		ALA		CYS		HIS		ASN		VAL		TYR		ILE		ARG		ASP		ILE		GLY		ALA		VAL		VAL		ASP		CYS		THR		LEU		HIS		GLY		GLY		GLY		LEU		ASP		TYR		PRO		TYR											

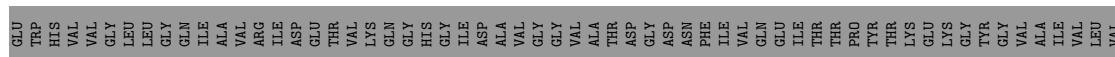


- Molecule 3: Pre-neck appendage protein

[illegible]

HIS	VAL	VAL	GLY	LEU	LEU	GLN	ILE	ALA	VAL	ARG	ILE	ASP	THR	VAL	LYS	GLN	GLY	HIS	GLY	ILE	ASP	ALA	VAL	GLY	GLY	VAL	ALA	THR	ASP	ASP	ASN	PHE	ILE	VAL	GLN	GLU	ILE	THR	THR	PRO	TYR	THR	LYS	GLU	LYS	GLY	TYR	GLY	VAL	ALA	ILE	VAL	LEU	VAL	VAL	LYS
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Chain d: 7% 92%

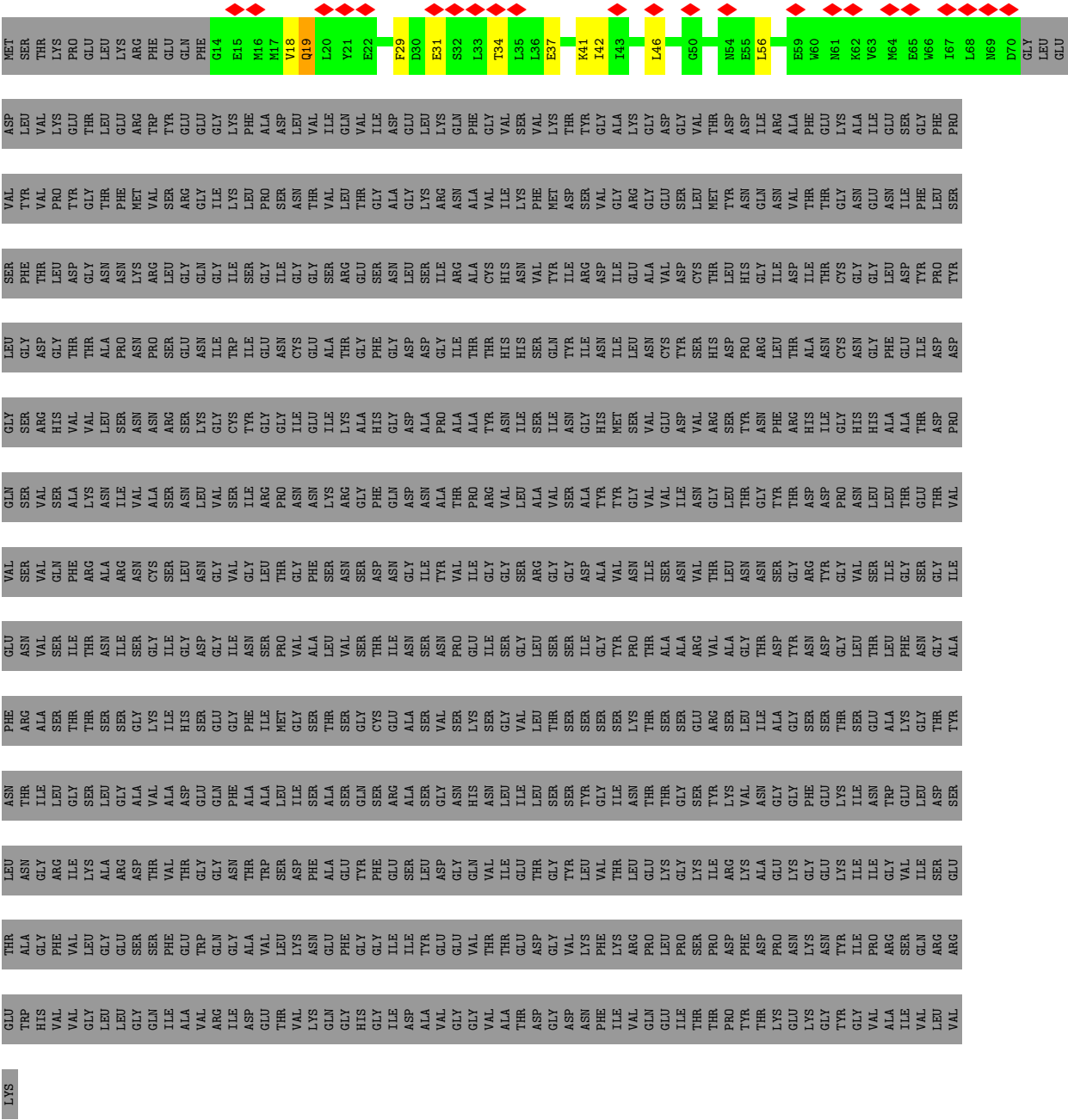


LYS

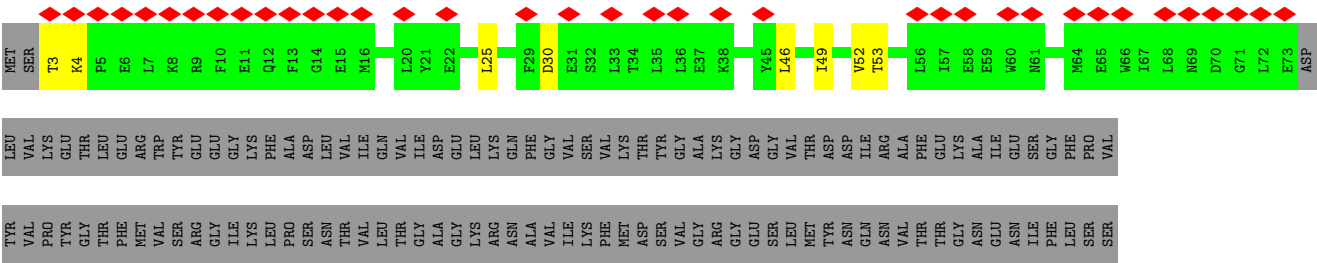
● Molecule 3: Pre-neck appendage protein



MET	THR	LYS	PRO	GLU	LEU	LYS	ARG	GLU	GLN	PHE	GLY	MET	VAL	GLN	LEU	Y21	E22	R23	Y24	L25	P26	E31	S32	L33	E37	K38	M39	I42	I43	H44	Y45	L46	M47	E48	E55	E58	E59	W60	N61	K62	V63	M64	E65	W66	I67	L68	N69	D70	G71	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
GLU	ASP	LEU	VAL	GLY	THR	LYS	GLU	TRP	TYR	GLY	GLY	GLY	ASP	LEU	VAL	THR	E22	E23	E24	E25	E26	E27	E28	E29	E30	E31	E32	E33	E34	E35	E36	E37	E38	E39	E40	E41	E42	E43	E44	E45	E46	E47	E48	E49	E50	E51	E52	E53	E54	E55	E56	E57	E58	E59	E60	E61	E62	E63	E64	E65	E66	E67	E68	E69	E70	E71	E72	E73	E74	E75	E76	E77	E78	E79	E80	E81	E82	E83	E84	E85	E86	E87	E88	E89	E90	E91	E92	E93	E94	E95	E96	E97	E98	E99	E100	E101	E102	E103	E104	E105	E106	E107	E108	E109	E110	E111	E112	E113	E114	E115	E116	E117	E118	E119	E120	E121	E122	E123	E124	E125	E126	E127	E128	E129	E130	E131	E132	E133	E134	E135	E136	E137	E138	E139	E140	E141	E142	E143	E144	E145	E146	E147	E148	E149	E150	E151	E152	E153	E154	E155	E156	E157	E158	E159	E160	E161	E162	E163	E164	E165	E166	E167	E168	E169	E170	E171	E172	E173	E174	E175	E176	E177	E178	E179	E180	E181	E182	E183	E184	E185	E186	E187	E188	E189	E190	E191	E192	E193	E194	E195	E196	E197	E198	E199	E200	E201	E202	E203	E204	E205	E206	E207	E208	E209	E210	E211	E212	E213	E214	E215	E216	E217	E218	E219	E220	E221	E222	E223	E224	E225	E226	E227	E228	E229	E230	E231	E232	E233	E234	E235	E236	E237	E238	E239	E240	E241	E242	E243	E244	E245	E246	E247	E248	E249	E250	E251	E252	E253	E254	E255	E256	E257	E258	E259	E260	E261	E262	E263	E264	E265	E266	E267	E268	E269	E270	E271	E272	E273	E274	E275	E276	E277	E278	E279	E280	E281	E282	E283	E284	E285	E286	E287	E288	E289	E290	E291	E292	E293	E294	E295	E296	E297	E298	E299	E300	E301	E302	E303	E304	E305	E306	E307	E308	E309	E310	E311	E312	E313	E314	E315	E316	E317	E318	E319	E320	E321	E322	E323	E324	E325	E326	E327	E328	E329	E330	E331	E332	E333	E334	E335	E336	E337	E338	E339	E340	E341	E342	E343	E344	E345	E346	E347	E348	E349	E350	E351	E352	E353	E354	E355	E356	E357	E358	E359	E360	E361	E362	E363	E364	E365	E366	E367	E368	E369	E370	E371	E372	E373	E374	E375	E376	E377	E378	E379	E380	E381	E382	E383	E384	E385	E386	E387	E388	E389	E390	E391	E392	E393	E394	E395	E396	E397	E398	E399	E400	E401	E402	E403	E404	E405	E406	E407	E408	E409	E410	E411	E412	E413	E414	E415	E416	E417	E418	E419	E420	E421	E422	E423	E424	E425	E426	E427	E428	E429	E430	E431	E432	E433	E434	E435	E436	E437	E438	E439	E440	E441	E442	E443	E444	E445	E446	E447	E448	E449	E450	E451	E452	E453	E454	E455	E456	E457	E458	E459	E460	E461	E462	E463	E464	E465	E466	E467	E468	E469	E470	E471	E472	E473	E474	E475	E476	E477	E478	E479	E480	E481	E482	E483	E484	E485	E486	E487	E488	E489	E490	E491	E492	E493	E494	E495	E496	E497	E498	E499	E500	E501	E502	E503	E504	E505	E506	E507	E508	E509	E510	E511	E512	E513	E514	E515	E516	E517	E518	E519	E520	E521	E522	E523	E524	E525	E526	E527	E528	E529	E530	E531	E532	E533	E534	E535	E536	E537	E538	E539	E540	E541	E542	E543	E544	E545	E546	E547	E548	E549	E550	E551	E552	E553	E554	E555	E556	E557	E558	E559	E560	E561	E562	E563	E564	E565	E566	E567	E568	E569	E570	E571	E572	E573	E574	E575	E576	E577	E578	E579	E580	E581	E582	E583	E584	E585	E586	E587	E588	E589	E590	E591	E592	E593	E594	E595	E596	E597	E598	E599	E600	E601	E602	E603	E604	E605	E606	E607	E608	E609	E610	E611	E612	E613	E614	E615	E616	E617	E618	E619	E620	E621	E622	E623	E624	E625	E626	E627	E628	E629	E630	E631	E632	E633	E634	E635	E636	E637	E638	E639	E640	E641	E642	E643	E644	E645	E646	E647	E648	E649	E650	E651	E652	E653	E654	E655	E656	E657	E658	E659	E660	E661	E662	E663	E664	E665	E666	E667	E668	E669	E670	E671	E672	E673	E674	E675	E676	E677	E678	E679	E680	E681	E682	E683	E684	E685	E686	E687	E688	E689	E690	E691	E692	E693	E694	E695	E696	E697	E698	E699	E700	E701	E702	E703	E704	E705	E706	E707	E708	E709	E710	E711	E712	E713	E714	E715	E716	E717	E718	E719	E720	E721	E722	E723	E724	E725	E726	E727	E728	E729	E730	E731	E732	E733	E734	E735	E736	E737	E738	E739	E740	E741	E742	E743	E744	E745	E746	E747	E748	E749	E750	E751	E752	E753	E754	E755	E756	E757	E758	E759	E760	E761	E762	E763	E764	E765	E766	E767	E768	E769	E770	E771	E772	E773	E774	E775	E776	E777	E778	E779	E780	E781	E782	E783	E784	E785	E786	E787	E788	E789	E790	E791	E792	E793	E794	E795	E796	E797	E798	E799	E800	E801	E802	E803	E804	E805	E806	E807	E808	E809	E810	E811	E812	E813	E814	E815	E816	E817	E818	E819	E820	E821	E822	E823	E824	E825	E826	E827	E828	E829	E830	E831	E832	E833	E834	E835	E836	E837	E838	E839	E840	E841	E842	E843	E844	E845	E846	E847	E848	E849	E850	E851	E852	E853	E854	E855	E856	E857	E858	E859	E860	E861	E862	E863	E864	E865	E866	E867	E868	E869	E870	E871	E872	E873	E874	E875	E876	E877	E878	E879	E880	E881	E882	E883	E884	E885	E886	E887	E888	E889	E890	E891	E892	E893	E894	E895	E896	E897	E898	E899	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E1000	E1001	E1002	E1003	E1004	E1005	E1006	E1007	E1008	E1009	E1010	E1011	E1012	E1013	E1014	E1015	E1016	E1017	E1018	E1019	E1020	E1021	E1022	E1023	E1024	E1025	E1026	E1027	E1028	E1029	E1030	E1031	E1032	E1033	E1034	E1035	E1036	E1037	E1038	E1039	E1040	E1041	E1042	E1043	E1044	E1045	E1046	E1047	E1048	E1049	E1050	E1051	E1052	E1053	E1054	E1055	E1056	E1057	E1058	E1059	E1060	E1061	E1062	E1063	E1064	E1065	E1066	E1067	E1068	E1069	E1070	E1071	E1072	E1073	E1074	E1075	E1076	E1077	E1078	E1079	E1080	E1081	E1082	E1083	E1084	E1085	E1086	E1087	E1088	E1089	E1090	E1091	E1092	E1093	E1094	E1095	E1096	E1097	E1098	E1099	E1100	E1101	E1102	E1103	E1104	E1105	E1106	E1107	E1108	E1109	E1110	E1111	E1112	E1113	E1114	E1115	E1116	E1117	E1118	E1119	E1120	E1121	E1122	E1123	E1124	E1125	E1126	E1127	E1128	E1129	E1130	E1131	E1132	E1133	E1134	E1135	E1136	E1137	E1138	E1139	E1140	E1141	E1142	E1143	E1144	E1145	E1146	E1147	E1148	E1149	E1150	E1151	E1152	E1153	E1154	E1155	E1156	E1157	E1158	E1159	E1160	E1161	E1162	E1163	E1164	E1165	E1166	E1167	E1168	E1169	E1170	E1171	E1172	E1173	E1174	E1175	E1176	E1177	E1178	E1179	E1180	E1181	E1182	E1183	E1184	E1185	E1186	E1187	E1188	E1189	E1190	E1191	E1192	E1193	E1194	E1195	E1196	E1197	E1198	E1199	E1200	E1201	E1202	E1203	E1204	E1205	E1206	E1207	E1208	E1209	E1210	E1211	E1212	E1213	E1214	E1215	E1216	E1217	E1218	E1219	E1220	E1221	E1222	E1223	E1224	E1225	E1226	E1227	E1228	E1229	E1230	E1231	E1232	E1233	E1234	E1235	E1236	E1237	E1238	E1239	E1240	E1241	E1242	E1243	E1244	E1245	E1246	E1247	E1248	E1249	E1250	E1251	E1252	E1253	E1254	E1255	E1256	E1257	E1258	E1259	E1260	E1261	E1262	E1263	E1264	E1265	E1266	E1267	E1268	E1269	E1270	E1271	E1272	E1273	E1274	E1275	E1276	E1277	E1278	E1279	E1280	E1281	E1282	E1283	E1284	E1285	E1286	E1287	E1288	E1289	E1290	E1291	E1292	E1293	E1294	E1295	E1296	E1297	E1298	E1299	E1300	E1301	E1302	E1303	E1304	E1305	E1306	E1307	E1308	E1309	E1310	E1311	E1312	E1313	E1314	E1315	E1316	E1317	E1318	E1319	E1320	E1321	E1322	E1323	E1324	E1325	E1326	E1327	E1328	E1329	E1330	E1331	E1332	E1333	E1334	E1335	E1336	E1337	E1338	E1339	E1340	E1341	E1342	E1343	E1344	E1345	E1346	E1347	E1348	E1349	E1350	E1351	E1352	E1353	E1354	E1355	E1356	E1357	E1358	E1359	E1360	E1361	E1362	E1363	E1364	E1365	E1366	E1367	E1368	E1369	E1370	E1371	E1372	E1373	E1374	E1375	E1376	E1377	E1378	E1379	E1380	E1381	E1382	E1383	E1384	E1385	E1386	E1387	E1388	E1389	E1390	E1391	E1392	E1393	E1394	E1395	E1396	E1397	E1398	E1399	E1400	E1401	E1402	E1403	E1404	E1405	E1406	E1407	E1408	E1409	E1410	E1411	E1412	E1413	E1414	E1415	E1416	E1417	E1418	E1419	E1420	E1421	E1422	E1423	E1424	E1425	E1426	E1427	E1428	E1429	E1430	E1431	E1432	E1433	E14



● Molecule 3: Pre-neck appendage protein



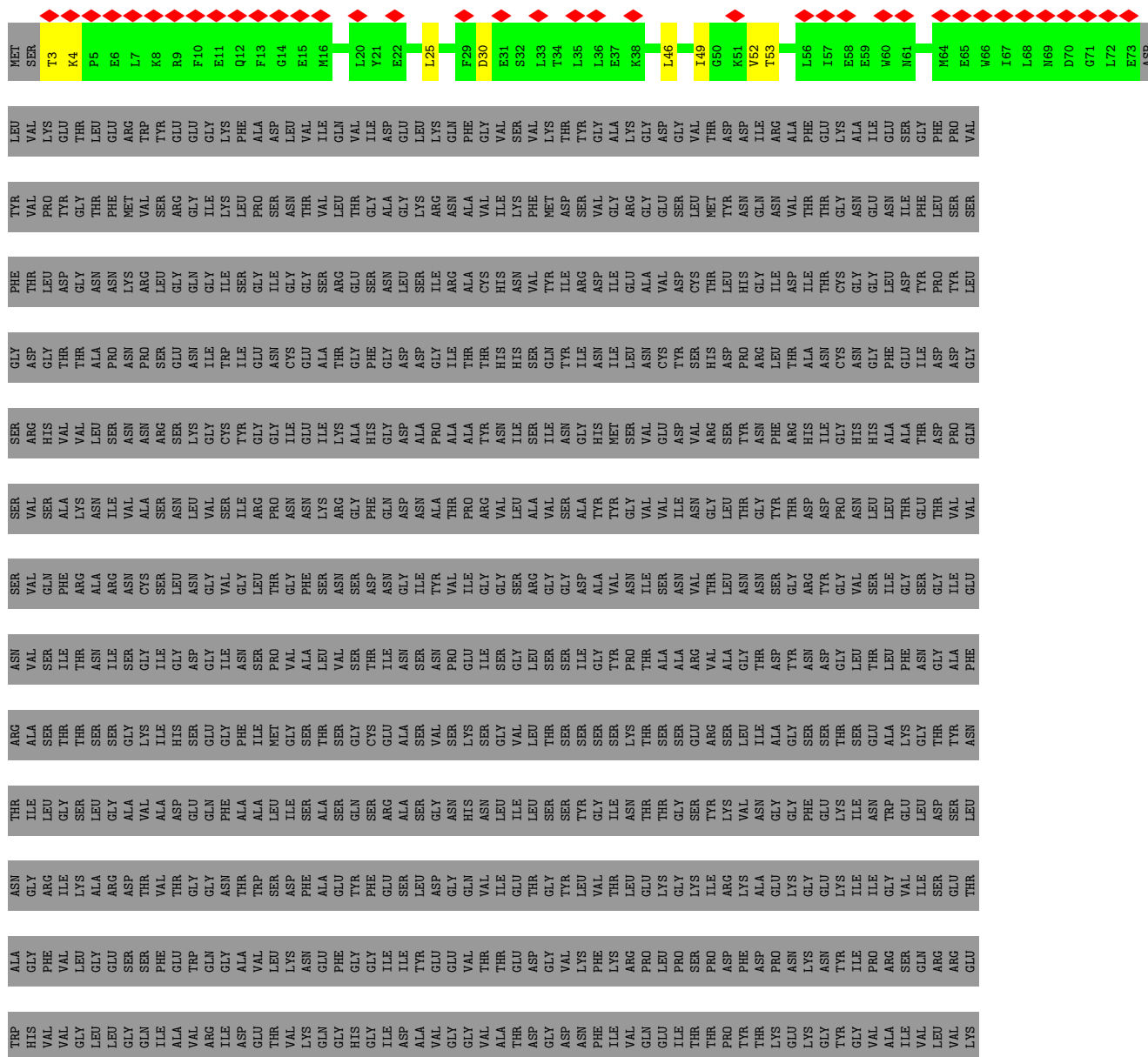


[illegible]

- Molecule 3: Pre-neck appendage protein

Chain i: 6% 93%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36370	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	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	120.855	Depositor
Minimum map value	-0.428	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.514	Depositor
Recommended contour level	6	Depositor
Map size ($\text{\AA}$)	740.8544, 740.8544, 740.8544	wwPDB
Map dimensions	572, 572, 572	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2952, 1.2952, 1.2952	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	0.23	0/2211	0.57	1/2996 (0.0%)
1	0b	0.23	0/2211	0.57	1/2996 (0.0%)
1	0c	0.23	0/2211	0.57	1/2996 (0.0%)
1	0d	0.23	0/2211	0.57	1/2996 (0.0%)
1	0e	0.23	0/2211	0.57	1/2996 (0.0%)
1	0f	0.23	0/2211	0.57	1/2996 (0.0%)
1	0g	0.23	0/2211	0.57	1/2996 (0.0%)
1	0h	0.23	0/2211	0.57	1/2996 (0.0%)
1	0i	0.23	0/2211	0.57	1/2996 (0.0%)
1	0j	0.23	0/2211	0.57	1/2996 (0.0%)
1	0k	0.23	0/2211	0.57	1/2996 (0.0%)
1	0l	0.23	0/2211	0.57	1/2996 (0.0%)
2	0A	0.31	0/2331	0.60	0/3144
2	0B	0.32	0/2331	0.60	0/3144
2	0C	0.32	0/2331	0.60	0/3144
2	0D	0.31	0/2331	0.60	0/3144
2	0E	0.32	0/2331	0.60	0/3144
2	0F	0.32	0/2331	0.60	0/3144
2	0G	0.32	0/2331	0.60	0/3144
2	0H	0.32	0/2331	0.60	0/3144
2	0I	0.32	0/2331	0.60	0/3144
2	0J	0.32	0/2331	0.61	0/3144
2	0K	0.32	0/2331	0.60	0/3144
2	0L	0.32	0/2331	0.60	0/3144
3	A	0.29	0/442	0.69	0/598
3	B	0.33	0/491	0.69	2/663 (0.3%)
3	C	0.23	0/615	0.59	0/828
3	D	0.29	0/442	0.69	0/598
3	E	0.30	0/491	0.68	2/663 (0.3%)
3	F	0.23	0/615	0.59	0/828
3	G	0.29	0/442	0.69	0/598
3	H	0.32	0/491	0.68	2/663 (0.3%)
3	I	0.23	0/615	0.59	0/828
3	J	0.29	0/442	0.69	0/598

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	K	0.32	0/491	0.68	2/663 (0.3%)
3	L	0.23	0/615	0.59	0/828
3	M	0.30	0/442	0.69	0/598
3	N	0.32	0/491	0.68	2/663 (0.3%)
3	O	0.23	0/615	0.59	0/828
3	P	0.30	0/442	0.69	0/598
3	Q	0.32	0/491	0.68	2/663 (0.3%)
3	R	0.23	0/615	0.59	0/828
3	S	0.30	0/442	0.70	0/598
3	T	0.31	0/491	0.68	2/663 (0.3%)
3	U	0.23	0/615	0.59	0/828
3	V	0.29	0/442	0.70	0/598
3	W	0.31	0/491	0.68	2/663 (0.3%)
3	X	0.23	0/615	0.59	0/828
3	Y	0.30	0/442	0.69	0/598
3	Z	0.31	0/491	0.69	2/663 (0.3%)
3	a	0.23	0/615	0.59	0/828
3	b	0.29	0/442	0.69	0/598
3	c	0.32	0/491	0.69	2/663 (0.3%)
3	d	0.23	0/615	0.59	0/828
3	e	0.30	0/442	0.71	0/598
3	f	0.29	0/491	0.68	2/663 (0.3%)
3	g	0.23	0/615	0.59	0/828
3	h	0.29	0/442	0.70	0/598
3	i	0.30	0/491	0.68	2/663 (0.3%)
3	j	0.23	0/615	0.59	0/828
All	All	0.28	0/73080	0.60	36/98748 (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
1	0a	0	1
1	0b	0	1
1	0c	0	1
1	0d	0	1
1	0e	0	1
1	0f	0	1
1	0g	0	1
1	0h	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	0i	0	1
1	0j	0	1
1	0k	0	1
1	0l	0	1
3	B	0	1
3	f	0	1
All	All	0	14

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0e	72	SER	N-CA-C	5.89	118.61	109.60
1	0b	72	SER	N-CA-C	5.88	118.60	109.60
1	0k	72	SER	N-CA-C	5.88	118.60	109.60
1	0g	72	SER	N-CA-C	5.88	118.60	109.60
1	0d	72	SER	N-CA-C	5.88	118.59	109.60

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0a	72	SER	Peptide
1	0b	72	SER	Peptide
1	0c	72	SER	Peptide
1	0d	72	SER	Peptide
1	0e	72	SER	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	0a	2163	0	2104	34	0
1	0b	2163	0	2104	36	0
1	0c	2163	0	2104	35	0
1	0d	2163	0	2104	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0e	2163	0	2104	37	0
1	0f	2163	0	2104	35	0
1	0g	2163	0	2104	33	0
1	0h	2163	0	2104	36	0
1	0i	2163	0	2104	37	0
1	0j	2163	0	2104	35	0
1	0k	2163	0	2104	37	0
1	0l	2163	0	2104	36	0
2	0A	2296	0	2143	56	0
2	0B	2296	0	2143	56	0
2	0C	2296	0	2143	38	0
2	0D	2296	0	2143	37	0
2	0E	2296	0	2143	38	0
2	0F	2296	0	2143	39	0
2	0G	2296	0	2143	37	0
2	0H	2296	0	2143	37	0
2	0I	2296	0	2143	51	0
2	0J	2296	0	2143	57	0
2	0K	2296	0	2143	47	0
2	0L	2296	0	2143	37	0
3	A	433	0	425	3	0
3	B	482	0	477	11	0
3	C	603	0	599	9	0
3	D	433	0	425	3	0
3	E	482	0	477	7	0
3	F	603	0	599	9	0
3	G	433	0	425	3	0
3	H	482	0	477	8	0
3	I	603	0	599	9	0
3	J	433	0	425	3	0
3	K	482	0	477	8	0
3	L	603	0	599	9	0
3	M	433	0	425	3	0
3	N	482	0	477	8	0
3	O	603	0	599	9	0
3	P	433	0	425	3	0
3	Q	482	0	477	8	0
3	R	603	0	599	9	0
3	S	433	0	425	3	0
3	T	482	0	477	9	0
3	U	603	0	599	9	0
3	V	433	0	425	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	W	482	0	477	8	0
3	X	603	0	599	9	0
3	Y	433	0	425	4	0
3	Z	482	0	477	10	0
3	a	603	0	599	9	0
3	b	433	0	425	4	0
3	c	482	0	477	8	0
3	d	603	0	599	9	0
3	e	433	0	425	4	0
3	f	482	0	477	6	0
3	g	603	0	599	8	0
3	h	433	0	425	4	0
3	i	482	0	477	8	0
3	j	603	0	599	8	0
All	All	71724	0	68976	928	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 7.

The worst 5 of 928 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)
2:0E:193:ILE:O	2:0E:194:GLU:HG3	1.88	0.74
2:0H:193:ILE:O	2:0H:194:GLU:HG3	1.88	0.74
2:0F:193:ILE:O	2:0F:194:GLU:HG3	1.88	0.74
2:0I:193:ILE:O	2:0I:194:GLU:HG3	1.88	0.74
2:0C:193:ILE:O	2:0C:194:GLU:HG3	1.88	0.73

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	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0b	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0c	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0d	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0e	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0f	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0g	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0h	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0i	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0j	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0k	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
1	0l	260/309 (84%)	243 (94%)	17 (6%)	0	100	100
2	0A	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0B	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0C	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0D	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0E	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0F	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0G	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0H	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0I	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0J	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0K	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
2	0L	289/293 (99%)	272 (94%)	17 (6%)	0	100	100
3	A	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	B	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	C	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	D	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	E	55/854 (6%)	51 (93%)	3 (6%)	1 (2%)	6	29
3	F	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	G	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	H	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	J	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	K	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	L	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	M	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	N	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	O	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	P	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	Q	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	R	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	S	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	T	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	U	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	V	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	W	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	X	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	Y	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	Z	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	a	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	b	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	c	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	d	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	e	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	f	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	g	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
3	h	49/854 (6%)	42 (86%)	7 (14%)	0	100	100
3	i	55/854 (6%)	52 (94%)	2 (4%)	1 (2%)	6	29
3	j	69/854 (8%)	63 (91%)	6 (9%)	0	100	100
All	All	8664/37968 (23%)	8063 (93%)	589 (7%)	12 (0%)	49	75

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	19	GLN
3	E	19	GLN
3	H	19	GLN
3	K	19	GLN
3	N	19	GLN

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	236/277 (85%)	236 (100%)	0	100	100
1	0b	236/277 (85%)	236 (100%)	0	100	100
1	0c	236/277 (85%)	236 (100%)	0	100	100
1	0d	236/277 (85%)	236 (100%)	0	100	100
1	0e	236/277 (85%)	236 (100%)	0	100	100
1	0f	236/277 (85%)	236 (100%)	0	100	100
1	0g	236/277 (85%)	236 (100%)	0	100	100
1	0h	236/277 (85%)	236 (100%)	0	100	100
1	0i	236/277 (85%)	236 (100%)	0	100	100
1	0j	236/277 (85%)	236 (100%)	0	100	100
1	0k	236/277 (85%)	236 (100%)	0	100	100
1	0l	236/277 (85%)	236 (100%)	0	100	100
2	0A	249/270 (92%)	249 (100%)	0	100	100
2	0B	249/270 (92%)	249 (100%)	0	100	100
2	0C	249/270 (92%)	249 (100%)	0	100	100
2	0D	249/270 (92%)	249 (100%)	0	100	100
2	0E	249/270 (92%)	249 (100%)	0	100	100
2	0F	249/270 (92%)	249 (100%)	0	100	100
2	0G	249/270 (92%)	249 (100%)	0	100	100
2	0H	249/270 (92%)	249 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	0I	249/270 (92%)	249 (100%)	0	100	100
2	0J	249/270 (92%)	249 (100%)	0	100	100
2	0K	249/270 (92%)	249 (100%)	0	100	100
2	0L	249/270 (92%)	249 (100%)	0	100	100
3	A	48/706 (7%)	48 (100%)	0	100	100
3	B	54/706 (8%)	54 (100%)	0	100	100
3	C	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (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	67/706 (10%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	b	48/706 (7%)	48 (100%)	0	100	100
3	c	54/706 (8%)	54 (100%)	0	100	100
3	d	67/706 (10%)	67 (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	67/706 (10%)	67 (100%)	0	100	100
3	h	48/706 (7%)	48 (100%)	0	100	100
3	i	54/706 (8%)	54 (100%)	0	100	100
3	j	67/706 (10%)	67 (100%)	0	100	100
All	All	7848/31980 (24%)	7848 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
3	Z	54	ASN
3	c	54	ASN
2	0E	162	ASN
2	0E	126	GLN
3	e	61	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.

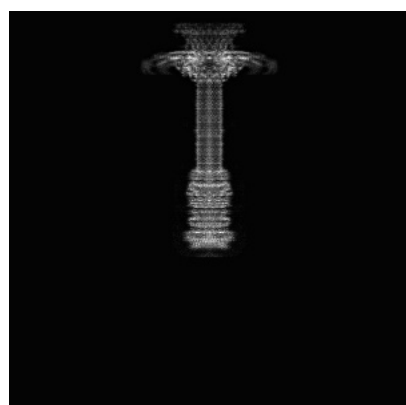
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4684. These allow visual inspection of the internal detail of the map and identification of artifacts.

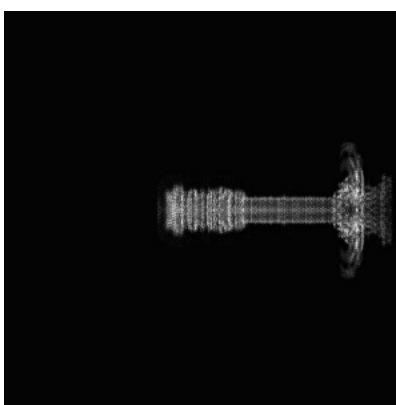
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

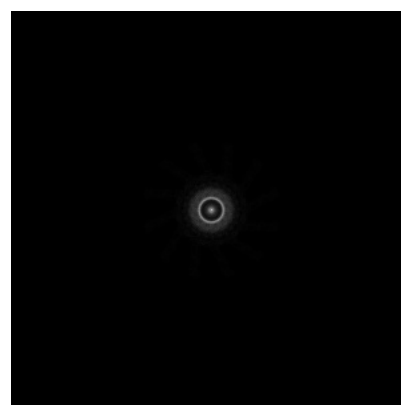
6.1.1 Primary map



X



Y

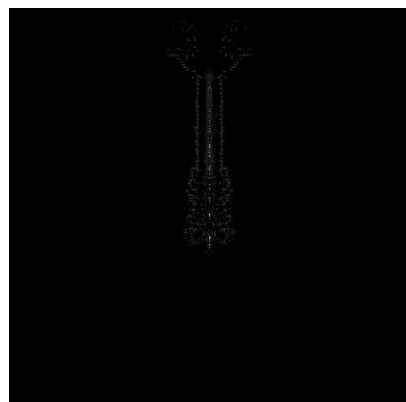


Z

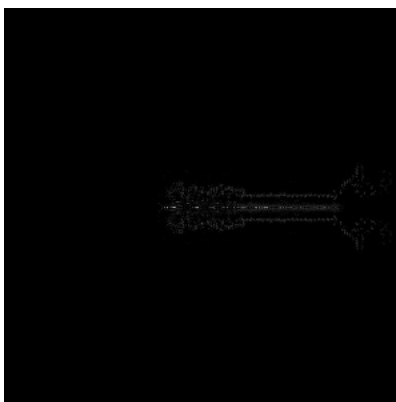
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

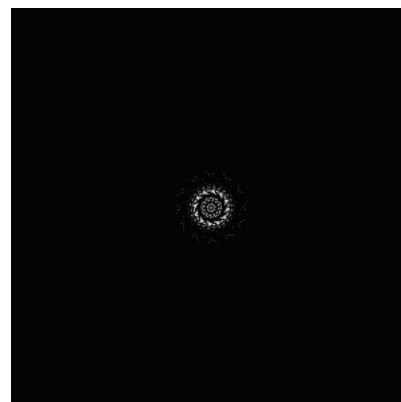
6.2.1 Primary map



X Index: 286



Y Index: 286

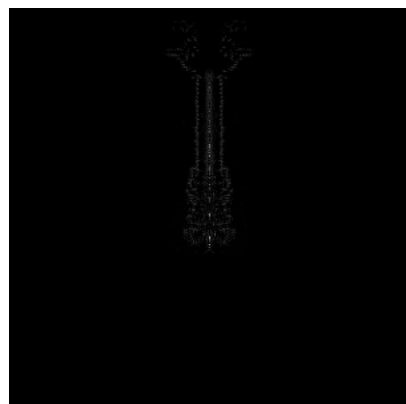


Z Index: 286

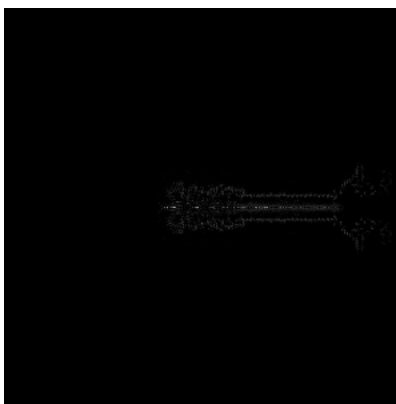
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

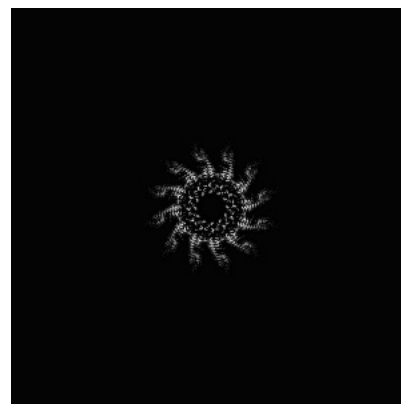
6.3.1 Primary map



X Index: 286



Y Index: 286

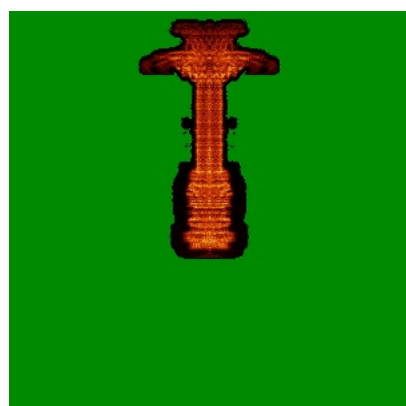


Z Index: 504

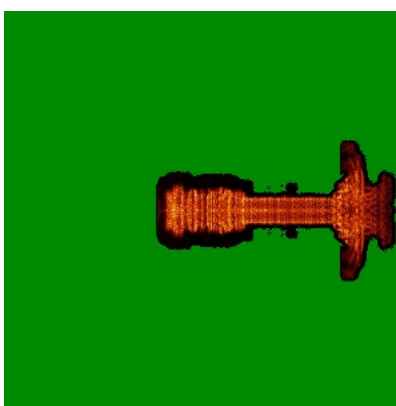
The images above show the largest variance slices of the map in three orthogonal directions.

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

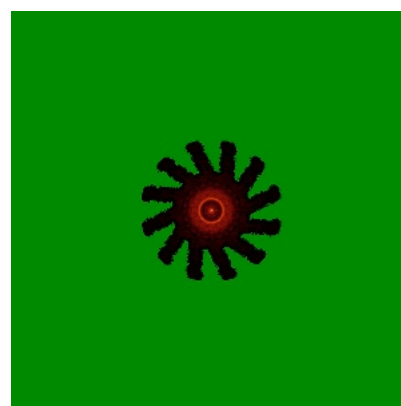
6.4.1 Primary map



X



Y

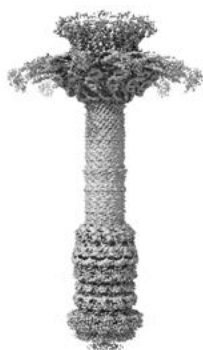


Z

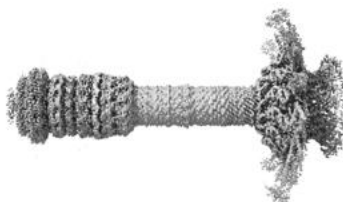
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

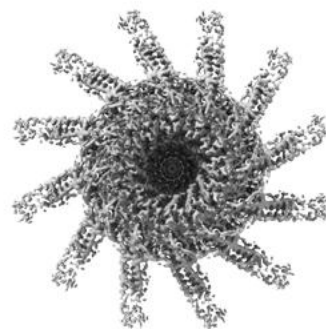
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

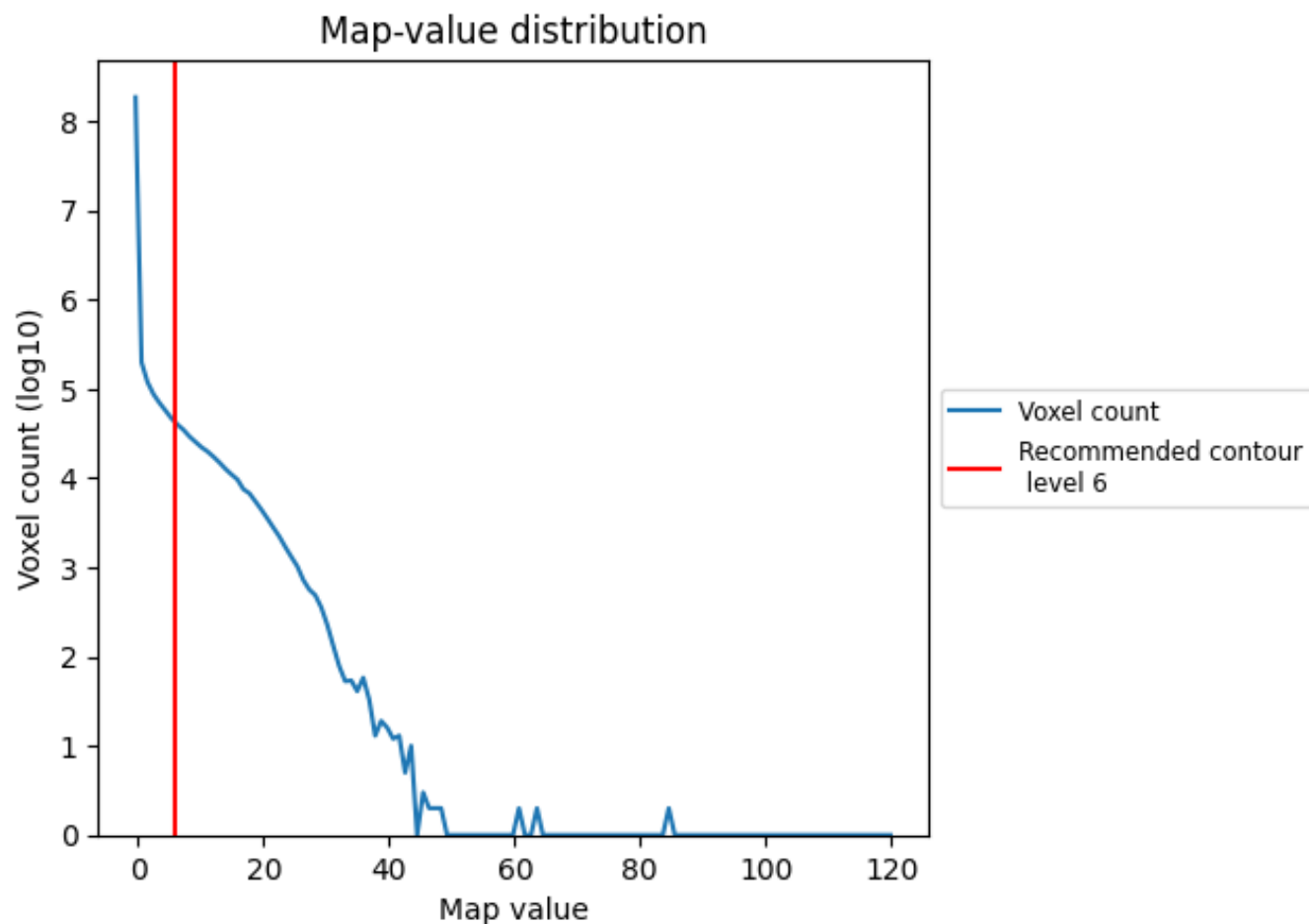
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

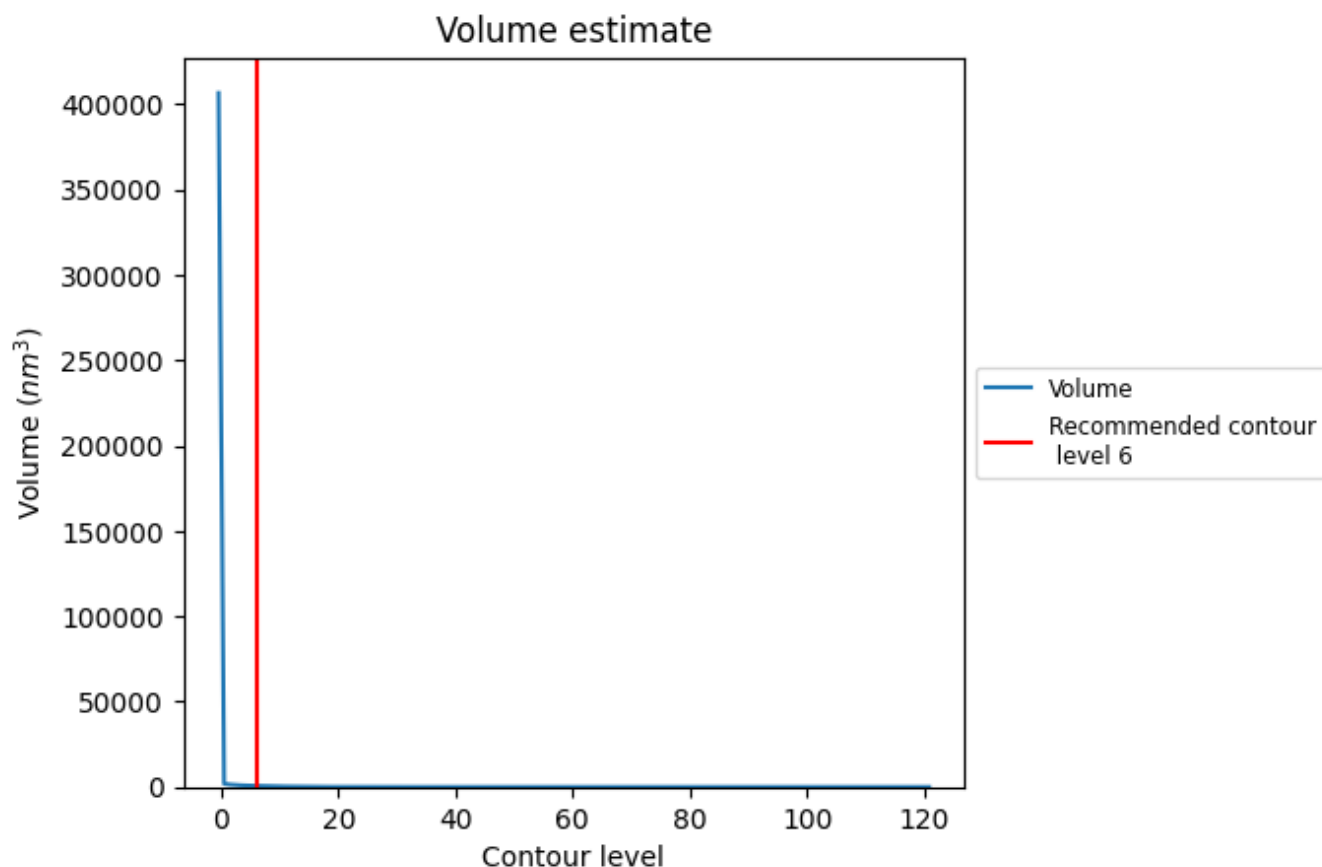
This section contains the results of statistical analysis of the map.

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.

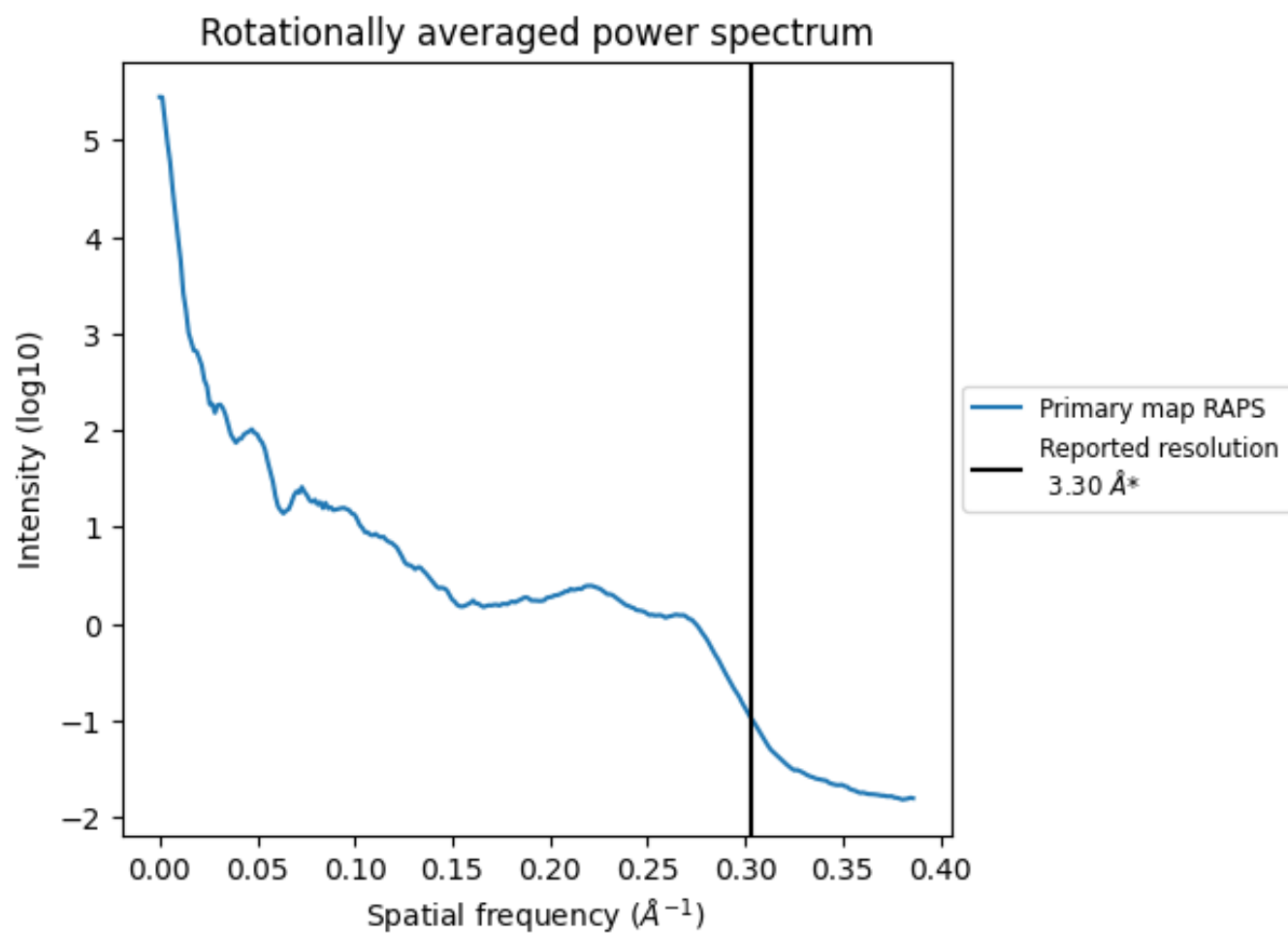
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 630 nm^3 ; this corresponds to an approximate mass of 569 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 0.303 Å⁻¹

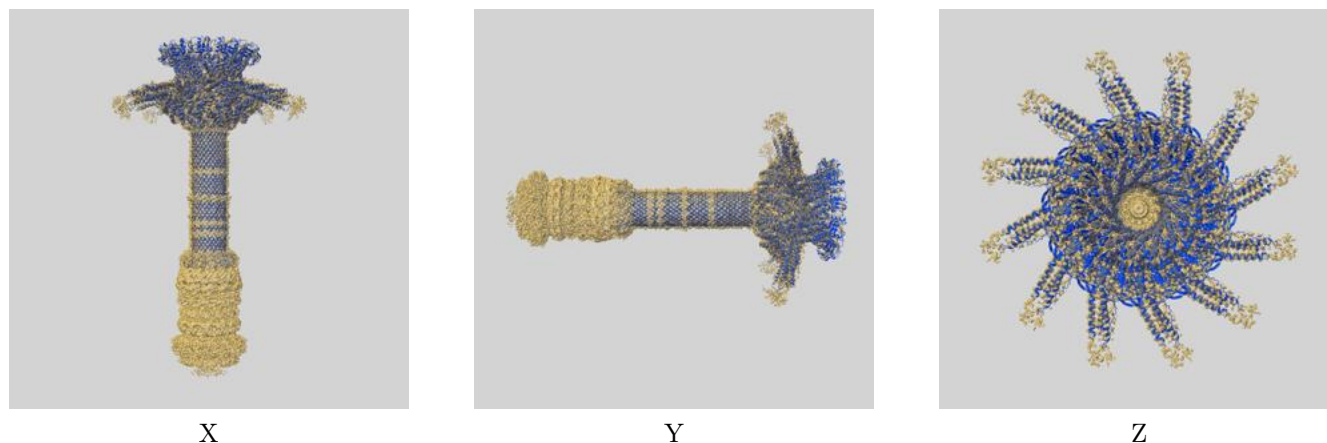
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

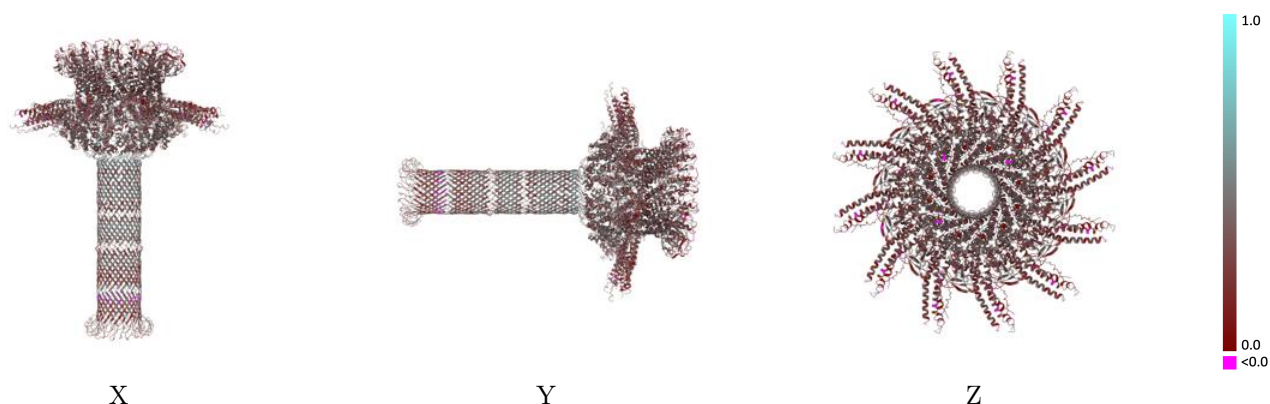
This section contains information regarding the fit between EMDB map EMD-4684 and PDB model 6QZ9. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 6.0 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](#)

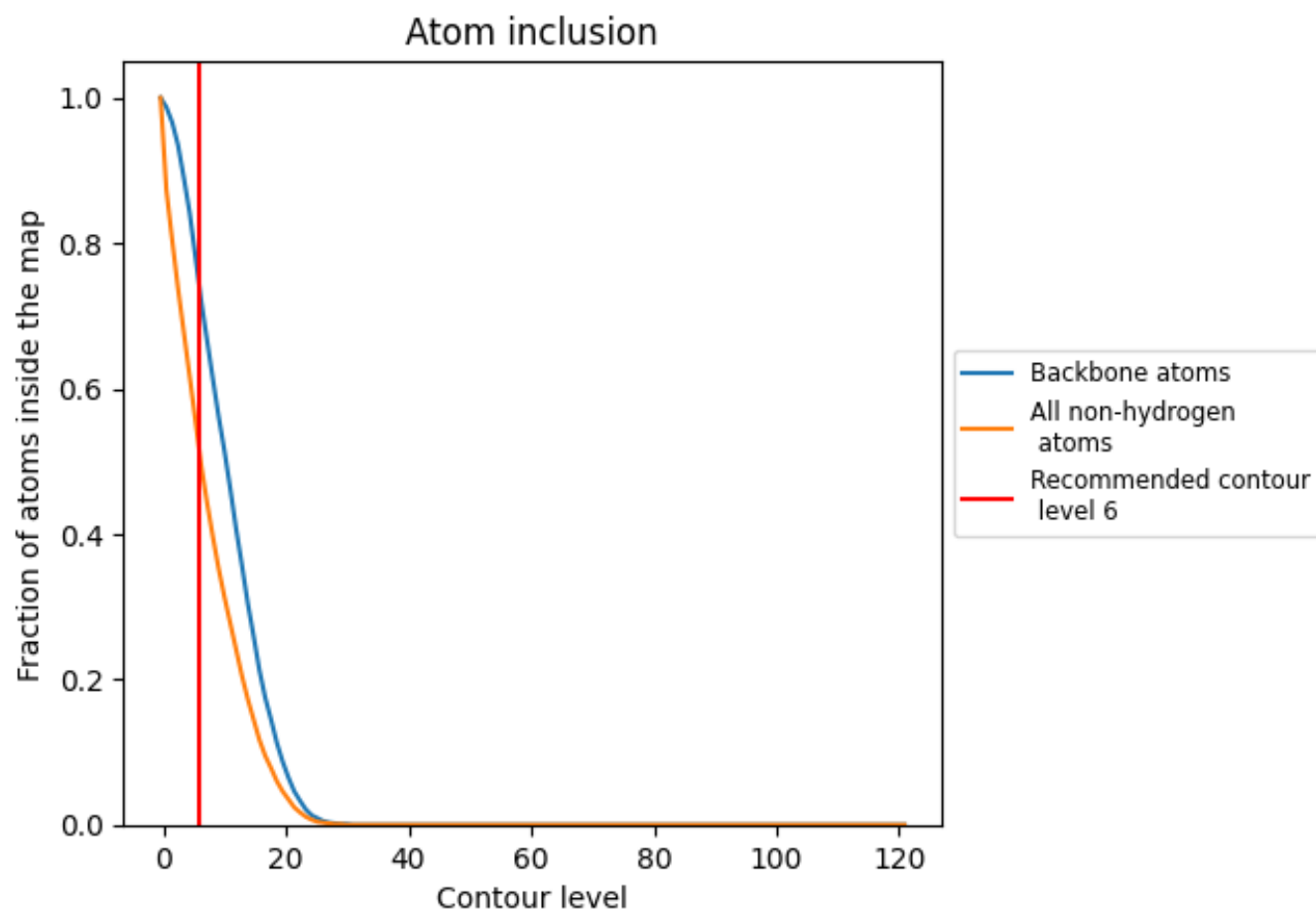


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 51% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5070	 0.3310
0A	 0.7320	 0.3750
0B	 0.7270	 0.3720
0C	 0.7330	 0.3750
0D	 0.7320	 0.3750
0E	 0.7330	 0.3750
0F	 0.7340	 0.3740
0G	 0.7320	 0.3730
0H	 0.7330	 0.3730
0I	 0.7320	 0.3730
0J	 0.7300	 0.3730
0K	 0.7250	 0.3710
0L	 0.7330	 0.3740
0a	 0.3370	 0.3190
0b	 0.3360	 0.3170
0c	 0.3380	 0.3160
0d	 0.3370	 0.3180
0e	 0.3370	 0.3170
0f	 0.3380	 0.3160
0g	 0.3370	 0.3180
0h	 0.3360	 0.3180
0i	 0.3370	 0.3170
0j	 0.3370	 0.3190
0k	 0.3360	 0.3180
0l	 0.3370	 0.3180
A	 0.4250	 0.2620
B	 0.4590	 0.2920
C	 0.3620	 0.3070
D	 0.4200	 0.2620
E	 0.4590	 0.2880
F	 0.3650	 0.3080
G	 0.4270	 0.2610
H	 0.4550	 0.2910
I	 0.3590	 0.3070
J	 0.4250	 0.2650



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Chain	Atom inclusion	Q-score
K	 0.4610	 0.2900
L	 0.3620	 0.3050
M	 0.4220	 0.2610
N	 0.4610	 0.2880
O	 0.3650	 0.3060
P	 0.4300	 0.2600
Q	 0.4530	 0.2880
R	 0.3590	 0.3040
S	 0.4250	 0.2640
T	 0.4610	 0.2910
U	 0.3640	 0.3030
V	 0.4200	 0.2600
W	 0.4610	 0.2870
X	 0.3670	 0.3060
Y	 0.4270	 0.2600
Z	 0.4480	 0.2880
a	 0.3640	 0.3020
b	 0.4200	 0.2580
c	 0.4610	 0.2880
d	 0.3620	 0.3060
e	 0.4150	 0.2610
f	 0.4550	 0.2880
g	 0.3720	 0.3020
h	 0.4270	 0.2570
i	 0.4530	 0.2910
j	 0.3620	 0.3050