



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:38 AM UTC

PDB ID : 7EY9 / pdb_00007ey9
EMDB ID : EMD-31319
Title : tail proteins
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2021-05-30
Resolution : 3.40 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:

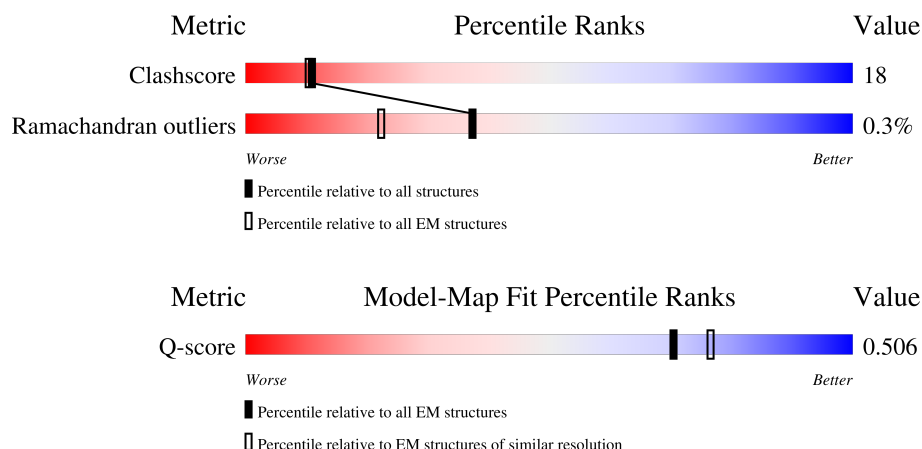
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	553	16% 9% . 75%
1	b	553	13% 10% . 76%
1	c	553	5% 16% 8% . 75%
1	d	553	16% 8% . 75%
1	e	553	13% 10% . 76%

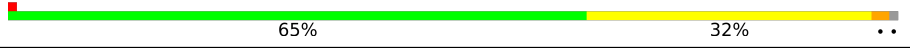
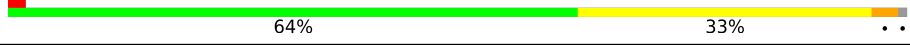
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Mol	Chain	Length	Quality of chain
1	f	553	
1	g	553	
1	h	553	
1	i	553	
1	j	553	
1	k	553	
1	l	553	
1	m	553	
1	n	553	
1	o	553	
1	p	553	
1	q	553	
1	r	553	
2	s	794	
2	t	794	
2	u	794	
2	v	794	
2	w	794	
2	x	794	
3	M	196	
3	N	196	
3	O	196	
3	P	196	
3	Q	196	
3	R	196	

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Mol	Chain	Length	Quality of chain
3	S	196	
3	T	196	
3	U	196	
3	V	196	
3	W	196	
3	X	196	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 76038 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 Tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	b	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	c	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	d	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	e	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	f	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	g	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	h	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	i	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	j	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	k	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	l	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	m	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	n	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	o	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	p	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	q	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		

- Molecule 2 is a protein called Tail tubular protein gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	t	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	u	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	v	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	w	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	x	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		

- Molecule 3 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	N	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	O	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	P	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	Q	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	R	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	S	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	T	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	U	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	V	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

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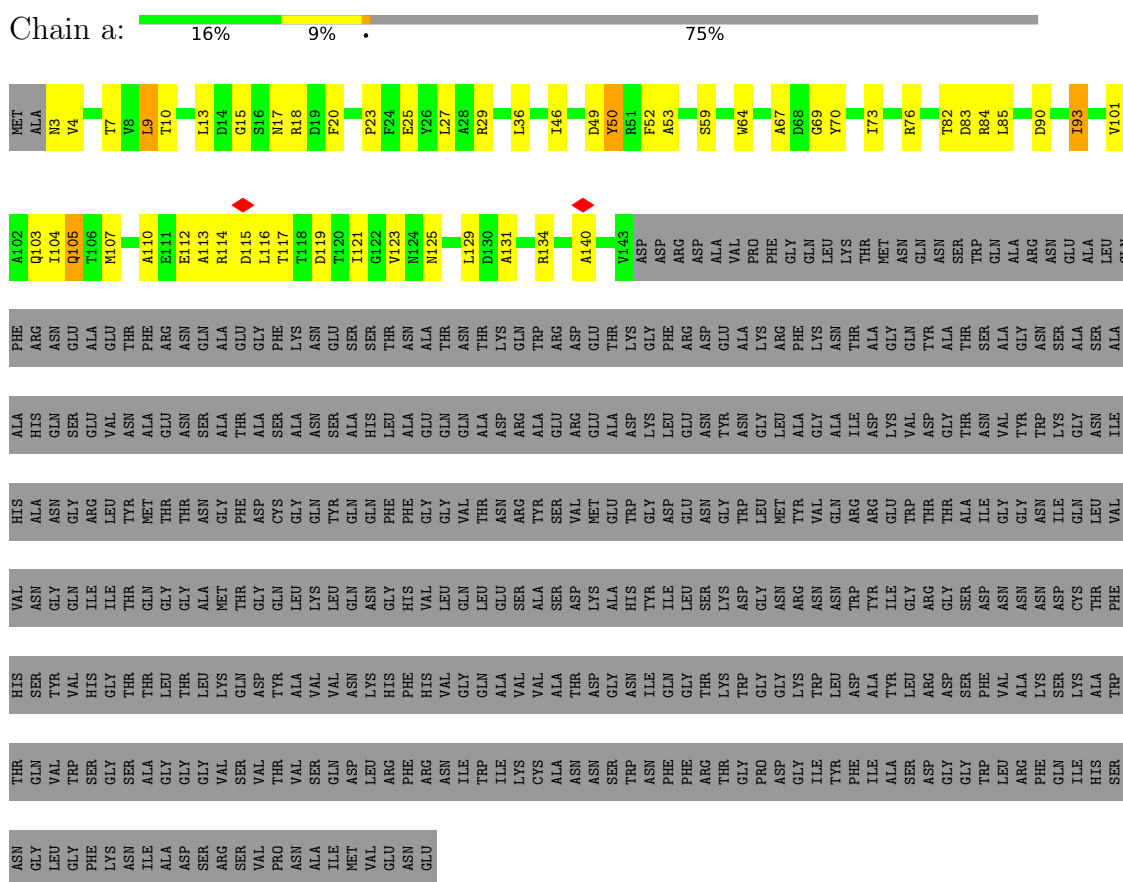
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	X	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

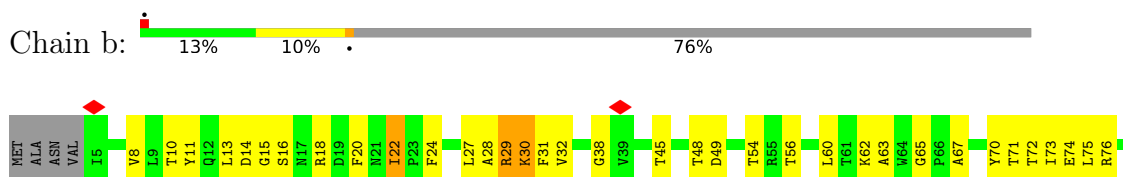
3 Residue-property plots

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.

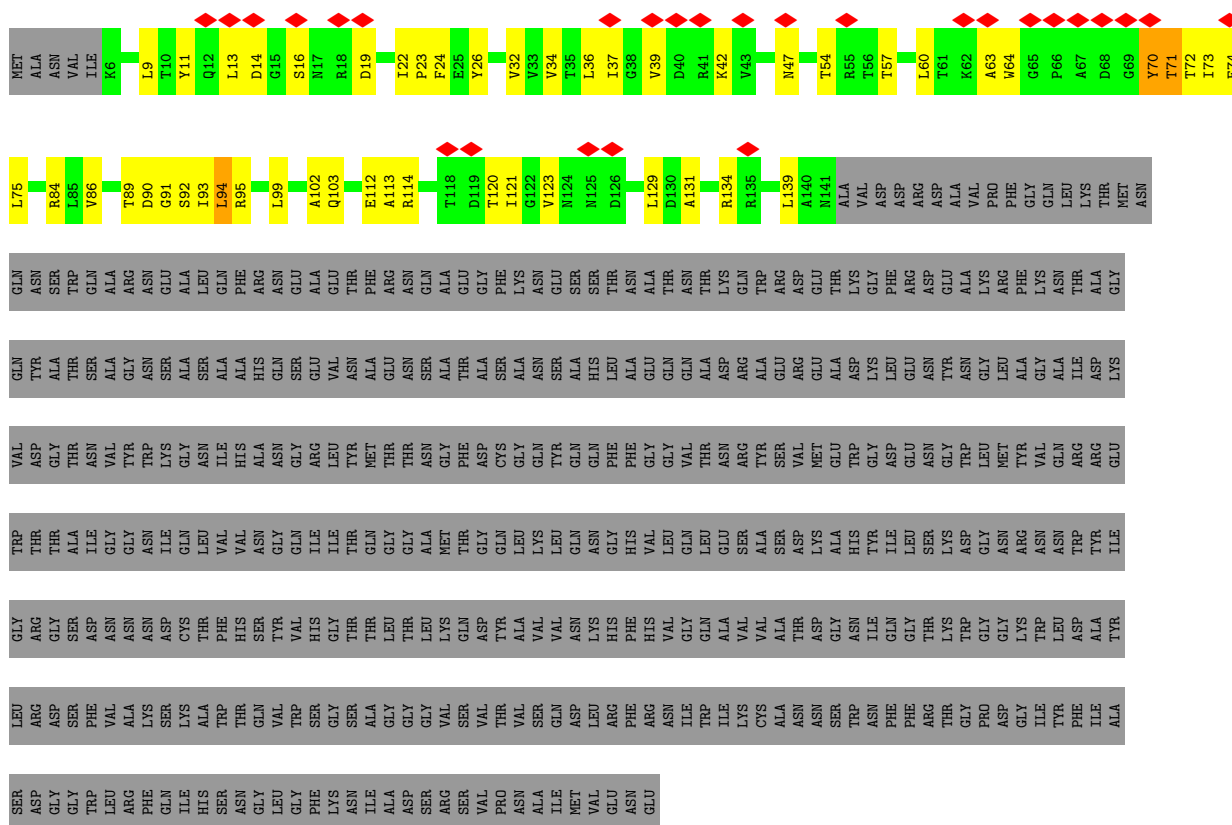
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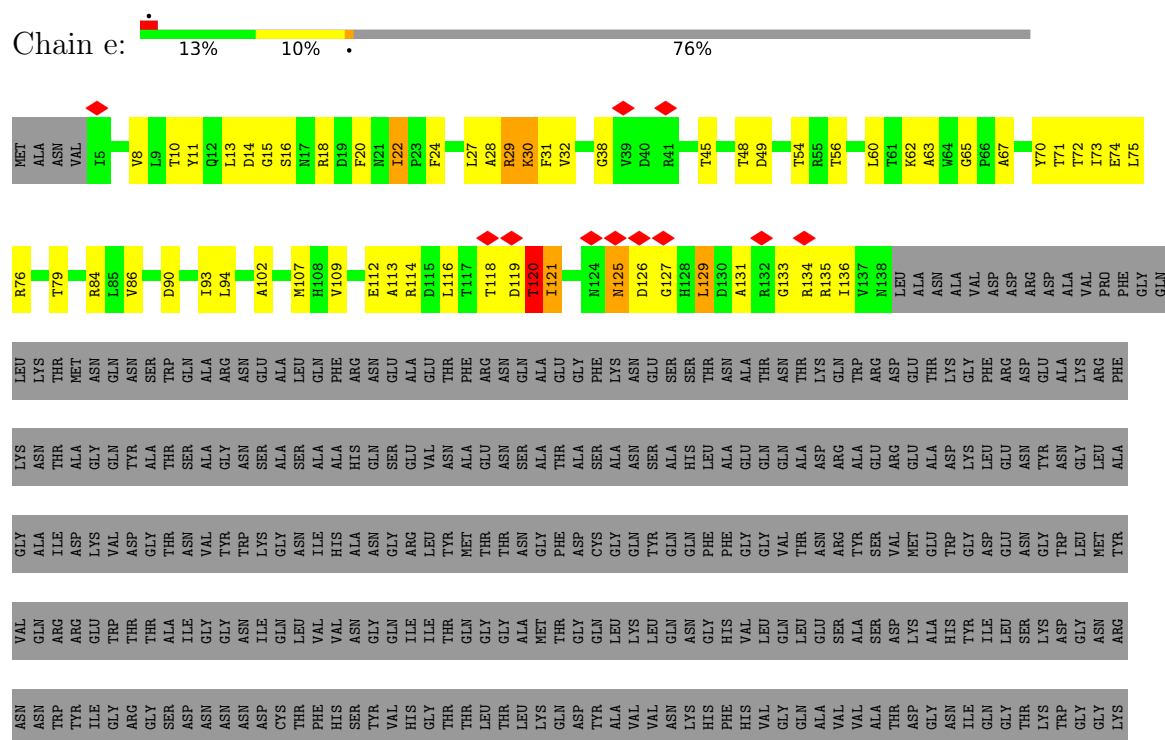
• Molecule 1: Tail fiber protein



- Molecule 1: Tail fiber protein

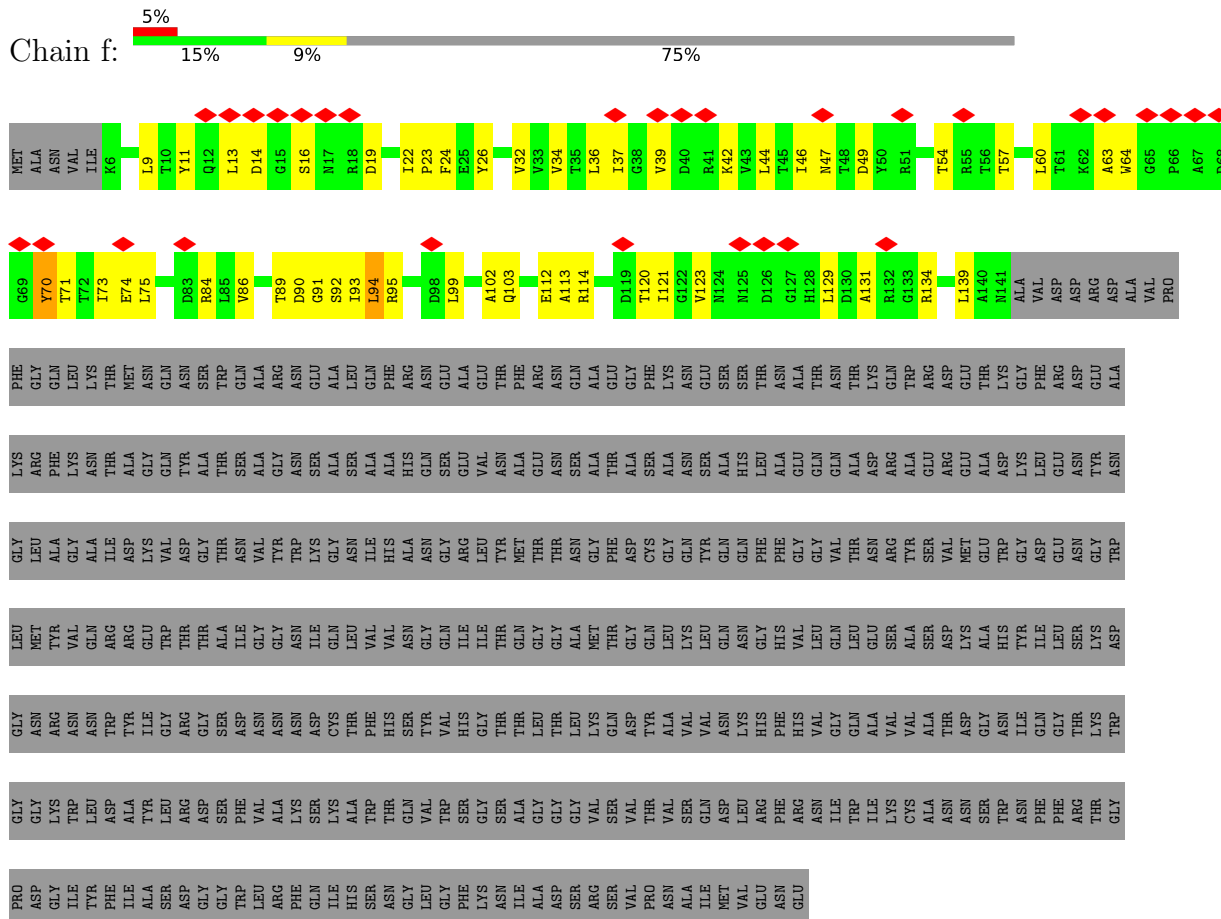


- Molecule 1: Tail fiber protein

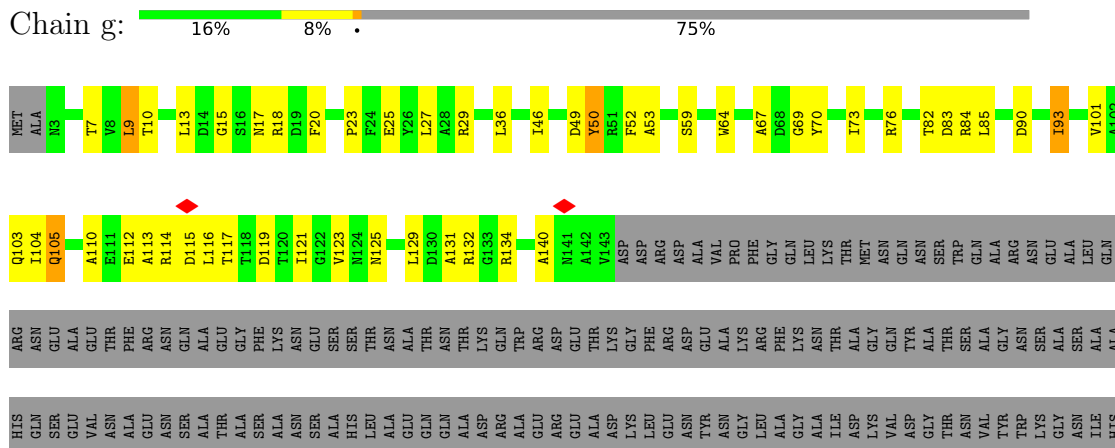


[illegible]

- Molecule 1: Tail fiber protein

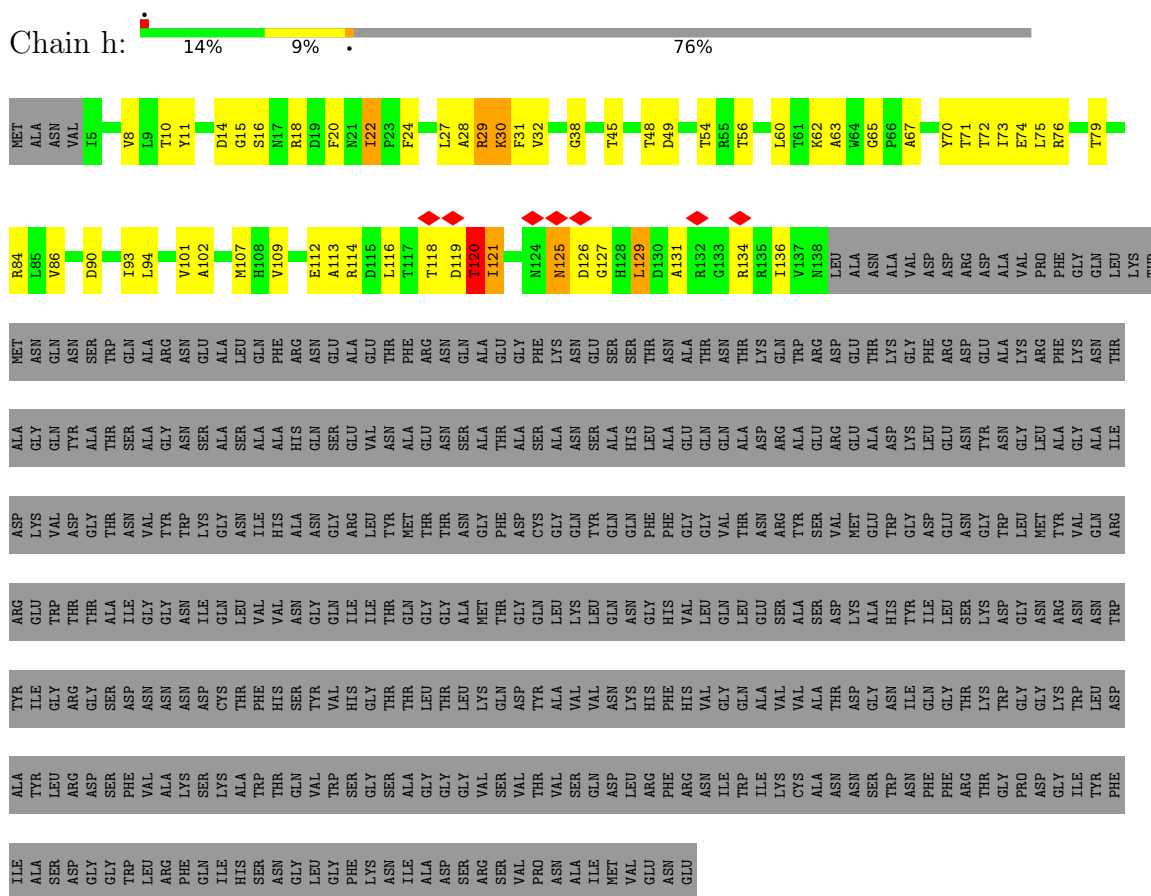


- Molecule 1: Tail fiber protein

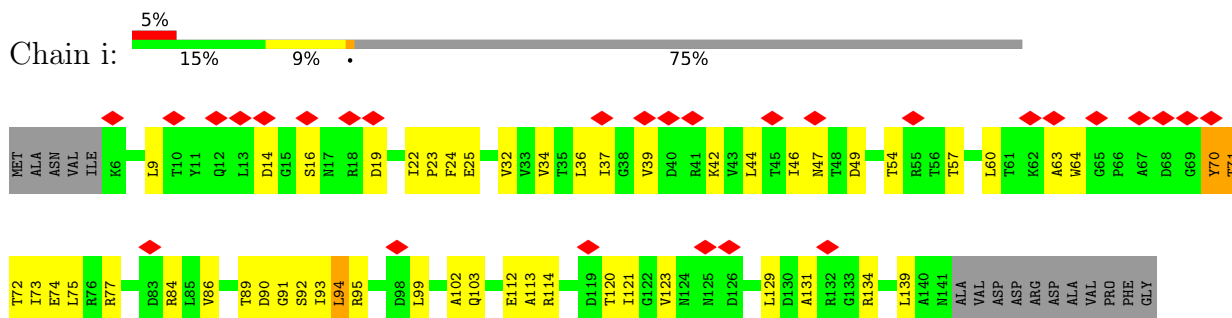


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- Molecule 1: Tail fiber protein



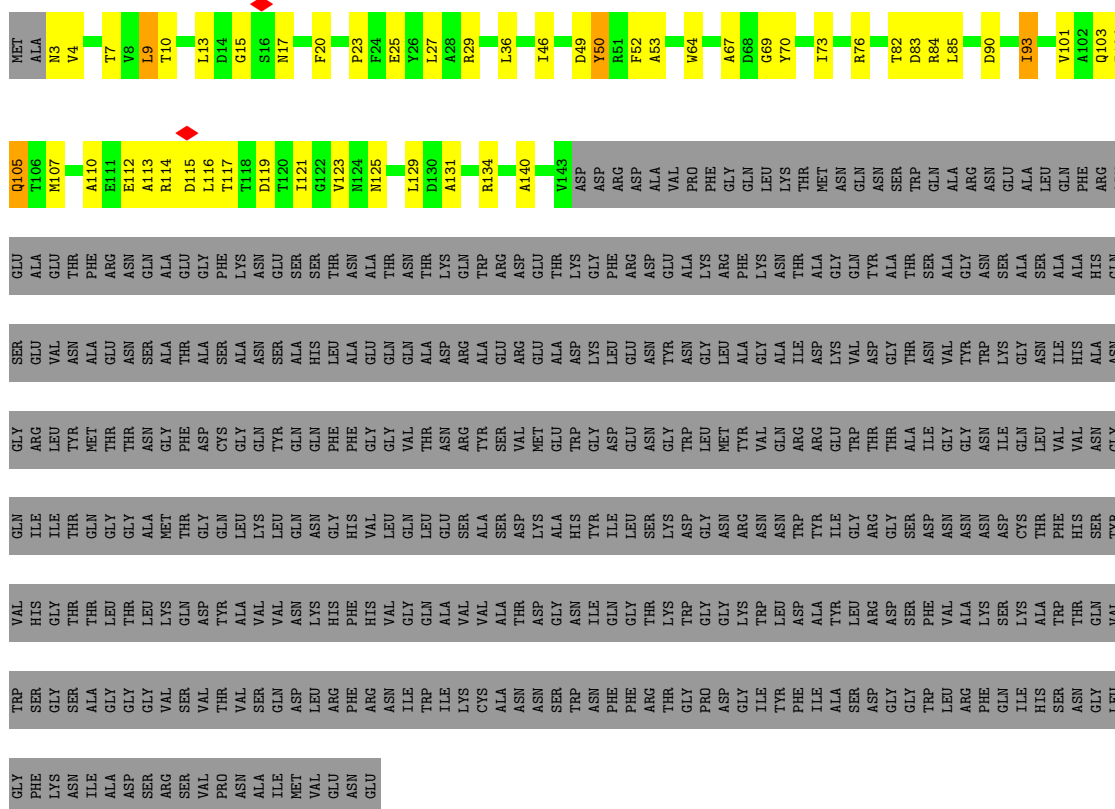
- Molecule 1: Tail fiber protein



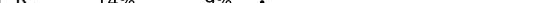
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ILE	THR	TRP	ASN	VAL	VAL	GLY	LYS	LEU
THR	LEU	LEU	ASN	GLN	GLN	ILE	ASN	LYS
PHE	ASP	TRP	TRP	ARG	ARG	ILE	THR	THR
ILE	ALA	ALA	TYR	THR	GLU	LYS	ALA	WET
ALA	TYR	ILE	ILE	GLU	GLU	VAL	GLN	ASN
SER	LEU	LEU	GLY	TRP	TRP	VAL	GLN	GLN
ASP	ASP	GLY	ARG	THR	THR	VAL	TYR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

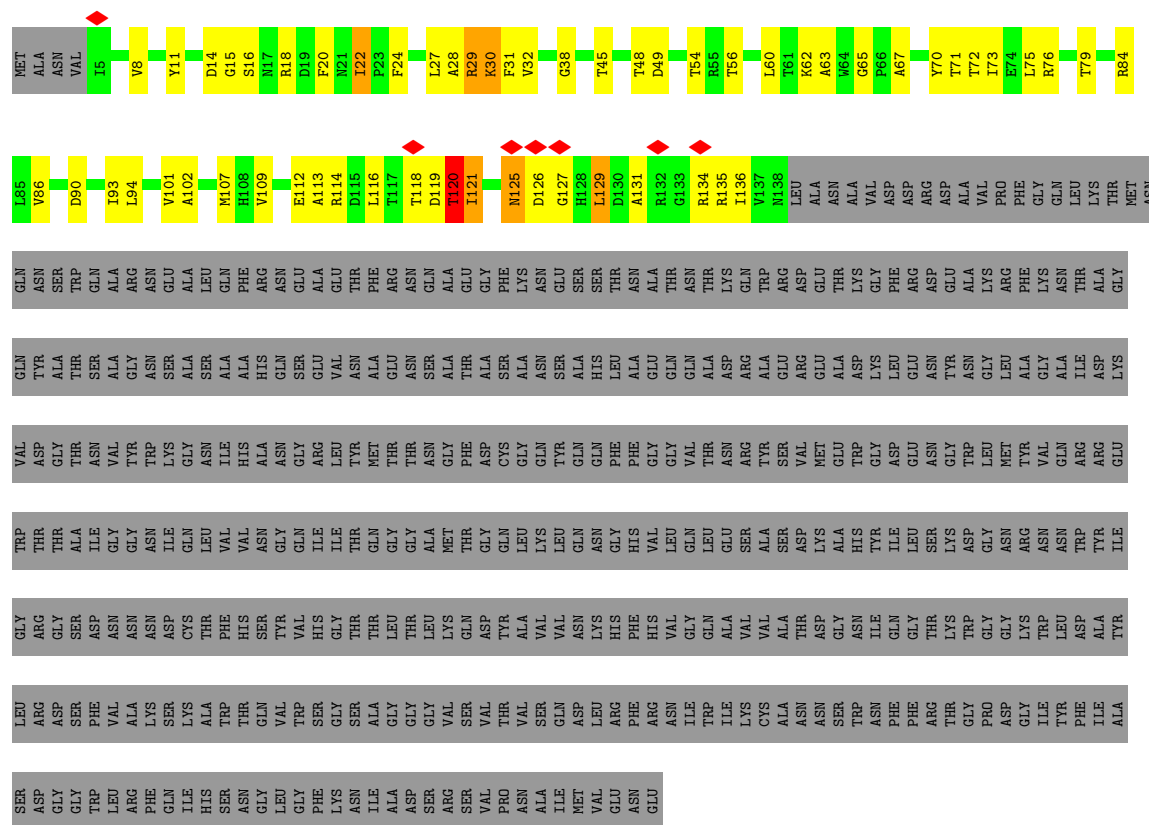
- Molecule 1: Tail fiber protein

Chain j:  16% 8% . 75%

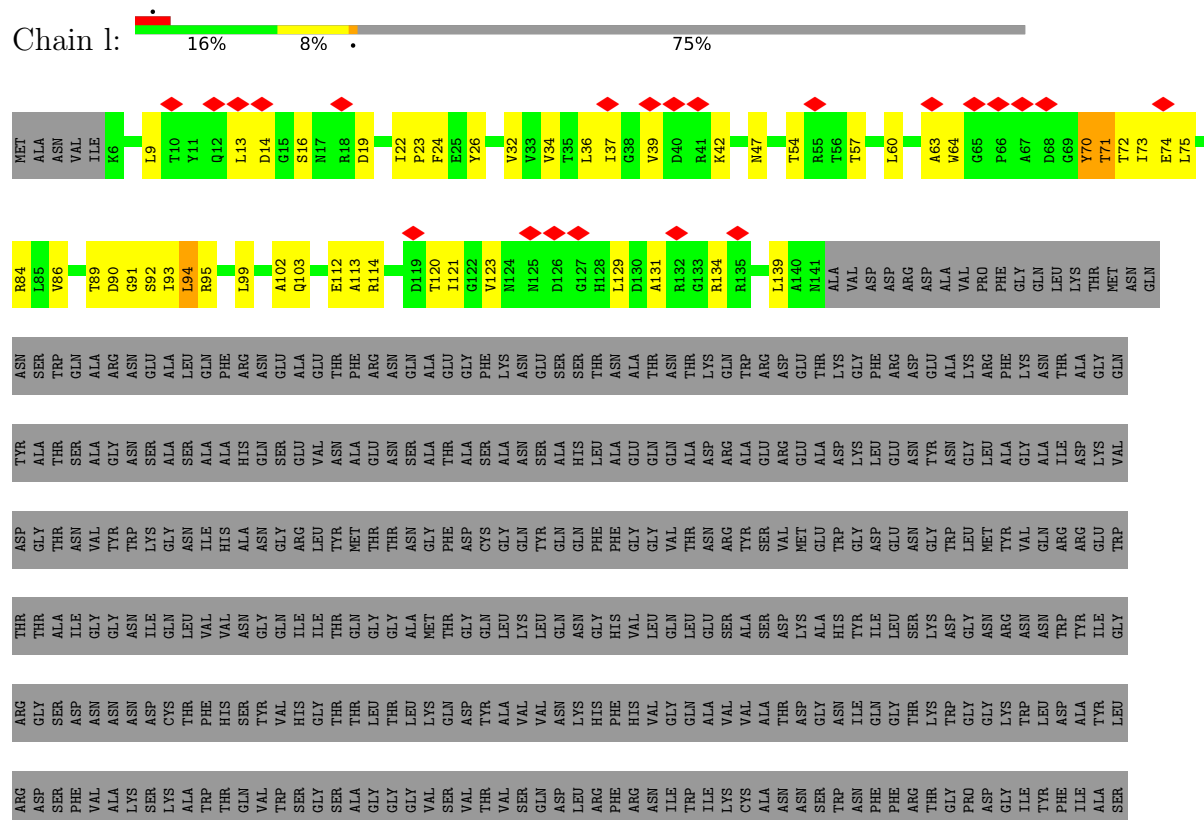


- Molecule 1: Tail fiber protein

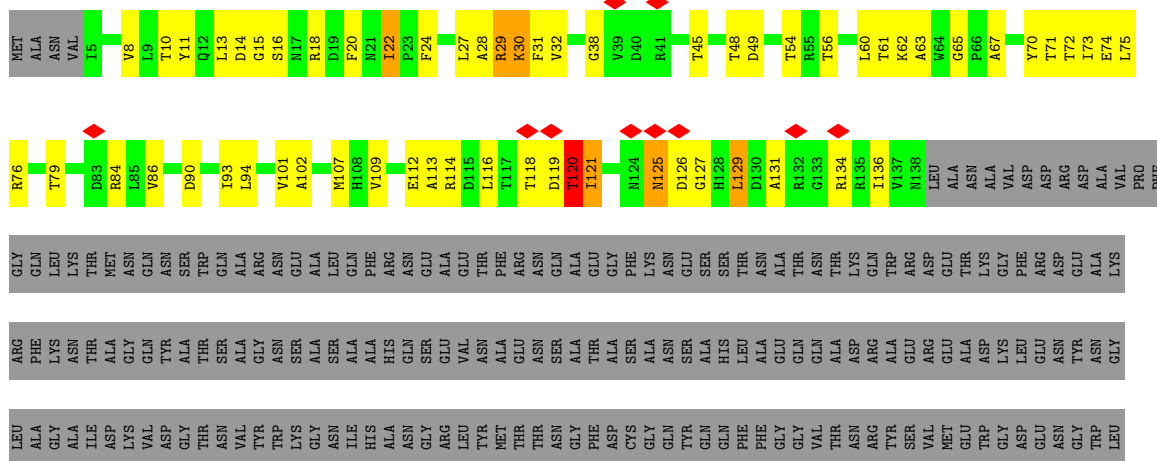
Chain k: 



• Molecule 1: Tail fiber protein

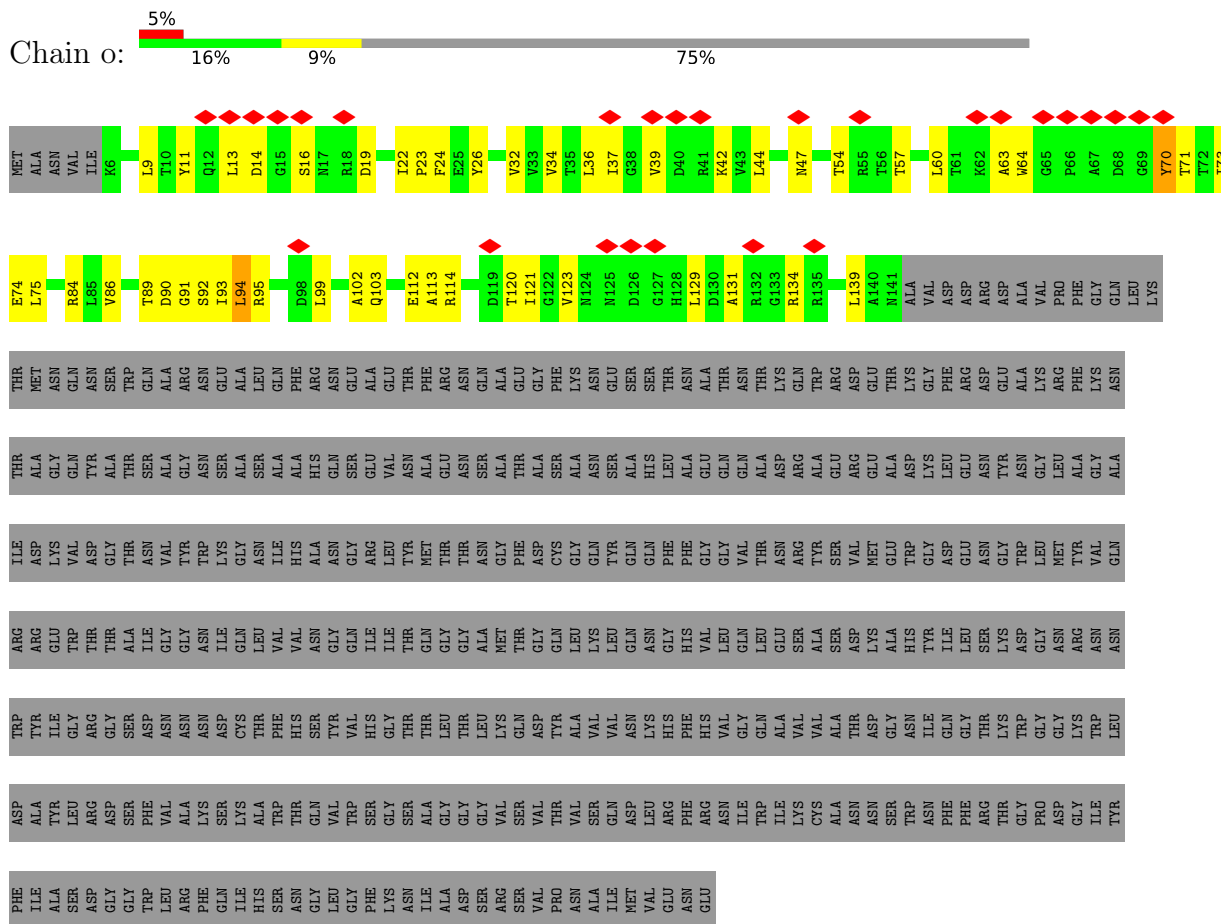


Chain m: 16% 8% 75%

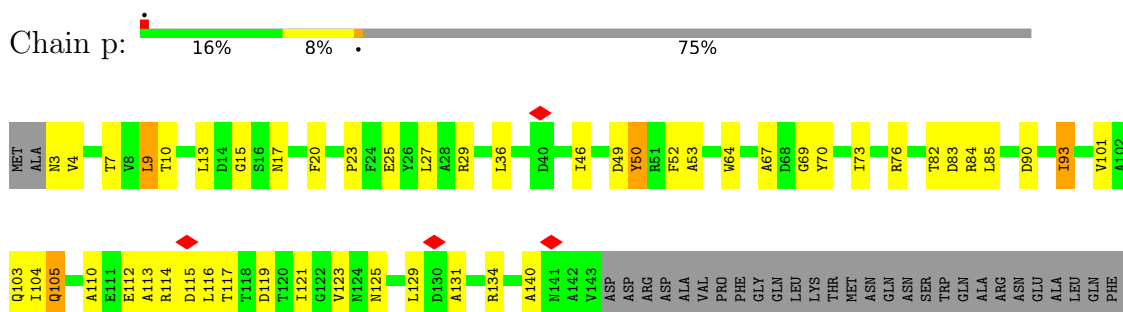


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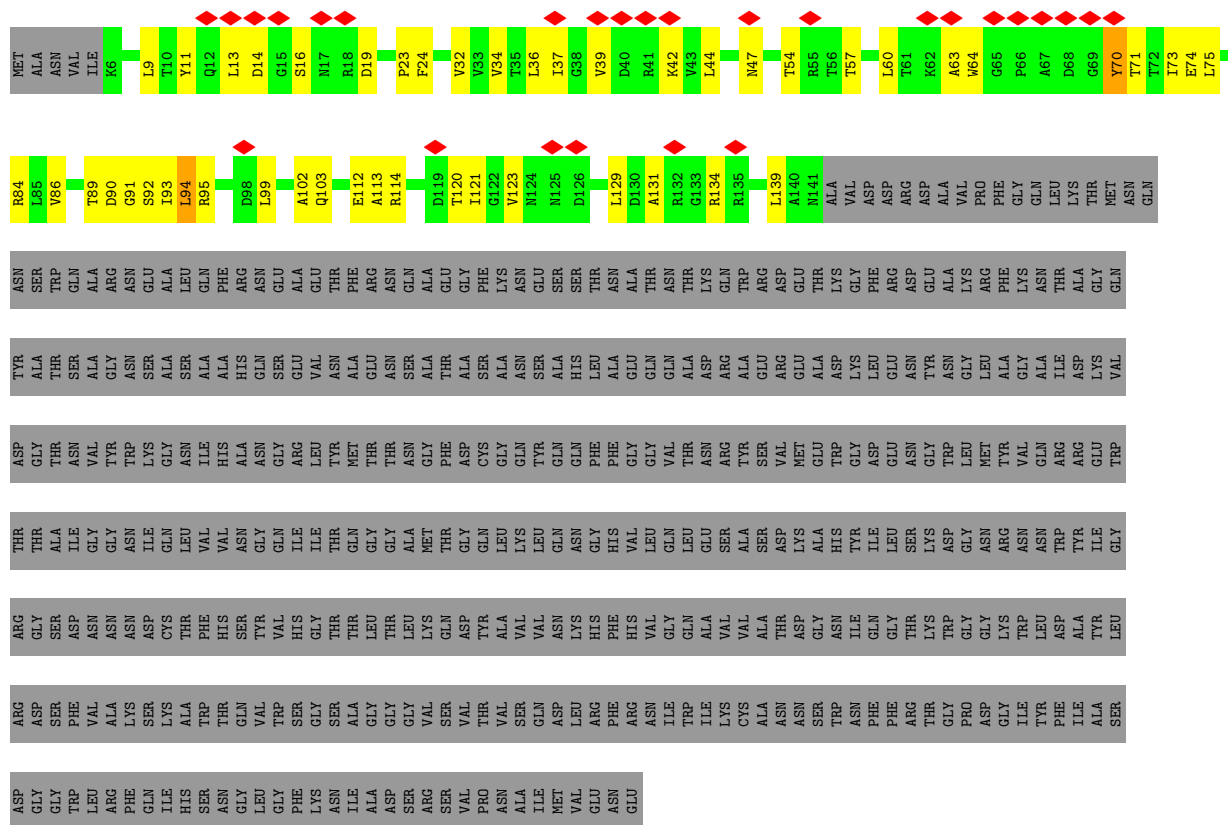
- Molecule 1: Tail fiber protein



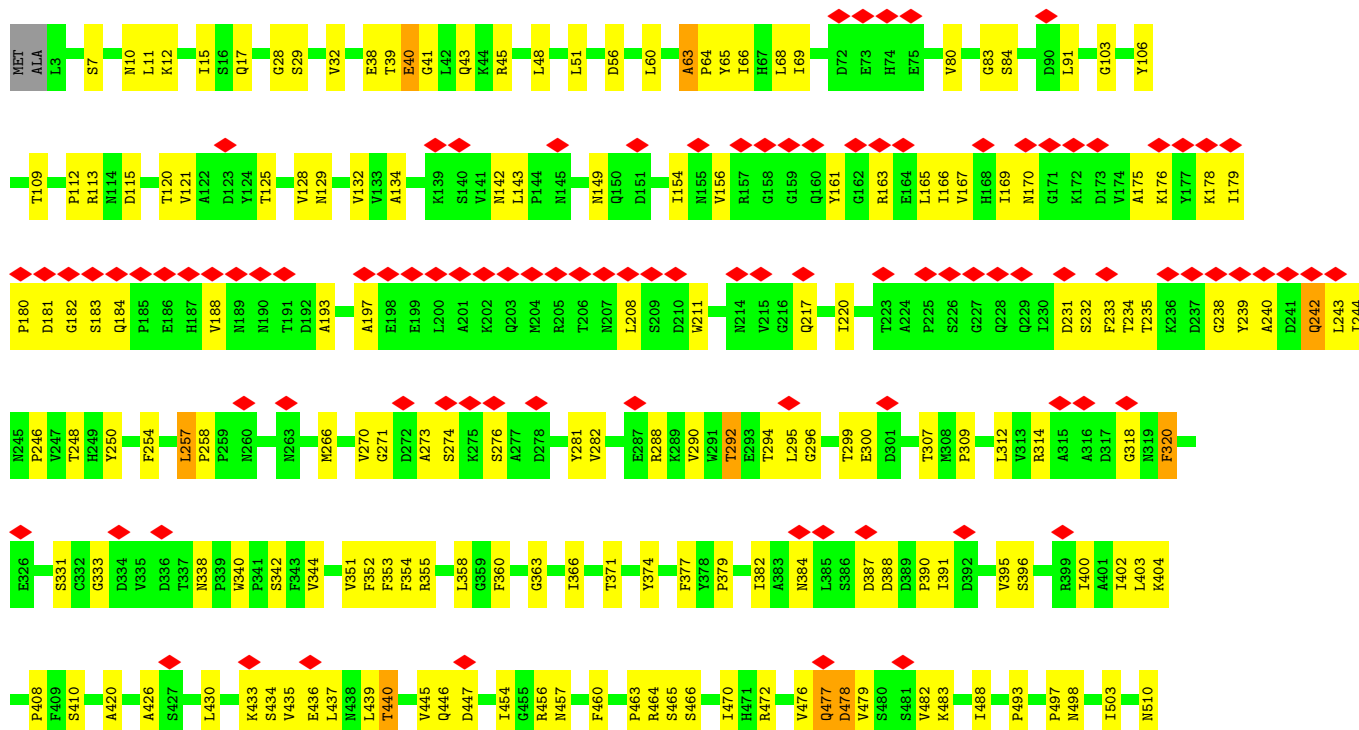
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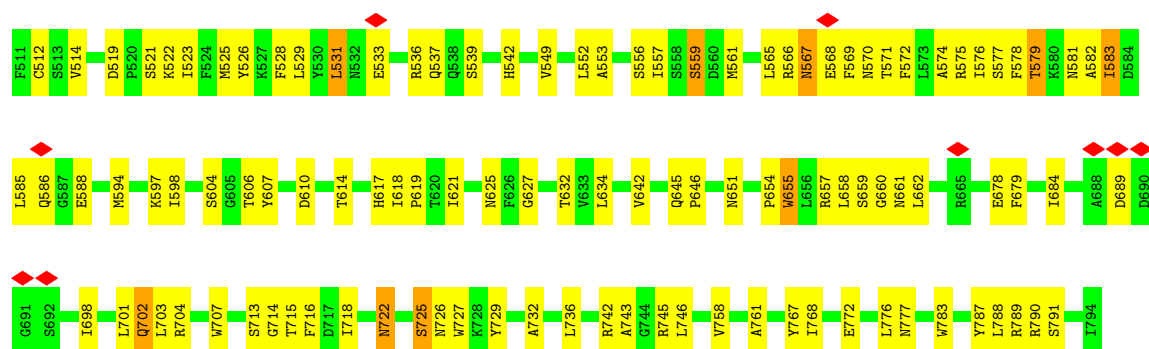




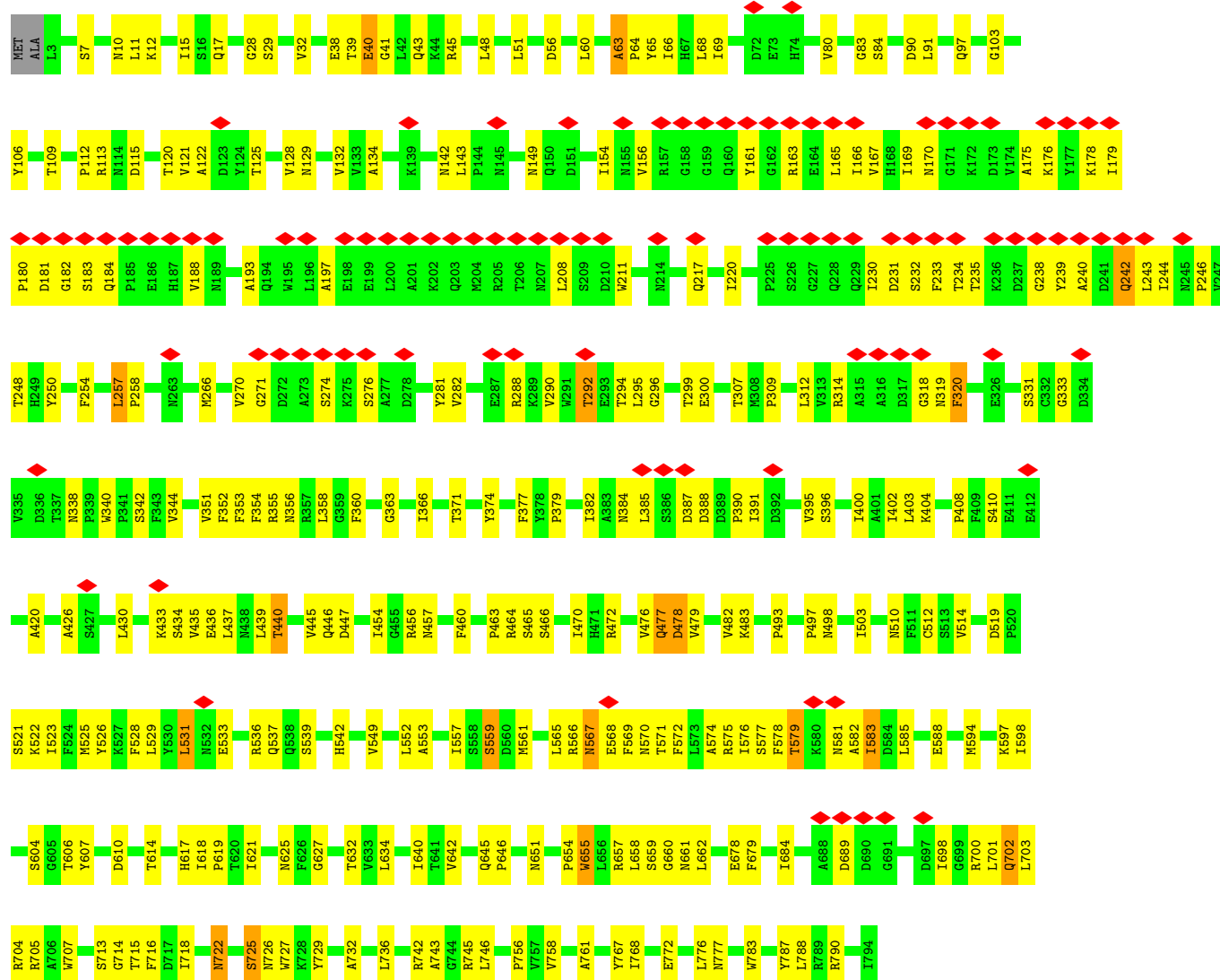


• Molecule 2: Tail tubular protein gp12



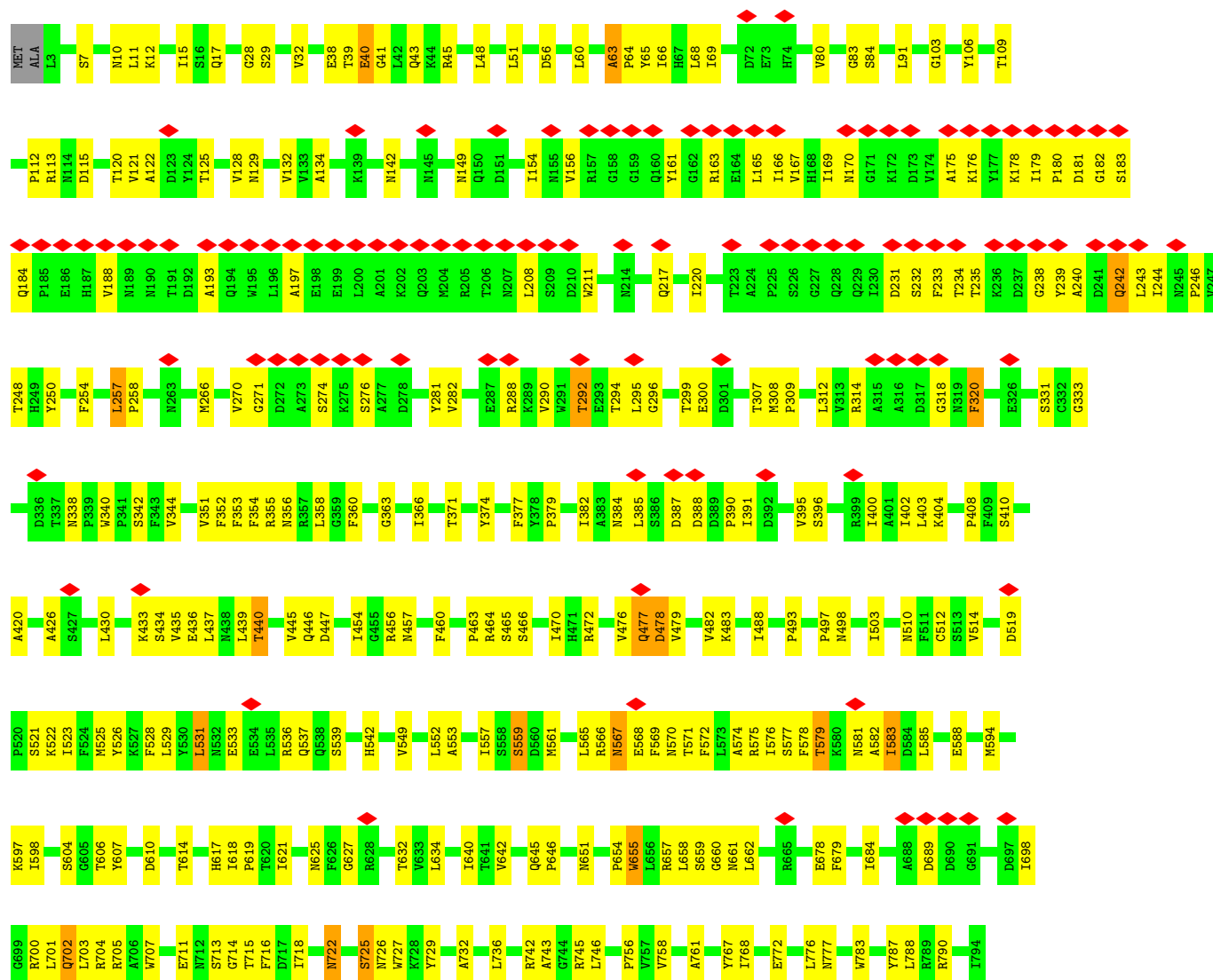


• Molecule 2: Tail tubular protein gp12

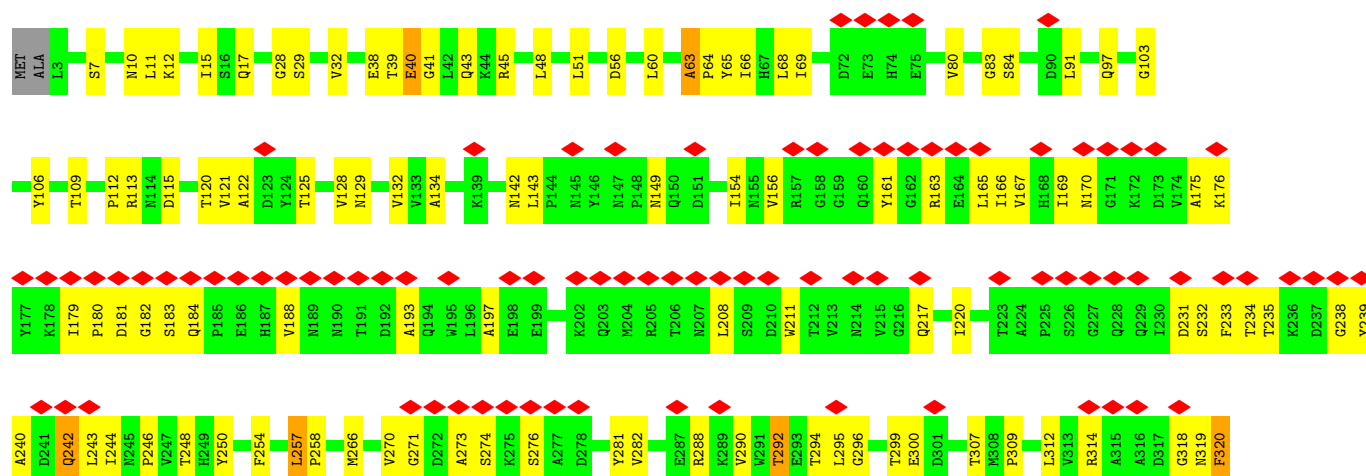


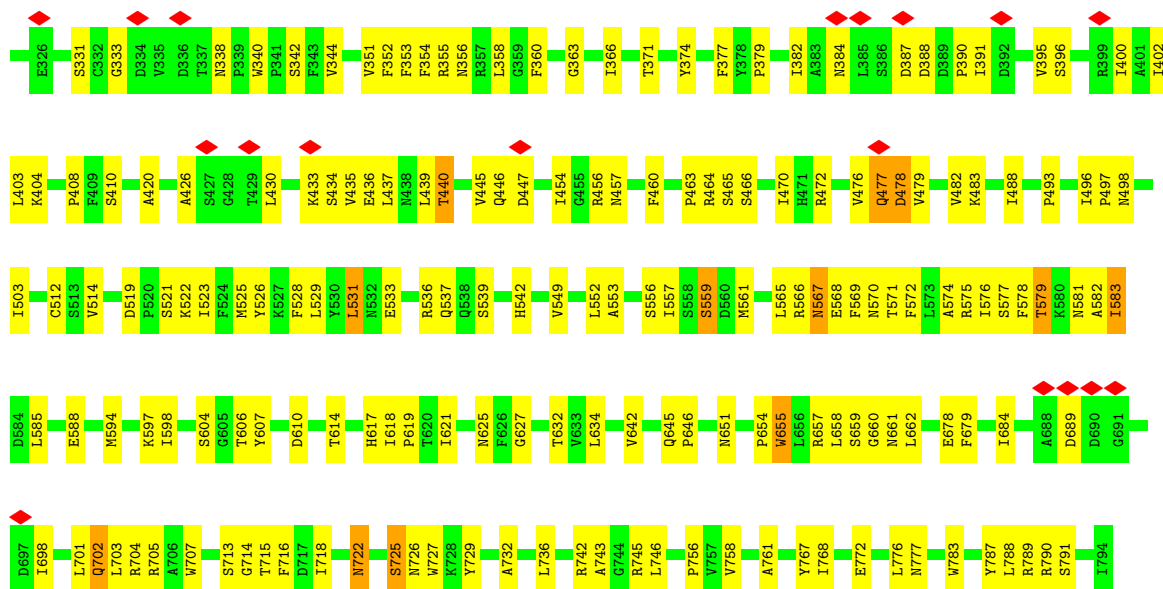
• Molecule 2: Tail tubular protein gp12



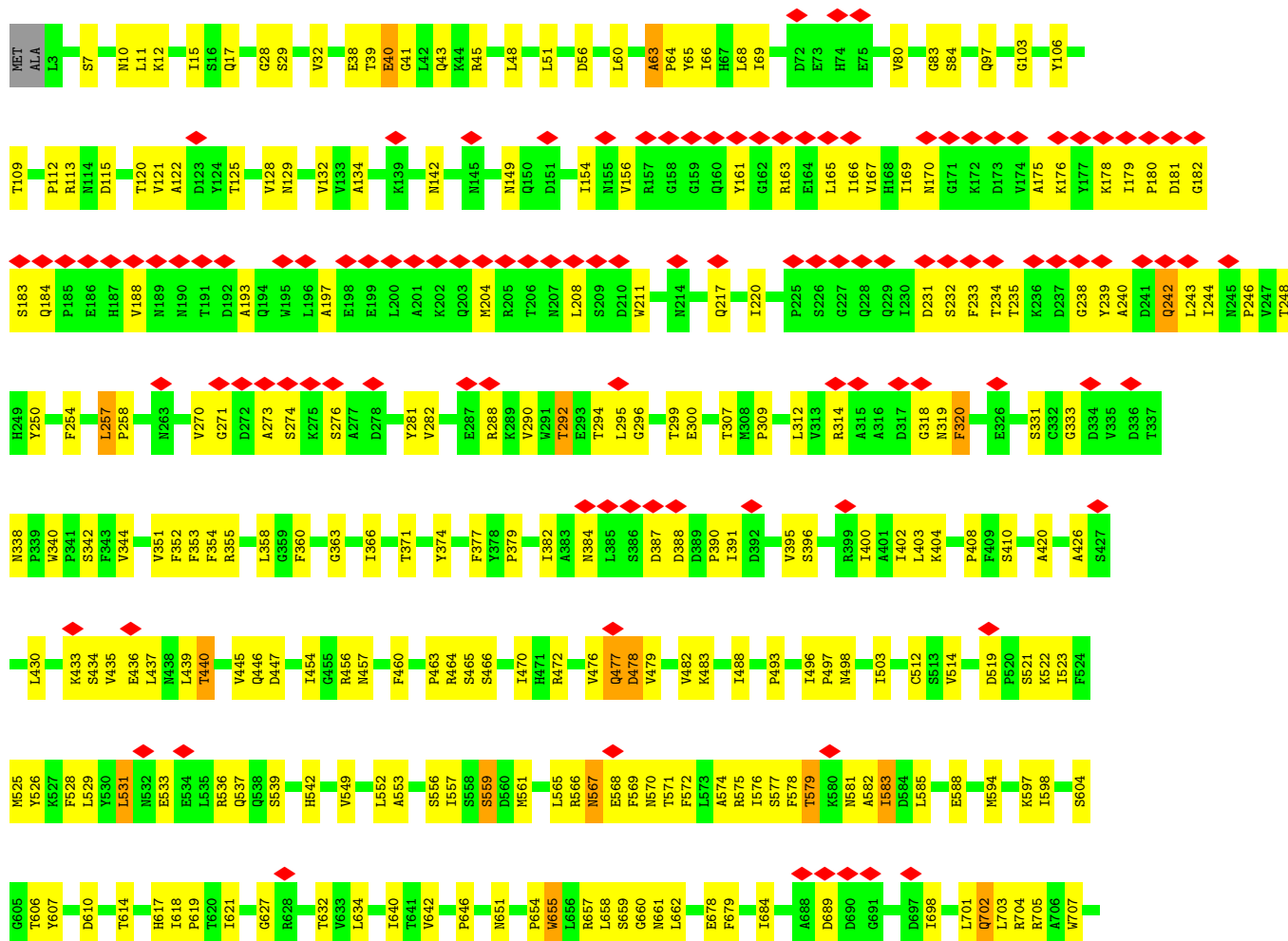


• Molecule 2: Tail tubular protein gp12



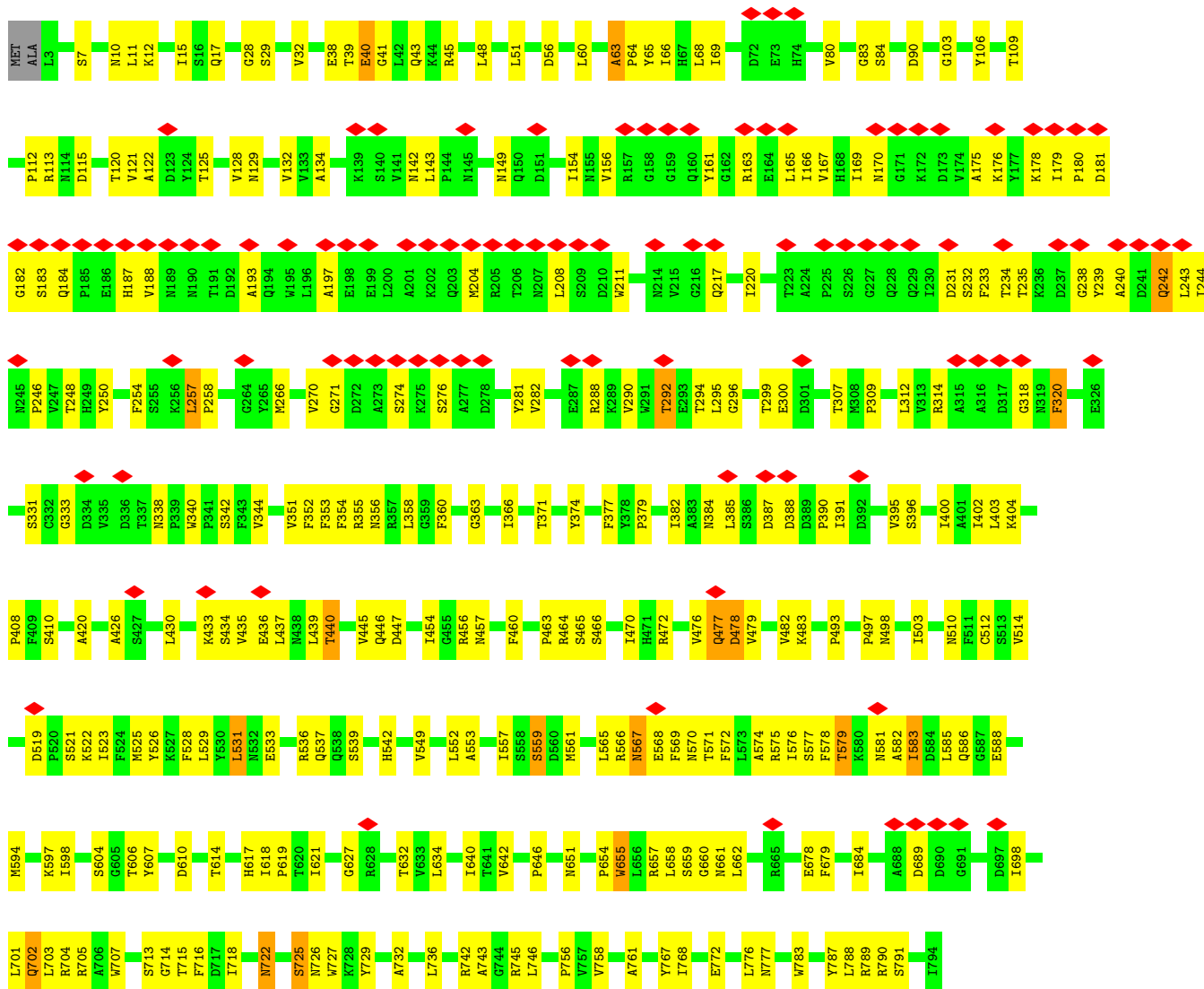


• Molecule 2: Tail tubular protein gp12

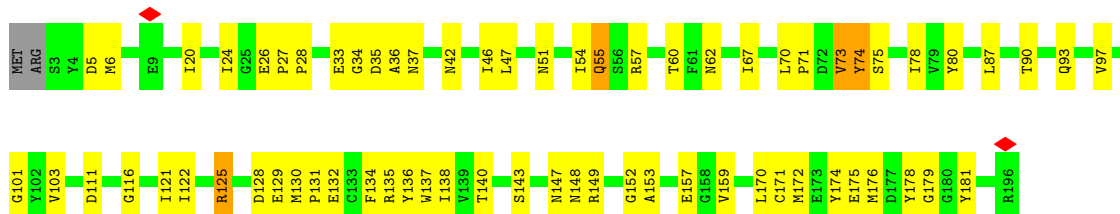




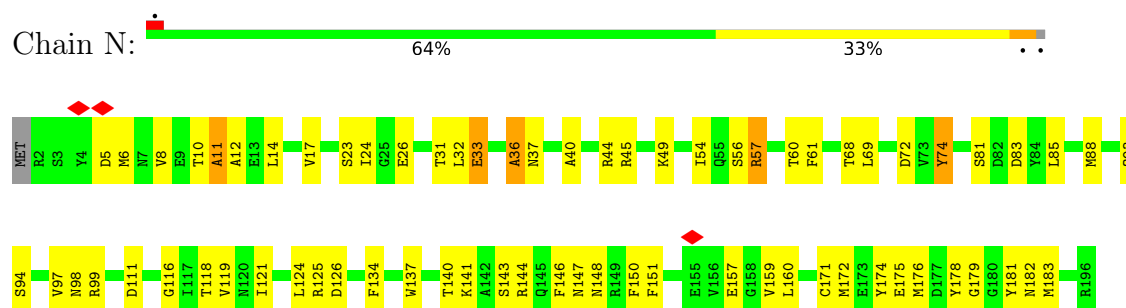
• Molecule 2: Tail tubular protein gp12



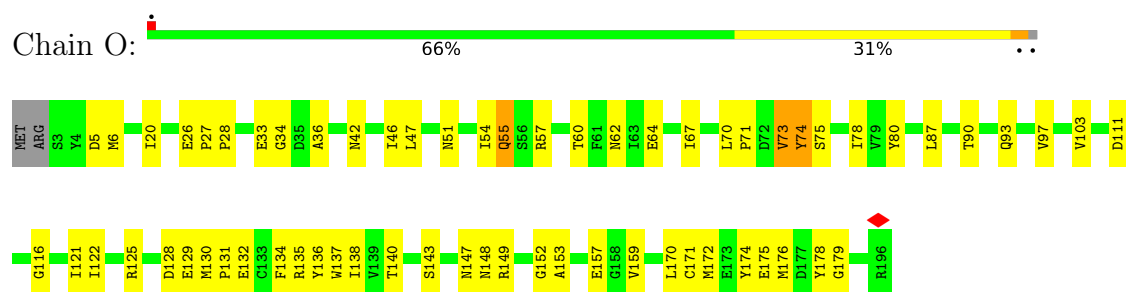
• Molecule 3: Tail tubular protein gp11



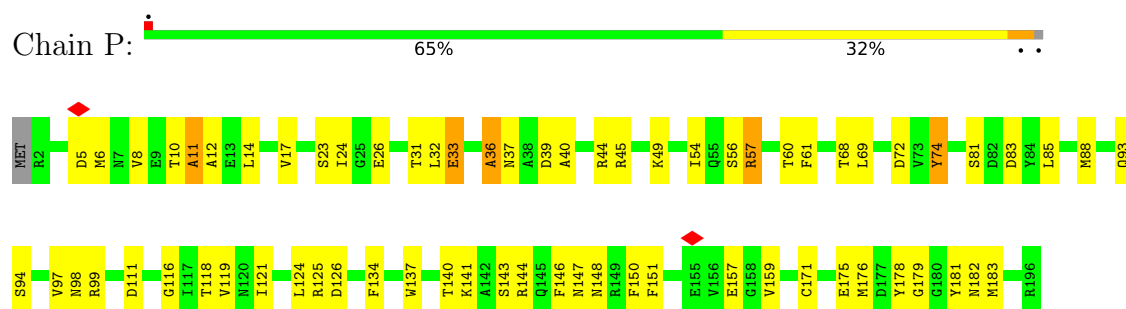
- Molecule 3: Tail tubular protein gp11



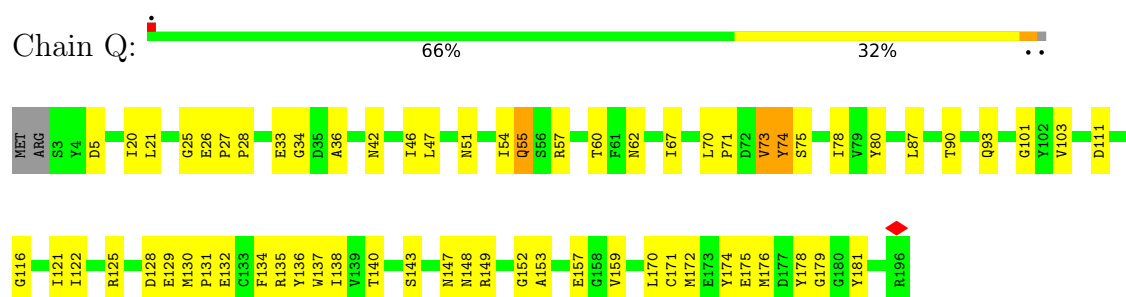
- Molecule 3: Tail tubular protein gp11



- Molecule 3: Tail tubular protein gp11

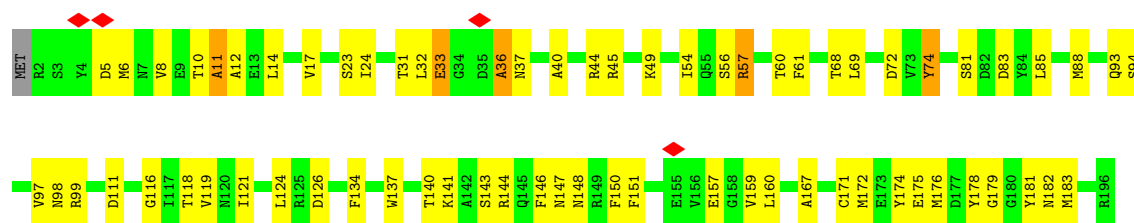


- Molecule 3: Tail tubular protein gp11

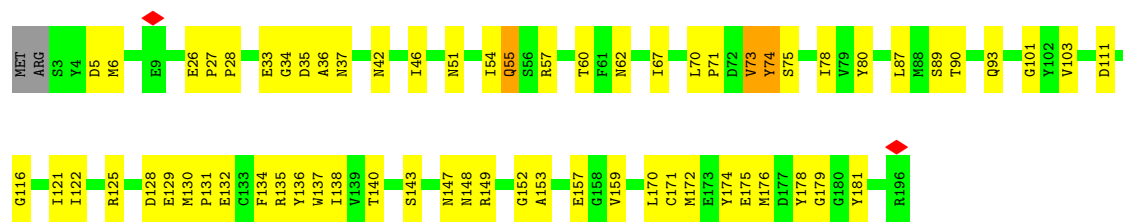


- Molecule 3: Tail tubular protein gp11

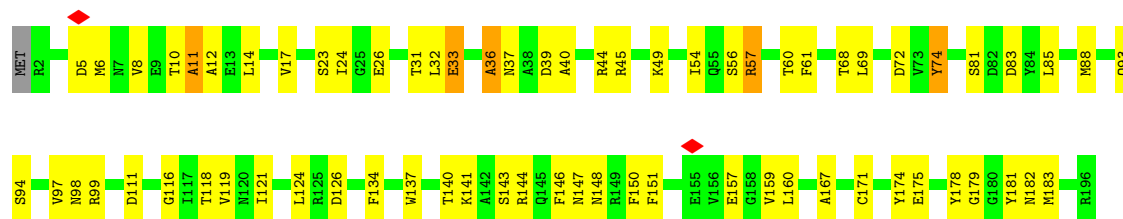




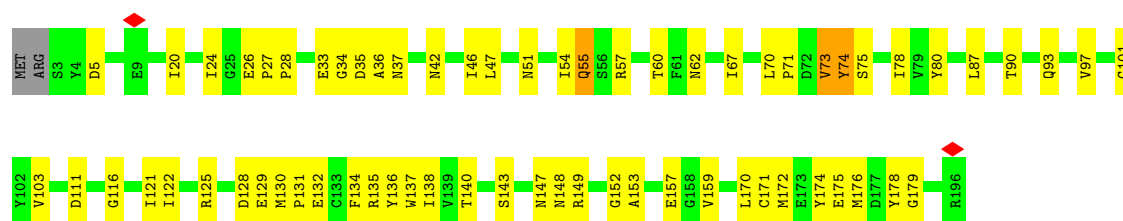
• Molecule 3: Tail tubular protein gp11



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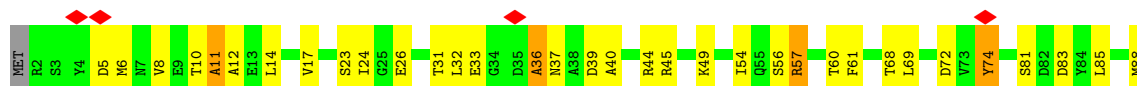




- Molecule 3: Tail tubular protein gp11



- Molecule 3: Tail tubular protein gp11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	75068	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	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	64.905	Depositor
Minimum map value	-38.213	Depositor
Average map value	0.014	Depositor
Map value standard deviation	2.892	Depositor
Recommended contour level	9	Depositor
Map size ($\text{\AA}$)	406.4, 406.4, 406.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.27, 1.27, 1.27	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	a	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	b	0.84	0/1082	1.10	14/1471 (1.0%)
1	c	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	d	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	e	0.84	0/1082	1.10	15/1471 (1.0%)
1	f	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	g	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	h	0.84	0/1082	1.10	14/1471 (1.0%)
1	i	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	j	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	k	0.84	0/1082	1.10	14/1471 (1.0%)
1	l	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	m	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	n	0.84	0/1082	1.10	14/1471 (1.0%)
1	o	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	p	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	q	0.84	0/1082	1.10	15/1471 (1.0%)
1	r	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
2	s	0.92	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	t	0.91	3/6468 (0.0%)	1.23	72/8797 (0.8%)
2	u	0.91	4/6468 (0.1%)	1.23	71/8797 (0.8%)
2	v	0.92	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	w	0.91	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	x	0.92	3/6468 (0.0%)	1.23	73/8797 (0.8%)
3	M	1.00	1/1573 (0.1%)	1.14	16/2129 (0.8%)
3	N	0.94	0/1584	1.12	12/2143 (0.6%)
3	O	1.00	0/1573	1.14	15/2129 (0.7%)
3	P	0.94	0/1584	1.12	11/2143 (0.5%)
3	Q	1.01	1/1573 (0.1%)	1.13	14/2129 (0.7%)
3	R	0.94	0/1584	1.12	12/2143 (0.6%)
3	S	1.00	2/1573 (0.1%)	1.13	15/2129 (0.7%)
3	T	0.94	0/1584	1.11	12/2143 (0.6%)
3	U	1.00	1/1573 (0.1%)	1.14	14/2129 (0.7%)
3	V	0.94	0/1584	1.11	12/2143 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	W	1.00	1/1573 (0.1%)	1.13	14/2129 (0.7%)
3	X	0.94	0/1584	1.11	12/2143 (0.6%)
All	All	0.93	43/77592 (0.1%)	1.20	824/105402 (0.8%)

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	j	9	LEU	CA-C	-6.33	1.45	1.52
1	p	9	LEU	CA-C	-6.27	1.45	1.52
1	d	9	LEU	CA-C	-6.13	1.45	1.52
1	m	9	LEU	CA-C	-6.12	1.45	1.52
2	x	577	SER	C-O	-6.10	1.17	1.24

The worst 5 of 824 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	d	69	GLY	N-CA-C	-15.06	89.05	112.84
1	j	69	GLY	N-CA-C	-15.00	89.14	112.84
1	p	69	GLY	N-CA-C	-14.99	89.15	112.84
1	a	69	GLY	N-CA-C	-14.99	89.16	112.84
1	m	69	GLY	N-CA-C	-14.97	89.18	112.84

There are no chirality outliers.

There are no planarity outliers.

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	a	1115	0	1122	59	0
1	b	1067	0	1071	72	0
1	c	1080	0	1082	52	0
1	d	1115	0	1122	55	0
1	e	1067	0	1071	73	0
1	f	1080	0	1082	51	0
1	g	1115	0	1122	58	0
1	h	1067	0	1071	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	i	1080	0	1082	54	0
1	j	1115	0	1122	56	0
1	k	1067	0	1071	73	0
1	l	1080	0	1082	51	0
1	m	1115	0	1122	56	0
1	n	1067	0	1071	74	0
1	o	1080	0	1082	50	0
1	p	1115	0	1122	57	0
1	q	1067	0	1071	73	0
1	r	1080	0	1082	49	0
2	s	6308	0	6070	292	0
2	t	6308	0	6070	300	0
2	u	6308	0	6070	298	0
2	v	6308	0	6070	293	0
2	w	6308	0	6070	288	0
2	x	6308	0	6070	289	0
3	M	1546	0	1460	78	0
3	N	1557	0	1473	104	0
3	O	1546	0	1460	72	0
3	P	1557	0	1473	102	0
3	Q	1546	0	1460	72	0
3	R	1557	0	1473	105	0
3	S	1546	0	1460	73	0
3	T	1557	0	1473	104	0
3	U	1546	0	1460	76	0
3	V	1557	0	1473	103	0
3	W	1546	0	1460	75	0
3	X	1557	0	1473	109	0
All	All	76038	0	73668	2755	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 2755 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:m:27:LEU:CD1	3:R:6:MET:HE3	1.43	1.49
1:p:27:LEU:CD1	3:P:6:MET:HE3	1.43	1.48
1:a:27:LEU:CD1	3:N:6:MET:HE3	1.43	1.47
1:d:27:LEU:CD1	3:X:6:MET:HE3	1.44	1.43
1:j:27:LEU:CD1	3:T:6:MET:HE3	1.48	1.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	b	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	c	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	d	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	e	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	f	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	g	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	h	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	i	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	j	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	k	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	l	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	m	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	n	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	o	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	p	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	q	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	r	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
2	s	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	t	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	u	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	v	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	w	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	x	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
3	M	192/196 (98%)	183 (95%)	8 (4%)	1 (0%)	24	54
3	N	193/196 (98%)	181 (94%)	12 (6%)	0	100	100
3	O	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	P	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	Q	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	R	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	S	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	T	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	U	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	V	193/196 (98%)	181 (94%)	12 (6%)	0	100	100
3	W	192/196 (98%)	183 (95%)	8 (4%)	1 (0%)	24	54
3	X	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
All	All	9480/17070 (56%)	8990 (95%)	460 (5%)	30 (0%)	37	65

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	29	ARG
1	b	120	THR
1	e	29	ARG
1	e	120	THR
1	h	29	ARG

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

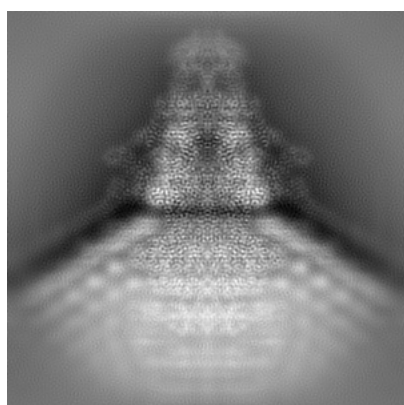
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31319. These allow visual inspection of the internal detail of the map and identification of artifacts.

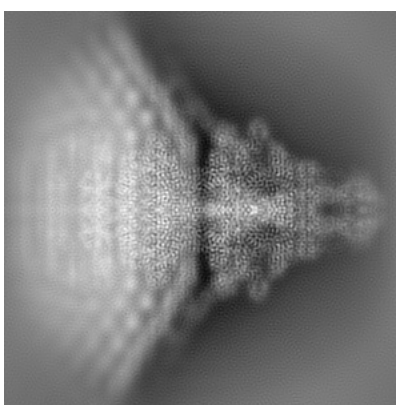
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

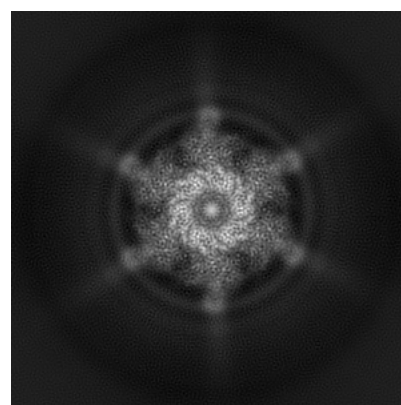
6.1.1 Primary map



X



Y

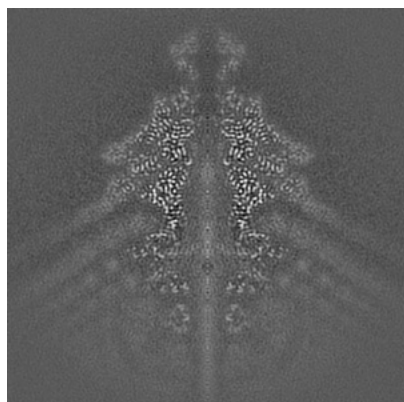


Z

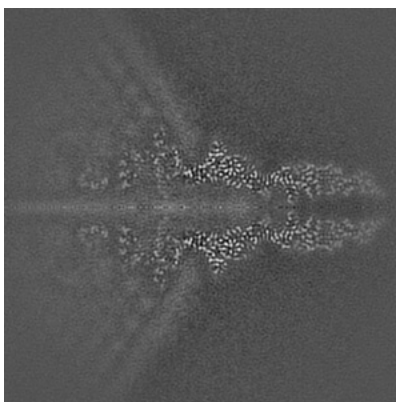
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

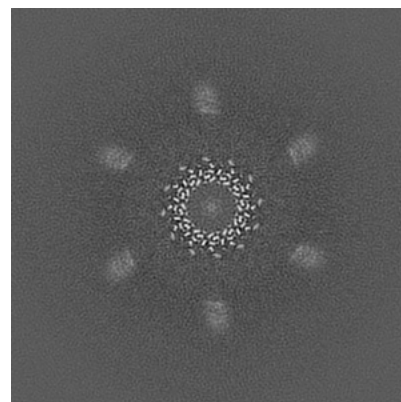
6.2.1 Primary map



X Index: 160



Y Index: 160

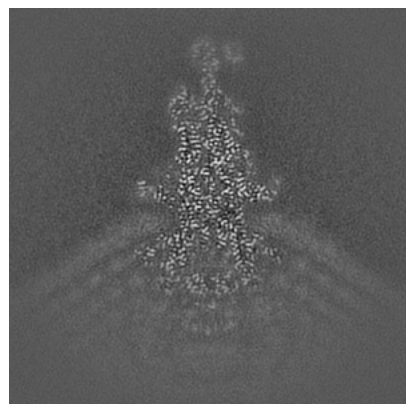


Z Index: 160

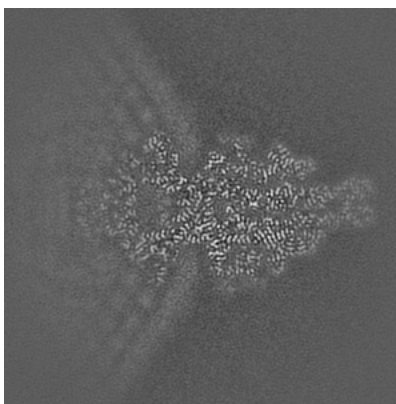
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

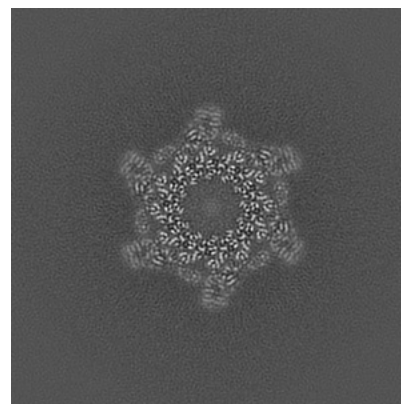
6.3.1 Primary map



X Index: 183



Y Index: 181

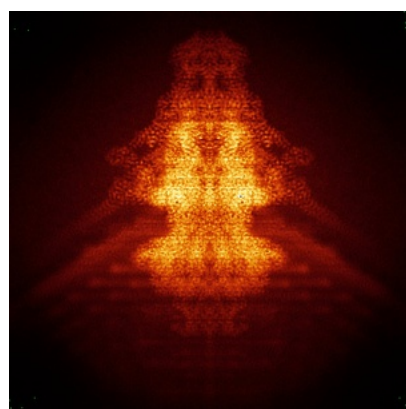


Z Index: 174

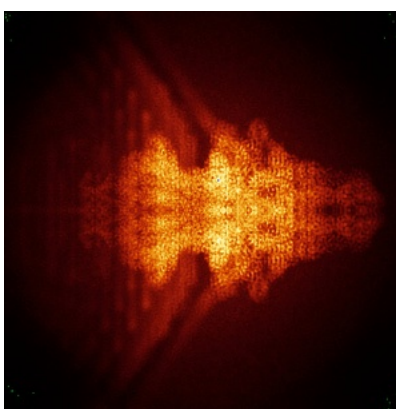
The images above show the largest variance slices of the map in three orthogonal directions.

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

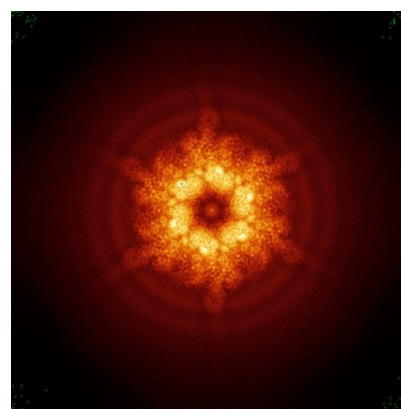
6.4.1 Primary map



X



Y

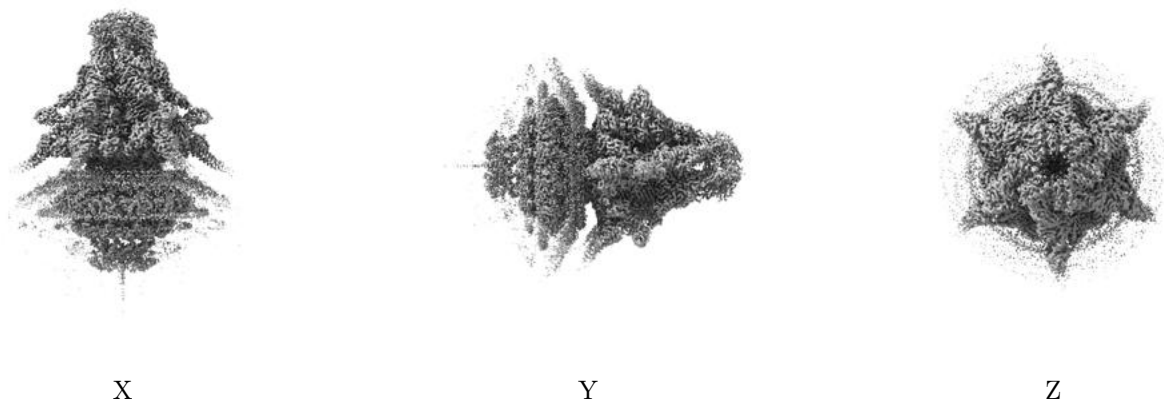


Z

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 9.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

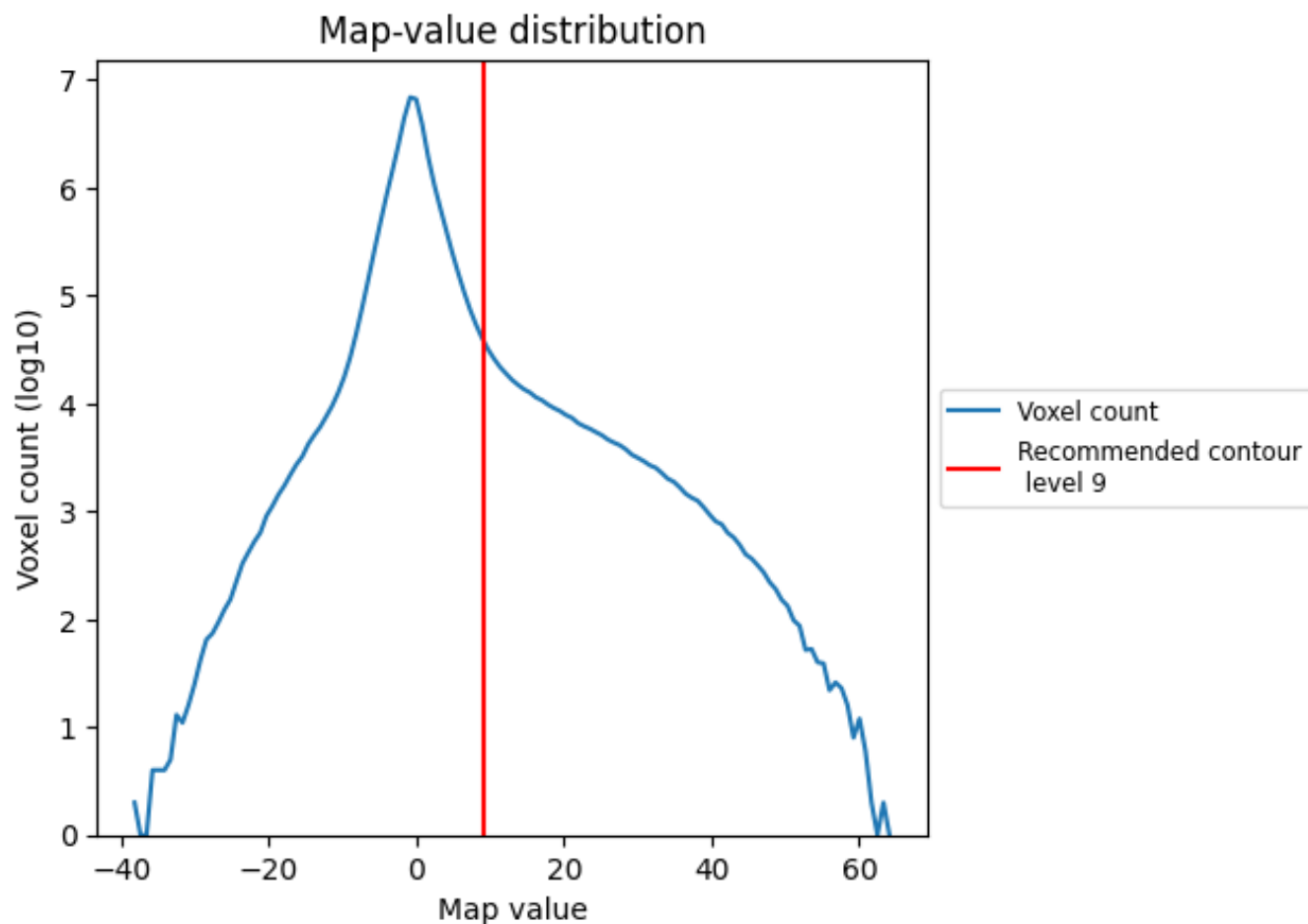
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

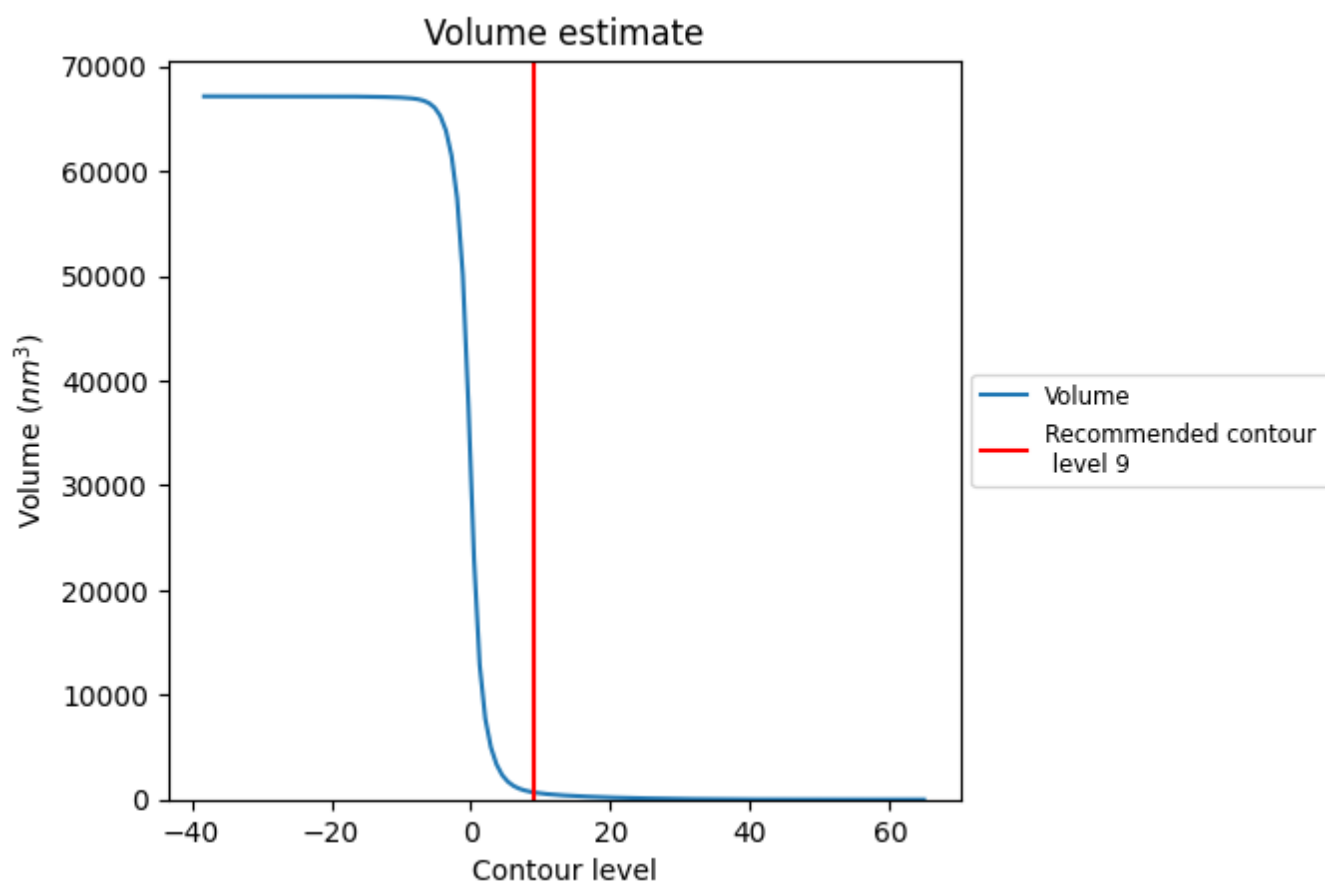
This section contains the results of statistical analysis of the map.

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.

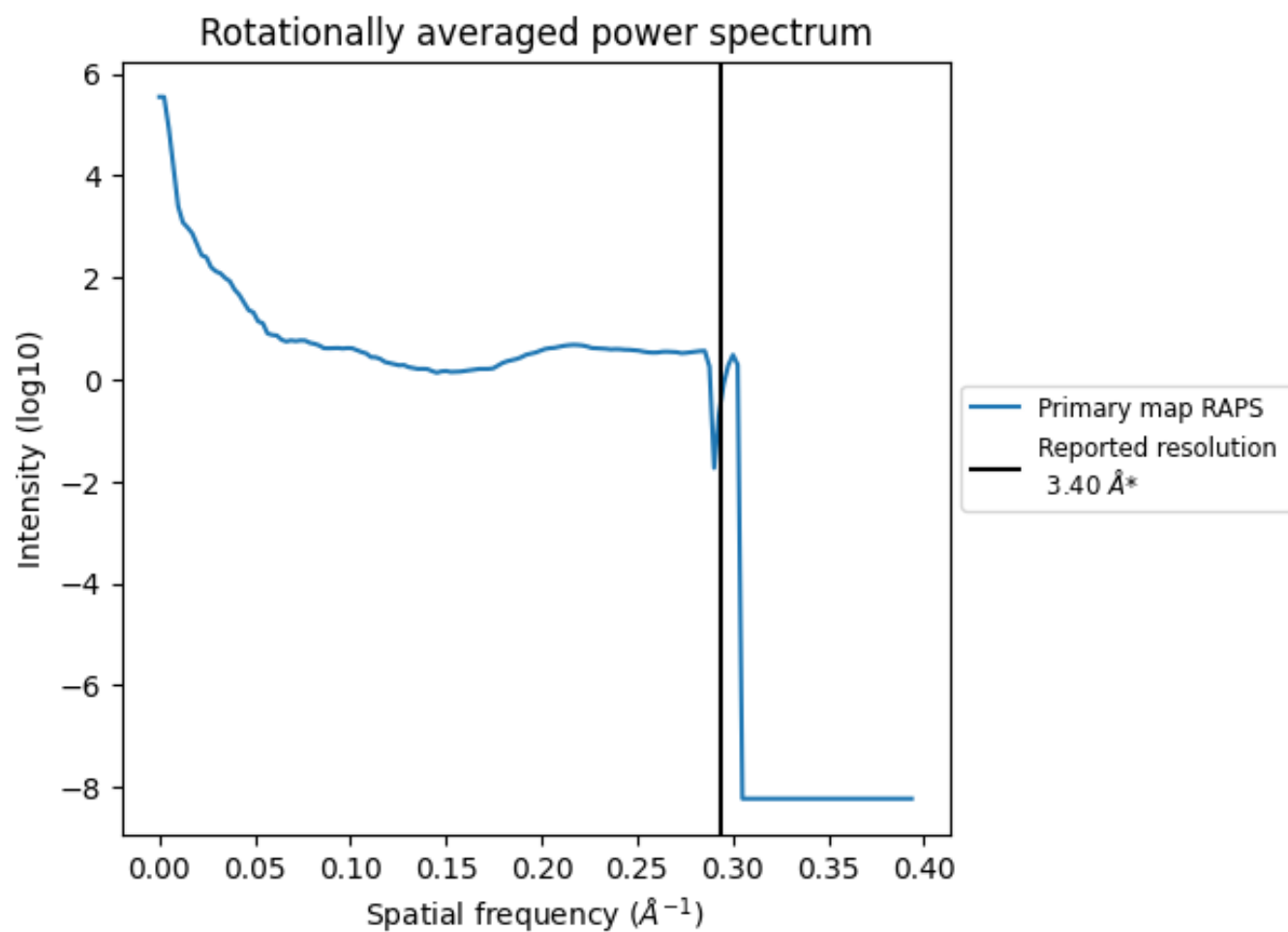
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690 nm³; this corresponds to an approximate mass of 624 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 0.294 Å⁻¹

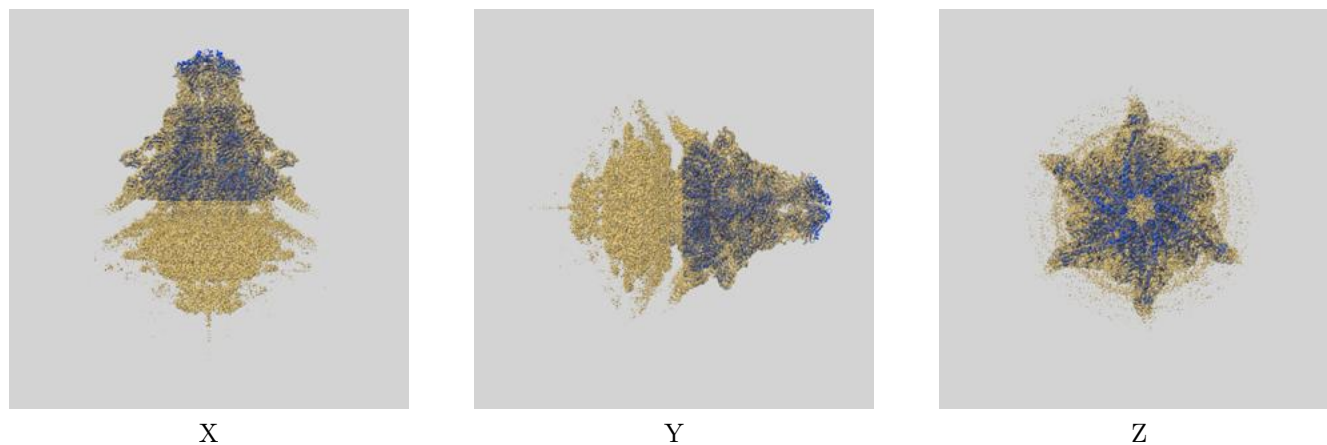
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

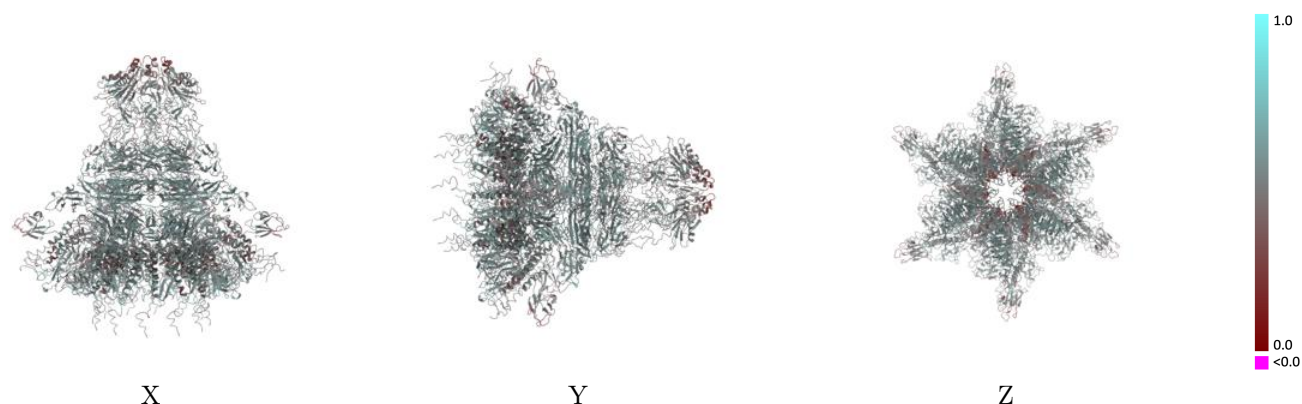
This section contains information regarding the fit between EMDB map EMD-31319 and PDB model 7EY9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



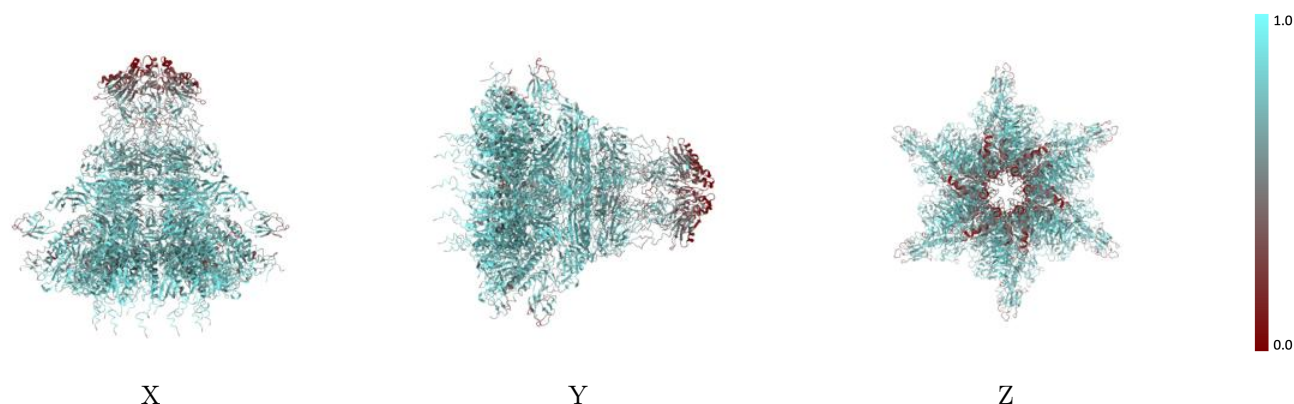
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



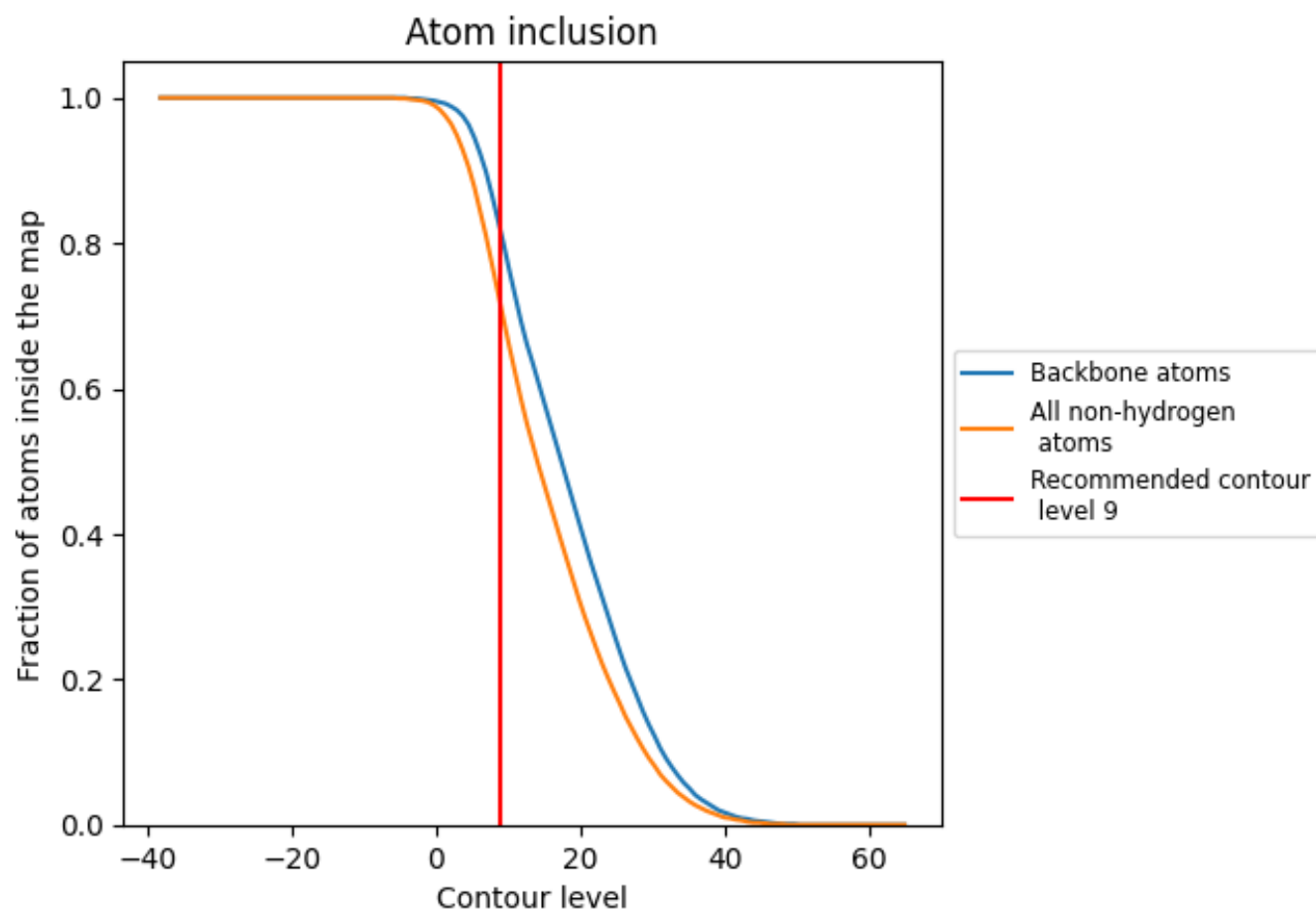
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 71% 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 (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7110	 0.5060
M	 0.7970	 0.5080
N	 0.7710	 0.5080
O	 0.7960	 0.5080
P	 0.7680	 0.5050
Q	 0.7990	 0.5040
R	 0.7720	 0.5060
S	 0.7990	 0.5070
T	 0.7730	 0.5070
U	 0.7950	 0.5070
V	 0.7700	 0.5070
W	 0.7960	 0.5060
X	 0.7700	 0.5060
a	 0.7760	 0.5280
b	 0.7260	 0.5080
c	 0.6300	 0.4610
d	 0.7680	 0.5180
e	 0.7240	 0.5020
f	 0.6060	 0.4490
g	 0.7730	 0.5200
h	 0.7340	 0.5010
i	 0.6140	 0.4520
j	 0.7650	 0.5260
k	 0.7230	 0.5050
l	 0.6330	 0.4610
m	 0.7550	 0.5200
n	 0.7240	 0.5030
o	 0.6200	 0.4510
p	 0.7680	 0.5210
q	 0.7360	 0.5010
r	 0.6150	 0.4460
s	 0.6840	 0.5190
t	 0.6780	 0.5100
u	 0.6750	 0.5080
v	 0.6840	 0.5150



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Chain	Atom inclusion	Q-score
w	 0.6760	 0.5090
x	 0.6750	 0.5090