



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:33 PM UTC

PDB ID : 7EY7 / pdb_00007ey7
EMDB ID : EMD-31321
Title : bacteriophage T7 tail complex
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2021-05-30
Resolution : 4.30 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:

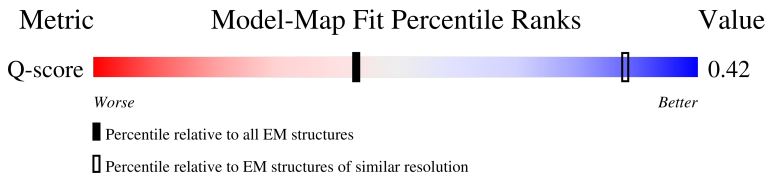
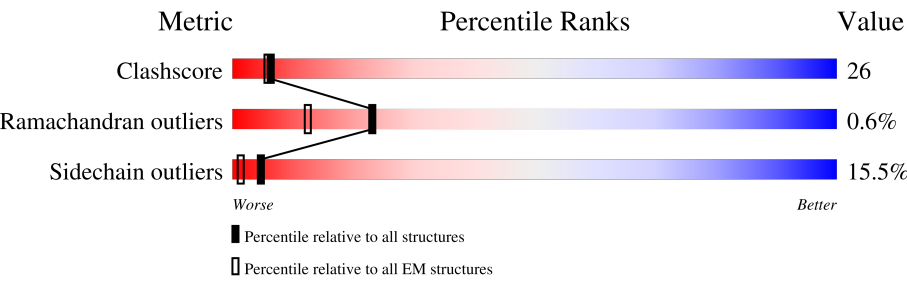
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.30 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.



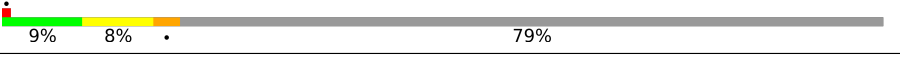
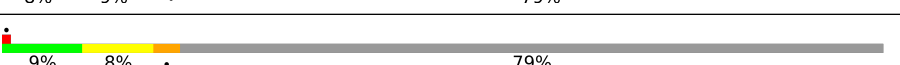
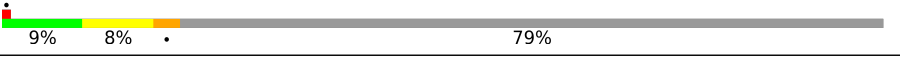
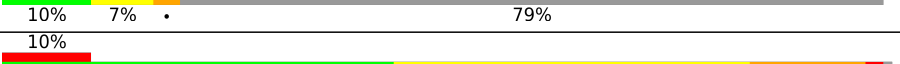
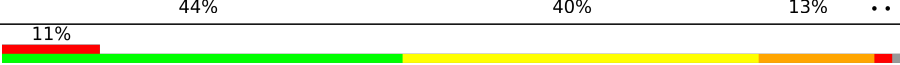
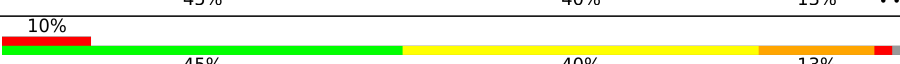
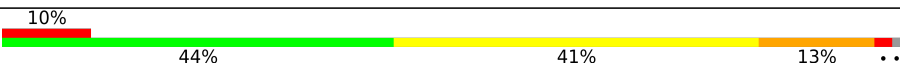
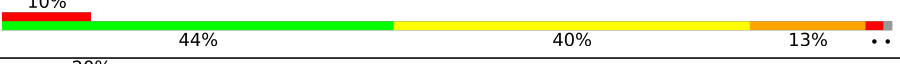
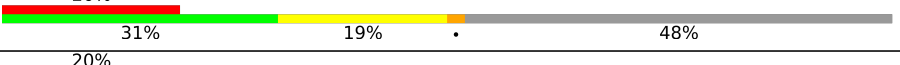
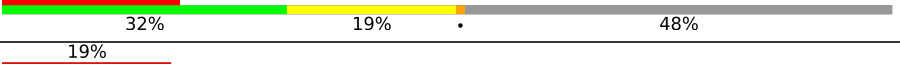
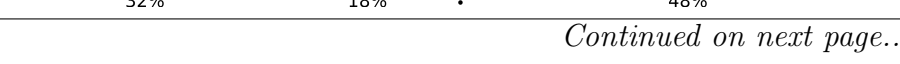
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	a	553	10%8%.. 79%
1	b	553	8%9%. 79%
1	c	553	9%8%. 79%
1	d	553	10%8%.. 79%

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Mol	Chain	Length	Quality of chain
1	e	553	 8% 9% . 79%
1	f	553	 9% 8% . 79%
1	g	553	 10% 7% . . 79%
1	h	553	 8% 9% . 79%
1	i	553	 9% 8% . 79%
1	j	553	 10% 7% . . 79%
1	k	553	 8% 9% . 79%
1	l	553	 9% 8% . 79%
1	m	553	 10% 7% . . 79%
1	n	553	 8% 9% . 79%
1	o	553	 9% 8% . 79%
1	p	553	 10% 7% . . 79%
1	q	553	 8% 9% . 79%
1	r	553	 10% 7% . 79%
2	s	794	 10% 44% 13% . .
2	t	794	 11% 45% 13% . .
2	u	794	 10% 45% 13% . .
2	v	794	 10% 44% 41% 13% . .
2	w	794	 11% 44% 40% 13% . .
2	x	794	 10% 44% 40% 13% . .
3	A	196	 20% 31% 19% . 48%
3	B	196	 20% 32% 19% . 48%
3	C	196	 19% 31% 18% . 48%
3	D	196	 17% 37% 14% . 48%
3	E	196	 20% 32% 18% . 48%

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Mol	Chain	Length	Quality of chain
3	F	196	
4	M	196	
4	N	196	
4	O	196	
4	P	196	
4	Q	196	
4	R	196	
4	S	196	
4	T	196	
4	U	196	
4	V	196	
4	W	196	
4	X	196	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 77574 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	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	b	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	c	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	d	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	e	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	f	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	g	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	h	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	i	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	j	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	k	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	l	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	m	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	n	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	o	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	p	115	Total 922	C 584	N 160	O 177	S 1	0	0
1	q	115	Total 922	C 584	N 160	O 177	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	115	Total	C	N	O	S	0	0
			922	584	160	177	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	t	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	u	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	v	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	w	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	x	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		

- Molecule 3 is a protein called Internal virion protein gp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	B	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	C	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	D	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	E	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	F	102	Total	C	N	O	S	0	0
			787	475	146	160	6		

- Molecule 4 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	N	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		

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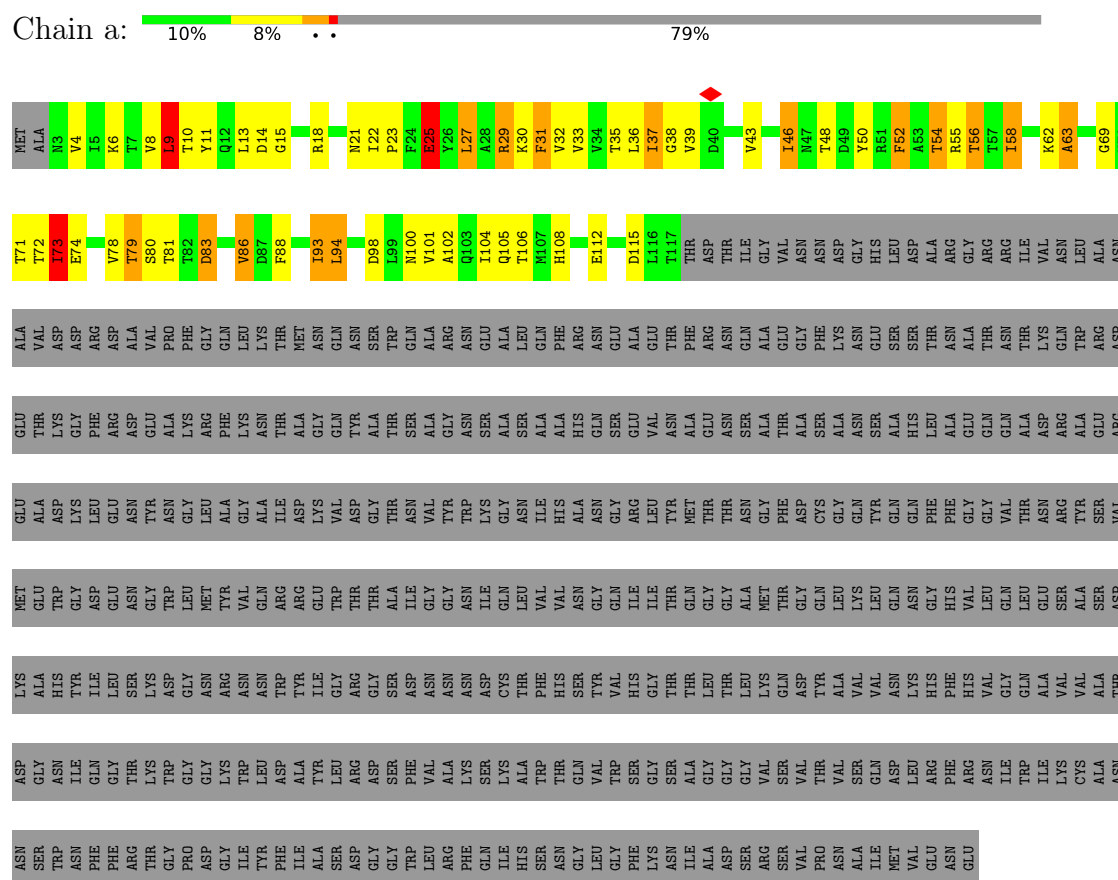
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Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	195	Total 1553	C 965	N 263	O 316	S 9	0	0
4	P	193	Total 1534	C 954	N 258	O 314	S 8	0	0
4	Q	195	Total 1553	C 965	N 263	O 316	S 9	0	0
4	R	193	Total 1534	C 954	N 258	O 314	S 8	0	0
4	S	195	Total 1553	C 965	N 263	O 316	S 9	0	0
4	T	193	Total 1534	C 954	N 258	O 314	S 8	0	0
4	U	195	Total 1553	C 965	N 263	O 316	S 9	0	0
4	V	193	Total 1534	C 954	N 258	O 314	S 8	0	0
4	W	195	Total 1553	C 965	N 263	O 316	S 9	0	0
4	X	193	Total 1534	C 954	N 258	O 314	S 8	0	0

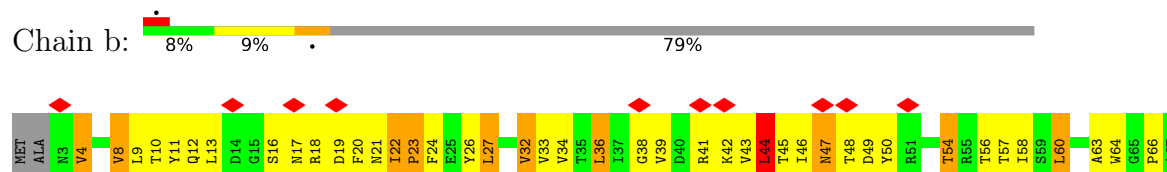
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Tail fiber protein

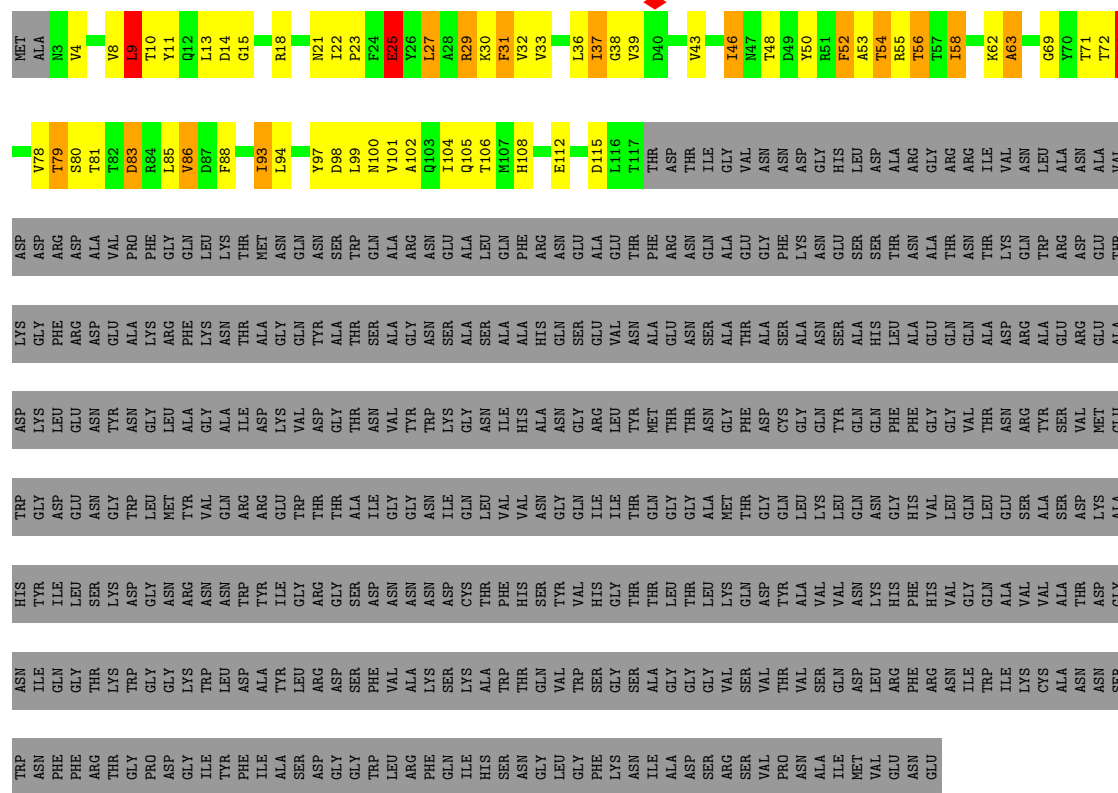


• Molecule 1: Tail fiber protein



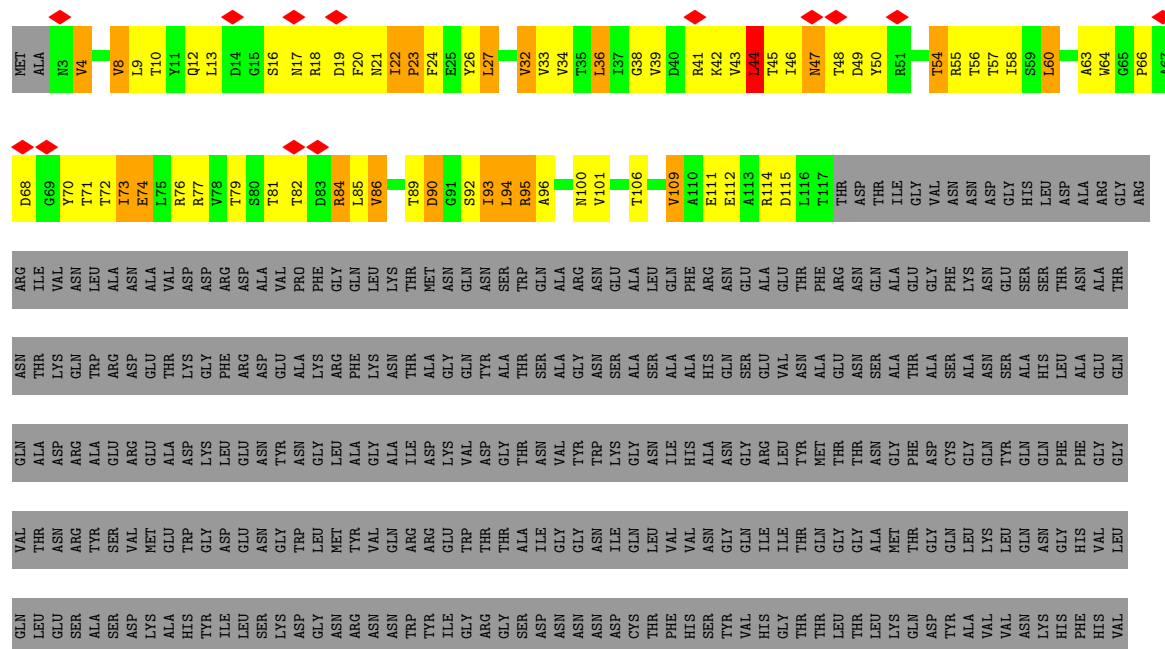


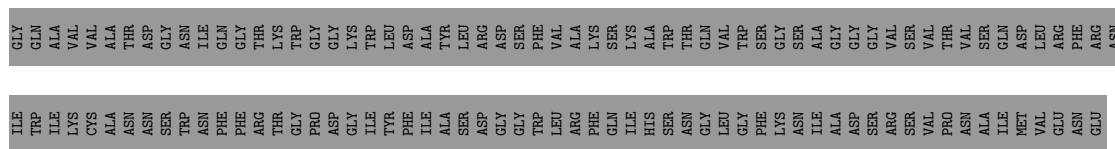
Chain d: 79%



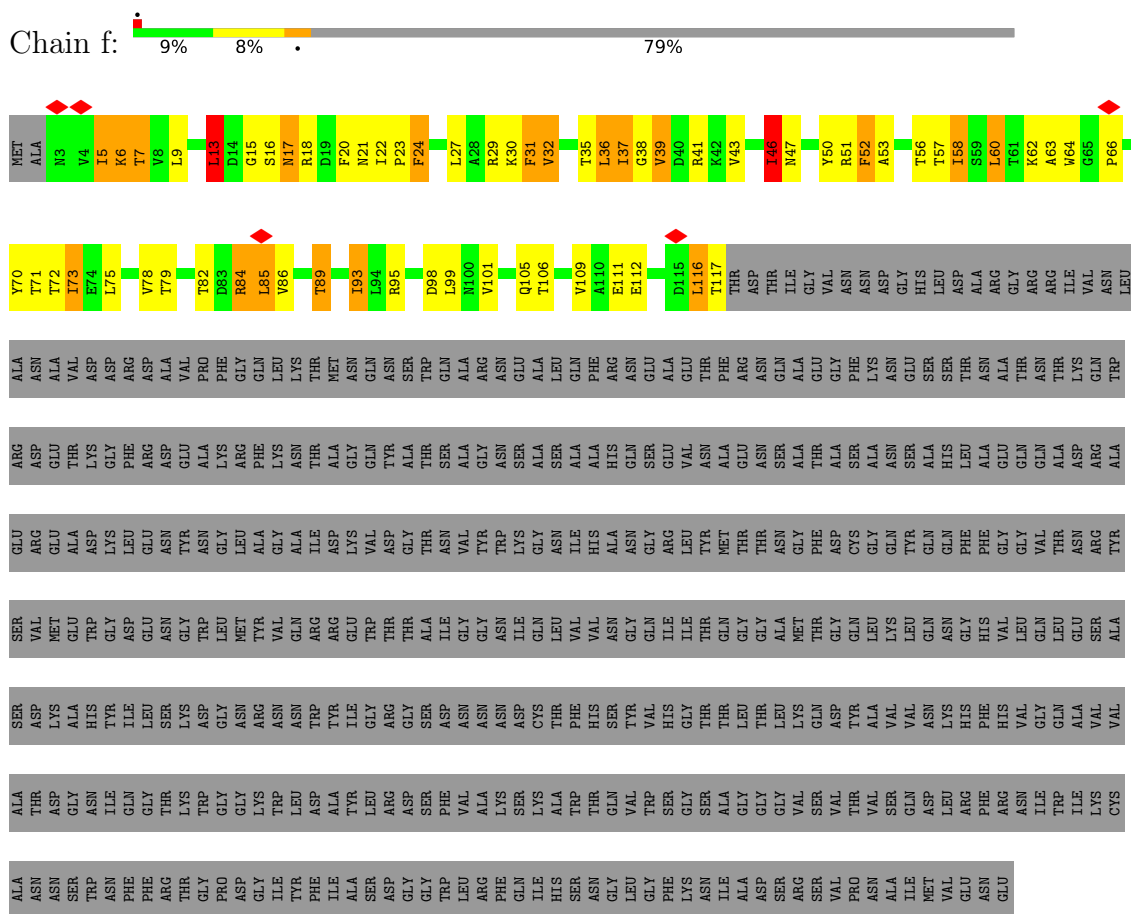
● Molecule 1: Tail fiber protein

Chain e: 79%

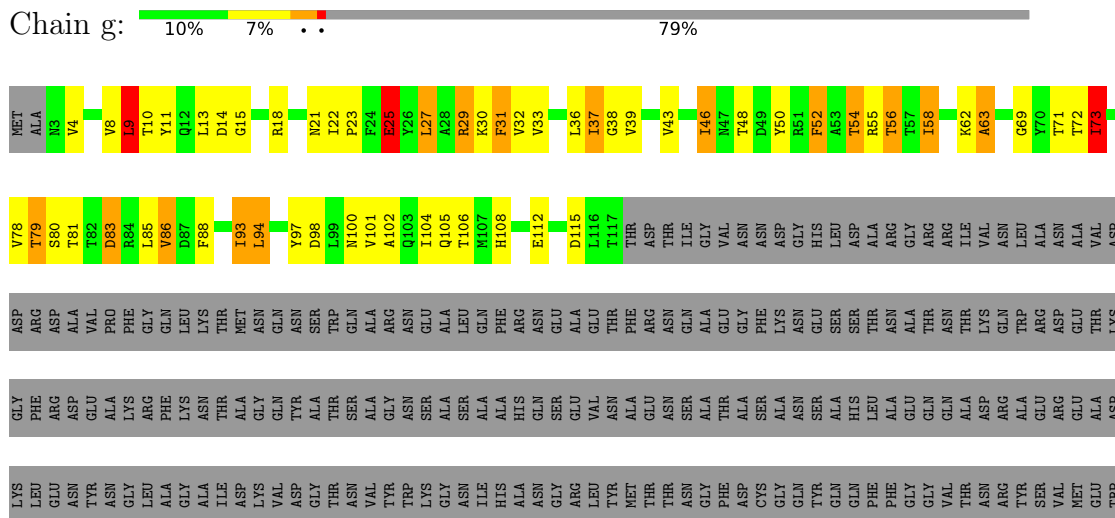




- Molecule 1: Tail fiber protein

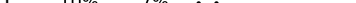


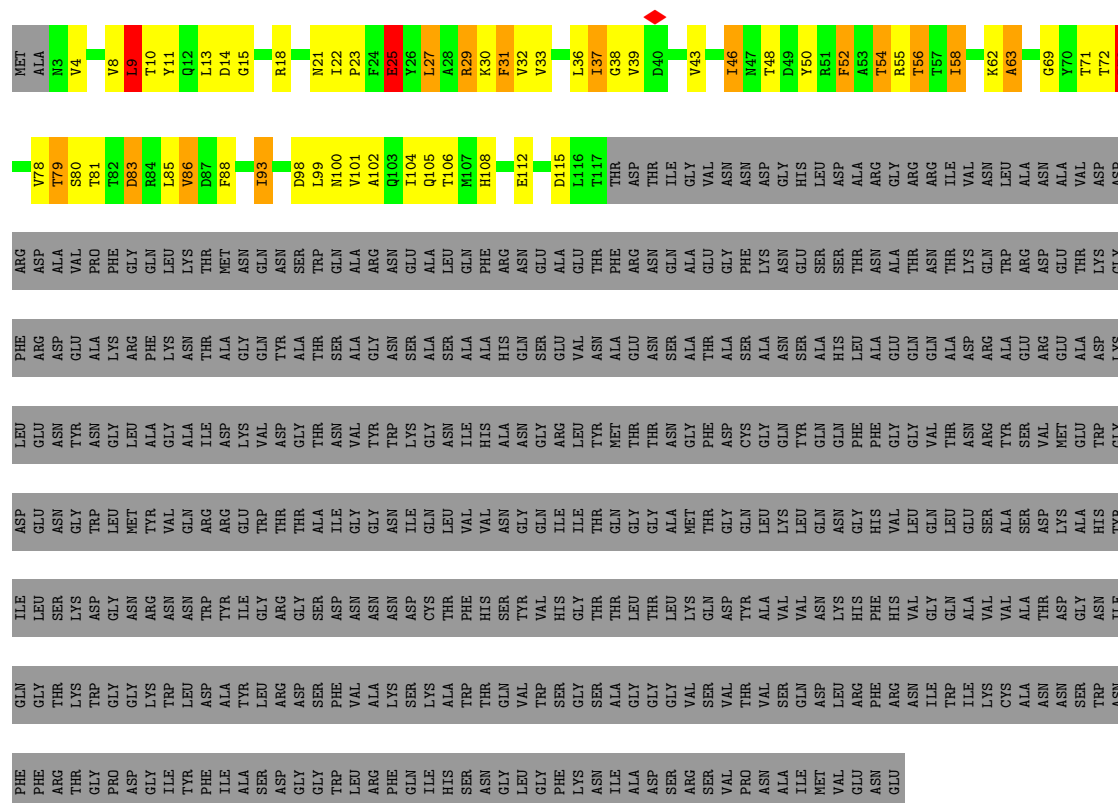
- Molecule 1: Tail fiber protein



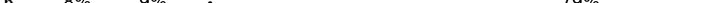
[illegible]

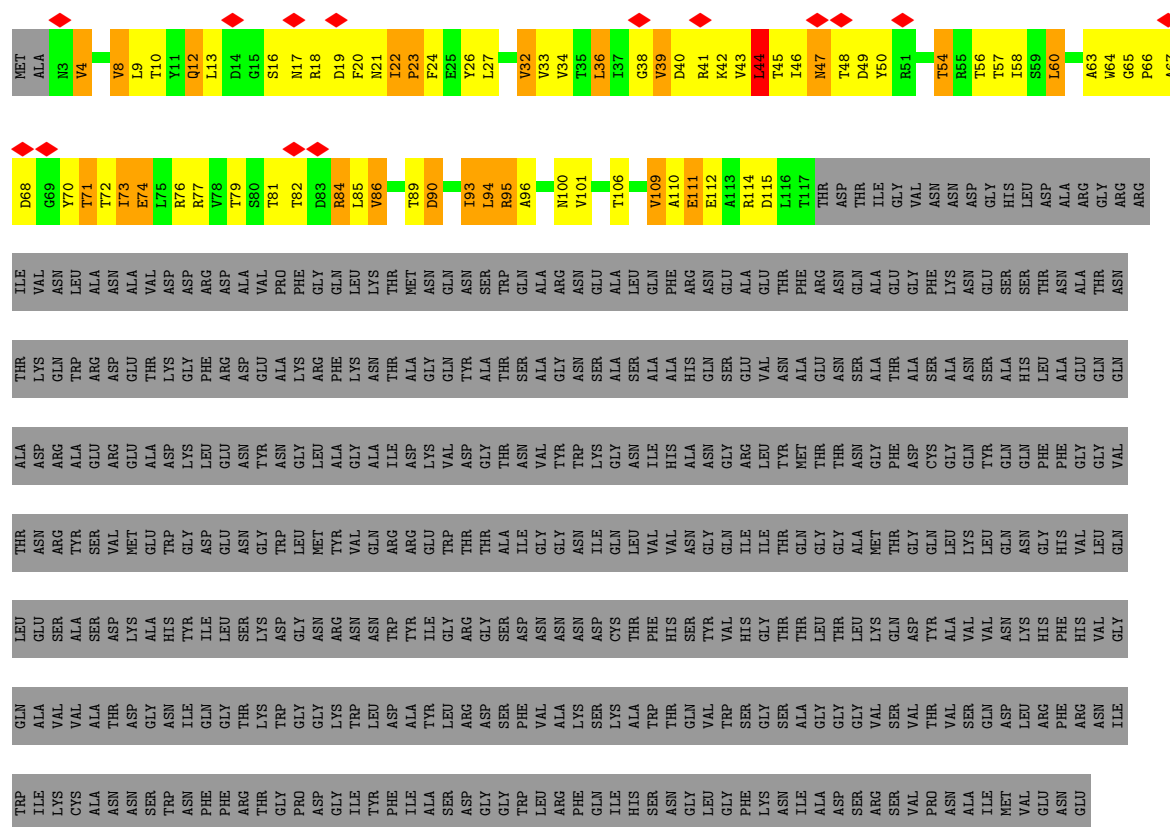
- Molecule 1: Tail fiber protein

Chain j:  10% 7% 3%

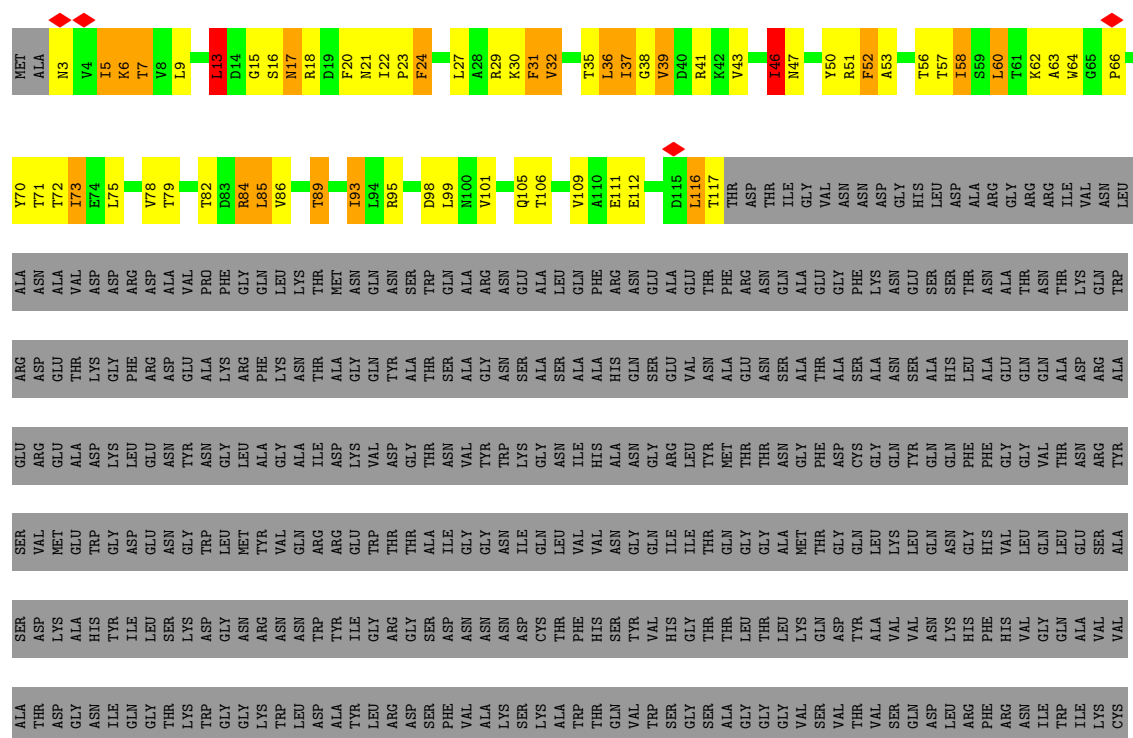


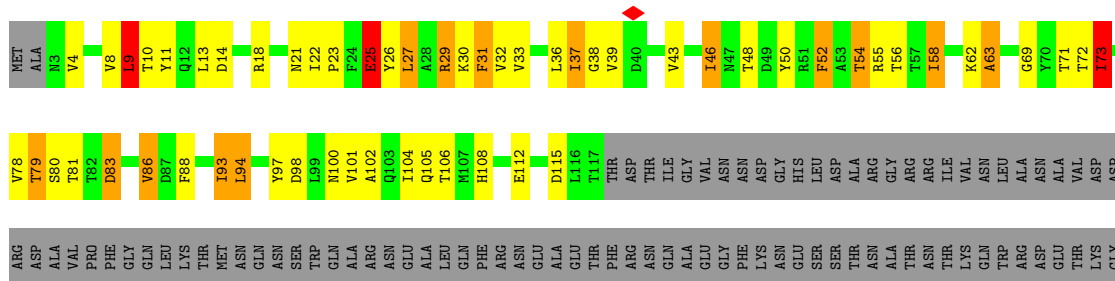
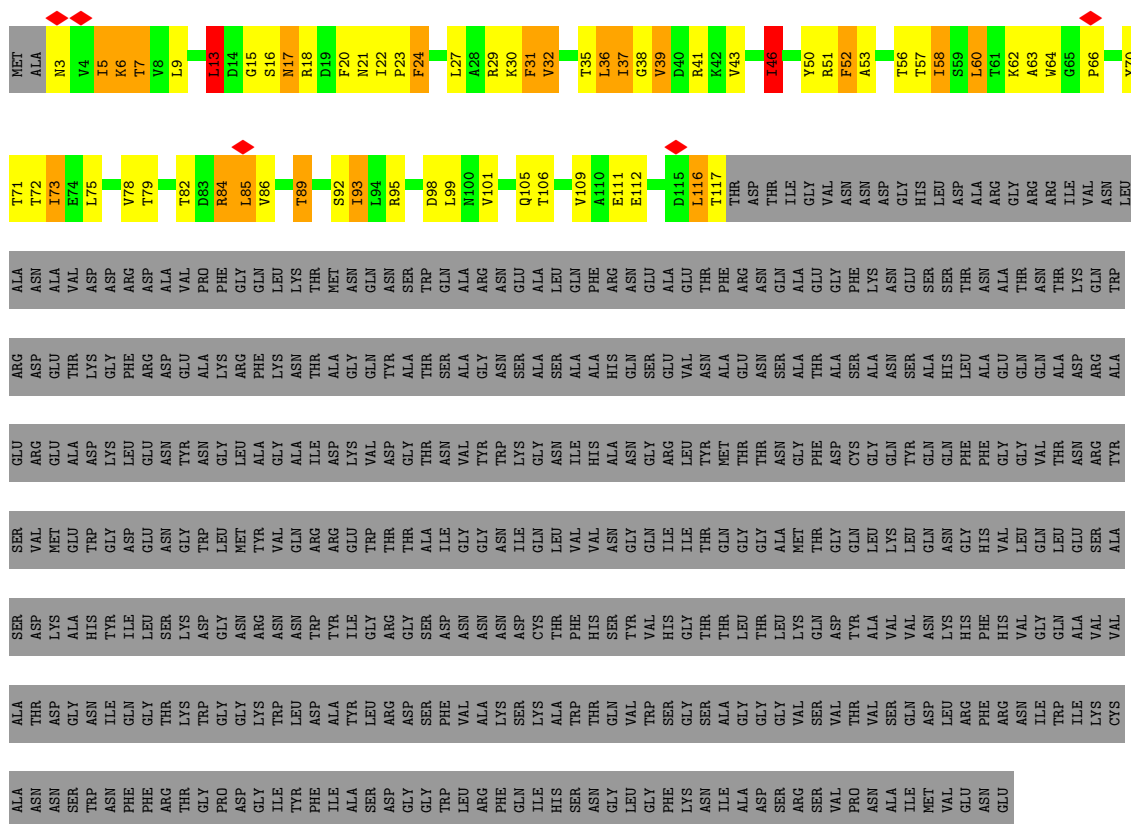
- Molecule 1: Tail fiber protein

Chain k:  8% 9% 79%

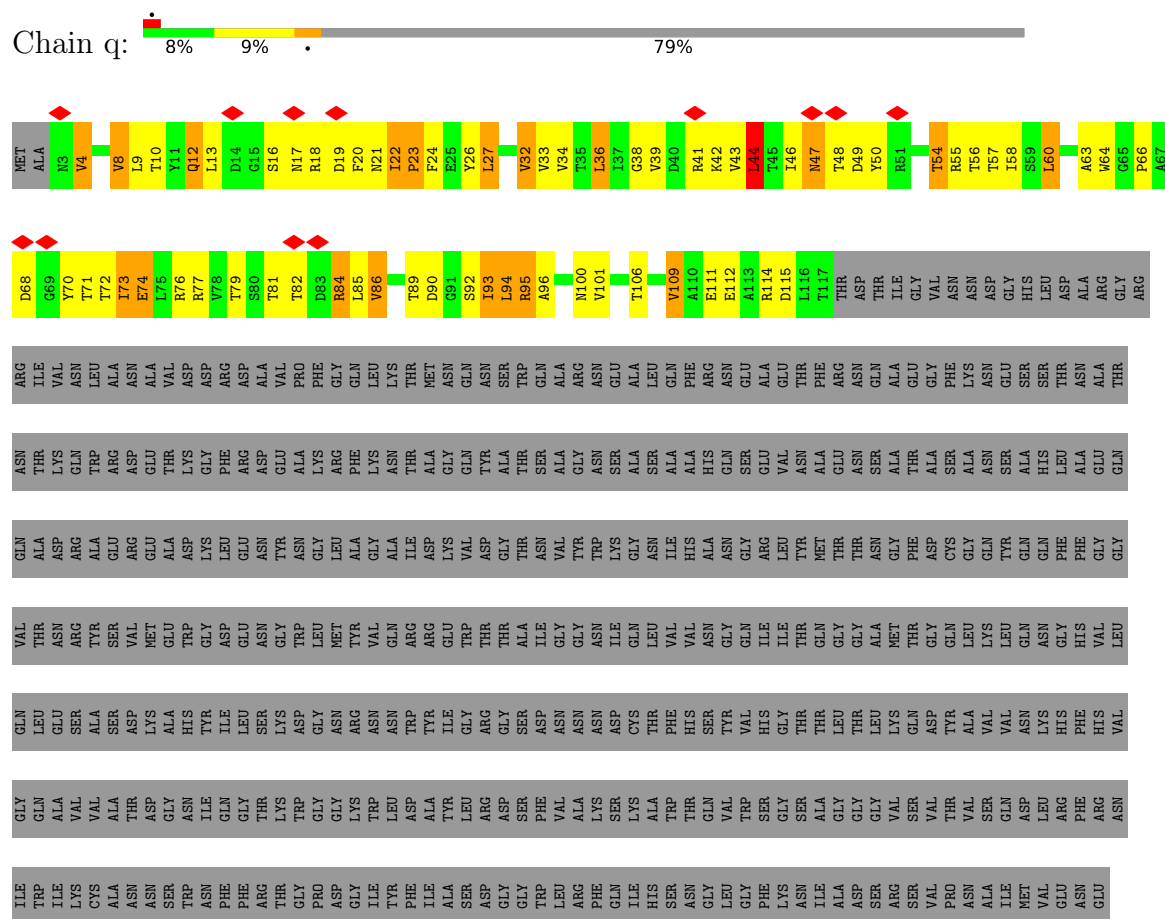


• Molecule 1: Tail fiber protein

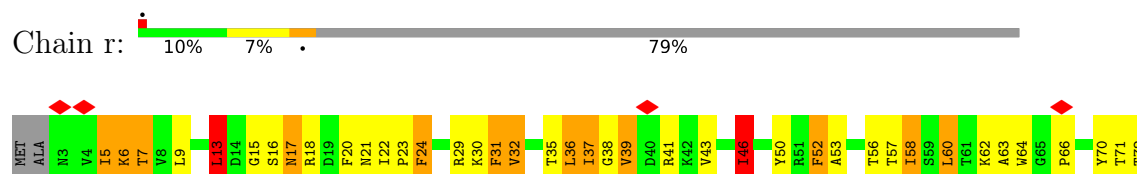


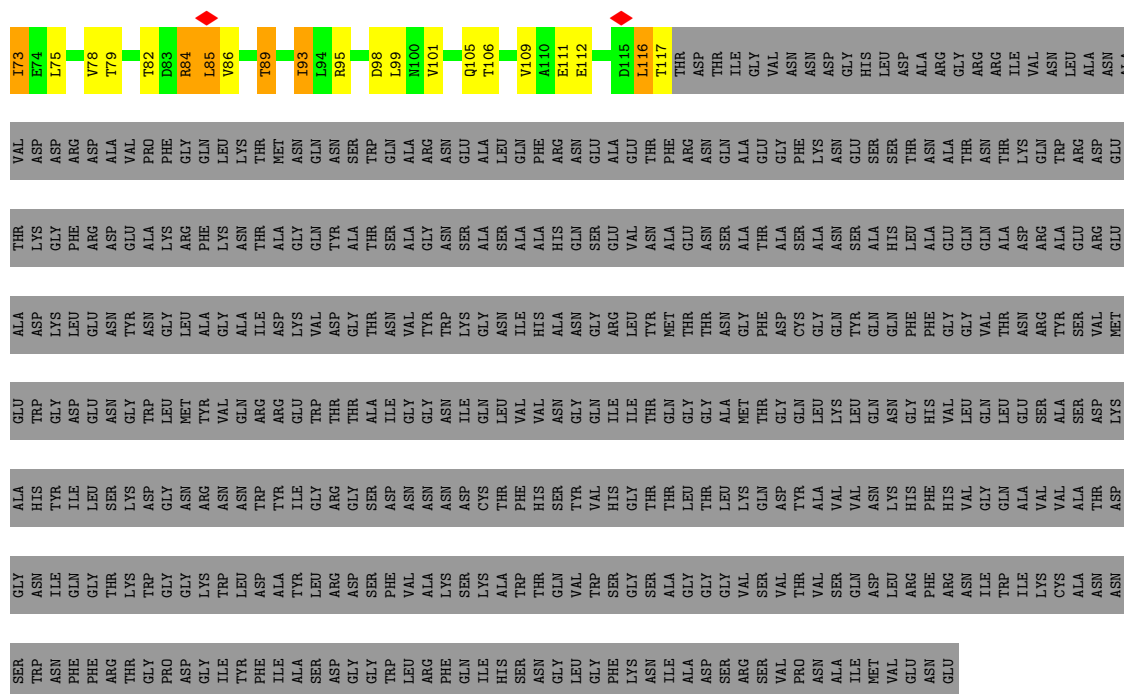


- Molecule 1: Tail fiber protein

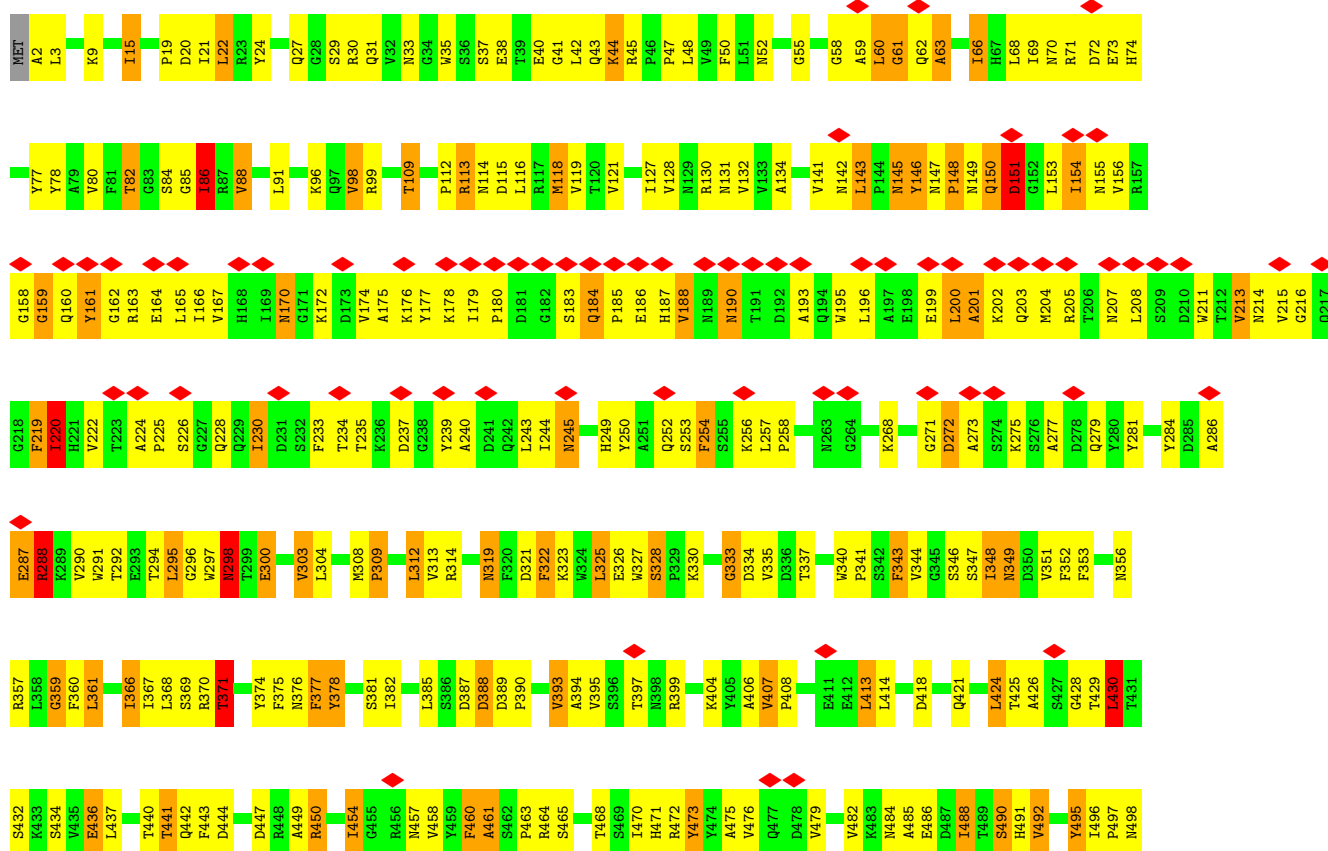


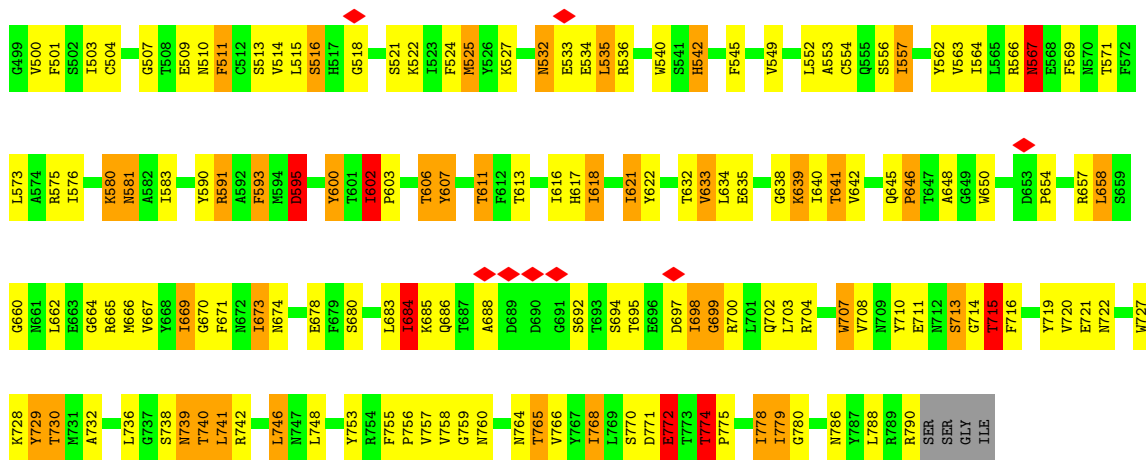
- Molecule 1: Tail fiber protein



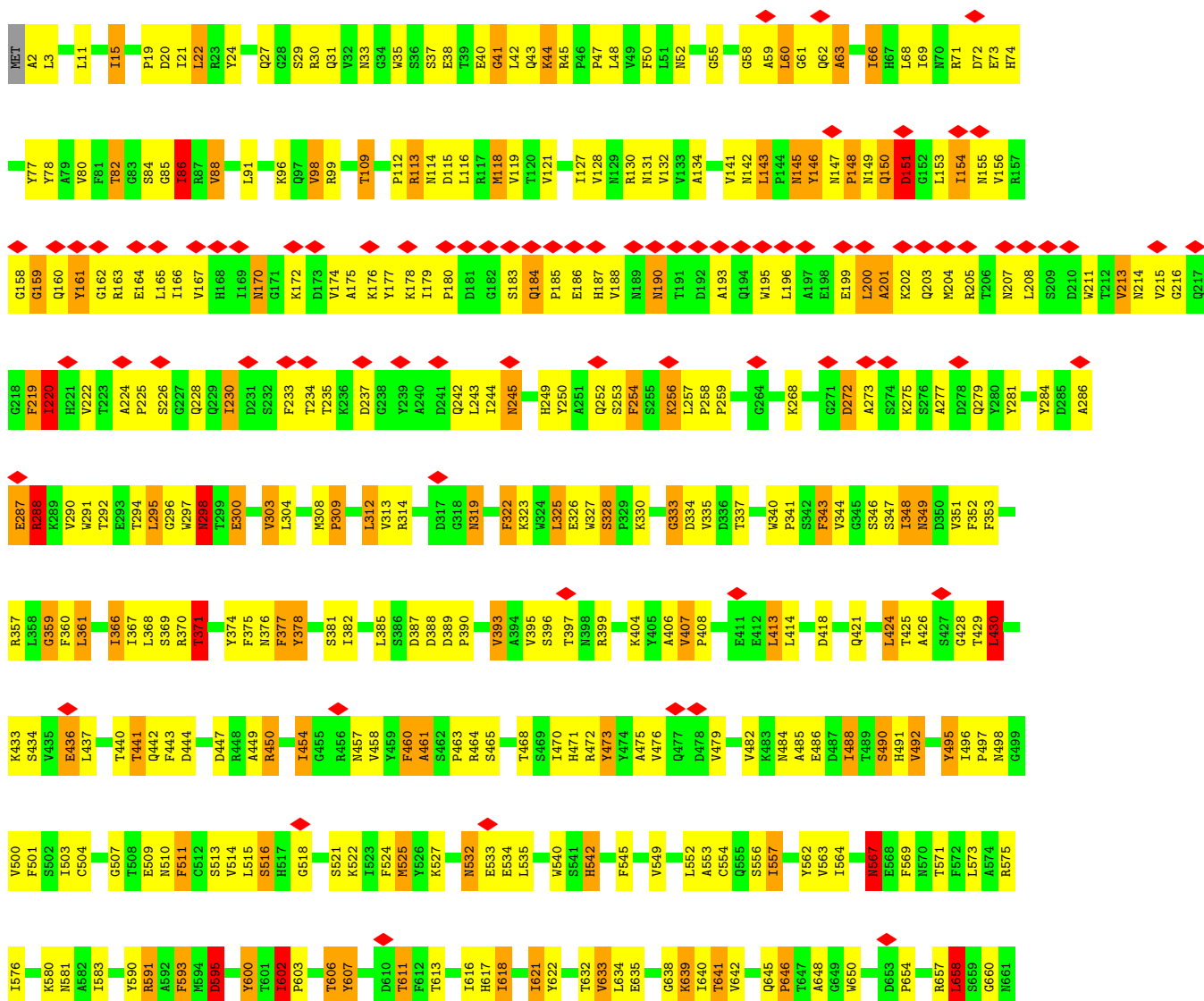
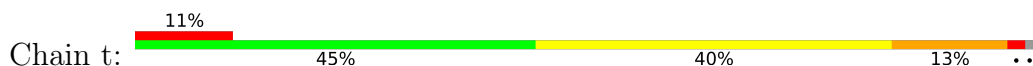


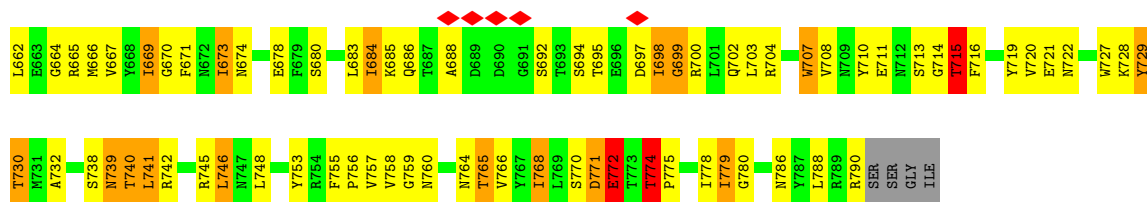
• Molecule 2: Tail tubular protein gp12



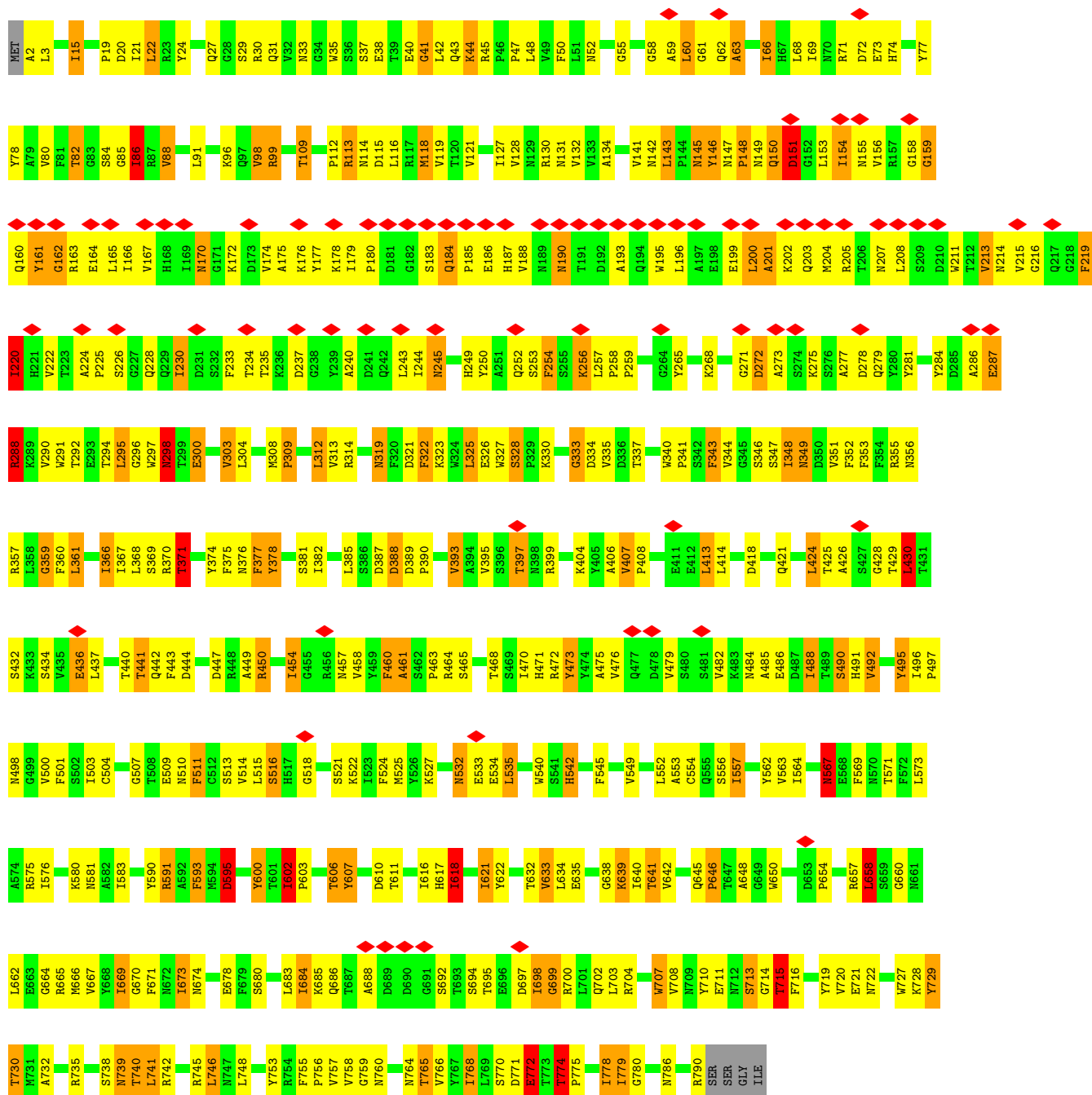


• Molecule 2: Tail tubular protein gp12

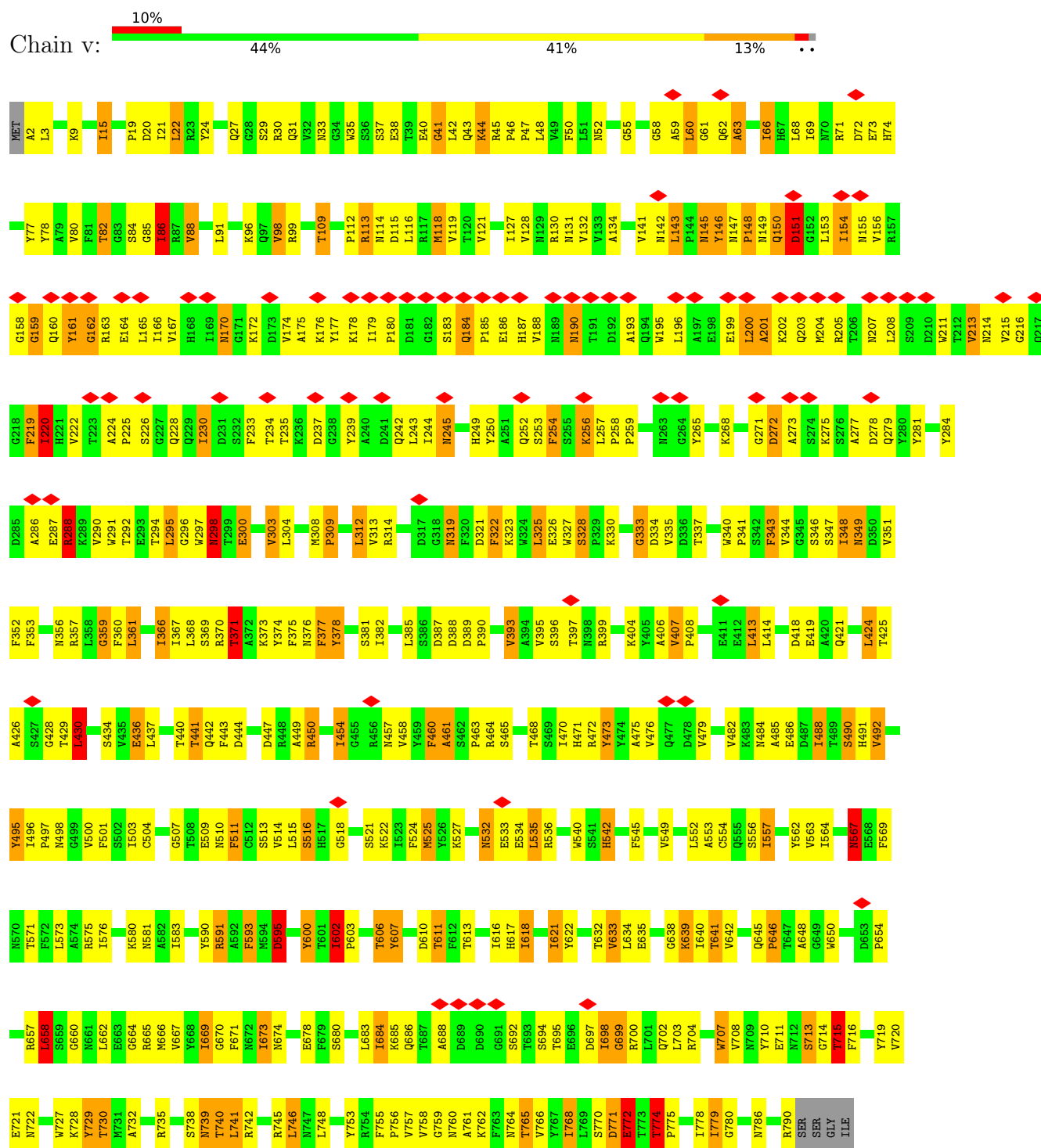


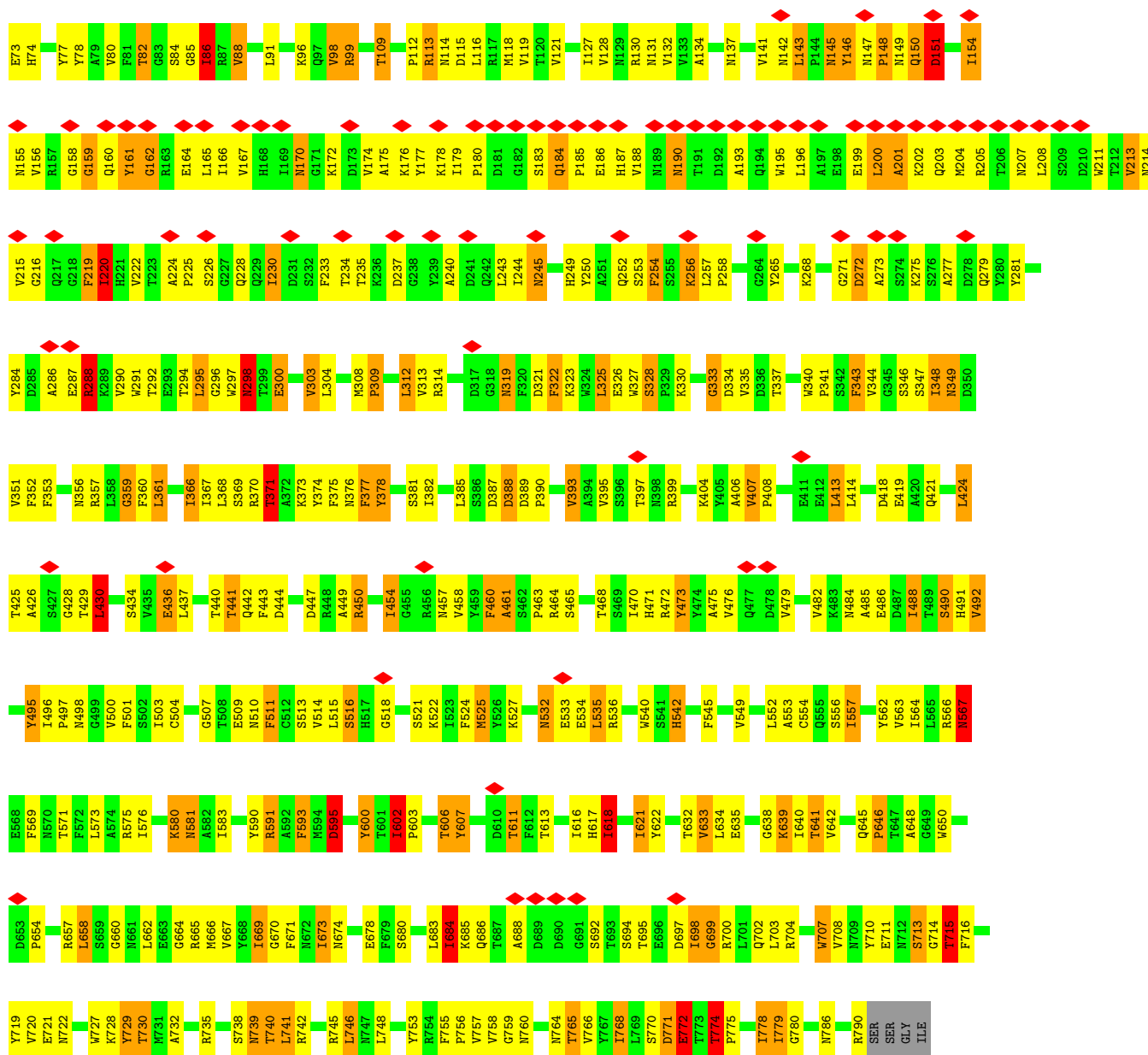


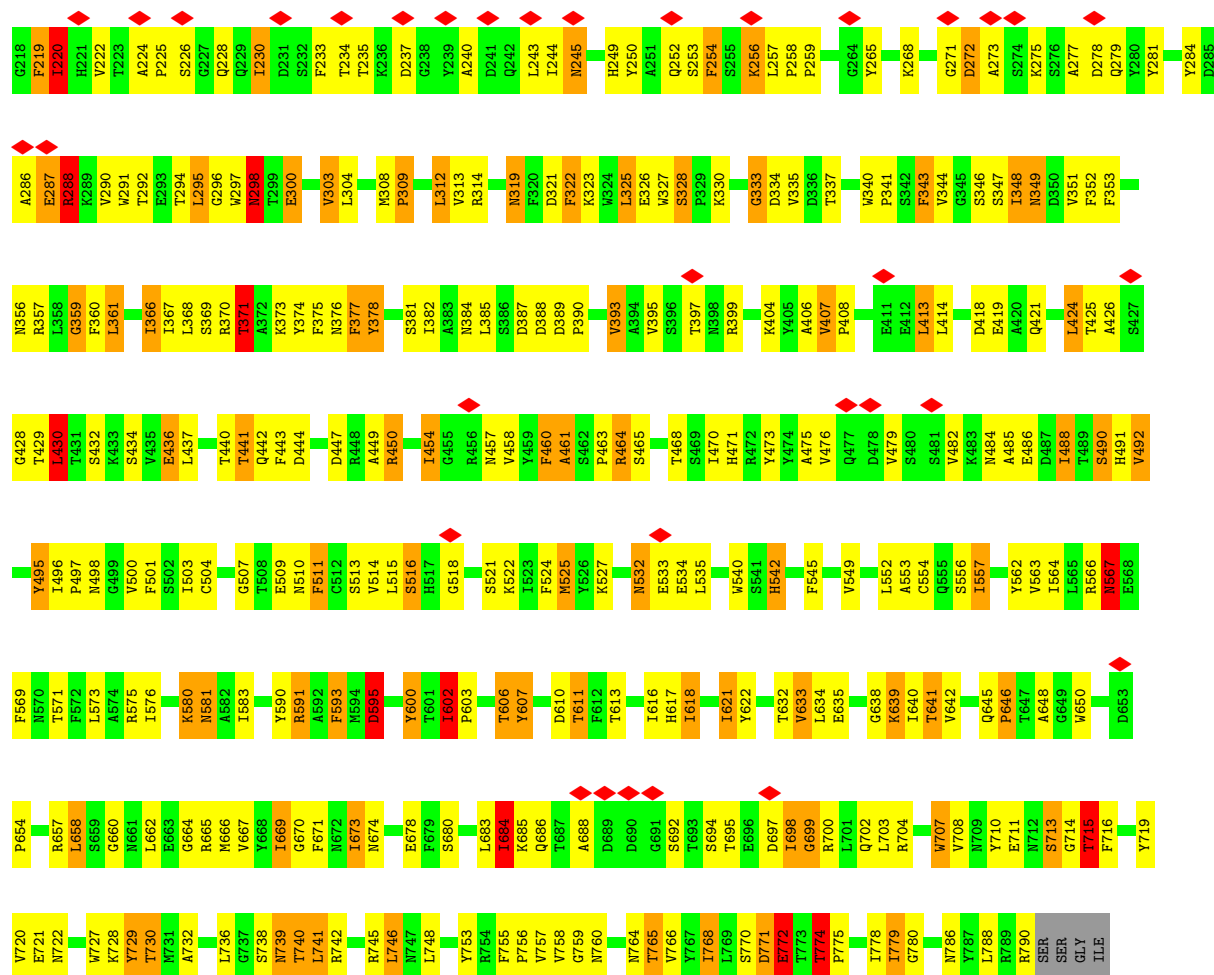
• Molecule 2: Tail tubular protein gp12



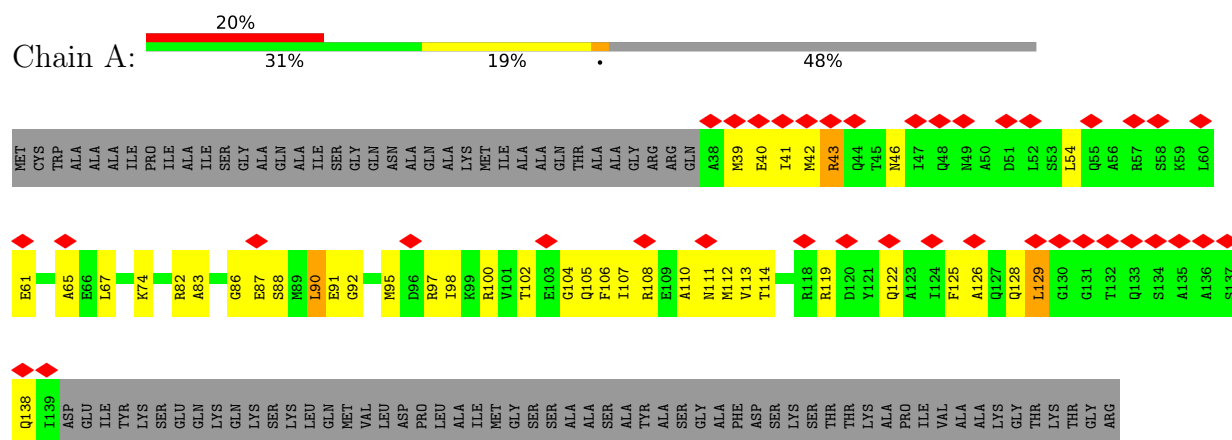
• Molecule 2: Tail tubular protein gp12



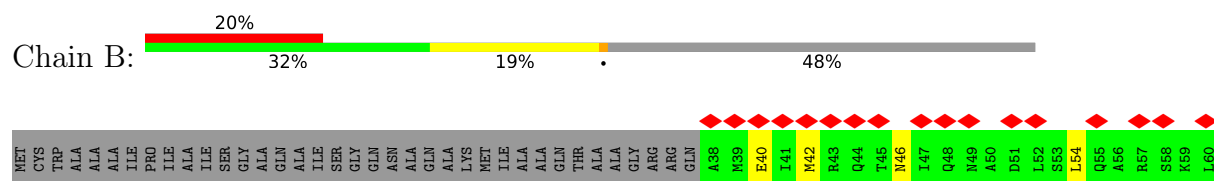




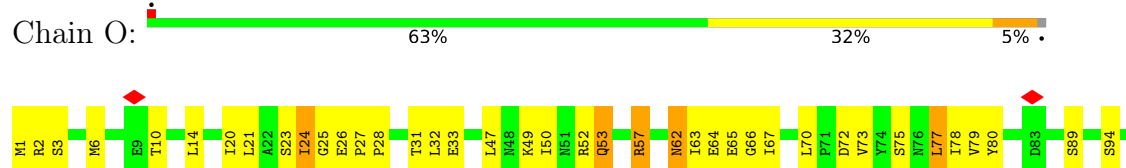
• Molecule 3: Internal virion protein gp14



• Molecule 3: Internal virion protein gp14

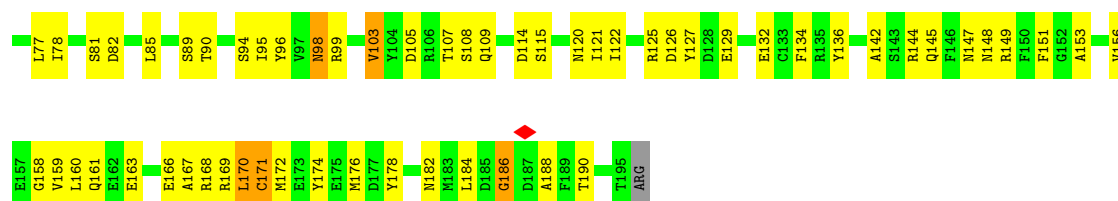
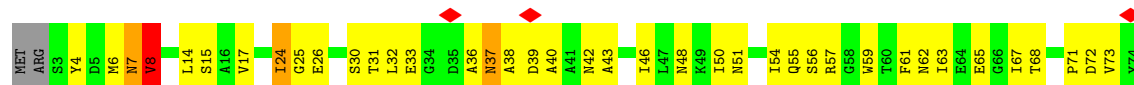


- Chain F:

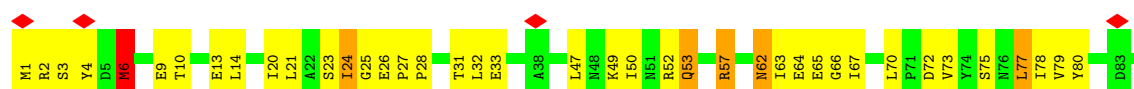




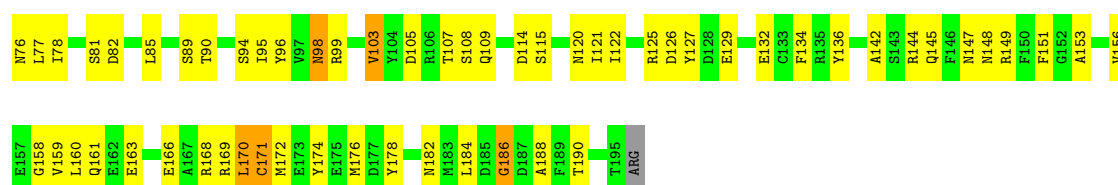
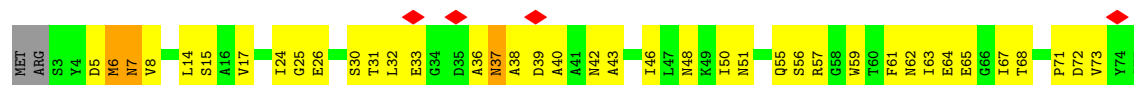
• Molecule 4: Tail tubular protein gp11



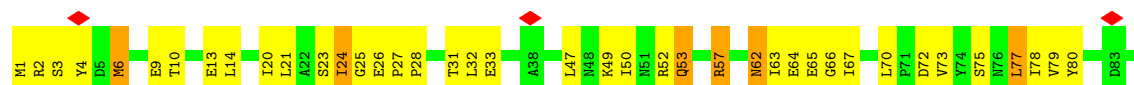
• Molecule 4: Tail tubular protein gp11



• Molecule 4: Tail tubular protein gp11

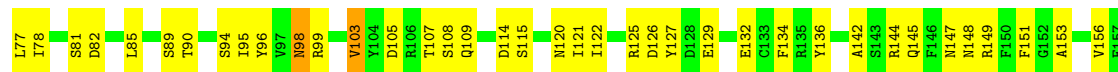


• Molecule 4: Tail tubular protein gp11

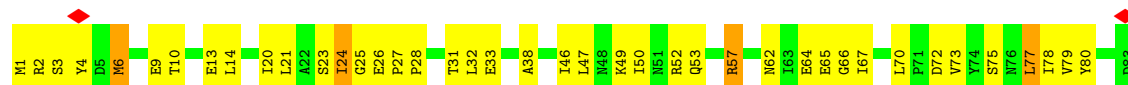




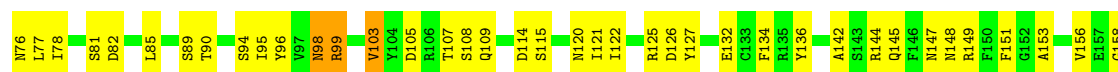
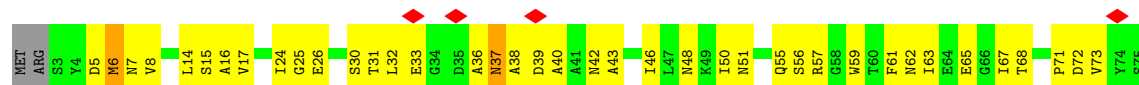
• Molecule 4: Tail tubular protein gp11



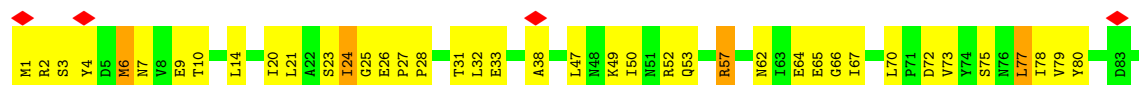
• Molecule 4: Tail tubular protein gp11

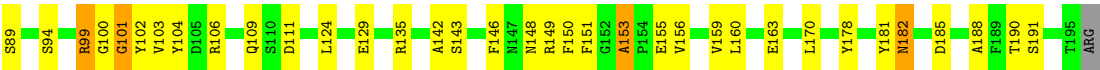


• Molecule 4: Tail tubular protein gp11

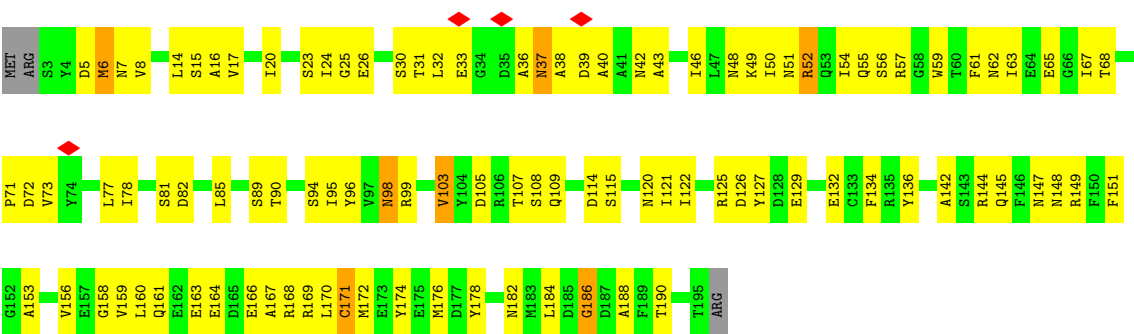


• Molecule 4: Tail tubular protein gp11





• Molecule 4: Tail tubular protein gp11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59985	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	43.195	Depositor
Minimum map value	-27.980	Depositor
Average map value	0.013	Depositor
Map value standard deviation	2.048	Depositor
Recommended contour level	8	Depositor
Map size ($\text{\AA}$)	508.0, 508.0, 508.0	wwPDB
Map dimensions	400, 400, 400	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	1.23	3/936 (0.3%)	1.47	20/1274 (1.6%)
1	b	1.21	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	c	1.13	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	d	1.22	3/936 (0.3%)	1.45	20/1274 (1.6%)
1	e	1.22	1/936 (0.1%)	1.63	29/1274 (2.3%)
1	f	1.14	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	g	1.23	3/936 (0.3%)	1.47	20/1274 (1.6%)
1	h	1.22	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	i	1.14	2/936 (0.2%)	1.51	20/1274 (1.6%)
1	j	1.22	4/936 (0.4%)	1.45	20/1274 (1.6%)
1	k	1.21	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	l	1.14	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	m	1.23	3/936 (0.3%)	1.46	20/1274 (1.6%)
1	n	1.22	1/936 (0.1%)	1.63	30/1274 (2.4%)
1	o	1.14	2/936 (0.2%)	1.54	21/1274 (1.6%)
1	p	1.23	4/936 (0.4%)	1.46	19/1274 (1.5%)
1	q	1.22	1/936 (0.1%)	1.63	30/1274 (2.4%)
1	r	1.13	3/936 (0.3%)	1.54	21/1274 (1.6%)
2	s	1.20	20/6449 (0.3%)	1.55	152/8772 (1.7%)
2	t	1.20	21/6449 (0.3%)	1.55	151/8772 (1.7%)
2	u	1.20	20/6449 (0.3%)	1.55	155/8772 (1.8%)
2	v	1.20	21/6449 (0.3%)	1.55	152/8772 (1.7%)
2	w	1.20	21/6449 (0.3%)	1.55	155/8772 (1.8%)
2	x	1.20	22/6449 (0.3%)	1.56	154/8772 (1.8%)
3	A	0.37	0/790	0.68	2/1056 (0.2%)
3	B	0.33	0/790	0.62	2/1056 (0.2%)
3	C	0.38	0/790	0.68	2/1056 (0.2%)
3	D	0.36	0/790	0.63	1/1056 (0.1%)
3	E	0.40	0/790	0.75	3/1056 (0.3%)
3	F	0.38	0/790	0.67	1/1056 (0.1%)
4	M	0.72	1/1580 (0.1%)	1.08	15/2139 (0.7%)
4	N	0.61	0/1561	0.96	8/2115 (0.4%)
4	O	0.72	1/1580 (0.1%)	1.05	12/2139 (0.6%)
4	P	0.60	0/1561	0.96	9/2115 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	Q	0.72	1/1580 (0.1%)	1.08	15/2139 (0.7%)
4	R	0.61	0/1561	0.96	9/2115 (0.4%)
4	S	0.73	1/1580 (0.1%)	1.07	13/2139 (0.6%)
4	T	0.61	0/1561	0.96	9/2115 (0.4%)
4	U	0.72	1/1580 (0.1%)	1.07	14/2139 (0.7%)
4	V	0.60	0/1561	0.95	8/2115 (0.4%)
4	W	0.72	1/1580 (0.1%)	1.07	15/2139 (0.7%)
4	X	0.60	0/1561	0.96	8/2115 (0.4%)
All	All	1.06	170/79128 (0.2%)	1.40	1485/107424 (1.4%)

The worst 5 of 170 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	99	ARG	CA-C	-6.99	1.46	1.53
4	O	99	ARG	CA-C	-6.98	1.46	1.53
4	M	99	ARG	CA-C	-6.97	1.46	1.53
4	S	99	ARG	CA-C	-6.97	1.46	1.53
4	U	99	ARG	CA-C	-6.97	1.46	1.53

The worst 5 of 1485 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	i	39	VAL	N-CA-C	-12.72	101.57	111.62
1	l	39	VAL	N-CA-C	-12.71	101.58	111.62
1	o	39	VAL	N-CA-C	-12.71	101.58	111.62
1	r	39	VAL	N-CA-C	-12.68	101.60	111.62
1	c	39	VAL	N-CA-C	-12.66	101.62	111.62

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	922	0	931	41	0
1	b	922	0	931	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	c	922	0	931	80	0
1	d	922	0	931	44	0
1	e	922	0	931	36	0
1	f	922	0	931	79	0
1	g	922	0	931	40	0
1	h	922	0	931	37	0
1	i	922	0	931	81	0
1	j	922	0	931	41	0
1	k	922	0	931	36	0
1	l	922	0	931	80	0
1	m	922	0	931	41	0
1	n	922	0	931	35	0
1	o	922	0	931	69	0
1	p	922	0	931	45	0
1	q	922	0	931	35	0
1	r	922	0	931	83	0
2	s	6289	0	6051	405	0
2	t	6289	0	6051	404	0
2	u	6289	0	6051	399	0
2	v	6289	0	6051	410	0
2	w	6289	0	6051	399	0
2	x	6289	0	6051	412	0
3	A	787	0	784	83	0
3	B	787	0	784	64	0
3	C	787	0	784	75	0
3	D	787	0	784	66	0
3	E	787	0	784	70	0
3	F	787	0	784	47	0
4	M	1553	0	1472	86	0
4	N	1534	0	1447	106	0
4	O	1553	0	1472	89	0
4	P	1534	0	1447	107	0
4	Q	1553	0	1472	84	0
4	R	1534	0	1447	103	0
4	S	1553	0	1472	82	0
4	T	1534	0	1447	100	0
4	U	1553	0	1472	82	0
4	V	1534	0	1447	103	0
4	W	1553	0	1472	83	0
4	X	1534	0	1447	110	0
All	All	77574	0	75282	3909	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 26.

The worst 5 of 3909 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:v:396:SER:HB2	3:A:91:GLU:CD	1.51	1.34
2:t:19:PRO:HG2	2:u:711:GLU:CD	1.57	1.28
2:s:711:GLU:CD	2:x:19:PRO:HG2	1.58	1.27
2:u:19:PRO:HG2	2:v:711:GLU:CD	1.59	1.27
2:v:19:PRO:HG2	2:w:711:GLU:CD	1.59	1.27

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	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49
1	b	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	c	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	49
1	d	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49
1	e	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	f	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	49
1	g	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49
1	h	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	i	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	49
1	j	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49
1	k	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	l	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	49
1	m	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	n	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	o	113/553 (20%)	108 (96%)	4 (4%)	1 (1%)	14	49
1	p	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	49
1	q	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	6	33
1	r	113/553 (20%)	107 (95%)	6 (5%)	0	100	100
2	s	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	52
2	t	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	52
2	u	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	52
2	v	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	52
2	w	787/794 (99%)	734 (93%)	47 (6%)	6 (1%)	16	52
2	x	787/794 (99%)	734 (93%)	47 (6%)	6 (1%)	16	52
3	A	100/196 (51%)	100 (100%)	0	0	100	100
3	B	100/196 (51%)	99 (99%)	1 (1%)	0	100	100
3	C	100/196 (51%)	100 (100%)	0	0	100	100
3	D	100/196 (51%)	99 (99%)	1 (1%)	0	100	100
3	E	100/196 (51%)	100 (100%)	0	0	100	100
3	F	100/196 (51%)	100 (100%)	0	0	100	100
4	M	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	N	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	O	193/196 (98%)	184 (95%)	9 (5%)	0	100	100
4	P	191/196 (97%)	179 (94%)	11 (6%)	1 (0%)	24	62
4	Q	193/196 (98%)	184 (95%)	9 (5%)	0	100	100
4	R	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	S	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	T	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	U	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
4	V	191/196 (97%)	179 (94%)	12 (6%)	0	100	100
4	W	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	X	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
All	All	9660/18246 (53%)	9080 (94%)	520 (5%)	60 (1%)	23	58

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	c	46	ILE
1	f	46	ILE
1	i	46	ILE
1	l	46	ILE
1	o	46	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	102/451 (23%)	77 (76%)	25 (24%)	1	4
1	b	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	c	102/451 (23%)	82 (80%)	20 (20%)	1	8
1	d	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	e	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	f	102/451 (23%)	82 (80%)	20 (20%)	1	8
1	g	102/451 (23%)	77 (76%)	25 (24%)	1	4
1	h	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	i	102/451 (23%)	82 (80%)	20 (20%)	1	8
1	j	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	k	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	l	102/451 (23%)	82 (80%)	20 (20%)	1	8
1	m	102/451 (23%)	77 (76%)	25 (24%)	1	4
1	n	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	o	102/451 (23%)	82 (80%)	20 (20%)	1	8
1	p	102/451 (23%)	77 (76%)	25 (24%)	1	4
1	q	102/451 (23%)	78 (76%)	24 (24%)	1	5
1	r	102/451 (23%)	82 (80%)	20 (20%)	1	8
2	s	684/688 (99%)	562 (82%)	122 (18%)	2	11
2	t	684/688 (99%)	562 (82%)	122 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	u	684/688 (99%)	562 (82%)	122 (18%)	2	11
2	v	684/688 (99%)	562 (82%)	122 (18%)	2	11
2	w	684/688 (99%)	562 (82%)	122 (18%)	2	11
2	x	684/688 (99%)	562 (82%)	122 (18%)	2	11
3	A	83/149 (56%)	79 (95%)	4 (5%)	23	45
3	B	83/149 (56%)	81 (98%)	2 (2%)	43	63
3	C	83/149 (56%)	78 (94%)	5 (6%)	17	40
3	D	83/149 (56%)	80 (96%)	3 (4%)	31	52
3	E	83/149 (56%)	79 (95%)	4 (5%)	23	45
3	F	83/149 (56%)	81 (98%)	2 (2%)	43	63
4	M	168/169 (99%)	158 (94%)	10 (6%)	17	40
4	N	166/169 (98%)	151 (91%)	15 (9%)	9	28
4	O	168/169 (99%)	158 (94%)	10 (6%)	17	40
4	P	166/169 (98%)	154 (93%)	12 (7%)	13	35
4	Q	168/169 (99%)	158 (94%)	10 (6%)	17	40
4	R	166/169 (98%)	152 (92%)	14 (8%)	10	30
4	S	168/169 (99%)	158 (94%)	10 (6%)	17	40
4	T	166/169 (98%)	153 (92%)	13 (8%)	11	32
4	U	168/169 (99%)	158 (94%)	10 (6%)	17	40
4	V	166/169 (98%)	153 (92%)	13 (8%)	11	32
4	W	168/169 (99%)	157 (94%)	11 (6%)	15	38
4	X	166/169 (98%)	152 (92%)	14 (8%)	10	30
All	All	8442/15168 (56%)	7136 (84%)	1306 (16%)	5	13

5 of 1306 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	w	220	ILE
3	A	90	LEU
2	w	385	LEU
2	w	215	VAL
2	x	170	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 244 such sidechains are listed below:

Mol	Chain	Res	Type
2	v	242	GLN
4	S	53	GLN
2	w	384	ASN
4	R	109	GLN
4	W	53	GLN

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.

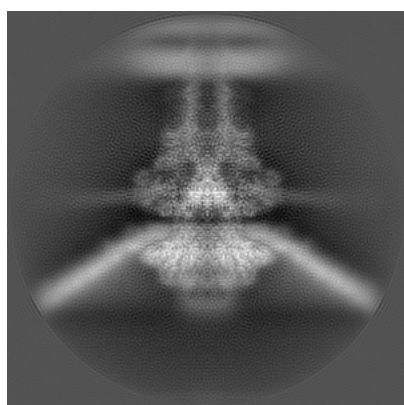
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31321. These allow visual inspection of the internal detail of the map and identification of artifacts.

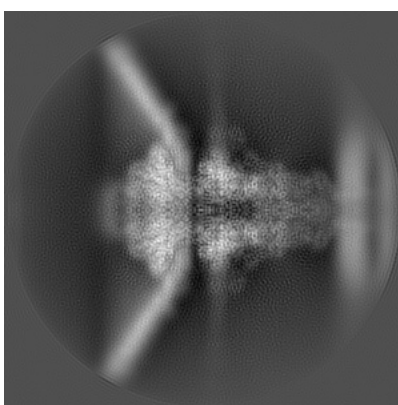
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

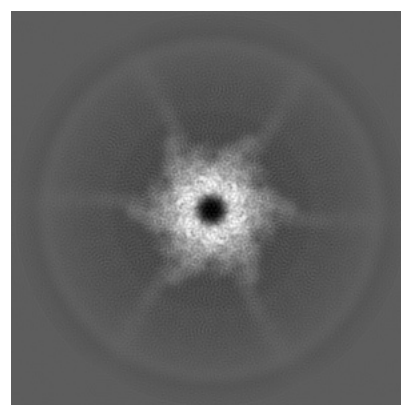
6.1.1 Primary map



X



Y

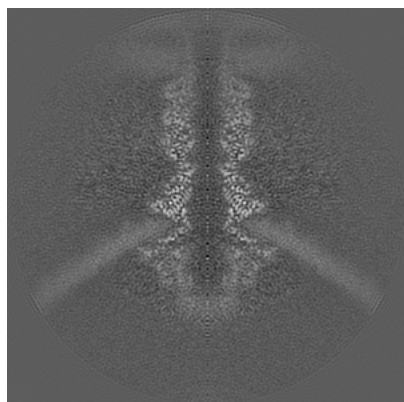


Z

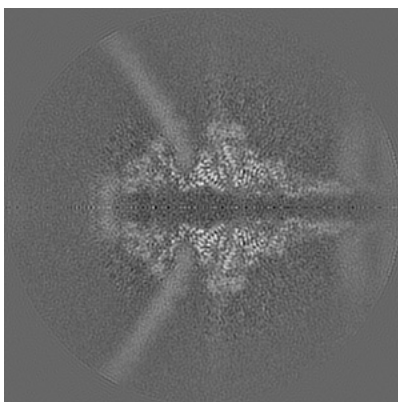
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

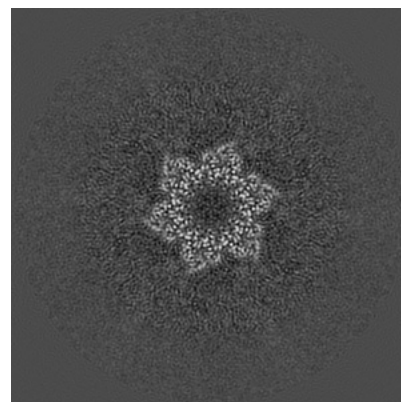
6.2.1 Primary map



X Index: 200



Y Index: 200

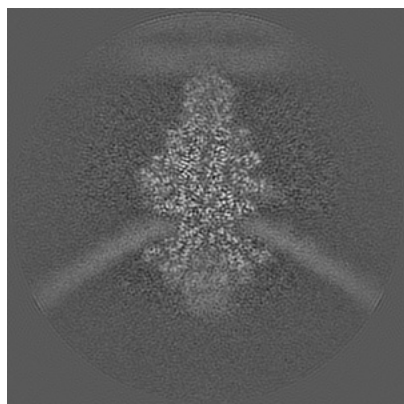


Z Index: 200

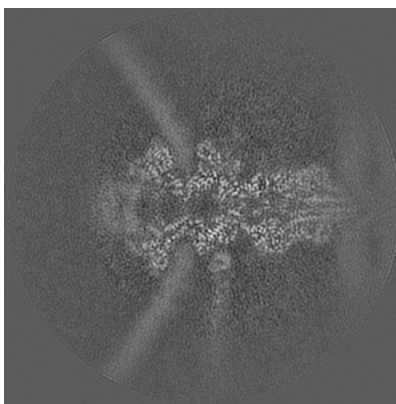
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

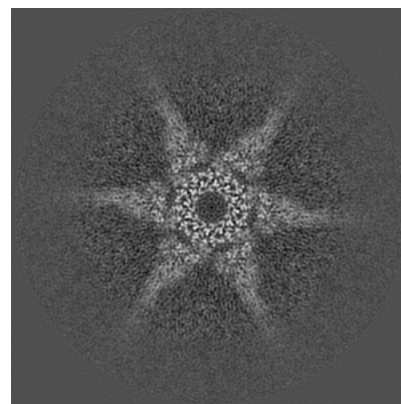
6.3.1 Primary map



X Index: 177



Y Index: 216

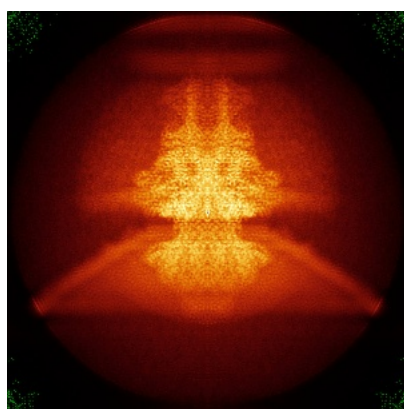


Z Index: 217

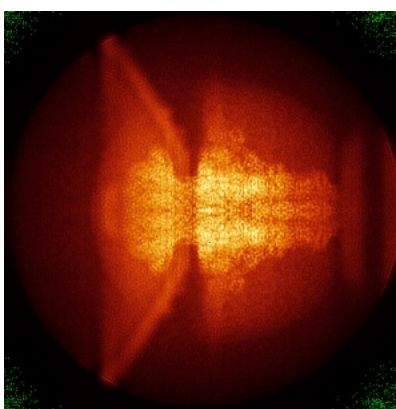
The images above show the largest variance slices of the map in three orthogonal directions.

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

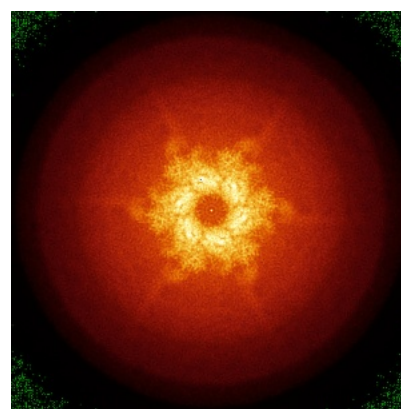
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

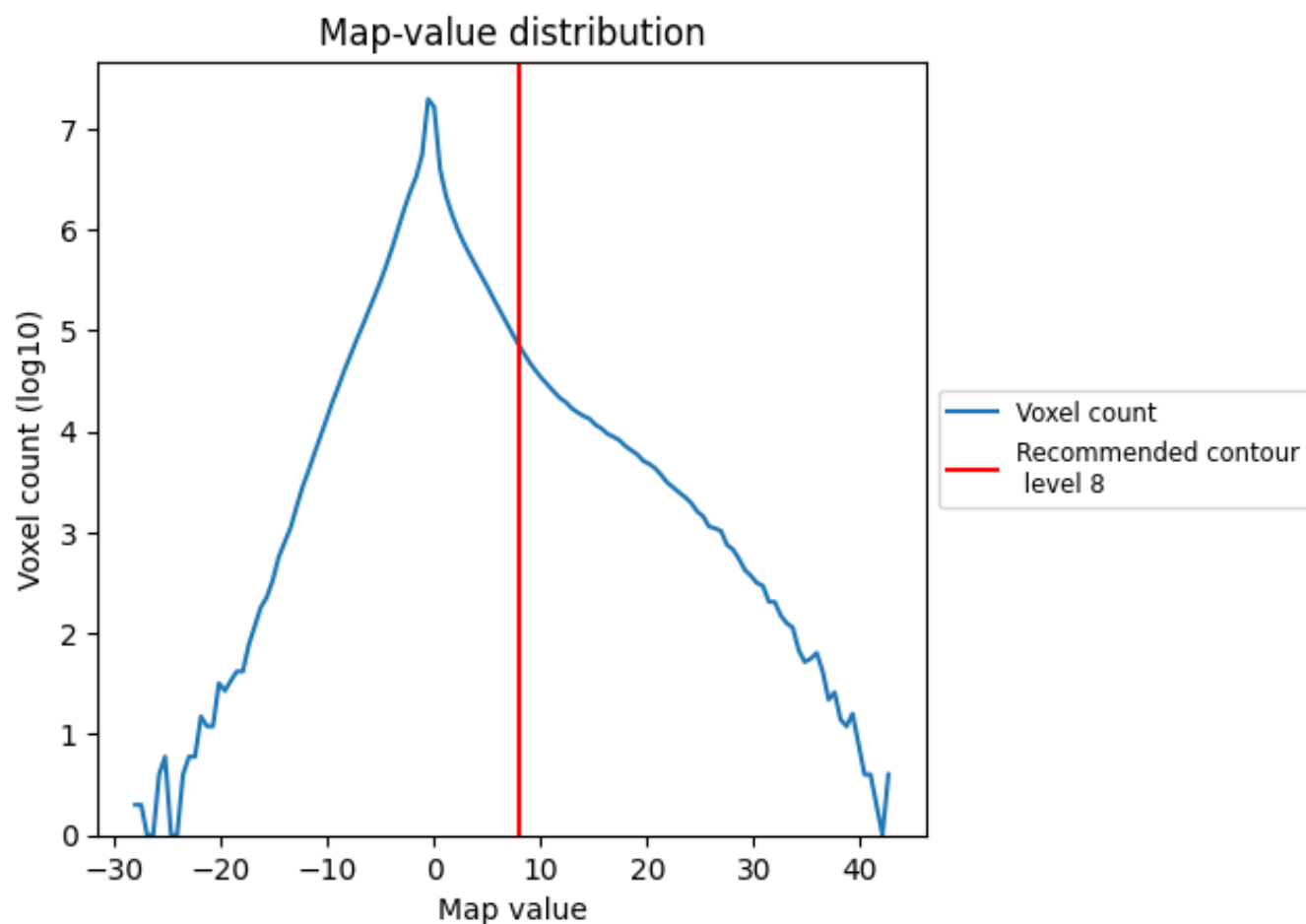
6.6 Mask visualisation

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

7 Map analysis [i](#)

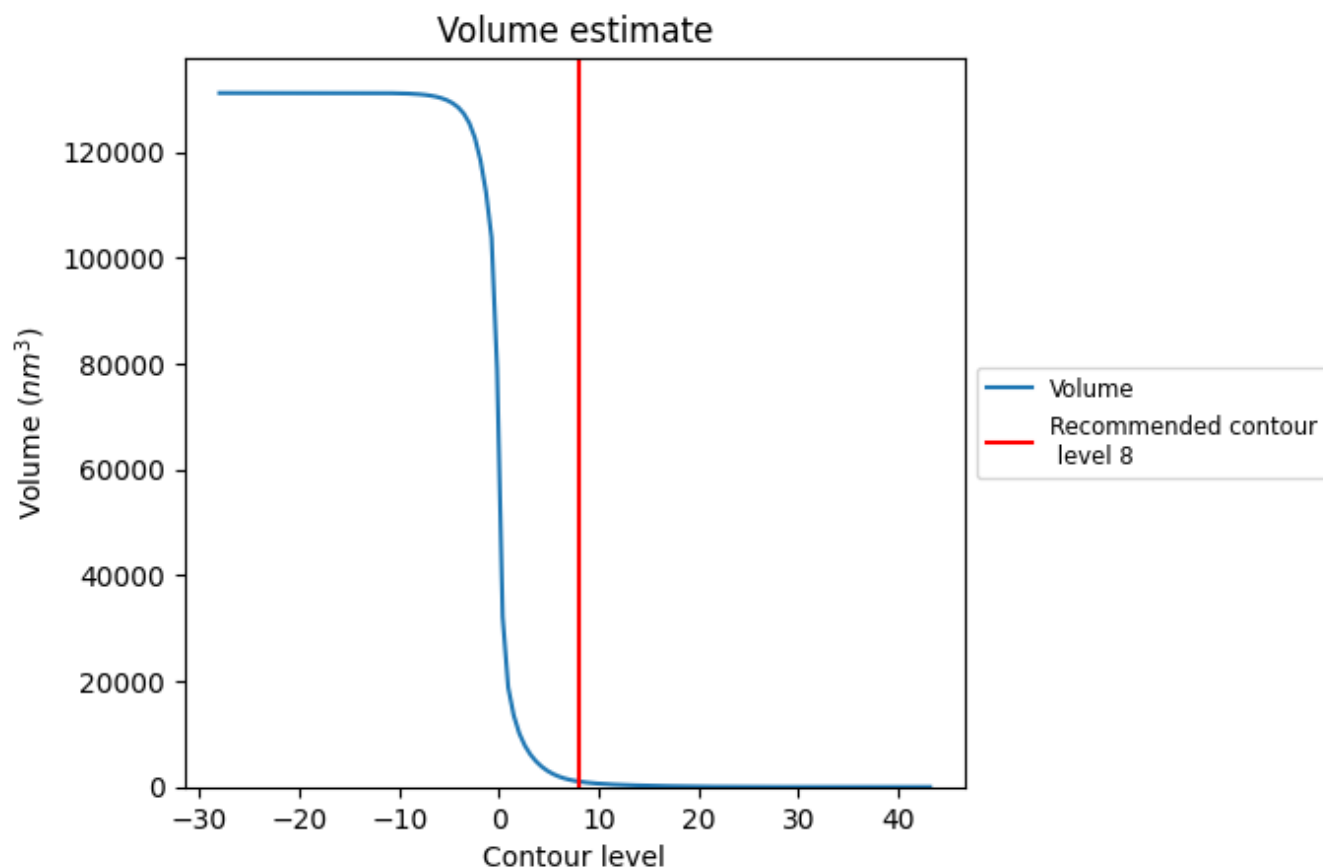
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

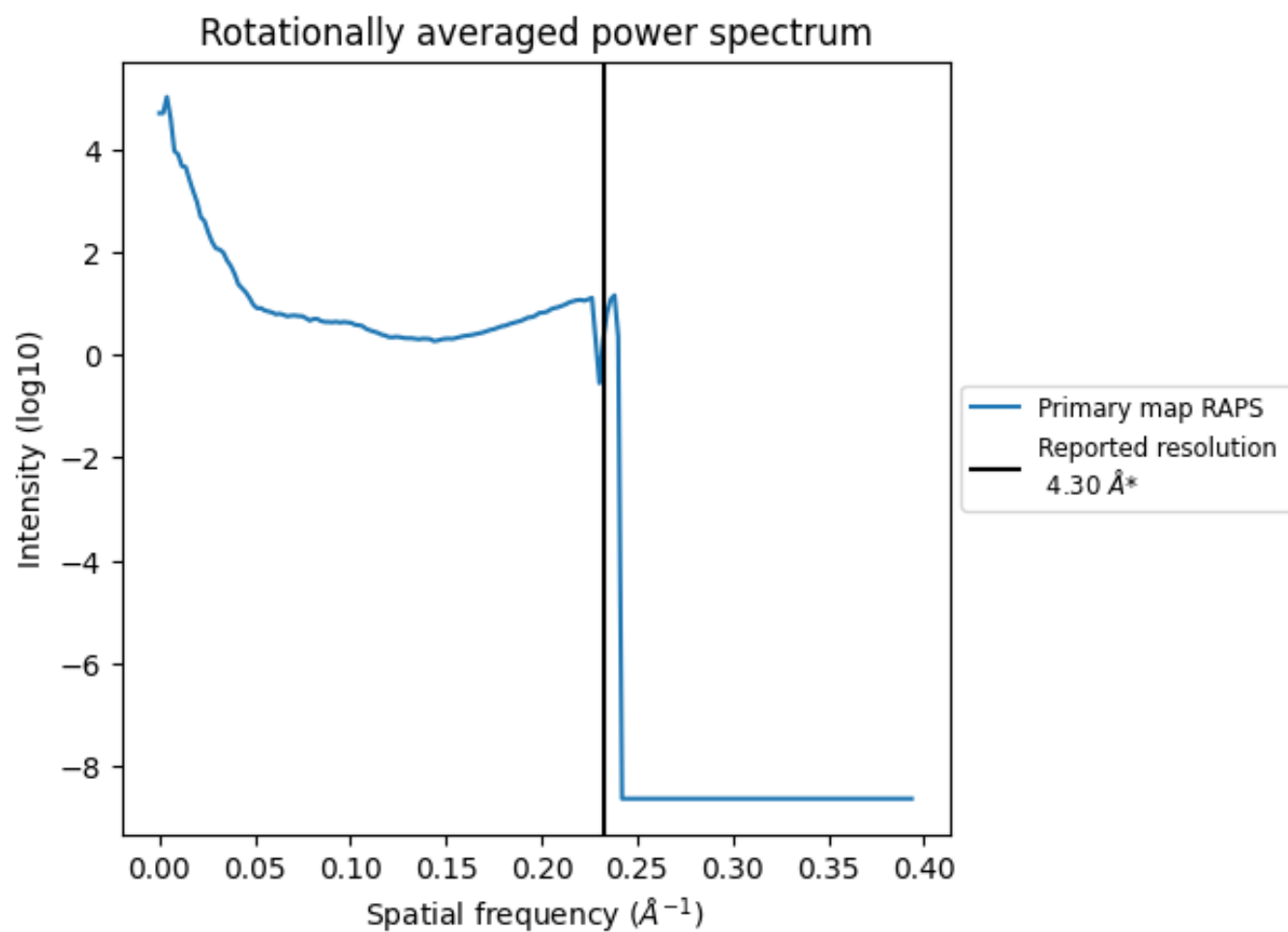
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1038 nm^3 ; this corresponds to an approximate mass of 938 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

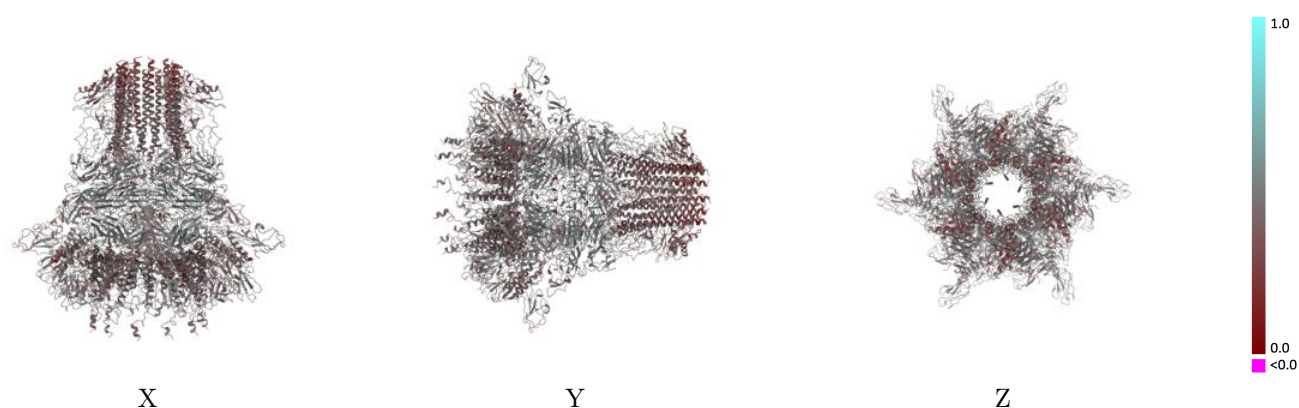
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31321 and PDB model 7EY7. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

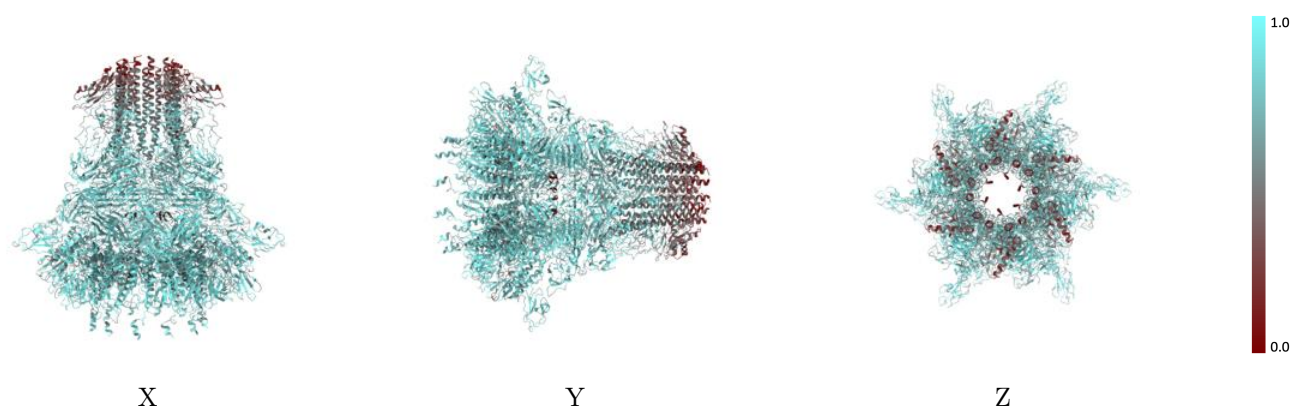
This section was not generated.

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



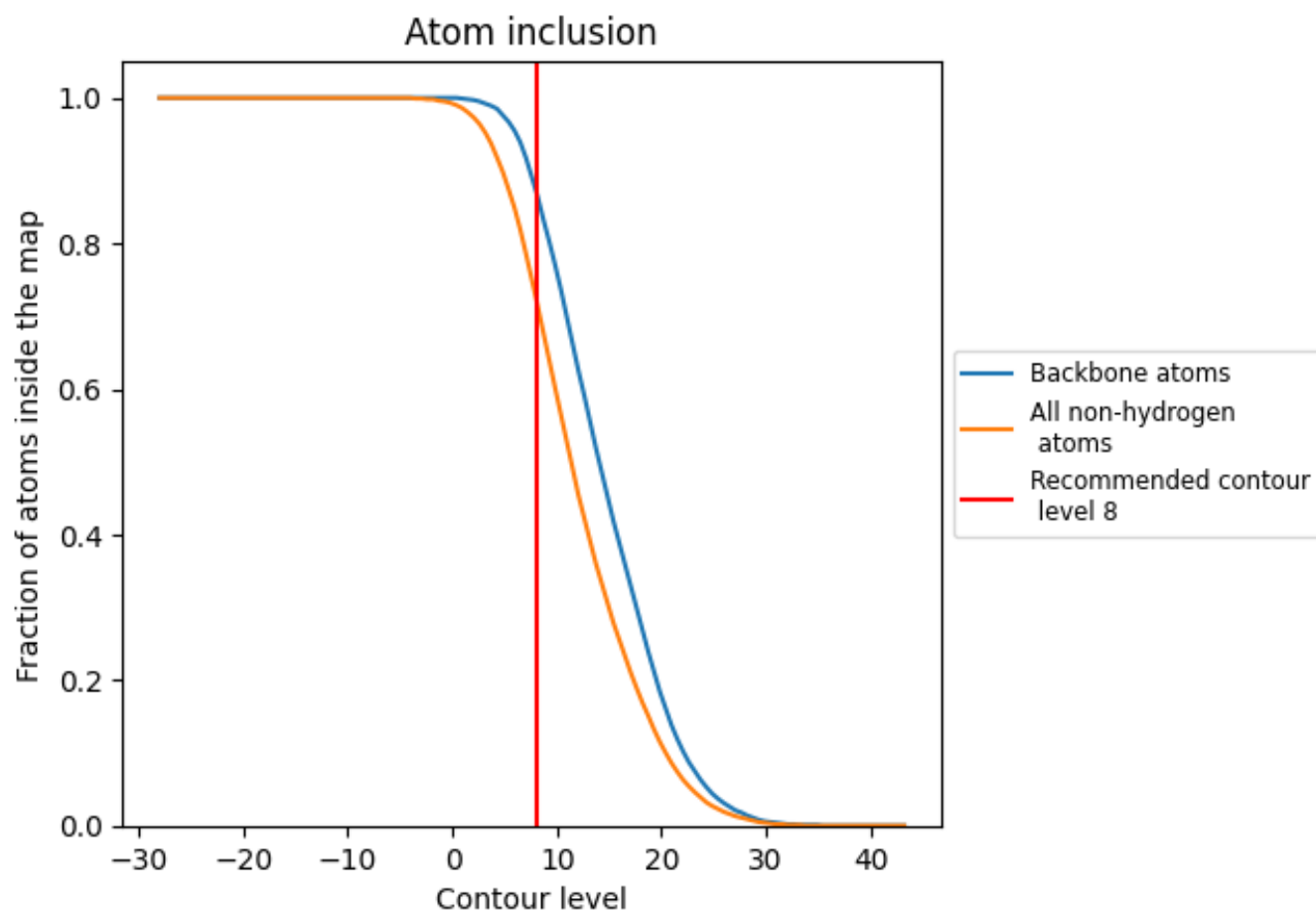
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 72% 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 (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.4200
A	 0.5180	 0.3430
B	 0.5150	 0.3450
C	 0.5190	 0.3450
D	 0.5400	 0.3540
E	 0.5160	 0.3450
F	 0.5200	 0.3530
M	 0.7660	 0.4190
N	 0.7750	 0.4130
O	 0.7650	 0.4190
P	 0.7740	 0.4120
Q	 0.7640	 0.4180
R	 0.7800	 0.4130
S	 0.7670	 0.4180
T	 0.7770	 0.4150
U	 0.7650	 0.4190
V	 0.7720	 0.4150
W	 0.7640	 0.4190
X	 0.7840	 0.4130
a	 0.7990	 0.4370
b	 0.6940	 0.4050
c	 0.7590	 0.4100
d	 0.7920	 0.4330
e	 0.6890	 0.4000
f	 0.7530	 0.4060
g	 0.7930	 0.4360
h	 0.6930	 0.4020
i	 0.7510	 0.4080
j	 0.7970	 0.4400
k	 0.6890	 0.4040
l	 0.7570	 0.4110
m	 0.7950	 0.4370
n	 0.6850	 0.4000
o	 0.7510	 0.4050
p	 0.7920	 0.4370



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Chain	Atom inclusion	Q-score
q	 0.6940	 0.4040
r	 0.7520	 0.4050
s	 0.7190	 0.4340
t	 0.7170	 0.4310
u	 0.7170	 0.4320
v	 0.7190	 0.4340
w	 0.7190	 0.4320
x	 0.7170	 0.4320