



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2025 – 02:09 am BST

PDB ID : 9GB5 / pdb_00009gb5
EMDB ID : EMD-51198
Title : Contracted phiCD508 neck
Authors : Wilson, J.S.; Fagan, R.P.; Bullough, P.A.
Deposited on : 2024-07-29
Resolution : 3.27 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

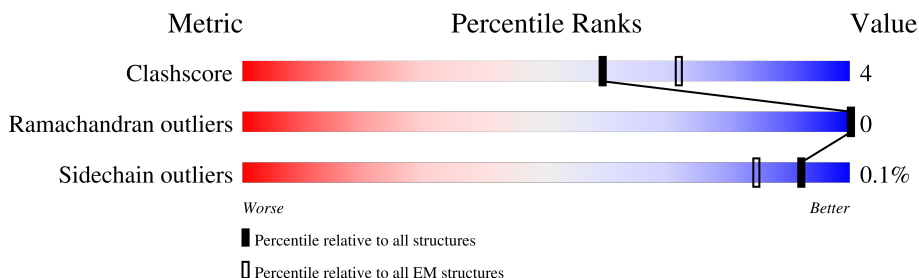
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.27 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.





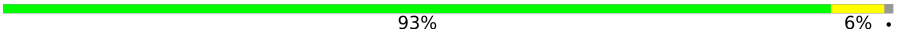






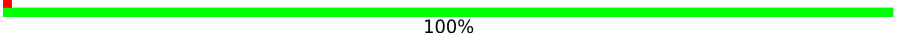

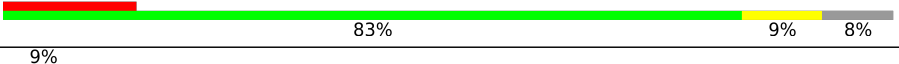
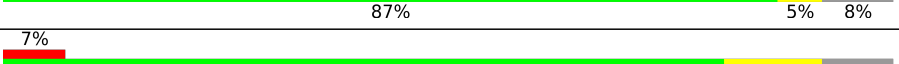
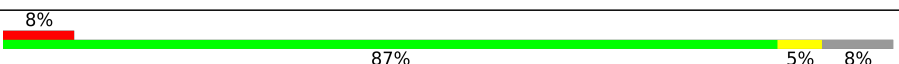
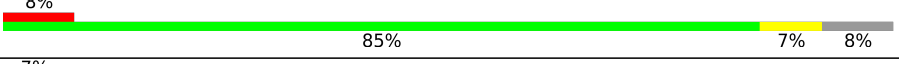
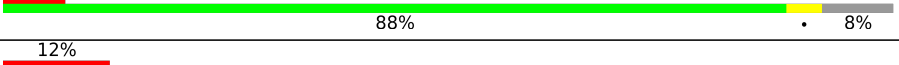

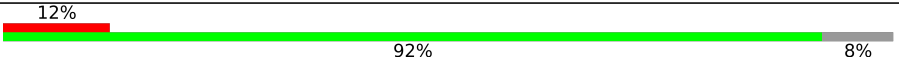
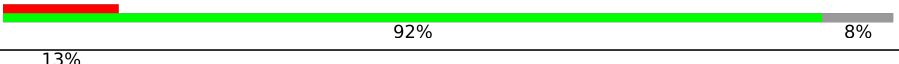
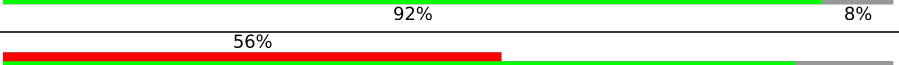





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	137	85% 9% 5%
1	B	137	81% 14% 5%
1	C	137	82% 13% 5%
1	D	137	80% 15% 5%
1	E	137	82% 12% 5%
1	F	137	86% 9% 5%
2	G	125	90% 10% .
2	K	125	86% 14% .

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Mol	Chain	Length	Quality of chain
2	M	125	
2	O	125	
2	Q	125	
2	X	125	
3	H	273	
3	L	273	
3	N	273	
3	P	273	
3	R	273	
3	d	273	
4	I	112	
4	J	112	
4	S	112	
4	T	112	
4	U	112	
4	V	112	
4	W	112	
4	Y	112	
4	Z	112	
4	a	112	
4	b	112	
4	c	112	
5	e	473	
5	f	473	
5	g	473	

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Mol	Chain	Length	Quality of chain
5	h	473	<div> <div>56%</div> <div>88%</div> <div>11%</div> </div>
5	i	473	<div> <div>55%</div> <div>88%</div> <div>11%</div> </div>
5	j	473	<div> <div>53%</div> <div>89%</div> <div>11%</div> </div>
6	k	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	l	500	<div> <div>25%</div> <div>89%</div> <div>11%</div> </div>
6	m	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	n	500	<div> <div>25%</div> <div>89%</div> <div>11%</div> </div>
6	o	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	p	500	<div> <div>25%</div> <div>89%</div> <div>11%</div> </div>
6	q	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	r	500	<div> <div>24%</div> <div>89%</div> <div>11%</div> </div>
6	s	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	t	500	<div> <div>25%</div> <div>89%</div> <div>11%</div> </div>
6	u	500	<div> <div>26%</div> <div>89%</div> <div>11%</div> </div>
6	v	500	<div> <div>25%</div> <div>89%</div> <div>11%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 193668 atoms, of which 96480 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 gp56 - Tail tube protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		
1	B	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		
1	C	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		
1	D	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		
1	E	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		
1	F	130	Total	C	H	N	O	S	0	0
			2060	652	1031	167	207	3		

- Molecule 2 is a protein called gp51 - Neck valve protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	G	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		
2	K	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		
2	M	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		
2	O	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		
2	Q	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		
2	X	124	Total	C	H	N	O	S	0	0
			2019	623	1021	172	197	6		

- Molecule 3 is a protein called gp53 - Tail adaptor protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	H	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	L	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		
3	N	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		
3	P	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		
3	R	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		
3	d	272	Total	C	H	N	O	S	0	0
			4462	1397	2247	380	426	12		

- Molecule 4 is a protein called gp50 - Portal adaptor protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	I	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	J	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	S	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	T	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	U	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	V	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	W	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	Y	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	Z	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	a	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	b	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		
4	c	103	Total	C	H	N	O	S	0	0
			1649	528	816	129	170	6		

- Molecule 5 is a protein called gp55 - Tail sheath protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	e	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		
5	f	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		
5	g	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		
5	h	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		
5	i	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		
5	j	420	Total	C	H	N	O	S	0	0
			6585	2089	3289	529	668	10		

- Molecule 6 is a protein called gp45 - Portal protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	k	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	l	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	m	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	n	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	o	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	p	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	q	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	r	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	s	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	t	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	u	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		
6	v	445	Total	C	H	N	O	S	0	0
			6927	2235	3430	579	668	15		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	51	ASN	LYS	conflict	UNP A0A069A478
k	419	CYS	SER	conflict	UNP A0A069A478
k	454	GLY	PRO	conflict	UNP A0A069A478
k	456	ARG	ILE	conflict	UNP A0A069A478
k	457	GLU	VAL	conflict	UNP A0A069A478
l	51	ASN	LYS	conflict	UNP A0A069A478
l	419	CYS	SER	conflict	UNP A0A069A478
l	454	GLY	PRO	conflict	UNP A0A069A478
l	456	ARG	ILE	conflict	UNP A0A069A478
l	457	GLU	VAL	conflict	UNP A0A069A478
m	51	ASN	LYS	conflict	UNP A0A069A478
m	419	CYS	SER	conflict	UNP A0A069A478
m	454	GLY	PRO	conflict	UNP A0A069A478
m	456	ARG	ILE	conflict	UNP A0A069A478
m	457	GLU	VAL	conflict	UNP A0A069A478
n	51	ASN	LYS	conflict	UNP A0A069A478
n	419	CYS	SER	conflict	UNP A0A069A478
n	454	GLY	PRO	conflict	UNP A0A069A478
n	456	ARG	ILE	conflict	UNP A0A069A478
n	457	GLU	VAL	conflict	UNP A0A069A478
o	51	ASN	LYS	conflict	UNP A0A069A478
o	419	CYS	SER	conflict	UNP A0A069A478
o	454	GLY	PRO	conflict	UNP A0A069A478
o	456	ARG	ILE	conflict	UNP A0A069A478
o	457	GLU	VAL	conflict	UNP A0A069A478
p	51	ASN	LYS	conflict	UNP A0A069A478
p	419	CYS	SER	conflict	UNP A0A069A478
p	454	GLY	PRO	conflict	UNP A0A069A478
p	456	ARG	ILE	conflict	UNP A0A069A478
p	457	GLU	VAL	conflict	UNP A0A069A478
q	51	ASN	LYS	conflict	UNP A0A069A478
q	419	CYS	SER	conflict	UNP A0A069A478
q	454	GLY	PRO	conflict	UNP A0A069A478
q	456	ARG	ILE	conflict	UNP A0A069A478
q	457	GLU	VAL	conflict	UNP A0A069A478
r	51	ASN	LYS	conflict	UNP A0A069A478
r	419	CYS	SER	conflict	UNP A0A069A478
r	454	GLY	PRO	conflict	UNP A0A069A478
r	456	ARG	ILE	conflict	UNP A0A069A478
r	457	GLU	VAL	conflict	UNP A0A069A478
s	51	ASN	LYS	conflict	UNP A0A069A478
s	419	CYS	SER	conflict	UNP A0A069A478
s	454	GLY	PRO	conflict	UNP A0A069A478

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Chain	Residue	Modelled	Actual	Comment	Reference
s	456	ARG	ILE	conflict	UNP A0A069A478
s	457	GLU	VAL	conflict	UNP A0A069A478
t	51	ASN	LYS	conflict	UNP A0A069A478
t	419	CYS	SER	conflict	UNP A0A069A478
t	454	GLY	PRO	conflict	UNP A0A069A478
t	456	ARG	ILE	conflict	UNP A0A069A478
t	457	GLU	VAL	conflict	UNP A0A069A478
u	51	ASN	LYS	conflict	UNP A0A069A478
u	419	CYS	SER	conflict	UNP A0A069A478
u	454	GLY	PRO	conflict	UNP A0A069A478
u	456	ARG	ILE	conflict	UNP A0A069A478
u	457	GLU	VAL	conflict	UNP A0A069A478
v	51	ASN	LYS	conflict	UNP A0A069A478
v	419	CYS	SER	conflict	UNP A0A069A478
v	454	GLY	PRO	conflict	UNP A0A069A478
v	456	ARG	ILE	conflict	UNP A0A069A478
v	457	GLU	VAL	conflict	UNP A0A069A478

3 Residue-property plots [i](#)


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: gp56 - Tail tube protein

Chain A: 




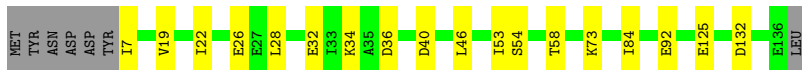
- Molecule 1: gp56 - Tail tube protein

Chain B: 




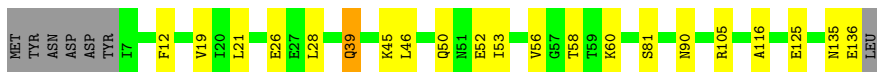
- Molecule 1: gp56 - Tail tube protein

Chain C: 




- Molecule 1: gp56 - Tail tube protein

Chain D: 




- Molecule 1: gp56 - Tail tube protein

Chain E: 




- Molecule 1: gp56 - Tail tube protein

Chain F:  86% 9% 5%




- Molecule 2: gp51 - Neck valve protein

Chain G:  90% 10% .




- Molecule 2: gp51 - Neck valve protein

Chain K:  86% 14% .




- Molecule 2: gp51 - Neck valve protein

Chain M:  83% 16% .



- Molecule 2: gp51 - Neck valve protein

Chain O:  90% 10% .




- Molecule 2: gp51 - Neck valve protein

Chain Q:  93% 6% .




- Molecule 2: gp51 - Neck valve protein

Chain X:  85% 14% .




- Molecule 3: gp53 - Tail adaptor protein

Chain H:  89% 11%



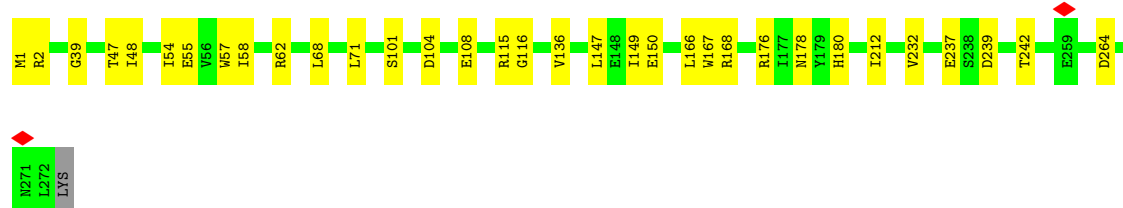
• Molecule 3: gp53 - Tail adaptor protein

Chain L:  88% 11%




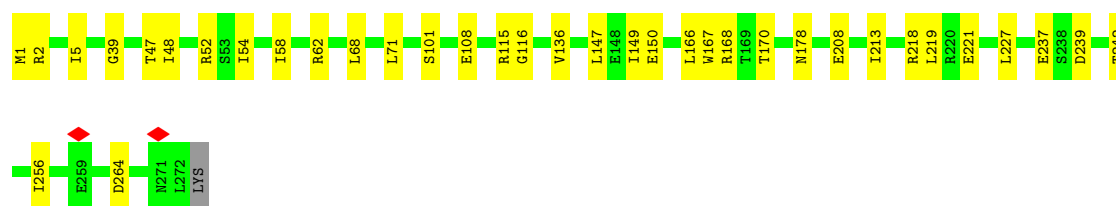
• Molecule 3: gp53 - Tail adaptor protein

Chain N:  88% 12%




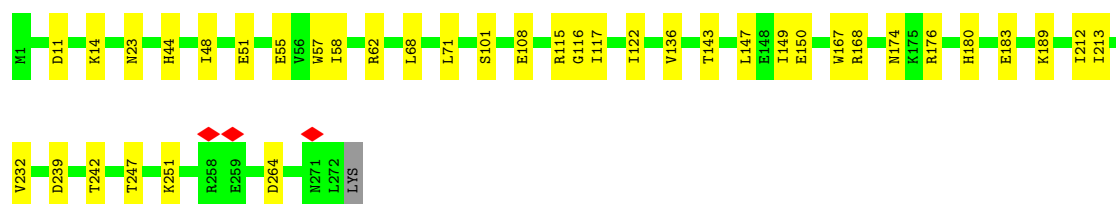
• Molecule 3: gp53 - Tail adaptor protein

Chain P:  86% 13%



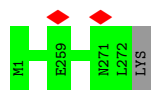
• Molecule 3: gp53 - Tail adaptor protein

Chain R:  86% 14%




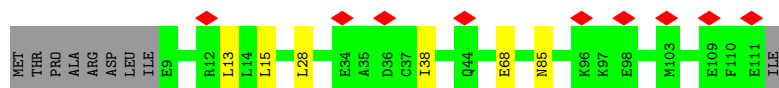
• Molecule 3: gp53 - Tail adaptor protein

Chain d:  100%




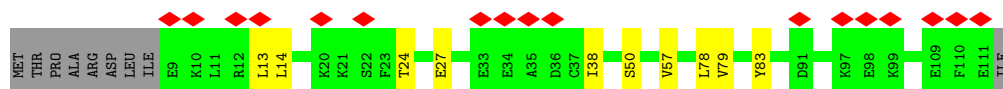
- Molecule 4: gp50 - Portal adaptor protein

Chain I:  8% 87% 5% 8%




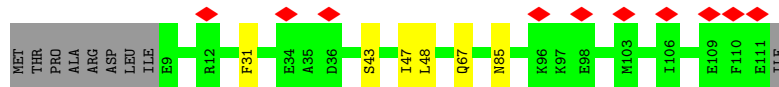
- Molecule 4: gp50 - Portal adaptor protein

Chain J:  15% 83% 9% 8%




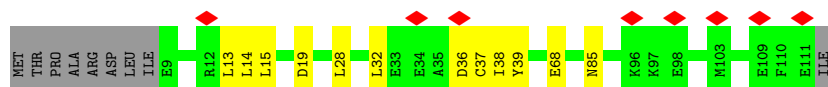
- Molecule 4: gp50 - Portal adaptor protein

Chain S:  9% 87% 5% 8%




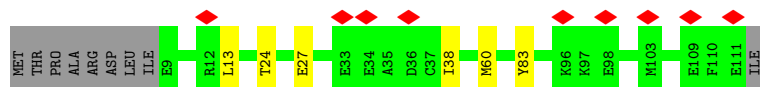
- Molecule 4: gp50 - Portal adaptor protein

Chain T:  7% 81% 11% 8%




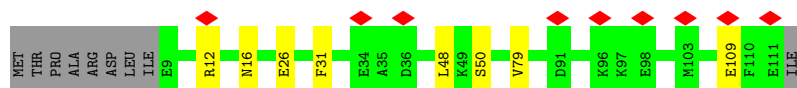
- Molecule 4: gp50 - Portal adaptor protein

Chain U:  8% 87% 5% 8%

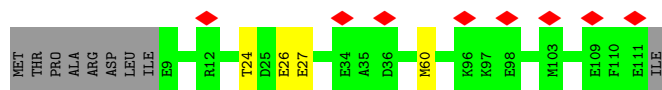
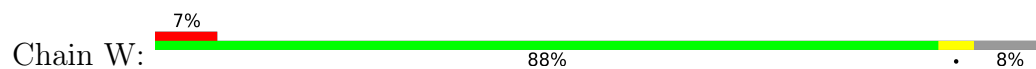


- Molecule 4: gp50 - Portal adaptor protein

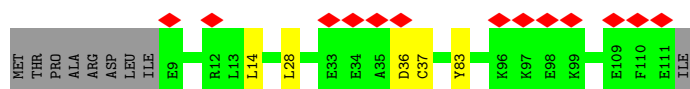
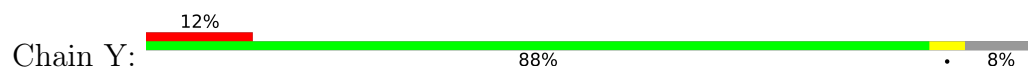
Chain V:  8% 85% 7% 8%



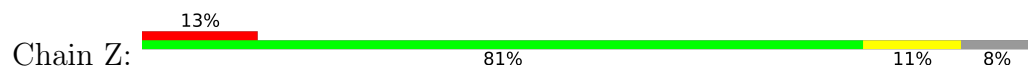
- Molecule 4: gp50 - Portal adaptor protein



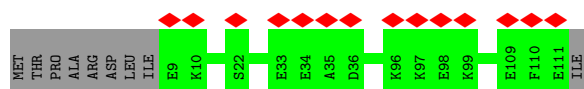
- Molecule 4: gp50 - Portal adaptor protein



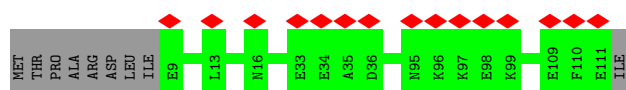
- Molecule 4: gp50 - Portal adaptor protein



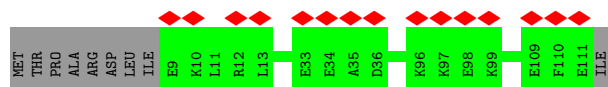
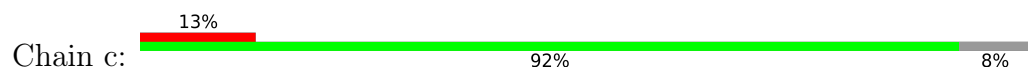
- Molecule 4: gp50 - Portal adaptor protein



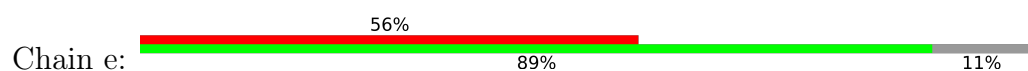
- Molecule 4: gp50 - Portal adaptor protein

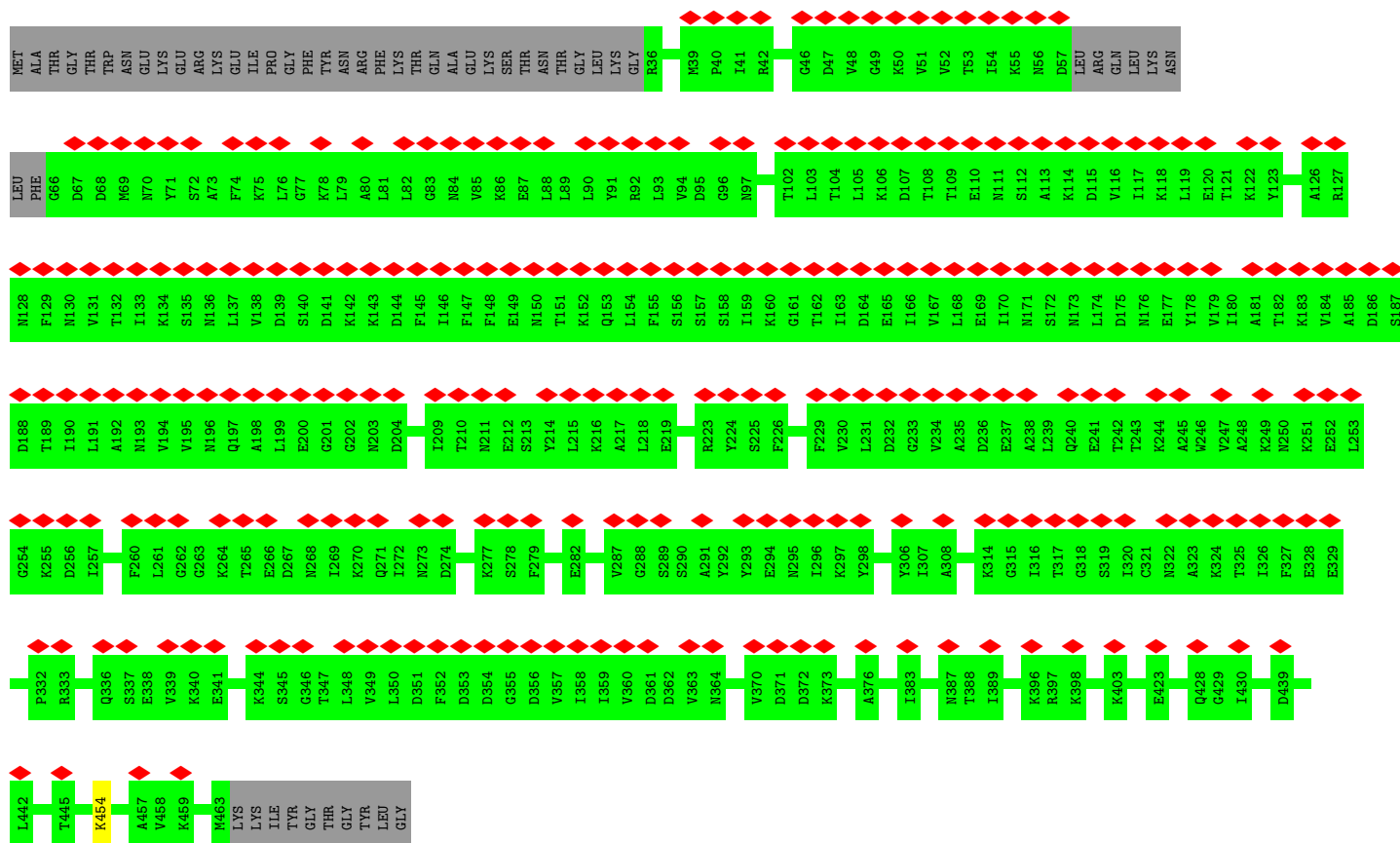


- Molecule 4: gp50 - Portal adaptor protein

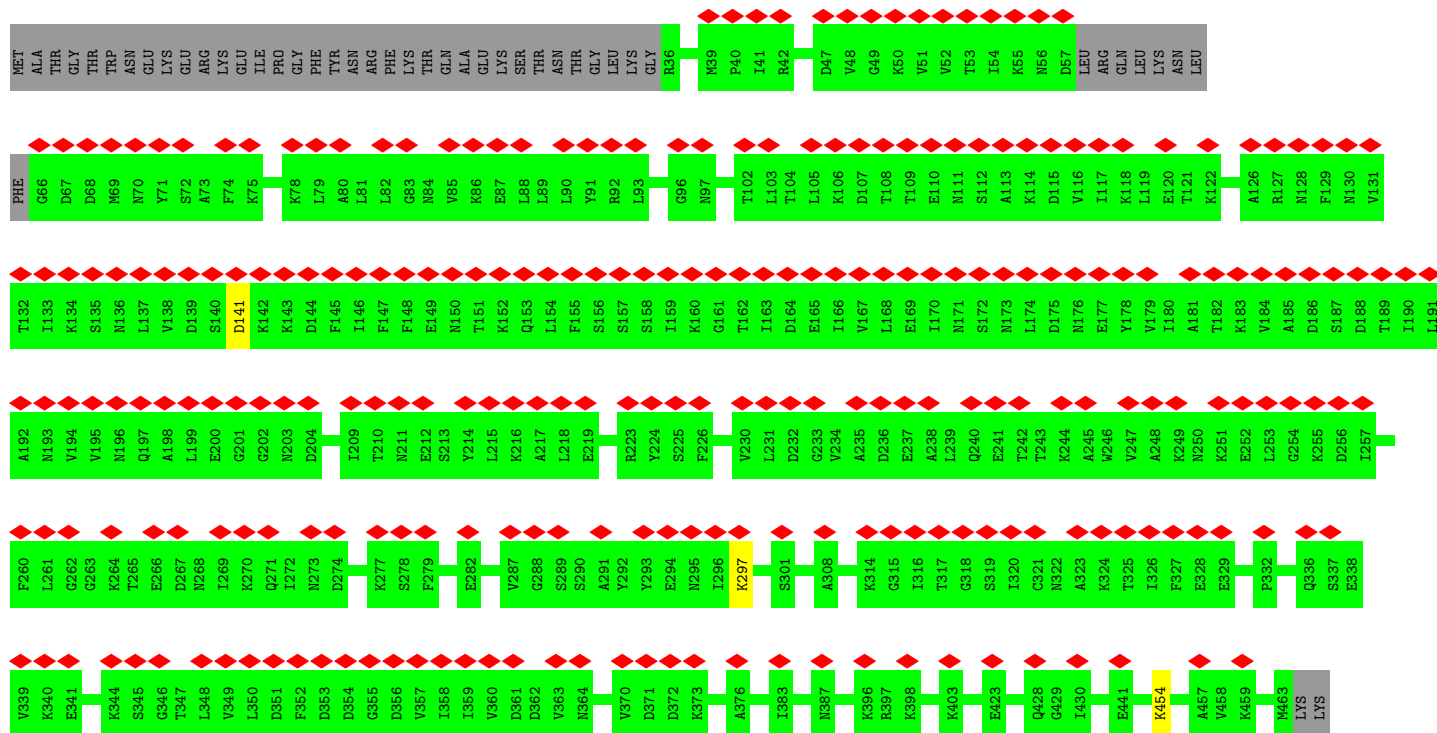
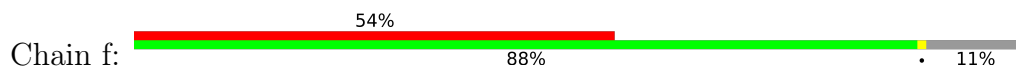


- Molecule 5: gp55 - Tail sheath protein






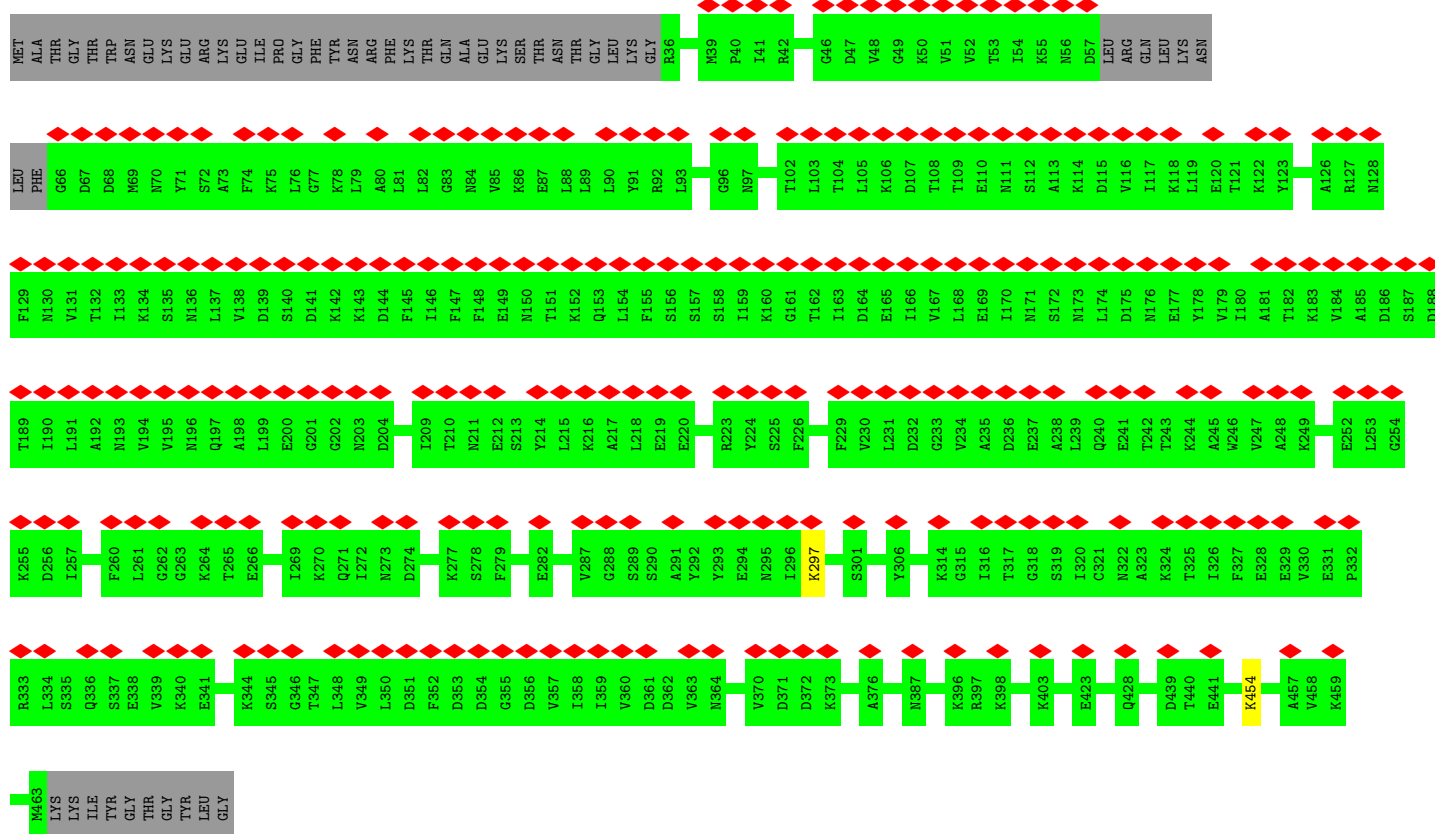
• Molecule 5: gp55 - Tail sheath protein




ILE
TYR
GLY
THR
GLY
TYR
LEU
GLY

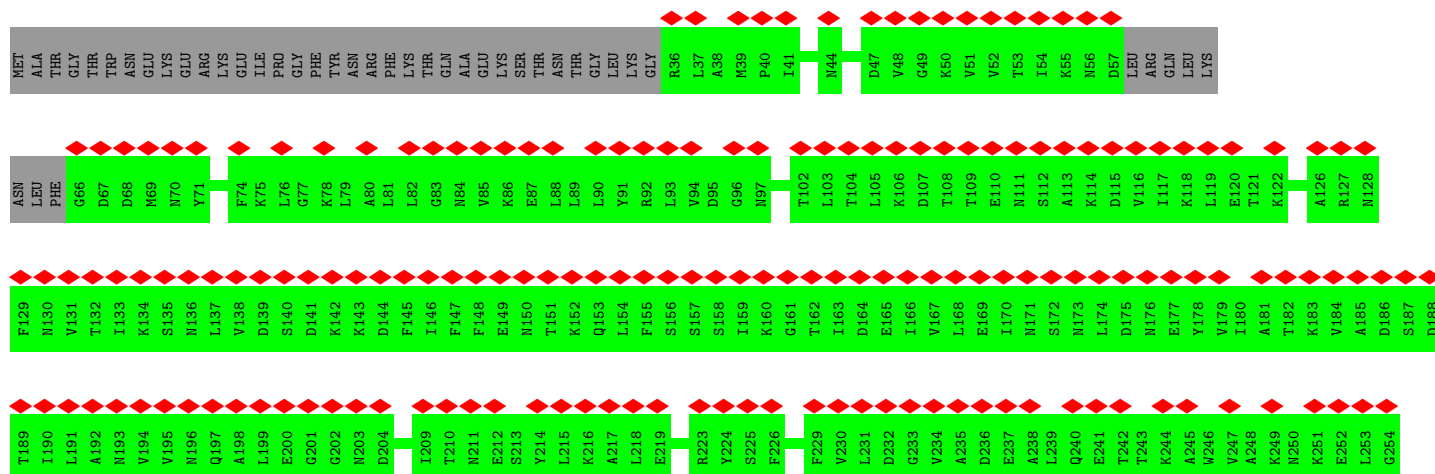
• Molecule 5: gp55 - Tail sheath protein

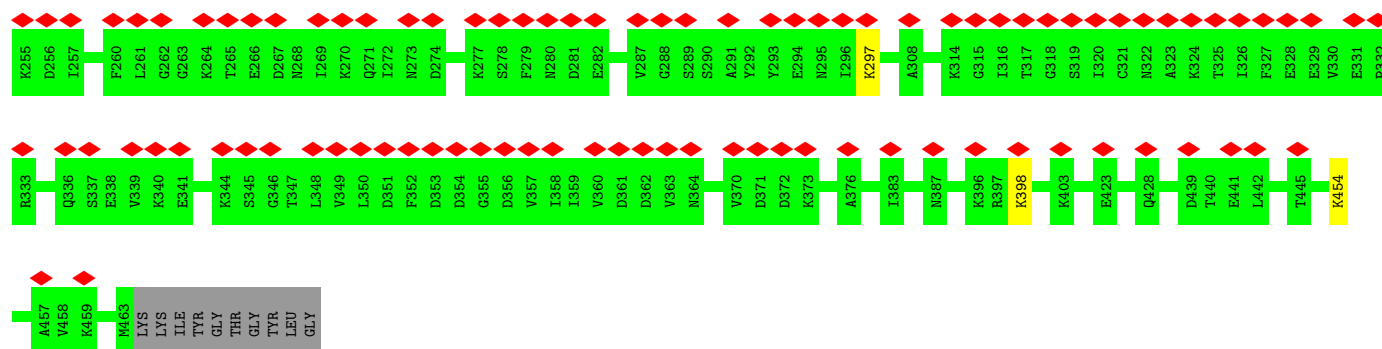
Chain g:  55% 88% 11%



• Molecule 5: gp55 - Tail sheath protein

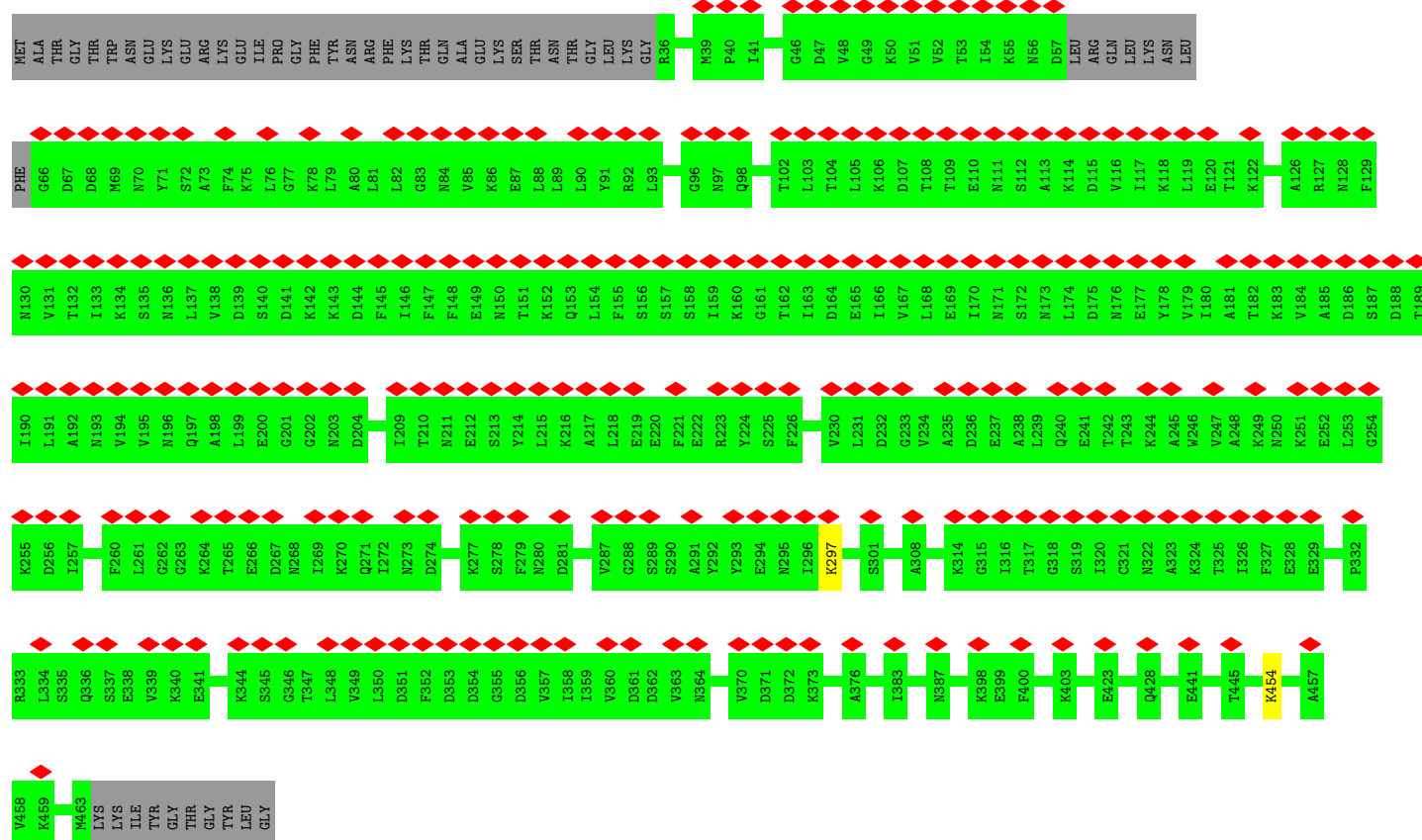
Chain h:  56% 88% 11%





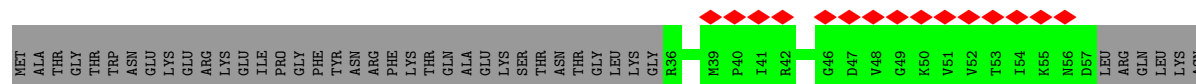
• Molecule 5: gp55 - Tail sheath protein

Chain i: 55% 88% 11%



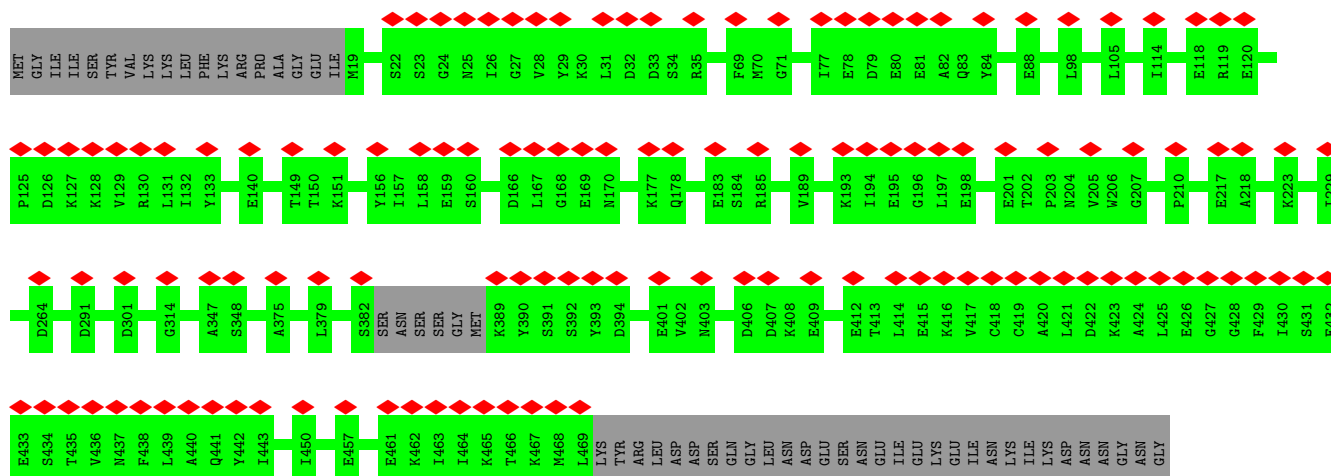
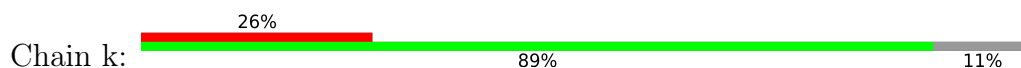
• Molecule 5: gp55 - Tail sheath protein

Chain j: 53% 89% 11%

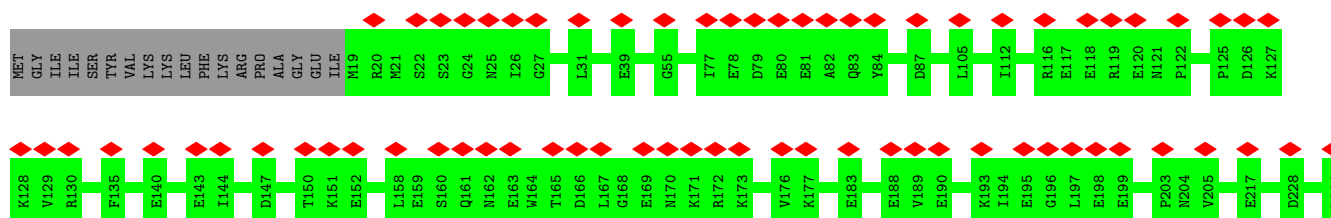
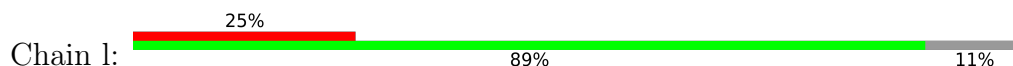


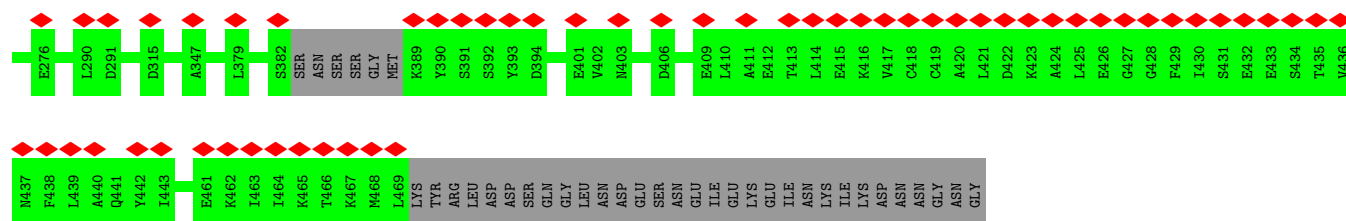


• Molecule 6: gp45 - Portal protein

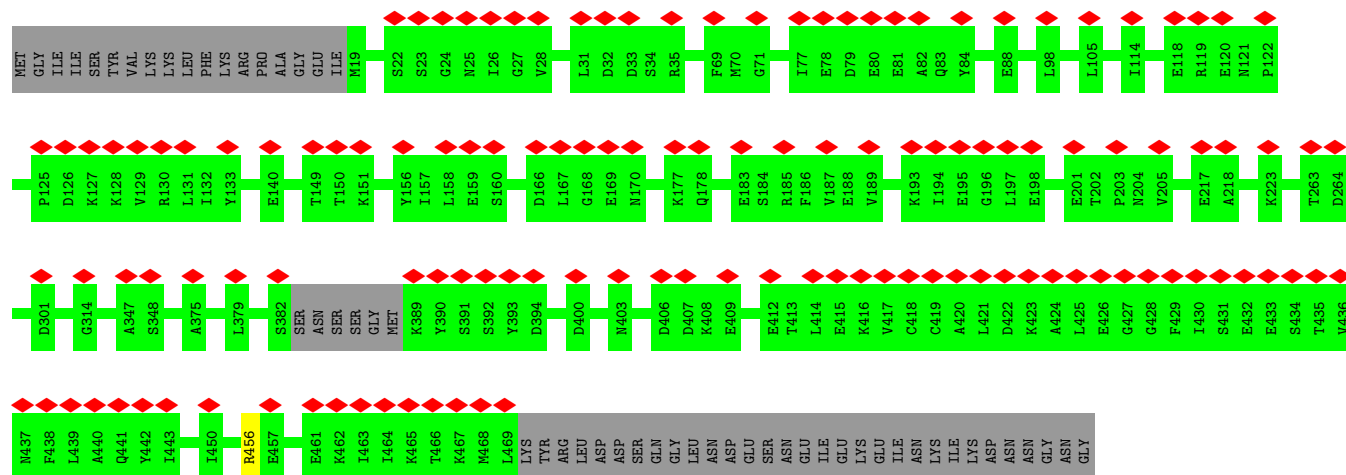
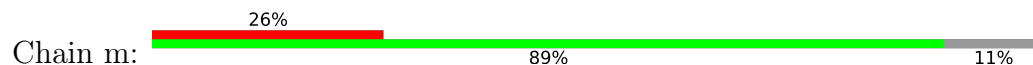


• Molecule 6: gp45 - Portal protein

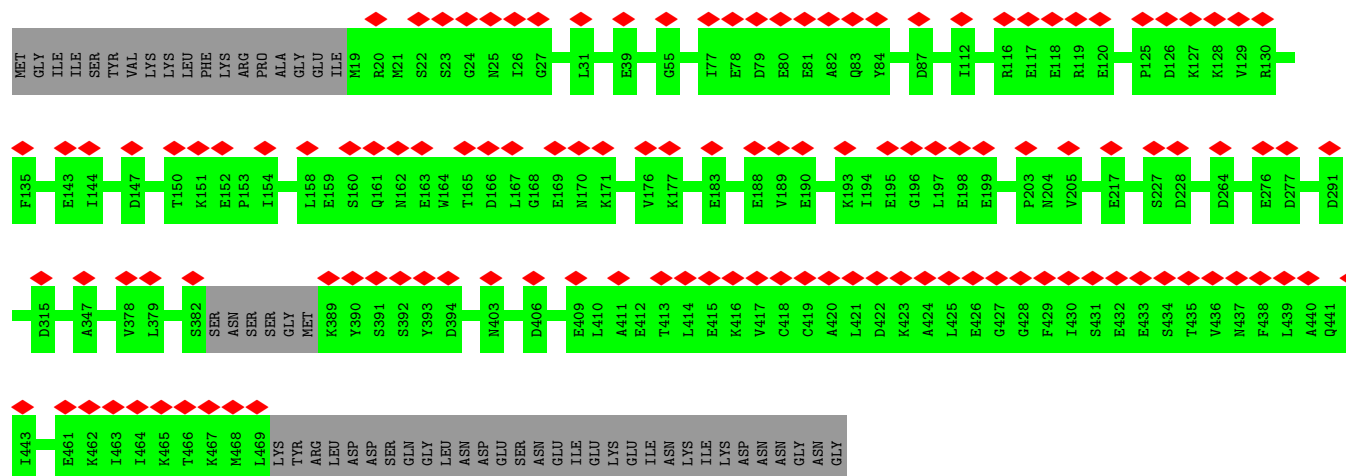
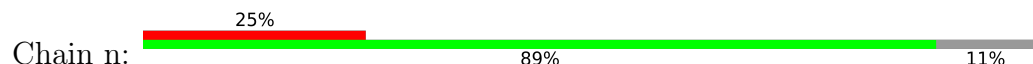




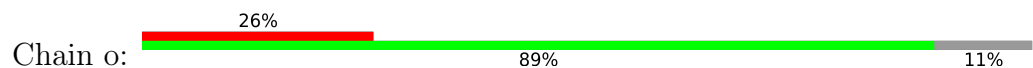
• Molecule 6: gp45 - Portal protein

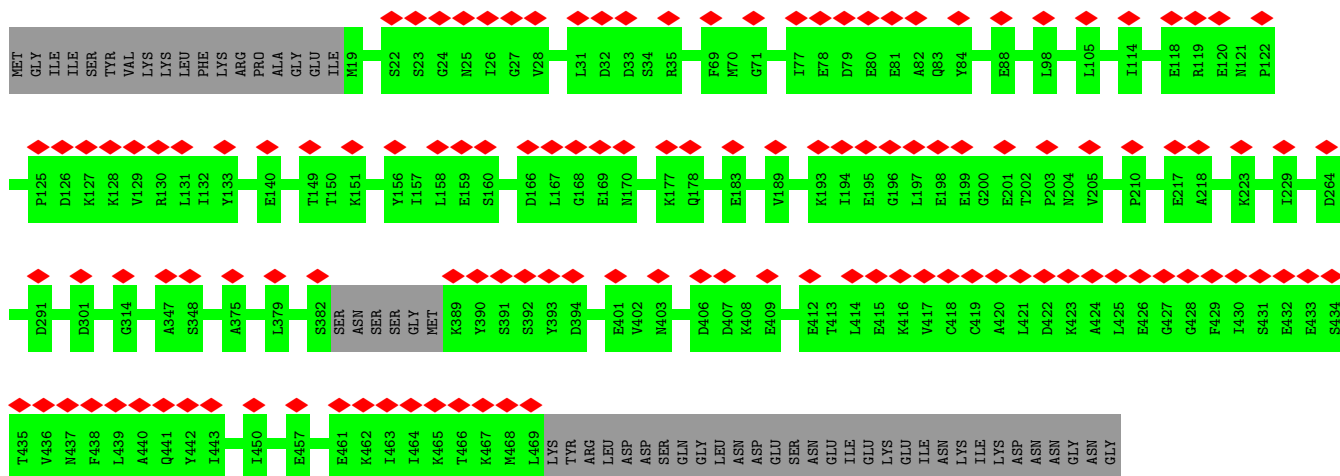


• Molecule 6: gp45 - Portal protein

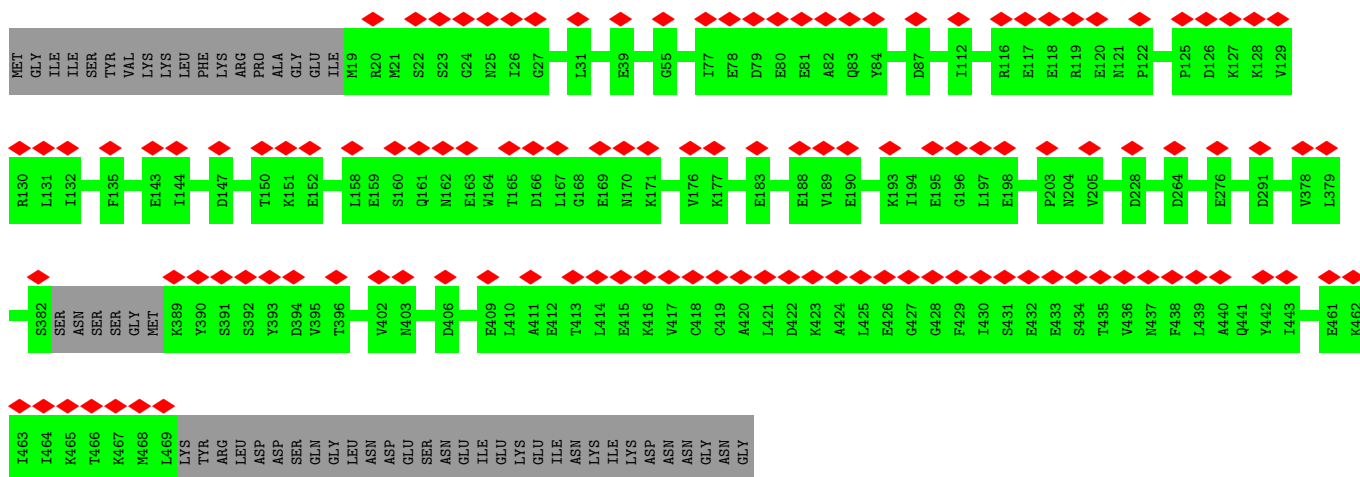
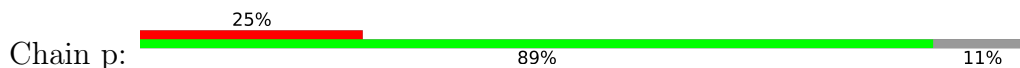


• Molecule 6: gp45 - Portal protein

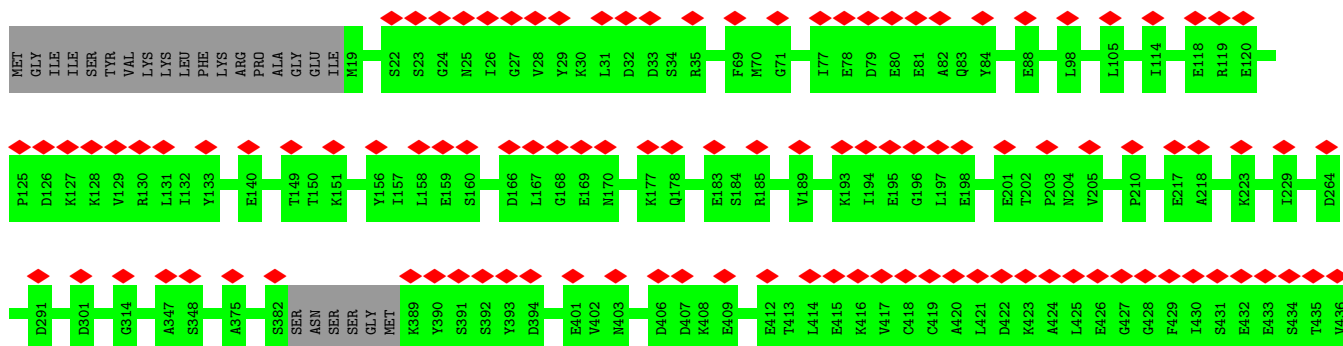
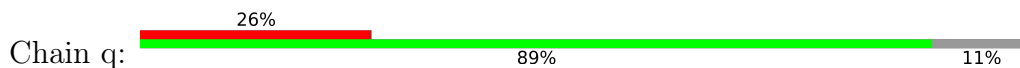


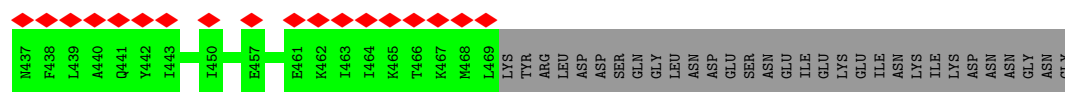


- Molecule 6: gp45 - Portal protein

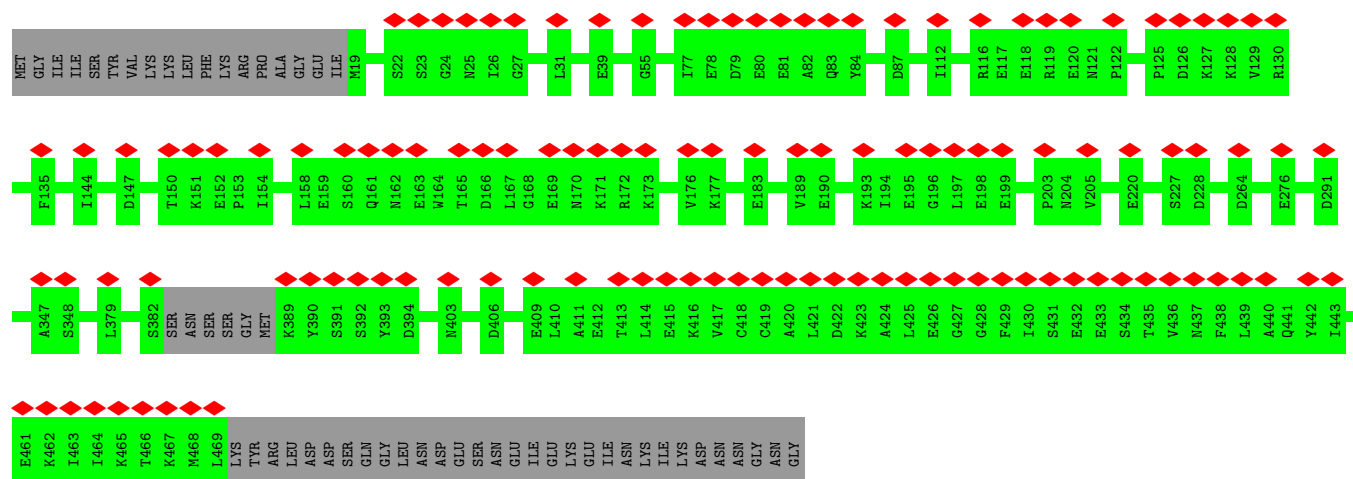
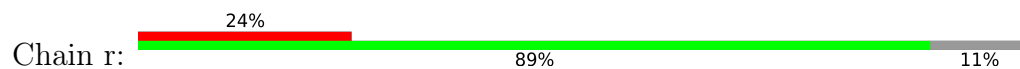


- Molecule 6: gp45 - Portal protein

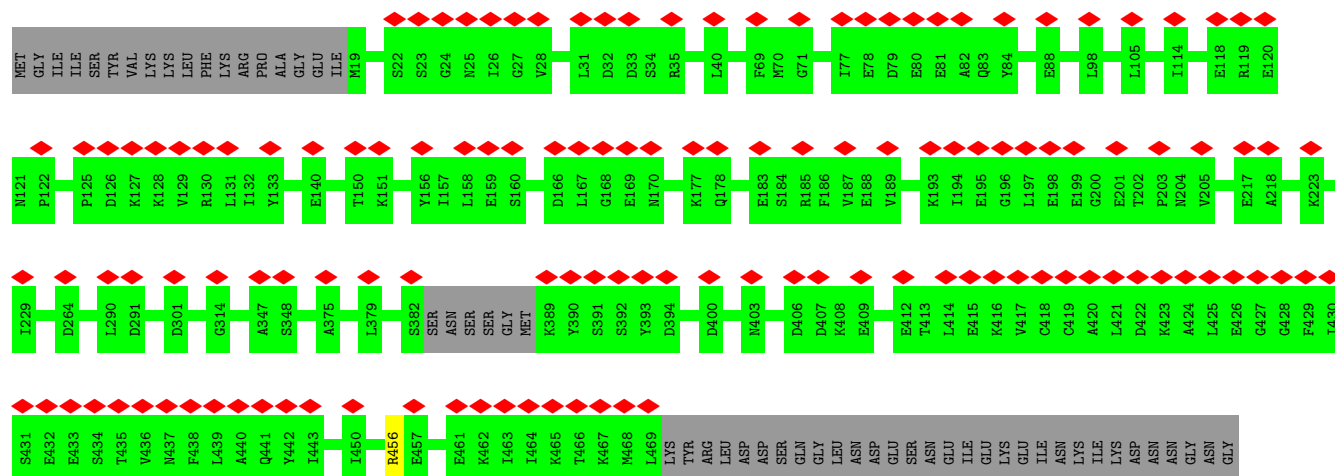
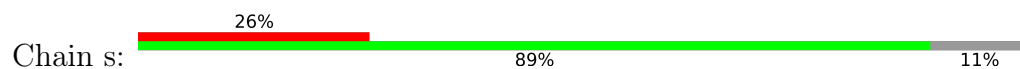




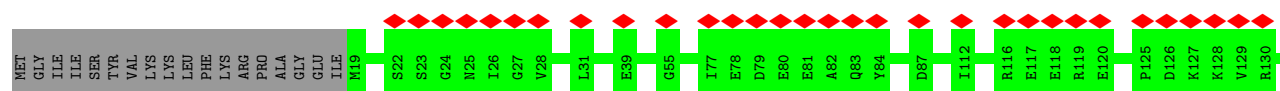
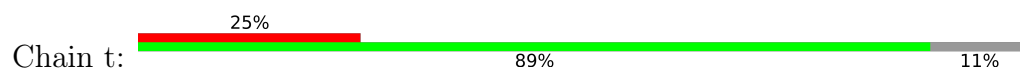
• Molecule 6: gp45 - Portal protein

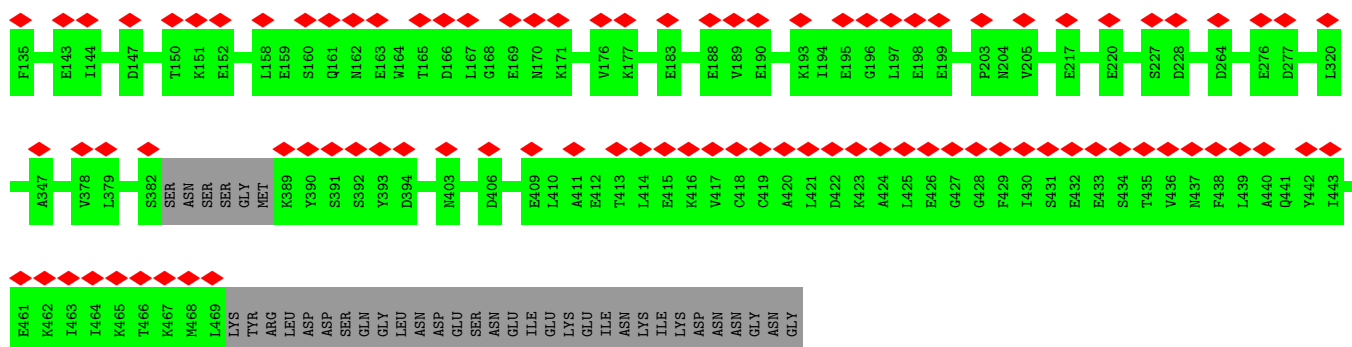


• Molecule 6: gp45 - Portal protein

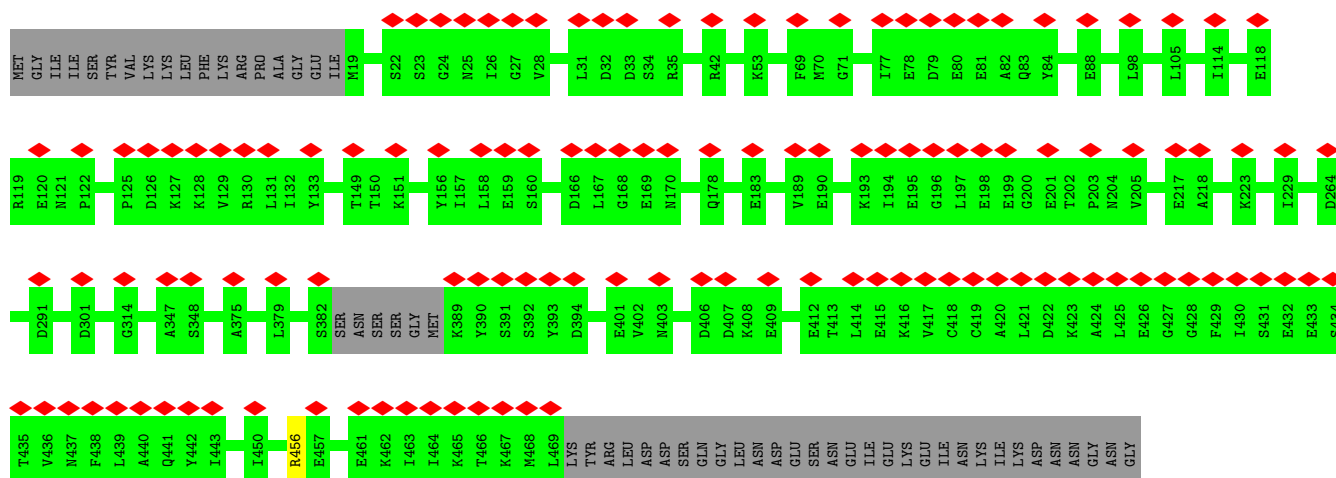
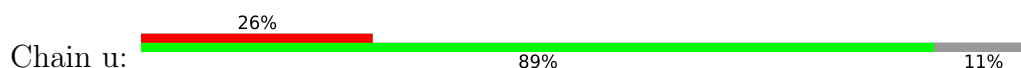


• Molecule 6: gp45 - Portal protein

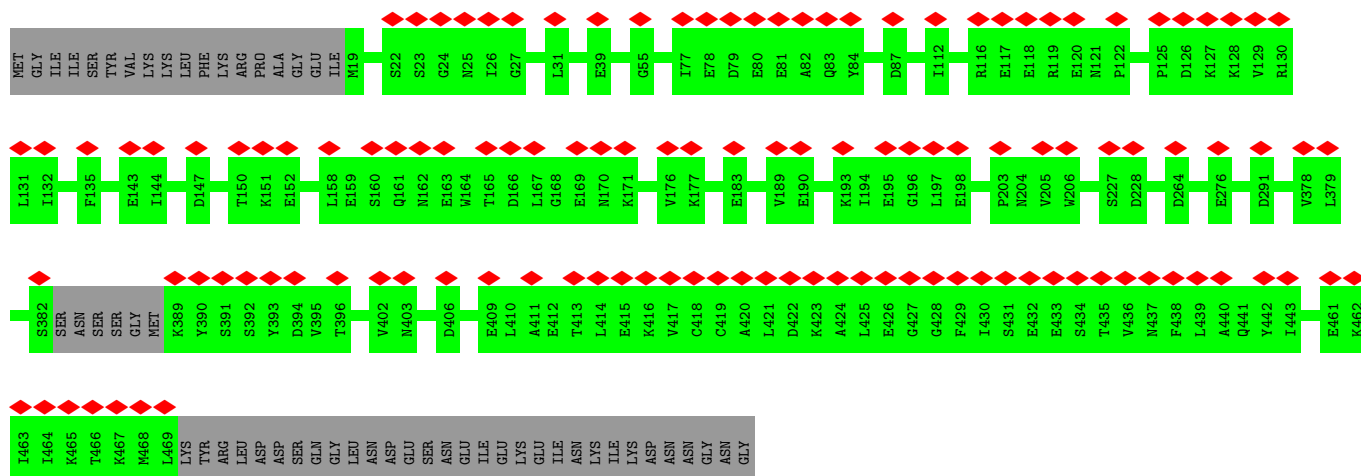
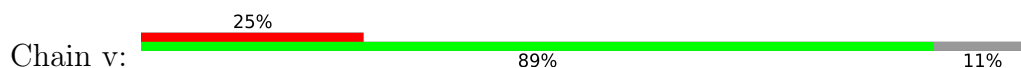




• Molecule 6: gp45 - Portal protein



• Molecule 6: gp45 - Portal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30325	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.428	Depositor
Minimum map value	-0.719	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.249	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.32	0/1041	0.58	0/1394
1	B	0.32	0/1041	0.57	0/1394
1	C	0.32	0/1041	0.57	0/1394
1	D	0.32	0/1041	0.57	0/1394
1	E	0.32	0/1041	0.58	0/1394
1	F	0.32	0/1041	0.58	0/1394
2	G	0.33	0/1007	0.60	0/1353
2	K	0.34	0/1007	0.61	0/1353
2	M	0.34	0/1007	0.60	0/1353
2	O	0.34	0/1007	0.61	0/1353
2	Q	0.34	0/1007	0.62	0/1353
2	X	0.34	0/1007	0.61	0/1353
3	H	0.34	0/2249	0.57	0/3030
3	L	0.34	0/2249	0.57	0/3030
3	N	0.33	0/2249	0.57	0/3030
3	P	0.34	0/2249	0.57	0/3030
3	R	0.34	0/2249	0.57	0/3030
3	d	0.33	0/2249	0.57	0/3030
4	I	0.34	0/845	0.49	0/1130
4	J	0.34	0/845	0.52	0/1130
4	S	0.34	0/845	0.51	0/1130
4	T	0.34	0/845	0.50	0/1130
4	U	0.34	0/845	0.49	0/1130
4	V	0.34	0/845	0.49	0/1130
4	W	0.34	0/845	0.50	0/1130
4	Y	0.34	0/845	0.51	0/1130
4	Z	0.35	0/845	0.52	0/1130
4	a	0.34	0/845	0.54	0/1130
4	b	0.34	0/845	0.54	0/1130
4	c	0.34	0/845	0.53	0/1130
5	e	0.26	0/3340	0.49	0/4508
5	f	0.28	0/3340	0.52	1/4508 (0.0%)
5	g	0.26	0/3340	0.49	0/4508
5	h	0.27	0/3340	0.49	0/4508

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	i	0.27	0/3340	0.49	0/4508
5	j	0.26	0/3340	0.49	0/4508
6	k	0.27	0/3566	0.50	0/4820
6	l	0.27	0/3566	0.50	0/4820
6	m	0.27	0/3566	0.50	0/4820
6	n	0.27	0/3566	0.51	0/4820
6	o	0.27	0/3566	0.50	0/4820
6	p	0.27	0/3566	0.51	0/4820
6	q	0.27	0/3566	0.50	0/4820
6	r	0.26	0/3566	0.51	0/4820
6	s	0.27	0/3566	0.49	0/4820
6	t	0.27	0/3566	0.51	0/4820
6	u	0.27	0/3566	0.50	0/4820
6	v	0.27	0/3566	0.50	0/4820
All	All	0.29	0/98754	0.52	1/133110 (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
4	T	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	f	141	ASP	CB-CG-OD1	8.18	125.66	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	T	19	ASP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1029	1031	1030	10	0
1	B	1029	1031	1030	15	0
1	C	1029	1031	1030	16	0
1	D	1029	1031	1030	18	0
1	E	1029	1031	1030	14	0
1	F	1029	1031	1030	11	0
2	G	998	1021	1020	7	0
2	K	998	1021	1020	11	0
2	M	998	1021	1020	13	0
2	O	998	1021	1020	9	0
2	Q	998	1021	1020	6	0
2	X	998	1021	1020	11	0
3	H	2215	2247	2244	23	0
3	L	2215	2247	2244	25	0
3	N	2215	2247	2244	25	0
3	P	2215	2247	2244	30	0
3	R	2215	2247	2244	29	0
3	d	2215	2247	2244	0	0
4	I	833	816	815	6	0
4	J	833	816	815	6	0
4	S	833	816	815	4	0
4	T	833	816	815	7	0
4	U	833	816	815	4	0
4	V	833	816	815	6	0
4	W	833	816	815	3	0
4	Y	833	816	815	3	0
4	Z	833	816	815	9	0
4	a	833	816	815	0	0
4	b	833	816	815	0	0
4	c	833	816	815	0	0
5	e	3296	3289	3287	0	0
5	f	3296	3289	3287	0	0
5	g	3296	3289	3287	0	0
5	h	3296	3289	3287	0	0
5	i	3296	3289	3287	0	0
5	j	3296	3289	3287	0	0
6	k	3497	3430	3424	0	0
6	l	3497	3430	3424	0	0
6	m	3497	3430	3424	0	0
6	n	3497	3430	3424	0	0
6	o	3497	3430	3424	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	p	3497	3430	3424	0	0
6	q	3497	3430	3424	0	0
6	r	3497	3430	3424	0	0
6	s	3497	3430	3424	0	0
6	t	3497	3430	3424	0	0
6	u	3497	3430	3424	0	0
6	v	3497	3430	3424	0	0
All	All	97188	96480	96354	265	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 4.

The worst 5 of 265 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)
4:U:13:LEU:HD22	4:U:38:ILE:HD13	1.59	0.82
4:T:13:LEU:HD22	4:T:38:ILE:HD13	1.62	0.81
1:A:46:LEU:HD23	1:A:53:ILE:HD13	1.68	0.73
4:T:85:ASN:OD1	4:Z:83:TYR:OH	2.06	0.72
4:U:24:THR:OG1	4:U:27:GLU:OE1	2.08	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	128/137 (93%)	124 (97%)	4 (3%)	0	100	100
1	B	128/137 (93%)	123 (96%)	5 (4%)	0	100	100
1	C	128/137 (93%)	124 (97%)	4 (3%)	0	100	100
1	D	128/137 (93%)	124 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	128/137 (93%)	122 (95%)	6 (5%)	0	100	100
1	F	128/137 (93%)	126 (98%)	2 (2%)	0	100	100
2	G	122/125 (98%)	118 (97%)	4 (3%)	0	100	100
2	K	122/125 (98%)	117 (96%)	5 (4%)	0	100	100
2	M	122/125 (98%)	120 (98%)	2 (2%)	0	100	100
2	O	122/125 (98%)	121 (99%)	1 (1%)	0	100	100
2	Q	122/125 (98%)	117 (96%)	5 (4%)	0	100	100
2	X	122/125 (98%)	120 (98%)	2 (2%)	0	100	100
3	H	270/273 (99%)	255 (94%)	15 (6%)	0	100	100
3	L	270/273 (99%)	258 (96%)	12 (4%)	0	100	100
3	N	270/273 (99%)	259 (96%)	11 (4%)	0	100	100
3	P	270/273 (99%)	256 (95%)	14 (5%)	0	100	100
3	R	270/273 (99%)	254 (94%)	16 (6%)	0	100	100
3	d	270/273 (99%)	255 (94%)	15 (6%)	0	100	100
4	I	101/112 (90%)	99 (98%)	2 (2%)	0	100	100
4	J	101/112 (90%)	98 (97%)	3 (3%)	0	100	100
4	S	101/112 (90%)	99 (98%)	2 (2%)	0	100	100
4	T	101/112 (90%)	98 (97%)	3 (3%)	0	100	100
4	U	101/112 (90%)	98 (97%)	3 (3%)	0	100	100
4	V	101/112 (90%)	99 (98%)	2 (2%)	0	100	100
4	W	101/112 (90%)	97 (96%)	4 (4%)	0	100	100
4	Y	101/112 (90%)	100 (99%)	1 (1%)	0	100	100
4	Z	101/112 (90%)	97 (96%)	4 (4%)	0	100	100
4	a	101/112 (90%)	98 (97%)	3 (3%)	0	100	100
4	b	101/112 (90%)	98 (97%)	3 (3%)	0	100	100
4	c	101/112 (90%)	99 (98%)	2 (2%)	0	100	100
5	e	416/473 (88%)	394 (95%)	22 (5%)	0	100	100
5	f	416/473 (88%)	392 (94%)	24 (6%)	0	100	100
5	g	416/473 (88%)	392 (94%)	24 (6%)	0	100	100
5	h	416/473 (88%)	393 (94%)	23 (6%)	0	100	100
5	i	416/473 (88%)	392 (94%)	24 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	j	416/473 (88%)	389 (94%)	27 (6%)	0	100	100
6	k	441/500 (88%)	433 (98%)	8 (2%)	0	100	100
6	l	441/500 (88%)	424 (96%)	17 (4%)	0	100	100
6	m	441/500 (88%)	432 (98%)	9 (2%)	0	100	100
6	n	441/500 (88%)	431 (98%)	10 (2%)	0	100	100
6	o	441/500 (88%)	432 (98%)	9 (2%)	0	100	100
6	p	441/500 (88%)	430 (98%)	11 (2%)	0	100	100
6	q	441/500 (88%)	431 (98%)	10 (2%)	0	100	100
6	r	441/500 (88%)	429 (97%)	12 (3%)	0	100	100
6	s	441/500 (88%)	431 (98%)	10 (2%)	0	100	100
6	t	441/500 (88%)	434 (98%)	7 (2%)	0	100	100
6	u	441/500 (88%)	433 (98%)	8 (2%)	0	100	100
6	v	441/500 (88%)	431 (98%)	10 (2%)	0	100	100
All	All	12120/13392 (90%)	11696 (96%)	424 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	115/122 (94%)	115 (100%)	0	100	100
1	B	115/122 (94%)	115 (100%)	0	100	100
1	C	115/122 (94%)	115 (100%)	0	100	100
1	D	115/122 (94%)	113 (98%)	2 (2%)	56	74
1	E	115/122 (94%)	115 (100%)	0	100	100
1	F	115/122 (94%)	115 (100%)	0	100	100
2	G	116/117 (99%)	116 (100%)	0	100	100
2	K	116/117 (99%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	116/117 (99%)	116 (100%)	0	100	100
2	O	116/117 (99%)	116 (100%)	0	100	100
2	Q	116/117 (99%)	116 (100%)	0	100	100
2	X	116/117 (99%)	116 (100%)	0	100	100
3	H	249/250 (100%)	249 (100%)	0	100	100
3	L	249/250 (100%)	249 (100%)	0	100	100
3	N	249/250 (100%)	249 (100%)	0	100	100
3	P	249/250 (100%)	249 (100%)	0	100	100
3	R	249/250 (100%)	249 (100%)	0	100	100
3	d	249/250 (100%)	249 (100%)	0	100	100
4	I	93/101 (92%)	93 (100%)	0	100	100
4	J	93/101 (92%)	93 (100%)	0	100	100
4	S	93/101 (92%)	93 (100%)	0	100	100
4	T	93/101 (92%)	93 (100%)	0	100	100
4	U	93/101 (92%)	93 (100%)	0	100	100
4	V	93/101 (92%)	93 (100%)	0	100	100
4	W	93/101 (92%)	93 (100%)	0	100	100
4	Y	93/101 (92%)	93 (100%)	0	100	100
4	Z	93/101 (92%)	93 (100%)	0	100	100
4	a	93/101 (92%)	93 (100%)	0	100	100
4	b	93/101 (92%)	93 (100%)	0	100	100
4	c	93/101 (92%)	93 (100%)	0	100	100
5	e	369/413 (89%)	368 (100%)	1 (0%)	91	94
5	f	369/413 (89%)	367 (100%)	2 (0%)	86	91
5	g	369/413 (89%)	367 (100%)	2 (0%)	86	91
5	h	369/413 (89%)	366 (99%)	3 (1%)	79	87
5	i	369/413 (89%)	367 (100%)	2 (0%)	86	91
5	j	369/413 (89%)	368 (100%)	1 (0%)	91	94
6	k	374/447 (84%)	374 (100%)	0	100	100
6	l	374/447 (84%)	374 (100%)	0	100	100
6	m	374/447 (84%)	373 (100%)	1 (0%)	91	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	n	374/447 (84%)	374 (100%)	0	100	100
6	o	374/447 (84%)	374 (100%)	0	100	100
6	p	374/447 (84%)	374 (100%)	0	100	100
6	q	374/447 (84%)	374 (100%)	0	100	100
6	r	374/447 (84%)	374 (100%)	0	100	100
6	s	374/447 (84%)	373 (100%)	1 (0%)	91	94
6	t	374/447 (84%)	374 (100%)	0	100	100
6	u	374/447 (84%)	373 (100%)	1 (0%)	91	94
6	v	374/447 (84%)	374 (100%)	0	100	100
All	All	10698/11988 (89%)	10682 (100%)	16 (0%)	92	96

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	s	456	ARG
6	m	456	ARG
5	h	398	LYS
5	j	454	LYS
5	h	297	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	K	108	GLN
2	K	118	GLN
6	p	216	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 [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.

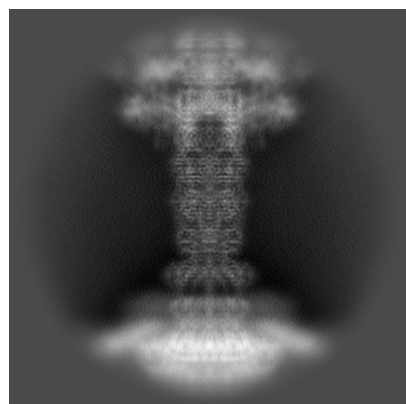
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51198. These allow visual inspection of the internal detail of the map and identification of artifacts.

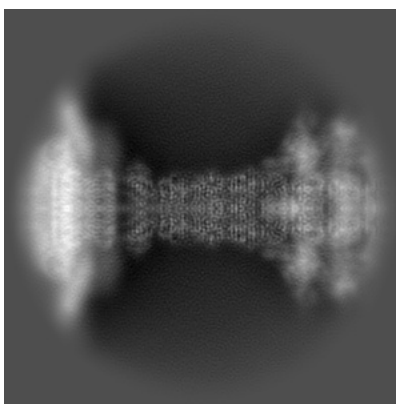
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

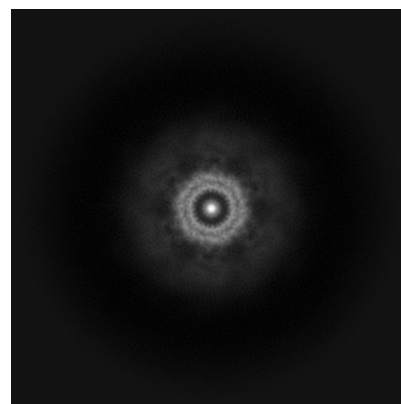
6.1.1 Primary map



X

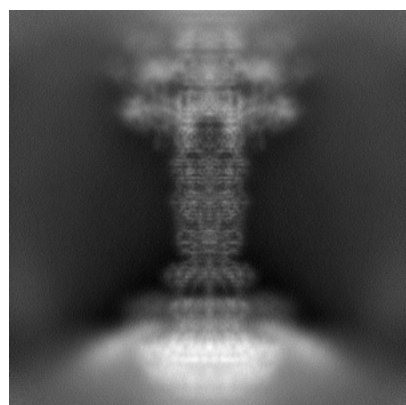


Y

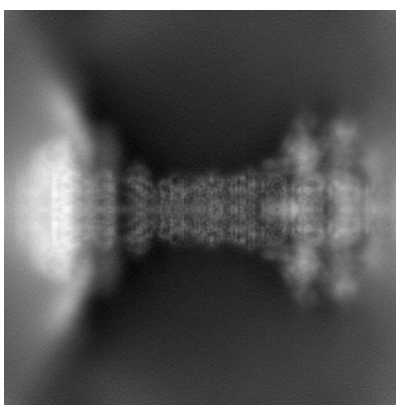


Z

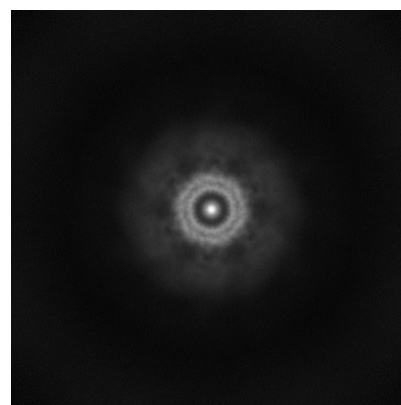
6.1.2 Raw map



X



Y

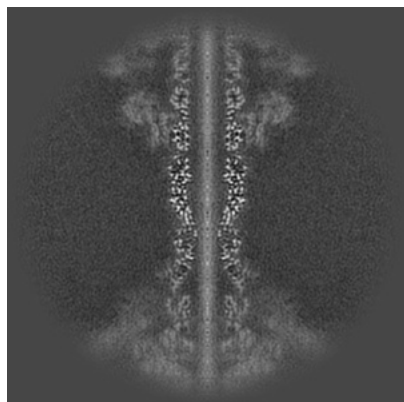


Z

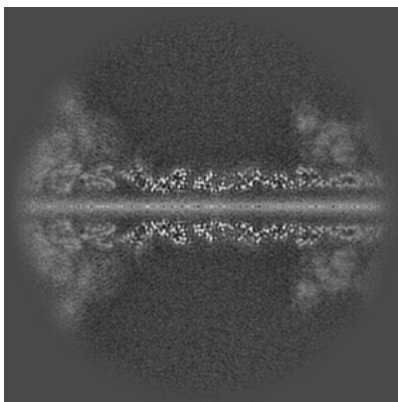
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

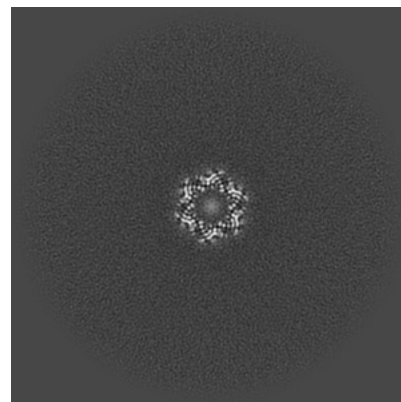
6.2.1 Primary map



X Index: 200

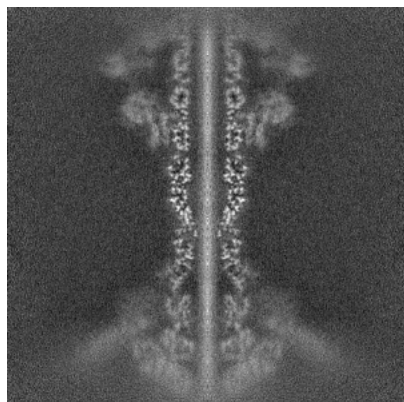


Y Index: 200

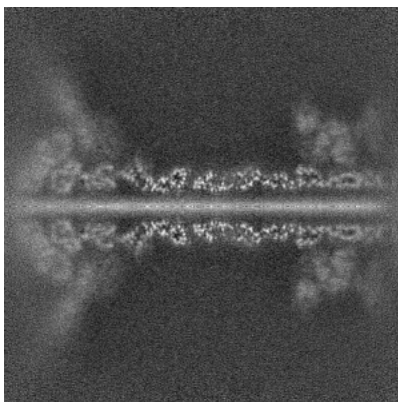


Z Index: 200

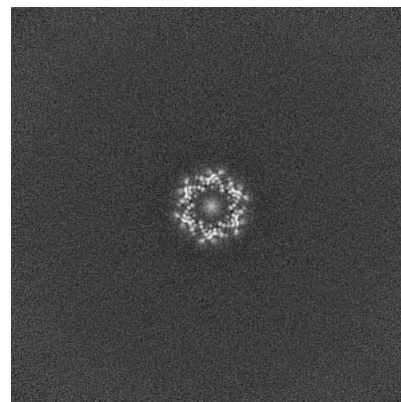
6.2.2 Raw map



X Index: 200



Y Index: 200

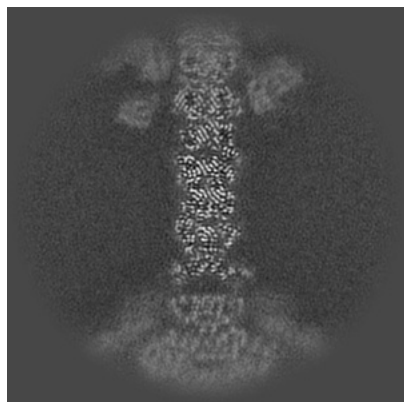


Z Index: 200

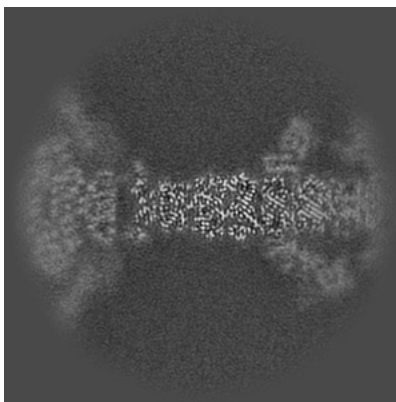
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

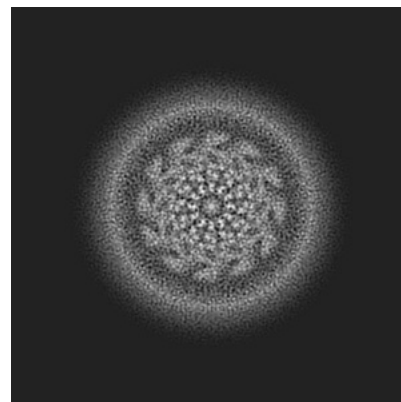
6.3.1 Primary map



X Index: 180

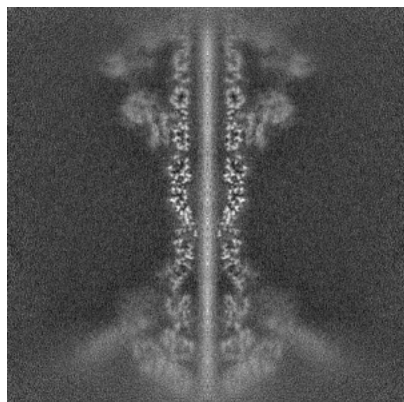


Y Index: 220

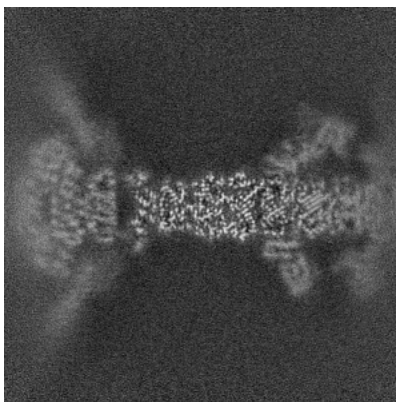


Z Index: 63

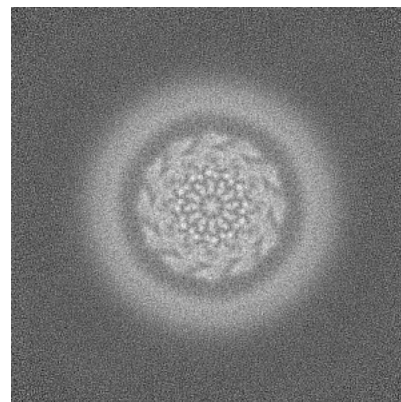
6.3.2 Raw map



X Index: 200



Y Index: 180

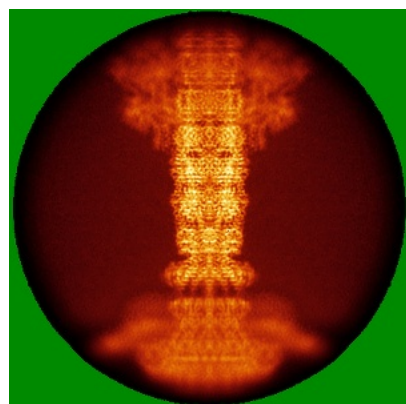


Z Index: 61

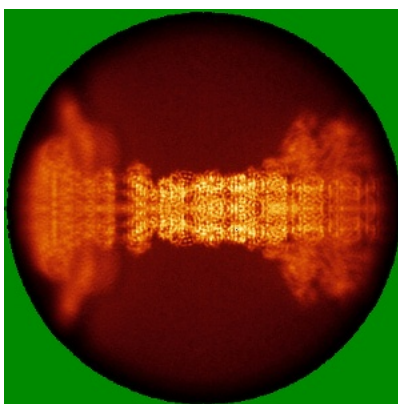
The images above show the largest variance slices of the map in three orthogonal directions.

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

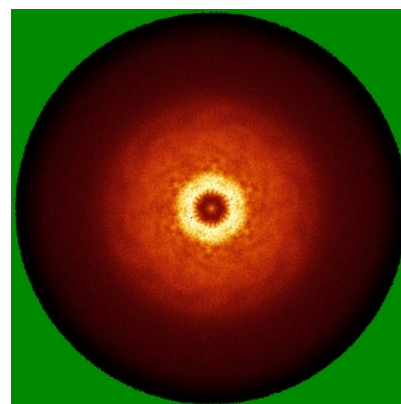
6.4.1 Primary map



X

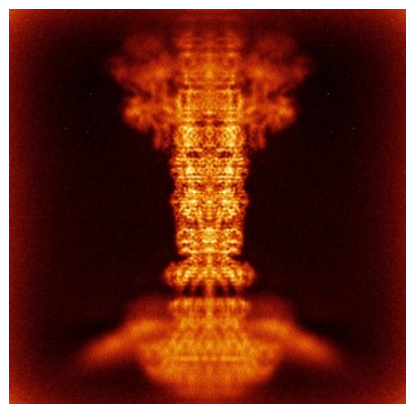


Y

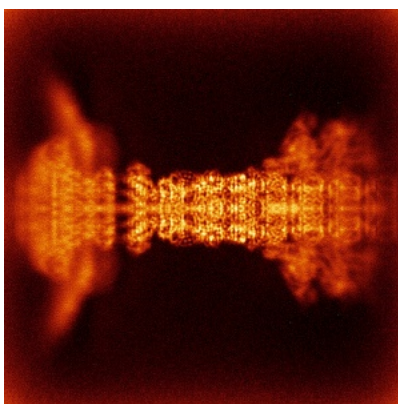


Z

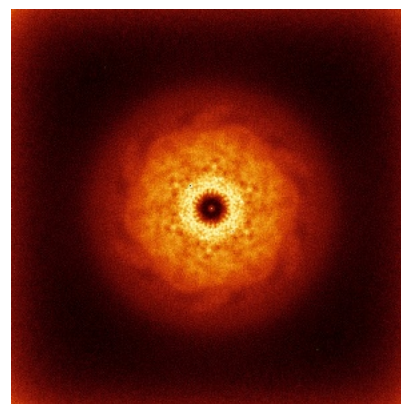
6.4.2 Raw map



X



Y

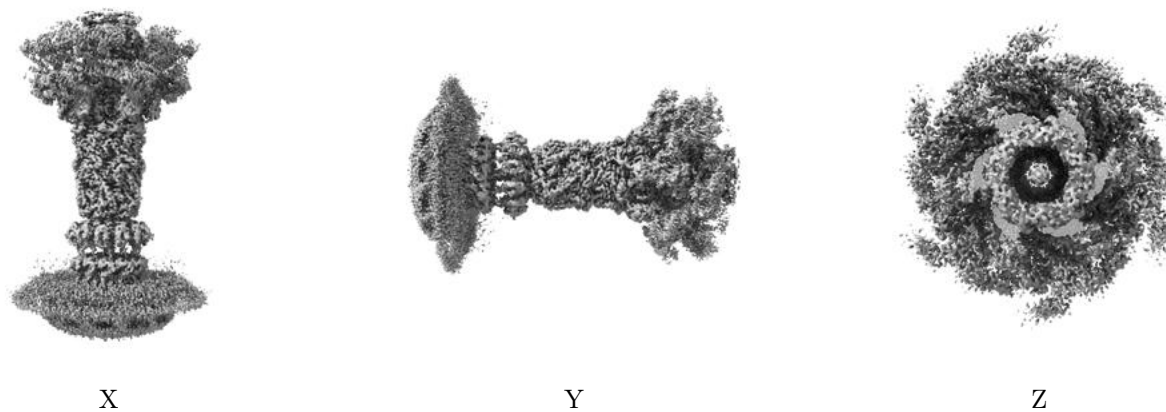


Z

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

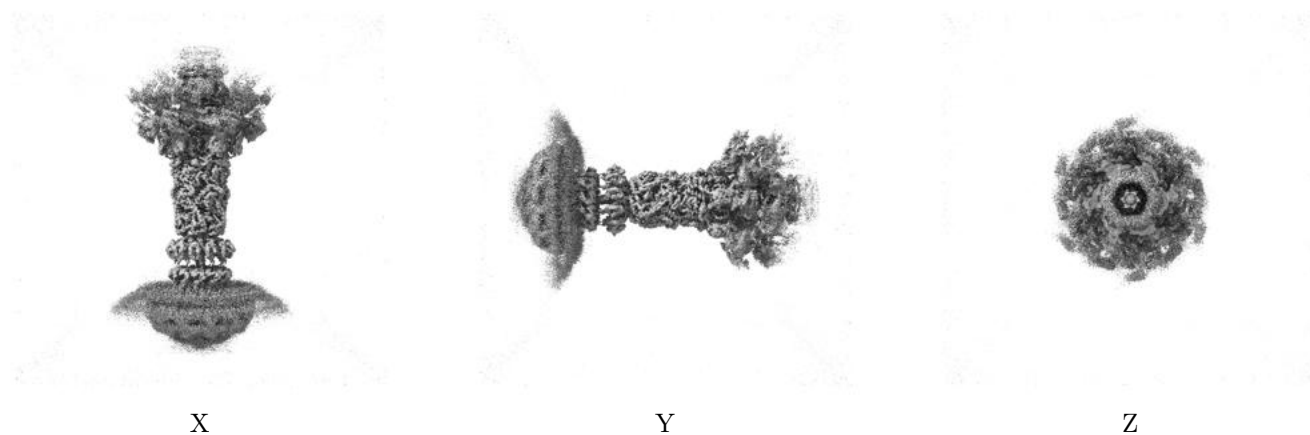
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.249. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

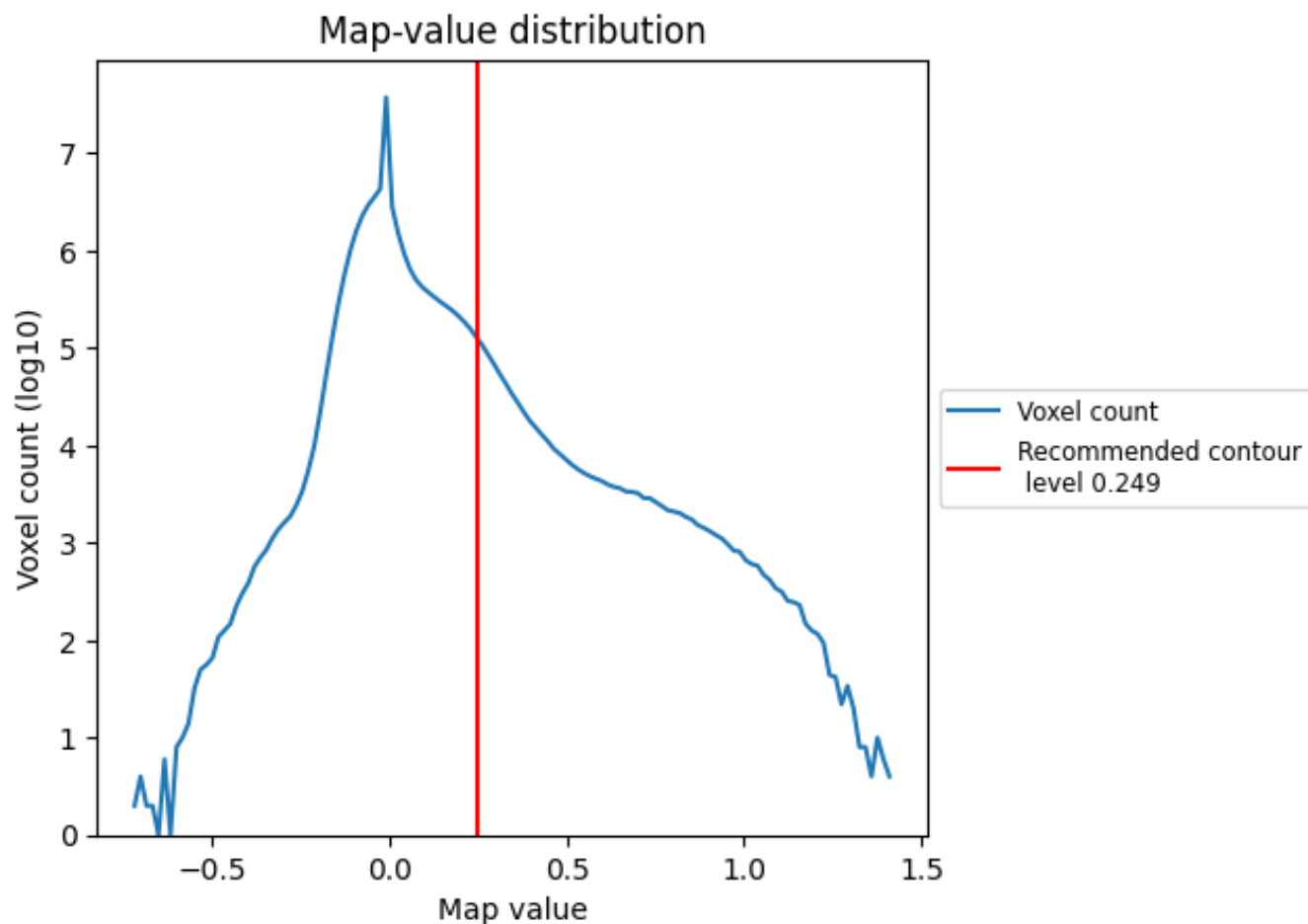
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

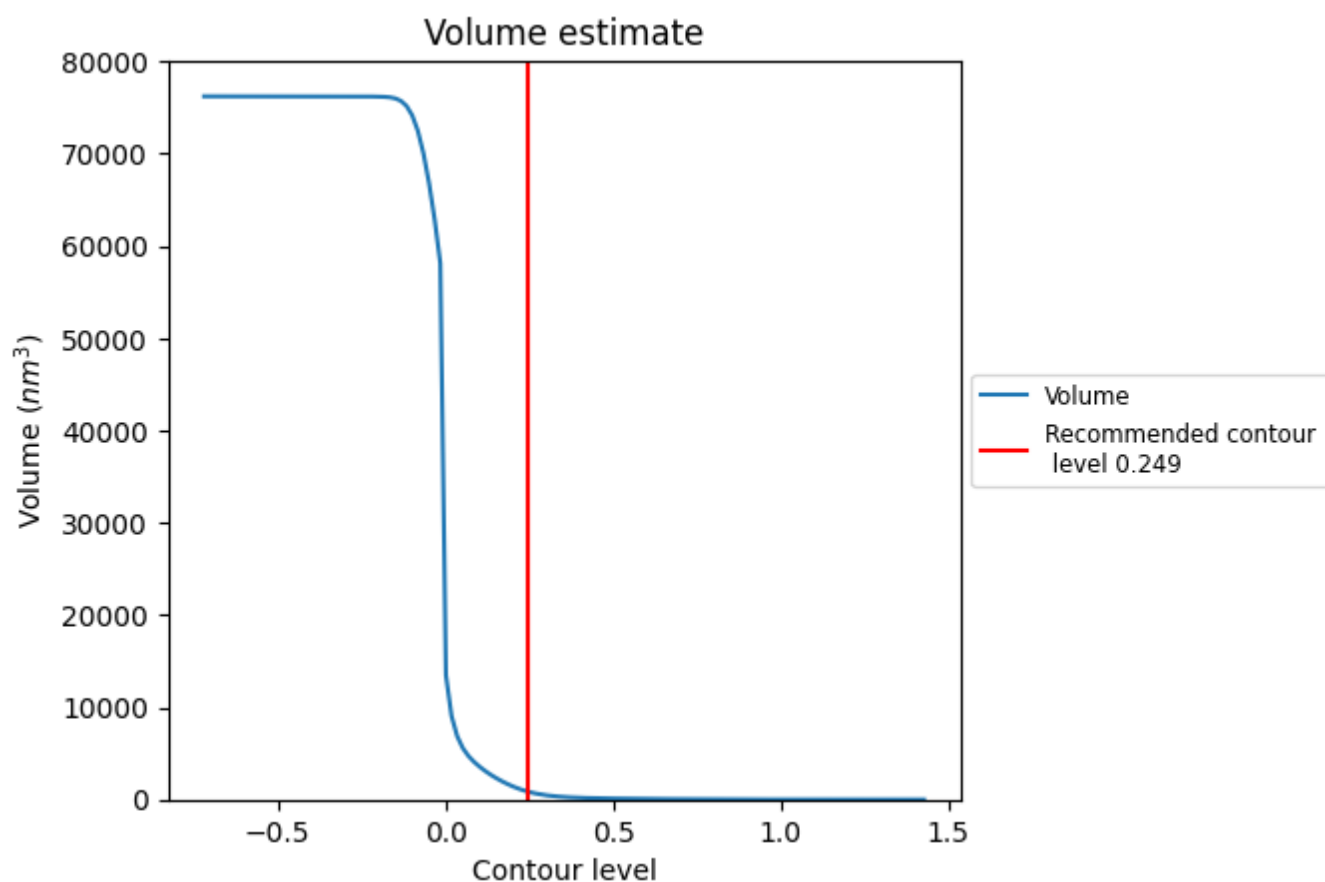
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

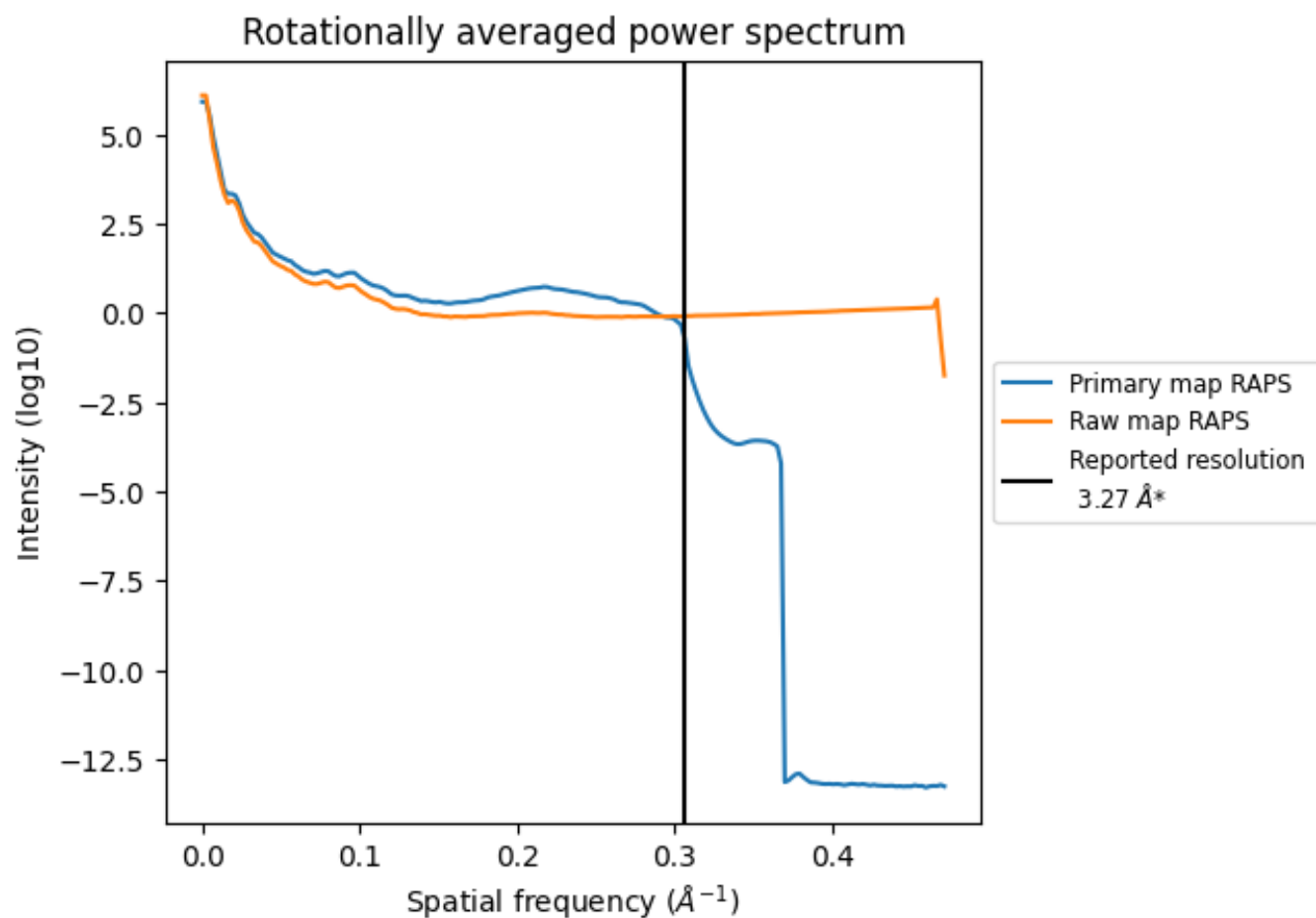
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 839 nm³; this corresponds to an approximate mass of 758 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 ⓘ

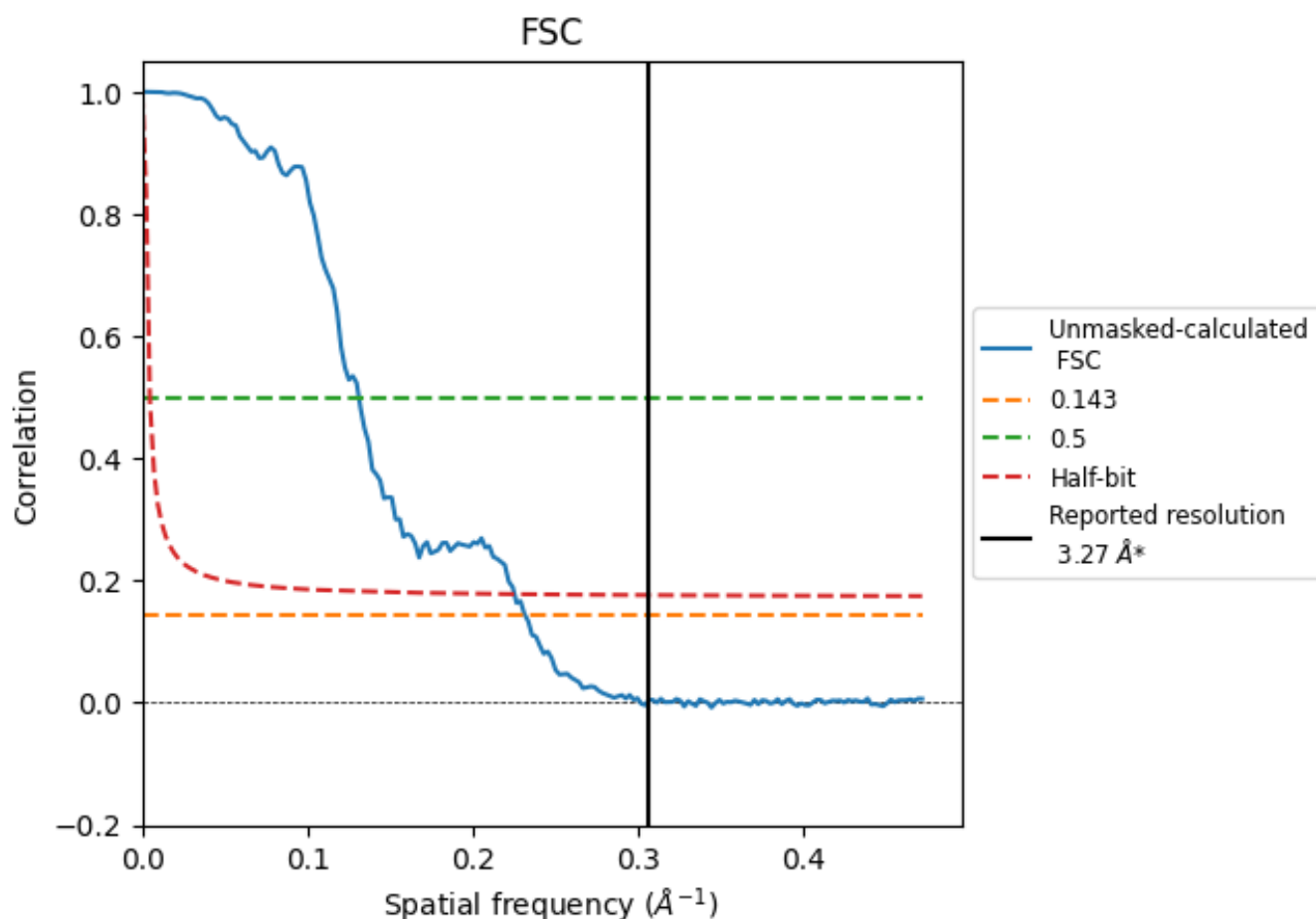


*Reported resolution corresponds to spatial frequency of 0.306 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.306 Å⁻¹

8.2 Resolution estimates [i](#)

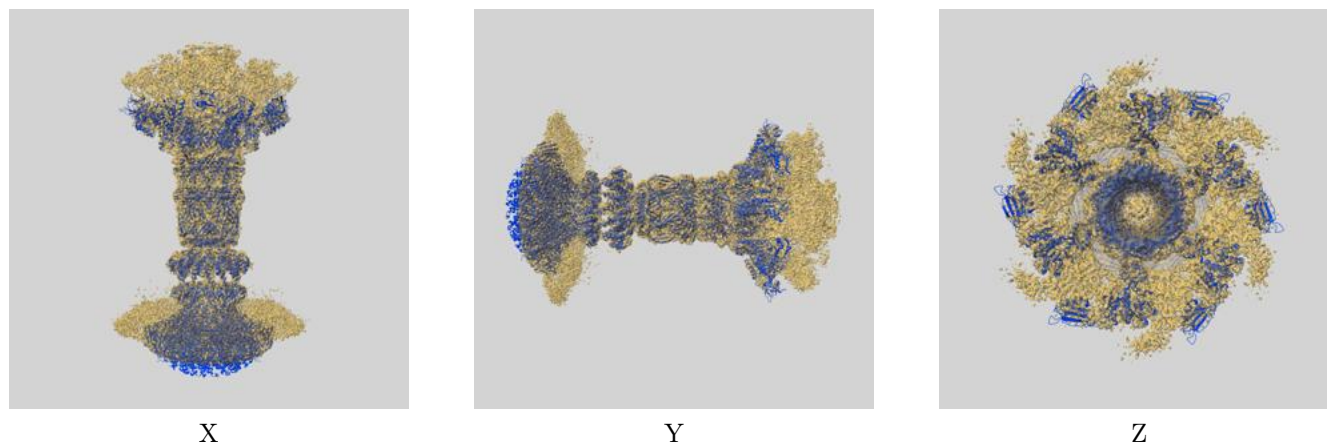
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.32	7.63	4.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.32 differs from the reported value 3.27 by more than 10 %

9 Map-model fit [i](#)

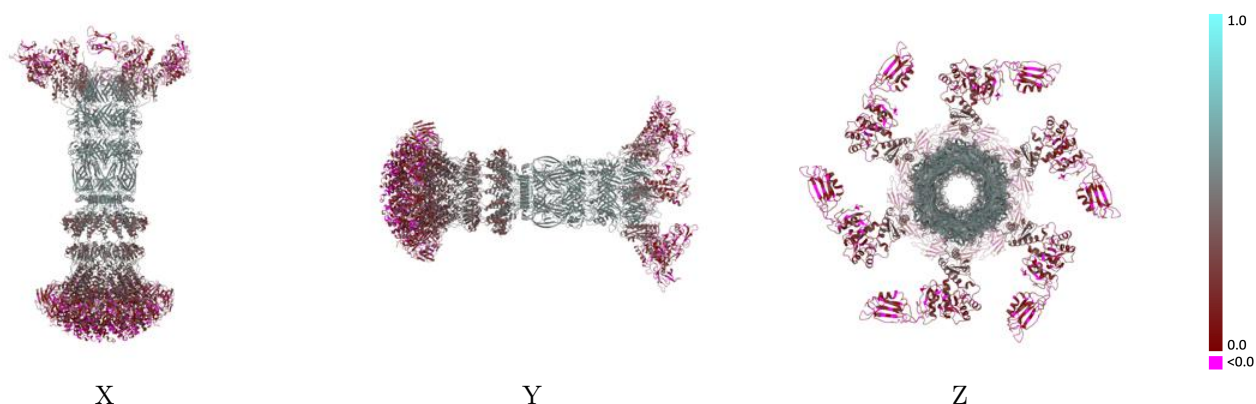
This section contains information regarding the fit between EMDB map EMD-51198 and PDB model 9GB5. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



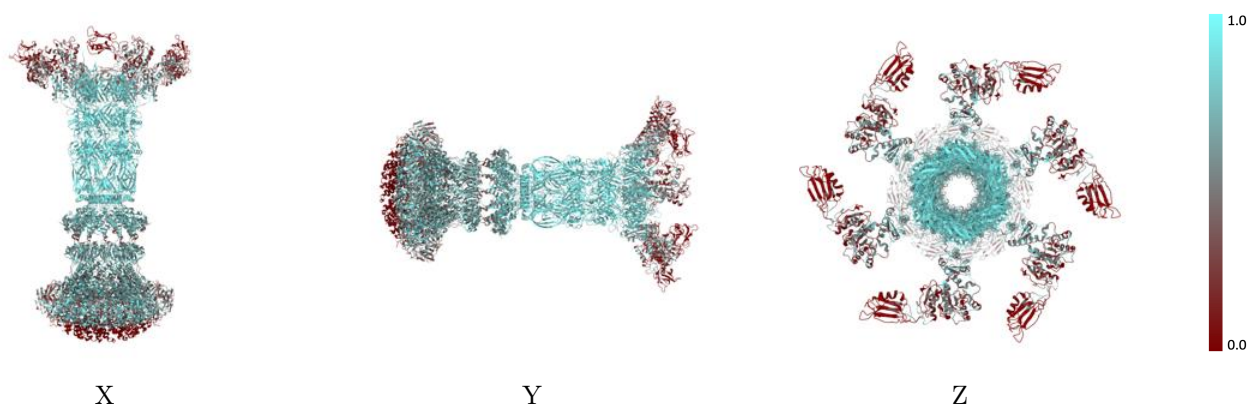
The images above show the 3D surface view of the map at the recommended contour level 0.249 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



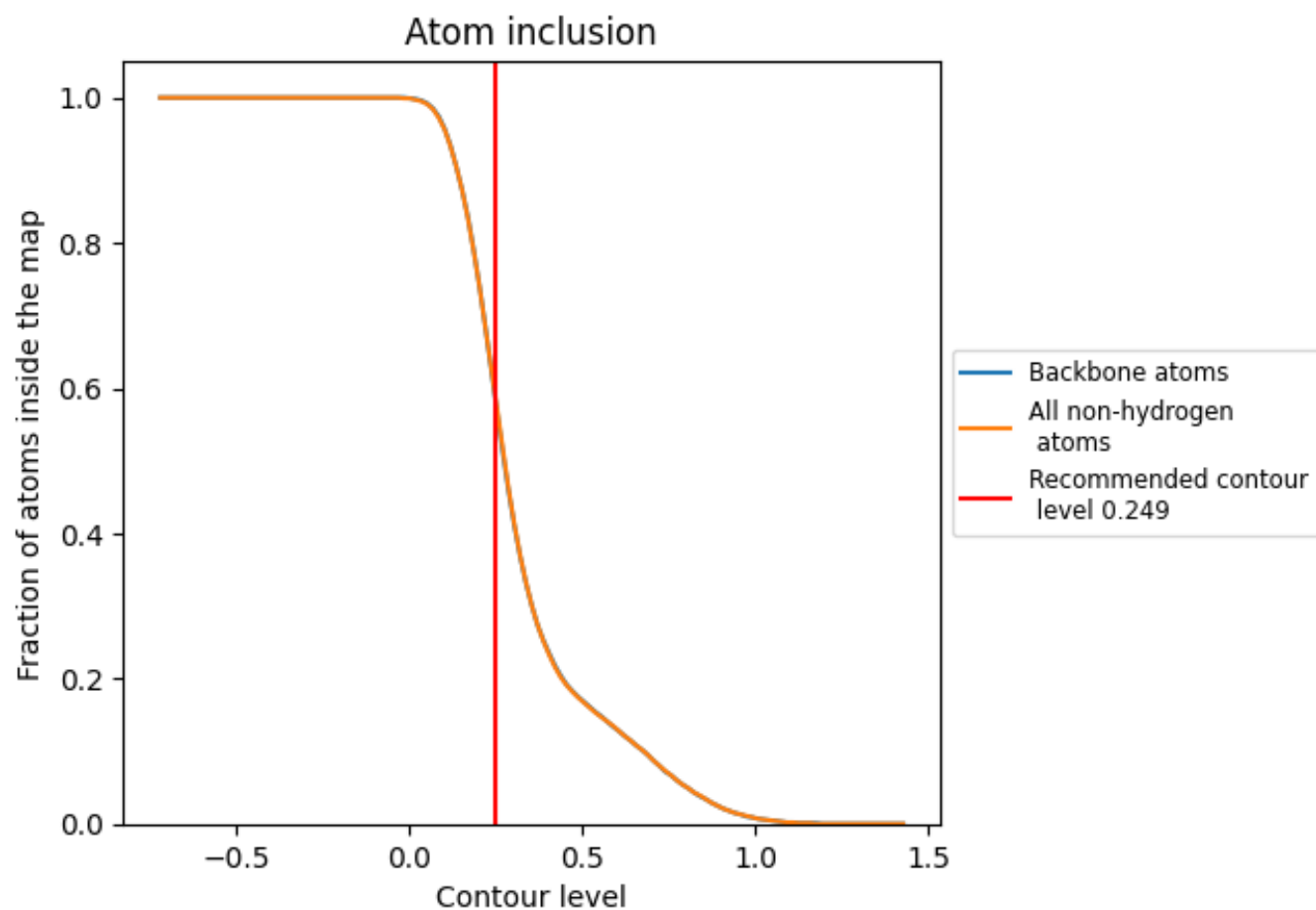
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.249).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





























The table lists the average atom inclusion at the recommended contour level (0.249) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5860	 0.3200
A	 0.8190	 0.5250
B	 0.8320	 0.5320
C	 0.8230	 0.5290
D	 0.8250	 0.5230
E	 0.8350	 0.5270
F	 0.8180	 0.5290
G	 0.8550	 0.5230
H	 0.8550	 0.5190
I	 0.7150	 0.4490
J	 0.6660	 0.4220
K	 0.8500	 0.5180
L	 0.8500	 0.5210
M	 0.8530	 0.5220
N	 0.8570	 0.5230
O	 0.8610	 0.5220
P	 0.8520	 0.5210
Q	 0.8550	 0.5180
R	 0.8510	 0.5200
S	 0.6910	 0.4390
T	 0.7040	 0.4420
U	 0.6980	 0.4450
V	 0.6890	 0.4360
W	 0.7060	 0.4460
X	 0.8600	 0.5210
Y	 0.6750	 0.4260
Z	 0.6580	 0.4160
a	 0.6720	 0.4270
b	 0.6660	 0.4300
c	 0.6670	 0.4280
d	 0.8550	 0.5220
e	 0.3170	 0.1920
f	 0.3210	 0.1960
g	 0.3150	 0.1900
h	 0.3140	 0.1900



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Chain	Atom inclusion	Q-score
i	 0.3150	 0.1890
j	 0.3210	 0.1910
k	 0.5520	 0.2370
l	 0.5300	 0.2210
m	 0.5570	 0.2350
n	 0.5340	 0.2250
o	 0.5530	 0.2360
p	 0.5320	 0.2230
q	 0.5540	 0.2340
r	 0.5360	 0.2230
s	 0.5520	 0.2370
t	 0.5370	 0.2260
u	 0.5540	 0.2350
v	 0.5330	 0.2240