



wwPDB EM Validation Summary Report ⓘ

Jun 10, 2026 – 11:36 pm BST

PDB ID : 3OYT / pdb_00003Oyt
EMDB ID : EMD-58150
Title : Capsid-connector assembly of the phage OE33PA
Authors : Goulet, A.; Cambillau, C.
Deposited on : 2026-05-18
Resolution : 3.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

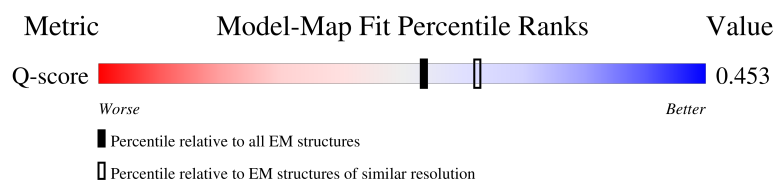
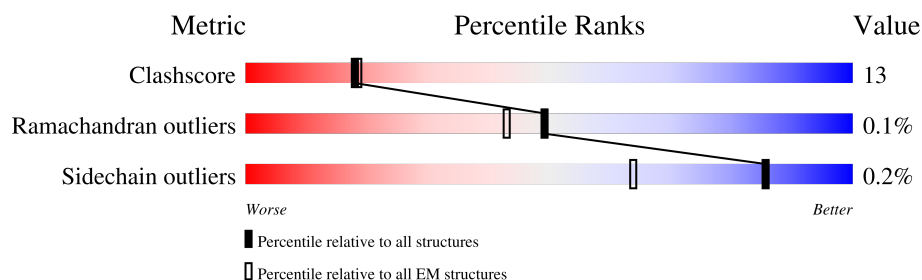
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	389	
1	B	389	
1	C	389	
1	D	389	



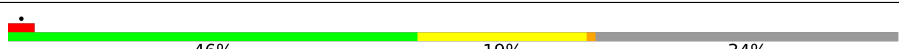
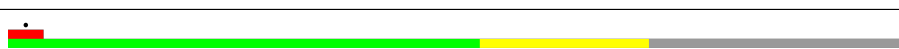
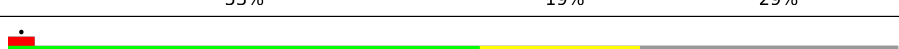
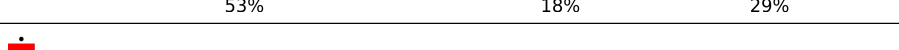
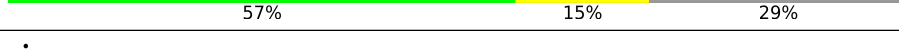

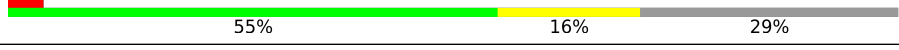




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Mol	Chain	Length	Quality of chain
1	E	389	
1	F	389	
1	G	389	
1	H	389	
1	I	389	
1	J	389	
1	K	389	
1	L	389	
2	M	413	
2	N	413	
2	O	413	
2	P	413	
2	Q	413	
2	R	413	
2	S	413	
2	T	413	
2	U	413	
2	V	413	
2	W	413	
2	X	413	
2	Y	413	
2	Z	413	
2	a	413	
2	b	413	
2	c	413	

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Mol	Chain	Length	Quality of chain
2	d	413	
2	e	413	
2	f	413	
2	g	413	
2	h	413	
2	i	413	
2	j	413	
2	k	413	
2	l	413	
2	m	413	
2	n	413	
2	o	413	
2	p	413	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 97192 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	330	Total	C	N	O	S	0	0
			2494	1573	424	486	11		
1	B	333	Total	C	N	O	S	0	0
			2531	1599	429	492	11		
1	C	316	Total	C	N	O	S	0	0
			2436	1541	411	473	11		
1	D	316	Total	C	N	O	S	0	0
			2427	1533	410	473	11		
1	E	336	Total	C	N	O	S	0	0
			2553	1609	433	500	11		
1	F	319	Total	C	N	O	S	0	0
			2454	1552	414	477	11		
1	G	315	Total	C	N	O	S	0	0
			2431	1538	410	472	11		
1	H	334	Total	C	N	O	S	0	0
			2547	1611	427	498	11		
1	I	342	Total	C	N	O	S	0	0
			2599	1639	436	513	11		
1	J	316	Total	C	N	O	S	0	0
			2430	1538	408	473	11		
1	K	334	Total	C	N	O	S	0	0
			2539	1604	424	500	11		
1	L	334	Total	C	N	O	S	0	0
			2565	1621	433	500	11		

- Molecule 2 is a protein called Major Capsid Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	N	293	Total	C	N	O	S	0	0
			2259	1424	376	452	7		
2	O	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		

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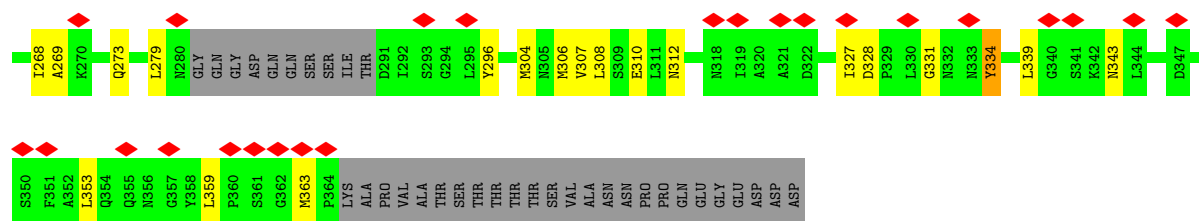
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	273	Total	C	N	O	S	0	0
			2121	1342	354	419	6		
2	Q	295	Total	C	N	O	S	0	0
			2272	1432	379	455	6		
2	R	295	Total	C	N	O	S	0	0
			2271	1432	378	454	7		
2	S	291	Total	C	N	O	S	0	0
			2246	1417	374	449	6		
2	T	292	Total	C	N	O	S	0	0
			2251	1419	375	451	6		
2	U	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	V	272	Total	C	N	O	S	0	0
			2113	1336	353	418	6		
2	W	295	Total	C	N	O	S	0	0
			2275	1434	379	455	7		
2	X	295	Total	C	N	O	S	0	0
			2271	1432	378	454	7		
2	Y	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	Z	274	Total	C	N	O	S	0	0
			2127	1352	354	415	6		
2	a	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	b	293	Total	C	N	O	S	0	0
			2256	1422	376	452	6		
2	c	295	Total	C	N	O	S	0	0
			2275	1434	379	455	7		
2	d	295	Total	C	N	O	S	0	0
			2271	1432	378	454	7		
2	e	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	f	273	Total	C	N	O	S	0	0
			2118	1339	355	418	6		
2	g	294	Total	C	N	O	S	0	0
			2263	1427	377	453	6		
2	h	293	Total	C	N	O	S	0	0
			2256	1422	376	452	6		
2	i	295	Total	C	N	O	S	0	0
			2267	1430	379	451	7		
2	j	295	Total	C	N	O	S	0	0
			2271	1432	378	454	7		

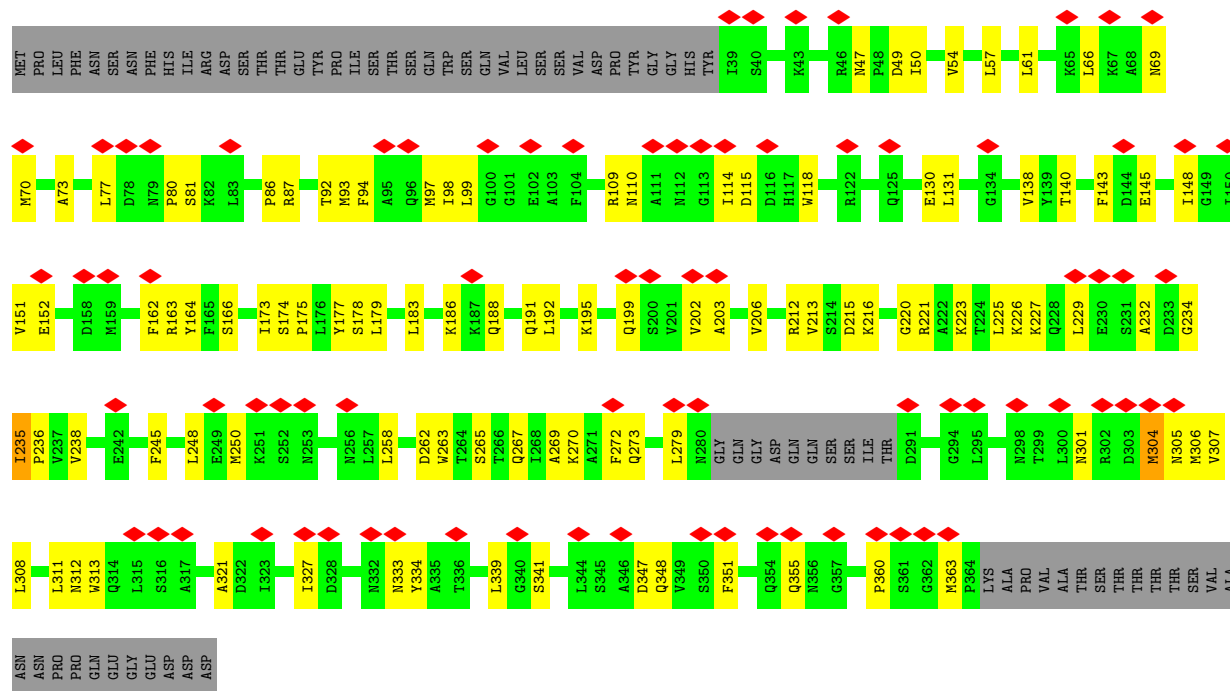
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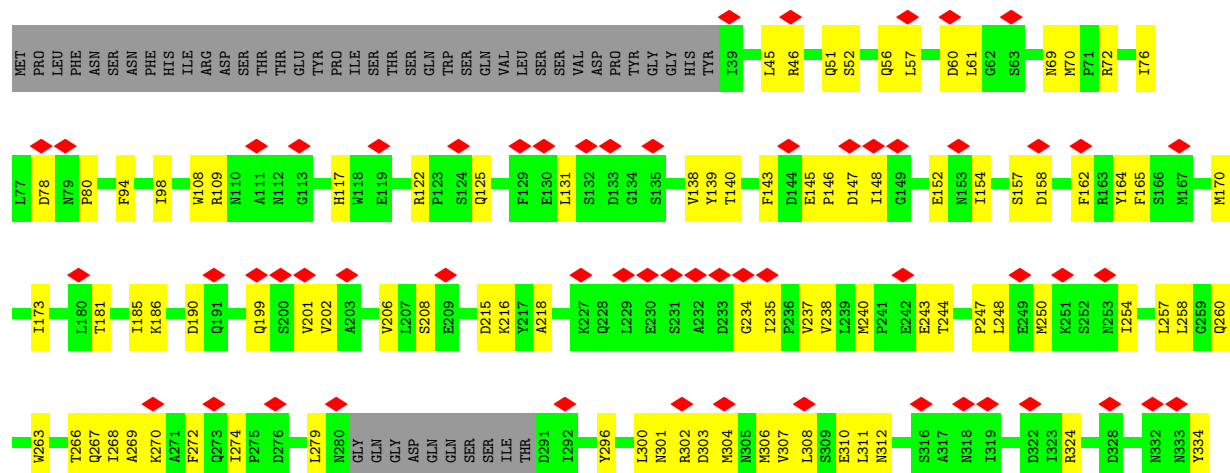
Mol	Chain	Residues	Atoms					AltConf	Trace
2	k	294	Total	C	N	O	S	0	0
			2258	1425	377	449	7		
2	l	293	Total	C	N	O	S	0	0
			2249	1419	373	450	7		
2	m	294	Total	C	N	O	S	0	0
			2266	1429	377	453	7		
2	n	274	Total	C	N	O	S	0	0
			2102	1329	354	413	6		
2	o	295	Total	C	N	O	S	0	0
			2272	1432	379	455	6		
2	p	295	Total	C	N	O	S	0	0
			2260	1424	377	453	6		

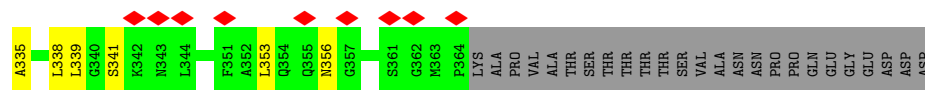


• Molecule 1: portal protein

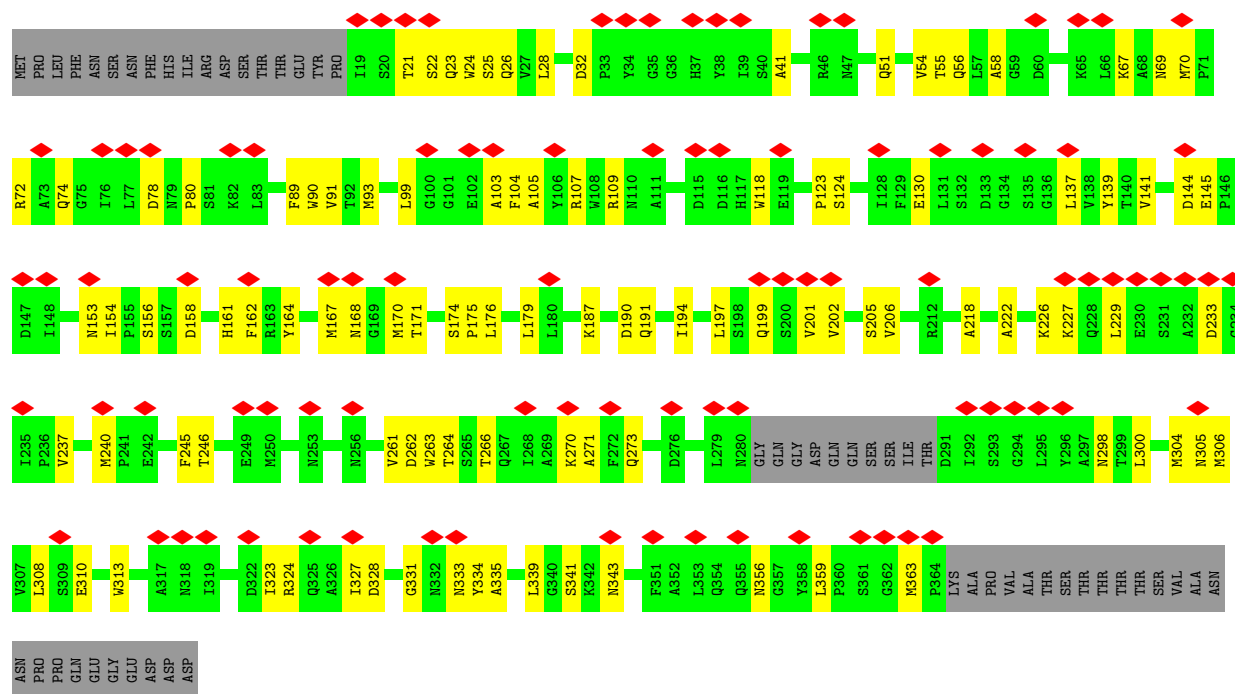


• Molecule 1: portal protein

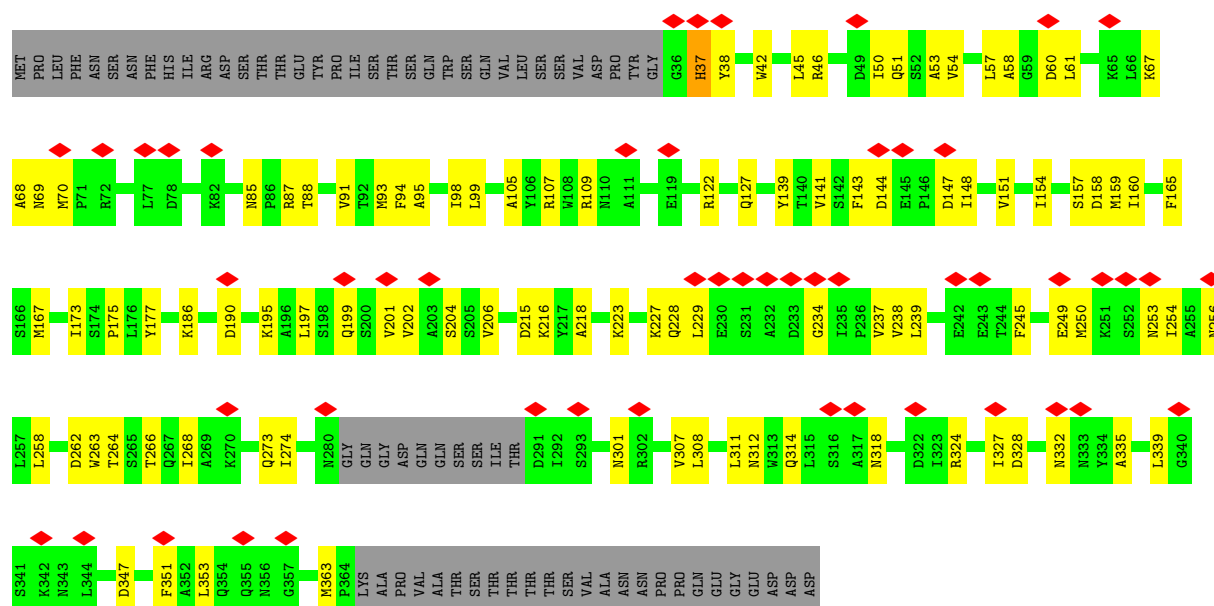




• Molecule 1: portal protein

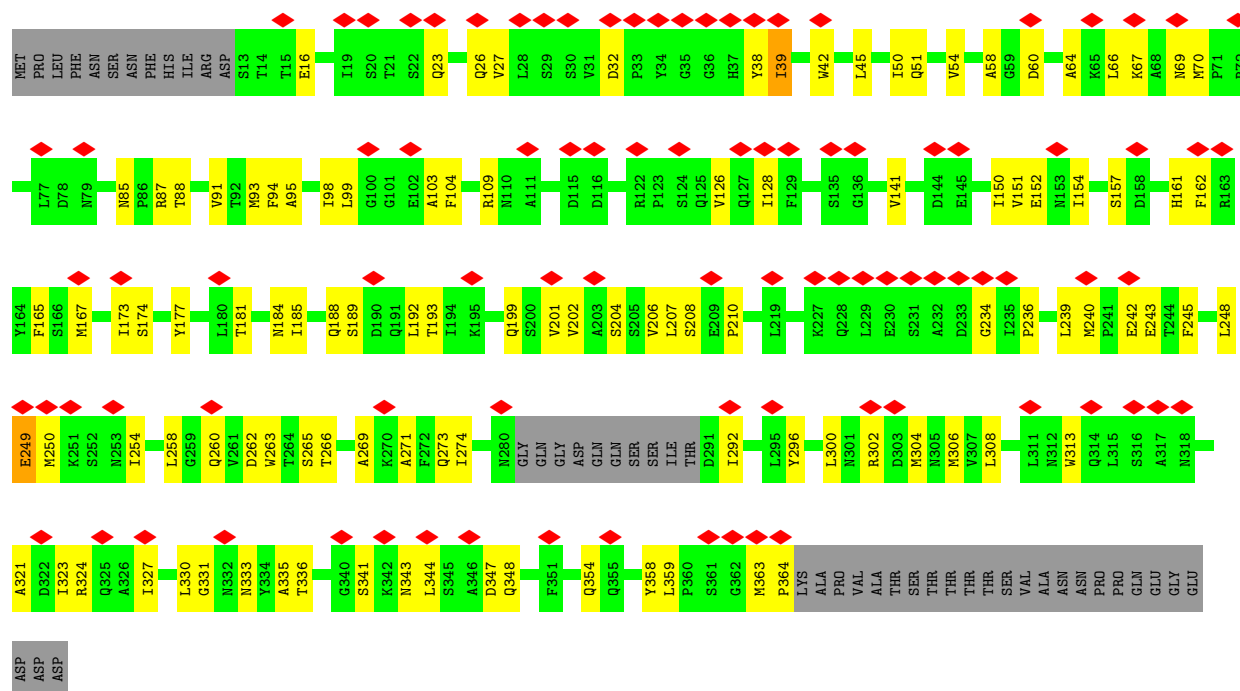


• Molecule 1: portal protein

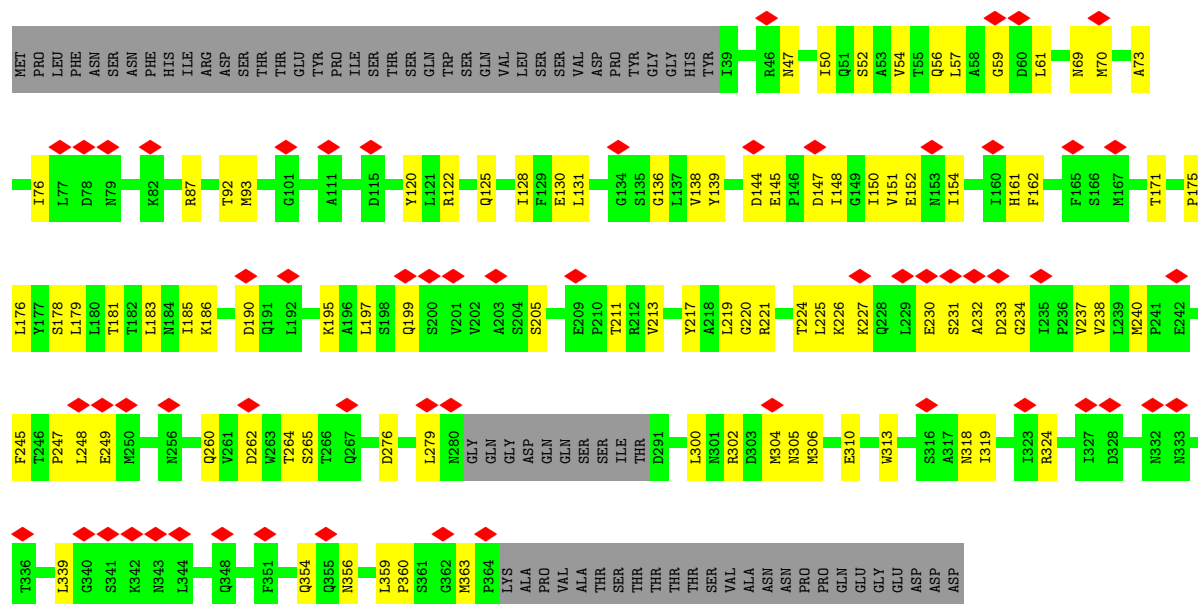


- Chain G:  19% 56% 24% 1%



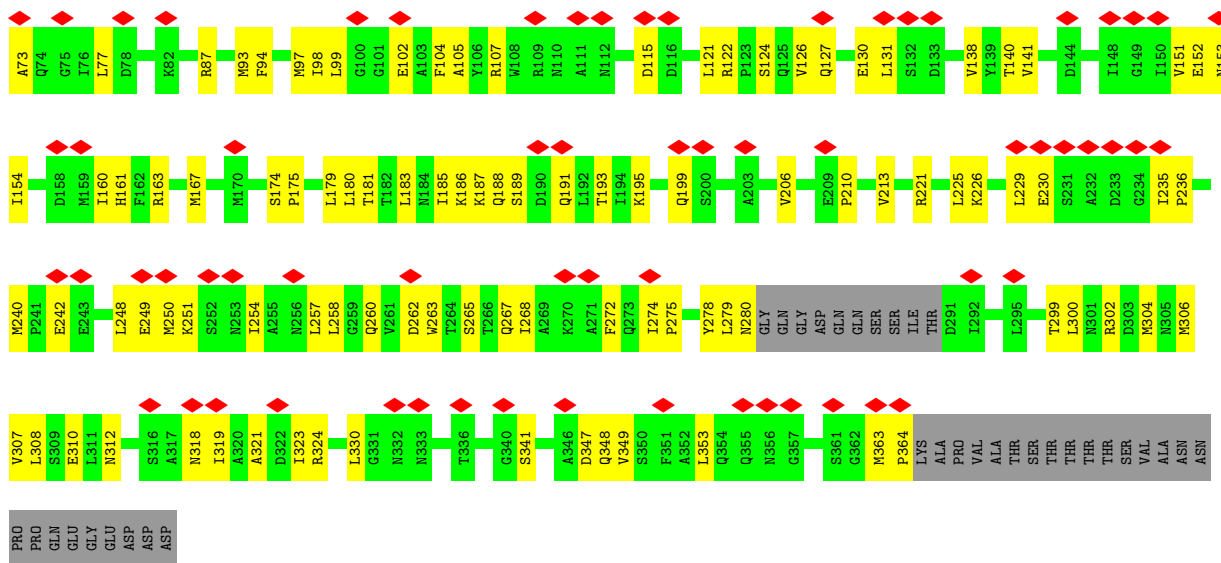


- Molecule 1: portal protein

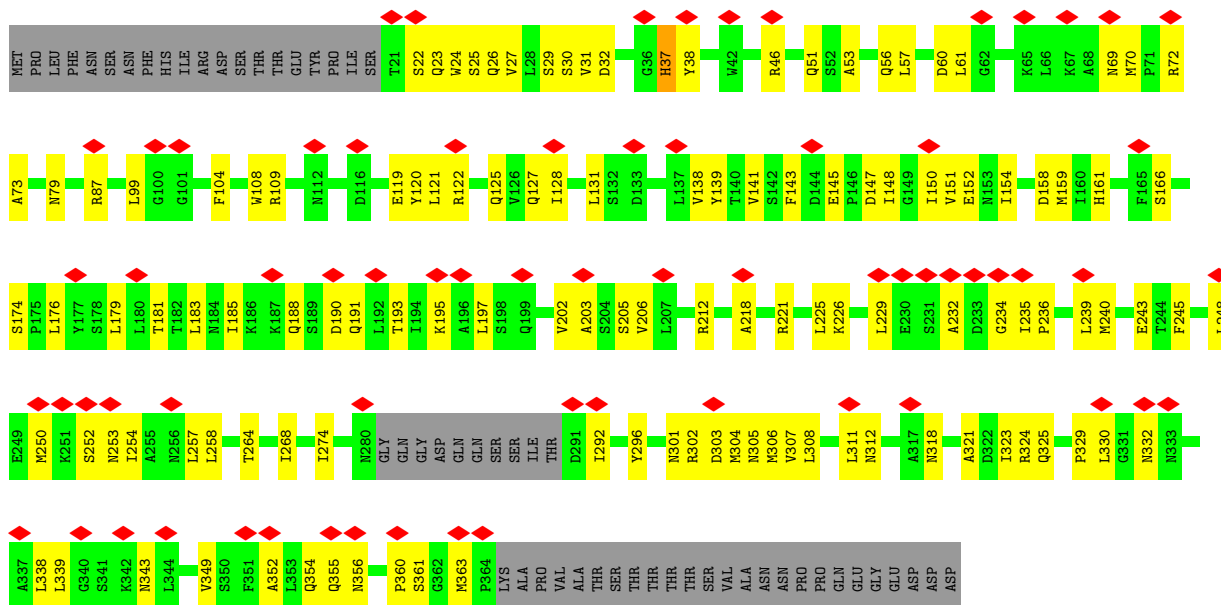


- Molecule 1: portal protein

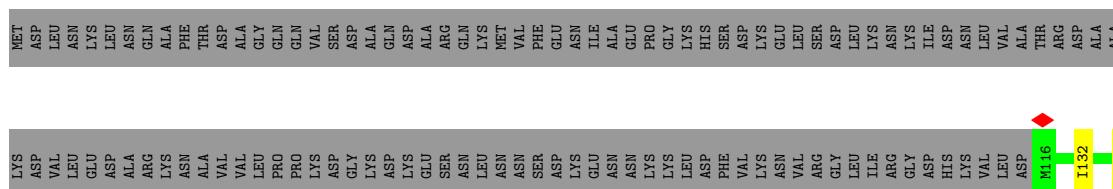




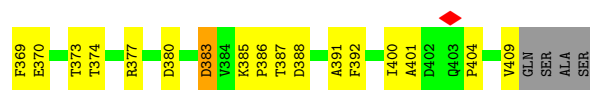
- Molecule 1: portal protein



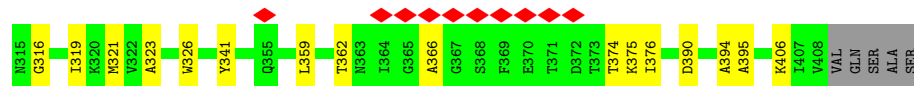
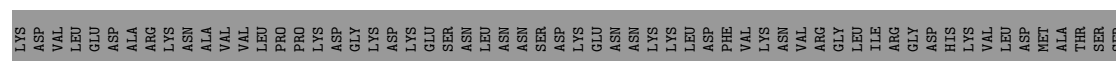
- Molecule 2: Major Capsid Protein



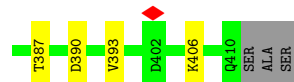
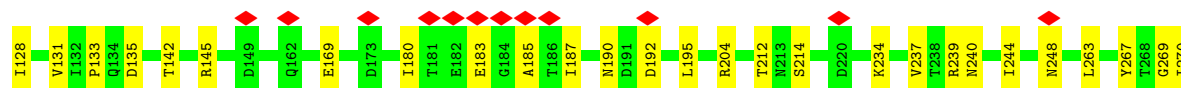
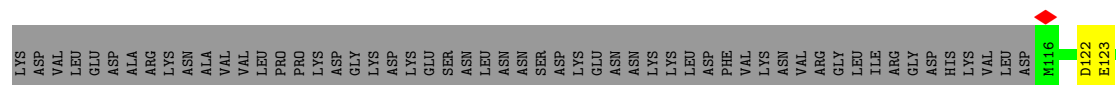




• Molecule 2: Major Capsid Protein

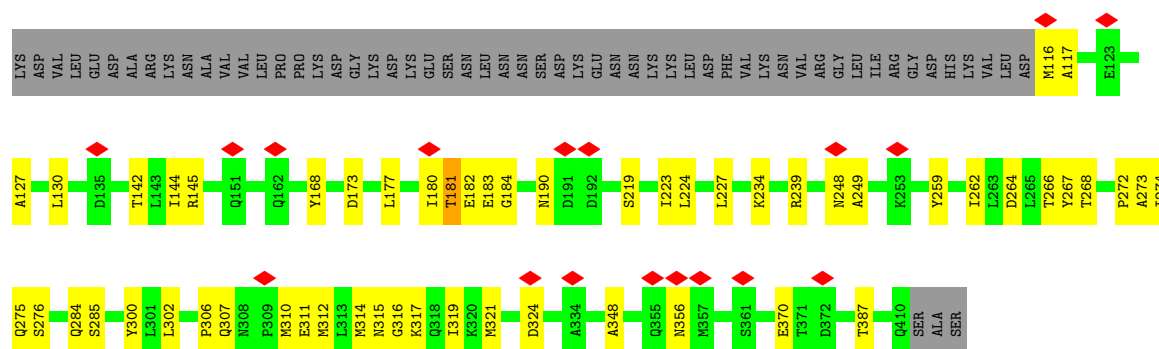


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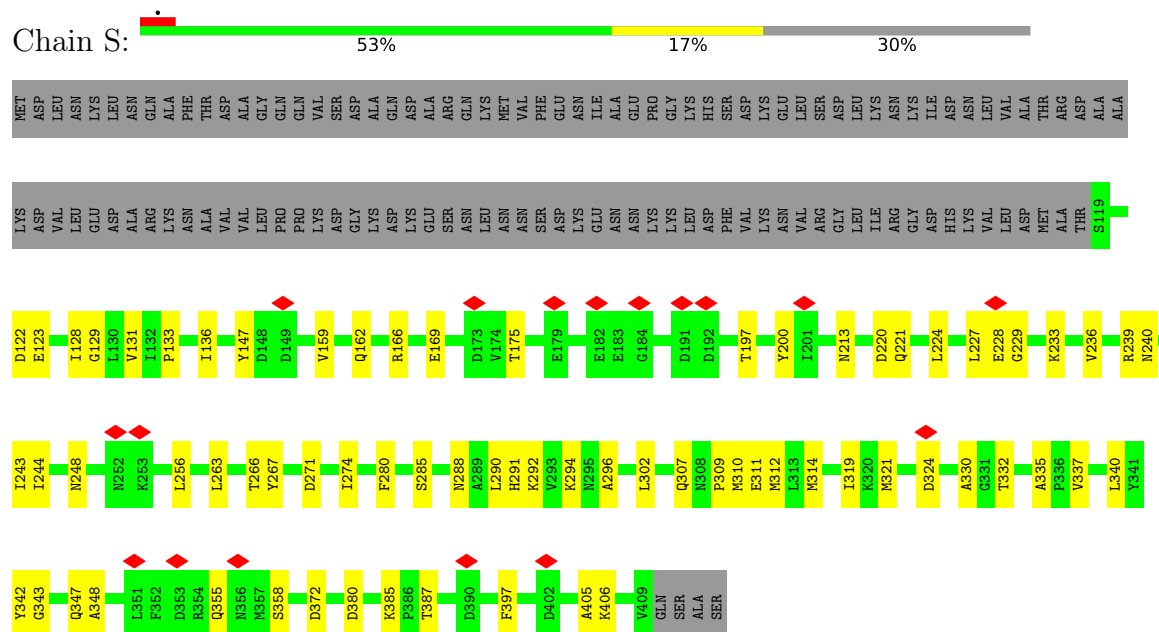


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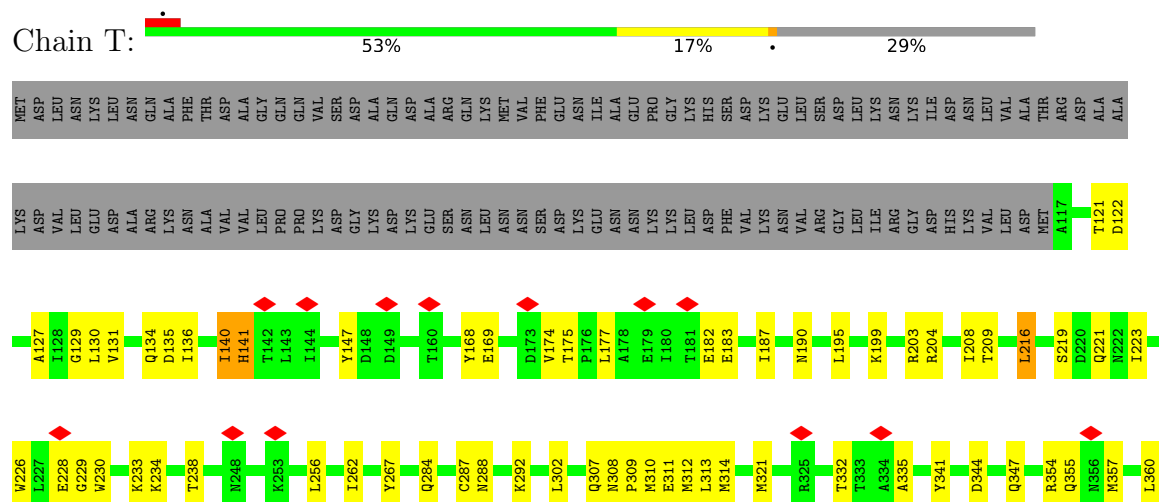


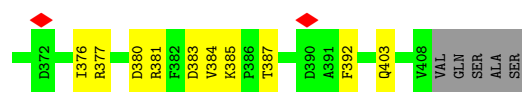


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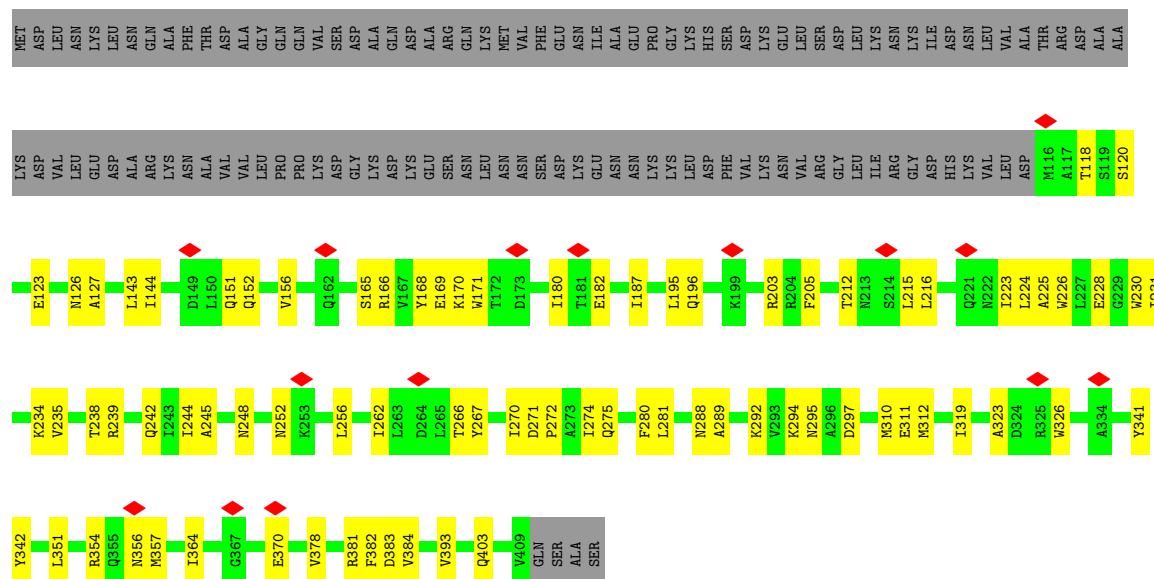


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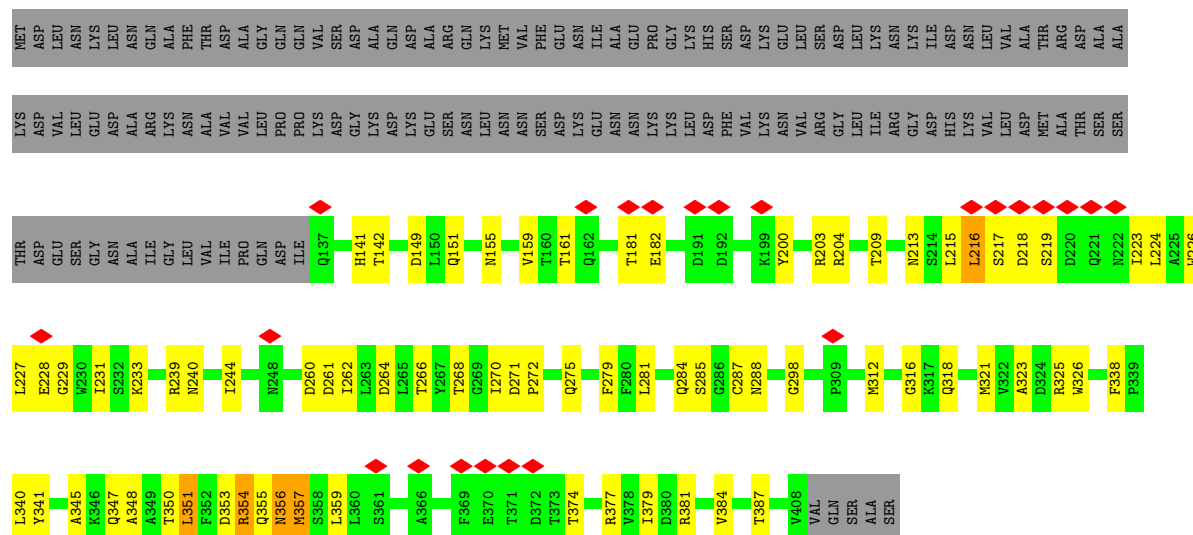




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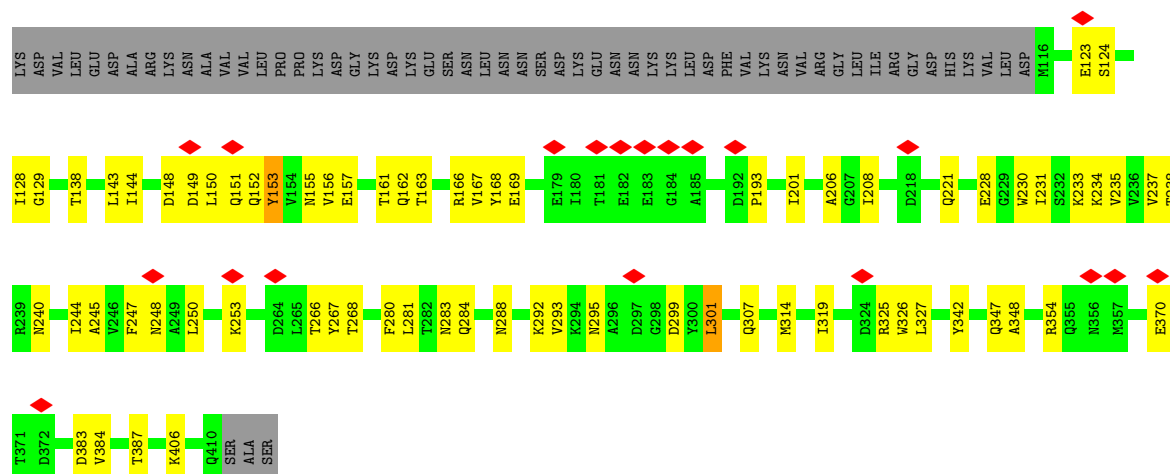


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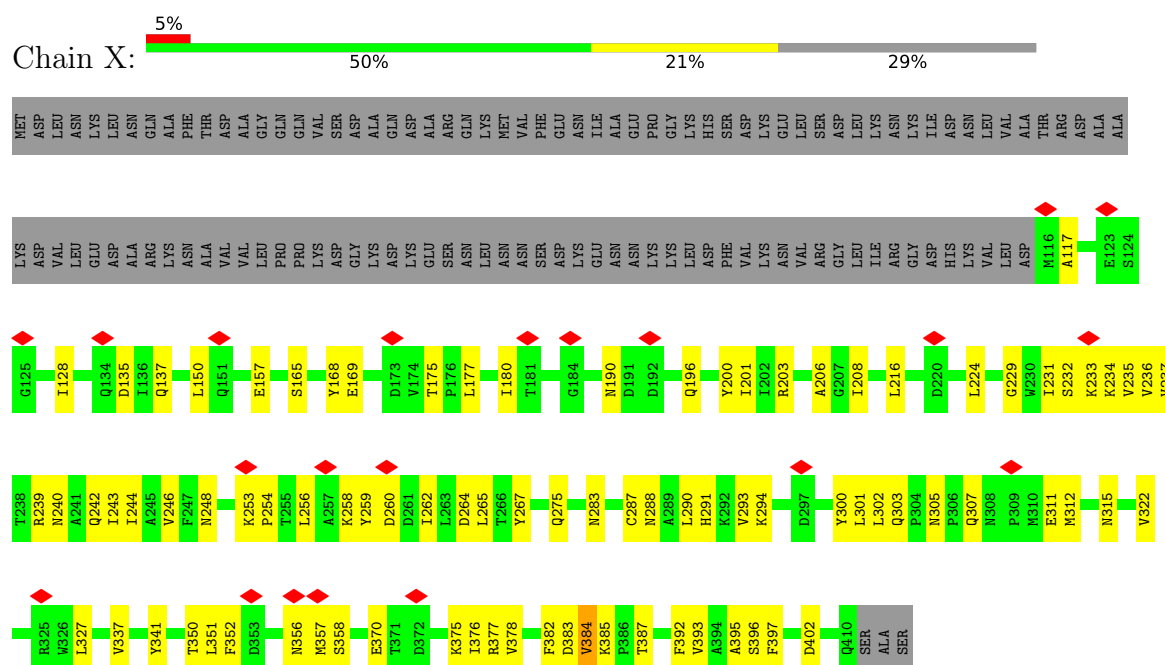


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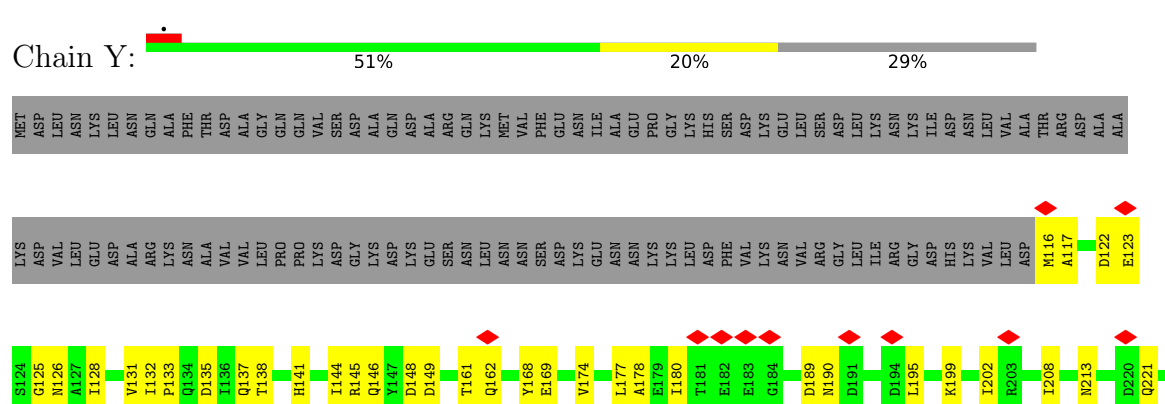


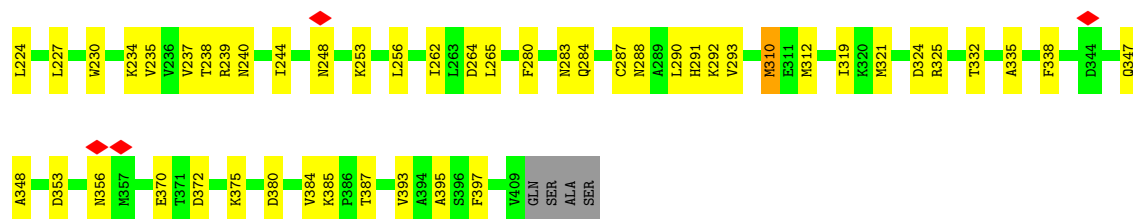


• Molecule 2: Major Capsid Protein

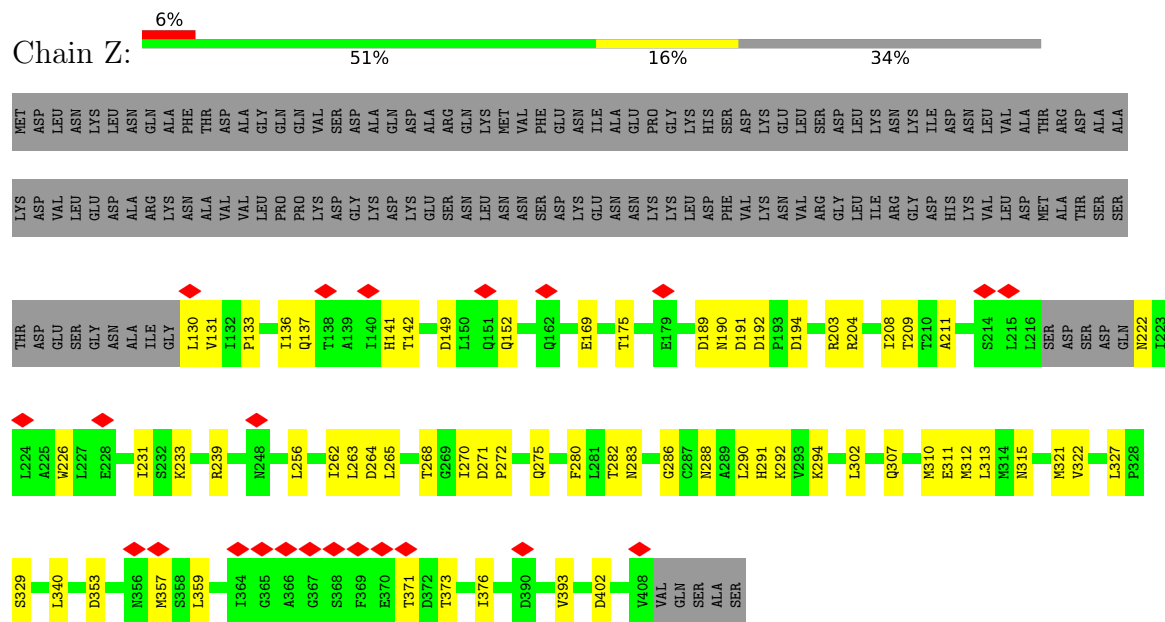


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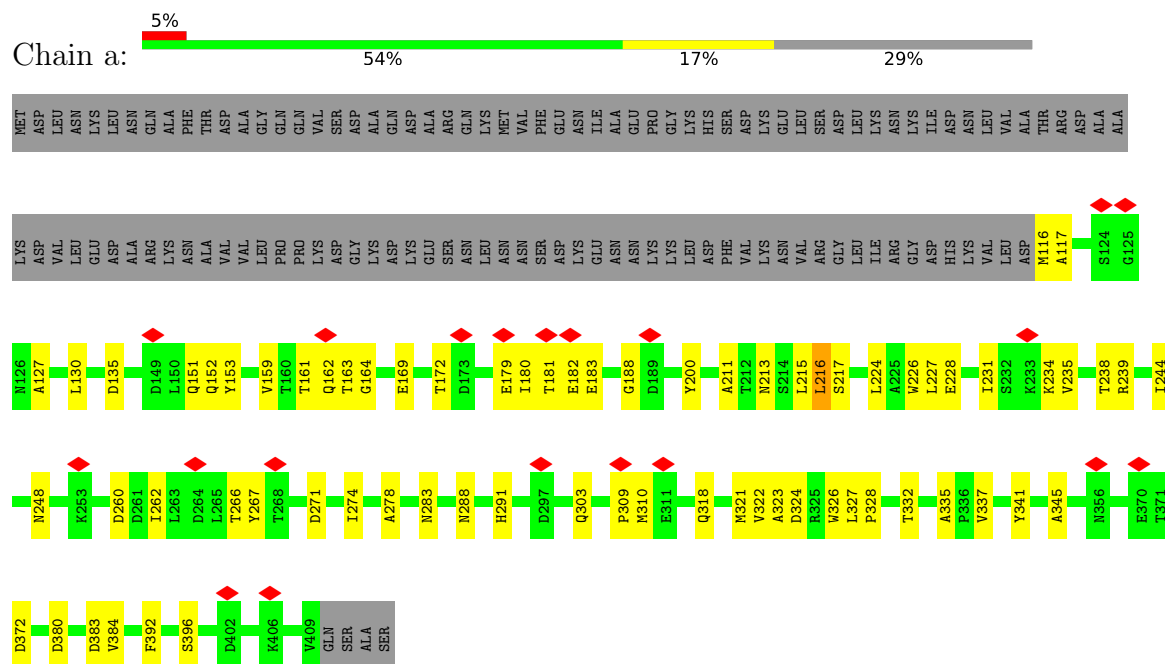




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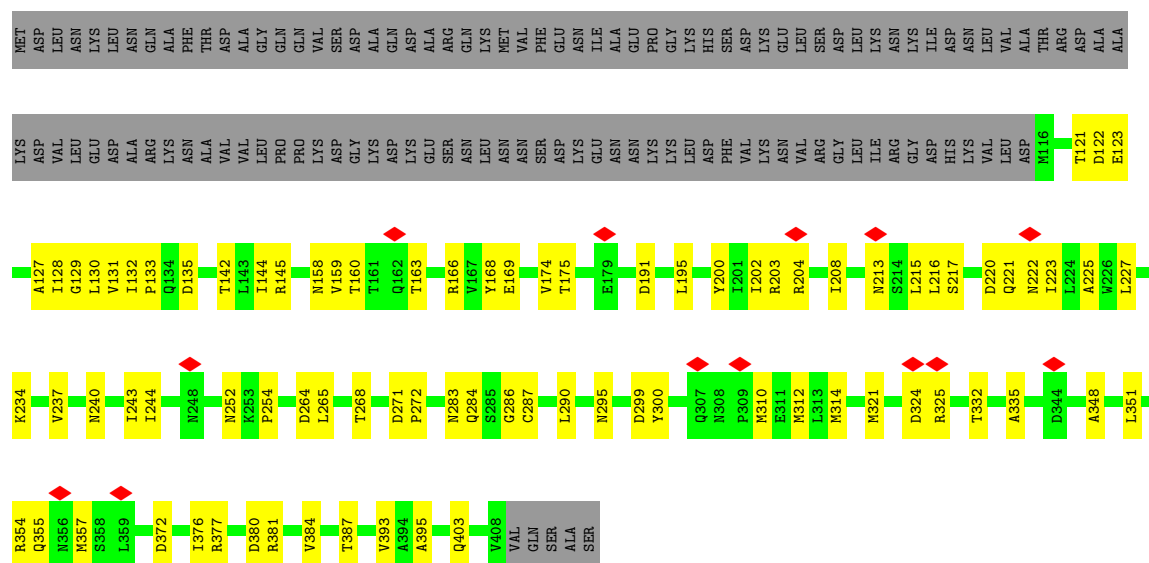


• Molecule 2: Major Capsid Protein



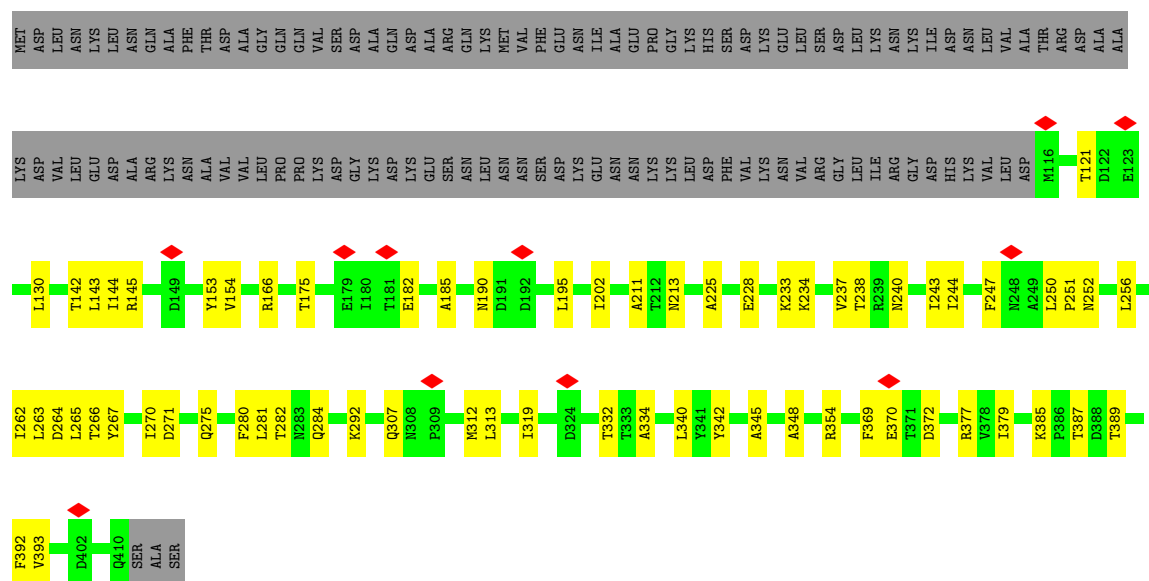
• Molecule 2: Major Capsid Protein

Chain b:  51% 20% 29%



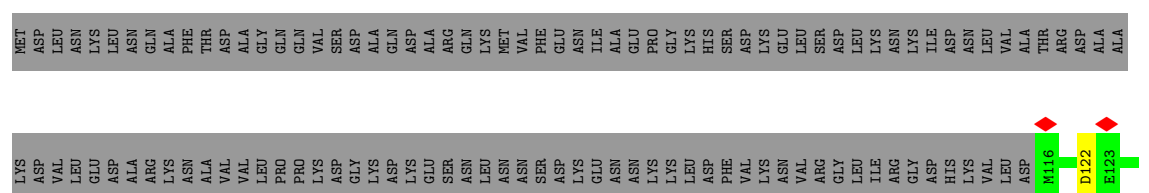
• Molecule 2: Major Capsid Protein

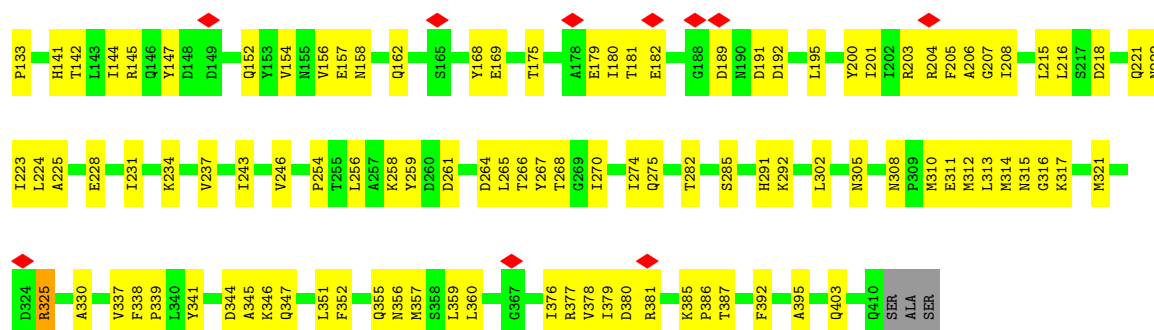
Chain c:  55% 16% 29%



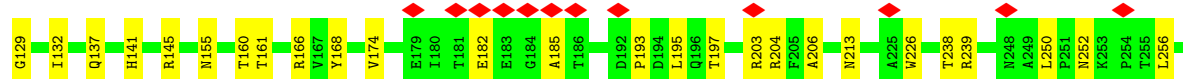
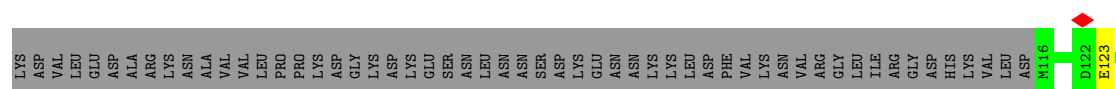
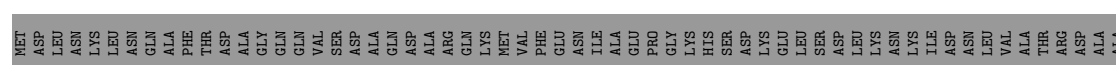
• Molecule 2: Major Capsid Protein

Chain d:  46% 25% 29%

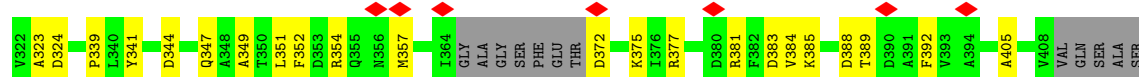
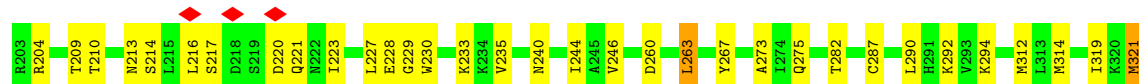
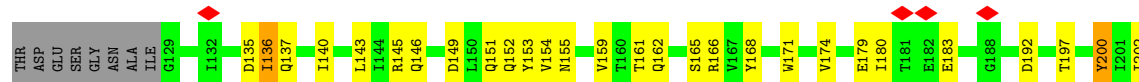
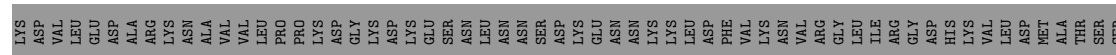
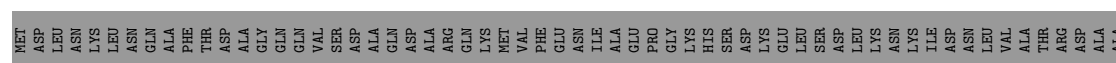




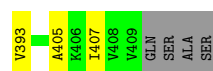
• Molecule 2: Major Capsid Protein



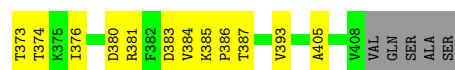
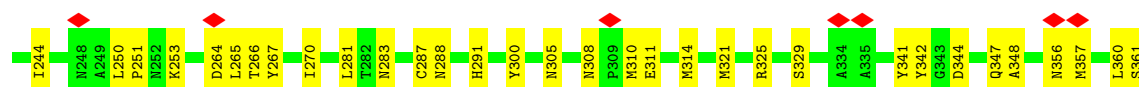
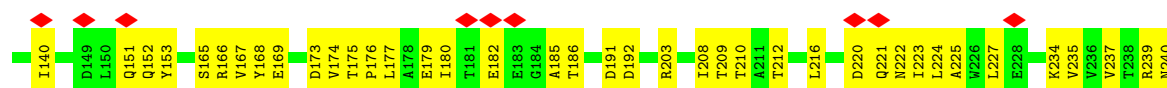
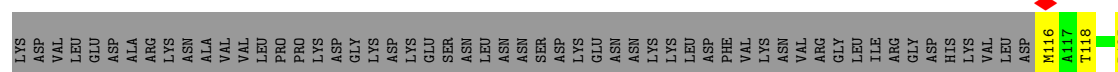
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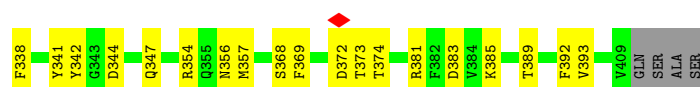
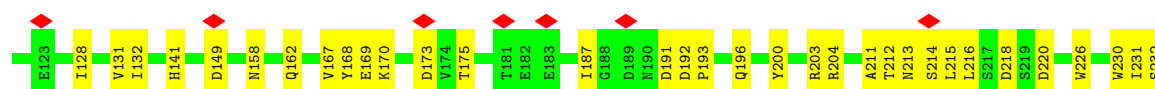
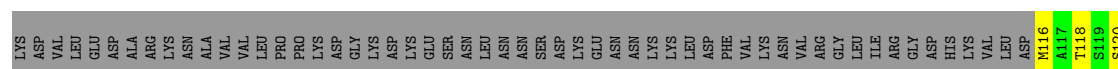




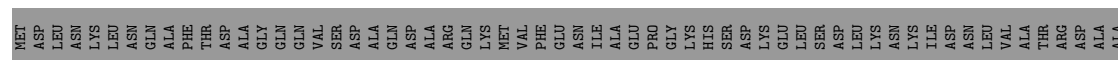
• Molecule 2: Major Capsid Protein

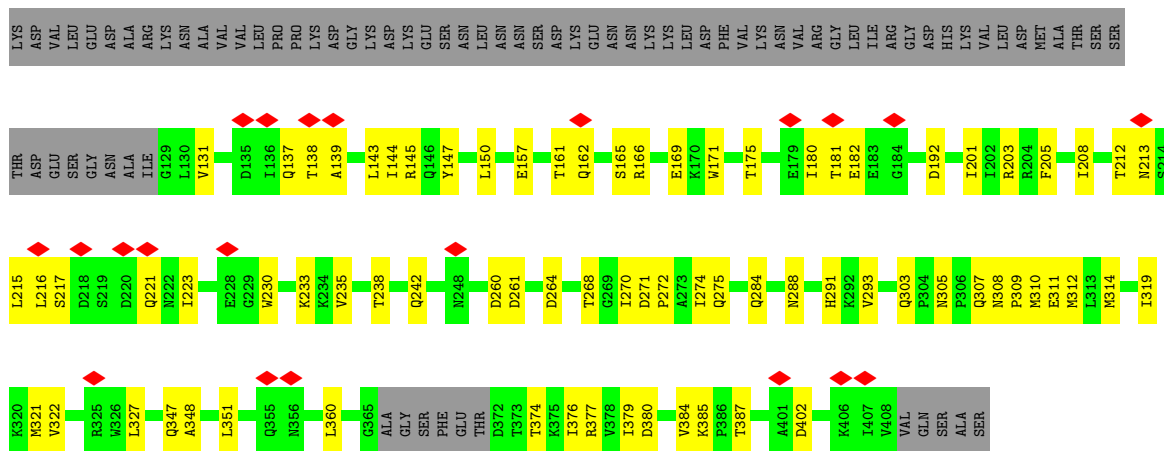


• Molecule 2: Major Capsid Protein

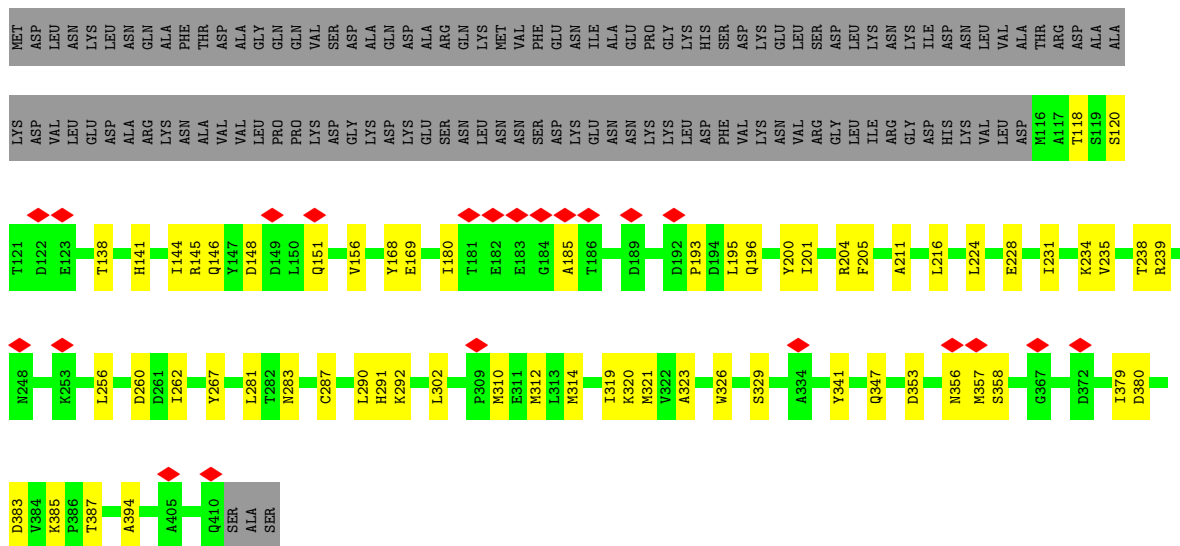


• Molecule 2: Major Capsid Protein

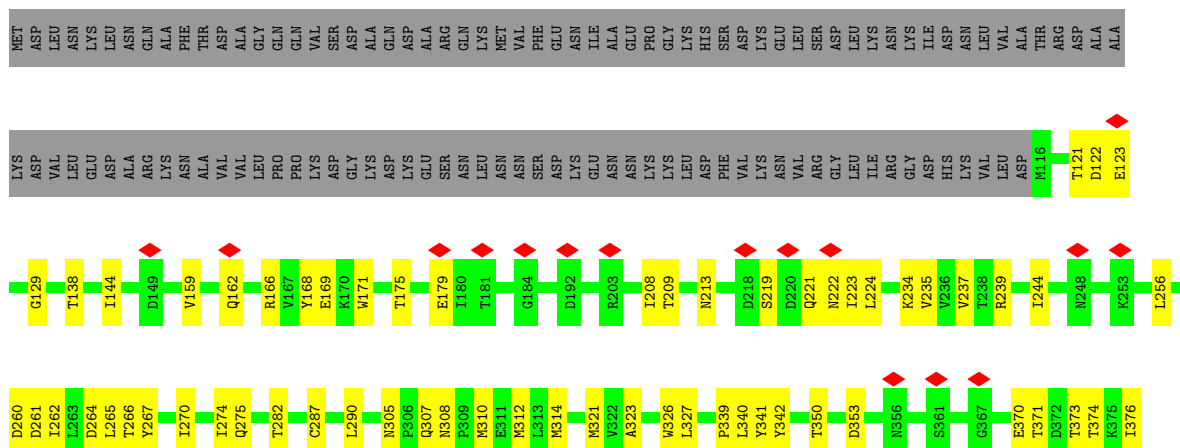




- Molecule 2: Major Capsid Protein



- Molecule 2: Major Capsid Protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5819	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.435	Depositor
Minimum map value	-0.249	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	563.808, 563.808, 563.808	wwPDB
Map dimensions	672, 672, 672	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.839, 0.839, 0.839	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	0.20	0/2540	0.42	0/3453
1	B	0.21	0/2579	0.48	1/3506 (0.0%)
1	C	0.22	0/2484	0.48	2/3376 (0.1%)
1	D	0.19	0/2473	0.39	0/3360
1	E	0.19	0/2601	0.43	0/3536
1	F	0.21	0/2503	0.45	0/3402
1	G	0.19	0/2479	0.41	0/3369
1	H	0.20	0/2598	0.43	0/3536
1	I	0.20	0/2650	0.43	1/3607 (0.0%)
1	J	0.18	0/2478	0.41	0/3369
1	K	0.21	0/2590	0.48	0/3528
1	L	0.22	0/2618	0.49	0/3562
2	M	0.19	0/2308	0.41	0/3151
2	N	0.20	0/2301	0.46	0/3141
2	O	0.19	0/2308	0.40	0/3151
2	P	0.19	0/2162	0.40	0/2951
2	Q	0.17	0/2314	0.37	0/3160
2	R	0.19	0/2313	0.42	0/3158
2	S	0.18	0/2288	0.41	0/3124
2	T	0.19	0/2293	0.44	0/3131
2	U	0.20	0/2308	0.42	0/3151
2	V	0.22	0/2154	0.55	4/2940 (0.1%)
2	W	0.20	0/2317	0.40	0/3163
2	X	0.18	0/2313	0.37	0/3158
2	Y	0.18	0/2308	0.39	0/3151
2	Z	0.18	0/2168	0.38	0/2960
2	a	0.17	0/2308	0.37	0/3151
2	b	0.18	0/2298	0.39	0/3138
2	c	0.17	0/2317	0.34	0/3163
2	d	0.20	0/2313	0.47	1/3158 (0.0%)
2	e	0.17	0/2308	0.36	0/3151
2	f	0.24	0/2158	0.51	1/2946 (0.0%)
2	g	0.18	0/2305	0.39	0/3148
2	h	0.21	0/2298	0.40	0/3138

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	0.17	0/2309	0.38	0/3153
2	j	0.18	0/2313	0.37	0/3158
2	k	0.17	0/2300	0.37	0/3141
2	l	0.17	0/2291	0.38	0/3129
2	m	0.18	0/2308	0.39	0/3151
2	n	0.19	0/2142	0.40	0/2925
2	o	0.19	0/2314	0.38	0/3160
2	p	0.20	0/2302	0.41	0/3144
All	All	0.19	0/99032	0.42	10/135048 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1
1	K	0	1
1	L	0	3
2	N	0	1
2	Q	0	1
2	Y	0	1
2	f	0	1
2	h	0	1
All	All	0	10

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	356	ASN	N-CA-C	-7.12	95.62	110.80
1	I	249	GLU	CA-CB-CG	6.01	126.12	114.10
2	V	355	GLN	CA-C-N	-5.83	110.40	121.54
2	V	355	GLN	C-N-CA	-5.83	110.40	121.54
2	V	354	ARG	CB-CG-CD	-5.60	98.42	111.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	37	HIS	Peptide

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Mol	Chain	Res	Type	Group
1	K	25	SER	Peptide
1	L	232	ALA	Peptide
1	L	25	SER	Peptide
1	L	37	HIS	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	2494	0	2429	90	0
1	B	2531	0	2462	80	0
1	C	2436	0	2411	116	0
1	D	2427	0	2403	86	0
1	E	2553	0	2497	98	0
1	F	2454	0	2416	97	0
1	G	2431	0	2409	84	0
1	H	2547	0	2481	102	0
1	I	2599	0	2532	100	0
1	J	2430	0	2400	81	0
1	K	2539	0	2472	105	0
1	L	2565	0	2512	122	0
2	M	2266	0	2238	64	0
2	N	2259	0	2229	67	0
2	O	2266	0	2238	85	0
2	P	2121	0	2098	61	0
2	Q	2272	0	2239	52	0
2	R	2271	0	2240	49	0
2	S	2246	0	2217	57	0
2	T	2251	0	2220	62	0
2	U	2266	0	2238	80	0
2	V	2113	0	2087	68	0
2	W	2275	0	2246	62	0
2	X	2271	0	2240	69	0
2	Y	2266	0	2238	71	0
2	Z	2127	0	2115	59	0
2	a	2266	0	2238	57	0
2	b	2256	0	2222	69	0
2	c	2275	0	2246	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	d	2271	0	2240	100	0
2	e	2266	0	2238	52	0
2	f	2118	0	2087	77	0
2	g	2263	0	2231	58	0
2	h	2256	0	2222	59	0
2	i	2267	0	2238	52	0
2	j	2271	0	2240	95	0
2	k	2258	0	2230	53	0
2	l	2249	0	2214	72	0
2	m	2266	0	2238	82	0
2	n	2102	0	2056	67	0
2	o	2272	0	2239	53	0
2	p	2260	0	2213	61	0
All	All	97192	0	95699	2573	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 13.

The worst 5 of 2573 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:K:210:PRO:HB3	1:K:242:GLU:HG2	1.36	1.04
2:i:372:ASP:OD2	2:o:204:ARG:NH1	1.97	0.97
1:H:65:LYS:HZ1	1:H:67:LYS:HE2	1.31	0.94
2:d:231:ILE:HG21	2:d:378:VAL:HG11	1.48	0.94
1:L:191:GLN:HE22	1:L:195:LYS:HE2	1.35	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	326/389 (84%)	311 (95%)	15 (5%)	0	100	100
1	B	329/389 (85%)	311 (94%)	17 (5%)	1 (0%)	36	65
1	C	312/389 (80%)	302 (97%)	10 (3%)	0	100	100
1	D	312/389 (80%)	302 (97%)	10 (3%)	0	100	100
1	E	332/389 (85%)	325 (98%)	7 (2%)	0	100	100
1	F	315/389 (81%)	302 (96%)	13 (4%)	0	100	100
1	G	311/389 (80%)	304 (98%)	7 (2%)	0	100	100
1	H	330/389 (85%)	311 (94%)	18 (6%)	1 (0%)	36	65
1	I	338/389 (87%)	320 (95%)	16 (5%)	2 (1%)	21	54
1	J	312/389 (80%)	306 (98%)	6 (2%)	0	100	100
1	K	330/389 (85%)	313 (95%)	16 (5%)	1 (0%)	36	65
1	L	330/389 (85%)	310 (94%)	20 (6%)	0	100	100
2	M	292/413 (71%)	265 (91%)	27 (9%)	0	100	100
2	N	291/413 (70%)	264 (91%)	27 (9%)	0	100	100
2	O	292/413 (71%)	262 (90%)	29 (10%)	1 (0%)	36	65
2	P	271/413 (66%)	248 (92%)	23 (8%)	0	100	100
2	Q	293/413 (71%)	268 (92%)	25 (8%)	0	100	100
2	R	293/413 (71%)	277 (94%)	15 (5%)	1 (0%)	36	65
2	S	289/413 (70%)	263 (91%)	26 (9%)	0	100	100
2	T	290/413 (70%)	267 (92%)	21 (7%)	2 (1%)	18	51
2	U	292/413 (71%)	276 (94%)	16 (6%)	0	100	100
2	V	270/413 (65%)	251 (93%)	18 (7%)	1 (0%)	30	61
2	W	293/413 (71%)	274 (94%)	19 (6%)	0	100	100
2	X	293/413 (71%)	280 (96%)	12 (4%)	1 (0%)	36	65
2	Y	292/413 (71%)	276 (94%)	15 (5%)	1 (0%)	36	65
2	Z	270/413 (65%)	247 (92%)	22 (8%)	1 (0%)	30	61
2	a	292/413 (71%)	274 (94%)	18 (6%)	0	100	100
2	b	291/413 (70%)	282 (97%)	9 (3%)	0	100	100
2	c	293/413 (71%)	286 (98%)	7 (2%)	0	100	100
2	d	293/413 (71%)	261 (89%)	32 (11%)	0	100	100
2	e	292/413 (71%)	275 (94%)	17 (6%)	0	100	100
2	f	269/413 (65%)	248 (92%)	20 (7%)	1 (0%)	30	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	g	292/413 (71%)	276 (94%)	16 (6%)	0	100	100
2	h	291/413 (70%)	271 (93%)	20 (7%)	0	100	100
2	i	293/413 (71%)	281 (96%)	12 (4%)	0	100	100
2	j	293/413 (71%)	280 (96%)	12 (4%)	1 (0%)	36	65
2	k	292/413 (71%)	274 (94%)	18 (6%)	0	100	100
2	l	291/413 (70%)	275 (94%)	16 (6%)	0	100	100
2	m	292/413 (71%)	279 (96%)	13 (4%)	0	100	100
2	n	270/413 (65%)	246 (91%)	23 (8%)	1 (0%)	30	61
2	o	293/413 (71%)	283 (97%)	10 (3%)	0	100	100
2	p	293/413 (71%)	278 (95%)	15 (5%)	0	100	100
All	All	12528/17058 (73%)	11804 (94%)	708 (6%)	16 (0%)	49	79

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	23	GLN
1	K	39	ILE
2	Z	137	GLN
2	f	136	ILE
2	j	159	VAL

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	265/334 (79%)	265 (100%)	0	100	100
1	B	269/334 (80%)	268 (100%)	1 (0%)	84	81
1	C	267/334 (80%)	267 (100%)	0	100	100
1	D	266/334 (80%)	266 (100%)	0	100	100
1	E	276/334 (83%)	275 (100%)	1 (0%)	84	81
1	F	267/334 (80%)	267 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	267/334 (80%)	265 (99%)	2 (1%)	76	78
1	H	275/334 (82%)	273 (99%)	2 (1%)	76	78
1	I	282/334 (84%)	282 (100%)	0	100	100
1	J	266/334 (80%)	266 (100%)	0	100	100
1	K	276/334 (83%)	275 (100%)	1 (0%)	84	81
1	L	280/334 (84%)	279 (100%)	1 (0%)	84	81
2	M	249/352 (71%)	249 (100%)	0	100	100
2	N	248/352 (70%)	248 (100%)	0	100	100
2	O	249/352 (71%)	249 (100%)	0	100	100
2	P	232/352 (66%)	232 (100%)	0	100	100
2	Q	249/352 (71%)	248 (100%)	1 (0%)	84	81
2	R	249/352 (71%)	249 (100%)	0	100	100
2	S	247/352 (70%)	247 (100%)	0	100	100
2	T	247/352 (70%)	246 (100%)	1 (0%)	84	81
2	U	249/352 (71%)	249 (100%)	0	100	100
2	V	231/352 (66%)	228 (99%)	3 (1%)	61	72
2	W	250/352 (71%)	248 (99%)	2 (1%)	73	77
2	X	249/352 (71%)	249 (100%)	0	100	100
2	Y	249/352 (71%)	249 (100%)	0	100	100
2	Z	232/352 (66%)	231 (100%)	1 (0%)	84	81
2	a	249/352 (71%)	248 (100%)	1 (0%)	84	81
2	b	247/352 (70%)	247 (100%)	0	100	100
2	c	250/352 (71%)	250 (100%)	0	100	100
2	d	249/352 (71%)	249 (100%)	0	100	100
2	e	249/352 (71%)	248 (100%)	1 (0%)	84	81
2	f	231/352 (66%)	229 (99%)	2 (1%)	70	76
2	g	248/352 (70%)	248 (100%)	0	100	100
2	h	247/352 (70%)	247 (100%)	0	100	100
2	i	248/352 (70%)	248 (100%)	0	100	100
2	j	249/352 (71%)	249 (100%)	0	100	100
2	k	247/352 (70%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	l	246/352 (70%)	246 (100%)	0	100	100
2	m	249/352 (71%)	249 (100%)	0	100	100
2	n	225/352 (64%)	224 (100%)	1 (0%)	84	81
2	o	249/352 (71%)	249 (100%)	0	100	100
2	p	245/352 (70%)	245 (100%)	0	100	100
All	All	10614/14568 (73%)	10593 (100%)	21 (0%)	85	85

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	W	301	LEU
2	e	252	ASN
2	n	157	GLU
2	f	263	LEU
2	a	216	LEU

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

Mol	Chain	Res	Type
2	l	318	GLN
2	n	151	GLN
2	O	126	ASN
2	N	162	GLN
2	n	284	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

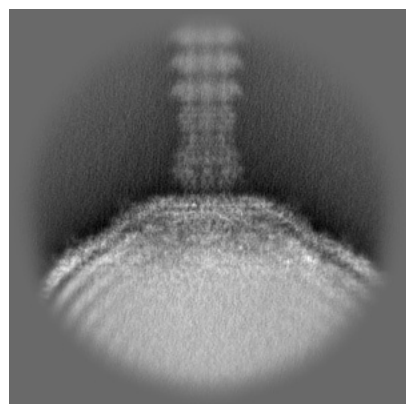
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-58150. These allow visual inspection of the internal detail of the map and identification of artifacts.

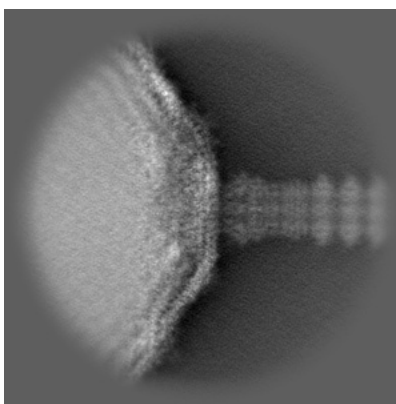
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

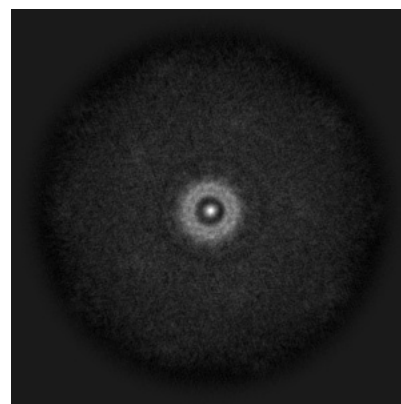
6.1.1 Primary map



X

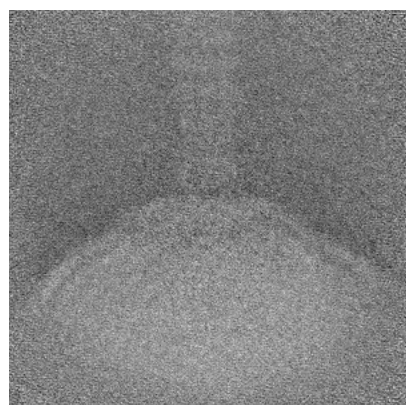


Y

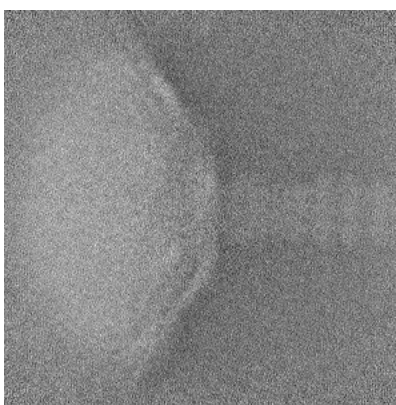


Z

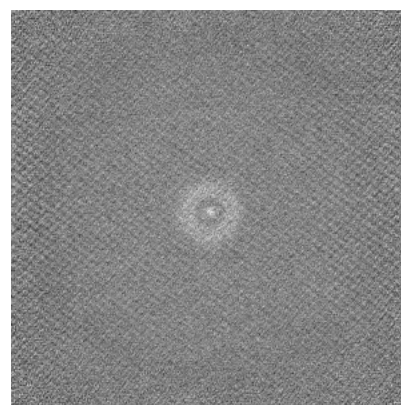
6.1.2 Raw map



X



Y

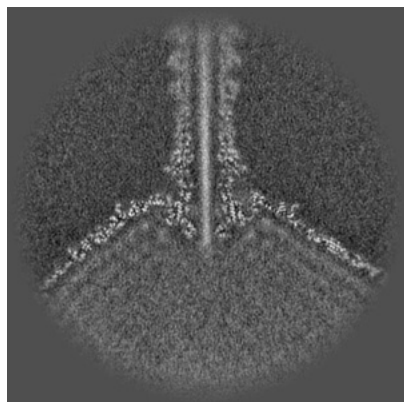


Z

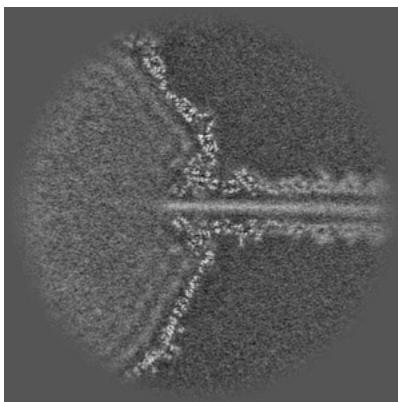
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

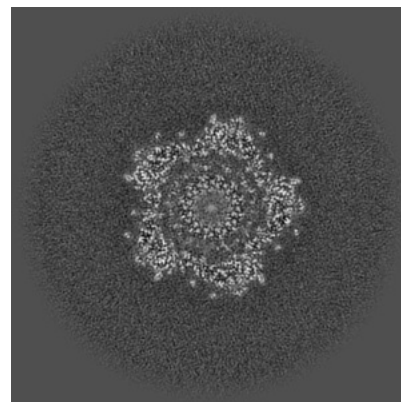
6.2.1 Primary map



X Index: 336

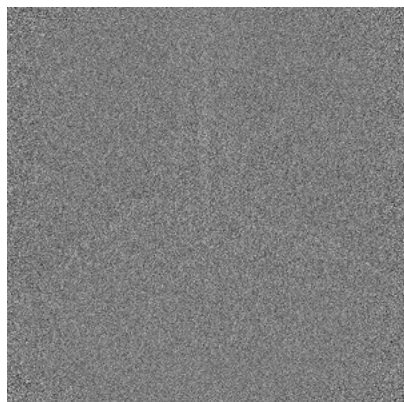


Y Index: 336

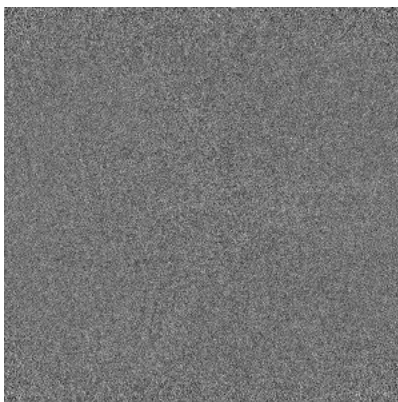


Z Index: 336

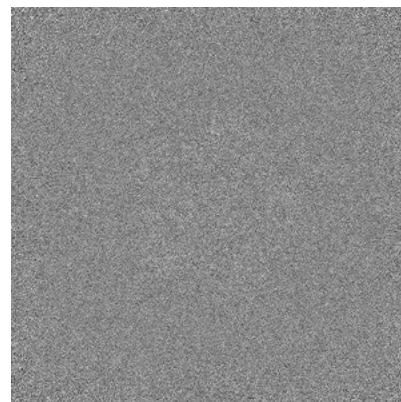
6.2.2 Raw map



X Index: 336



Y Index: 336

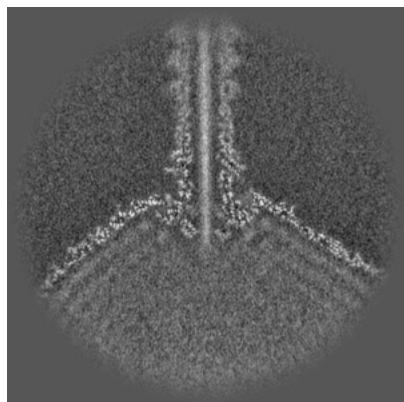


Z Index: 336

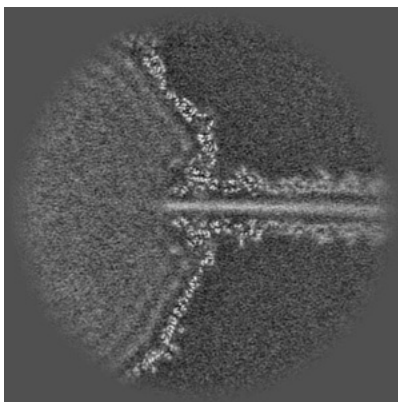
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

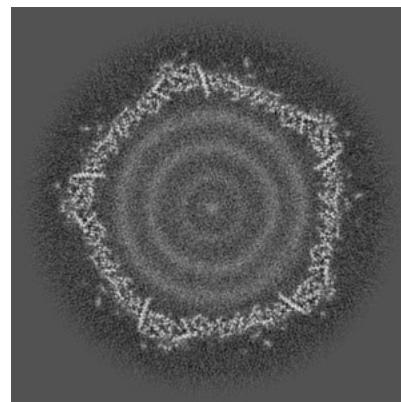
6.3.1 Primary map



X Index: 334

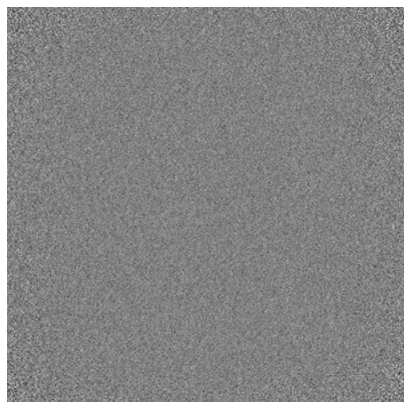


Y Index: 335

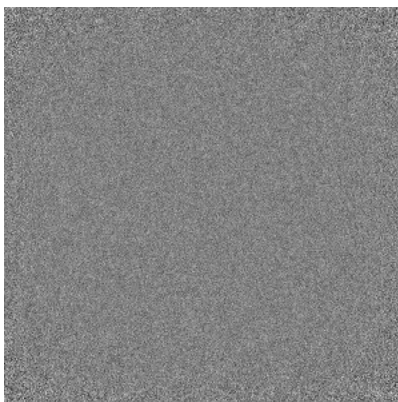


Z Index: 271

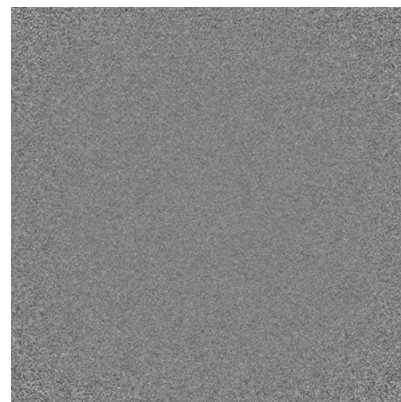
6.3.2 Raw map



X Index: 0



Y Index: 0

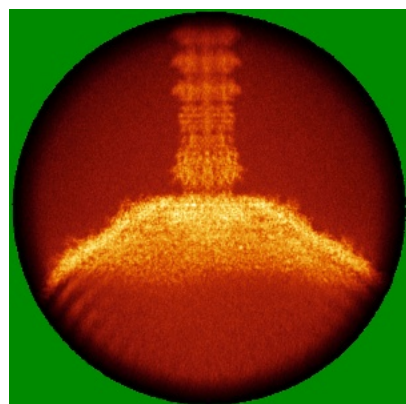


Z Index: 0

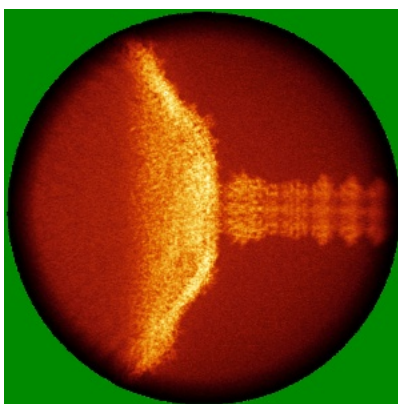
The images above show the largest variance slices of the map in three orthogonal directions.

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

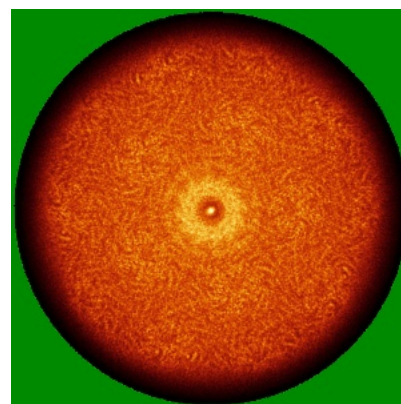
6.4.1 Primary map



X

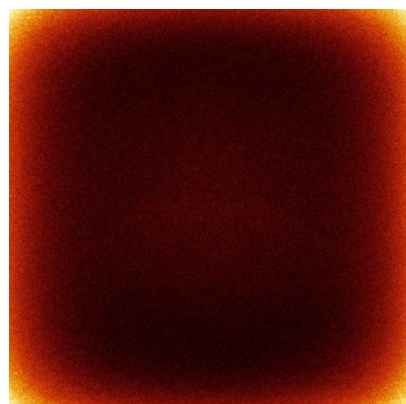


Y

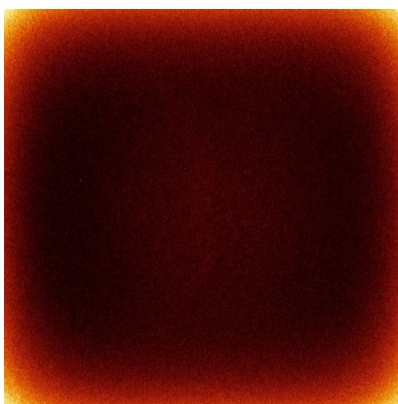


Z

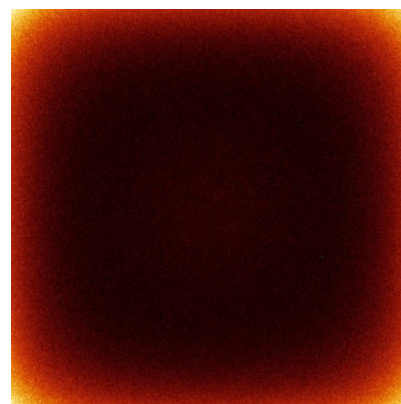
6.4.2 Raw map



X



Y

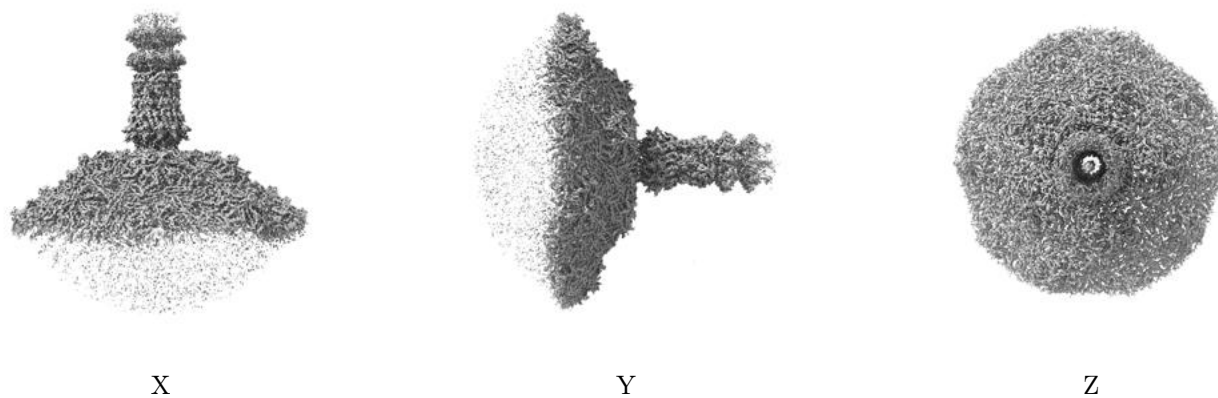


Z

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.

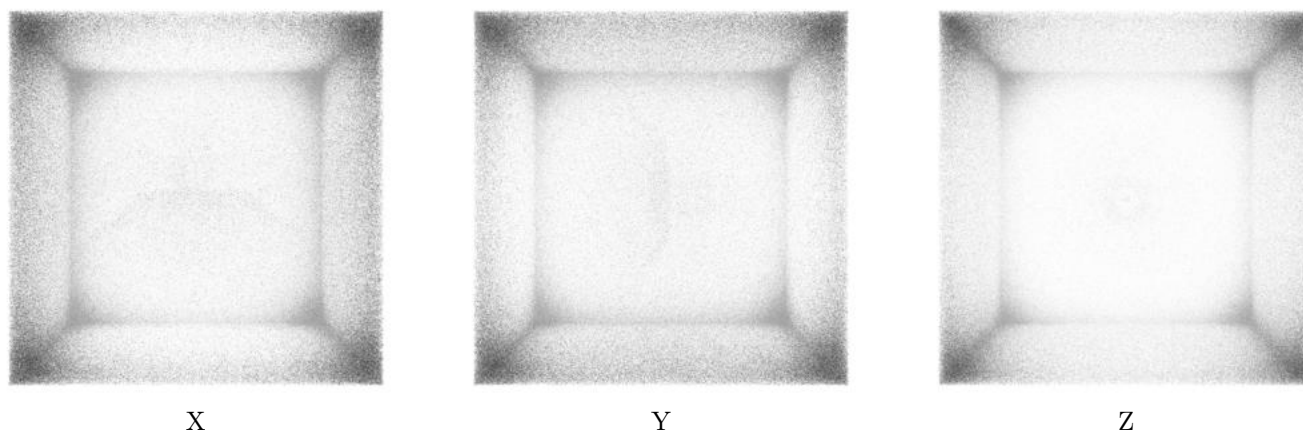
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. 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.

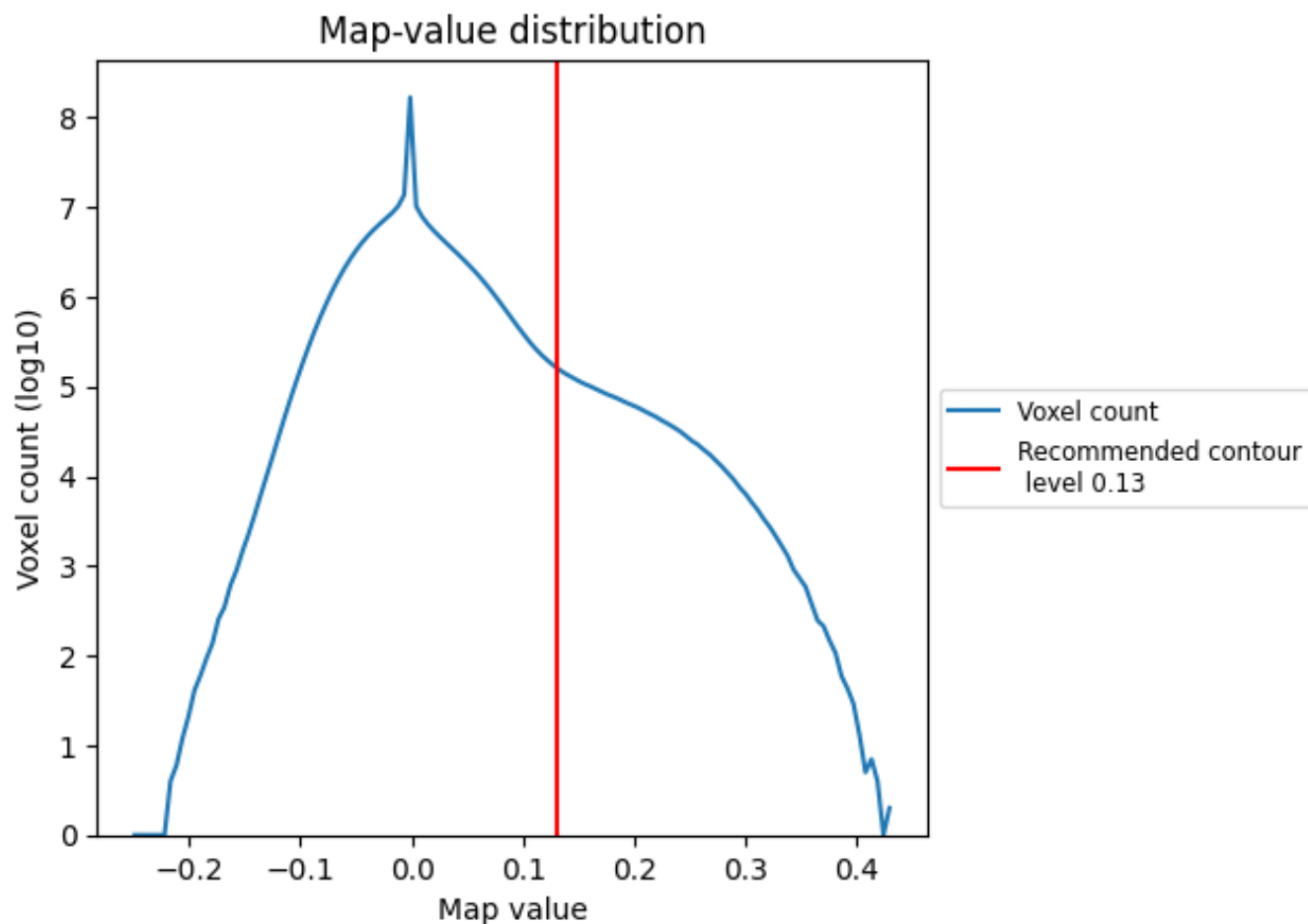
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

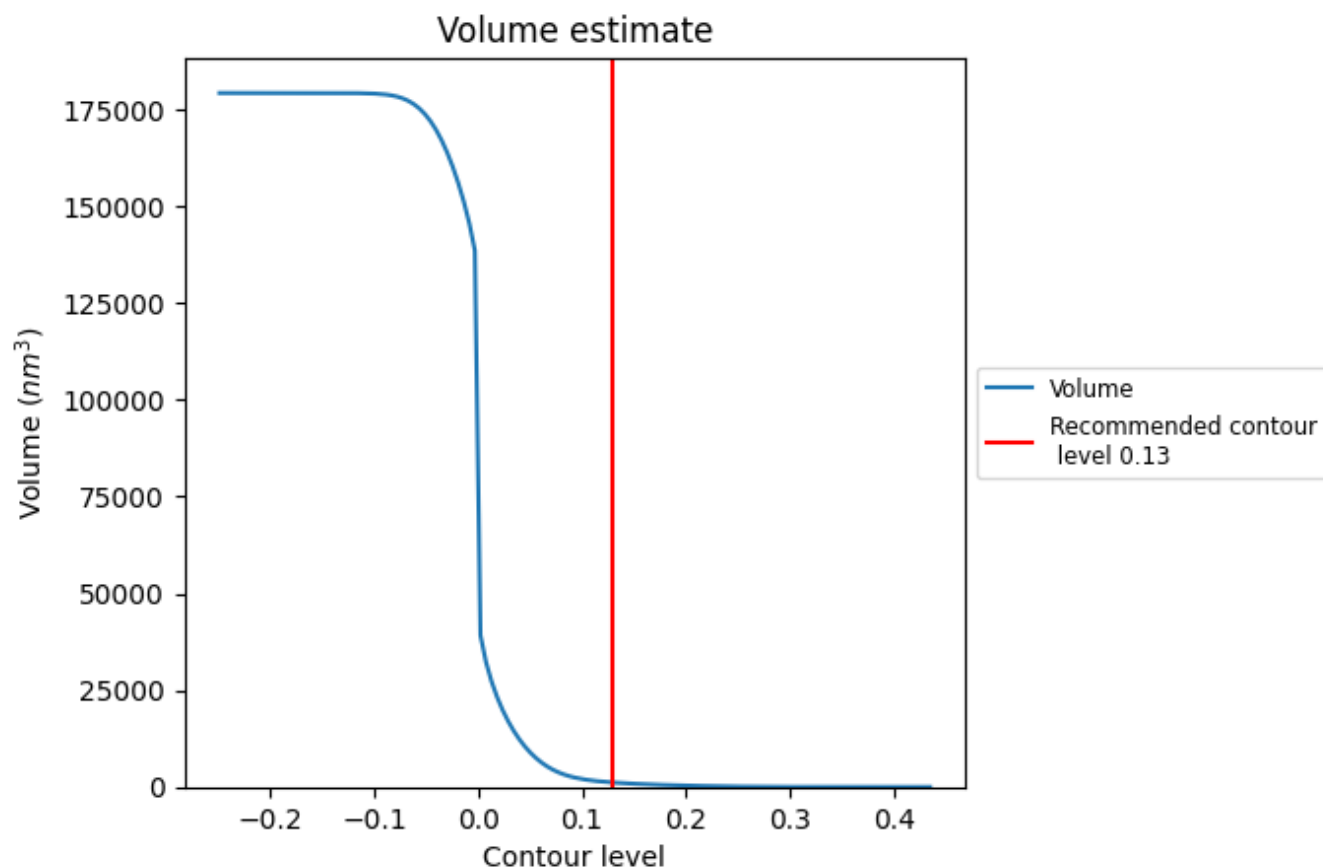
This section contains the results of statistical analysis of the map.

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.

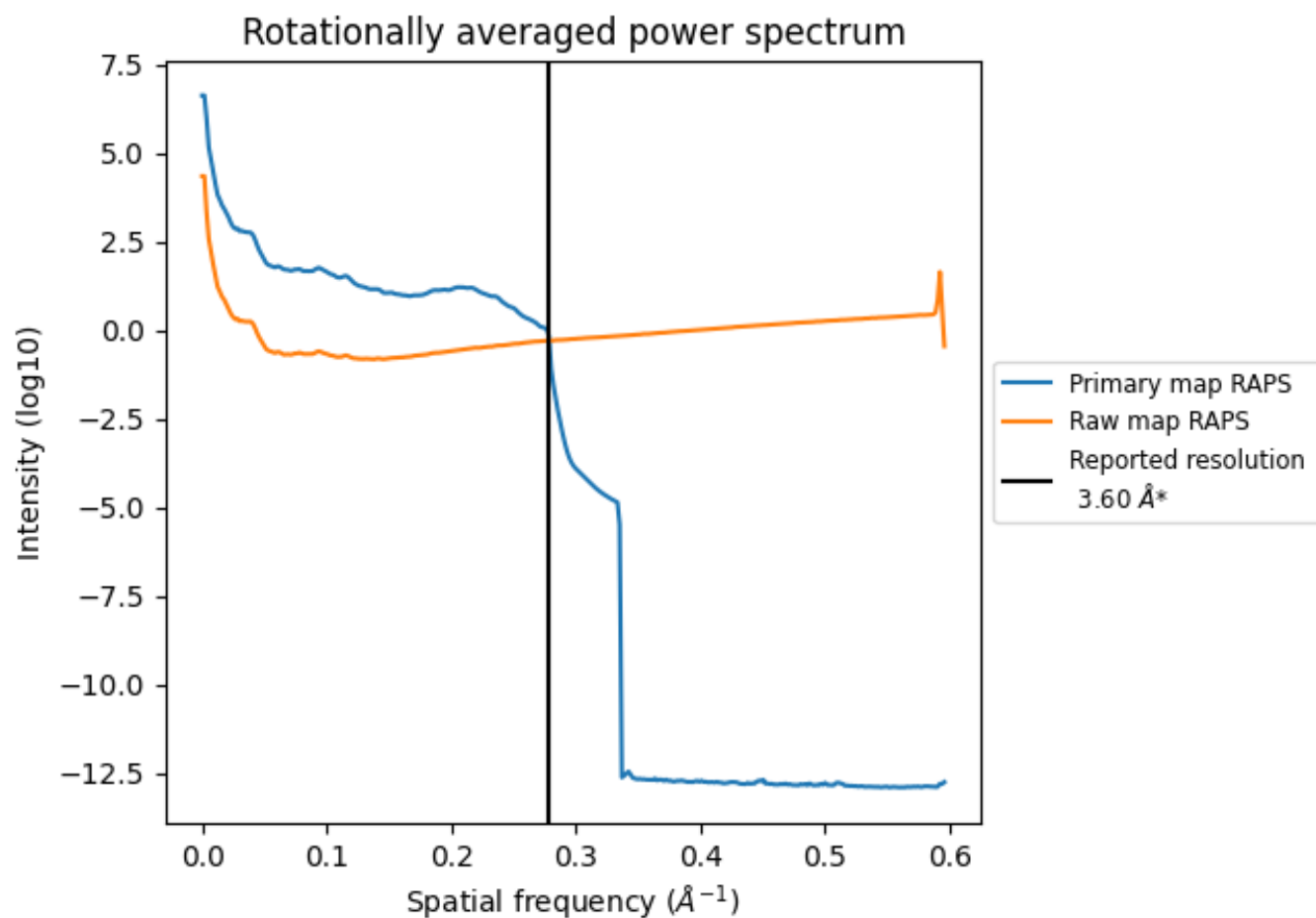
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1145 nm^3 ; this corresponds to an approximate mass of 1035 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 ⓘ

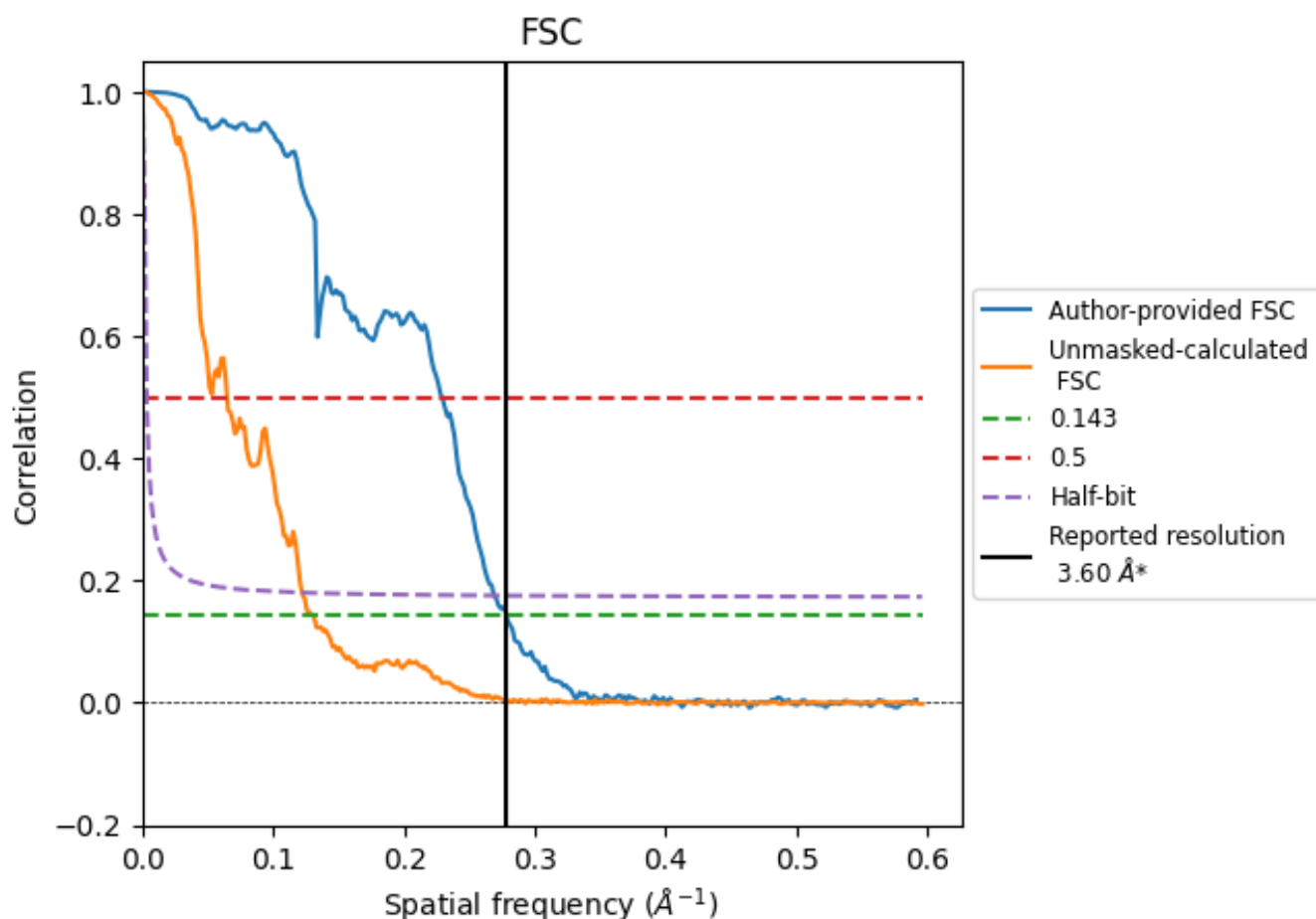


*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

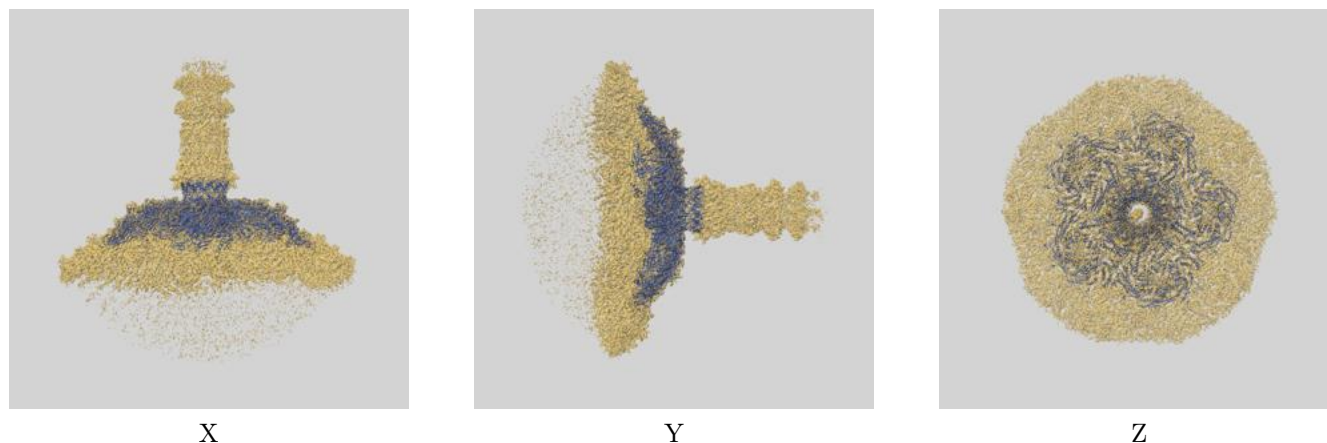
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.37	3.72
Unmasked-calculated*	7.70	15.43	8.19

*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 7.70 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

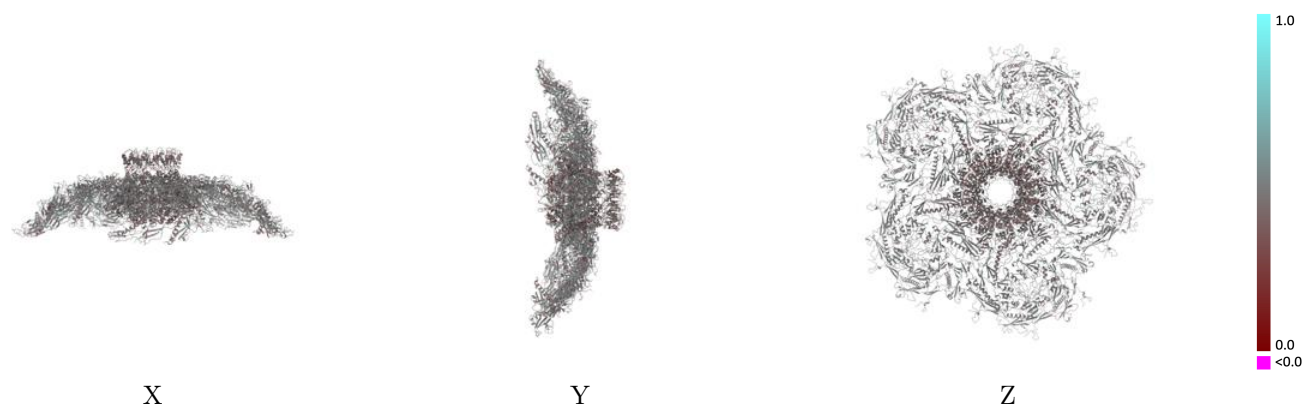
This section contains information regarding the fit between EMDB map EMD-58150 and PDB model 30YT. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



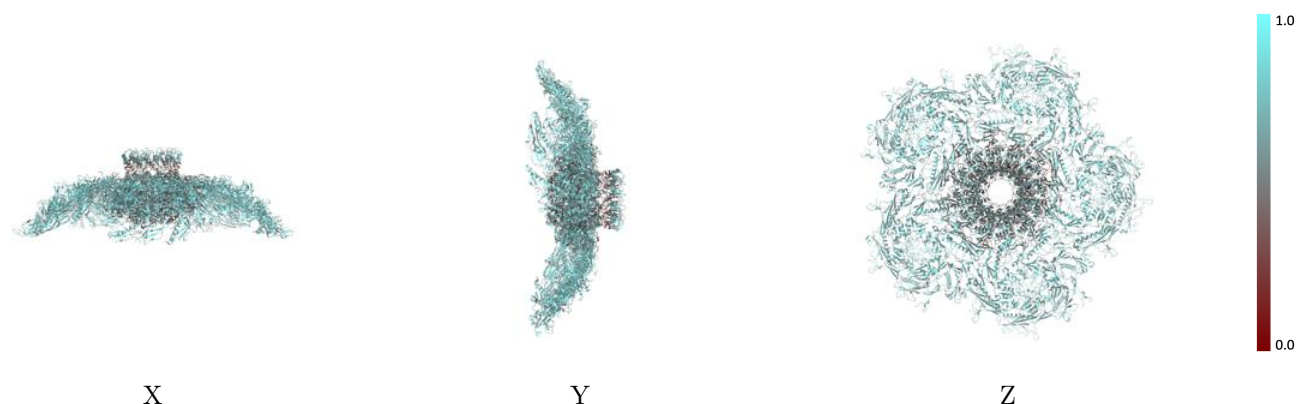
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



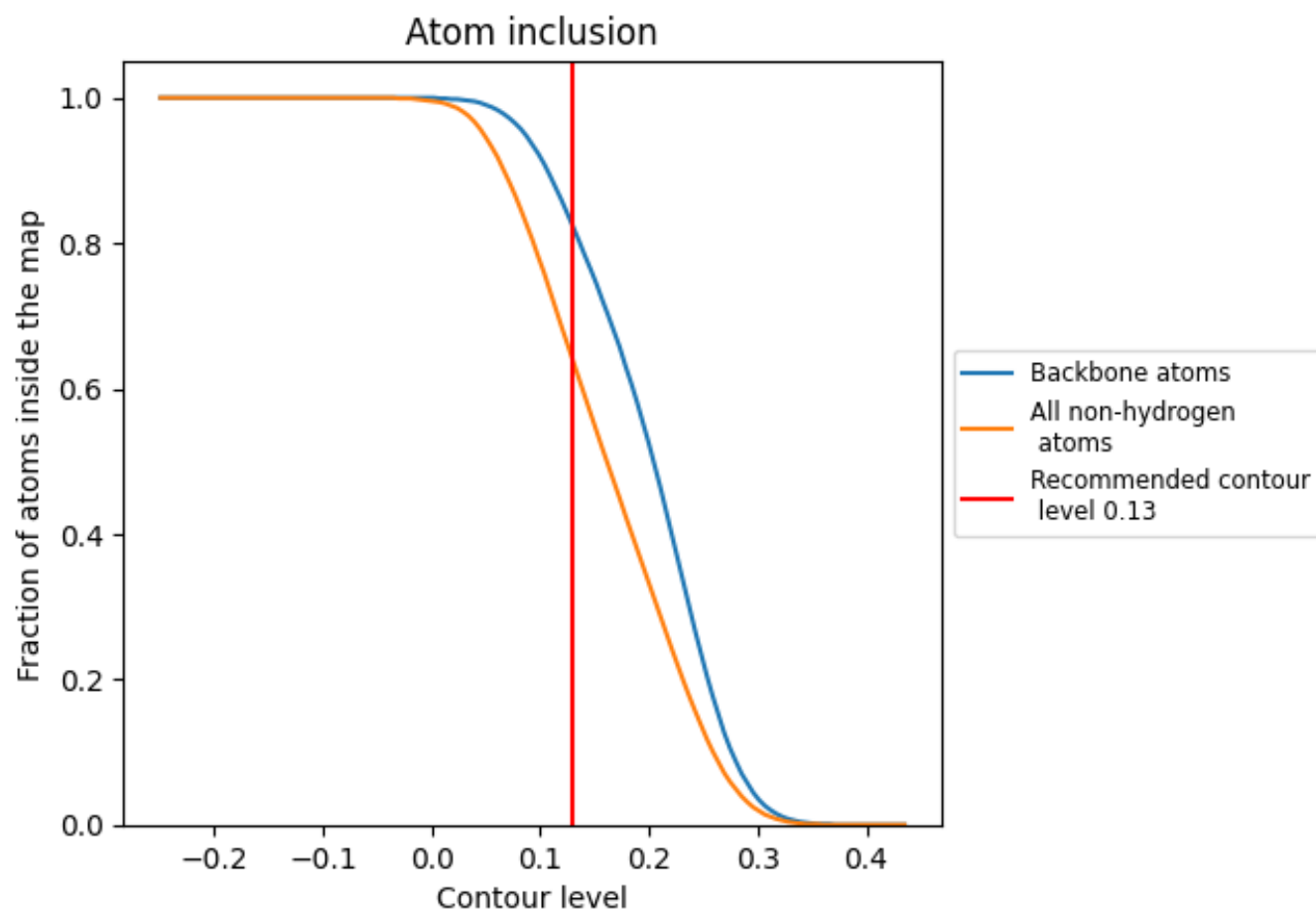
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 64% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.4530
A	 0.5590	 0.4300
B	 0.5600	 0.4380
C	 0.5370	 0.4260
D	 0.5530	 0.4320
E	 0.5120	 0.4190
F	 0.5760	 0.4400
G	 0.5300	 0.4290
H	 0.5640	 0.4340
I	 0.5250	 0.4220
J	 0.5530	 0.4290
K	 0.5430	 0.4260
L	 0.5510	 0.4270
M	 0.6990	 0.4640
N	 0.6860	 0.4580
O	 0.6780	 0.4570
P	 0.6570	 0.4600
Q	 0.6740	 0.4670
R	 0.6780	 0.4610
S	 0.6870	 0.4720
T	 0.6760	 0.4570
U	 0.6820	 0.4640
V	 0.6720	 0.4640
W	 0.6920	 0.4700
X	 0.6650	 0.4540
Y	 0.6810	 0.4700
Z	 0.6720	 0.4620
a	 0.6710	 0.4600
b	 0.6690	 0.4580
c	 0.7040	 0.4770
d	 0.6860	 0.4670
e	 0.6820	 0.4700
f	 0.6720	 0.4650
g	 0.6670	 0.4590
h	 0.6770	 0.4620



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Chain	Atom inclusion	Q-score
i	 0.6870	 0.4740
j	 0.6900	 0.4710
k	 0.6920	 0.4670
l	 0.6710	 0.4650
m	 0.6940	 0.4650
n	 0.6770	 0.4550
o	 0.6820	 0.4700
p	 0.6760	 0.4580