



wwPDB EM Validation Summary Report ⓘ

Aug 8, 2026 – 09:49 AM EDT

PDB ID : 11ML / pdb_000011ml
EMDB ID : EMD-75837
Title : Bacteriophage Goslar Empty Capsid Asymmetric Unit
Authors : Basu, D.; Gu, Y.; Corbett, K.D.
Deposited on : 2026-03-05
Resolution : 5.16 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.dev133
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) : 2.50

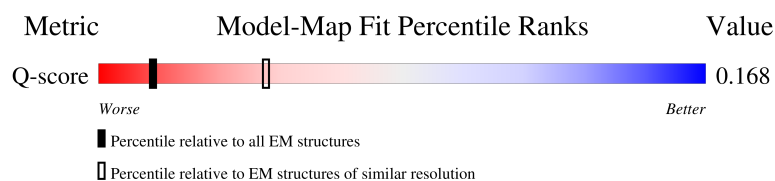
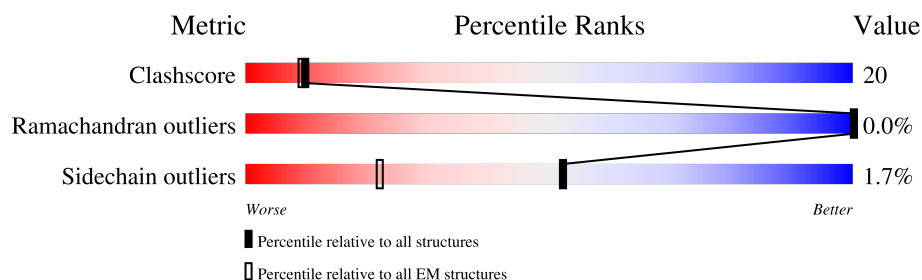
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.16 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.



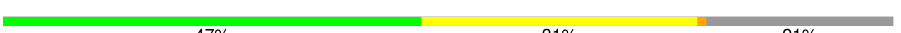
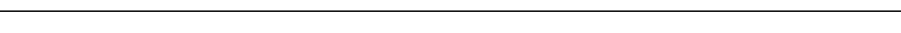
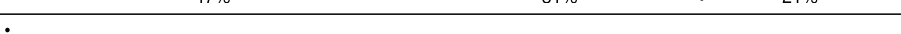
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	690 (4.66 - 5.65)

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	A0	740	 46% 32% • 21%
1	A1	740	 46% 32% • 21%
1	A2	740	 52% 26% • 21%
1	A3	740	 52% 26% 21%

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Mol	Chain	Length	Quality of chain
1	A4	740	
1	A5	740	
1	A6	740	
1	A7	740	
1	A8	740	
1	A9	740	
1	Ar	740	
1	As	740	
1	At	740	
1	Au	740	
1	Av	740	
1	Aw	740	
1	Ax	740	
1	Ay	740	
1	Az	740	
1	BA	740	
1	BB	740	
1	BC	740	
1	BD	740	
1	BE	740	
1	BF	740	
1	BG	740	
1	BH	740	
2	B	104	
3	G	212	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 127476 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A1	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A2	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A3	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A4	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A5	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A6	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A7	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A8	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	A9	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	Ar	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	As	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	At	576	Total	C	N	O	S	0	0
			4593	2902	799	875	17		
1	Au	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	Av	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	Aw	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	Ax	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ay	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	Az	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BA	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BB	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BC	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BD	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BE	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BF	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BG	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
1	BH	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		

- Molecule 2 is a protein called Capsid Latch gp146.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	96	Total	C	N	O	S	0	0
			759	470	137	150	2		

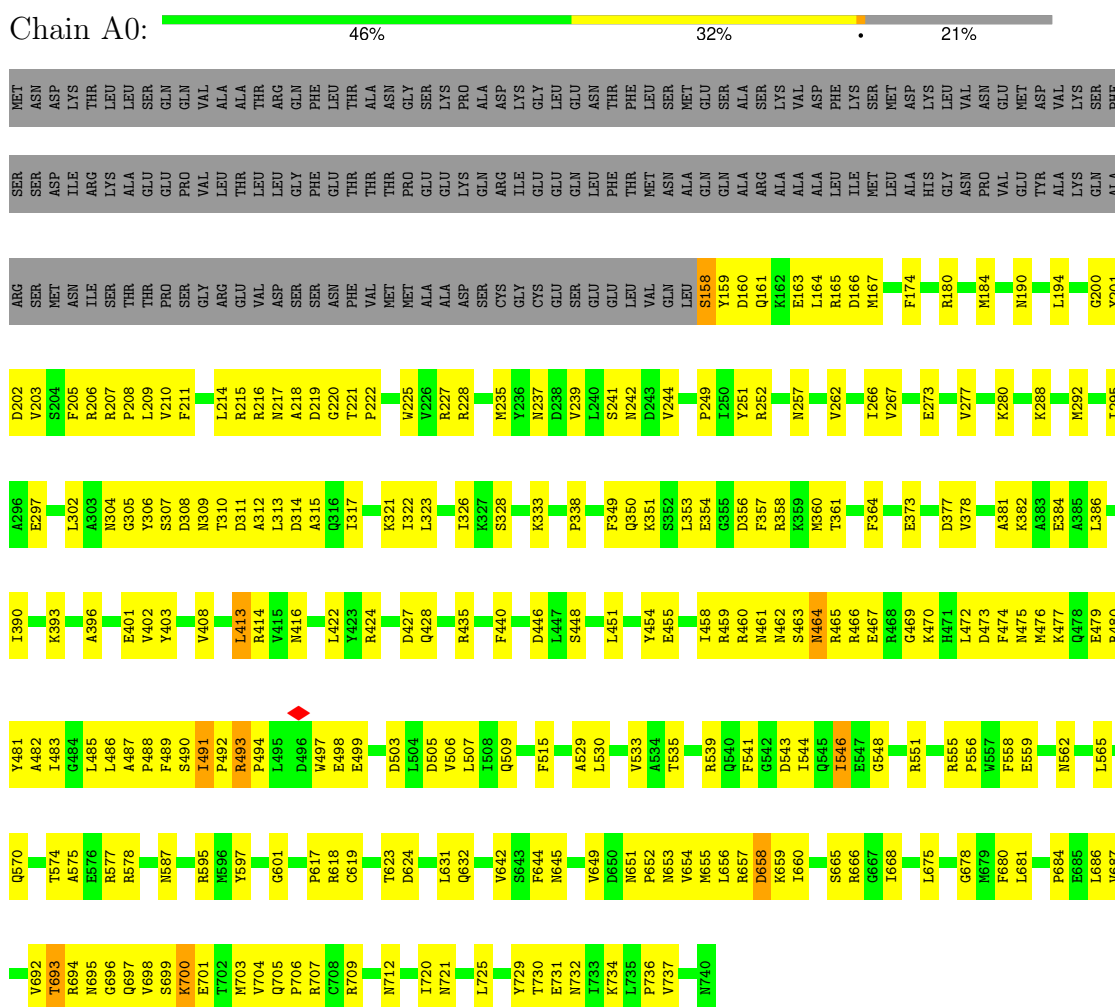
- Molecule 3 is a protein called Capsid Decorator gp77.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	147	Total	C	N	O	S	0	0
			1198	763	212	216	7		

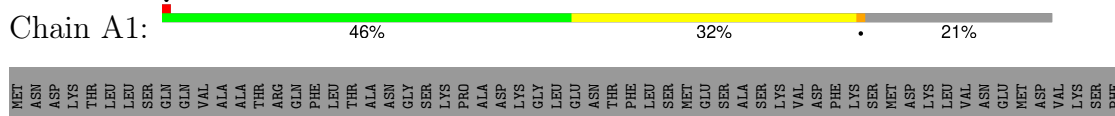
3 Residue-property plots

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

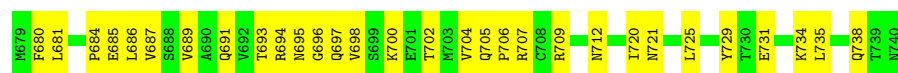
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein

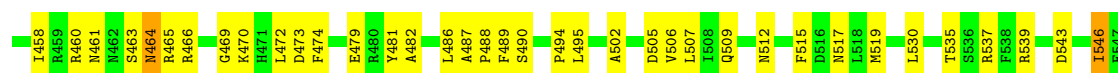
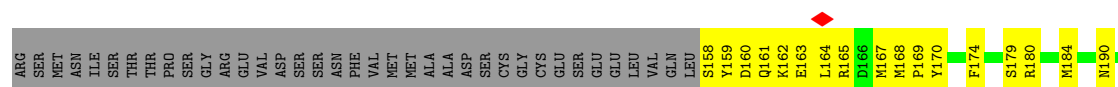
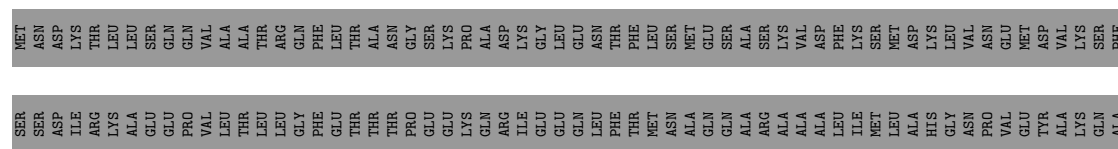


SER	SER	ARG	F205	T293	A381	G469	N557	I668	SER	ARG	N190	I301	L451	D543
SER	ASP	SER	R206	G294	K382	K470	F558	L675	SER	SER	L194	L302	Y454	I546
ASP	MET	MET	R207	I295	A383	H471	E559	L676	ASP	MET	L199	G305	I458	E547
ILE	ASN	ASN	F208	A296	E384	L472	N562	G678	ILE	ASP	G200	Y306	G548	G548
ARG	ARG	ILE	L209	E297	A385	F473	N565	N679	ARG	SER	Y201	S307	R459	G548
LYS	SER	SER	V210	D298	L386	F474	L566	F680	LYS	THR	Y202	D314	R460	R551
ALA	THR	THR	F211	D299	T390	H475	T572	L681	ALA	THR	D203	A315	M464	R555
GLU	GLU	THR	H212	S300	T393	H476	T573	L682	GLU	PRO	D204	A316	R465	R556
PRO	PRO	THR	H213	I301	K393	H477	T574	L683	GLN	GLN	D205	A317	R466	R557
VAL	GLY	GLY	R216	L302	K394	E478	T575	P684	VAL	VAL	R206	I322	R467	G678
LEU	ARG	ARG	N217	A303	E479	R480	T576	L685	LEU	GLU	R207	L323	R468	N562
THR	GLU	GLU	K218	N304	Y401	Y481	R577	P686	THR	THR	P208	S328	R469	L565
LEU	VAL	VAL	D219	G305	Y402	A482	R578	L687	LEU	LEU	L209	Y307	R470	T572
GLY	ASP	ASP	T221	Y306	Y403	A483	R579	S688	GLY	ASP	V210	S307	K471	T573
PHE	SER	SER	G220	D307	G404	G484	A583	A690	PHE	GLN	F211	K333	L472	A575
GLU	ASN	ASN	T225	D308	S405	L485	A584	Q691	GLU	THR	D212	P338	D473	R577
THR	ASN	ASN	R228	T310	N407	L486	N587	V692	THR	THR	H213	F338	F474	T572
THR	PHE	PHE	R229	D311	V408	A487	V588	T693	THR	THR	R216	F349	H475	T573
THR	VAL	VAL	R230	A312	E409	P488	V589	R694	THR	THR	R217	Q350	M476	T574
THR	MET	MET	R231	L313	L413	F489	R595	R695	THR	THR	A218	K351	E479	A576
PRO	MET	MET	R232	D314	R414	S490	R596	Q696	PRO	PRO	D219	Y307	R480	R577
GLU	ALA	ALA	R233	Q316	N415	L491	R597	V698	GLU	GLU	G220	R358	Y481	R578
LYS	ASP	ASP	R234	T317	N416	P492	Y597	S699	LYS	LYS		K359	I482	N587
GLN	SER	SER	R235	T318	G417	P493	G601	K700	GLN	GLN		F364	I483	R585
ARG	CYS	CYS	R236	L319	A418	P494	P617	E701	ARG	ARG		Q350	G484	R586
ILE	GLY	GLY	R237	I322	E421	D496	R618	T702	ILE	ILE		K351	L485	G601
GLU	CYS	CYS	R238	I323	R424	D503	T623	M703	GLU	GLU		E373	L486	P617
GLN	GLU	GLU	R239	K327	R425	L504	D624	Q705	GLU	GLN		D377	P488	P618
LEU	SER	SER	R240	S328	D427	D505	R625	P706	LEU	LEU		V378	S490	T623
PHE	GLU	GLU	R241	K333	Q428	L507	R626	R707	PHE	THR		A381	I491	D624
THR	LEU	LEU	R242	K334	Q429	L508	R627	C708	THR	THR		E384	P492	L631
MET	VAL	VAL	R243	P338	R435	Q509	R628	N712	MET	ASN		I380	R493	L632
MET	GLN	GLN	R244	P339	R436	Q510	R629	N713	ASN	ALA		L390	P494	L633
ASN	ALA	ALA	R245	T346	F440	F515	R630	T720	ALA	ALA		A396	L495	V642
ALA	GLN	GLN	R246	Q350	D447	D516	R631	N721	GLN	GLN		Y260	D496	S643
ALA	ARG	ARG	R247	K351	S448	N517	R632	N722	ALA	ALA		F261	W497	P644
ALA	ALA	ALA	R248	S352	S449	L530	R633	L725	ALA	ALA		V262	D505	V649
ALA	ALA	ALA	R249	L353	L451	T535	R634	R726	ALA	ALA		R266	V506	D650
LEU	LEU	LEU	R250	D356	Y454	R539	R635	Y729	LEU	LEU		V267	Q509	N651
ILE	ILE	ILE	R251	F357	E455	R540	R636	T730	ILE	ILE		R270	N512	P652
MET	MET	MET	R252	R358	L456	F541	R637	T731	MET	SER		R271	M167	L656
LEU	LEU	LEU	R253	K359	R457	F542	R638	N732	LEU	LEU		R272	M168	R657
ALA	ALA	ALA	R254	K360	I458	G543	R639	N733	ALA	ASP		T281	P169	D658
HIS	HIS	HIS	R255	T361	R459	D543	R640	K734	ASP	LYS		K288	Y170	K659
GLY	GLY	GLY	R256	L362	R460	L544	R641	L735	LYS	LEU		L289	S171	I660
PRO	PRO	PRO	R257	A363	N461	Q545	R642	L736	VAL	VAL		D427	V172	I661
VAL	VAL	VAL	R258	F364	N462	I546	R643	V737	ASN	ASN		Q428	V173	R666
GLU	GLU	GLU	R259	S463	S464	R547	R644	N740	GLU	GLU		R435	F174	G667
TYR	TYR	TYR	R260	E373	R465	G548	R645	N741	NET	NET		D446	S179	I668
ALA	ALA	ALA	R261	D377	R466	R551	R646	N742	ASP	ASP		D447	R180	L675
LYS	LYS	LYS	R262	V378	R467	R552	R647	N743	VAL	VAL		D448	R181	G678
GLN	GLN	GLN	R263	S377	R468	R553	R648	N744	LYS	LYS		D449	R182	
ALA	ALA	ALA	R264	V379	R469	R554	R649	N745	SER	SER		D450	R183	
			R265	S380	R470	R555	R650	N746	PHE	PHE		D451	R184	
			R266	S381	R471	R556	R651	N747				D452	R185	
			R267	S382	R472	R557	R652	N748				D453	R186	
			R268	S383	R473	R558	R653	N749				D454	R187	
			R269	S384	R474	R559	R654	N750				D455	R188	
			R270	S385	R475	R560	R655	N751				D456	R189	
			R271	S386	R476	R561	R656	N752				D457	R190	
			R272	S387	R477	R562	R657	N753				D458	R191	
			R273	S388	R478	R563	R658	N754				D459	R192	
			R274	S389	R479	R564	R659	N755				D460	R193	
			R275	S390	R480	R565	R660	N756				D461	R194	
			R276	S391	R481	R566	R661	N757				D462	R195	
			R277	S392	R482	R567	R662	N758				D463	R196	
			R278	S393	R483	R568	R663	N759				D464	R197	
			R279	S394	R484	R569	R664	N760				D465	R198	
			R280	S395	R485	R570	R665	N761				D466	R199	
			R281	S396	R486	R571	R666	N762				D467	R200	
			R282	S397	R487	R572	R667	N763				D468	R201	
			R283	S398	R488	R573	R668	N764				D469	R202	
			R284	S399	R489	R574	R669	N765				D470	R203	
			R285	S400	R490	R575	R670	N766				D471	R204	
			R286	S401	R491	R576	R671	N767				D472	R205	
			R287	S402	R492	R577	R672	N768				D473	R206	
			R288	S403	R493	R578	R673	N769				D474	R207	
			R289	S404	R494	R579	R674	N770				D475	R208	
			R290	S405	R495	R580	R675	N771				D476	R209	
			R291	S406	R496	R581	R676	N772				D477	R210	
			R292	S407	R497	R582	R677	N773				D478	R211	
			R293	S408	R498	R583	R678	N774				D479	R212	
			R294	S409	R499	R584	R679	N775				D480	R213	
			R295	S410	R500	R585	R680	N776				D481	R214	
			R296	S411	R501	R586	R681	N777				D482	R215	
			R297	S412	R502	R587	R682	N778				D483	R216	
			R298	S413	R503	R588	R683	N779				D484	R217	
			R299	S414	R504	R589	R684	N780				D485	R218	
			R300	S415	R505	R590	R685	N781				D486	R219	
			R301	S416	R506	R591	R686	N782				D487	R220	
			R302	S417	R507	R592	R687	N783				D488	R221	
			R303	S418	R508	R593	R688	N784				D489	R222	
			R304	S419	R509	R594	R689	N785				D490	R223	
			R305	S420	R510	R595	R690	N786				D491	R224	
			R306	S421	R511	R596	R691	N787				D492	R225	
			R307	S422	R512	R597	R692	N788				D493	R226	
			R308	S423	R513	R598	R693	N789				D494	R227	
			R309	S424	R514	R599	R694	N790				D495	R228	
			R310	S425	R515	R600	R695	N791				D496	R229	
			R311	S426	R516	R601	R696	N792				D497	R230	
			R312	S427	R517	R602	R697	N793				D498	R231	
			R313	S428	R518	R603	R698	N794				D499	R232	
			R314	S429	R519	R604	R699	N795				D500	R233	
			R315	S430	R520	R605	R700	N796				D501	R234	
			R316	S431	R521	R606	R701	N797				D502	R235	
			R317	S432	R522	R607	R702	N798				D503	R236	
			R318	S433	R523	R608	R703	N799				D504	R237	
			R319	S434	R524	R609	R704	N800				D505	R238	
			R320	S435	R525	R610	R705	N801				D506	R239	
			R321	S436	R526	R611	R706	N802				D507	R240	
			R322	S437	R527	R612	R707	N803				D508	R241	
			R323	S438	R528	R613	R708	N804				D509	R242	
			R324	S439	R529	R614	R709	N805				D510	R243	
			R325	S440	R530	R615	R710	N806				D511	R244	
			R326	S441	R531	R616	R711	N807				D512	R245	
			R327	S442	R532	R617	R712	N808				D513	R246	
			R328	S443	R533	R618	R							



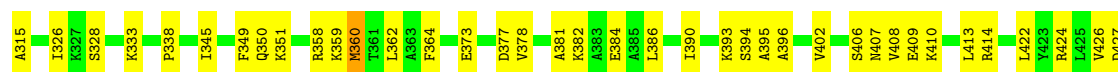
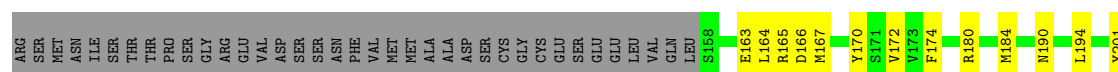
• Molecule 1: Major capsid protein

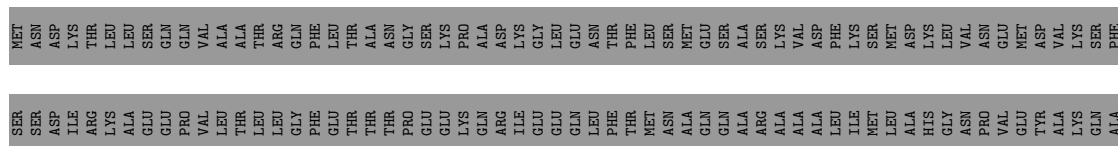
Chain A3: 52% 26% 21%



• Molecule 1: Major capsid protein

Chain A4: 51% 28% 21%





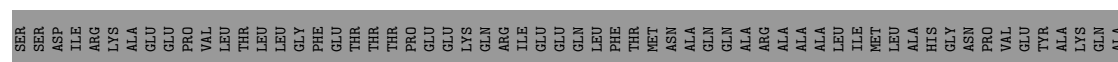


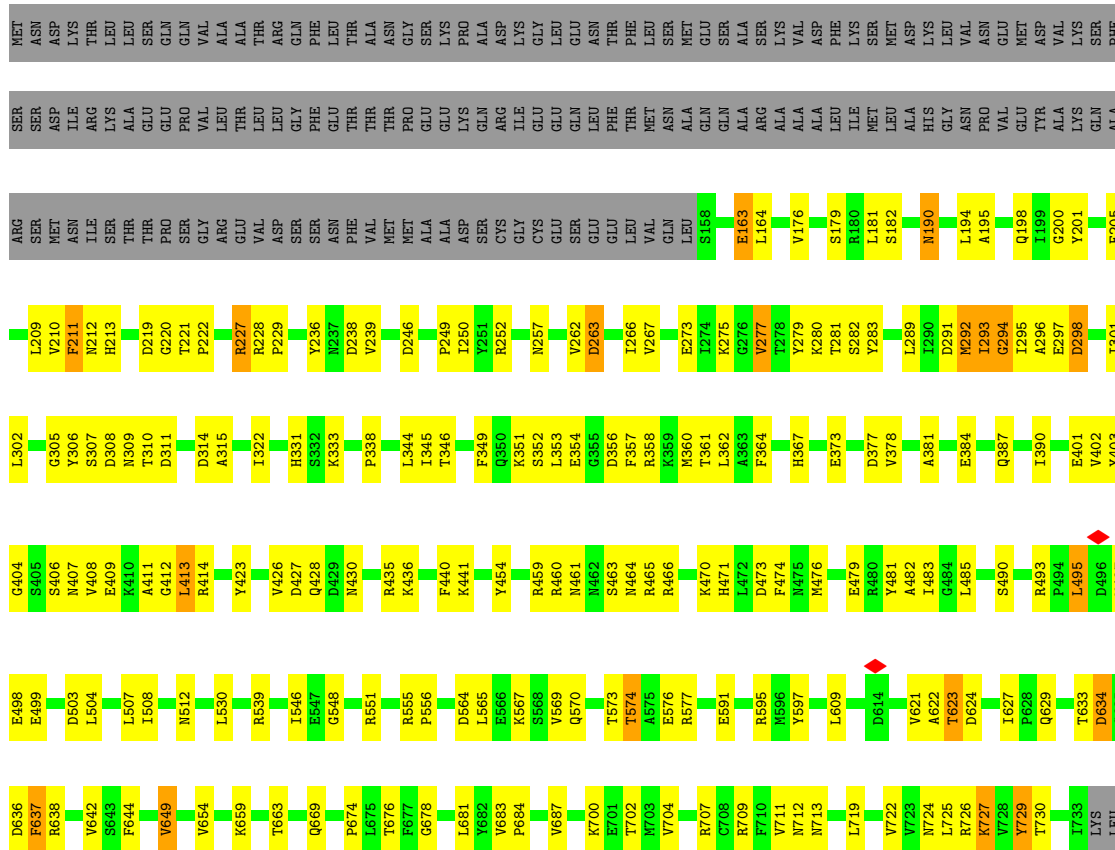
Response	Percentage
Yes	49%
No	29%
Don't know	21%

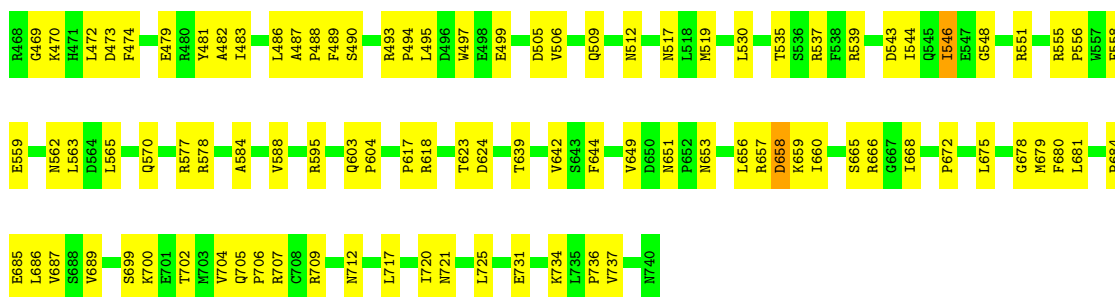
- Molecule 1: Major capsid protein

Response	Percentage
Yes	47%
No	31%
Don't know	21%

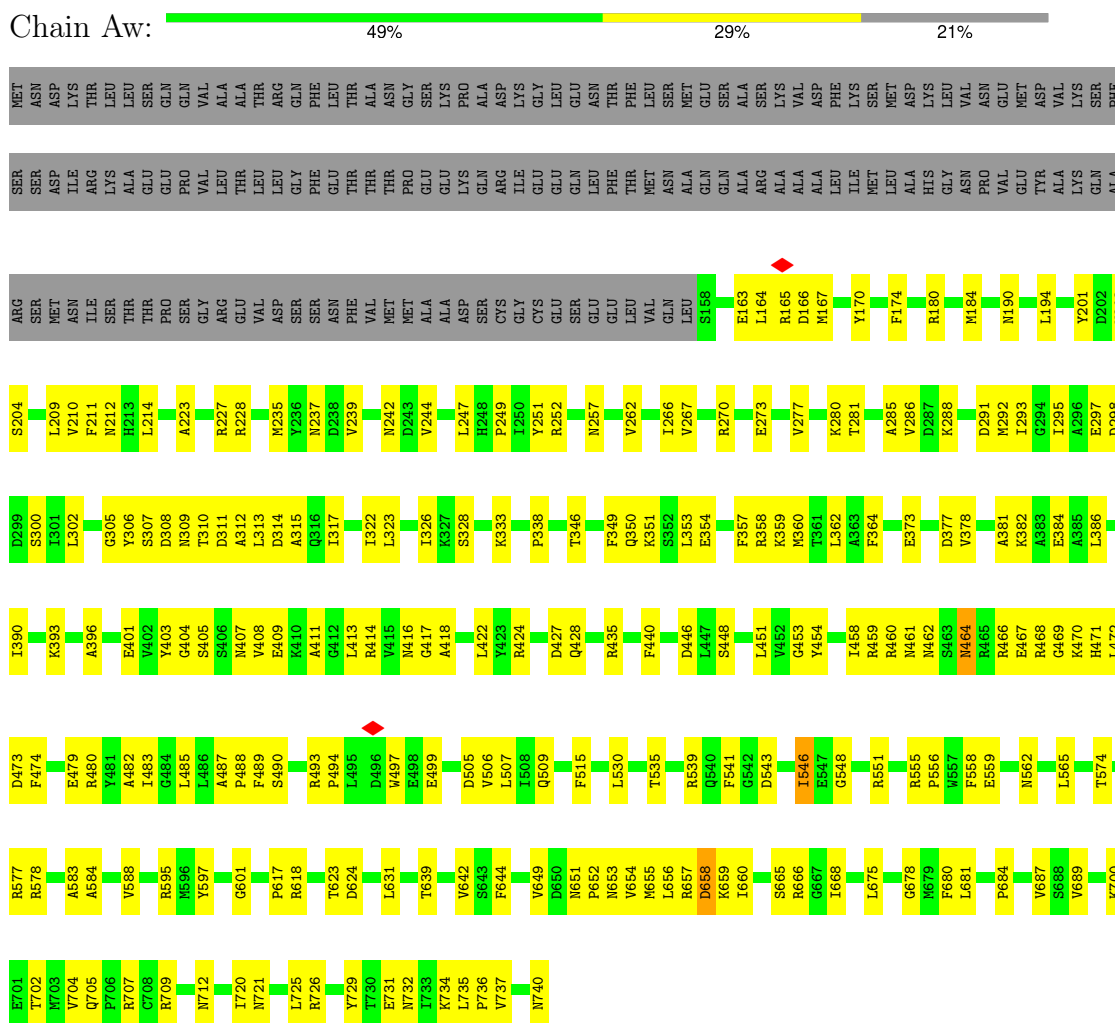




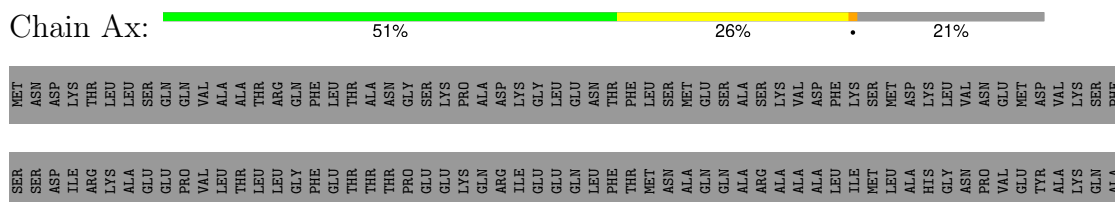


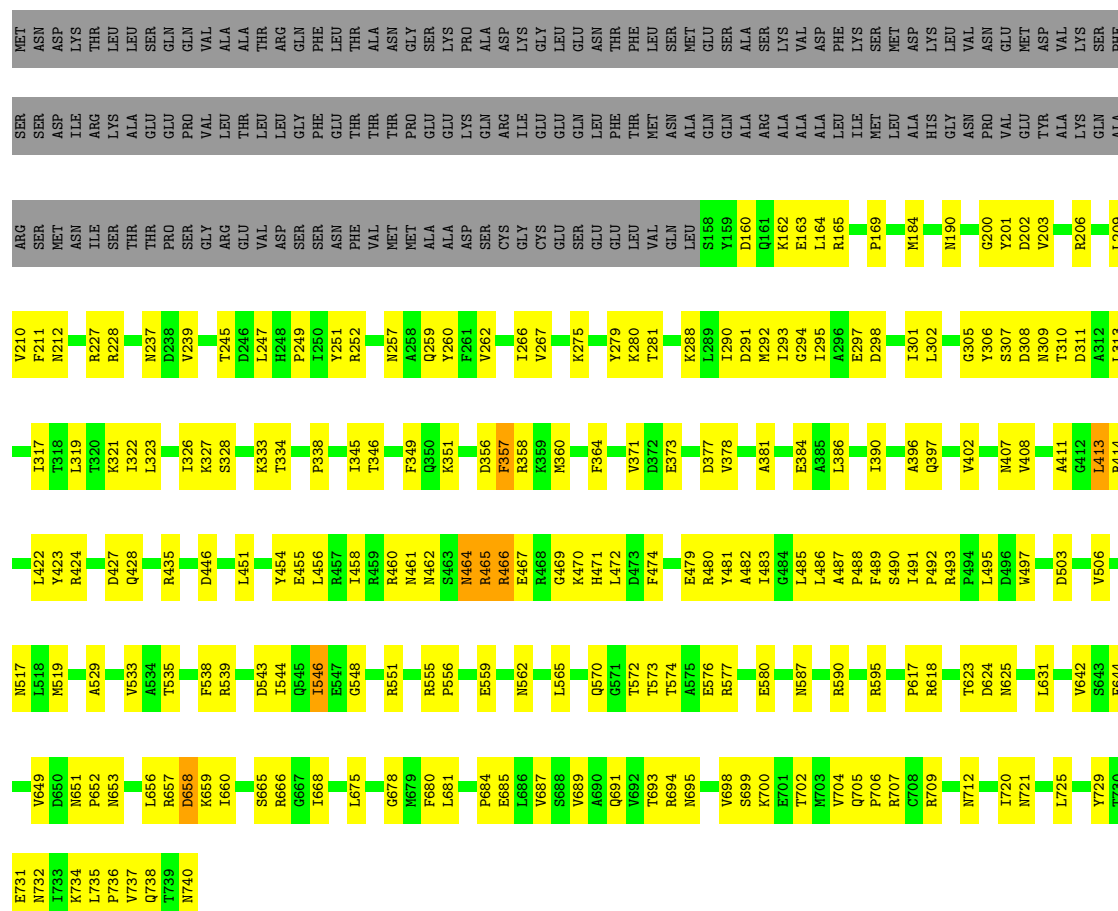


- Molecule 1: Major capsid protein

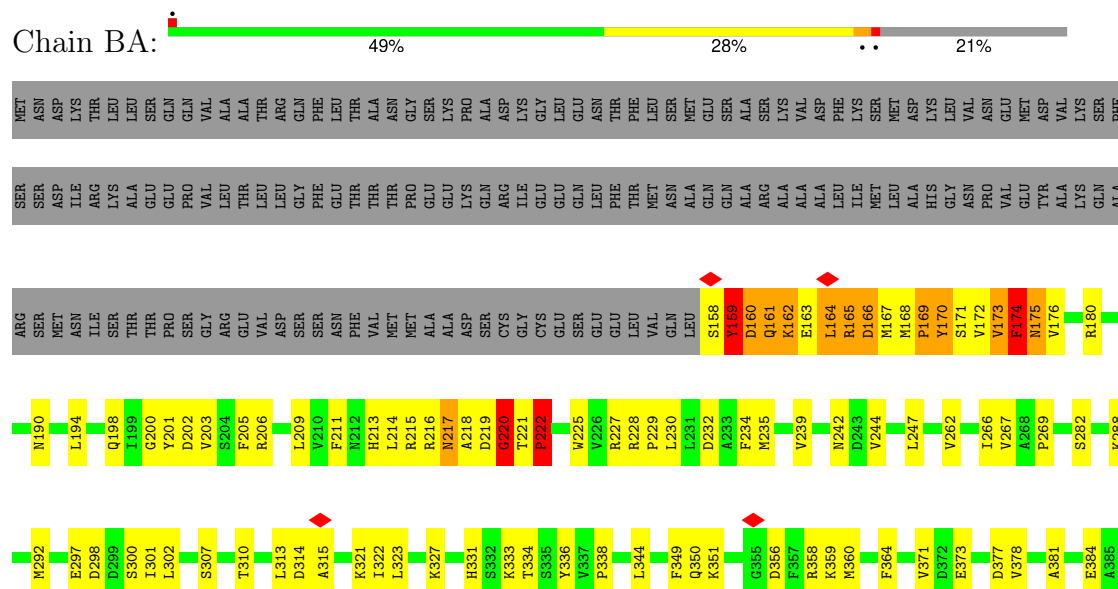
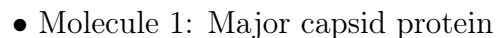


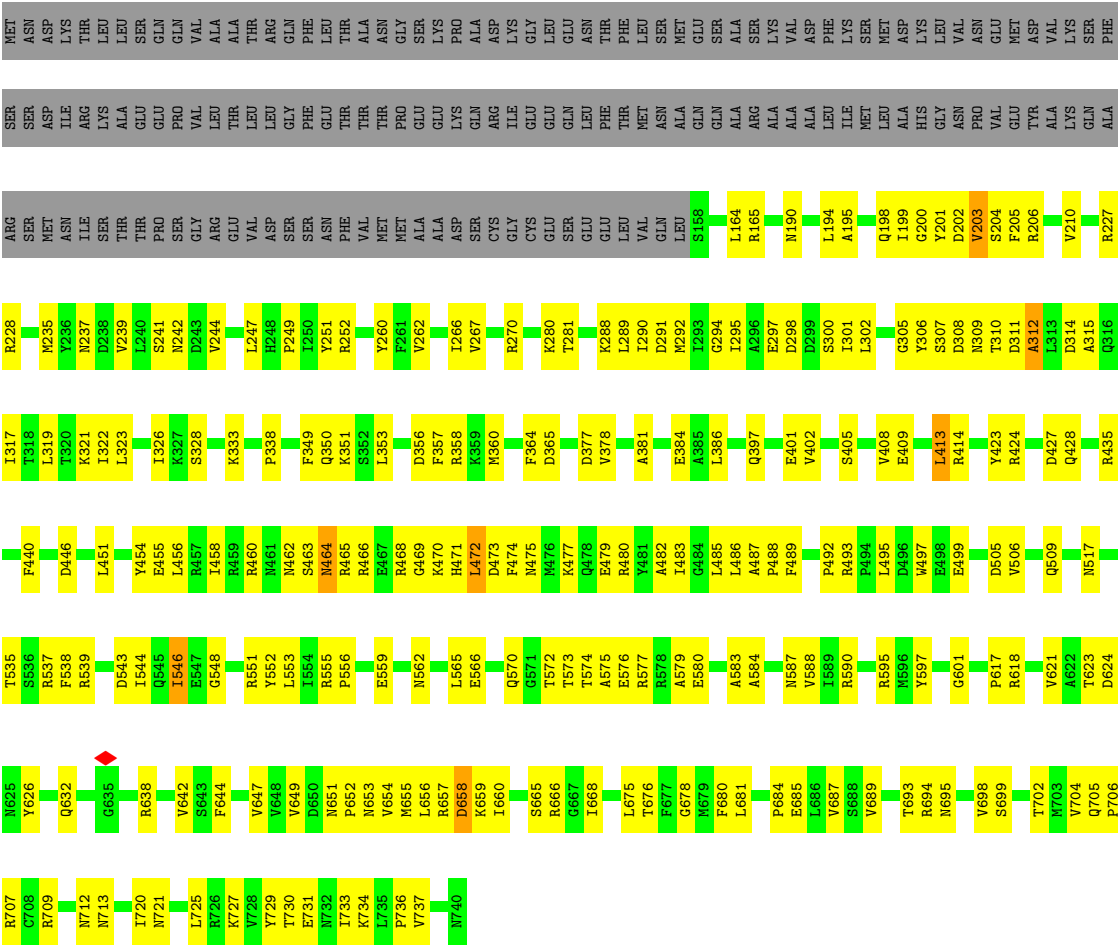
- Molecule 1: Major capsid protein



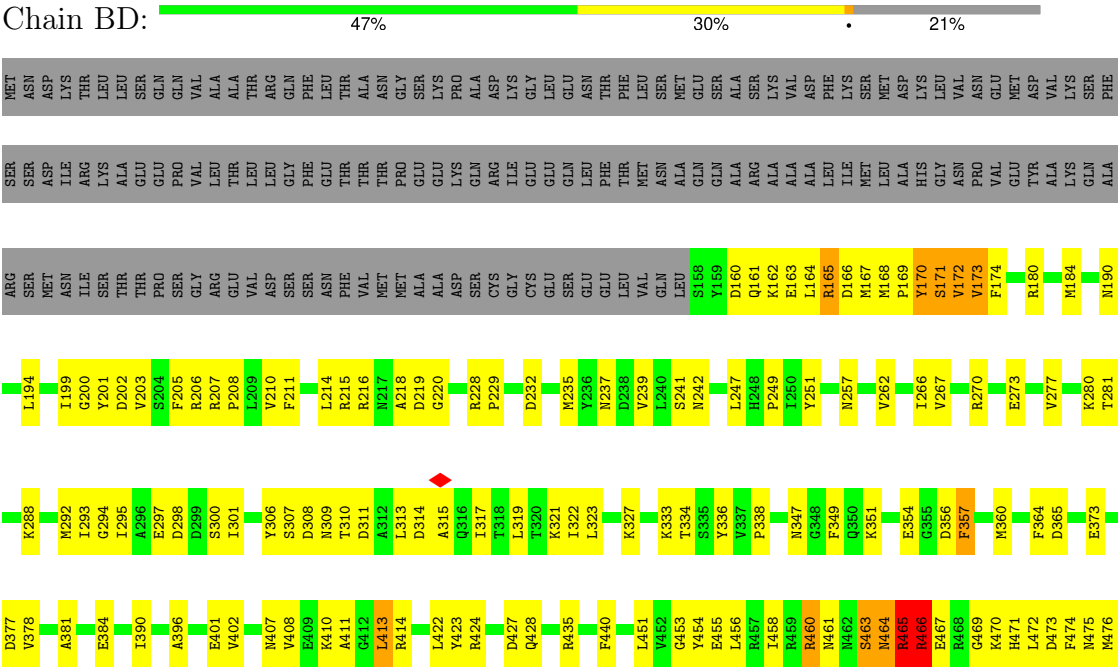


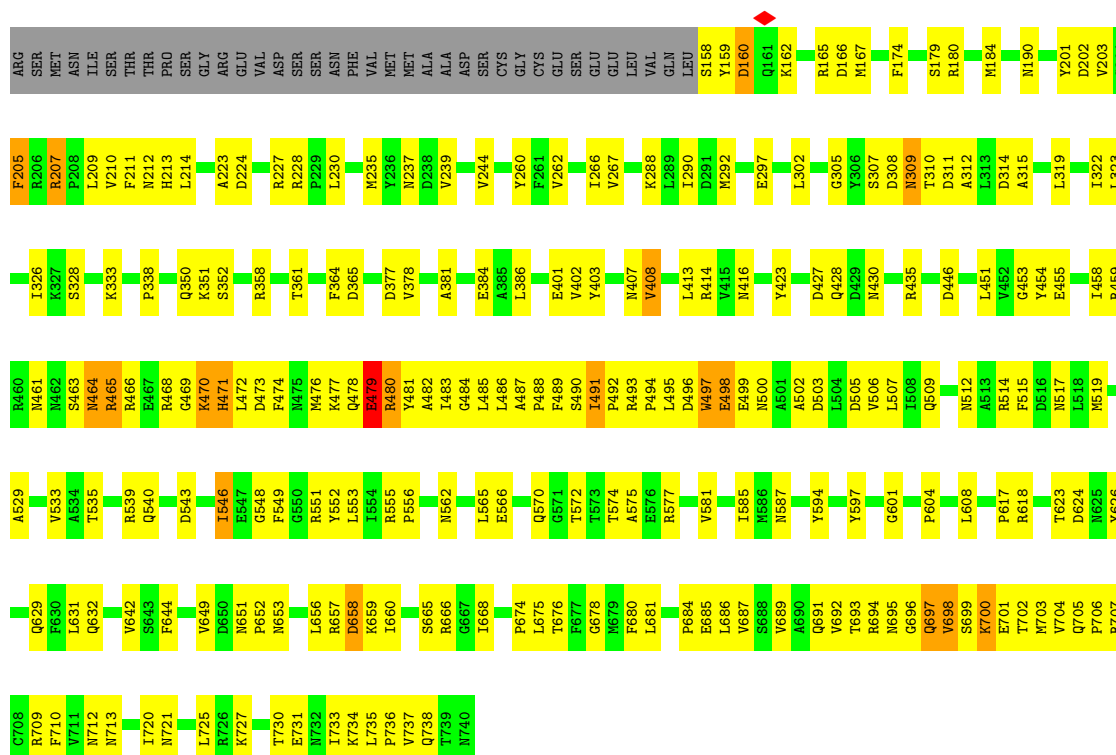
Chain Az:





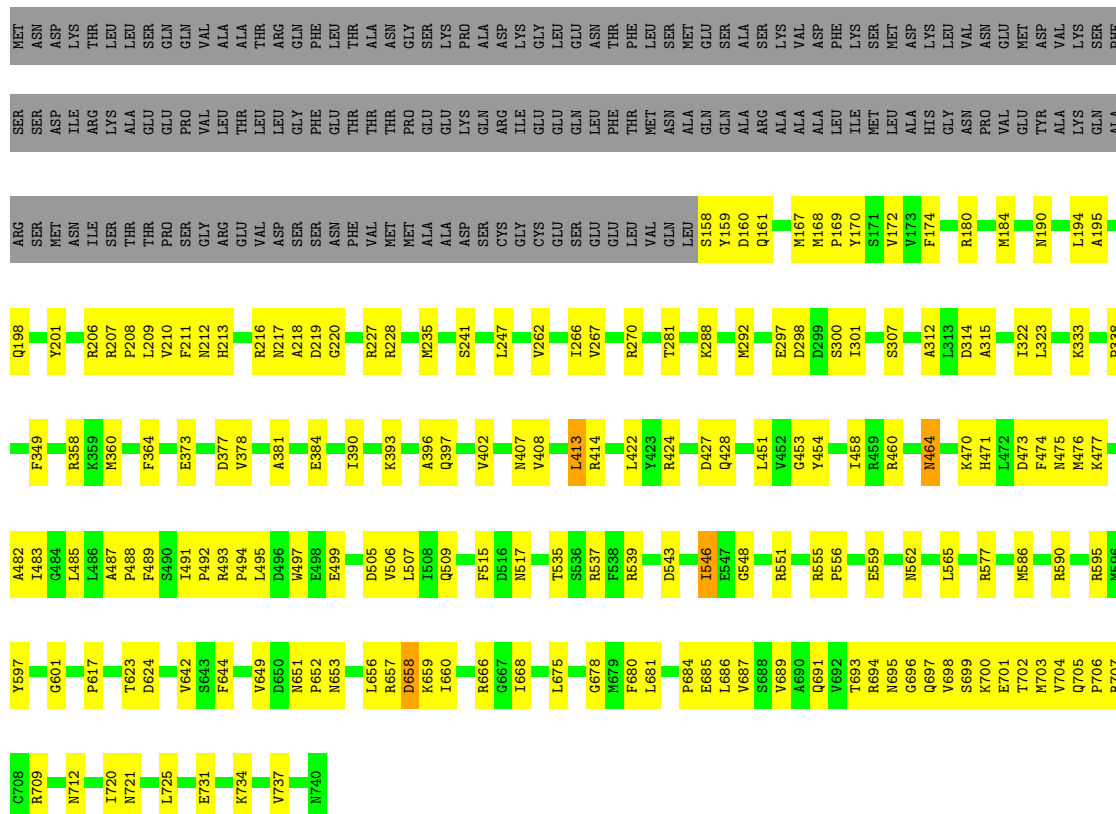
● Molecule 1: Major capsid protein



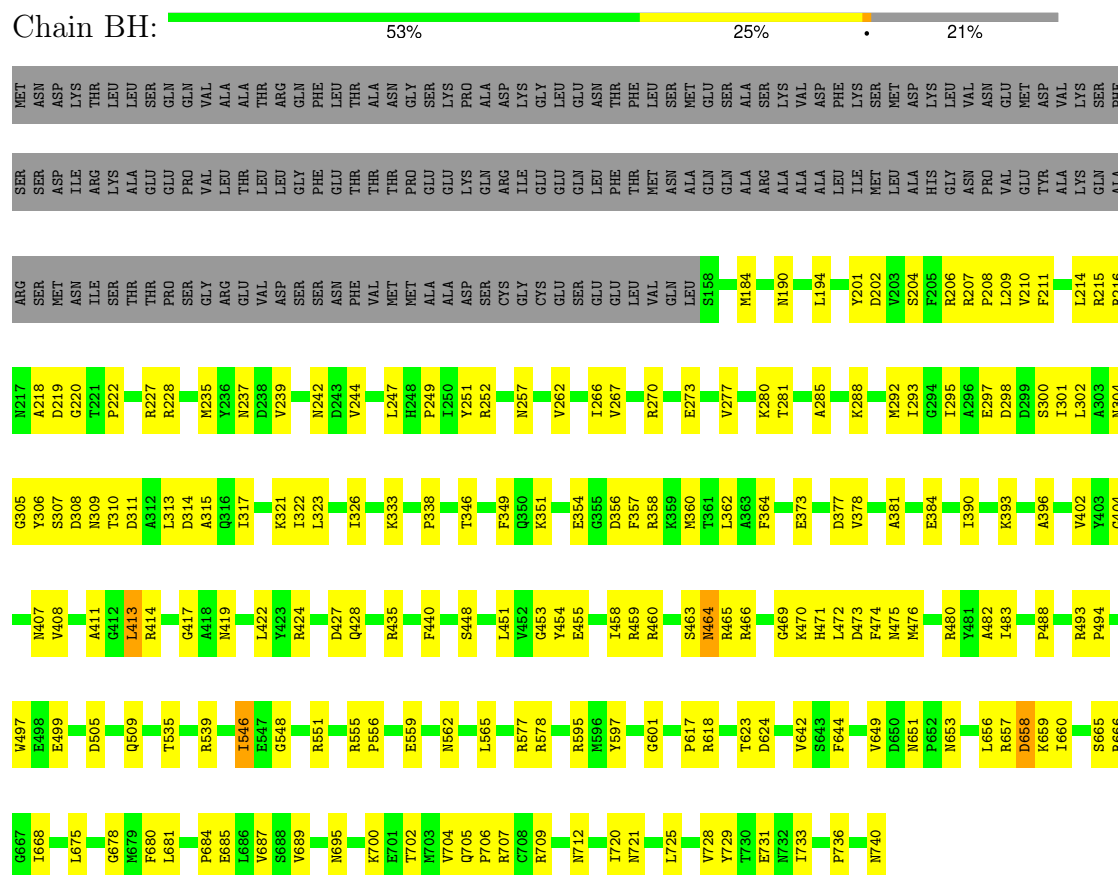


• Molecule 1: Major capsid protein

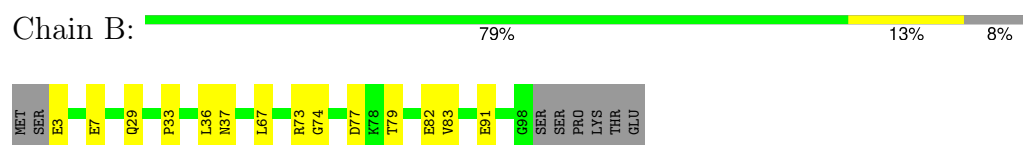
Chain BG: 55% 23% 21%



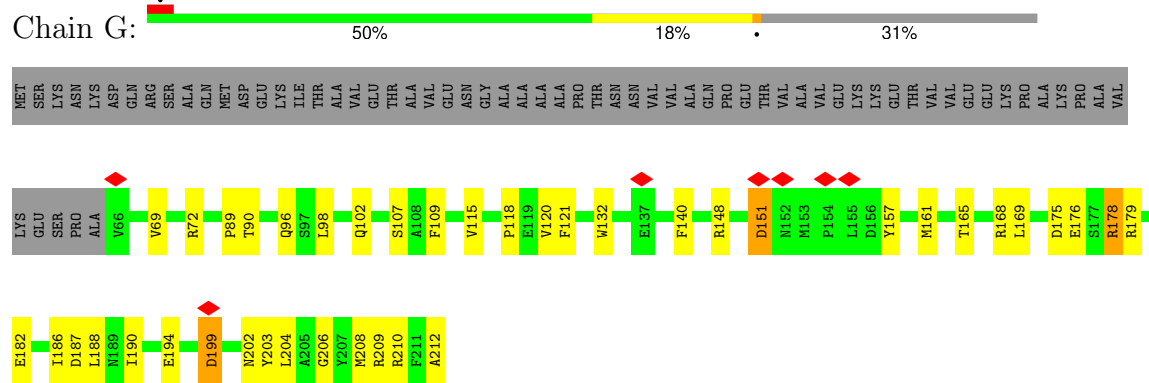
- Molecule 1: Major capsid protein



- Molecule 2: Capsid Latch gp146



- Molecule 3: Capsid Decorator gp77



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4535	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.562	Depositor
Minimum map value	-0.473	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.132	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	1708.6875, 1708.6875, 1708.6875	wwPDB
Map dimensions	701, 701, 701	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.4375, 2.4375, 2.4375	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	A0	0.28	0/4735	0.55	5/6411 (0.1%)
1	A1	0.27	0/4735	0.61	5/6411 (0.1%)
1	A2	0.20	0/4735	0.45	0/6411
1	A3	0.18	0/4735	0.41	0/6411
1	A4	0.20	0/4735	0.48	2/6411 (0.0%)
1	A5	0.21	0/4735	0.47	1/6411 (0.0%)
1	A6	0.20	0/4735	0.46	0/6411
1	A7	0.19	0/4735	0.41	0/6411
1	A8	0.24	1/4735 (0.0%)	0.52	6/6411 (0.1%)
1	A9	0.25	0/4735	0.53	2/6411 (0.0%)
1	Ar	0.22	0/4735	0.51	2/6411 (0.0%)
1	As	0.22	0/4735	0.47	0/6411
1	At	0.28	2/4676 (0.0%)	0.54	4/6330 (0.1%)
1	Au	0.18	0/4735	0.40	0/6411
1	Av	0.19	0/4735	0.39	0/6411
1	Aw	0.20	0/4735	0.44	1/6411 (0.0%)
1	Ax	0.28	0/4735	0.57	5/6411 (0.1%)
1	Ay	0.26	0/4735	0.58	5/6411 (0.1%)
1	Az	0.24	0/4735	0.51	1/6411 (0.0%)
1	BA	0.41	4/4735 (0.1%)	0.81	31/6411 (0.5%)
1	BB	0.24	0/4735	0.54	0/6411
1	BC	0.94	1/4735 (0.0%)	0.57	3/6411 (0.0%)
1	BD	0.58	6/4735 (0.1%)	0.66	16/6411 (0.2%)
1	BE	0.37	3/4735 (0.1%)	0.77	19/6411 (0.3%)
1	BF	0.31	0/4735	0.76	23/6411 (0.4%)
1	BG	0.18	0/4735	0.40	0/6411
1	BH	0.18	0/4735	0.40	0/6411
2	B	0.18	0/766	0.37	0/1027
3	G	0.11	0/1224	0.30	0/1656
All	All	0.32	17/129776 (0.0%)	0.54	131/175699 (0.1%)

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	A0	0	1
1	A5	0	1
1	Av	0	1
1	Ax	0	1
1	Az	0	1
1	BA	0	3
1	BE	0	1
1	BF	0	2
All	All	0	11

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BC	203	VAL	CB-CG2	62.74	3.59	1.52
1	BD	170	TYR	CD1-CE1	17.96	1.92	1.38
1	BD	170	TYR	CD2-CE2	16.15	1.87	1.38
1	BD	170	TYR	CE2-CZ	14.00	1.71	1.38
1	BD	170	TYR	CE1-CZ	13.83	1.71	1.38

The worst 5 of 131 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BA	160	ASP	CA-C-N	14.52	150.57	123.13
1	BA	160	ASP	C-N-CA	14.52	150.57	123.13
1	BD	170	TYR	CA-CB-CG	12.32	136.07	113.90
1	BC	203	VAL	CA-CB-CG2	11.09	129.25	110.40
1	BE	296	ALA	N-CA-C	10.76	127.24	108.52

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A0	158	SER	Peptide
1	A5	159	TYR	Peptide
1	Av	159	TYR	Peptide
1	Ax	158	SER	Peptide
1	Az	158	SER	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	A0	4651	0	4633	325	0
1	A1	4651	0	4633	365	0
1	A2	4651	0	4633	227	0
1	A3	4651	0	4633	201	0
1	A4	4651	0	4633	209	0
1	A5	4651	0	4633	252	0
1	A6	4651	0	4633	185	0
1	A7	4651	0	4633	179	0
1	A8	4651	0	4633	261	0
1	A9	4651	0	4633	270	0
1	Ar	4651	0	4633	260	0
1	As	4651	0	4633	245	0
1	At	4593	0	4562	203	0
1	Au	4651	0	4633	159	0
1	Av	4651	0	4633	162	0
1	Aw	4651	0	4633	215	0
1	Ax	4651	0	4633	274	0
1	Ay	4651	0	4633	252	0
1	Az	4651	0	4633	266	0
1	BA	4651	0	4633	393	0
1	BB	4651	0	4633	255	0
1	BC	4651	0	4633	293	0
1	BD	4651	0	4633	359	0
1	BE	4651	0	4633	409	0
1	BF	4651	0	4633	338	0
1	BG	4651	0	4633	155	0
1	BH	4651	0	4633	178	0
2	B	759	0	770	12	0
3	G	1198	0	1190	26	0
All	All	127476	0	126980	4996	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 20.

The worst 5 of 4996 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:BD:170:TYR:CD2	1:BD:170:TYR:CE2	1.87	1.62
1:BD:170:TYR:CE1	1:BD:170:TYR:CD1	1.92	1.55
1:A8:466:ARG:NE	1:Ax:697:GLN:O	1.82	1.12
1:BA:161:GLN:N	1:BE:294:GLY:H	1.49	1.11
1:BC:408:VAL:HG13	1:BE:164:LEU:HG	1.32	1.11

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	A0	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	A1	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	A2	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	A3	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	A4	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	A5	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	A6	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	A7	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	A8	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	A9	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	Ar	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	As	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
1	At	574/740 (78%)	529 (92%)	43 (8%)	2 (0%)	36	71
1	Au	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	Av	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
1	Aw	581/740 (78%)	568 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ax	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	Ay	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	Az	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
1	BA	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
1	BB	581/740 (78%)	564 (97%)	17 (3%)	0	100	100
1	BC	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
1	BD	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
1	BE	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	BF	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
1	BG	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
1	BH	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	B	94/104 (90%)	93 (99%)	1 (1%)	0	100	100
3	G	145/212 (68%)	141 (97%)	4 (3%)	0	100	100
All	All	15919/20296 (78%)	15500 (97%)	417 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	At	642	VAL
1	At	292	MET

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	A0	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A1	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A2	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A3	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A4	509/644 (79%)	502 (99%)	7 (1%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A5	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	A6	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A7	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	A8	509/644 (79%)	500 (98%)	9 (2%)	51	67
1	A9	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	Ar	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	As	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	At	500/644 (78%)	473 (95%)	27 (5%)	20	41
1	Au	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	Av	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	Aw	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	Ax	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	Ay	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	Az	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	BA	509/644 (79%)	500 (98%)	9 (2%)	51	67
1	BB	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	BC	509/644 (79%)	501 (98%)	8 (2%)	55	69
1	BD	509/644 (79%)	498 (98%)	11 (2%)	45	64
1	BE	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	BF	509/644 (79%)	500 (98%)	9 (2%)	51	67
1	BG	509/644 (79%)	502 (99%)	7 (1%)	59	72
1	BH	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	B	83/91 (91%)	83 (100%)	0	100	100
3	G	125/177 (71%)	119 (95%)	6 (5%)	23	44
All	All	13942/17656 (79%)	13711 (98%)	231 (2%)	52	68

5 of 231 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Au	413	LEU
1	BH	546	ILE
1	Ay	262	VAL
1	BH	413	LEU
1	BE	642	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 144 such sidechains are listed below:

Mol	Chain	Res	Type
1	BD	304	ASN
3	G	101	HIS
1	BD	651	ASN
1	BF	651	ASN
1	A9	651	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

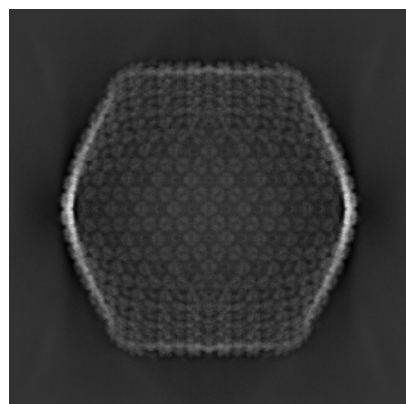
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75837. These allow visual inspection of the internal detail of the map and identification of artifacts.

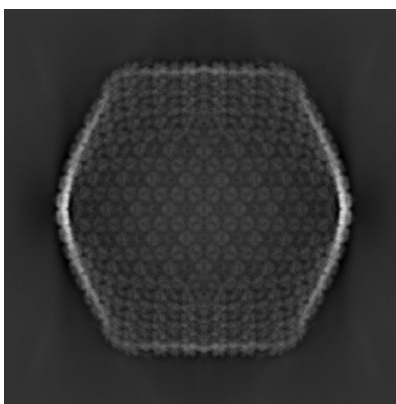
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

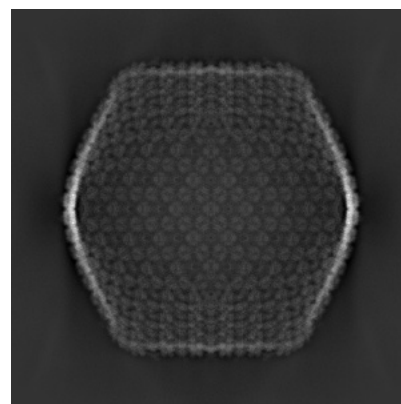
6.1.1 Primary map



X

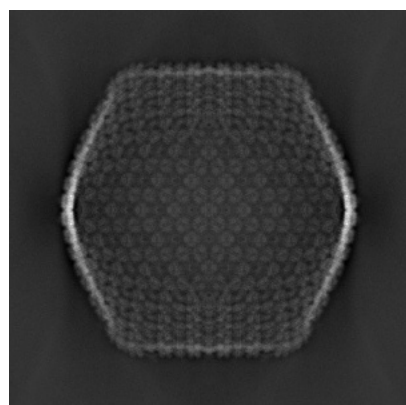


Y

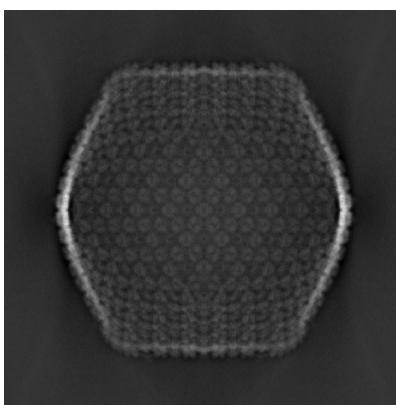


Z

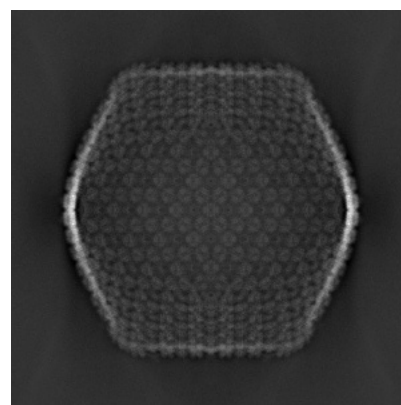
6.1.2 Raw map



X



Y

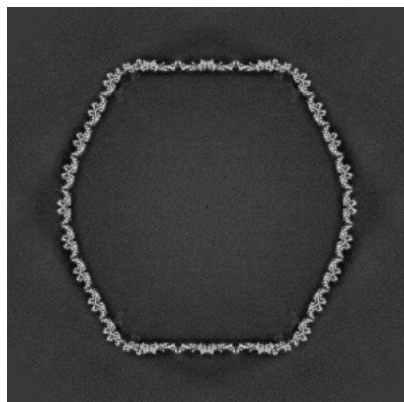


Z

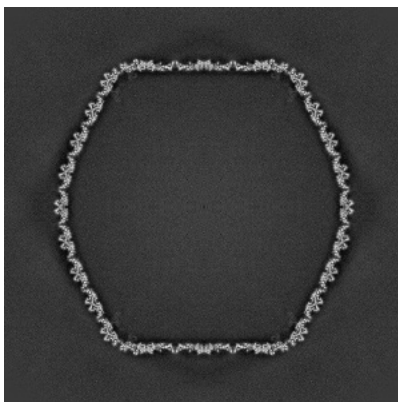
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

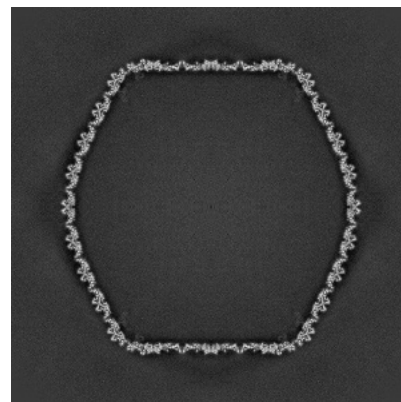
6.2.1 Primary map



X Index: 350

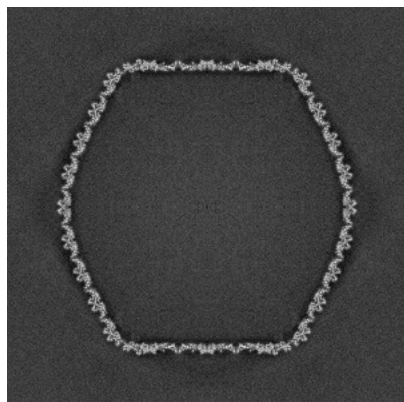


Y Index: 350

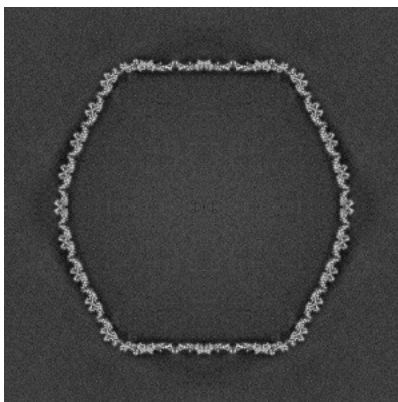


Z Index: 350

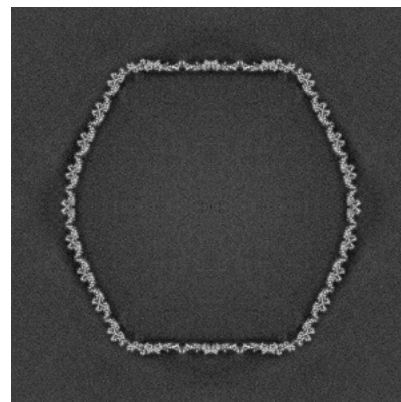
6.2.2 Raw map



X Index: 350



Y Index: 350

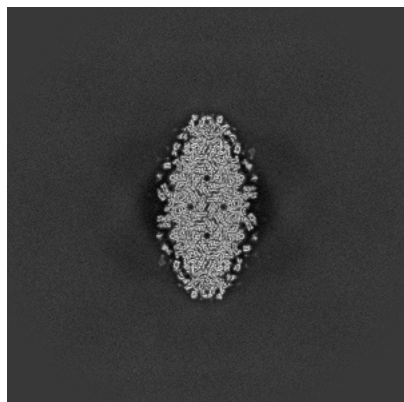


Z Index: 350

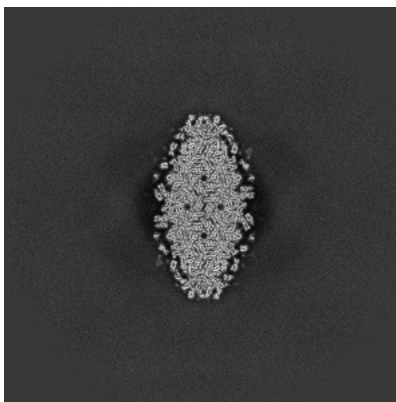
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

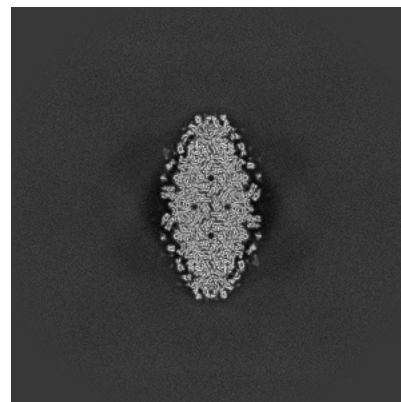
6.3.1 Primary map



X Index: 109

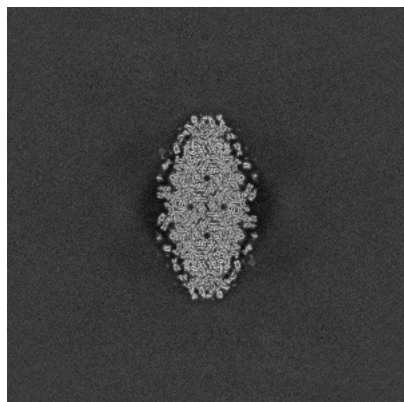


Y Index: 109

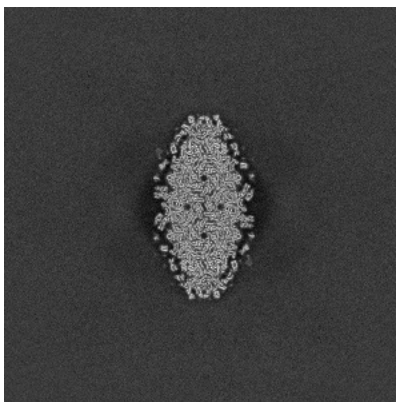


Z Index: 591

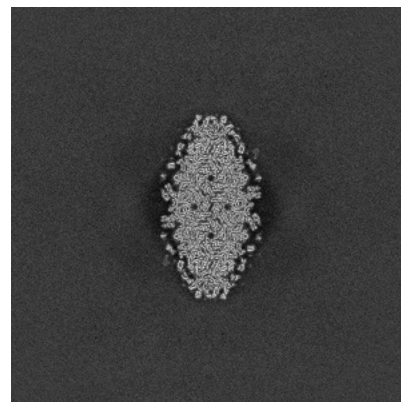
6.3.2 Raw map



X Index: 591



Y Index: 591

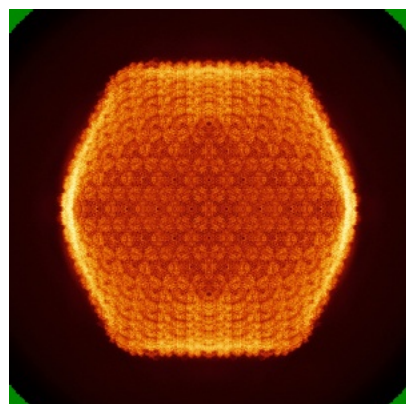


Z Index: 109

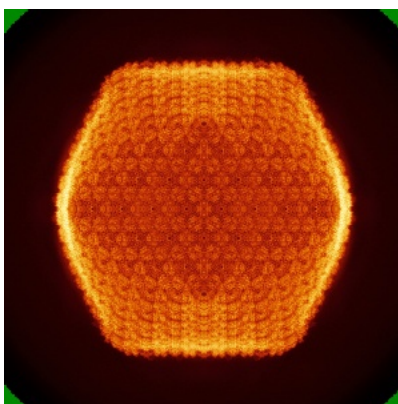
The images above show the largest variance slices of the map in three orthogonal directions.

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

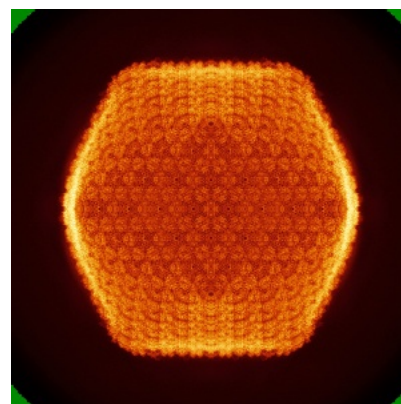
6.4.1 Primary map



X

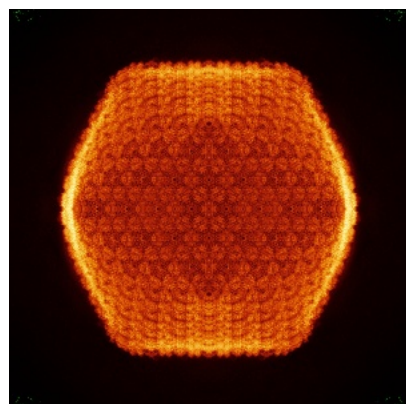


Y

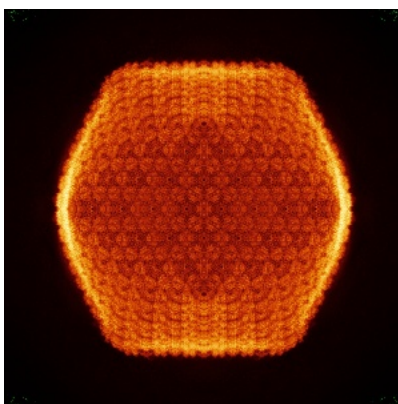


Z

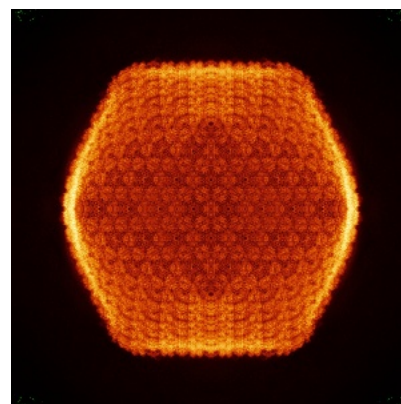
6.4.2 Raw map



X



Y

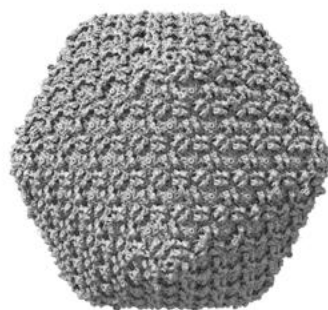


Z

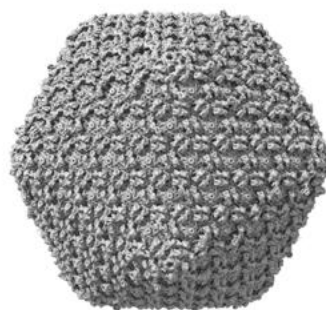
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

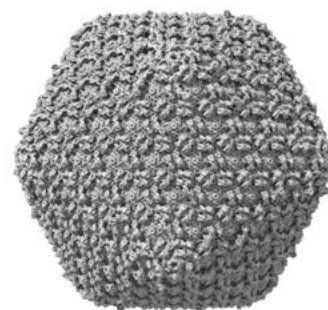
6.5.1 Primary map



X



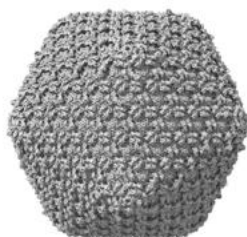
Y



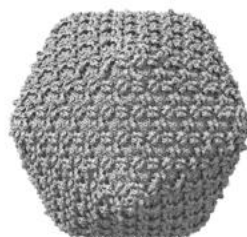
Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

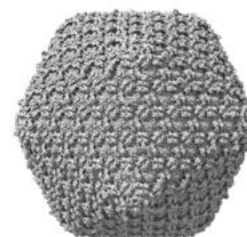
6.5.2 Raw map



X



Y



Z

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.

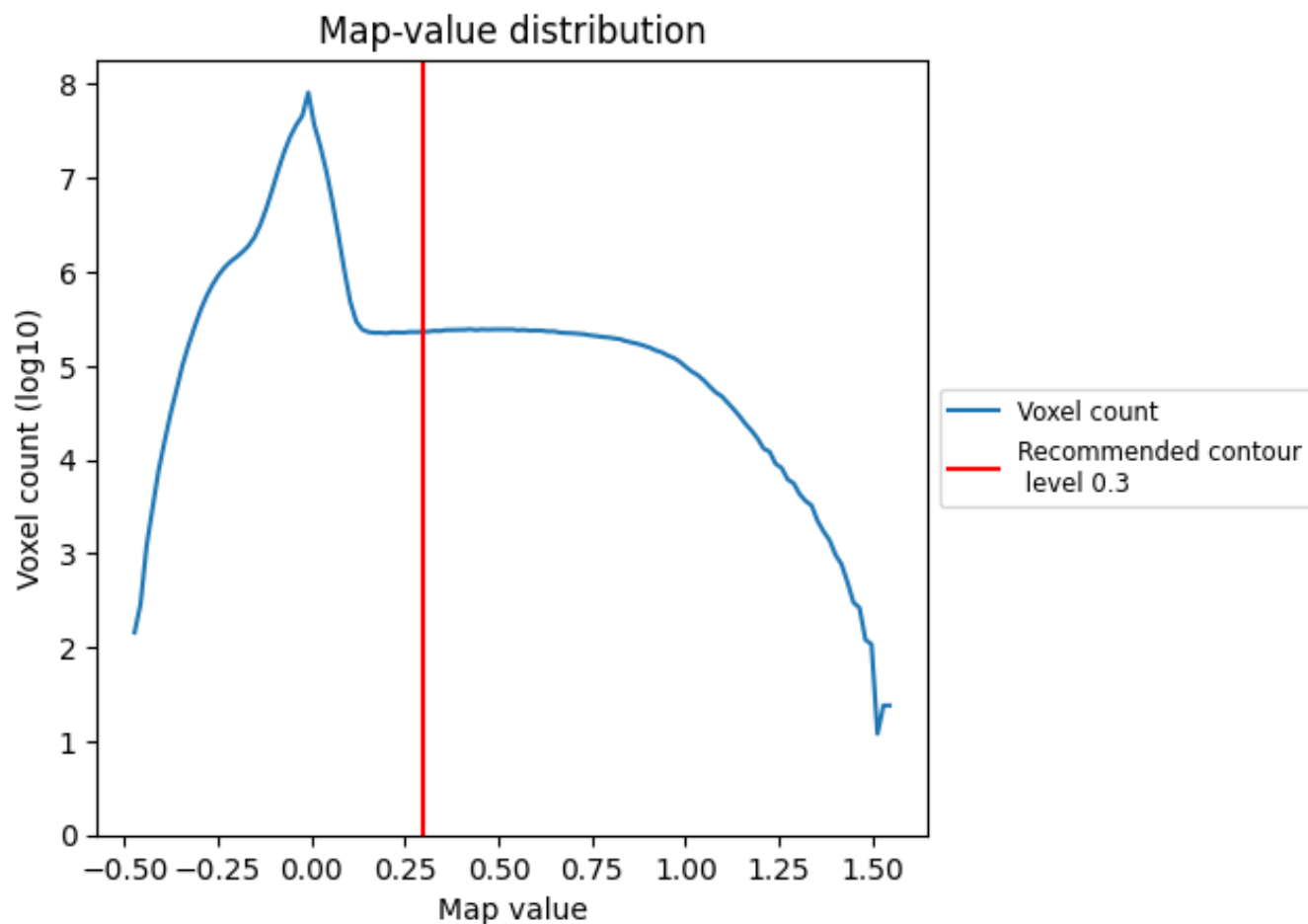
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

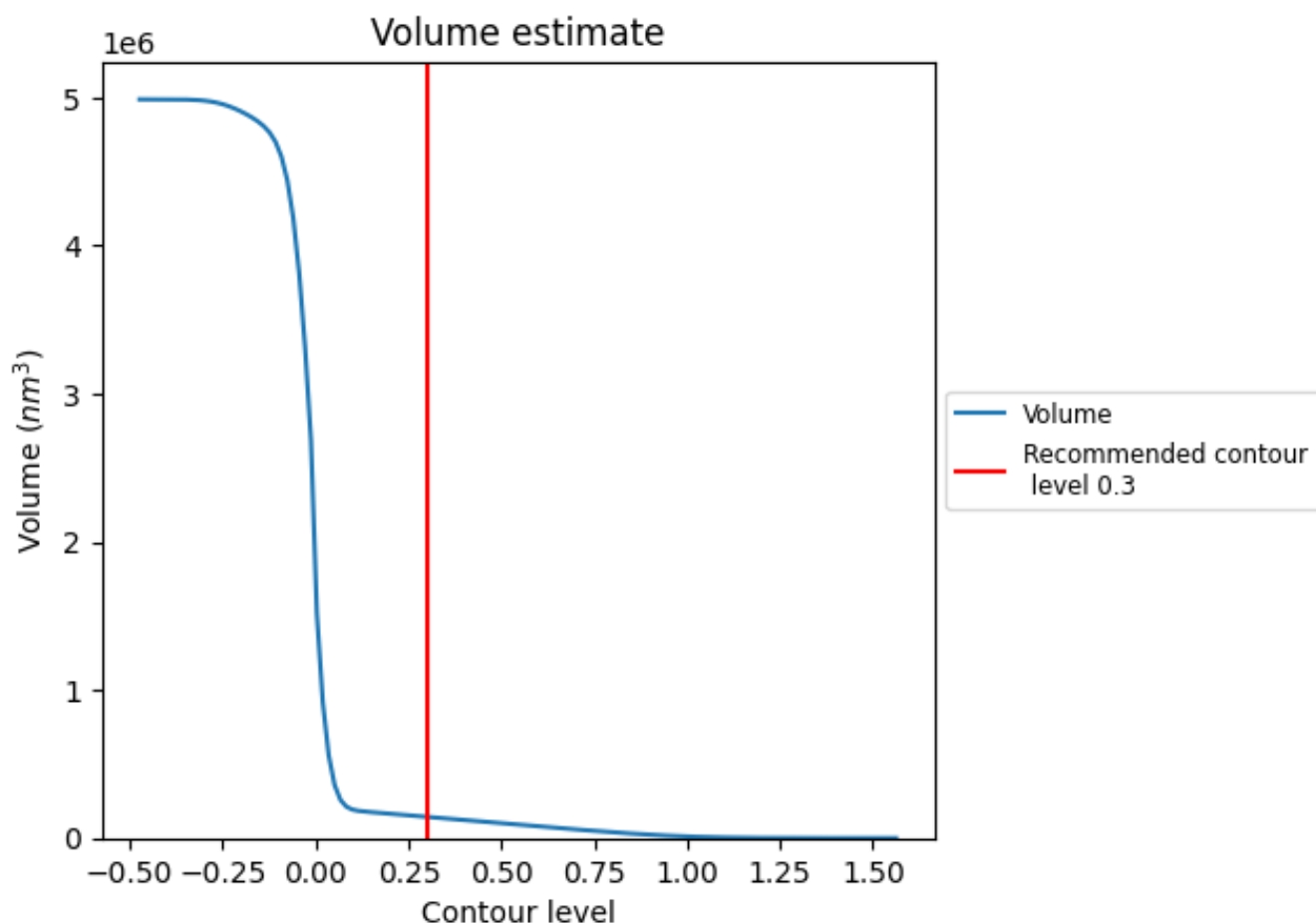
This section contains the results of statistical analysis of the map.

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.

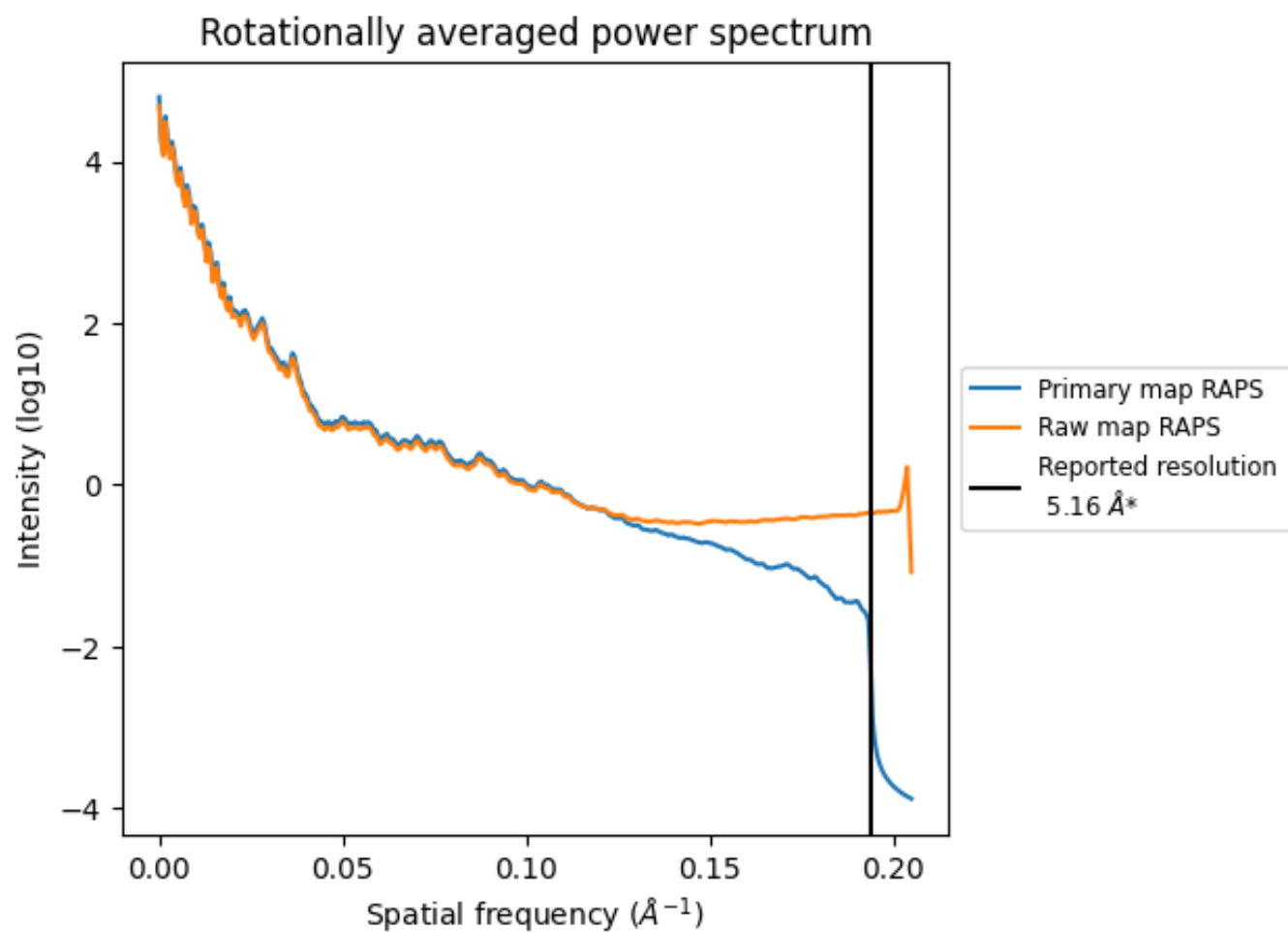
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 144456 nm^3 ; this corresponds to an approximate mass of 130491 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 ⓘ

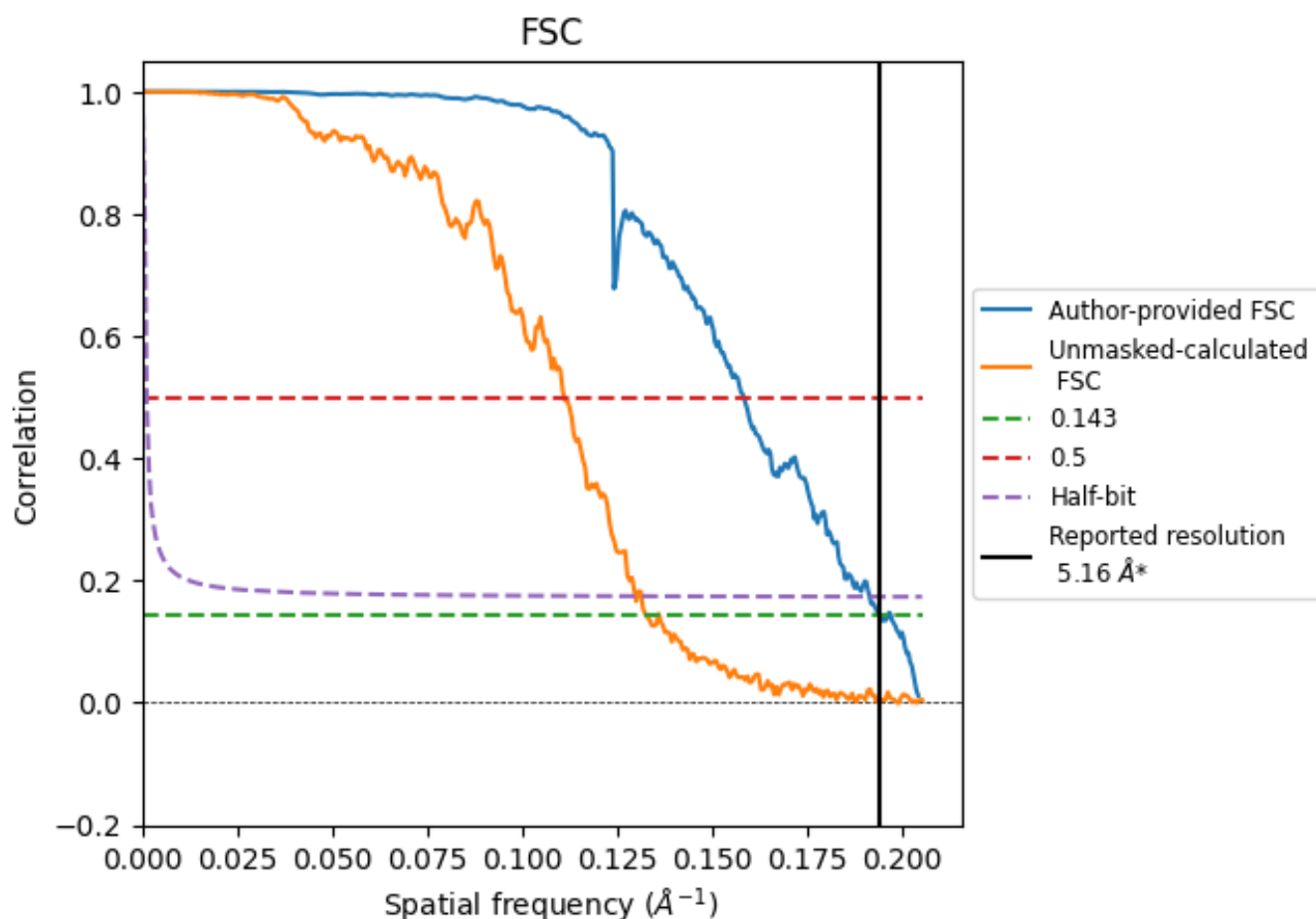


*Reported resolution corresponds to spatial frequency of 0.194 Å⁻¹

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 $0.194 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

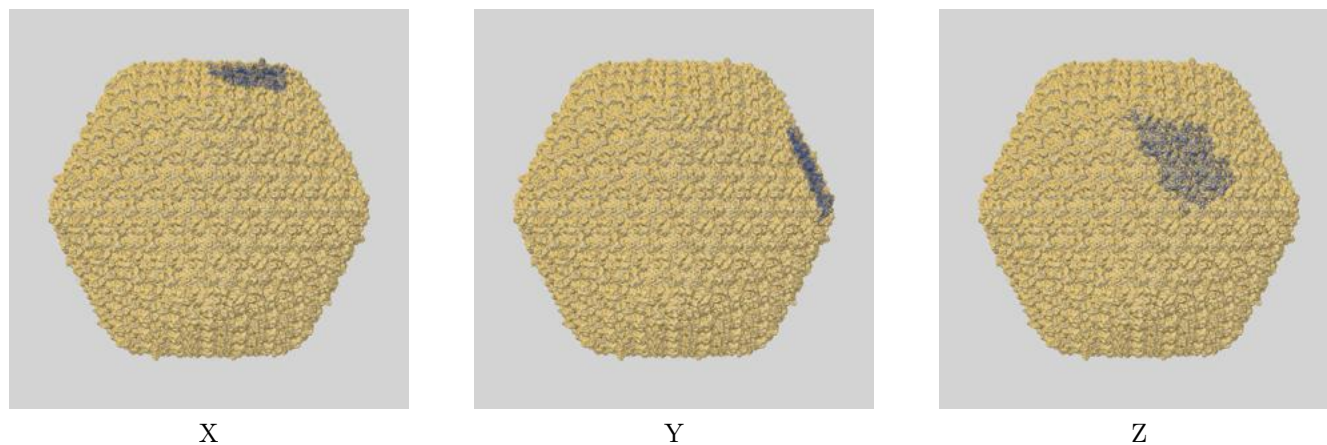
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.16	-	-
Author-provided FSC curve	5.16	6.32	5.23
Unmasked-calculated*	7.55	9.01	7.71

*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 7.55 differs from the reported value 5.16 by more than 10 %

9 Map-model fit [i](#)

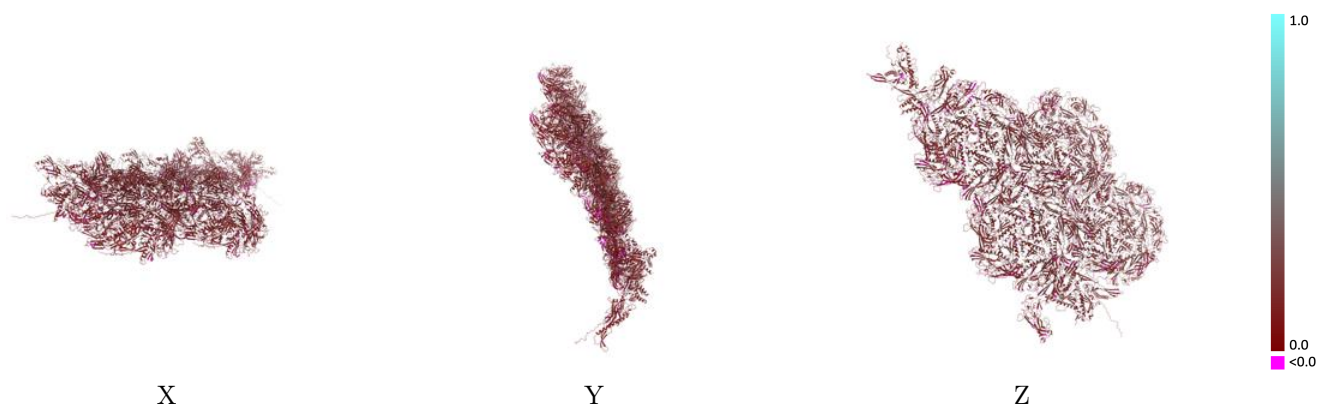
This section contains information regarding the fit between EMDB map EMD-75837 and PDB model 11ML. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



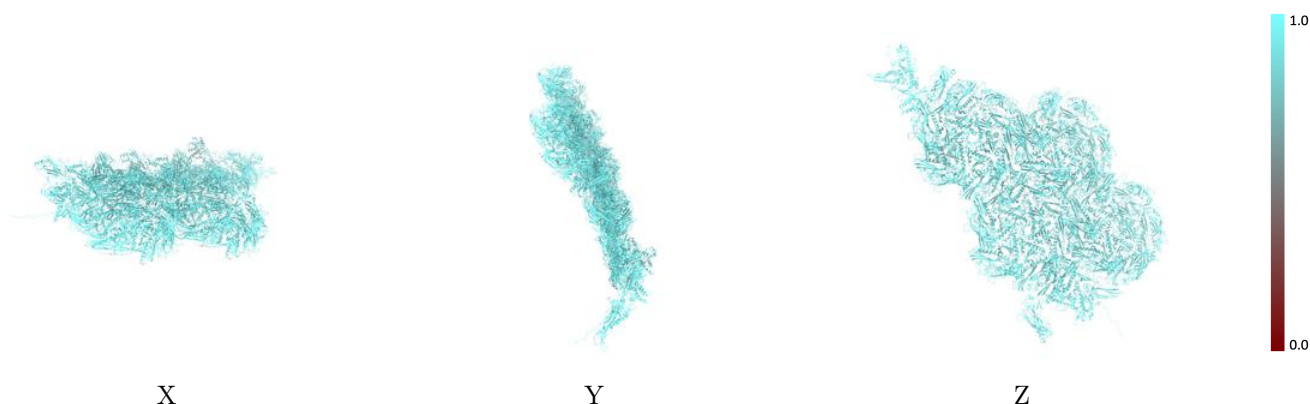
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



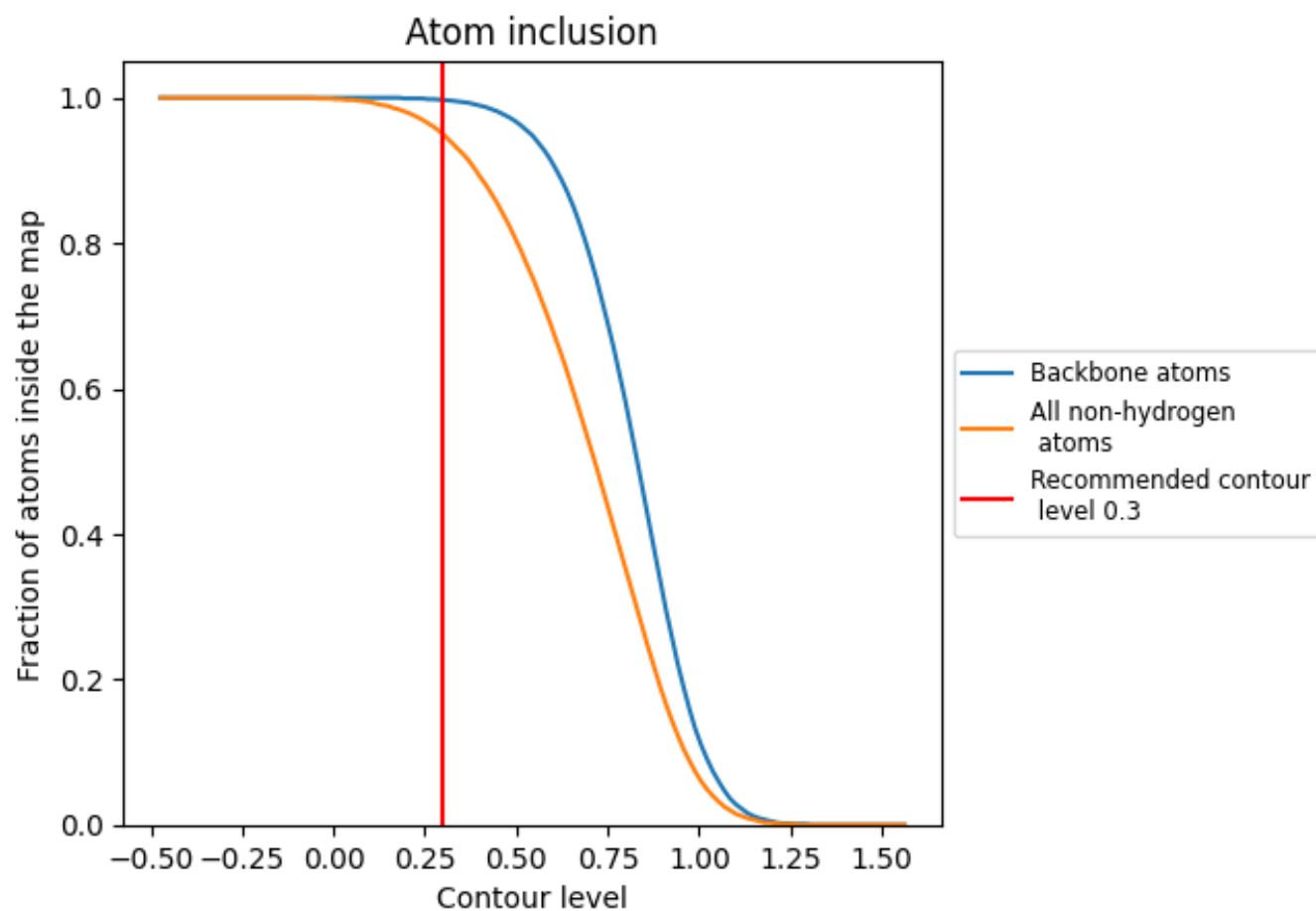
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 95% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.1680
A0	 0.9460	 0.1720
A1	 0.9450	 0.1630
A2	 0.9620	 0.1720
A3	 0.9550	 0.1720
A4	 0.9440	 0.1660
A5	 0.9540	 0.1740
A6	 0.9460	 0.1630
A7	 0.9540	 0.1670
A8	 0.9570	 0.1700
A9	 0.9530	 0.1730
Ar	 0.9580	 0.1710
As	 0.9510	 0.1690
At	 0.9520	 0.1780
Au	 0.9680	 0.1700
Av	 0.9620	 0.1710
Aw	 0.9510	 0.1640
Ax	 0.9520	 0.1640
Ay	 0.9590	 0.1720
Az	 0.9540	 0.1770
B	 0.9650	 0.1860
BA	 0.9370	 0.1490
BB	 0.9270	 0.1580
BC	 0.9460	 0.1630
BD	 0.9560	 0.1720
BE	 0.9390	 0.1670
BF	 0.9370	 0.1590
BG	 0.9630	 0.1710
BH	 0.9580	 0.1700
G	 0.7610	 0.1830

