



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:30 AM UTC

PDB ID : 6XF8 / pdb_00006xf8
EMDB ID : EMD-22166
Title : DLP 5 fold
Authors : Sutton, G.; Sun, D.P.; Fu, X.F.; Kotecha, A.; Hecksel, G.W.; Clare, D.K.;
Zhang, P.; Stuart, D.; Boyce, M.
Deposited on : 2020-06-15
Resolution : 6.50 Å(reported)

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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

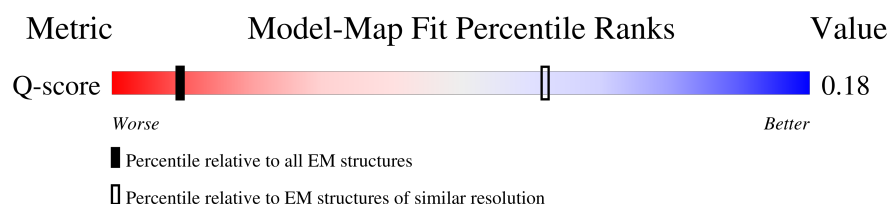
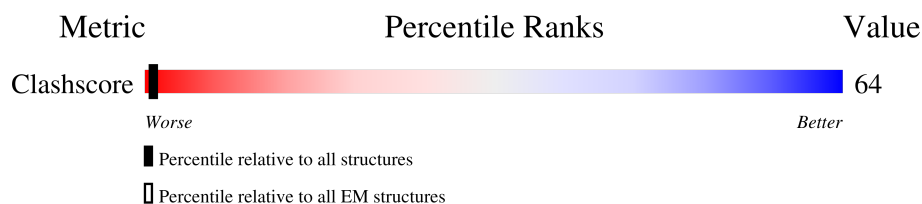
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

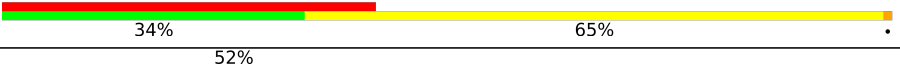
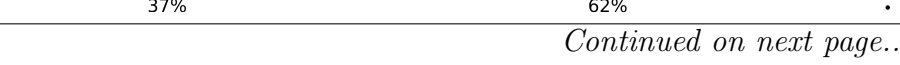
The reported resolution of this entry is 6.50 Å.

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	-
Q-score	-	25397	556 (6.00 - 7.00)

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	F	633	
1	K	633	
2	G	365	
2	H	365	
2	I	365	
3	E	417	

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Mol	Chain	Length	Quality of chain
4	B	1059	 55% 38% 59%
4	C	1059	 50% 37% 62%
5	A	1288	 45% 30% 69%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 47830 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 Outer capsid protein mu-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	608	Total	C	N	O	S	0	0
			4641	2950	770	903	18		
1	F	608	Total	C	N	O	S	0	0
			4641	2950	770	903	18		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	344	LEU	PRO	conflict	UNP P11077
K	359	PHE	LEU	conflict	UNP P11077
F	344	LEU	PRO	conflict	UNP P11077
F	359	PHE	LEU	conflict	UNP P11077

- Molecule 2 is a protein called Outer capsid protein sigma-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	365	Total	C	N	O	S	0	0
			2885	1818	508	531	28		
2	H	365	Total	C	N	O	S	0	0
			2885	1818	508	531	28		
2	G	365	Total	C	N	O	S	0	0
			2885	1818	508	531	28		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	104	CYS	ALA	conflict	UNP P07939
I	325	ASN	ASP	conflict	UNP P07939
H	104	CYS	ALA	conflict	UNP P07939
H	325	ASN	ASP	conflict	UNP P07939
G	104	CYS	ALA	conflict	UNP P07939
G	325	ASN	ASP	conflict	UNP P07939

- Molecule 3 is a protein called Inner capsid protein sigma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	417	Total	C	N	O	S	0	0
			3313	2092	600	604	17		

- Molecule 4 is a protein called Inner capsid protein lambda-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	1051	Total	C	N	O	S	0	0
			8311	5314	1407	1540	50		
4	B	1031	Total	C	N	O	S	0	0
			8143	5208	1375	1510	50		

- Molecule 5 is a protein called mRNA (guanine-N(7)-)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	1284	Total	C	N	O	S	0	0
			10126	6468	1699	1917	42		

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	ASN	THR	conflict	UNP Q91RA5
A	78	ALA	VAL	conflict	UNP Q91RA5
A	97	VAL	ILE	conflict	UNP Q91RA5
A	108	ASN	SER	conflict	UNP Q91RA5
A	151	ALA	VAL	conflict	UNP Q91RA5
A	231	HIS	ASN	conflict	UNP Q91RA5
A	277	THR	ALA	conflict	UNP Q91RA5
A	365	THR	ALA	conflict	UNP Q91RA5
A	370	VAL	ILE	conflict	UNP Q91RA5
A	407	MET	VAL	conflict	UNP Q91RA5
A	425	ASP	GLU	conflict	UNP Q91RA5
A	508	SER	ALA	conflict	UNP Q91RA5
A	509	ARG	GLY	conflict	UNP Q91RA5
A	559	ILE	VAL	conflict	UNP Q91RA5
A	599	LEU	PHE	conflict	UNP Q91RA5
A	622	PRO	THR	conflict	UNP Q91RA5
A	661	HIS	GLN	conflict	UNP Q91RA5
A	775	ILE	VAL	conflict	UNP Q91RA5
A	799	SER	ALA	conflict	UNP Q91RA5
A	889	MET	ILE	conflict	UNP Q91RA5
A	916	LYS	ARG	conflict	UNP Q91RA5

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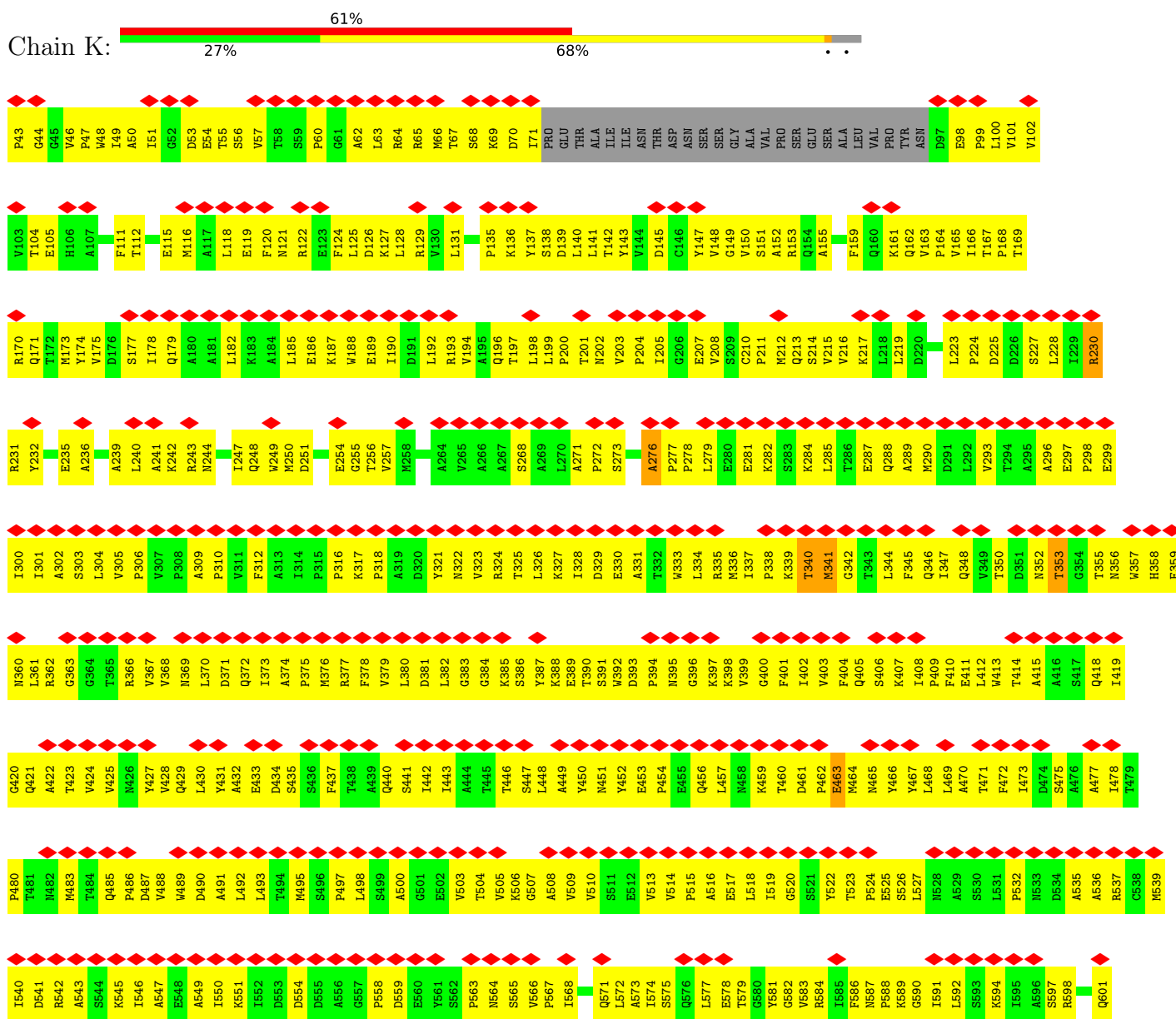
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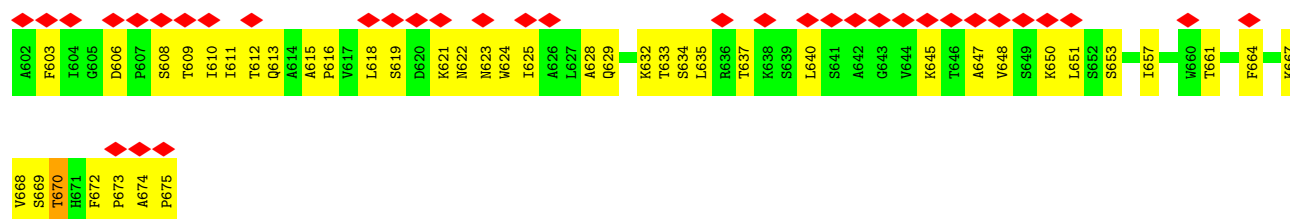
Chain	Residue	Modelled	Actual	Comment	Reference
A	944	SER	ALA	conflict	UNP Q91RA5
A	950	ARG	LYS	conflict	UNP Q91RA5
A	964	ASP	GLY	conflict	UNP Q91RA5
A	982	VAL	ILE	conflict	UNP Q91RA5
A	991	THR	ALA	conflict	UNP Q91RA5
A	992	ARG	LYS	conflict	UNP Q91RA5
A	1008	ILE	VAL	conflict	UNP Q91RA5
A	1031	ARG	GLN	conflict	UNP Q91RA5
A	1052	VAL	ILE	conflict	UNP Q91RA5
A	1083	THR	ALA	conflict	UNP Q91RA5
A	1119	VAL	ILE	conflict	UNP Q91RA5
A	1155	THR	ALA	conflict	UNP Q91RA5
A	1263	VAL	ILE	conflict	UNP Q91RA5
A	1274	ILE	LEU	conflict	UNP Q91RA5

3 Residue-property plots

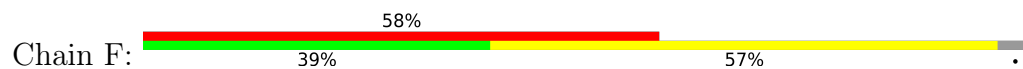
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Outer capsid protein mu-1





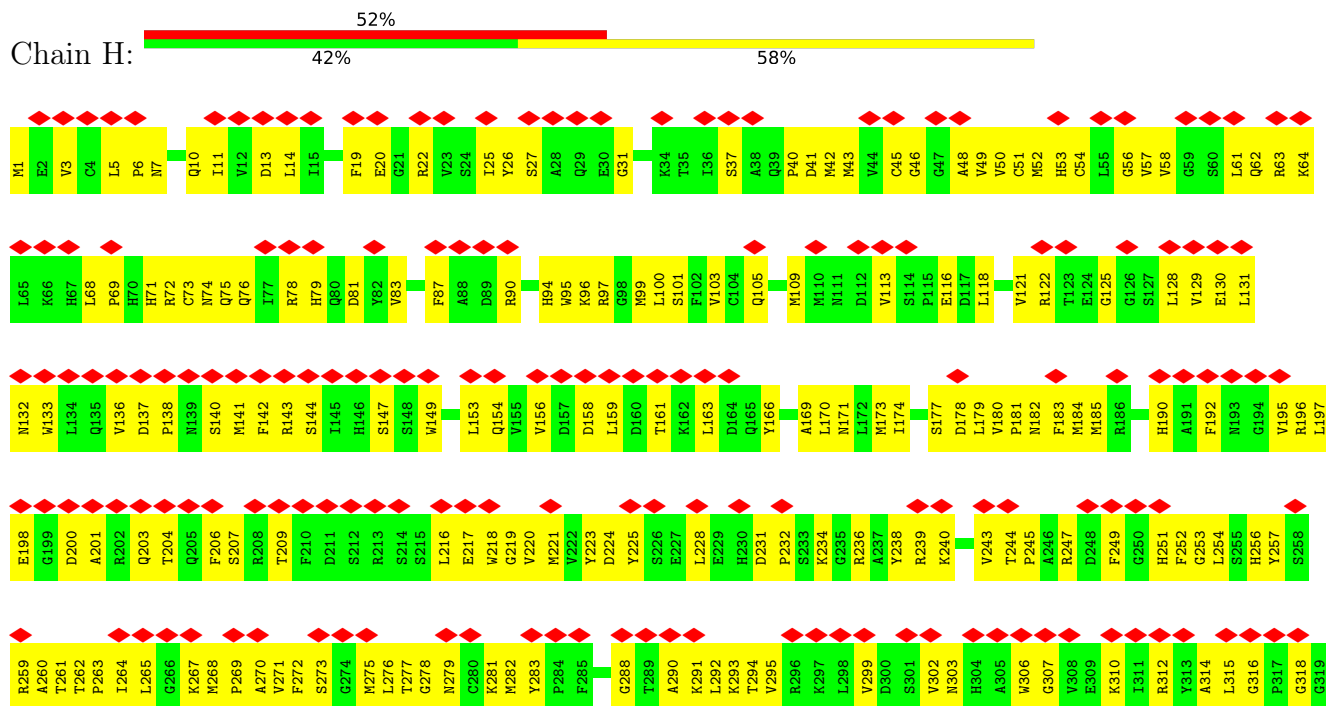
• Molecule 1: Outer capsid protein mu-1

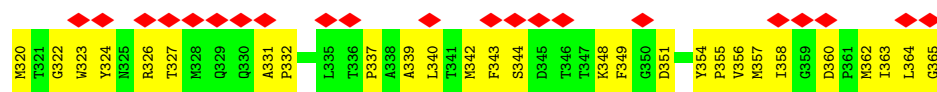


- Molecule 2: Outer capsid protein sigma-3

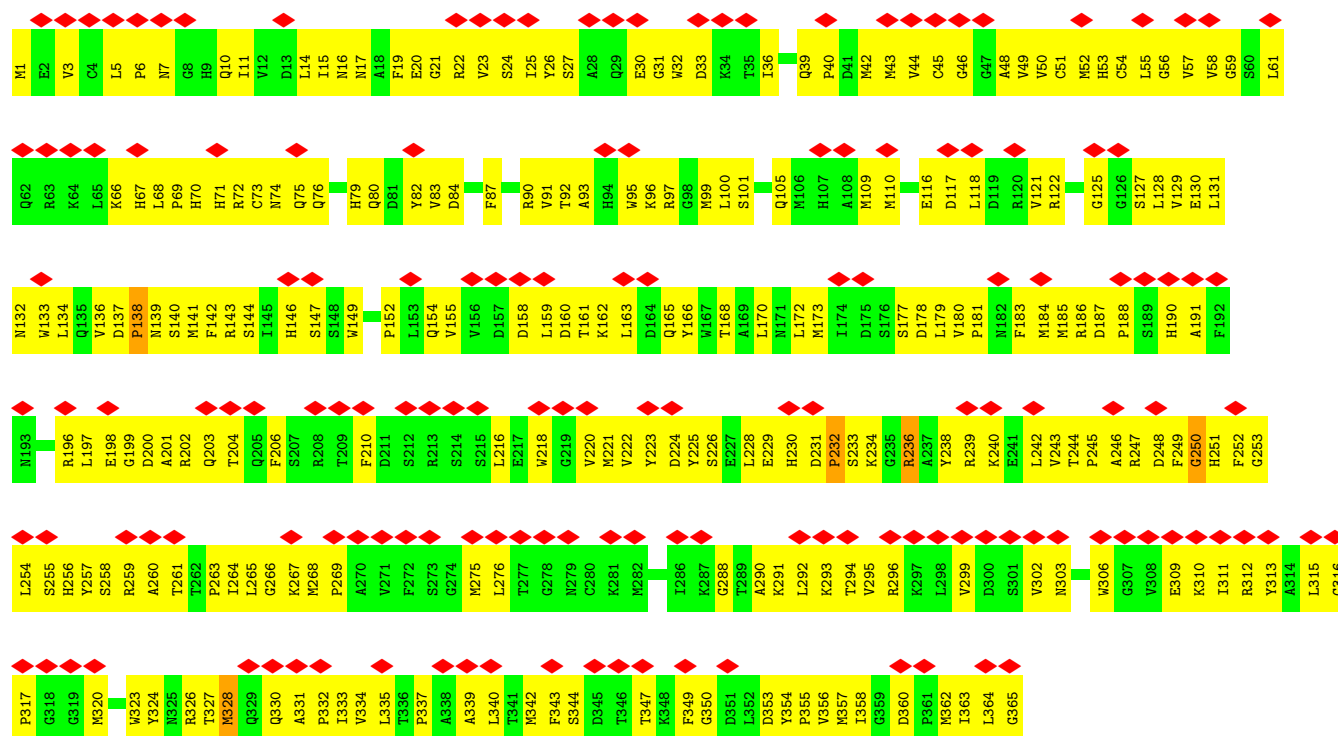


- Molecule 2: Outer capsid protein sigma-3

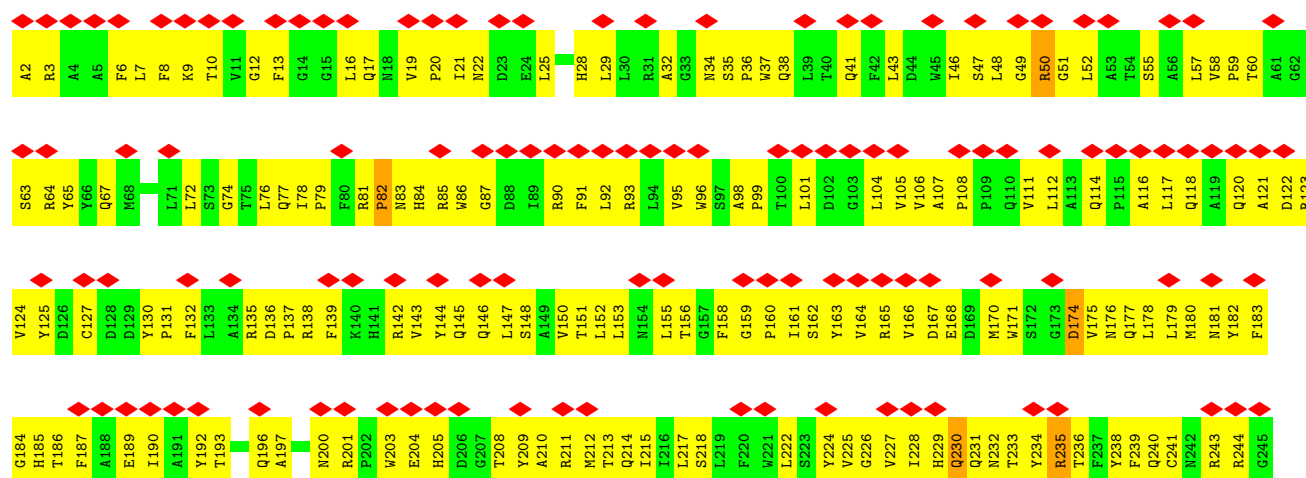


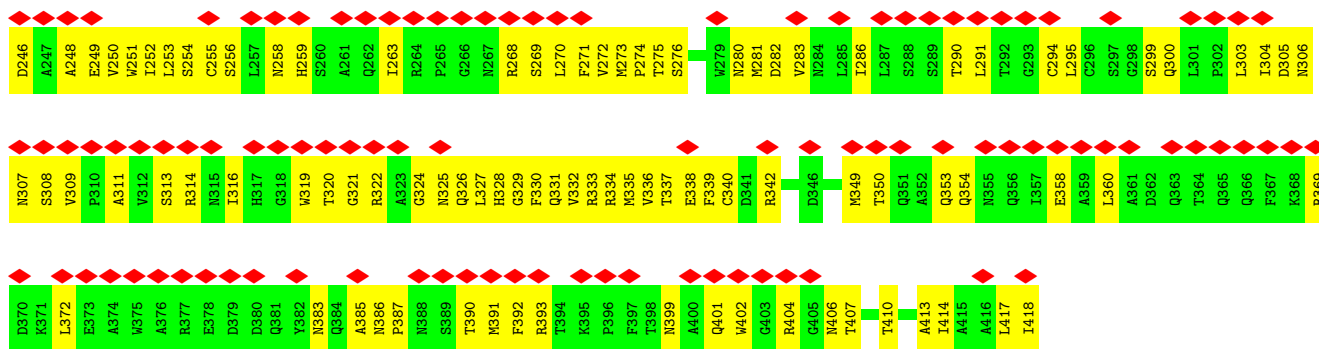


• Molecule 2: Outer capsid protein sigma-3

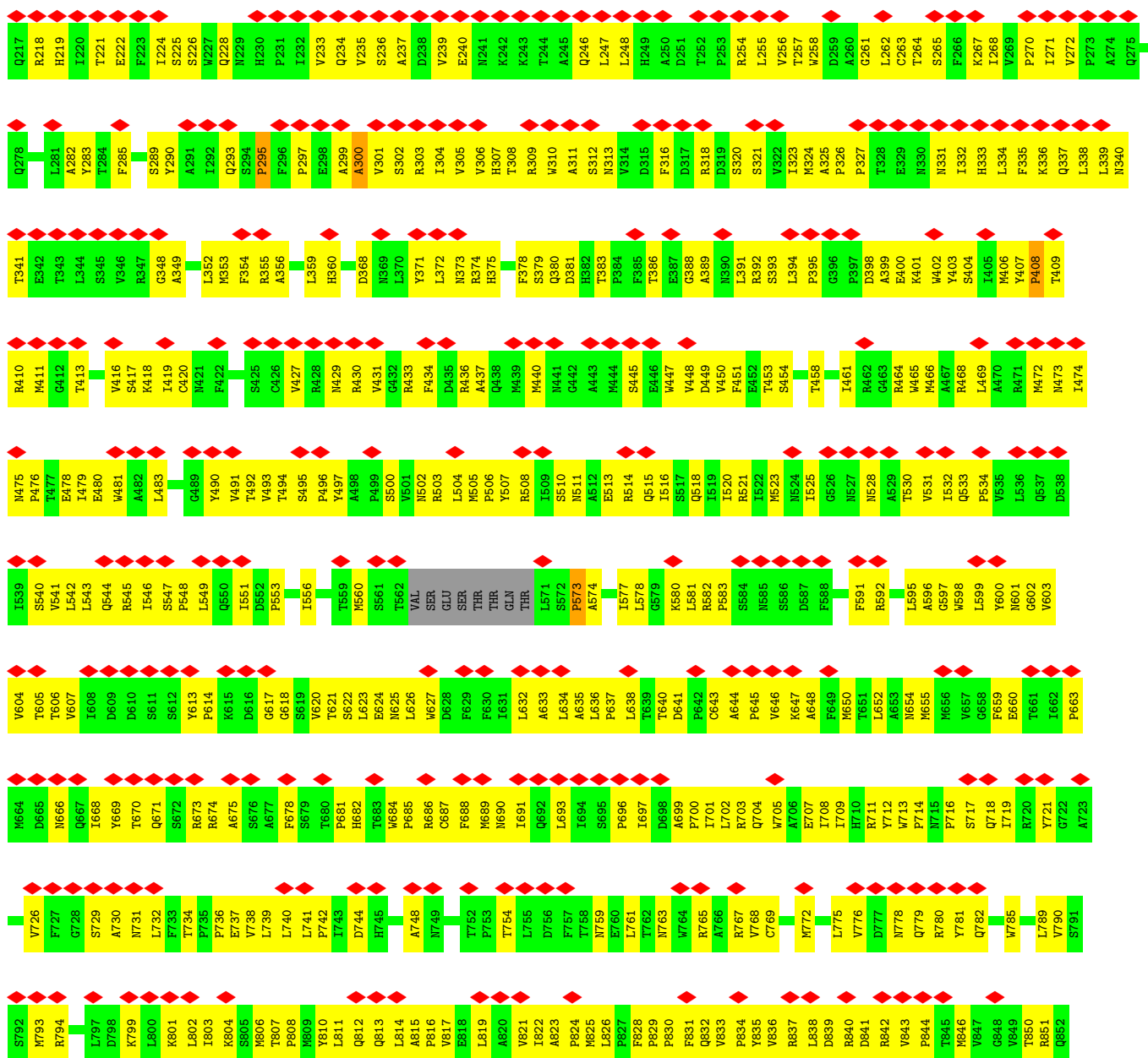


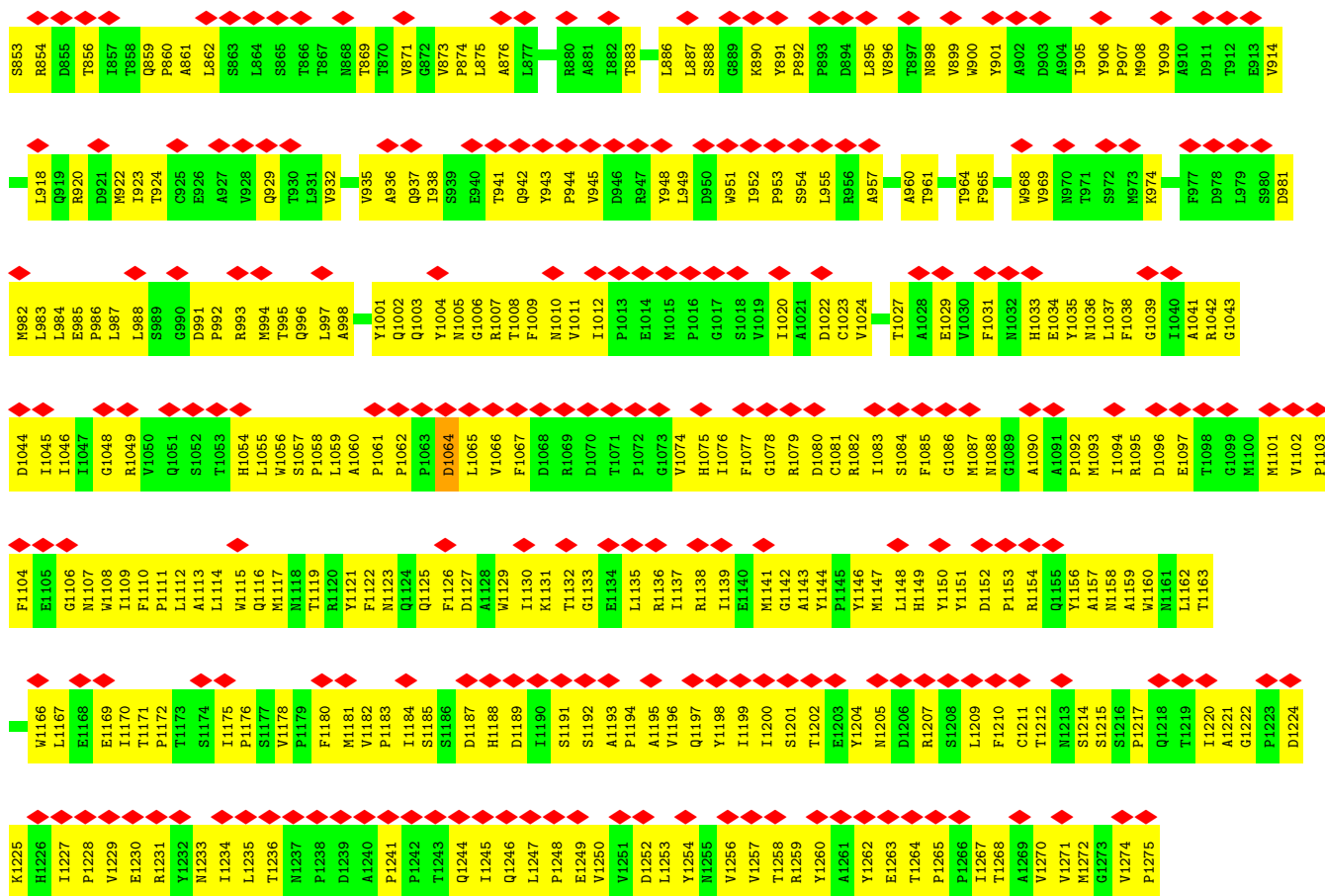
• Molecule 3: Inner capsid protein sigma-2

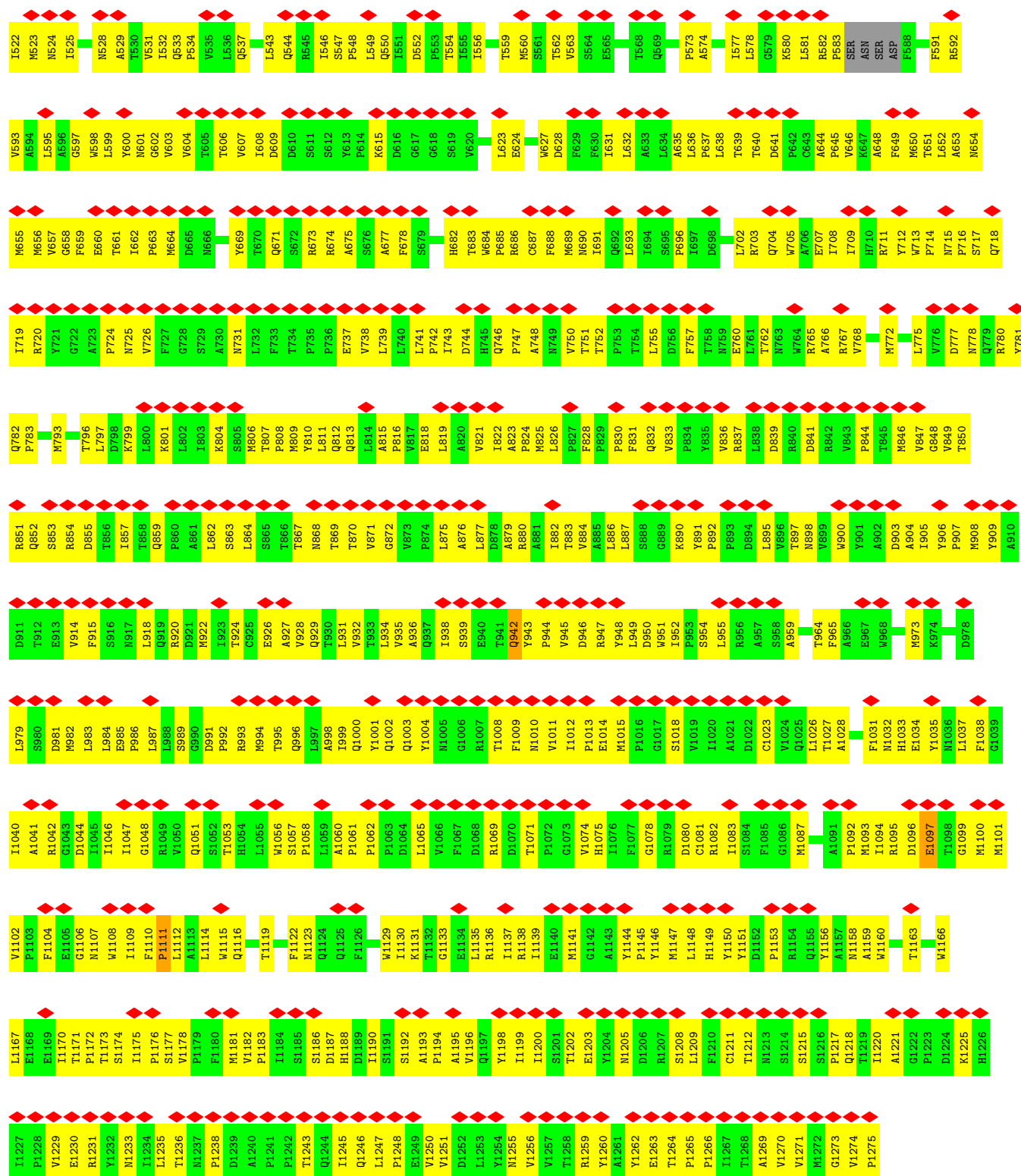




• Molecule 4: Inner capsid protein lambda-1







- Molecule 5: mRNA (guanine-N(7)-)-methyltransferase



F813	E814	V815	S816	V819	Y820	D821	G822	D823	V824	W825	L826	D827	L828	G829	T830	G831	P832	E833	A834	K835	I836	L837	E838	L839	I840	P841	A842	T843	S844	P845	V846	T847	C848	V849	D850	I851	R852	P853	T854	A855	P856	P857	S858	G859	W861	N862	V863	R864	T865	T866	F867	L868	E869	L870	D871	Y872	L873		
L684	S685	T686	I687	S688	R689	Q690	L691	P692	R693	S694	P695	F696	Q697	P698	S699	D699	G700	S701	W702	T703	T704	G705	I706	E707	L708	T709	S710	I711	E712	P713	W714	G715	F716	S717	W718	M719	T720	Q721	R724	I725	L730	C731	A732	W733	V734	G735	V736	A737	R738	F739	L740	A741	A742	I743	Y744	E745	A749		
R750	V751	L752	T753	I754	T755	T756	R757	R758	S759	P760	A761	S762	R765	R768	L769	R770	Y771	L772	P773	L774	I775	D776	P777	L778	S779	L780	E781	V782	Q783	A784	R785	T786	L787	L788	P789	A790	D791	P792	W793	L794	F795	E796	N797	V798	S799	Q800	A801	H804	W805	C806	T807	M808	M809	M810	Y811	N812			
V623	W624	H625	V626	I627	Q628	Q629	K630	L631	L632	P633	N634	L635	T636	S637	Y638	L639	L640	K641	K642	F644	V645	T646	N647	N648	V649	E650	L651	F652	F653	V654	A655	F656	G657	V658	H659	Q660	H661	S662	S663	L664	T665	W666	T667	S668	G669	V670	Y671	F672	F673	L674	V675	D676	H677	F678	T679	Y681			
D561	L562	A563	R564	P565	F566	Q567	S568	G569	D570	Y571	Q572	F573	Y574	Y575	S576	F577	V578	D579	Q580	Y581	V582	D583	G584	H585	D586	D587	L588	S589	L590	S591	S592	G593	L594	V595	E596	S597	L598	L599	M603	H604	A605	W606	T607	A607	P608	G609	O610	S611	F612	F613	V614	L615	L616	M617	F618	P619	T620	R621	P622
Y438	V439	D440	Y441	N442	R443	S444	H445	R446	V447	V448	L449	S450	S451	E452	L453	P454	Q455	L456	P457	D458	T459	Y460	F461	D462	G463	D464	E465	Q466	R469	S470	L471	F472	S473	L474	A475	R476	K477	L478	G479	P480	R481	S482	L483	V484	K485	D486	T487	L488	V489	K491	Y494	Q495	A496	L497	D498	P499			
Q374	L375	R376	L377	G378	K379	R380	L381	A383	Q385	S388	D389	T390	P391	S392	P393	V394	Q395	Q399	Y400	T401	L402	D403	Q404	A405	A406	M407	D408	E409	Q410	D411	L412	M413	V414	L417	T418	Q419	L420	P421	L422	R423	P424	D425	Y426	G427	M428	L429	W430	V431	G432	D433	A434	L435	S436	Y437					
Y312	Q313	L314	A315	R316	P317	L318	P319	R320	Q321	L322	T323	N324	R325	W326	L327	F330	V331	S332	Q333	T334	K335	D337	G338	V339	N340	E341	T342	P343	L344	W345	P346	Q347	E348	R349	Y350	V351	Q352	L353	A354	P358	S359	V360	V361	D362	G363	L366	A364	T365	Q366	G367	Y369	V370	R371	K372	N373				
T247	L248	T249	N250	T252	M255	L256	L257	L261	E262	Q263	F264	S265	A266	A270	R271	Q274	P275	V276	T277	R278	L279	D280	L281	Q281	C282	S283	H284	L285	R286	W287	G288	A289	Q290	Y291	V292	G293	E294	D295	L296	S296	L297	T298	Y299	R300	L301	G302	V303	L304	S305	L306	L307	A308	T309	N310	G311				
L187	F188	K189	D191	L192	S193	D194	Y195	A196	K197	A198	F199	Y200	D202	T203	Y204	E205	G206	L207	D208	R209	F210	F211	W212	T213	H214	D215	L216	S216	S217	A218	G219	V222	H223	Y224	D225	V226	T227	N229	Q230	H231	H232	Y233	L234	L235	G236	T237	L238	T239	Q240	M241	Y242	S243	A244	P245					
Q127	A128	F129	Y130	D131	L132	L133	P134	L135	L136	L137	I138	L139	D140	T141	M142	I143	G144	D145	L146	L147	G148	T149	G150	L151	S152	L153	S154	Q155	F156	F157	Q158	S159	H160	G161	D162	V163	L164	E165	V166	A167	G169	L170	K171	Y172	L173	Q174	M175	E176	N177	Y178	S179	N180	D182	D183	P185	P186			
Q84	G85	L86	V87	L88	D89	Q71	L72	Y73	G74	F75	P76	G77	A78	F79	D80	D81	W82	E83	R84	R87	E88	K89	V92	L93	K94	Y95	E96	R99	I100	Y101	P102	I103	G104	N105	E106	S107	N108	E109	H110	V111	V112	V113	F114	V115	A116	N117	A118	L119	V120	G121	A122	F123	L124	S125	N126				
N3	V4	W5	G6	V7	R8	L9	A10	D11	S12	L13	S14	S15	P16	T17	I18	E19	T20	R21	T22	R23	Q24	Y25	T26	L27	H28	D29	L30	L34	D35	A36	N37	P38	G39	R40	E41	P42	W43	K44	P45	L46	N48	Q49	T51	N52	N53	I54	V55	A56	V57	Q58	L59	F60	R61	P62	L63				



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of subtomograms used	625	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.955	Depositor
Minimum map value	-5.801	Depositor
Average map value	0.054	Depositor
Map value standard deviation	0.430	Depositor
Recommended contour level	2.7	Depositor
Map size (Å)	648.0, 648.0, 648.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.8, 1.8, 1.8	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	F	0.95	0/4737	1.26	5/6466 (0.1%)
1	K	0.94	0/4737	1.28	11/6466 (0.2%)
2	G	0.94	0/2957	1.29	8/4005 (0.2%)
2	H	0.92	0/2957	1.25	2/4005 (0.0%)
2	I	0.93	0/2957	1.26	2/4005 (0.0%)
3	E	0.89	0/3398	1.28	5/4626 (0.1%)
4	B	0.93	0/8363	1.27	8/11454 (0.1%)
4	C	0.94	0/8537	1.27	8/11693 (0.1%)
5	A	0.93	0/10384	1.25	15/14170 (0.1%)
All	All	0.93	0/49027	1.27	64/66890 (0.1%)

There are no bond length outliers.

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	408	PRO	N-CA-C	-9.08	102.04	113.84
1	K	276	ALA	N-CA-C	7.43	114.68	108.07
3	E	50	ARG	N-CA-C	-7.27	104.14	113.16
4	B	659	PHE	N-CA-C	-7.06	103.28	112.68
4	B	414	PRO	N-CA-C	-6.68	104.45	113.40

There are no chirality outliers.

There are no planarity outliers.

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	F	4641	0	4668	618	0
1	K	4641	0	4655	966	0
2	G	2885	0	2806	479	0
2	H	2885	0	2813	307	0
2	I	2885	0	2813	272	0
3	E	3313	0	3214	583	0
4	B	8143	0	8056	1028	0
4	C	8311	0	8205	1058	0
5	A	10126	0	9903	1442	0
All	All	47830	0	47133	6083	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 64.

The worst 5 of 6083 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)
3:E:180:MET:HE2	4:B:497:TYR:CD2	1.31	1.65
1:K:506:LYS:HG3	2:G:313:TYR:CG	1.26	1.65
1:K:584:ARG:HB2	2:G:70:HIS:CD2	1.27	1.63
3:E:258:ASN:HB2	4:C:854:ARG:CZ	1.30	1.61
1:K:504:THR:HG22	2:G:317:PRO:CG	1.13	1.60

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

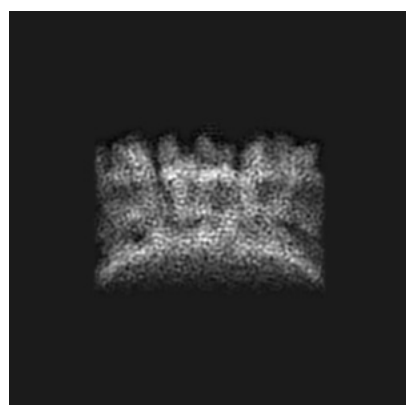
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22166. These allow visual inspection of the internal detail of the map and identification of artifacts.

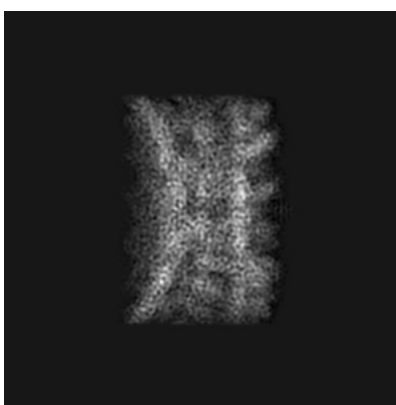
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

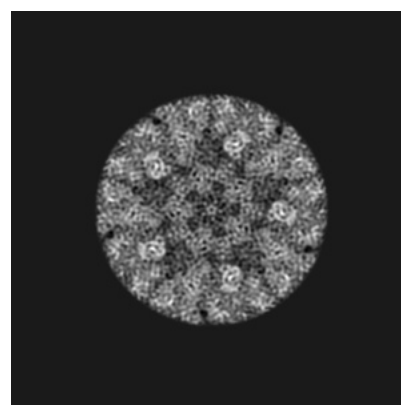
6.1.1 Primary map



X



Y

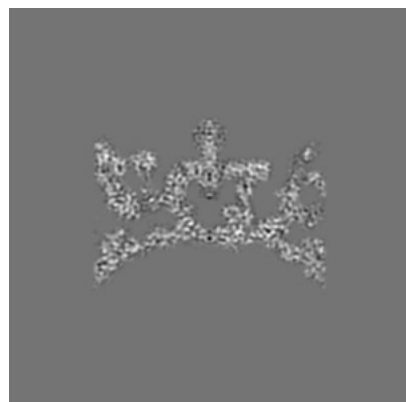


Z

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

6.2 Central slices [i](#)

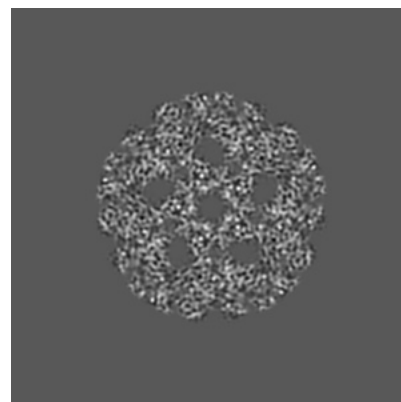
6.2.1 Primary map



X Index: 180



Y Index: 180



Z Index: 180

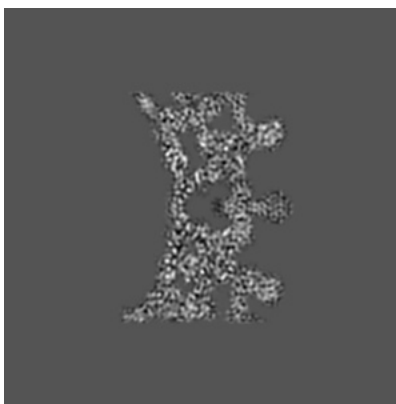
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

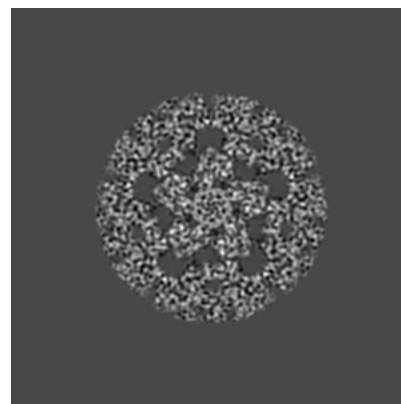
6.3.1 Primary map



X Index: 195



Y Index: 176

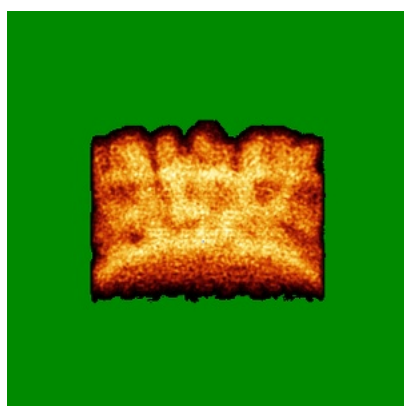


Z Index: 213

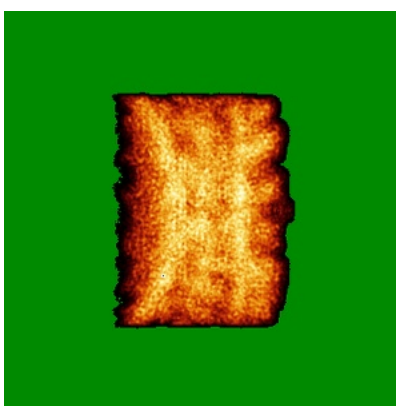
The images above show the largest variance slices of the map in three orthogonal directions.

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

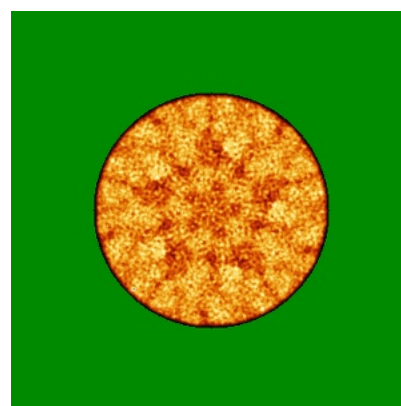
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

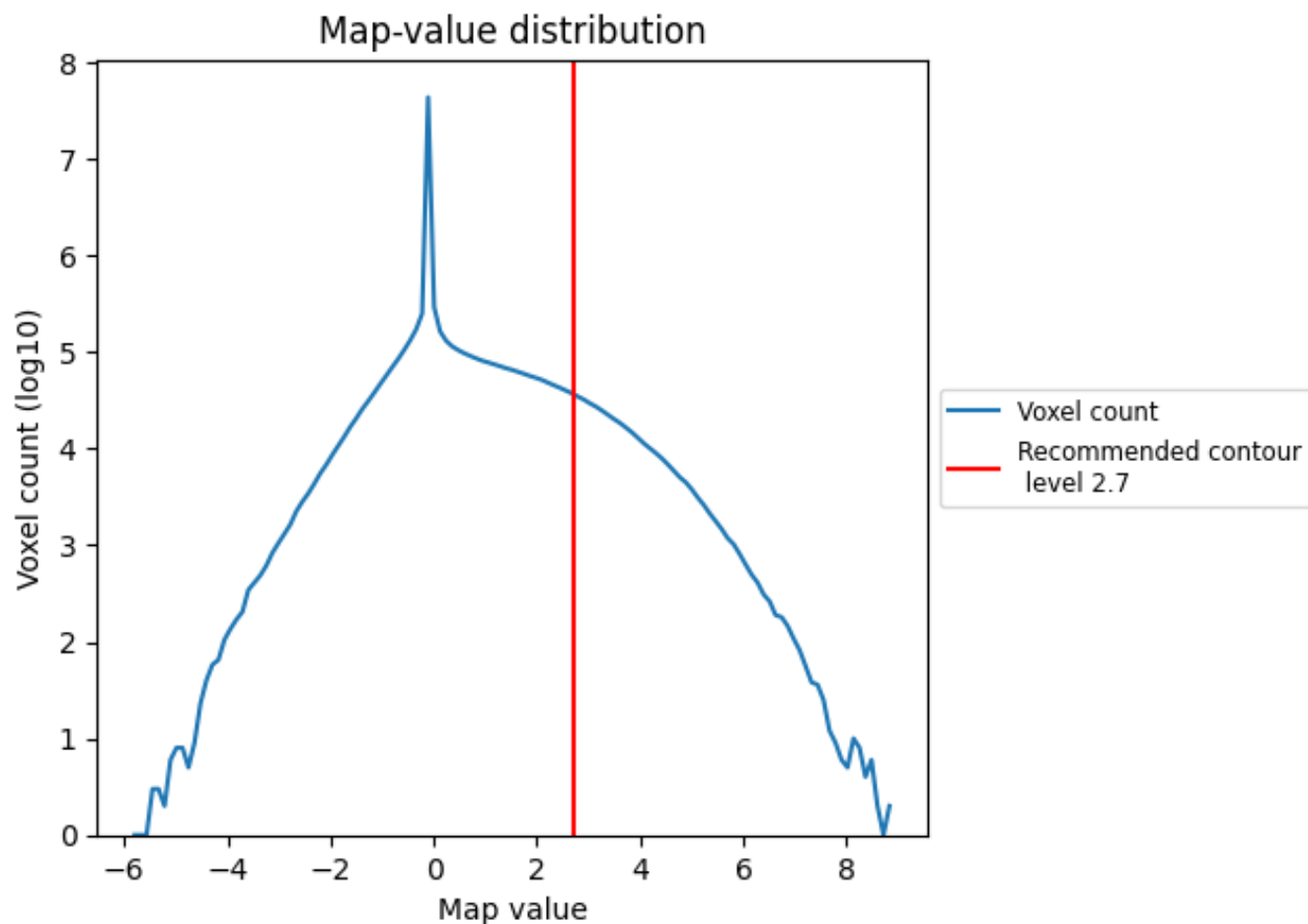
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

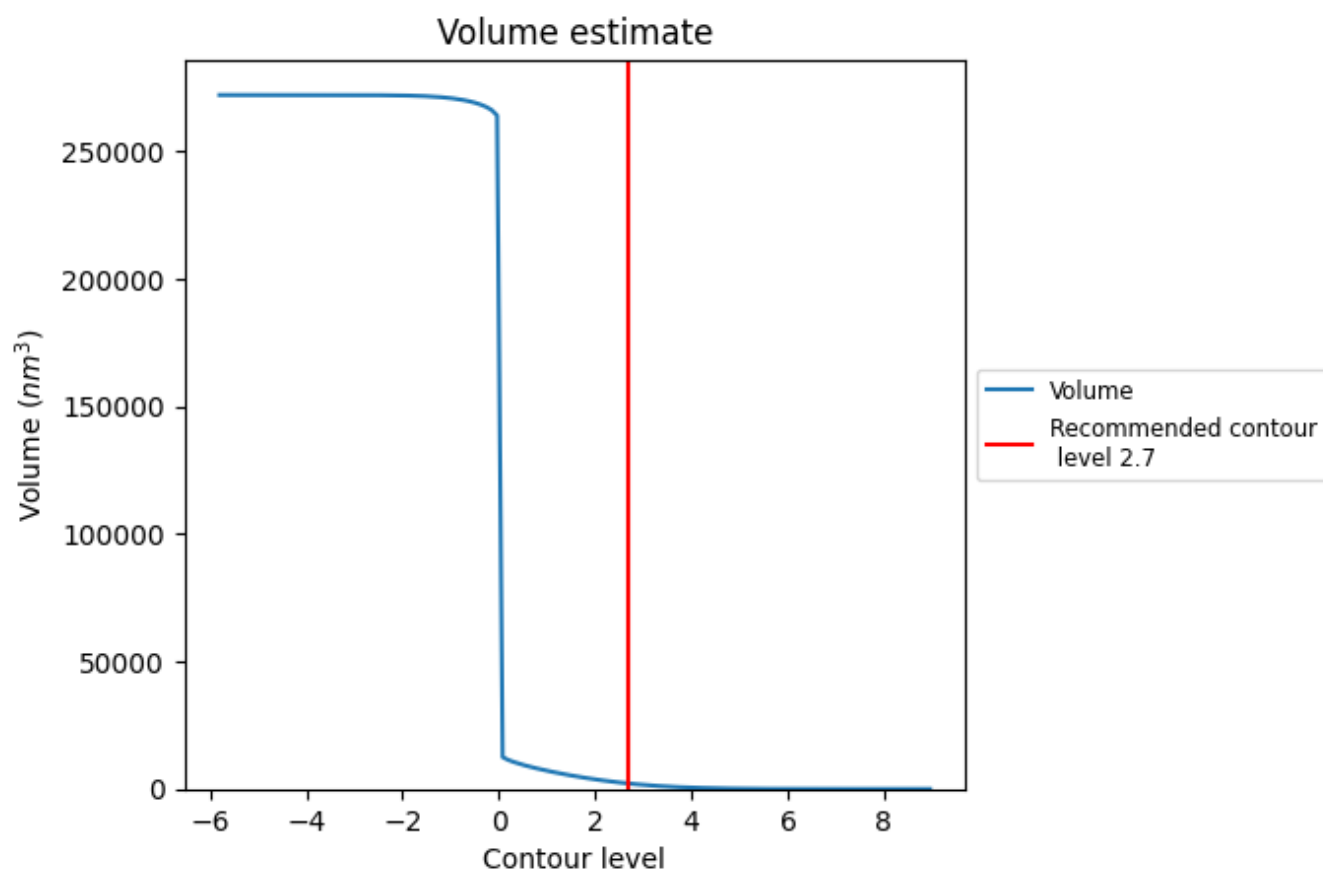
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

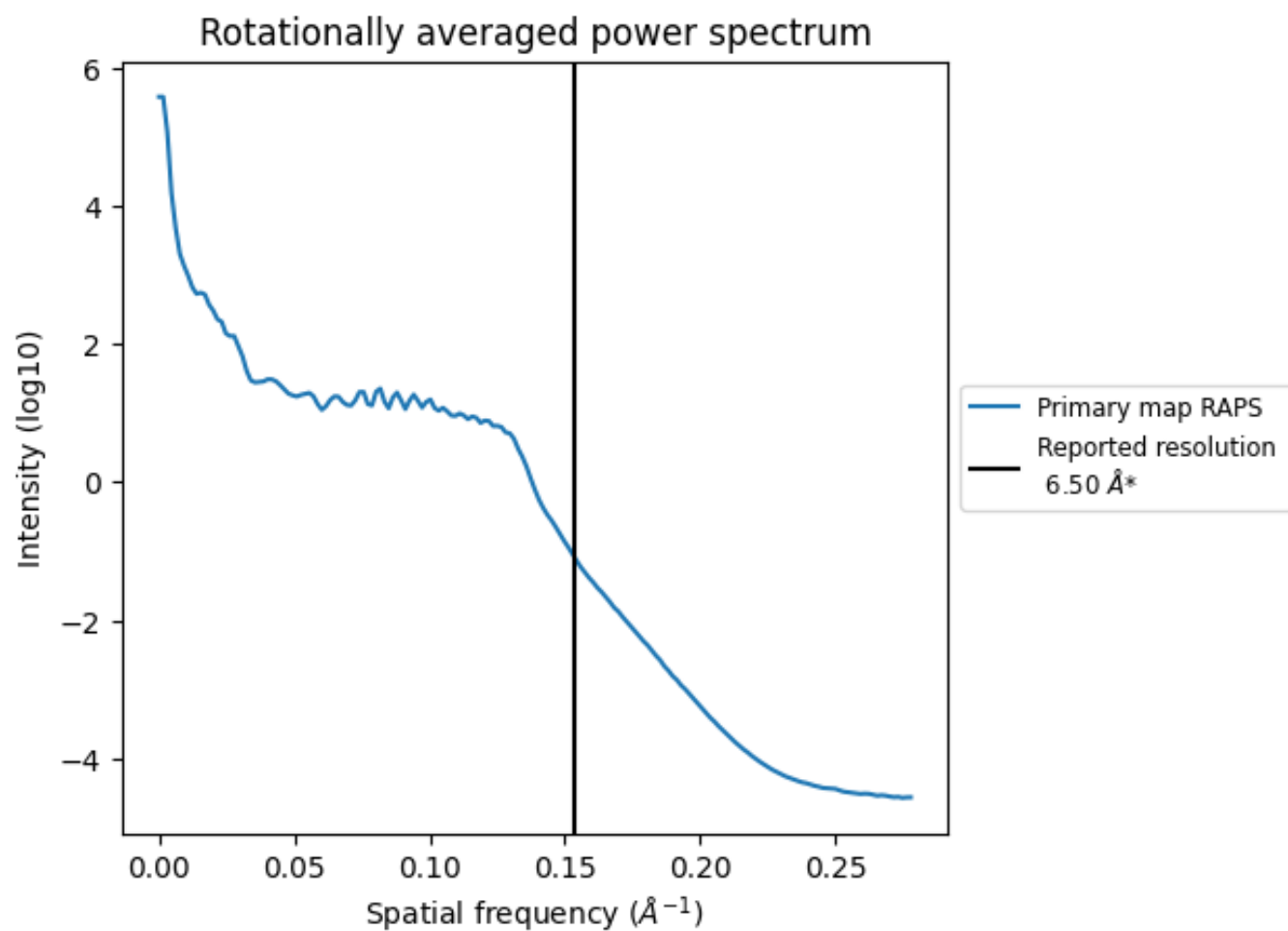
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2134 nm³; this corresponds to an approximate mass of 1928 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 0.154 Å⁻¹

8 Fourier-Shell correlation

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

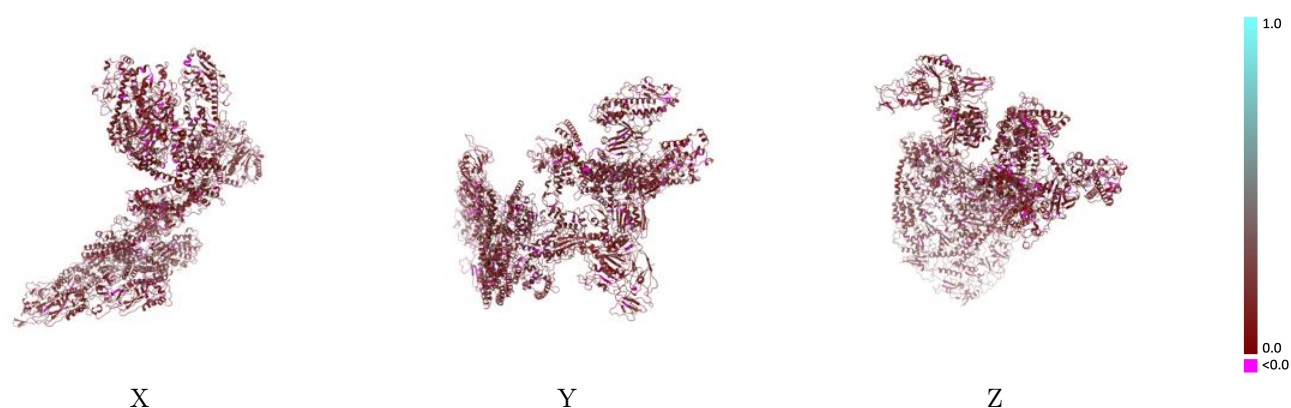
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-22166 and PDB model 6XF8. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

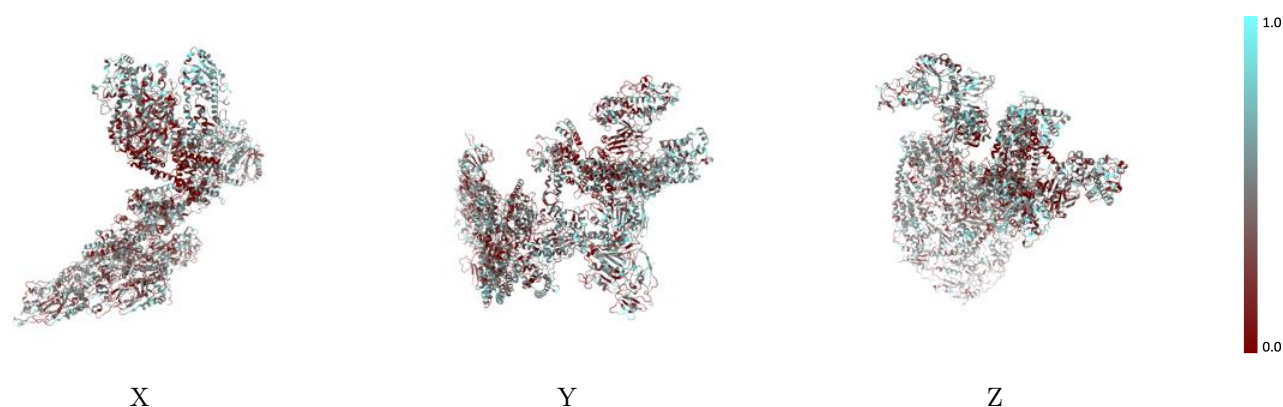
This section was not generated.

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



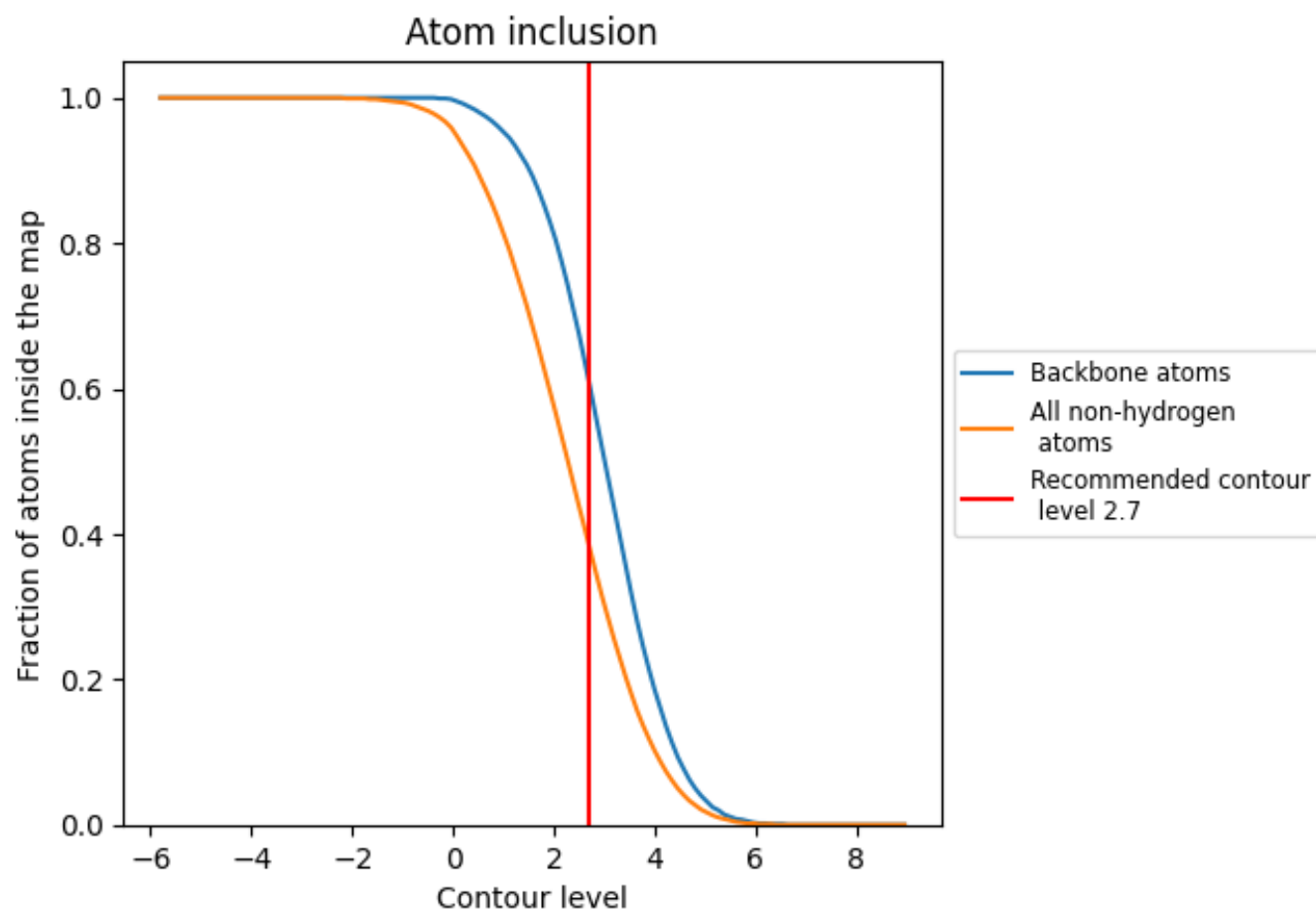
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 38% 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 (2.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3830	0.1800
A	0.4180	0.1900
B	0.3490	0.1770
C	0.3920	0.1840
E	0.3840	0.1770
F	0.3240	0.1690
G	0.4760	0.1890
H	0.3860	0.1640
I	0.4830	0.1750
K	0.2910	0.1760

1.0

0.0

<0.0