



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 07:50 PM UTC

PDB ID : 8HEY / pdb_00008hey
EMDB ID : EMD-34704
Title : One CVSC-binding penton vertex in HCMV B-capsid
Authors : Li, Z.; Yu, X.
Deposited on : 2022-11-09
Resolution : 4.10 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

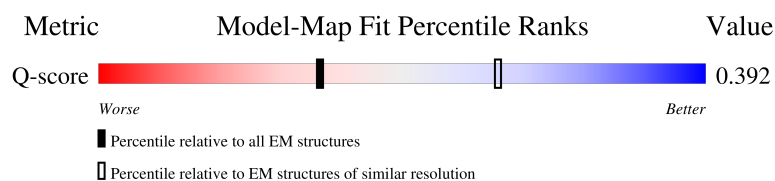
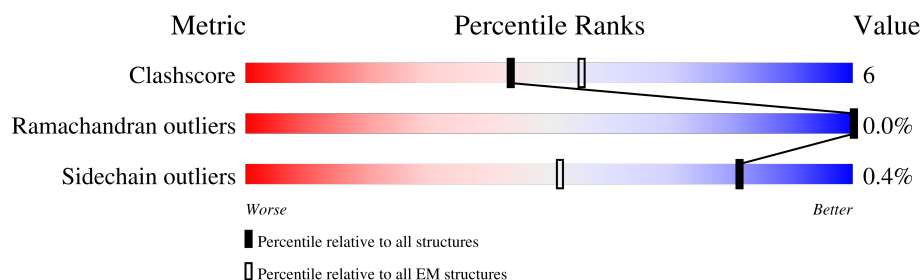
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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.



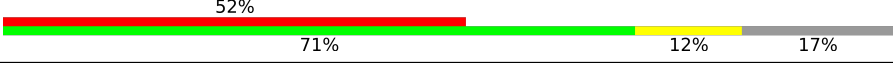
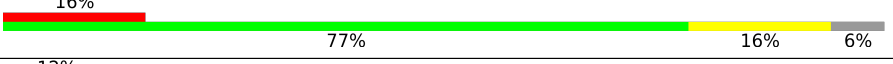
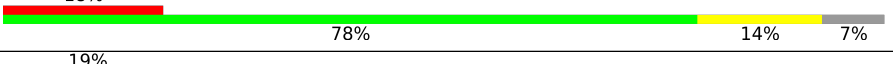
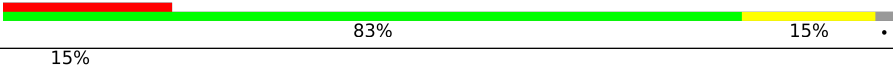
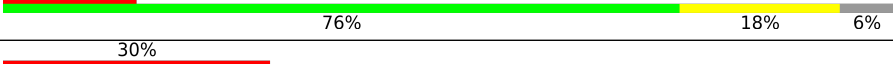
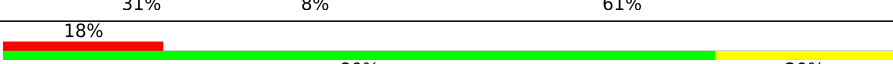
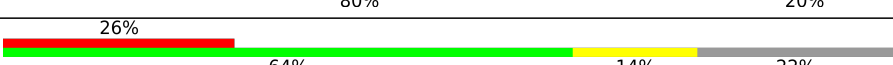
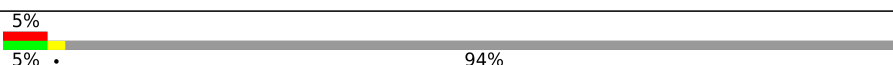
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	Q	75	56% 52% 7% 41%
1	R	75	53% 60% 13% 27%
1	S	75	51% 64% 8% 27%
1	T	75	19% 31% 69%

Continued on next page...

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Mol	Chain	Length	Quality of chain
1	i	75	
1	j	75	
2	A	1370	
2	B	1370	
2	C	1370	
2	D	1370	
2	Y	1370	
2	Z	1370	
2	a	1370	
3	I	306	
3	h	306	
3	n	306	
3	o	306	
4	g	290	
4	m	290	
5	M	594	
6	N	642	
6	O	642	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 90223 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 Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T	23	Total	C	N	O	S	0	0
			192	121	38	31	2		
1	i	56	Total	C	N	O	S	0	0
			446	282	80	80	4		
1	j	58	Total	C	N	O	S	0	0
			467	294	87	82	4		
1	Q	44	Total	C	N	O	S	0	0
			352	221	65	62	4		
1	R	55	Total	C	N	O	S	0	0
			436	276	77	79	4		
1	S	55	Total	C	N	O	S	0	0
			436	276	77	79	4		

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	1281	Total	C	N	O	S	0	0
			10125	6444	1760	1864	57		
2	D	1270	Total	C	N	O	S	0	0
			10054	6409	1745	1843	57		
2	Y	1347	Total	C	N	O	S	0	0
			10676	6799	1850	1966	61		
2	Z	1326	Total	C	N	O	S	0	0
			10498	6687	1820	1933	58		
2	A	1142	Total	C	N	O	S	0	0
			9105	5832	1576	1648	49		
2	B	1282	Total	C	N	O	S	0	0
			10164	6479	1760	1866	59		
2	C	1300	Total	C	N	O	S	0	0
			10291	6562	1785	1885	59		

- Molecule 3 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	290	Total	C	N	O	S	0	0
			2304	1481	397	409	17		
3	I	277	Total	C	N	O	S	0	0
			2209	1418	381	393	17		
3	n	295	Total	C	N	O	S	0	0
			2334	1501	402	412	19		
3	o	289	Total	C	N	O	S	0	0
			2291	1473	393	407	18		

- Molecule 4 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	g	112	Total	C	N	O	S	0	0
			929	596	164	165	4		
4	m	290	Total	C	N	O	S	0	0
			2325	1485	411	417	12		

- Molecule 5 is a protein called Capsid vertex component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	464	Total	C	N	O	S	0	0
			3813	2388	733	678	14		

- Molecule 6 is a protein called Capsid vertex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	51	Total	C	N	O	S	0	0
			432	269	87	73	3		
6	O	41	Total	C	N	O	S	0	0
			344	223	62	57	2		

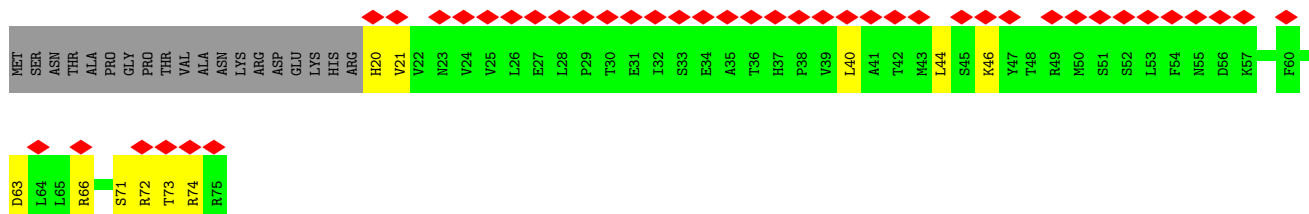
3 Residue-property plots [i](#)

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

- Molecule 1: Small capsomere-interacting protein



- Molecule 1: Small capsomere-interacting protein

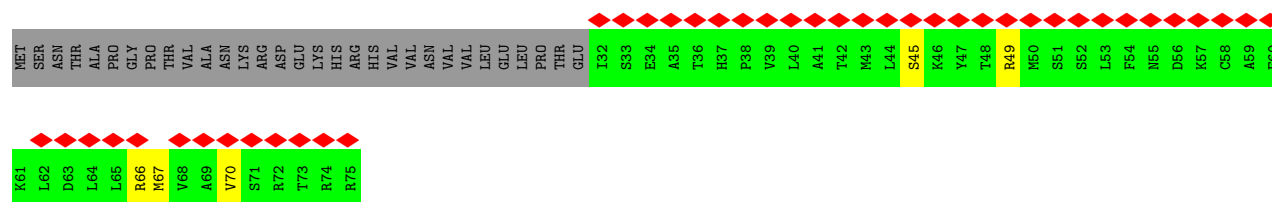


- Molecule 1: Small capsomere-interacting protein

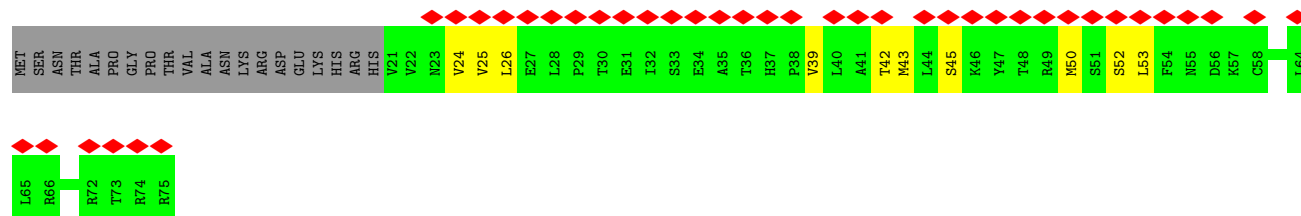


- Molecule 1: Small capsomere-interacting protein

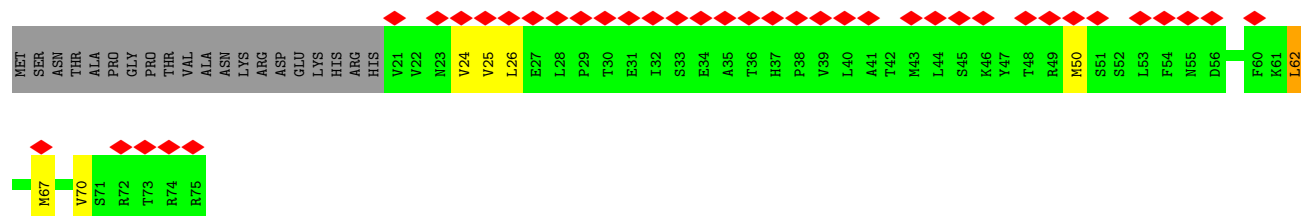




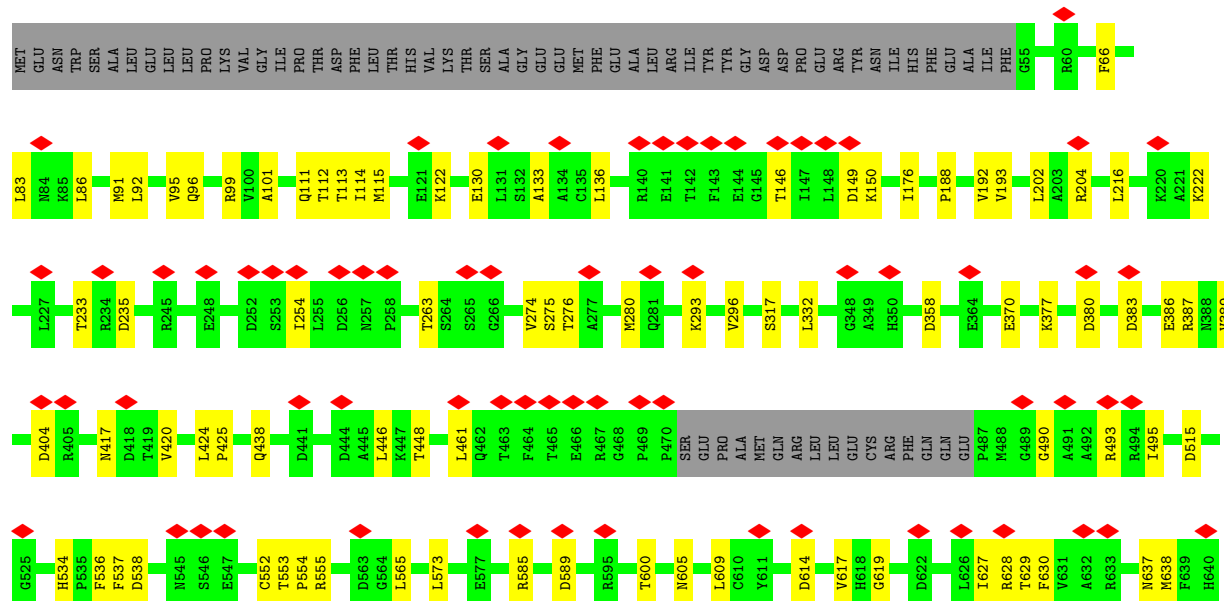
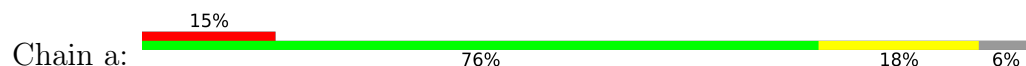
• Molecule 1: Small capsomere-interacting protein

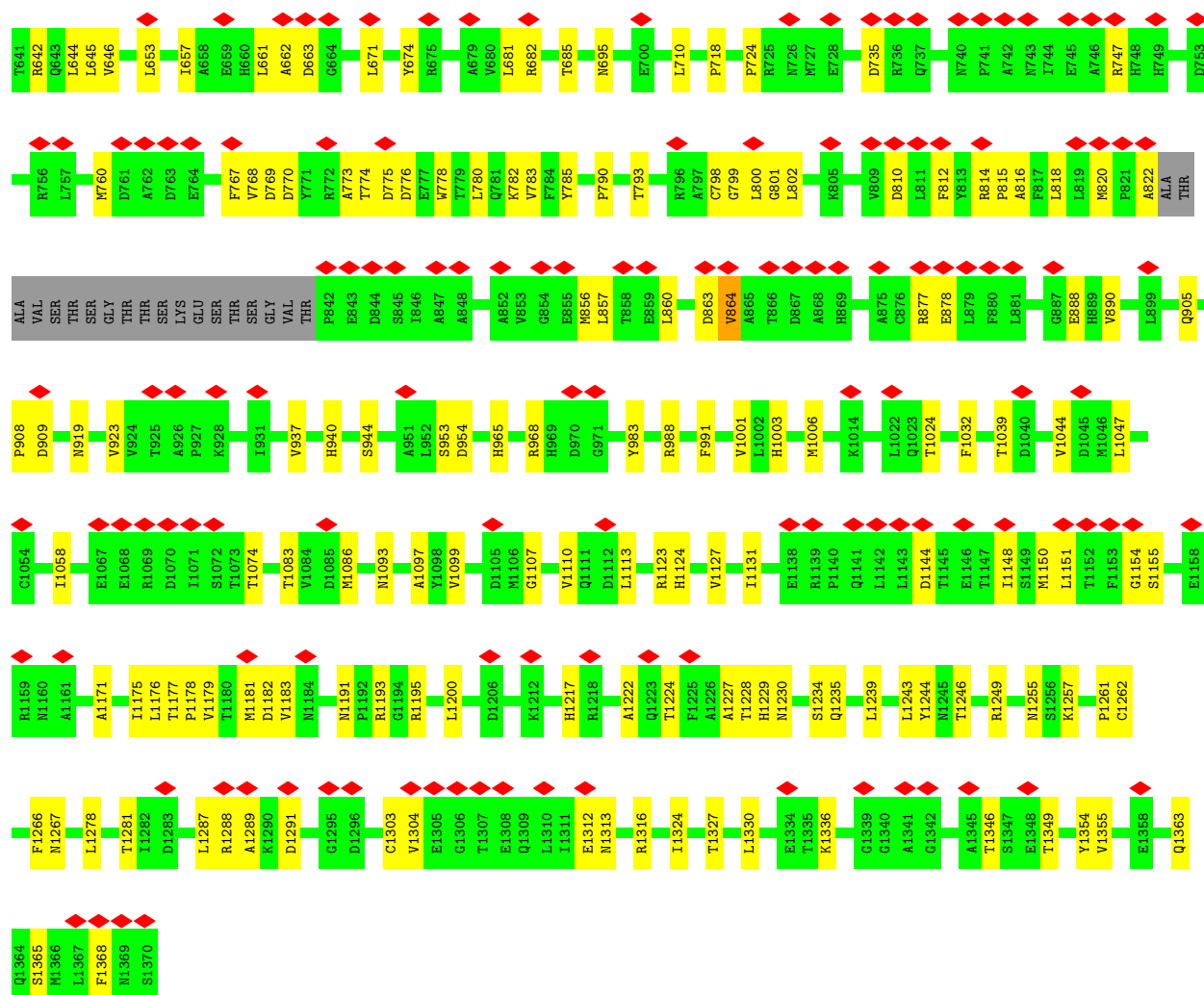


• Molecule 1: Small capsomere-interacting protein

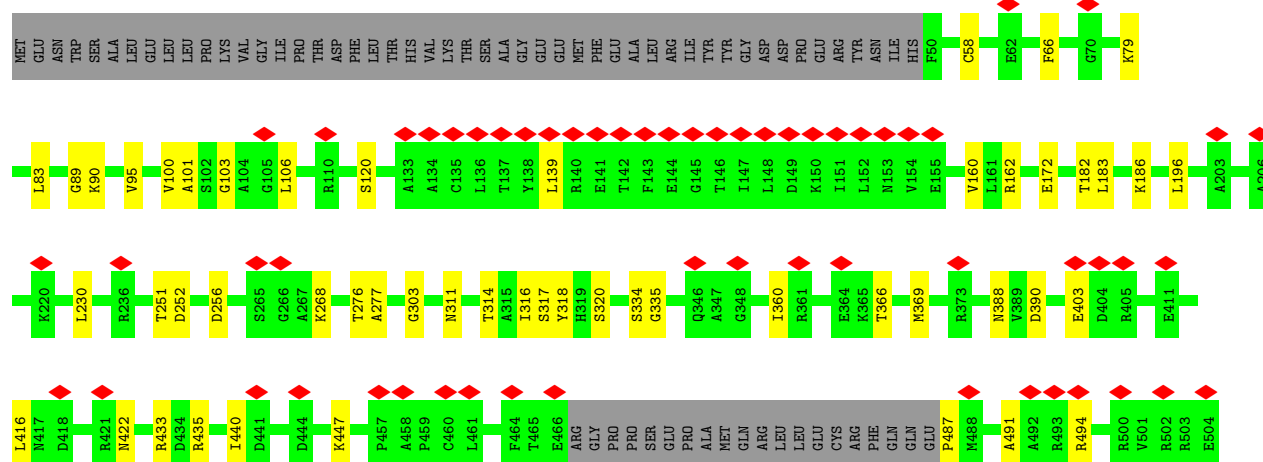
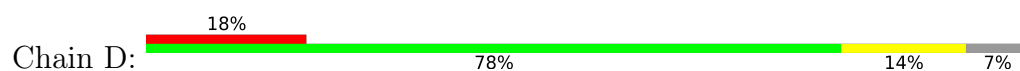


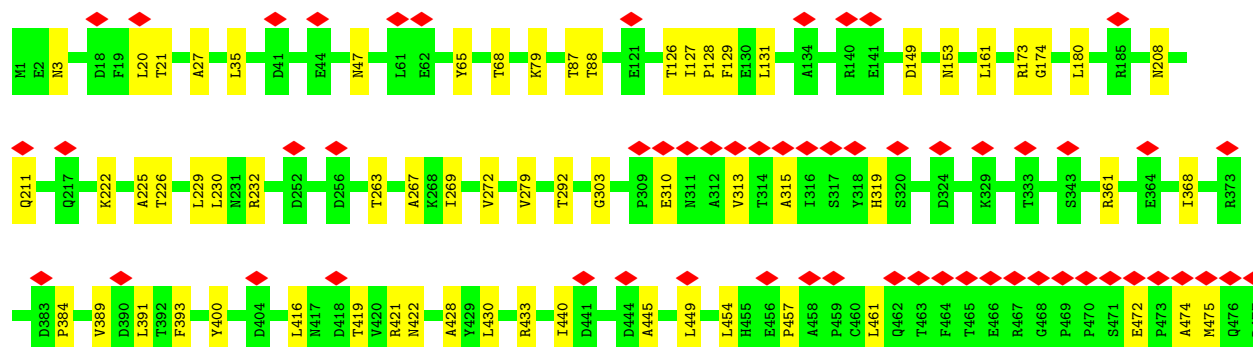
• Molecule 2: Major capsid protein

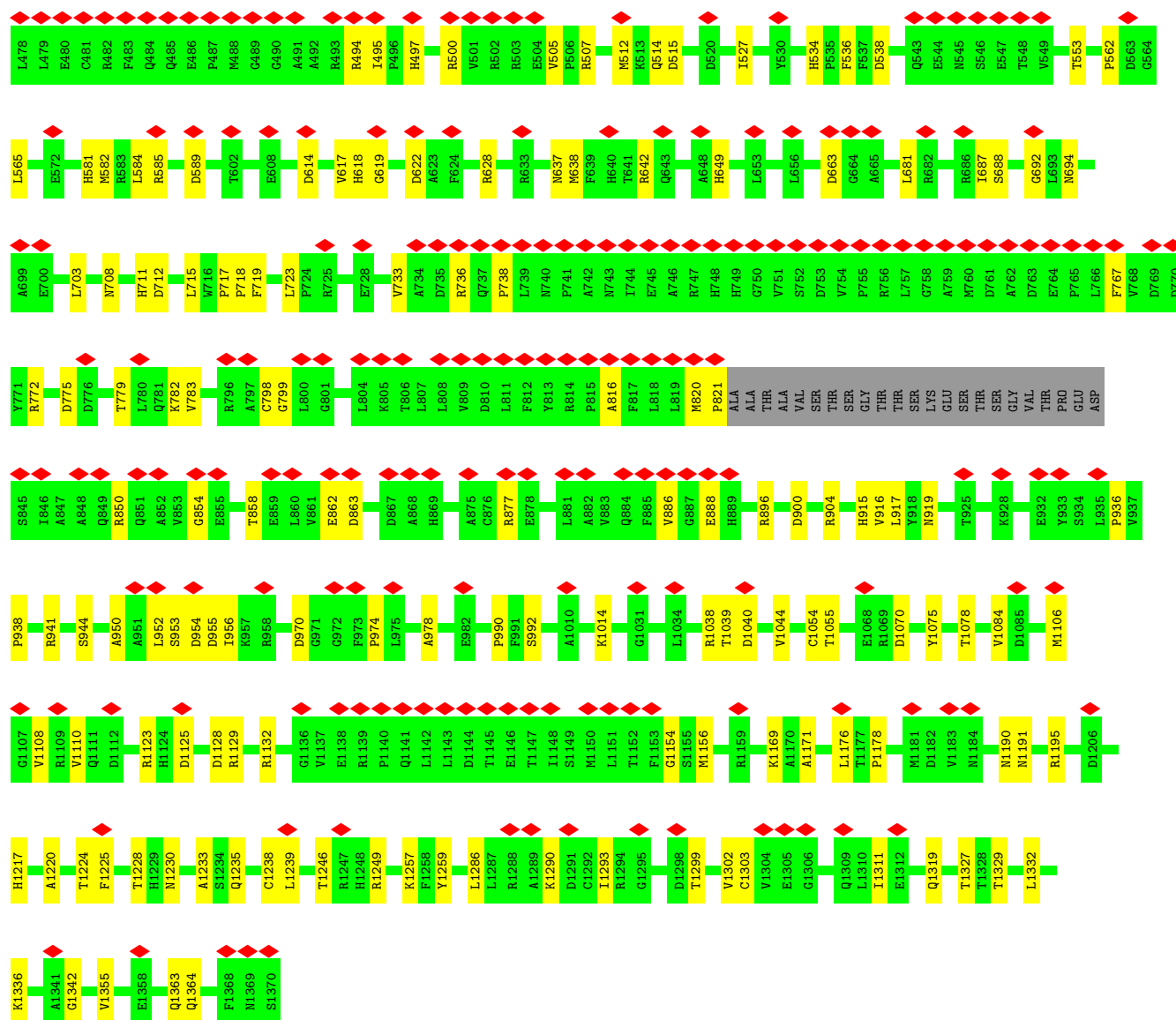




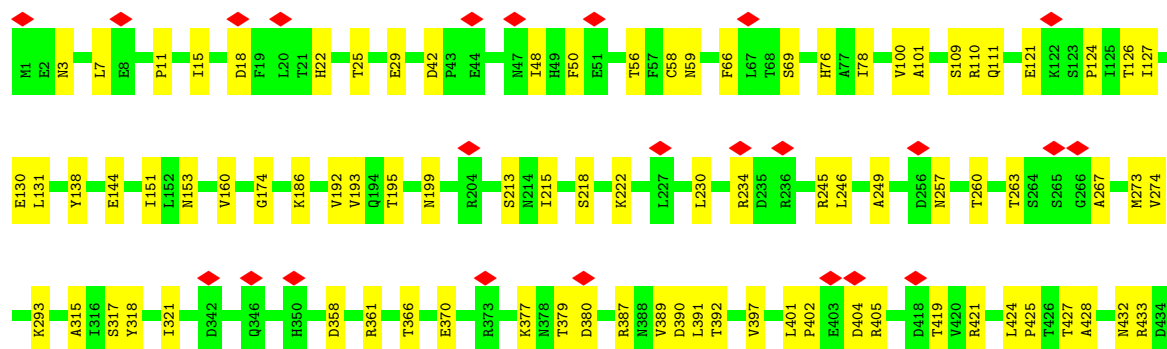
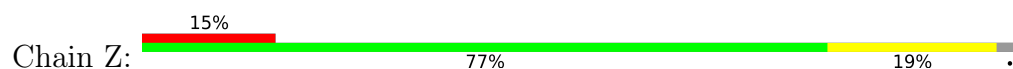
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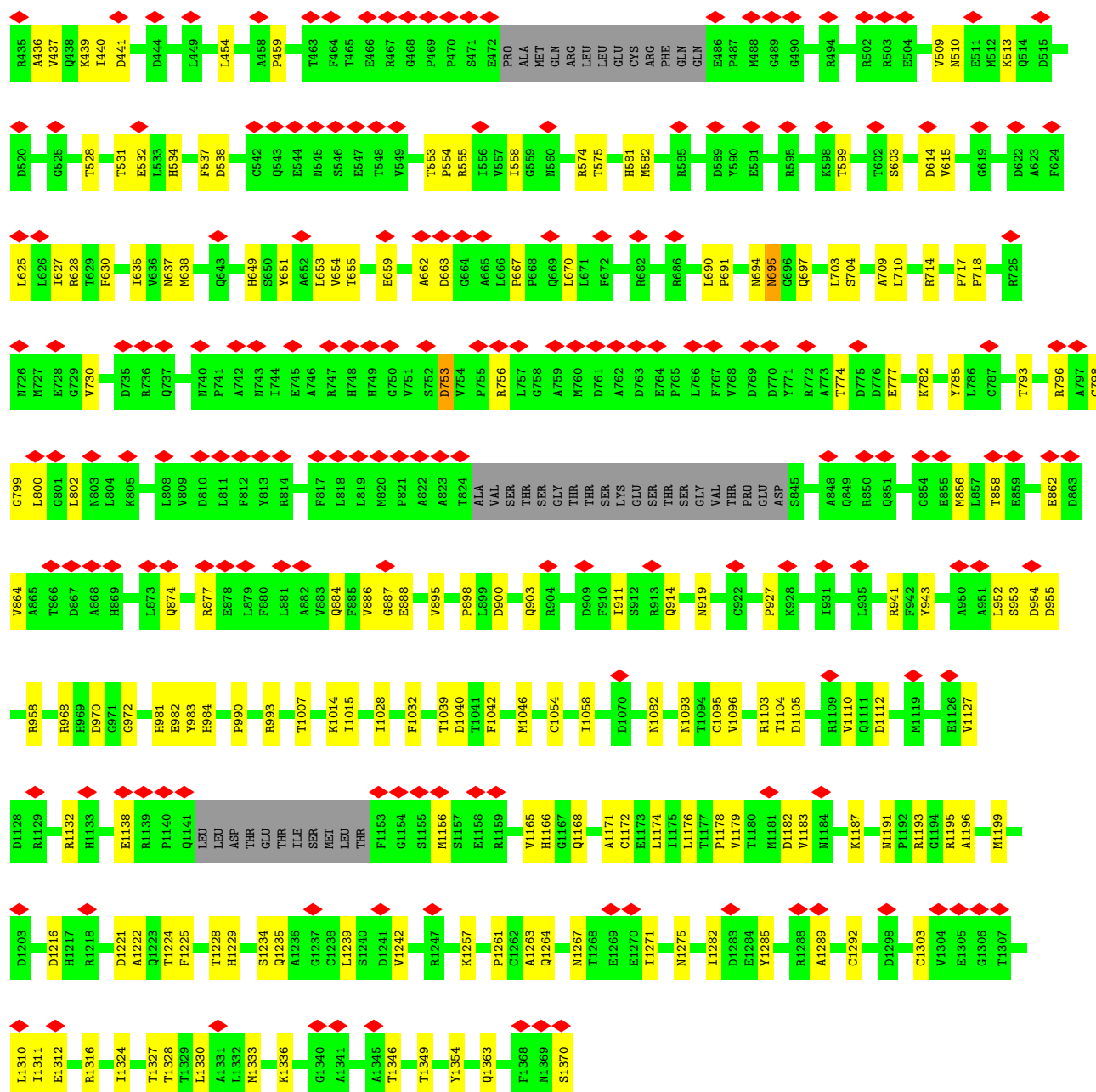




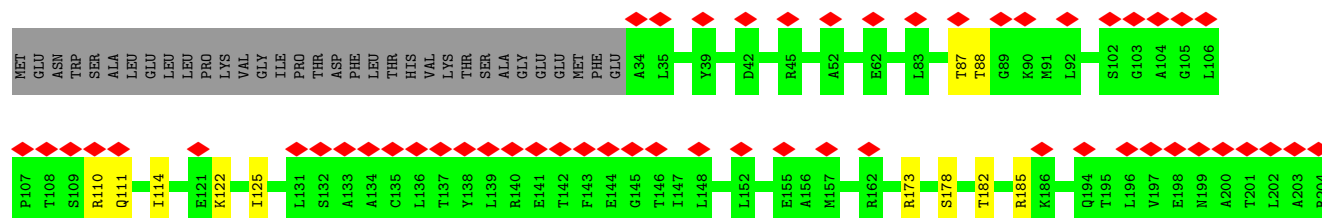
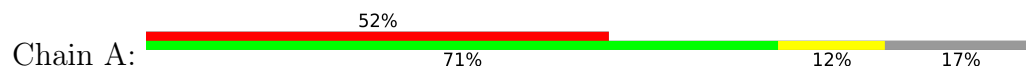


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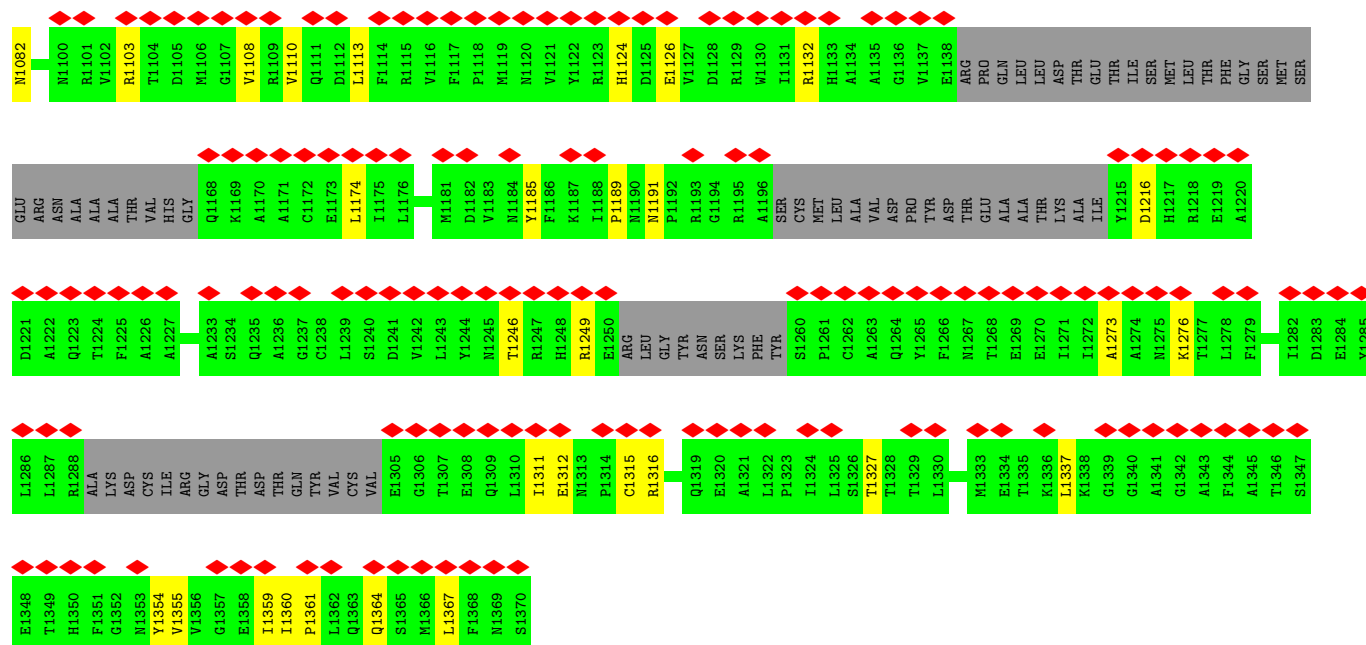




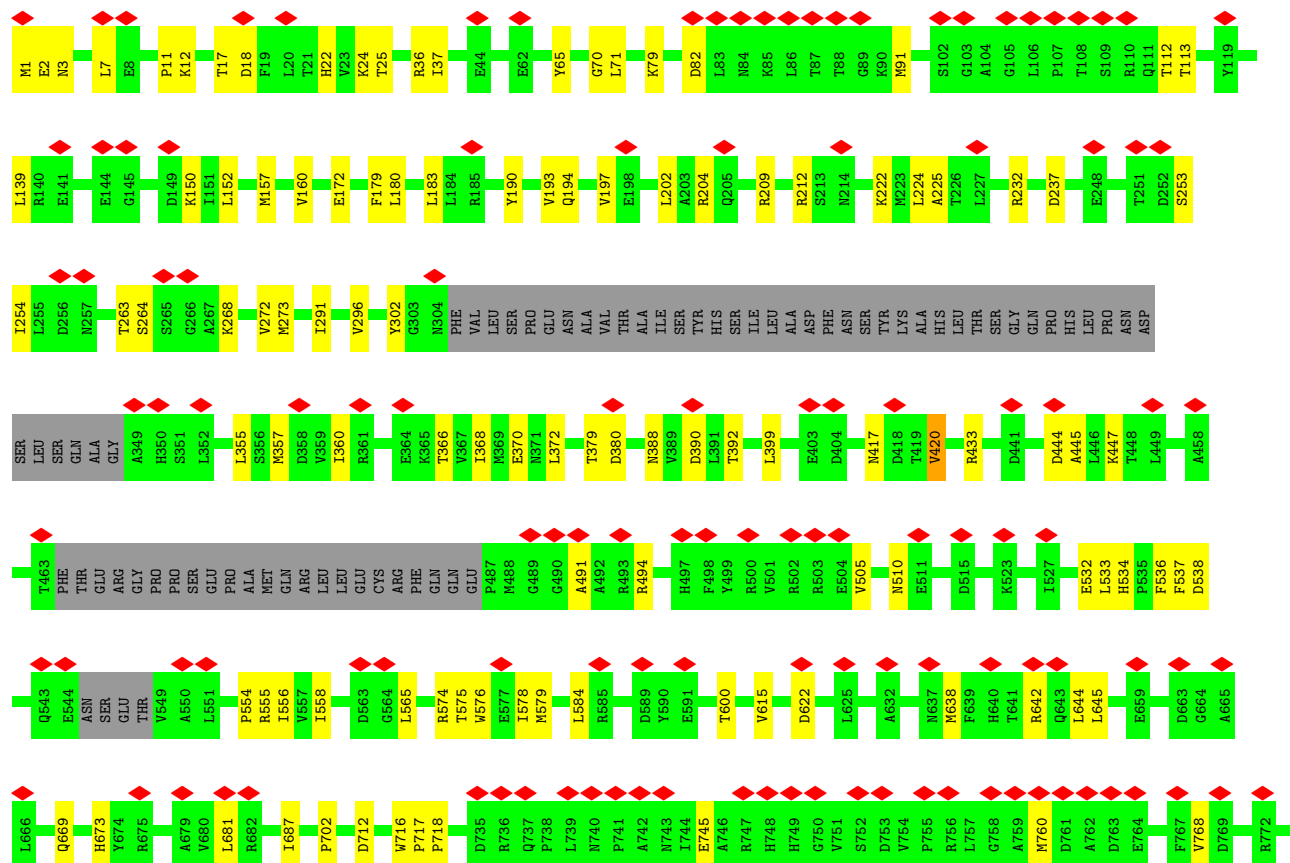
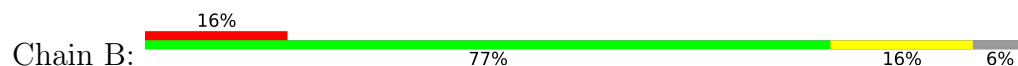
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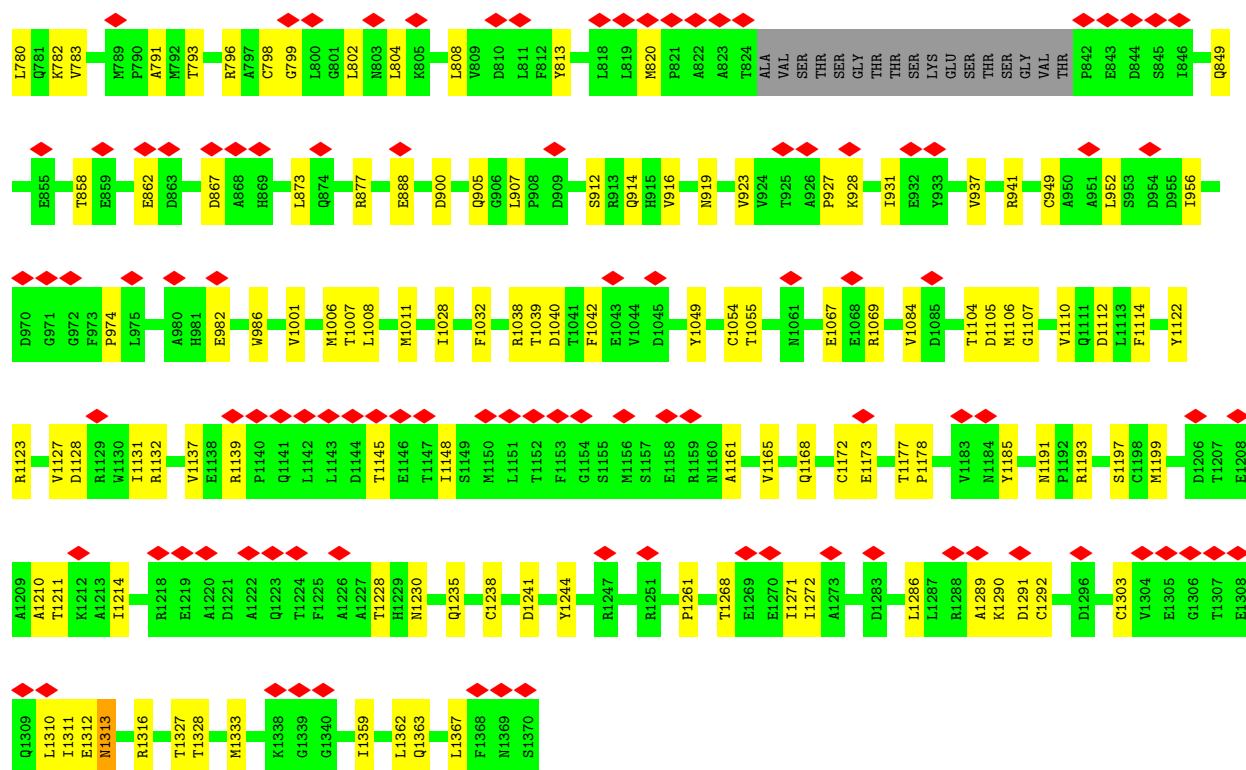


A996	A1000	V1001	V1005	M1006	T1007	L1008	A1009	A1010	M1011	L1012	Y1013	K1014	L1020	V1021	L1022	K1025	A1026	H1027	H1028	H1029	P1030	G1031	F1032	A1033	L1034	T1035	R1038	T1039	R968	D1040	E1043	V1044	D1045	M1046	S1050	G1051	M1060	M1061	V1064	T1065	K1066	E1067	E1068	R1069	D1070	I1071	S1072	T1073	V1077													
P936	V937	P938	F939	H940	R941	F942	Y943	S944	N945	P946	T947	I948	C949	A950	R891	L892	S893	E894	D954	D955	I956	K957	R958	Y959	Y960	T961	E962	F963	P964	H965	Y966	H967	R968	H969	F970	I911	S912	G971	G972	F973	P974	L975	P976	T977	A978	F979	A980	H981	E982	Y983	H984	T985	A926	L987	R988	S989	P990	F991	S992	R993	Y994	S995
A816	F817	L818	L819	M820	P821	A822	ALA	THR	ALA	VAL	SER	THR	GLY	THR	THR	SER	LYS	GLU	SER	THR	SER	GLY	VAL	THR	PRO	THR	PRO	GLU	ASP	S845	T846	A847	A848	Q849	R850	Q851	A852	V853	G854	E855	M856	L857	T858	E859	L860	E862	D863	V864	A865	T866	D867	A868	H869	T870	P871	L872	L873	Q874	A875			
C876	R877	E878	L879	F880	L881	A882	V883	Q884	F885	V886	G887	E888	H889	V890	K891	V892	L893	E894	D954	D955	I956	K957	R958	Y959	Y960	T961	E962	F963	P964	H965	Y966	H967	R968	H969	F910	I911	S912	G971	G972	F973	P974	L975	P976	T977	A978	F979	A980	H981	E982	Y983	H984	T985	A926	L987	R988	S989	P990	F991	S992	R993	Y994	S995
GLY	D697	L698	A699	MET	E700	F701	L703	S704	A705	V706	V707	W708	A709	L710	H711	D712	T774	D775	D776	E777	W778	T779	L780	Q781	K782	V783	F784	V785	L786	C787	L788	W789	P790	A791	W792	T793	W794	W795	R796	A797	G798	G799	L800	C801	L802	N803	L804	D805	T806	L807	L808	W809	D810	L811	F812	Y813	R814	P815				
V636	N637	N638	F639	H640	T641	R642	Q643	L644	L645	V646	F647	A648	H649	S650	Y651	A652	L653	V654	T655	L656	T657	A658	E659	H660	L661	A662	D663	G664	A665	L666	P667	P668	Q669	L670	L671	F672	H673	V674	H675	N676	L677	V678	A679	V680	L681	H682	L683	V684	T685	H686	T687	S688	ALA	LEU	PRO	GLY	LEU	ASN	ASN			
W576	E577	L578	M579	E580	H581	M582	R583	L584	R585	P586	P587	P588	D589	Y590	E591	E592	T593	L594	R595	L596	F597	K598	T599	T600	V601	T602	S603	G604	N605	Y606	P607	E608	H641	C542	GLN	GLU	ASN	SER	GLU	THR	V549	C552	T553	P554	R555	I556	V557	L558	G559	N560	D563	G564	L565	A566	E572	T575	I635					
E504	V505	P506	R507	T508	V509	M510	E511	M512	K513	Q514	D515	F516	V517	Y522	K523	V524	G525	Q462	T463	F464	THR	GLU	THR	ARG	GLY	THR	THR	VAL	GLU	SER	LYS	VAL	PRO	ALA	MET	GLN	ARG	LEU	GLU	CYS	ARG	PHE	GLN	GLU	PRO	MET	GLY	A491	A492	R493	R494	I495	F498	Y499	R500	V501	R502	R503				
T379	D380	T381	K382	R387	N388	V389	L390	H391	T392	F395	P396	V397	G398	L399	Y400	L401	P402	E403	ASP	ARG	GLY	THR	THR	THR	VAL	GLU	SER	LYS	ASN	ASP	VAL	PRO	ALA	LEU	SER	ASN	GLN	ALA	T419	V420	A349	H950	A423	L424	D358	V359	I360	R361	L362	G363	E364	I368	R373	R374	V375	Y376	K377	N378	D441	F442		
S285	L286	L287	S288	I291	T295	A300	L307	E310	N311	N326	SER	TYR	LYS	ALA	HIS	LEU	THR	SER	GLY	THR	GLN	PRO	HIS	LEU	PRO	ASN	ASP	LYS	VAL	LEU	SER	ASN	GLN	ALA	G348	A349	H950	S356	M357	D358	V359	I360	R361	L362	G363	E364	I368	R373	R374	V375	Y376	K377	N378	S275	T276	Q281	M284					

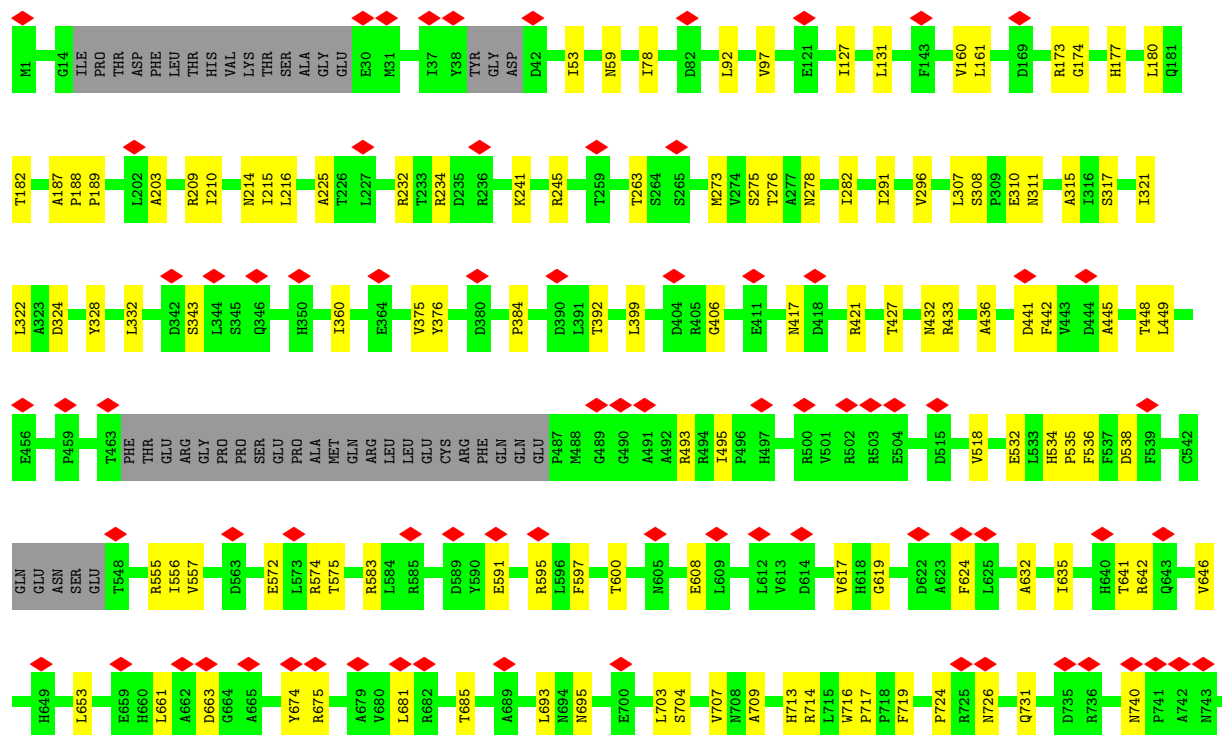
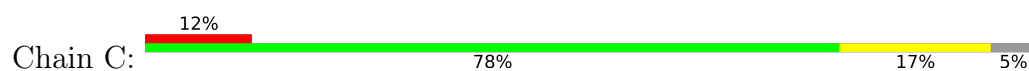


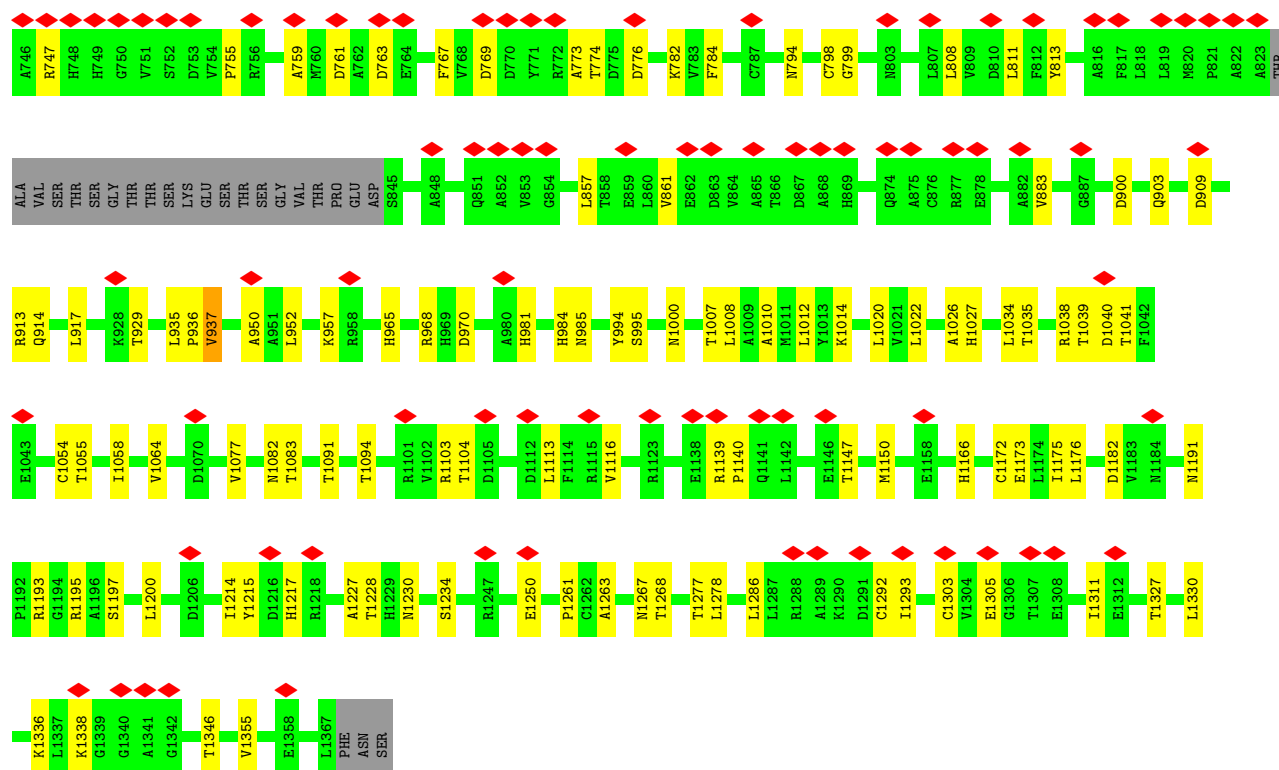
• Molecule 2: Major capsid protein



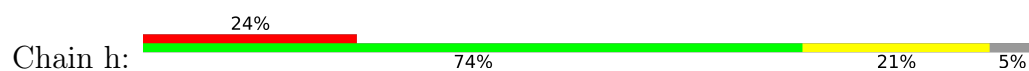


• Molecule 2: Major capsid protein

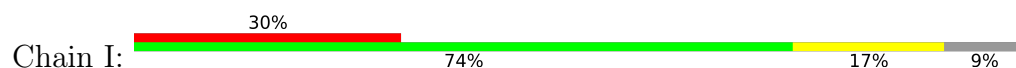


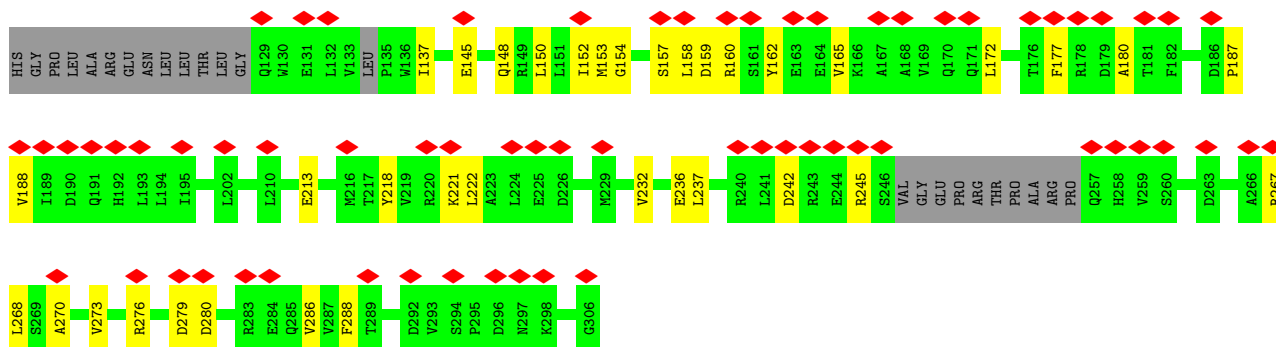


• Molecule 3: Triplex capsid protein 2

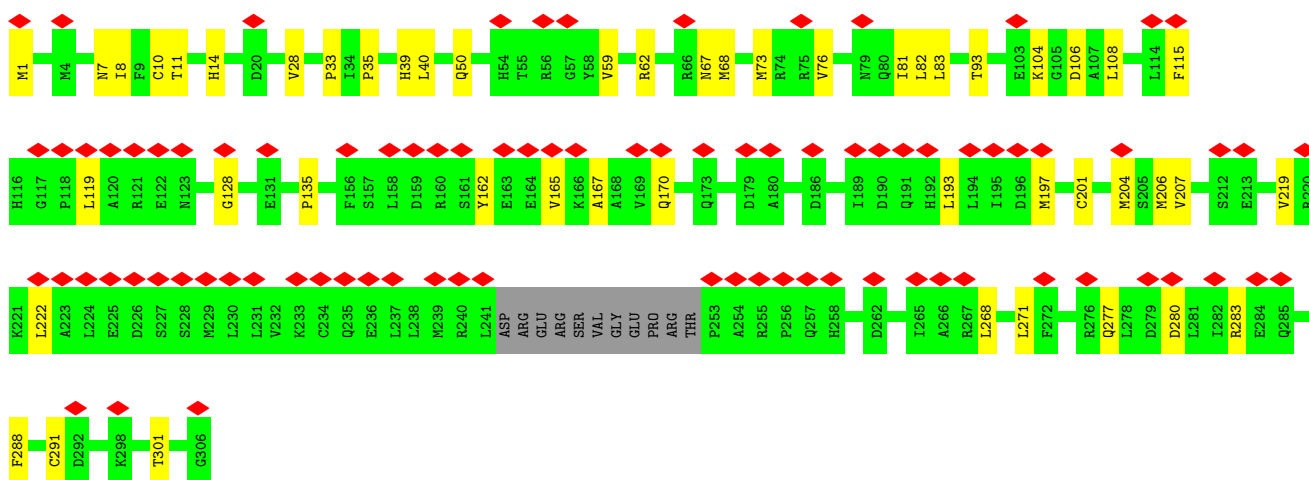
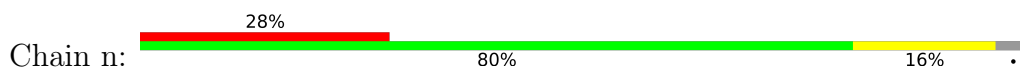


• Molecule 3: Triplex capsid protein 2

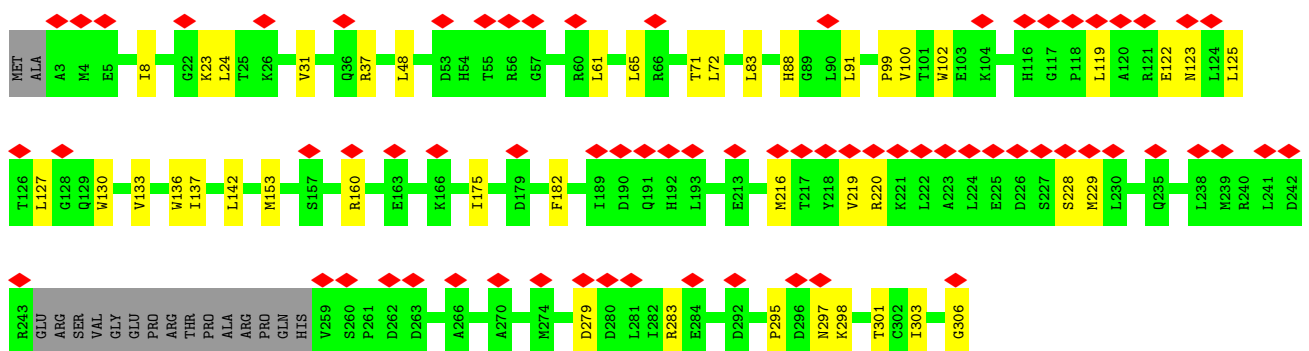
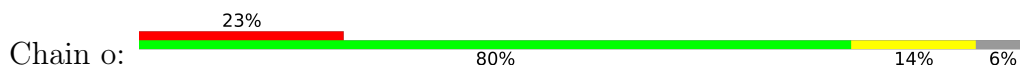




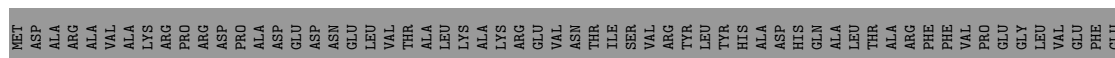
• Molecule 3: Triplex capsid protein 2



• Molecule 3: Triplex capsid protein 2



• Molecule 4: Triplex capsid protein 1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40903	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	416.0, 416.0, 416.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.625, 1.625, 1.625	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	Q	0.17	0/356	0.48	0/475
1	R	0.20	0/441	0.54	0/594
1	S	0.20	0/441	0.56	0/594
1	T	0.20	0/193	0.56	0/254
1	i	0.19	0/452	0.49	0/609
1	j	0.18	0/474	0.48	0/638
2	A	0.22	0/9319	0.55	0/12686
2	B	0.27	0/10403	0.57	3/14166 (0.0%)
2	C	0.26	0/10533	0.54	0/14346
2	D	0.25	0/10292	0.53	2/14019 (0.0%)
2	Y	0.25	0/10932	0.55	2/14892 (0.0%)
2	Z	0.26	0/10750	0.53	3/14644 (0.0%)
2	a	0.27	0/10365	0.55	0/14122
3	I	0.23	0/2248	0.56	0/3046
3	h	0.25	0/2348	0.58	0/3189
3	n	0.25	0/2379	0.54	0/3230
3	o	0.24	0/2333	0.52	0/3167
4	g	0.20	0/951	0.49	0/1288
4	m	0.26	0/2374	0.58	0/3221
5	M	0.24	0/3900	0.63	2/5284 (0.0%)
6	N	0.25	0/439	0.76	2/588 (0.3%)
6	O	0.22	0/353	0.64	0/480
All	All	0.25	0/92276	0.55	14/125532 (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
2	C	0	1
2	D	0	1
2	Y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	M	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Z	1127	VAL	N-CA-C	-7.33	106.34	113.53
2	Z	753	ASP	CA-C-N	6.35	124.24	120.24
2	Z	753	ASP	C-N-CA	6.35	124.24	120.24
6	N	28	GLU	CA-C-N	6.31	133.60	121.54
6	N	28	GLU	C-N-CA	6.31	133.60	121.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	1303	CYS	Peptide
2	D	585	ARG	Peptide
5	M	511	LEU	Peptide
5	M	66	ALA	Peptide
2	Y	585	ARG	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	Q	352	0	373	3	0
1	R	436	0	463	7	0
1	S	436	0	463	5	0
1	T	192	0	207	0	0
1	i	446	0	470	8	0
1	j	467	0	490	5	0
2	A	9105	0	9096	99	0
2	B	10164	0	10131	148	0
2	C	10291	0	10265	152	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	10054	0	10026	123	0
2	Y	10676	0	10618	131	0
2	Z	10498	0	10431	179	0
2	a	10125	0	10087	159	0
3	I	2209	0	2289	36	0
3	h	2304	0	2391	48	0
3	n	2334	0	2431	34	0
3	o	2291	0	2383	25	0
4	g	929	0	922	12	0
4	m	2325	0	2363	39	0
5	M	3813	0	3741	52	0
6	N	432	0	436	10	0
6	O	344	0	346	6	0
All	All	90223	0	90422	1175	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 6.

The worst 5 of 1175 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:324:ASP:HB2	2:C:343:SER:HB3	1.73	0.71
5:M:170:ARG:HB3	5:M:315:ARG:HH22	1.57	0.70
2:Z:144:GLU:H	4:m:36:ARG:HH21	1.40	0.69
2:Y:820:MET:HE3	2:Y:821:PRO:HD2	1.76	0.67
2:A:553:THR:HG21	2:A:983:TYR:HB3	1.76	0.66

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	Q	42/75 (56%)	42 (100%)	0	0	100	100
1	R	53/75 (71%)	52 (98%)	1 (2%)	0	100	100
1	S	53/75 (71%)	53 (100%)	0	0	100	100
1	T	21/75 (28%)	20 (95%)	1 (5%)	0	100	100
1	i	54/75 (72%)	54 (100%)	0	0	100	100
1	j	56/75 (75%)	55 (98%)	1 (2%)	0	100	100
2	A	1118/1370 (82%)	1058 (95%)	60 (5%)	0	100	100
2	B	1272/1370 (93%)	1192 (94%)	80 (6%)	0	100	100
2	C	1288/1370 (94%)	1216 (94%)	72 (6%)	0	100	100
2	D	1262/1370 (92%)	1184 (94%)	78 (6%)	0	100	100
2	Y	1343/1370 (98%)	1262 (94%)	81 (6%)	0	100	100
2	Z	1318/1370 (96%)	1235 (94%)	83 (6%)	0	100	100
2	a	1275/1370 (93%)	1202 (94%)	73 (6%)	0	100	100
3	I	269/306 (88%)	261 (97%)	8 (3%)	0	100	100
3	h	286/306 (94%)	266 (93%)	20 (7%)	0	100	100
3	n	291/306 (95%)	271 (93%)	20 (7%)	0	100	100
3	o	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
4	g	108/290 (37%)	102 (94%)	6 (6%)	0	100	100
4	m	288/290 (99%)	268 (93%)	20 (7%)	0	100	100
5	M	458/594 (77%)	417 (91%)	41 (9%)	0	100	100
6	N	49/642 (8%)	44 (90%)	5 (10%)	0	100	100
6	O	39/642 (6%)	32 (82%)	6 (15%)	1 (3%)	4	28
All	All	11228/13722 (82%)	10554 (94%)	673 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	O	27	PRO

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	Q	40/68 (59%)	40 (100%)	0	100	100
1	R	51/68 (75%)	51 (100%)	0	100	100
1	S	51/68 (75%)	50 (98%)	1 (2%)	48	66
1	T	21/68 (31%)	21 (100%)	0	100	100
1	i	52/68 (76%)	52 (100%)	0	100	100
1	j	54/68 (79%)	54 (100%)	0	100	100
2	A	1001/1192 (84%)	999 (100%)	2 (0%)	87	87
2	B	1116/1192 (94%)	1110 (100%)	6 (0%)	81	82
2	C	1130/1192 (95%)	1124 (100%)	6 (0%)	81	82
2	D	1106/1192 (93%)	1099 (99%)	7 (1%)	78	80
2	Y	1174/1192 (98%)	1172 (100%)	2 (0%)	87	87
2	Z	1152/1192 (97%)	1145 (99%)	7 (1%)	78	80
2	a	1115/1192 (94%)	1110 (100%)	5 (0%)	84	83
3	I	251/273 (92%)	251 (100%)	0	100	100
3	h	261/273 (96%)	260 (100%)	1 (0%)	84	83
3	n	263/273 (96%)	263 (100%)	0	100	100
3	o	259/273 (95%)	258 (100%)	1 (0%)	84	83
4	g	101/252 (40%)	101 (100%)	0	100	100
4	m	252/252 (100%)	252 (100%)	0	100	100
5	M	391/500 (78%)	388 (99%)	3 (1%)	73	77
6	N	45/526 (9%)	45 (100%)	0	100	100
6	O	38/526 (7%)	37 (97%)	1 (3%)	40	61
All	All	9924/11900 (83%)	9882 (100%)	42 (0%)	81	83

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1001	VAL
2	C	883	VAL
2	B	1084	VAL
2	C	97	VAL
2	C	1292	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 206 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	96	ASN
2	A	618	HIS
5	M	120	GLN
3	I	191	GLN
3	o	191	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

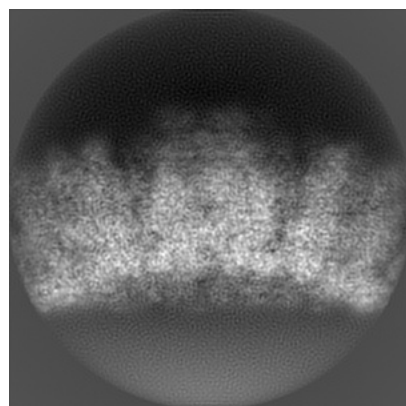
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34704. These allow visual inspection of the internal detail of the map and identification of artifacts.

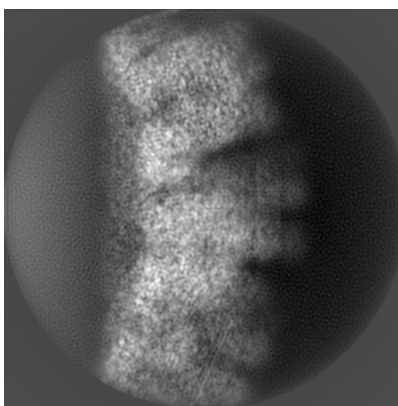
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

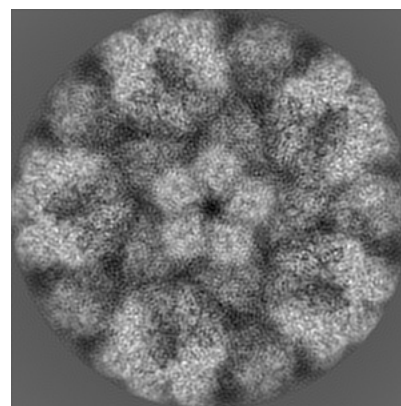
6.1.1 Primary map



X

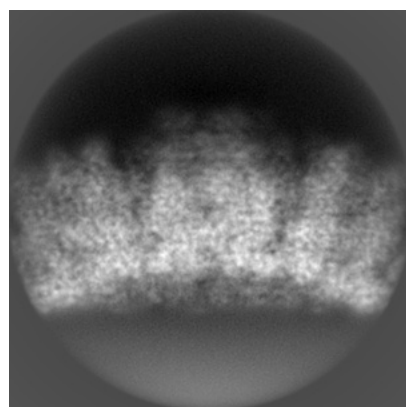


Y

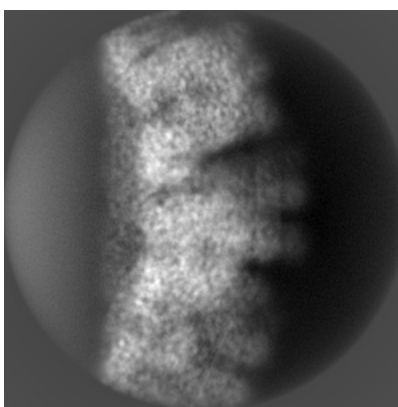


Z

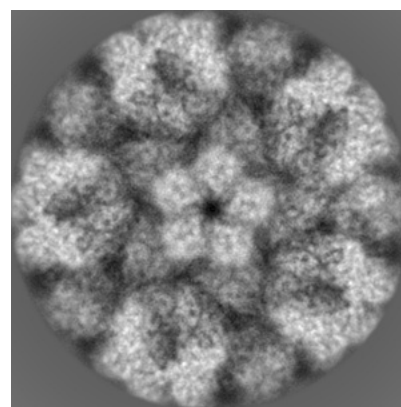
6.1.2 Raw map



X



Y

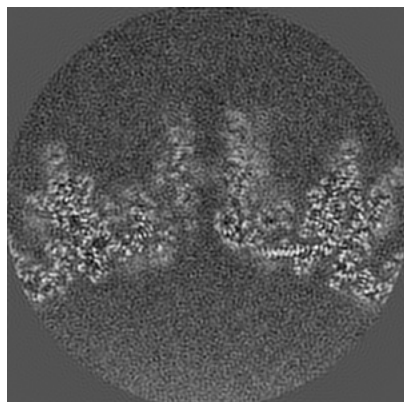


Z

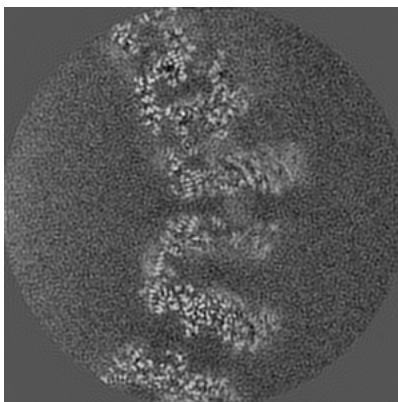
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

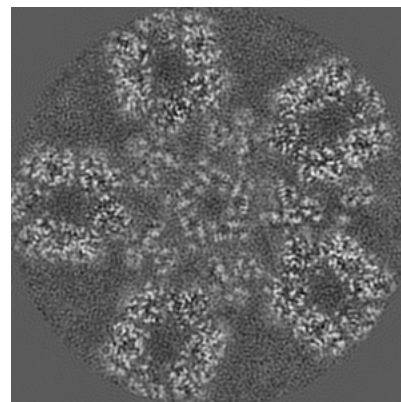
6.2.1 Primary map



X Index: 128

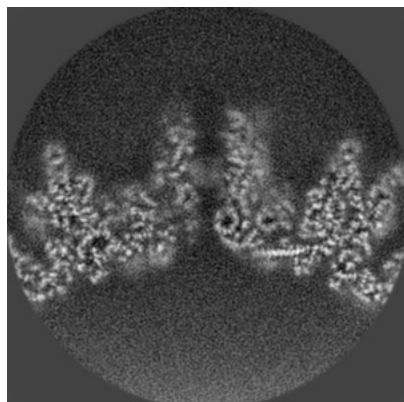


Y Index: 128

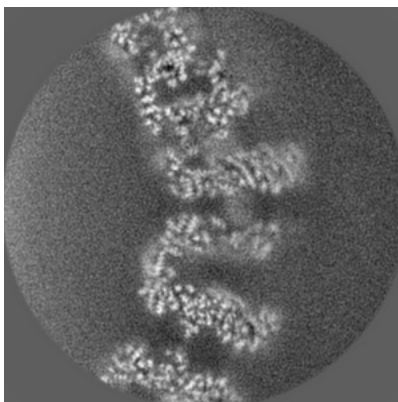


Z Index: 128

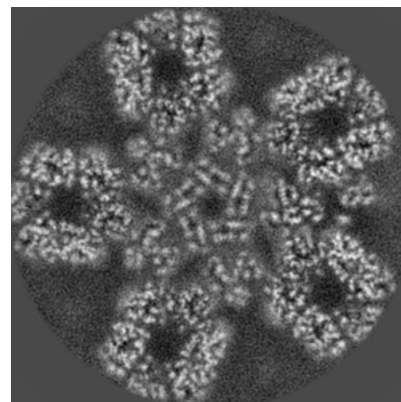
6.2.2 Raw map



X Index: 128



Y Index: 128

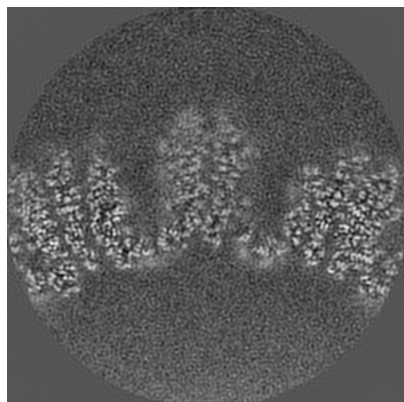


Z Index: 128

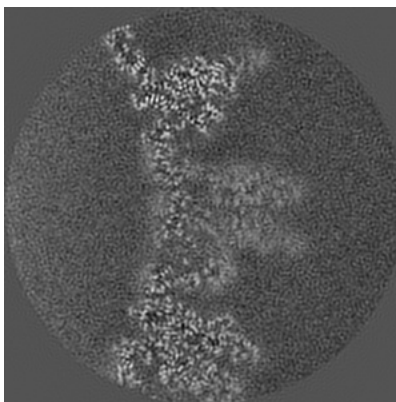
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

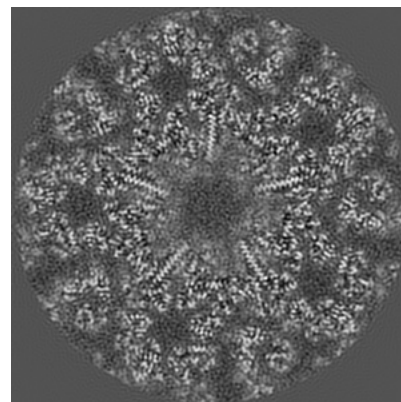
6.3.1 Primary map



X Index: 116

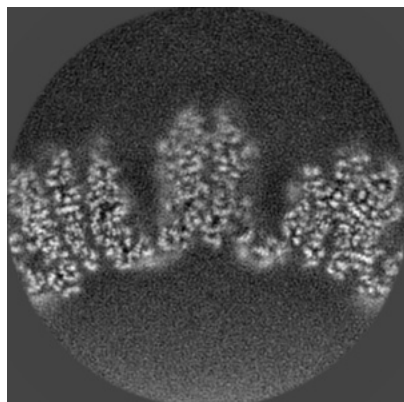


Y Index: 104

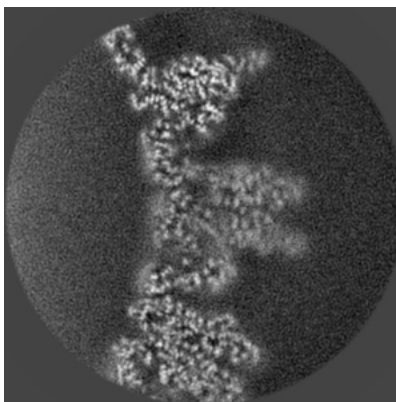


Z Index: 98

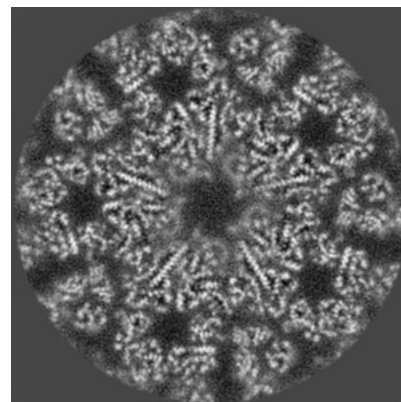
6.3.2 Raw map



X Index: 116



Y Index: 104

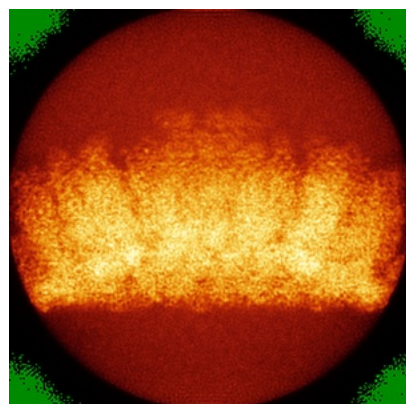


Z Index: 99

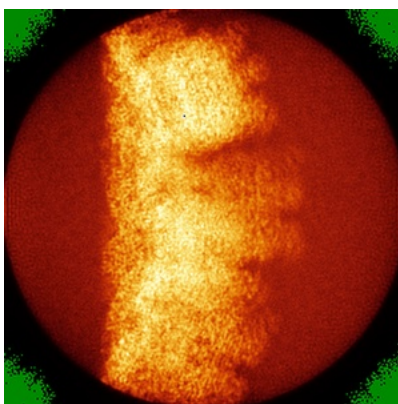
The images above show the largest variance slices of the map in three orthogonal directions.

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

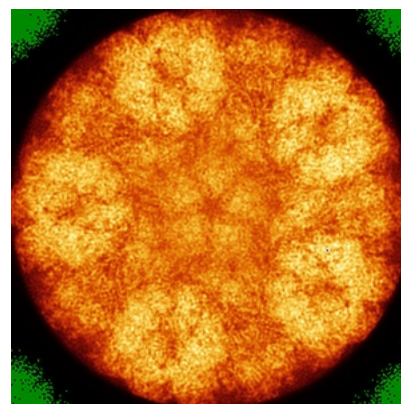
6.4.1 Primary map



X

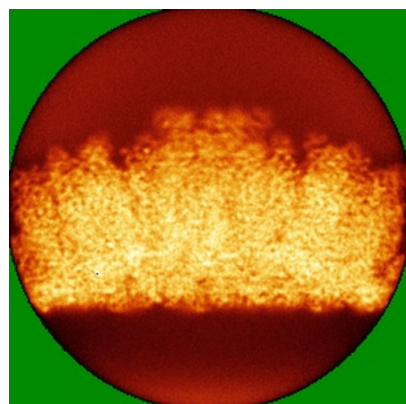


Y

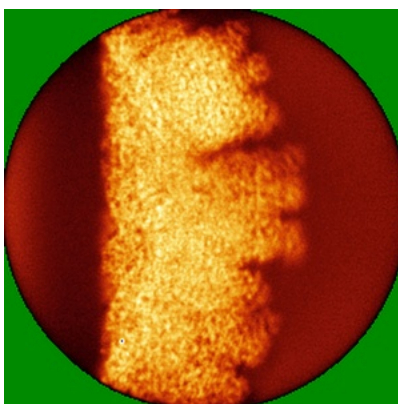


Z

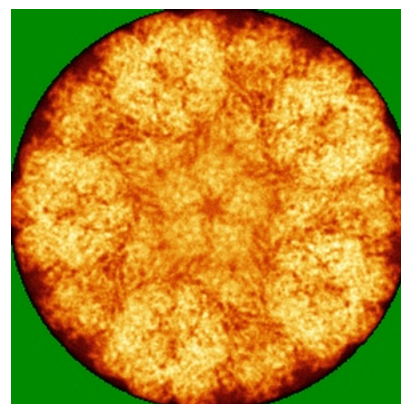
6.4.2 Raw map



X



Y

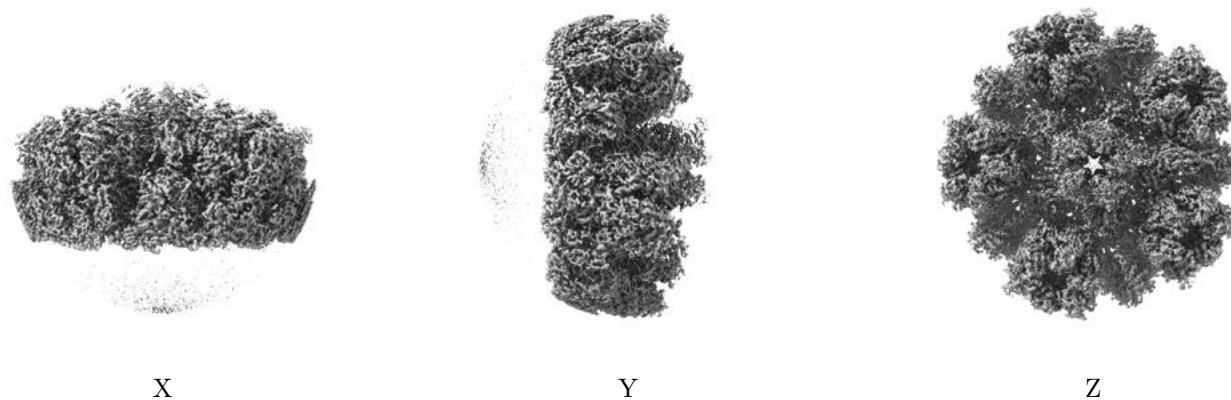


Z

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.

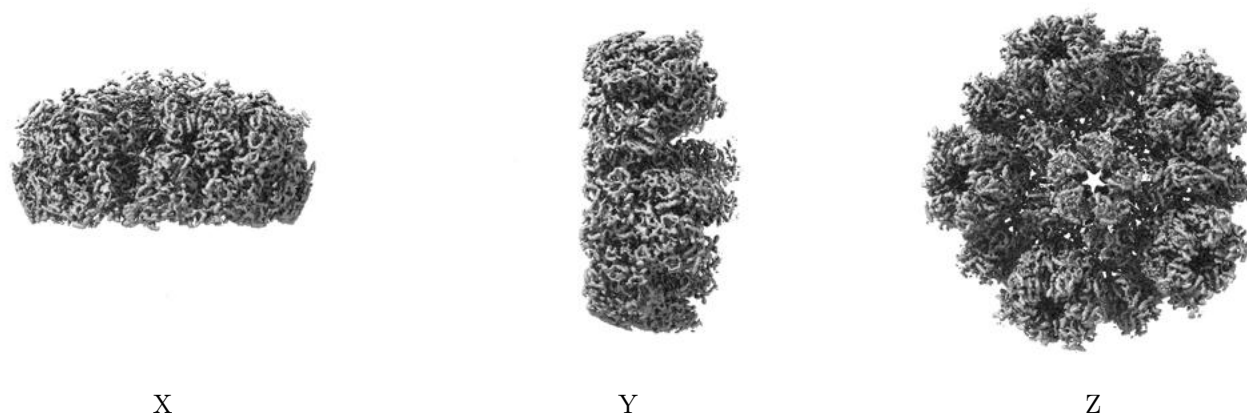
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

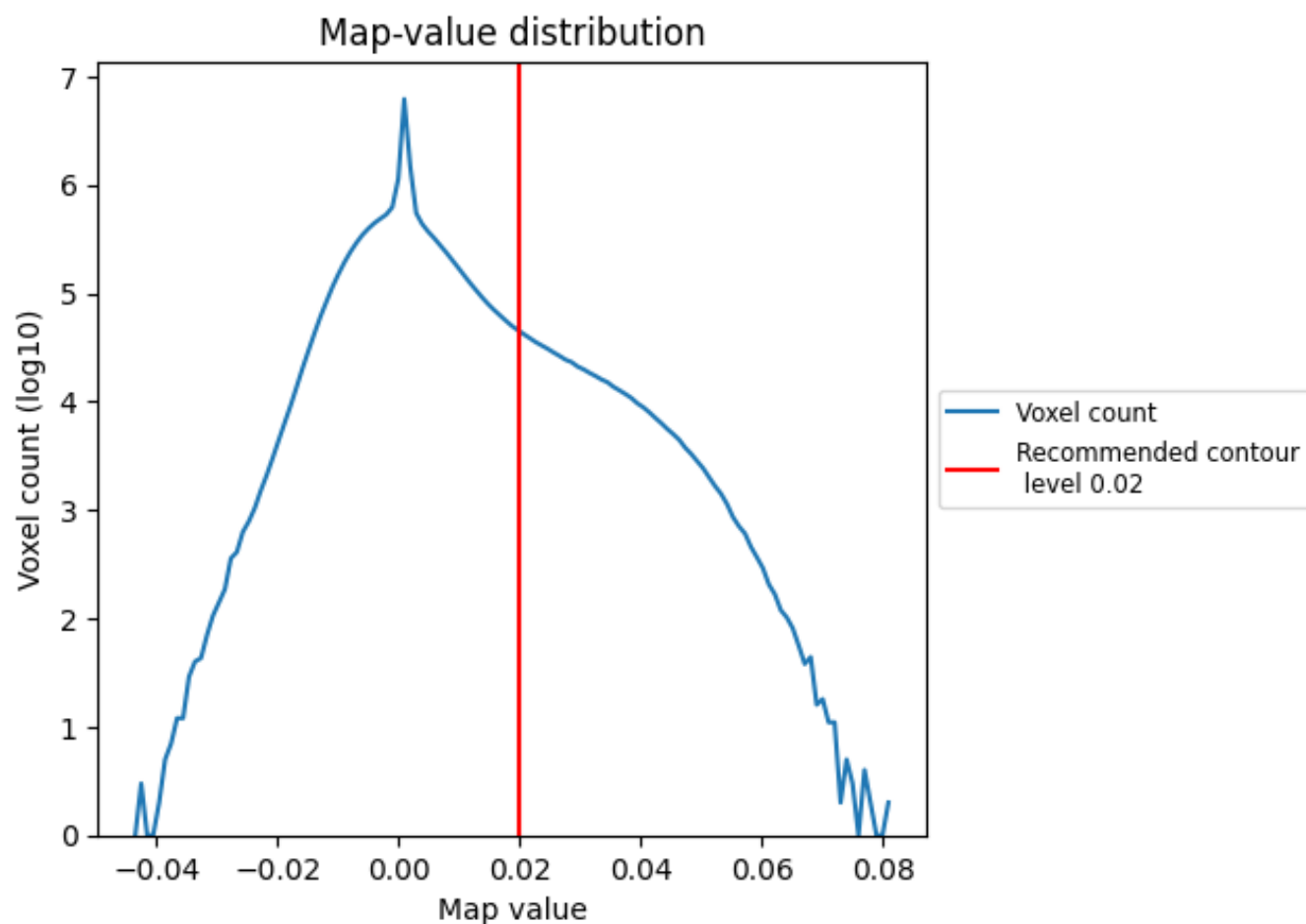
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

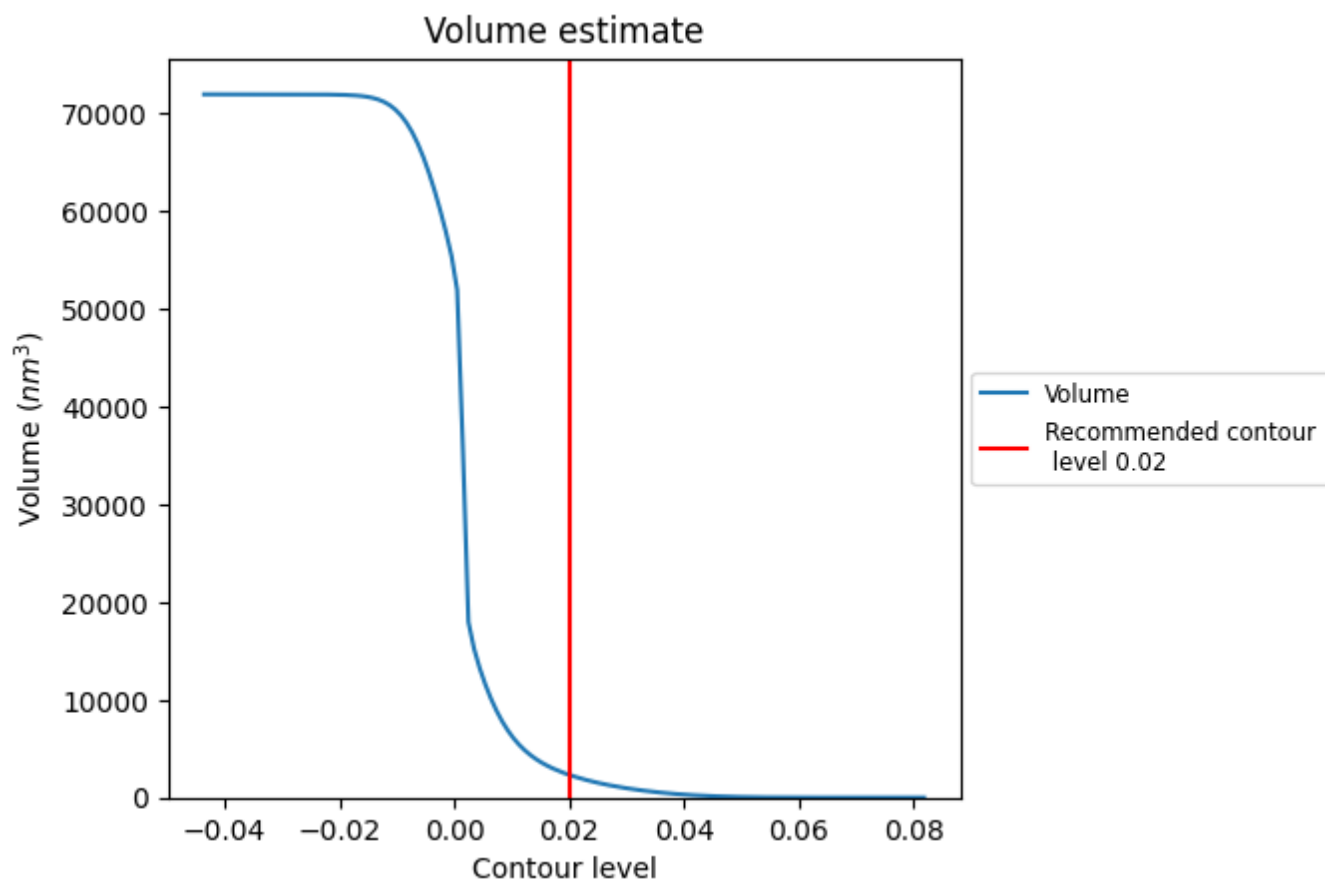
This section contains the results of statistical analysis of the map.

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.

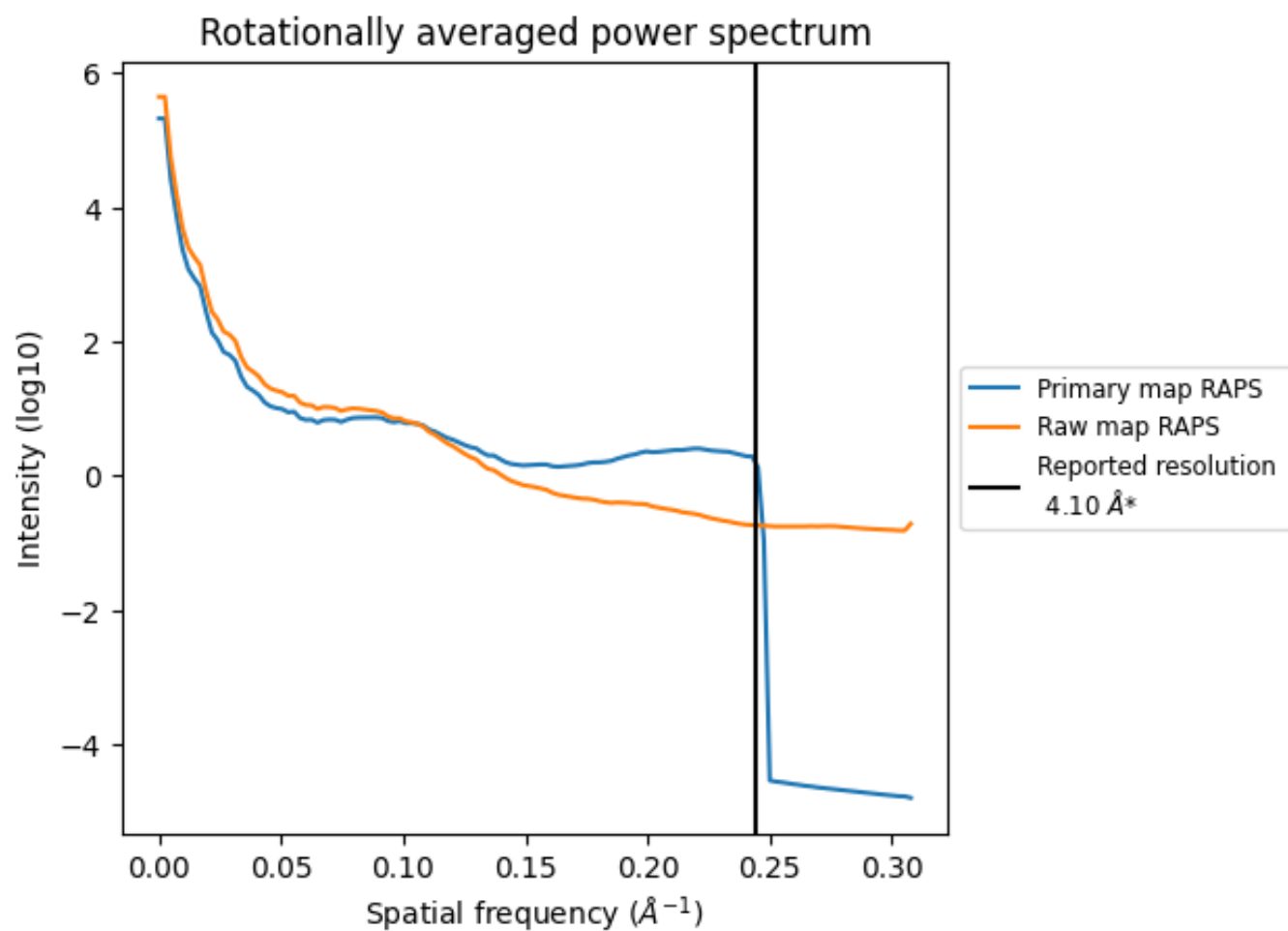
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2336 nm³; this corresponds to an approximate mass of 2110 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 ⓘ

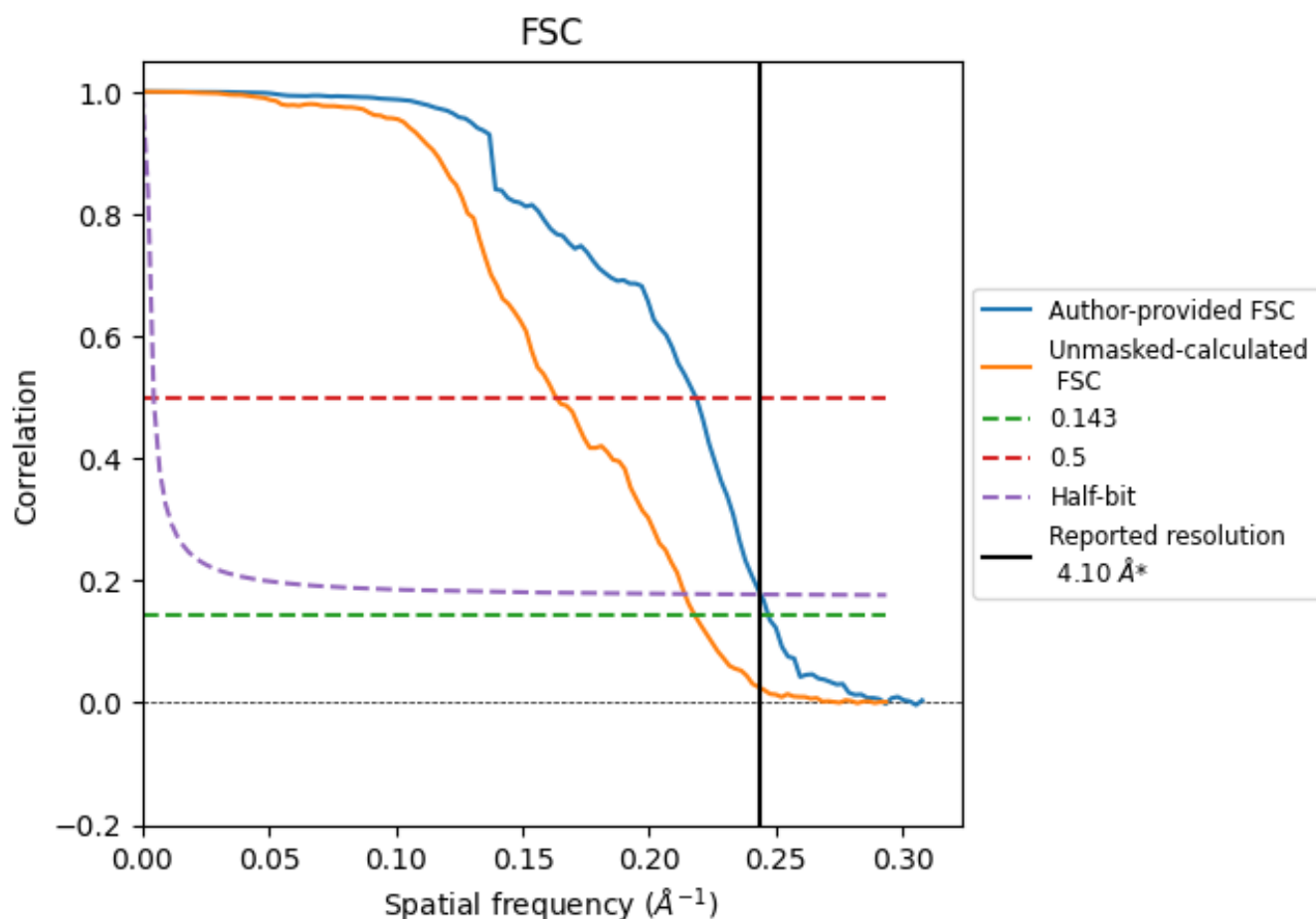


*Reported resolution corresponds to spatial frequency of 0.244 $\text{\AA}^{-1}$

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 0.244 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.05	4.58	4.10
Unmasked-calculated*	4.59	6.13	4.67

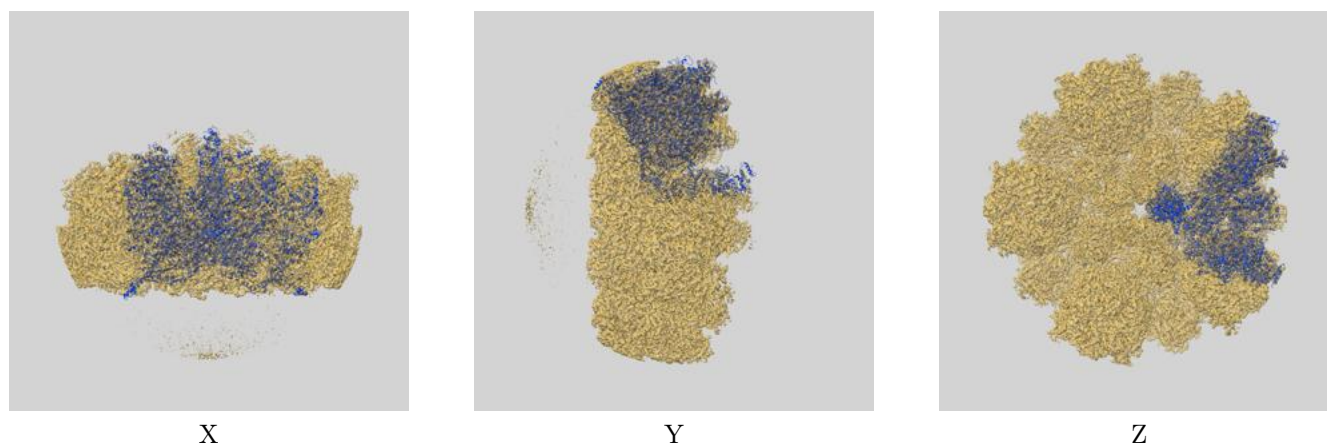
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.59 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

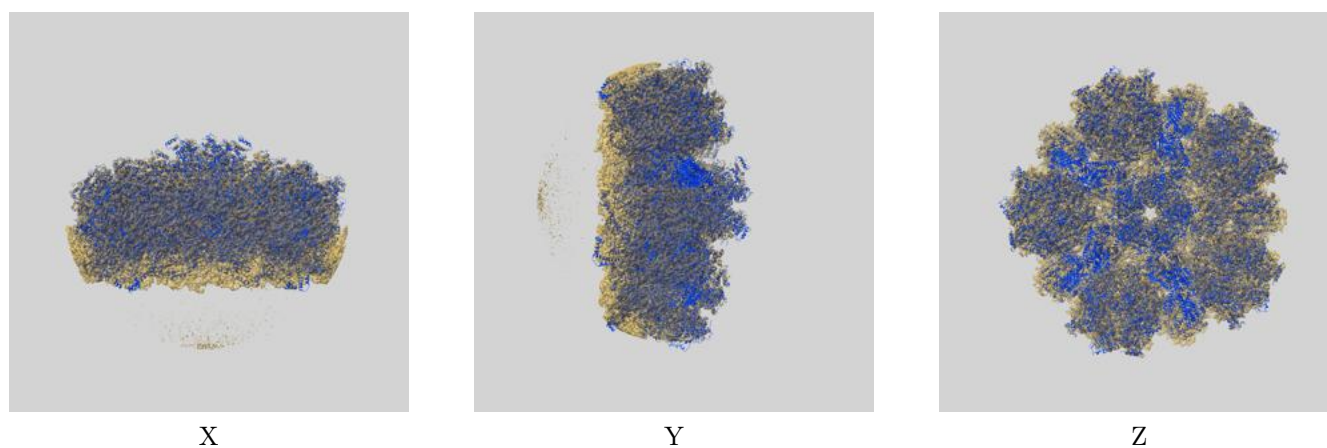
This section contains information regarding the fit between EMDB map EMD-34704 and PDB model 8HEY. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

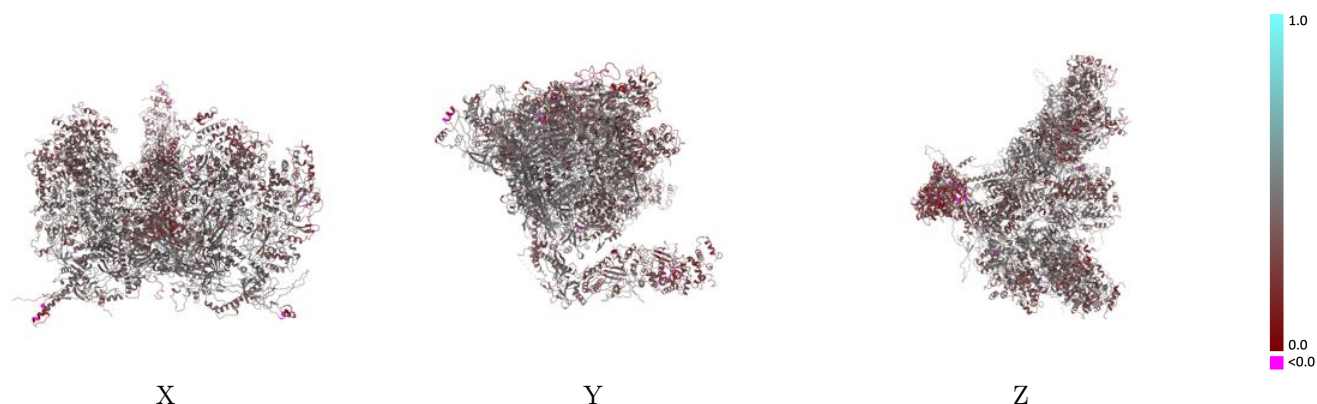


9.1.2 Map-model assembly overlay [i](#)



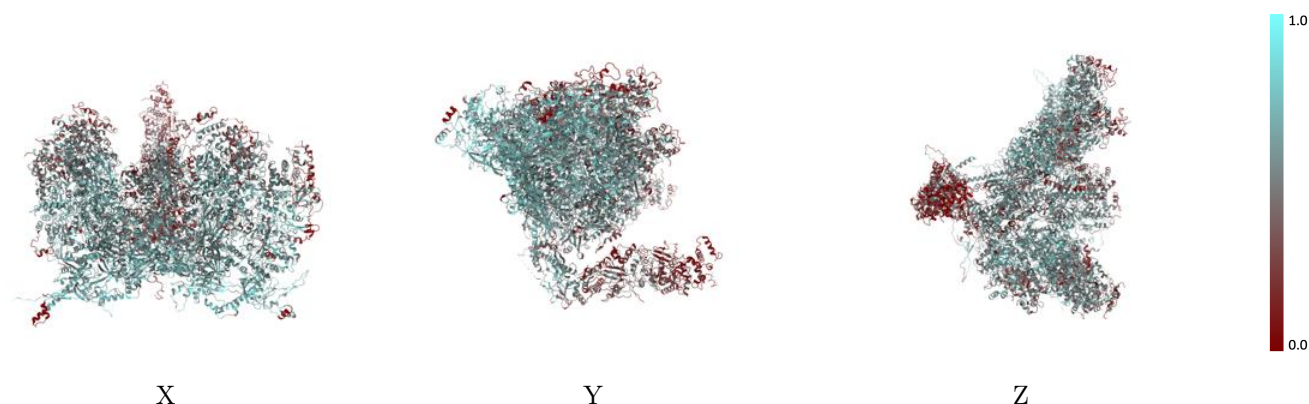
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



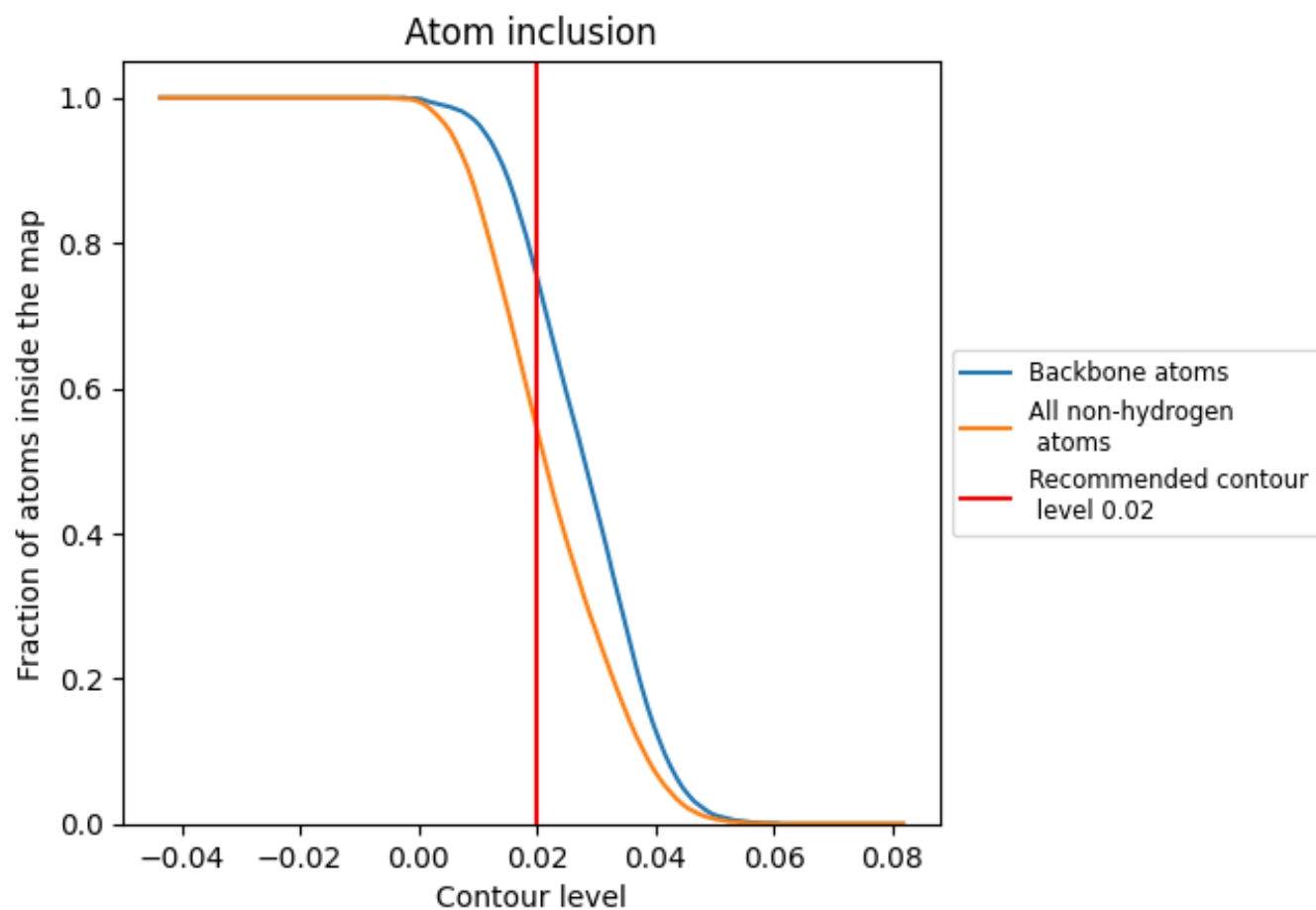
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 54% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5440	 0.3920
A	 0.3210	 0.3210
B	 0.5870	 0.4150
C	 0.6310	 0.4190
D	 0.5820	 0.4070
I	 0.4820	 0.3780
M	 0.5010	 0.3930
N	 0.3320	 0.2850
O	 0.2730	 0.2800
Q	 0.0650	 0.2280
R	 0.2470	 0.3080
S	 0.2940	 0.2930
T	 0.3210	 0.2940
Y	 0.5720	 0.3890
Z	 0.6060	 0.4140
a	 0.6090	 0.4140
g	 0.4890	 0.3740
h	 0.5410	 0.3830
i	 0.2320	 0.2540
j	 0.2910	 0.3010
m	 0.5800	 0.3990
n	 0.5060	 0.3780
o	 0.5390	 0.3770

