



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:43 PM UTC

PDB ID : 6F9D / pdb_00006f9d
EMDB ID : EMD-4199
Title : Model of the Rift Valley fever virus glycoprotein hexamer type 2
Authors : Halldorsson, S.; Bowden, T.A.; Huiskonen, J.T.
Deposited on : 2017-12-14
Resolution : 13.30 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:

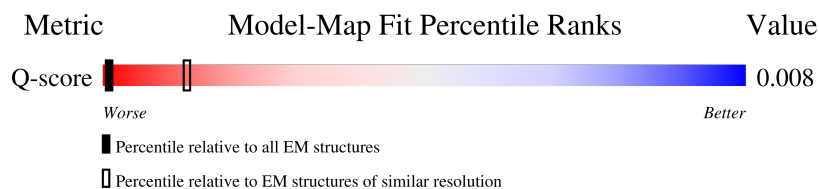
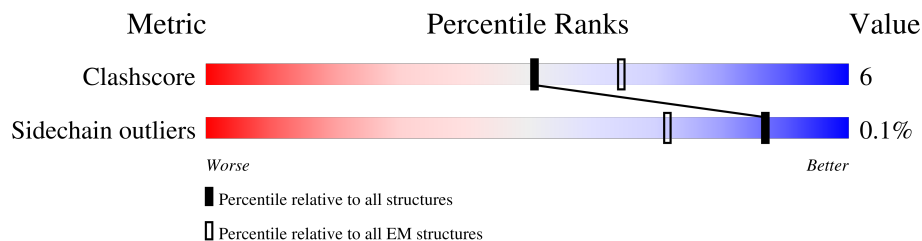
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 13.30 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	62 (12.80 - 13.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	316	57% (Poor fit), 81% (0 outliers), 14% (1 outlier), 5% (2 outliers), 5% (3+ outliers)
1	C	316	56% (Poor fit), 85% (0 outliers), 10% (1 outlier), 5% (2 outliers), 5% (3+ outliers)
1	E	316	53% (Poor fit), 82% (0 outliers), 14% (1 outlier), 5% (2 outliers), 5% (3+ outliers)
1	G	316	54% (Poor fit), 80% (0 outliers), 15% (1 outlier), 5% (2 outliers), 5% (3+ outliers)
1	I	316	51% (Poor fit), 80% (0 outliers), 15% (1 outlier), 5% (2 outliers), 5% (3+ outliers)

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Mol	Chain	Length	Quality of chain
1	K	316	<p>52% 82% 13% 5%</p>
2	B	431	<p>100% 84% 16%</p>
2	D	431	<p>100% 86% 14%</p>
2	F	431	<p>100% 83% 17%</p>
2	H	431	<p>100% 88% 12%</p>
2	J	431	<p>100% 85% 15%</p>
2	L	431	<p>100% 87% 13%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 33048 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 Glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	301	2284	1437	400	441	6	0	0
1	C	301	2284	1437	400	441	6	0	0
1	E	301	2284	1437	400	441	6	0	0
1	G	301	2284	1437	400	441	6	0	0
1	I	301	2284	1437	400	441	6	0	0
1	K	301	2284	1437	400	441	6	0	0

- Molecule 2 is a protein called Glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	431	3224	2006	561	652	5	0	0
2	D	431	3224	2006	561	652	5	0	0
2	F	431	3224	2006	561	652	5	0	0
2	H	431	3224	2006	561	652	5	0	0
2	J	431	3224	2006	561	652	5	0	0
2	L	431	3224	2006	561	652	5	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	688	ASP	-	expression tag	UNP A2T072
B	689	PRO	-	expression tag	UNP A2T072

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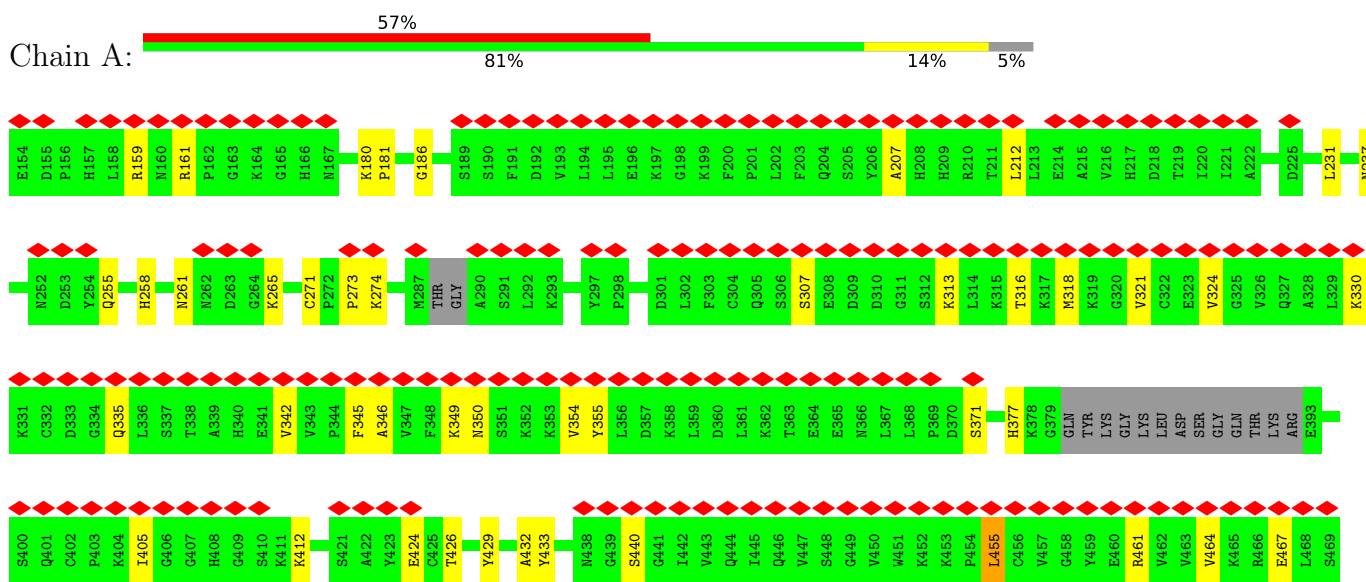
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Chain	Residue	Modelled	Actual	Comment	Reference
B	690	GLY	-	expression tag	UNP A2T072
D	688	ASP	-	expression tag	UNP A2T072
D	689	PRO	-	expression tag	UNP A2T072
D	690	GLY	-	expression tag	UNP A2T072
F	688	ASP	-	expression tag	UNP A2T072
F	689	PRO	-	expression tag	UNP A2T072
F	690	GLY	-	expression tag	UNP A2T072
H	688	ASP	-	expression tag	UNP A2T072
H	689	PRO	-	expression tag	UNP A2T072
H	690	GLY	-	expression tag	UNP A2T072
J	688	ASP	-	expression tag	UNP A2T072
J	689	PRO	-	expression tag	UNP A2T072
J	690	GLY	-	expression tag	UNP A2T072
L	688	ASP	-	expression tag	UNP A2T072
L	689	PRO	-	expression tag	UNP A2T072
L	690	GLY	-	expression tag	UNP A2T072

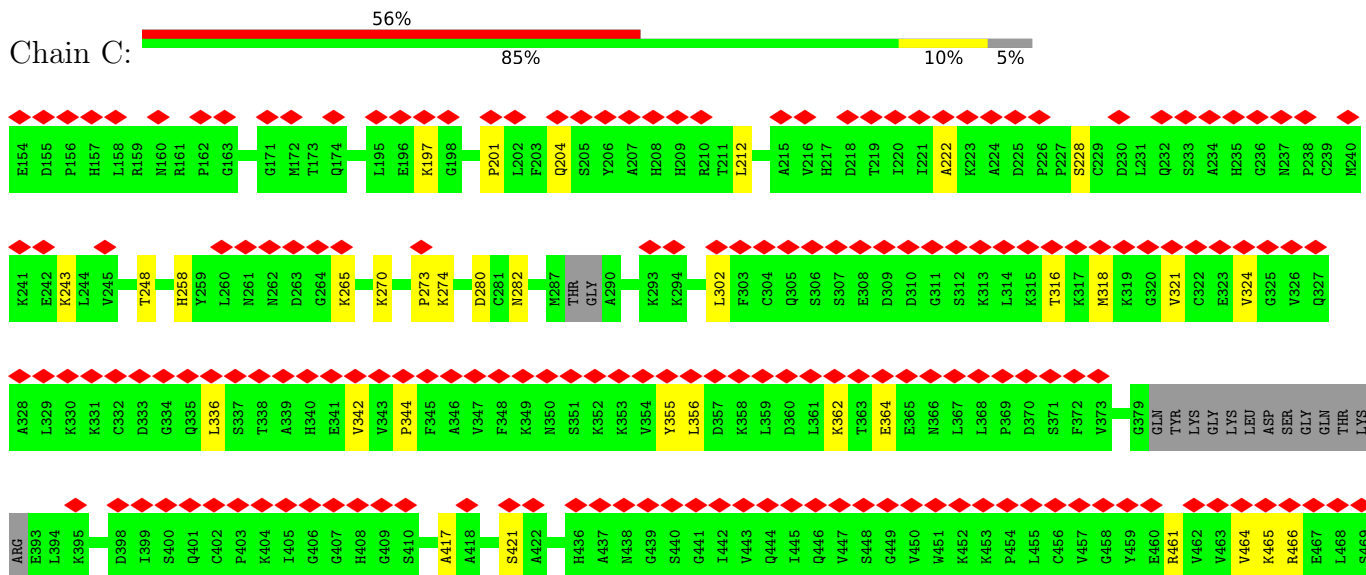
3 Residue-property plots [i](#)

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.

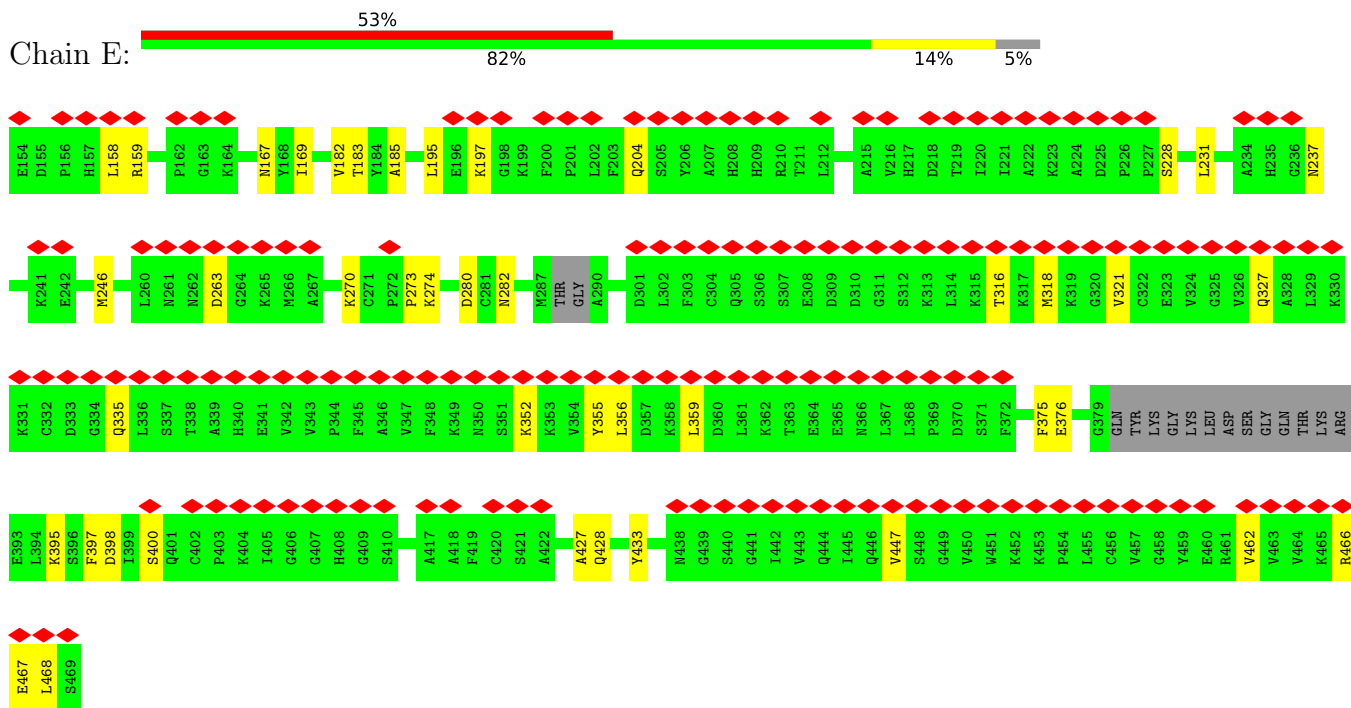
- Molecule 1: Glycoprotein



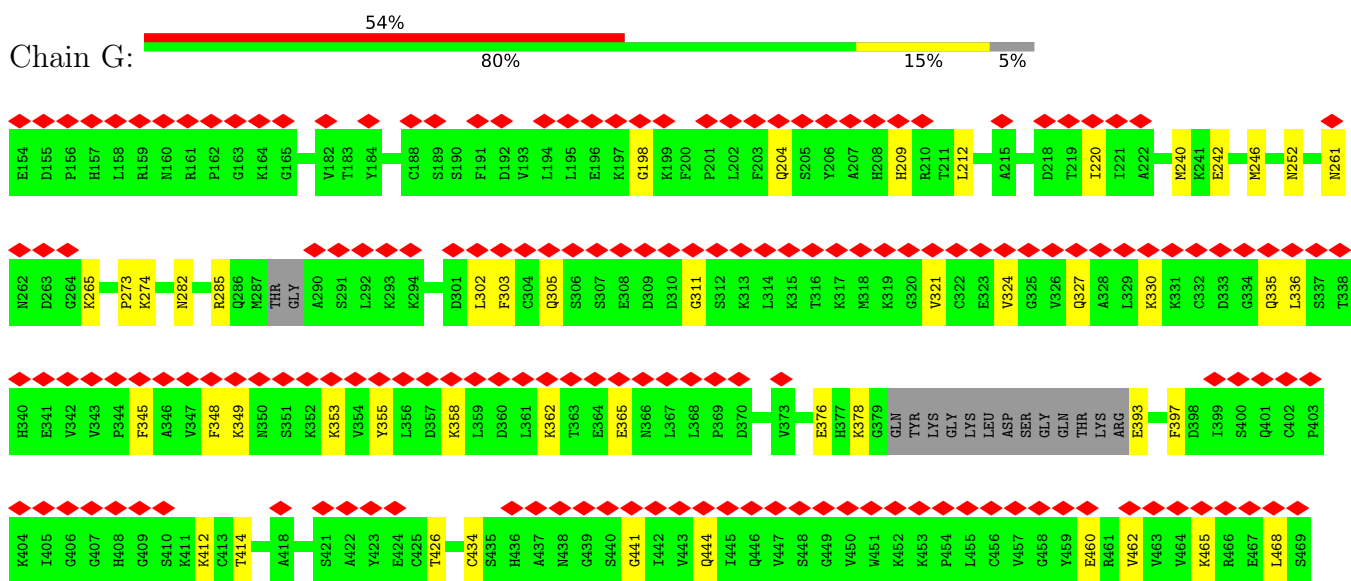
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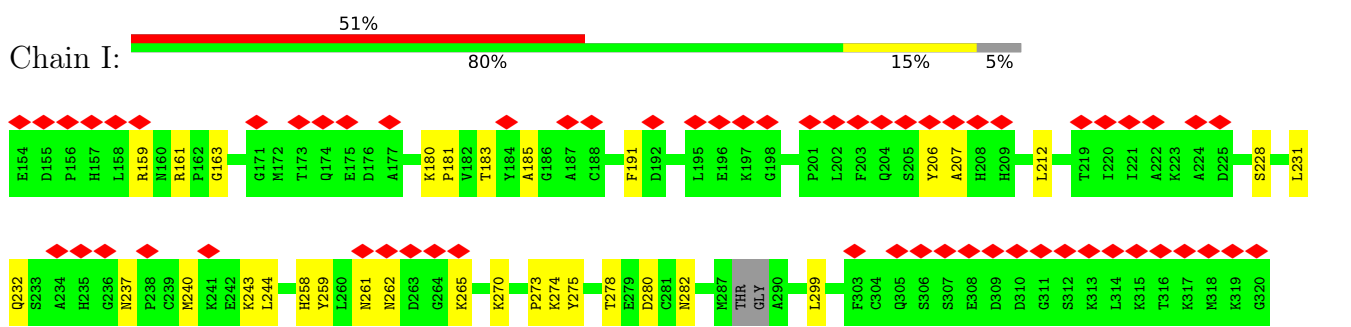
- Molecule 1: Glycoprotein

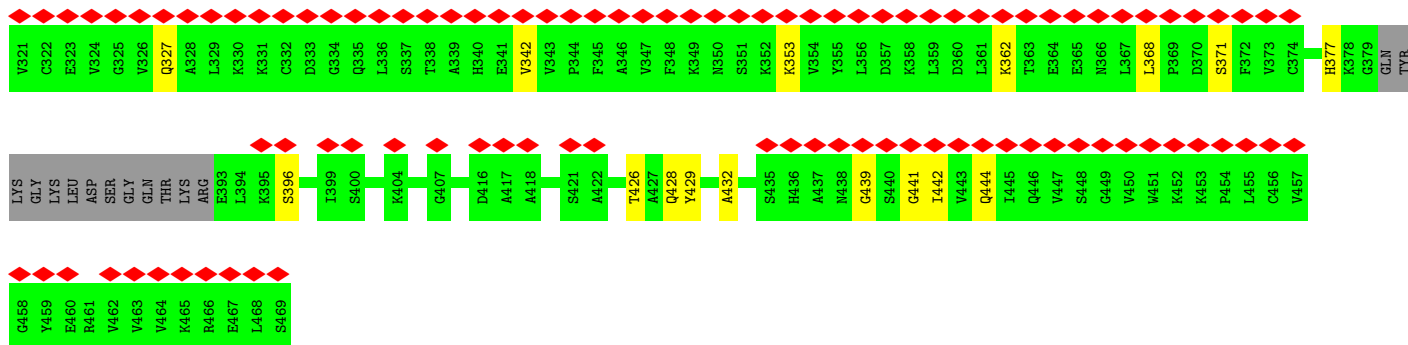


• Molecule 1: Glycoprotein

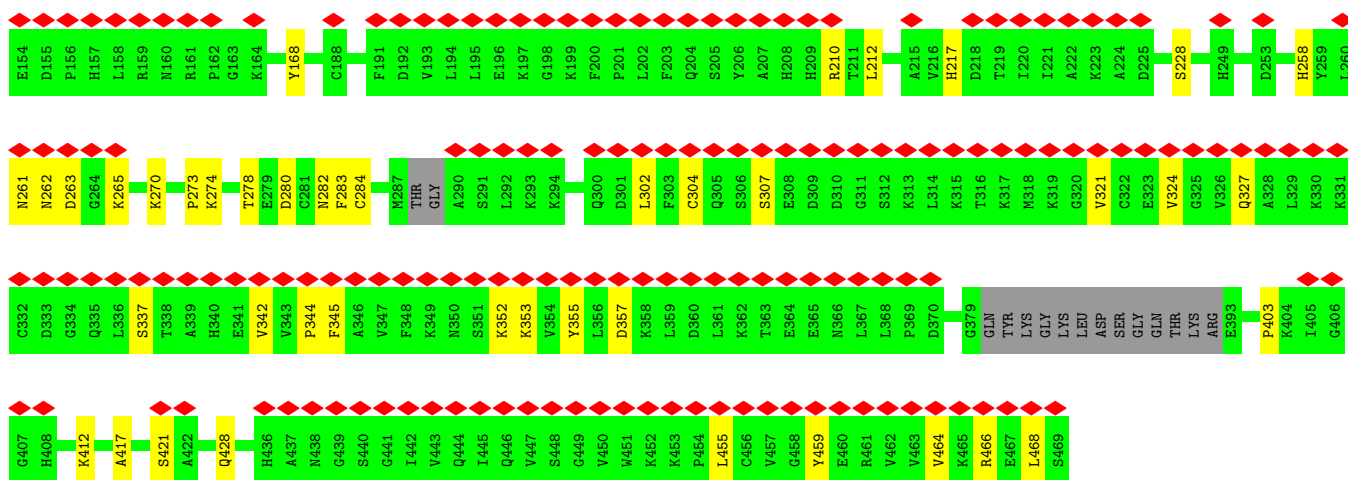
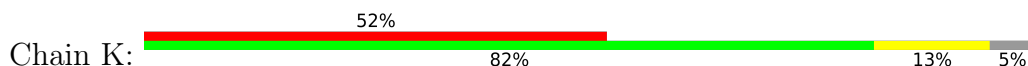


• Molecule 1: Glycoprotein

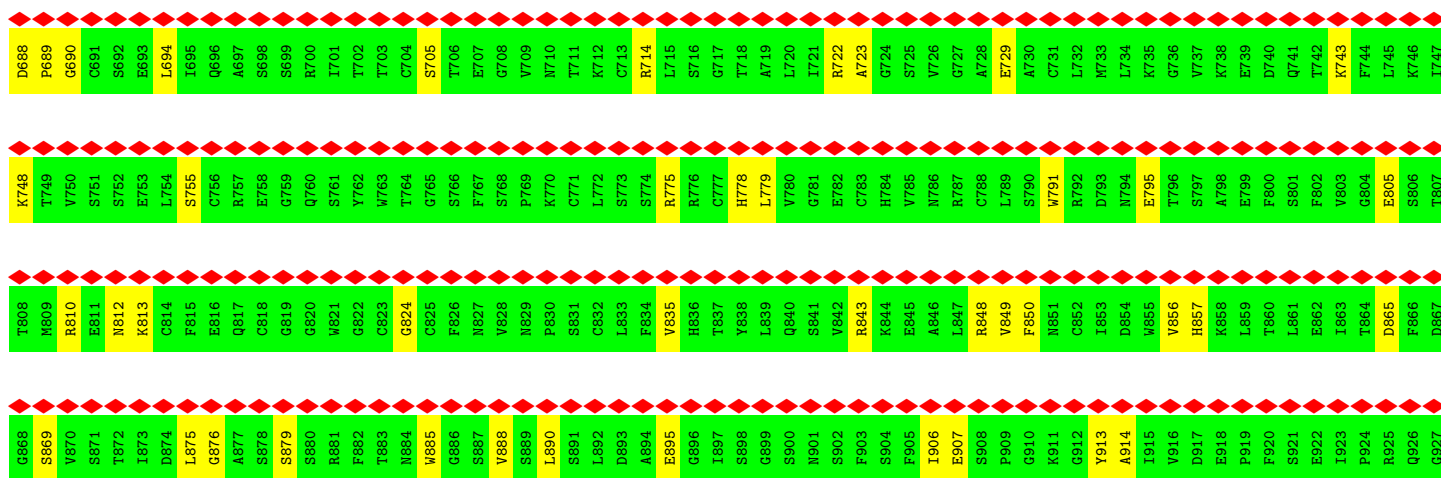
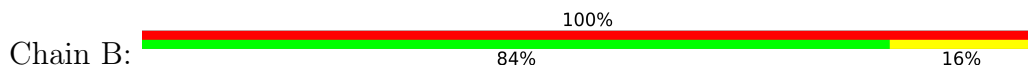




• Molecule 1: Glycoprotein



• Molecule 2: Glycoprotein



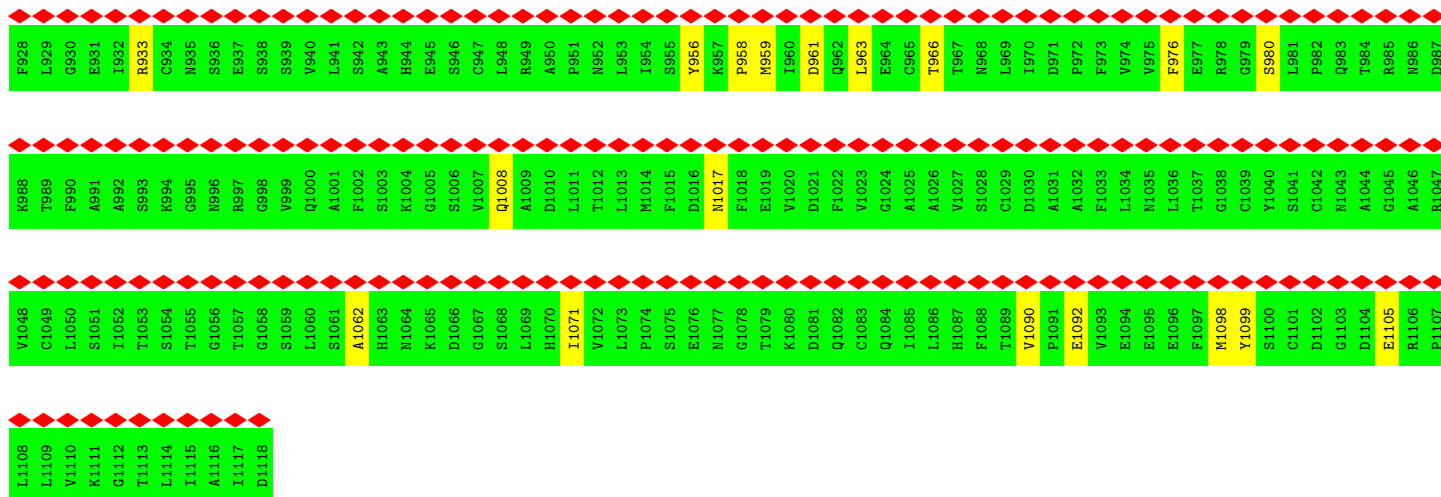


D688	P689	G690	C691	S692	E693	L694	I695	Q696	A697	S698	S699	R700	I701	T702	T703	C704	S705	T706	E707	G708	V709	M710	T711	K712	C713	R714	L715	S716	G717	T718	A719	L720	I721	R722	A723	G724	S725	V726	G727	A728	E729	A730	C731	L732	M733	L734	K735	G736	V737	K738	E739	D740	Q741	T742	K743	F744	L745	K746	I747
K748	T749	V750	S751	F752	E753	L754	S755	C756	R757	E758	G759	Q760	S761	Y762	W763	T764	G765	S766	F767	S768	W769	K770	C771	L772	S773	S774	R775	K776	C777	H778	L779	V780	G781	E782	C783	H784	V785	N786	R787	C788	L789	S790	W791	R792	D793	M794	E795	T796	S797	A798	E799	F800	S801	F802	V803	G804	E805	S806	T807
M809	R810	E811	N812	K813	C814	F815	E816	Q817	C818	G819	S820	W821	G822	C823	G824	C825	F826	N827	W828	N829	P830	S831	C832	L833	F834	V835	H836	T837	Y838	L839	Q840	S841	V842	R843	K844	F845	A846	L847	R848	V849	F850	N851	C852	D853	D854	W855	V856	H857	K858	L859	T860	S861	E862	I863	T864	D865	F866	D867	
G868	S869	V870	S871	T872	I873	D874	L875	G876	A877	S878	S879	S880	R881	F882	T883	N884	W885	G886	S887	V888	S889	L890	S891	L892	D893	A894	E895	G896	I897	S898	G899	S900	N901	S902	F903	S904	F905	I906	E907	S908	P909	G910	K911	G912	Y913	A914	I915	V916	D917	E918	P919	F920	L921	P922	I923	P924	R925	Q926	G927
L929	G930	E931	I932	R933	C934	N935	S936	S937	S938	S939	V940	N941	S942	A943	H944	E945	S946	C947	L948	R949	A950	P951	N952	L953	I954	S955	Y956	K957	P958	M959	I960	D961	Q962	L963	E964	C965	T966	T967	N968	L969	I970	D971	P972	F973	Y974	V975	F976	E977	R978	G979	S980	L981	P982	Q983	T984	R985	N986	D987	
F988	T989	F990	A991	A992	S993	K994	G995	H996	G998	W999	Q1000	A1001	F1002	S1003	K1004	G1005	S1006	V1007	Q1008	A1009	D1010	L1011	T1012	L1013	M1014	F1015	D1016	N1017	F1018	E1019	V1020	D1021	F1022	V1023	G1024	A1025	A1026	V1027	S1028	C1029	T1030	A1031	A1032	F1033	L1034	N1035	L1036	T1037	G1038	C1039	Y1040	S1041	C1042	N1043	A1044	G1045	A1046	R1047	
V1048	C1049	L1050	S1051	T1052	T1053	S1054	T1055	G1056	T1057	G1058	S1059	L1060	S1061	A1062	H1063	N1064	K1065	D1066	G1067	S1068	L1069	H1070	I1071	T1072	L1073	P1074	S1075	E1076	N1077	G1078	T1079	K1080	D1081	Q1082	C1083	Q1084	I1085	L1086	H1087	F1088	T1089	V1090	P1091	E1092	V1093	E1094	E1095	L1096	T1097	M1098	Y1099	S1100	C1101	D1102	N1103	D1104	E1105	R1106	P1107
L1108	L1109	V1110	K1111	G1112	T1113	L1114	I1115	A1116	T1117	D1118																																																	

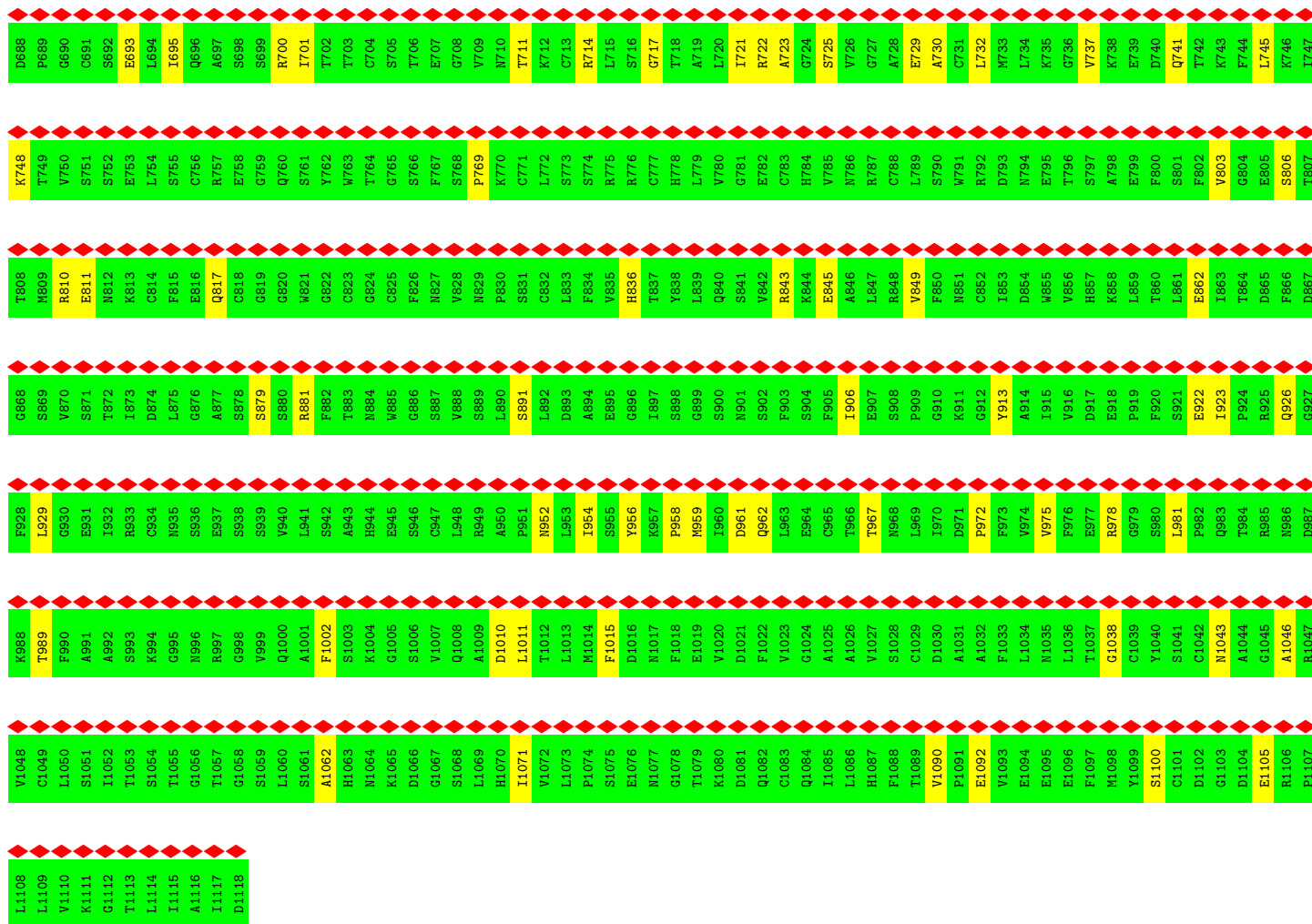
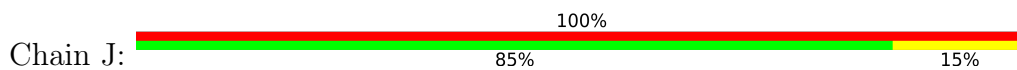
● Molecule 2: Glycoprotein



D688	P689	G690	C691	S692	E693	L694	I695	Q696	A697	S698	S699	R700	I701	T702	T703	C704	S705	T706	E707	G708	V709	M710	T711	K712	C713	R714	L715	S716	G717	T718	A719	L720	I721	R722	A723	G724	S725	V726	G727	A728	E729	A730	C731	L732	M733	L734	K735	G736	V737	K738	E739	D740	Q741	T742	K743	F744	L745	K746	I747
K748	T749	V750	S751	F752	E753	L754	S755	C756	R757	E758	G759	Q760	S761	Y762	W763	T764	G765	S766	F767	S768	W769	K770	C771	L772	S773	S774	R775	K776	C777	H778	L779	V780	G781	E782	C783	H784	V785	N786	R787	C788	L789	S790	W791	R792	D793	M794	E795	T796	S797	A798	E799	F800	S801	F802	V803	G804	E805	S806	T807
M809	R810	E811	N812	K813	C814	F815	E816	Q817	C818	G819	S820	W821	G822	C823	G824	C825	F826	N827	W828	N829	P830	S831	C832	L833	F834	V835	H836	T837	Y838	L839	Q840	S841	V842	R843	K844	F845	A846	L847	R848	V849	F850	N851	C852	D853	D854	W855	V856	H857	K858	L859	T860	S861	E862	I863	T864	D865	F866	D867	
G868	S869	V870	S871	T872	I873	D874	L875	G876	A877	S878	S879	S880	R881	F882	T883	N884	W885	G886	S887	V888	S889	L890	S891	L892	D893	A894	E895	G896	I897	S898	G899	S900	N901	S902	F903	S904	F905	I906	E907	S908	P909	G910	K911	G912	Y913	A914	I915	V916	D917	E918	P919	F920	L921	P922	I923	P924	R925	Q926	G927



• Molecule 2: Glycoprotein



• Molecule 2: Glycoprotein

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2995	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	22	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	0.101	Depositor
Minimum map value	-0.072	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	345.6, 345.6, 345.6	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7, 2.7, 2.7	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	A	0.08	0/2333	0.25	0/3136
1	C	0.08	0/2333	0.24	0/3136
1	E	0.09	0/2333	0.26	0/3136
1	G	0.08	0/2333	0.22	0/3136
1	I	0.07	0/2333	0.21	0/3136
1	K	0.08	0/2333	0.23	0/3136
2	B	0.08	0/3284	0.24	0/4431
2	D	0.08	0/3284	0.23	0/4431
2	F	0.08	0/3284	0.23	0/4431
2	H	0.08	0/3284	0.24	0/4431
2	J	0.08	0/3284	0.23	0/4431
2	L	0.08	0/3284	0.23	0/4431
All	All	0.08	0/33702	0.24	0/45402

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2284	0	2205	27	0
1	C	2284	0	2205	19	0
1	E	2284	0	2205	28	0
1	G	2284	0	2205	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	2284	0	2205	28	0
1	K	2284	0	2205	26	0
2	B	3224	0	3071	38	0
2	D	3224	0	3071	36	0
2	F	3224	0	3071	44	0
2	H	3224	0	3071	29	0
2	J	3224	0	3071	38	0
2	L	3224	0	3071	34	0
All	All	33048	0	31656	356	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 356 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:212:LEU:HB2	1:K:302:LEU:HD11	1.77	0.66
2:D:748:LYS:HB3	2:D:862:GLU:HB3	1.79	0.65
2:B:1062:ALA:HB3	2:B:1071:ILE:HB	1.79	0.64
2:F:805:GLU:OE2	2:F:810:ARG:NH2	2.30	0.64
2:H:1062:ALA:HB3	2:H:1071:ILE:HB	1.78	0.64

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](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	241/271 (89%)	240 (100%)	1 (0%)	84	84
1	C	241/271 (89%)	241 (100%)	0	100	100
1	E	241/271 (89%)	241 (100%)	0	100	100
1	G	241/271 (89%)	241 (100%)	0	100	100
1	I	241/271 (89%)	241 (100%)	0	100	100
1	K	241/271 (89%)	241 (100%)	0	100	100
2	B	347/371 (94%)	347 (100%)	0	100	100
2	D	347/371 (94%)	346 (100%)	1 (0%)	86	86
2	F	347/371 (94%)	347 (100%)	0	100	100
2	H	347/371 (94%)	347 (100%)	0	100	100
2	J	347/371 (94%)	347 (100%)	0	100	100
2	L	347/371 (94%)	346 (100%)	1 (0%)	86	86
All	All	3528/3852 (92%)	3525 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	455	LEU
2	D	892	LEU
2	L	873	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	327	GLN
1	K	428	GLN
2	L	968	ASN
2	F	784	HIS
1	E	428	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.

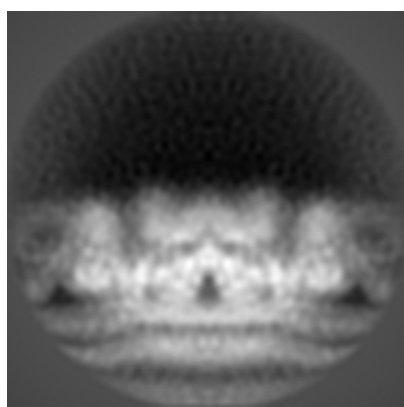
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4199. These allow visual inspection of the internal detail of the map and identification of artifacts.

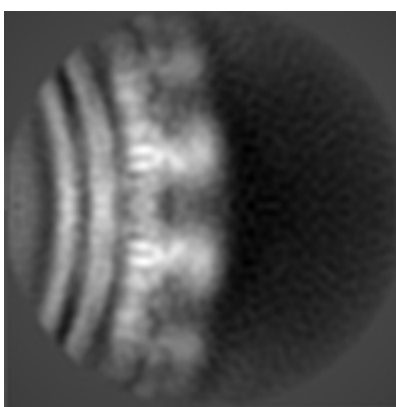
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

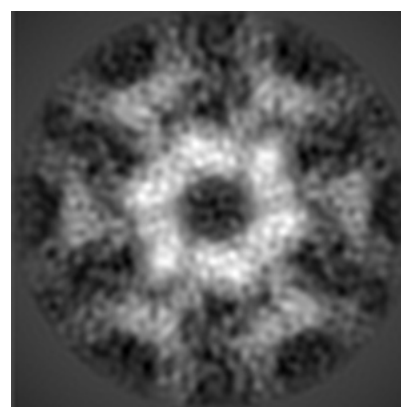
6.1.1 Primary map



X



Y

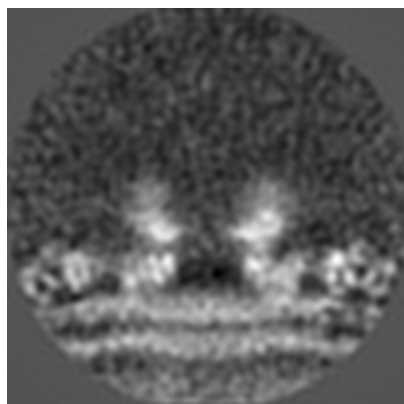


Z

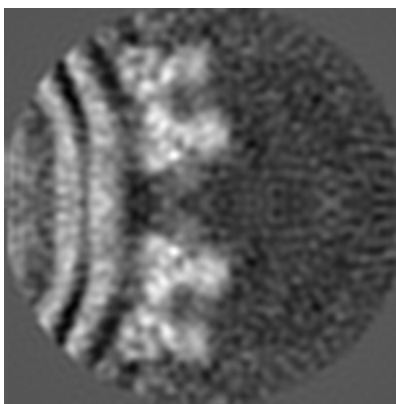
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

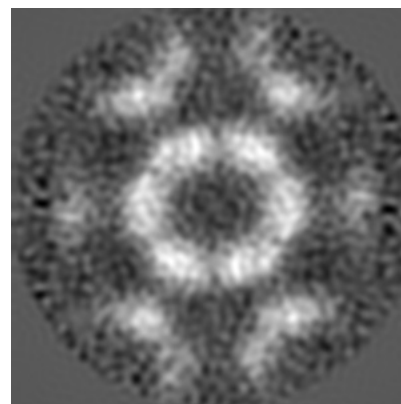
6.2.1 Primary map



X Index: 64



Y Index: 64

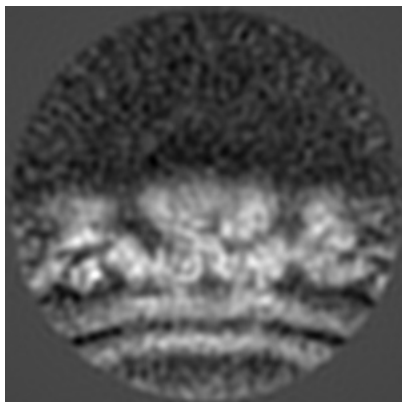


Z Index: 64

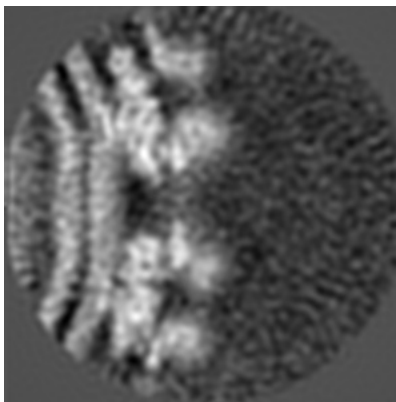
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

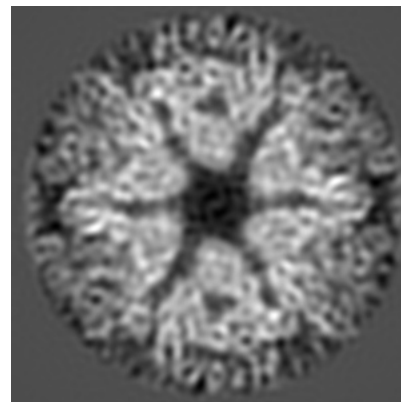
6.3.1 Primary map



X Index: 83



Y Index: 58

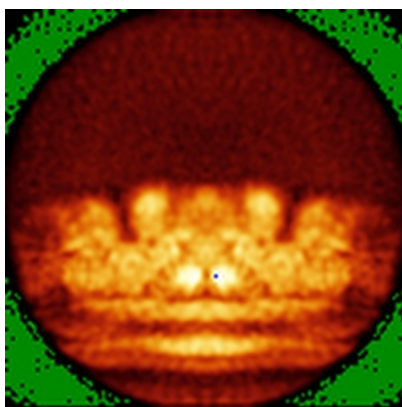


Z Index: 42

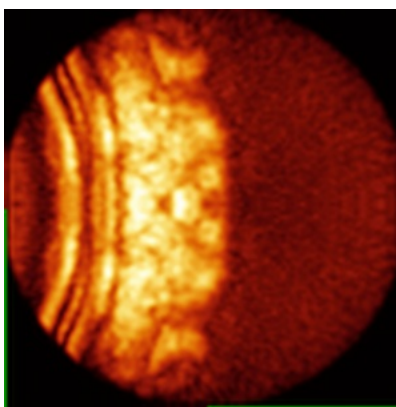
The images above show the largest variance slices of the map in three orthogonal directions.

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

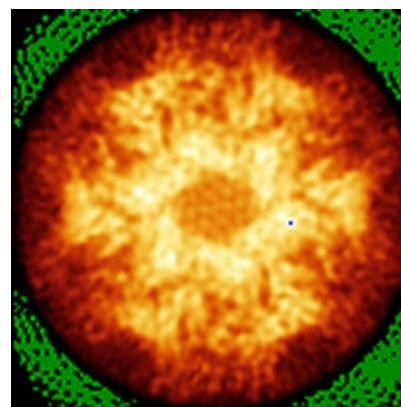
6.4.1 Primary map



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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

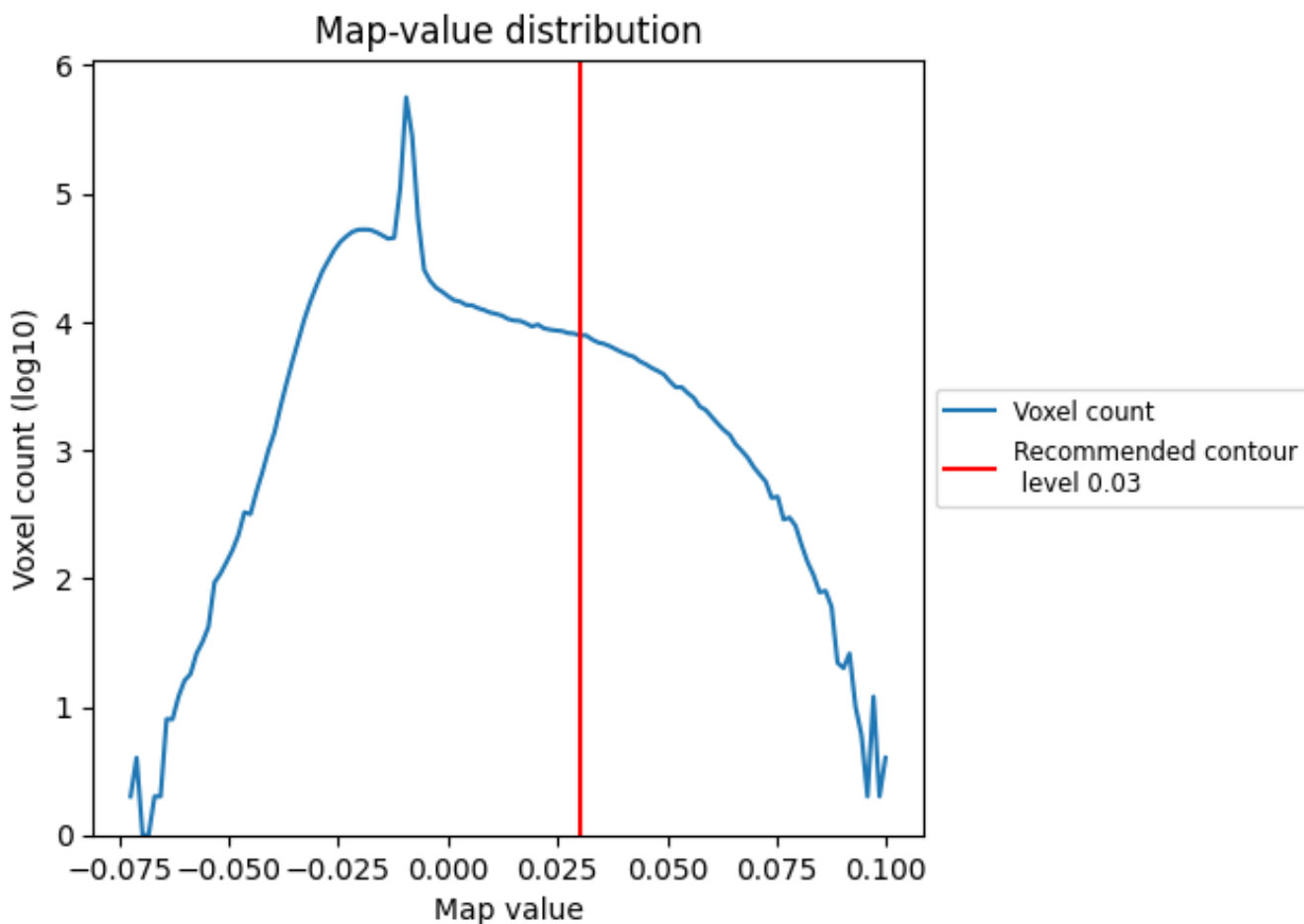
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

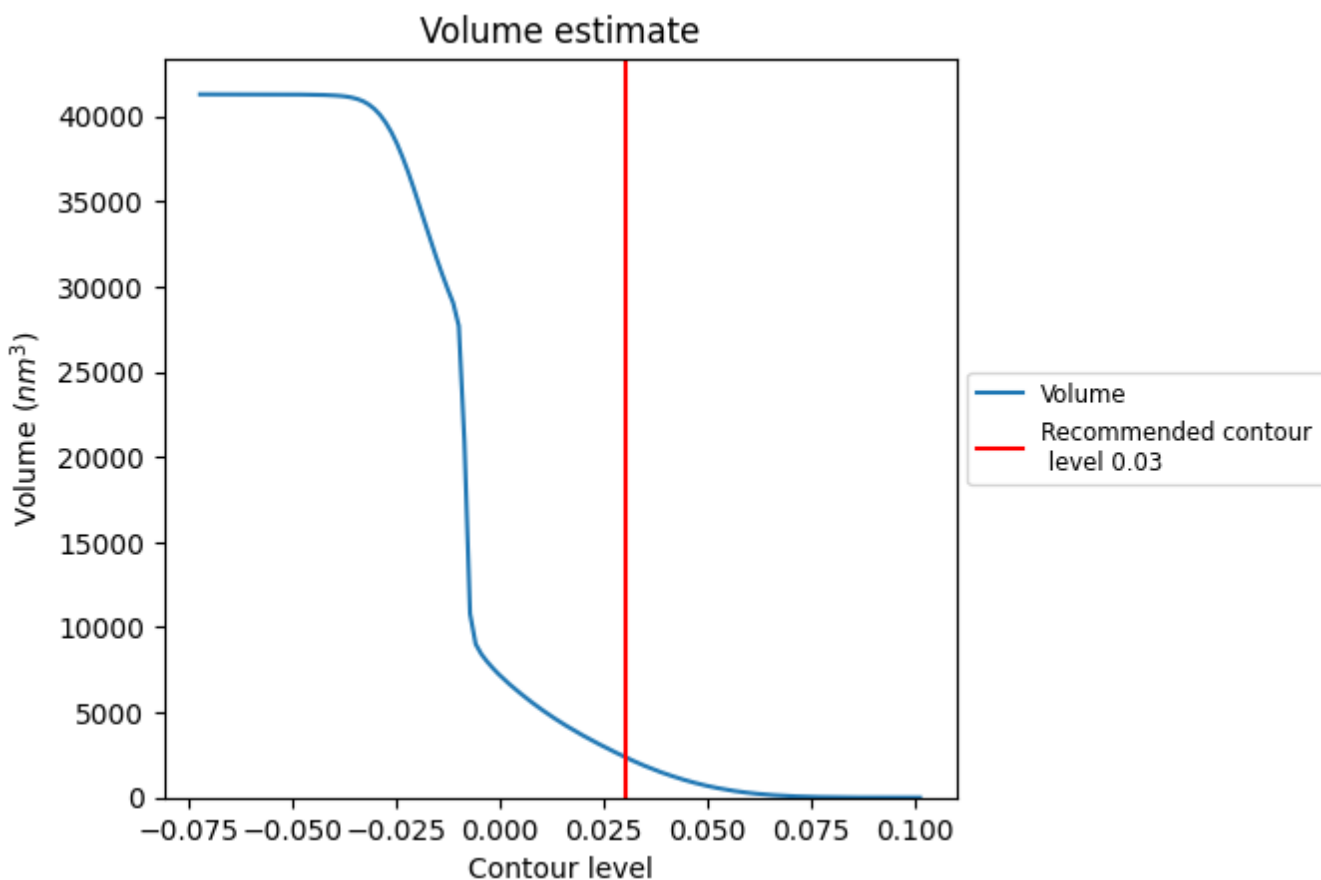
This section contains the results of statistical analysis of the map.

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.

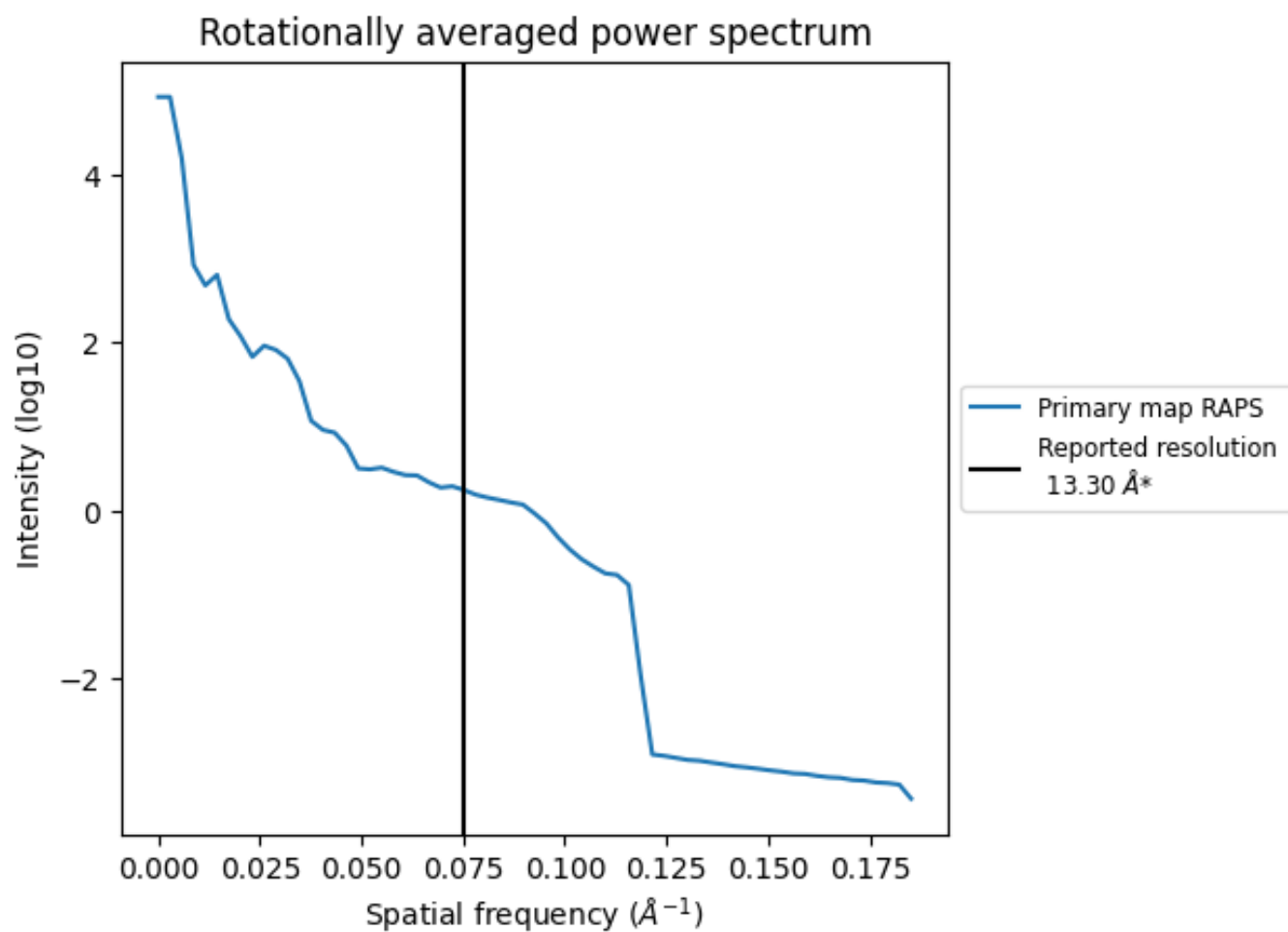
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2388 nm³; this corresponds to an approximate mass of 2157 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 [i](#)

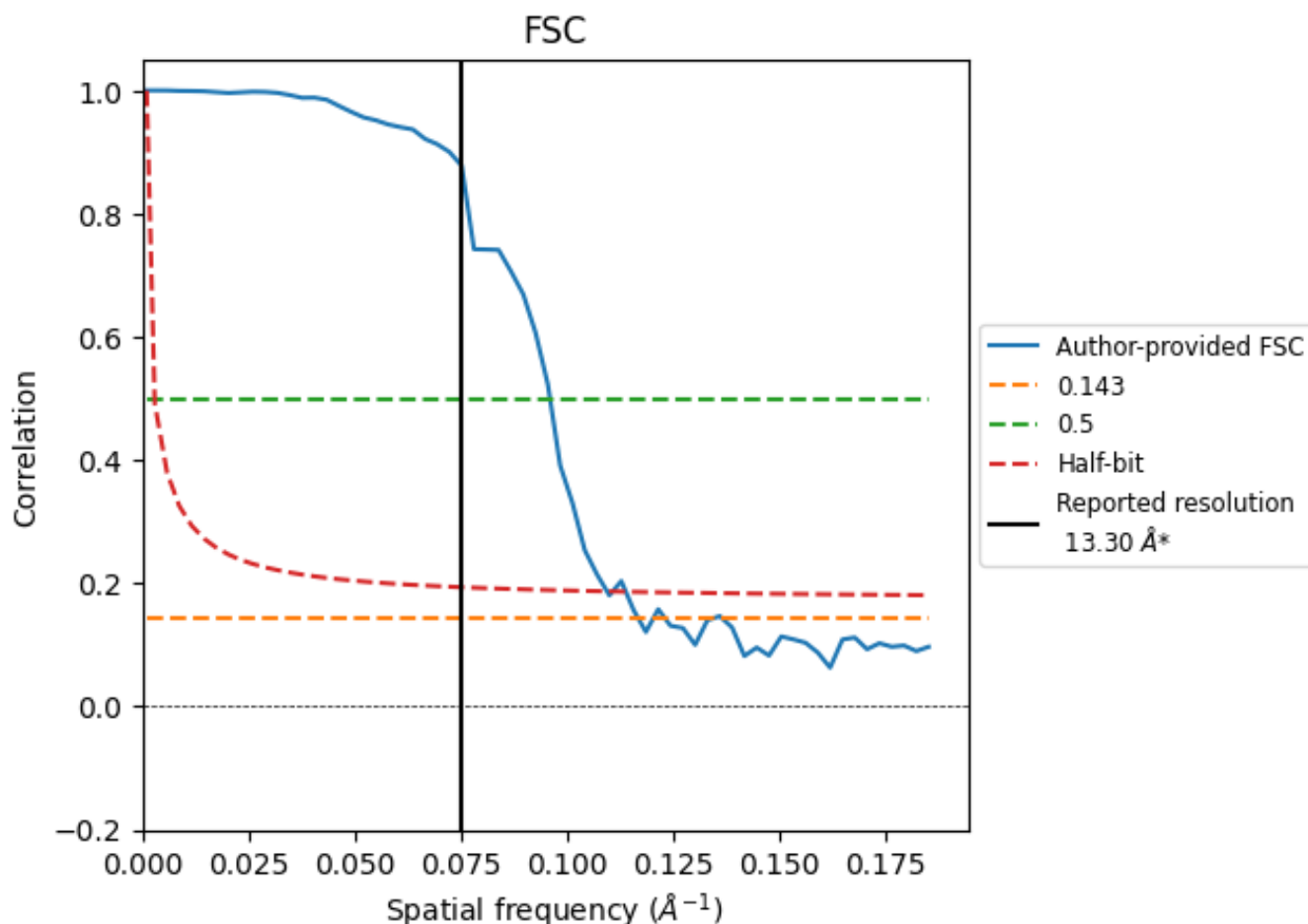


*Reported resolution corresponds to spatial frequency of 0.075 Å⁻¹

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 0.075 Å⁻¹

8.2 Resolution estimates [i](#)

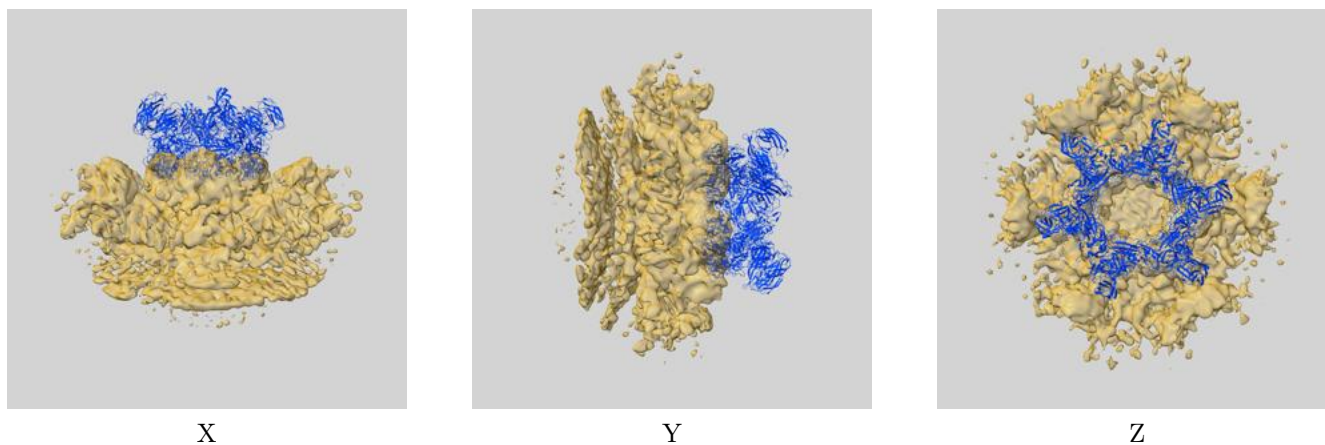
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	13.30	-	-
Author-provided FSC curve	8.56	10.42	9.14
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.56 differs from the reported value 13.3 by more than 10 %

9 Map-model fit [i](#)

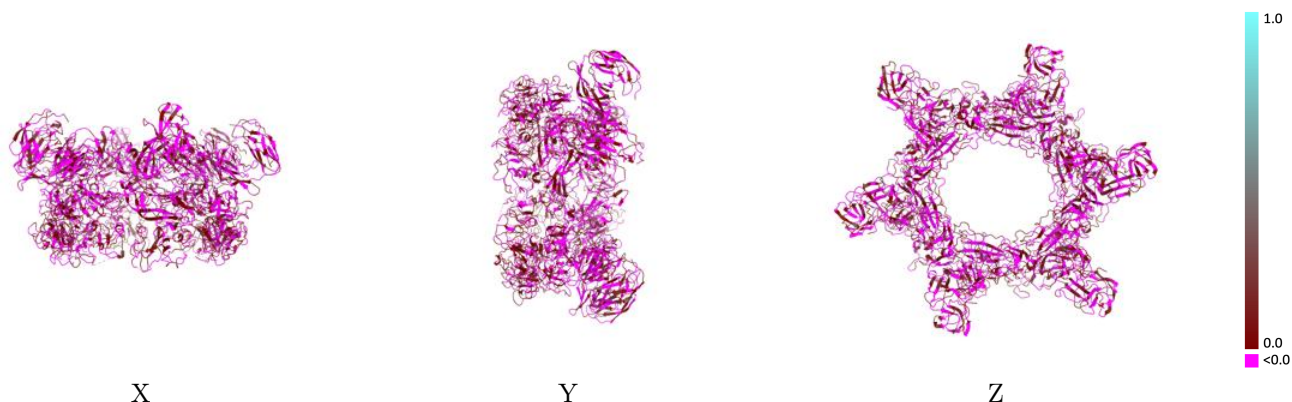
This section contains information regarding the fit between EMDB map EMD-4199 and PDB model 6F9D. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



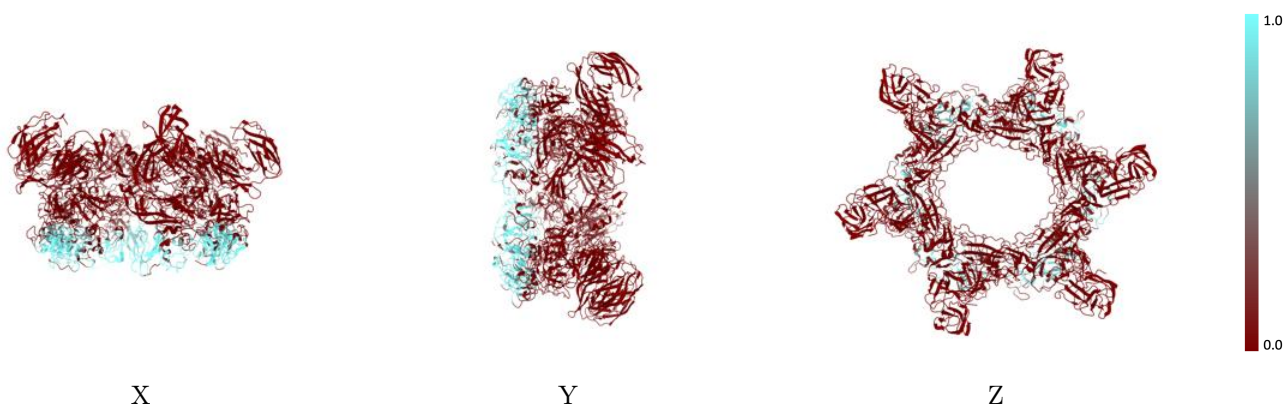
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



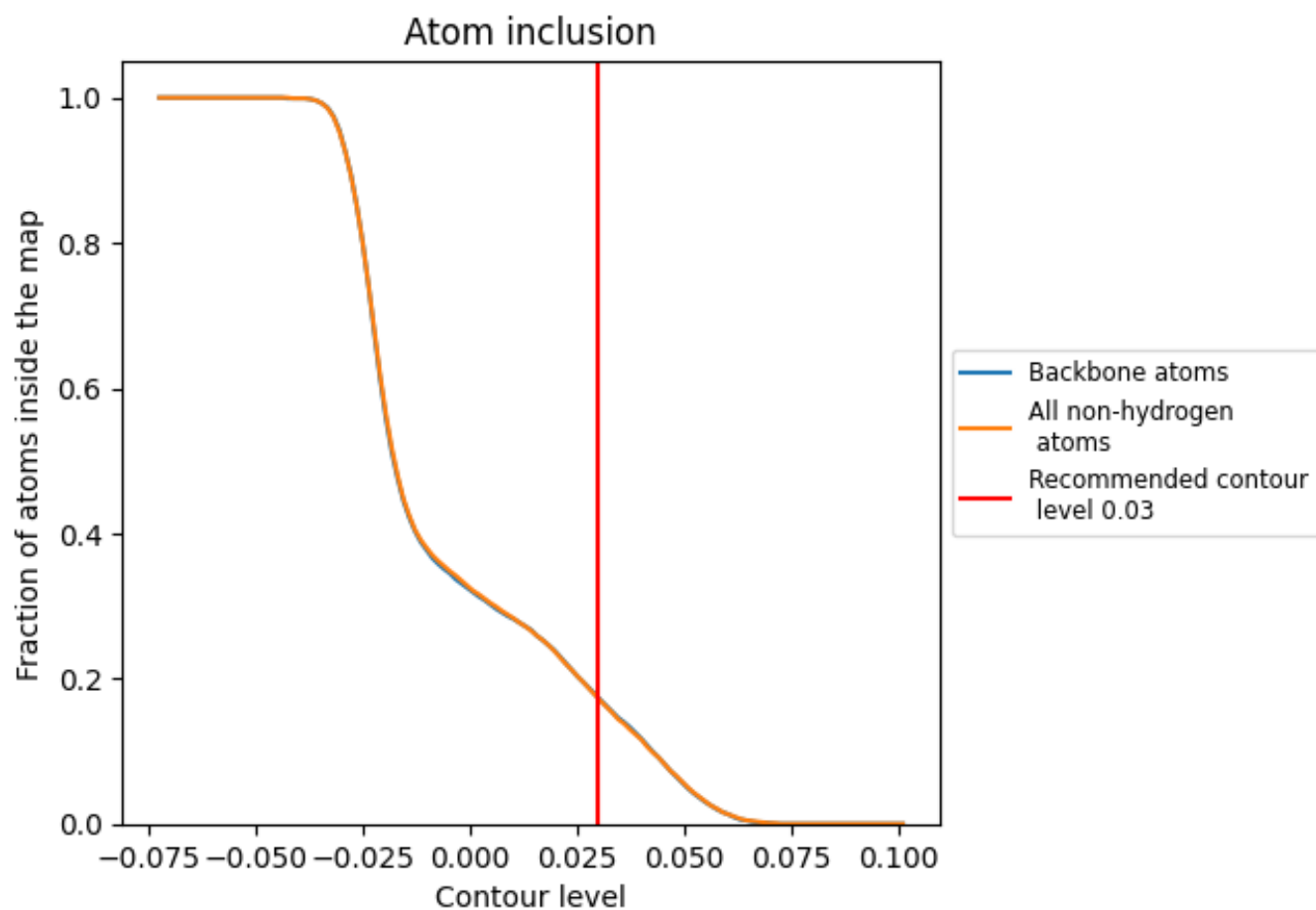
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 17% of all backbone atoms, 17% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.1730	 0.0080
A	 0.3810	 0.0150
B	 0.0000	 0.0020
C	 0.4000	 0.0300
D	 0.0000	 0.0010
E	 0.4180	 0.0220
F	 0.0000	 0.0030
G	 0.4200	 0.0260
H	 0.0000	 -0.0070
I	 0.4490	 0.0250
J	 0.0000	 -0.0040
K	 0.4260	 0.0180
L	 0.0000	 -0.0110

