



## wwPDB EM Validation Summary Report ⓘ

Dec 26, 2024 – 07:44 AM EST

PDB ID : 6F9D  
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](mailto: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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

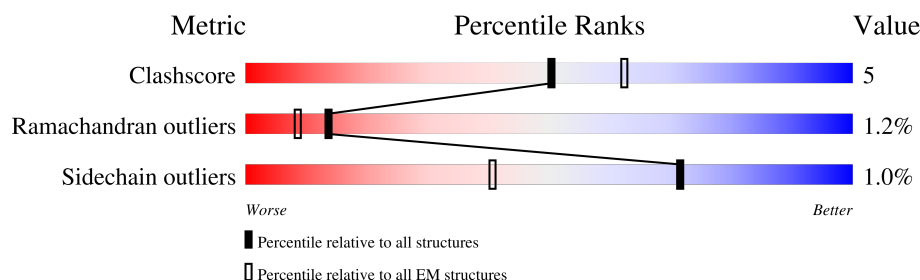
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	<div> <div>57%</div> <div>79% 15% 5%</div> </div>
1	C	316	<div> <div>56%</div> <div>83% 12% 5%</div> </div>
1	E	316	<div> <div>53%</div> <div>80% 15% 5%</div> </div>
1	G	316	<div> <div>54%</div> <div>80% 15% 5%</div> </div>
1	I	316	<div> <div>51%</div> <div>79% 16% 5%</div> </div>
1	K	316	<div> <div>52%</div> <div>80% 16% 5%</div> </div>
2	B	431	<div> <div>100%</div> <div>83% 16%</div> </div>
2	D	431	<div> <div>100%</div> <div>84% 16%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	431	<div><div></div><div>100%</div><div>81%18%</div></div>
2	H	431	<div><div></div><div>100%</div><div>87%13%</div></div>
2	J	431	<div><div></div><div>100%</div><div>84%16%</div></div>
2	L	431	<div><div></div><div>100%</div><div>85%14%</div></div>

## 2 Entry composition

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
1	A	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		
1	C	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		
1	E	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		
1	G	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		
1	I	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		
1	K	301	Total	C	N	O	S	0	0
			2284	1437	400	441	6		

- Molecule 2 is a protein called Glycoprotein.

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

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

*Continued on next page...*

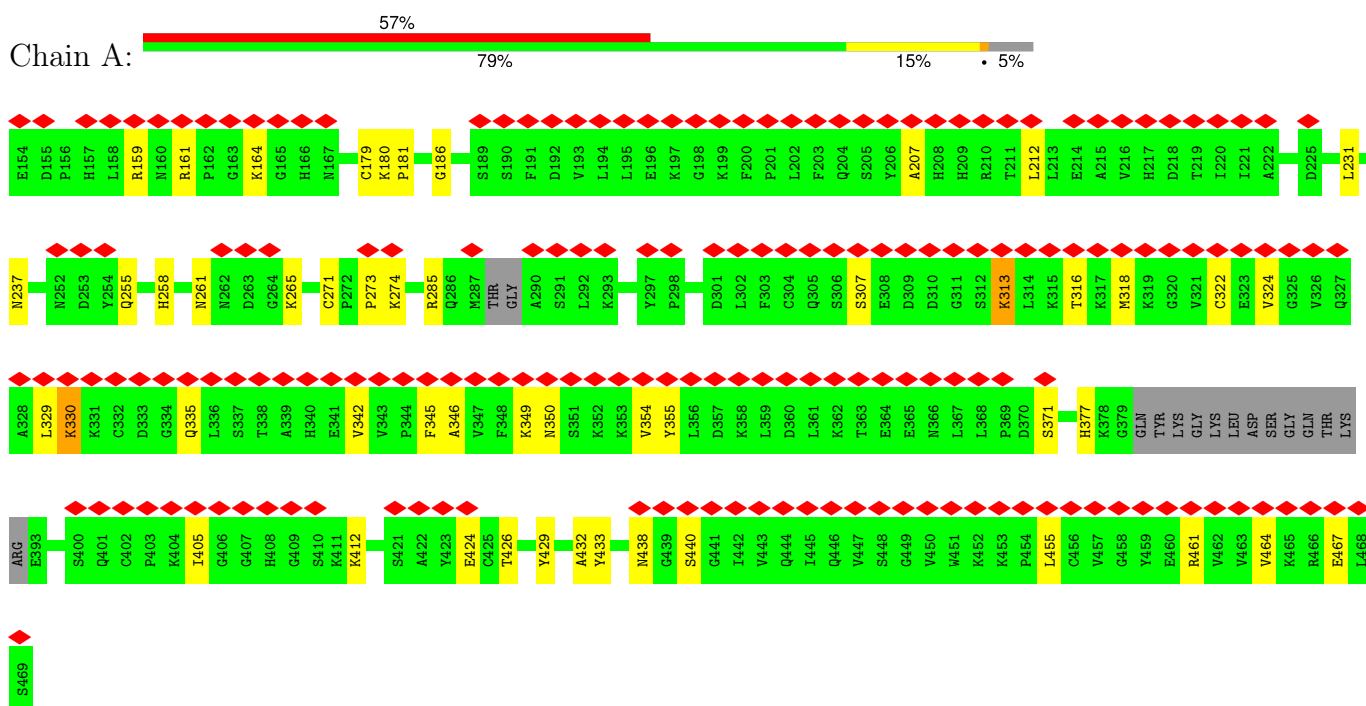
*Continued from previous page...*

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

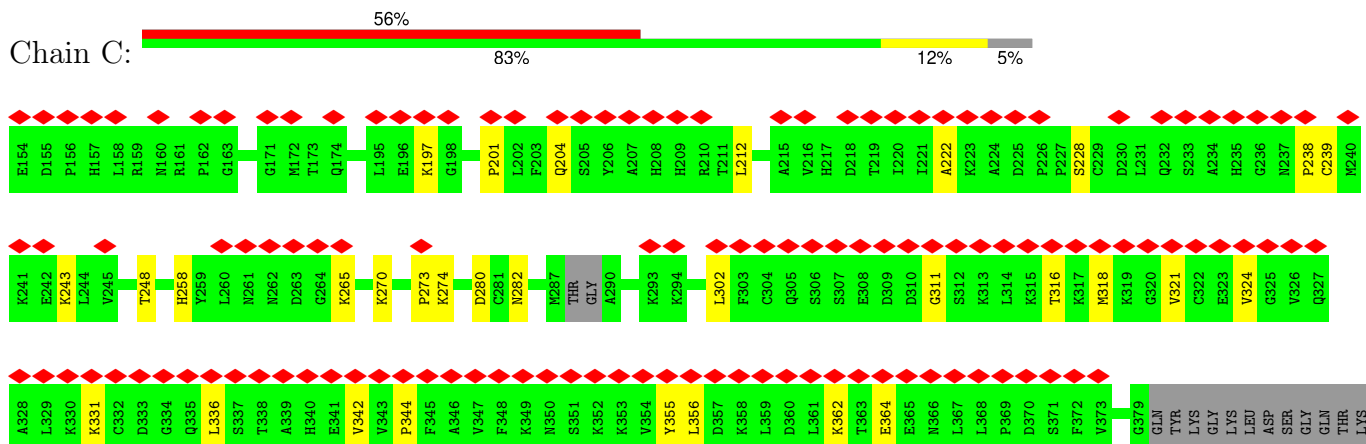
### 3 Residue-property plots

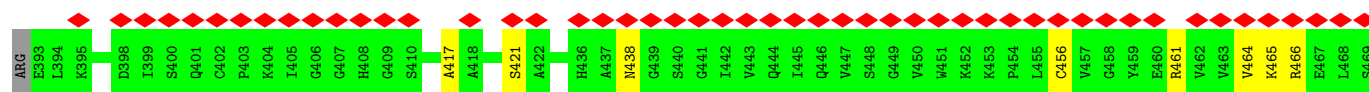
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

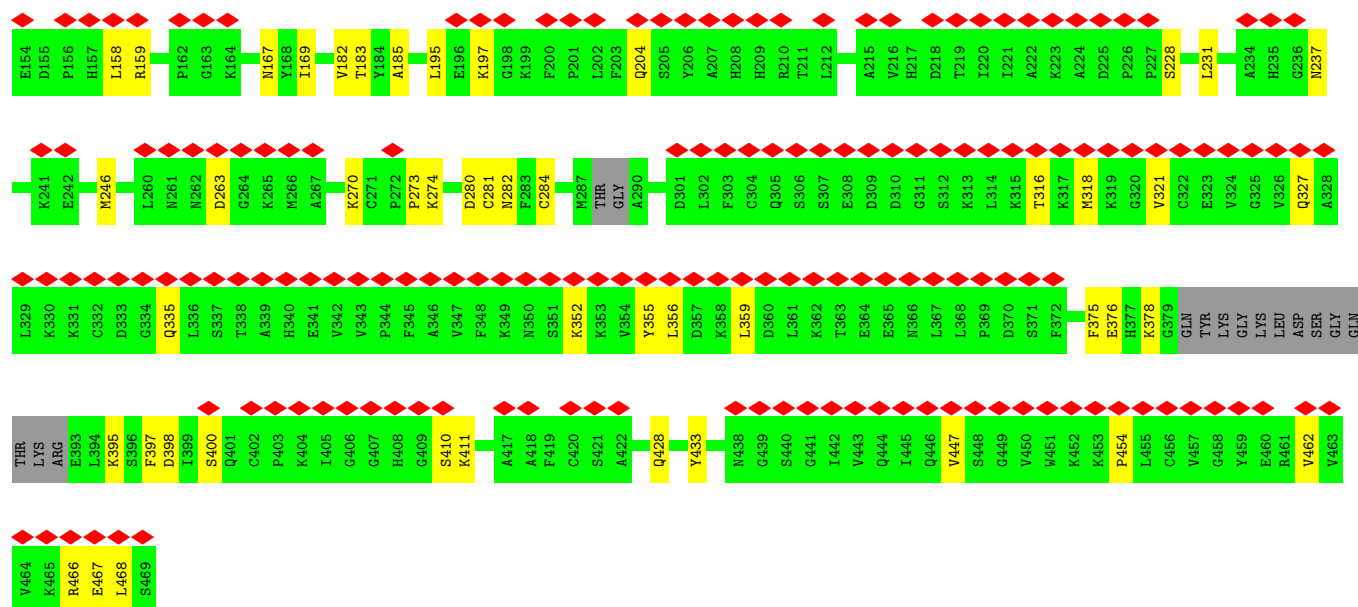
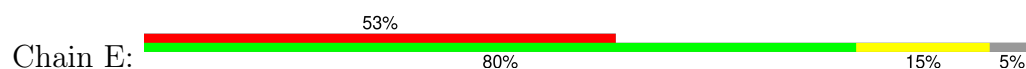


#### • Molecule 1: Glycoprotein

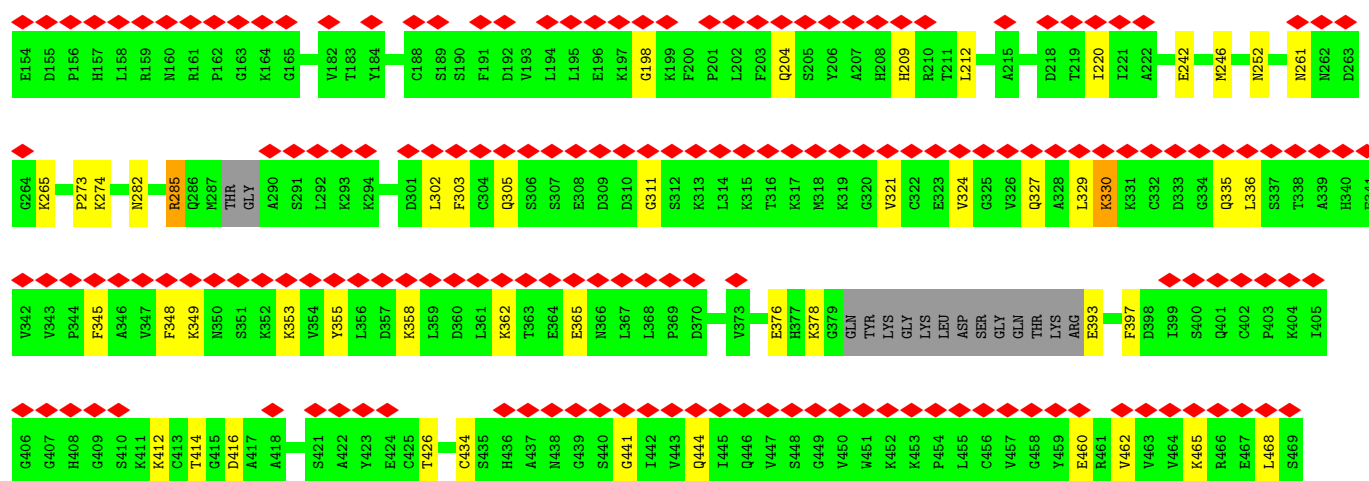
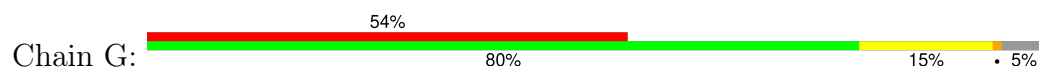




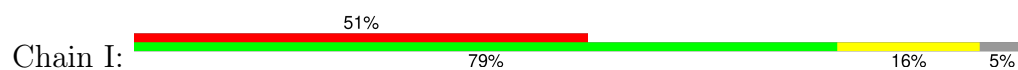
• Molecule 1: Glycoprotein

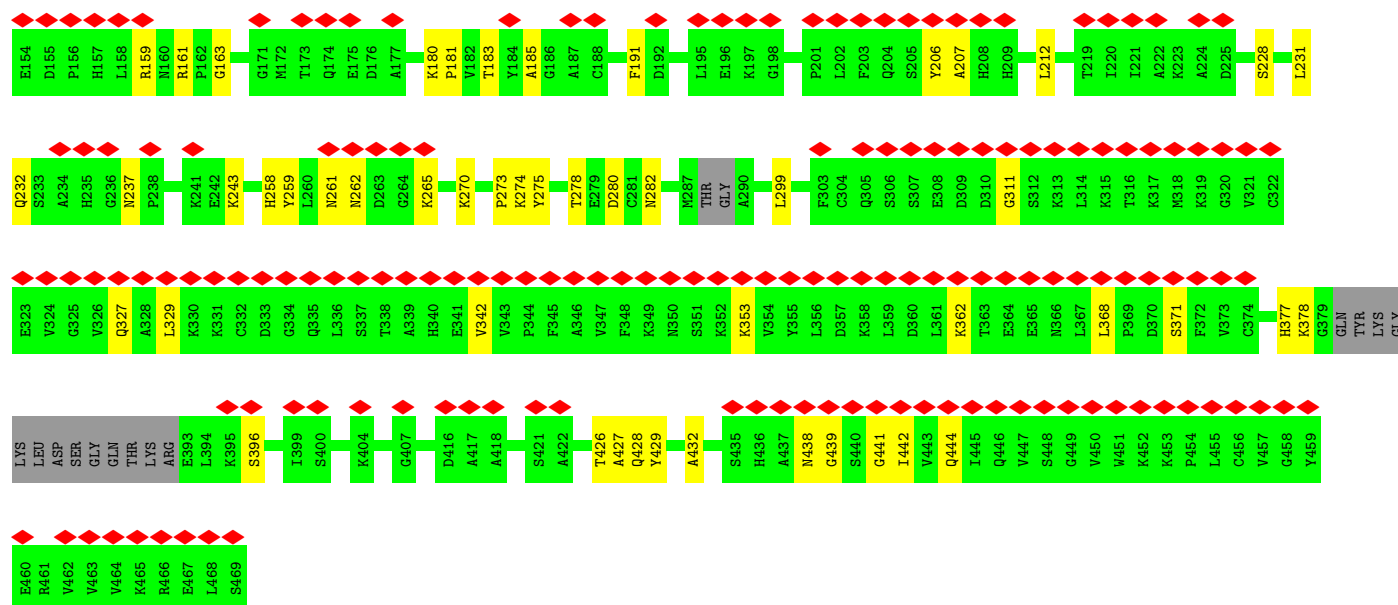


• Molecule 1: Glycoprotein

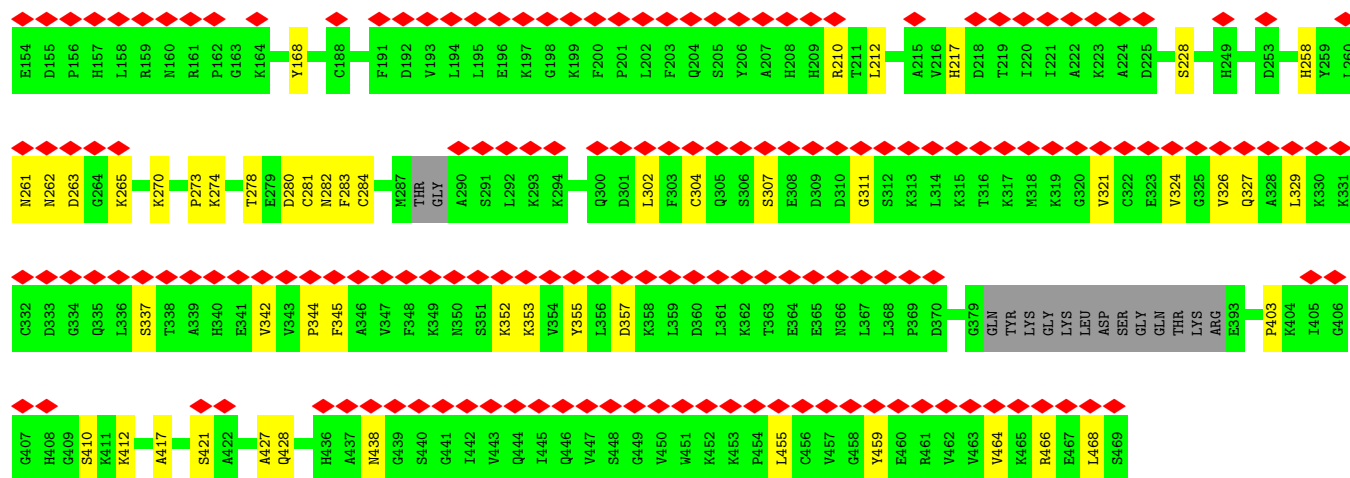
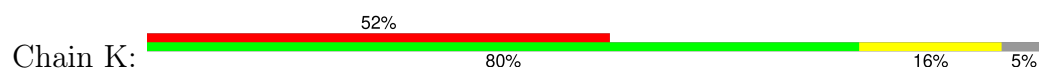


• Molecule 1: Glycoprotein

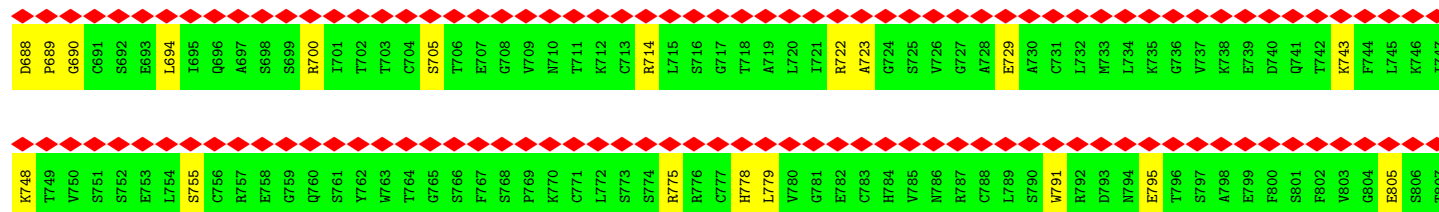
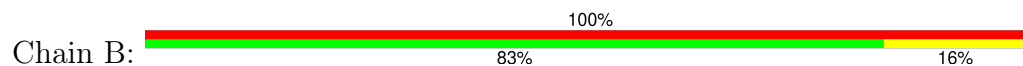




• Molecule 1: Glycoprotein

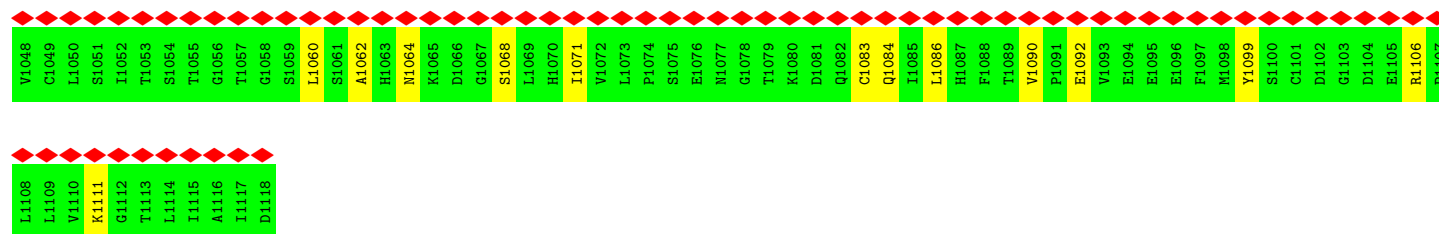


• Molecule 2: Glycoprotein

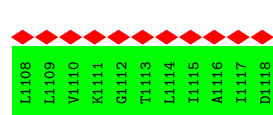
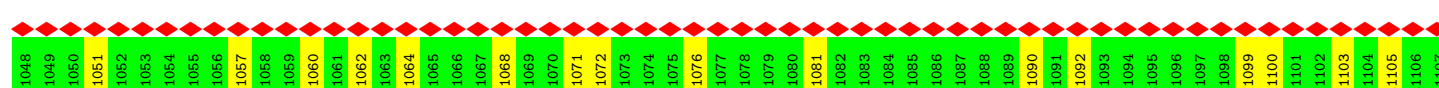
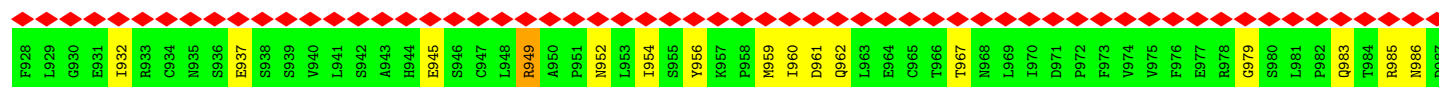
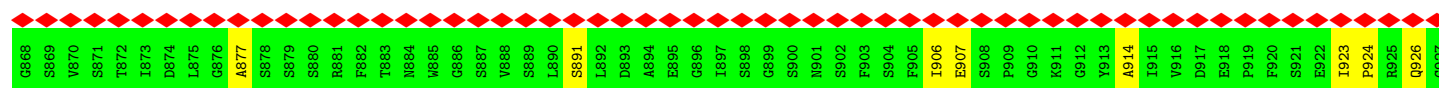
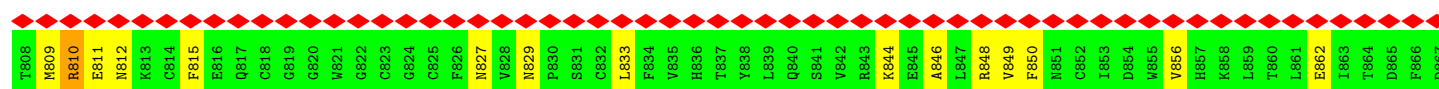
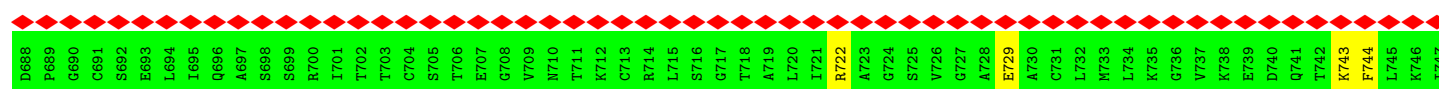
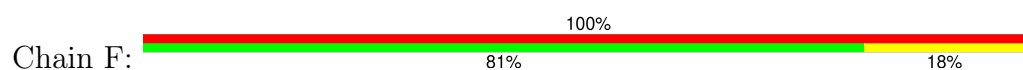




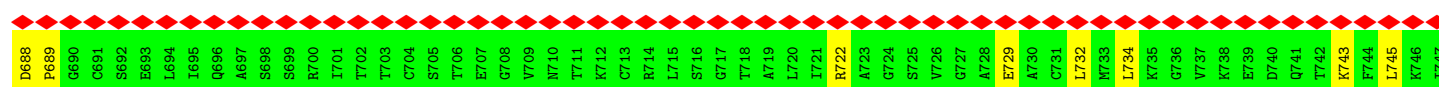
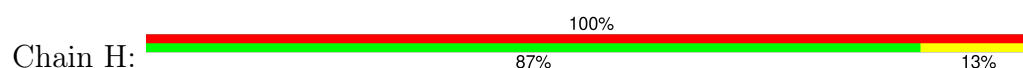
L1108	V1048	K988	F928	G868	T808
L1109	C1049	T989	L929	S869	M809
V1110	L1050	F990	G930	V870	R810
K1111	S1051	A991	E931	S871	E811
G1112	I1052	A992	I932	T872	N812
T1113	T1053	S993	R933	I873	K813
L1114	S1054	K994	C934	D874	C814
I1115	T1055	G995	N935	L875	F815
A1116	G1056	N996	S936	G876	E816
I1117	T1057	R997	E937	A877	Q817
D1118	G1058	G998	S938	S878	C818
	S1059	V999	S939	S879	G819
	L1060	Q1000	V940	S880	G820
	S1061	A1001	L941	R881	W821
	A1062	F1002	S942	F882	G822
	H1063	S1003	A943	T883	C823
	N1064	K1004	H944	H884	G824
	K1065	G1005	E945	W885	C825
	D1066	S1006	S946	G886	F826
	G1067	V1007	C947	S887	N827
	S1068	Q1008	L948	V888	V828
	L1069	A1009	R949	S889	N829
	H1070	D1010	A950	L890	P830
	T1071	L1011	P951	S891	S831
	V1072	T1012	N952	L892	C832
	L1073	L1013	L953	D893	L833
	P1074	M1014	I954	A894	F834
	S1075	F1015	S955	E895	V835
	E1076	D1016	Y956	G896	H836
	N1077	M1017	K957	T897	T837
	G1078	F1018	P958	S898	Y838
	T1079	E1019	M959	G899	L839
	K1080	V1020	I960	S900	Q840
	D1081	D1021	D961	N901	S841
	Q1082	F1022	Q962	S902	V842
	C1083	V1023	L963	F903	R843
	Q1084	G1024	E964	S904	K844
	I1085	A1025	C965	F905	E845
	L1086	A1026	T966	I906	A846
	H1087	V1027	T967	E907	L847
	F1088	S1028	N968	S908	R848
	T1089	C1029	L969	P909	V849
	V1090	D1030	I970	G910	F850
	P1091	A1031	D971	K911	N851
	E1092	A1032	P972	G912	C852
	V1093	F1033	F973	Y913	I853
	E1094	L1034	V974	A914	D854
	E1095	M1035	V975	I915	W855
	E1096	L1036	F976	V916	V856
	F1097	T1037	E977	D917	H857
	M1098	G1038	R978	E918	K858
	Y1099	C1039	G979	P919	L859
	S1100	Y1040	S980	F920	T860
	C1101	S1041	L981	S921	L861
	D1102	C1042	P982	E922	E862
	G1103	M1043	Q983	I923	I863
	D1104	A1044	T984	P924	T864
	E1105	G1045	R985	R925	D865
	P1106	A1046	N986	Q926	F866
	R1107	R1047	D987	G927	D867



• Molecule 2: Glycoprotein

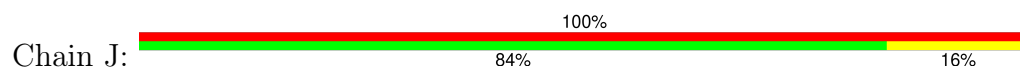


• Molecule 2: Glycoprotein

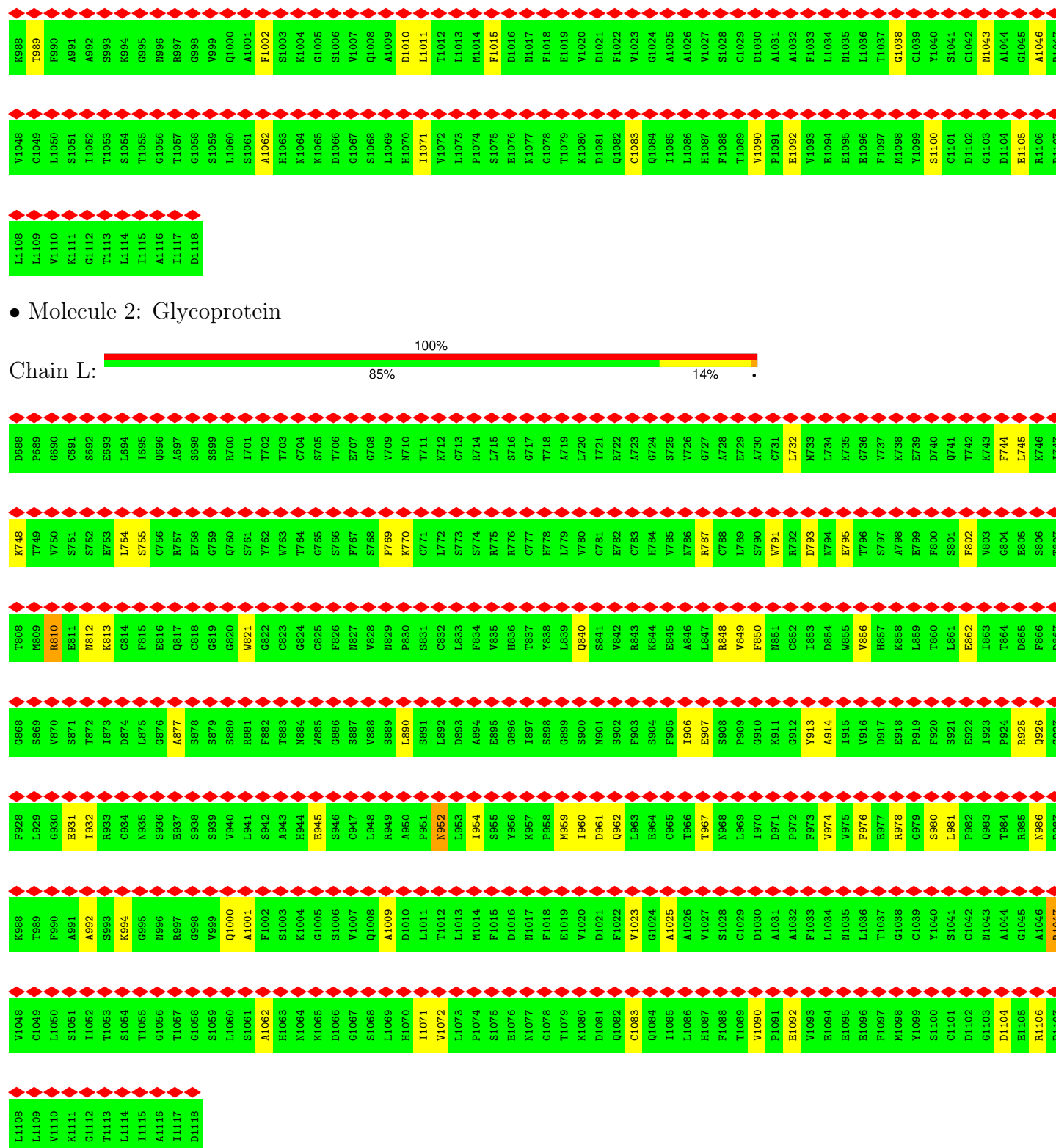


K748	T808	G868	F928	K988	V1048	L1108
T749	M809	S869	L929	T989	C1049	L1109
V750	R810	V870	G930	F990	L1050	V1110
S751	E811	S871	E931	A991	S1051	K1111
S752	N812	T872	R932	A992	T1052	T1112
E753	K813	I873	R933	S993	T1053	T1113
L754	C814	D874	C934	K994	S1054	L1114
S755	F815	L875	N935	G995	T1055	I1115
C756	E816	G876	S936	N996	G1056	A1116
R757	Q817	A877	E937	R997	T1057	I1117
E758	C818	S878	S938	G998	G1058	D1118
G759	G819	S879	S939	V999	S1059	
Q760	G820	S880	V940	Q1000	L1060	
S761	W821	R881	L941	A1001	S1061	
Y762	G822	F882	S942	F1002	A1062	
W763	C823	T883	A943	S1003	H1063	
T764	G824	N884	H944	K1004	N1064	
G765	C825	W885	E945	G1005	K1065	
S766	F826	G886	S946	S1006	D1066	
F767	N827	S887	C947	T1007	G1067	
S768	V828	W888	L948	Q1008	S1068	
P769	N829	S889	R949	A1009	L1069	
K770	P830	L890	A950	D1010	H1070	
C771	S831	S891	P951	L1011	T1071	
L772	C832	L892	N952	T1012	V1072	
S773	F833	D893	L953	L1013	L1073	
R774	A894	A894	I954	M1014	P1074	
R775	V835	E895	S955	F1015	S1075	
R776	H836	G896	Y956	D1016	E1076	
C777	T837	I897	K957	N1017	M1077	
H778	Y838	S898	P958	F1018	G1078	
L779	L839	G899	M959	E1019	T1079	
V780	Q840	S900	I960	V1020	K1080	
G781	S841	N901	D961	D1021	L1081	
E782	V842	S902	Q962	F1022	Q1082	
C783	R843	F903	L963	V1023	Q1083	
H784	K844	S904	E964	G1024	Q1084	
V785	E845	F905	C965	A1025	I1085	
N786	A846	I906	T966	A1026	L1086	
R787	L847	E907	T967	V1027	H1087	
C788	R848	S908	N968	S1028	F1088	
L789	V849	P909	L969	C1029	T1089	
S790	F850	G910	I970	D1030	V1090	
W791	N851	K911	D971	A1031	C1091	
R792	C852	G912	F972	A1032	E1092	
D793	I853	Y913	F973	F1033	V1093	
N794	D854	A914	V974	L1034	E1094	
E795	W855	I915	V975	M1035	E1095	
T796	V856	V916	F976	L1036	E1096	
S797	H857	D917	E977	T1037	F1097	
A798	K858	E918	R978	G1038	M1098	
E799	L859	P919	G979	C1039	Y1099	
F800	T860	F920	S980	Y1040	S1100	
S801	L861	S921	L981	C1041	G1101	
F802	E862	E922	P982	C1042	D1102	
V803	I863	I923	Q983	M1043	G1103	
G804	T864	P924	T984	A1044	D1104	
E805	D865	R925	N985	G1045	L1105	
S806	F866	Q926	N986	A1046	R1106	
T807	D867	G927	D987	R1047	P1107	

• Molecule 2: Glycoprotein



D688	K748	T808	G868	F928	V1048	L1108
P689	T749	M809	S869	L929	C1049	L1109
G690	V750	R810	V870	G930	L1050	V1110
C691	S751	E811	S871	E931	S1051	K1111
S692	S752	N812	T872	R932	T1052	T1112
E693	E753	K813	I873	R933	T1053	T1113
L694	L754	C814	D874	C934	S1054	L1114
I695	S755	F815	L875	N935	T1055	I1115
Q696	C756	E816	G876	S936	G1056	A1116
A697	R757	Q817	A877	E937	T1057	I1117
S698	E758	C818	S878	S938	G1058	D1118
S699	G759	G819	S879	S939	S1059	
R700	Q760	G820	S880	V940	L1060	
I701	S761	W821	R881	L941	S1061	
T702	Y762	G822	F882	S942	A1062	
T703	W763	C823	T883	A943	H1063	
C704	T764	G824	N884	H944	N1064	
S705	G765	C825	W885	E945	K1065	
T706	S766	F826	G886	S946	D1066	
E707	F767	N827	S887	C947	G1067	
G708	S768	V828	W888	L948	S1068	
V709	P769	N829	S889	R949	L1069	
W710	K770	P830	L890	A950	H1070	
T711	C771	S831	S891	D1010	T1071	
K712	L772	C832	L892	T1012	V1072	
C713	S773	L833	D893	L1013	L1073	
R714	S774	F834	A894	M1014	P1074	
L715	R775	V835	E895	F1015	S1075	
S716	R776	H836	G896	D1016	E1076	
G717	C777	T837	I897	N1017	M1077	
T718	H778	Y838	S898	F1018	G1078	
A719	L779	L839	G899	E1019	T1079	
L720	V780	Q840	S900	V1020	K1080	
L721	G781	S841	N901	D1021	L1081	
R722	E782	V842	S902	F1022	Q1082	
A723	C783	R843	F903	V1023	Q1083	
G724	H784	K844	S904	G1024	Q1084	
S725	V785	E845	F905	A1025	I1085	
V726	N786	A846	I906	A1026	L1086	
G727	R787	L847	E907	V1027	H1087	
A728	C788	R848	S908	S1028	F1088	
E729	L789	V849	P909	C1029	T1089	
A730	S790	F850	G910	D1030	V1090	
C731	W791	N851	K911	A1031	C1091	
L732	R792	C852	G912	A1032	E1092	
M733	D793	I853	Y913	F1033	V1093	
L734	N794	D854	A914	L1034	E1094	
K735	E795	W855	I915	M1035	E1095	
G736	T796	V856	V916	L1036	E1096	
V737	S797	H857	D917	T1037	F1097	
K738	A798	K858	E918	G1038	M1098	
E739	E799	L859	P919	C1039	Y1099	
D740	F800	T860	F920	Y1040	S1100	
Q741	S801	L861	S921	C1041	G1101	
T742	F802	E862	E922	C1042	D1102	
K743	V803	I863	I923	M1043	G1103	
F744	G804	T864	P924	A1044	D1104	
L745	E805	D865	R925	G1045	L1105	
K746	S806	F866	Q926	A1046	R1106	
I747	T807	D867	G927	R1047	P1107	



• Molecule 2: Glycoprotein

Chain L:



## 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 ( $\text{\AA}$ )	345.6, 345.6, 345.6	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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	0.24	0/2333	0.41	0/3136
1	C	0.24	0/2333	0.40	0/3136
1	E	0.24	0/2333	0.42	0/3136
1	G	0.24	0/2333	0.41	0/3136
1	I	0.24	0/2333	0.41	0/3136
1	K	0.24	0/2333	0.40	0/3136
2	B	0.24	0/3284	0.41	0/4431
2	D	0.24	0/3284	0.42	0/4431
2	F	0.24	0/3284	0.42	0/4431
2	H	0.24	0/3284	0.42	0/4431
2	J	0.24	0/3284	0.43	0/4431
2	L	0.24	0/3284	0.43	0/4431
All	All	0.24	0/33702	0.42	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	26	0
1	C	2284	0	2205	19	0
1	E	2284	0	2205	27	0
1	G	2284	0	2205	26	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	2284	0	2205	26	0
1	K	2284	0	2205	26	0
2	B	3224	0	3071	38	0
2	D	3224	0	3071	35	0
2	F	3224	0	3071	43	0
2	H	3224	0	3071	28	0
2	J	3224	0	3071	36	0
2	L	3224	0	3071	34	0
All	All	33048	0	31656	348	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 5.

The worst 5 of 348 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](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	295/316 (93%)	254 (86%)	37 (12%)	4 (1%)	9	41
1	C	295/316 (93%)	250 (85%)	41 (14%)	4 (1%)	9	41
1	E	295/316 (93%)	260 (88%)	32 (11%)	3 (1%)	13	49

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	295/316 (93%)	254 (86%)	39 (13%)	2 (1%)	19	57
1	I	295/316 (93%)	256 (87%)	36 (12%)	3 (1%)	13	49
1	K	295/316 (93%)	261 (88%)	28 (10%)	6 (2%)	6	32
2	B	429/431 (100%)	380 (89%)	44 (10%)	5 (1%)	11	44
2	D	429/431 (100%)	378 (88%)	47 (11%)	4 (1%)	14	52
2	F	429/431 (100%)	380 (89%)	43 (10%)	6 (1%)	9	41
2	H	429/431 (100%)	382 (89%)	42 (10%)	5 (1%)	11	44
2	J	429/431 (100%)	376 (88%)	48 (11%)	5 (1%)	11	44
2	L	429/431 (100%)	382 (89%)	43 (10%)	4 (1%)	14	52
All	All	4344/4482 (97%)	3813 (88%)	480 (11%)	51 (1%)	14	44

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1083	CYS
1	C	239	CYS
2	D	1083	CYS
1	E	281	CYS
1	E	284	CYS

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	241/271 (89%)	237 (98%)	4 (2%)	56	72
1	C	241/271 (89%)	239 (99%)	2 (1%)	79	85
1	E	241/271 (89%)	240 (100%)	1 (0%)	89	91
1	G	241/271 (89%)	239 (99%)	2 (1%)	79	85
1	I	241/271 (89%)	239 (99%)	2 (1%)	79	85
1	K	241/271 (89%)	240 (100%)	1 (0%)	89	91
2	B	347/371 (94%)	344 (99%)	3 (1%)	75	83

Continued on next page...



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	347/371 (94%)	339 (98%)	8 (2%)	45	64
2	F	347/371 (94%)	344 (99%)	3 (1%)	75	83
2	H	347/371 (94%)	345 (99%)	2 (1%)	84	88
2	J	347/371 (94%)	346 (100%)	1 (0%)	91	92
2	L	347/371 (94%)	342 (99%)	5 (1%)	62	75
All	All	3528/3852 (92%)	3494 (99%)	34 (1%)	71	82

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	438	ASN
2	L	810	ARG
2	L	994	LYS
2	D	949	ARG
2	D	925	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	1000	GLN
1	K	428	GLN
2	J	1043	ASN
1	K	166	HIS
2	L	952	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

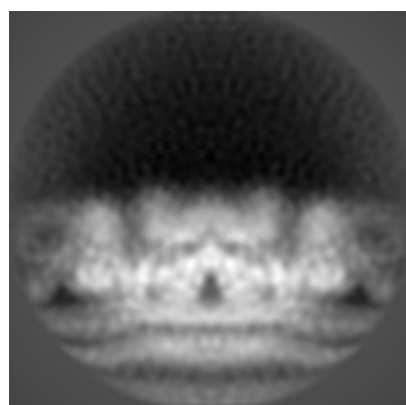
## 6 Map visualisation [i](#)

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

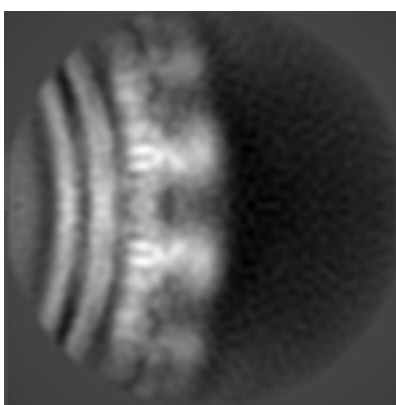
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

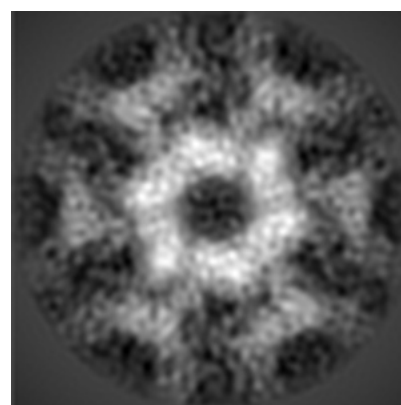
#### 6.1.1 Primary map



X



Y

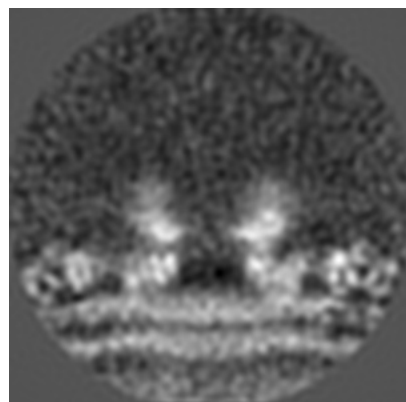


Z

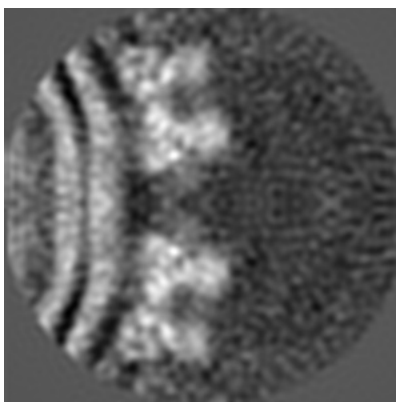
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

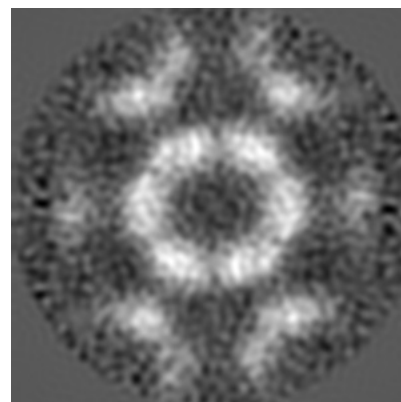
#### 6.2.1 Primary map



X Index: 64



Y Index: 64

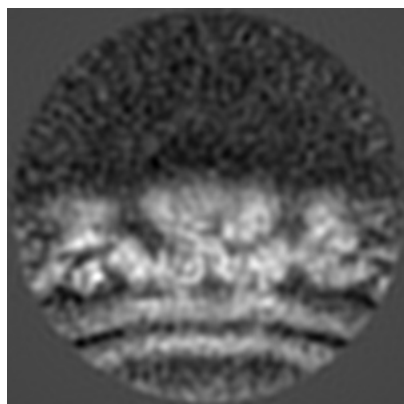


Z Index: 64

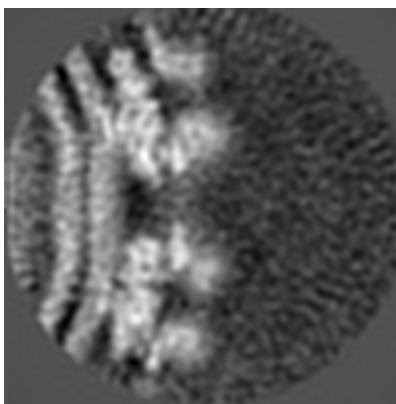
The images above show central slices of the map in three orthogonal directions.

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

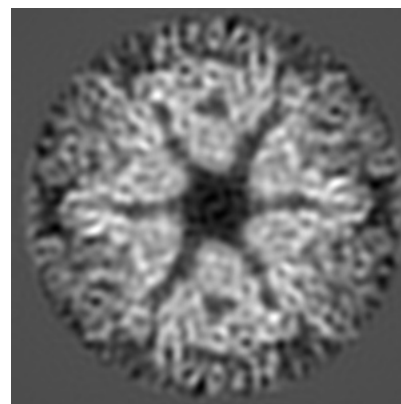
### 6.3.1 Primary map



X Index: 83



Y Index: 58

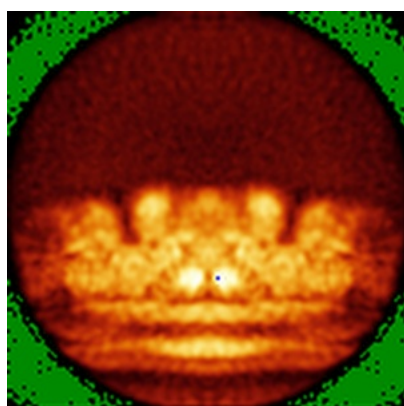


Z Index: 42

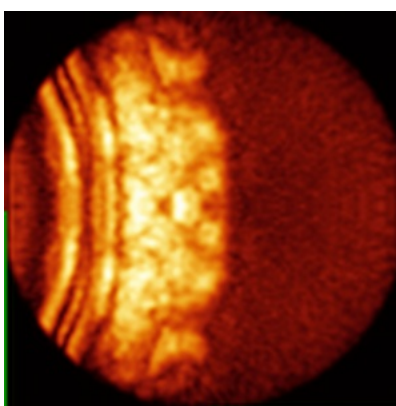
The images above show the largest variance slices of the map in three orthogonal directions.

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

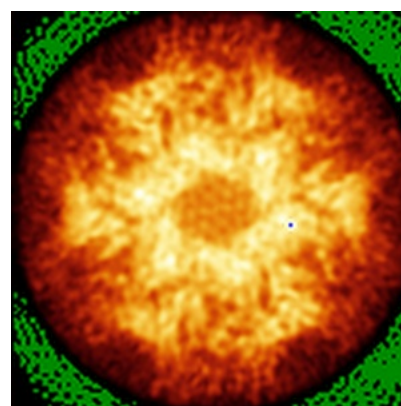
### 6.4.1 Primary map



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.

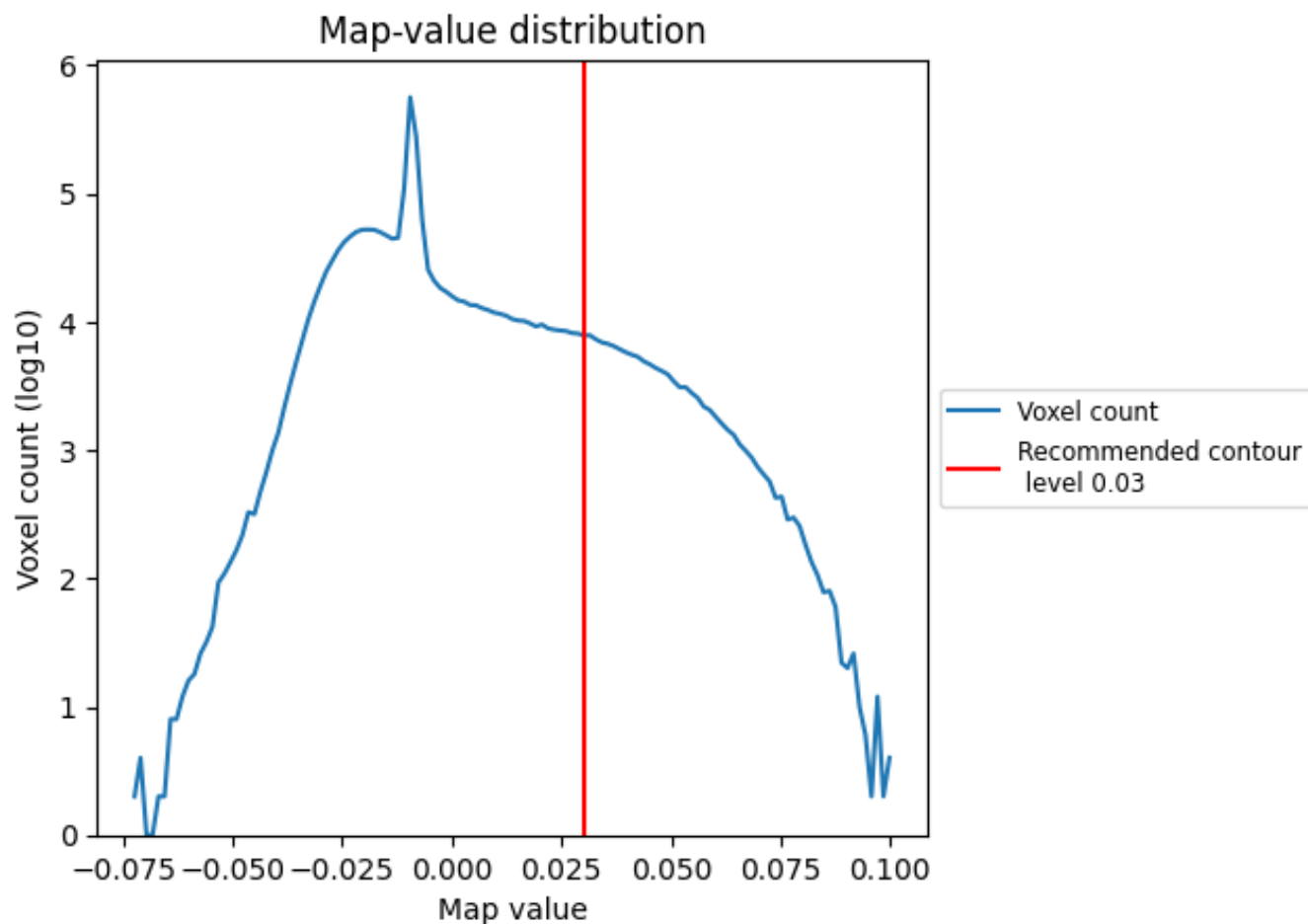
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

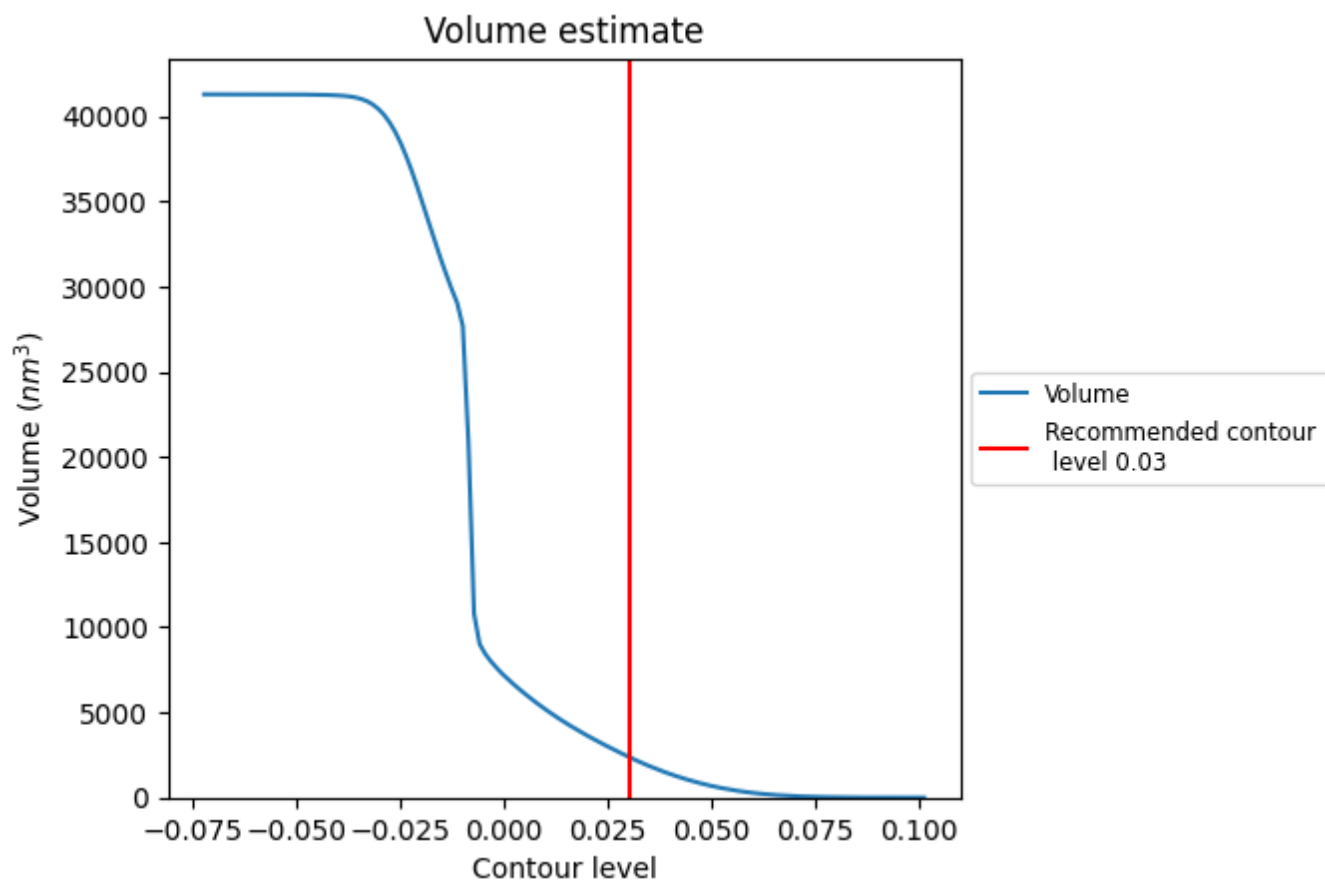
This section contains the results of statistical analysis of the map.

### 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.

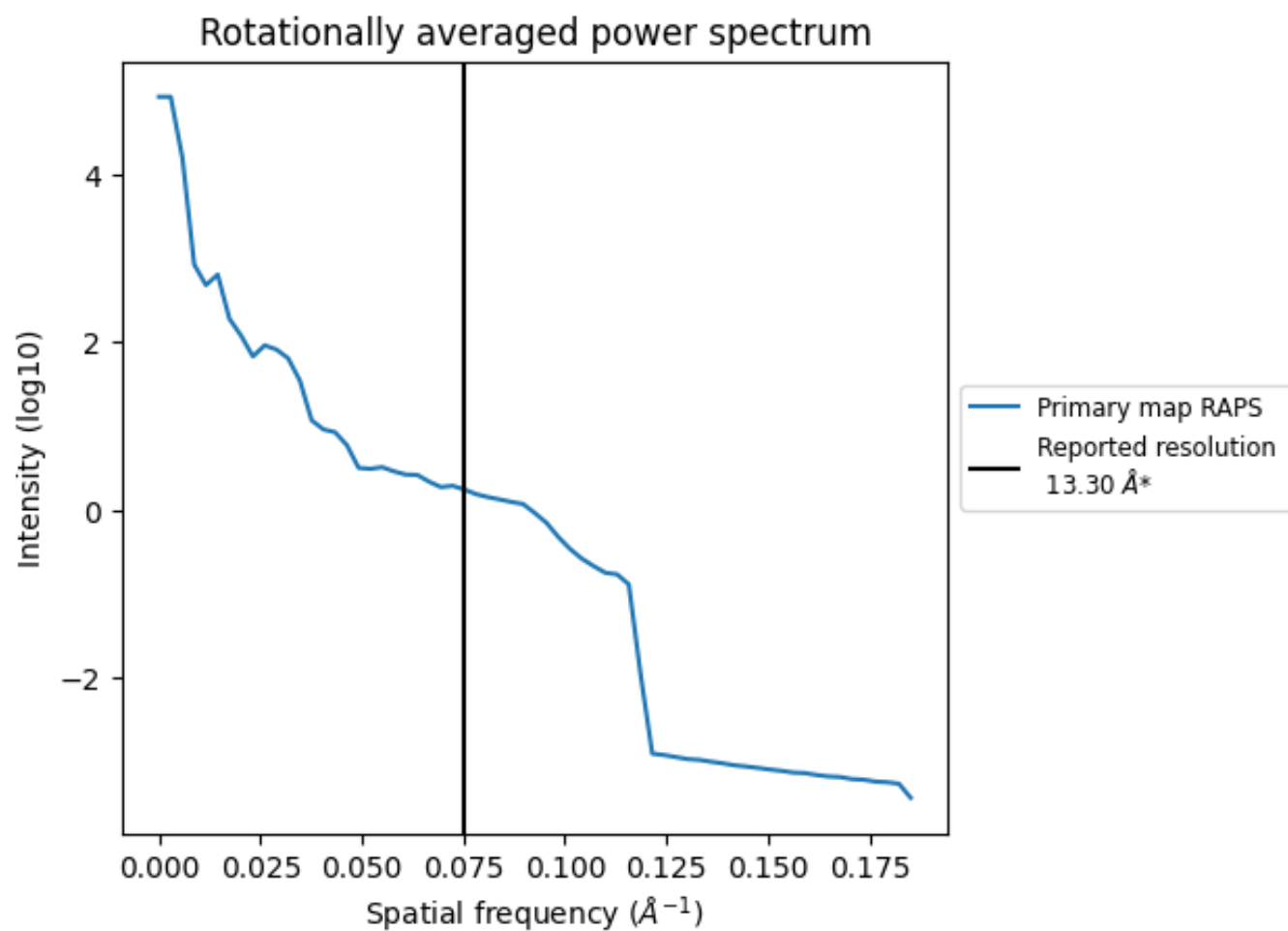
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2388 nm<sup>3</sup>; 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 ⓘ



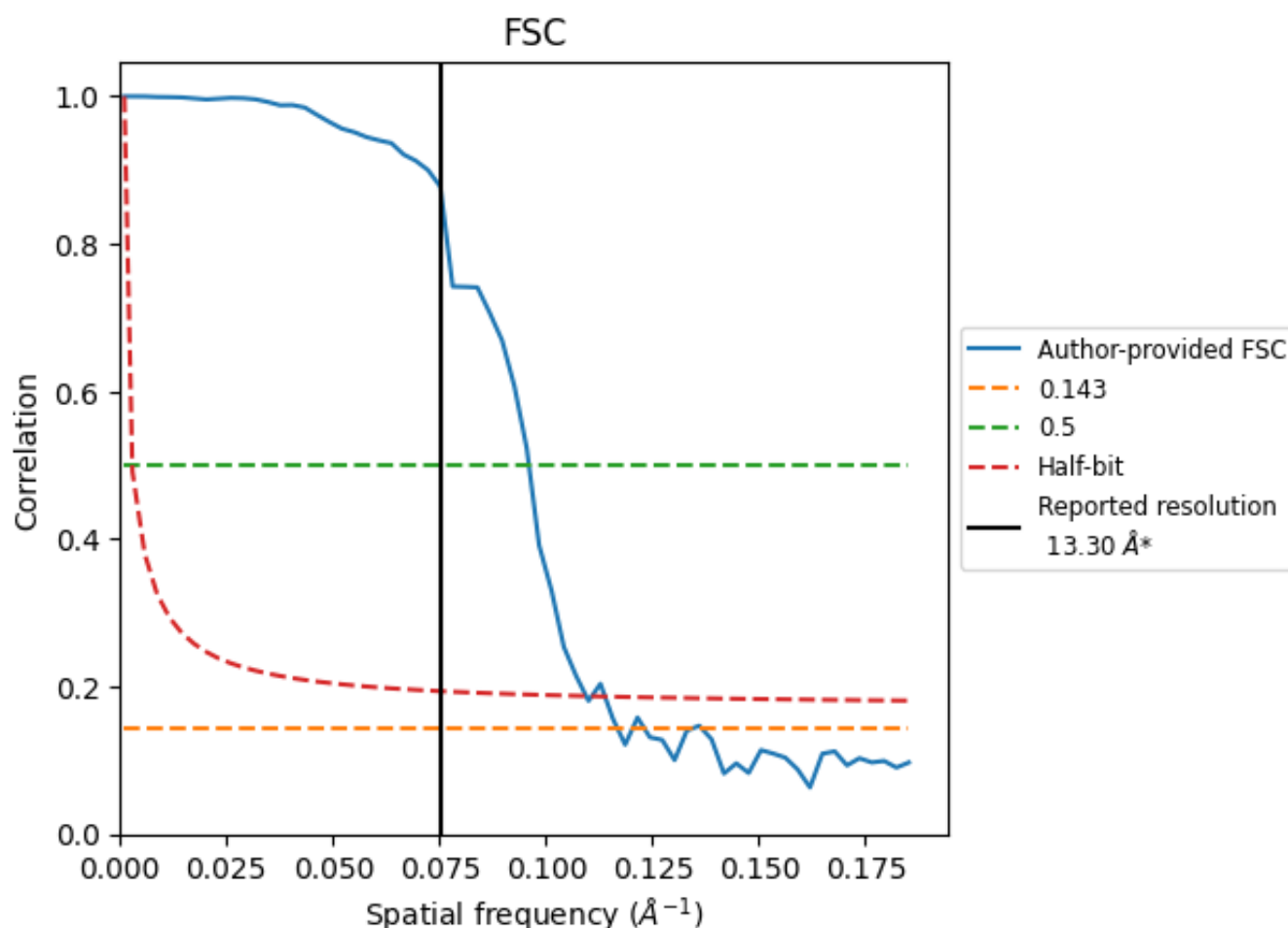
\*Reported resolution corresponds to spatial frequency of 0.075 Å<sup>-1</sup>



## 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<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

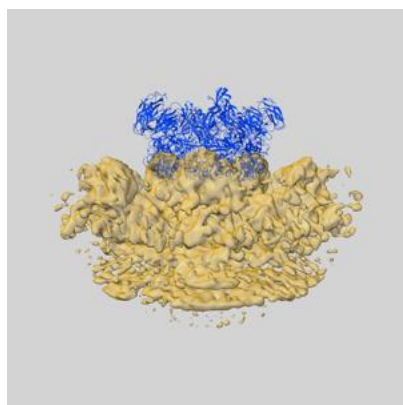
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	13.30	-	-
Author-provided FSC curve	8.56	10.42	9.14
Unmasked-calculated*	-	-	-

\*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 %

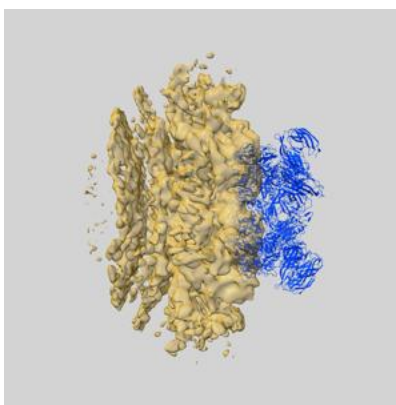
## 9 Map-model fit [i](#)

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](#).

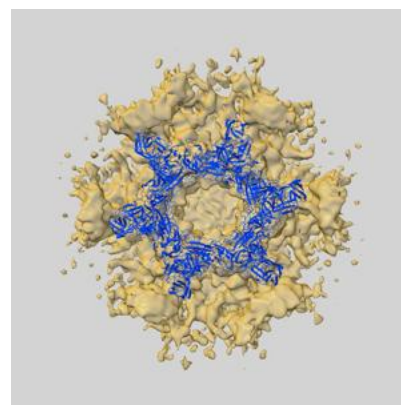
### 9.1 Map-model overlay [i](#)



X



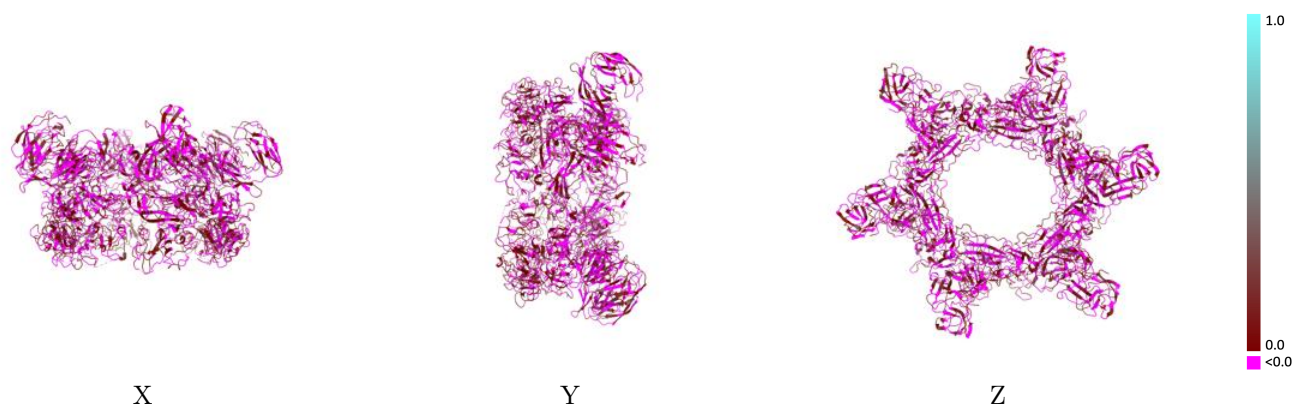
Y



Z

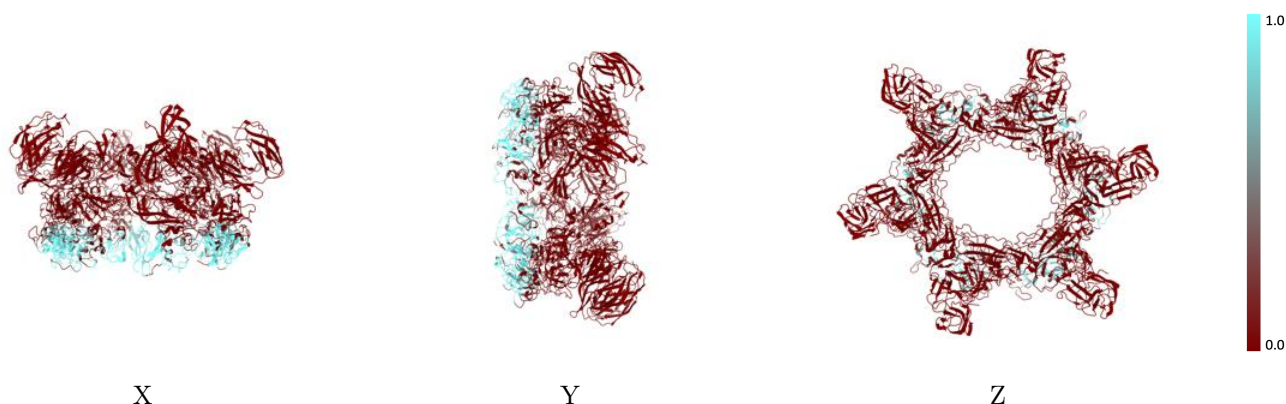
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



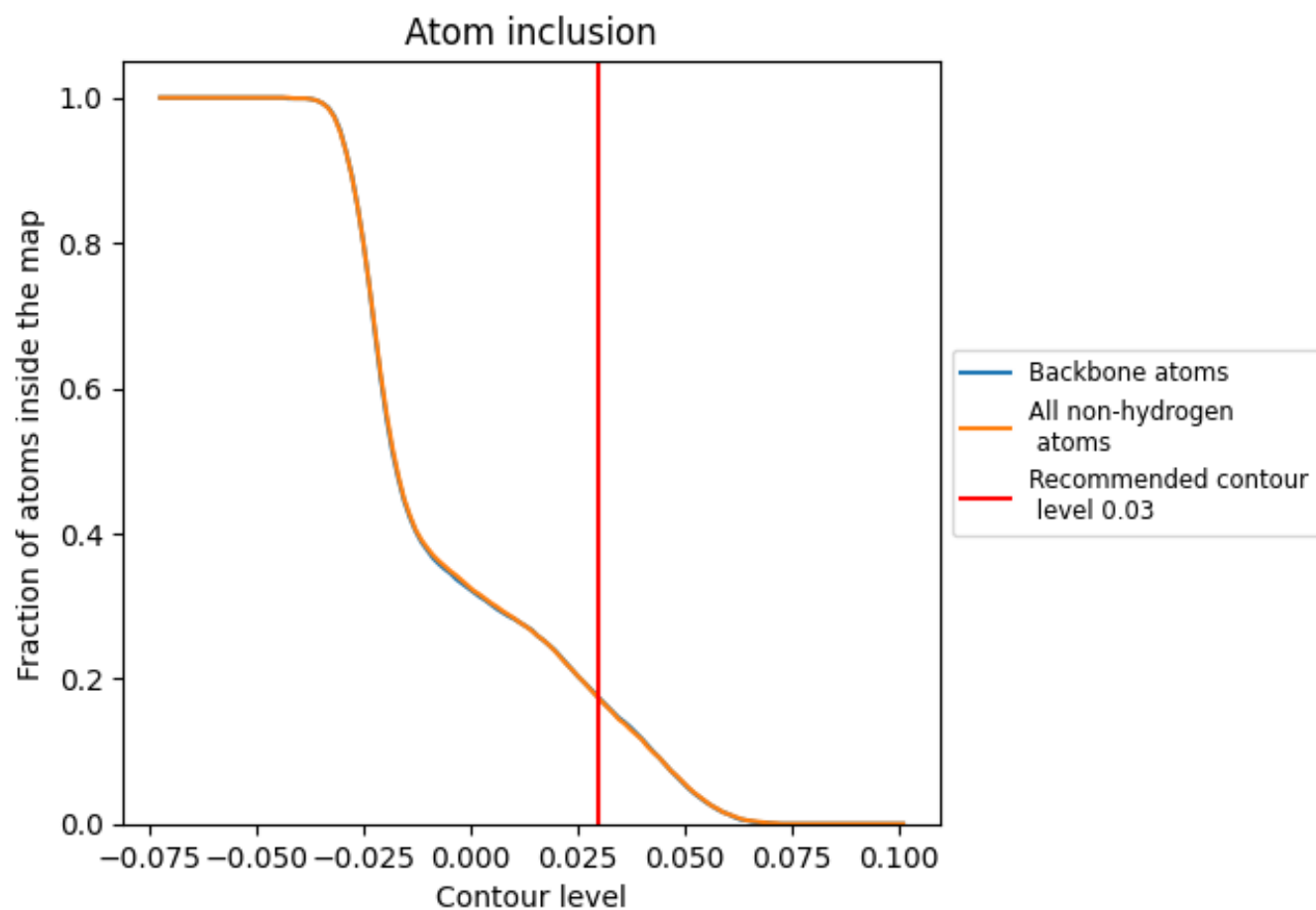
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	<div></div> 0.1730	<div></div> 0.0080
A	<div></div> 0.3810	<div></div> 0.0150
B	<div></div> 0.0000	<div></div> 0.0020
C	<div></div> 0.4000	<div></div> 0.0300
D	<div></div> 0.0000	<div></div> 0.0010
E	<div></div> 0.4180	<div></div> 0.0220
F	<div></div> 0.0000	<div></div> 0.0030
G	<div></div> 0.4200	<div></div> 0.0260
H	<div></div> 0.0000	<div></div> -0.0070
I	<div></div> 0.4490	<div></div> 0.0250
J	<div></div> 0.0000	<div></div> -0.0040
K	<div></div> 0.4260	<div></div> 0.0180
L	<div></div> 0.0000	<div></div> -0.0110

1.0

0.0

<0.0