



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:26 PM UTC

PDB ID : 9G8N / pdb_00009g8n
EMDB ID : EMD-51133
Title : 80S-bound human Ski2-exosome complex
Authors : Koegel, A.; Keidel, A.; Loukeri, M.J.; Kuhn, C.C.; Langer, L.M.; Schaefer, I.B.; Conti, E.
Deposited on : 2024-07-23
Resolution : 3.70 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:

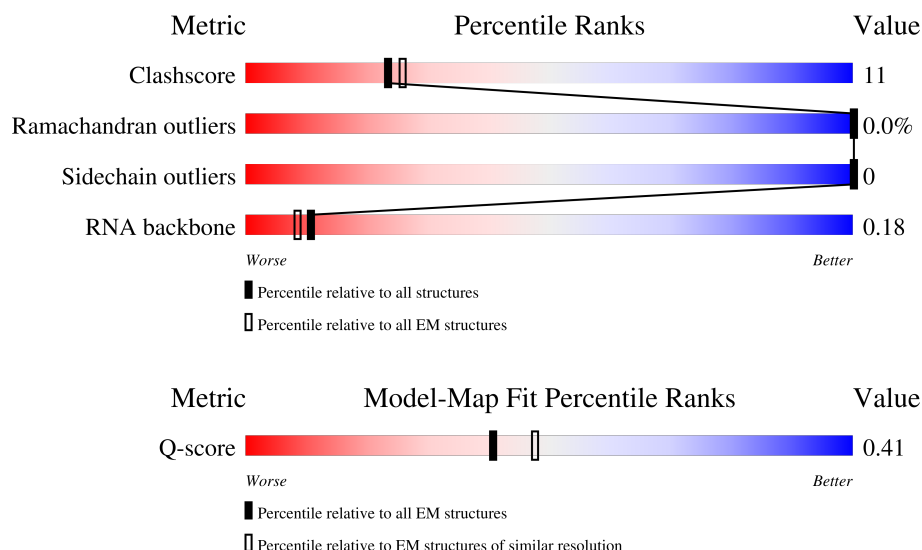
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	L	245	
2	N	280	
3	O	239	

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Mol	Chain	Length	Quality of chain
4	F	295	
5	H	279	
6	J	199	
7	X	44	
8	A	1246	
9	G	272	
10	I	297	
11	E	274	
12	K	443	
13	M	1056	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 34405 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 Exosome complex component RRP41.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	241	Total	C	N	O	S	0	0
			1819	1123	343	344	9		

- Molecule 2 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	265	Total	C	N	O	S	0	0
			2020	1272	337	397	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-3	GLY	-	expression tag	UNP Q96B26
N	-2	PRO	-	expression tag	UNP Q96B26
N	-1	ASP	-	expression tag	UNP Q96B26
N	0	SER	-	expression tag	UNP Q96B26

- Molecule 3 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	O	208	Total	C	N	O	S	0	0
			1566	979	278	297	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-3	GLY	-	expression tag	UNP Q9NQ4
O	-2	PRO	-	expression tag	UNP Q9NQ4
O	-1	ASP	-	expression tag	UNP Q9NQ4
O	0	SER	-	expression tag	UNP Q9NQ4

- Molecule 4 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	286	Total	C	N	O	S	0	0
			2194	1373	374	432	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP Q15024
F	-2	PRO	-	expression tag	UNP Q15024
F	-1	ASP	-	expression tag	UNP Q15024
F	0	SER	-	expression tag	UNP Q15024

- Molecule 5 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	237	Total	C	N	O	S	0	0
			1806	1136	329	329	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-3	GLY	-	expression tag	UNP Q9NQT5
H	-2	PRO	-	expression tag	UNP Q9NQT5
H	-1	ASP	-	expression tag	UNP Q9NQT5
H	0	SER	-	expression tag	UNP Q9NQT5
H	225	HIS	TYR	variant	UNP Q9NQT5

- Molecule 6 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	184	Total	C	N	O	S	0	0
			1414	889	248	267	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLY	-	expression tag	UNP Q9Y3B2
J	-2	PRO	-	expression tag	UNP Q9Y3B2
J	-1	ASP	-	expression tag	UNP Q9Y3B2
J	0	SER	-	expression tag	UNP Q9Y3B2

- Molecule 7 is a RNA chain called CrPV-IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	X	44	Total	C	N	O	P	0	0
			841	376	82	339	44		

- Molecule 8 is a protein called Helicase SKI2W.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	949	Total	C	N	O	S	0	0
			7438	4710	1316	1370	42		

- Molecule 9 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	251	Total	C	N	O	S	0	0
			1852	1149	352	344	7		

- Molecule 10 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	289	Total	C	N	O	S	0	0
			2263	1424	405	419	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	GLY	-	expression tag	UNP Q13868
I	-2	PRO	-	expression tag	UNP Q13868
I	-1	ASP	-	expression tag	UNP Q13868
I	0	SER	-	expression tag	UNP Q13868

- Molecule 11 is a protein called Isoform 2 of HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	66	Total	C	N	O	S	0	0
			525	340	89	95	1		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	365	GLY	-	expression tag	UNP Q9Y450
E	366	PRO	-	expression tag	UNP Q9Y450
E	367	ASP	-	expression tag	UNP Q9Y450
E	368	SER	-	expression tag	UNP Q9Y450

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Chain	Residue	Modelled	Actual	Comment	Reference
E	633	LEU	-	expression tag	UNP Q9Y450
E	634	GLU	-	expression tag	UNP Q9Y450
E	635	VAL	-	expression tag	UNP Q9Y450
E	636	LEU	-	expression tag	UNP Q9Y450
E	637	PHE	-	expression tag	UNP Q9Y450
E	638	GLN	-	expression tag	UNP Q9Y450

- Molecule 12 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	353	Total	C	N	O	S	0	0
			2764	1734	482	529	19		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	GLY	-	expression tag	UNP Q06265
K	-2	PRO	-	expression tag	UNP Q06265
K	-1	ASP	-	expression tag	UNP Q06265
K	0	SER	-	expression tag	UNP Q06265

- Molecule 13 is a protein called DIS3-like exonuclease 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	975	Total	C	N	O	S	0	0
			7903	4986	1405	1471	41		

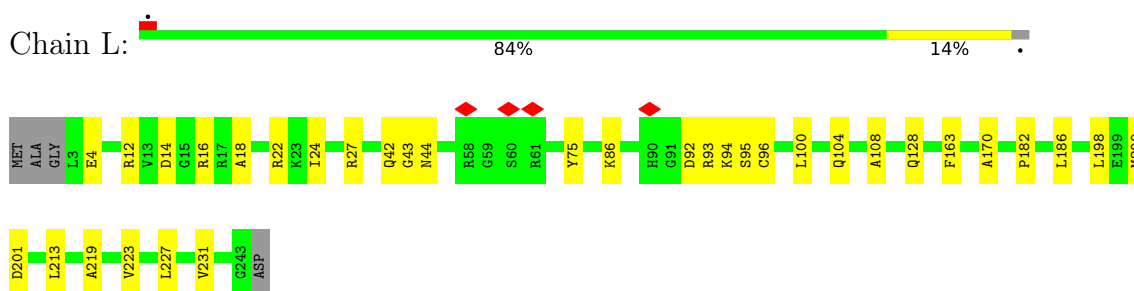
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-1	GLY	-	expression tag	UNP Q8TF46
M	0	PRO	-	expression tag	UNP Q8TF46
M	486	ASN	ASP	conflict	UNP Q8TF46

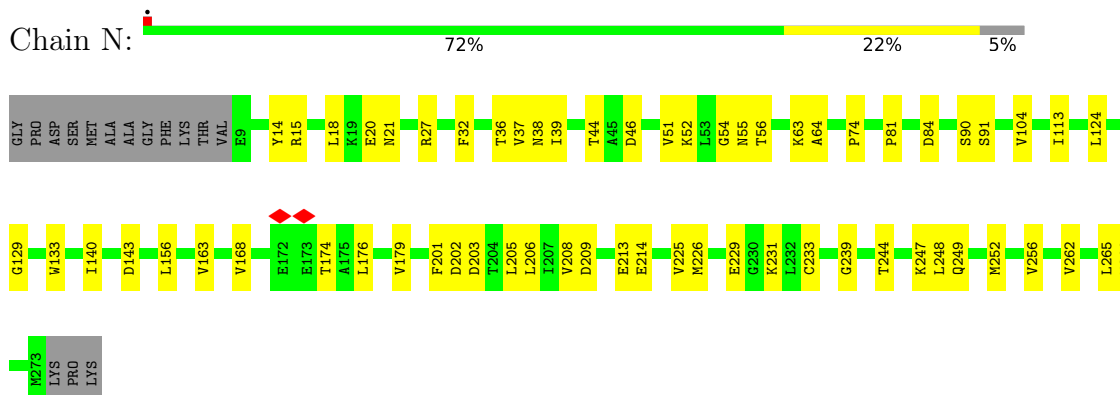
3 Residue-property plots [i](#)

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.

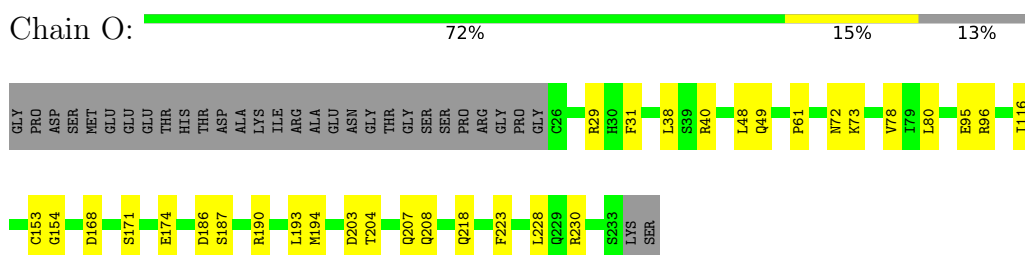
- Molecule 1: Exosome complex component RRP41



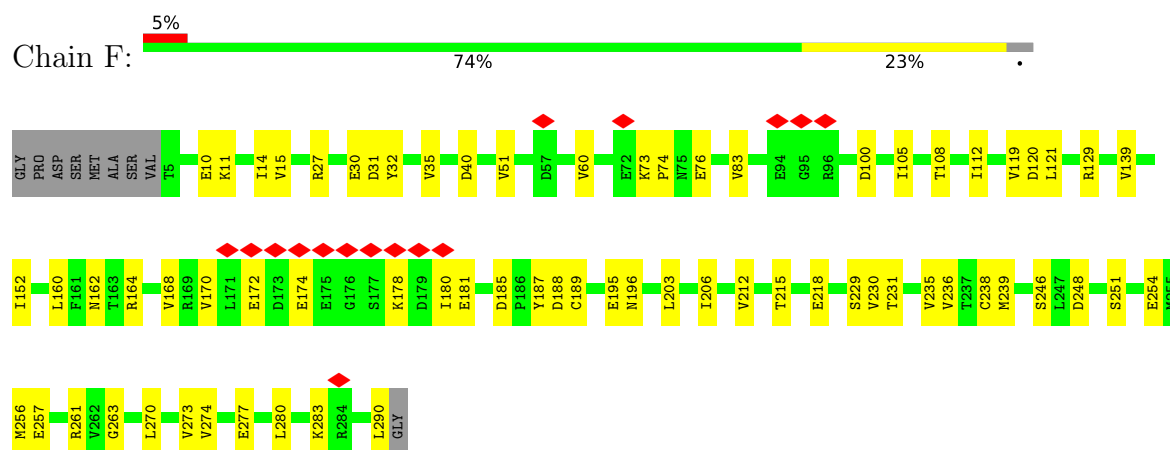
- Molecule 2: Exosome complex component RRP43



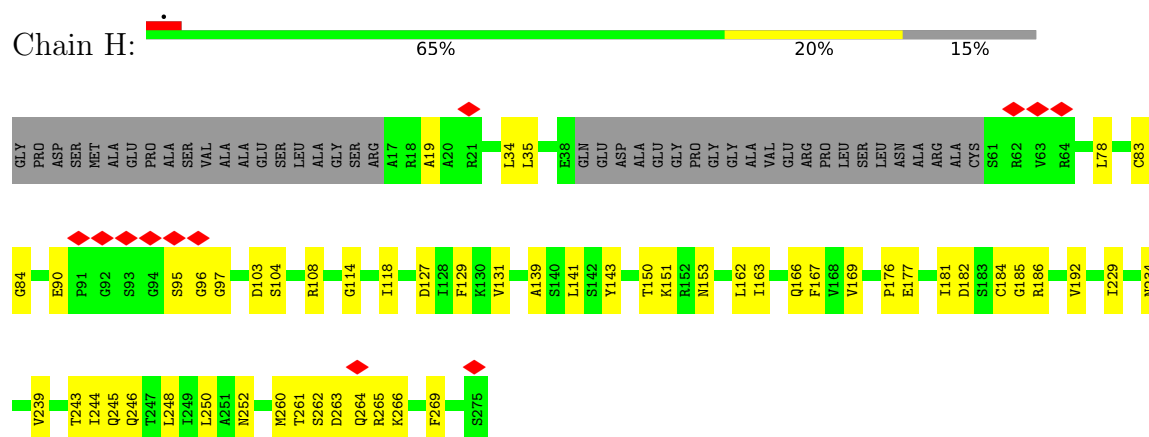
- Molecule 3: Exosome complex component RRP46



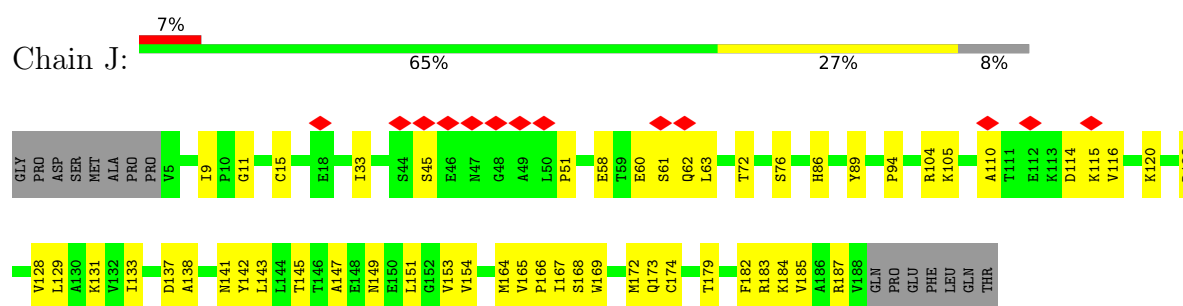
- Molecule 4: Exosome complex component RRP42



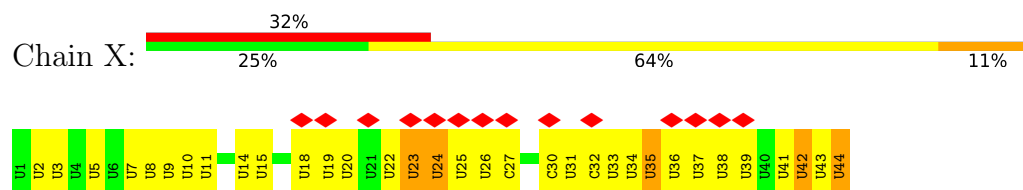
• Molecule 5: Exosome complex component RRP40



• Molecule 6: Exosome complex component CSL4

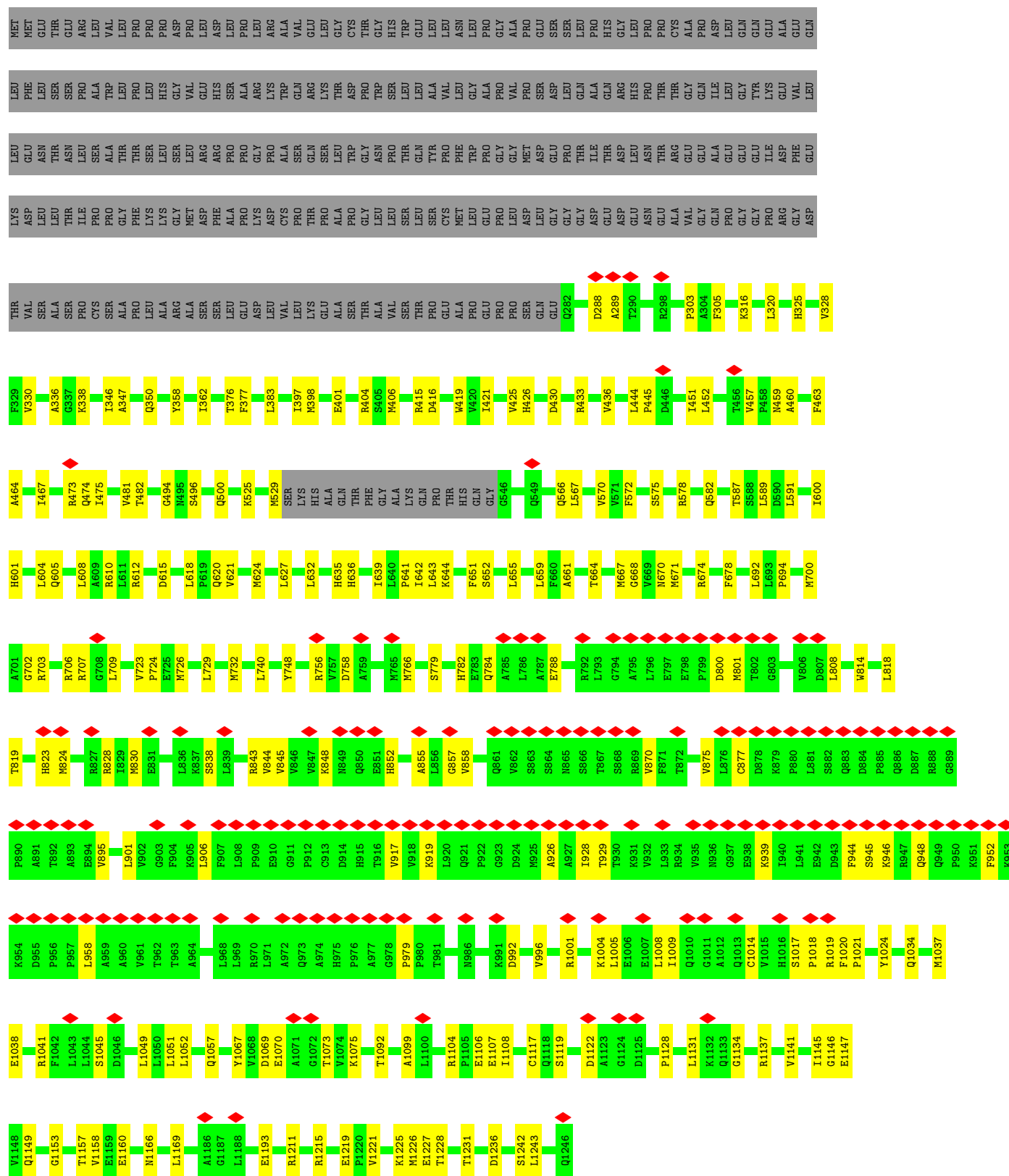


• Molecule 7: CrPV-IRES RNA

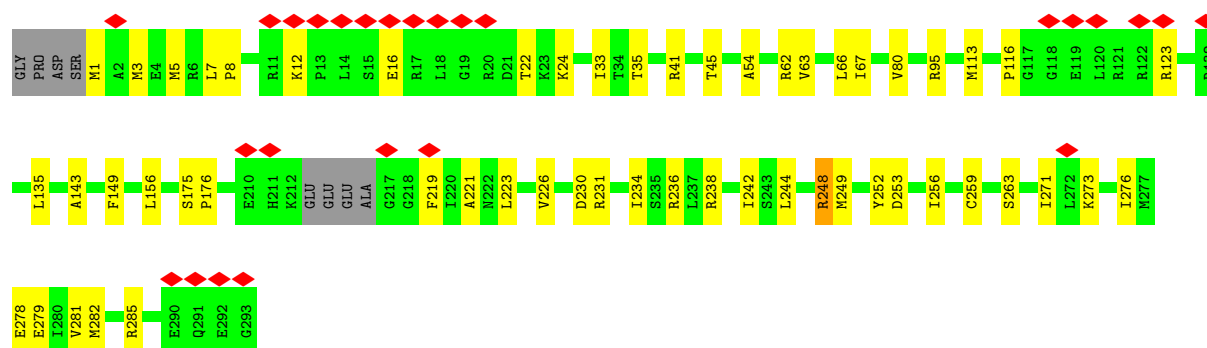
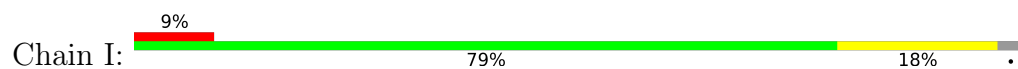


• Molecule 8: Helicase SKI2W

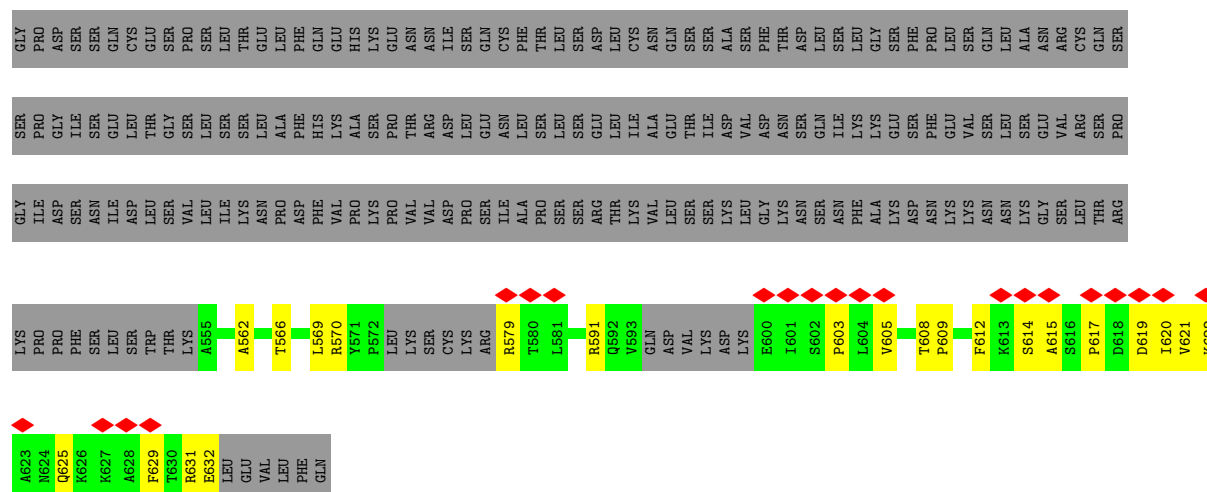




- Molecule 10: Exosome complex component RRP4



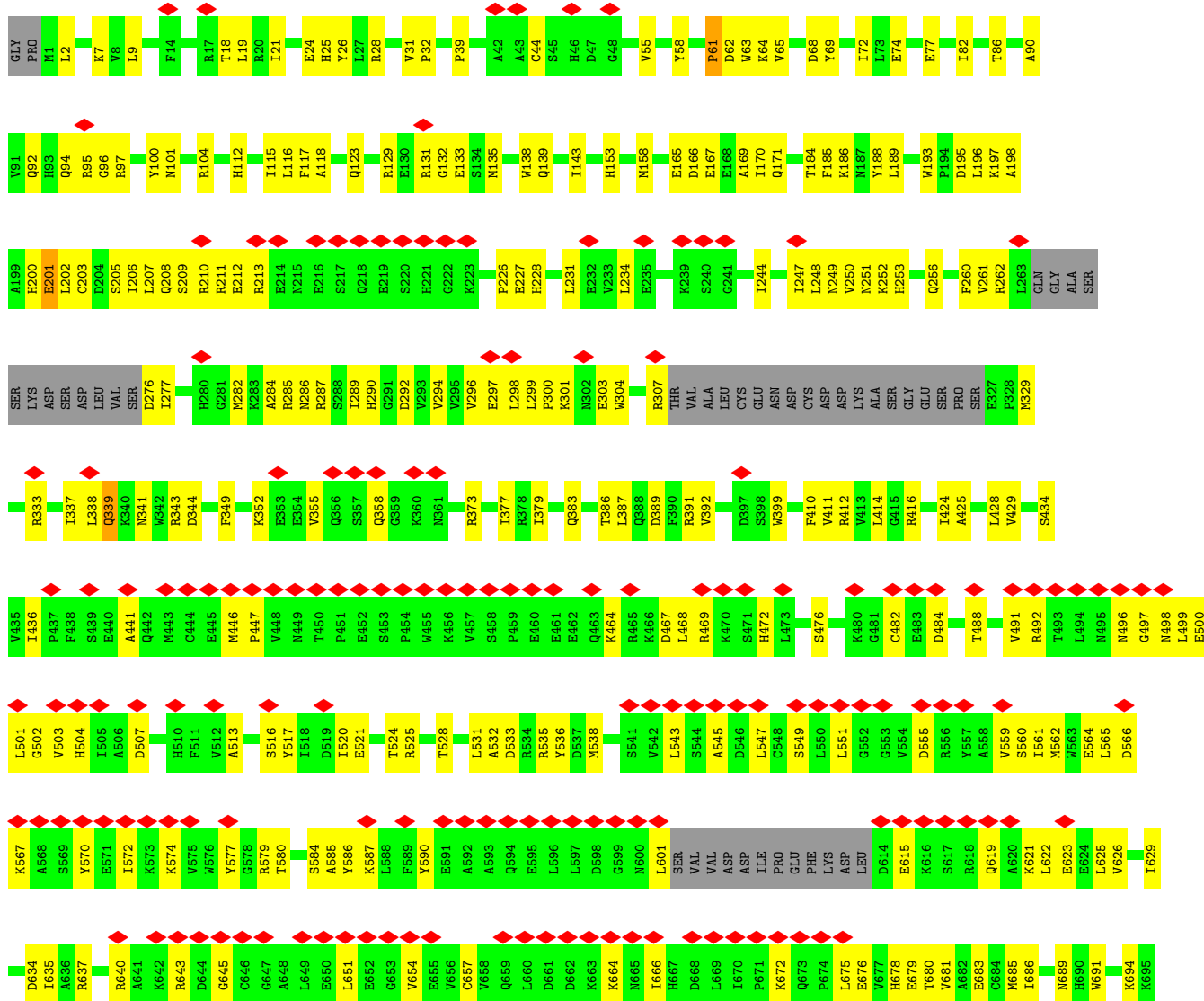
- Molecule 11: Isoform 2 of HBS1-like protein



- Molecule 12: Exosome complex component RRP45



- Molecule 13: DIS3-like exonuclease 1



LEU	I696	T763	D832	S912	N1016	Y1022	R1026	L1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
ILE	W697	Q763	L833	C913	I1017	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
HIS	E598	Q764	E334	G914	I1018	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	E599	A765	E335	P915	I1019	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
SER	F700	M766	L836	D916	I1020	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
PRO	P701	S767	C837	S917	I1021	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LEU	H702	A769	R938	C918	I1022	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LEU	Q703	L770	H839	S919	I1023	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	A704	Y771	I940	C918	I1024	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	L705	G775	N841	S919	I1025	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	L706	S776	N842	S920	I1026	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LEU	R707	C777	R843	E920	I1027	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
VAL	Q708	A778	N844	W921	I1028	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	P712	E779	Q845	K922	I1029	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	H713	E780	H849	P923	I1030	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
VAL	Q714	E781	F958	G924	I1031	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	E715	E781	M861	S925	I1032	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
THR	H716	H784	Y862	L926	I1033	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	F717	Y785	F863	Q927	I1034	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
SER	F718	G786	K864	R928	I1035	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	S719	L787	D865	F929	I1036	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
ALA	E720	A788	K866	K932	I1037	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	L720	Y792	D867	T936	I1038	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LEU	R721	T793	P868	T937	I1039	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
ALA	E722	Y794	A869	T938	I1040	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	A724	F795	T870	T939	I1041	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	K725	I799	E871	D940	I1042	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
VAL	A726	Y802	E872	E941	I1043	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	K727	S803	E872	S942	I1044	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	F728	D804	I875	S942	I1045	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	G729	I805	S876	L947	I1046	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	F730	V806	D877	F948	I1047	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	I731	V807	I880	T952	I1048	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	D732	I881	Y881	V953	I1049	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	T733	L810	S882	R954	I1050	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	R734	L811	I883	T955	I1051	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	S735	M812	I883	S956	I1052	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	N736	M812	G887	I957	I1053	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	K737	A813	V888	R961	I1054	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	T738	A814	L889	D965	I1055	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	L739	I815	L890	T966	I1056	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	A740	S816	F891	I967	I1057	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLN	D741	D817	I892	R968	I1058	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	S742	K818	G896	L969	I1059	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	L743	K819	I897	E970	I1060	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	D744	K820	K898	I971	I1061	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	N745	M821	G899	I972	I1062	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	A746	E822	G899	I973	I1063	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	N747	I823	A900	N974	I1064	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	D748	K824	A901	S977	I1065	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	P749	G825	K906	Y977	I1066	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	H750	G826	D907	K978	I1067	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	D751	N826	L909	I979	I1068	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	P752	L827	G908	P980	I1069	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	I753	F828	L909	N981	I1070	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	V754	S829	T982	T982	I1071	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
LYS	N755	N830	E983	E983	I1072	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE
GLU	R756	K831	L909	E983	I1073	Q1023	Y1022	I1037	I1040	L1046	N1050	ASN	TYR	GLY	ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	79353	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 ($e^-/\text{\AA}^2$)	64.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.038	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	708.19836, 708.19836, 708.19836	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8512, 0.8512, 0.8512	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.12	0/1843	0.35	0/2492
2	N	0.11	0/2053	0.33	0/2786
3	O	0.13	0/1586	0.36	0/2145
4	F	0.13	0/2225	0.41	0/3007
5	H	0.12	0/1832	0.43	0/2467
6	J	0.13	0/1438	0.48	0/1942
7	X	0.12	0/923	0.36	0/1424
8	A	0.13	0/7577	0.40	0/10257
9	G	0.13	0/1881	0.38	0/2551
10	I	0.13	0/2296	0.50	2/3092 (0.1%)
11	E	0.20	0/535	0.83	0/722
12	K	0.15	0/2807	0.57	4/3792 (0.1%)
13	M	0.15	0/8072	0.58	5/10916 (0.0%)
All	All	0.13	0/35068	0.47	11/47593 (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
9	G	0	1
10	I	0	1
11	E	0	1
12	K	0	1
13	M	0	4
All	All	0	8

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	63	VAL	CA-C-N	10.39	141.38	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	63	VAL	C-N-CA	10.39	141.38	121.54
13	M	61	PRO	CA-C-N	-7.17	110.13	120.89
13	M	61	PRO	C-N-CA	-7.17	110.13	120.89
12	K	304	ASP	CA-C-N	-5.71	111.71	122.27

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	E	614	SER	Peptide
9	G	91	ALA	Peptide
10	I	248	ARG	Peptide
12	K	303	ILE	Peptide
13	M	339	GLN	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	L	1819	0	1818	30	0
2	N	2020	0	2035	40	0
3	O	1566	0	1605	26	0
4	F	2194	0	2205	51	0
5	H	1806	0	1865	45	0
6	J	1414	0	1441	46	0
7	X	841	0	425	13	0
8	A	7438	0	7568	150	0
9	G	1852	0	1881	33	0
10	I	2263	0	2337	37	0
11	E	525	0	536	27	0
12	K	2764	0	2790	77	0
13	M	7903	0	7833	266	0
All	All	34405	0	34339	754	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 11.

The worst 5 of 754 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)
6:J:164:MET:HE3	6:J:165:VAL:H	1.31	0.95
11:E:615:ALA:HB1	11:E:620:ILE:HD11	1.48	0.93
3:O:119:VAL:HG21	12:K:85:MET:HB3	1.57	0.86
8:A:621:VAL:HG23	8:A:643:LEU:HD11	1.57	0.85
8:A:1034:GLN:HA	8:A:1037:MET:SD	2.21	0.81

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	L	239/245 (98%)	237 (99%)	2 (1%)	0	100	100
2	N	263/280 (94%)	260 (99%)	3 (1%)	0	100	100
3	O	206/239 (86%)	206 (100%)	0	0	100	100
4	F	284/295 (96%)	271 (95%)	12 (4%)	1 (0%)	30	60
5	H	233/279 (84%)	226 (97%)	6 (3%)	1 (0%)	30	60
6	J	182/199 (92%)	174 (96%)	8 (4%)	0	100	100
8	A	945/1246 (76%)	934 (99%)	11 (1%)	0	100	100
9	G	247/272 (91%)	246 (100%)	1 (0%)	0	100	100
10	I	285/297 (96%)	275 (96%)	10 (4%)	0	100	100
11	E	60/274 (22%)	50 (83%)	10 (17%)	0	100	100
12	K	351/443 (79%)	326 (93%)	25 (7%)	0	100	100
13	M	965/1056 (91%)	884 (92%)	81 (8%)	0	100	100
All	All	4260/5125 (83%)	4089 (96%)	169 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	H	263	ASP
4	F	248	ASP

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	L	183/186 (98%)	183 (100%)	0	100	100
2	N	227/238 (95%)	227 (100%)	0	100	100
3	O	172/196 (88%)	172 (100%)	0	100	100
4	F	249/255 (98%)	249 (100%)	0	100	100
5	H	196/224 (88%)	196 (100%)	0	100	100
6	J	160/173 (92%)	160 (100%)	0	100	100
8	A	813/1062 (77%)	813 (100%)	0	100	100
9	G	178/188 (95%)	178 (100%)	0	100	100
10	I	251/257 (98%)	251 (100%)	0	100	100
11	E	57/251 (23%)	57 (100%)	0	100	100
12	K	307/384 (80%)	307 (100%)	0	100	100
13	M	873/945 (92%)	873 (100%)	0	100	100
All	All	3666/4359 (84%)	3666 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	208	GLN
13	M	383	GLN
13	M	1019	GLN
13	M	280	HIS
13	M	619	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	X	43/44 (97%)	25 (58%)	2 (4%)

5 of 25 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	X	2	U
7	X	3	U
7	X	5	U
7	X	9	U
7	X	10	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	X	8	U
7	X	38	U

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.

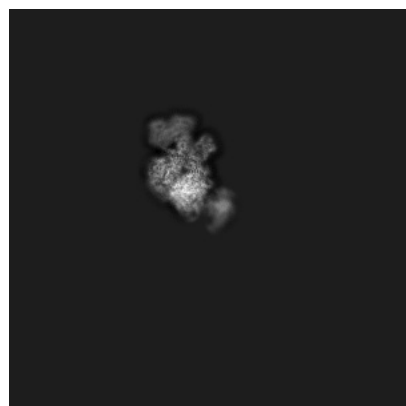
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51133. These allow visual inspection of the internal detail of the map and identification of artifacts.

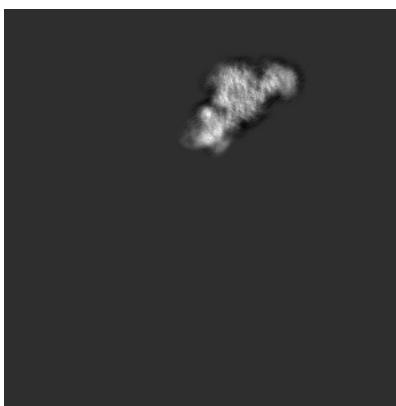
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

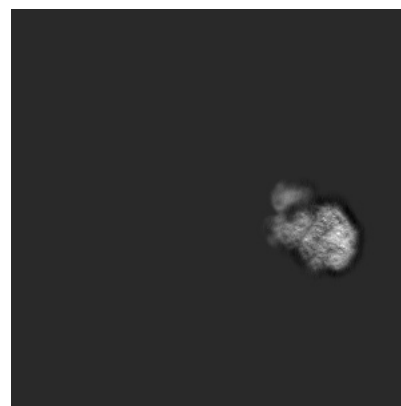
6.1.1 Primary map



X

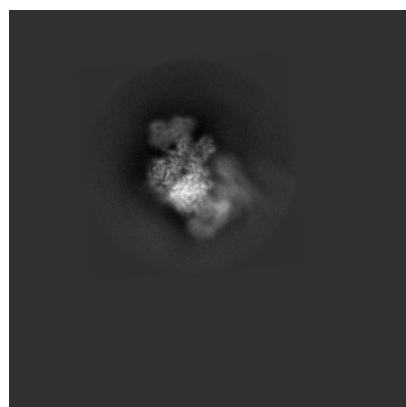


Y

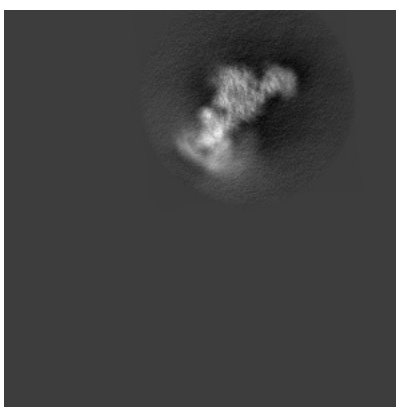


Z

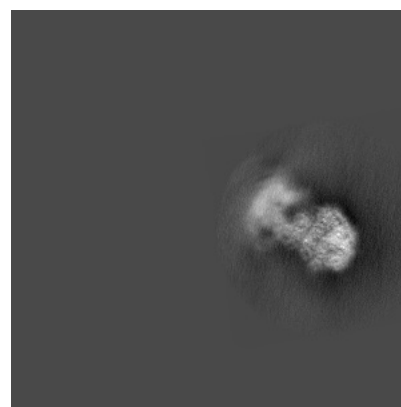
6.1.2 Raw map



X



Y

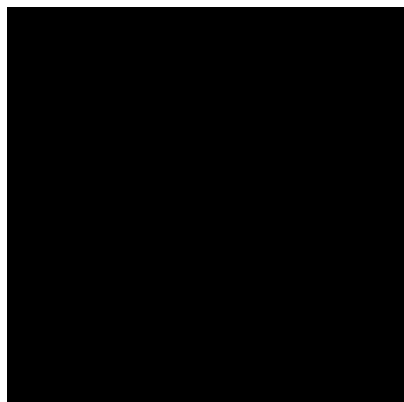


Z

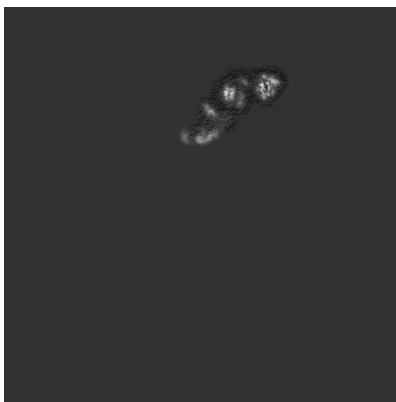
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

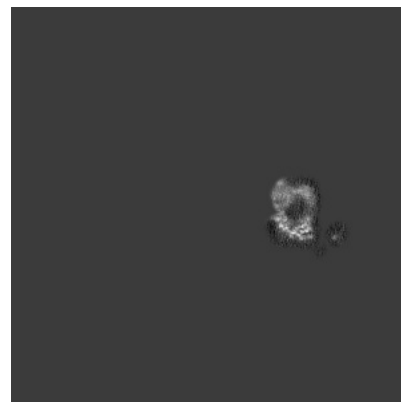
6.2.1 Primary map



X Index: 416



Y Index: 416

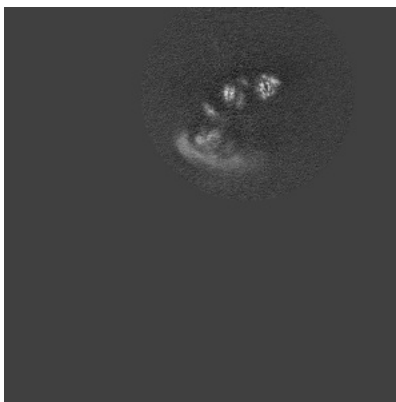


Z Index: 416

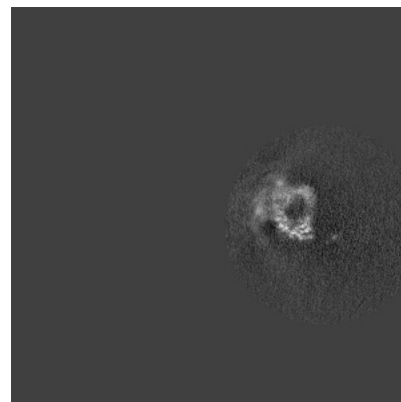
6.2.2 Raw map



X Index: 416



Y Index: 416

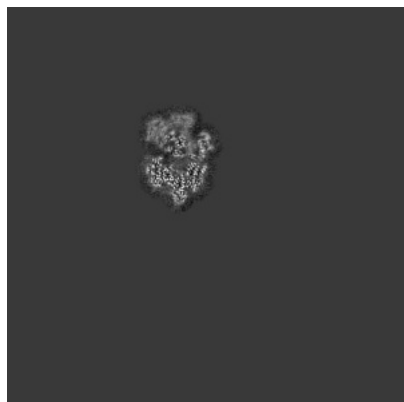


Z Index: 416

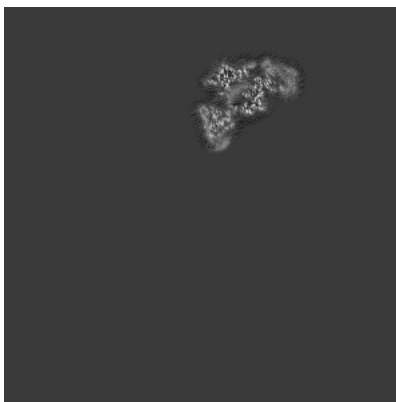
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

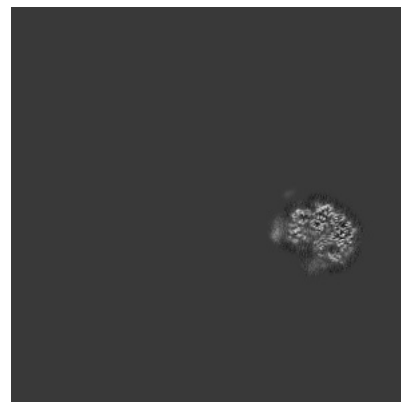
6.3.1 Primary map



X Index: 679

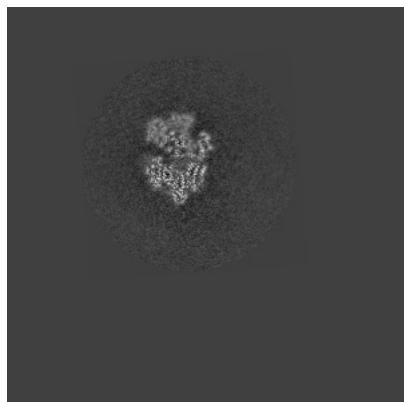


Y Index: 354

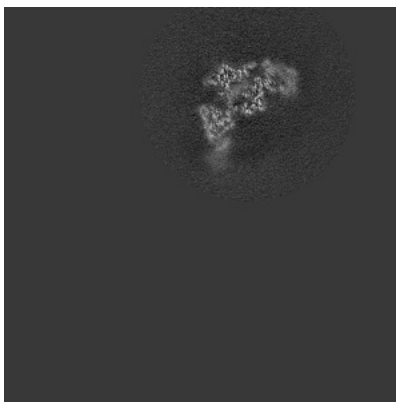


Z Index: 463

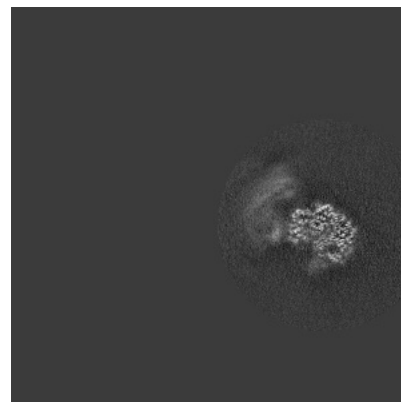
6.3.2 Raw map



X Index: 680



Y Index: 354

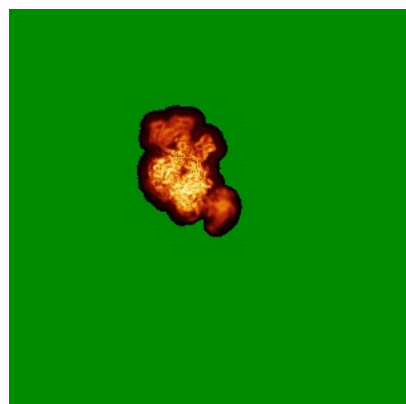


Z Index: 463

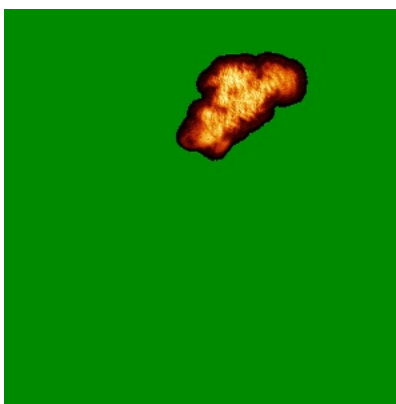
The images above show the largest variance slices of the map in three orthogonal directions.

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

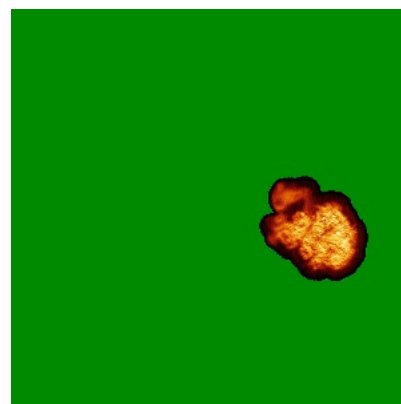
6.4.1 Primary map



X

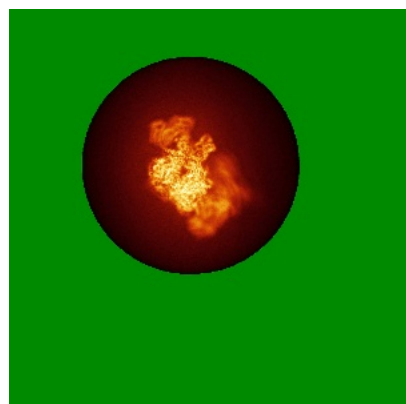


Y

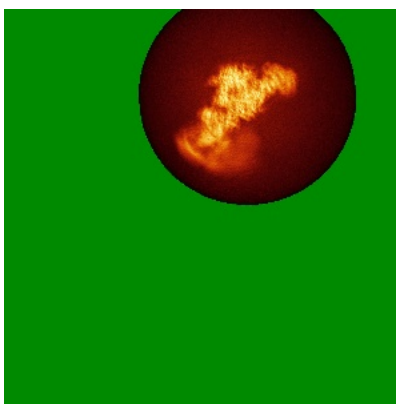


Z

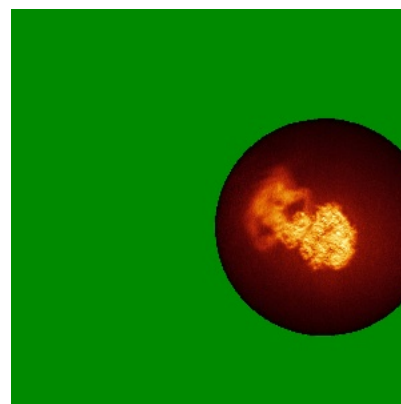
6.4.2 Raw map



X



Y

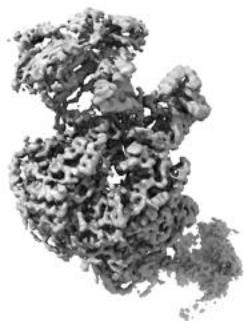


Z

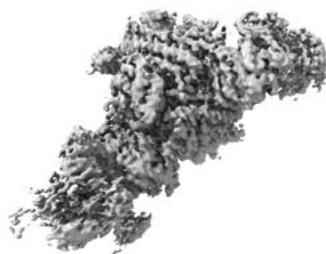
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

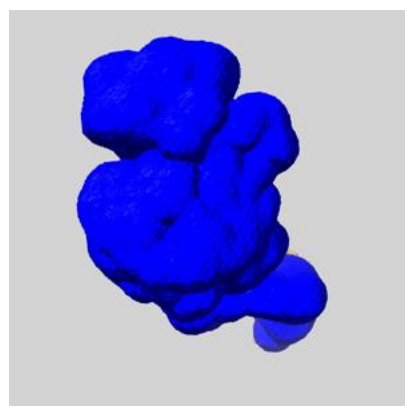
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

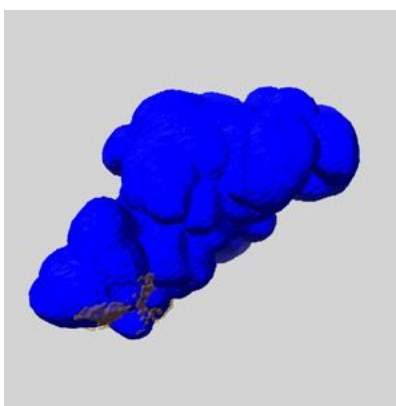
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

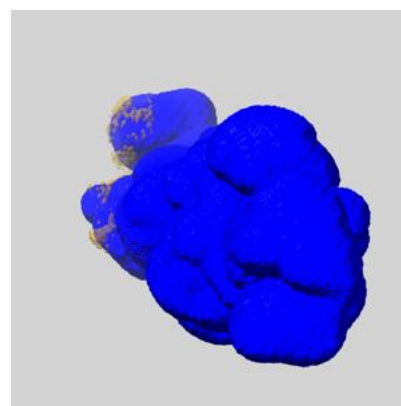
6.6.1 emd_51133_msk_1.map [i](#)



X



Y

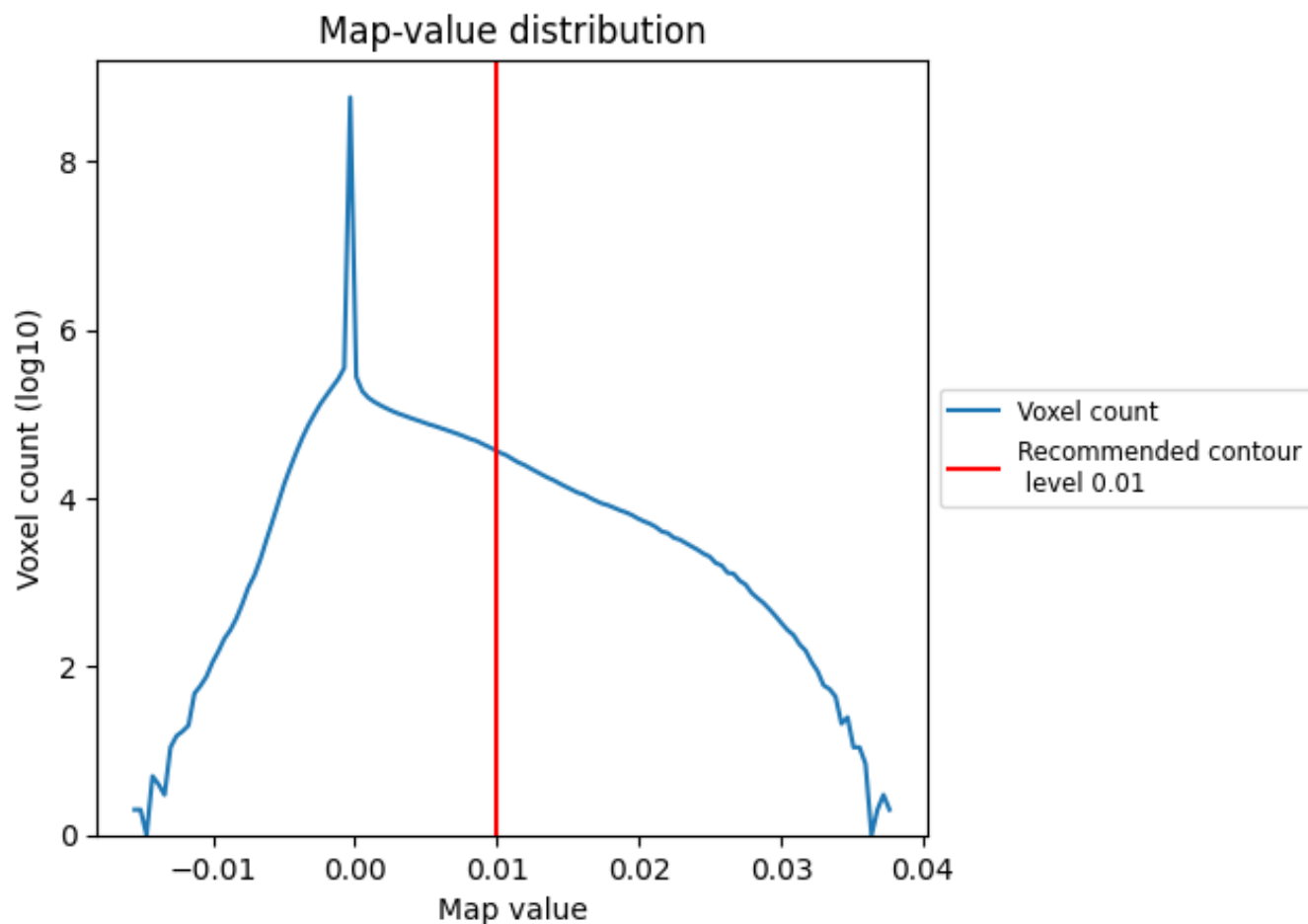


Z

7 Map analysis [i](#)

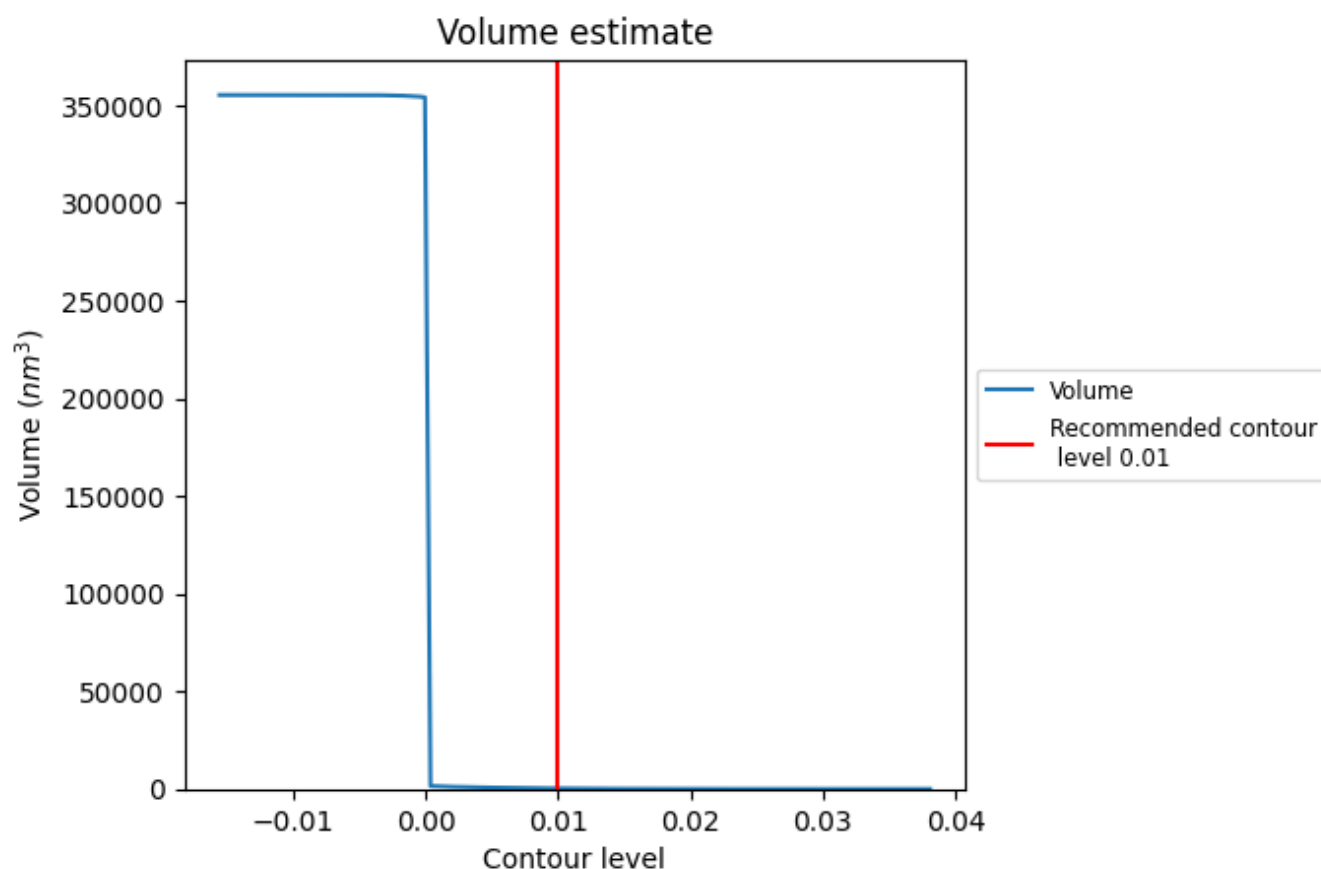
This section contains the results of statistical analysis of the map.

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.

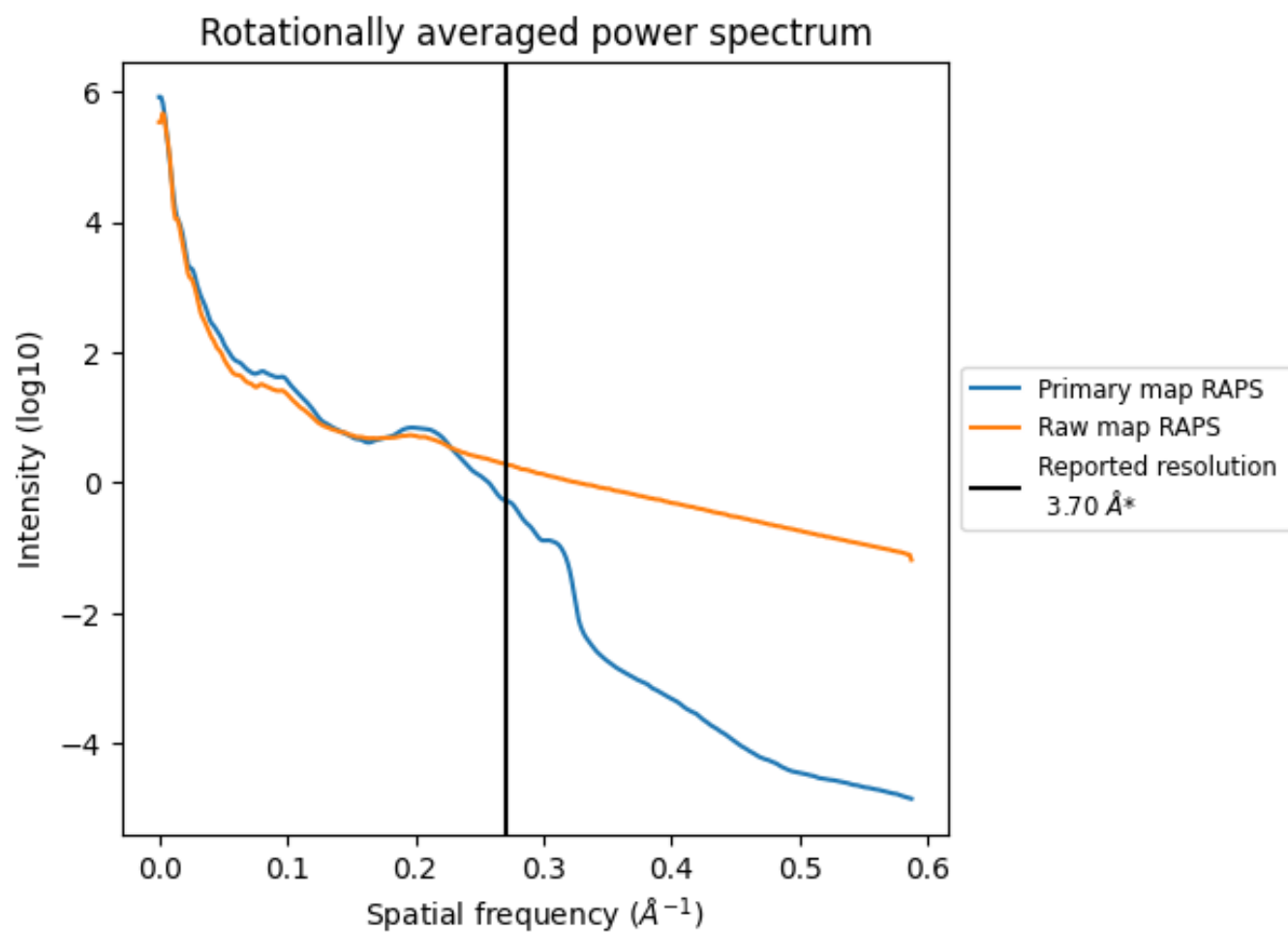
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 278 nm^3 ; this corresponds to an approximate mass of 251 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 ⓘ

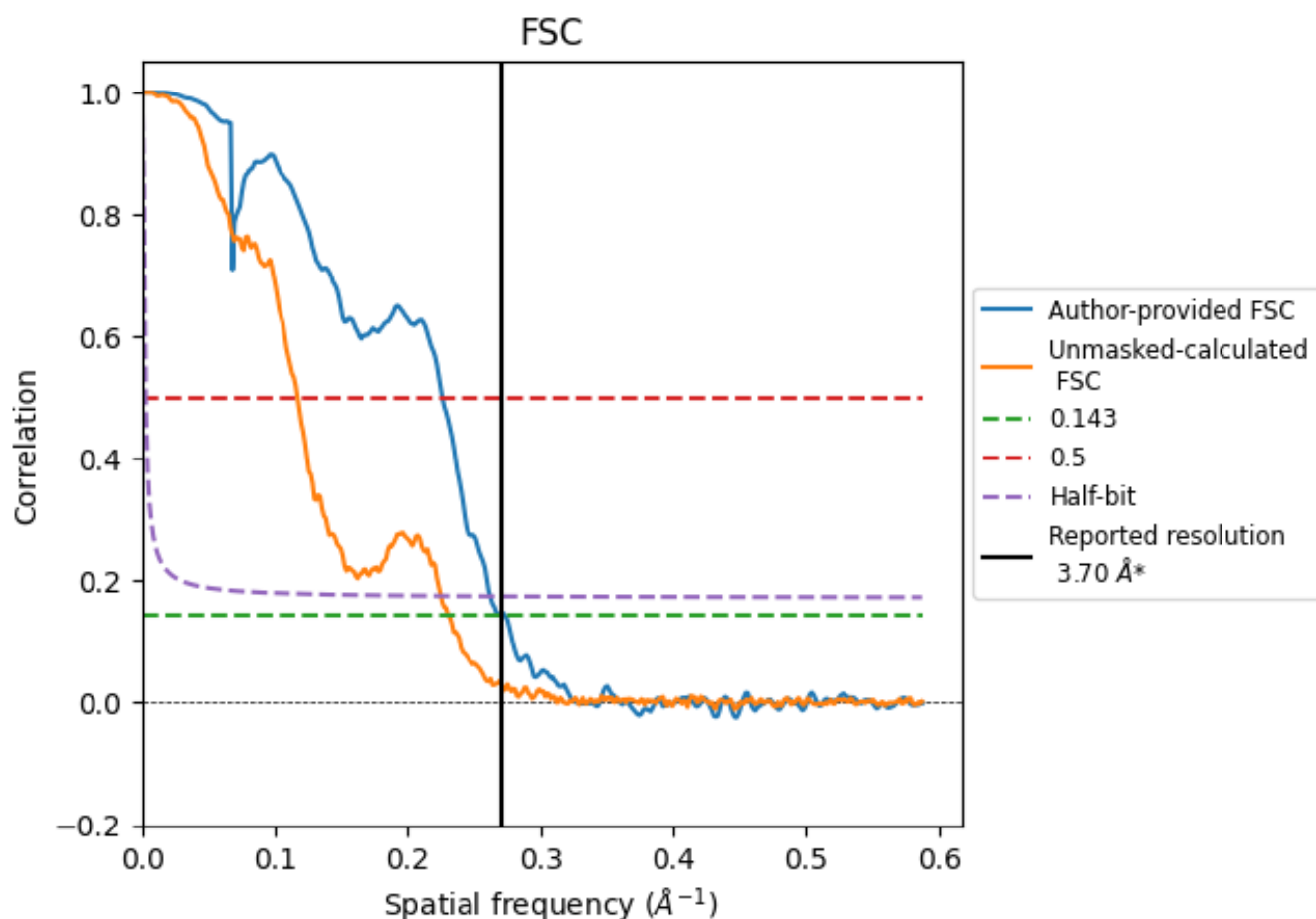


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

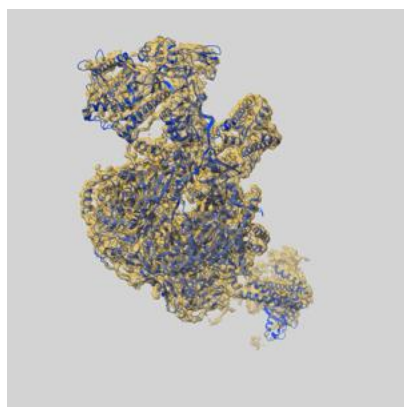
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.66	4.43	3.81
Unmasked-calculated*	4.35	8.54	4.45

*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 4.35 differs from the reported value 3.7 by more than 10 %

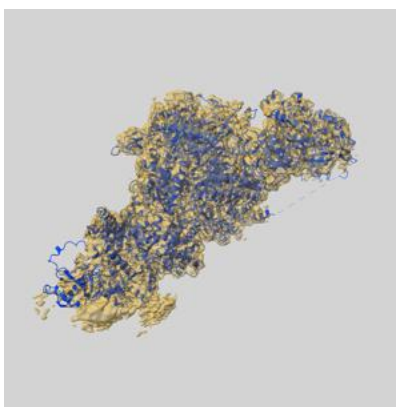
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51133 and PDB model 9G8N. Per-residue inclusion information can be found in section [3](#) on page [8](#).

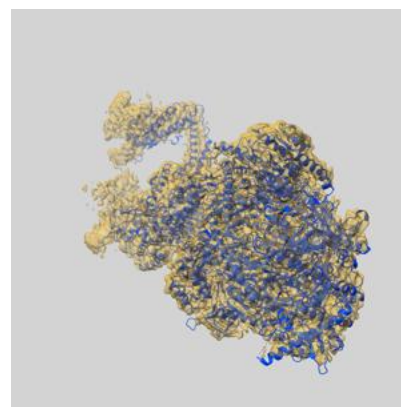
9.1 Map-model overlay [i](#)



X



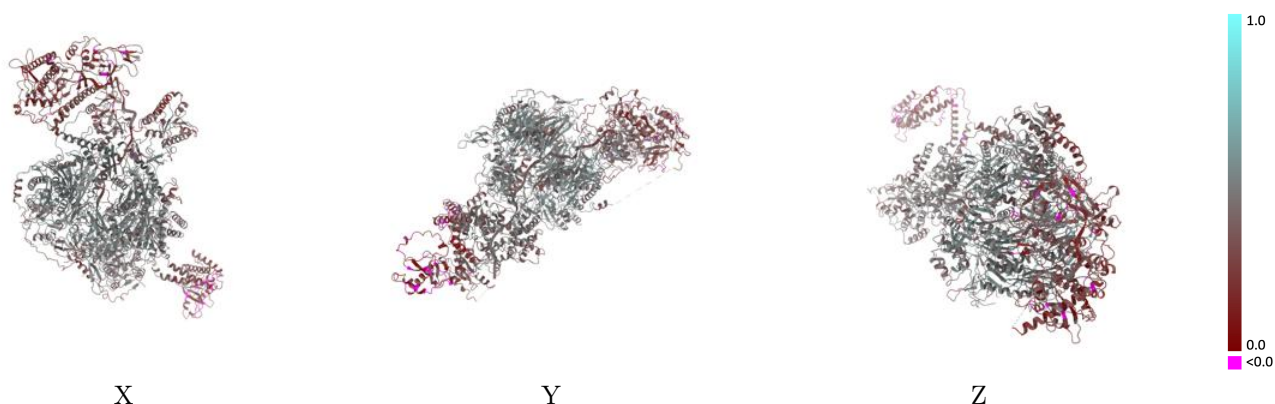
Y



Z

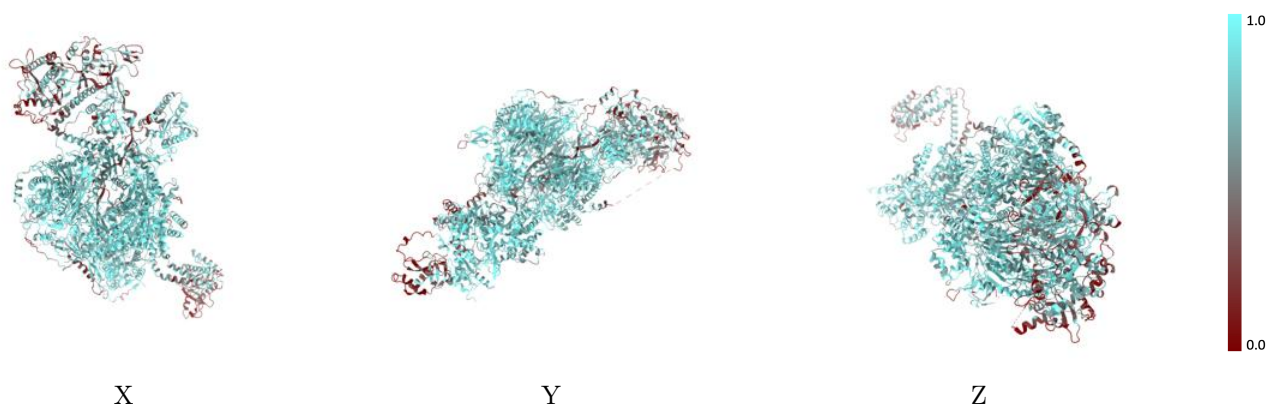
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



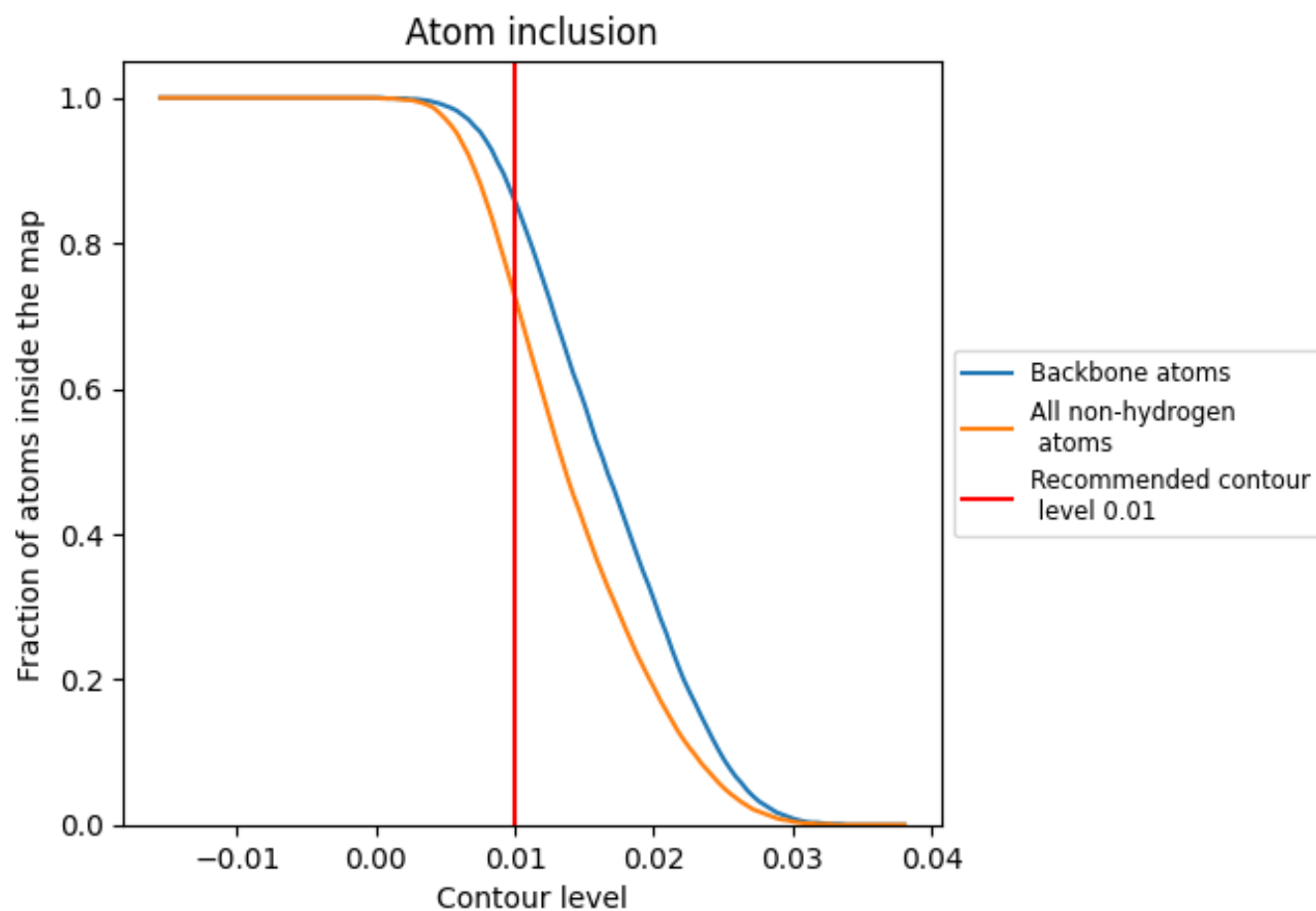
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 73% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7270	 0.4100
A	 0.7210	 0.3520
E	 0.5820	 0.3870
F	 0.7960	 0.4600
G	 0.8290	 0.4890
H	 0.8190	 0.4760
I	 0.7700	 0.4590
J	 0.7600	 0.4590
K	 0.7960	 0.4800
L	 0.8170	 0.4970
M	 0.5720	 0.3210
N	 0.8560	 0.4820
O	 0.8510	 0.5060
X	 0.6140	 0.3410

