



## wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 02:11 PM JST

PDB ID : 5X0Y  
EMDB ID : EMD-6700  
Title : Complex of Snf2-Nucleosome complex with Snf2 bound to SHL2 of the nucleosome  
Authors : Li, M.; Liu, X.; Xia, X.; Chen, Z.; Li, X.  
Deposited on : 2017-01-23  
Resolution : 4.69 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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

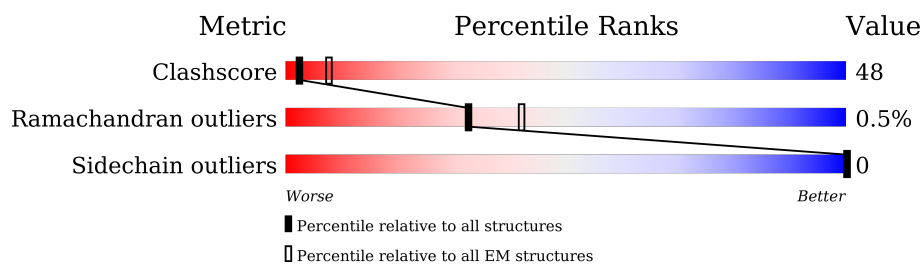
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.69 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	135	<div> <div>22%</div> <div>30%</div> <div>42%</div> <div>27%</div> </div>
1	E	135	<div> <div>19%</div> <div>33%</div> <div>36%</div> <div>30%</div> </div>
2	B	102	<div> <div>25%</div> <div>33%</div> <div>51%</div> <div>15%</div> </div>
2	F	102	<div> <div>23%</div> <div>46%</div> <div>38%</div> <div>16%</div> </div>
3	C	129	<div> <div>35%</div> <div>40%</div> <div>42%</div> <div>17%</div> </div>
3	G	129	<div> <div>23%</div> <div>43%</div> <div>40%</div> <div>17%</div> </div>
4	D	122	<div> <div>17%</div> <div>46%</div> <div>30%</div> <div>24%</div> </div>
4	H	122	<div> <div>7%</div> <div>41%</div> <div>35%</div> <div>24%</div> </div>

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Mol	Chain	Length	Quality of chain
5	I	167	<div><div><div></div><div></div><div></div></div><div>10%9%75%13%</div></div>
6	J	167	<div><div><div></div><div></div><div></div></div><div>11%5%79%13%</div></div>
7	O	735	<div><div><div></div><div></div><div></div></div><div>41%18%61%21%</div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16798 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 Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	98	Total	C	N	O	S	0	0
			800	505	153	139	3		
1	E	95	Total	C	N	O	S	0	0
			778	491	148	136	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	F	86	Total	C	N	O	S	0	0
			672	424	130	117	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O		0	0
			811	510	158	143			
3	G	107	Total	C	N	O		0	0
			815	513	159	143			

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			718	451	128	137	2		
4	H	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	SER	see sequence details	UNP P02281

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Chain	Residue	Modelled	Actual	Comment	Reference
H	29	THR	SER	see sequence details	UNP P02281

- Molecule 5 is a DNA chain called DNA (167-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		

- Molecule 6 is a DNA chain called DNA (167-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		

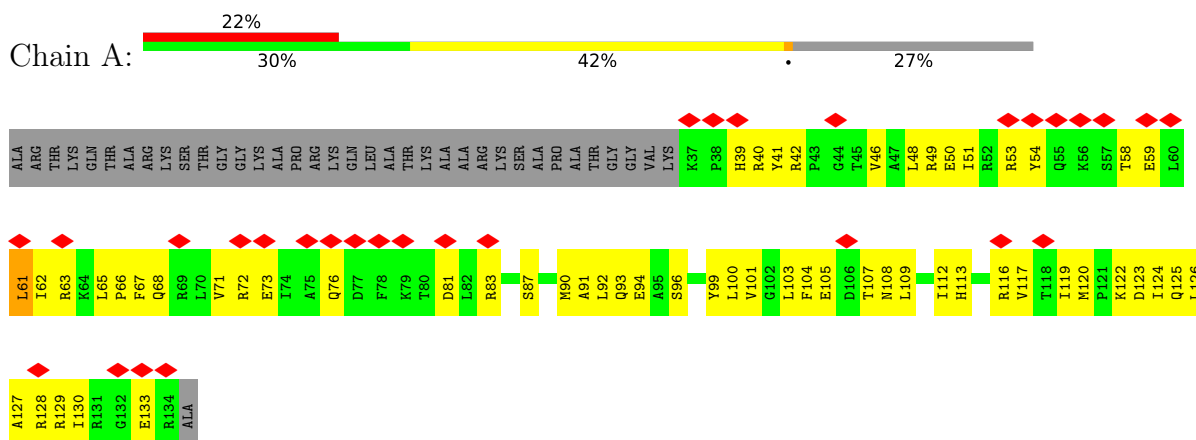
- Molecule 7 is a protein called Transcription regulatory protein SNF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	583	Total	C	N	O	S	0	0
			4789	3045	846	881	17		

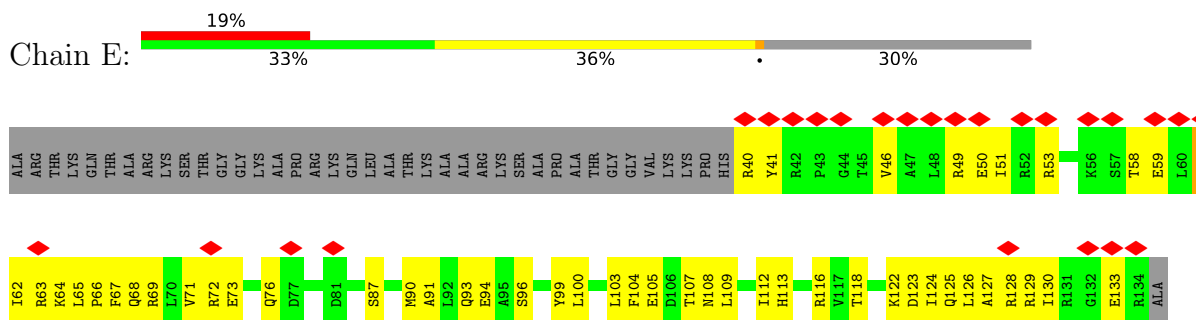
### 3 Residue-property plots [i](#)

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.

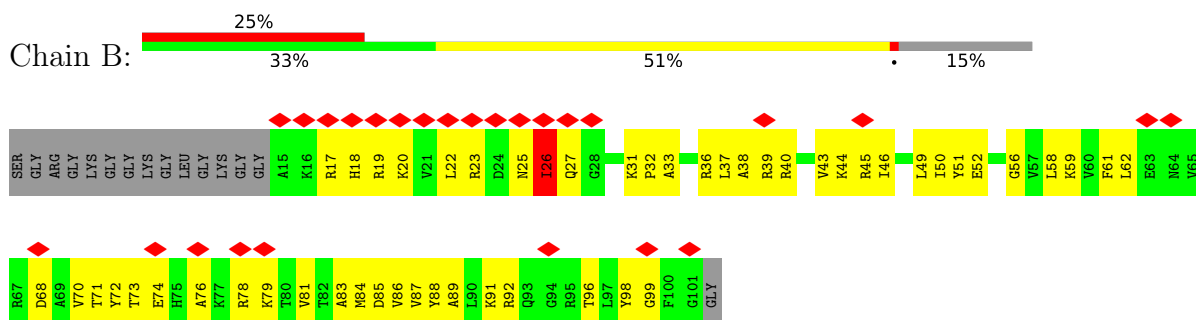
#### • Molecule 1: Histone H3.2



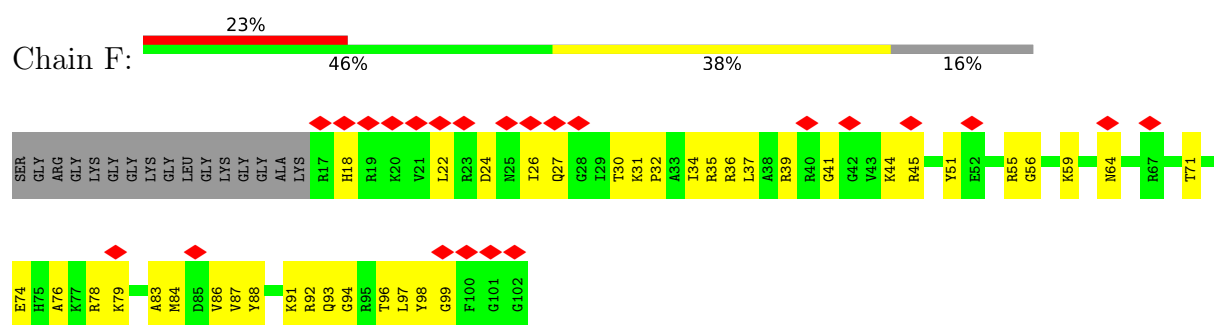
#### • Molecule 1: Histone H3.2



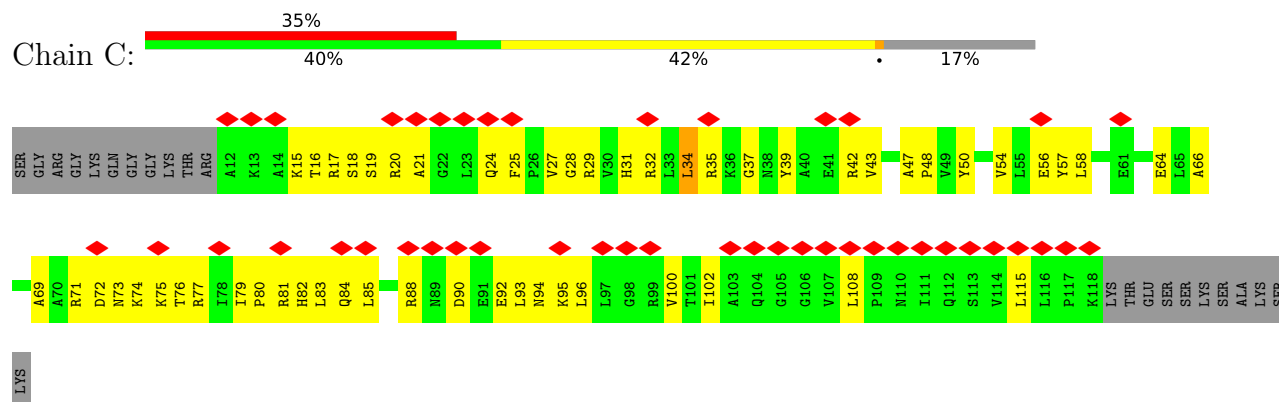
#### • Molecule 2: Histone H4



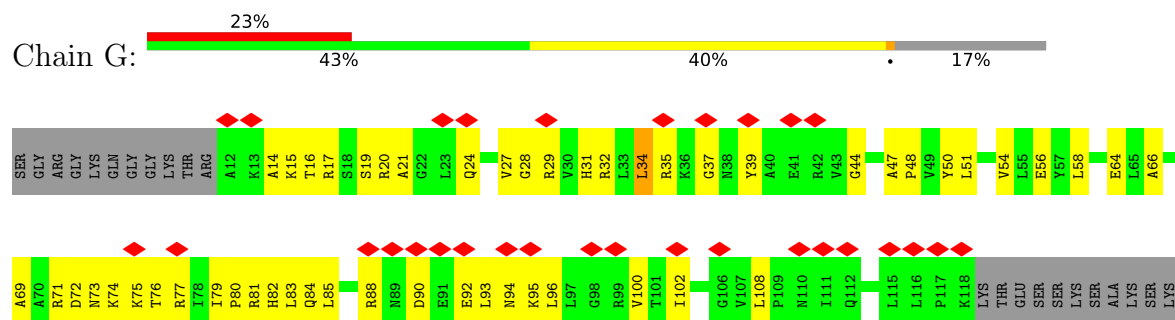
#### • Molecule 2: Histone H4



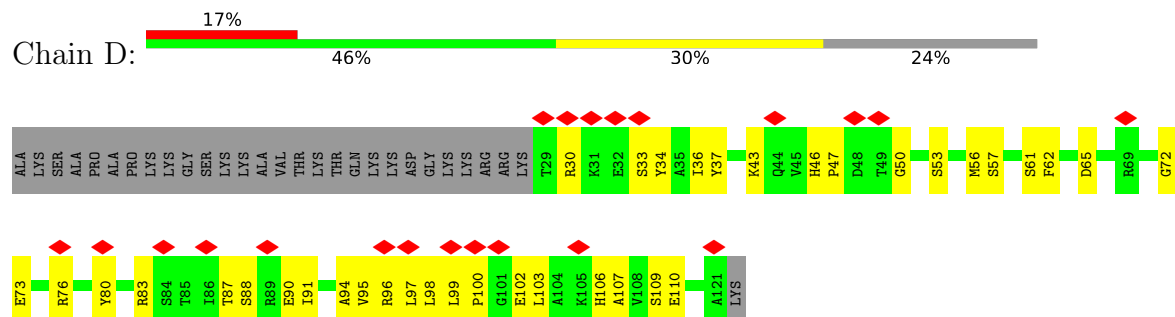
- Molecule 3: Histone H2A



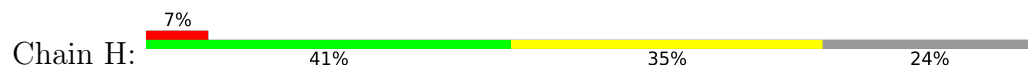
- Molecule 3: Histone H2A



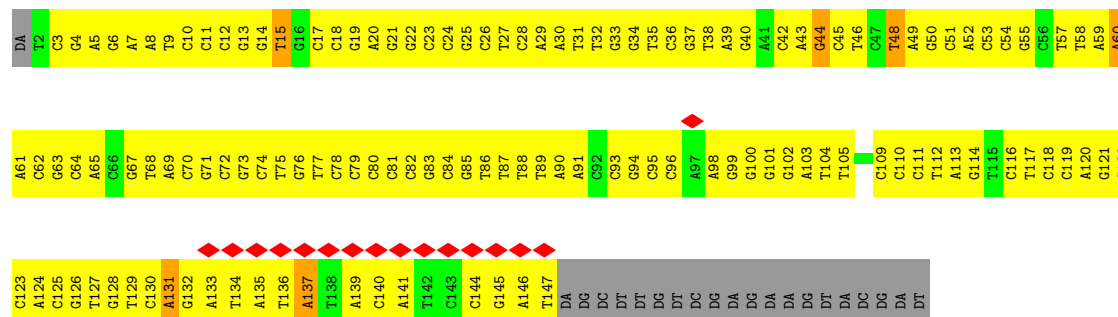
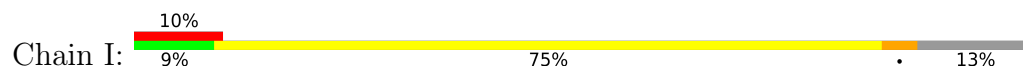
- Molecule 4: Histone H2B 1.1



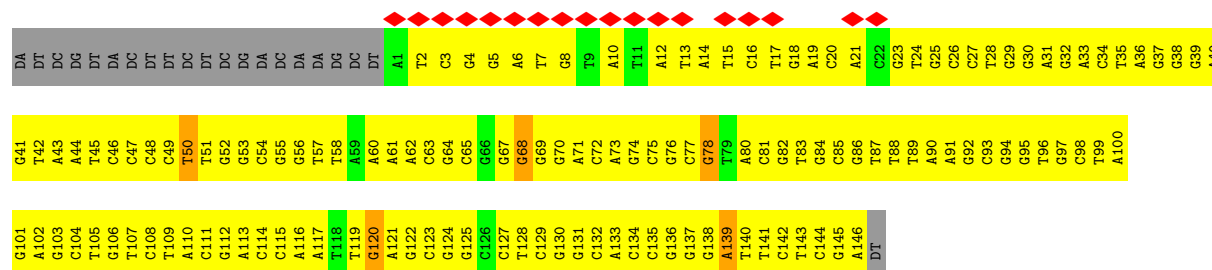
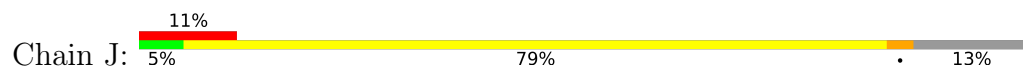
- Molecule 4: Histone H2B 1.1



- Molecule 5: DNA (167-MER)



- Molecule 6: DNA (167-MER)



- Molecule 7: Transcription regulatory protein SNF2





THR	ARG	E1269	L1209	F1149	K1088	L1027	D967	S907	F847
	ASP	SER	R1210	N1150	F1089	K1028	K968	L908	K848
	ILE	GLY	L1211	A1151	E1090	Y1029	T909	T909	G849
	GLU	VAL	L1212	P1152	L1091	R1030	T969	L910	S850
	GLU	GLU	L1213	D1153	D1093	L1031	E970	N911	P851
	LEU	GLU	T1214	S1154	R1094	L1032	L971	T912	P852
	GLU	GLU	N1215	E1155	L1095	PHE	S972	H913	N852
	ALA	E1277	S1216	L1156	L1096	ILE	E973	H914	E853
	ILE	L1278	V1217	L1157	L1097	GLY	E974	H915	R854
	ASP	K1279	E1218	C1158	K1098	ASP	E975	A916	K855
GLY	ASP	E1280	E1219	F1159	L1099	GLN	T976	A916	A956
	S1340	V1220	F1160	T1102	ASN	ASN	L977	D917	K857
	E1341	L1221	L1161	G1103	ASN	ASN	L977	Y918	K858
	S1342	E1223	G1104	H1104	LYS	LYS	R919	A859	K860
	A1343	R1224	T1163	R1105	LYS	W979	L920	I861	I861
	A1344	A1225	R1164	V1106	VAL	VAL	T980	I921	R862
	V1345	V1226	A1165	L1107	GLY	GLY	R981	L922	A863
	V1346	K1227	G1166	T1108	LEU	LEU	R982	T923	G864
	N1347	L1287	L1228	F1109	R1046	R984	G924	G924	E865
	G1348	L1289	L1229	F1110	G1047	K985	T925	T925	F866
	R1349	R1290	L1230	Q1111	F1048	K985	P926	P926	D867
	GLY	D1291	I1231	M1112	N1050	R986	L927	Q928	V868
	ALA	E1292	G1232	T1113	K1051	R988	N929	N929	V869
	ARG	M1294	A1238	Q1114	I1052	P989	L931	L931	T871
	GLU	A1295	K1234	L1172	M1053	F990	P932	P932	T872
	ARG	V1296	V1235	T1173	M1063	L991	E833	E833	F873
	LYS	L1297	L1236	T1174	Q1054	L992	L934	L934	E874
	THR	T1298	Q1237	A1175	K1055	R993	W935	W935	W935
	R1299	E1299	A1238	M1119	K1056	R994	L837	L837	I876
	THR	M1300	G1239	D1176	E1120	K1057	L995	L995	I877
	D1301	K1240	T1177	D1121	I1058	C1059	K996	K996	K878
	ASN	E1302	D1241	F1122	L1123	N1060	R997	R997	E879
	D1303	D1242	I1180	L1123	H1061	V999	F940	F940	R880
	R1304	N1243	F1181	Y1125	E1000	L941	L941	L941	A881
	S1305	S1244	D1182	N1126	F1062	L942	P943	P943	L882
	GLU	S1245	T1183	N1127	M1063	L001	L883	L883	L883
	T1246	S1246	D1184	I1128	F1064	E1002	K944	K944	S884
	K1307	S1247	W1185	K1129	F1065	L1003	L945	L945	K885
	E1308	E1248	P1187	Y1130	E1066	P1004	F946	F946	V886
	LEU	E1309	E1249	L1131	E1067	D1005	N947	N947	K887
	GLU	LEU	E1249	R1132	E1068	K1006	S948	S948	W888
	GLY	GLY	Q1250	L1133	D1070	V1007	V889	V889	V889
	VAL	E1251	D1251	G1135	Q1071	E1008	K950	K950	H890
	VAL	A1252	L1191	H1136	T1072	K1009	M891	M891	M891
	S1314	L1253	L1190	G1135	V1010	F952	F952	F952	I892
	SER	L1254	A1193	T1137	P1074	V1011	E893	E893	I893
	ASP	R1254	Q1194	K1138	T1075	C1013	E954	E954	D894
	ASP	R1255	R1255	S1139	E1076	K1014	F956	F956	G896
	LYS	L1257	L1257	D1140	E1077	M1015	R897	R897	G896
	ASN	E1319	L1258	E1141	D1080	M1015	S1016	S1016	N957
	GLN	K1320	A1260	H1198	I1082	A1017	T958	T958	R898
	SER	SER	E1261	R1199	S1143	L1018	P959	P959	M899
	GLU	GLU	E1262	R1142	W1083	Q1019	F960	F960	K900
	ARG	LEU	E1263	S1143	I1083	T1021	ALA	ALA	ASN
	ARG	PRO	E1263	R1147	V1085	M1022	THR	THR	A902
	LYS	ASP	R1264	K1203	A1086	Y1023	GLY	GLY	Q903
	GLN	ILE	R1265	N1204	G1087	Q1024	GLY	GLY	S904
	TYR	TYR	K1266	E1205	G1087	M1025	GLN	GLN	K905
	SER	SER	K1267	T1206					L906
			R1268	T1207					
			T1208						

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90725	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0341	Depositor
Map size (Å)	337.92, 337.92, 337.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	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	A	0.57	0/812	0.67	1/1091 (0.1%)
1	E	0.57	0/788	0.67	1/1057 (0.1%)
2	B	0.62	0/711	0.68	0/950
2	F	0.62	0/680	0.66	0/912
3	C	0.49	0/821	0.63	1/1112 (0.1%)
3	G	0.48	0/825	0.64	1/1116 (0.1%)
4	D	0.59	0/729	0.61	0/985
4	H	0.59	0/737	0.62	0/993
5	I	1.34	0/3333	1.11	6/5137 (0.1%)
6	J	1.36	1/3381 (0.0%)	1.04	4/5221 (0.1%)
7	O	0.45	0/4864	0.65	2/6536 (0.0%)
All	All	0.93	1/17681 (0.0%)	0.85	16/25110 (0.1%)

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
1	A	0	1
1	E	0	1
2	B	0	1
7	O	0	5
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	68	DG	C3'-O3'	-5.87	1.36	1.44

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	120	DG	O4'-C4'-C3'	-7.85	101.29	106.00
5	I	15	DT	O4'-C4'-C3'	-7.37	101.55	104.50
5	I	48	DT	O4'-C4'-C3'	-7.21	101.61	104.50
5	I	60	DA	O4'-C1'-N9	6.42	112.50	108.00
5	I	44	DG	O4'-C4'-C3'	-6.09	102.06	104.50

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	58	THR	Peptide
2	B	26	ILE	Peptide
1	E	58	THR	Peptide
7	O	768	LYS	Peptide
7	O	839	ALA	Peptide

## 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	800	0	829	60	0
1	E	778	0	813	45	0
2	B	703	0	757	74	0
2	F	672	0	698	44	0
3	C	811	0	849	62	0
3	G	815	0	860	51	0
4	D	718	0	725	53	0
4	H	726	0	747	45	0
5	I	2975	0	1639	262	0
6	J	3011	0	1639	309	0
7	O	4789	0	4882	638	0
All	All	16798	0	14438	1477	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 48.

The worst 5 of 1477 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)
7:O:1233:GLY:O	7:O:1237:GLN:HB2	1.22	1.32
7:O:876:ILE:O	7:O:880:ARG:HB2	1.41	1.17
7:O:1232:ASP:O	7:O:1236:ILE:HB	1.42	1.16
7:O:1301:ASP:O	7:O:1305:SER:HB2	1.60	1.02
5:I:111:DC:O2	6:J:37:DG:N2	1.93	1.01

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	96/135 (71%)	88 (92%)	8 (8%)	0	100	100
1	E	93/135 (69%)	85 (91%)	8 (9%)	0	100	100
2	B	85/102 (83%)	69 (81%)	15 (18%)	1 (1%)	13	50
2	F	84/102 (82%)	81 (96%)	3 (4%)	0	100	100
3	C	105/129 (81%)	99 (94%)	6 (6%)	0	100	100
3	G	105/129 (81%)	99 (94%)	6 (6%)	0	100	100
4	D	91/122 (75%)	83 (91%)	8 (9%)	0	100	100
4	H	91/122 (75%)	83 (91%)	8 (9%)	0	100	100
7	O	569/735 (77%)	483 (85%)	81 (14%)	5 (1%)	17	56
All	All	1319/1711 (77%)	1170 (89%)	143 (11%)	6 (0%)	32	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	26	ILE
7	O	1163	THR
7	O	958	THR
7	O	979	VAL
7	O	679	ILE

### 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	84/110 (76%)	84 (100%)	0	100	100
1	E	82/110 (74%)	82 (100%)	0	100	100
2	B	72/78 (92%)	72 (100%)	0	100	100
2	F	67/78 (86%)	67 (100%)	0	100	100
3	C	81/101 (80%)	81 (100%)	0	100	100
3	G	82/101 (81%)	82 (100%)	0	100	100
4	D	77/102 (76%)	77 (100%)	0	100	100
4	H	79/102 (78%)	79 (100%)	0	100	100
7	O	525/667 (79%)	525 (100%)	0	100	100
All	All	1149/1449 (79%)	1149 (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 23 such sidechains are listed below:

Mol	Chain	Res	Type
7	O	929	ASN
7	O	1051	GLN
7	O	1025	GLN
7	O	1054	GLN
2	F	93	GLN

### 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 [i](#)

There are no monosaccharides 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.

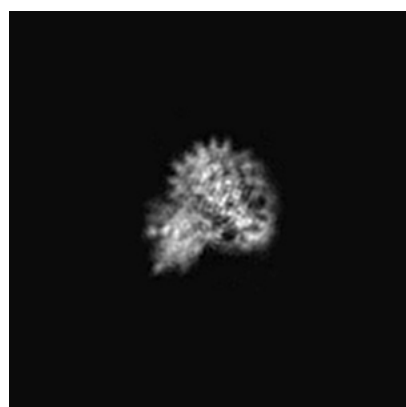
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6700. These allow visual inspection of the internal detail of the map and identification of artifacts.

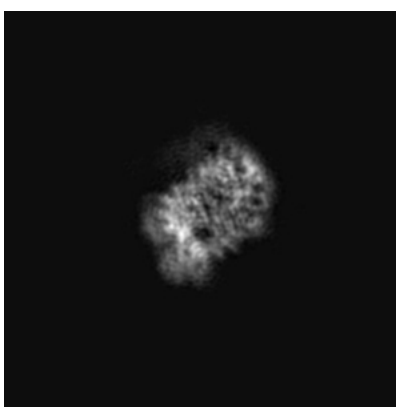
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

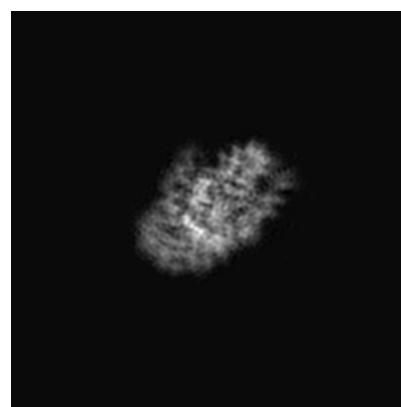
#### 6.1.1 Primary map



X



Y

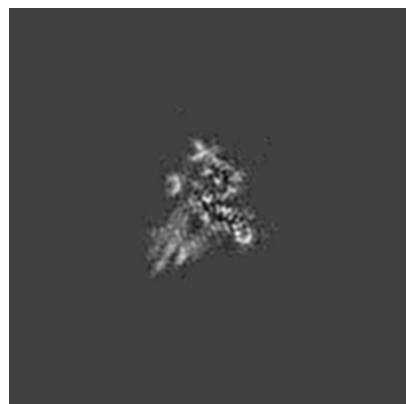


Z

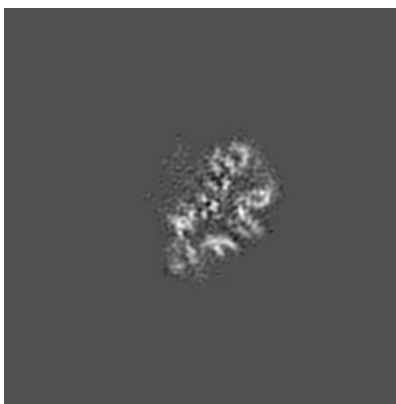
The images above show the map projected in three orthogonal directions.

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

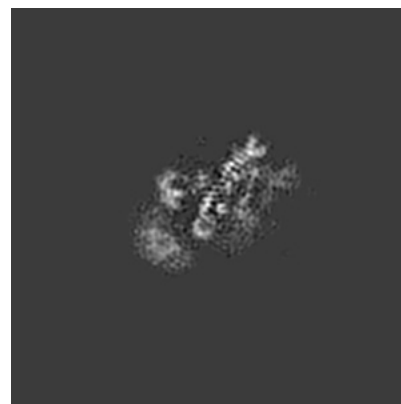
#### 6.2.1 Primary map



X Index: 128



Y Index: 128



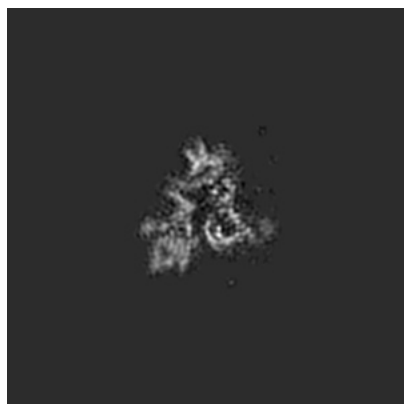
Z Index: 128



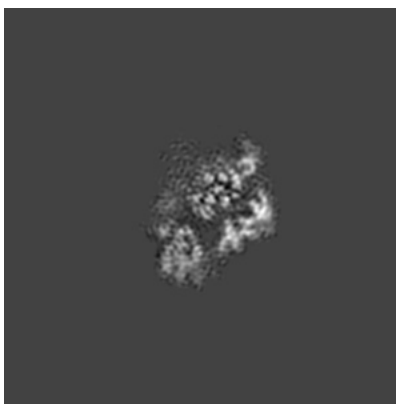
The images above show central slices of the map in three orthogonal directions.

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

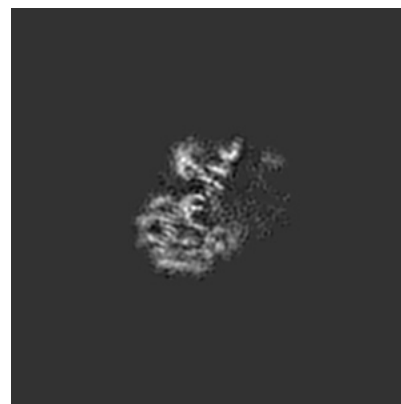
### 6.3.1 Primary map



X Index: 118



Y Index: 122

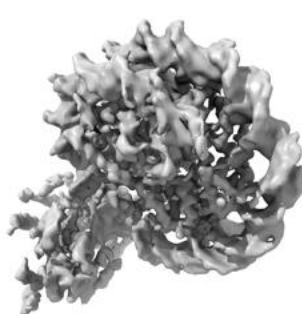


Z Index: 113

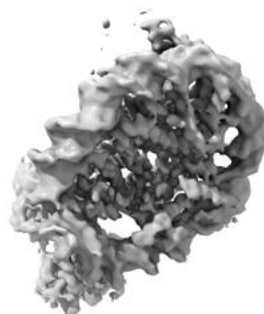
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

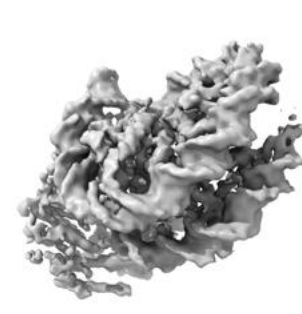
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0341. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

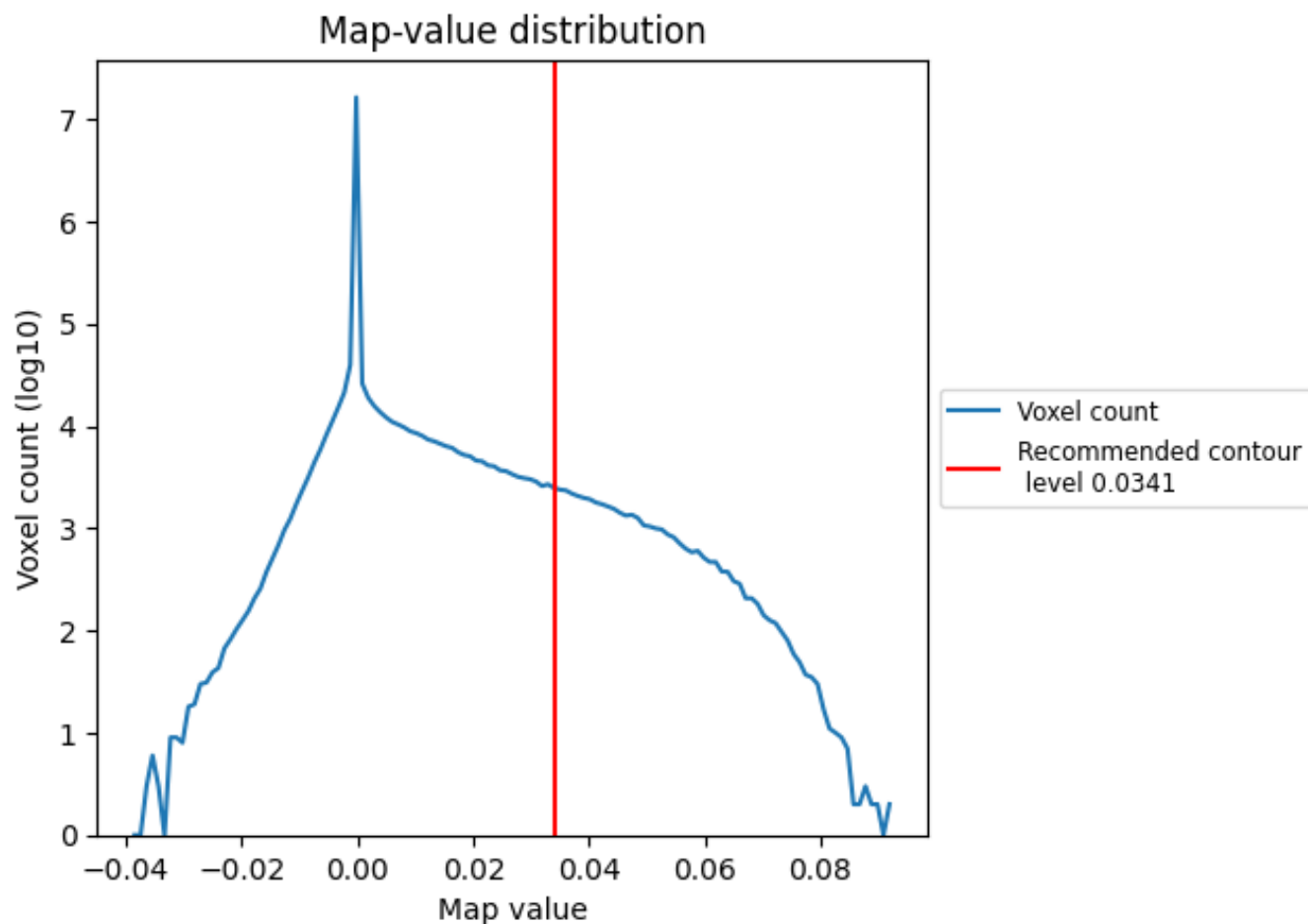
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

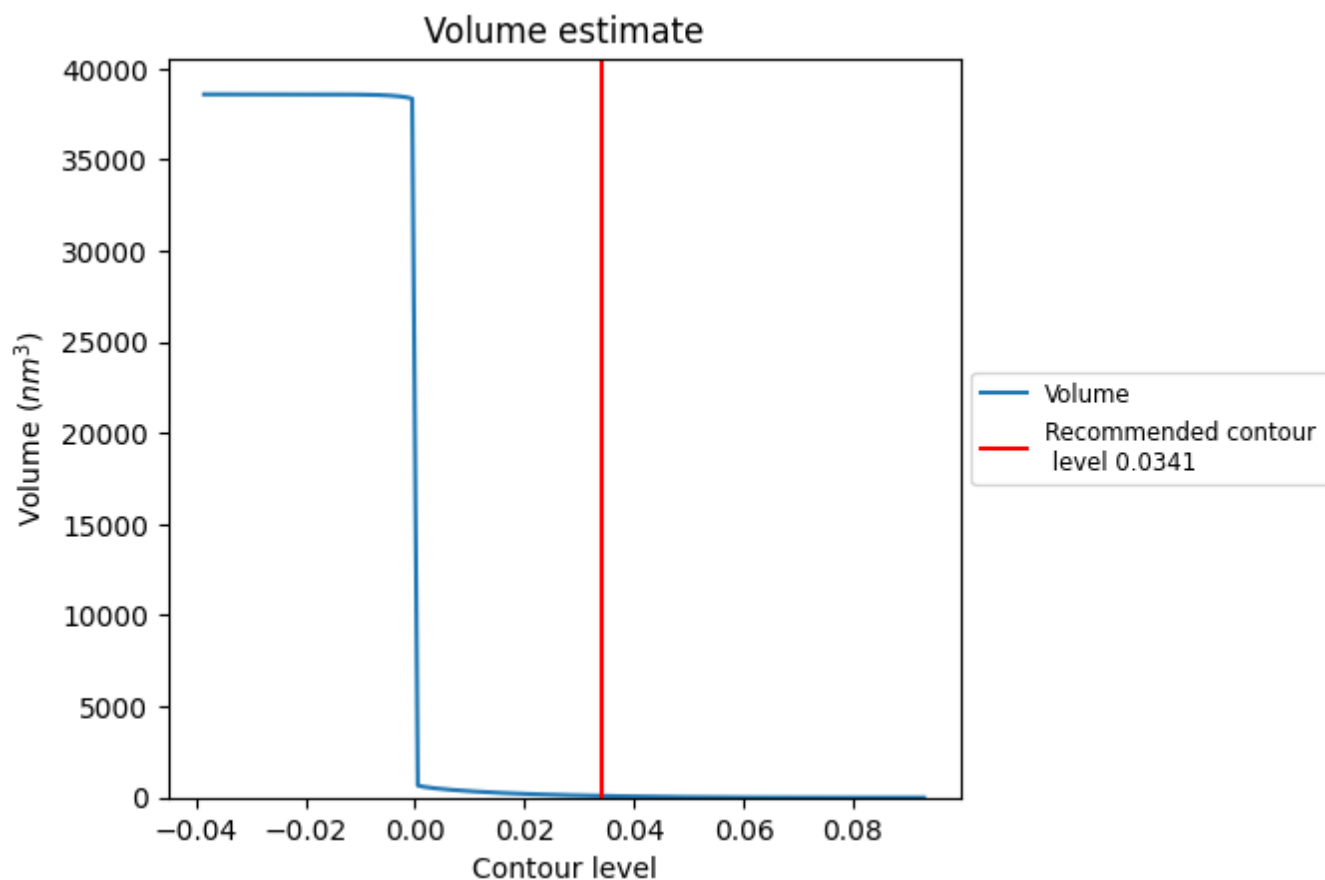
This section contains the results of statistical analysis of the map.

### 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.

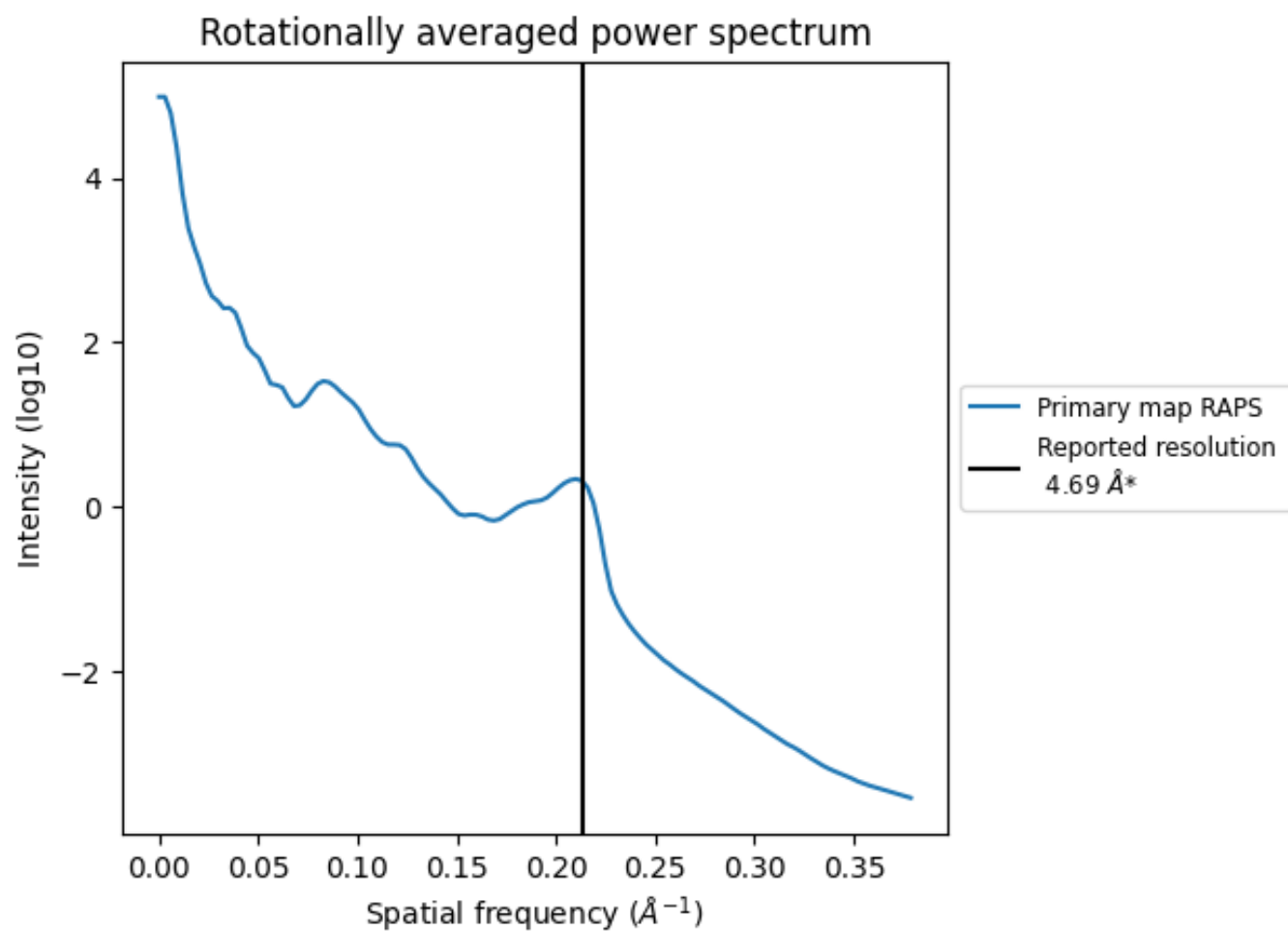
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 91 nm<sup>3</sup>; this corresponds to an approximate mass of 82 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 0.213 Å<sup>-1</sup>

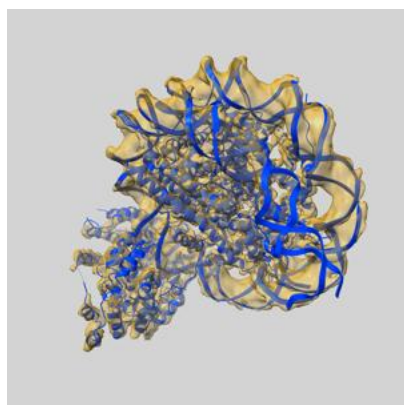
## 8 Fourier-Shell correlation ⓘ

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

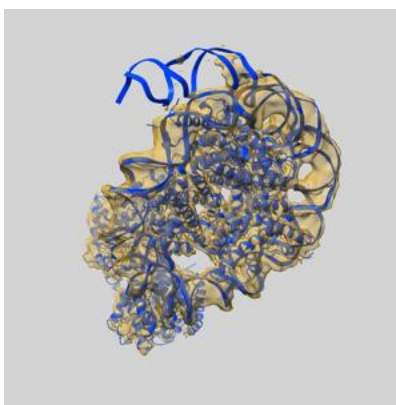
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6700 and PDB model 5X0Y. Per-residue inclusion information can be found in section [3](#) on page [6](#).

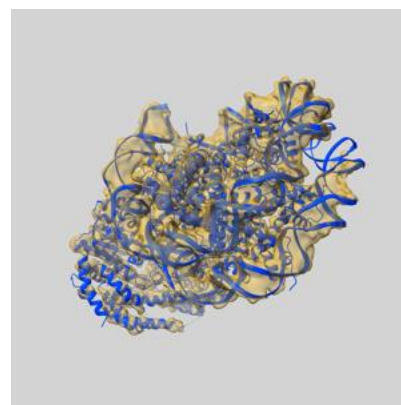
### 9.1 Map-model overlay [i](#)



X



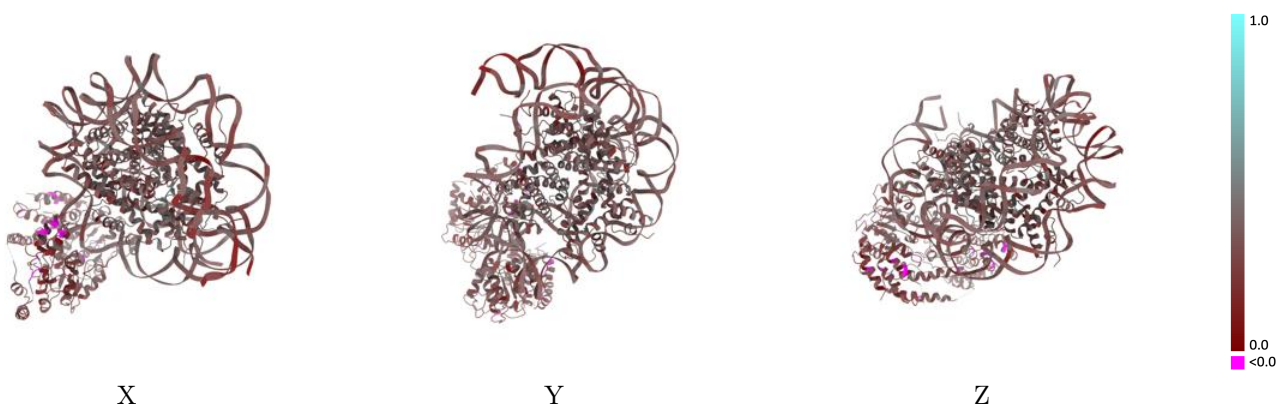
Y



Z

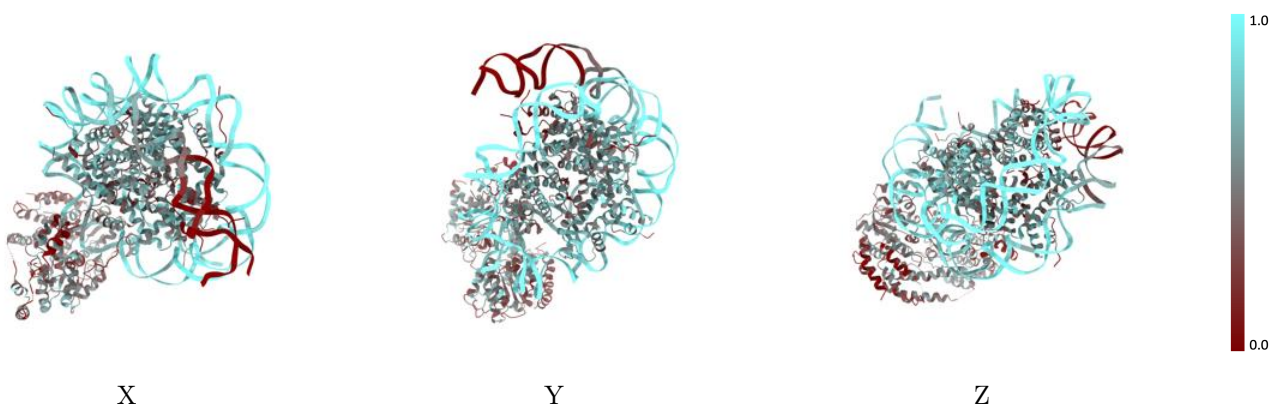
The images above show the 3D surface view of the map at the recommended contour level 0.0341 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

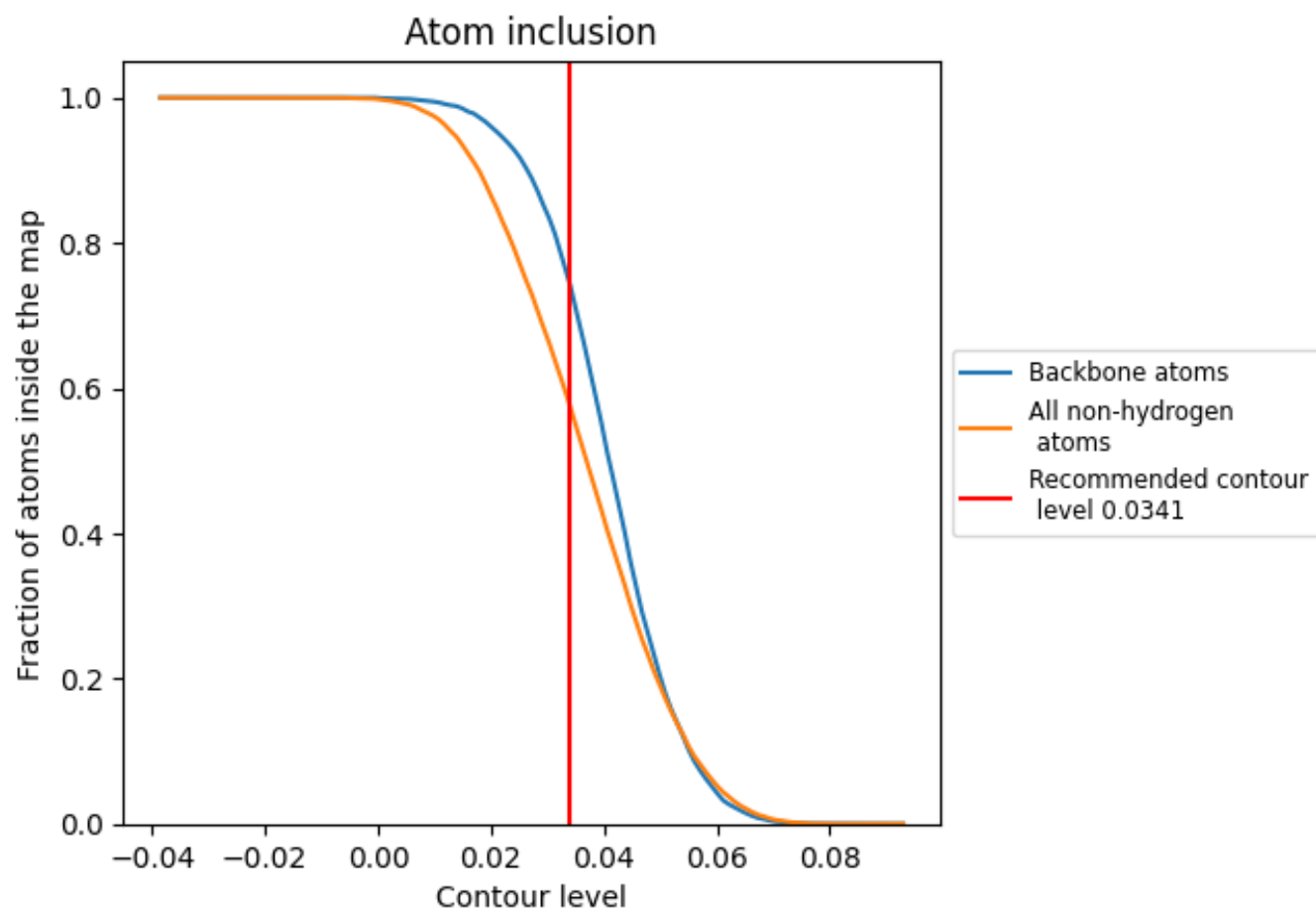
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.0341).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 57% 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 (0.0341) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5737	<div></div> 0.3150
A	<div></div> 0.5318	<div></div> 0.3630
B	<div></div> 0.5201	<div></div> 0.3700
C	<div></div> 0.4377	<div></div> 0.3190
D	<div></div> 0.5492	<div></div> 0.3320
E	<div></div> 0.5073	<div></div> 0.3590
F	<div></div> 0.5293	<div></div> 0.3620
G	<div></div> 0.5443	<div></div> 0.3520
H	<div></div> 0.6008	<div></div> 0.3590
I	<div></div> 0.7782	<div></div> 0.3240
J	<div></div> 0.7811	<div></div> 0.3270
O	<div></div> 0.3692	<div></div> 0.2570

1.0

0.0

<0.0