



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:19 PM UTC

PDB ID : 8G4W / pdb_00008g4w
EMDB ID : EMD-29732
Title : Cryo-EM consensus structure of Escherichia coli que-PEC (paused elongation complex) RNA Polymerase plus preQ1 ligand
Authors : Porta, J.C.; Chauvier, A.; Deb, I.; Ellinger, E.; Frank, A.T.; Meze, K.; Ohi, M.D.; Walter, N.G.
Deposited on : 2023-02-10
Resolution : 3.80 Å (reported)
Based on initial model : 6ASX

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

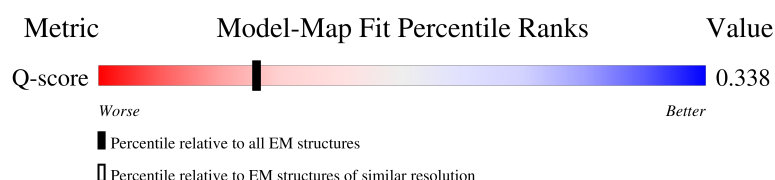
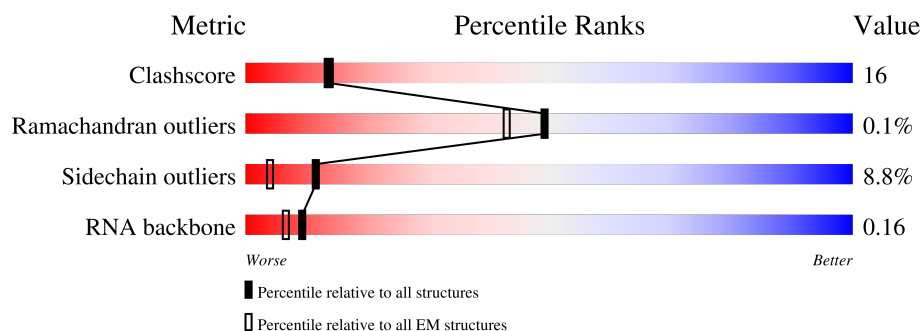
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	A	39	
2	B	31	

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Mol	Chain	Length	Quality of chain
3	G	235	23%61%33%6%
3	H	235	42%38%40%15%7%
4	K	79	52%57%35%8%
5	R	47	83%40%49%6%
6	I	1340	41%63%33%..
7	J	1358	45%61%36%..

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 26842 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 DNA chain called DNA (39-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	19	Total	C	N	O	P	0	0
			388	186	78	107	17		

- Molecule 2 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	31	Total	C	N	O	P	0	0
			631	301	107	192	31		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	221	Total	C	N	O	S	0	0
			1708	1069	303	330	6		
3	H	219	Total	C	N	O	S	0	0
			1693	1058	298	331	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	235	GLU	-	expression tag	UNP A0A5B9AW69
H	235	GLU	-	expression tag	UNP A0A5B9AW69

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a RNA chain called RNA (47-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	47	Total	C	N	O	P	0	0
			997	449	185	317	46		

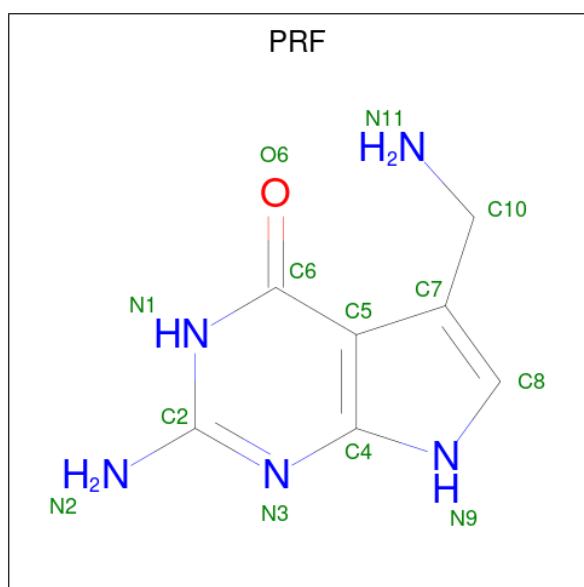
- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	1316	Total	C	N	O	S	0	0
			10381	6514	1810	2014	43		

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	1337	Total	C	N	O	S	0	0
			10403	6536	1856	1961	50		

- Molecule 8 is 7-DEAZA-7-AMINOMETHYL-GUANINE (CCD ID: PRF) (formula: $C_7H_9N_5O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
8	R	1	Total	C	N	O	0
			13	7	5	1	

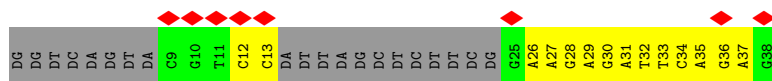
- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	J	1	Total	Mg	0
			1	1	

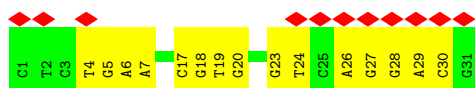
3 Residue-property plots

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.

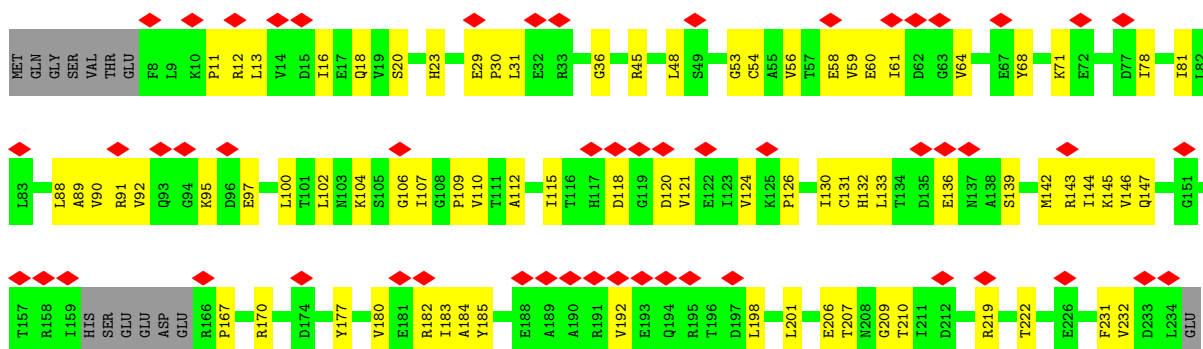
- Molecule 1: DNA (39-mer)



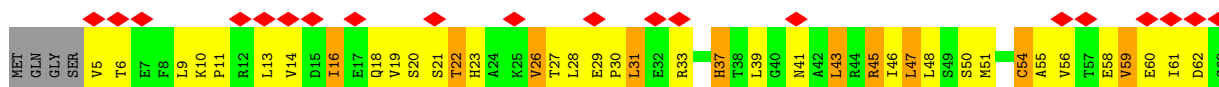
- Molecule 2: DNA (31-MER)



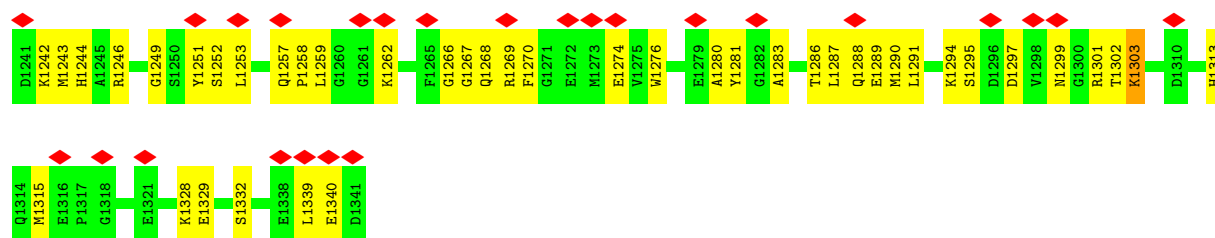
- Molecule 3: DNA-directed RNA polymerase subunit alpha



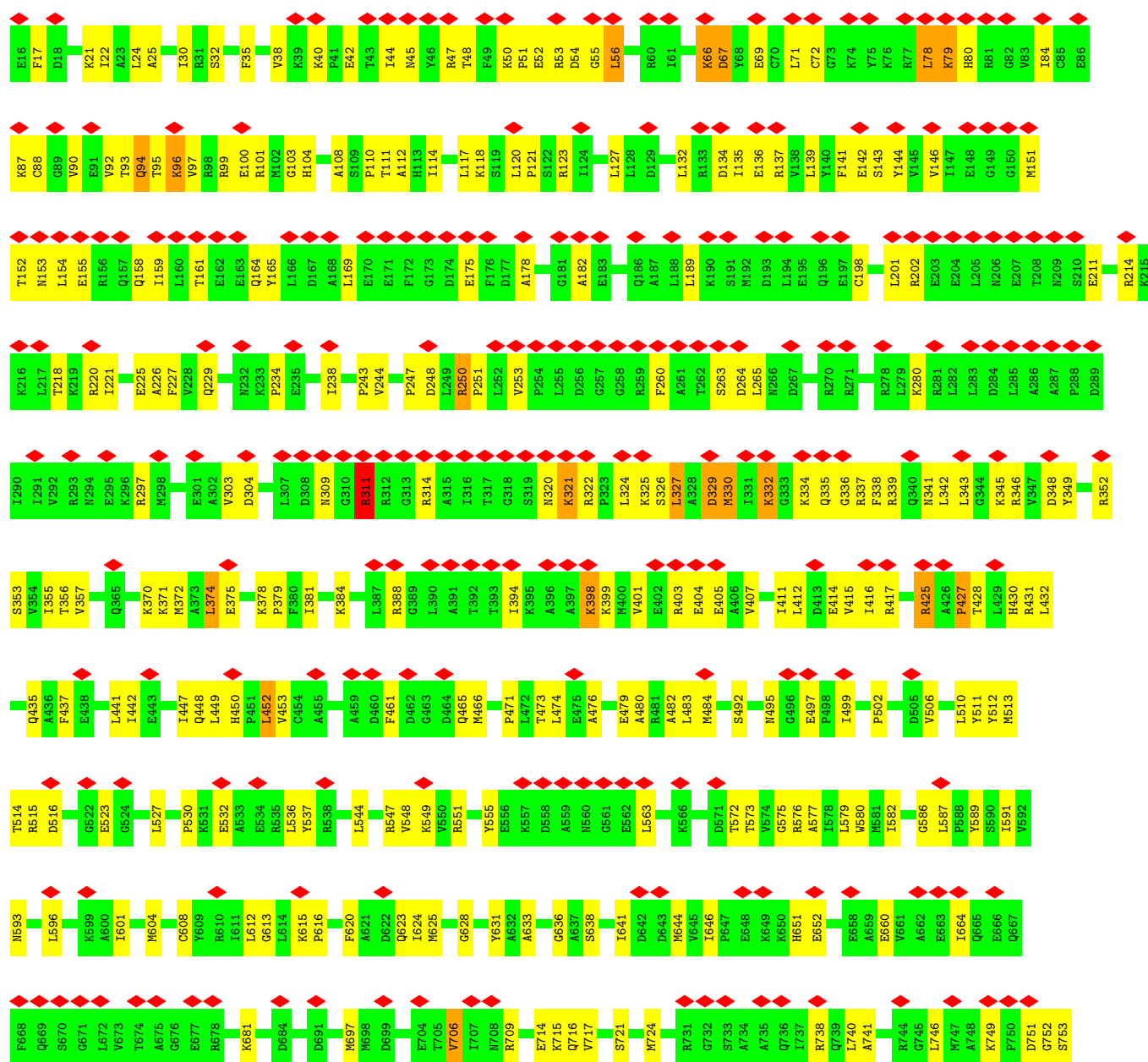
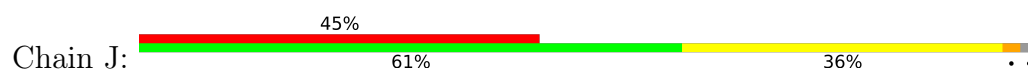
- Molecule 3: DNA-directed RNA polymerase subunit alpha







• Molecule 7: DNA-directed RNA polymerase subunit beta'



R1372	R1373	M1295	G1296	K1297	V1298	G1299	A1300	T1301	Y1302	D1305	L1306	K1311	L1314	A1315	T1316	E1317	A1322	F1325	Q1326	E1327	R1330	F1334	V1337	A1338	G1339	K1340	R1341	D1342	E1343	L1344	R1345	G1346	L1347	K1348	E1349	F1350	V1351	I1352	V1353	G1354	R1355	L1356	I1357	Y1363	A1364	Y1365	H1366	Q1367	D1368	R1369	M1370	R1371									
		R1222	L1223	R1224	G1225	V1226	H1227	A1228	V1229	T1230	R1231	E1236	V1237	Q1238	D1239	V1240	Y1241	R1242	L1243	Q1244	G1245	D1250	I1253	T1256	V1257	R1258	Q1259	R1262	K1263	I1266	V1267	H1268	A1269	G1270	S1271	S1272	D1273	F1274	L1275	E1276	G1277	E1278	Q1279	V1280	E1281	Y1282	S1283	R1284	V1285	K1286	H1289	E1293	A1294								
		G1161	I1162	V1163	S1164	F1165	G1166	K1167	E1168	T1169	K1170	G1171	K1172	R1173	R1174	L1175	T1178	P1179	V1180	D1181	G1182	S1183	D1184	P1185	V1186	E1187	F1188	M1189	I1190	P1191	K1192	V1193	R1194	Q1195	L1196	N1197	V1198	F1199	E1200	G1201	E1202	R1203	V1204	E1205	R1206	G1207	D1208	V1209	I1210	S1211	D1212	G1213	P1214	E1215	A1216	P1217	H1218	D1219	I1220	L1221	
		Q1098	Y1099	F1100	L1101	P1102	G1103	K1104	A1105	I1106	V1107	Q1108	L1109	E1110	D1111	G1112	V1113	Q1114	I1115	S1116	S1117	G1118	D1119	T1120	L1121	A1122	R1123	I1124	P1125	GLU	SER	GLY	GLY	THR	LYS	ASP	T1134	T1135	G1136	G1137	L1138	P1139	D1143	E1146	A1147	R1148	R1149	P1150	K1151	E1152	P1153	A1154	T1155	L1156	A1157	E1158	I1159	S1160			
		T1038	D1039	M1040	I1041	D1042	G1043	Q1044	T1045	I1046	T1047	R1048	Q1049	T1050	D1051	E1052	L1053	T1054	G1055	L1056	S1057	S1058	L1059	V1060	V1061	L1062	D1063	S1064	A1065	E1066	R1067	T1068	A1069	G1070	V1071	K1072	D1073	L1074	R1075	P1076	A1077	L1078	K1079	I1080	V1081	D1082	A1083	Q1084	G1085	N1086	D1087	V1088	L1089	T1090	P1091	G1092	T1093	D1094	M1095	P1096	A1097
		R978	N979	T980	E981	L982	K983	L984	I985	D986	E987	F988	G989	R990	T991	K992	E993	S994	Y995	K996	V997	P998	Y999	G1000	A1001	V1002	L1003	A1004	K1005	G1006	D1007	G1008	E1009	Q1010	V1011	A1012	G1013	G1014	E1015	T1016	V1017	A1018	N1019	V1020	D1021	P1022	H1023	T1024	M1025	P1026	V1027	I1028	T1029	E1030	V1031	S1032	G1033	F1034	V1035	R1036	F1037
		N910	K911	G912	E913	I918	I923	G924	E925	Q929	L930	T931	N932	R933	THR	PHE	HIS	ILE	GLY	GLY	ALA	ALA	SER	ARG	ALA	ALA	GLU	S948	S949	I950	Q951	V952	K953	N954	K955	G956	S957	I958	K959	L960	S961	N962	V963	K964	S965	V966	V967	N968	S969	T970	G971	K972	L973	V974	T976	S977					
		G829	D830	V831	K832	E833	P834	L835	R836	D837	R838	V839	A845	E846	D847	V848	L849	K850	P851	G852	T853	A854	D855	I856	L857	V858	H865	E866	Q867	D870	L871	L872	E873	E874	V877	D878	A879	R883	C888	D889	T890	S891	F892	C895	C898	R901	D902	I826	E827	G828											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51824	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 ($e^-/\text{\AA}^2$)	62.00	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.135	Depositor
Minimum map value	-0.541	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	300.0, 300.0, 300.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PRF

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	0.22	0/436	0.39	0/670
2	B	0.19	0/704	0.38	0/1084
3	G	0.16	0/1728	0.32	0/2341
3	H	0.95	0/1712	1.31	1/2320 (0.0%)
4	K	0.86	0/629	1.28	0/847
5	R	1.80	21/1116 (1.9%)	1.51	19/1736 (1.1%)
6	I	0.37	0/10547	0.59	6/14232 (0.0%)
7	J	0.42	0/10560	0.64	3/14257 (0.0%)
All	All	0.57	21/27432 (0.1%)	0.74	29/37487 (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
5	R	0	13

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	24	U	O3'-P	-7.26	1.50	1.61
5	R	27	A	P-O5'	-7.13	1.49	1.59
5	R	3	A	C5'-C4'	6.94	1.61	1.51
5	R	14	C	C5'-C4'	6.79	1.61	1.51
5	R	20	C	C3'-C2'	6.69	1.62	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	3	A	P-O5'-C5'	9.04	134.47	120.90
5	R	17	C	P-O5'-C5'	7.03	131.45	120.90
5	R	32	A	P-O5'-C5'	6.25	130.28	120.90
5	R	19	C	C5'-C4'-O4'	6.17	119.05	109.80
5	R	11	U	C1'-O4'-C4'	-6.07	103.83	109.90

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	R	1	G	Sidechain
5	R	10	C	Sidechain
5	R	4	G	Sidechain
5	R	7	G	Sidechain
5	R	9	U	Sidechain

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	A	388	0	216	11	0
2	B	631	0	352	13	0
3	G	1708	0	1752	53	0
3	H	1693	0	1727	66	0
4	K	627	0	634	11	0
5	R	997	0	511	10	0
6	I	10381	0	10391	341	0
7	J	10403	0	10636	385	0
8	R	13	0	9	0	0
9	J	1	0	0	0	0
All	All	26842	0	26228	820	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 16.

The worst 5 of 820 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)
3:H:16:ILE:CG2	3:H:26:VAL:HG13	1.63	1.25
7:J:1048:ARG:HG2	7:J:1059:LEU:CD2	1.68	1.21
7:J:1048:ARG:CG	7:J:1059:LEU:CD2	2.19	1.19
7:J:118:LYS:CE	7:J:136:GLU:OE2	1.90	1.19
6:I:1294:LYS:HG2	7:J:348:ASP:OD1	1.44	1.15

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	
3	G	217/235 (92%)	212 (98%)	5 (2%)	0	100	100
3	H	215/235 (92%)	204 (95%)	9 (4%)	2 (1%)	14	45
4	K	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
6	I	1312/1340 (98%)	1271 (97%)	40 (3%)	1 (0%)	48	79
7	J	1331/1358 (98%)	1293 (97%)	37 (3%)	1 (0%)	48	79
All	All	3152/3247 (97%)	3055 (97%)	93 (3%)	4 (0%)	49	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	30	PRO
3	H	90	VAL
6	I	58	PRO
7	J	427	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	189/202 (94%)	189 (100%)	0	100	100
3	H	188/202 (93%)	96 (51%)	92 (49%)	0	0
4	K	67/67 (100%)	39 (58%)	28 (42%)	0	0
6	I	1135/1155 (98%)	1080 (95%)	55 (5%)	23	47
7	J	1122/1134 (99%)	1060 (94%)	62 (6%)	19	45
All	All	2701/2760 (98%)	2464 (91%)	237 (9%)	11	33

5 of 237 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	K	68	GLU
7	J	407	VAL
6	I	978	VAL
7	J	404	GLU
7	J	1046	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
7	J	419	HIS
7	J	1086	ASN
7	J	424	ASN
7	J	465	GLN
7	J	1195	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	R	47/47 (100%)	27 (57%)	2 (4%)

5 of 27 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	R	2	C
5	R	3	A
5	R	8	U

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Mol	Chain	Res	Type
5	R	9	U
5	R	10	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	R	1	G
5	R	15	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	PRF	R	101	-	14,14,14	0.66	0	14,20,20	1.54	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PRF	R	101	-	-	0/0/2/2	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
8	R	101	PRF	C7-C5-C4	-5.20	106.71	112.68

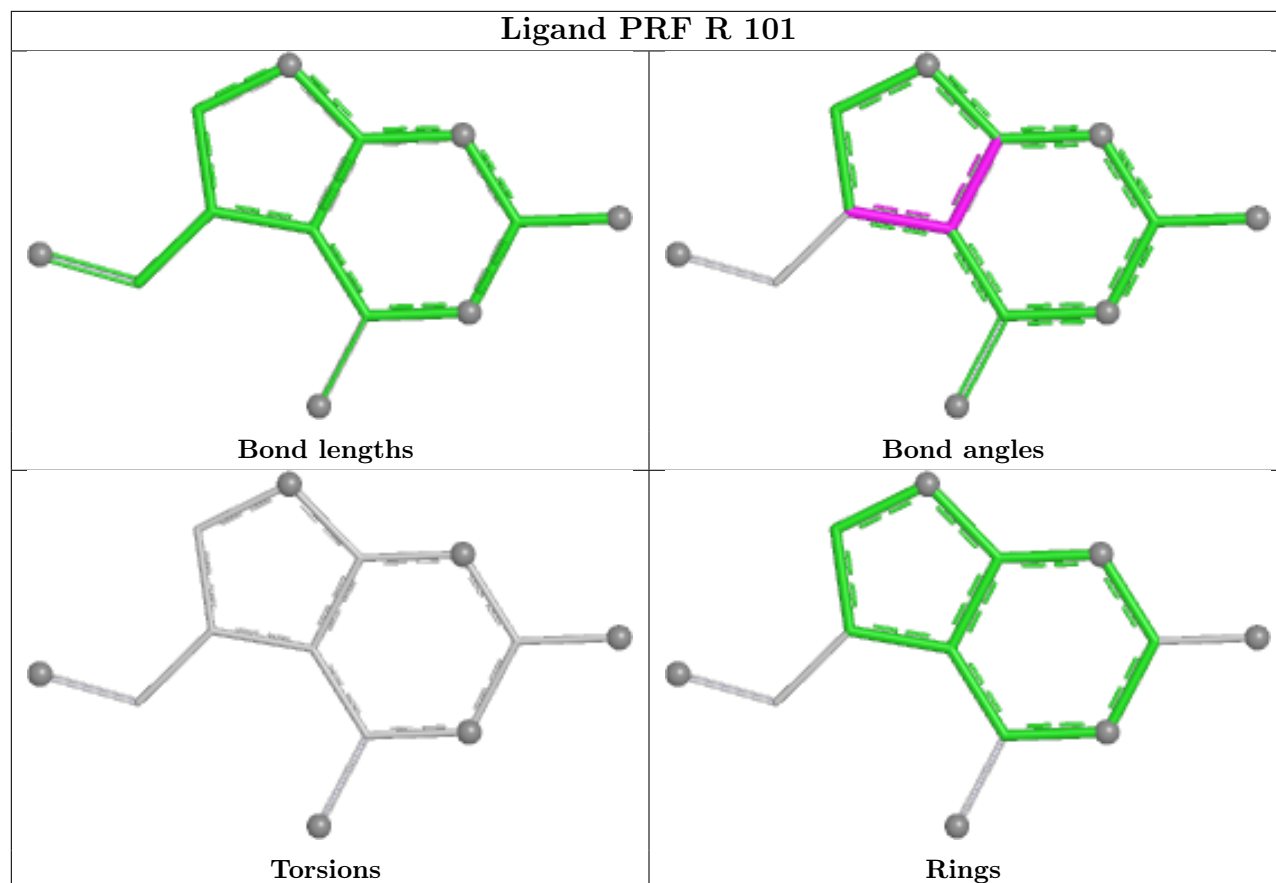
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

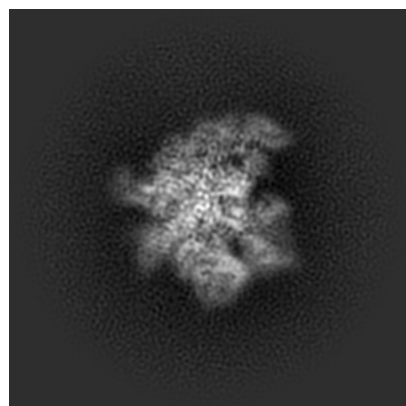
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29732. These allow visual inspection of the internal detail of the map and identification of artifacts.

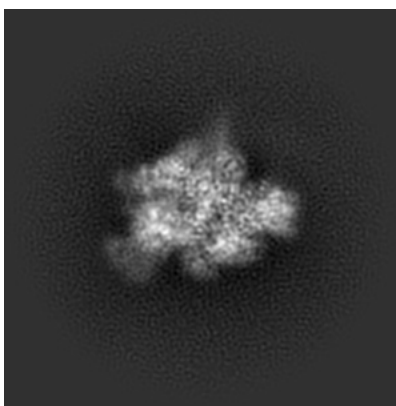
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

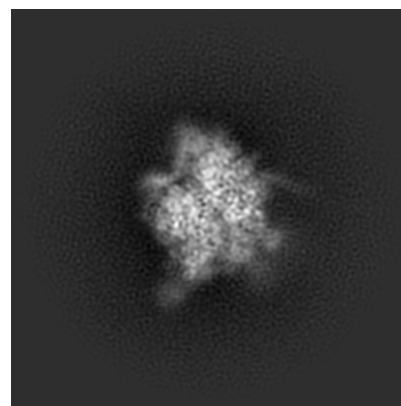
6.1.1 Primary map



X

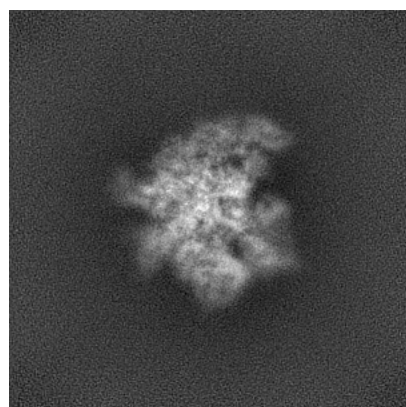


Y

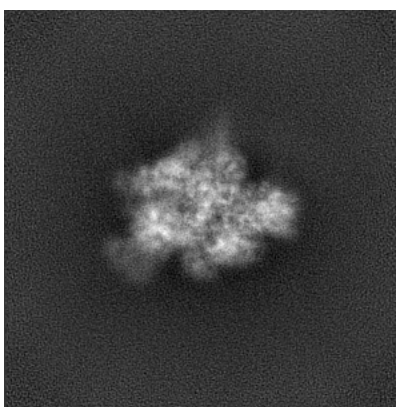


Z

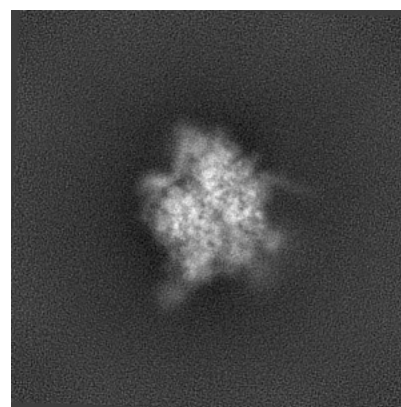
6.1.2 Raw map



X



Y

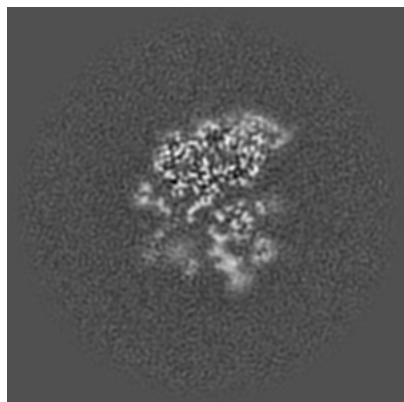


Z

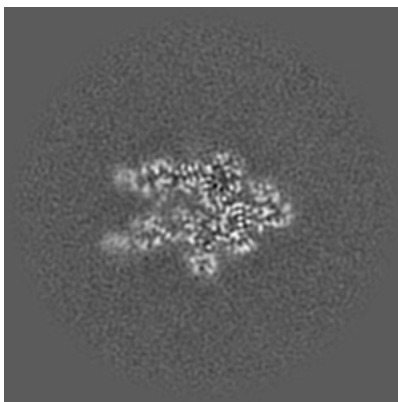
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

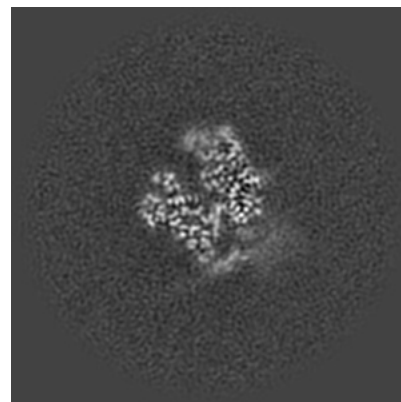
6.2.1 Primary map



X Index: 150

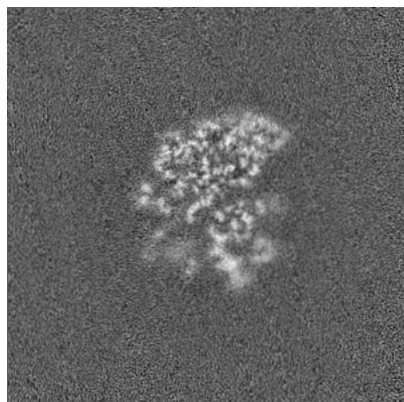


Y Index: 150

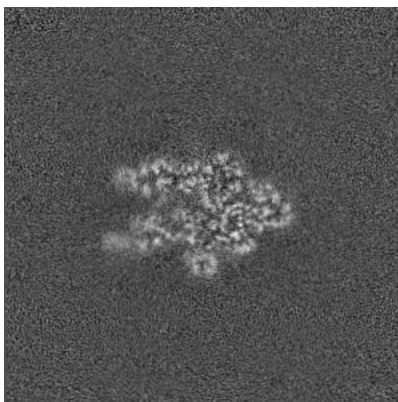


Z Index: 150

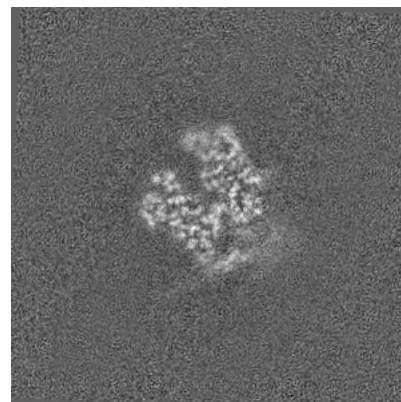
6.2.2 Raw map



X Index: 150



Y Index: 150

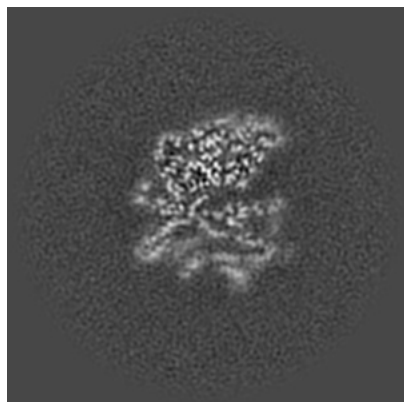


Z Index: 150

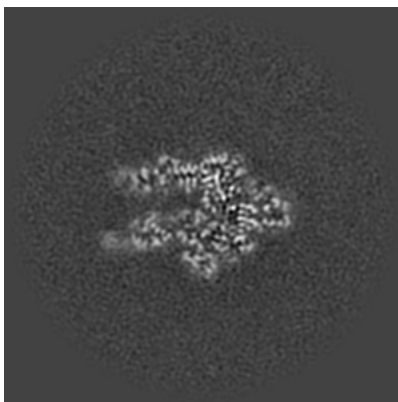
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

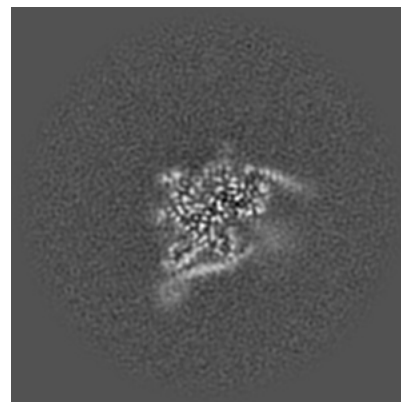
6.3.1 Primary map



X Index: 146

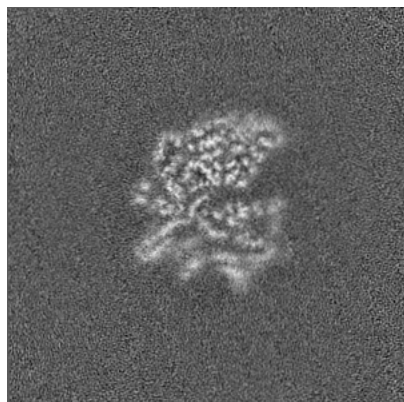


Y Index: 148

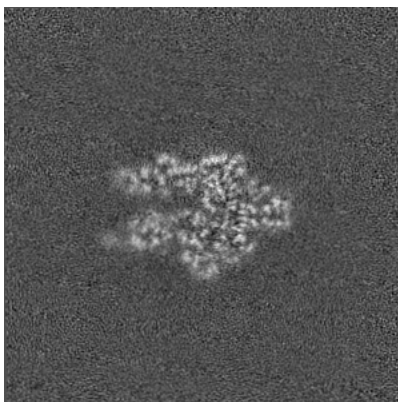


Z Index: 165

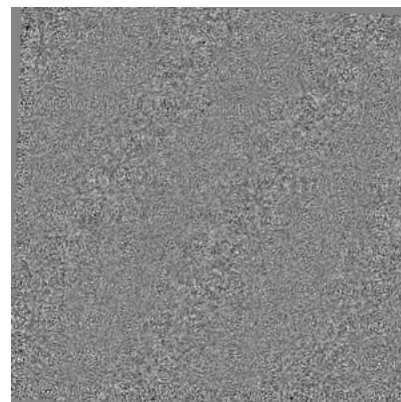
6.3.2 Raw map



X Index: 146



Y Index: 147

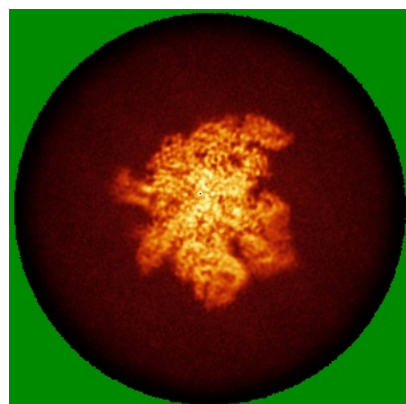


Z Index: 297

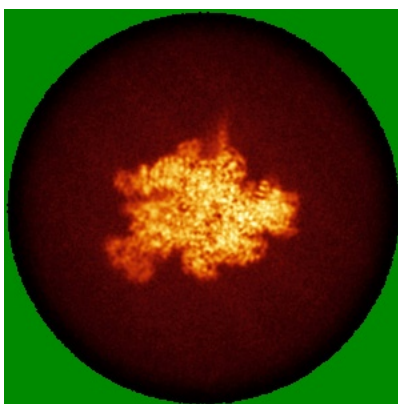
The images above show the largest variance slices of the map in three orthogonal directions.

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

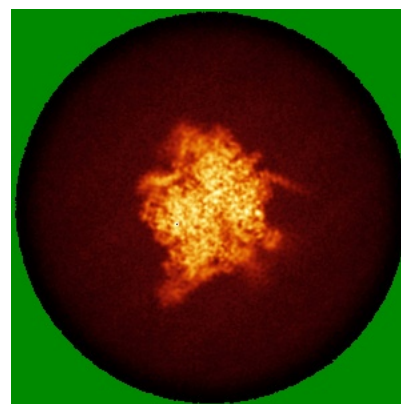
6.4.1 Primary map



X

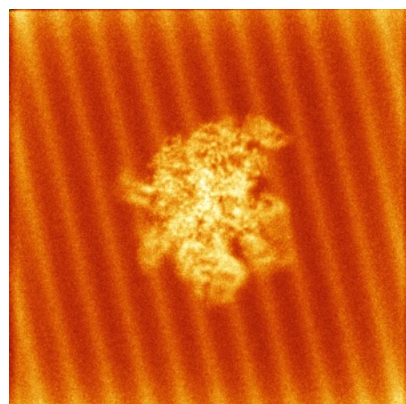


Y

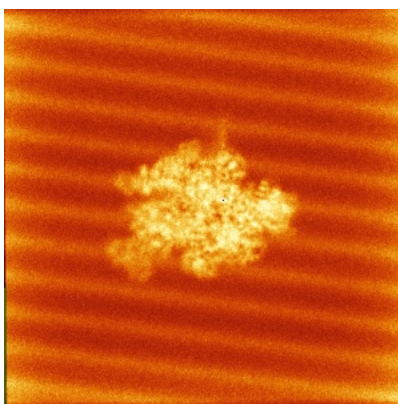


Z

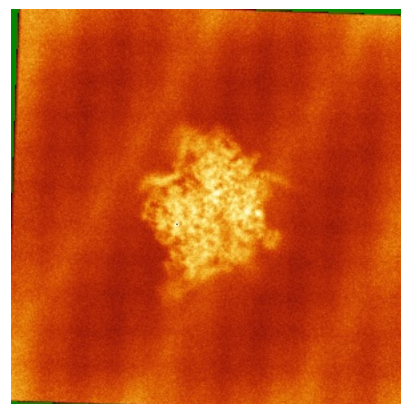
6.4.2 Raw map



X



Y

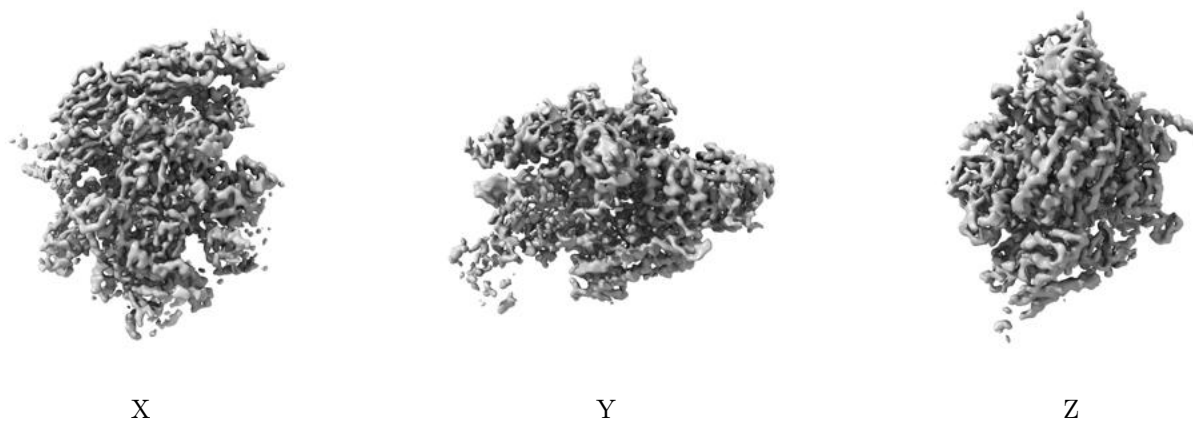


Z

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

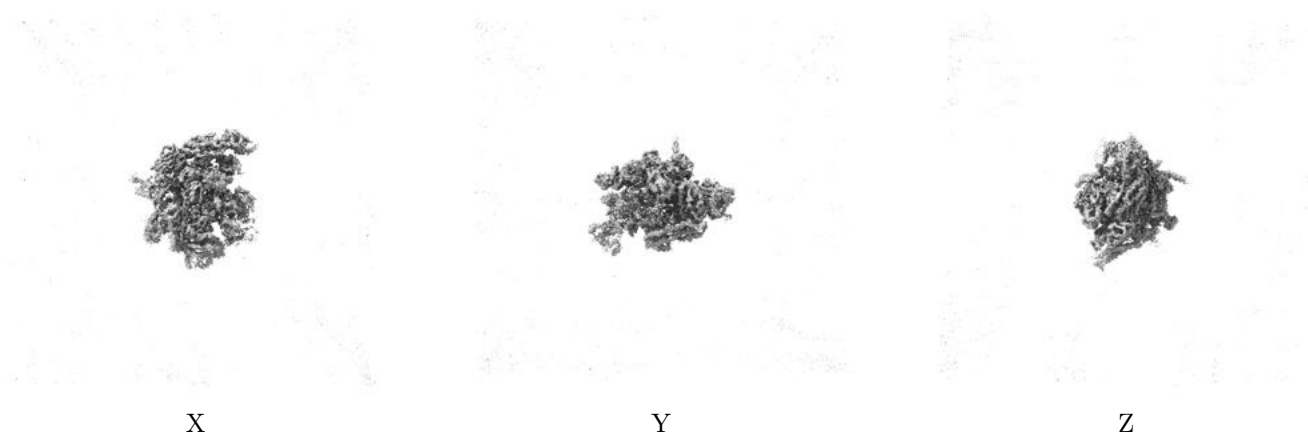
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

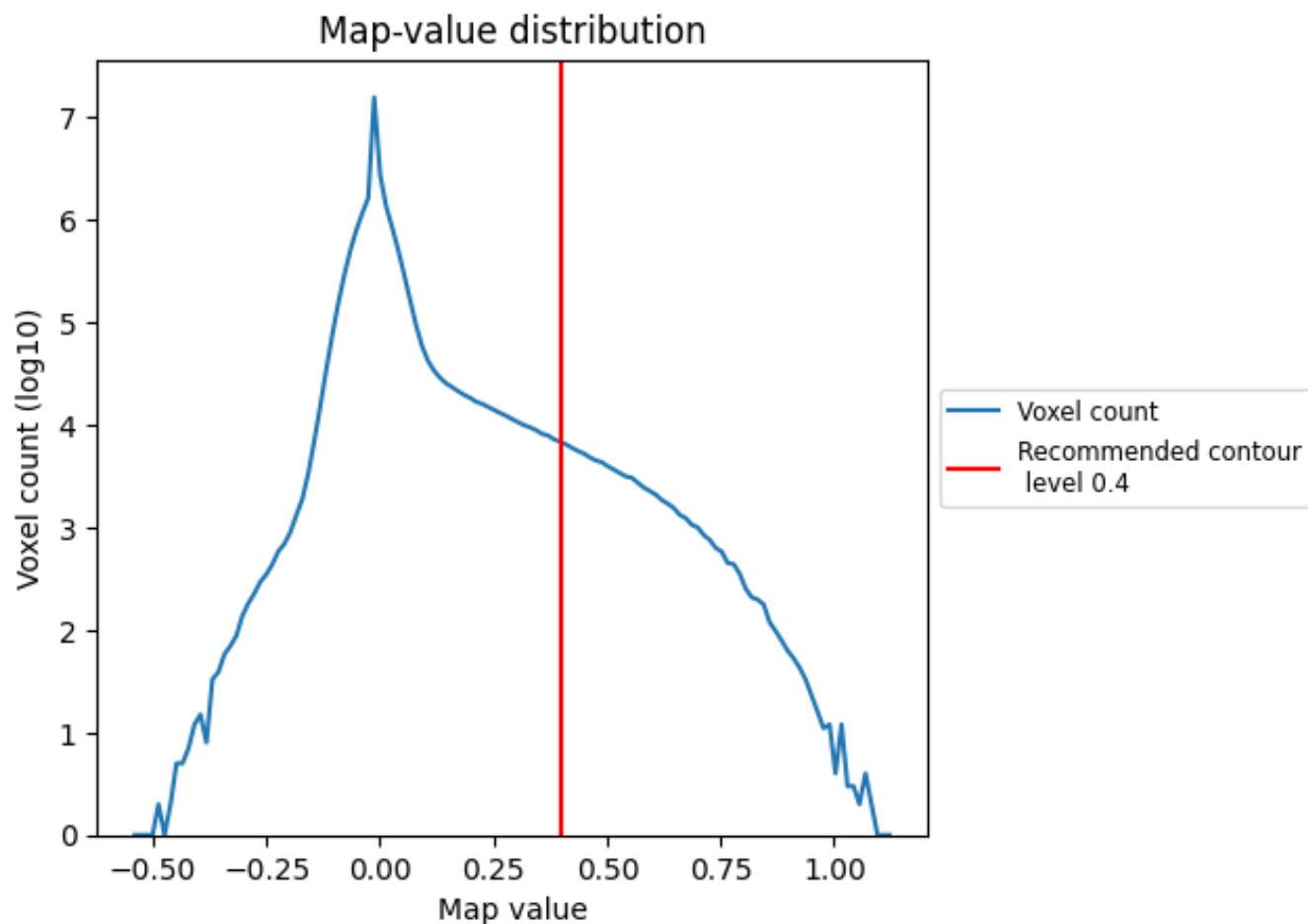
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

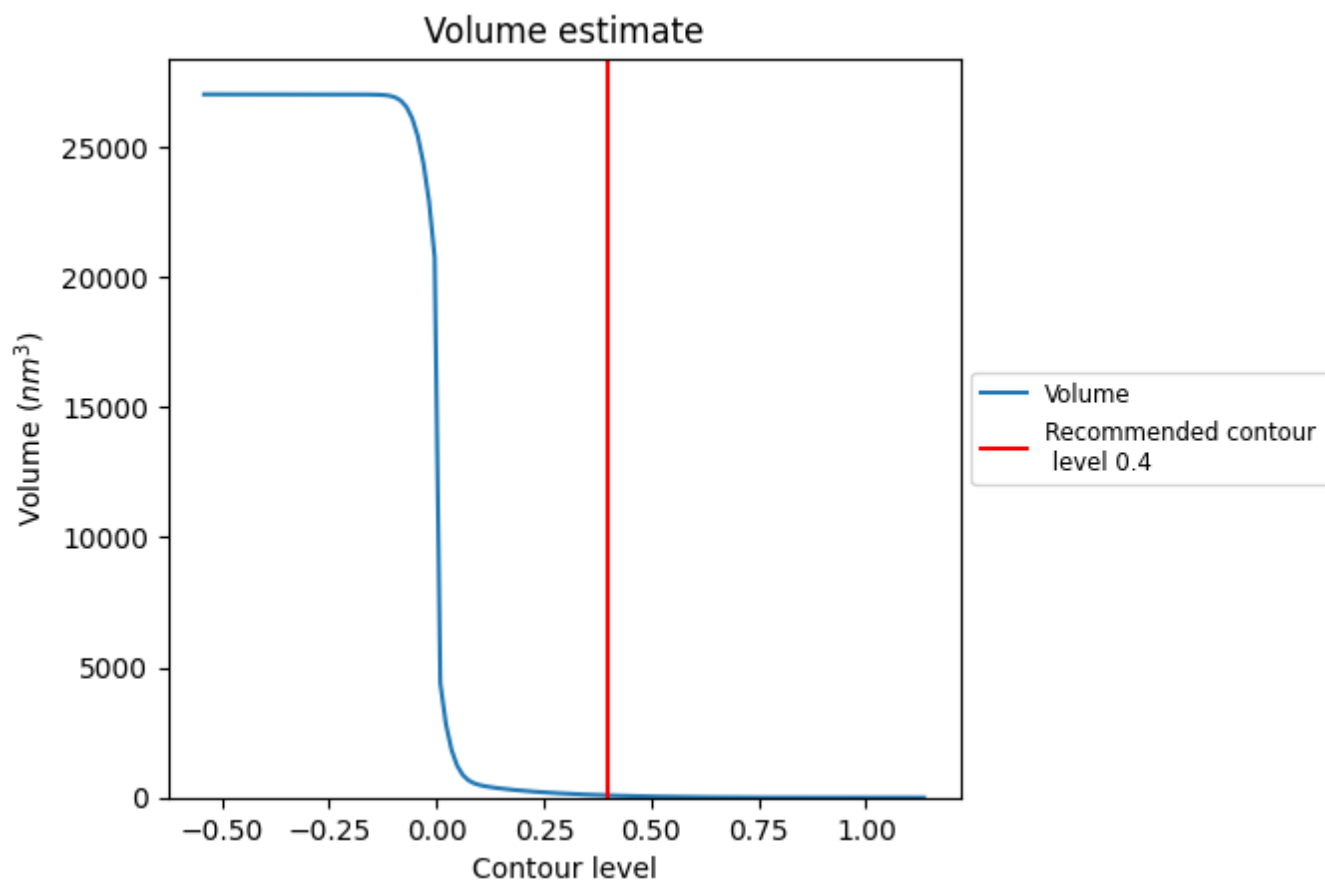
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

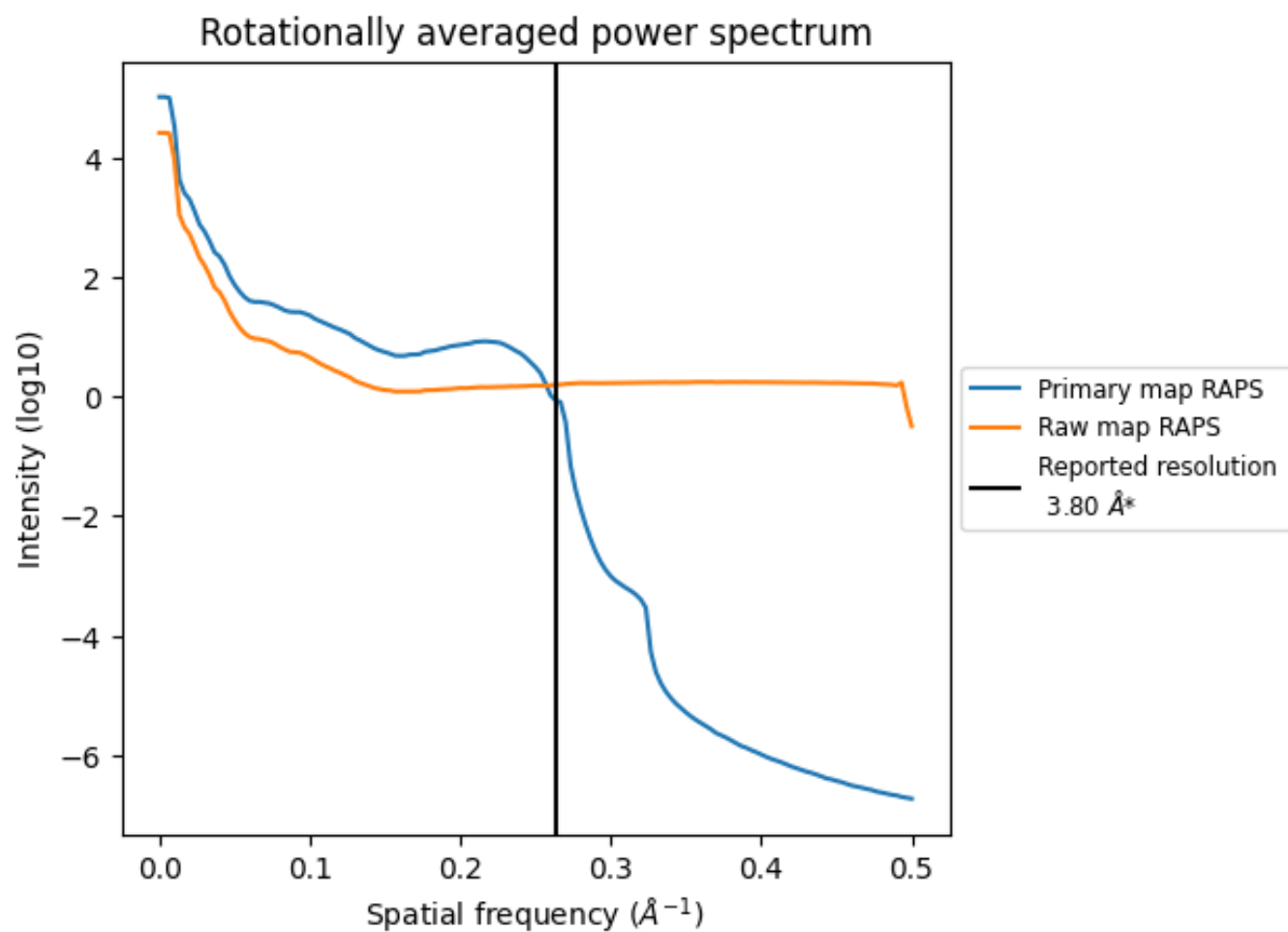
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm³; this corresponds to an approximate mass of 76 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 ⓘ

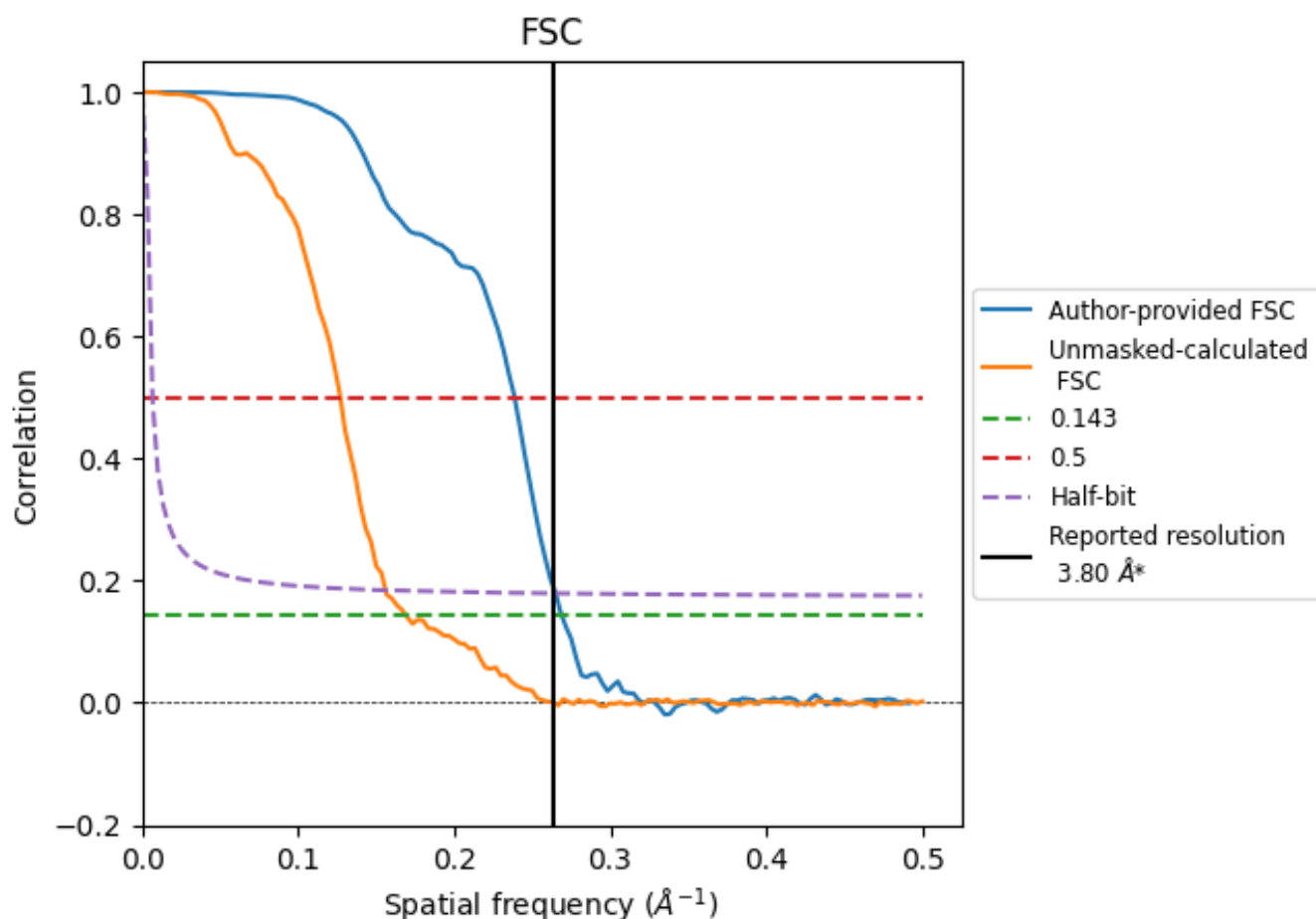


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

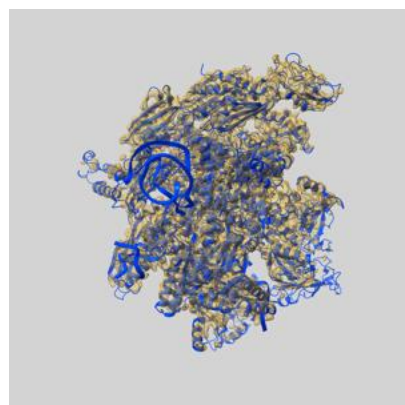
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.72	4.19	3.77
Unmasked-calculated*	5.91	7.87	6.41

*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 5.91 differs from the reported value 3.8 by more than 10 %

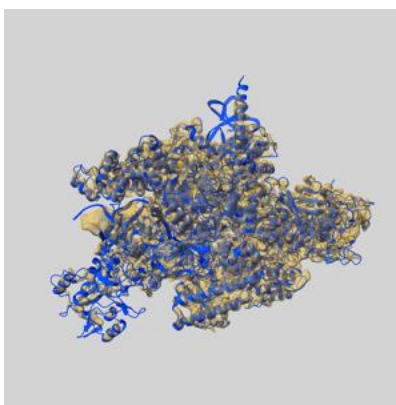
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29732 and PDB model 8G4W. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

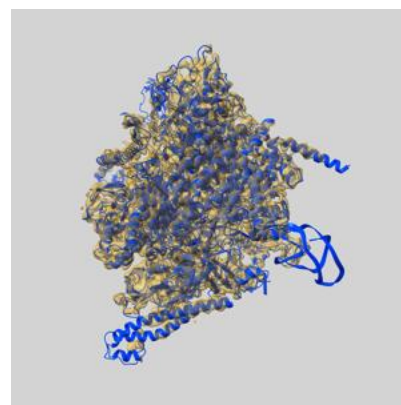
9.1 Map-model overlay [i](#)



X



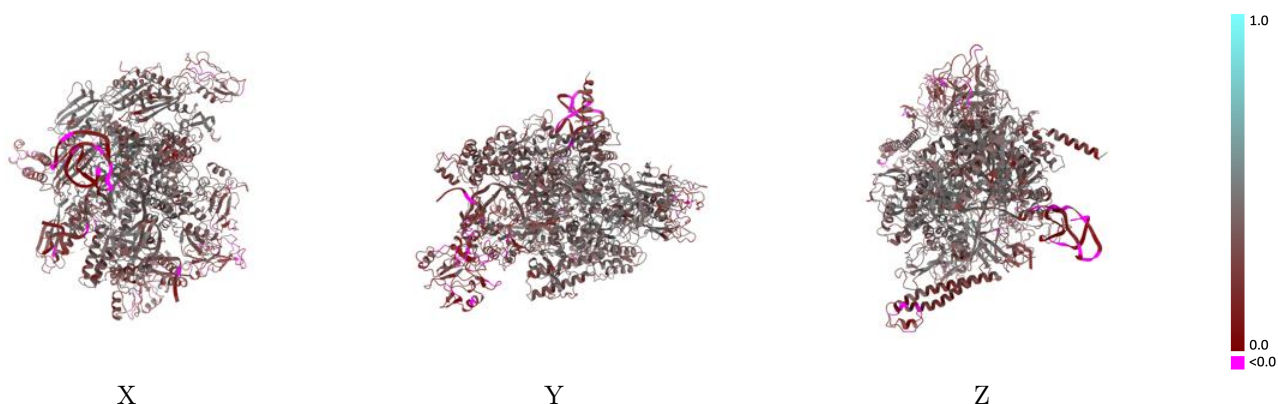
Y



Z

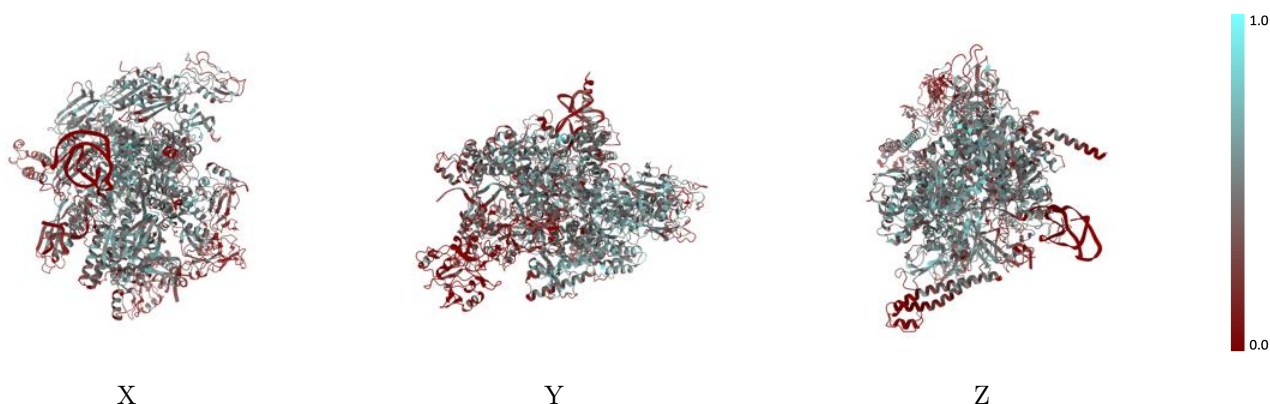
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



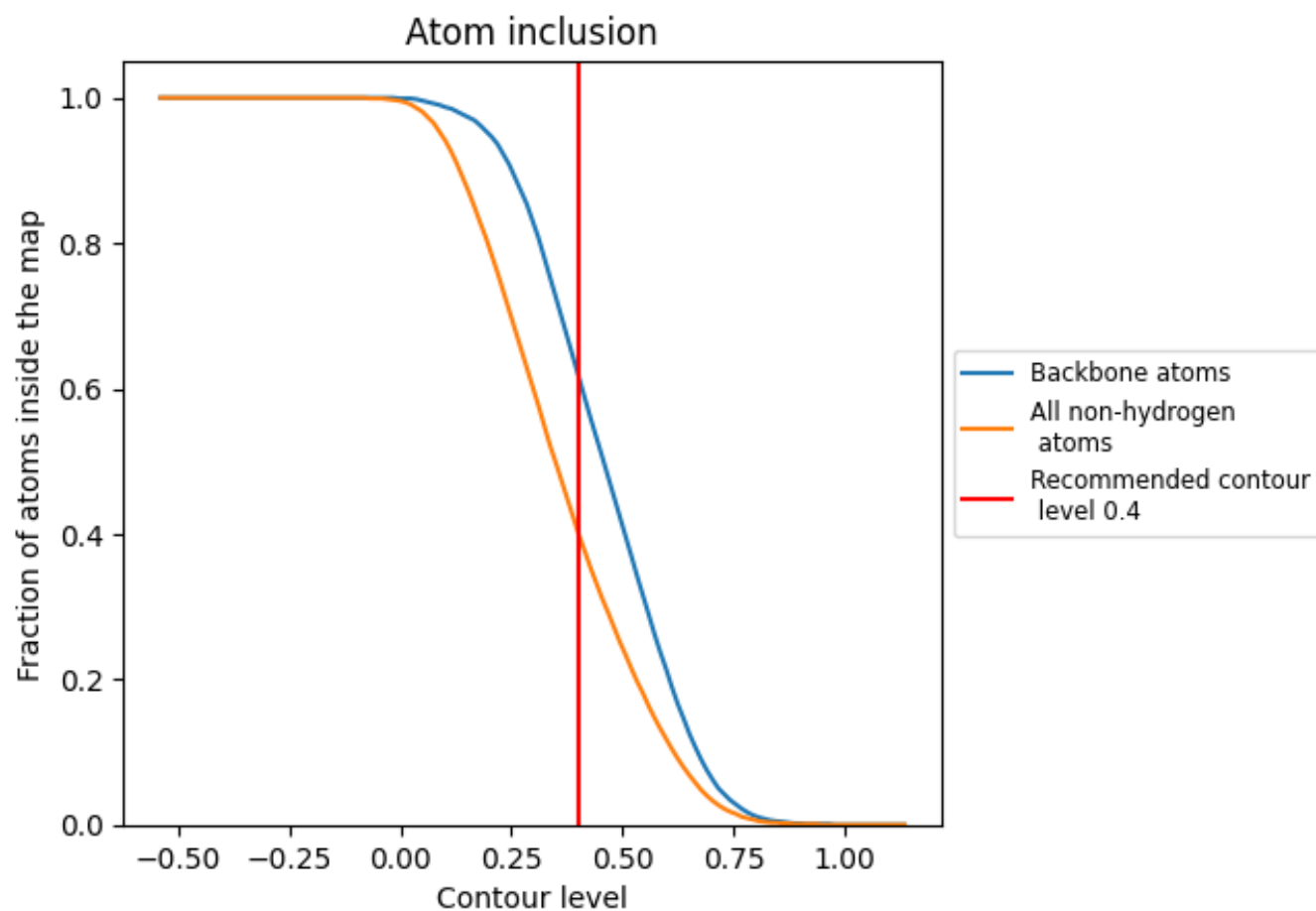
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 40% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4020	0.3380
A	0.4200	0.2700
B	0.4470	0.2870
G	0.5080	0.4040
H	0.3990	0.3080
I	0.4160	0.3580
J	0.3970	0.3410
K	0.3630	0.3290
R	0.1210	0.1030

1.0

0.0

<0.0