



Full wwPDB EM Validation Report ⓘ

Dec 7, 2022 – 12:41 PM JST

PDB ID : 7DZX
EMDB ID : EMD-30918
Title : Spike protein from SARS-CoV2 with Fab fragment of enhancing antibody 8D2
Authors : Liu, Y.; Soh, W.T.; Li, S.; Kishikawa, J.; Hirose, M.; Kato, T.; Standley, D.;
Okada, M.; Arase, H.
Deposited on : 2021-01-26
Resolution : 3.53 Å (reported)
Based on initial models : 7K8W, 5X8M

This is a Full wwPDB EM Validation 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.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) : 2.31.3

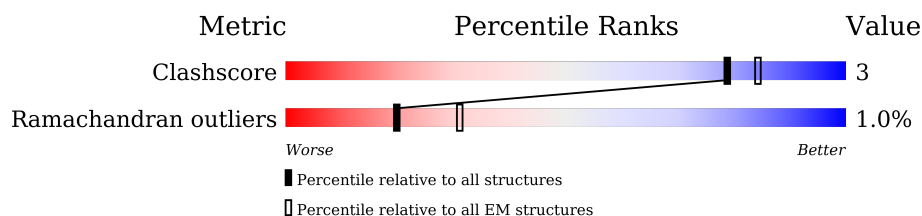
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.53 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

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	1249	<div> <div>13%</div> <div>88%</div> <div>10%</div> </div>
1	B	1249	<div> <div>15%</div> <div>88%</div> <div>10%</div> </div>
1	C	1249	<div> <div>8%</div> <div>88%</div> <div>10%</div> </div>
2	H	227	<div> <div>40%</div> <div>98%</div> <div>.</div> </div>
3	L	213	<div> <div>54%</div> <div>99%</div> <div>.</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15212 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	1121	Total	C	N	O	0	0
			4484	2242	1121	1121		
1	B	1121	Total	C	N	O	0	0
			4484	2242	1121	1121		
1	C	1121	Total	C	N	O	0	0
			4484	2242	1121	1121		

There are 402 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	GLN	-	expression tag	UNP P0DTC2
A	15	CYS	-	expression tag	UNP P0DTC2
A	16	VAL	-	expression tag	UNP P0DTC2
A	17	ASN	-	expression tag	UNP P0DTC2
A	18	LEU	-	expression tag	UNP P0DTC2
A	19	THR	-	expression tag	UNP P0DTC2
A	20	THR	-	expression tag	UNP P0DTC2
A	21	ARG	-	expression tag	UNP P0DTC2
A	22	THR	-	expression tag	UNP P0DTC2
A	23	GLN	-	expression tag	UNP P0DTC2
A	24	LEU	-	expression tag	UNP P0DTC2
A	25	PRO	-	expression tag	UNP P0DTC2
A	26	PRO	-	expression tag	UNP P0DTC2
A	614	GLY	ASP	engineered mutation	UNP P0DTC2
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	GLY	ARG	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1148	PHE	-	expression tag	UNP P0DTC2
A	1149	LYS	-	expression tag	UNP P0DTC2
A	1150	GLU	-	expression tag	UNP P0DTC2
A	1151	GLU	-	expression tag	UNP P0DTC2
A	1152	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1153	ASP	-	expression tag	UNP P0DTC2
A	1154	LYS	-	expression tag	UNP P0DTC2
A	1155	TYR	-	expression tag	UNP P0DTC2
A	1156	PHE	-	expression tag	UNP P0DTC2
A	1157	LYS	-	expression tag	UNP P0DTC2
A	1158	ASN	-	expression tag	UNP P0DTC2
A	1159	HIS	-	expression tag	UNP P0DTC2
A	1160	THR	-	expression tag	UNP P0DTC2
A	1161	SER	-	expression tag	UNP P0DTC2
A	1162	PRO	-	expression tag	UNP P0DTC2
A	1163	ASP	-	expression tag	UNP P0DTC2
A	1164	VAL	-	expression tag	UNP P0DTC2
A	1165	ASP	-	expression tag	UNP P0DTC2
A	1166	LEU	-	expression tag	UNP P0DTC2
A	1167	GLY	-	expression tag	UNP P0DTC2
A	1168	ASP	-	expression tag	UNP P0DTC2
A	1169	ILE	-	expression tag	UNP P0DTC2
A	1170	SER	-	expression tag	UNP P0DTC2
A	1171	GLY	-	expression tag	UNP P0DTC2
A	1172	ILE	-	expression tag	UNP P0DTC2
A	1173	ASN	-	expression tag	UNP P0DTC2
A	1174	ALA	-	expression tag	UNP P0DTC2
A	1175	SER	-	expression tag	UNP P0DTC2
A	1176	VAL	-	expression tag	UNP P0DTC2
A	1177	VAL	-	expression tag	UNP P0DTC2
A	1178	ASN	-	expression tag	UNP P0DTC2
A	1179	ILE	-	expression tag	UNP P0DTC2
A	1180	GLN	-	expression tag	UNP P0DTC2
A	1181	LYS	-	expression tag	UNP P0DTC2
A	1182	GLU	-	expression tag	UNP P0DTC2
A	1183	ILE	-	expression tag	UNP P0DTC2
A	1184	ASP	-	expression tag	UNP P0DTC2
A	1185	ARG	-	expression tag	UNP P0DTC2
A	1186	LEU	-	expression tag	UNP P0DTC2
A	1187	ASN	-	expression tag	UNP P0DTC2
A	1188	GLU	-	expression tag	UNP P0DTC2
A	1189	VAL	-	expression tag	UNP P0DTC2
A	1190	ALA	-	expression tag	UNP P0DTC2
A	1191	LYS	-	expression tag	UNP P0DTC2
A	1192	ASN	-	expression tag	UNP P0DTC2
A	1193	LEU	-	expression tag	UNP P0DTC2
A	1194	ASN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1195	GLU	-	expression tag	UNP P0DTC2
A	1196	SER	-	expression tag	UNP P0DTC2
A	1197	LEU	-	expression tag	UNP P0DTC2
A	1198	ILE	-	expression tag	UNP P0DTC2
A	1199	ASP	-	expression tag	UNP P0DTC2
A	1200	LEU	-	expression tag	UNP P0DTC2
A	1201	GLN	-	expression tag	UNP P0DTC2
A	1202	GLU	-	expression tag	UNP P0DTC2
A	1203	LEU	-	expression tag	UNP P0DTC2
A	1204	GLY	-	expression tag	UNP P0DTC2
A	1205	LYS	-	expression tag	UNP P0DTC2
A	1206	TYR	-	expression tag	UNP P0DTC2
A	1207	GLU	-	expression tag	UNP P0DTC2
A	1208	GLN	-	expression tag	UNP P0DTC2
A	1209	TYR	-	expression tag	UNP P0DTC2
A	1210	ILE	-	expression tag	UNP P0DTC2
A	1211	LYS	-	expression tag	UNP P0DTC2
A	1212	GLY	-	expression tag	UNP P0DTC2
A	1213	SER	-	expression tag	UNP P0DTC2
A	1214	GLY	-	expression tag	UNP P0DTC2
A	1215	ARG	-	expression tag	UNP P0DTC2
A	1216	GLU	-	expression tag	UNP P0DTC2
A	1217	ASN	-	expression tag	UNP P0DTC2
A	1218	LEU	-	expression tag	UNP P0DTC2
A	1219	TYR	-	expression tag	UNP P0DTC2
A	1220	PHE	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	GLY	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	GLY	-	expression tag	UNP P0DTC2
A	1225	GLY	-	expression tag	UNP P0DTC2
A	1226	SER	-	expression tag	UNP P0DTC2
A	1227	GLY	-	expression tag	UNP P0DTC2
A	1228	TYR	-	expression tag	UNP P0DTC2
A	1229	ILE	-	expression tag	UNP P0DTC2
A	1230	PRO	-	expression tag	UNP P0DTC2
A	1231	GLU	-	expression tag	UNP P0DTC2
A	1232	ALA	-	expression tag	UNP P0DTC2
A	1233	PRO	-	expression tag	UNP P0DTC2
A	1234	ARG	-	expression tag	UNP P0DTC2
A	1235	ASP	-	expression tag	UNP P0DTC2
A	1236	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1237	GLN	-	expression tag	UNP P0DTC2
A	1238	ALA	-	expression tag	UNP P0DTC2
A	1239	TYR	-	expression tag	UNP P0DTC2
A	1240	VAL	-	expression tag	UNP P0DTC2
A	1241	ARG	-	expression tag	UNP P0DTC2
A	1242	LYS	-	expression tag	UNP P0DTC2
A	1243	ASP	-	expression tag	UNP P0DTC2
A	1244	GLY	-	expression tag	UNP P0DTC2
A	1245	GLU	-	expression tag	UNP P0DTC2
A	1246	TRP	-	expression tag	UNP P0DTC2
A	1247	VAL	-	expression tag	UNP P0DTC2
A	1248	LEU	-	expression tag	UNP P0DTC2
A	1249	LEU	-	expression tag	UNP P0DTC2
A	1250	SER	-	expression tag	UNP P0DTC2
A	1251	THR	-	expression tag	UNP P0DTC2
A	1252	PHE	-	expression tag	UNP P0DTC2
A	1253	LEU	-	expression tag	UNP P0DTC2
A	1254	GLY	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	HIS	-	expression tag	UNP P0DTC2
A	1259	HIS	-	expression tag	UNP P0DTC2
A	1260	HIS	-	expression tag	UNP P0DTC2
A	1261	HIS	-	expression tag	UNP P0DTC2
A	1262	HIS	-	expression tag	UNP P0DTC2
B	14	GLN	-	expression tag	UNP P0DTC2
B	15	CYS	-	expression tag	UNP P0DTC2
B	16	VAL	-	expression tag	UNP P0DTC2
B	17	ASN	-	expression tag	UNP P0DTC2
B	18	LEU	-	expression tag	UNP P0DTC2
B	19	THR	-	expression tag	UNP P0DTC2
B	20	THR	-	expression tag	UNP P0DTC2
B	21	ARG	-	expression tag	UNP P0DTC2
B	22	THR	-	expression tag	UNP P0DTC2
B	23	GLN	-	expression tag	UNP P0DTC2
B	24	LEU	-	expression tag	UNP P0DTC2
B	25	PRO	-	expression tag	UNP P0DTC2
B	26	PRO	-	expression tag	UNP P0DTC2
B	614	GLY	ASP	engineered mutation	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	685	GLY	ARG	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1148	PHE	-	expression tag	UNP P0DTC2
B	1149	LYS	-	expression tag	UNP P0DTC2
B	1150	GLU	-	expression tag	UNP P0DTC2
B	1151	GLU	-	expression tag	UNP P0DTC2
B	1152	LEU	-	expression tag	UNP P0DTC2
B	1153	ASP	-	expression tag	UNP P0DTC2
B	1154	LYS	-	expression tag	UNP P0DTC2
B	1155	TYR	-	expression tag	UNP P0DTC2
B	1156	PHE	-	expression tag	UNP P0DTC2
B	1157	LYS	-	expression tag	UNP P0DTC2
B	1158	ASN	-	expression tag	UNP P0DTC2
B	1159	HIS	-	expression tag	UNP P0DTC2
B	1160	THR	-	expression tag	UNP P0DTC2
B	1161	SER	-	expression tag	UNP P0DTC2
B	1162	PRO	-	expression tag	UNP P0DTC2
B	1163	ASP	-	expression tag	UNP P0DTC2
B	1164	VAL	-	expression tag	UNP P0DTC2
B	1165	ASP	-	expression tag	UNP P0DTC2
B	1166	LEU	-	expression tag	UNP P0DTC2
B	1167	GLY	-	expression tag	UNP P0DTC2
B	1168	ASP	-	expression tag	UNP P0DTC2
B	1169	ILE	-	expression tag	UNP P0DTC2
B	1170	SER	-	expression tag	UNP P0DTC2
B	1171	GLY	-	expression tag	UNP P0DTC2
B	1172	ILE	-	expression tag	UNP P0DTC2
B	1173	ASN	-	expression tag	UNP P0DTC2
B	1174	ALA	-	expression tag	UNP P0DTC2
B	1175	SER	-	expression tag	UNP P0DTC2
B	1176	VAL	-	expression tag	UNP P0DTC2
B	1177	VAL	-	expression tag	UNP P0DTC2
B	1178	ASN	-	expression tag	UNP P0DTC2
B	1179	ILE	-	expression tag	UNP P0DTC2
B	1180	GLN	-	expression tag	UNP P0DTC2
B	1181	LYS	-	expression tag	UNP P0DTC2
B	1182	GLU	-	expression tag	UNP P0DTC2
B	1183	ILE	-	expression tag	UNP P0DTC2
B	1184	ASP	-	expression tag	UNP P0DTC2
B	1185	ARG	-	expression tag	UNP P0DTC2
B	1186	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1187	ASN	-	expression tag	UNP P0DTC2
B	1188	GLU	-	expression tag	UNP P0DTC2
B	1189	VAL	-	expression tag	UNP P0DTC2
B	1190	ALA	-	expression tag	UNP P0DTC2
B	1191	LYS	-	expression tag	UNP P0DTC2
B	1192	ASN	-	expression tag	UNP P0DTC2
B	1193	LEU	-	expression tag	UNP P0DTC2
B	1194	ASN	-	expression tag	UNP P0DTC2
B	1195	GLU	-	expression tag	UNP P0DTC2
B	1196	SER	-	expression tag	UNP P0DTC2
B	1197	LEU	-	expression tag	UNP P0DTC2
B	1198	ILE	-	expression tag	UNP P0DTC2
B	1199	ASP	-	expression tag	UNP P0DTC2
B	1200	LEU	-	expression tag	UNP P0DTC2
B	1201	GLN	-	expression tag	UNP P0DTC2
B	1202	GLU	-	expression tag	UNP P0DTC2
B	1203	LEU	-	expression tag	UNP P0DTC2
B	1204	GLY	-	expression tag	UNP P0DTC2
B	1205	LYS	-	expression tag	UNP P0DTC2
B	1206	TYR	-	expression tag	UNP P0DTC2
B	1207	GLU	-	expression tag	UNP P0DTC2
B	1208	GLN	-	expression tag	UNP P0DTC2
B	1209	TYR	-	expression tag	UNP P0DTC2
B	1210	ILE	-	expression tag	UNP P0DTC2
B	1211	LYS	-	expression tag	UNP P0DTC2
B	1212	GLY	-	expression tag	UNP P0DTC2
B	1213	SER	-	expression tag	UNP P0DTC2
B	1214	GLY	-	expression tag	UNP P0DTC2
B	1215	ARG	-	expression tag	UNP P0DTC2
B	1216	GLU	-	expression tag	UNP P0DTC2
B	1217	ASN	-	expression tag	UNP P0DTC2
B	1218	LEU	-	expression tag	UNP P0DTC2
B	1219	TYR	-	expression tag	UNP P0DTC2
B	1220	PHE	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	GLY	-	expression tag	UNP P0DTC2
B	1223	GLY	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	GLY	-	expression tag	UNP P0DTC2
B	1226	SER	-	expression tag	UNP P0DTC2
B	1227	GLY	-	expression tag	UNP P0DTC2
B	1228	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1229	ILE	-	expression tag	UNP P0DTC2
B	1230	PRO	-	expression tag	UNP P0DTC2
B	1231	GLU	-	expression tag	UNP P0DTC2
B	1232	ALA	-	expression tag	UNP P0DTC2
B	1233	PRO	-	expression tag	UNP P0DTC2
B	1234	ARG	-	expression tag	UNP P0DTC2
B	1235	ASP	-	expression tag	UNP P0DTC2
B	1236	GLY	-	expression tag	UNP P0DTC2
B	1237	GLN	-	expression tag	UNP P0DTC2
B	1238	ALA	-	expression tag	UNP P0DTC2
B	1239	TYR	-	expression tag	UNP P0DTC2
B	1240	VAL	-	expression tag	UNP P0DTC2
B	1241	ARG	-	expression tag	UNP P0DTC2
B	1242	LYS	-	expression tag	UNP P0DTC2
B	1243	ASP	-	expression tag	UNP P0DTC2
B	1244	GLY	-	expression tag	UNP P0DTC2
B	1245	GLU	-	expression tag	UNP P0DTC2
B	1246	TRP	-	expression tag	UNP P0DTC2
B	1247	VAL	-	expression tag	UNP P0DTC2
B	1248	LEU	-	expression tag	UNP P0DTC2
B	1249	LEU	-	expression tag	UNP P0DTC2
B	1250	SER	-	expression tag	UNP P0DTC2
B	1251	THR	-	expression tag	UNP P0DTC2
B	1252	PHE	-	expression tag	UNP P0DTC2
B	1253	LEU	-	expression tag	UNP P0DTC2
B	1254	GLY	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	HIS	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
C	14	GLN	-	expression tag	UNP P0DTC2
C	15	CYS	-	expression tag	UNP P0DTC2
C	16	VAL	-	expression tag	UNP P0DTC2
C	17	ASN	-	expression tag	UNP P0DTC2
C	18	LEU	-	expression tag	UNP P0DTC2
C	19	THR	-	expression tag	UNP P0DTC2
C	20	THR	-	expression tag	UNP P0DTC2
C	21	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	22	THR	-	expression tag	UNP P0DTC2
C	23	GLN	-	expression tag	UNP P0DTC2
C	24	LEU	-	expression tag	UNP P0DTC2
C	25	PRO	-	expression tag	UNP P0DTC2
C	26	PRO	-	expression tag	UNP P0DTC2
C	614	GLY	ASP	engineered mutation	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	GLY	ARG	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1148	PHE	-	expression tag	UNP P0DTC2
C	1149	LYS	-	expression tag	UNP P0DTC2
C	1150	GLU	-	expression tag	UNP P0DTC2
C	1151	GLU	-	expression tag	UNP P0DTC2
C	1152	LEU	-	expression tag	UNP P0DTC2
C	1153	ASP	-	expression tag	UNP P0DTC2
C	1154	LYS	-	expression tag	UNP P0DTC2
C	1155	TYR	-	expression tag	UNP P0DTC2
C	1156	PHE	-	expression tag	UNP P0DTC2
C	1157	LYS	-	expression tag	UNP P0DTC2
C	1158	ASN	-	expression tag	UNP P0DTC2
C	1159	HIS	-	expression tag	UNP P0DTC2
C	1160	THR	-	expression tag	UNP P0DTC2
C	1161	SER	-	expression tag	UNP P0DTC2
C	1162	PRO	-	expression tag	UNP P0DTC2
C	1163	ASP	-	expression tag	UNP P0DTC2
C	1164	VAL	-	expression tag	UNP P0DTC2
C	1165	ASP	-	expression tag	UNP P0DTC2
C	1166	LEU	-	expression tag	UNP P0DTC2
C	1167	GLY	-	expression tag	UNP P0DTC2
C	1168	ASP	-	expression tag	UNP P0DTC2
C	1169	ILE	-	expression tag	UNP P0DTC2
C	1170	SER	-	expression tag	UNP P0DTC2
C	1171	GLY	-	expression tag	UNP P0DTC2
C	1172	ILE	-	expression tag	UNP P0DTC2
C	1173	ASN	-	expression tag	UNP P0DTC2
C	1174	ALA	-	expression tag	UNP P0DTC2
C	1175	SER	-	expression tag	UNP P0DTC2
C	1176	VAL	-	expression tag	UNP P0DTC2
C	1177	VAL	-	expression tag	UNP P0DTC2
C	1178	ASN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1179	ILE	-	expression tag	UNP P0DTC2
C	1180	GLN	-	expression tag	UNP P0DTC2
C	1181	LYS	-	expression tag	UNP P0DTC2
C	1182	GLU	-	expression tag	UNP P0DTC2
C	1183	ILE	-	expression tag	UNP P0DTC2
C	1184	ASP	-	expression tag	UNP P0DTC2
C	1185	ARG	-	expression tag	UNP P0DTC2
C	1186	LEU	-	expression tag	UNP P0DTC2
C	1187	ASN	-	expression tag	UNP P0DTC2
C	1188	GLU	-	expression tag	UNP P0DTC2
C	1189	VAL	-	expression tag	UNP P0DTC2
C	1190	ALA	-	expression tag	UNP P0DTC2
C	1191	LYS	-	expression tag	UNP P0DTC2
C	1192	ASN	-	expression tag	UNP P0DTC2
C	1193	LEU	-	expression tag	UNP P0DTC2
C	1194	ASN	-	expression tag	UNP P0DTC2
C	1195	GLU	-	expression tag	UNP P0DTC2
C	1196	SER	-	expression tag	UNP P0DTC2
C	1197	LEU	-	expression tag	UNP P0DTC2
C	1198	ILE	-	expression tag	UNP P0DTC2
C	1199	ASP	-	expression tag	UNP P0DTC2
C	1200	LEU	-	expression tag	UNP P0DTC2
C	1201	GLN	-	expression tag	UNP P0DTC2
C	1202	GLU	-	expression tag	UNP P0DTC2
C	1203	LEU	-	expression tag	UNP P0DTC2
C	1204	GLY	-	expression tag	UNP P0DTC2
C	1205	LYS	-	expression tag	UNP P0DTC2
C	1206	TYR	-	expression tag	UNP P0DTC2
C	1207	GLU	-	expression tag	UNP P0DTC2
C	1208	GLN	-	expression tag	UNP P0DTC2
C	1209	TYR	-	expression tag	UNP P0DTC2
C	1210	ILE	-	expression tag	UNP P0DTC2
C	1211	LYS	-	expression tag	UNP P0DTC2
C	1212	GLY	-	expression tag	UNP P0DTC2
C	1213	SER	-	expression tag	UNP P0DTC2
C	1214	GLY	-	expression tag	UNP P0DTC2
C	1215	ARG	-	expression tag	UNP P0DTC2
C	1216	GLU	-	expression tag	UNP P0DTC2
C	1217	ASN	-	expression tag	UNP P0DTC2
C	1218	LEU	-	expression tag	UNP P0DTC2
C	1219	TYR	-	expression tag	UNP P0DTC2
C	1220	PHE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	GLY	-	expression tag	UNP P0DTC2
C	1223	GLY	-	expression tag	UNP P0DTC2
C	1224	GLY	-	expression tag	UNP P0DTC2
C	1225	GLY	-	expression tag	UNP P0DTC2
C	1226	SER	-	expression tag	UNP P0DTC2
C	1227	GLY	-	expression tag	UNP P0DTC2
C	1228	TYR	-	expression tag	UNP P0DTC2
C	1229	ILE	-	expression tag	UNP P0DTC2
C	1230	PRO	-	expression tag	UNP P0DTC2
C	1231	GLU	-	expression tag	UNP P0DTC2
C	1232	ALA	-	expression tag	UNP P0DTC2
C	1233	PRO	-	expression tag	UNP P0DTC2
C	1234	ARG	-	expression tag	UNP P0DTC2
C	1235	ASP	-	expression tag	UNP P0DTC2
C	1236	GLY	-	expression tag	UNP P0DTC2
C	1237	GLN	-	expression tag	UNP P0DTC2
C	1238	ALA	-	expression tag	UNP P0DTC2
C	1239	TYR	-	expression tag	UNP P0DTC2
C	1240	VAL	-	expression tag	UNP P0DTC2
C	1241	ARG	-	expression tag	UNP P0DTC2
C	1242	LYS	-	expression tag	UNP P0DTC2
C	1243	ASP	-	expression tag	UNP P0DTC2
C	1244	GLY	-	expression tag	UNP P0DTC2
C	1245	GLU	-	expression tag	UNP P0DTC2
C	1246	TRP	-	expression tag	UNP P0DTC2
C	1247	VAL	-	expression tag	UNP P0DTC2
C	1248	LEU	-	expression tag	UNP P0DTC2
C	1249	LEU	-	expression tag	UNP P0DTC2
C	1250	SER	-	expression tag	UNP P0DTC2
C	1251	THR	-	expression tag	UNP P0DTC2
C	1252	PHE	-	expression tag	UNP P0DTC2
C	1253	LEU	-	expression tag	UNP P0DTC2
C	1254	GLY	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	HIS	-	expression tag	UNP P0DTC2
C	1259	HIS	-	expression tag	UNP P0DTC2
C	1260	HIS	-	expression tag	UNP P0DTC2
C	1261	HIS	-	expression tag	UNP P0DTC2
C	1262	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Fab Heavy chain of enhancing antibody.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	H	227	Total	C	N	O	0	0
			908	454	227	227		

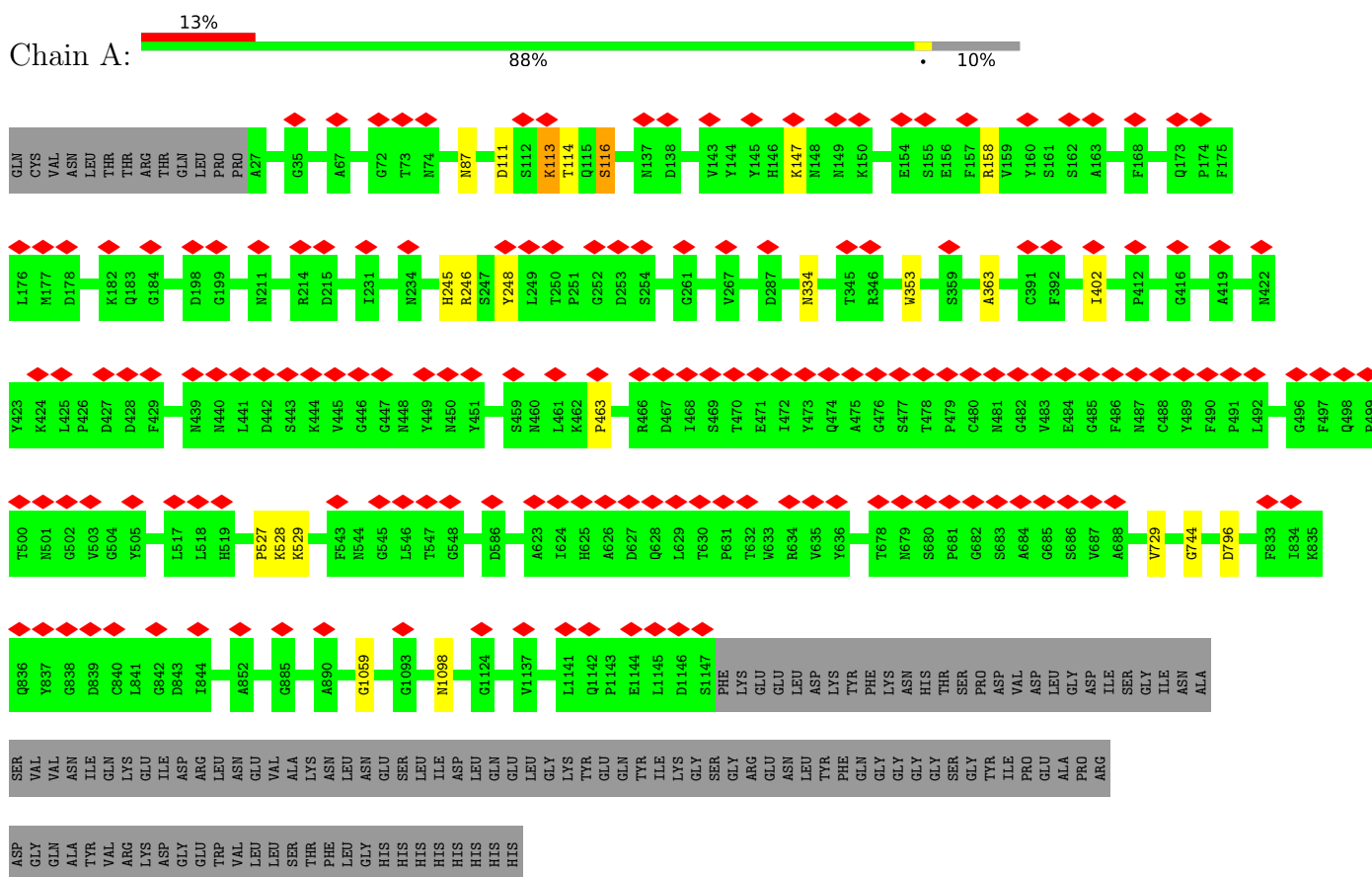
- Molecule 3 is a protein called Fab light chain of enhancing antibody.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	L	213	Total	C	N	O	0	0
			852	426	213	213		

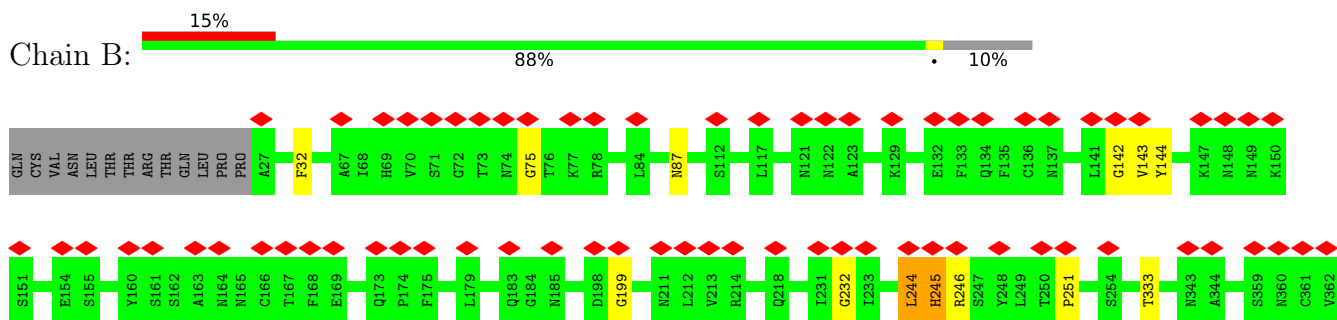
3 Residue-property plots

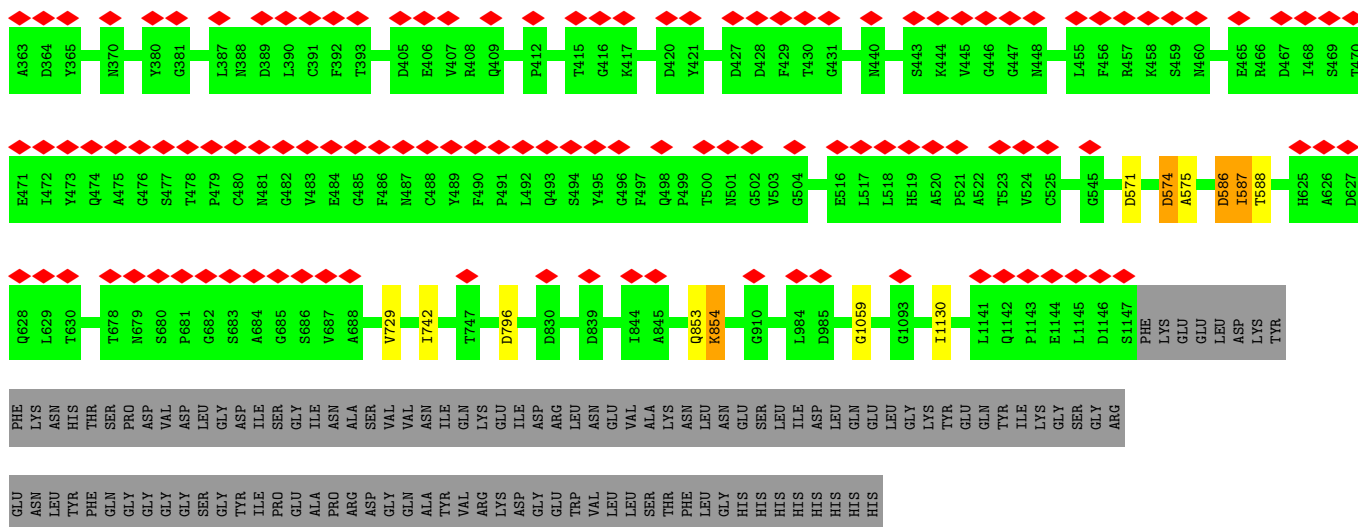
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

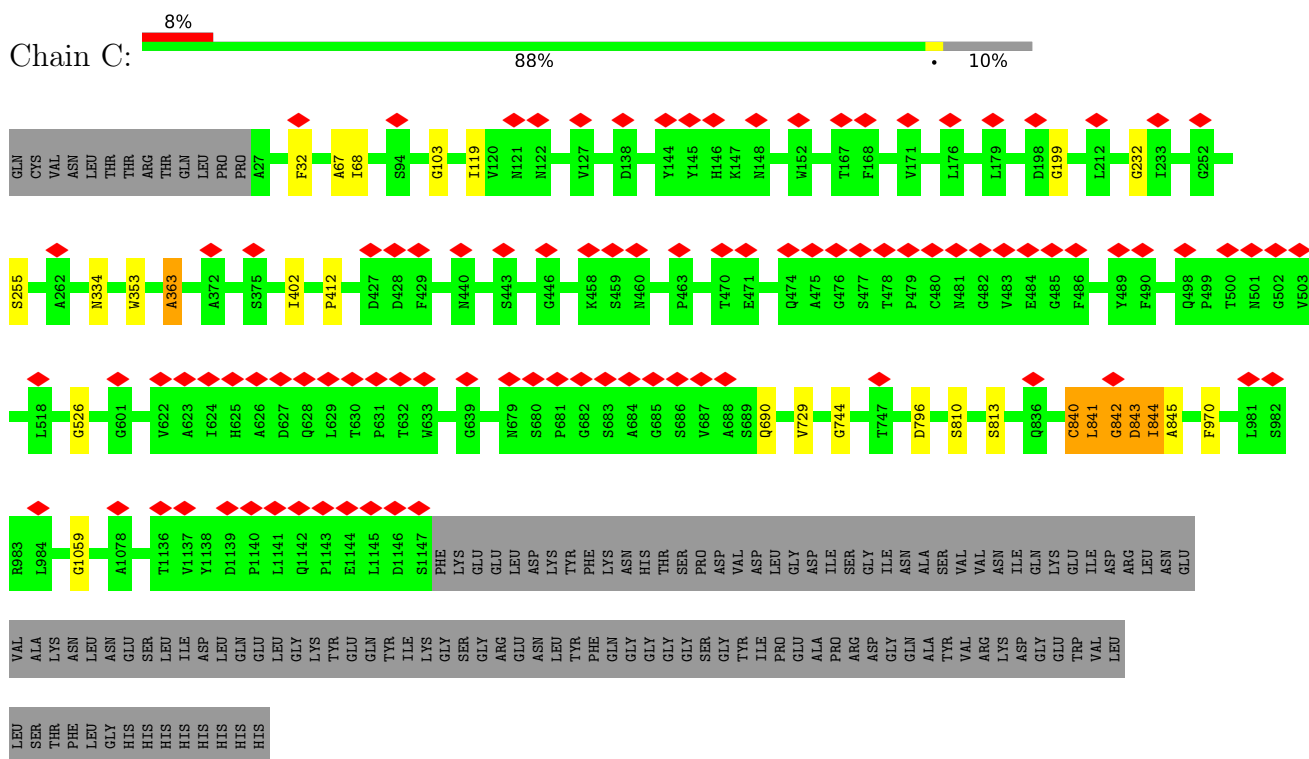


• Molecule 1: Spike glycoprotein

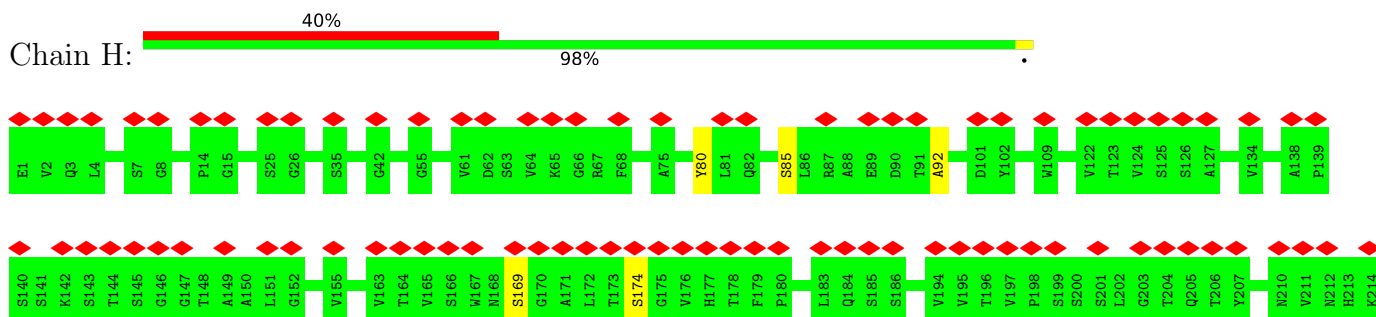




- Molecule 1: Spike glycoprotein

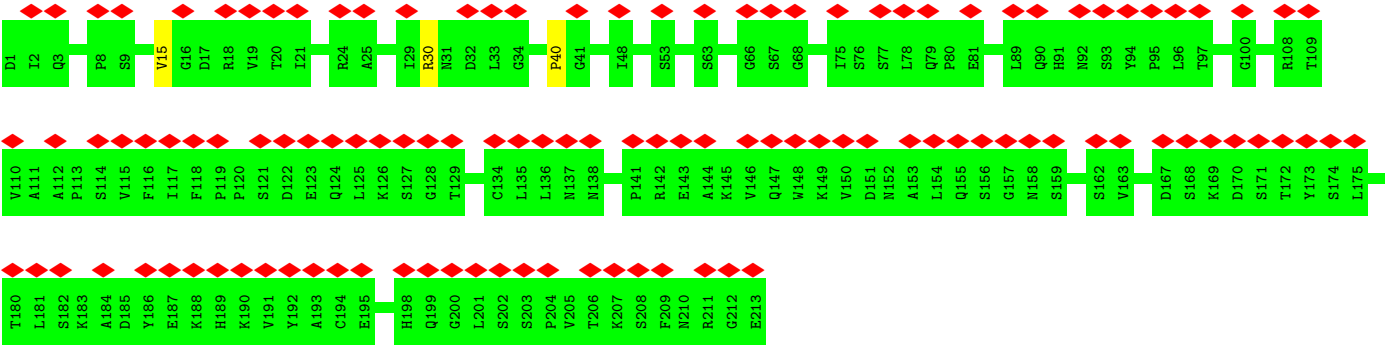


- Molecule 2: Fab Heavy chain of enhancing antibody





• Molecule 3: Fab light chain of enhancing antibody



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	169524	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.929	Depositor
Minimum map value	-0.325	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	387.2, 387.2, 387.2	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88000005, 0.88000005, 0.88000005	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	0.91	0/4483	0.89	6/5602 (0.1%)
1	B	0.92	3/4483 (0.1%)	0.92	10/5602 (0.2%)
1	C	0.97	9/4483 (0.2%)	0.96	17/5602 (0.3%)
2	H	0.92	0/907	0.89	1/1132 (0.1%)
3	L	0.87	0/851	0.78	0/1062
All	All	0.93	12/15207 (0.1%)	0.91	34/19000 (0.2%)

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	B	0	1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	841	LEU	N-CA	9.29	1.65	1.46
1	C	842	GLY	CA-C	8.15	1.64	1.51
1	C	843	ASP	CA-C	7.78	1.73	1.52
1	C	840	CYS	C-N	7.19	1.50	1.34
1	C	841	LEU	C-N	6.94	1.45	1.33
1	B	587	ILE	N-CA	6.75	1.59	1.46
1	C	841	LEU	CA-C	5.68	1.67	1.52
1	C	843	ASP	C-N	5.60	1.47	1.34
1	B	586	ASP	C-N	5.35	1.46	1.34
1	B	854	LYS	CA-C	-5.20	1.39	1.52
1	C	843	ASP	N-CA	5.14	1.56	1.46
1	C	840	CYS	N-CA	-5.07	1.36	1.46

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	574	ASP	C-N-CA	16.39	162.68	121.70
1	C	840	CYS	CA-C-O	-13.97	90.75	120.10
1	B	854	LYS	C-N-CA	-10.92	94.39	121.70
1	B	586	ASP	C-N-CA	9.85	146.32	121.70
1	C	843	ASP	C-N-CA	9.77	146.14	121.70
1	C	840	CYS	CA-C-N	9.47	138.04	117.20
1	C	841	LEU	C-N-CA	9.13	141.47	122.30
1	C	841	LEU	N-CA-C	8.40	133.67	111.00
1	C	840	CYS	C-N-CA	8.26	142.34	121.70
1	C	842	GLY	C-N-CA	8.00	141.69	121.70
1	C	843	ASP	N-CA-C	7.64	131.63	111.00
1	B	244	LEU	C-N-CA	7.10	139.45	121.70
1	B	587	ILE	N-CA-C	6.69	129.06	111.00
1	B	574	ASP	N-CA-C	6.52	128.61	111.00
1	C	844	ILE	N-CA-C	6.14	127.58	111.00
1	A	1098	ASN	N-CA-C	-5.88	95.12	111.00
1	C	970	PHE	O-C-N	-5.87	113.22	123.20
1	C	843	ASP	CA-C-N	5.86	130.08	117.20
1	B	586	ASP	CA-C-O	-5.69	108.16	120.10
1	C	843	ASP	O-C-N	-5.54	113.83	122.70
1	B	245	HIS	C-N-CA	-5.46	108.05	121.70
1	A	245	HIS	C-N-CA	-5.35	108.33	121.70
1	C	840	CYS	O-C-N	5.32	131.21	122.70
2	H	85	SER	N-CA-C	-5.29	96.73	111.00
1	A	363	ALA	C-N-CA	5.25	134.81	121.70
1	C	844	ILE	O-C-N	-5.22	114.34	122.70
1	A	527	PRO	C-N-CA	5.18	134.65	121.70
1	C	363	ALA	C-N-CA	5.12	134.51	121.70
1	B	251	PRO	N-CA-C	-5.11	98.80	112.10
1	C	67	ALA	C-N-CA	5.11	134.48	121.70
1	A	246	ARG	C-N-CA	5.08	134.39	121.70
1	B	742	ILE	C-N-CA	5.04	134.31	121.70
1	A	113	LYS	C-N-CA	-5.03	109.12	121.70
1	C	842	GLY	O-C-N	-5.03	114.66	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	853	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	A	4484	0	1220	5	0
1	B	4484	0	1219	43	0
1	C	4484	0	1220	35	0
2	H	908	0	262	0	0
3	L	852	0	234	0	0
All	All	15212	0	4155	54	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 3.

All (54) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:ILE:CA	1:C:841:LEU:CA	2.55	0.84
1:B:575:ALA:N	1:C:844:ILE:N	2.28	0.81
1:B:142:GLY:HA2	1:B:244:LEU:N	2.00	0.77
1:B:199:GLY:O	1:B:232:GLY:HA2	1.87	0.75
1:B:143:VAL:C	1:B:245:HIS:H	1.93	0.71
1:C:729:VAL:H	1:C:1059:GLY:HA2	1.57	0.70
1:B:143:VAL:N	1:B:245:HIS:H	1.91	0.69
1:B:575:ALA:N	1:C:844:ILE:H	1.92	0.67
1:B:575:ALA:N	1:C:843:ASP:N	2.44	0.65
1:C:199:GLY:HA2	1:C:232:GLY:HA2	1.79	0.65
1:B:575:ALA:CA	1:C:844:ILE:H	2.10	0.65
1:B:729:VAL:H	1:B:1059:GLY:HA2	1.62	0.64
1:B:587:ILE:N	1:C:840:CYS:O	2.32	0.63
1:B:587:ILE:CA	1:C:842:GLY:H	2.12	0.63
1:B:587:ILE:CA	1:C:842:GLY:N	2.62	0.63
1:C:363:ALA:O	1:C:526:GLY:HA2	2.00	0.61
1:B:143:VAL:N	1:B:245:HIS:N	2.50	0.59
1:B:574:ASP:C	1:C:845:ALA:H	2.06	0.58
1:A:729:VAL:H	1:A:1059:GLY:HA2	1.71	0.55
1:B:143:VAL:CA	1:B:245:HIS:H	2.20	0.54
1:B:575:ALA:N	1:C:843:ASP:CA	2.71	0.54
1:B:587:ILE:C	1:C:840:CYS:C	2.67	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:574:ASP:N	1:C:843:ASP:CA	2.71	0.53
1:B:575:ALA:N	1:C:843:ASP:C	2.62	0.52
1:B:575:ALA:C	1:C:843:ASP:N	2.62	0.52
1:A:147:LYS:CA	1:A:248:TYR:CA	2.88	0.51
1:B:575:ALA:C	1:C:843:ASP:H	2.14	0.51
1:C:729:VAL:N	1:C:1059:GLY:HA2	2.25	0.51
1:B:142:GLY:HA3	1:B:244:LEU:C	2.32	0.50
1:B:574:ASP:O	1:B:587:ILE:N	2.37	0.48
1:C:199:GLY:CA	1:C:232:GLY:HA2	2.43	0.48
1:A:114:THR:C	1:A:116:SER:H	2.16	0.47
1:B:588:THR:N	1:C:841:LEU:CA	2.78	0.47
1:A:111:ASP:C	1:A:113:LYS:H	2.18	0.47
1:B:574:ASP:CA	1:C:843:ASP:C	2.83	0.47
1:B:142:GLY:HA2	1:B:244:LEU:CA	2.45	0.47
1:B:586:ASP:O	1:C:841:LEU:N	2.47	0.46
1:B:142:GLY:CA	1:B:244:LEU:N	2.74	0.46
1:B:574:ASP:H	1:C:843:ASP:CA	2.30	0.44
1:B:575:ALA:O	1:C:843:ASP:CA	2.66	0.44
1:B:587:ILE:N	1:C:842:GLY:N	2.66	0.44
1:B:588:THR:N	1:C:841:LEU:N	2.66	0.44
1:B:575:ALA:CA	1:C:843:ASP:N	2.81	0.44
1:B:729:VAL:N	1:B:1059:GLY:HA2	2.32	0.43
1:B:575:ALA:N	1:C:842:GLY:C	2.72	0.43
1:B:587:ILE:N	1:C:841:LEU:CA	2.81	0.43
1:B:587:ILE:CA	1:C:841:LEU:N	2.83	0.42
1:C:103:GLY:HA3	1:C:119:ILE:O	2.20	0.42
1:B:143:VAL:C	1:B:245:HIS:N	2.68	0.42
1:B:586:ASP:O	1:C:841:LEU:CA	2.68	0.42
1:B:144:TYR:CA	1:B:246:ARG:N	2.83	0.42
1:B:587:ILE:N	1:C:841:LEU:C	2.74	0.41
1:A:729:VAL:N	1:A:1059:GLY:HA2	2.33	0.41
1:B:574:ASP:H	1:C:843:ASP:C	2.24	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1119/1249 (90%)	1067 (95%)	41 (4%)	11 (1%)	15	55
1	B	1119/1249 (90%)	1076 (96%)	35 (3%)	8 (1%)	22	62
1	C	1119/1249 (90%)	1051 (94%)	56 (5%)	12 (1%)	14	54
2	H	225/227 (99%)	216 (96%)	5 (2%)	4 (2%)	8	43
3	L	211/213 (99%)	205 (97%)	3 (1%)	3 (1%)	11	48
All	All	3793/4187 (91%)	3615 (95%)	140 (4%)	38 (1%)	20	55

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	463	PRO
1	A	528	LYS
1	A	529	LYS
1	A	796	ASP
1	B	75	GLY
1	B	571	ASP
1	B	854	LYS
1	C	68	ILE
1	C	353	TRP
1	C	796	ASP
1	C	810	SER
2	H	174	SER
1	A	116	SER
1	A	334	ASN
1	A	744	GLY
1	B	87	ASN
1	B	796	ASP
1	B	1130	ILE
1	C	744	GLY
2	H	80	TYR
3	L	15	VAL
1	A	158	ARG
1	B	32	PHE
1	C	334	ASN
1	C	402	ILE
1	C	412	PRO
1	C	690	GLN

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Mol	Chain	Res	Type
3	L	30	ARG
1	A	353	TRP
1	B	333	THR
1	C	32	PHE
1	C	813	SER
2	H	169	SER
3	L	40	PRO
1	A	87	ASN
1	C	255	SER
2	H	92	ALA
1	A	402	ILE

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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 ⓘ

There are no chain breaks in this entry.

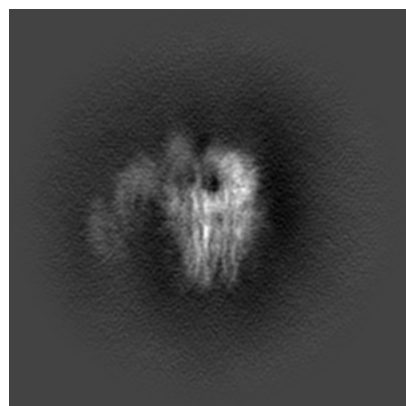
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30918. These allow visual inspection of the internal detail of the map and identification of artifacts.

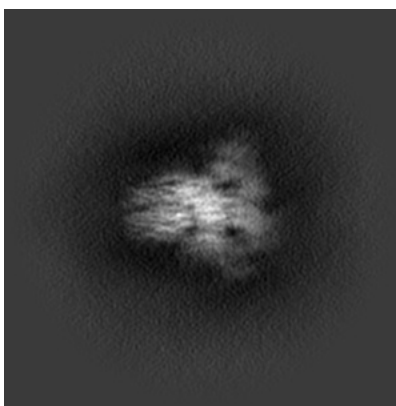
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

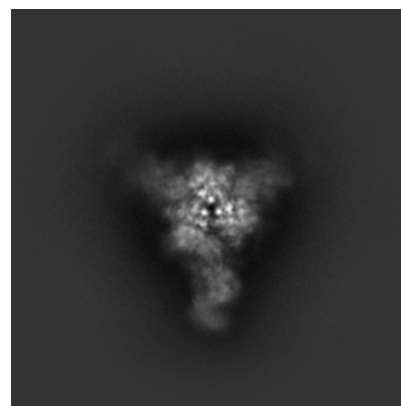
6.1.1 Primary map



X

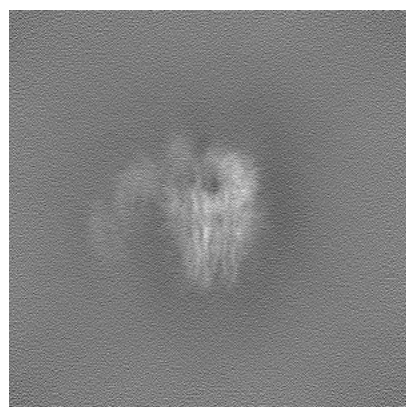


Y

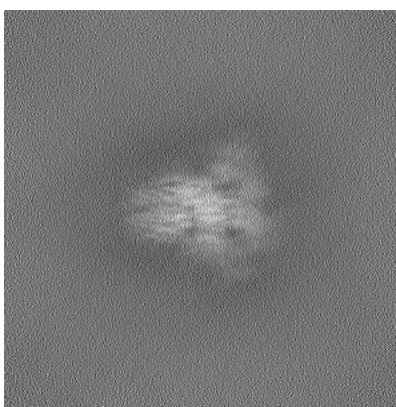


Z

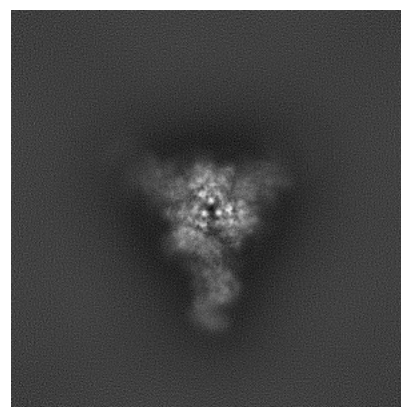
6.1.2 Raw map



X



Y

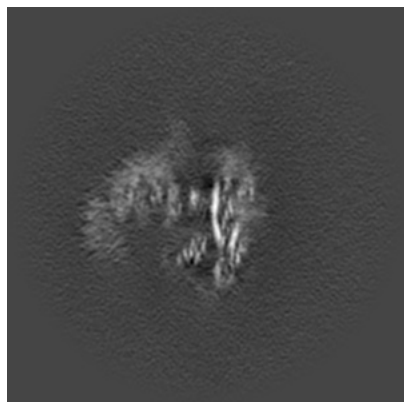


Z

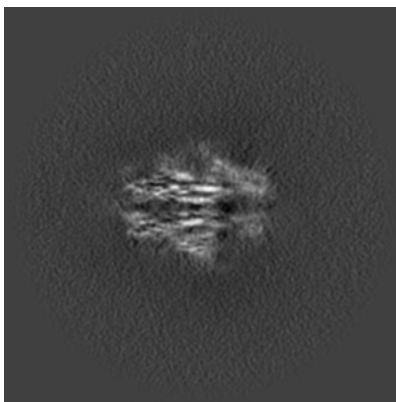
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

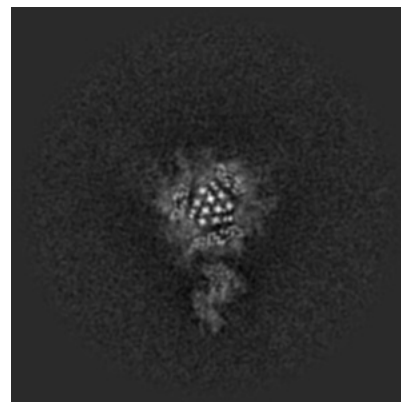
6.2.1 Primary map



X Index: 220

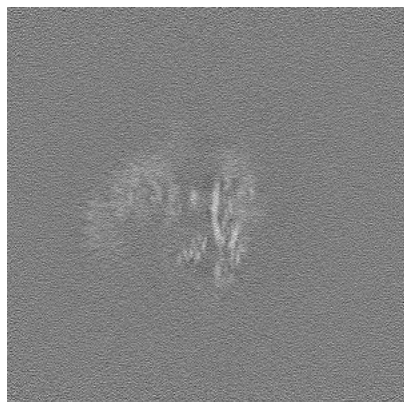


Y Index: 220

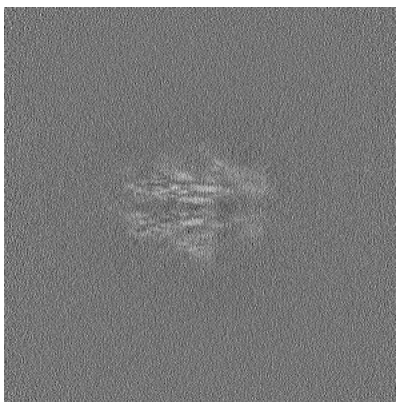


Z Index: 220

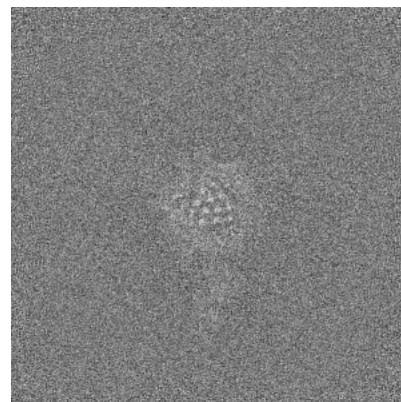
6.2.2 Raw map



X Index: 220



Y Index: 220

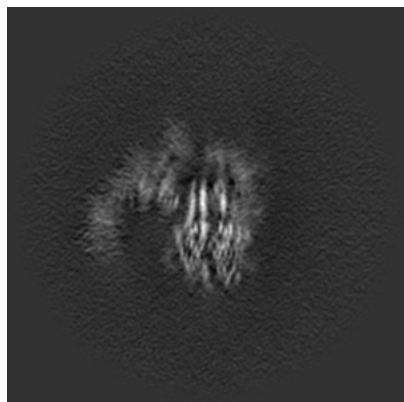


Z Index: 220

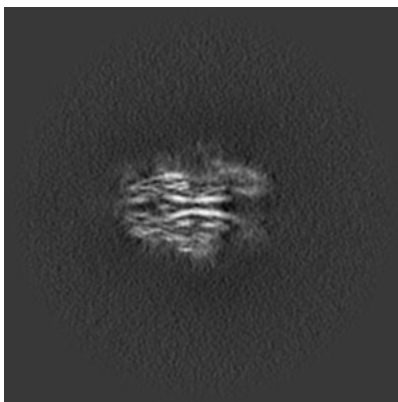
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

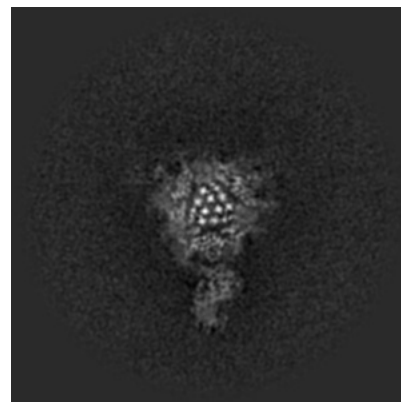
6.3.1 Primary map



X Index: 212

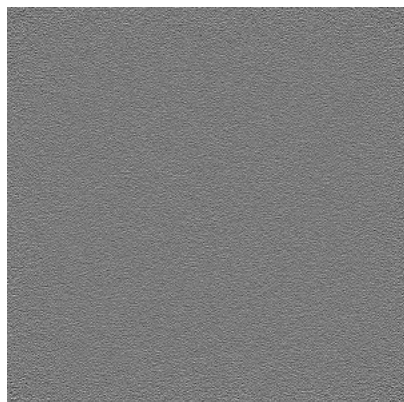


Y Index: 216

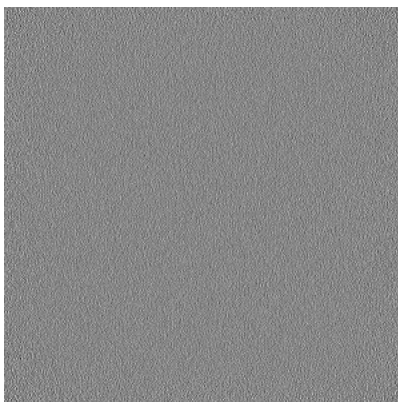


Z Index: 224

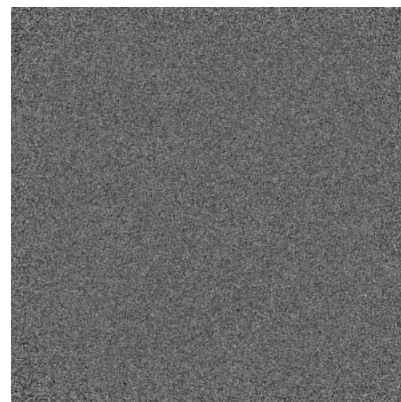
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

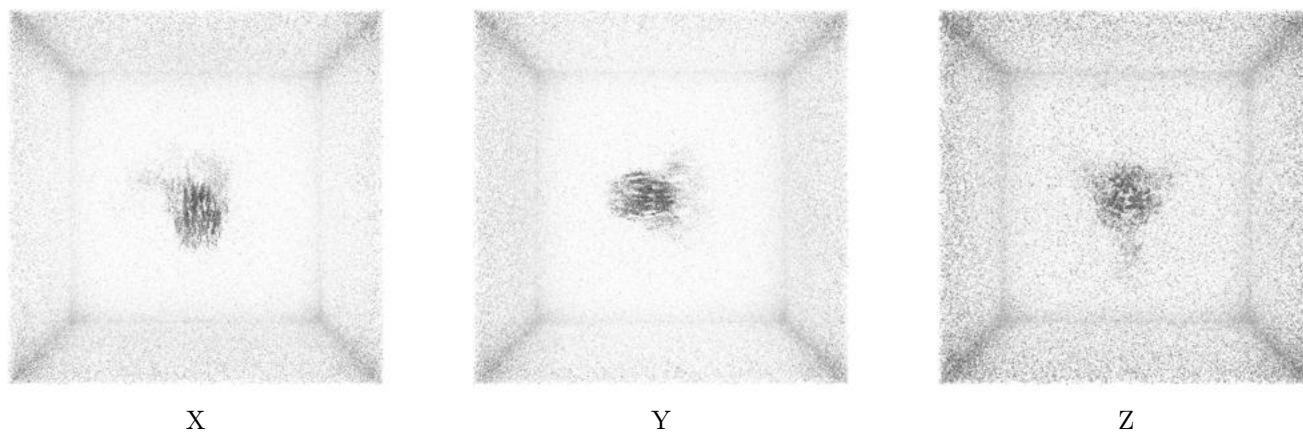
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

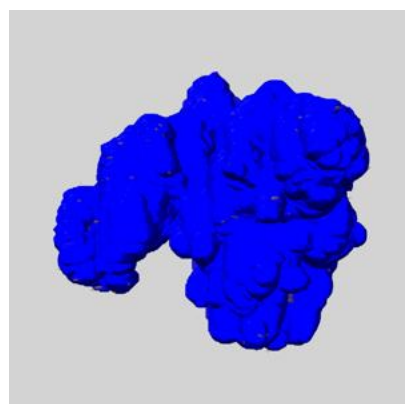
6.5 Mask visualisation [i](#)

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

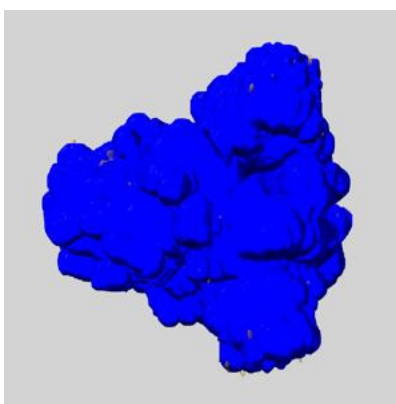
A mask typically either:

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

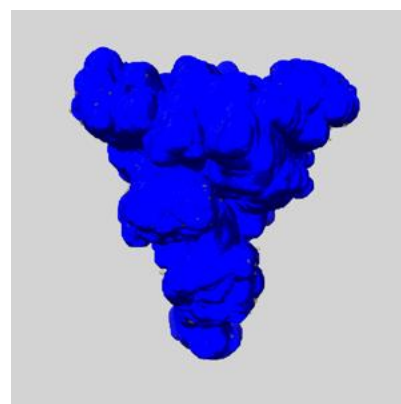
6.5.1 emd_30918_msk_1.map [i](#)



X



Y

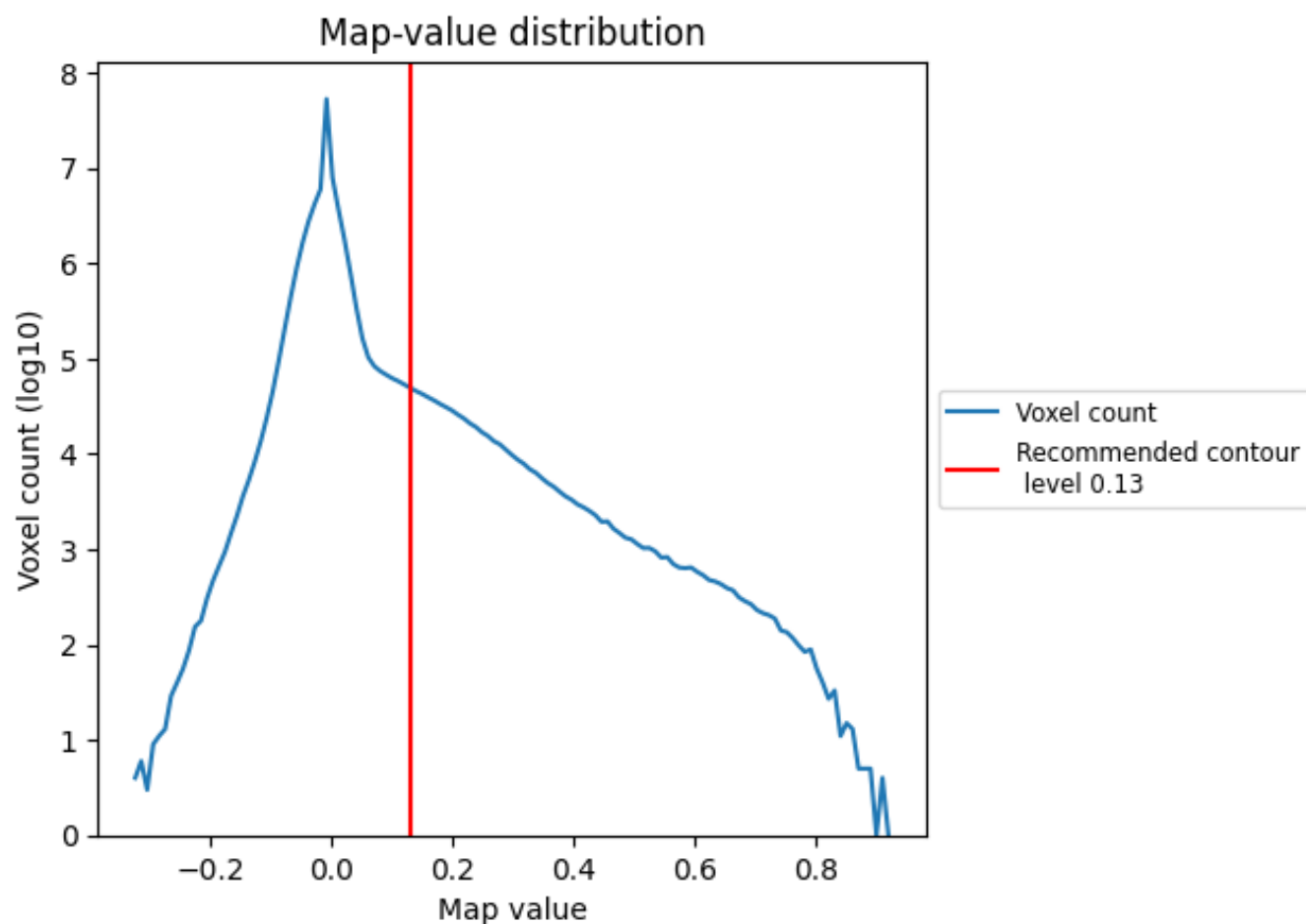


Z

7 Map analysis [i](#)

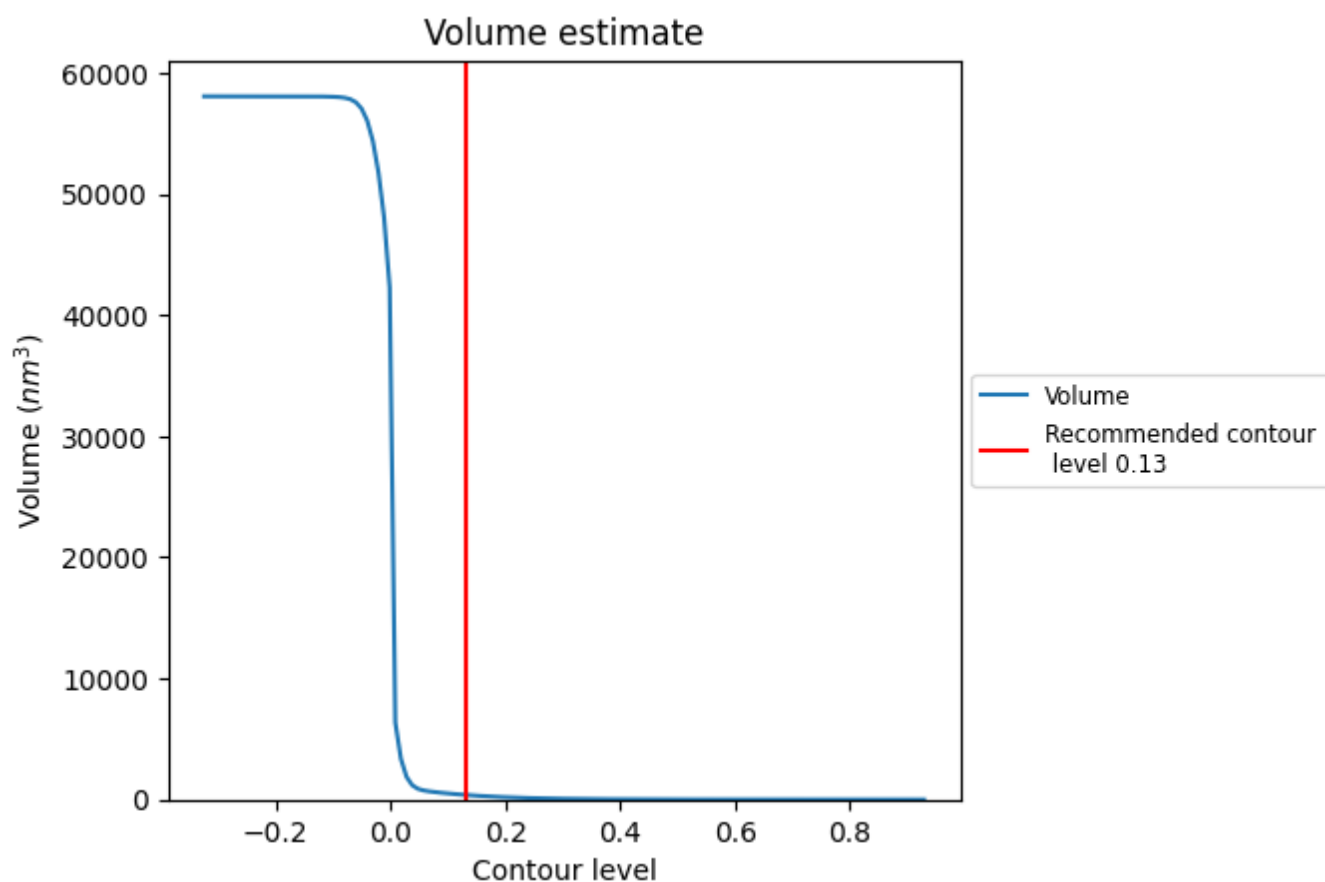
This section contains the results of statistical analysis of the map.

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.

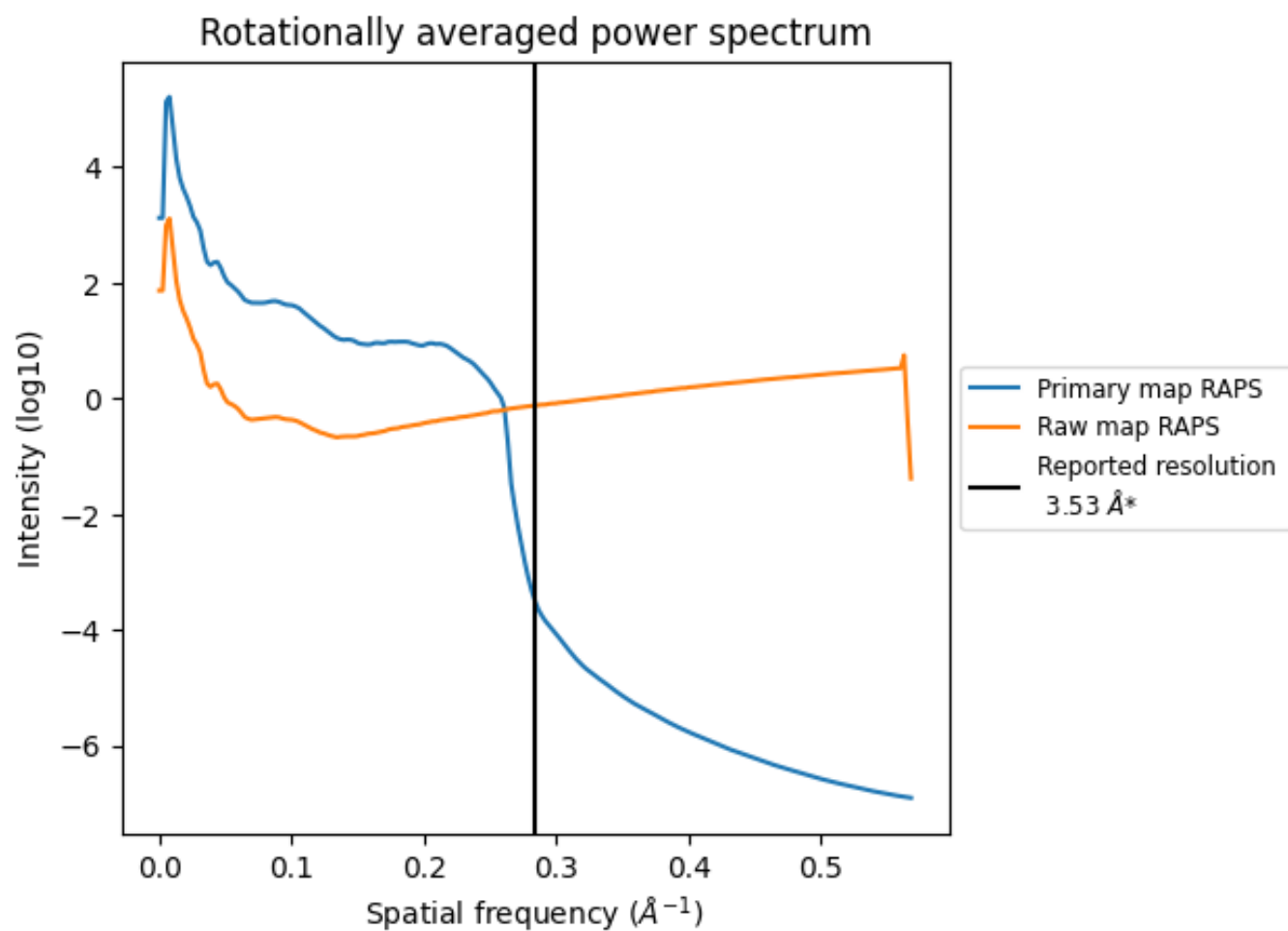
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 385 nm³; this corresponds to an approximate mass of 347 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

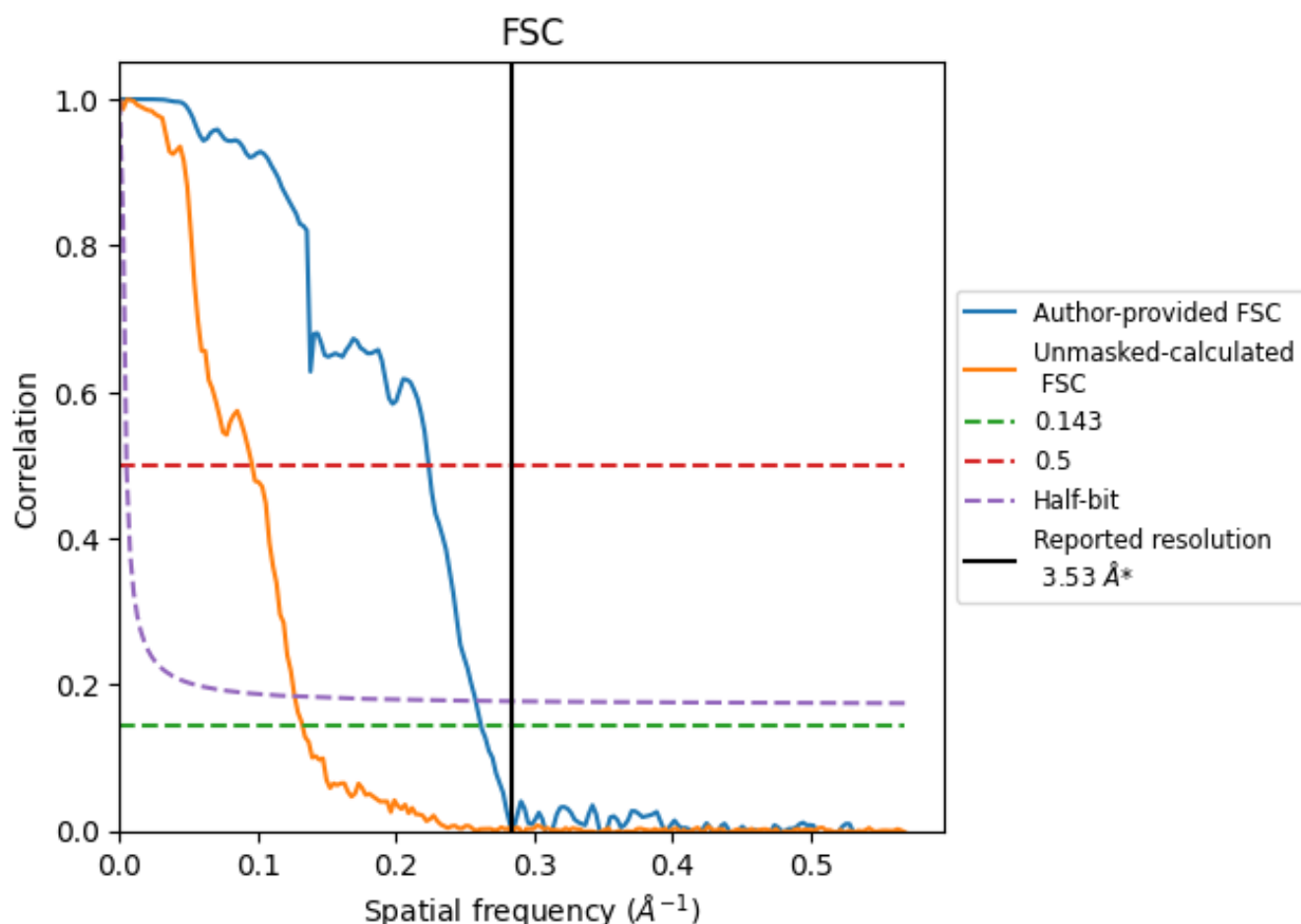


*Reported resolution corresponds to spatial frequency of 0.283 \AA^{-1}

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 0.283 Å⁻¹

8.2 Resolution estimates [i](#)

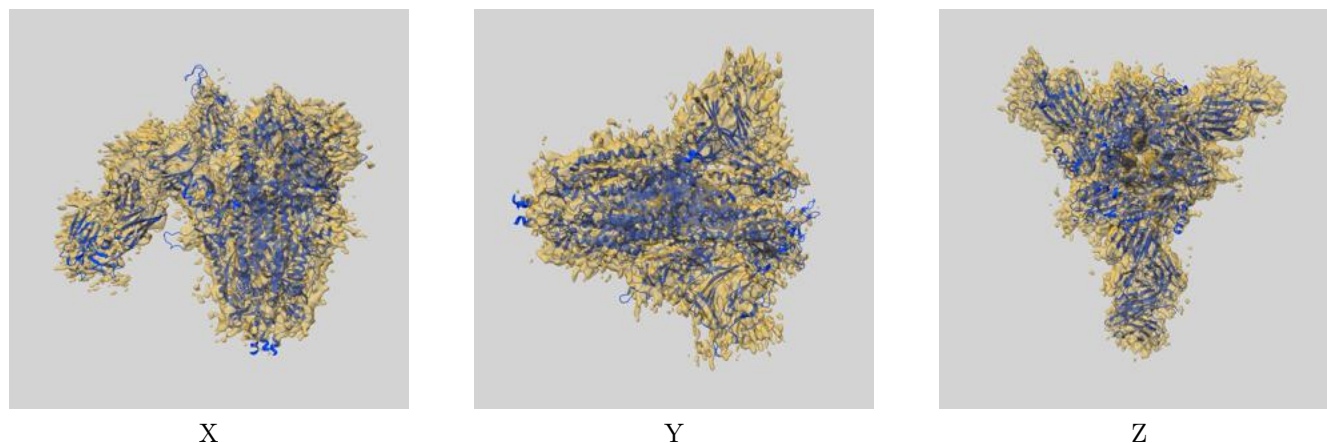
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.53	-	-
Author-provided FSC curve	3.82	4.47	3.88
Unmasked-calculated*	7.55	10.43	7.89

*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 7.55 differs from the reported value 3.53 by more than 10 %

9 Map-model fit [i](#)

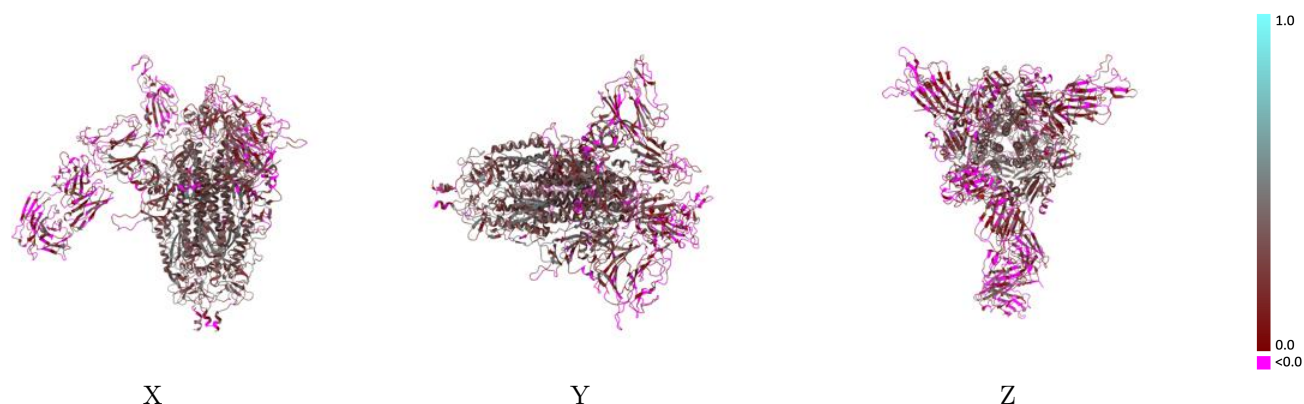
This section contains information regarding the fit between EMDB map EMD-30918 and PDB model 7DZX. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



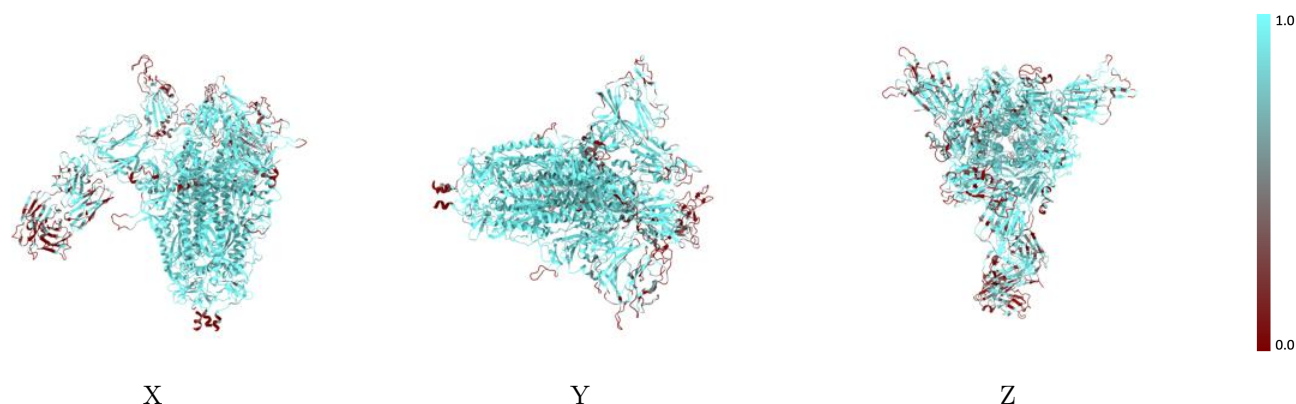
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



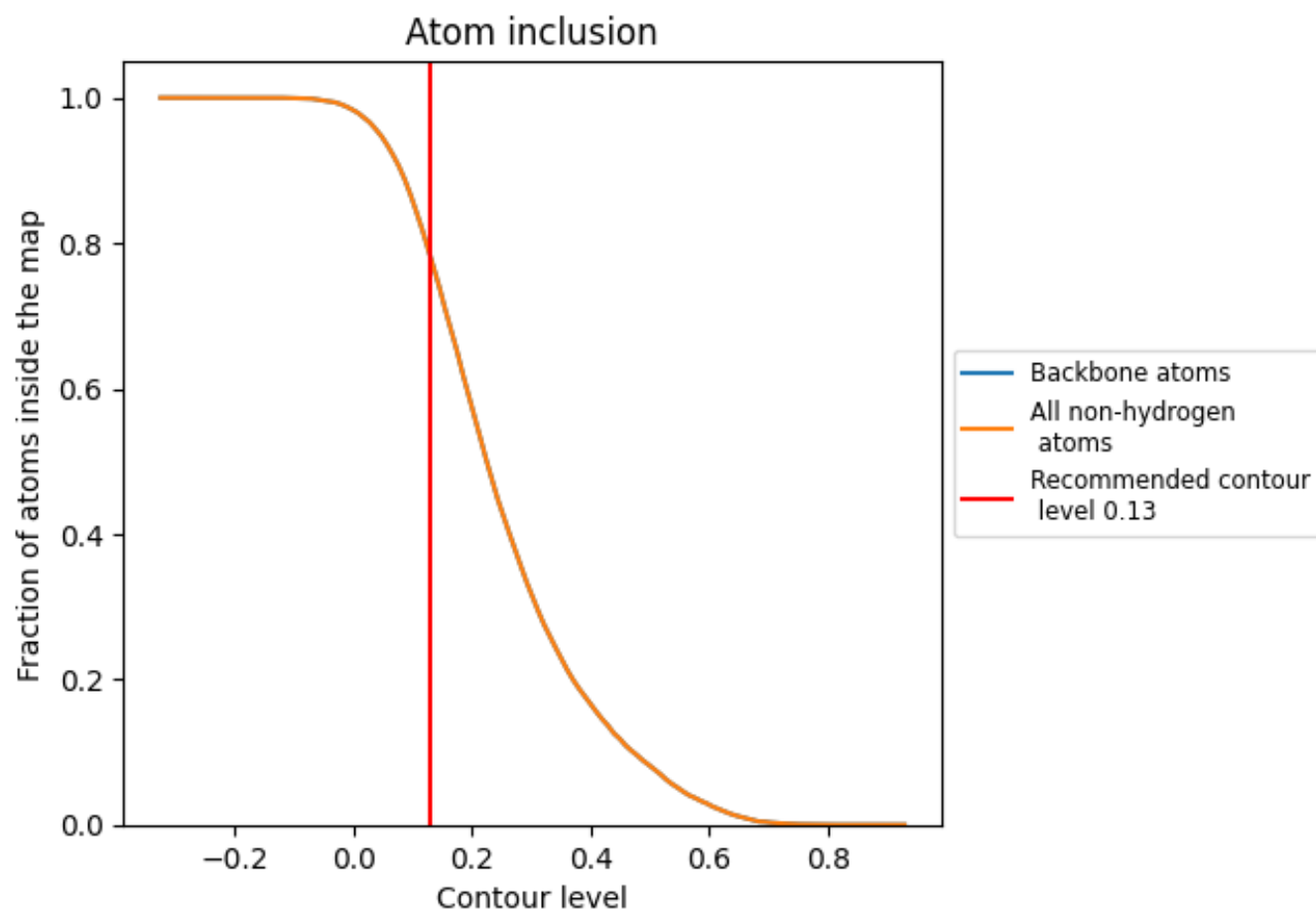
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 78% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7823	<div></div> 0.2200
A	<div></div> 0.8113	<div></div> 0.2390
B	<div></div> 0.7859	<div></div> 0.2170
C	<div></div> 0.8698	<div></div> 0.2560
H	<div></div> 0.5430	<div></div> 0.0750
L	<div></div> 0.4061	<div></div> 0.0920

