



Full wwPDB EM Validation Report ⓘ

Apr 16, 2026 – 04:39 pm BST

PDB ID : 9TPW / pdb_00009tpw
EMDB ID : EMD-56117
Title : cryo-ET structure of mTOR complex 2 on a PIP2-containing membrane
Authors : Hay, I.M.; Ahsan, B.; Williams, R.L.
Deposited on : 2025-12-18
Resolution : 6.40 Å(reported)

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.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

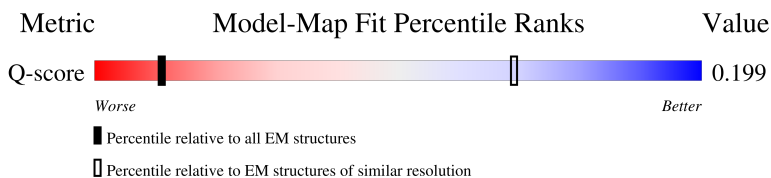
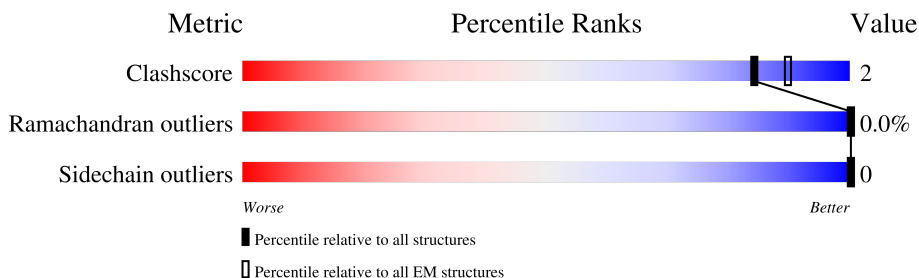
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.40 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	-
Q-score	-	25397	544 (5.90 - 6.90)

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	2590	<div> <div>35%</div> <div>82% 6% 13%</div> </div>
1	B	2590	<div> <div>36%</div> <div>81% 6% 13%</div> </div>
2	C	326	<div> <div>66%</div> <div>88% 8% .</div> </div>
2	D	326	<div> <div>67%</div> <div>89% 8% .</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	1734	<div><div><div>24%</div><div>60%</div><div>5%</div><div>35%</div></div></div>
3	F	1734	<div><div><div>22%</div><div>60%</div><div>•</div><div>35%</div></div></div>
4	G	522	<div><div><div>17%</div><div>22%</div><div>•</div><div>77%</div></div></div>
4	H	522	<div><div><div>17%</div><div>22%</div><div>•</div><div>77%</div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 61288 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 Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2265	Total	C	N	O	S	0	0
			18242	11626	3206	3284	126		
1	B	2263	Total	C	N	O	S	0	0
			18230	11619	3204	3282	125		

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-40	MET	-	initiating methionine	UNP P42345
A	-39	ALA	-	expression tag	UNP P42345
A	-38	SER	-	expression tag	UNP P42345
A	-37	TRP	-	expression tag	UNP P42345
A	-36	SER	-	expression tag	UNP P42345
A	-35	HIS	-	expression tag	UNP P42345
A	-34	PRO	-	expression tag	UNP P42345
A	-33	GLN	-	expression tag	UNP P42345
A	-32	PHE	-	expression tag	UNP P42345
A	-31	GLU	-	expression tag	UNP P42345
A	-30	LYS	-	expression tag	UNP P42345
A	-29	GLY	-	expression tag	UNP P42345
A	-28	GLY	-	expression tag	UNP P42345
A	-27	GLY	-	expression tag	UNP P42345
A	-26	ALA	-	expression tag	UNP P42345
A	-25	ARG	-	expression tag	UNP P42345
A	-24	GLY	-	expression tag	UNP P42345
A	-23	GLY	-	expression tag	UNP P42345
A	-22	SER	-	expression tag	UNP P42345
A	-21	GLY	-	expression tag	UNP P42345
A	-20	GLY	-	expression tag	UNP P42345
A	-19	GLY	-	expression tag	UNP P42345
A	-18	SER	-	expression tag	UNP P42345
A	-17	TRP	-	expression tag	UNP P42345
A	-16	SER	-	expression tag	UNP P42345
A	-15	HIS	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	PRO	-	expression tag	UNP P42345
A	-13	GLN	-	expression tag	UNP P42345
A	-12	PHE	-	expression tag	UNP P42345
A	-11	GLU	-	expression tag	UNP P42345
A	-10	LYS	-	expression tag	UNP P42345
A	-9	GLY	-	expression tag	UNP P42345
A	-8	GLU	-	expression tag	UNP P42345
A	-7	ASN	-	expression tag	UNP P42345
A	-6	LEU	-	expression tag	UNP P42345
A	-5	TYR	-	expression tag	UNP P42345
A	-4	PHE	-	expression tag	UNP P42345
A	-3	GLN	-	expression tag	UNP P42345
A	-2	GLY	-	expression tag	UNP P42345
A	-1	GLY	-	expression tag	UNP P42345
A	0	THR	-	expression tag	UNP P42345
B	-40	MET	-	initiating methionine	UNP P42345
B	-39	ALA	-	expression tag	UNP P42345
B	-38	SER	-	expression tag	UNP P42345
B	-37	TRP	-	expression tag	UNP P42345
B	-36	SER	-	expression tag	UNP P42345
B	-35	HIS	-	expression tag	UNP P42345
B	-34	PRO	-	expression tag	UNP P42345
B	-33	GLN	-	expression tag	UNP P42345
B	-32	PHE	-	expression tag	UNP P42345
B	-31	GLU	-	expression tag	UNP P42345
B	-30	LYS	-	expression tag	UNP P42345
B	-29	GLY	-	expression tag	UNP P42345
B	-28	GLY	-	expression tag	UNP P42345
B	-27	GLY	-	expression tag	UNP P42345
B	-26	ALA	-	expression tag	UNP P42345
B	-25	ARG	-	expression tag	UNP P42345
B	-24	GLY	-	expression tag	UNP P42345
B	-23	GLY	-	expression tag	UNP P42345
B	-22	SER	-	expression tag	UNP P42345
B	-21	GLY	-	expression tag	UNP P42345
B	-20	GLY	-	expression tag	UNP P42345
B	-19	GLY	-	expression tag	UNP P42345
B	-18	SER	-	expression tag	UNP P42345
B	-17	TRP	-	expression tag	UNP P42345
B	-16	SER	-	expression tag	UNP P42345
B	-15	HIS	-	expression tag	UNP P42345
B	-14	PRO	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	GLN	-	expression tag	UNP P42345
B	-12	PHE	-	expression tag	UNP P42345
B	-11	GLU	-	expression tag	UNP P42345
B	-10	LYS	-	expression tag	UNP P42345
B	-9	GLY	-	expression tag	UNP P42345
B	-8	GLU	-	expression tag	UNP P42345
B	-7	ASN	-	expression tag	UNP P42345
B	-6	LEU	-	expression tag	UNP P42345
B	-5	TYR	-	expression tag	UNP P42345
B	-4	PHE	-	expression tag	UNP P42345
B	-3	GLN	-	expression tag	UNP P42345
B	-2	GLY	-	expression tag	UNP P42345
B	-1	GLY	-	expression tag	UNP P42345
B	0	THR	-	expression tag	UNP P42345

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	315	Total	C	N	O	S	0	0
			2443	1518	434	473	18		
2	D	315	Total	C	N	O	S	0	0
			2443	1518	434	473	18		

- Molecule 3 is a protein called Rapamycin-insensitive companion of mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	1119	Total	C	N	O	S	0	0
			8990	5732	1584	1625	49		
3	F	1119	Total	C	N	O	S	0	0
			8990	5732	1584	1625	49		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-25	MET	-	initiating methionine	UNP Q6R327
E	-24	ALA	-	expression tag	UNP Q6R327
E	-23	ASP	-	expression tag	UNP Q6R327
E	-22	TYR	-	expression tag	UNP Q6R327
E	-21	LYS	-	expression tag	UNP Q6R327
E	-20	ASP	-	expression tag	UNP Q6R327
E	-19	HIS	-	expression tag	UNP Q6R327
E	-18	ASP	-	expression tag	UNP Q6R327

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-17	GLY	-	expression tag	UNP Q6R327
E	-16	ASP	-	expression tag	UNP Q6R327
E	-15	TYR	-	expression tag	UNP Q6R327
E	-14	LYS	-	expression tag	UNP Q6R327
E	-13	ASP	-	expression tag	UNP Q6R327
E	-12	HIS	-	expression tag	UNP Q6R327
E	-11	ASP	-	expression tag	UNP Q6R327
E	-10	ILE	-	expression tag	UNP Q6R327
E	-9	ASP	-	expression tag	UNP Q6R327
E	-8	TYR	-	expression tag	UNP Q6R327
E	-7	LYS	-	expression tag	UNP Q6R327
E	-6	ASP	-	expression tag	UNP Q6R327
E	-5	ASP	-	expression tag	UNP Q6R327
E	-4	ASP	-	expression tag	UNP Q6R327
E	-3	ASP	-	expression tag	UNP Q6R327
E	-2	LYS	-	expression tag	UNP Q6R327
E	-1	GLY	-	expression tag	UNP Q6R327
E	0	THR	-	expression tag	UNP Q6R327
F	-25	MET	-	initiating methionine	UNP Q6R327
F	-24	ALA	-	expression tag	UNP Q6R327
F	-23	ASP	-	expression tag	UNP Q6R327
F	-22	TYR	-	expression tag	UNP Q6R327
F	-21	LYS	-	expression tag	UNP Q6R327
F	-20	ASP	-	expression tag	UNP Q6R327
F	-19	HIS	-	expression tag	UNP Q6R327
F	-18	ASP	-	expression tag	UNP Q6R327
F	-17	GLY	-	expression tag	UNP Q6R327
F	-16	ASP	-	expression tag	UNP Q6R327
F	-15	TYR	-	expression tag	UNP Q6R327
F	-14	LYS	-	expression tag	UNP Q6R327
F	-13	ASP	-	expression tag	UNP Q6R327
F	-12	HIS	-	expression tag	UNP Q6R327
F	-11	ASP	-	expression tag	UNP Q6R327
F	-10	ILE	-	expression tag	UNP Q6R327
F	-9	ASP	-	expression tag	UNP Q6R327
F	-8	TYR	-	expression tag	UNP Q6R327
F	-7	LYS	-	expression tag	UNP Q6R327
F	-6	ASP	-	expression tag	UNP Q6R327
F	-5	ASP	-	expression tag	UNP Q6R327
F	-4	ASP	-	expression tag	UNP Q6R327
F	-3	ASP	-	expression tag	UNP Q6R327
F	-2	LYS	-	expression tag	UNP Q6R327

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLY	-	expression tag	UNP Q6R327
F	0	THR	-	expression tag	UNP Q6R327

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit MAPKAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	120	Total	C	N	O	S	0	0
			974	603	182	185	4		
4	H	120	Total	C	N	O	S	0	0
			974	603	182	185	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	1	ACE	-	acetylation	UNP Q9BPZ7
H	1	ACE	-	acetylation	UNP Q9BPZ7

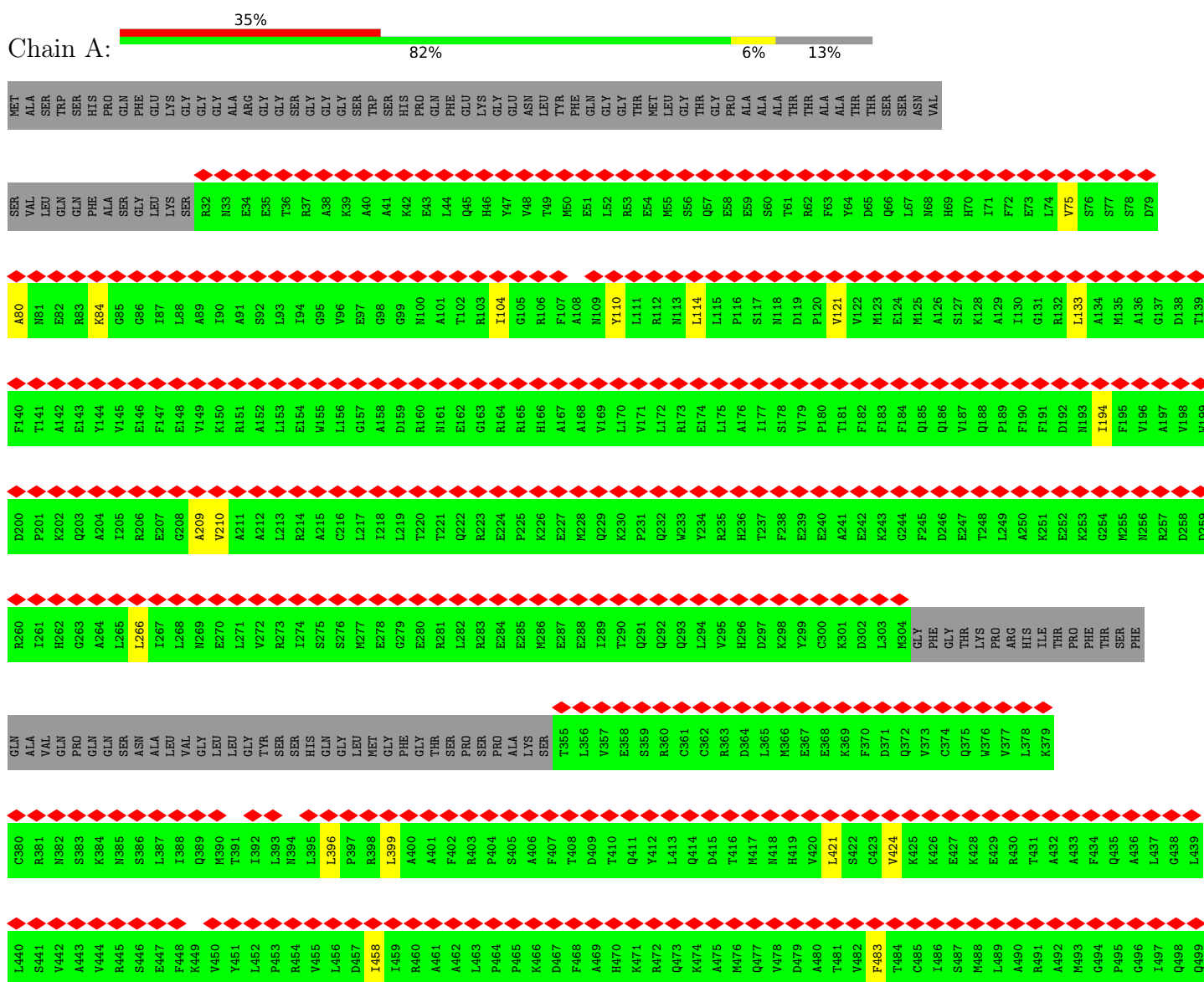
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
5	E	1	Total	Zn	0
			1	1	
5	F	1	Total	Zn	0
			1	1	

3 Residue-property plots

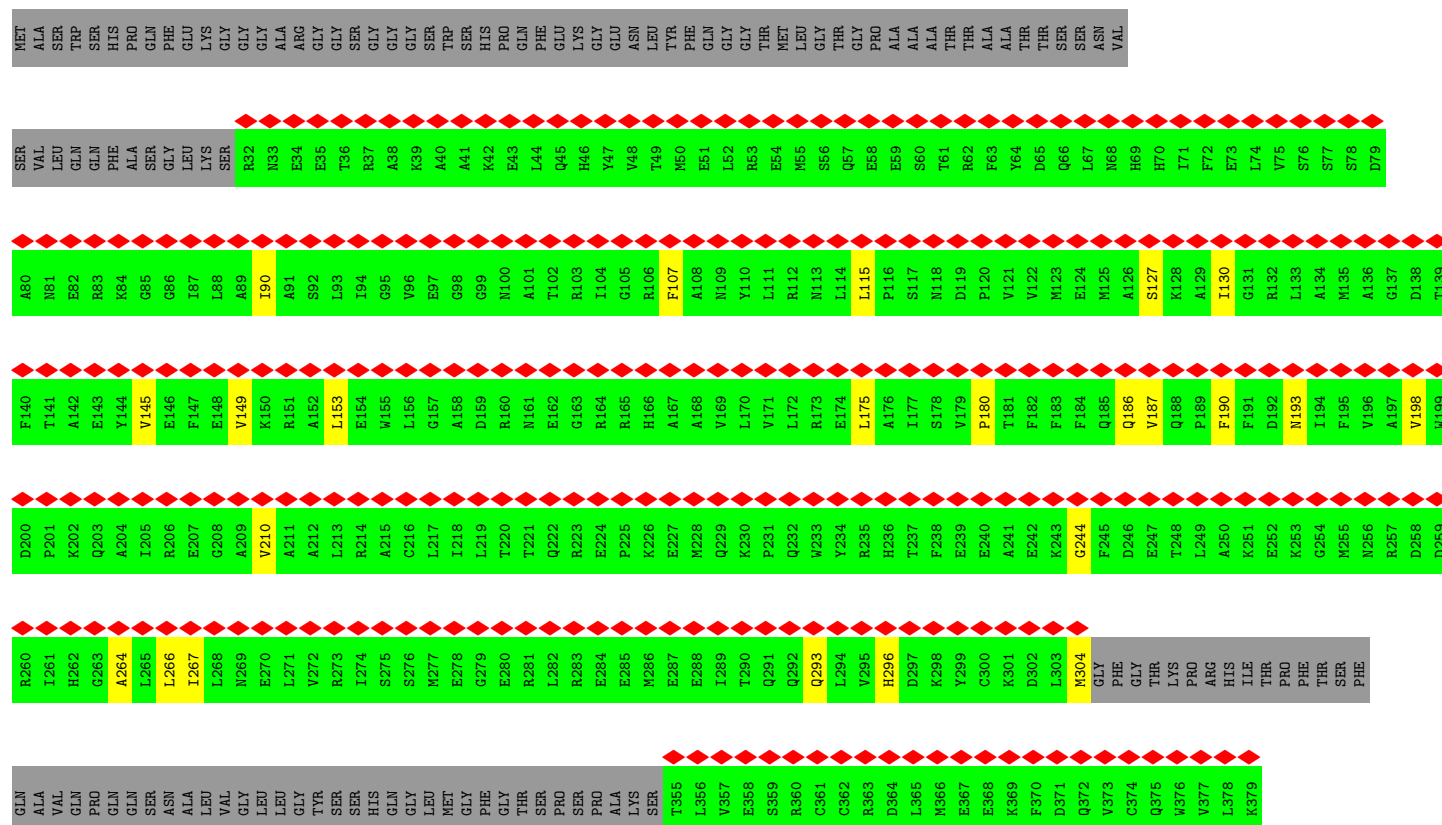
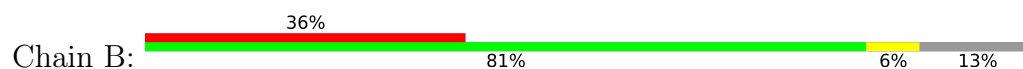
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

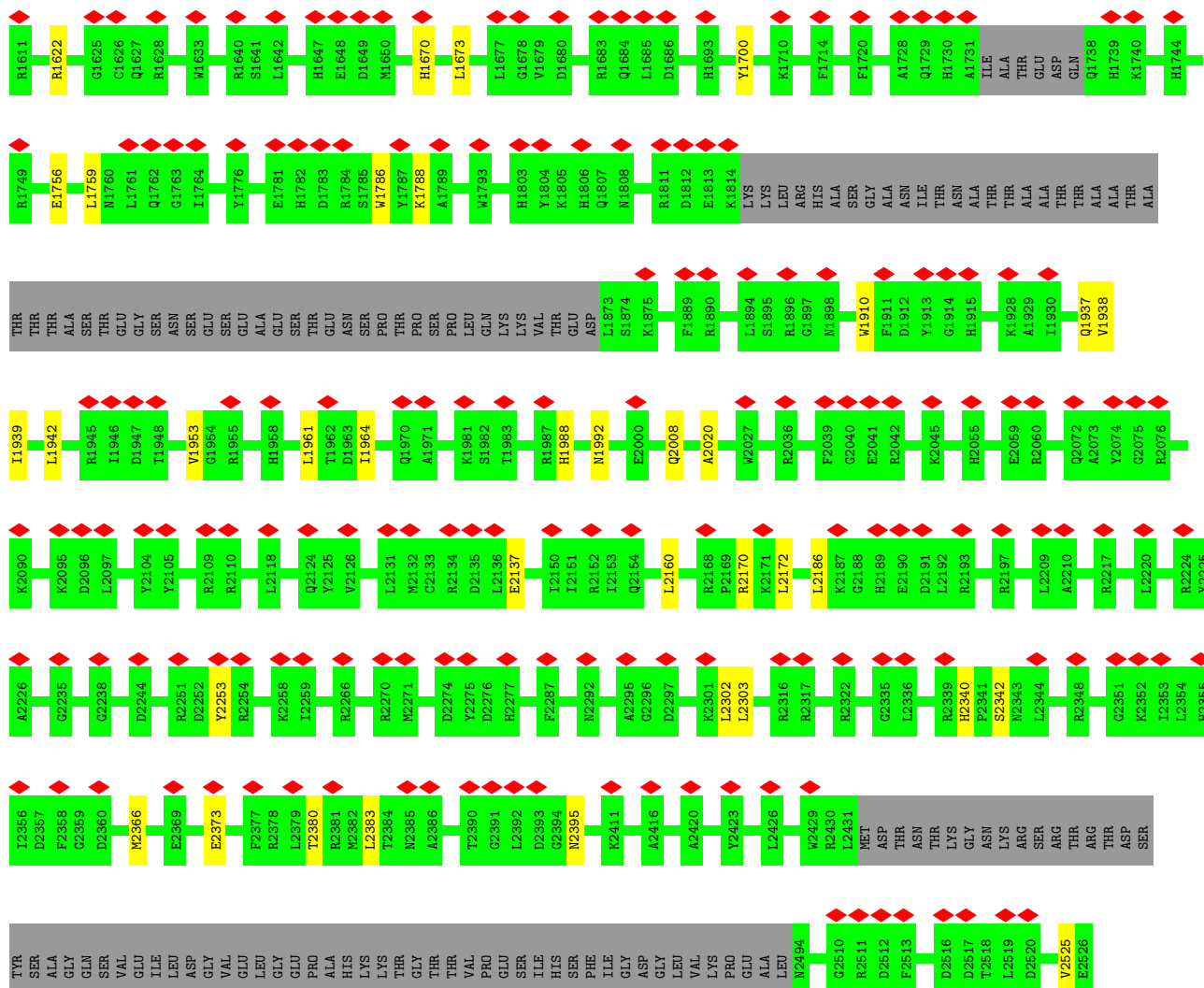




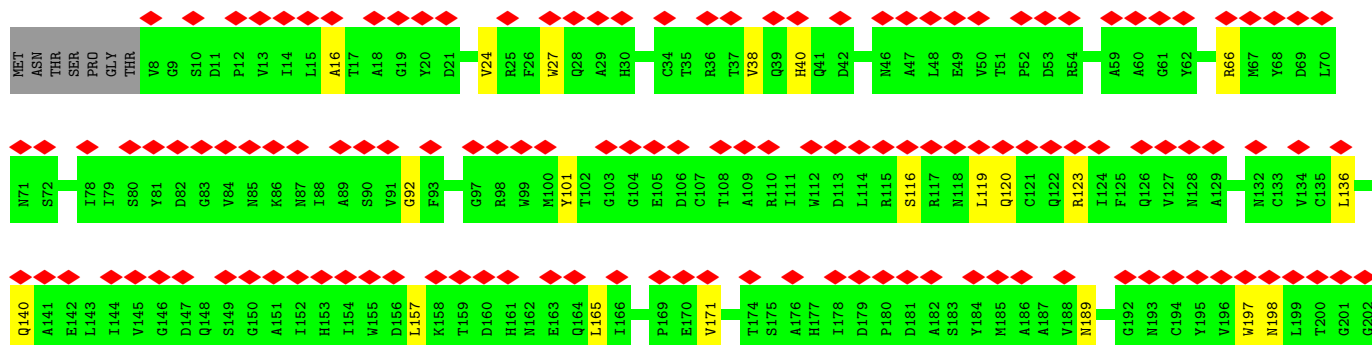
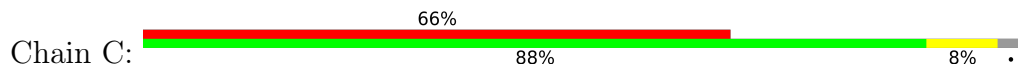
- Molecule 1: Serine/threonine-protein kinase mTOR



C380	R381	N382	S383	N384	N385	S386	L387	I388	Q389	M390	T391	I392	L393	N394	L395	L396	P397	R398	L399	A400	A401	F402	R403	P404	S405	A406	F407	T408	D409	T410	Q411	Y412	L413	Q414	D415	T416	M417	N418	H419	V420	L421	S422	C423	V424	K425	K426	E427	K428	E429	R430	T431	A432	F434	Q435	A436	G438	L439																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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D500	I501	K502	E503	L504	E505	P507	M508	L509	A510	V511	G512	L513	P514	S515	A516	L517	T518	A519	V520	L521	Y522	D523	L524	S525	R526	Q527	I528	P529	Q530	L531	K532	K533	D534	I535	Q536	D537	G538	L539	L540	K541	M542	L543	R544	L545	V546	L547	M548	H549	K550	P551	L552	R553	H554	P555	G556	M557	P558	K559																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G560	L561	A562	H563	Q564	L565	A566	S567	P568	G569	L570	T571	L572	L573	P574	E575	A576	S577	D578	V579	S580	S581	I582	T583	L584	A585	L586	T587	T588	L589	G590	S591	F592	E593	F594	G595	G596	H597	S598	L599	T600	Q601	F602	V603	R604	H605	D608	H609	F610	L611	N612	S613	E614	R619	M620	E621	R624																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
R628	L629	T631	P630	S631	I632	L633	H634	S635	L636	G637	H638	L639	V640	S641	T642	L643	V644	S645	L646	T647	P648	S649	L650	A651	L652	T653	P654	L655	S656	T657	F658	E659	L660	H661	G662	L663	T664	S665	P666	L667	T668	R669	L670	S671	L672	T673	P674	L675	S676	T677	F678	L679	G680	H681	L682	T683	P684	L685	S686	T687	R688	L689	T690	S691	L692	T693	P694	L695	S696	T697	R698	L699	T700	S701	L702	T703	P704	L705	S706	T707	R708	L709	T710	S711	L712	T713	P714	L715	S716	T717	R718	L719	T720	S721	L722	T723	P724	L725	S726	T727	R728	L729	T730	P731	L732	S733	T734	R735	L736	T737	P738	L739	S740	T741	R742	L743	T744	S745	T746	P747	L748	T749	S750	T751	R752	L753	T754	P755	L756	S757	T758	R759	L760	T761	S762	T763	P764	L765	S766	T767	R768	L769	T770	S771	T772	P773	L774	S775	T776	R777	L778	T779	S780	T781	P782	L783	S784	T785	R786	L787	T788	P789	L790	S791	T792	R793	L794	T795	P796	L797	S798	T799	R800	L801	T802	P803	L804	S805	T806	R807	L808	T809	P810	L811	S812	T813	R814	L815	T816	P817	L818	S819	T820	R821	L822	T823	P824	L825	S826	T827	R828	L829	T830	P831	L832	S833	T834	R835	L836	T837	P838	L839	S840	T841	R842	L843	T844	P845	L846	S847	T848	R849	L850	T851	P852	L853	S854	T855	R856	L857	T858	P859	L860	S861	T862	R863	L864	T865	P866	L867	S868	T869	R870	L871	T872	P873	L874	S875	T876	R877	L878	T879	P880	L881	S882	T883	R884	L885	T886	P887	L888	S889	T890	R891	L892	T893	P894	L895	S896	T897	R898	L899	T900	P901	L902	S903	T904	R905	L906	T907	P908	L909	S910	T911	R912	L913	T914	P915	L916	S917	T918	R919	L920	T921	P922	L923	S924	T925	R926	L927	T928	P929	L930	S931	T932	R933	L934	T935	P936	L937	S938	T939	R940	L941	T942	P943	L944	S945	T946	R947	L948	T949	P950	L951	S952	T953	R954	L955	T956	P957	L958	S959	T960	R961	L962	T963	P964	L965	S966	T967	R968	L969	T969	P970	L971	S972	T973	R974	L975	T976	P977	L978	S979	T980	R981	L982	T983	P984	L985	S986	T987	R988	L989	T990	P991	L992	S993	T994	R995	L996	T997	P998	L999	S1000	T1001	R1002	L1003	T1004	P1005	L1006	T1007	P1008	L1009	T1010	P1011	L1012	T1013	P1014	L1015	T1016	P1017	L1018	T1019	P1020	L1021	T1022	P1023	L1024	T1025	P1026	L1027	T1028	P1029	L1030	T1031	P1032	L1033	T1034	P1035	L1036	T1037	P1038	L1039	T1040	P1041	L1042	T1043	P1044	L1045	T1046	P1047	L1048	T1049	P1050	L1051	T1052	P1053	L1054	T1055	P1056	L1057	T1058	P1059	L1060	T1061	P1062	L1063	T1064	P1065	L1066	T1067	P1068	L1069	T1070	P1071	L1072	T1073	P1074	L1075	T1076	P1077	L1078	T1079	P1080	L1081	T1082	P1083	L1084	T1085	P1086	L1087	T1088	P1089	L1090	T1091	P1092	L1093	T1094	P1095	L1096	T1097	P1098	L1099	T1100	P1101	L1102	T1103	P1104	L1105	T1106	P1107	L1108	T1109	P1110	L1111	T1112	P1113	L1114	T1115	P1116	L1117	T1118	P1119	L1120	T1121	P1122	L1123	T1124	P1125	L1126	T1127	P1128	L1129	T1130	P1131	L1132	T1133	P1134	L1135	T1136	P1137	L1138	T1139	P1140	L1141	T1142	P1143	L1144	T1145	P1146	L1147	T1148	P1149	L1150	T1151	P1152	L1153	T1154	P1155	L1156	T1157	P1158	L1159	T1160	P1161	L1162	T1163	P1164	L1165	T1166	P1167	L1168	T1169	P1170	L1171	T1172	P1173	L1174	T1175	P1176	L1177	T1178	P1179	L1180	T1181	P1182	L1183	T1184	P1185	L1186	T1187	P1188	L1189	T1189	P1190	L1191	T1192	P1193	L1194	T1195	P1196	L1197	T1198	P1199	L1200	T1201	P1202	L1203	T1204	P1205	L1206	T1207	P1208	L1209	T1210	P1211	L1212	T1213	P1214	L1215	T1216	P1217	L1218	T1219	P1220	L1221	T1222	P1223	L1224	T1225	P1226	L1227	T1228	P1229	L1230	T1231	P1232	L1233	T1234	P1235	L1236	T1237	P1238	L1239	T1240	P1241	L1242	T1243	P1244	L1245	T1246	P1247	L1248	T1249	P1250	L1251	T1252	P1253	L1254	T1255	P1256	L1257	T1258	P1259	L1260	T1261	P1262	L1263	T1264	P1265	L1266	T1267	P1268	L1269	T1270	P1271	L1272	T1273	P1274	L1275	T1276	P1277	L1278	T1279	P1280	L1281	T1282	P1283	L1284	T1285	P1286	L1287	T1288	P1289	L1290	T1291	P1292	L1293	T1294	P1295	L1296	T1297	P1298	L1299	T1300	P1301	L1302	T1303	P1304	L1305	T1306	P1307	L1308	T1309	P1310	L1311	T1312	P1313	L1314	T1315	P1316	L1317	T1318	P1319	L1320	T1321	P1322	L1323	T1324	P1325	L1326	T1327	P1328	L1329	T1330	P1331	L1332	T1333	P1334	L1335	T1336	P1337	L1338	T1339	P1340	L1341	T1342	P1343	L1344	T1345	P1346	L1347	T1348	P1349	L1350	T1351	P1352	L1353	T1354	P1355	L1356	T1357	P1358	L1359	T1360	P1361	L1362	T1363	P1364	L1365	T1366	P1367	L1368	T1369	P1370	L1371	T1372	P1373	L1374	T1375	P1376	L1377	T1378	P1379	L1380	T1381	P1382	L1383	T1384	P1385	L1386	T1386	P1387	L1388	T1389	P1390	L1391	T1392	P1393	L1394	T1395	P1396	L1397	T1398	P1399	L1400	T1401	P1402	L1403	T1404	P1405	L1406	T1407	P1408	L1409	T1410	P1411	L1412	T1413	P1414	L1415	T1416	P1417	L1418	T1419	P1420	L1421	T1422	P1423	L1424	T1425	P1426	L1427	T1428	P1429	L1430	T1431	P1432	L1433	T1434	P1435	L1436	T1437	P1438	L1439	T1440	P1441	L1442	T1443	P1444	L1445	T1446	P1447	L1448	T1449	P1450	L1451	T1452	P1453	L1454	T1455	P1456	L1457	T1458	P1459	L1460	T1461	P1462	L1463	T1464	P1465	L1466	T1467	P1468	L1469	T1470	P1471	L1472	T1473	P1474	L1475	T1476	P1477	L1478	T1479	P1480	L1481	T1482	P1483	L1484	T1485	P1486	L1487	T1488	P1489	L1490	T1491	P1492	L1493	T1494	P1495	L1496	T1497	P1498	L1499	T1500	P1501	L1502	T1503	P1504	L1505	T1506	P1507	L1508	T1509	P1510	L1511	T1512	P1513	L1514	T1515	P1516	L1517	T1518	P1519	L1520	T1521	P1522	L1523	T1524	P1525	L1526	T1527	P1528	L1529	T1530	P1531	L1532	T1533	P1534	L1535	T1536	P1537	L1538	T1539	P1540	L1541	T1542	P1543	L1544	T1545	P1546	L1547	T1548	P1549	L1550	T1551	P1552	L1553	T1554	P1555	L1556	T1557	P1558	L1559	T1560	P1561	L1562	T1563	P1564	L1565	T1566	P1567	L1568	T1569	P1570	L1571	T1572	P1573	L1574	T1575	P1576	L1577	T1578	P1579	L1580	T1581	P1582	L1583	T1584	P1585	L1586	T1587	P1588	L1589	T1590	P1591	L1592	T1593	P1594	L1595	T1596	P1597	L1598	T1599	P1600	L1601	T1602	P1603	L1604	T1605	P1606	L1607	T1608	P1609	L1610	T1611	P1612	L1613	T1614	P1615	L1616	T1617	P1618	L1619	T1620	P1621	L1622	T1623	P1624	L1625	T1626	P1627	L1628	T1629	P1630	L1631	T1632	P1633	L1634	T1635	P1636	L1637	T1638	P1639	L1640	T1641	P1642	L1643	T1644	P1645	L1646	T1647	P1648	L1649	T1650	P1651	L1652	T1653	P1654	L1655	T1656	P1657	L1658	T1659	P1660	L1661	T1662	P1663	L1664	T1665	P1666	L1667	T1668	P1669	L1670	T1671	P1672	L1673	T1674	P1675	L1676	T1677	P1678	L1679	T1680	P1681	L1682	T1683	P1684	L1685	T1686	P1687	L1688	T1689	P1690	L1691	T1692	P1693	L1694	T1695	P1696	L1697	T1698	P1699	L1700	T1701	P1702	L1703	T1704	P1705	L1706	T1707	P1708	L1709	T1710	P1711	L1712	T1713	P1714	L1715	T1716	P1717	L1718	T1719	P1720	L1721	T1722	P1723	L1724	T1725	P1726	L1727	T1728	P1729	L1730	T1731	P1732	L1733	T1734	P1735	L1736	T1737	P1738	L1739	T1740	P1741	L1742	T1743	P1744	L1745	T1746	P1747	L1748	T1749	P1750	L1751	T1752	P1753	L1754	T1755	P1756	L1757	T1758	P1759	L1760	T1761	P1762	L1763	T1764	P1765	L1766	T1767	P1768	L1769	T1770	P1771	L1772	T1773	P1774	L1775	T1776	P1777	L1778	T1779	P1780	L1781	T1782	P1783	L1784	T1785	P1786	L1787	T1788	P1789	L1790	T1791	P1792	L1793	T1794	P1795	L1796	T1797	P1798	L1799	T1800	P1801	L1802	T1803	P1804	L1805	T1806	P1807	L1808	T1809	P1810	L1811	T1812	P181

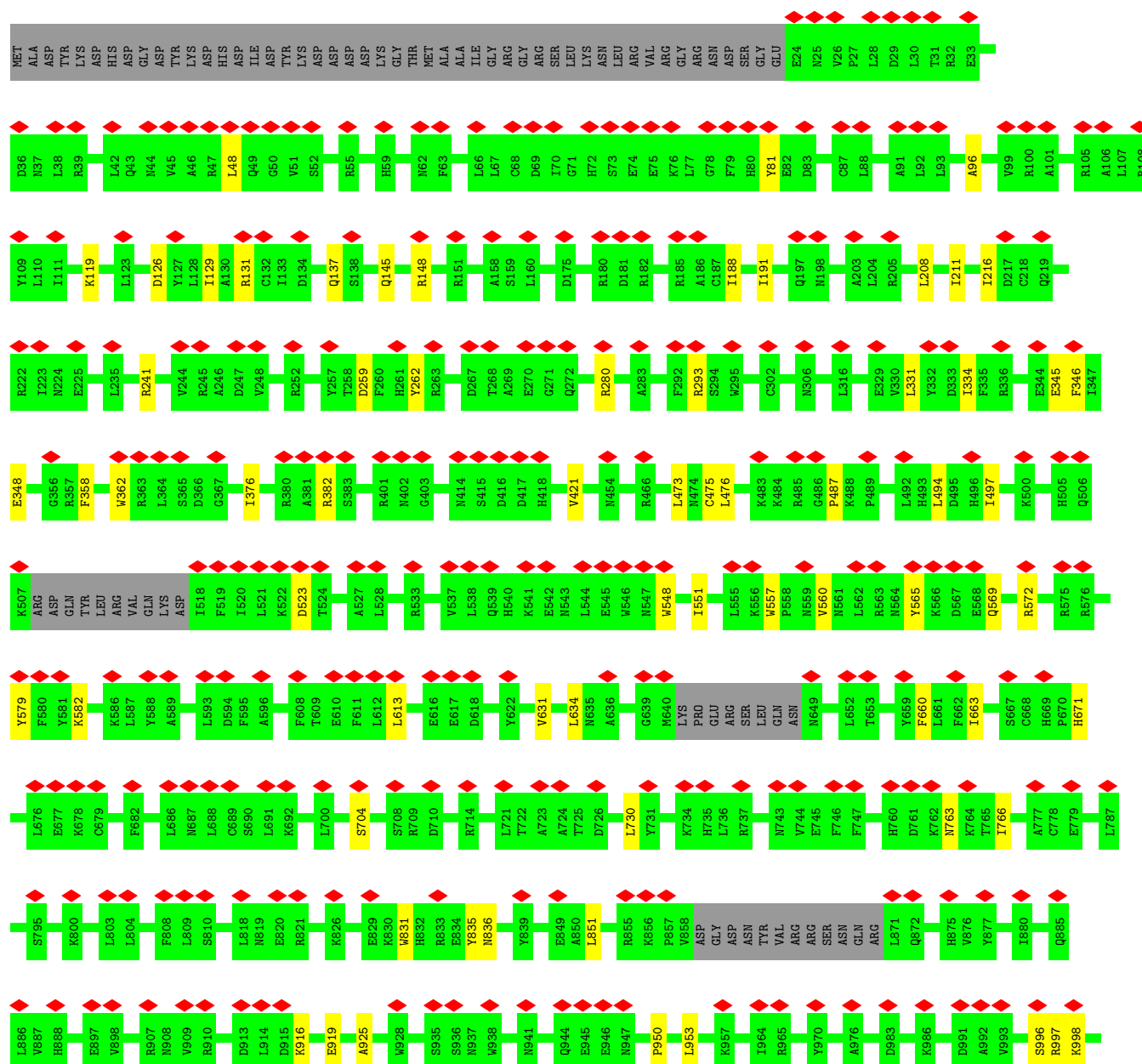


• Molecule 2: Target of rapamycin complex subunit LST8

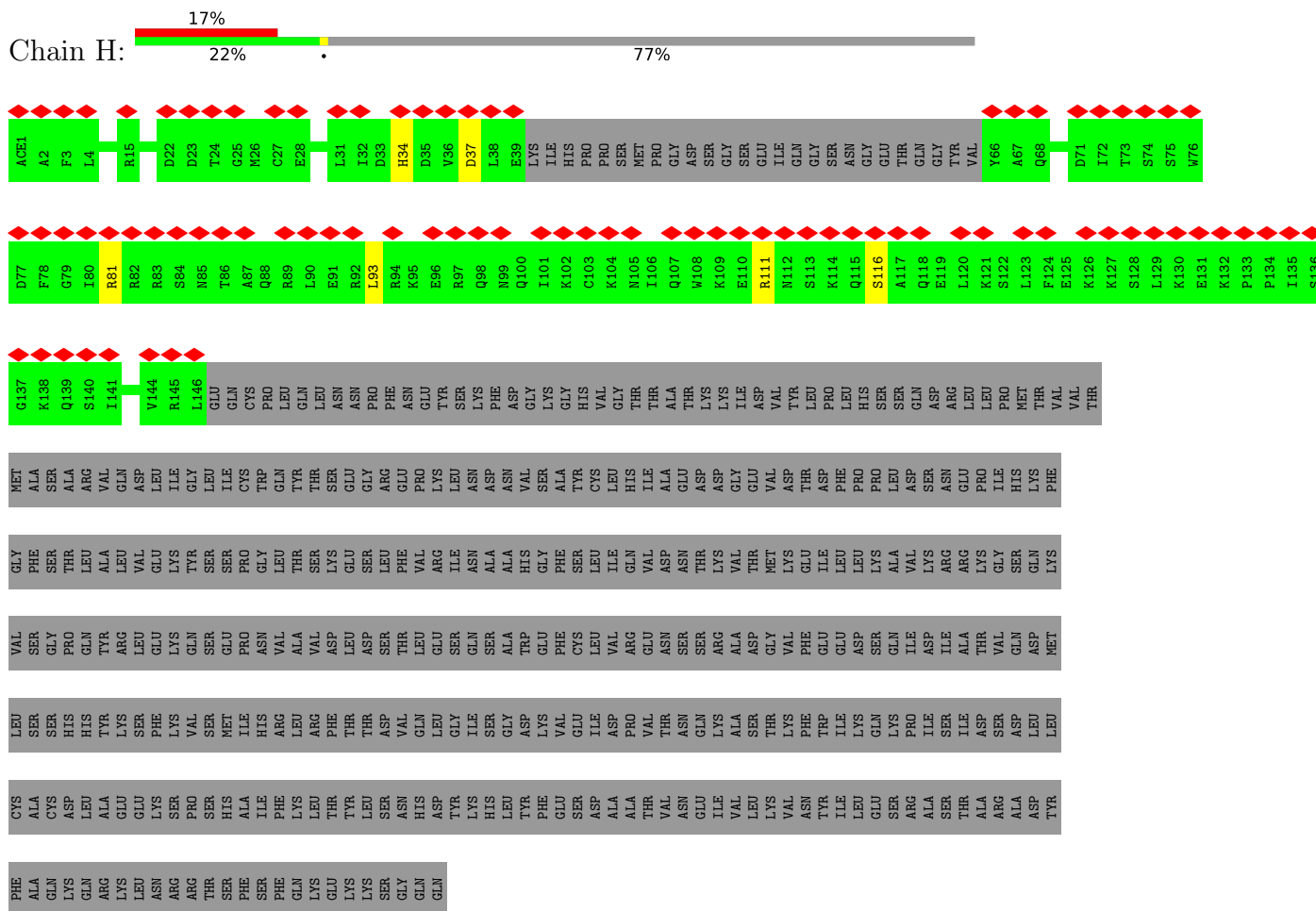




- Molecule 3: Rapamycin-insensitive companion of mTOR



- Molecule 4: Target of rapamycin complex 2 subunit MAPKAP1



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	38469	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	140	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.030	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	532.92804, 532.92804, 532.92804	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.514, 1.514, 1.514	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.35	0/18617	0.79	0/25184
1	B	0.35	0/18604	0.81	0/25166
2	C	0.35	0/2501	0.78	0/3408
2	D	0.34	0/2501	0.79	0/3408
3	E	0.34	0/9154	0.77	0/12384
3	F	0.34	0/9154	0.79	0/12384
4	G	0.32	0/984	0.81	0/1318
4	H	0.31	0/984	0.83	0/1318
All	All	0.34	0/62499	0.80	0/84570

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	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1132	ARG	Sidechain
1	B	1132	ARG	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	18242	0	18471	80	0
1	B	18230	0	18458	84	0
2	C	2443	0	2327	15	0
2	D	2443	0	2327	15	0
3	E	8990	0	9187	43	0
3	F	8990	0	9187	44	0
4	G	974	0	993	4	0
4	H	974	0	993	4	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
All	All	61288	0	61943	282	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 2.

All (282) 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:153:LEU:HD22	1:B:193:ASN:HB2	1.78	0.66
2:D:50:VAL:HG21	2:D:321:ASN:HB2	1.80	0.64
1:A:722:ASN:HD21	3:F:1001:TRP:HB3	1.63	0.62
1:A:2022:LEU:HD13	1:A:2066:LYS:HE2	1.82	0.60
3:E:1541:CYS:HA	3:E:1608:CYS:HB2	1.83	0.60
1:A:2185:LEU:HB2	1:A:2237:ILE:HB	1.84	0.60
3:F:345:GLU:HG2	3:F:348:GLU:H	1.67	0.59
1:B:1160:VAL:HA	1:B:1163:LEU:HD12	1.85	0.58
1:B:783:LEU:HD23	1:B:823:ILE:HD13	1.86	0.58
1:B:210:VAL:HG21	1:B:266:LEU:HB3	1.84	0.57
3:F:208:LEU:HA	3:F:211:ILE:HD12	1.87	0.57
1:A:1115:LEU:HD21	1:A:1155:ILE:HD11	1.87	0.57
3:F:145:GLN:HE22	3:F:148:ARG:HH11	1.53	0.57
3:E:46:ALA:HB1	3:E:1690:GLU:HG2	1.86	0.56
3:F:950:PRO:HA	3:F:953:LEU:HD12	1.87	0.56
3:F:293:ARG:HD2	3:F:851:LEU:HD22	1.88	0.56
1:A:2535:HIS:HA	1:A:2538:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1427:GLU:HG2	1:B:2395:ASN:HA	1.88	0.56
1:B:962:GLN:HE22	1:B:1000:VAL:HG13	1.71	0.56
1:B:2535:HIS:HA	1:B:2538:LEU:HD12	1.87	0.55
1:A:934:MET:HG2	1:A:953:VAL:HG21	1.89	0.55
3:E:730:LEU:HD13	3:E:766:ILE:HG12	1.88	0.55
1:A:424:VAL:HG11	1:A:458:ILE:HG12	1.89	0.55
1:B:90:ILE:HG23	1:B:107:PHE:HB3	1.89	0.54
3:E:950:PRO:HA	3:E:953:LEU:HD12	1.89	0.54
1:A:75:VAL:HG21	1:A:110:TYR:HB3	1.90	0.54
3:F:631:VAL:HA	3:F:634:LEU:HD12	1.89	0.54
1:B:741:LEU:HG	1:B:782:LYS:HE3	1.90	0.53
3:F:831:TRP:HA	3:F:835:TYR:HB2	1.89	0.53
1:B:1274:ARG:HD3	1:B:1279:ASP:HB3	1.90	0.53
1:B:1547:ARG:HA	1:B:1550:LEU:HD12	1.91	0.53
2:D:111:ILE:HD12	2:D:123:ARG:HB3	1.91	0.53
3:E:887:VAL:HG12	3:E:936:SER:HB2	1.89	0.53
3:E:825:ALA:HA	3:E:828:LEU:HD12	1.90	0.53
3:E:916:LYS:HB2	3:E:919:GLU:HG2	1.91	0.53
3:F:126:ASP:HA	3:F:129:ILE:HD12	1.91	0.53
1:A:2121:LEU:HB2	1:A:2160:LEU:HD12	1.91	0.53
3:E:126:ASP:HA	3:E:129:ILE:HD12	1.91	0.52
1:B:869:LEU:HA	1:B:872:LEU:HD13	1.92	0.52
1:A:1596:LEU:HA	1:A:1599:LEU:HD12	1.91	0.52
3:E:345:GLU:HG2	3:E:348:GLU:H	1.74	0.52
3:E:937:ASN:HA	3:E:940:LEU:HD12	1.92	0.52
1:B:2170:ARG:HB2	1:B:2186:LEU:HB3	1.90	0.52
3:E:380:ARG:HD3	3:E:741:ARG:HA	1.92	0.52
1:A:1272:ALA:HB1	1:A:1274:ARG:HG2	1.90	0.52
1:A:1988:HIS:CE1	1:A:1992:ASN:HD21	2.28	0.52
1:B:244:GLY:HA3	1:B:264:ALA:HB2	1.92	0.52
3:F:376:ILE:HG23	3:F:487:PRO:HB2	1.90	0.52
2:C:27:TRP:HH2	2:C:310:GLY:H	1.58	0.51
1:B:2366:MET:HG2	1:B:2373:GLU:HB2	1.92	0.51
3:F:569:GLN:HG2	3:F:572:ARG:HH21	1.75	0.51
4:H:111:ARG:HD2	4:H:116:SER:HB3	1.92	0.51
1:A:656:LEU:HA	1:A:659:LEU:HD12	1.92	0.51
1:B:955:LEU:HD22	1:B:971:VAL:HG13	1.92	0.51
1:B:1939:ILE:HA	1:B:1942:LEU:HD12	1.92	0.51
1:B:2253:TYR:HB2	1:B:2302:LEU:HD13	1.92	0.51
1:A:697:PHE:HA	1:A:700:LEU:HD12	1.93	0.51
1:B:486:ILE:HG23	1:B:504:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:81:TYR:HD2	3:F:119:LYS:HZ2	1.59	0.51
1:A:1010:GLU:HG2	1:A:1048:ILE:HG13	1.93	0.51
3:F:494:LEU:HA	3:F:497:ILE:HD12	1.93	0.51
2:C:198:ASN:HB2	2:C:213:LYS:HD2	1.93	0.51
3:F:331:LEU:HA	3:F:334:ILE:HD12	1.92	0.51
2:C:230:PRO:HG2	2:C:280:GLY:HA2	1.94	0.50
2:D:284:TYR:HB3	2:D:296:LEU:HD11	1.92	0.50
3:E:344:GLU:HG2	3:E:418:HIS:HB3	1.93	0.50
2:C:116:SER:HB2	2:C:119:LEU:HB2	1.93	0.50
3:E:179:GLU:HG3	3:E:1667:LEU:HD23	1.94	0.50
3:F:96:ALA:HB2	4:H:81:ARG:HH22	1.75	0.50
3:F:473:LEU:HA	3:F:476:LEU:HD12	1.94	0.50
1:A:2154:GLN:HE21	1:A:2177:SER:HA	1.76	0.50
1:B:463:LEU:HD22	1:B:507:PRO:HB2	1.94	0.50
1:A:1477:MET:HE2	1:A:1500:LYS:HE2	1.94	0.50
2:D:50:VAL:HG13	2:D:319:ALA:HB1	1.93	0.50
1:B:872:LEU:HB3	1:B:1576:THR:HG22	1.94	0.50
3:E:831:TRP:HA	3:E:835:TYR:HB2	1.93	0.50
3:F:131:ARG:HH12	3:F:1677:PHE:HB2	1.77	0.50
1:A:2137:GLU:HA	1:A:2152:ARG:HD3	1.93	0.49
1:B:1988:HIS:CE1	1:B:1992:ASN:HD21	2.30	0.49
3:F:216:ILE:HG22	3:F:280:ARG:HH11	1.77	0.49
1:A:2118:LEU:HD21	1:A:2121:LEU:HD21	1.94	0.49
2:D:86:LYS:HB3	2:D:105:GLU:HB2	1.94	0.49
2:C:123:ARG:HH22	2:C:157:LEU:HA	1.77	0.49
1:A:2340:HIS:CE1	1:A:2342:SER:HB2	2.47	0.49
3:E:144:THR:HG23	4:G:30:VAL:HG22	1.93	0.49
1:B:1206:HIS:HE1	1:B:1208:ARG:HB3	1.77	0.49
1:A:194:ILE:HG13	1:A:209:ALA:HB1	1.94	0.49
3:E:259:ASP:HB3	3:E:262:TYR:HB2	1.95	0.49
1:A:2525:VAL:HA	1:A:2528:LEU:HD12	1.93	0.49
1:B:1355:GLN:HE22	1:B:1392:ALA:HB2	1.77	0.49
1:B:1380:ILE:HG23	1:B:1399:TYR:HB3	1.95	0.49
1:A:607:ALA:HA	1:A:611:LEU:HD12	1.95	0.49
1:A:1400:LYS:HE2	1:A:1415:SER:HB3	1.94	0.49
3:F:241:ARG:HD2	3:F:1442:ILE:HD12	1.94	0.49
1:A:1364:MET:HG3	1:A:1372:LEU:HB2	1.95	0.48
2:C:120:GLN:HB3	4:G:116:SER:HB2	1.95	0.48
2:D:122:GLN:HE21	2:D:124:ILE:HD11	1.77	0.48
1:A:802:ILE:HA	1:A:805:LEU:HD12	1.94	0.48
1:A:872:LEU:HD21	1:A:1575:LEU:HG	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1160:VAL:HA	1:A:1163:LEU:HD12	1.95	0.48
1:A:1291:LEU:HB3	1:A:1321:ALA:HB1	1.95	0.48
1:B:712:ILE:HD11	1:B:760:LEU:HD13	1.96	0.48
1:B:799:LEU:HG	1:B:843:THR:HG21	1.94	0.48
1:B:1091:ILE:HA	1:B:1094:ILE:HD12	1.96	0.48
1:B:1937:GLN:HG3	1:B:1938:VAL:HG13	1.96	0.48
1:B:2525:VAL:HA	1:B:2528:LEU:HD12	1.94	0.48
3:F:560:VAL:HA	3:F:565:TYR:HE2	1.79	0.48
1:B:385:ASN:HB3	1:B:388:ILE:HD12	1.95	0.48
1:B:965:SER:HA	1:B:968:HIS:CG	2.48	0.48
2:D:57:ILE:HB	2:D:70:LEU:HD11	1.96	0.48
3:F:579:TYR:HA	3:F:582:LYS:HD3	1.95	0.48
3:F:916:LYS:HB2	3:F:919:GLU:HG2	1.96	0.48
3:E:548:TRP:HA	3:E:551:ILE:HD12	1.96	0.48
3:E:331:LEU:HD23	3:E:334:ILE:HD12	1.95	0.48
1:A:104:ILE:HA	1:A:133:LEU:HD11	1.96	0.47
3:F:523:ASP:HA	3:F:557:TRP:HE1	1.79	0.47
1:A:976:THR:HA	1:A:1019:LEU:HD21	1.95	0.47
1:B:424:VAL:HA	1:B:430:ARG:HG3	1.96	0.47
1:A:1072:PRO:HA	1:A:1075:ILE:HD12	1.96	0.47
3:F:259:ASP:HB3	3:F:262:TYR:HB2	1.96	0.47
1:B:293:GLN:HA	1:B:515:PRO:HB2	1.96	0.47
1:A:1427:GLU:HG2	1:A:2395:ASN:HA	1.96	0.47
1:B:854:VAL:HG11	1:B:1622:ARG:HG2	1.96	0.47
2:D:66:ARG:HD2	2:D:77:PRO:HG3	1.97	0.47
3:E:111:ILE:HA	3:E:116:ILE:HG21	1.97	0.47
1:A:1421:ASN:HD21	1:A:1452:LYS:HB3	1.81	0.46
3:F:548:TRP:HA	3:F:551:ILE:HD12	1.98	0.46
1:A:1265:LEU:HD21	1:A:1294:ASP:HB2	1.97	0.46
1:B:1421:ASN:HD21	1:B:1452:LYS:HB3	1.80	0.46
3:F:137:GLN:HE22	3:F:1678:GLN:HE22	1.63	0.46
3:F:613:LEU:HD11	3:F:671:HIS:HB2	1.98	0.46
3:E:376:ILE:HG23	3:E:487:PRO:HB2	1.97	0.46
3:F:1636:LEU:HA	3:F:1639:ILE:HD12	1.97	0.46
1:A:1400:LYS:HE3	1:A:1412:ILE:HG23	1.96	0.46
2:C:16:ALA:HB3	2:C:319:ALA:HB3	1.98	0.46
3:E:81:TYR:HD2	3:E:119:LYS:HZ2	1.62	0.46
3:E:241:ARG:HD2	3:E:1442:ILE:HD12	1.96	0.46
3:E:682:PHE:HA	3:E:685:LEU:HD12	1.98	0.46
2:C:274:TRP:HE1	2:C:290:SER:HB3	1.81	0.46
4:H:34:HIS:HA	4:H:37:ASP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2141:PRO:HD3	1:A:2153:ILE:HD11	1.96	0.46
1:B:630:LEU:HD22	1:B:652:VAL:HG13	1.97	0.46
1:B:802:ILE:HA	1:B:805:LEU:HD12	1.98	0.45
3:F:996:SER:HA	3:F:1425:ILE:HG23	1.98	0.45
1:B:127:SER:HA	1:B:130:ILE:HD12	1.98	0.45
1:B:1010:GLU:HG2	1:B:1048:ILE:HG13	1.98	0.45
1:B:1125:PRO:HA	1:B:1132:ARG:HH22	1.82	0.45
1:A:80:ALA:HB1	1:A:84:LYS:HE3	1.99	0.45
1:B:2380:THR:H	1:B:2383:LEU:HD12	1.81	0.45
1:A:2387:MET:HE1	1:A:2392:LEU:HA	1.98	0.45
3:E:304:PRO:HG3	3:E:1438:GLN:HE22	1.80	0.45
4:G:76:TRP:CD1	4:G:76:TRP:H	2.29	0.45
1:A:690:ALA:HA	1:A:693:LEU:HD12	1.98	0.45
1:A:1939:ILE:HA	1:A:1942:LEU:HD12	1.99	0.45
1:B:1670:HIS:HA	1:B:1673:LEU:HD12	1.99	0.45
3:E:245:ARG:HB2	3:E:249:GLU:HG3	1.98	0.45
3:F:331:LEU:HD23	3:F:334:ILE:HD12	1.98	0.45
3:F:1637:LEU:HB3	4:H:93:LEU:HD22	1.99	0.45
1:B:293:GLN:HG2	1:B:516:ALA:HA	1.99	0.45
1:B:776:LEU:HA	1:B:779:LEU:HD12	1.99	0.45
2:C:92:GLY:HA3	2:C:101:TYR:CZ	2.52	0.45
3:F:660:PHE:HA	3:F:663:ILE:HD12	1.98	0.45
2:D:23:THR:HG22	2:D:39:GLN:HE22	1.82	0.45
3:F:346:PHE:HD1	3:F:421:VAL:HG13	1.81	0.44
1:A:1786:TRP:CZ2	1:A:1788:LYS:HD2	2.52	0.44
1:B:1031:MET:HA	1:B:1034:ILE:HD12	1.98	0.44
2:D:40:HIS:CE1	2:D:66:ARG:HH21	2.36	0.44
2:D:234:LEU:HD11	2:D:255:MET:HE2	1.99	0.44
1:A:1932:ILE:HA	1:A:1935:TRP:HD1	1.82	0.44
1:B:296:HIS:NE2	1:B:587:ARG:HD2	2.32	0.44
3:E:337:LEU:HD13	3:E:429:GLU:HB3	2.00	0.44
1:B:1961:LEU:HA	1:B:1964:ILE:HD12	2.00	0.44
1:B:145:VAL:HG13	1:B:175:LEU:HD13	2.00	0.44
1:B:656:LEU:HD23	1:B:659:LEU:HD12	1.98	0.44
1:A:1217:VAL:HG21	3:E:521:LEU:HD11	2.00	0.44
1:A:84:LYS:HE2	1:A:121:VAL:HB	2.00	0.44
1:A:885:ILE:HA	1:A:888:LEU:HD12	2.00	0.44
1:B:393:LEU:HB3	1:B:436:ALA:HB2	1.99	0.44
1:B:952:MET:HA	1:B:955:LEU:HD12	1.99	0.44
1:A:1684:GLN:HB3	1:A:1687:HIS:CE1	2.52	0.44
1:A:2411:LYS:HG3	1:A:2508:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:852:THR:HG21	4:G:4:LEU:HD11	1.99	0.43
1:A:75:VAL:HG22	1:A:114:LEU:HD11	1.99	0.43
1:A:1044:MET:HA	1:A:1049:GLN:NE2	2.34	0.43
3:E:124:LYS:HE3	3:E:1519:ASN:HA	2.00	0.43
1:B:656:LEU:HA	1:B:659:LEU:HD12	2.00	0.43
2:C:24:VAL:HB	2:C:38:VAL:HG22	2.00	0.43
3:E:121:LEU:HD11	3:E:160:LEU:HB3	1.99	0.43
1:A:483:PHE:HB3	1:A:520:VAL:HG21	2.00	0.43
1:A:1976:LEU:HB3	1:A:1995:LEU:HD21	2.01	0.43
2:C:136:LEU:HD11	2:C:140:GLN:HA	2.01	0.43
1:B:304:MET:HA	1:B:580:GLY:H	1.83	0.43
1:B:2008:GLN:HE22	1:B:2137:GLU:H	1.67	0.43
1:A:1500:LYS:HG3	1:A:1504:VAL:HB	2.00	0.43
1:B:1477:MET:HG3	1:B:1500:LYS:HE2	2.00	0.43
3:E:295:TRP:HZ3	3:E:394:LEU:HD13	1.83	0.43
3:E:785:HIS:HA	3:E:788:ILE:HD12	2.00	0.43
3:F:358:PHE:HA	3:F:362:TRP:CZ3	2.54	0.43
3:F:763:ASN:HB3	3:F:766:ILE:HD12	2.01	0.43
1:A:2048:PHE:CE2	1:A:2085:CYS:HB3	2.54	0.43
3:F:346:PHE:CZ	3:F:475:CYS:HB3	2.54	0.43
1:A:421:LEU:HD23	1:A:458:ILE:HD11	2.01	0.43
1:A:2380:THR:H	1:A:2383:LEU:HD12	1.83	0.43
1:A:630:LEU:HD22	1:A:652:VAL:HG13	2.01	0.42
2:D:14:ILE:HG23	2:D:54:ARG:HH21	1.84	0.42
1:B:746:ILE:HG22	1:B:749:ILE:H	1.84	0.42
3:E:169:LEU:HB3	3:E:191:ILE:HD11	2.01	0.42
1:A:825:MET:HE1	1:A:864:LEU:HD22	2.01	0.42
1:B:1910:TRP:CD1	1:B:1953:VAL:HG13	2.54	0.42
3:E:917:TRP:HA	3:E:920:ILE:HD12	2.01	0.42
1:A:1879:MET:HE3	1:A:1880:TYR:CZ	2.54	0.42
1:B:1101:GLN:HG3	1:B:1138:THR:HG23	2.02	0.42
1:A:776:LEU:HA	1:A:779:LEU:HD12	2.01	0.42
1:B:846:GLN:HE22	1:B:886:ARG:HH22	1.68	0.42
3:E:613:LEU:HD11	3:E:671:HIS:HB2	2.01	0.42
1:A:965:SER:HA	1:A:968:HIS:CG	2.55	0.42
1:B:2020:ALA:HA	1:B:2186:LEU:HD21	2.00	0.42
1:A:853:TYR:CE2	1:A:857:PRO:HD3	2.55	0.42
1:A:1274:ARG:HB2	1:A:1280:TRP:CE2	2.55	0.42
1:A:541:LYS:HA	1:A:552:LEU:HB2	2.02	0.42
1:A:1954:GLY:HA2	1:A:1957:ILE:HD12	2.02	0.42
2:D:40:HIS:CG	2:D:66:ARG:HH21	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:730:LEU:HD13	3:F:766:ILE:HG12	2.01	0.42
2:C:165:LEU:HD21	2:C:197:TRP:CE2	2.55	0.42
1:A:1751:PHE:HA	1:A:1754:LEU:HD12	2.01	0.42
1:B:396:LEU:HD13	1:B:416:THR:HG23	2.01	0.42
2:C:171:VAL:HG11	2:C:189:ASN:HD22	1.85	0.42
3:E:547:ASN:HB3	3:E:550:LEU:HD12	2.01	0.42
3:F:188:ILE:HA	3:F:191:ILE:HD12	2.02	0.42
1:A:210:VAL:HG21	1:A:266:LEU:HB3	2.01	0.41
3:E:794:LEU:HD12	3:E:805:LEU:HD13	2.02	0.41
1:A:656:LEU:HA	1:A:656:LEU:HD23	1.88	0.41
1:A:1374:LEU:HD12	1:A:1383:LEU:HD11	2.02	0.41
1:B:149:VAL:HG11	1:B:186:GLN:HB3	2.02	0.41
1:B:1786:TRP:CZ2	1:B:1788:LYS:HD2	2.55	0.41
2:C:136:LEU:HD21	2:C:140:GLN:HG2	2.01	0.41
3:E:270:GLU:HA	3:E:273:LEU:HG	2.02	0.41
1:B:198:VAL:HG11	1:B:267:ILE:HD11	2.01	0.41
3:F:836:ASN:HB3	3:F:925:ALA:HB1	2.01	0.41
1:A:681:GLU:HG2	1:A:717:ARG:HD2	2.02	0.41
1:B:1272:ALA:HB1	1:B:1274:ARG:HG2	2.02	0.41
1:B:2160:LEU:HD22	1:B:2172:LEU:HA	2.01	0.41
1:A:1477:MET:HE3	1:A:1477:MET:HB3	1.85	0.41
1:B:2340:HIS:CE1	1:B:2342:SER:HB2	2.55	0.41
2:D:180:PRO:HG3	2:D:230:PRO:HA	2.03	0.41
1:A:1643:VAL:HG23	1:A:1644:VAL:HG23	2.02	0.41
1:B:1196:ASN:HA	1:B:1199:LEU:HD12	2.03	0.41
1:B:1198:VAL:HG22	1:B:1201:ARG:HH22	1.86	0.41
1:B:1533:THR:HA	1:B:1536:ILE:HD12	2.03	0.41
1:A:746:ILE:HB	1:A:749:ILE:HD12	2.03	0.41
1:B:1042:TRP:CD1	1:B:1049:GLN:HG2	2.55	0.41
3:F:48:LEU:HD22	3:F:1686:HIS:CD2	2.56	0.41
3:F:473:LEU:HD23	3:F:476:LEU:HD12	2.03	0.41
1:A:1544:ALA:HB3	1:A:1567:ALA:HB2	2.03	0.41
1:B:2170:ARG:HB2	1:B:2186:LEU:HD23	2.03	0.41
2:D:136:LEU:HD11	2:D:140:GLN:HA	2.03	0.41
1:A:2034:ALA:HB1	1:A:2047:MET:HG3	2.02	0.41
1:B:693:LEU:HD23	1:B:696:LEU:HD12	2.03	0.41
1:B:1552:LEU:HD21	1:B:1602:VAL:HG11	2.03	0.41
1:B:1673:LEU:HD13	1:B:1700:TYR:HD1	1.85	0.41
1:B:2527:LEU:HD23	1:B:2530:LYS:HD2	2.02	0.41
3:F:382:ARG:HA	3:F:997:ARG:HB2	2.03	0.41
3:F:660:PHE:HB3	3:F:704:SER:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2194:GLN:HG3	1:A:2421:PHE:HZ	1.86	0.41
1:B:115:LEU:HD21	1:B:130:ILE:HD11	2.03	0.41
3:E:199:PRO:HG3	3:E:240:THR:HG22	2.02	0.41
1:A:663:GLY:HA3	1:A:675:VAL:HG11	2.02	0.40
1:A:1613:GLU:HG2	1:A:1616:ARG:NH2	2.36	0.40
1:B:825:MET:HE1	1:B:864:LEU:HD13	2.02	0.40
1:A:2022:LEU:HB2	1:A:2024:HIS:CE1	2.56	0.40
1:B:1089:GLY:HA2	1:B:1128:PRO:HG3	2.03	0.40
2:C:40:HIS:CD2	2:C:66:ARG:HH21	2.38	0.40
3:E:990:TRP:CZ2	3:E:1430:PRO:HG3	2.55	0.40
1:A:396:LEU:HD23	1:A:399:LEU:HD12	2.04	0.40
1:B:1756:GLU:HA	1:B:1759:LEU:HD12	2.03	0.40
3:E:633:TRP:CZ2	3:E:656:SER:HB2	2.56	0.40
3:F:382:ARG:CZ	3:F:998:LYS:HG3	2.51	0.40
1:B:187:VAL:HA	1:B:190:PHE:HB3	2.04	0.40
1:B:1119:VAL:HA	1:B:1122:PHE:CE2	2.56	0.40
1:B:2303:LEU:HD23	1:B:2303:LEU:HA	1.90	0.40
3:E:293:ARG:HD2	3:E:851:LEU:HD22	2.03	0.40
3:E:635:ASN:HA	3:E:640:MET:HE3	2.04	0.40

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	2245/2590 (87%)	2185 (97%)	59 (3%)	1 (0%)	100	100
1	B	2241/2590 (86%)	2184 (98%)	56 (2%)	1 (0%)	100	100
2	C	313/326 (96%)	301 (96%)	12 (4%)	0	100	100
2	D	313/326 (96%)	302 (96%)	11 (4%)	0	100	100
3	E	1103/1734 (64%)	1079 (98%)	24 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	1103/1734 (64%)	1076 (98%)	27 (2%)	0	100	100
4	G	116/522 (22%)	111 (96%)	5 (4%)	0	100	100
4	H	116/522 (22%)	107 (92%)	9 (8%)	0	100	100
All	All	7550/10344 (73%)	7345 (97%)	203 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	180	PRO
1	A	569	GLY

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	1991/2248 (89%)	1991 (100%)	0	100	100
1	B	1990/2248 (88%)	1990 (100%)	0	100	100
2	C	267/276 (97%)	267 (100%)	0	100	100
2	D	267/276 (97%)	267 (100%)	0	100	100
3	E	1005/1562 (64%)	1005 (100%)	0	100	100
3	F	1005/1562 (64%)	1005 (100%)	0	100	100
4	G	111/470 (24%)	111 (100%)	0	100	100
4	H	111/470 (24%)	111 (100%)	0	100	100
All	All	6747/9112 (74%)	6747 (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. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	A	722	ASN
1	A	743	HIS
1	A	791	ASN
1	A	1049	GLN
1	A	1207	GLN
1	A	1348	GLN
1	A	1405	GLN
1	A	1421	ASN
1	A	1693	HIS
1	A	1715	GLN
1	A	1791	HIS
1	A	1803	HIS
1	A	1958	HIS
1	A	1992	ASN
1	A	2003	ASN
1	A	2007	GLN
1	A	2024	HIS
1	A	2028	HIS
1	A	2071	ASN
1	A	2148	GLN
1	A	2154	GLN
1	A	2180	HIS
1	A	2410	HIS
1	B	68	ASN
1	B	736	GLN
1	B	846	GLN
1	B	899	HIS
1	B	962	GLN
1	B	1077	HIS
1	B	1207	GLN
1	B	1311	ASN
1	B	1355	GLN
1	B	1366	HIS
1	B	1405	GLN
1	B	1424	GLN
1	B	1494	HIS
1	B	1553	HIS
1	B	1730	HIS
1	B	1739	HIS
1	B	1803	HIS
1	B	1808	ASN
1	B	1937	GLN

Continued on next page...

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Mol	Chain	Res	Type
1	B	1992	ASN
1	B	2003	ASN
1	B	2007	GLN
1	B	2117	GLN
1	B	2154	GLN
1	B	2223	GLN
1	B	2282	GLN
1	B	2531	GLN
2	C	30	HIS
2	C	71	ASN
2	C	198	ASN
2	D	39	GLN
2	D	122	GLN
2	D	283	GLN
3	E	178	GLN
3	E	233	HIS
3	E	242	GLN
3	E	300	ASN
3	E	432	HIS
3	E	435	ASN
3	E	559	ASN
3	E	658	HIS
3	E	694	GLN
3	E	900	ASN
3	E	958	GLN
3	E	1438	GLN
3	E	1485	GLN
3	E	1494	ASN
3	E	1632	HIS
3	E	1658	HIS
3	F	145	GLN
3	F	233	HIS
3	F	242	GLN
3	F	300	ASN
3	F	432	HIS
3	F	435	ASN
3	F	454	ASN
3	F	480	HIS
3	F	505	HIS
3	F	540	HIS
3	F	900	ASN
3	F	908	ASN

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Mol	Chain	Res	Type
3	F	947	ASN
3	F	988	HIS
3	F	999	HIS
3	F	1494	ASN
3	F	1658	HIS
3	F	1678	GLN
3	F	1686	HIS
4	G	18	HIS
4	G	115	GLN
4	H	18	HIS
4	H	88	GLN
4	H	139	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

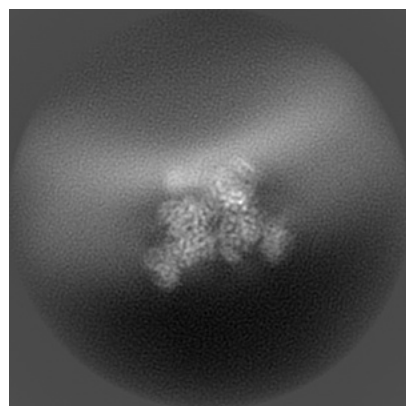
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56117. These allow visual inspection of the internal detail of the map and identification of artifacts.

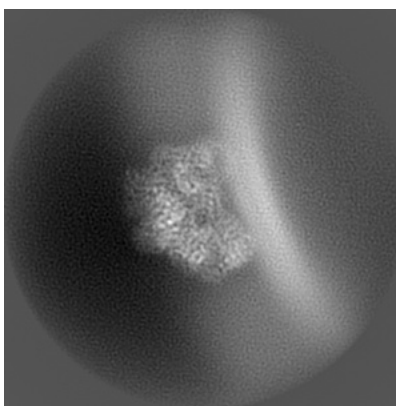
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

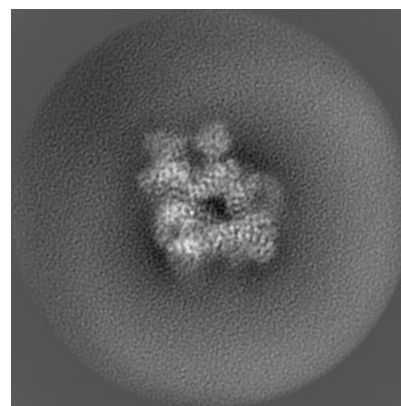
6.1.1 Primary map



X

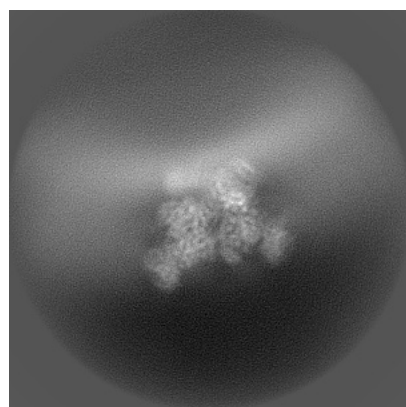


Y

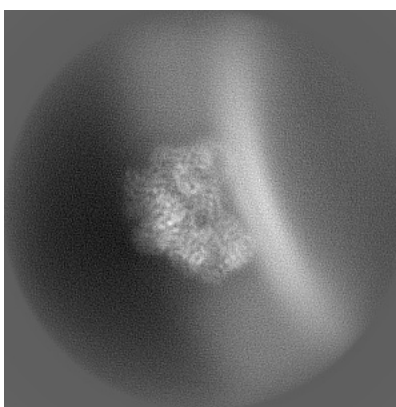


Z

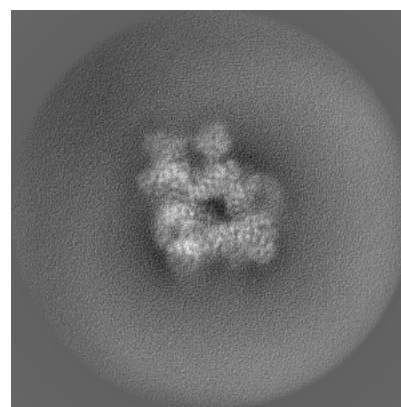
6.1.2 Raw map



X



Y

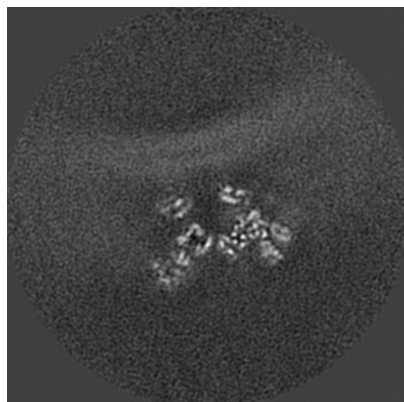


Z

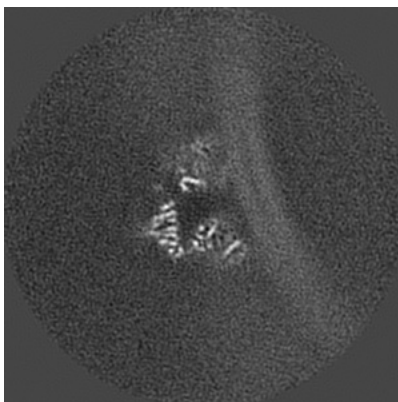
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

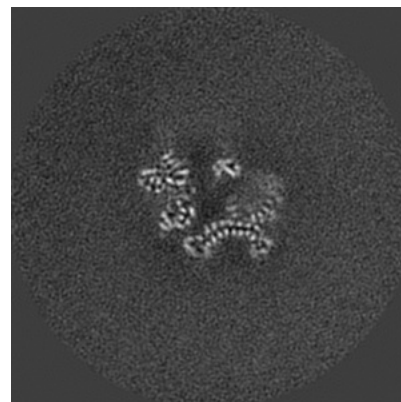
6.2.1 Primary map



X Index: 176

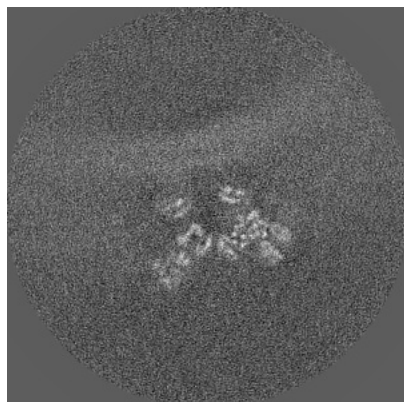


Y Index: 176

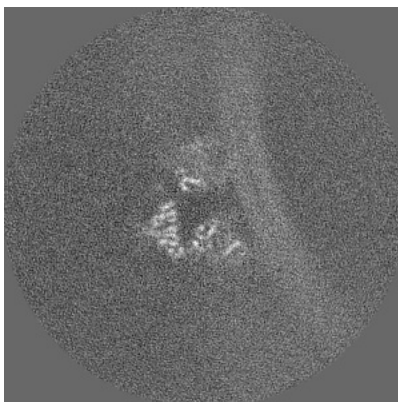


Z Index: 176

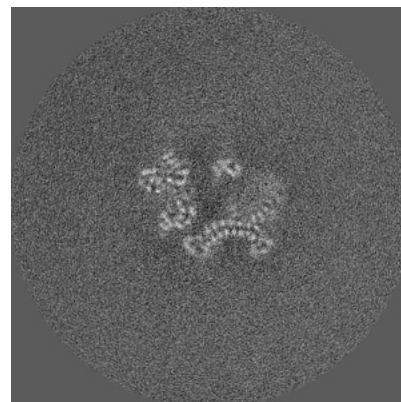
6.2.2 Raw map



X Index: 176



Y Index: 176

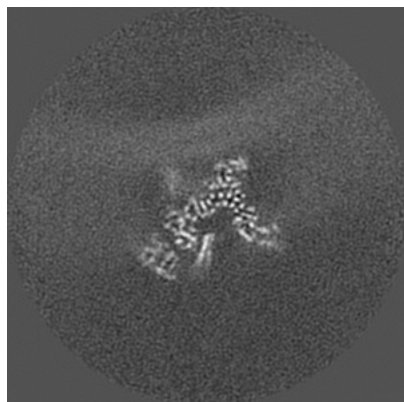


Z Index: 176

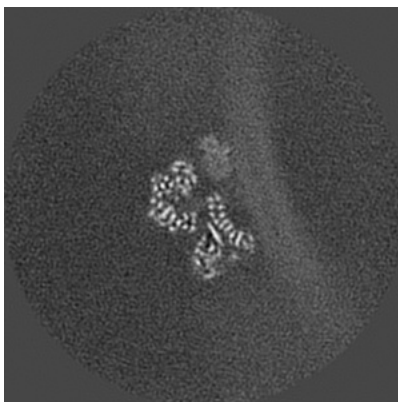
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

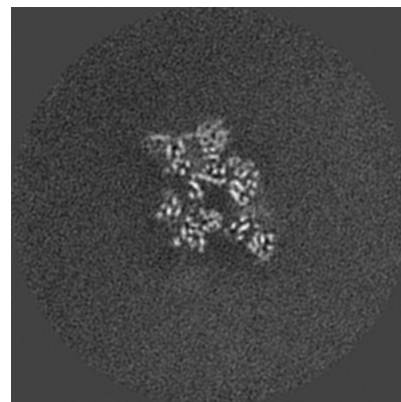
6.3.1 Primary map



X Index: 151

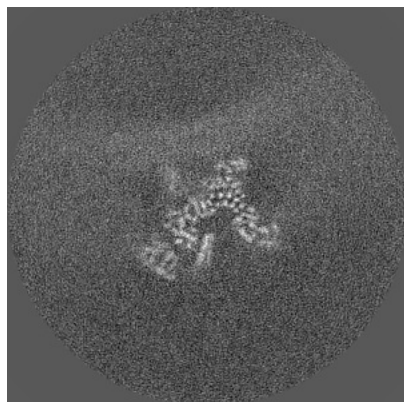


Y Index: 195

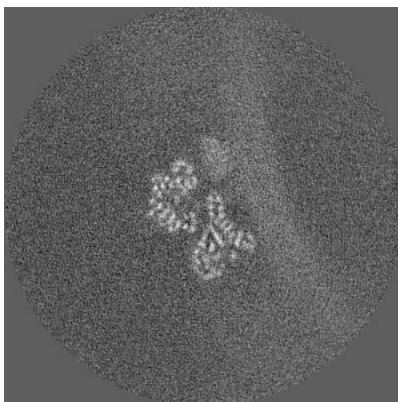


Z Index: 153

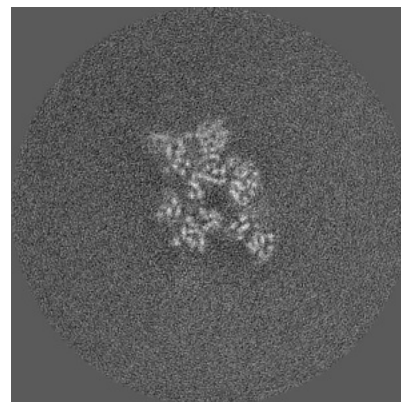
6.3.2 Raw map



X Index: 151



Y Index: 196

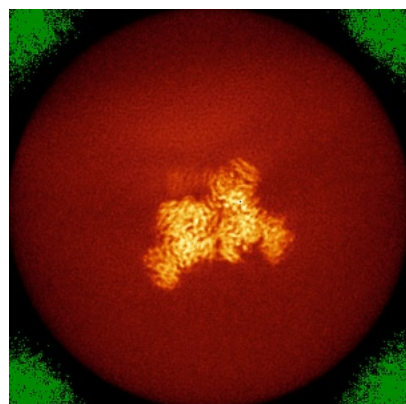


Z Index: 153

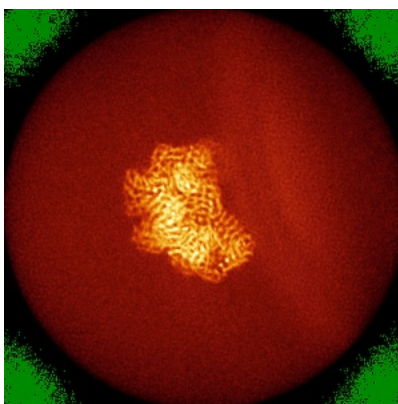
The images above show the largest variance slices of the map in three orthogonal directions.

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

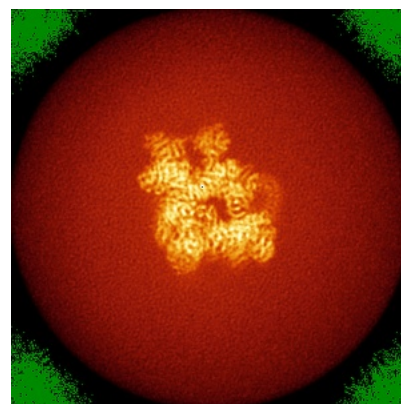
6.4.1 Primary map



X

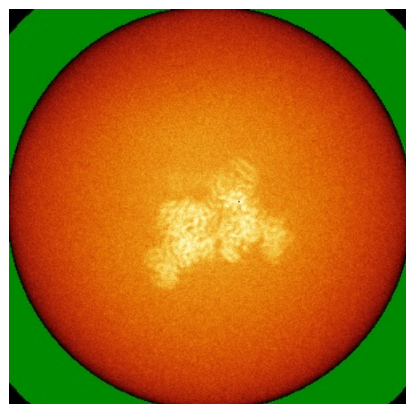


Y

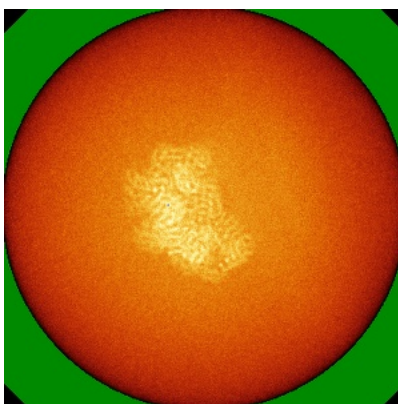


Z

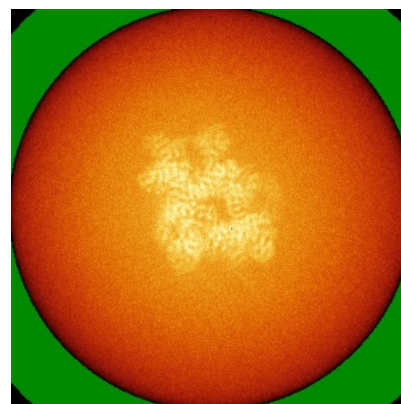
6.4.2 Raw map



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.

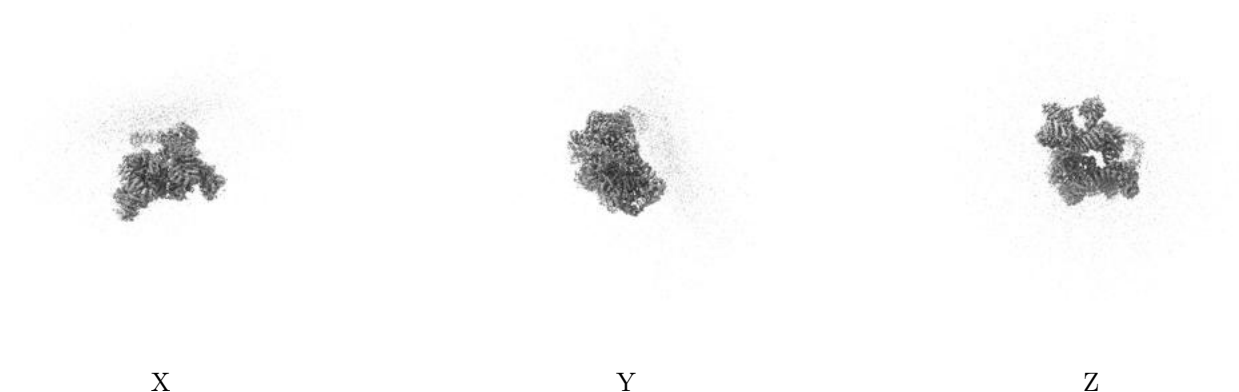
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

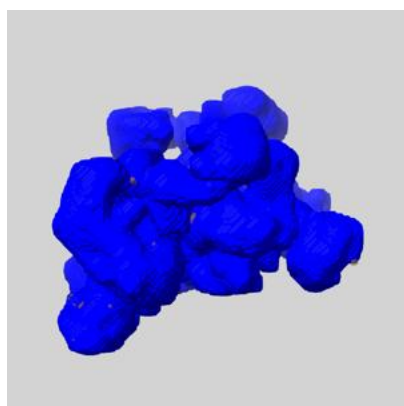
6.6 Mask visualisation [i](#)

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

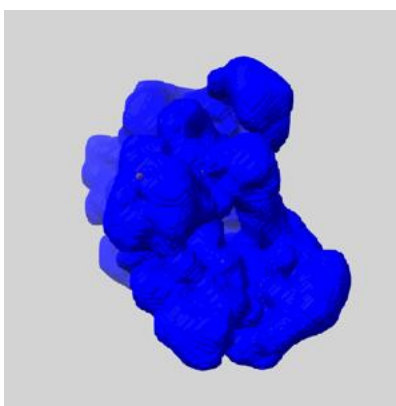
A mask typically either:

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

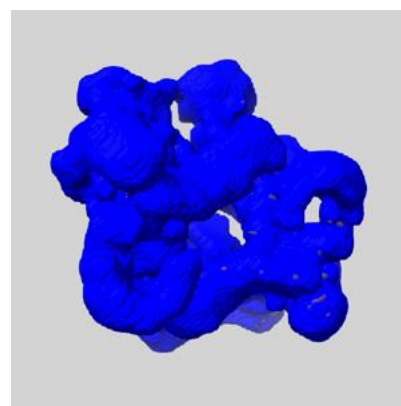
6.6.1 emd_56117_msk_1.map [i](#)



X



Y

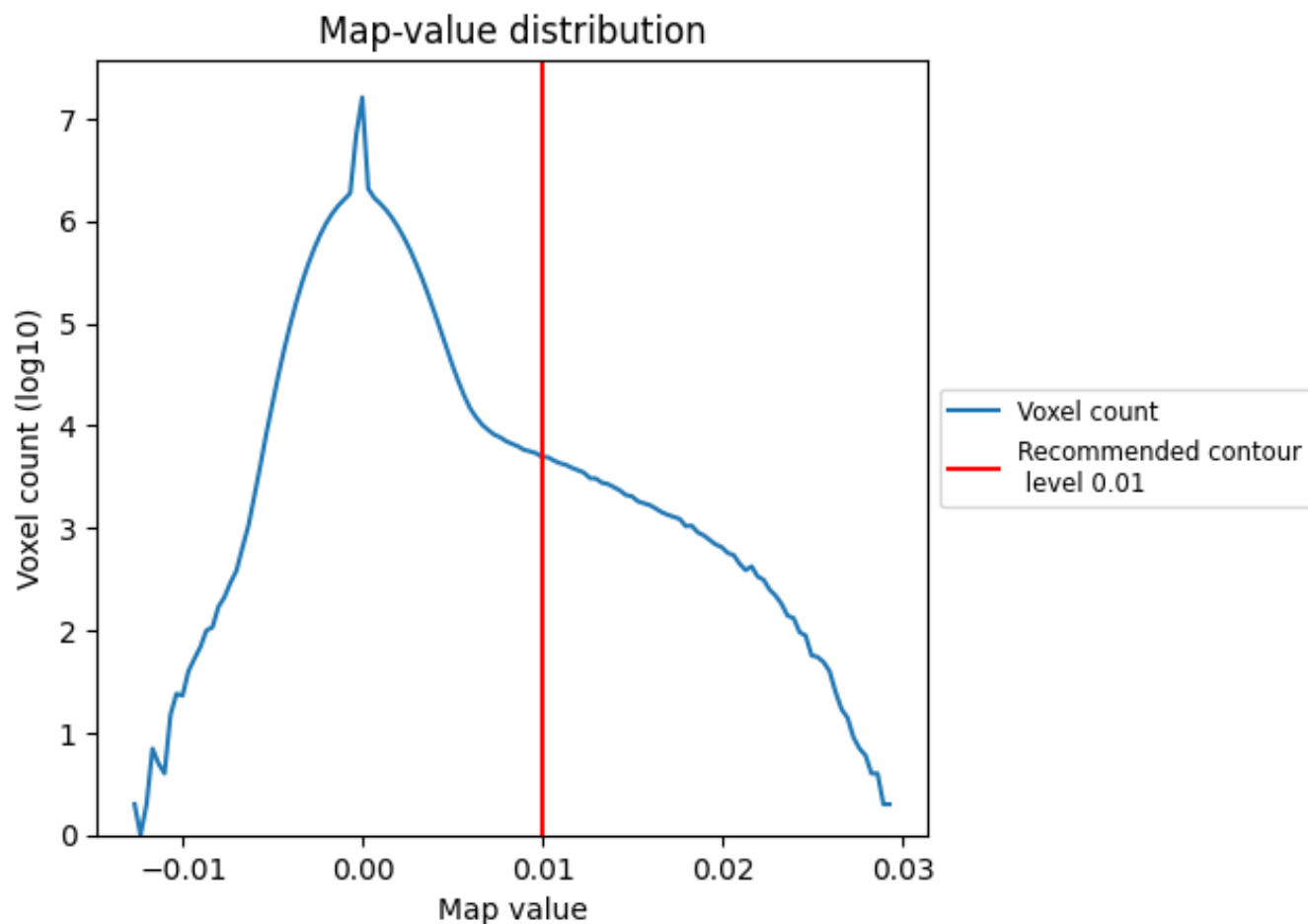


Z

7 Map analysis [i](#)

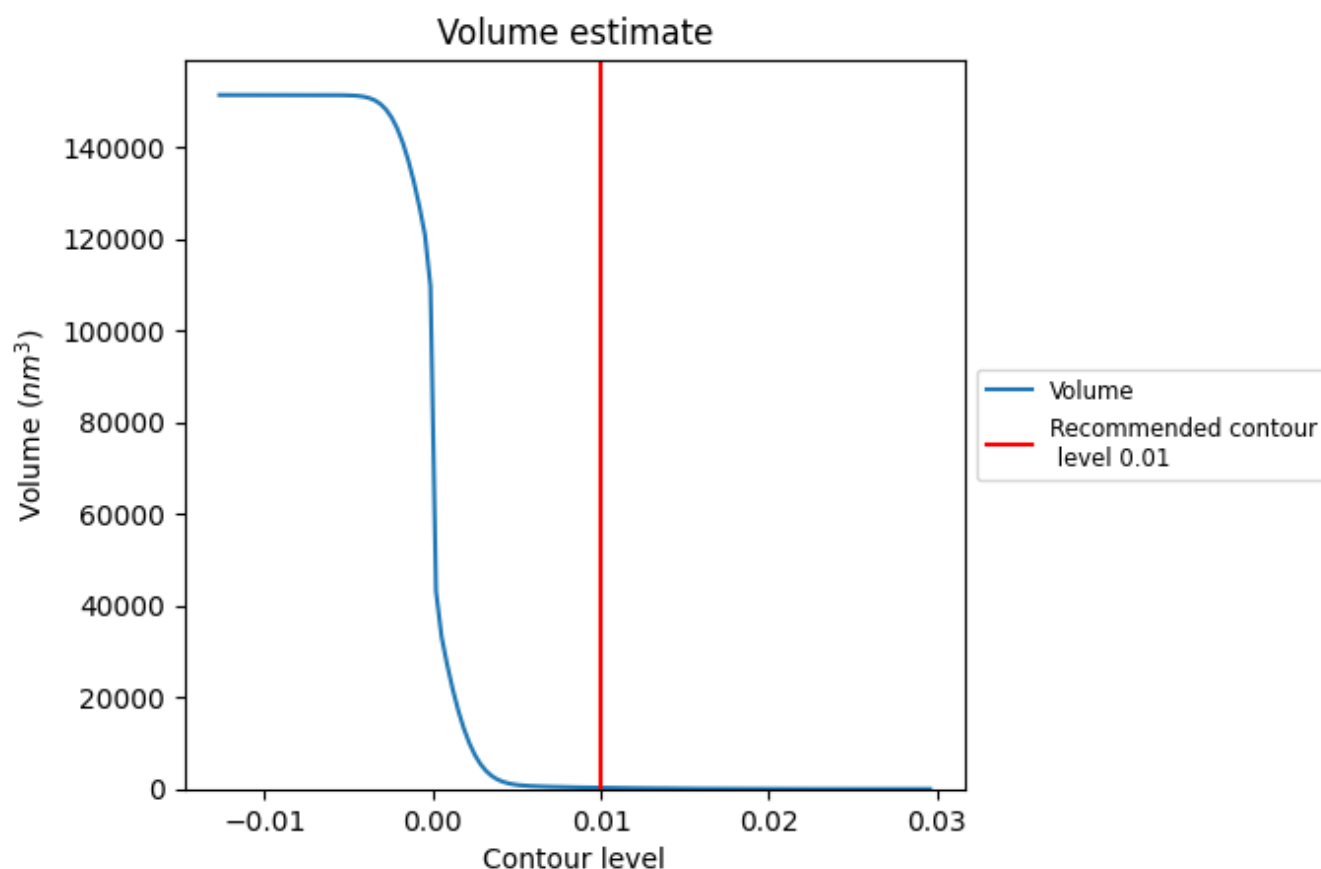
This section contains the results of statistical analysis of the map.

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.

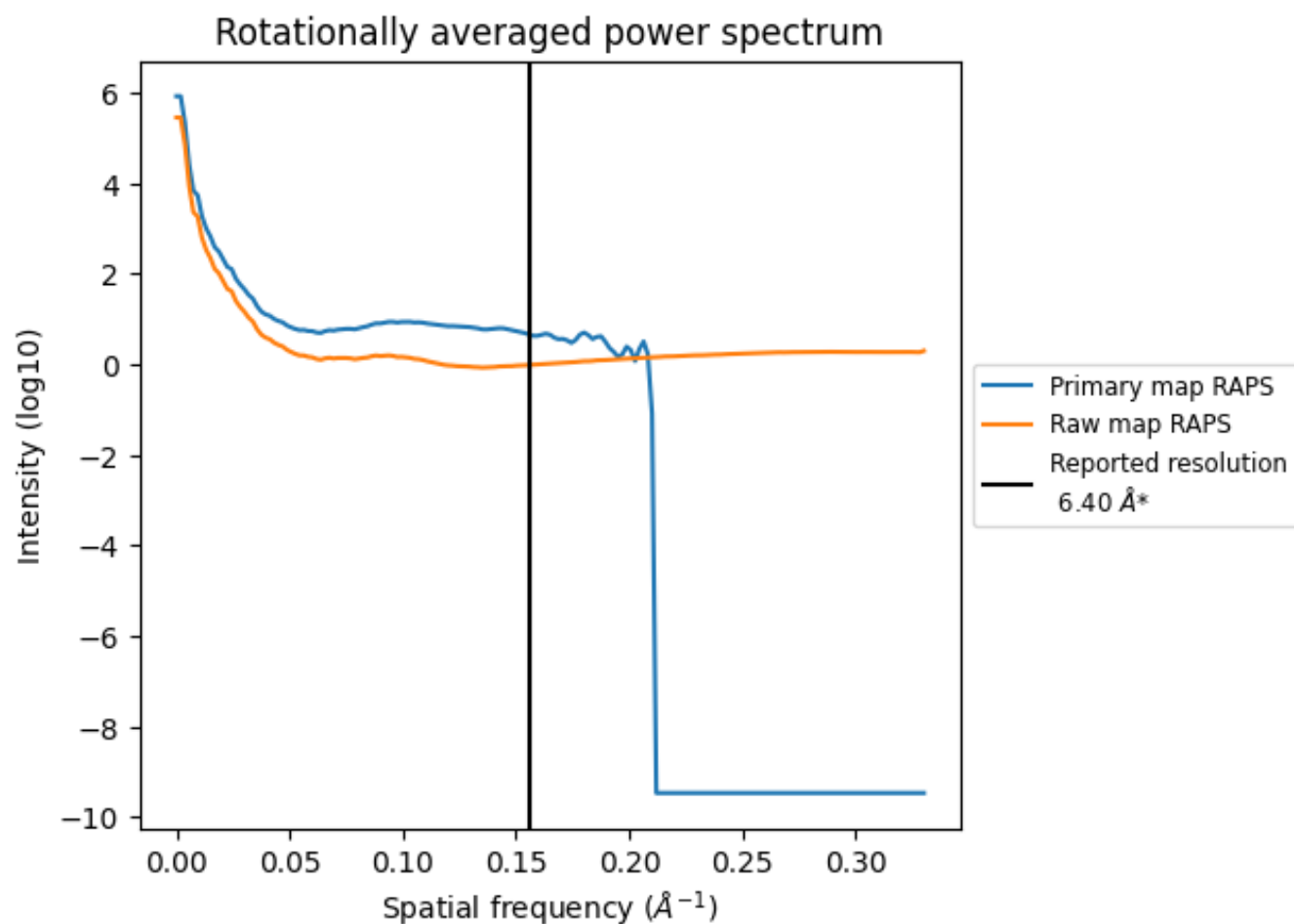
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 265 nm^3 ; this corresponds to an approximate mass of 239 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 ⓘ

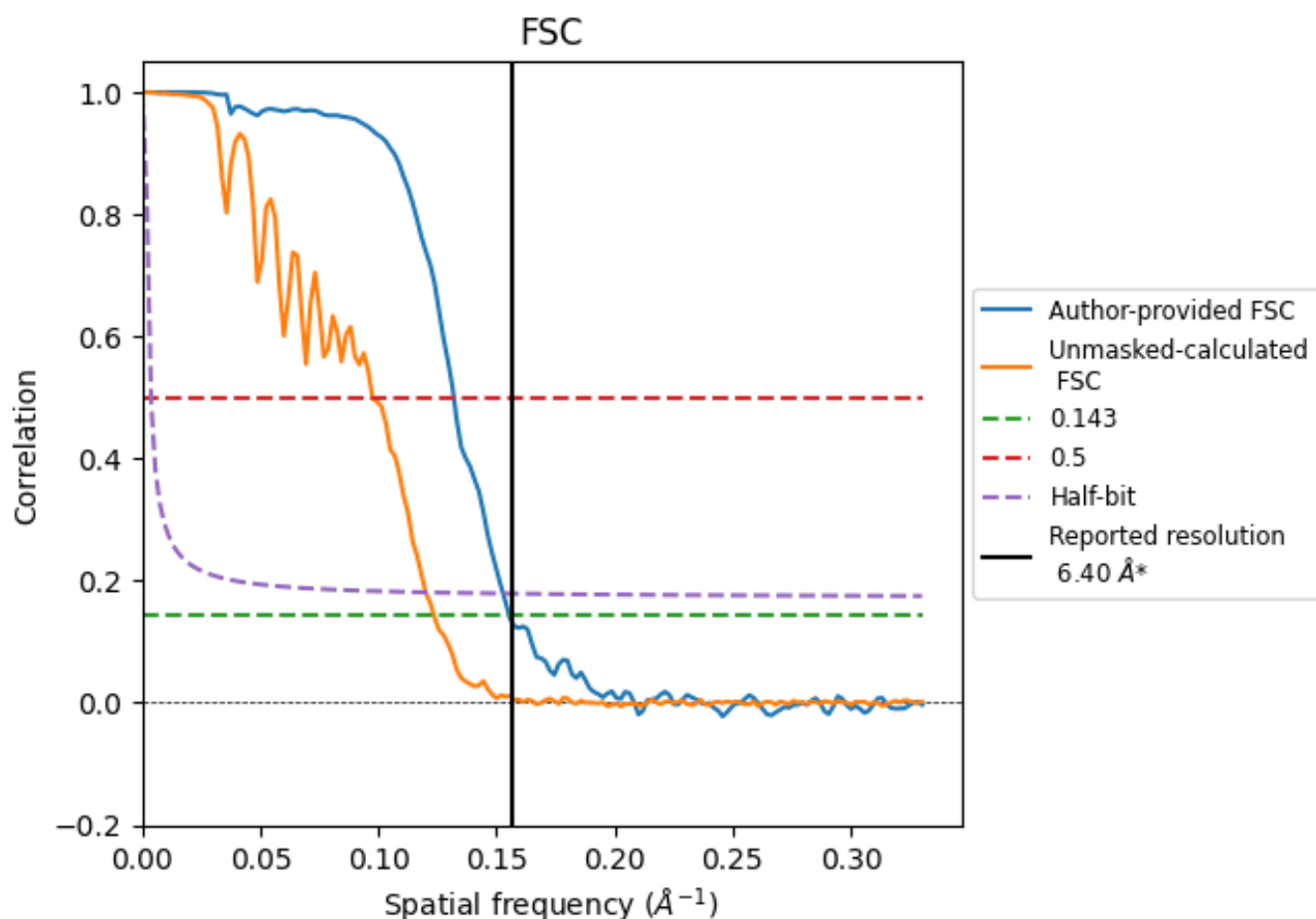


*Reported resolution corresponds to spatial frequency of 0.156 Å⁻¹

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 0.156 \AA^{-1}

8.2 Resolution estimates [i](#)

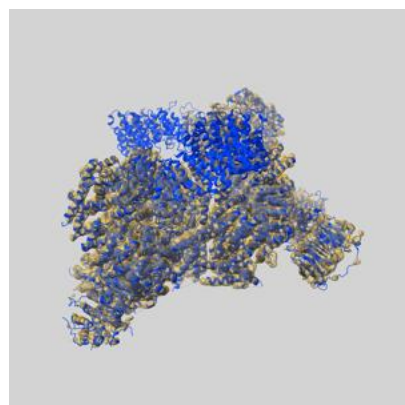
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.40	-	-
Author-provided FSC curve	6.44	7.58	6.54
Unmasked-calculated*	8.09	10.26	8.33

*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 8.09 differs from the reported value 6.4 by more than 10 %

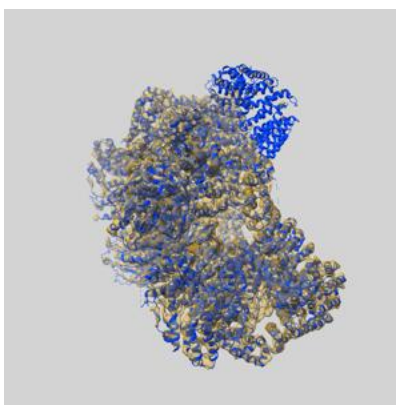
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-56117 and PDB model 9TPW. Per-residue inclusion information can be found in section [3](#) on page [9](#).

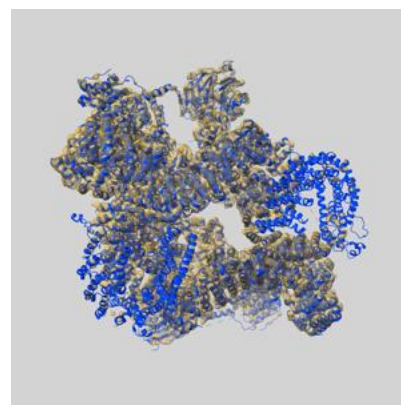
9.1 Map-model overlay [i](#)



X



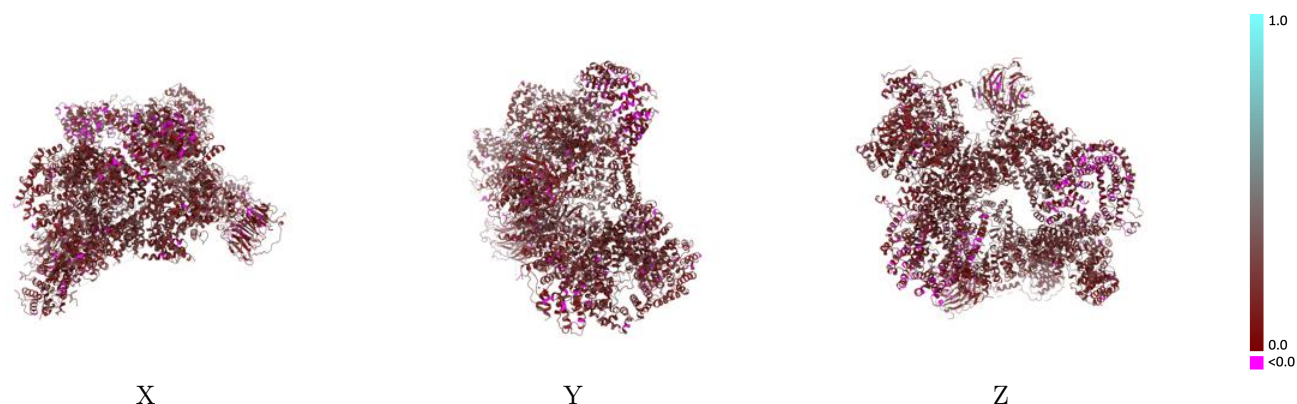
Y



Z

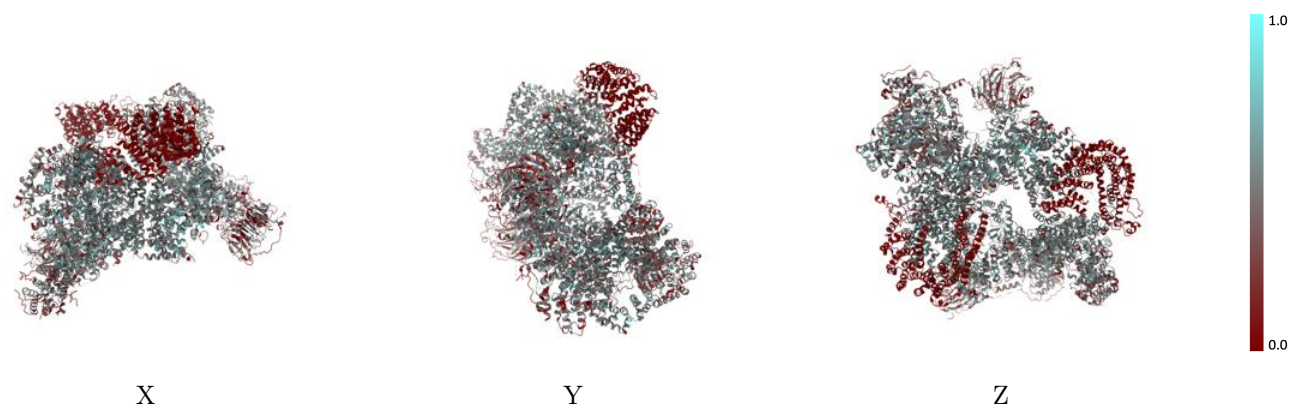
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



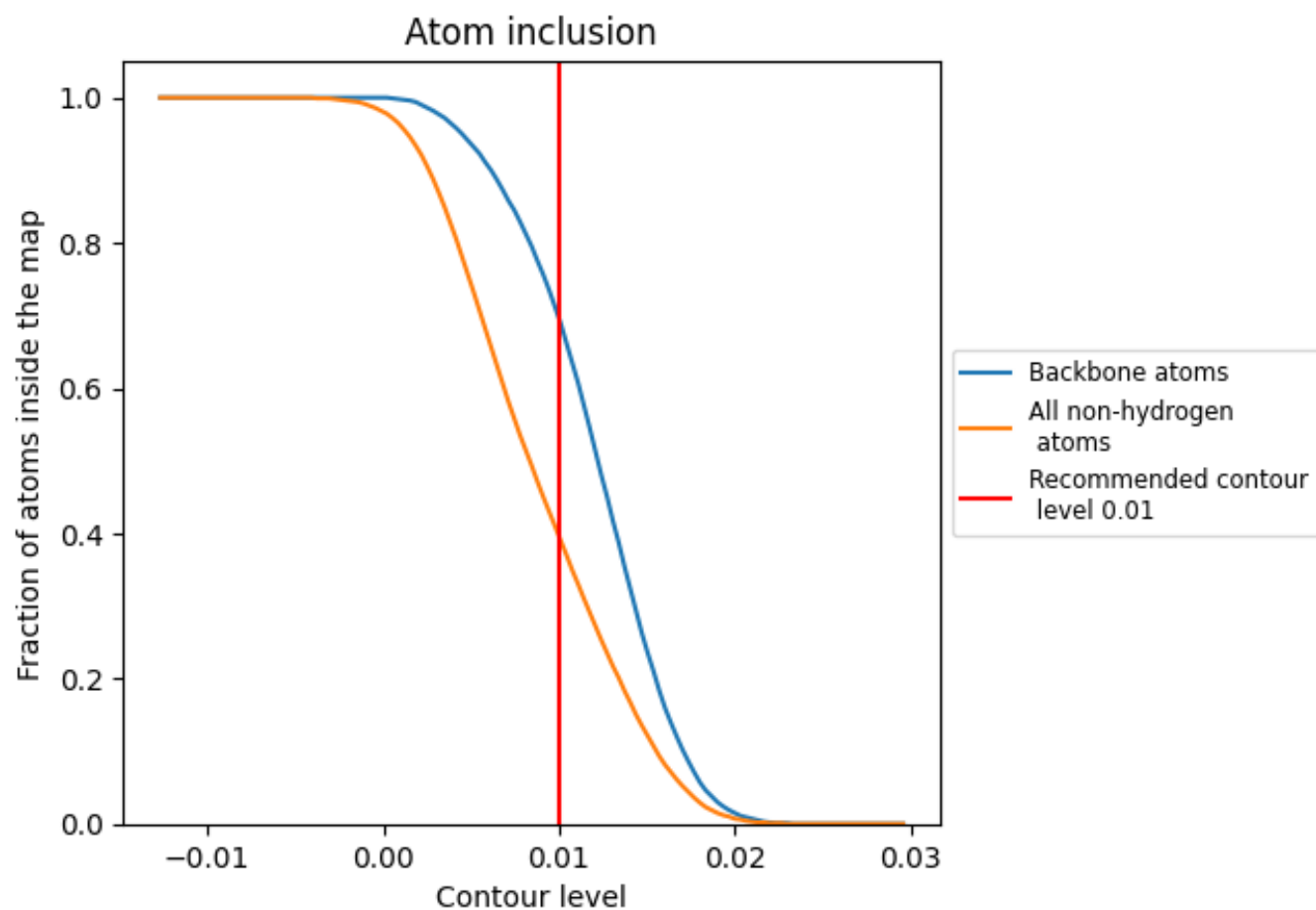
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3960	<div></div> 0.1990
A	<div></div> 0.3940	<div></div> 0.1930
B	<div></div> 0.3900	<div></div> 0.1950
C	<div></div> 0.3030	<div></div> 0.1990
D	<div></div> 0.3120	<div></div> 0.1920
E	<div></div> 0.4350	<div></div> 0.2030
F	<div></div> 0.4540	<div></div> 0.2060
G	<div></div> 0.2340	<div></div> 0.2260
H	<div></div> 0.2560	<div></div> 0.2380

1.0

0.0

<0.0