



Full wwPDB EM Validation Report ⓘ

Jan 27, 2025 – 12:49 PM JST

PDB ID : 8I7J
EMDB ID : EMD-35216
Title : Yeast 40S-eIF4B - partially open conformation of the 40S head
Authors : Datey, A.; Khaja, F.T.; Hussain, T.
Deposited on : 2023-01-31
Resolution : 4.60 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:

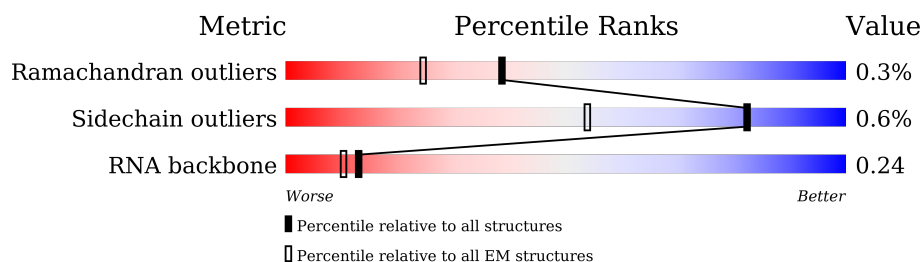
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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.



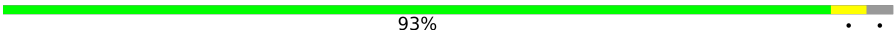
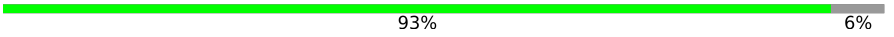
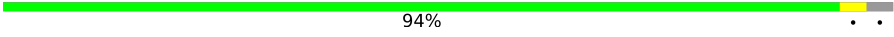

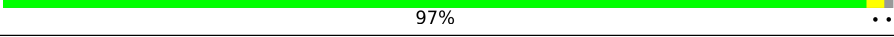

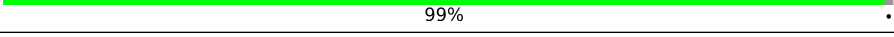
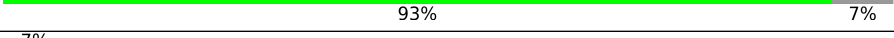
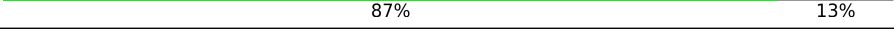
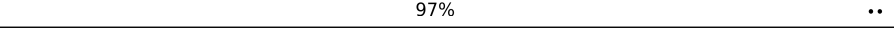
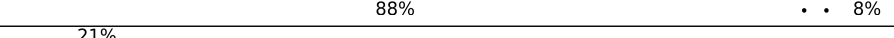
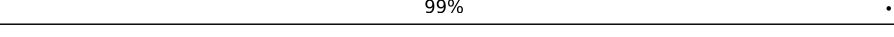
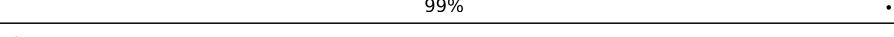
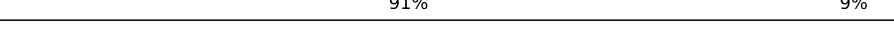
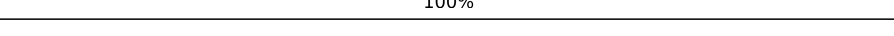
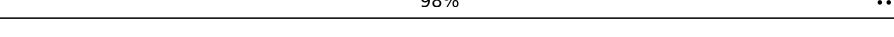
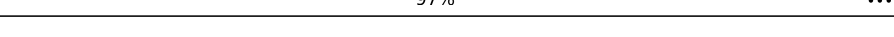
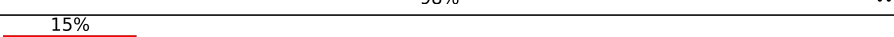
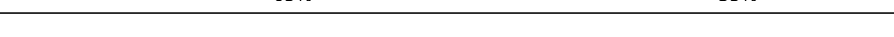






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	1799	
2	A	254	
3	B	255	
4	C	259	
5	D	237	
6	E	261	
7	F	227	
8	G	236	

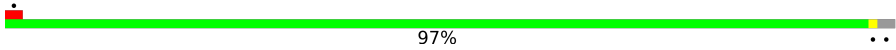
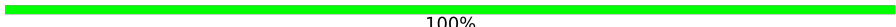
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Mol	Chain	Length	Quality of chain
9	H	190	
10	I	201	
11	J	188	
12	K	106	
13	L	156	
14	M	134	
15	N	151	
16	O	137	
17	P	142	
18	Q	143	
19	R	136	
20	S	146	
21	T	144	
22	U	117	
23	V	87	
24	W	130	
25	X	145	
26	Y	135	
27	Z	108	
28	a	119	
29	b	82	
30	c	67	
31	d	56	
32	e	63	
33	f	150	

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Mol	Chain	Length	Quality of chain
34	g	326	 97%
35	h	25	 100%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 76299 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 RNA chain called RNA (1780-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

- Molecule 2 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	208	Total	C	N	O	S	0	0
			1626	1040	286	298	2		

- Molecule 3 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	223	Total	C	N	O	S	0	0
			1774	1120	325	326	3		

- Molecule 4 is a protein called KLLA0F09812p.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	217	Total	C	N	O	S	0	0
			1629	1041	287	297	4		

- Molecule 5 is a protein called KLLA0D08305p.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	223	Total	C	N	O	S	0	0
			1744	1108	313	318	5		

- Molecule 6 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 7 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	226	Total	C	N	O	S	0	0
			1812	1134	348	326	4		

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	184	Total	C	N	O	S	0	0
			1483	950	270	263			

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 11 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 12 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 13 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	M	122	Total	C	N	O	0	0
			922	575	167	180		

- Molecule 15 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 17 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	123	Total	C	N	O	S	0	0
			980	628	179	168	5		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	141	Total	C	N	O	0	0
			1105	709	204	192		

- Molecule 19 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	125	Total	C	N	O	S	0	0
			991	619	182	187	3		

- Molecule 20 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 21 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	143	Total	C	N	O	0	0
			1110	693	210	207		

- Molecule 22 is a protein called KLLA0F25542p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 24 is a protein called KLLA0B07931p.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 25 is a protein called KLLA0B11231p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Y	134	Total	C	N	O	0	0
			1061	665	207	189		

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 28 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	98	Total	C	N	O	S	0	0
			779	480	165	129	5		

- Molecule 29 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 31 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 32 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	53	Total	C	N	O	S	0	0
			428	268	87	72	1		

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	69	Total	C	N	O	S	0	0
			549	352	102	91	4		

- Molecule 34 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 35 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	2	2	Total	Mg	0
			2	2	

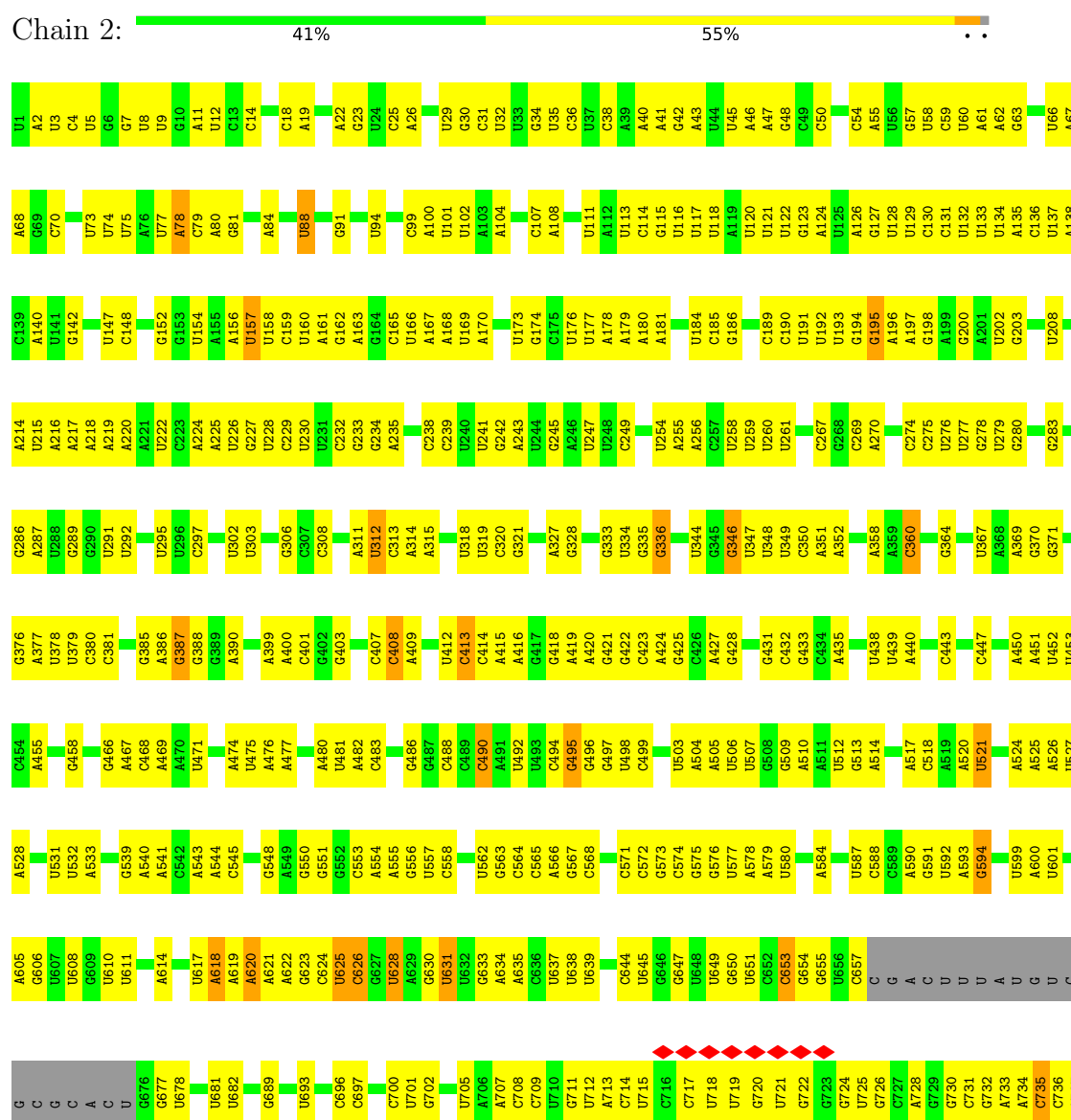
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	a	1	Total	Zn	0
			1	1	
37	b	1	Total	Zn	0
			1	1	
37	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.

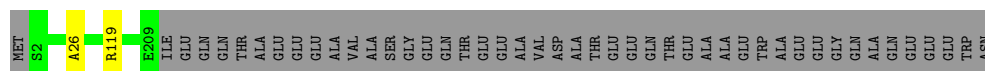
• Molecule 1: RNA (1780-MER)




A1798	C1722	U1648	C1578	G1436	U1352	G1266	G1198		A1112	A1042	U967	A891	G822	A740
	A1649	G1600	C1579	G1427	G1353	G1267	A1201	A1113	U1043	C968	C968	G894	G823	C741
	C1650	A1501	U1428	U1428	G1356	U1288	A1202	G1117	C1044	A969	A970	U894	U824	U742
	U1726	G1502	U1502	C1429	G1357	G1289	A1203	U1116		U895		U895	U825	U743
	C1727	A1581	G1581	U1430	G1358	A1274	C1204	G1117	U1047	C896	C897	C896	C826	U744
	G1653	G1504	C1431	U1431	A1359	A1274	U1205	G1118	U1048	A897	A898	G898	U827	U745
	U1654	G1505	U1432	U1432	A1359	C1278			G1049	C974	C975	U899	U828	
	U1655	U1506	G1433	G1433	C1360	C1279	G1211	C1122	G1050	G975	G976	G900	U829	U749
	G1656	C1507	U1434	U1434	U1361	G1280	G1212	G1120	U1051	A976	A977	U900	U830	U750
	U1585	U1508			G1362	U1281	G1213	A1123	G1052	G979	G980	U901	U831	G751
	C1587	G1509	C1438	C1438	U1363	U1282	U1214	A1124	U1053	U980	U981	U902	U832	A752
	G1588		U1440	U1440	C1364	C1283	G1215	G1125	U1054	U982	U983	G903	G833	A753
	C1589	A1513	U1441	U1441	C1365	C1284	C1216	G1126	U1055	U984	U985	A904	U834	A754
		A1514	U1442	U1442	G1366	U1284	A1216		U1056	A982	A983	A905	U835	A755
	U1593	C1594	G1443	G1443	U1367	U1285	G1217	G1129	U1057	G983	G984	A906	G836	A756
	C1594	C1515	U1444	U1444	U1368	A1286	A1218	A1130	C1058	C989	C990	U907	G837	A757
	U1595	C1516	C1445	C1445	U1369	G1287	C1219	G1131	U1059	U908	U909	U908	U838	U758
	U1596	G1519	C1446	C1446	G1370	G1288	A1220	A1137	U1060	C909	C910	U909	U839	U759
	C1597	U1520	U1446	U1446	A1371	G1288	C1221	G1138	A1061	U910	U911	U910	U840	A760
	U1598	G1521	U1447	U1447	C1374	G1289	A1222	G1139	U1062	A991	A992	U911	C841	
	G1600	A1522	U1448	U1448	U1375	G1292	A1223	G1140	G1063	A993	A994	G912	U842	G765
	C1601	C1525			U1376	G1293	A1224	G1145	U1064	G995	G996	G913	U843	U766
	U1602	G1531	C1453	C1453	U1377	G1294	A1225	G1146	C1065	U995	U996	A914	G844	U767
	G1603	U1532	C1454	C1454	U1378	G1298	A1226	G1147	C1066	U995	U996	U915	G845	
	C1604	G1533	C1455	C1455	U1379	G1298	G1227	G1148	C1067	C999	C999	U916	A846	A771
	U1606	U1534	C1456	C1456	A1380	U1306	A1229	G1149	A1068	U1000	U1001	U920	C847	G772
		C1535	C1457	C1457	G1384	U1309	U1230	A1150	U1070	G1001	G1002	U921	C848	A774
	U1611	U1536	C1459	C1459	G1385	U1313	U1231	A1151	G1073	A1004	A1005	G924	U850	
	A1612	G1537	C1460	C1460	A1386	U1314	G1232	G1152	C1074	C1006	C1007	A925	U853	G778
	C1613	U1538	C1461	C1461	C1387	U1314	A1233	G1153	A1075	C1008	C1009	C926	U854	A779
	G1614	G1539	C1462	C1462	U1388	C1316	C1234	G1154		C1010	C1011	C927	A855	A780
		U1540	G1463	C1463	A1389	G1317	A1235	C1155	U1079	A1012	A1013	A928	A856	A781
	C1617	C1541	G1464	C1464	U1392	G1317	G1236	C1157	C1081	U1014	U1015	C930	U857	G782
		U1542			G1393	A1320	G1240	G1158	G1082	G1015	G1016	A932	A858	C785
	G1620	A1543	C1468	C1468	U1396	A1321	A1241	A1159	A1085	C1020	C1021	C933	A861	G786
	C1621	U1544	C1470	C1470	C1397	C1322	G1242	A1162	A1086	G1022	G1023	U934	A862	A787
	U1622	A1545	U1471	U1471	U1397	G1326	A1243	C1172	A1087	A1024	A1025	G935	U863	U789
	U1623	G1551	G1475	C1475	G1400	G1327	C1245	C1173	U1088	G941	G942	U944	A864	A790
	U1624	U1552	G1476	C1476	C1401	A1328	C1247	U1174	C1089	C943	C944	U945	G865	A791
		A1553			A1404	A1386	U1248		A1090	A1026	A1027	U946	G866	A792
	A1629	U1554	C1479	C1479	U1405	C1387	U1249	G1177	U1091	C1032	C1033	U947	G870	U793
	C1630	U1555			U1406	C1388	U1250	G1178	A1092	U1028	U1029	U948	G871	C797
	A1631	U1556	C1483	C1483	A1408	U1339	U1253	C1179	U1093	A950	A951	U949	G872	
	C1632	A1557	G1484	C1484	A1409	U1340	G1254	A1182	C1095	U1030	U1031	U950	G873	G800
	A1633	U1562	A1485	C1485	G1410	C1341	A1255	A1183	U1096	G1031	G1032	C955	G874	G801
	C1634		U1487	C1486	U1411	U1342	U1256	U1184	U1097	C1033	C1034	U951	G875	A802
	C1635	U1565	U1487	C1486	U1412	A1343	U1257	U1185	U1098	C1035	C1036	U952	G876	
	G1636	C1566	U1488	C1488	U1413	A1344	U1258	C1191	U1099	A1035	A1036	U953	G877	A811
		A1567	A1489	C1489	U1413	A1345	U1259	A1192	G1100	U1037	U1038	U954	G878	U812
	C1639	U1568	A1490	C1490	U1413	A1346	U1260	A1193	G1101	A1038	A1039	U955	G879	A813
	A1640	A1569	A1491	C1491	U1413	A1347	G1261	A1194	U1102	U1039	U1040	U956	G880	G814
	U1641	C1570	C1492	C1492	U1421	A1348	G1262	C1195	U1103	G1041	G1042	U957	G881	G815
	C1642	A1571	C1493	C1493	A1422	G1349	G1263	A1196	C1104	U1041	U1042	U958	G882	
	G1643	G1572	U1494	C1494	A1423	G1350	G1264	A1197	G1108			U959	G883	U819
	U1644		U1495	C1495	A1425	U1351	U1265	G1197				U960	U884	U820
		A1575										U961	U885	U821

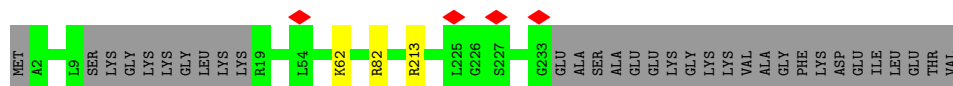
• Molecule 2: 40S ribosomal protein S0

Chain A:  81% 18%




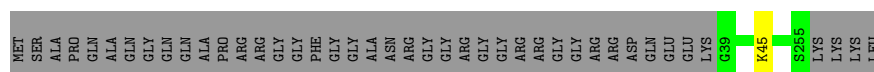
- Molecule 3: 40S ribosomal protein S1

Chain B:  86% 13%



- Molecule 4: KLLA0F09812p

Chain C:  83% 16%



- Molecule 5: KLLA0D08305p

Chain D:  93% 6%




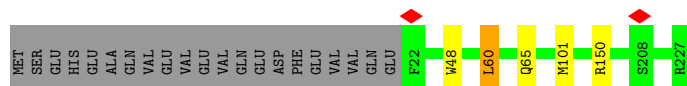
- Molecule 6: 40S ribosomal protein S4

Chain E:  98% 0%



- Molecule 7: KLLA0D10659p

Chain F:  89% 9%



- Molecule 8: 40S ribosomal protein S6

Chain G:  95% 0%



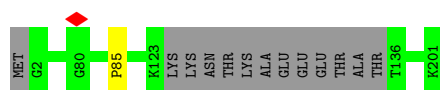
- Molecule 9: 40S ribosomal protein S7

Chain H:  93% ..



- Molecule 10: 40S ribosomal protein S8

Chain I:  93% 6%




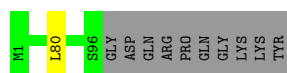
- Molecule 11: KLLA0E23673p

Chain J:  94% ..



- Molecule 12: KLLA0B08173p

Chain K:  90% 9%




- Molecule 13: KLLA0A10483p

Chain L:  97% ..



- Molecule 14: 40S ribosomal protein S12

Chain M:  13% 90% 9%



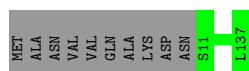
- Molecule 15: KLLA0F18040p

Chain N:  99% .




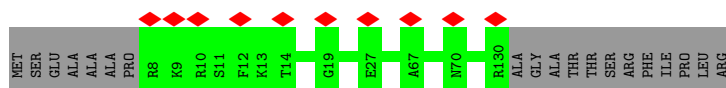
- Molecule 16: 40S ribosomal protein S14

Chain O:  93% 7%



- Molecule 17: KLLA0F07843p

Chain P:  7% 87% 13%



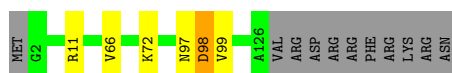
- Molecule 18: 40S ribosomal protein S16

Chain Q:  97% ..



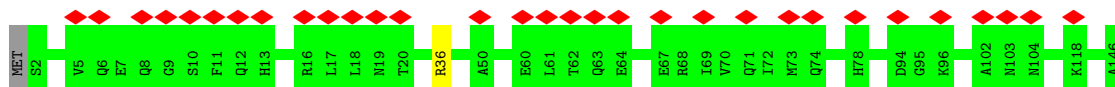
- Molecule 19: KLLA0B01474p

Chain R:  88% .. 8%



- Molecule 20: KLLA0B01562p

Chain S:  21% 99% ..




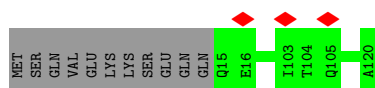
- Molecule 21: KLLA0A07194p

Chain T:  99% .



- Molecule 22: KLLA0F25542p

Chain U:  91% 9%



- Molecule 23: 40S ribosomal protein S21

Chain V:  100%

There are no outlier residues recorded for this chain.

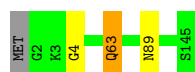
- Molecule 24: KLLA0B07931p

Chain W:  98% ..



- Molecule 25: KLLA0B11231p

Chain X:  97% ...



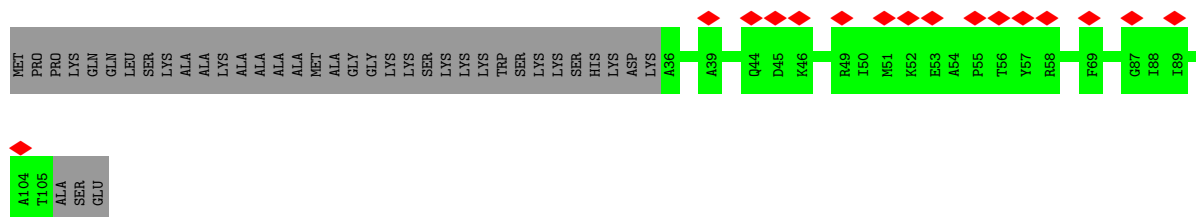
- Molecule 26: 40S ribosomal protein S24

Chain Y:  98% ..




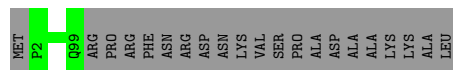
- Molecule 27: 40S ribosomal protein S25

Chain Z:  15% 65% 35%



- Molecule 28: 40S ribosomal protein S26

Chain a:  82% 18%



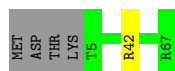
- Molecule 29: 40S ribosomal protein S27

Chain b:  99% .



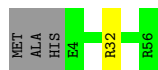
- Molecule 30: 40S ribosomal protein S28

Chain c:  93% • 6%




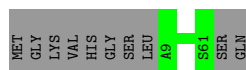
- Molecule 31: 40S ribosomal protein S29

Chain d:  93% • 5%



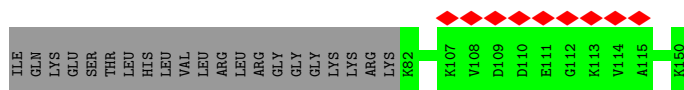
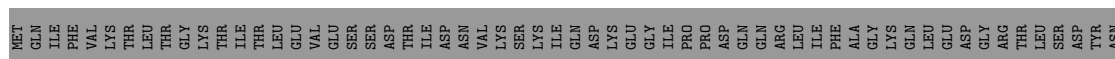
- Molecule 32: 40S ribosomal protein S30

Chain e:  84% 16%



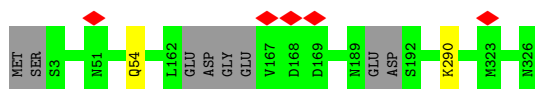
- Molecule 33: Ubiquitin-40S ribosomal protein S27a

Chain f:  6% 46% 54%



- Molecule 34: KLLA0E12277p

Chain g:  97% • •



- Molecule 35: 60S ribosomal protein L41-A

Chain h:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108616	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	421.19998, 421.19998, 421.19998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.17, 1.17, 1.17	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, MG

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	2	0.73	4/42269 (0.0%)	1.16	166/65862 (0.3%)
2	A	0.39	0/1666	0.56	0/2279
3	B	0.37	0/1798	0.59	0/2421
4	C	0.40	0/1659	0.59	0/2252
5	D	0.32	0/1769	0.55	0/2378
6	E	0.41	0/2122	0.60	0/2861
7	F	0.31	0/1628	0.53	0/2198
8	G	0.35	0/1835	0.54	0/2451
9	H	0.38	0/1507	0.59	2/2028 (0.1%)
10	I	0.37	0/1515	0.56	0/2029
11	J	0.37	0/1495	0.61	0/2001
12	K	0.36	0/831	0.59	1/1123 (0.1%)
13	L	0.44	0/1276	0.57	0/1718
14	M	0.26	0/929	0.54	0/1255
15	N	0.36	0/1210	0.55	0/1628
16	O	0.34	0/953	0.59	0/1279
17	P	0.31	0/1000	0.53	0/1343
18	Q	0.31	0/1125	0.52	0/1510
19	R	0.35	0/1002	0.63	0/1346
20	S	0.26	0/1212	0.51	0/1629
21	T	0.32	0/1129	0.51	0/1520
22	U	0.32	0/857	0.56	0/1158
23	V	0.38	0/696	0.58	0/938
24	W	0.46	0/1039	0.64	0/1399
25	X	0.40	0/1137	0.59	0/1516
26	Y	0.38	0/1075	0.54	0/1433
27	Z	0.27	0/567	0.51	0/762
28	a	0.41	0/791	0.59	0/1059
29	b	0.36	0/619	0.61	0/837
30	c	0.30	0/496	0.56	0/666
31	d	0.37	0/457	0.53	0/607
32	e	0.39	0/435	0.60	0/579

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.29	0/562	0.56	0/751
34	g	0.32	0/2521	0.52	0/3431
35	h	0.27	0/234	0.62	0/300
All	All	0.58	4/81416 (0.0%)	0.94	169/118547 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1
3	B	0	1
5	D	0	1
7	F	0	2
8	G	0	1
9	H	0	1
11	J	0	2
13	L	0	1
14	M	0	1
18	Q	0	1
19	R	0	3
25	X	0	2
26	Y	0	1
34	g	0	1
All	All	0	19

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1151	A	O3'-P	5.51	1.67	1.61
1	2	1453	G	N9-C4	-5.46	1.33	1.38
1	2	100	A	N7-C5	-5.11	1.36	1.39
1	2	618	A	N9-C4	-5.05	1.34	1.37

All (169) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1531	C	N1-C2-O2	10.33	125.10	118.90
1	2	1630	C	N3-C2-O2	-9.55	115.21	121.90
1	2	1630	C	C2-N1-C1'	8.89	128.58	118.80
1	2	1630	C	N1-C2-O2	8.82	124.19	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1079	U	C2-N1-C1'	8.76	128.21	117.70
1	2	1531	C	N3-C2-O2	-8.70	115.81	121.90
1	2	1387	C	C2-N1-C1'	8.62	128.28	118.80
1	2	1620	G	N1-C6-O6	-8.45	114.83	119.90
1	2	826	C	C2-N1-C1'	-8.37	109.59	118.80
1	2	1502	G	O4'-C1'-N9	8.26	114.81	108.20
1	2	1453	G	N3-C4-N9	-8.21	121.07	126.00
1	2	847	C	N1-C2-O2	7.82	123.59	118.90
1	2	826	C	C6-N1-C1'	7.80	130.16	120.80
1	2	626	C	C2-N1-C1'	7.58	127.14	118.80
1	2	31	C	N3-C2-O2	-7.53	116.63	121.90
1	2	1292	U	N3-C2-O2	-7.48	116.97	122.20
1	2	1338	C	N3-C2-O2	-7.38	116.73	121.90
1	2	408	C	N3-C2-O2	-7.31	116.78	121.90
1	2	1453	G	N3-C4-C5	7.27	132.23	128.60
1	2	1292	U	N1-C2-O2	7.22	127.86	122.80
1	2	1525	C	N1-C2-O2	7.18	123.21	118.90
1	2	1531	C	N3-C4-N4	-7.11	113.03	118.00
1	2	1794	C	C2-N1-C1'	7.08	126.59	118.80
1	2	1617	C	C2-N1-C1'	6.95	126.45	118.80
1	2	1079	U	N1-C2-O2	6.88	127.62	122.80
1	2	1617	C	C5-C6-N1	6.84	124.42	121.00
1	2	1584	A	N7-C8-N9	6.76	117.18	113.80
1	2	1620	G	O4'-C1'-N9	6.72	113.58	108.20
1	2	620	A	N1-C6-N6	-6.72	114.57	118.60
1	2	1033	C	C2-N1-C1'	6.70	126.17	118.80
1	2	509	G	N3-C4-N9	-6.63	122.02	126.00
1	2	1737	C	N3-C2-O2	-6.58	117.29	121.90
1	2	1472	G	N3-C2-N2	6.56	124.50	119.90
1	2	964	U	C4-C5-C6	6.56	123.64	119.70
1	2	1316	C	N1-C2-O2	6.55	122.83	118.90
1	2	847	C	N3-C2-O2	-6.51	117.34	121.90
1	2	1079	U	N3-C2-O2	-6.43	117.69	122.20
1	2	844	G	C5-C6-O6	6.43	132.46	128.60
1	2	1525	C	N3-C2-O2	-6.42	117.40	121.90
1	2	31	C	N1-C2-O2	6.42	122.75	118.90
1	2	1673	C	N3-C2-O2	-6.41	117.41	121.90
1	2	1322	C	N3-C2-O2	-6.41	117.41	121.90
1	2	1365	C	C5-C6-N1	6.41	124.21	121.00
1	2	1387	C	C6-N1-C1'	-6.37	113.15	120.80
1	2	1583	U	C2-N1-C1'	6.37	125.34	117.70
1	2	979	G	N3-C4-N9	6.31	129.79	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1454	C	C2-N1-C1'	6.31	125.75	118.80
1	2	935	G	C8-N9-C1'	-6.26	118.87	127.00
1	2	1630	C	C6-N1-C1'	-6.24	113.31	120.80
1	2	1794	C	N1-C2-O2	6.21	122.62	118.90
1	2	571	C	N3-C2-O2	-6.17	117.58	121.90
1	2	1322	C	N1-C2-O2	6.16	122.60	118.90
12	K	80	LEU	CB-CG-CD2	-6.16	100.54	111.00
1	2	1030	U	N3-C4-O4	-6.15	115.09	119.40
1	2	1387	C	C5-C6-N1	6.11	124.06	121.00
1	2	79	C	C2-N1-C1'	6.08	125.49	118.80
1	2	914	A	N7-C8-N9	6.06	116.83	113.80
1	2	631	U	C2-N3-C4	-6.06	123.36	127.00
1	2	1589	C	C2-N1-C1'	6.06	125.46	118.80
1	2	495	G	N3-C4-N9	-5.99	122.41	126.00
1	2	1620	G	C2-N3-C4	5.98	114.89	111.90
1	2	1472	G	C5-C6-O6	5.96	132.18	128.60
1	2	1620	G	C5-C6-N1	5.95	114.47	111.50
9	H	98	ILE	C-N-CA	-5.94	106.84	121.70
1	2	1621	C	C6-N1-C2	-5.94	117.92	120.30
1	2	1033	C	C6-N1-C1'	-5.93	113.68	120.80
1	2	1454	C	N1-C2-O2	5.93	122.46	118.90
1	2	897	A	C2-N3-C4	-5.92	107.64	110.60
1	2	909	C	N3-C2-O2	-5.88	117.79	121.90
1	2	1472	G	N1-C6-O6	-5.85	116.39	119.90
1	2	935	G	N3-C4-N9	5.83	129.50	126.00
1	2	1468	C	C2-N1-C1'	5.81	125.19	118.80
1	2	1292	U	C2-N1-C1'	5.77	124.62	117.70
1	2	935	G	C4-N9-C1'	5.77	134.00	126.50
1	2	1079	U	C6-N1-C1'	-5.76	113.14	121.20
1	2	1594	C	C2-N1-C1'	5.74	125.11	118.80
1	2	1086	A	C6-N1-C2	-5.71	115.17	118.60
1	2	1630	C	C6-N1-C2	-5.69	118.02	120.30
1	2	591	G	C8-N9-C4	-5.67	104.13	106.40
1	2	898	G	N3-C4-N9	-5.63	122.62	126.00
1	2	1015	C	C2-N1-C1'	5.63	124.99	118.80
1	2	1118	G	C8-N9-C4	-5.62	104.15	106.40
1	2	346	G	C4-N9-C1'	5.62	133.81	126.50
1	2	976	A	N1-C2-N3	5.62	132.11	129.30
1	2	1191	C	N1-C2-O2	5.61	122.27	118.90
1	2	1453	G	N3-C2-N2	-5.59	115.99	119.90
1	2	121	U	C2-N3-C4	-5.59	123.65	127.00
1	2	1030	U	C5-C4-O4	5.59	129.25	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1453	G	C4-N9-C1'	-5.58	119.25	126.50
1	2	1316	C	N3-C2-O2	-5.58	118.00	121.90
1	2	625	U	C2-N1-C1'	5.57	124.38	117.70
1	2	336	G	C8-N9-C4	5.56	108.62	106.40
1	2	346	G	C8-N9-C1'	-5.54	119.80	127.00
1	2	521	U	C2-N1-C1'	5.53	124.34	117.70
1	2	1338	C	C6-N1-C2	-5.53	118.09	120.30
1	2	1594	C	C6-N1-C2	-5.52	118.09	120.30
1	2	826	C	N3-C4-N4	-5.52	114.14	118.00
1	2	628	U	N3-C2-O2	-5.50	118.35	122.20
1	2	1438	C	N1-C2-O2	5.50	122.20	118.90
1	2	1172	C	N3-C2-O2	-5.49	118.06	121.90
1	2	413	C	N3-C2-O2	-5.49	118.06	121.90
1	2	626	C	C6-N1-C1'	-5.48	114.22	120.80
1	2	898	G	C4-N9-C1'	-5.47	119.39	126.50
1	2	964	U	C2-N3-C4	-5.47	123.72	127.00
1	2	735	C	N1-C2-O2	5.47	122.18	118.90
1	2	388	G	C8-N9-C4	-5.45	104.22	106.40
1	2	1583	U	N1-C2-O2	5.43	126.60	122.80
1	2	408	C	N1-C2-N3	5.42	122.99	119.20
1	2	942	C	C5-C6-N1	-5.41	118.30	121.00
1	2	100	A	C4-C5-C6	5.40	119.70	117.00
1	2	1453	G	C2-N3-C4	-5.40	109.20	111.90
1	2	964	U	N1-C2-N3	5.39	118.14	114.90
1	2	900	G	O4'-C1'-N9	-5.39	103.89	108.20
1	2	1672	C	N1-C2-O2	5.39	122.13	118.90
1	2	157	U	OP1-P-O3'	5.38	117.05	105.20
1	2	1033	C	N1-C2-O2	5.38	122.13	118.90
1	2	1461	C	N1-C2-O2	5.38	122.13	118.90
1	2	79	C	C6-N1-C2	-5.36	118.16	120.30
1	2	1253	U	C2-N1-C1'	5.35	124.12	117.70
1	2	1620	G	C6-N1-C2	-5.32	121.91	125.10
1	2	408	C	C6-N1-C2	-5.32	118.17	120.30
1	2	1617	C	C6-N1-C1'	-5.31	114.43	120.80
1	2	974	C	N3-C2-O2	-5.30	118.19	121.90
1	2	966	A	C8-N9-C4	-5.29	103.68	105.80
1	2	979	G	N3-C4-C5	-5.29	125.95	128.60
1	2	509	G	N3-C4-C5	5.29	131.24	128.60
1	2	1617	C	N1-C2-O2	5.28	122.07	118.90
1	2	1015	C	N1-C2-O2	5.28	122.07	118.90
1	2	844	G	N1-C6-O6	-5.28	116.73	119.90
1	2	1531	C	C5-C4-N4	5.27	123.89	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	871	G	N3-C4-C5	-5.26	125.97	128.60
1	2	631	U	C5-C6-N1	-5.26	120.07	122.70
1	2	306	G	C6-C5-N7	-5.25	127.25	130.40
1	2	1472	G	N1-C2-N2	-5.25	111.47	116.20
1	2	873	C	C2-N1-C1'	5.24	124.57	118.80
1	2	620	A	C5-C6-N6	5.24	127.89	123.70
1	2	1594	C	N1-C2-O2	5.20	122.02	118.90
1	2	1221	C	N1-C2-O2	5.19	122.02	118.90
1	2	1594	C	N3-C2-O2	-5.17	118.28	121.90
1	2	1326	C	N3-C2-O2	-5.17	118.28	121.90
1	2	107	C	C2-N1-C1'	5.16	124.48	118.80
1	2	360	C	C2-N1-C1'	5.16	124.47	118.80
1	2	91	G	C4-N9-C1'	5.15	133.20	126.50
1	2	1794	C	N3-C2-O2	-5.15	118.29	121.90
1	2	826	C	C5-C4-N4	5.14	123.80	120.20
1	2	1794	C	C6-N1-C2	-5.14	118.24	120.30
1	2	1461	C	N3-C2-O2	-5.14	118.30	121.90
1	2	490	C	C2-N3-C4	-5.13	117.33	119.90
1	2	312	U	C5-C6-N1	-5.13	120.14	122.70
1	2	1678	G	O4'-C1'-N9	5.13	112.30	108.20
9	H	87	ASP	CB-CG-OD1	5.11	122.89	118.30
1	2	900	G	C4-N9-C1'	5.10	133.13	126.50
1	2	653	C	C2-N1-C1'	5.09	124.40	118.80
1	2	387	G	C4-C5-N7	5.08	112.83	110.80
1	2	1159	A	C6-N1-C2	-5.08	115.55	118.60
1	2	88	U	C6-N1-C1'	-5.08	114.08	121.20
1	2	594	G	N1-C2-N2	-5.05	111.65	116.20
1	2	1350	G	N9-C4-C5	-5.05	103.38	105.40
1	2	1036	C	C2-N1-C1'	5.03	124.33	118.80
1	2	1737	C	N1-C2-O2	5.03	121.92	118.90
1	2	1269	G	N3-C4-N9	5.03	129.02	126.00
1	2	898	G	C8-N9-C1'	5.03	133.54	127.00
1	2	926	C	N3-C2-O2	-5.03	118.38	121.90
1	2	1126	G	C8-N9-C4	-5.03	104.39	106.40
1	2	195	G	O4'-C1'-N9	5.02	112.22	108.20
1	2	78	A	N1-C2-N3	5.02	131.81	129.30
1	2	624	C	C6-N1-C2	-5.02	118.29	120.30
1	2	1583	U	N3-C2-O2	-5.01	118.69	122.20
1	2	1065	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	26	ALA	Peptide
3	B	213	ARG	Peptide
5	D	219	GLU	Peptide
7	F	101	MET	Peptide
7	F	60	LEU	Peptide
8	G	68	LEU	Peptide
9	H	130	VAL	Peptide
11	J	134	ILE	Peptide
11	J	8	TYR	Peptide
13	L	103	ARG	Peptide
14	M	101	GLY	Peptide
18	Q	40	GLN	Peptide
19	R	66	VAL	Peptide
19	R	97	ASN	Peptide
19	R	98	ASP	Peptide
25	X	63	GLN	Peptide
25	X	89	ASN	Peptide
26	Y	29	HIS	Peptide
34	g	290	LYS	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	206/254 (81%)	164 (80%)	42 (20%)	0	100	100
3	B	219/255 (86%)	183 (84%)	36 (16%)	0	100	100
4	C	215/259 (83%)	181 (84%)	33 (15%)	1 (0%)	25	64
5	D	221/237 (93%)	188 (85%)	33 (15%)	0	100	100
6	E	258/261 (99%)	195 (76%)	62 (24%)	1 (0%)	30	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	F	204/227 (90%)	164 (80%)	39 (19%)	1 (0%)	25	64
8	G	224/236 (95%)	186 (83%)	37 (16%)	1 (0%)	30	68
9	H	182/190 (96%)	144 (79%)	36 (20%)	2 (1%)	12	46
10	I	184/201 (92%)	147 (80%)	36 (20%)	1 (0%)	25	64
11	J	180/188 (96%)	135 (75%)	43 (24%)	2 (1%)	12	46
12	K	94/106 (89%)	78 (83%)	16 (17%)	0	100	100
13	L	153/156 (98%)	117 (76%)	36 (24%)	0	100	100
14	M	120/134 (90%)	97 (81%)	23 (19%)	0	100	100
15	N	148/151 (98%)	126 (85%)	22 (15%)	0	100	100
16	O	125/137 (91%)	95 (76%)	30 (24%)	0	100	100
17	P	121/142 (85%)	102 (84%)	19 (16%)	0	100	100
18	Q	139/143 (97%)	120 (86%)	19 (14%)	0	100	100
19	R	123/136 (90%)	91 (74%)	29 (24%)	3 (2%)	5	28
20	S	143/146 (98%)	116 (81%)	27 (19%)	0	100	100
21	T	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
22	U	104/117 (89%)	90 (86%)	14 (14%)	0	100	100
23	V	85/87 (98%)	65 (76%)	20 (24%)	0	100	100
24	W	127/130 (98%)	101 (80%)	26 (20%)	0	100	100
25	X	142/145 (98%)	97 (68%)	43 (30%)	2 (1%)	9	40
26	Y	132/135 (98%)	109 (83%)	22 (17%)	1 (1%)	16	54
27	Z	68/108 (63%)	53 (78%)	15 (22%)	0	100	100
28	a	96/119 (81%)	67 (70%)	29 (30%)	0	100	100
29	b	79/82 (96%)	57 (72%)	22 (28%)	0	100	100
30	c	61/67 (91%)	50 (82%)	11 (18%)	0	100	100
31	d	51/56 (91%)	39 (76%)	12 (24%)	0	100	100
32	e	51/63 (81%)	41 (80%)	10 (20%)	0	100	100
33	f	67/150 (45%)	46 (69%)	21 (31%)	0	100	100
34	g	312/326 (96%)	267 (86%)	45 (14%)	0	100	100
35	h	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4798/5313 (90%)	3858 (80%)	925 (19%)	15 (0%)	38	72

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	R	98	ASP
4	C	45	LYS
19	R	72	LYS
25	X	4	GLY
26	Y	35	VAL
7	F	60	LEU
8	G	149	LYS
9	H	15	GLU
9	H	63	PRO
11	J	122	VAL
6	E	201	HIS
19	R	99	VAL
11	J	101	VAL
25	X	63	GLN
10	I	85	PRO

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	
2	A	174/211 (82%)	173 (99%)	1 (1%)	84	88
3	B	198/228 (87%)	196 (99%)	2 (1%)	73	81
4	C	176/203 (87%)	176 (100%)	0	100	100
5	D	185/196 (94%)	183 (99%)	2 (1%)	70	80
6	E	223/224 (100%)	221 (99%)	2 (1%)	75	83
7	F	174/194 (90%)	171 (98%)	3 (2%)	56	72
8	G	192/200 (96%)	192 (100%)	0	100	100
9	H	164/170 (96%)	162 (99%)	2 (1%)	67	79
10	I	147/159 (92%)	147 (100%)	0	100	100
11	J	153/158 (97%)	152 (99%)	1 (1%)	81	87
12	K	88/96 (92%)	88 (100%)	0	100	100
13	L	136/137 (99%)	134 (98%)	2 (2%)	60	75
14	M	97/109 (89%)	96 (99%)	1 (1%)	73	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	127/128 (99%)	127 (100%)	0	100	100
16	O	96/104 (92%)	96 (100%)	0	100	100
17	P	105/119 (88%)	105 (100%)	0	100	100
18	Q	117/119 (98%)	116 (99%)	1 (1%)	75	83
19	R	112/124 (90%)	111 (99%)	1 (1%)	75	83
20	S	128/129 (99%)	127 (99%)	1 (1%)	79	84
21	T	117/118 (99%)	117 (100%)	0	100	100
22	U	96/107 (90%)	96 (100%)	0	100	100
23	V	73/73 (100%)	73 (100%)	0	100	100
24	W	110/111 (99%)	109 (99%)	1 (1%)	75	83
25	X	119/120 (99%)	119 (100%)	0	100	100
26	Y	108/109 (99%)	108 (100%)	0	100	100
27	Z	60/88 (68%)	60 (100%)	0	100	100
28	a	83/100 (83%)	83 (100%)	0	100	100
29	b	71/72 (99%)	71 (100%)	0	100	100
30	c	55/59 (93%)	54 (98%)	1 (2%)	54	71
31	d	46/48 (96%)	45 (98%)	1 (2%)	47	65
32	e	47/55 (86%)	47 (100%)	0	100	100
33	f	58/133 (44%)	58 (100%)	0	100	100
34	g	265/272 (97%)	264 (100%)	1 (0%)	89	90
35	h	23/23 (100%)	23 (100%)	0	100	100
All	All	4123/4496 (92%)	4100 (99%)	23 (1%)	82	88

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	119	ARG
3	B	62	LYS
3	B	82	ARG
5	D	76	ARG
5	D	117	ARG
6	E	108	ARG
6	E	198	ARG
7	F	48	TRP
7	F	65	GLN

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Mol	Chain	Res	Type
7	F	150	ARG
9	H	88	ARG
9	H	111	LYS
11	J	171	ARG
13	L	15	LYS
13	L	67	ARG
14	M	116	ASN
18	Q	102	LYS
19	R	11	ARG
20	S	36	ARG
24	W	57	ARG
30	c	42	ARG
31	d	32	ARG
34	g	54	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	30	GLN
2	A	33	GLN
2	A	109	ASN
3	B	178	ASN
3	B	183	GLN
6	E	224	ASN
7	F	36	GLN
7	F	39	GLN
8	G	10	ASN
8	G	81	HIS
10	I	116	HIS
11	J	38	ASN
12	K	14	HIS
12	K	47	GLN
16	O	24	ASN
19	R	48	ASN
20	S	44	ASN
21	T	43	ASN
21	T	101	ASN
29	b	49	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1778/1799 (98%)	979 (55%)	57 (3%)

All (979) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	5	U
1	2	7	G
1	2	8	U
1	2	9	U
1	2	11	A
1	2	12	U
1	2	14	C
1	2	18	C
1	2	19	A
1	2	22	A
1	2	23	G
1	2	25	C
1	2	26	A
1	2	29	U
1	2	30	G
1	2	32	U
1	2	34	G
1	2	35	U
1	2	36	C
1	2	38	C
1	2	40	A
1	2	41	A
1	2	42	G
1	2	43	A
1	2	45	U
1	2	46	A
1	2	47	A
1	2	48	G
1	2	50	C
1	2	54	C
1	2	55	A
1	2	57	G
1	2	58	U
1	2	59	C
1	2	60	U

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Mol	Chain	Res	Type
1	2	61	A
1	2	62	A
1	2	63	G
1	2	66	U
1	2	67	A
1	2	68	A
1	2	70	C
1	2	73	U
1	2	74	U
1	2	75	U
1	2	77	U
1	2	78	A
1	2	80	A
1	2	81	G
1	2	84	A
1	2	88	U
1	2	94	U
1	2	99	C
1	2	101	U
1	2	102	U
1	2	104	A
1	2	108	A
1	2	111	U
1	2	113	U
1	2	114	C
1	2	115	G
1	2	116	U
1	2	117	U
1	2	118	U
1	2	120	U
1	2	122	U
1	2	123	G
1	2	124	A
1	2	126	A
1	2	127	G
1	2	128	U
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U

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Mol	Chain	Res	Type
1	2	135	A
1	2	136	C
1	2	137	U
1	2	138	A
1	2	140	A
1	2	142	G
1	2	147	U
1	2	148	C
1	2	152	G
1	2	154	U
1	2	156	A
1	2	158	U
1	2	159	C
1	2	160	U
1	2	161	A
1	2	162	G
1	2	163	A
1	2	165	C
1	2	166	U
1	2	167	A
1	2	168	A
1	2	169	U
1	2	170	A
1	2	173	U
1	2	174	G
1	2	176	U
1	2	177	U
1	2	178	A
1	2	179	A
1	2	180	A
1	2	181	A
1	2	184	U
1	2	185	C
1	2	186	G
1	2	189	C
1	2	190	C
1	2	191	U
1	2	192	U
1	2	193	U
1	2	194	G
1	2	195	G
1	2	196	A

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Mol	Chain	Res	Type
1	2	197	A
1	2	198	G
1	2	200	G
1	2	203	G
1	2	208	U
1	2	215	U
1	2	216	A
1	2	217	A
1	2	218	A
1	2	219	A
1	2	220	A
1	2	222	U
1	2	224	A
1	2	225	A
1	2	226	U
1	2	227	G
1	2	228	U
1	2	229	C
1	2	230	U
1	2	232	C
1	2	233	G
1	2	234	G
1	2	235	A
1	2	238	C
1	2	239	C
1	2	241	U
1	2	242	G
1	2	243	A
1	2	245	G
1	2	247	U
1	2	249	C
1	2	254	U
1	2	255	A
1	2	256	A
1	2	258	U
1	2	259	U
1	2	260	U
1	2	261	U
1	2	267	C
1	2	270	A
1	2	274	C
1	2	275	C

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Mol	Chain	Res	Type
1	2	276	U
1	2	277	U
1	2	278	G
1	2	279	U
1	2	280	G
1	2	283	G
1	2	286	G
1	2	287	A
1	2	289	G
1	2	291	U
1	2	292	U
1	2	295	U
1	2	297	C
1	2	302	U
1	2	303	U
1	2	308	C
1	2	311	A
1	2	312	U
1	2	313	C
1	2	314	A
1	2	315	A
1	2	318	U
1	2	319	U
1	2	320	C
1	2	321	G
1	2	327	A
1	2	328	G
1	2	333	G
1	2	335	G
1	2	336	G
1	2	344	U
1	2	346	G
1	2	348	U
1	2	349	U
1	2	350	C
1	2	351	A
1	2	352	A
1	2	358	A
1	2	360	C
1	2	364	G
1	2	367	U
1	2	369	A

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Mol	Chain	Res	Type
1	2	370	G
1	2	371	G
1	2	376	G
1	2	377	A
1	2	378	U
1	2	379	U
1	2	380	C
1	2	381	C
1	2	385	G
1	2	386	A
1	2	387	G
1	2	390	A
1	2	399	A
1	2	400	A
1	2	401	C
1	2	403	G
1	2	407	C
1	2	408	C
1	2	409	A
1	2	412	U
1	2	413	C
1	2	414	C
1	2	415	A
1	2	416	A
1	2	418	G
1	2	419	A
1	2	420	A
1	2	421	G
1	2	422	G
1	2	423	C
1	2	424	A
1	2	425	G
1	2	427	A
1	2	428	G
1	2	431	G
1	2	432	C
1	2	433	G
1	2	435	A
1	2	438	U
1	2	439	U
1	2	440	A
1	2	443	C

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Mol	Chain	Res	Type
1	2	447	C
1	2	450	A
1	2	451	A
1	2	452	U
1	2	453	U
1	2	455	A
1	2	458	G
1	2	466	G
1	2	467	A
1	2	468	C
1	2	469	A
1	2	471	U
1	2	474	A
1	2	475	U
1	2	476	A
1	2	477	A
1	2	480	A
1	2	481	U
1	2	482	A
1	2	483	C
1	2	486	G
1	2	488	C
1	2	490	C
1	2	492	U
1	2	494	C
1	2	495	G
1	2	496	G
1	2	497	G
1	2	498	U
1	2	499	C
1	2	503	U
1	2	504	A
1	2	505	A
1	2	506	U
1	2	507	U
1	2	510	A
1	2	512	U
1	2	513	G
1	2	514	A
1	2	517	A
1	2	518	C
1	2	520	A

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Mol	Chain	Res	Type
1	2	521	U
1	2	524	A
1	2	525	A
1	2	526	A
1	2	527	U
1	2	528	A
1	2	531	U
1	2	532	U
1	2	533	A
1	2	539	G
1	2	540	A
1	2	541	A
1	2	543	A
1	2	544	A
1	2	545	C
1	2	548	G
1	2	550	G
1	2	551	G
1	2	553	C
1	2	554	A
1	2	555	A
1	2	556	G
1	2	557	U
1	2	558	C
1	2	563	G
1	2	565	C
1	2	566	A
1	2	567	G
1	2	568	C
1	2	572	C
1	2	573	G
1	2	574	C
1	2	575	G
1	2	576	G
1	2	577	U
1	2	578	A
1	2	579	A
1	2	580	U
1	2	584	A
1	2	587	U
1	2	588	C
1	2	590	A

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Mol	Chain	Res	Type
1	2	592	U
1	2	593	A
1	2	594	G
1	2	599	U
1	2	600	A
1	2	601	U
1	2	605	A
1	2	606	G
1	2	608	U
1	2	610	U
1	2	611	U
1	2	614	A
1	2	617	U
1	2	618	A
1	2	619	A
1	2	620	A
1	2	621	A
1	2	622	A
1	2	623	G
1	2	625	U
1	2	626	C
1	2	628	U
1	2	630	G
1	2	631	U
1	2	633	G
1	2	634	A
1	2	635	A
1	2	637	U
1	2	638	U
1	2	639	U
1	2	644	C
1	2	645	U
1	2	647	G
1	2	649	U
1	2	650	G
1	2	651	U
1	2	653	C
1	2	654	G
1	2	655	G
1	2	657	C
1	2	677	G
1	2	678	U

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Mol	Chain	Res	Type
1	2	681	U
1	2	682	U
1	2	689	G
1	2	693	U
1	2	696	C
1	2	697	C
1	2	700	C
1	2	701	U
1	2	702	G
1	2	705	U
1	2	707	A
1	2	708	C
1	2	709	C
1	2	711	G
1	2	712	U
1	2	713	A
1	2	714	C
1	2	715	U
1	2	717	C
1	2	718	U
1	2	719	U
1	2	720	G
1	2	721	U
1	2	722	G
1	2	724	G
1	2	725	U
1	2	726	G
1	2	728	A
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	737	A
1	2	738	G
1	2	740	A
1	2	741	C
1	2	742	U
1	2	743	U
1	2	745	U
1	2	749	U

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Mol	Chain	Res	Type
1	2	752	A
1	2	753	A
1	2	755	A
1	2	756	A
1	2	758	U
1	2	760	A
1	2	765	G
1	2	766	U
1	2	767	U
1	2	771	A
1	2	772	G
1	2	773	C
1	2	774	A
1	2	778	G
1	2	779	A
1	2	780	A
1	2	781	A
1	2	782	G
1	2	785	C
1	2	786	G
1	2	787	A
1	2	788	A
1	2	790	A
1	2	791	U
1	2	792	A
1	2	793	U
1	2	797	C
1	2	800	G
1	2	802	A
1	2	811	A
1	2	812	U
1	2	813	A
1	2	814	G
1	2	815	G
1	2	819	U
1	2	820	U
1	2	822	G
1	2	823	G
1	2	824	U
1	2	825	U
1	2	826	C
1	2	827	U

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Mol	Chain	Res	Type
1	2	828	A
1	2	829	U
1	2	830	U
1	2	831	U
1	2	832	U
1	2	833	G
1	2	834	U
1	2	835	U
1	2	836	G
1	2	837	G
1	2	838	U
1	2	840	U
1	2	841	C
1	2	842	U
1	2	843	A
1	2	845	G
1	2	849	A
1	2	850	U
1	2	853	U
1	2	854	A
1	2	856	U
1	2	858	A
1	2	861	A
1	2	862	A
1	2	863	U
1	2	864	A
1	2	866	G
1	2	870	G
1	2	872	U
1	2	875	G
1	2	876	G
1	2	877	G
1	2	878	G
1	2	882	C
1	2	883	A
1	2	887	U
1	2	888	U
1	2	891	A
1	2	894	G
1	2	896	C
1	2	897	A
1	2	898	G

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Mol	Chain	Res	Type
1	2	899	A
1	2	902	U
1	2	903	G
1	2	904	A
1	2	905	A
1	2	907	U
1	2	908	U
1	2	909	C
1	2	911	U
1	2	912	G
1	2	913	G
1	2	915	U
1	2	916	U
1	2	920	U
1	2	924	G
1	2	925	A
1	2	928	A
1	2	930	C
1	2	931	U
1	2	932	A
1	2	934	U
1	2	941	G
1	2	942	C
1	2	944	U
1	2	945	U
1	2	946	U
1	2	950	A
1	2	955	C
1	2	958	U
1	2	959	U
1	2	962	A
1	2	963	U
1	2	965	A
1	2	967	U
1	2	968	C
1	2	969	A
1	2	970	A
1	2	973	A
1	2	976	A
1	2	979	G
1	2	980	U
1	2	982	A

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Mol	Chain	Res	Type
1	2	983	G
1	2	989	C
1	2	990	G
1	2	992	A
1	2	993	G
1	2	994	A
1	2	995	U
1	2	996	G
1	2	999	C
1	2	1000	A
1	2	1001	G
1	2	1004	A
1	2	1005	C
1	2	1006	C
1	2	1012	A
1	2	1014	U
1	2	1015	C
1	2	1020	C
1	2	1022	A
1	2	1023	U
1	2	1024	A
1	2	1026	A
1	2	1027	C
1	2	1028	U
1	2	1030	U
1	2	1031	G
1	2	1033	C
1	2	1034	G
1	2	1035	A
1	2	1036	C
1	2	1038	A
1	2	1039	G
1	2	1041	G
1	2	1042	A
1	2	1044	C
1	2	1047	G
1	2	1049	G
1	2	1050	G
1	2	1051	U
1	2	1052	G
1	2	1053	U
1	2	1055	U

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Mol	Chain	Res	Type
1	2	1057	U
1	2	1058	C
1	2	1059	U
1	2	1061	A
1	2	1062	U
1	2	1064	A
1	2	1065	C
1	2	1066	C
1	2	1068	A
1	2	1070	U
1	2	1073	G
1	2	1075	A
1	2	1079	U
1	2	1080	A
1	2	1081	C
1	2	1082	G
1	2	1085	A
1	2	1086	A
1	2	1088	U
1	2	1089	C
1	2	1090	A
1	2	1091	A
1	2	1092	A
1	2	1093	G
1	2	1095	C
1	2	1096	U
1	2	1097	U
1	2	1098	U
1	2	1099	G
1	2	1101	G
1	2	1102	U
1	2	1103	U
1	2	1104	C
1	2	1108	G
1	2	1112	A
1	2	1113	G
1	2	1116	U
1	2	1117	G
1	2	1122	C
1	2	1123	A
1	2	1125	G
1	2	1129	G

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Mol	Chain	Res	Type
1	2	1130	A
1	2	1137	A
1	2	1139	G
1	2	1140	G
1	2	1145	G
1	2	1146	A
1	2	1148	G
1	2	1151	A
1	2	1153	G
1	2	1154	G
1	2	1155	C
1	2	1156	A
1	2	1157	C
1	2	1162	A
1	2	1173	C
1	2	1174	U
1	2	1177	G
1	2	1178	G
1	2	1179	C
1	2	1182	A
1	2	1184	U
1	2	1185	U
1	2	1191	C
1	2	1193	A
1	2	1194	C
1	2	1195	A
1	2	1196	C
1	2	1198	G
1	2	1201	A
1	2	1202	A
1	2	1203	A
1	2	1204	C
1	2	1205	U
1	2	1211	G
1	2	1212	G
1	2	1214	C
1	2	1216	A
1	2	1217	G
1	2	1218	A
1	2	1219	C
1	2	1220	A
1	2	1223	A

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Mol	Chain	Res	Type
1	2	1225	A
1	2	1226	A
1	2	1227	G
1	2	1228	G
1	2	1229	A
1	2	1231	U
1	2	1233	A
1	2	1234	C
1	2	1235	A
1	2	1236	G
1	2	1240	G
1	2	1241	A
1	2	1242	G
1	2	1243	A
1	2	1244	G
1	2	1245	C
1	2	1246	U
1	2	1247	C
1	2	1249	U
1	2	1250	U
1	2	1254	G
1	2	1255	A
1	2	1256	U
1	2	1258	U
1	2	1259	U
1	2	1261	U
1	2	1262	G
1	2	1264	G
1	2	1265	U
1	2	1266	G
1	2	1268	U
1	2	1269	G
1	2	1274	A
1	2	1278	C
1	2	1280	G
1	2	1282	U
1	2	1283	C
1	2	1284	U
1	2	1285	U
1	2	1287	G
1	2	1290	G
1	2	1292	U

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Mol	Chain	Res	Type
1	2	1294	G
1	2	1298	G
1	2	1306	U
1	2	1309	U
1	2	1313	U
1	2	1314	U
1	2	1316	C
1	2	1317	G
1	2	1320	A
1	2	1321	A
1	2	1322	C
1	2	1328	A
1	2	1336	A
1	2	1339	U
1	2	1340	A
1	2	1342	U
1	2	1343	A
1	2	1344	A
1	2	1345	A
1	2	1346	U
1	2	1348	G
1	2	1349	G
1	2	1350	G
1	2	1351	U
1	2	1353	G
1	2	1356	G
1	2	1358	C
1	2	1359	A
1	2	1361	U
1	2	1363	G
1	2	1364	C
1	2	1366	G
1	2	1368	U
1	2	1369	U
1	2	1370	G
1	2	1371	A
1	2	1374	C
1	2	1375	U
1	2	1376	U
1	2	1378	U
1	2	1380	A
1	2	1384	G

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Mol	Chain	Res	Type
1	2	1385	G
1	2	1386	A
1	2	1387	C
1	2	1388	U
1	2	1389	A
1	2	1392	G
1	2	1393	G
1	2	1396	U
1	2	1397	C
1	2	1400	G
1	2	1401	C
1	2	1404	A
1	2	1405	U
1	2	1408	A
1	2	1409	A
1	2	1410	G
1	2	1411	U
1	2	1412	U
1	2	1413	U
1	2	1419	A
1	2	1421	U
1	2	1422	A
1	2	1425	A
1	2	1427	G
1	2	1428	U
1	2	1429	C
1	2	1430	U
1	2	1431	G
1	2	1433	G
1	2	1434	A
1	2	1440	U
1	2	1442	A
1	2	1443	G
1	2	1444	A
1	2	1445	C
1	2	1446	G
1	2	1448	U
1	2	1455	C
1	2	1456	G
1	2	1457	C
1	2	1458	A
1	2	1459	C

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Mol	Chain	Res	Type
1	2	1461	C
1	2	1463	C
1	2	1464	G
1	2	1468	C
1	2	1469	A
1	2	1470	C
1	2	1471	U
1	2	1472	G
1	2	1475	G
1	2	1476	G
1	2	1479	C
1	2	1483	C
1	2	1484	G
1	2	1485	A
1	2	1487	U
1	2	1488	A
1	2	1489	C
1	2	1490	A
1	2	1492	C
1	2	1494	U
1	2	1495	U
1	2	1499	C
1	2	1502	G
1	2	1503	A
1	2	1504	G
1	2	1506	U
1	2	1508	U
1	2	1509	G
1	2	1513	A
1	2	1514	A
1	2	1515	U
1	2	1516	C
1	2	1519	G
1	2	1521	G
1	2	1522	A
1	2	1531	C
1	2	1532	G
1	2	1533	U
1	2	1534	G
1	2	1535	C
1	2	1537	G
1	2	1539	G

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Mol	Chain	Res	Type
1	2	1540	G
1	2	1541	A
1	2	1542	U
1	2	1543	A
1	2	1544	G
1	2	1545	A
1	2	1551	G
1	2	1553	A
1	2	1555	U
1	2	1557	A
1	2	1562	U
1	2	1565	U
1	2	1566	C
1	2	1567	A
1	2	1568	A
1	2	1569	C
1	2	1570	G
1	2	1571	A
1	2	1572	G
1	2	1575	A
1	2	1578	C
1	2	1580	U
1	2	1582	G
1	2	1583	U
1	2	1585	A
1	2	1587	C
1	2	1589	C
1	2	1593	U
1	2	1595	A
1	2	1596	U
1	2	1598	A
1	2	1599	G
1	2	1600	C
1	2	1602	U
1	2	1603	G
1	2	1605	G
1	2	1606	U
1	2	1611	U
1	2	1614	G
1	2	1622	C
1	2	1623	C
1	2	1624	U

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Mol	Chain	Res	Type
1	2	1625	U
1	2	1629	A
1	2	1631	A
1	2	1632	C
1	2	1633	A
1	2	1634	C
1	2	1636	G
1	2	1639	C
1	2	1641	U
1	2	1642	C
1	2	1643	G
1	2	1644	C
1	2	1645	U
1	2	1648	U
1	2	1650	C
1	2	1651	C
1	2	1652	G
1	2	1653	A
1	2	1655	U
1	2	1656	G
1	2	1657	A
1	2	1658	A
1	2	1660	G
1	2	1665	A
1	2	1669	A
1	2	1673	C
1	2	1674	U
1	2	1678	G
1	2	1680	U
1	2	1684	C
1	2	1685	U
1	2	1687	A
1	2	1688	G
1	2	1690	G
1	2	1691	A
1	2	1692	A
1	2	1693	G
1	2	1694	G
1	2	1697	G
1	2	1698	C
1	2	1699	A
1	2	1701	C

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Mol	Chain	Res	Type
1	2	1702	U
1	2	1703	C
1	2	1704	C
1	2	1705	A
1	2	1706	U
1	2	1707	C
1	2	1708	U
1	2	1710	A
1	2	1712	A
1	2	1717	A
1	2	1718	G
1	2	1719	A
1	2	1720	A
1	2	1721	U
1	2	1722	C
1	2	1725	G
1	2	1727	C
1	2	1732	U
1	2	1733	U
1	2	1734	G
1	2	1736	U
1	2	1737	C
1	2	1738	A
1	2	1739	U
1	2	1740	U
1	2	1742	A
1	2	1743	G
1	2	1744	A
1	2	1746	G
1	2	1747	A
1	2	1751	A
1	2	1752	A
1	2	1753	A
1	2	1754	A
1	2	1755	G
1	2	1758	G
1	2	1759	U
1	2	1760	A
1	2	1761	A
1	2	1762	C
1	2	1764	A
1	2	1765	G

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Mol	Chain	Res	Type
1	2	1766	G
1	2	1767	U
1	2	1768	U
1	2	1773	U
1	2	1777	U
1	2	1778	G
1	2	1779	A
1	2	1781	C
1	2	1784	G
1	2	1785	C
1	2	1789	A
1	2	1790	G
1	2	1791	G
1	2	1792	A
1	2	1793	U
1	2	1794	C
1	2	1798	A

All (57) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	57	G
1	2	157	U
1	2	158	U
1	2	161	A
1	2	184	U
1	2	202	U
1	2	214	A
1	2	217	A
1	2	234	G
1	2	269	C
1	2	291	U
1	2	334	U
1	2	347	U
1	2	378	U
1	2	413	C
1	2	418	G
1	2	480	A
1	2	498	U
1	2	544	A
1	2	562	U
1	2	564	C

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Mol	Chain	Res	Type
1	2	573	G
1	2	599	U
1	2	610	U
1	2	735	C
1	2	751	G
1	2	790	A
1	2	821	U
1	2	898	G
1	2	903	G
1	2	941	G
1	2	994	A
1	2	1013	G
1	2	1025	A
1	2	1032	C
1	2	1067	C
1	2	1139	G
1	2	1150	A
1	2	1195	A
1	2	1243	A
1	2	1254	G
1	2	1315	G
1	2	1343	A
1	2	1344	A
1	2	1360	C
1	2	1427	G
1	2	1470	C
1	2	1491	A
1	2	1501	A
1	2	1566	C
1	2	1579	C
1	2	1613	C
1	2	1624	U
1	2	1720	A
1	2	1765	G
1	2	1788	A
1	2	1791	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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.

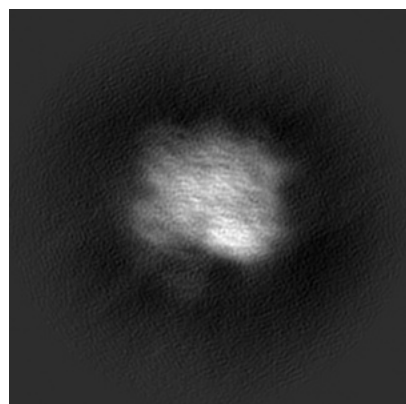
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35216. These allow visual inspection of the internal detail of the map and identification of artifacts.

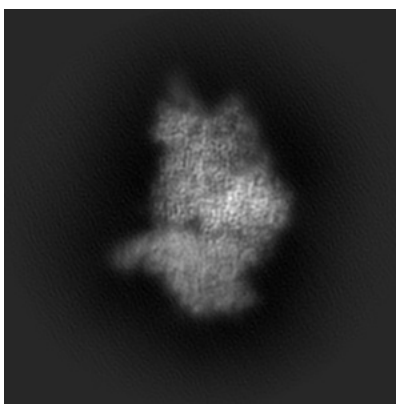
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

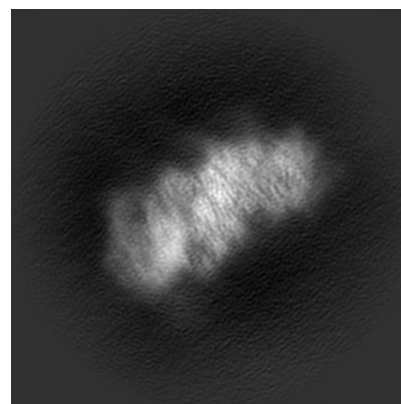
6.1.1 Primary map



X

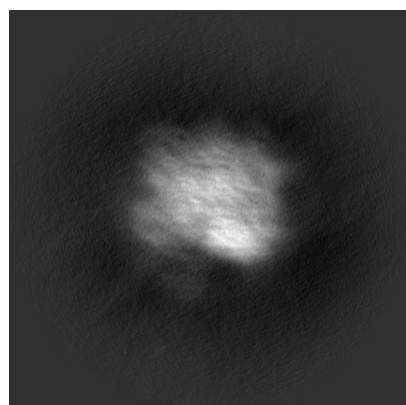


Y

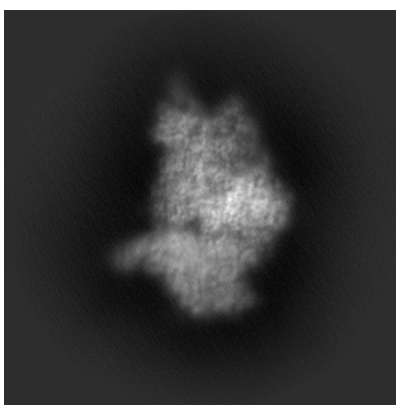


Z

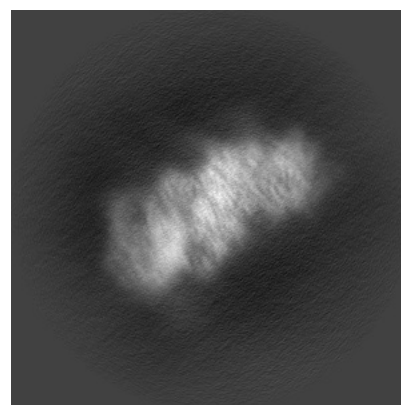
6.1.2 Raw map



X



Y

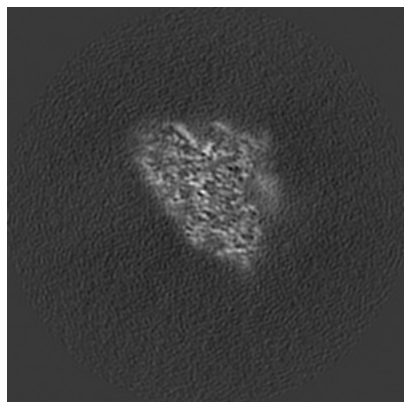


Z

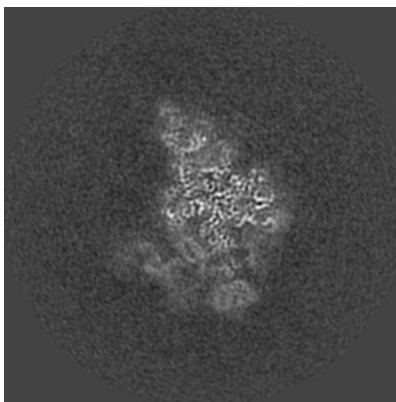
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

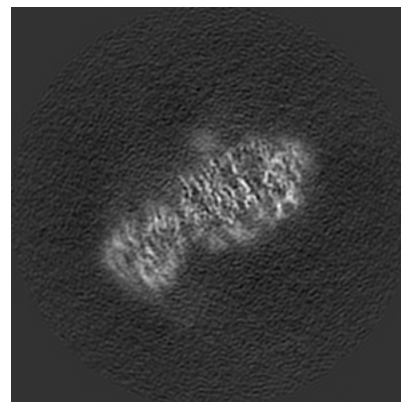
6.2.1 Primary map



X Index: 180

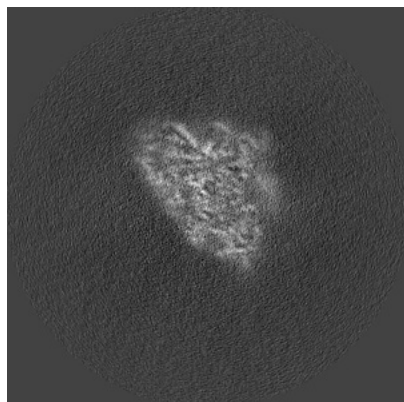


Y Index: 180

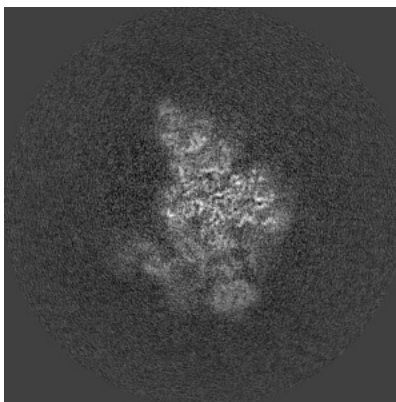


Z Index: 180

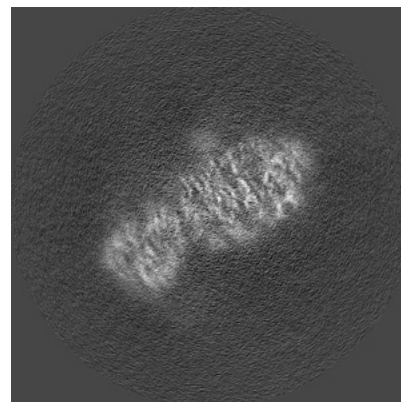
6.2.2 Raw map



X Index: 180



Y Index: 180

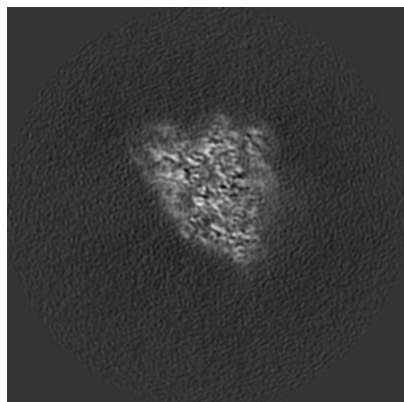


Z Index: 180

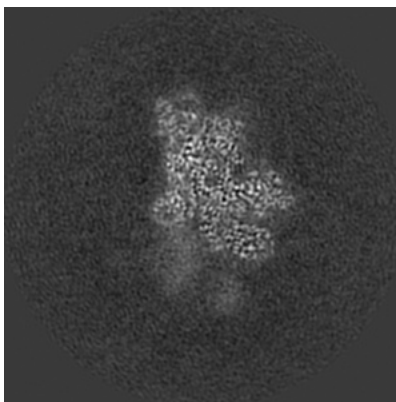
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

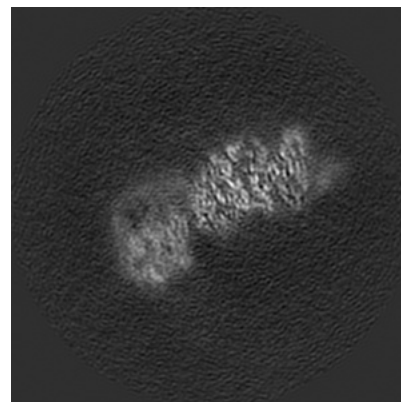
6.3.1 Primary map



X Index: 187

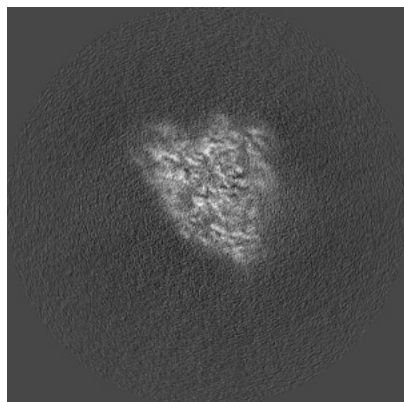


Y Index: 195

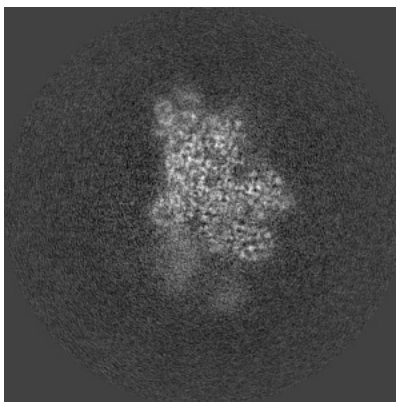


Z Index: 160

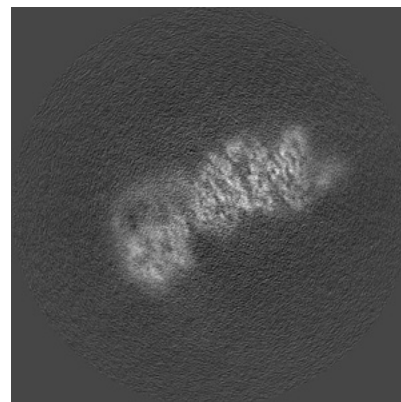
6.3.2 Raw map



X Index: 187



Y Index: 196

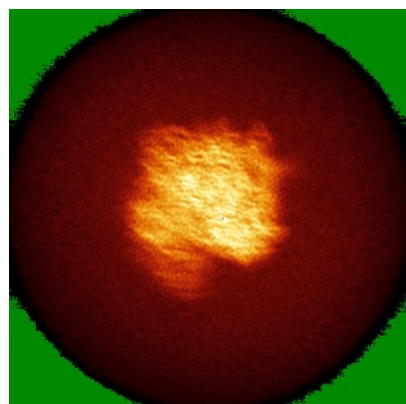


Z Index: 159

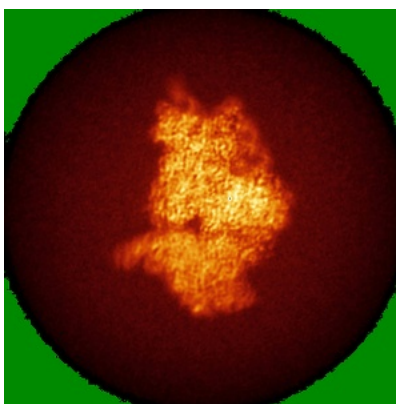
The images above show the largest variance slices of the map in three orthogonal directions.

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

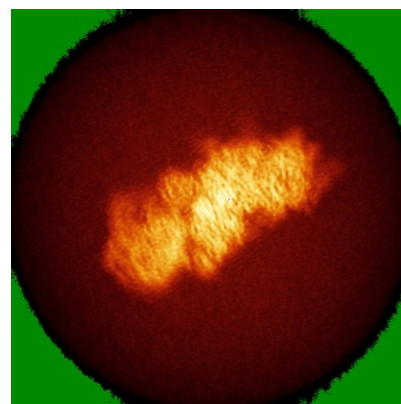
6.4.1 Primary map



X

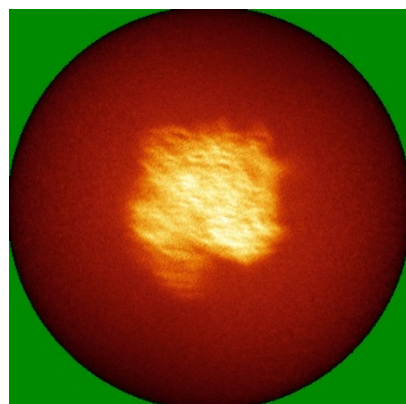


Y

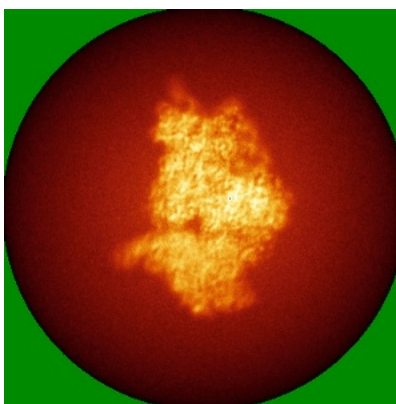


Z

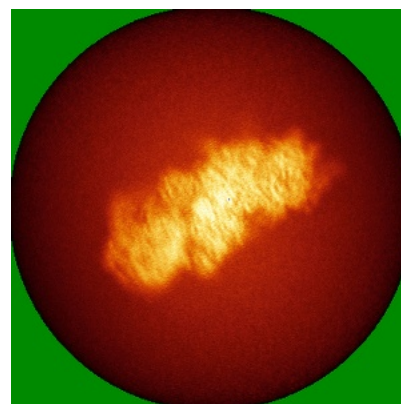
6.4.2 Raw map



X



Y

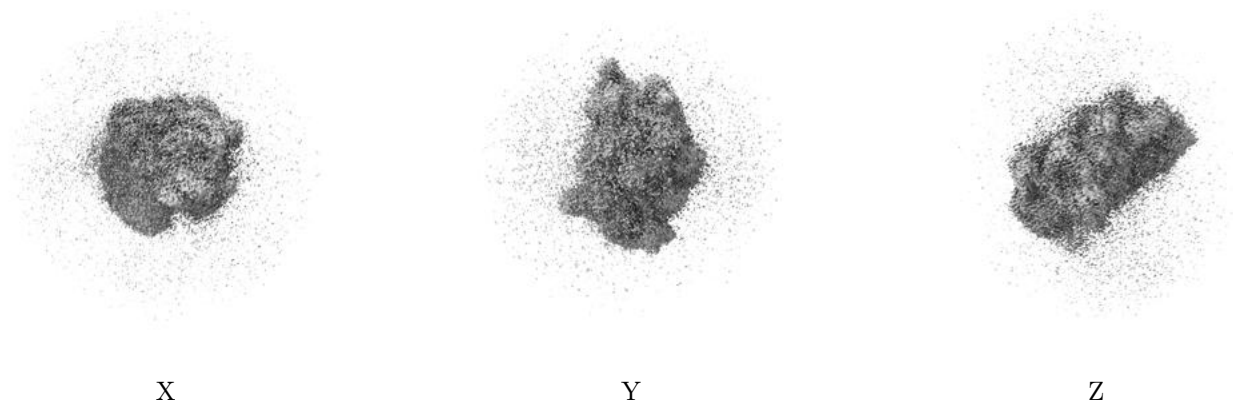


Z

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.

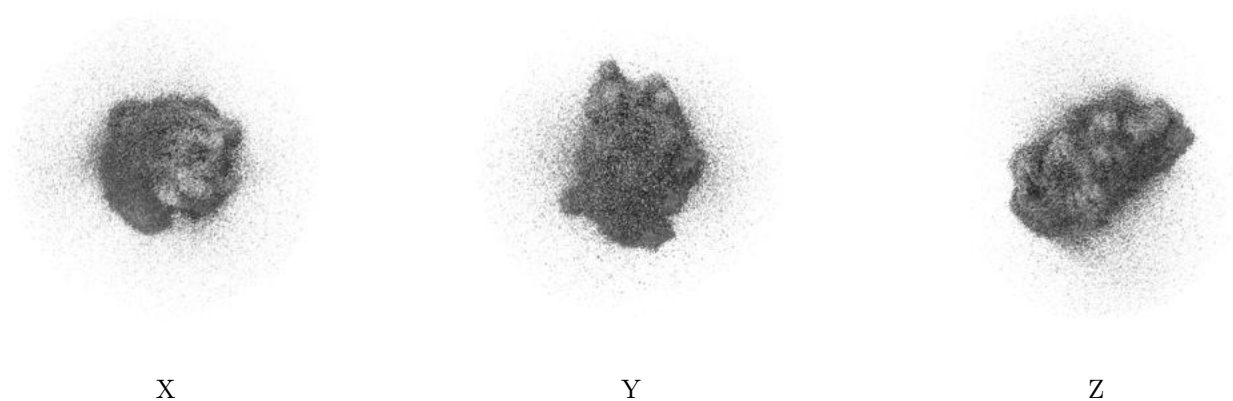
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

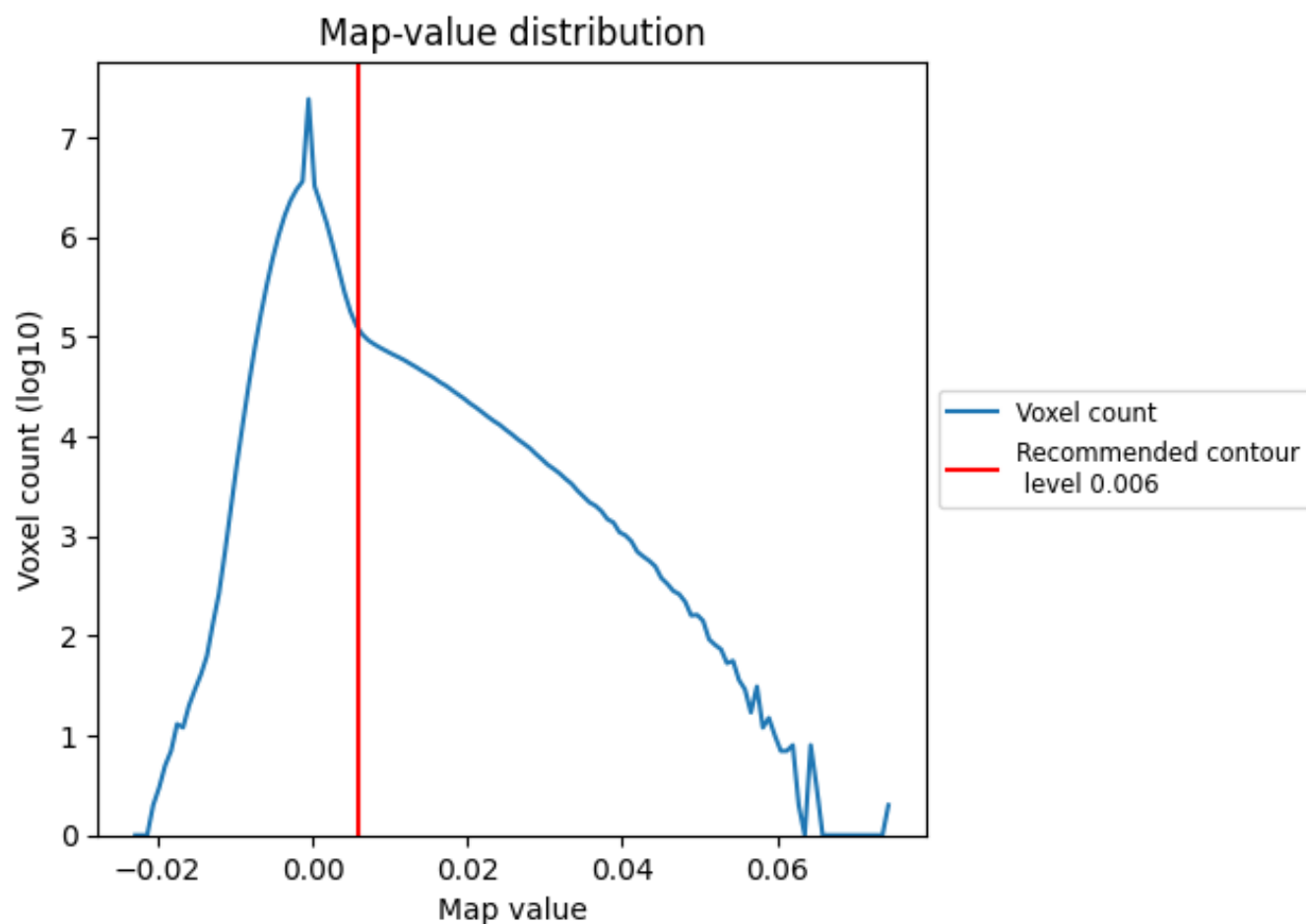
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

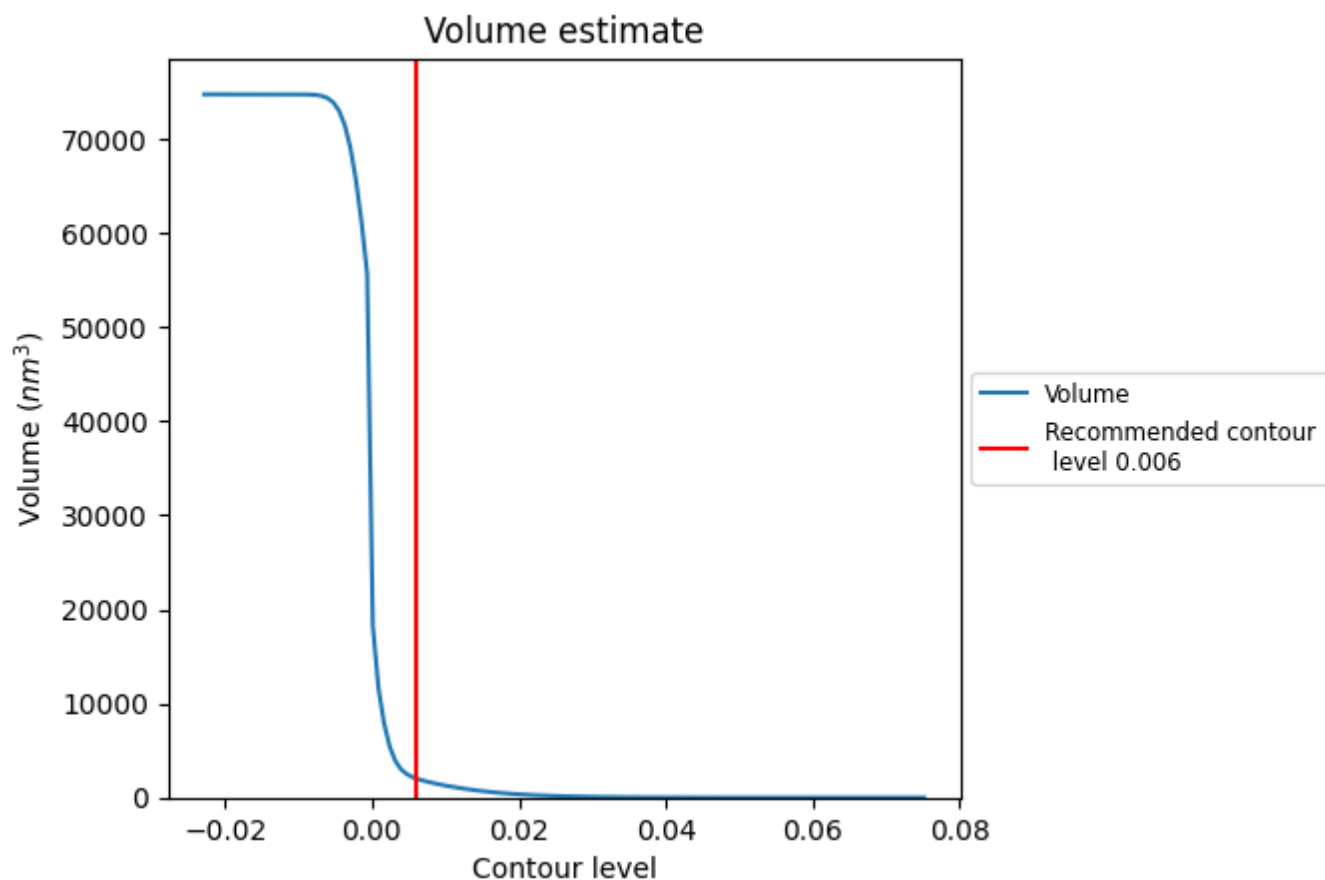
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

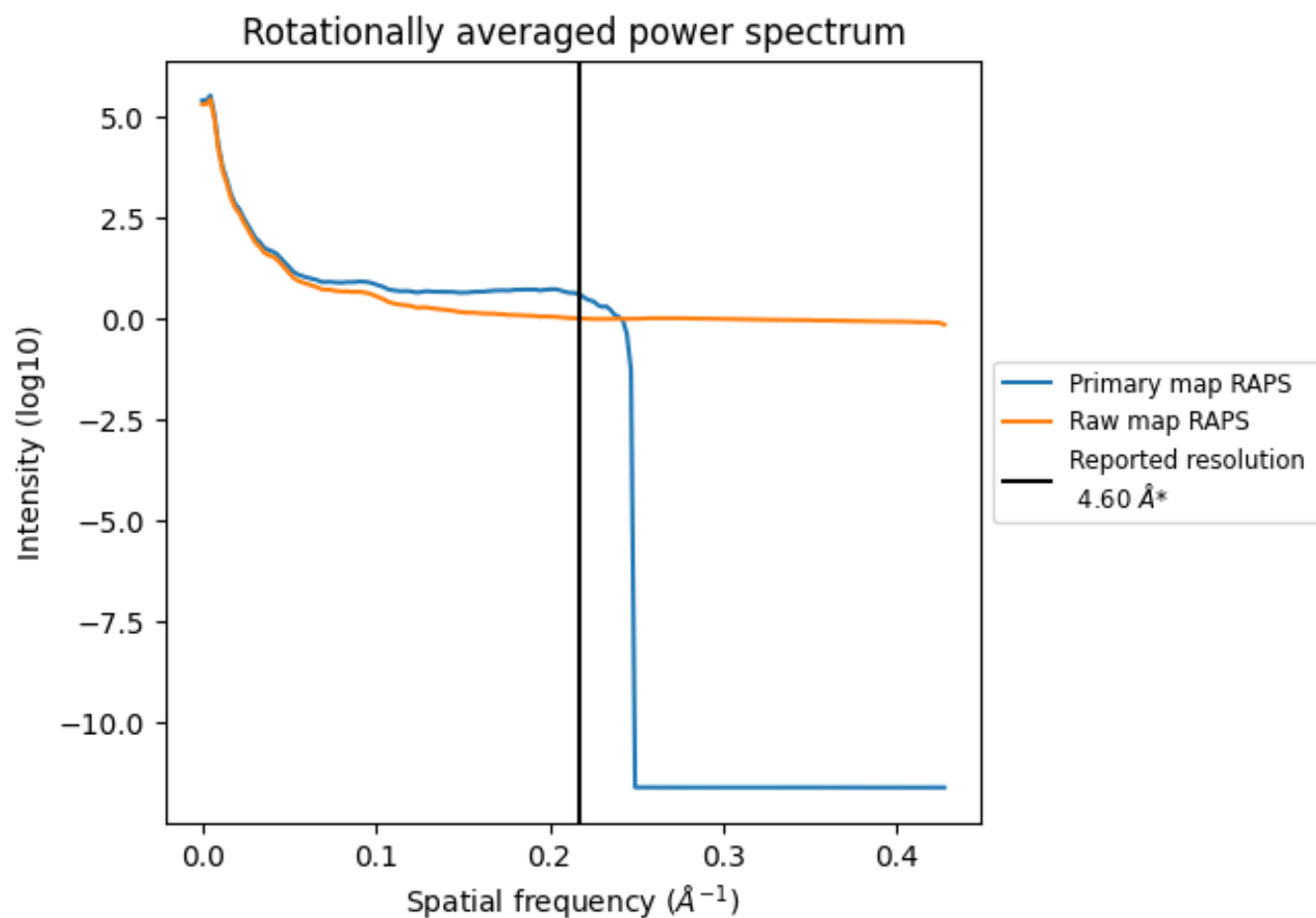
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2040 nm^3 ; this corresponds to an approximate mass of 1843 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 ⓘ

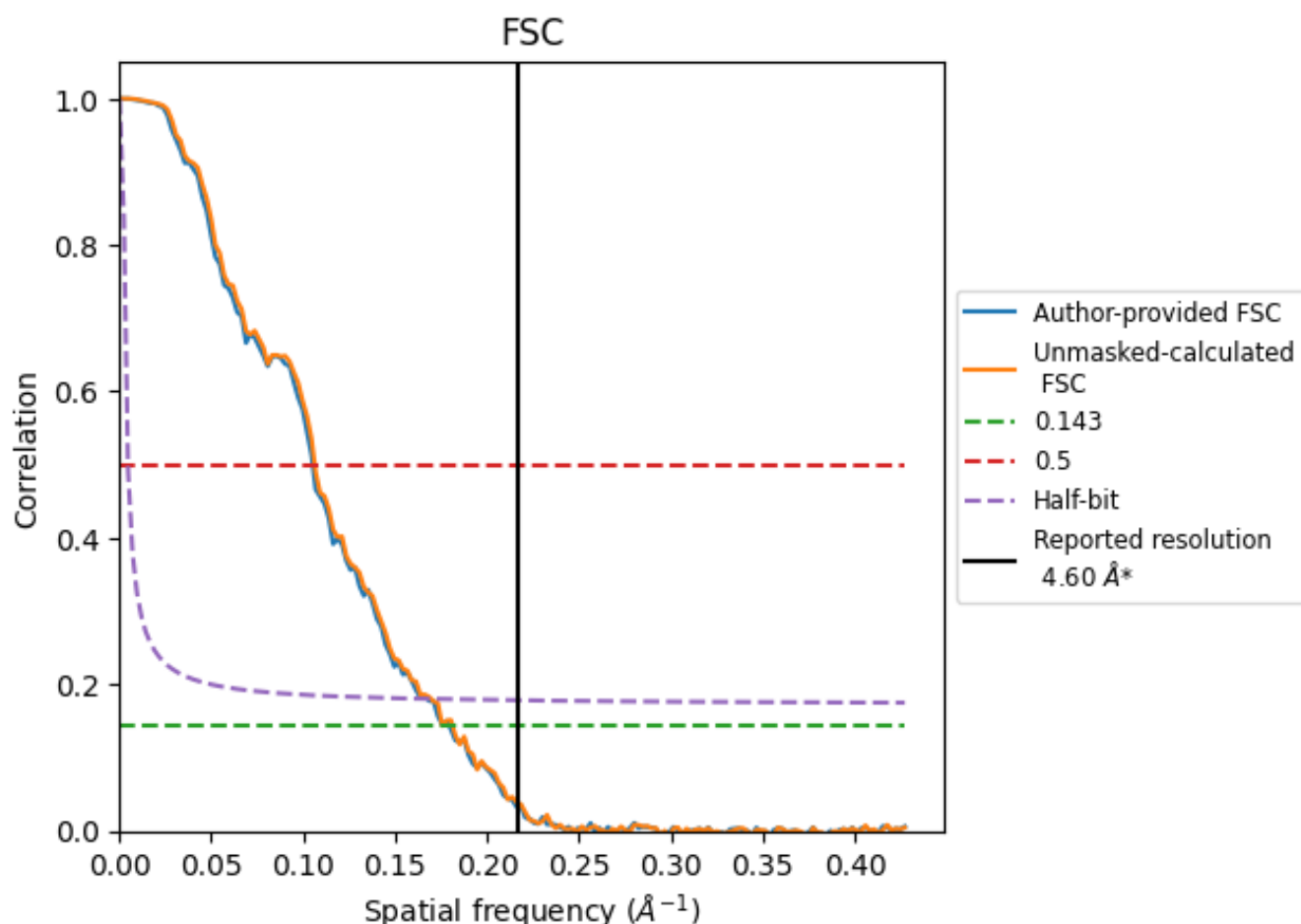


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	5.57	9.51	5.97
Unmasked-calculated*	5.51	9.41	5.89

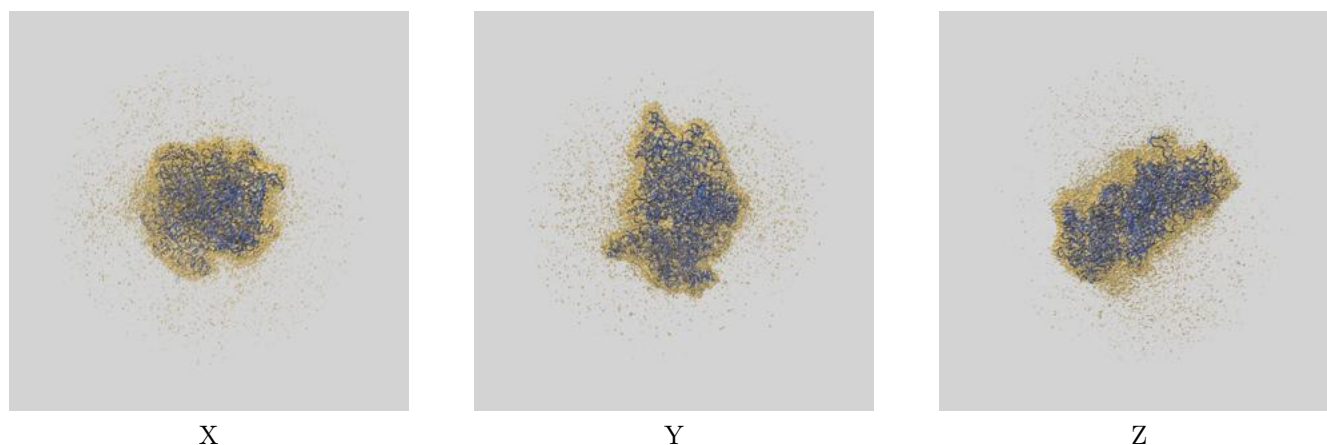
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.57 differs from the reported value 4.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.51 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

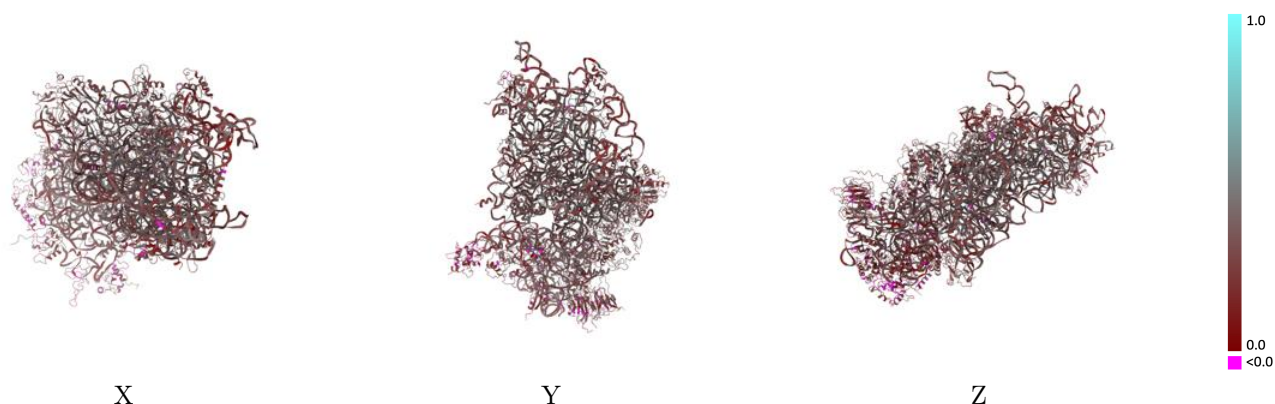
This section contains information regarding the fit between EMDB map EMD-35216 and PDB model 8I7J. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



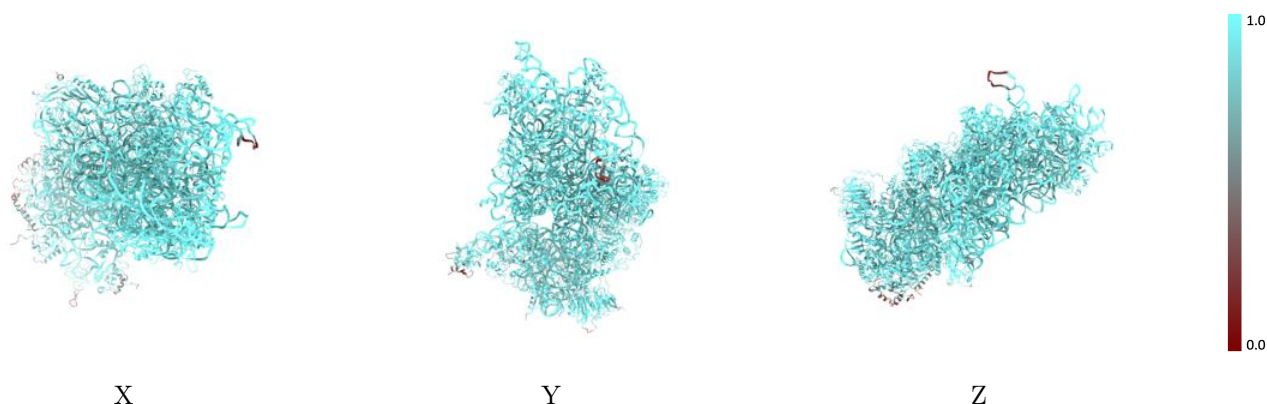
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



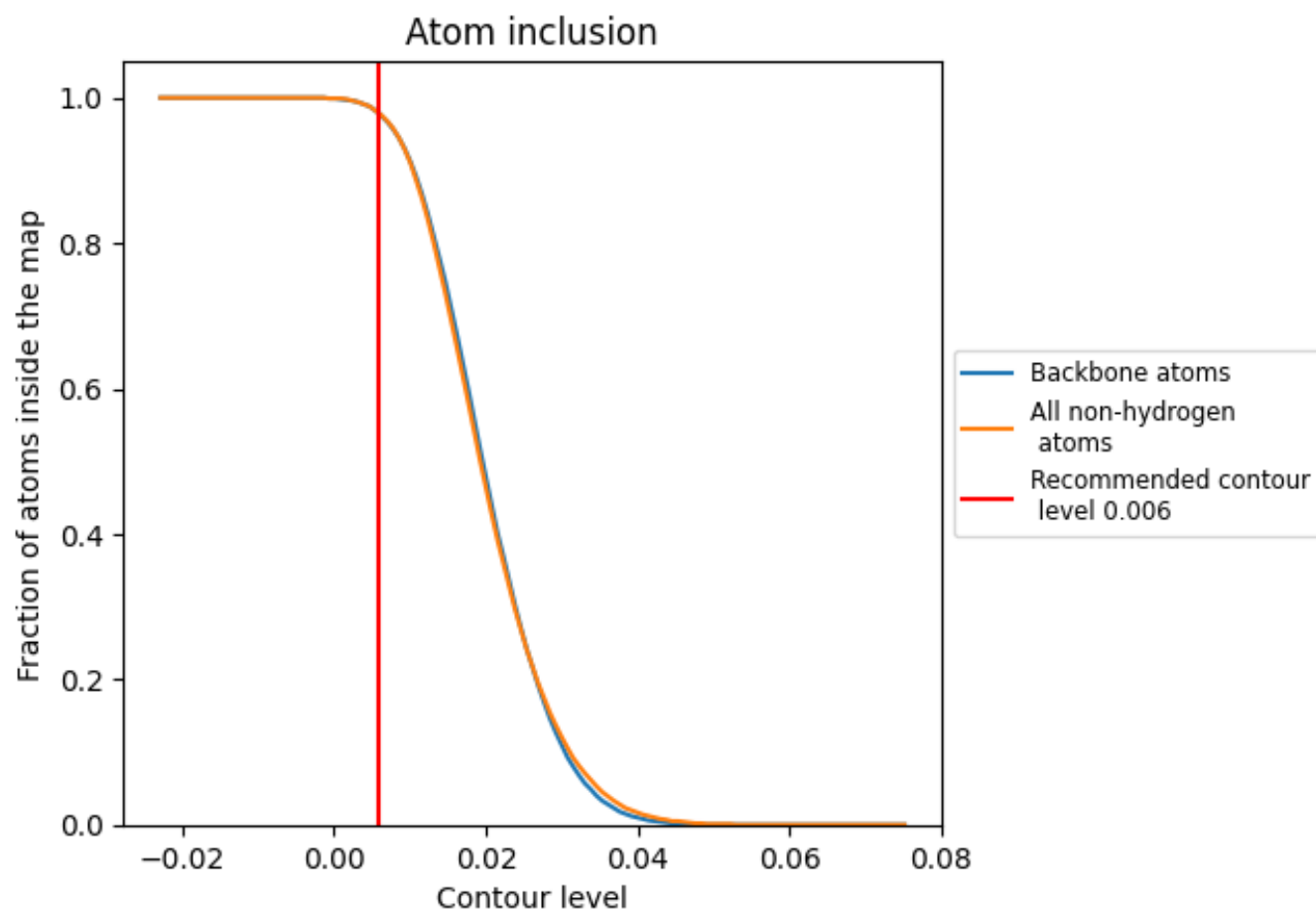
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9780	 0.3160
2	 0.9950	 0.3290
A	 0.9870	 0.3510
B	 0.9700	 0.3220
C	 0.9930	 0.3530
D	 0.9460	 0.2720
E	 0.9970	 0.3640
F	 0.9770	 0.2430
G	 0.9940	 0.3160
H	 0.9830	 0.3310
I	 0.9920	 0.3490
J	 0.9950	 0.3530
K	 0.9790	 0.2530
L	 0.9840	 0.3780
M	 0.8200	 0.1930
N	 0.9890	 0.3600
O	 0.9910	 0.3180
P	 0.8770	 0.2160
Q	 1.0000	 0.2870
R	 0.9790	 0.3240
S	 0.7490	 0.1600
T	 0.9970	 0.2510
U	 0.9140	 0.2590
V	 0.9930	 0.3530
W	 0.9910	 0.3810
X	 0.9910	 0.3920
Y	 0.9990	 0.3400
Z	 0.6630	 0.1020
a	 0.9960	 0.3620
b	 0.9970	 0.3760
c	 0.9680	 0.2080
d	 1.0000	 0.2730
e	 1.0000	 0.3180
f	 0.8200	 0.1190
g	 0.9640	 0.2700
h	 0.9430	 0.1670

