



wwPDB EM Validation Summary 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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

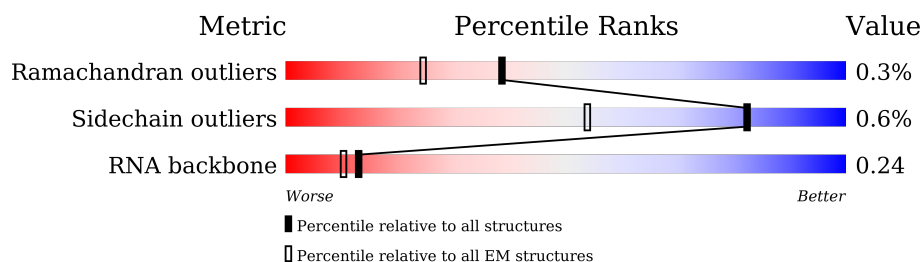
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :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




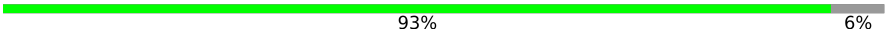
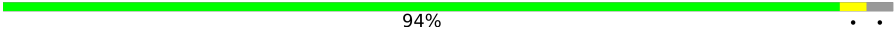

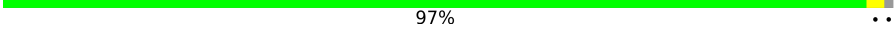

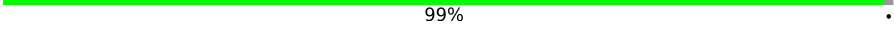
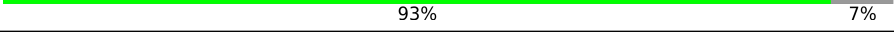

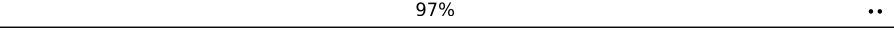

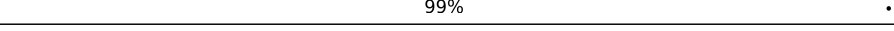
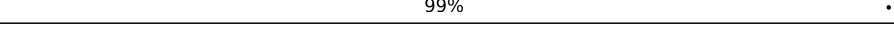

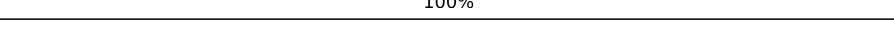
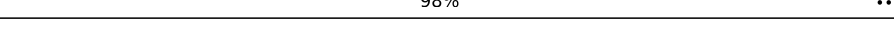
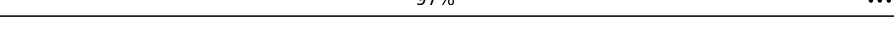
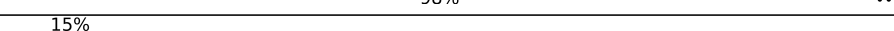

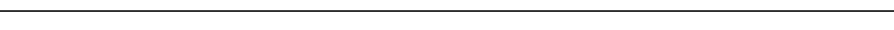

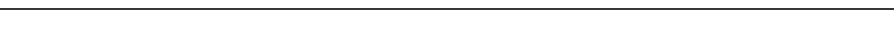
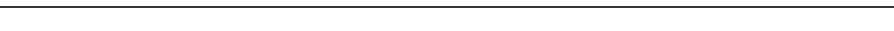


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	

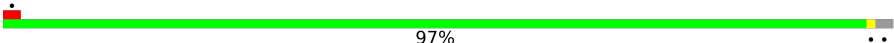

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Mol	Chain	Length	Quality of chain
9	H	190	 93% . .
10	I	201	 93% 6%
11	J	188	 94% . .
12	K	106	 90% . 9%
13	L	156	 97% ..
14	M	134	 13% 90% . 9%
15	N	151	 99% .
16	O	137	 93% 7%
17	P	142	 7% 87% 13%
18	Q	143	 97% ..
19	R	136	 88% . . 8%
20	S	146	 21% 99% ..
21	T	144	 99% .
22	U	117	 91% 9%
23	V	87	 100%
24	W	130	 98% ..
25	X	145	 97% ...
26	Y	135	 98% ..
27	Z	108	 15% 65% 35%
28	a	119	 82% 18%
29	b	82	 99% .
30	c	67	 93% . 6%
31	d	56	 93% . 5%
32	e	63	 84% 16%
33	f	150	 6% 46% 54%

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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	

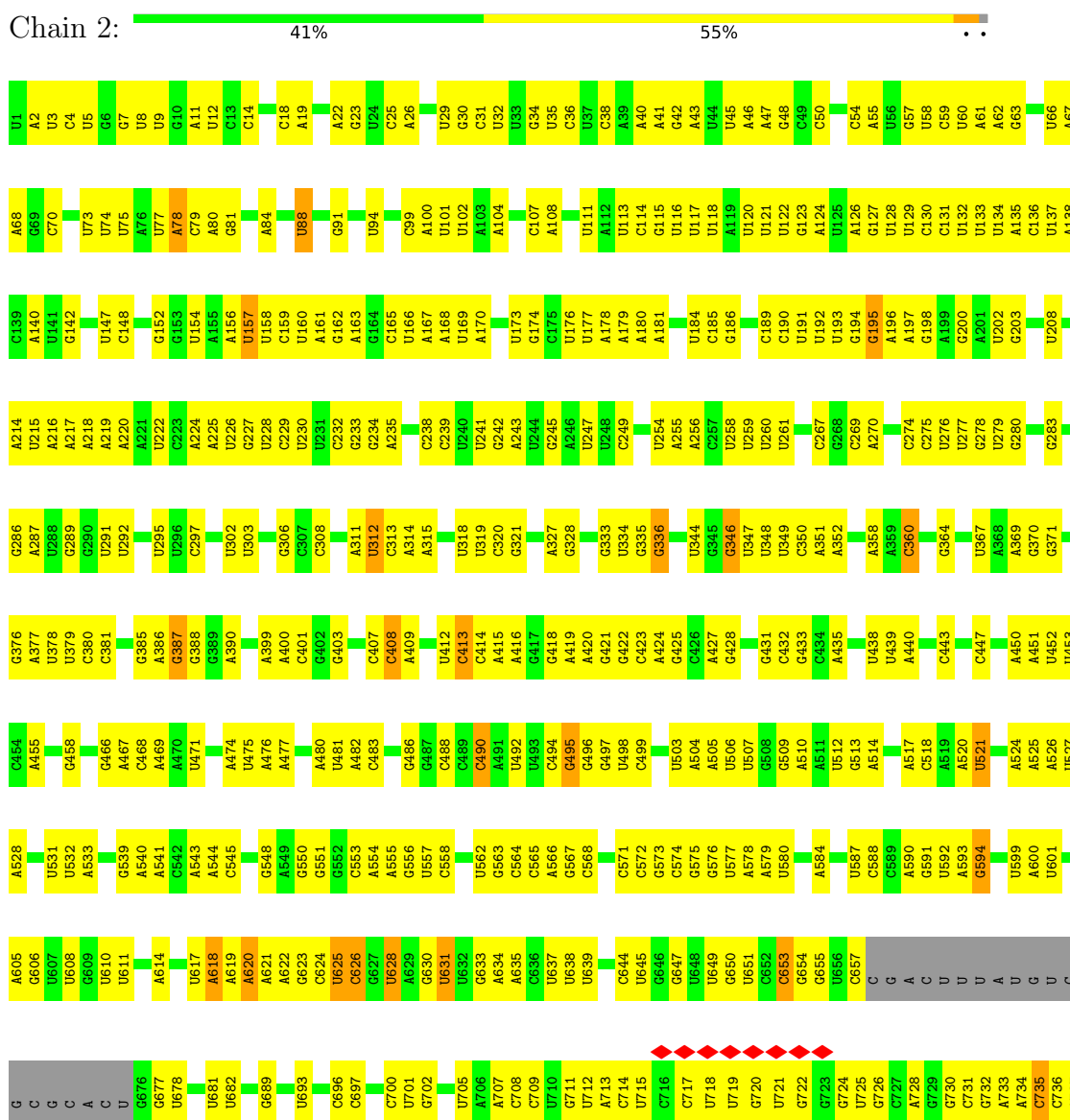
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

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.

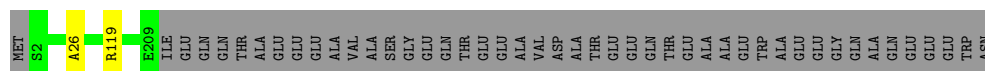
• Molecule 1: RNA (1780-MER)




A1798	C1722	U1648	C1578	C1499	G1426	U1362	G1266	G1198		A1112	A1042	U967	A891	G822	A740
	A1649	G1650	C1579	G1500	G1427	G1353	G1267	A1201	A1113	C1043	C968	C968	G894	G823	C741
	C1650	U1580	C1579	G1501	U1428	G1356	U1268	A1202	G1113	C1044	A969	A970	G895	U824	U742
	G1652	A1581	U1580	G1502	U1429	G1357	G1269	A1203	U1116	G1047	C896	C896	G896	U825	U743
	A1653	G1582	G1582	G1504	G1431	C1358	A1274	C1204	G1117	U1048	A973	A973	A897	G826	U744
	U1654	U1583	U1583	G1505	U1432	A1359		U1205	G1118	U1048	C974	C974	A898	U827	U745
	C1655	A1584	A1584	G1506	G1433	C1360	C1278	G1211		G1049	G975	G975	A899	A828	U749
	G1657	A1585	G1507	U1508	A1434	U1361	C1279	G1212	C1122	G1050	A976	A976	G900	U829	U750
	U1658	G1586	U1508	G1507		U1362	U1280	U1123	A1123	G1051	G901	G901	G901	U830	G751
	C1659	G1587	G1587	G1509	C1438	G1363	U1281	U1213	A1124	U1053	G879	G879	U902	U832	A752
	G1660	C1589	C1589		U1439	C1364	U1282	C1214	G1125	U1054	U980	U980	G903	U833	A753
	A1665			A1513	U1440	C1365	C1283	C1215	G1126	U1055	U981	U981	A904	G833	A754
		U1593	U1593	U1514	U1441	G1366	U1284	A1216	G1125	U1056	A982	A982	A905	U835	A755
	A1669	C1594	C1594	C1516	A1442	G1367	U1285	G1217	G1129	U1057	G983	G983	A906	G836	A756
	G1743	A1595	A1595	G1519	G1443	U1368	A1286	A1218	A1130	C1058	U907	U907	U907	G837	A757
	C1672	U1596	U1596	G1520	A1444	U1369	G1287	C1219	A1137	U1059	C989	C989	U908	U838	U758
	U1674	C1597	C1597	U1520	U1446	A1371	G1290	A1220	A1137	U1060	G990	G990	C909	U839	U759
		C1673	U1598	G1521	U1447	U1371	G1291	C1221	A1138	A1061	A991	A991	U910	U840	A760
	A1747	U1674	U1599	A1522	U1448	C1374	U1292	A1223	G1139	U1062	A992	A992	U911	C841	
			C1600			U1375	G1293	U1224	G1140	G1063	G993	G993	G912	U842	G765
	G1678	U1601	U1601	C1525	G1453	U1376	G1294	A1225	G1145	C1065	A994	A994	G913	A843	U766
	A1679	U1602	U1602	C1531	C1454	U1377		A1226	A1146	C1066	U995	U995	A914	G844	U767
	U1680	G1603	C1603	U1532	C1455	U1378	G1298	G1227	C1147	C1067	C999	C999	U916	G845	
	A1753	C1604	G1604	U1533	G1456	U1379		G1228	G1148	A1068	C999	C999	U920	C847	A771
	G1684	U1605	G1605	G1534	C1457	A1380	U1306	A1229	G1149	C1069	A1000	A1000	U920	C847	C772
	U1685	U1606	U1606	U1535	U1458	A1381		U1230	A1150	U1070	G1001	G1001	A849	A774	
	U1688			U1536	C1459	G1384	U1309	U1231	A1151		G824	G824	A825	U850	
	A1687	U1611	U1611	U1537	G1460	G1385		G1232	G1152	G1073	A1004	A1004	C925	U853	G778
	G1688	C1612	C1612	G1537	C1461	A1386	U1313	A1233	G1153	C1074	C1005	C1005	C926	U853	A779
	A1760	G1613	G1613	U1538	G1462	C1387	U1314	C1234	G1154	A1075	C1006	C1006	U927	A854	A780
	G1690	U1614	G1614	G1539	C1463	U1388	G1315	A1235	C1155		A781	A781	A928	A855	A781
	A1691			G1540	G1464	A1389	C1316	G1236	A1156	U1079	A1012	A1012	A929	U856	G782
	G1692	C1617	C1617	A1541		A1389	G1317		C1157	A1080	G1013	G1013	C930	G857	
	C1693			U1542	C1468	G1392		G1240	C1158	C1081	U1014	U1014	U931	A858	C785
	A1764	G1693	G1693	U1543	A1469	G1393	A1320	A1241	A1159	U1082	C1015	C1015	A932	G861	G786
	G1765			A1543	C1470	U1396	A1321	G1242	A1162	A1085	C1020	C1020	C933	A862	A787
	U1767	C1697	C1697	A1545	U1471	C1397	C1322	A1243	C1172	U1086	A1021	A1021	U934	A861	A788
	G1768	U1623	C1623	U1547	G1472	U1405	G1326	G1244	C1173	A1087	G1022	G1022	G935	U789	
		A1699	U1624	G1551		U1405	U1326	C1245	C1174	U1088	U1023	U1023	A941	A864	A790
	U1773	A1700	U1625	U1552	G1475	G1400	G1327	U1246	C1179	C1089	A1024	A1024	C942	G865	U791
		C1701	A1553	U1553	G1476	C1401	A1328	C1247		U1089	A1025	A1025	C942	G866	A792
	U1777	U1702	A1554	A1554		A1404		U1248		C1089	A1026	A1026	A943	G870	U793
	G1778	C1703	C1630	U1555	C1479	U1405	A1336	U1249	G1177	A1090	C1027	C1027	U945	G871	C797
	A1779	G1704	A1631	U1556		U1405	C1337	U1250	G1178	A1091	U1028	U1028	U946	U872	
	U1780	A1705	C1632	U1557	G1483	U1408	U1338	U1251	C1179	U1092	G1033	G1033	U946	U872	
	C1781	U1706	A1633	A1557	C1484	U1409	U1339	U1252		U1093	A1029	A1029		G871	
		C1707	U1634		G1485	A1408	U1339	U1253	A1182	C1095	U1030	U1030	A950	C873	G800
	G1784	U1708	C1635	U1558	U1486	U1410	A1409	G1254	A1183	U1096	A1031	A1031	U950	G874	G801
	C1785	C1709	G1636	U1559	G1487	C1411	U1410	A1255	A1184	U1096	C1032	C1032	C955	G875	A802
		U1710	U1566	U1566	U1488	U1412	A1343	U1256	U1185	U1097	G1033	G1033	C955	G876	
	A1788	G1711	C1639	U1567	C1489	U1413	A1344	U1258		G1098	A1034	A1034	U958	G877	A811
	U1789	A1712	G1640	A1568	A1490	U1419	A1345	U1259	C1191	G1100	A1035	A1035	U959	G878	A813
	G1790		U1641	C1569	A1491	A1420	U1346	G1260	A1192	U1101	C1036	C1036	A962	C882	A813
	A1717		C1642	U1570	C1492	A1421	A1347	U1261	A1193	U1102	U1037	U1037	A962	A883	G814
	G1718		G1643	U1571	C1493	U1421	G1348	G1262	C1194	U1102	A1038	A1038	U963	G815	
	U1792		C1644	A1572	G1494	A1422	G1349	G1263	C1195	C1104	G1039	G1039	U964	U887	U819
	C1794		U1645	U1495	U1495	U1425	G1350	G1264	C1196		G1040	G1040	A965	U888	
			A1575			A1426	U1351	U1265	C1197	C1103			A966	U820	U820

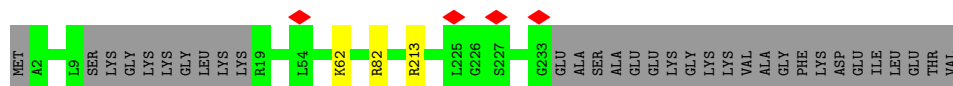
- Molecule 2: 40S ribosomal protein S0

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%




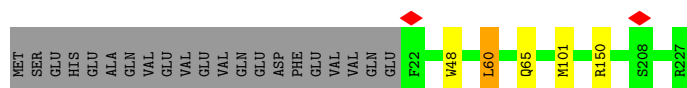
- Molecule 6: 40S ribosomal protein S4

Chain E:  98%



- Molecule 7: KLLA0D10659p

Chain F:  89% 9%



- Molecule 8: 40S ribosomal protein S6

Chain G:  95%



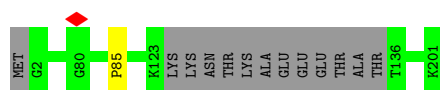
- Molecule 9: 40S ribosomal protein S7

Chain H:  93% ..



- Molecule 10: 40S ribosomal protein S8

Chain I:  93% 6%




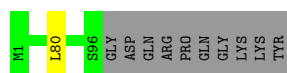
- Molecule 11: KLLA0E23673p

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%



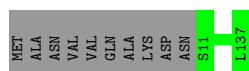
- Molecule 15: KLLA0F18040p

Chain N:  99% .




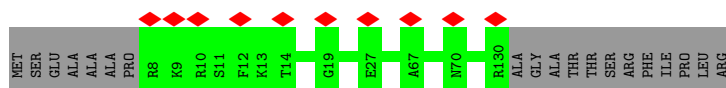
- Molecule 16: 40S ribosomal protein S14

Chain O:  93% 7%



- Molecule 17: KLLA0F07843p

Chain P:  7% 87% 13%




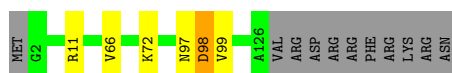
- Molecule 18: 40S ribosomal protein S16

Chain Q:  97% ..



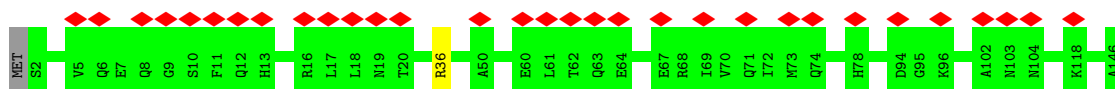
- Molecule 19: KLLA0B01474p

Chain R:  88% .. 8%



- Molecule 20: KLLA0B01562p

Chain S:  21% 99% ..




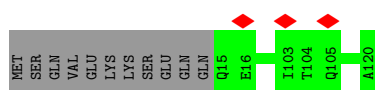
- Molecule 21: KLLA0A07194p

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.

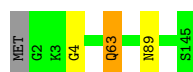
- Molecule 24: KLLA0B07931p

Chain W:  98%



- Molecule 25: KLLA0B11231p

Chain X:  97%



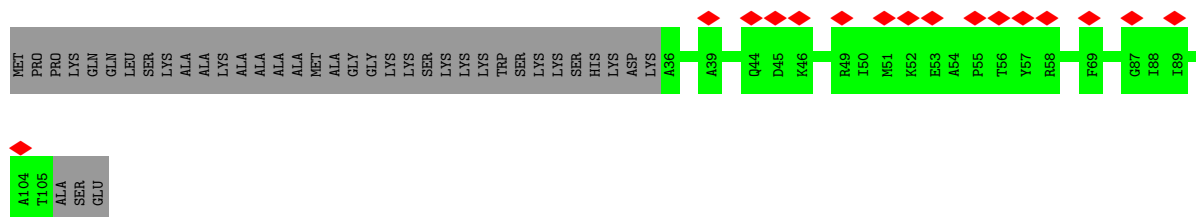
- Molecule 26: 40S ribosomal protein S24

Chain Y:  98%




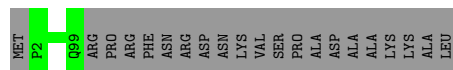
- Molecule 27: 40S ribosomal protein S25

Chain Z:  15% 65% 35%



- Molecule 28: 40S ribosomal protein S26

Chain a:  82% 18%



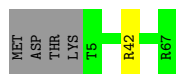
- Molecule 29: 40S ribosomal protein S27

Chain b:  99%



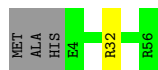
- Molecule 30: 40S ribosomal protein S28

Chain c:  93% • 6%




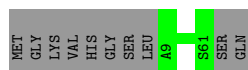
- Molecule 31: 40S ribosomal protein S29

Chain d:  93% • 5%



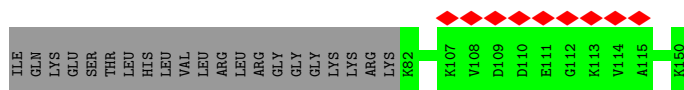
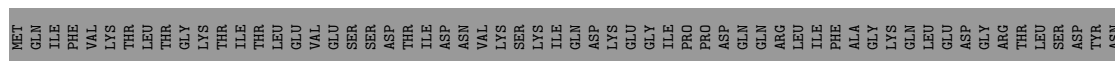
- Molecule 32: 40S ribosomal protein S30

Chain e:  84% 16%



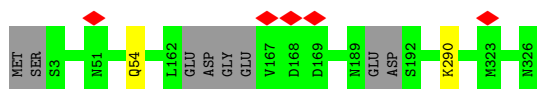
- Molecule 33: Ubiquitin-40S ribosomal protein S27a

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

The worst 5 of 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

There are no chirality outliers.

5 of 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

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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	R	98	ASP
4	C	45	LYS
19	R	72	LYS

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Mol	Chain	Res	Type
25	X	4	GLY
26	Y	35	VAL

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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	67	ARG
19	R	11	ARG
18	Q	102	LYS
20	S	36	ARG
6	E	198	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
16	O	24	ASN
21	T	43	ASN
29	b	49	HIS
21	T	101	ASN
7	F	36	GLN

5.3.3 RNA [i](#)

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

5 of 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

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	898	G
1	2	1788	A
1	2	1067	C
1	2	1765	G
1	2	1566	C

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

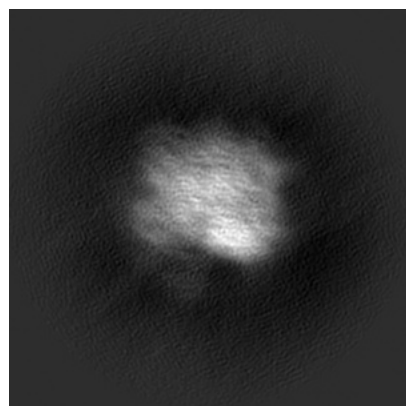
6 Map visualisation [i](#)

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

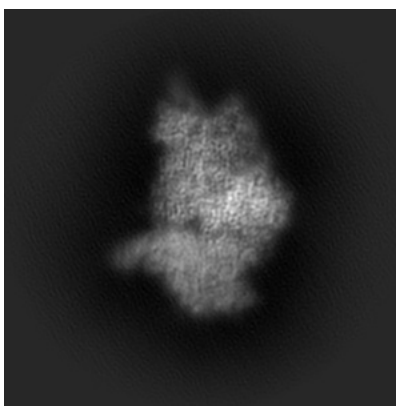
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

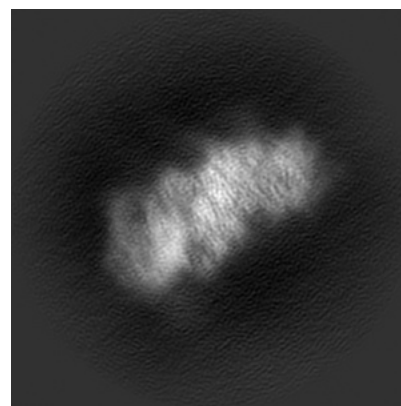
6.1.1 Primary map



X

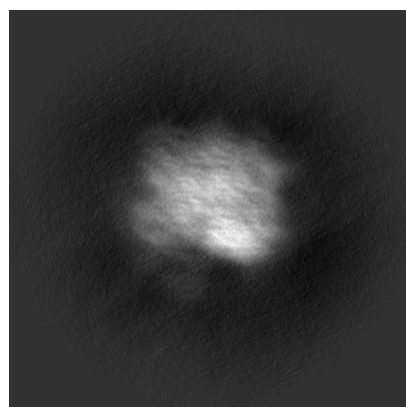


Y

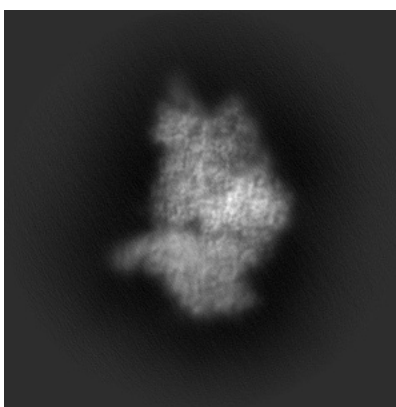


Z

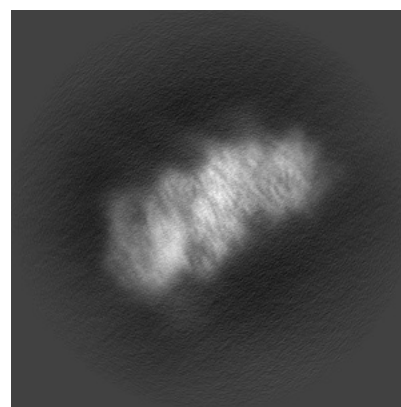
6.1.2 Raw map



X



Y

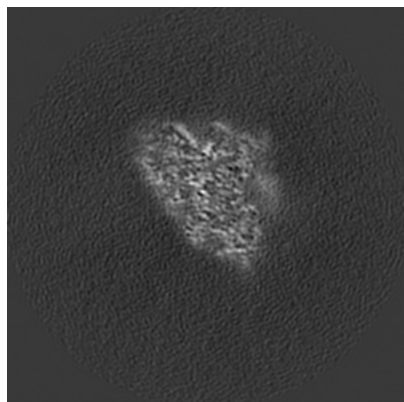


Z

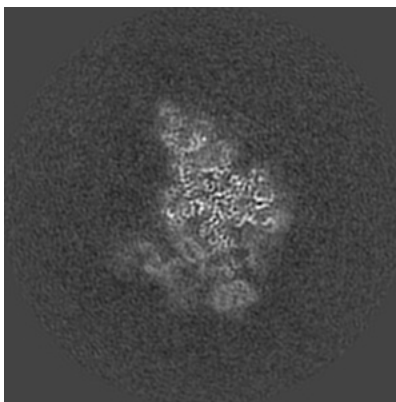
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

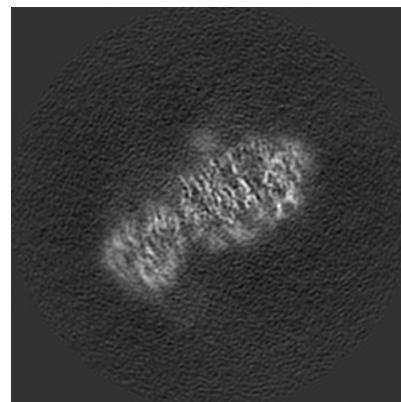
6.2.1 Primary map



X Index: 180

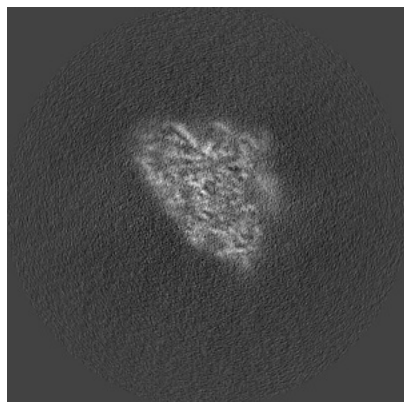


Y Index: 180

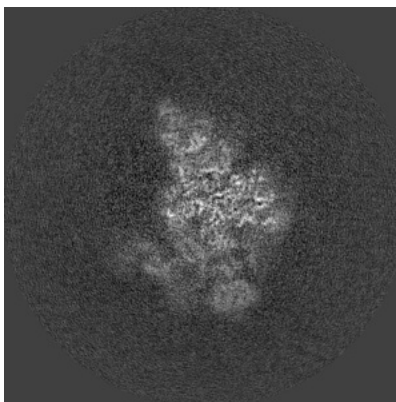


Z Index: 180

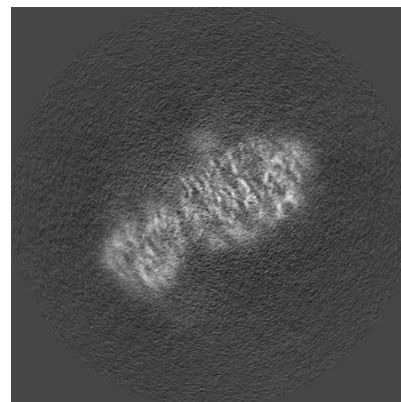
6.2.2 Raw map



X Index: 180



Y Index: 180

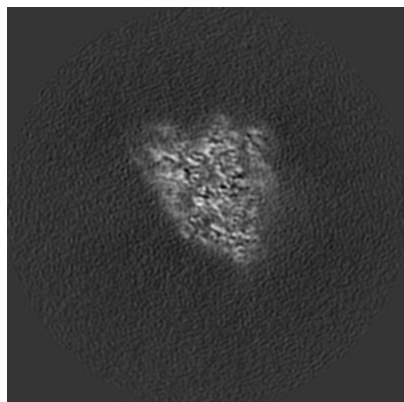


Z Index: 180

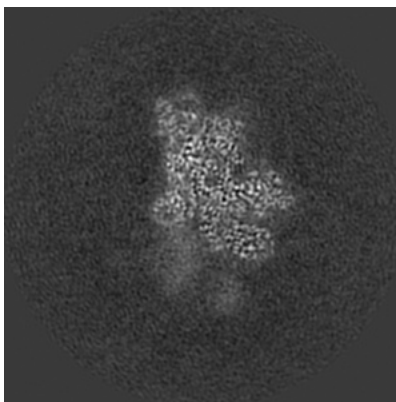
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

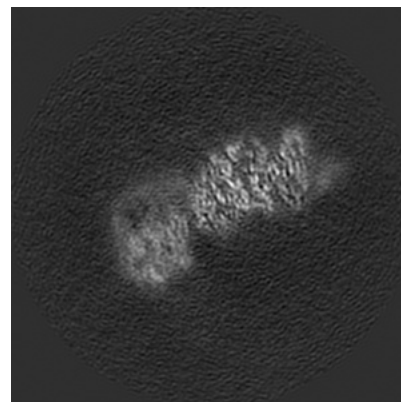
6.3.1 Primary map



X Index: 187

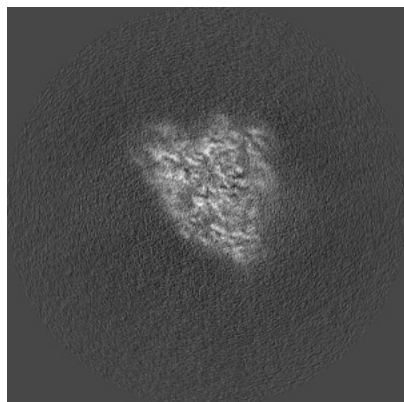


Y Index: 195

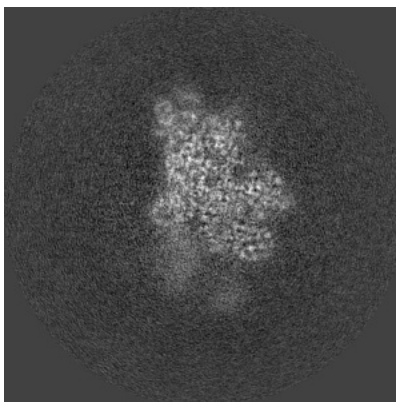


Z Index: 160

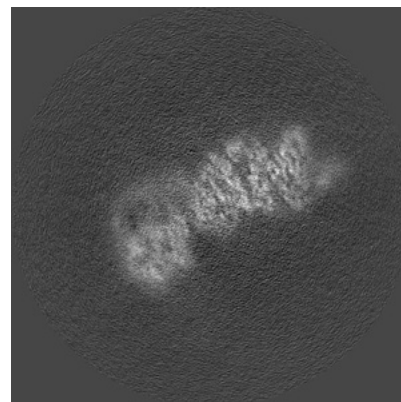
6.3.2 Raw map



X Index: 187



Y Index: 196

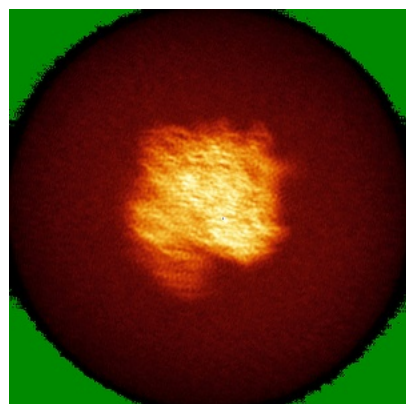


Z Index: 159

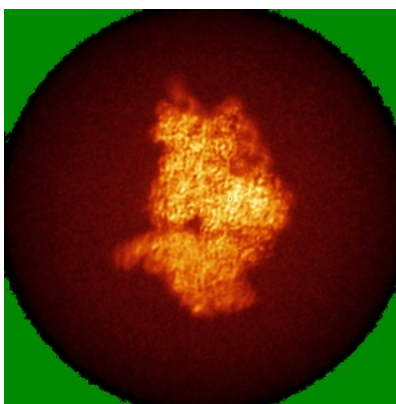
The images above show the largest variance slices of the map in three orthogonal directions.

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

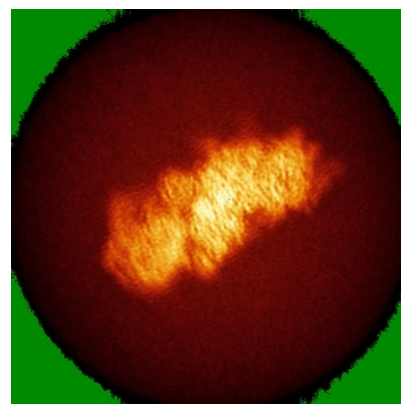
6.4.1 Primary map



X

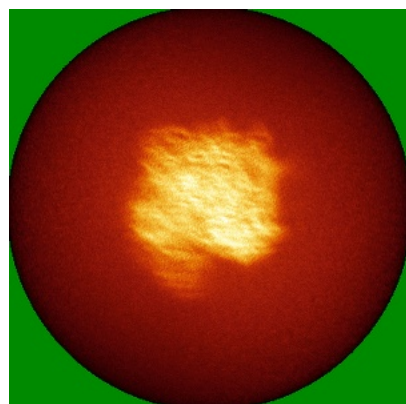


Y

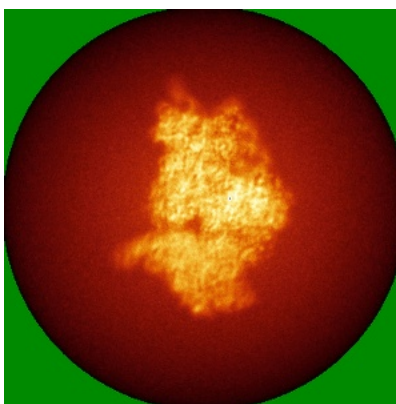


Z

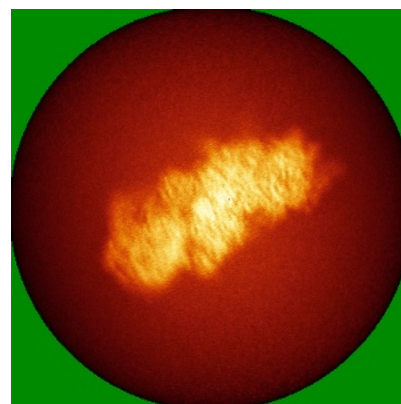
6.4.2 Raw map



X



Y

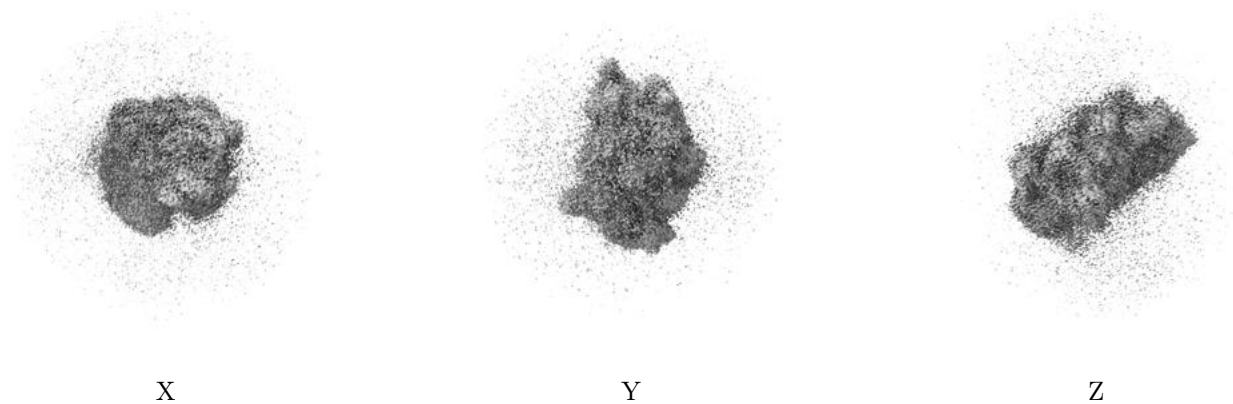


Z

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.

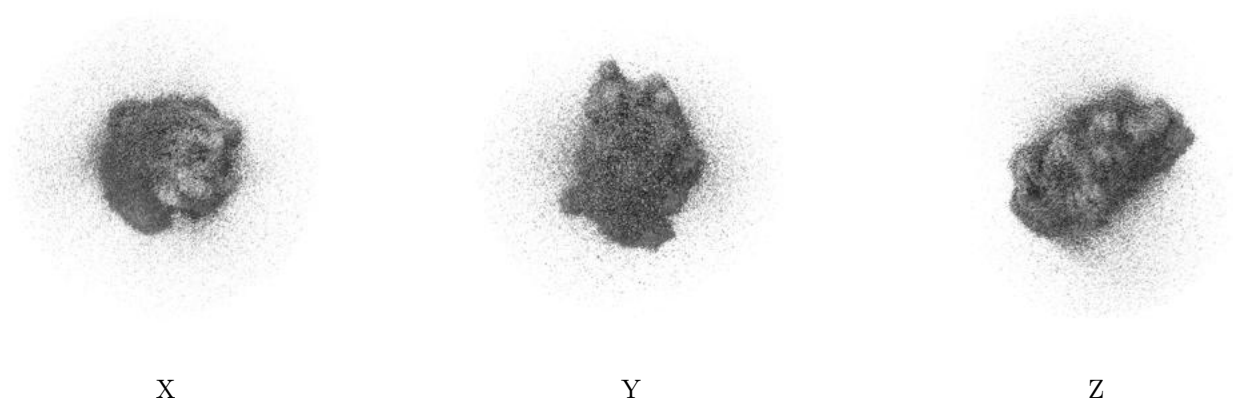
6.5 Orthogonal surface views [i](#)

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.

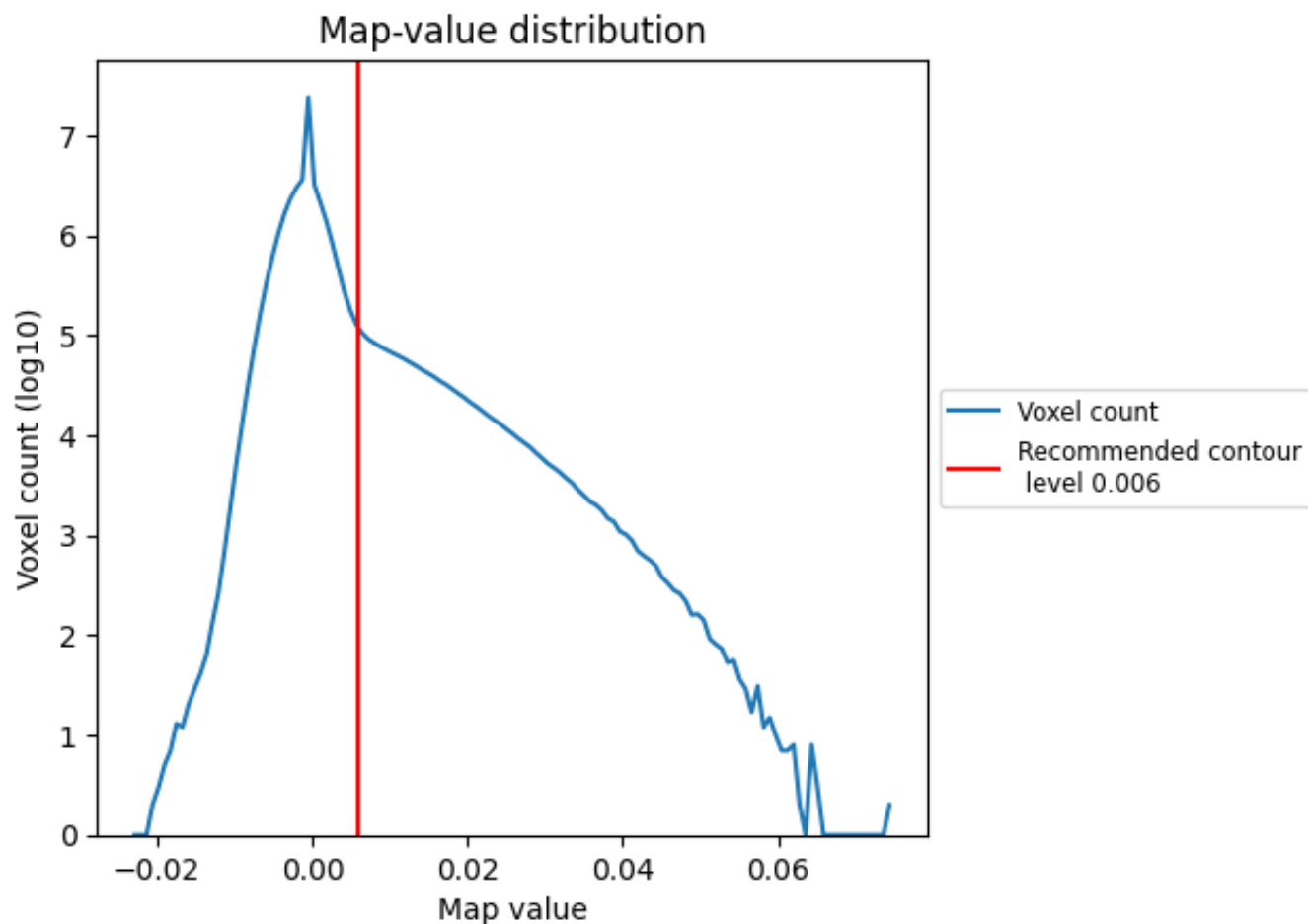
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

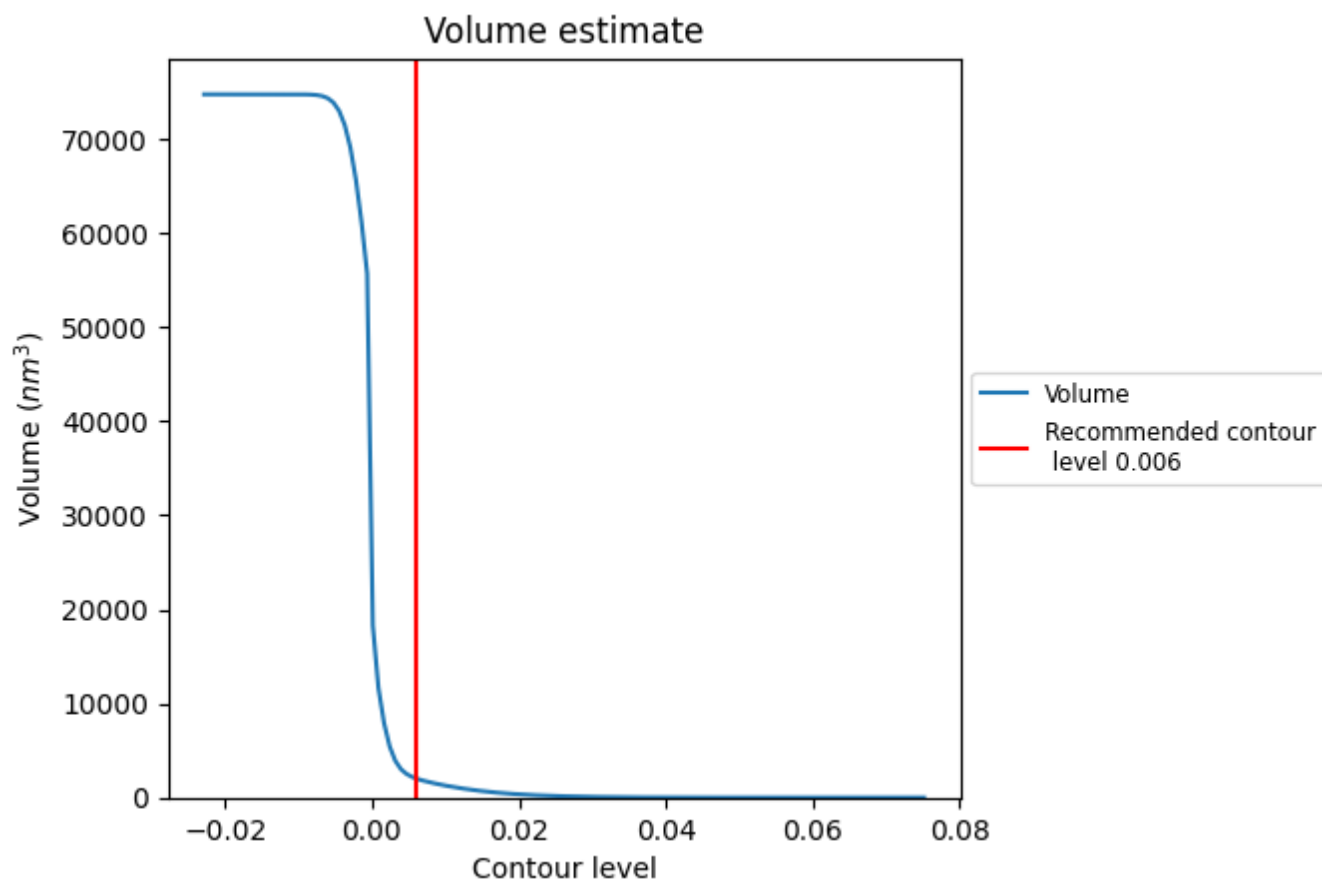
This section contains the results of statistical analysis of the map.

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.

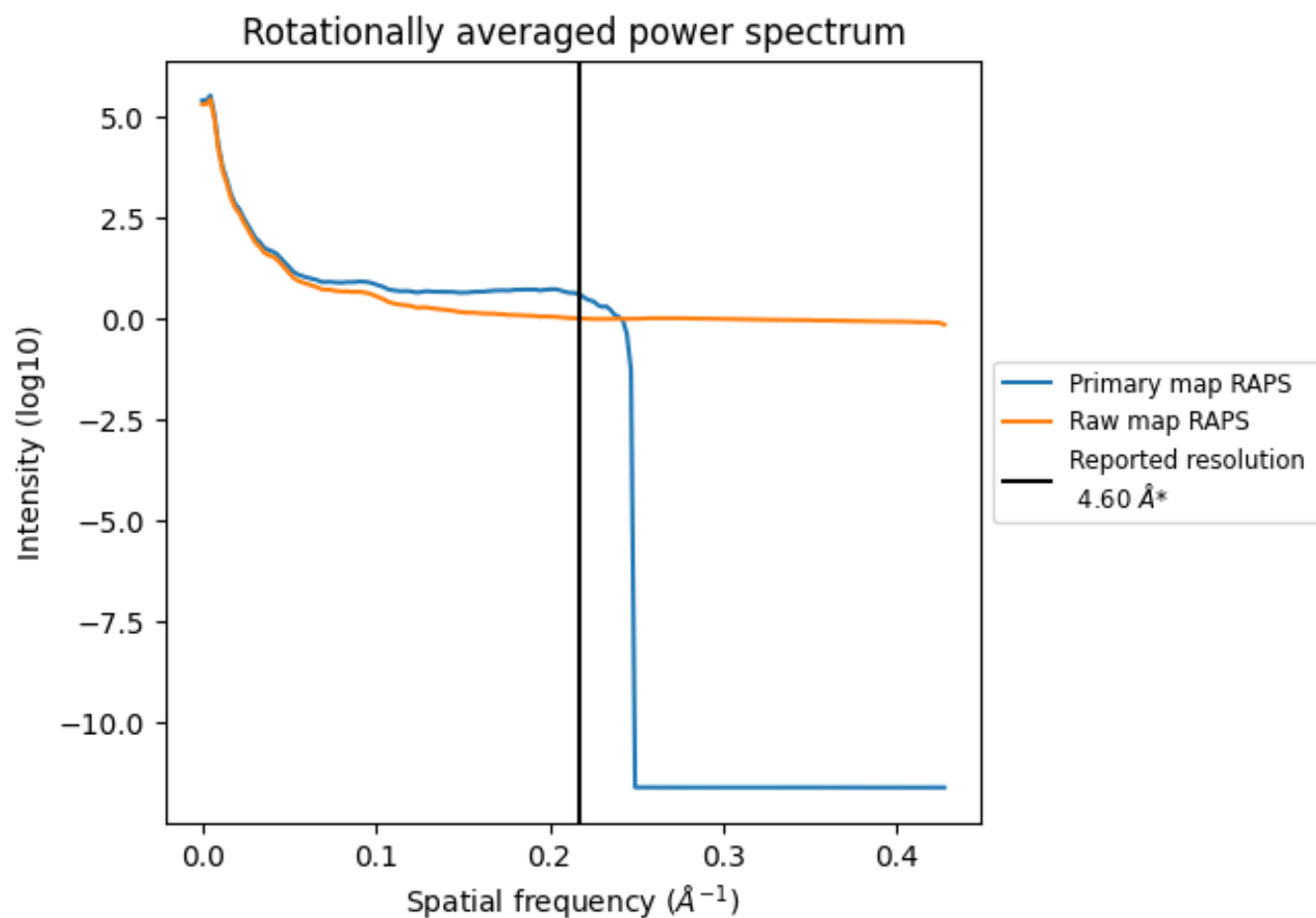
7.2 Volume estimate [i](#)



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 ⓘ

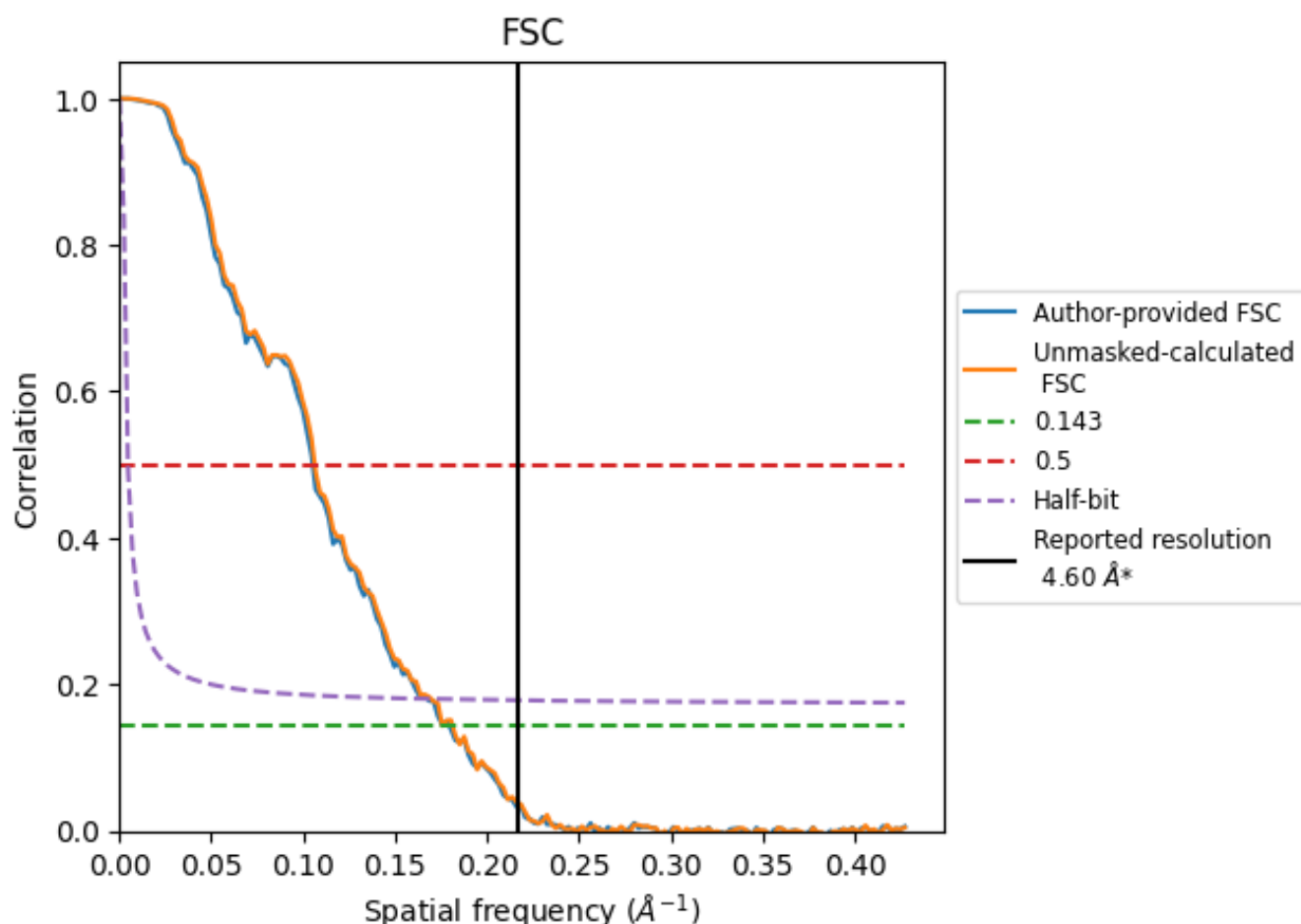


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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

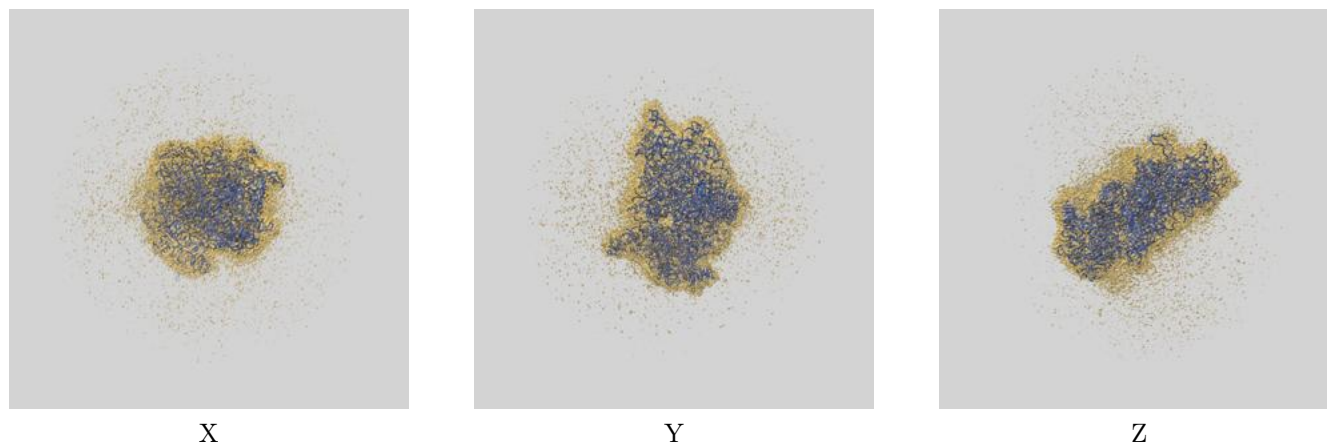
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.57 differs from the reported value 4.6 by more than 10 %

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](#)

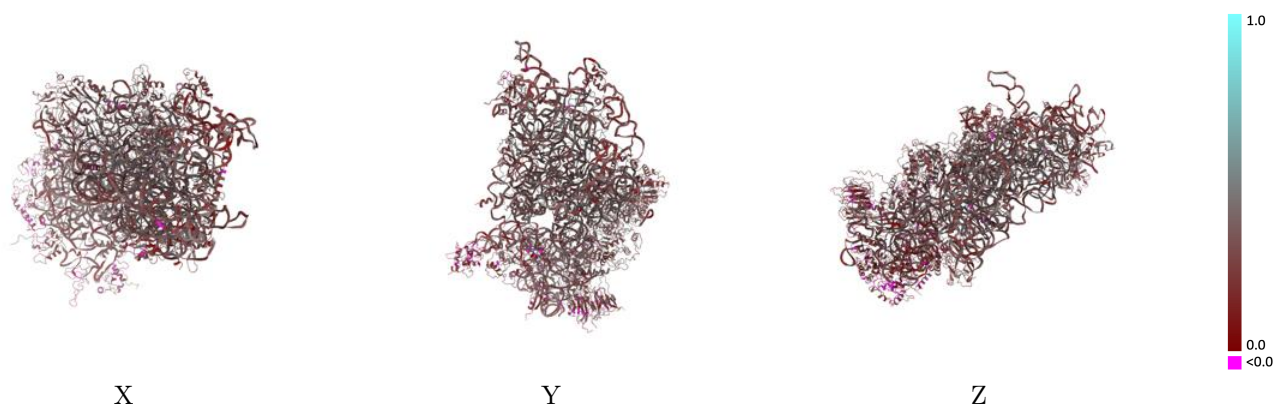
This section contains information regarding the fit between EMDB map EMD-35216 and PDB model 8I7J. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



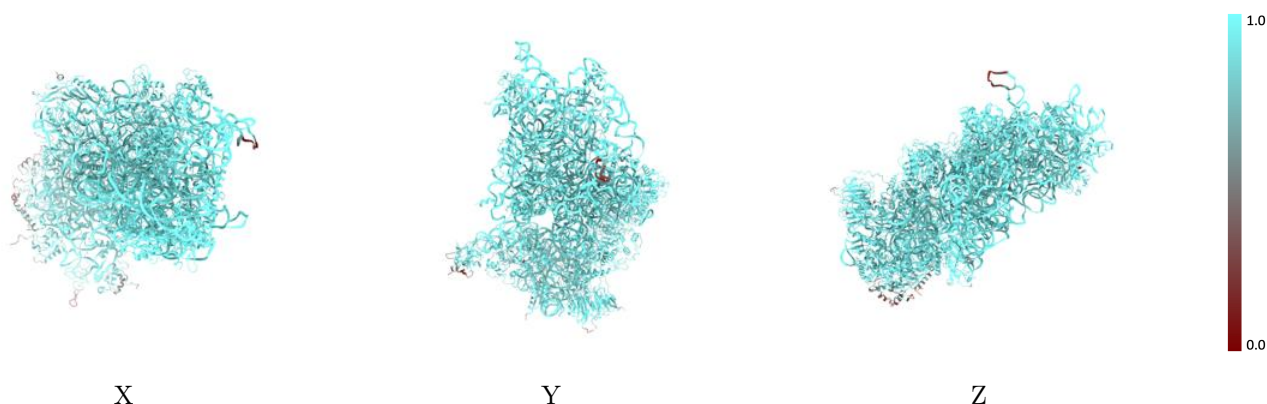
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



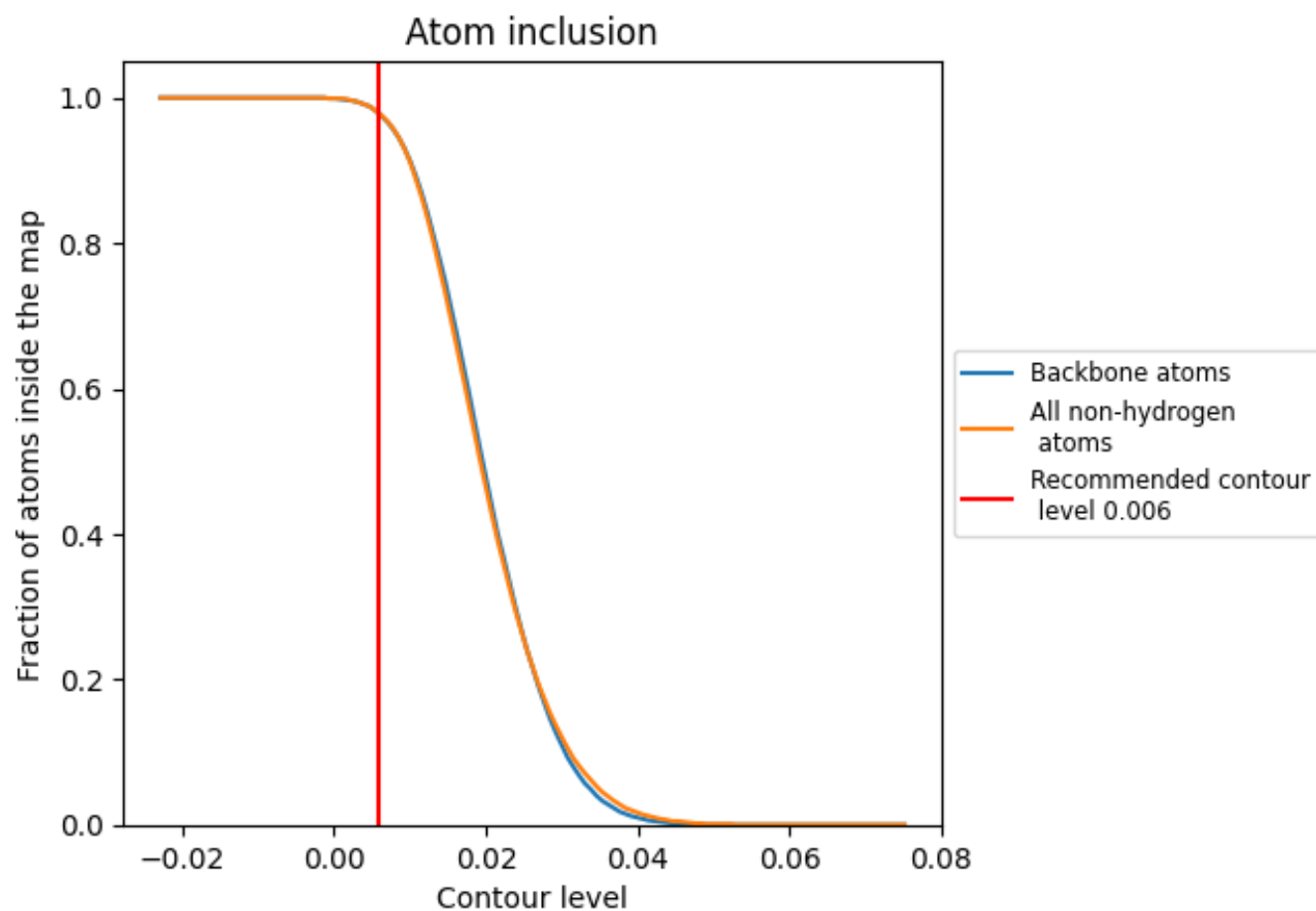
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

