



wwPDB EM Validation Summary Report ⓘ

Jul 21, 2024 – 12:45 PM JST

PDB ID : 8XZ3
EMDB ID : EMD-38788
Title : Mycobacterium smegmatis 50S ribosomal subunit with Erythromycin
Authors : Srinivasan, K.; Banerjee, A.; Sengupta, J.
Deposited on : 2024-01-20
Resolution : 3.60 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.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

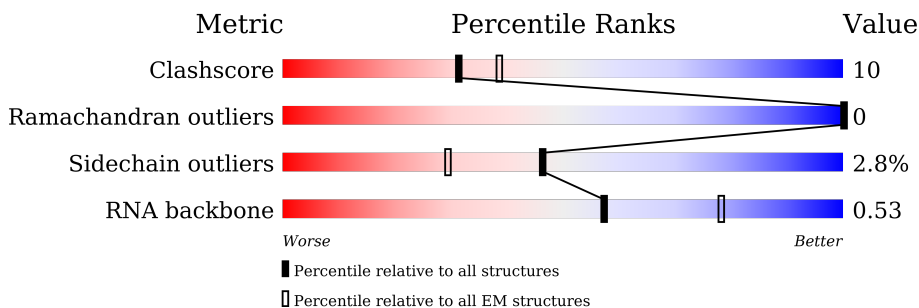
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.







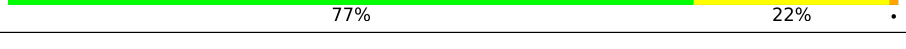
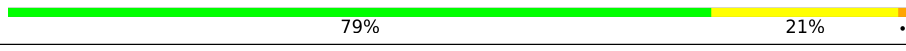


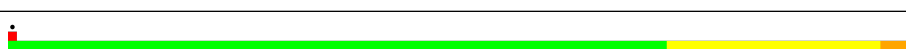
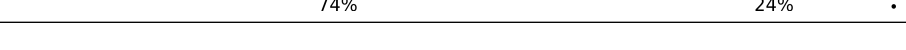
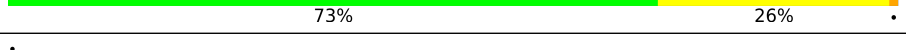
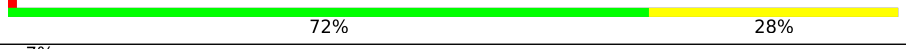



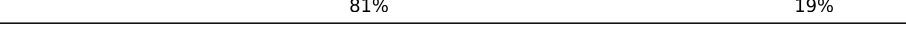



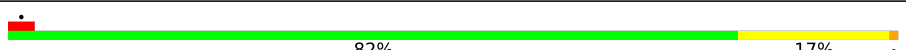

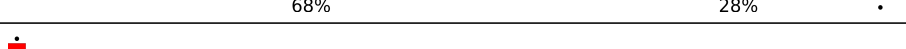


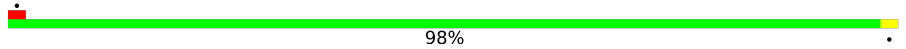
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	3	23	
2	A	3119	
3	B	118	
4	C	275	
5	D	214	
6	E	209	
7	F	182	


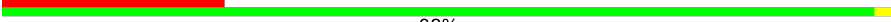
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Mol	Chain	Length	Quality of chain
8	G	176	
9	H	151	
10	I	126	
11	J	133	
12	K	146	
13	L	122	
14	M	145	
15	N	136	
16	O	118	
17	P	126	
18	Q	113	
19	R	124	
20	S	100	
21	T	114	
22	U	97	
23	V	105	
24	W	192	
25	X	79	
26	Y	63	
27	Z	64	
28	a	59	
29	b	54	
30	c	49	
31	d	46	
32	e	63	

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Mol	Chain	Length	Quality of chain
33	f	37	 100%
34	g	48	 25% 98%

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 97741 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3119	Total	C	N	O	P	1	0
			67003	29864	12318	21701	3120		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 14 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 15 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 16 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 17 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 19 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 20 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 21 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 22 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 29 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 31 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 35 is ERYTHROMYCIN A (three-letter code: ERY) (formula: C₃₇H₆₇NO₁₃) (labeled as "Ligand of Interest" by depositor).

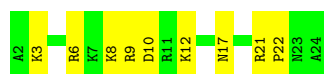


3 Residue-property plots

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.

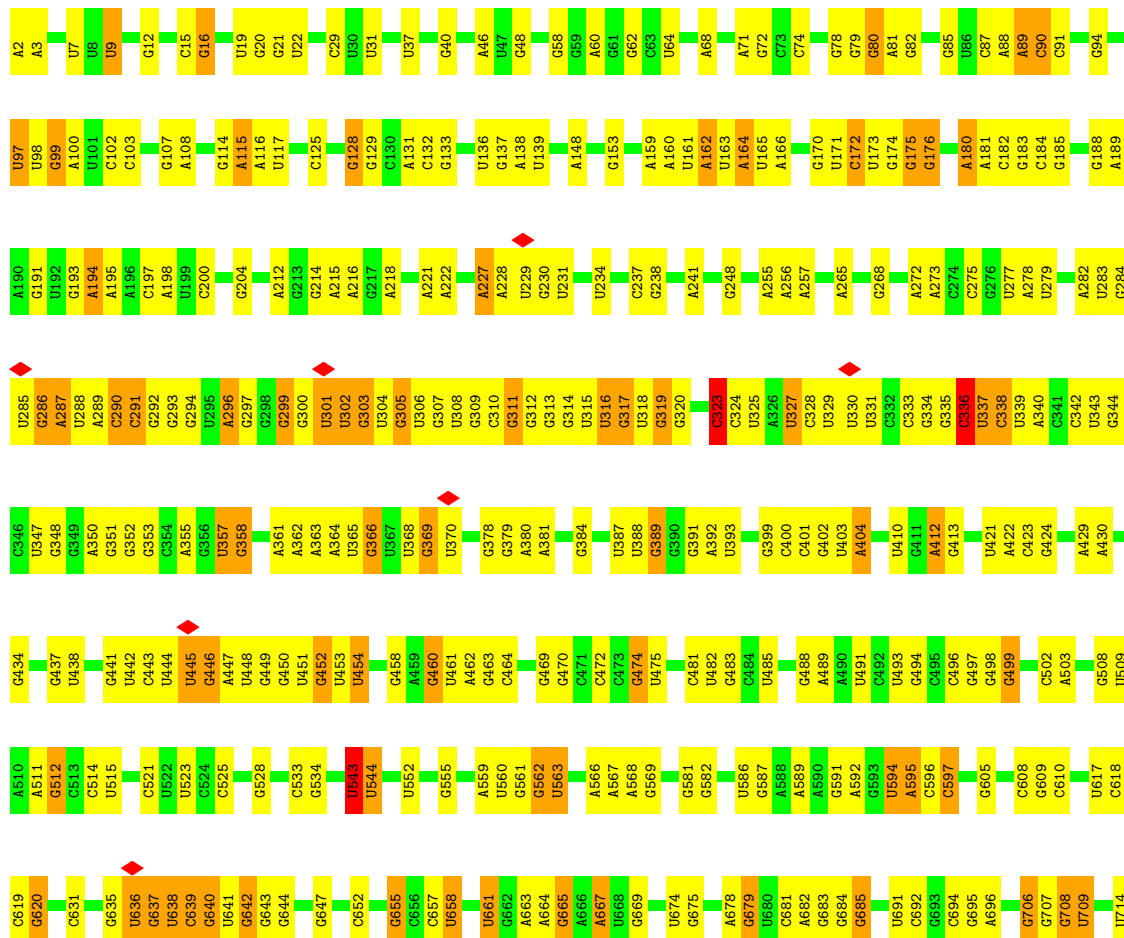
- Molecule 1: 50S ribosomal protein bL37

Chain 3: 

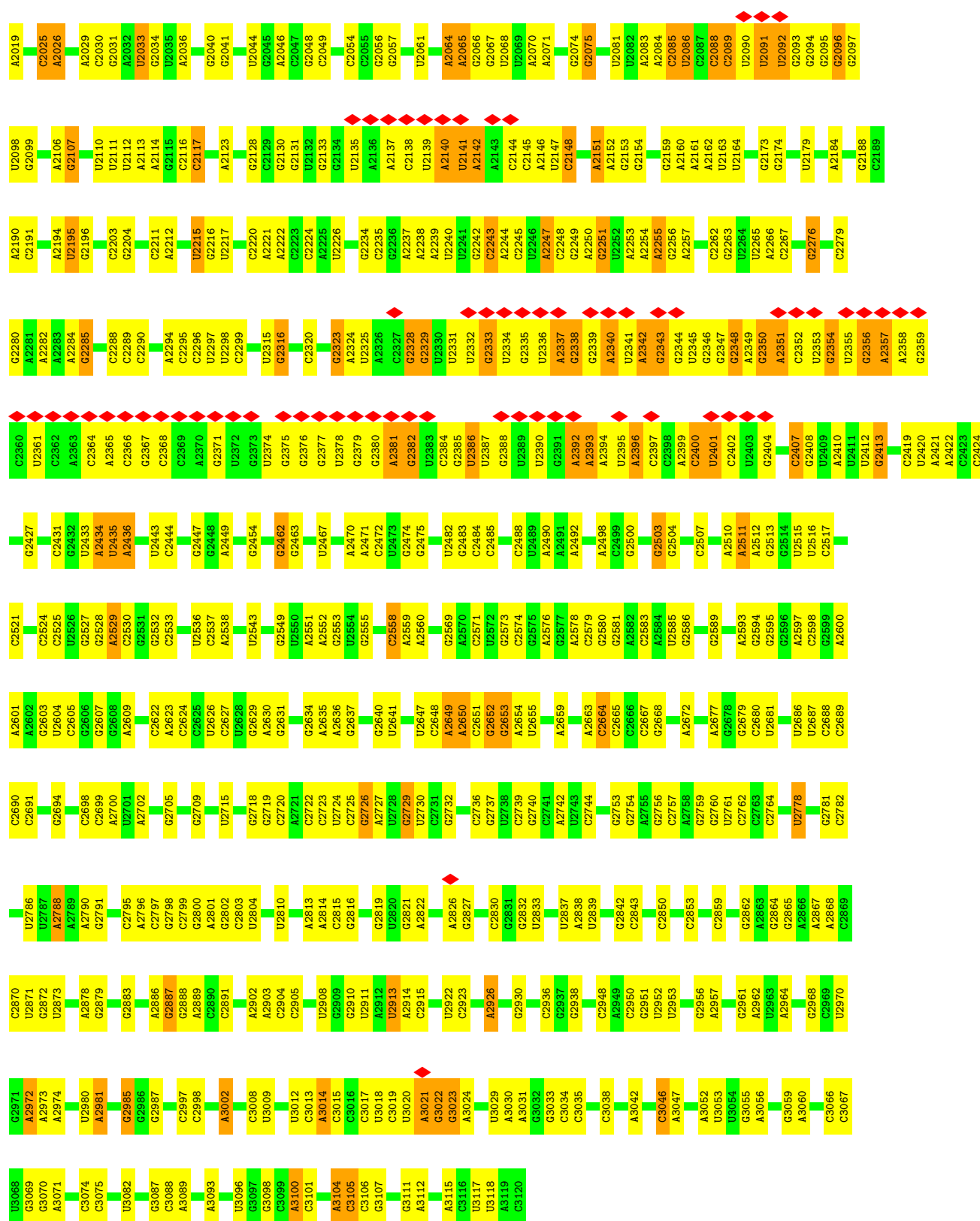


- Molecule 2: 23S rRNA

Chain A: 



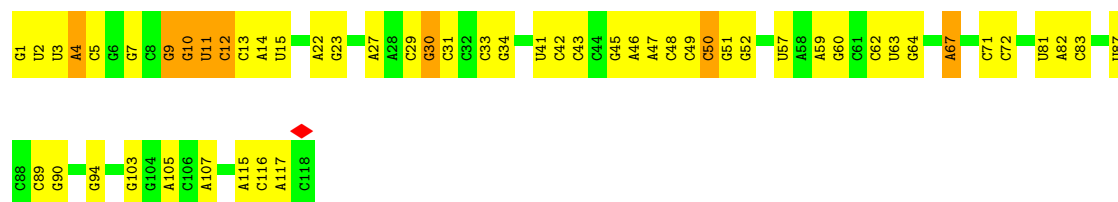
G1893	U1771	G1688	G1604	U1544	G1443	G1353	G1254	U1183	A1101	C1001	G916	A804	A721
G1905	G1780	U1689	G1605	C1545	U1444	A1362	G1255	U1184	G1102	C1002	G917	C805	G722
U1906	A1690	G1547	G1606	A1546	C1448	G1363	G1256	A1185	C1103	A1003	U918	A808	C723
A1916	C1784	A1691	C1607	C1548	C1449	U1364	G1257	A1186	C1104	C1004	G919	G811	G724
G1922	G1785	G1696	U1608	G1549	U1455	A1365	U1259	A1187	G1111	A1005	G920	C812	A727
G1923	A1787	G1703	G1609	G1550	G1456	G1367	A1261	A1188	C1112	G1006	C927	G819	G728
U1937	A1789	U1704	G1610	U1551	G1457	A1368	A1262	C1190	G1113	G1007	U928	G730	G729
G1938	U1798	A1708	G1611	A1552	U1463	A1369	A1267	A1191	G1114	U1008	C929	A731	A731
U1946	G1803	U1709	G1612	U1553	A1464	U1370	A1270	G1192	A1118	A934	A934	C825	G732
U1947	G1804	G1710	G1613	U1554	G1465	G1371	G1271	C1193	A1119	A935	A935	G826	G733
A1948	G1805	G1711	U1618	A1555	G1466	A1377	G1272	C1194	C1012	U1010	A936	G827	U735
C1949	A1806	G1712	U1619	C1556	A1467	U1378	G1273	A1195	U1013	A937	U937	G828	C734
C1952	G1814	U1713	U1620	U1557	A1468	G1379	A1274	C1196	C1123	G938	A938	U829	U736
C1953	C1817	C1718	U1621	A1558	G1470	A1380	A1275	C1197	C1124	C939	A939	A830	G737
A1956	G1822	C1719	G1622	U1559	G1471	G1381	G1276	C1198	C1125	A940	U941	A831	A738
G1959	C1823	U1720	U1623	U1560	C1472	U1382	G1288	U1208	U1132	A1025	U942	A832	U739
G1963	C1824	G1724	U1624	C1562	G1473	A1383	A1284	A1202	A1127	C1030	U943	A740	A740
U1964	A1826	U1725	G1625	A1563	G1476	G1384	G1285	A1203	A1128	C949	U944	G742	G742
C1973	G1840	U1726	U1626	A1564	C1477	C1385	C1286	A1204	G1129	A1033	G948	G743	C744
A1974	U1727	A1729	G1627	A1565	G1478	G1386	A1287	A1205	C1130	A950	U949	U838	A738
A1975	U1730	U1730	U1628	A1566	G1479	U1389	A1288	U1209	G1131	G951	G841	U839	U739
U1981	U1731	G1731	U1629	A1567	A1480	C1393	C1290	G1209	G1132	U857	A858	A858	A747
C1984	U1732	A1732	U1630	C1571	U1487	A1394	G1291	U1212	U1137	U854	G844	A751	U748
G1845	C1733	C1733	U1631	C1572	A1493	G1395	G1292	A1213	A1138	C955	C845	C752	C752
A1990	C1734	C1734	U1632	U1573	U1494	U1397	U1293	U1214	A1048	U860	U857	A753	A753
C1991	U1735	U1735	U1633	U1574	A1499	C1403	C1298	U1215	U1141	A1058	U962	A756	A756
U1992	G1736	A1736	U1634	C1575	A1500	G1407	G1301	C1220	A1139	G1063	U966	G757	G757
C1998	A1737	U1737	U1635	C1576	C1501	C1408	G1302	A1221	U1142	A1064	C967	A758	A758
U1996	G1746	G1746	U1636	C1577	G1502	U1411	U1303	U1222	G1143	C968	U969	G759	G759
A1997	A1747	A1747	U1639	U1578	U1507	C1412	C1314	U1223	U1151	G1089	A972	U760	U760
U1999	U1748	U1748	U1640	C1579	A1508	G1414	C1315	G1224	G1152	G1072	G973	G872	U761
C2000	A1749	A1749	U1641	U1580	A1510	A1415	U1316	G1225	G1153	A1076	G974	G873	U762
A2001	G1754	G1754	U1642	C1581	G1522	A1416	G1317	A1228	U1154	U1077	U975	G766	G766
A2002	A1755	A1755	U1645	U1582	U1528	G1425	G1326	G1230	G1162	G1078	A976	G768	G768
A2003	G1756	G1756	U1646	U1583	U1529	G1426	G1332	U1231	A1163	U1079	G979	U772	U772
C2004	U1757	U1757	U1647	U1584	G1530	U1427	G1335	G1232	A1164	U1080	C980	G773	G773
A2005	G1758	G1758	U1648	U1585	C1531	U1428	G1336	U1233	A1165	U1083	U981	G774	G774
A2006	A1759	A1759	U1649	U1586	G1532	C1429	G1339	U1234	U1084	A982	C983	U779	U779
C2007	C1762	C1762	U1650	G1587	U1533	U1431	G1344	U1235	A1172	G1085	C984	A790	A790
U2011	G1763	G1763	U1651	U1588	C1534	G1434	A1344	U1236	G1173	C1086	C992	A896	A896
C2012	A1764	A1764	U1652	U1589	C1535	U1435	G1345	U1237	G1174	U1087	G993	A897	A897
C2013	U1765	U1765	U1653	G1590	U1536	G1436	U1346	G1238	A1175	C1088	A994	A898	G784
G2014	G1766	G1766	U1654	U1591	U1537	A1437	G1347	U1239	G1176	C1089	U995	G899	A790
U2015	U1767	U1767	U1655	U1592	A1538	G1438	U1349	G1240	G1177	U1090	C996	A908	G794
G2016	C1768	C1768	U1656	U1593	U1539	G1439	U1350	A1244	U1178	A1091	G997	A909	A909
C2017	G1769	G1769	U1657	U1594	G1541	C1440	G1351	U1248	U1179	G1092	C998	C910	C910
G2018	G1770	G1770	U1658	U1595	A1542	U1443	A1352	U1250	G1181	G1096	U911	U801	U801
			U1659	C1596	A1543			A1261	C1182	A1099	C1000		
			U1681	C1597				G1252		C1100			
			U1598	U1597				C1253					
			U1599	U1598									
			G1600	U1599									
			U1601	G1600									
			U1602	U1601									
			G1603	U1602									



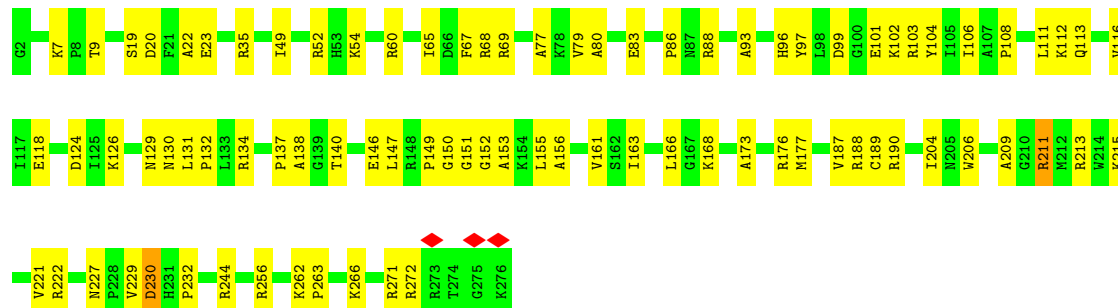
• Molecule 3: 5S rRNA

Chain B:

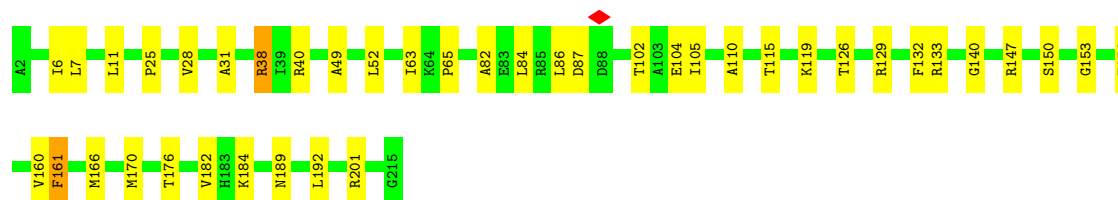
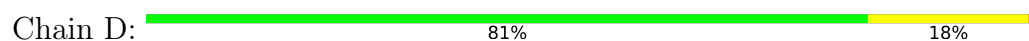




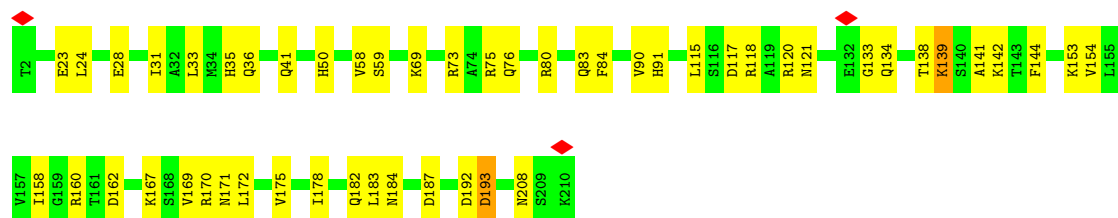
- Molecule 4: Large ribosomal subunit protein uL2



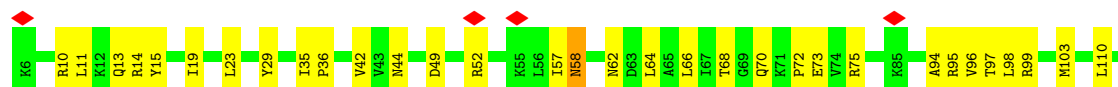
- Molecule 5: Large ribosomal subunit protein uL3

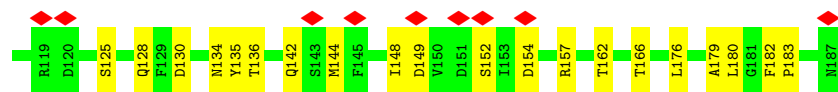


- Molecule 6: Large ribosomal subunit protein uL4

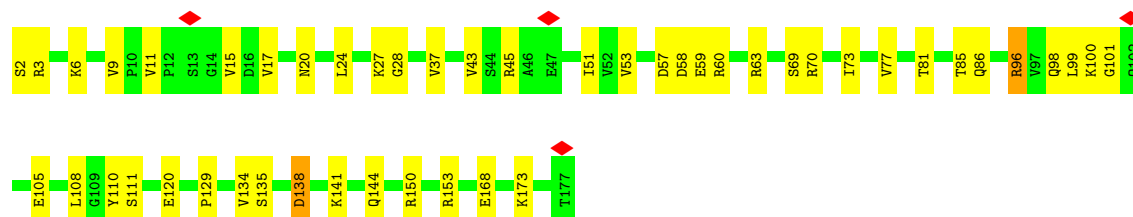


- Molecule 7: Large ribosomal subunit protein uL5

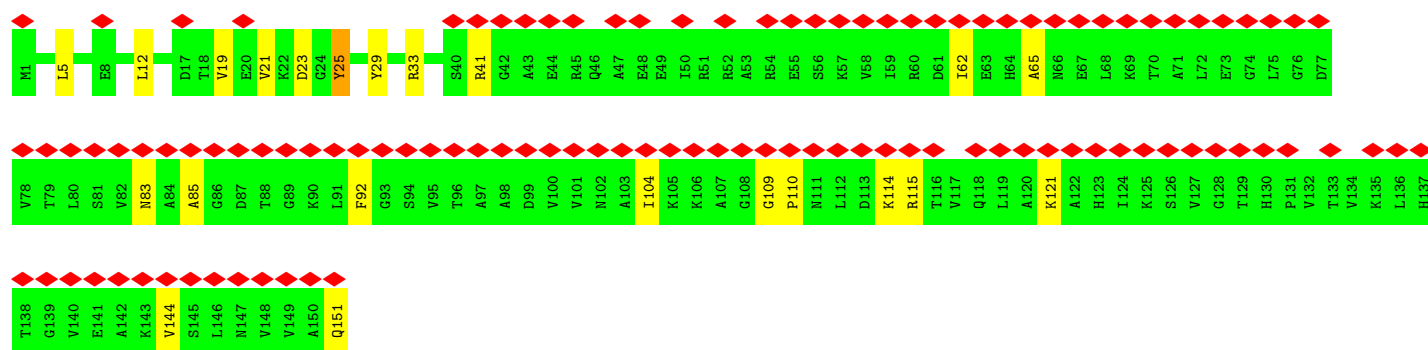
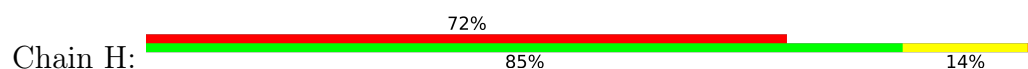




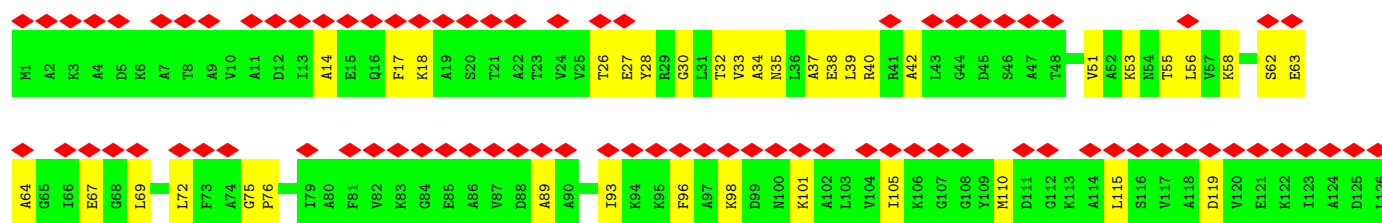
- Molecule 8: Large ribosomal subunit protein uL6



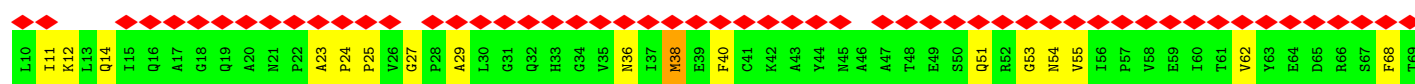
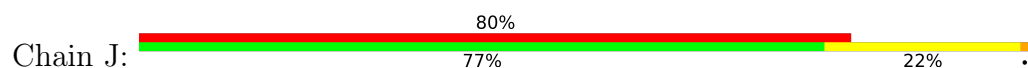
- Molecule 9: 50S ribosomal protein L9

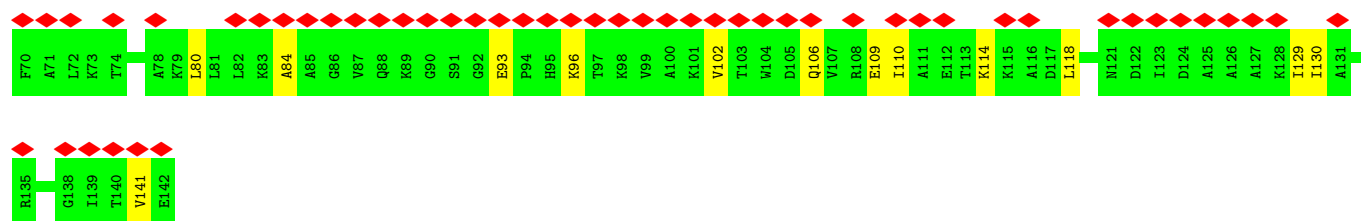


- Molecule 10: Large ribosomal subunit protein uL10



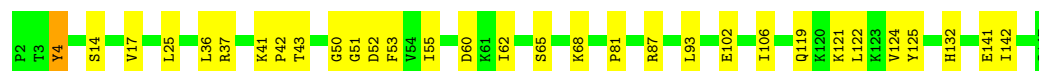
- Molecule 11: Large ribosomal subunit protein uL11





- Molecule 12: Large ribosomal subunit protein uL13

Chain K: 79% 21%



- Molecule 13: 50S ribosomal protein L14

Chain L: 73% 24%



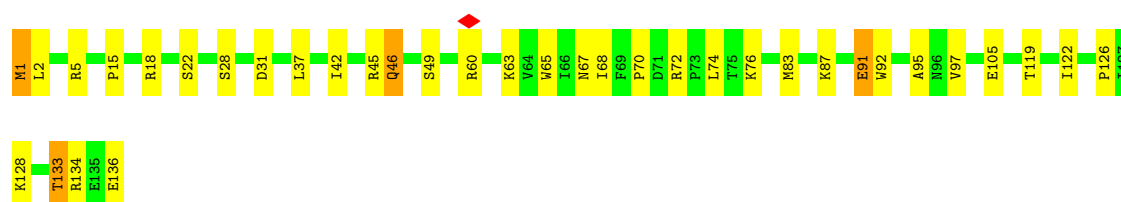
- Molecule 14: Large ribosomal subunit protein uL15

Chain M: 80% 19%



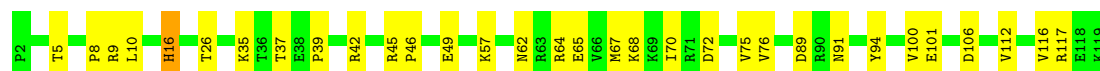
- Molecule 15: Large ribosomal subunit protein uL16

Chain N: 74% 24%



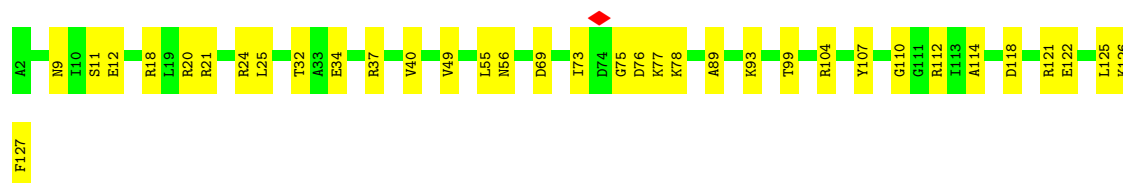
- Molecule 16: Large ribosomal subunit protein bL17

Chain O: 73% 26%

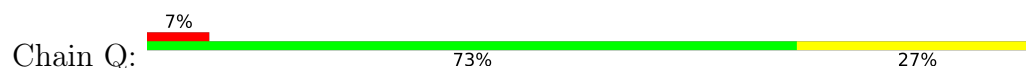


- Molecule 17: Large ribosomal subunit protein uL18

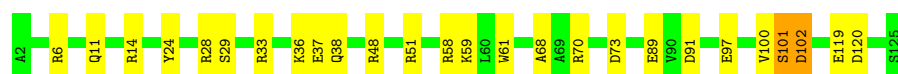
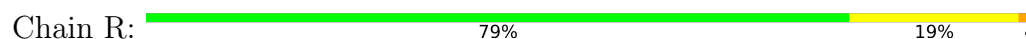
Chain P: 72% 28%



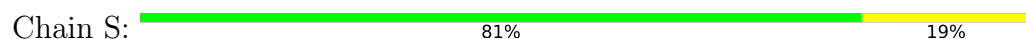
- Molecule 18: 50S ribosomal protein L19



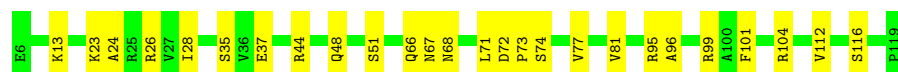
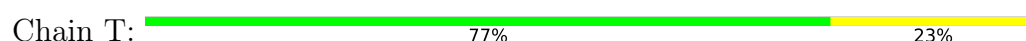
- Molecule 19: Large ribosomal subunit protein bL20



- Molecule 20: Large ribosomal subunit protein bL21



- Molecule 21: Large ribosomal subunit protein uL22

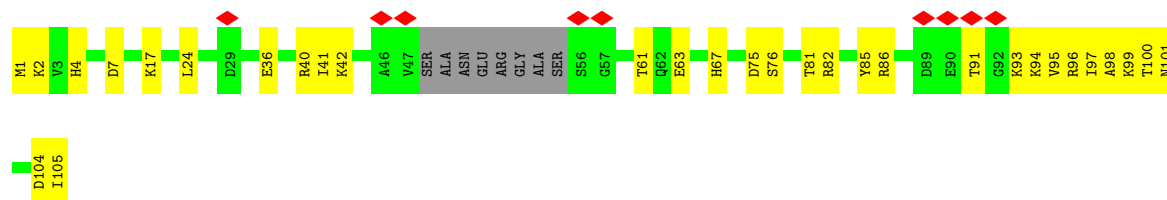


- Molecule 22: Large ribosomal subunit protein uL23

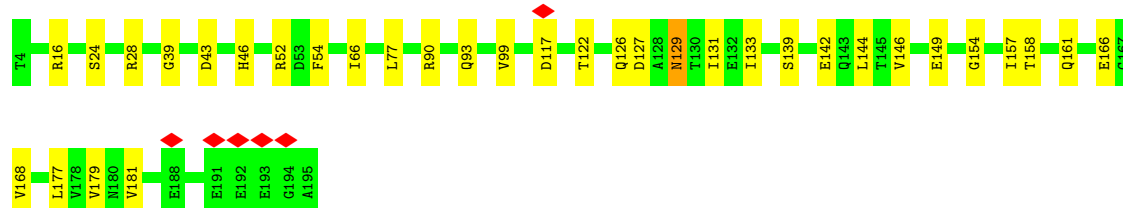
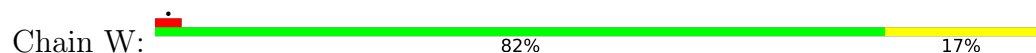


- Molecule 23: Large ribosomal subunit protein uL24

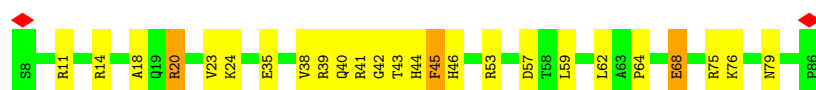




- Molecule 24: Large ribosomal subunit protein bL25



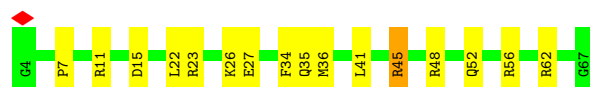
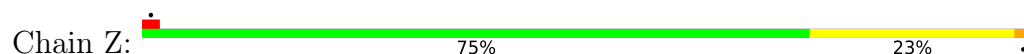
- Molecule 25: Large ribosomal subunit protein bL27



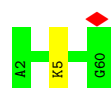
- Molecule 26: Large ribosomal subunit protein bL28



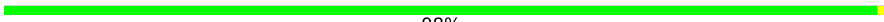
- Molecule 27: Large ribosomal subunit protein uL29



- Molecule 28: Large ribosomal subunit protein uL30



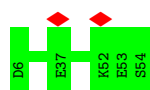
- Molecule 29: Large ribosomal subunit protein bL32

Chain b:  98%



- Molecule 30: Large ribosomal subunit protein bL33A

Chain c:  100%



- Molecule 31: Large ribosomal subunit protein bL34

Chain d:  98%



- Molecule 32: Large ribosomal subunit protein bL35

Chain e:  97%



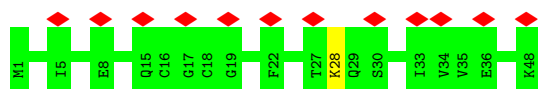
- Molecule 33: 50S ribosomal protein L36

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: Large ribosomal subunit protein bL31

Chain g:  98%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28.75	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	30.405	Depositor
Minimum map value	-14.822	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.6	Depositor
Map size (\AA)	449.40002, 449.40002, 449.40002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	3	0.31	0/191	0.63	0/247
2	A	0.70	0/75026	0.87	45/117066 (0.0%)
3	B	0.57	0/2821	0.88	2/4396 (0.0%)
4	C	0.43	0/2153	0.59	0/2895
5	D	0.43	0/1609	0.58	0/2165
6	E	0.38	0/1592	0.53	0/2153
7	F	0.30	0/1467	0.57	0/1973
8	G	0.34	0/1369	0.57	0/1848
9	H	0.26	0/1027	0.49	0/1398
10	I	0.27	0/925	0.49	0/1246
11	J	0.25	0/1006	0.47	0/1364
12	K	0.43	0/1157	0.54	0/1567
13	L	0.43	0/946	0.62	0/1268
14	M	0.40	0/1091	0.57	0/1457
15	N	0.38	0/1118	0.58	0/1506
16	O	0.41	0/945	0.55	0/1267
17	P	0.33	0/966	0.60	1/1298 (0.1%)
18	Q	0.40	0/921	0.55	0/1236
19	R	0.45	0/1000	0.60	1/1341 (0.1%)
20	S	0.41	0/764	0.52	0/1030
21	T	0.42	0/887	0.59	0/1204
22	U	0.39	0/766	0.54	0/1030
23	V	0.35	0/738	0.58	0/987
24	W	0.31	0/1443	0.55	0/1970
25	X	0.40	0/595	0.61	0/798
26	Y	0.40	0/478	0.59	0/641
27	Z	0.36	0/534	0.64	0/713
28	a	0.39	0/477	0.61	0/640
29	b	0.37	0/427	0.65	0/572
30	c	0.32	0/413	0.56	0/553
31	d	0.38	0/380	0.70	0/500
32	e	0.26	0/507	0.64	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.38	0/303	0.60	0/401
34	g	0.32	0/372	0.51	0/503
All	All	0.63	0/106414	0.81	49/159905 (0.0%)

There are no bond length outliers.

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	323	C	C2-N1-C1'	7.45	127.00	118.80
2	A	2243	C	C2-N1-C1'	7.19	126.70	118.80
2	A	1973	C	C2-N3-C4	-6.50	116.65	119.90
2	A	975	U	C2-N1-C1'	6.31	125.28	117.70
2	A	1428	U	C2-N1-C1'	6.19	125.13	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	189	0	205	8	0
2	A	67003	0	33711	978	0
3	B	2522	0	1285	39	0
4	C	2110	0	2165	63	0
5	D	1587	0	1630	29	0
6	E	1569	0	1607	41	0
7	F	1445	0	1476	39	0
8	G	1348	0	1399	38	0
9	H	1018	0	988	15	0
10	I	918	0	959	28	0
11	J	990	0	1021	21	0
12	K	1130	0	1167	28	0
13	L	938	0	1000	22	0
14	M	1078	0	1151	27	0
15	N	1092	0	1128	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	O	928	0	972	24	0
17	P	956	0	991	26	0
18	Q	907	0	938	19	0
19	R	988	0	1038	19	0
20	S	754	0	802	14	0
21	T	873	0	909	16	0
22	U	756	0	802	19	0
23	V	732	0	782	24	0
24	W	1428	0	1443	22	0
25	X	586	0	601	18	0
26	Y	470	0	484	11	0
27	Z	531	0	541	11	0
28	a	474	0	500	0	0
29	b	423	0	463	0	0
30	c	405	0	411	0	0
31	d	377	0	411	0	0
32	e	502	0	541	0	0
33	f	299	0	324	0	0
34	g	364	0	352	0	0
35	A	51	0	67	4	0
All	All	97741	0	64264	1450	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 1450 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:279:U:H3	2:A:307:G:H1	0.95	0.93
2:A:1547:G:H1	2:A:1623:U:H3	1.11	0.93
2:A:2131:G:H1	2:A:2147:U:H3	1.14	0.89
2:A:1367:G:N7	19:R:36:LYS:NZ	2.24	0.86
22:U:8:ARG:NE	27:Z:27:GLU:OE2	2.09	0.86

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	21/23 (91%)	21 (100%)	0	0	100	100
4	C	273/275 (99%)	257 (94%)	16 (6%)	0	100	100
5	D	212/214 (99%)	196 (92%)	16 (8%)	0	100	100
6	E	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
7	F	180/182 (99%)	172 (96%)	8 (4%)	0	100	100
8	G	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
9	H	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
10	I	124/126 (98%)	117 (94%)	7 (6%)	0	100	100
11	J	131/133 (98%)	127 (97%)	4 (3%)	0	100	100
12	K	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
13	L	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
14	M	143/145 (99%)	127 (89%)	16 (11%)	0	100	100
15	N	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
16	O	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
17	P	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
18	Q	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
19	R	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
20	S	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
21	T	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
22	U	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
23	V	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
24	W	190/192 (99%)	184 (97%)	6 (3%)	0	100	100
25	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
26	Y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
27	Z	62/64 (97%)	61 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	a	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
29	b	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
30	c	47/49 (96%)	43 (92%)	4 (8%)	0	100	100
31	d	44/46 (96%)	44 (100%)	0	0	100	100
32	e	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
33	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
34	g	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
All	All	3615/3689 (98%)	3442 (95%)	173 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	18/18 (100%)	17 (94%)	1 (6%)	21	56
4	C	215/215 (100%)	210 (98%)	5 (2%)	50	76
5	D	160/160 (100%)	154 (96%)	6 (4%)	33	66
6	E	169/169 (100%)	164 (97%)	5 (3%)	41	71
7	F	151/151 (100%)	148 (98%)	3 (2%)	55	79
8	G	148/148 (100%)	145 (98%)	3 (2%)	55	79
9	H	90/116 (78%)	88 (98%)	2 (2%)	52	77
10	I	89/89 (100%)	88 (99%)	1 (1%)	73	88
11	J	102/102 (100%)	99 (97%)	3 (3%)	42	72
12	K	119/119 (100%)	117 (98%)	2 (2%)	60	82
13	L	100/100 (100%)	95 (95%)	5 (5%)	24	59
14	M	112/112 (100%)	110 (98%)	2 (2%)	59	81
15	N	114/114 (100%)	106 (93%)	8 (7%)	15	48
16	O	97/97 (100%)	94 (97%)	3 (3%)	40	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	P	93/93 (100%)	92 (99%)	1 (1%)	73	88
18	Q	100/100 (100%)	97 (97%)	3 (3%)	41	71
19	R	97/97 (100%)	92 (95%)	5 (5%)	23	58
20	S	81/81 (100%)	81 (100%)	0	100	100
21	T	90/90 (100%)	88 (98%)	2 (2%)	52	77
22	U	83/83 (100%)	80 (96%)	3 (4%)	35	67
23	V	81/86 (94%)	81 (100%)	0	100	100
24	W	155/155 (100%)	152 (98%)	3 (2%)	57	80
25	X	58/58 (100%)	53 (91%)	5 (9%)	10	41
26	Y	50/50 (100%)	48 (96%)	2 (4%)	31	65
27	Z	58/58 (100%)	56 (97%)	2 (3%)	37	69
28	a	52/52 (100%)	51 (98%)	1 (2%)	57	80
29	b	43/43 (100%)	42 (98%)	1 (2%)	50	76
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	35/35 (100%)	34 (97%)	1 (3%)	42	72
32	e	53/53 (100%)	51 (96%)	2 (4%)	33	66
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/43 (100%)	42 (98%)	1 (2%)	50	76
All	All	2938/2969 (99%)	2857 (97%)	81 (3%)	46	72

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	R	120	ASP
26	Y	54	SER
21	T	67	ASN
24	W	139	SER
28	a	5	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
7	F	62	ASN
8	G	144	GLN
11	J	51	GLN

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Mol	Chain	Res	Type
17	P	9	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3117/3119 (99%)	637 (20%)	24 (0%)
3	B	117/118 (99%)	18 (15%)	1 (0%)
All	All	3234/3237 (99%)	655 (20%)	25 (0%)

5 of 655 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	7	U
2	A	9	U
2	A	12	G
2	A	16	G
2	A	19	U

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1084	U
2	A	1597	G
3	B	10	G
2	A	1535	C
2	A	1730	U

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
35	ERY	A	3201	-	53,53,53	1.23	3 (5%)	82,82,82	1.83	25 (30%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	ERY	A	3201	-	-	20/72/107/107	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	A	3201	ERY	C6-C5	3.01	1.61	1.55
35	A	3201	ERY	C22-C23	2.73	1.60	1.52
35	A	3201	ERY	O10-C6	-2.61	1.40	1.44

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	3201	ERY	O3-C3-C4	5.39	114.72	108.22
35	A	3201	ERY	O7-C5-C6	4.57	112.02	106.39
35	A	3201	ERY	O6-C17-C16	-4.30	103.08	111.12
35	A	3201	ERY	O7-C5-C4	-3.22	106.72	111.54
35	A	3201	ERY	C6-C5-C4	-3.07	109.70	114.05

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	A	3201	ERY	C9-C10-C11-C12
35	A	3201	ERY	C9-C10-C11-O12
35	A	3201	ERY	C34-C10-C11-C12

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Continued from previous page...

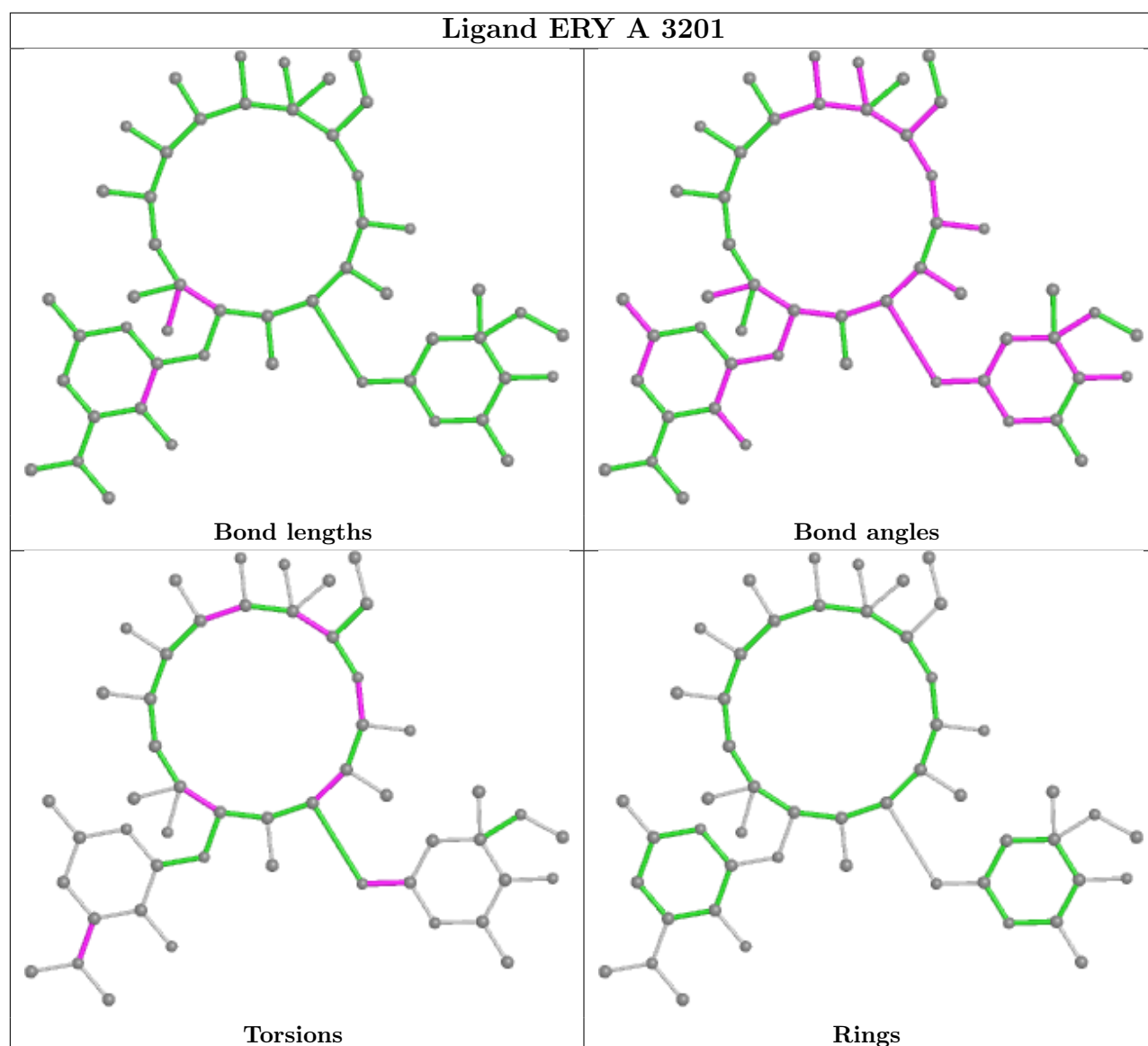
Mol	Chain	Res	Type	Atoms
35	A	3201	ERY	C34-C10-C11-O12
35	A	3201	ERY	C11-C12-C13-O2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	A	3201	ERY	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

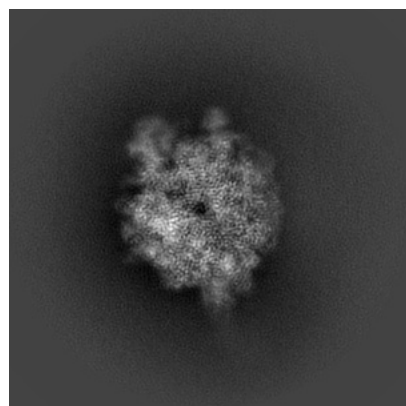
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38788. These allow visual inspection of the internal detail of the map and identification of artifacts.

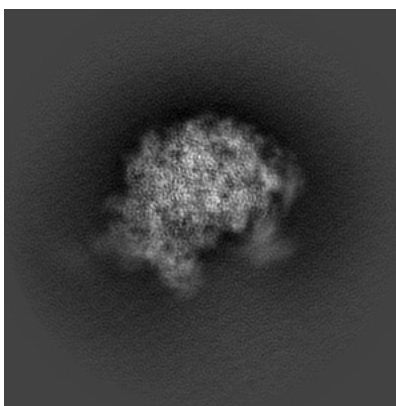
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

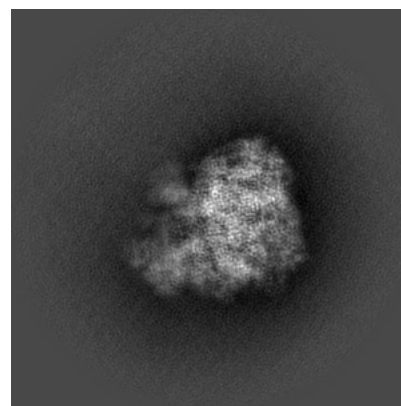
6.1.1 Primary map



X

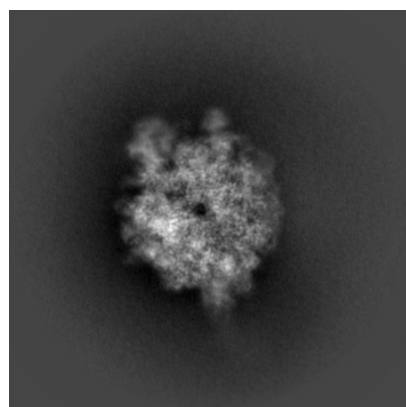


Y

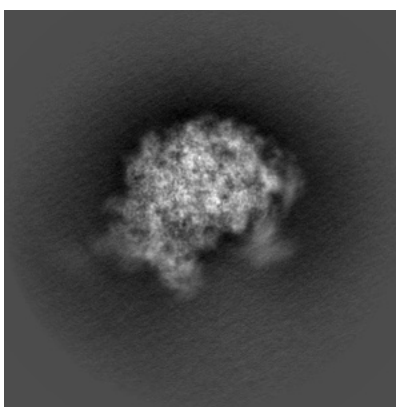


Z

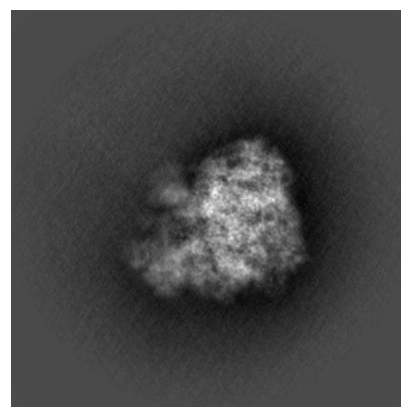
6.1.2 Raw map



X



Y

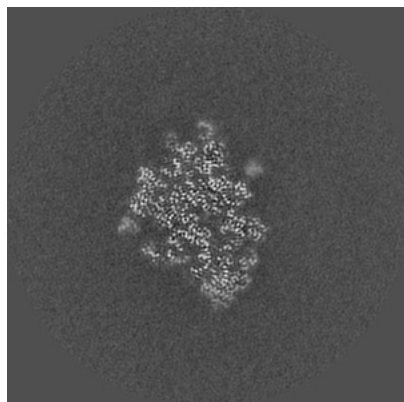


Z

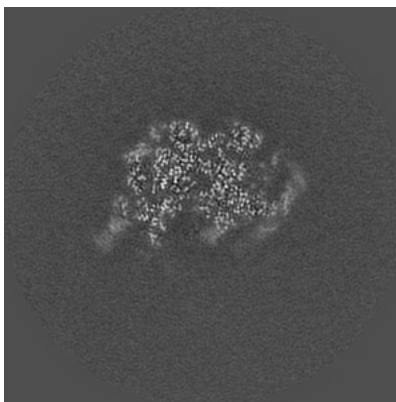
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

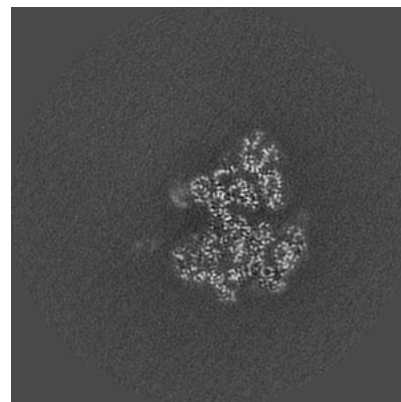
6.2.1 Primary map



X Index: 210

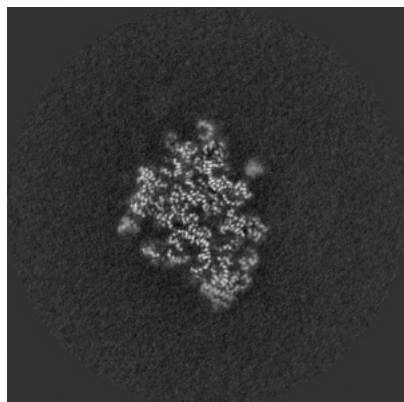


Y Index: 210

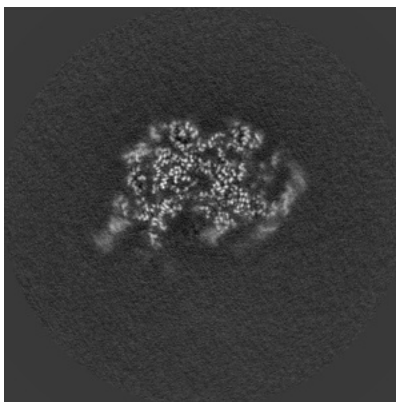


Z Index: 210

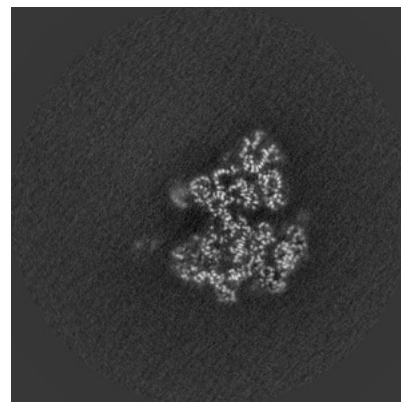
6.2.2 Raw map



X Index: 210



Y Index: 210

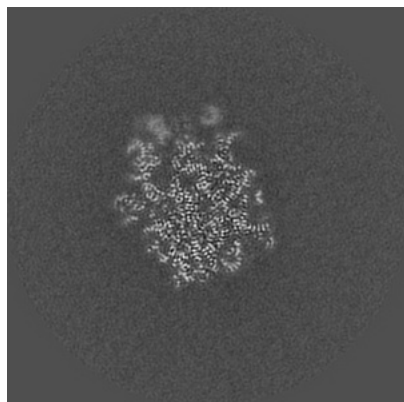


Z Index: 210

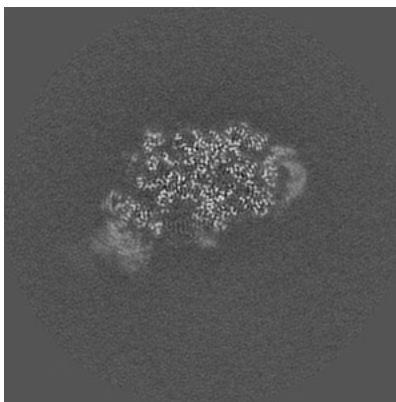
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

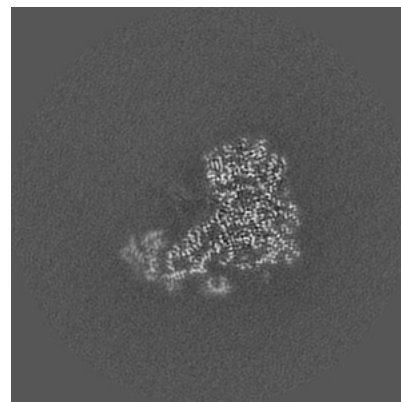
6.3.1 Primary map



X Index: 230

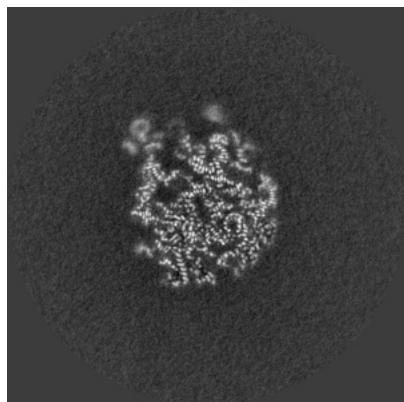


Y Index: 219

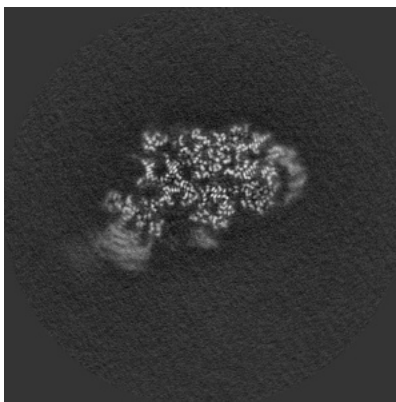


Z Index: 191

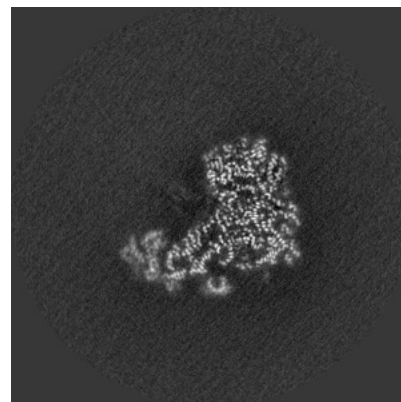
6.3.2 Raw map



X Index: 245



Y Index: 222

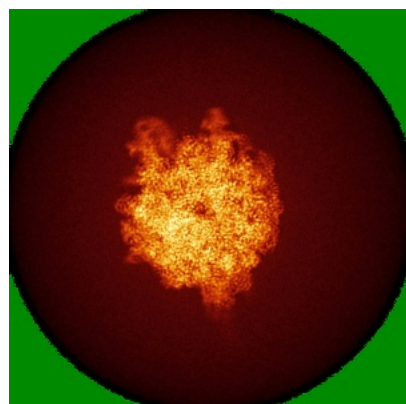


Z Index: 191

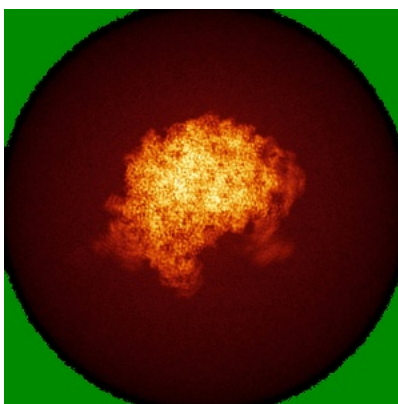
The images above show the largest variance slices of the map in three orthogonal directions.

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

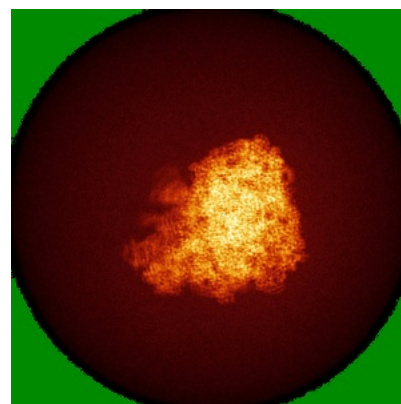
6.4.1 Primary map



X

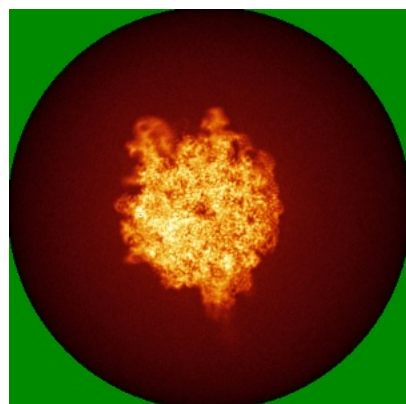


Y

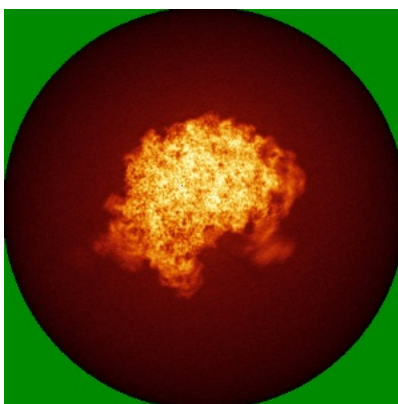


Z

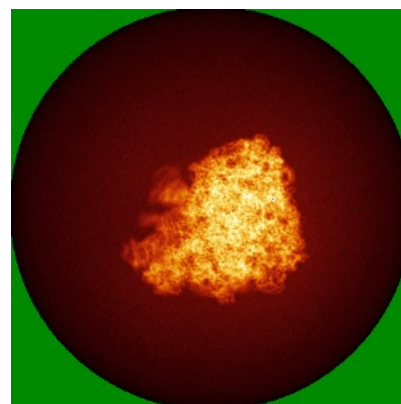
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.6. 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



X



Y



Z

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.

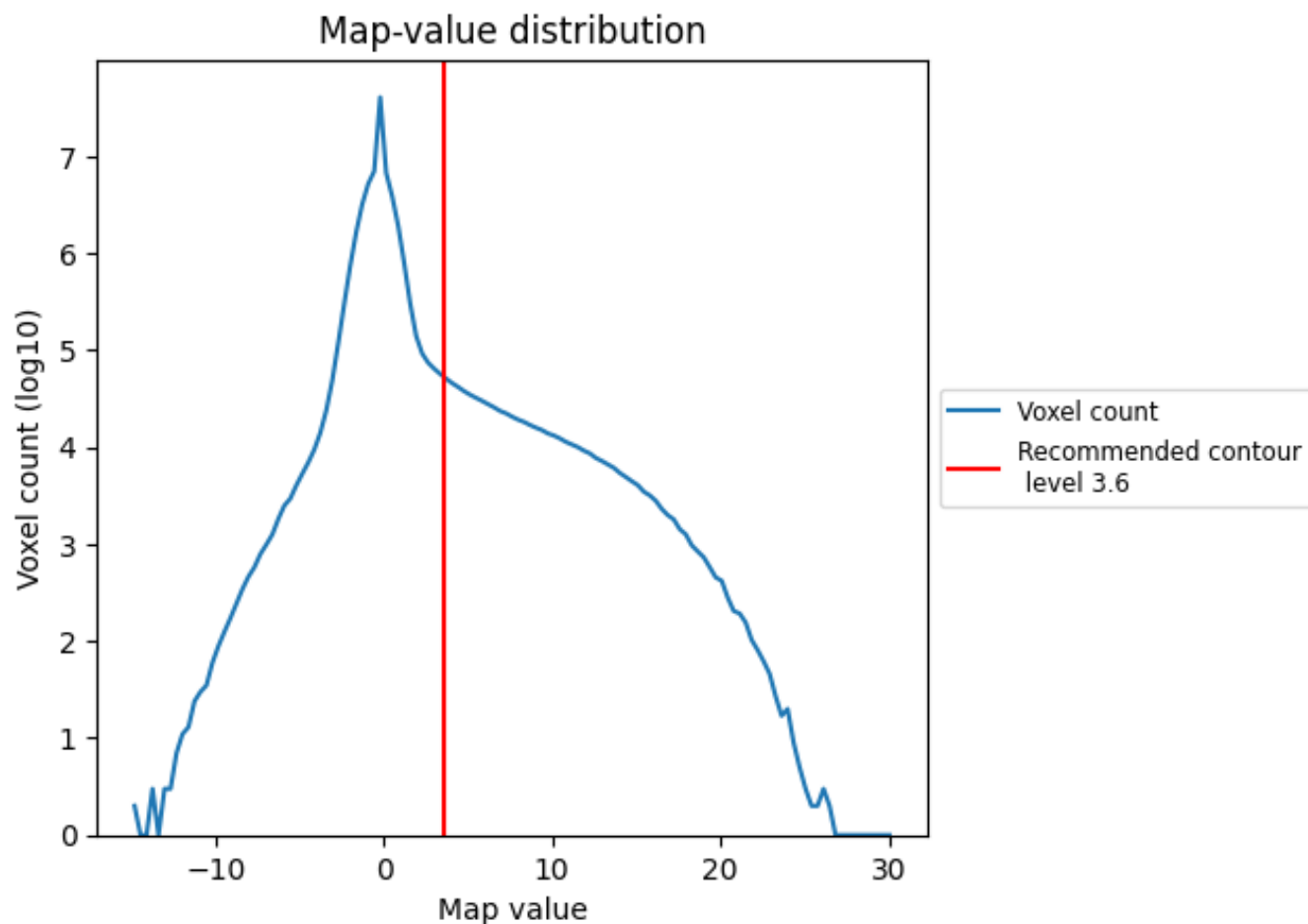
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

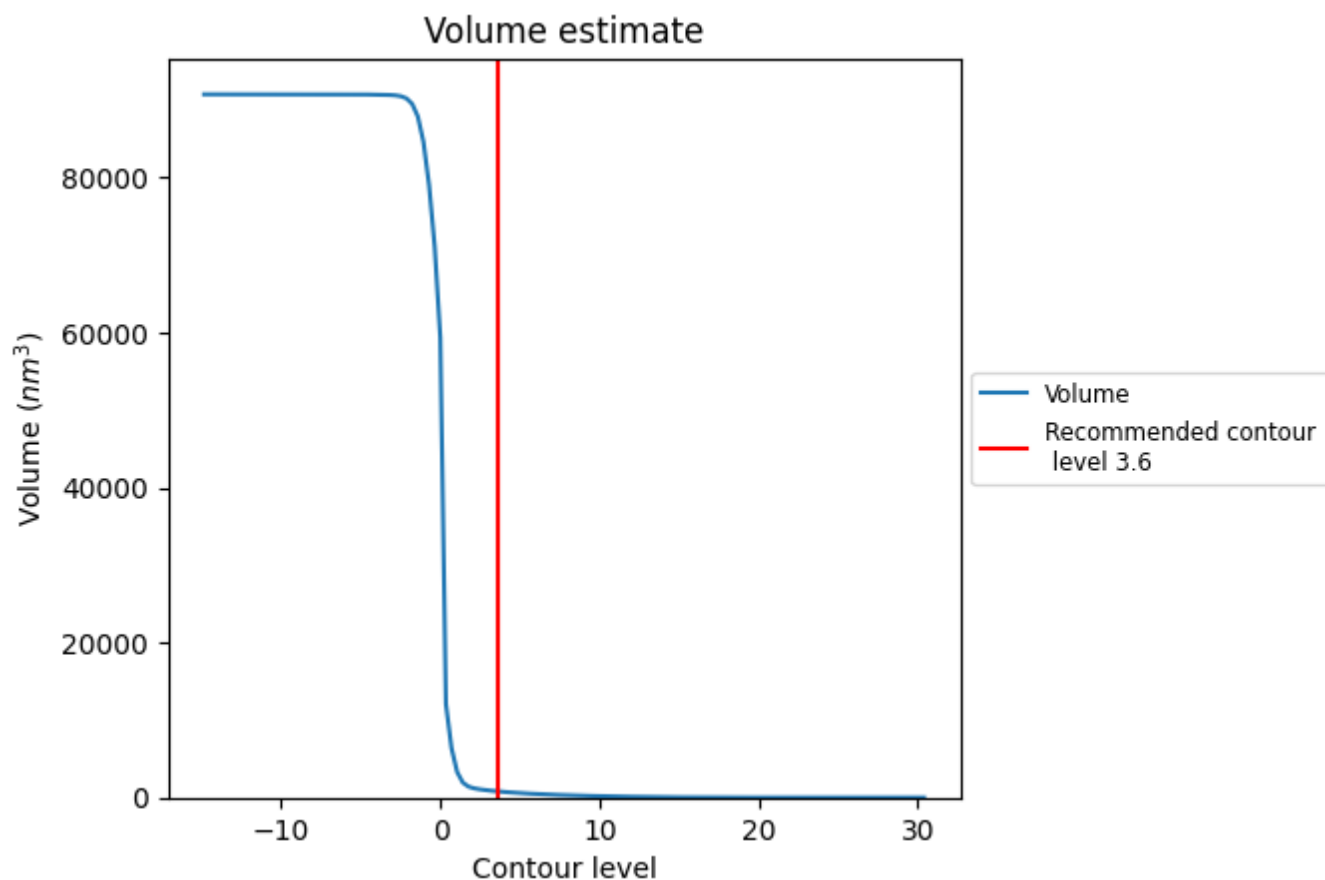
This section contains the results of statistical analysis of the map.

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.

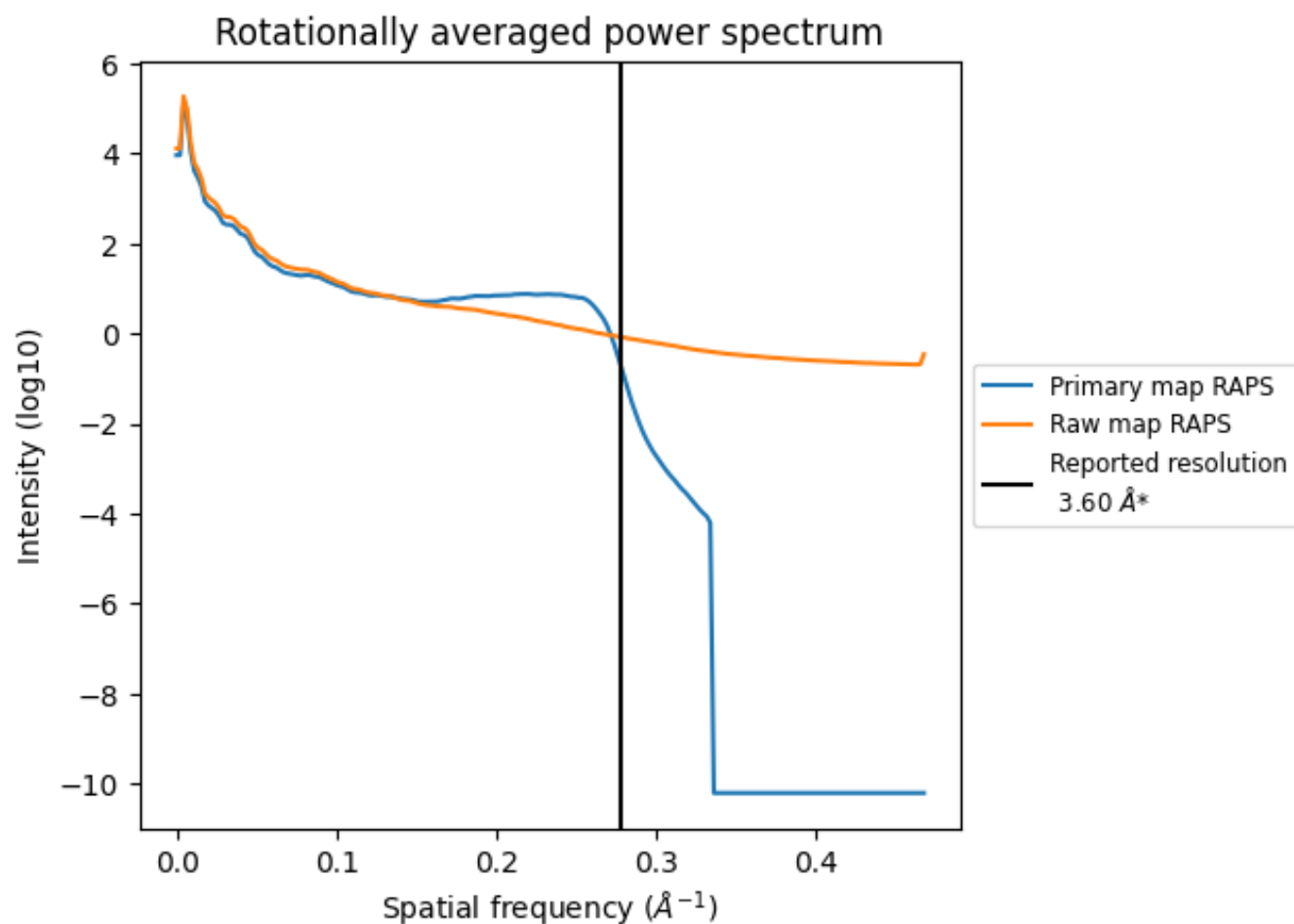
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 803 nm^3 ; this corresponds to an approximate mass of 725 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 ⓘ

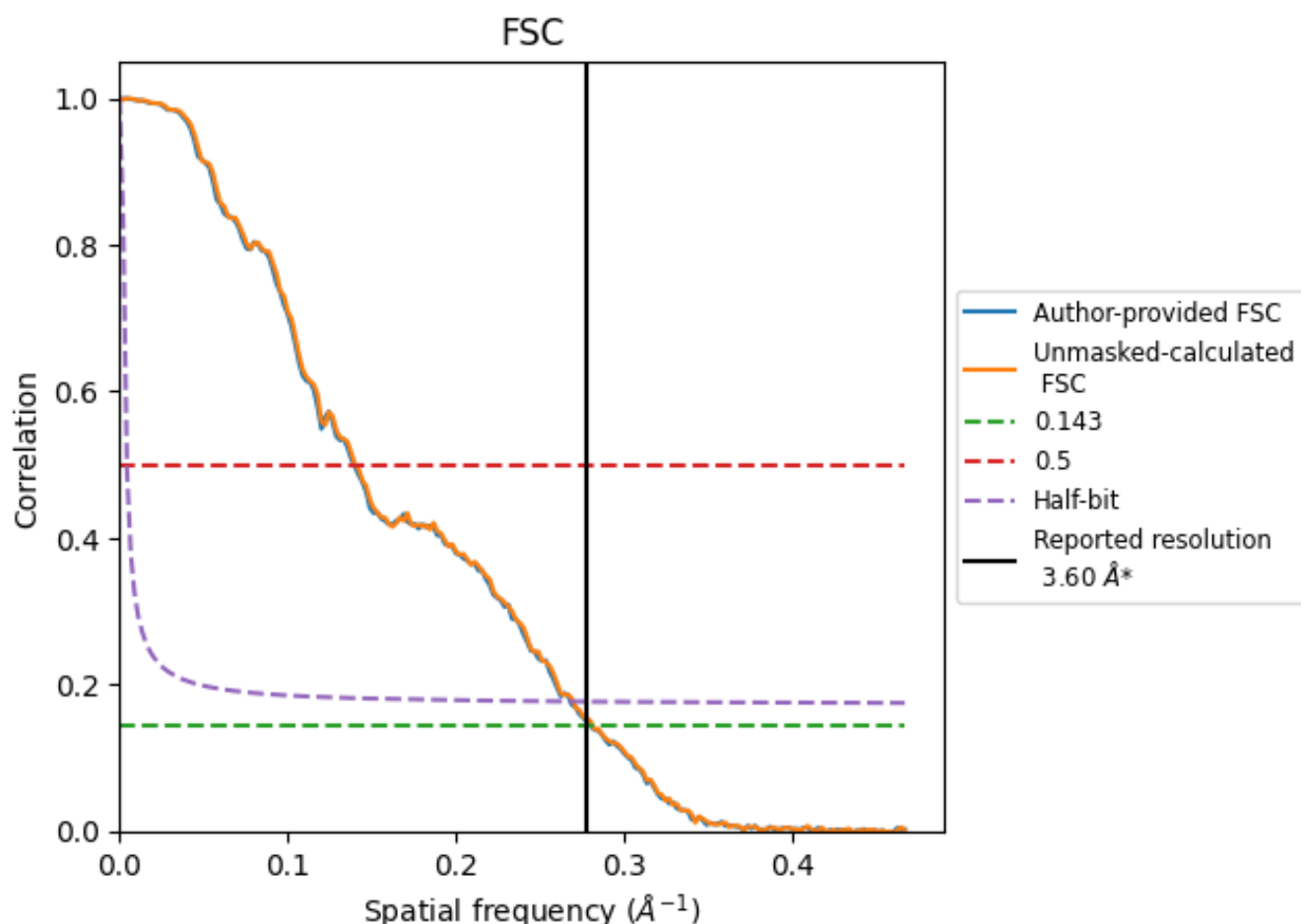


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

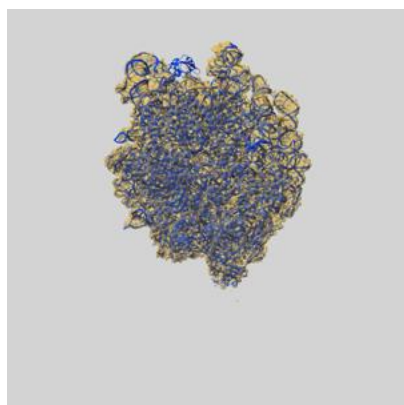
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.56	7.17	3.73
Unmasked-calculated*	3.55	7.13	3.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

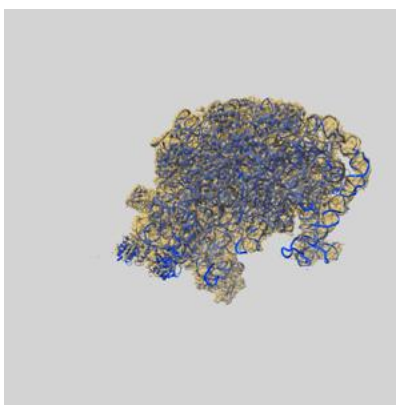
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38788 and PDB model 8XZ3. Per-residue inclusion information can be found in section [3](#) on page [11](#).

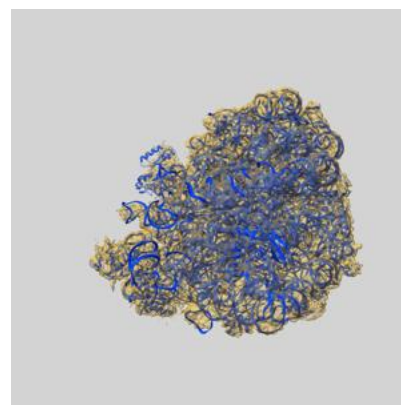
9.1 Map-model overlay [i](#)



X



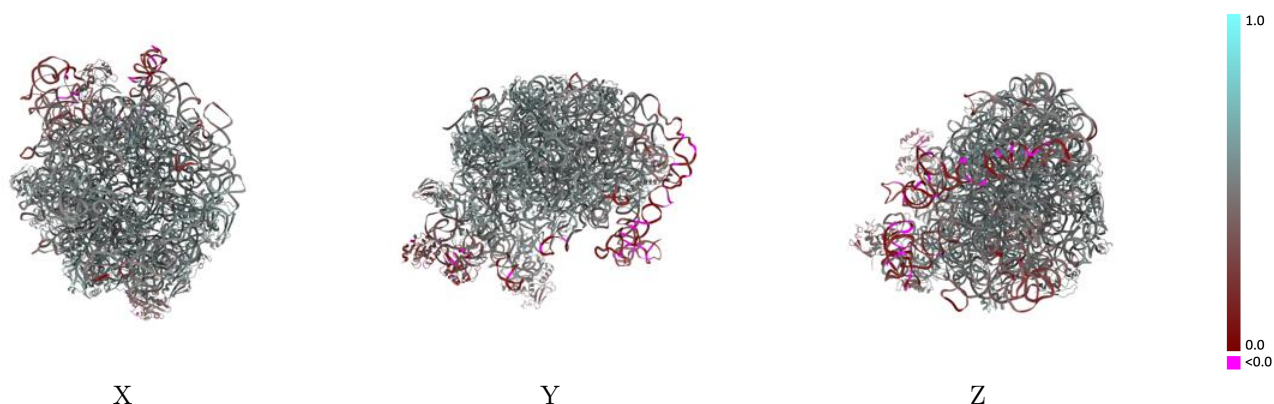
Y



Z

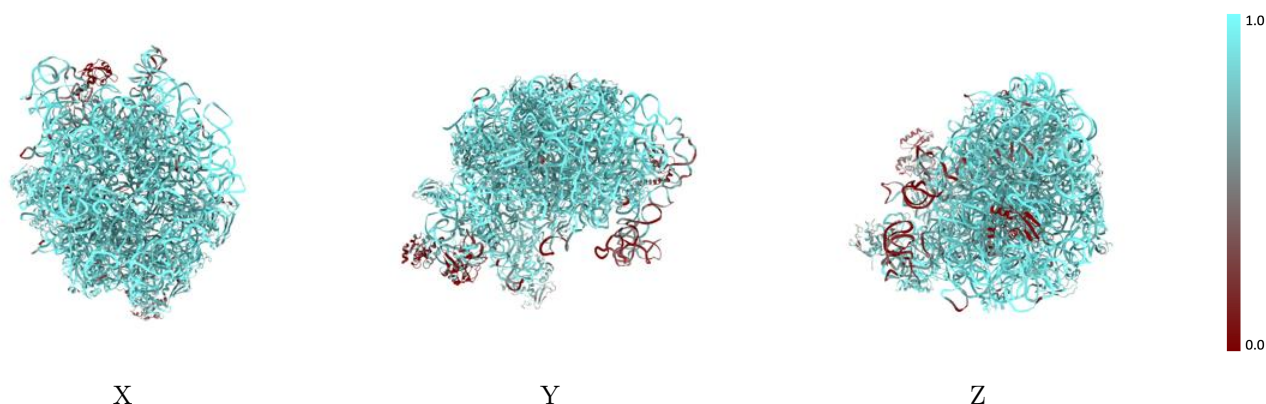
The images above show the 3D surface view of the map at the recommended contour level 3.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



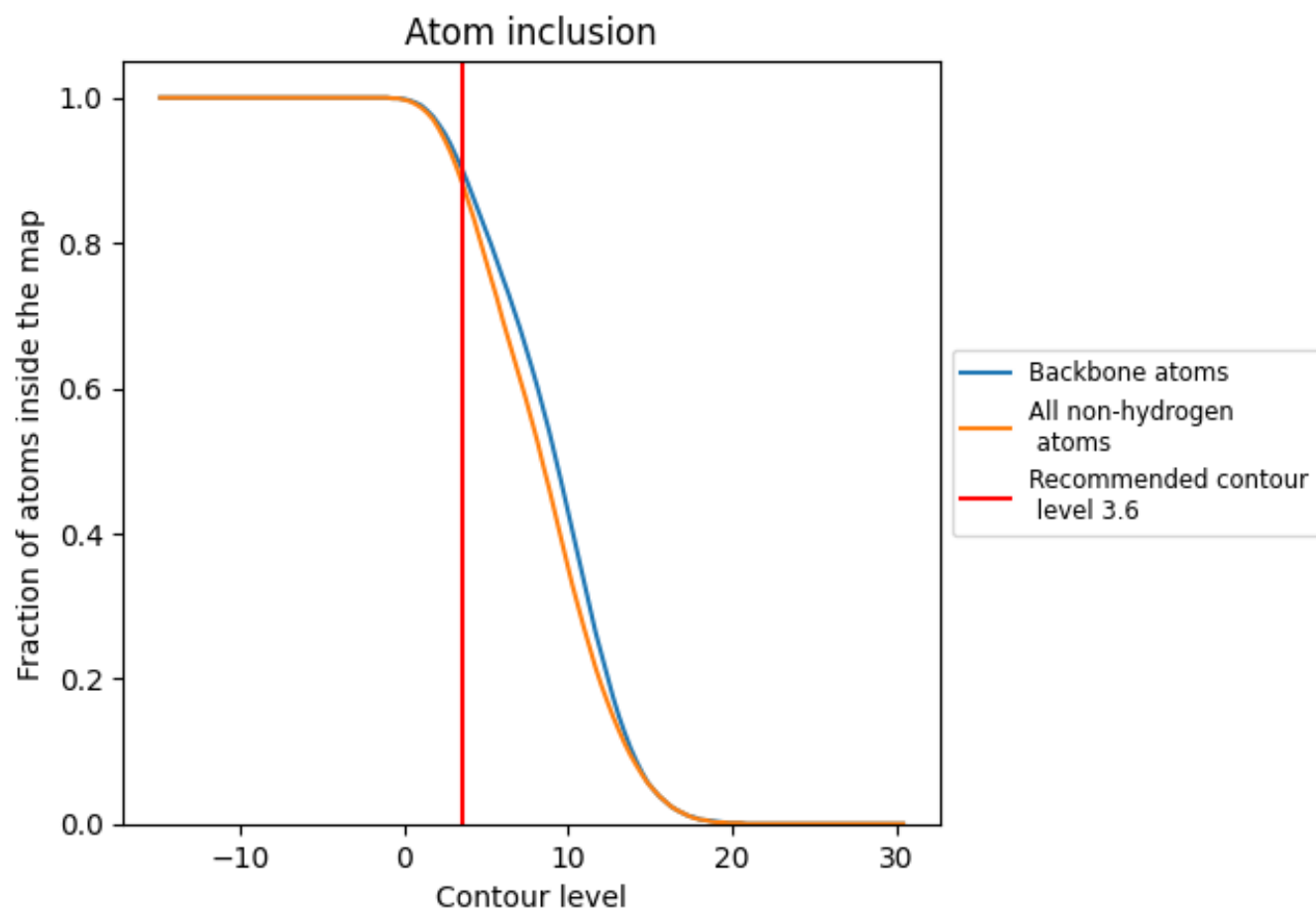
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.6).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (3.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.4730
3	 0.8440	 0.5460
A	 0.9100	 0.4610
B	 0.9600	 0.4680
C	 0.9030	 0.5450
D	 0.9100	 0.5490
E	 0.8730	 0.5280
F	 0.7480	 0.4200
G	 0.8430	 0.4760
H	 0.2490	 0.4160
I	 0.3230	 0.2700
J	 0.2280	 0.2490
K	 0.9150	 0.5500
L	 0.8770	 0.5380
M	 0.8870	 0.5330
N	 0.8650	 0.5440
O	 0.8990	 0.5460
P	 0.8970	 0.5020
Q	 0.8160	 0.5270
R	 0.9310	 0.5420
S	 0.9070	 0.5540
T	 0.9040	 0.5510
U	 0.8450	 0.5220
V	 0.8000	 0.4990
W	 0.8050	 0.5100
X	 0.8900	 0.5390
Y	 0.8850	 0.5290
Z	 0.8750	 0.5130
a	 0.9150	 0.5410
b	 0.9000	 0.5490
c	 0.8120	 0.5400
d	 0.9170	 0.5610
e	 0.7060	 0.5440
f	 0.9060	 0.5600
g	 0.5750	 0.3330

