



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:29 AM UTC

PDB ID : 6WNT / pdb_00006wnt
EMDB ID : EMD-21856
Title : 50S ribosomal subunit without free 5S rRNA and perturbed PTC
Authors : Loveland, A.B.; Korostelev, A.A.; Mankin, A.S.; Huang, S.; Aleksashin, N.A.; Klepacki, D.; Reier, K.; Kefi, A.; Szal, A.; Remme, J.; Jaeger, L.; Vazquez-Laslop, N.
Deposited on : 2020-04-23
Resolution : 3.10 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

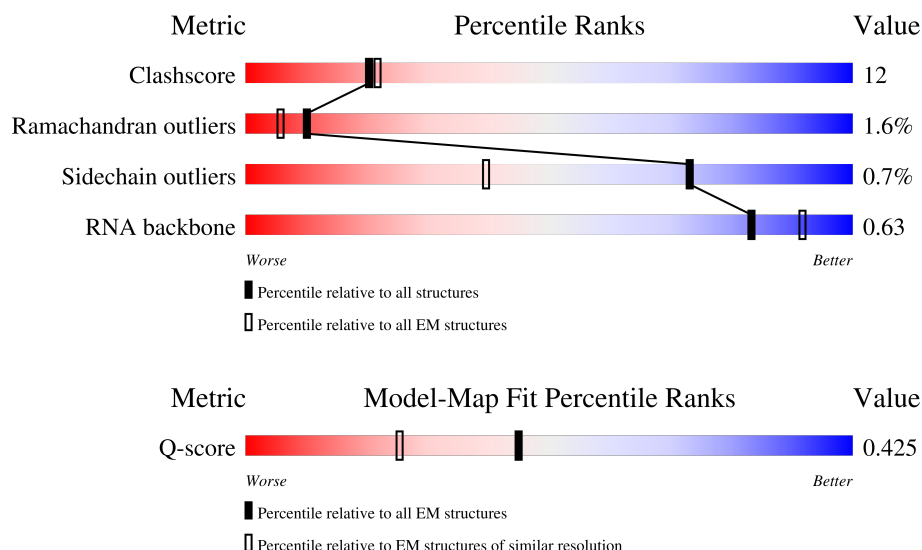
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



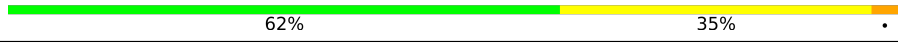
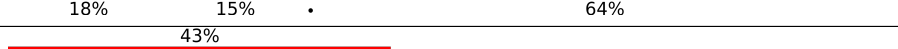
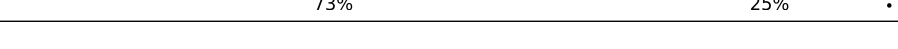
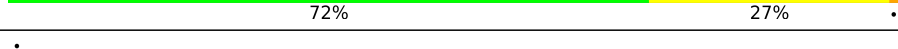
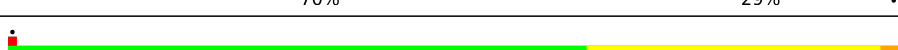
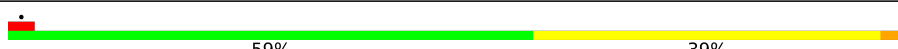
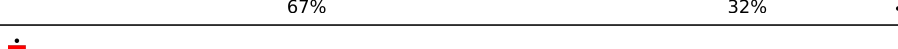
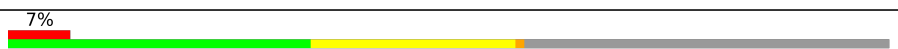
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	b	271	
2	c	209	
3	d	201	

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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	n	120	
13	o	116	
14	p	114	
15	q	117	
16	r	103	
17	s	110	
18	t	93	
19	u	102	
20	v	94	
21	w	75	
22	x	77	
23	y	63	
24	z	58	
25	A	70	
26	B	56	
27	D	46	
28	E	64	

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Mol	Chain	Length	Quality of chain
29	F	38	76%18%5%
30	a	223	42%39%19%40%
31	4	3031	51%42%6%

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 91164 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	53	Total	C	N	O	S	0	0
			409	261	74	73	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	o	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	p	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	q	117	Total	C	N	O		0	0
			946	604	192	150			

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	r	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	75	Total	C	N	O	S	0	0
			574	356	116	101	1		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	x	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 25 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	41	Total	C	N	O	S	0	0
			315	192	57	60	6		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	E	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 30 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

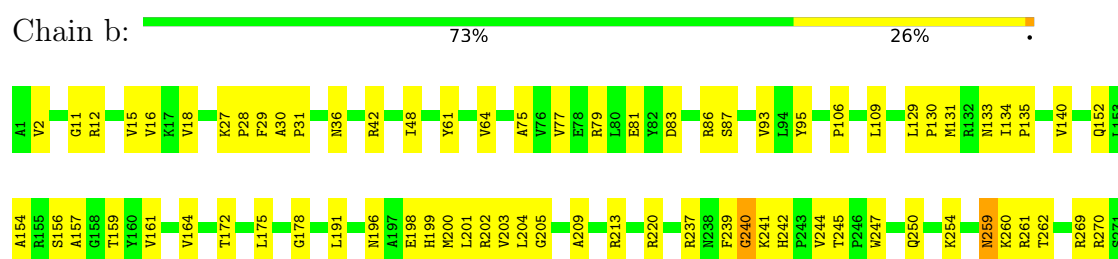
- Molecule 31 is a RNA chain called 23s-5s joint ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	3025	Total	C	N	O	P	0	0
			64925	28962	11938	21001	3024		

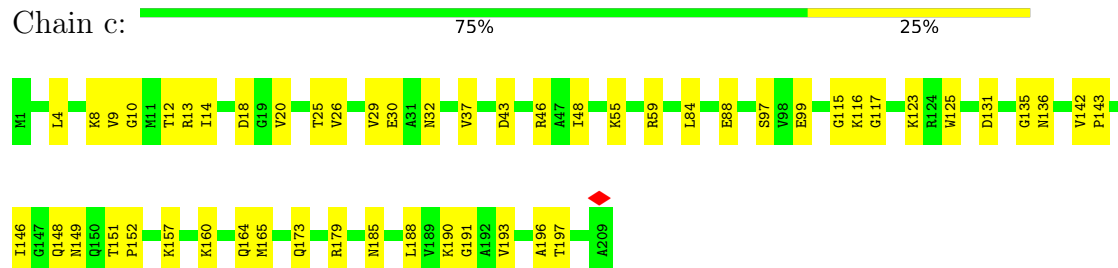
3 Residue-property plots [i](#)

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.

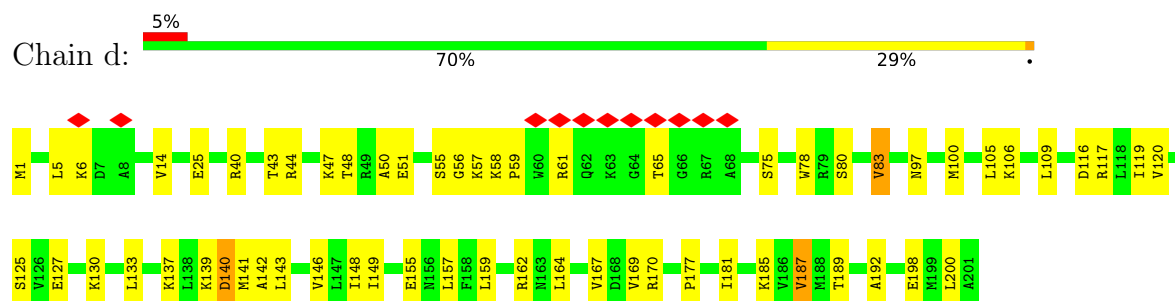
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

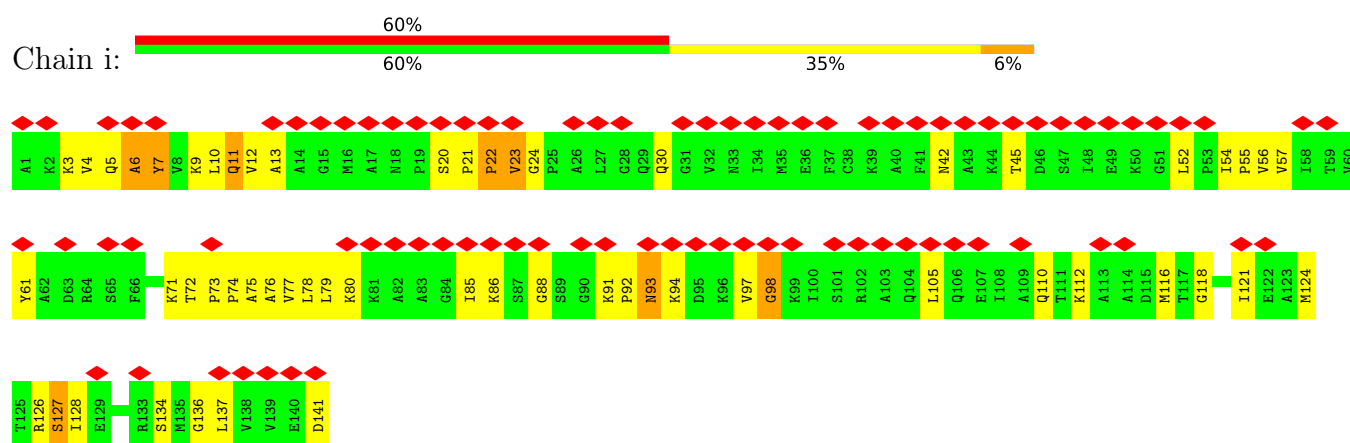


• Molecule 3: 50S ribosomal protein L4

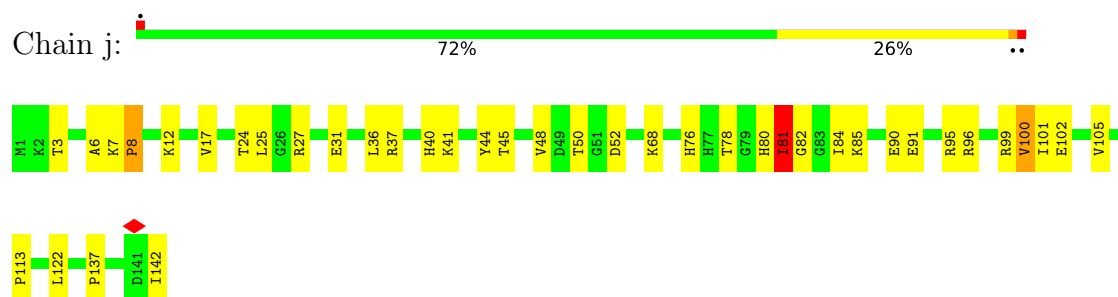


• Molecule 4: 50S ribosomal protein L5

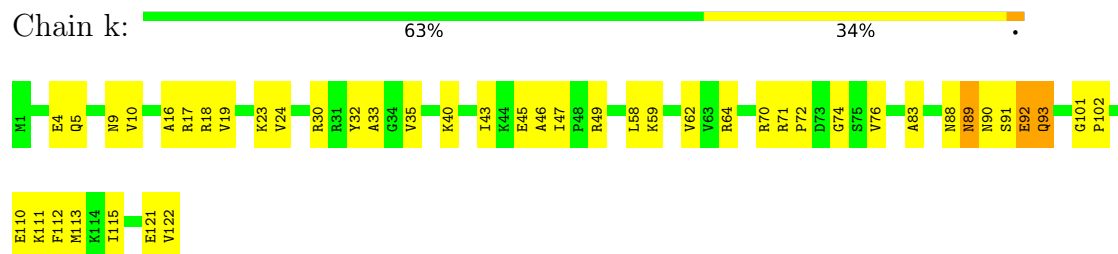




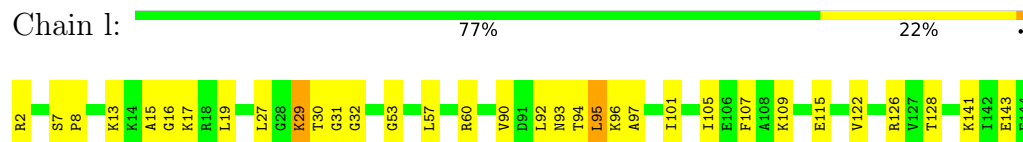
- Molecule 9: 50S ribosomal protein L13



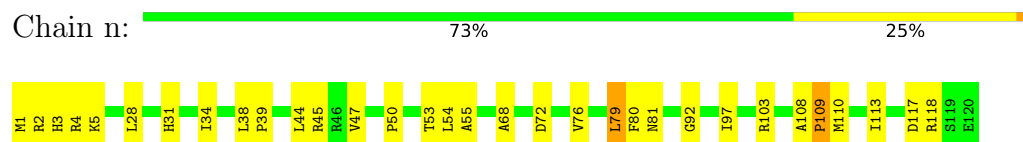
- Molecule 10: 50S ribosomal protein L14



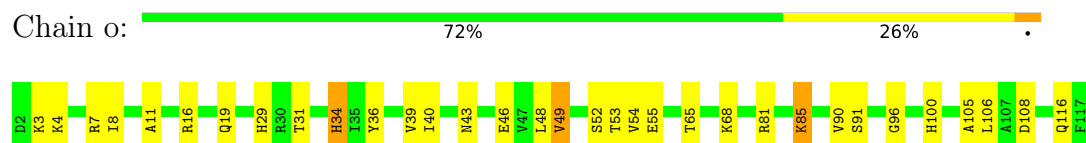
- Molecule 11: 50S ribosomal protein L15



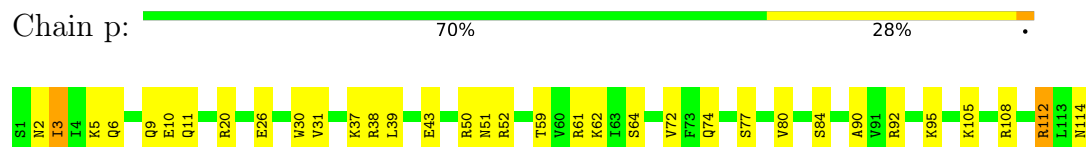
- Molecule 12: 50S ribosomal protein L17



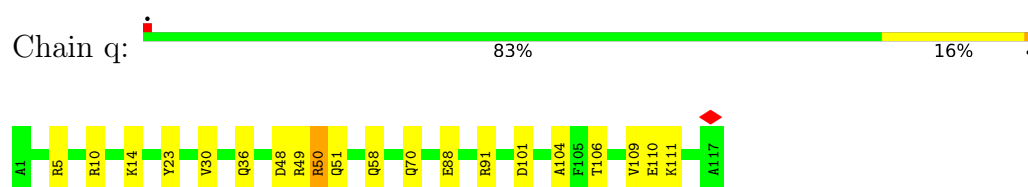
- Molecule 13: 50S ribosomal protein L18



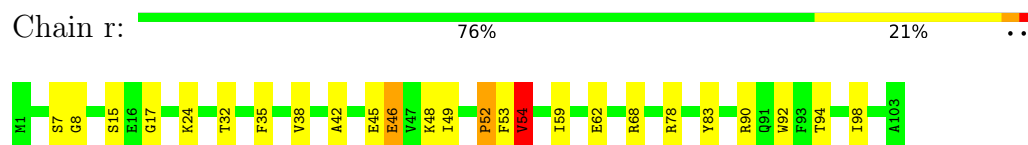
- Molecule 14: 50S ribosomal protein L19



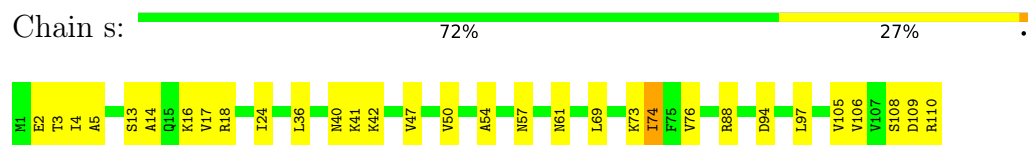
- Molecule 15: 50S ribosomal protein L20



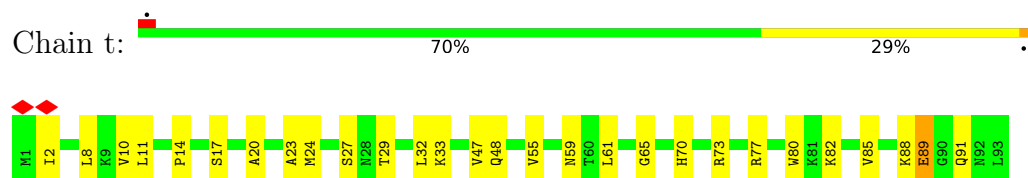
- Molecule 16: 50S ribosomal protein L21



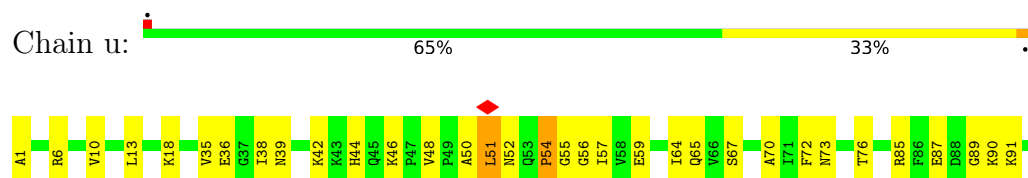
- Molecule 17: 50S ribosomal protein L22



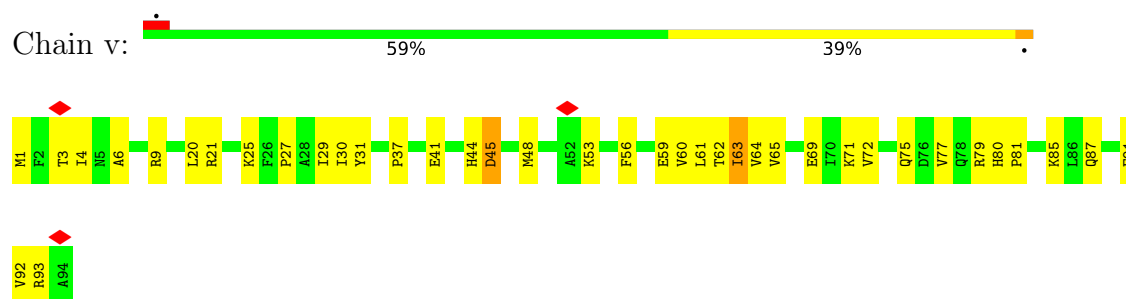
- Molecule 18: 50S ribosomal protein L23



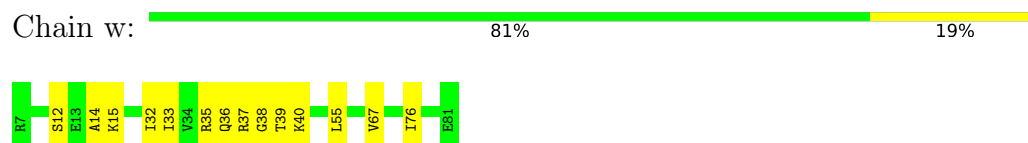
- Molecule 19: 50S ribosomal protein L24



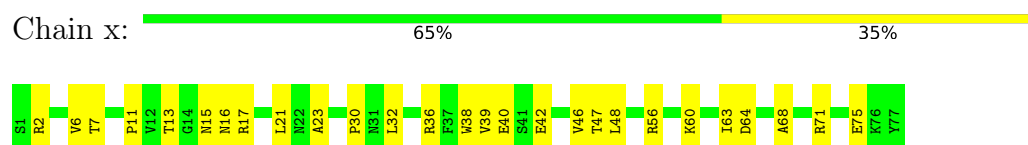
- Molecule 20: 50S ribosomal protein L25



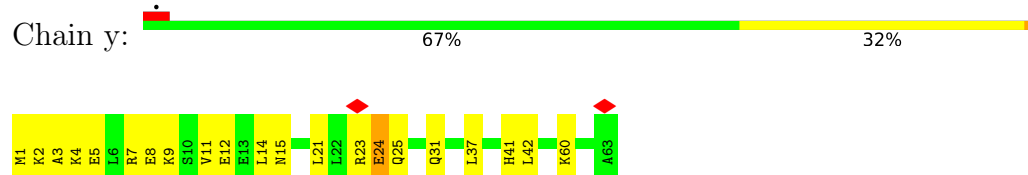
- Molecule 21: 50S ribosomal protein L27



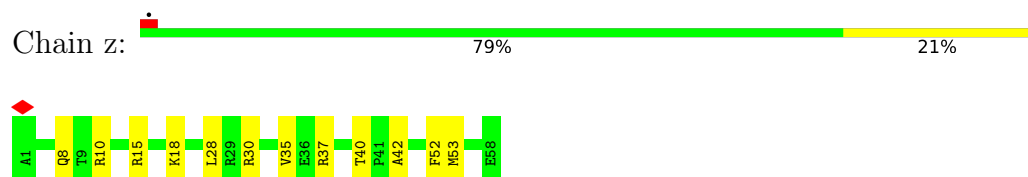
- Molecule 22: 50S ribosomal protein L28



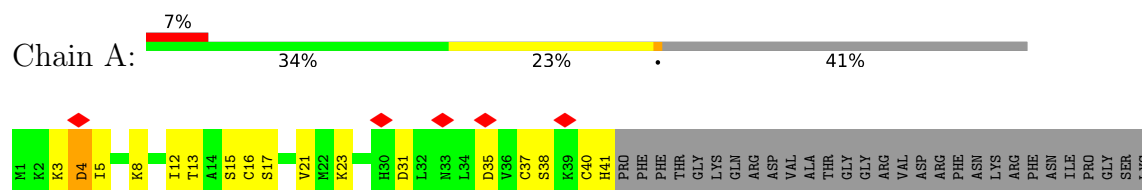
- Molecule 23: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L30

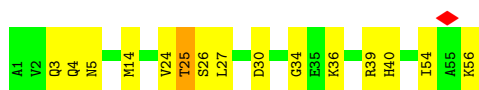


- Molecule 25: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L32

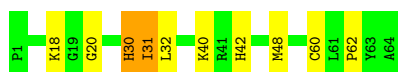
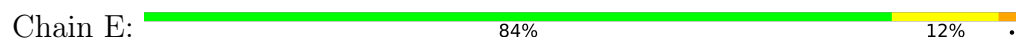




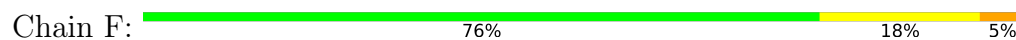
- Molecule 27: 50S ribosomal protein L34



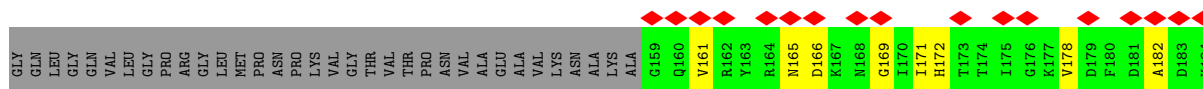
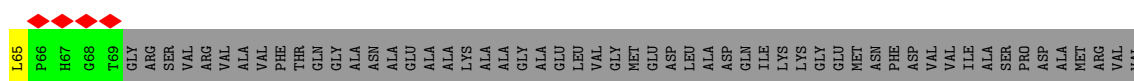
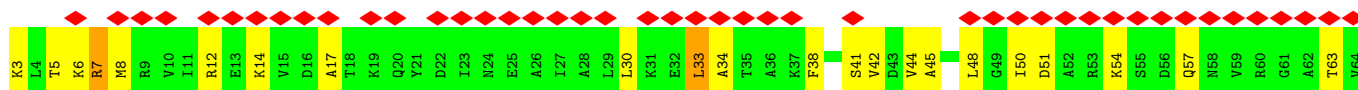
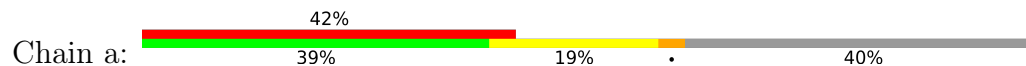
- Molecule 28: 50S ribosomal protein L35



- Molecule 29: 50S ribosomal protein L36



- Molecule 30: 50S ribosomal protein L1



- Molecule 31: 23s-5s joint ribosomal RNA



G1380	A1275	C1204	G1127	U1045	G954	C876	G797	U709	A609	G520	A415	A320	G215	U120
A1381	U1276	A1205	G1131	A1046	U955	A877	G798	U710	A613	U521	U416	U321	A216	G121
G1384	C1277	G1206	U1132	G1047	G956	A878		U714	A614	A522	U419	A322	A217	A127
G1394	C1278	C1207	G1133	G1048	G957	A879		G715	U615	A221	C420	A324	A222	U133
U1395	A1279	A1208	G1136	A1050	U958	G882	C806	A716		A222	C421	G327	G225	G134
A1396	C1280	U1209	G1137	A1051	A960	G883	U810	C717		C225	G424	U328	A226	U138
A1397	C1281	U1210	G1138	C1052	C961	C885	U811	A718		A226		G329	A227	U139
C1398	A1284	U1211	G1139	U1053	G962	A886	C812	C719		G530	C435	A330	C228	C140
G1399	U1287	A1212	U1140	G963	U963	U887	U813	A720		A532	C436	C331	C229	G141
A1400	G1288	G1213	U1141	C1064	A973	U888	C814	A721		G533	U437	G332	G230	
	C1289	G1215	G1058	U1065	G974	C889	C815	A722		U534	G438	C335	G231	
G1407	G1290	A1216	G1059	C968	A975	C890	C816	G726		G535	A439	A340	A231	A149
		A1217	C1060	G969	G970	G891	C817	A727		G536	C440	C341	G232	U150
C1417	C1295	A1218	U1061	U970	G971	A892	G818	G728		G537	U441		C151	U151
C1418	G1296	G1219	U1062	A893	A972	C893	A819	G729		A538	G442		A152	
C1419	A1297	C1220	U1063	U894	A973	C894		A730		G539	A443	C353	G242	
G1420		G1221	C1064	U895	A974	U895	U826	A731		G543	C444	A354	G248	A155
		G1222	U1065	C896	A975	A896	U827	A732		C544	C445	U355	C249	A156
C1425	U1301	A1223	G1066	C897	A979	C898	U828	G738		U545	G446	G356		
	U1302	G1224	U1067	G1068	A979	A899	A829	A739		U546		C357	G254	A161
G1428	A1303	U1225	G1159	U1068	A979	A899	G830	A743		C650	U451	U358	A255	U162
A1429	U1304	A1226	A1160	C1069	C982	A900	G831	U744		A547		G359	C163	C164
	G1305	G1227	U1161	U1070	A983	C901	U832	G745		G548	C456	U360	G266	
	C1306	C1228	G1162	C1070	A983	C902	A833	G746		G549	A457	C361		
G1437	G1307	U1229	U1067	A1081	C987	G903	G834	C747		A654	G458	A362	C275	A167
	U1308	C1230	G1164	G1082	A988	G904				A655		G363	U276	G168
C1447	U1309	A1231	G1168	C1085	C995	U905	U839	A752		U554	G467	A368	G277	G169
C1448	G1169	C1232	U1086	G1086	A996	U906	C840	A753		G555	G468	U369	A278	U170
U1454	C1170	U1233	G1170	G996	C997	C907	G841	U754		U558	G469	U370	A279	U171
A1455	C1171	G1234	C1172	C908	A998	C908	U842	A755		C559		G371	U280	A172
A1456	G1313	G1235	C1173	U1091	A1001	A910	G843	A756			G473	A371	C281	
A1457	U1314	U1236	C1174	A1001	A1002	A911	A844	A757		U562	G474	U372	A282	G176
C1458	G1315	C1237	U1174	A1002	G1002	A912	A845	C671		A563		A374	G283	U177
	A1317	G1238	C1097	U1098	A1009	C912	U846	G757		U573	G481	G375	U284	
	G1318	A1239	G1099	U1098	A1009	U913	U847	G760		A574	A482	G375	G285	A181
G1469	G1319	G1240	A1100	G1099	A1009	U913	C848	A761		A575			U286	
		U1241	C1101	C1101	U1012	A917	A849	A762			C490	G381	G287	C184
U1472	C1242	C1243	C1102	C1102	C1013	A918	U850	G763		G578	C491	A382	G287	
	G1243		G1184	G1184	A1020	U929	U852	C765		G579	A492	G386	A294	G189
U1480	G1248	G1249	U1185	C1108	G1021	U929	C853	U766		U580	G493	U387	G297	A190
A1481	C1248	C1249	U1186	G1109	G1022	U932	C854	U767		C581	G494		G298	A191
G1483	G1253	G1254	U1187	G1110	U1023	A933	G855	G768		A582	G495	C394		C192
G1484	C1339	A1254	U1188	A1111	G1024	U934	G858	U769		G585	G497	U395	G301	A195
C1485	G1340	G1255	U1189	C1112	G1025	C935	G859	G770		U588	G498	G396	C302	A196
G1486	A1255	G1256	G1191	U1114	G1026	A936	U860	G771		A503	U503	G400	G303	A197
A1487	C1341		C1192	C1115	C1027	C937		G776		A504	G401	A401	A198	C198
			U1193	A1116	U1028					A505	A402	A402	A199	U200
G1488	G1346	U1260	U1194	G1117	G1029	G940	G864	U779		A506	A403	U403	C201	
G1489	G1364	A1261	A1118	C1030	U1031	A941	C865			G506	U404	A404	U202	G198
	A1365	C1263	A1119	G1031	C1032	G942	G869	A782		A507	U405	G406	G312	A196
A1493	G1196		G1120	C1032		G946	U870	A783		A508	G406		G313	A203
A1494	C1366	G1266	U1121	U1033		A947	U871	G784		U511	G411		G314	A207
A1495	A1198	G1267	A1122	C1038		A947	U872	G785		G512	A412		G315	C208
G1496	G1199	C1268	A1123	C1039		C948	U873			G518	C413		G316	
	C1200		A1124	G949		G949	G874	A794		G518	C413		G317	
A1501	A1201	U1269	A1125	C1043		G953	G875	G795					G318	A213
A1506	C1378	A1270	C1126	G1044				G796					G319	G214

C2640	U2551	G2458	A2394	G2314	G2248	C2171	G2073	A1994	A1912	A1818	C1692	U1604	U1507
C2641	C2555	G2459	A2395	U2315	G2249	C2172	U2074	G1995	A1913	C1819	C1693	U1605	A1511
C2642	C2556	G2460	A2396	U2316	U2250	C2173	C2075	G1996	A1914	A1829	A1697	G1610	C1514
C2643	C2557	U2462	A2397	U2317	G2251	G2174	G2076	C1996	C1918	G1830	A1698	U1613	A1515
C2644	A2558	G2463	A2400	U2322	G2252	C2175	U2083	C2002	C1919	C1831	A1699	U1614	G1516
C2645	A2563	A2468	U2400	U2323	A2254	G2176	G2092	C2003	G1920	C1832	A1700	U1615	
U2646	A2401	G2469	A2401	C2324	G2255	A2180	C2093	A2004	C1921	A1833	U1704	A1618	U1522
U2647	A2402	U2470	A2402	U2325	G2256	C2183	C2094	U2008	C1922	G1837	C1706	C1526	
C2648	A2406	U2471	A2406	U2326	C2257	C2184	C2094	C2009	C1923	G1838	U1705		
C2649	A2407	U2472	A2407	A2327	U2258	G2185	C2095	U2010	C1924	C1839	C1706		
U2650	G2407	C2473	G2407	C2328	U2259	A2186	A2098		G1925	G1843	A1719	U1533	
G2651	G2408	A2474	G2408	G2329	U2260	G2187	U2099		U1926	C1627	C1720	U1534	
	A2409	G2475	A2409	U2330	G2261	A2188	G2100	A2013	G1927				
	G2410		G2410	U2331	G2262	G2189	G2101		C1928				
	C2411		C2411	G2332	G2263	A2190	U2107	A2018	A1929	U1853	C1723	C1542	
	C2412		C2412	A2333	A2264	C2191	U2108	G2019	G1934	C1854	A1724	G1543	
	C2413		C2413	C2334	G2265	C2192	C2108		G1935	C1855	A1632	G1544	
	G2414		G2414	C2335	U2266	C2193	G2117	A2027	A1936	U1857	G1729	U1634	
	A2415		A2415	C2336	G2267	C2194	C2118	A2028	A1937	C1858	U1730	C1635	A1547
	A2416		A2416	U2337	U2267	C2194	U2119	A2029	A1938	G1859	U1731	A1636	A1548
				U2338			U2120		A1939	C1860	A1736	A1637	
				A2339			U2121	C2033		U1864	A1736	G1638	C1556
	U2419		U2419	A2340	A2270	G2197	U2121	G2034	C1944	G1865	C1739		G1557
	G2420		G2420		C2271	A2198		G2035	G1945	U1867	A1744	A1643	G1558
	G2421		G2421		C2272	A2199		C2036	G1946	C1866			A1559
				G2345	C2273	C2200	C2124	C2037	U1947	A1661			G1560
	U2424		U2424	U2346	A2274	C2201	C2125	C2038	U1948	C1868	A1769	U1651	A1561
	A2425		A2425	G2347	C2275	U2202	A2126	U2039	A1949	C1869	G1770	G1652	G1562
	A2426		A2426	U2348	G2276	U2203	C2127	A2040	U1949		G1771	A1653	A1563
	A2427		A2427	C2349	U2277		C2128		A1949		C1772	G1654	G1564
	C2428		C2428	C2350	U2278	C2206	C2129	A2041	C1950	A1872	A1765	C1655	C1565
	G2429		G2429	G2351	U2279	U2207		C2042	G1951	A1873	A1766	C1656	C1566
	U2430		U2430	G2352	U2280	A2208	G2138	U2043	G1952	A1874	A1666	U1567	
	G2431		G2431	C2353	C2281	U2209	U2139	A2044	U1953	U1875	G1770	A1667	A1567
	G2432		G2432	C2354	U2282		G2140	U2045	G1954		G1771	C1659	G1568
	U2433		U2433		U2283	G2214	A2141		U1955	G1881	C1772	A1660	U1570
	G2434		G2434	U2357	U2284	G2215			G1956	A1882	G1773	C1661	U1571
	G2435		G2435	G2358	G2285		U2145	C2047	A1957	A1883	C1774	A1662	G1572
	G2436		G2436		U2286	U2220	G2146	G2048	C1965	G1884	U1775	C1663	G1573
	A2437		A2437	U2361	G2287	G2221	A2147	G2049		A1885	C1776	C1664	C1574
	C2438		C2438	G2362	A2286	A2222	C2148	G2050	G1970	U1886	U1776	G1665	C1575
	A2439		A2439		G2287	A2223	C2149	C2051	C1971	A1887	U1785	G1666	C1576
	U2440		U2440	G2366	C2288		U2150	C2052		C1889	C1786	G1667	G1577
	C2441		C2441		C2289	U2226	C2151	C2053	G1974	A1890	G1668	G1668	G1578
	A2442		A2442	U2371	A2291	U2227	G2152	U2054		G1891	C1669	C1579	
	G2443		G2443	U2372	C2292		U2156	G2057	A1975	C1892	U1790	C1582	
	G2444		G2444	U2373	C2293	C2231	G2157	C2058	A1976	G1893	U1791		
	A2445		A2445	G2374	U2294	C2232	A2158	U2059	G1977	G1894	G1794	A1672	
	G2446		G2446	A2375		U2233	A2159	A2060	G1978	G1895	G1795	A1673	U1586
	G2447		G2447	C2376		U2234		G2061	U1979	C1896			U1587
	U2448		U2448	U2377	A2298	G2235			U1980		C1798	A1676	U1588
	U2449		U2449	G2378	U2300		U2162	G2062	A1981	A1901	C1799	A1677	C1589
	A2450		A2450	U2379	A2301	C2238	G2163	A2063	A1982	C1902	U1799	G1683	U1596
	G2451		G2451	C2380	A2302	U2239	C2164	A2065	U1983	G1903	G1802		A1597
	G2452		G2452	G2381	C2302	U2240	A2165	A2066	U1984	G1904			A1598
	U2453		U2453	C2382	C2303	U2241	A2166	U2067	G1985			G1688	
	C2454		C2454	A2304	A2304	A2242	U2167	U2068	A1986	U1808	U1602	G1689	U1602
	A2455		A2455		G2307	U2246	G2168		G1990	G1810	U1603	G1690	U1603
	A2456		A2456	U2308	U2307		U2169	U2071					
	U2457		U2457	U2309	U2309	A2247	A2170	U2072					
					U2313								

U2989	G2990	G2903	C2809	G2725
G2995	A2906	A2907	A2810	A2726
A2996	U2907	U2912	C2811	G2727
G2997	U2912	C2913	U2812	A2728
C2998	C2913	U2914	G2813	C2729
U2999	U2914	C2915	U2814	A2730
A3000	C2915	C2916	U2815	G2731
A3001	C2916	C2917	G2816	U2732
C3002	C2917	U2918	U2817	U2733
A3007	U2918	G2919	C2818	C2734
C3008	G2919	C2923	G2820	
A3011	U2924	U2924	G2821	U2737
U3012	U2925	U2925	G2822	C2738
G3013	U2926	U2926	U2823	C2739
C3024	A2927	A2927	U2826	C2740
U3025	A2928	A2928	C2827	A2742
U3026	G2929	G2929	C2831	U2743
A3027	G2930	G2930	C2832	
C3030	U2932	U2932	C2838	C2747
U3031	C2933	C2933	G2842	
	C2934	C2934		G2751
	U2935	U2935	G2846	G2752
	G2936	G2936		G2753
	A2937	A2937	A2849	C2754
	A2938	A2938	G2850	G2755
	G2939	G2939	C2851	C2756
	G2940	G2940	U2856	U2757
	A2941	A2941	G2857	
			C2858	C2764
	U2946	U2946	G2859	U2765
	G2947	G2947	G2860	U2766
	A2948	A2948	A2861	A2767
	A2949	A2949		G2768
			U2871	G2769
	G2953	G2953	G2872	A2770
	A2954	A2954	C2873	G2771
			U2874	
	C2958	C2958	G2875	C2774
			A2876	U2775
	G2962	G2962	G2877	G2776
	A2963	A2963	A2878	C2777
	U2964	U2964	G2879	C2778
	A2965	A2965		
	G2966	G2966	C2883	A2782
	G2967	G2967		G2783
	C2968	C2968	C2888	U2784
	C2969	C2969	A2889	
	G2970	G2970		A2788
	G2971	G2971	A2892	A2789
			A2893	A2790
	G2974	G2974		G2792
	U2975	U2975	C2900	A2793
	G2976	G2976	C2901	C2794
	U2977	U2977	C2902	
				G2802
				A2807
				U2808

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21705	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.138	Depositor
Minimum map value	-6.456	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.774	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.35	0/2121	0.92	7/2852 (0.2%)
2	c	0.34	0/1585	0.86	0/2134
3	d	0.38	0/1570	0.86	3/2113 (0.1%)
4	e	0.44	0/1434	0.90	6/1926 (0.3%)
5	f	0.41	0/1342	0.87	5/1816 (0.3%)
6	g	0.43	0/414	1.01	3/556 (0.5%)
7	h	0.56	0/1001	1.09	8/1350 (0.6%)
8	i	0.58	0/1045	1.04	3/1410 (0.2%)
9	j	0.34	0/1151	0.86	3/1551 (0.2%)
10	k	0.36	0/947	0.92	2/1268 (0.2%)
11	l	0.35	0/1053	0.98	5/1403 (0.4%)
12	n	0.32	0/973	0.91	3/1301 (0.2%)
13	o	0.34	0/901	0.90	3/1209 (0.2%)
14	p	0.33	0/928	0.83	2/1242 (0.2%)
15	q	0.32	0/959	0.89	4/1278 (0.3%)
16	r	0.37	0/828	0.87	3/1107 (0.3%)
17	s	0.32	0/863	0.86	1/1156 (0.1%)
18	t	0.34	0/744	0.83	0/994
19	u	0.35	0/787	0.92	2/1051 (0.2%)
20	v	0.40	0/765	0.85	2/1025 (0.2%)
21	w	0.31	0/581	0.81	0/769
22	x	0.32	0/634	0.87	1/848 (0.1%)
23	y	0.34	0/509	0.83	0/677
24	z	0.31	0/452	0.79	0/605
25	A	0.41	0/319	0.82	2/426 (0.5%)
26	B	0.31	0/449	0.78	0/599
27	D	0.34	0/379	0.86	0/498
28	E	0.33	0/512	0.85	1/676 (0.1%)
29	F	0.30	0/303	0.81	0/397
30	a	0.53	0/1033	0.94	7/1387 (0.5%)
31	4	0.46	0/72710	0.50	5/113431 (0.0%)
All	All	0.44	0/99292	0.62	81/149055 (0.1%)

There are no bond length outliers.

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	10	ALA	N-CA-C	8.18	121.15	110.43
5	f	47	ASN	N-CA-C	-8.15	102.37	112.88
11	l	95	LEU	N-CA-C	-7.49	104.28	113.41
12	n	68	ALA	N-CA-C	-7.49	103.12	111.28
7	h	58	THR	N-CA-C	7.43	121.19	112.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	b	2082	0	2157	57	0
2	c	1564	0	1616	41	0
3	d	1551	0	1619	42	0
4	e	1410	0	1447	77	0
5	f	1322	0	1374	49	0
6	g	409	0	429	15	0
7	h	988	0	1025	57	0
8	i	1031	0	1088	60	0
9	j	1128	0	1162	30	0
10	k	938	0	1012	32	0
11	l	1044	0	1117	22	0
12	n	960	0	1000	19	0
13	o	891	0	923	25	0
14	p	916	0	965	29	0
15	q	946	0	1022	19	0
16	r	815	0	839	17	0
17	s	856	0	922	25	0
18	t	738	0	807	19	0
19	u	779	0	834	22	0
20	v	752	0	780	30	0
21	w	574	0	592	11	0
22	x	624	0	655	21	0
23	y	508	0	543	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	z	448	0	491	9	0
25	A	315	0	318	9	0
26	B	443	0	461	13	0
27	D	376	0	418	13	0
28	E	503	0	574	8	0
29	F	302	0	343	11	0
30	a	1026	0	1092	41	0
31	4	64925	0	32667	1219	0
All	All	91164	0	60292	1840	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 12.

The worst 5 of 1840 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)
31:4:1024:G:H3'	31:4:1025:G:H2'	1.29	1.14
31:4:1307:G:H2'	31:4:1308:U:H4'	1.24	1.14
31:4:45:G:H5''	31:4:46:G:H5'	1.21	1.12
20:v:62:THR:HG22	20:v:69:GLU:HG2	1.32	1.10
8:i:4:VAL:HG21	31:4:1227:G:H5''	1.35	1.09

There are no symmetry-related clashes.

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	
1	b	269/271 (99%)	237 (88%)	29 (11%)	3 (1%)	11	39
2	c	207/209 (99%)	187 (90%)	19 (9%)	1 (0%)	24	57
3	d	199/201 (99%)	177 (89%)	20 (10%)	2 (1%)	12	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	e	175/177 (99%)	150 (86%)	23 (13%)	2 (1%)	11	39
5	f	174/176 (99%)	157 (90%)	15 (9%)	2 (1%)	11	39
6	g	51/149 (34%)	37 (72%)	11 (22%)	3 (6%)	1	8
7	h	129/131 (98%)	97 (75%)	26 (20%)	6 (5%)	2	11
8	i	139/141 (99%)	114 (82%)	20 (14%)	5 (4%)	2	16
9	j	140/142 (99%)	131 (94%)	7 (5%)	2 (1%)	9	34
10	k	120/122 (98%)	99 (82%)	18 (15%)	3 (2%)	4	21
11	l	141/143 (99%)	122 (86%)	16 (11%)	3 (2%)	5	25
12	n	118/120 (98%)	104 (88%)	11 (9%)	3 (2%)	4	21
13	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	44
14	p	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	44
15	q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
16	r	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	6	25
17	s	108/110 (98%)	98 (91%)	8 (7%)	2 (2%)	6	27
18	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	39
19	u	100/102 (98%)	85 (85%)	11 (11%)	4 (4%)	2	13
20	v	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
21	w	73/75 (97%)	65 (89%)	7 (10%)	1 (1%)	9	34
22	x	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
23	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	30
24	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
25	A	39/70 (56%)	35 (90%)	4 (10%)	0	100	100
26	B	54/56 (96%)	47 (87%)	6 (11%)	1 (2%)	6	27
27	D	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
28	E	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7	30
29	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	20
30	a	130/223 (58%)	114 (88%)	14 (11%)	2 (2%)	8	32
All	All	3325/3601 (92%)	2925 (88%)	347 (10%)	53 (2%)	10	30

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	30	GLU

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Mol	Chain	Res	Type
3	d	83	VAL
5	f	174	LYS
6	g	9	VAL
7	h	80	THR

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	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	78
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	72
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	82
6	g	42/114 (37%)	42 (100%)	0	100	100
7	h	100/100 (100%)	100 (100%)	0	100	100
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	73
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	80
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	79
11	l	102/102 (100%)	102 (100%)	0	100	100
12	n	100/100 (100%)	100 (100%)	0	100	100
13	o	86/86 (100%)	85 (99%)	1 (1%)	63	78
14	p	99/99 (100%)	99 (100%)	0	100	100
15	q	89/89 (100%)	89 (100%)	0	100	100
16	r	84/84 (100%)	83 (99%)	1 (1%)	63	78
17	s	93/93 (100%)	93 (100%)	0	100	100
18	t	80/80 (100%)	79 (99%)	1 (1%)	61	77
19	u	83/83 (100%)	83 (100%)	0	100	100
20	v	78/78 (100%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	w	57/57 (100%)	56 (98%)	1 (2%)	51	73
22	x	67/67 (100%)	67 (100%)	0	100	100
23	y	55/55 (100%)	55 (100%)	0	100	100
24	z	48/48 (100%)	48 (100%)	0	100	100
25	A	38/62 (61%)	37 (97%)	1 (3%)	40	68
26	B	47/47 (100%)	47 (100%)	0	100	100
27	D	38/38 (100%)	37 (97%)	1 (3%)	40	68
28	E	51/51 (100%)	51 (100%)	0	100	100
29	F	34/34 (100%)	33 (97%)	1 (3%)	37	66
30	a	110/174 (63%)	108 (98%)	2 (2%)	51	73
All	All	2739/2899 (94%)	2720 (99%)	19 (1%)	73	82

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	A	35	ASP
30	a	33	LEU
30	a	214	ILE
29	F	36	ARG
9	j	81	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
23	y	58	ASN
30	a	57	GLN
25	A	41	HIS
28	E	30	HIS
10	k	3	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	4	3023/3031 (99%)	371 (12%)	9 (0%)

5 of 371 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	4	10	A
31	4	12	U
31	4	34	U
31	4	35	G
31	4	46	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	4	2632	U
31	4	3001	A
31	4	1025	G
31	4	2424	U
31	4	2430	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

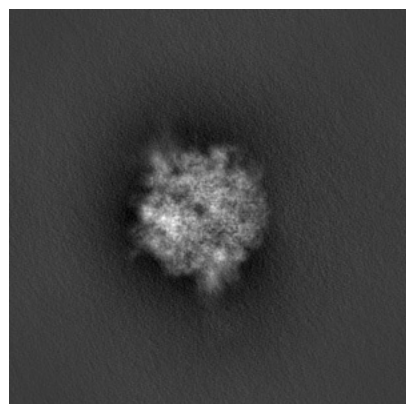
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21856. These allow visual inspection of the internal detail of the map and identification of artifacts.

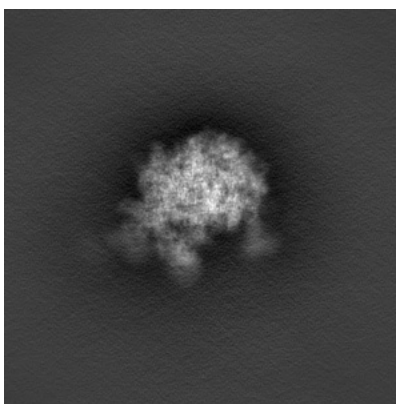
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

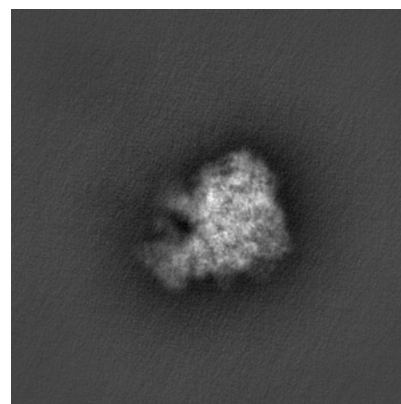
6.1.1 Primary map



X

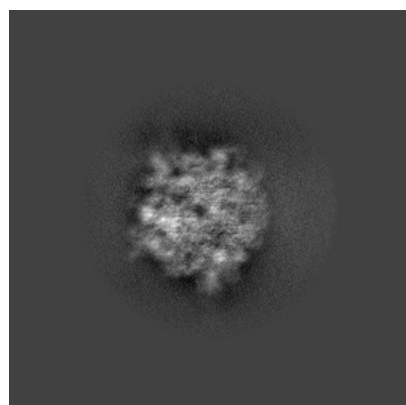


Y

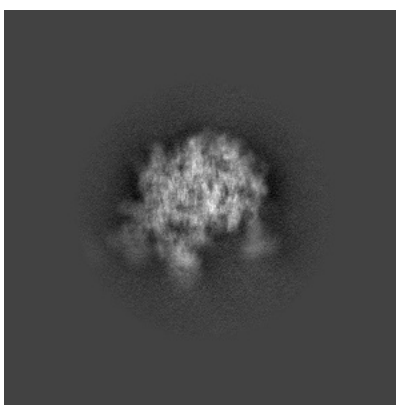


Z

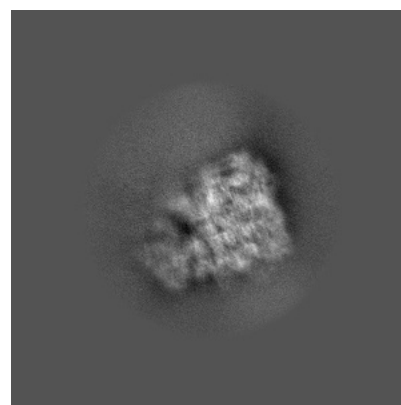
6.1.2 Raw map



X



Y

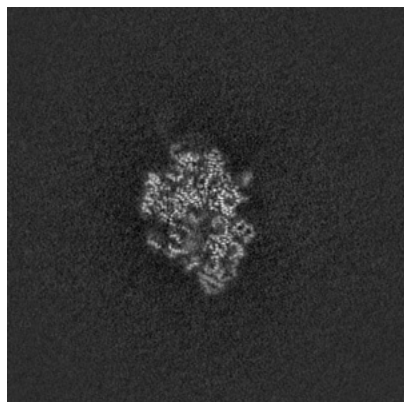


Z

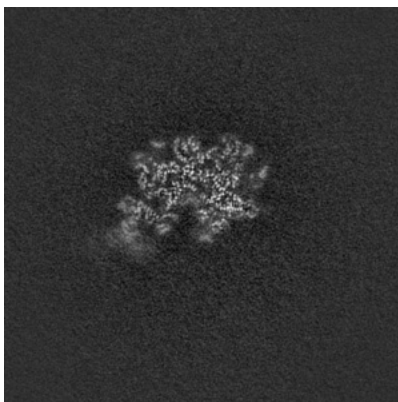
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

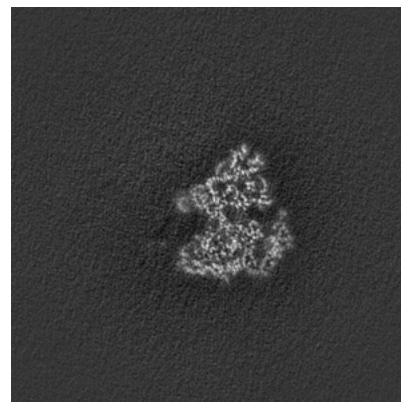
6.2.1 Primary map



X Index: 304

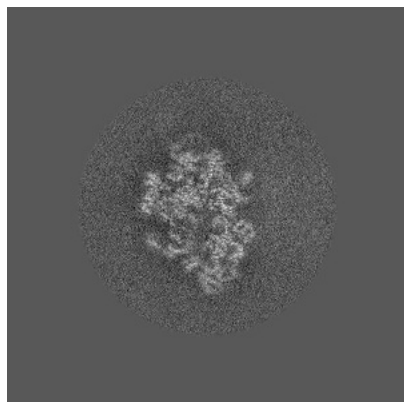


Y Index: 304

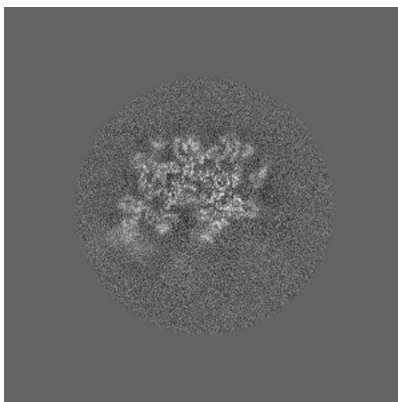


Z Index: 304

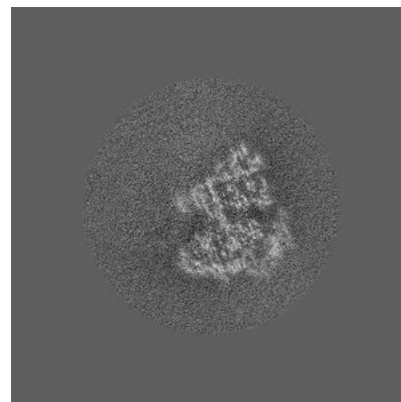
6.2.2 Raw map



X Index: 304



Y Index: 304

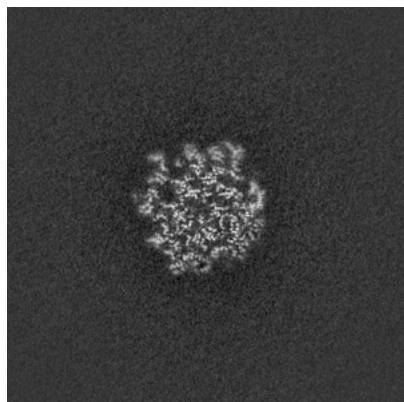


Z Index: 304

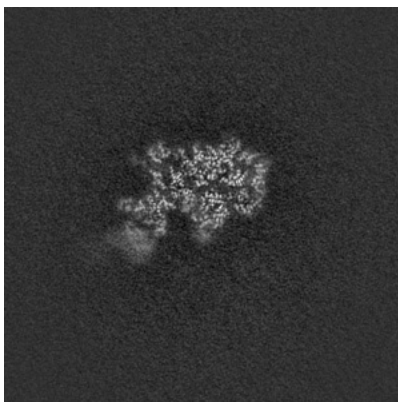
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

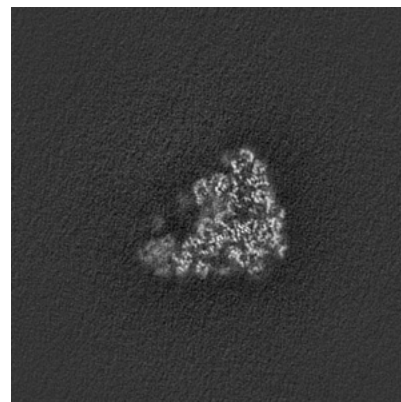
6.3.1 Primary map



X Index: 339

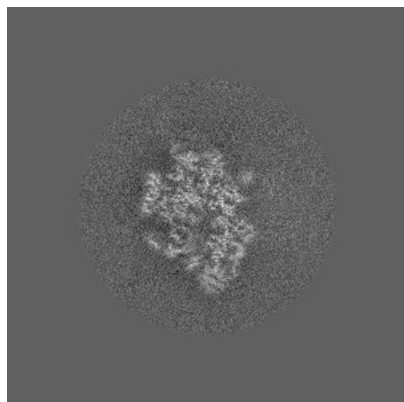


Y Index: 316

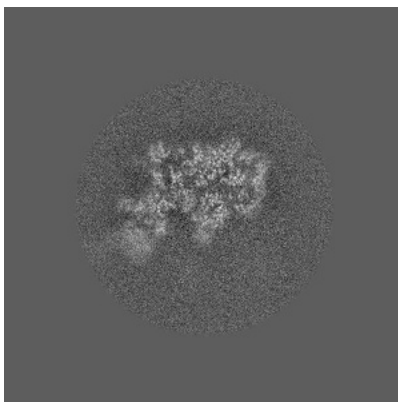


Z Index: 290

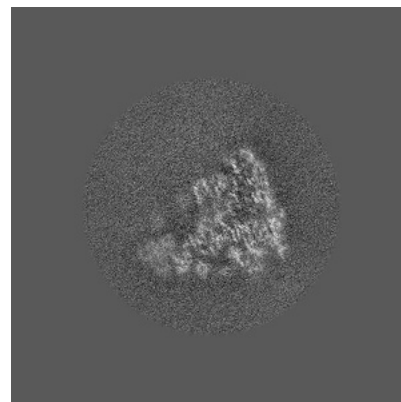
6.3.2 Raw map



X Index: 303



Y Index: 316

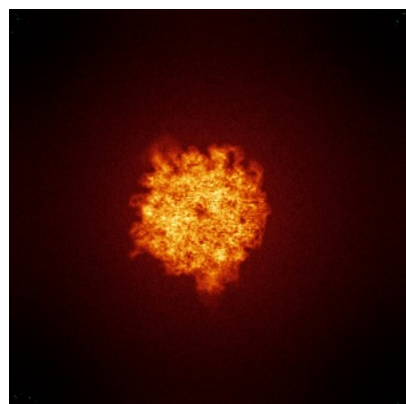


Z Index: 290

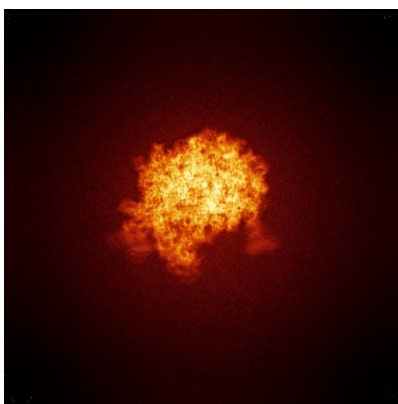
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

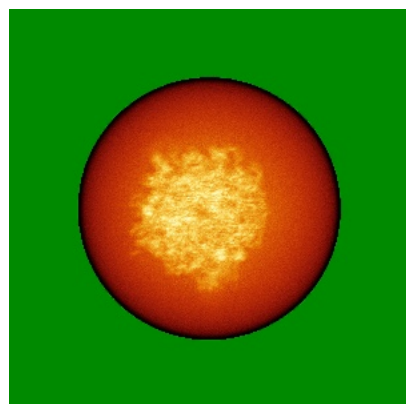


Y

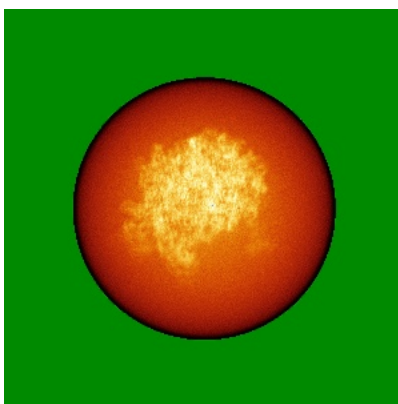


Z

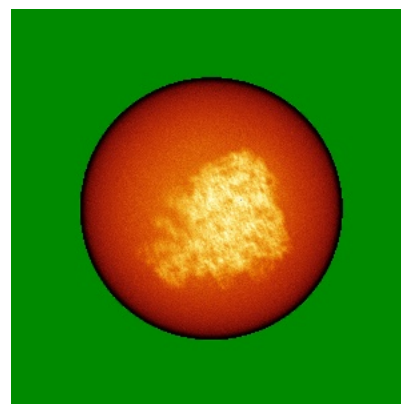
6.4.2 Raw map



X



Y

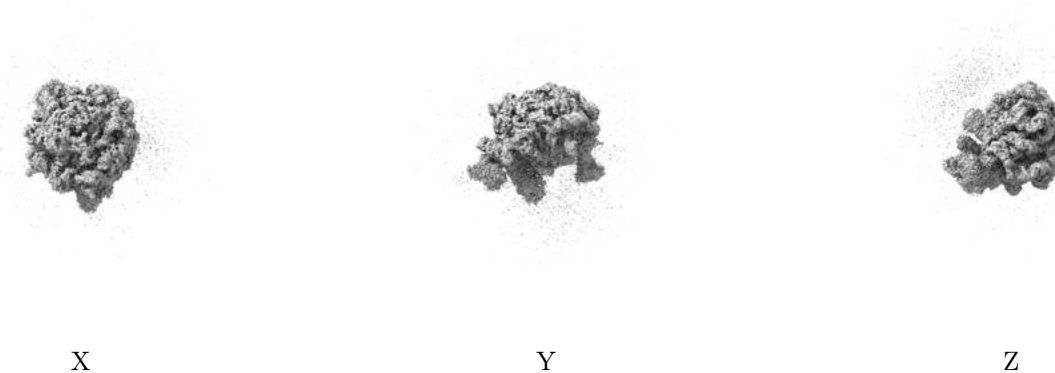


Z

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.

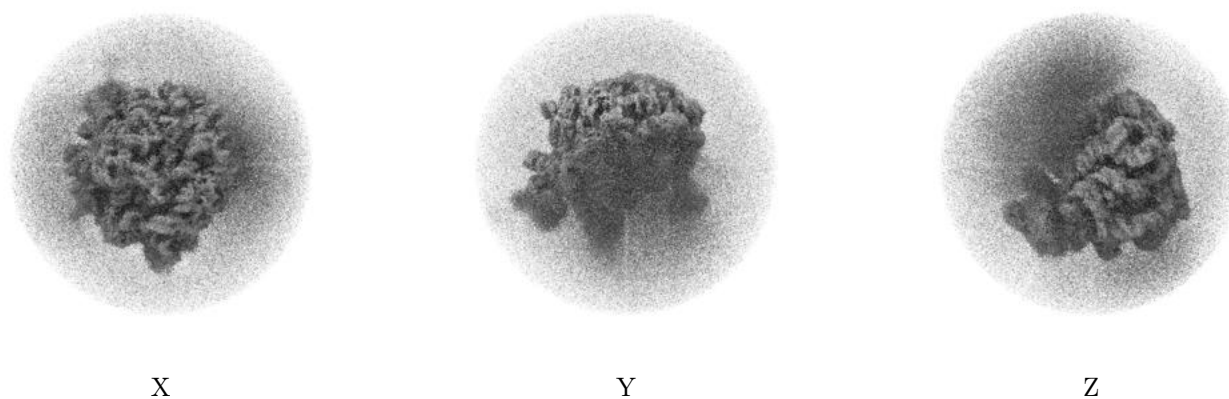
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. 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.

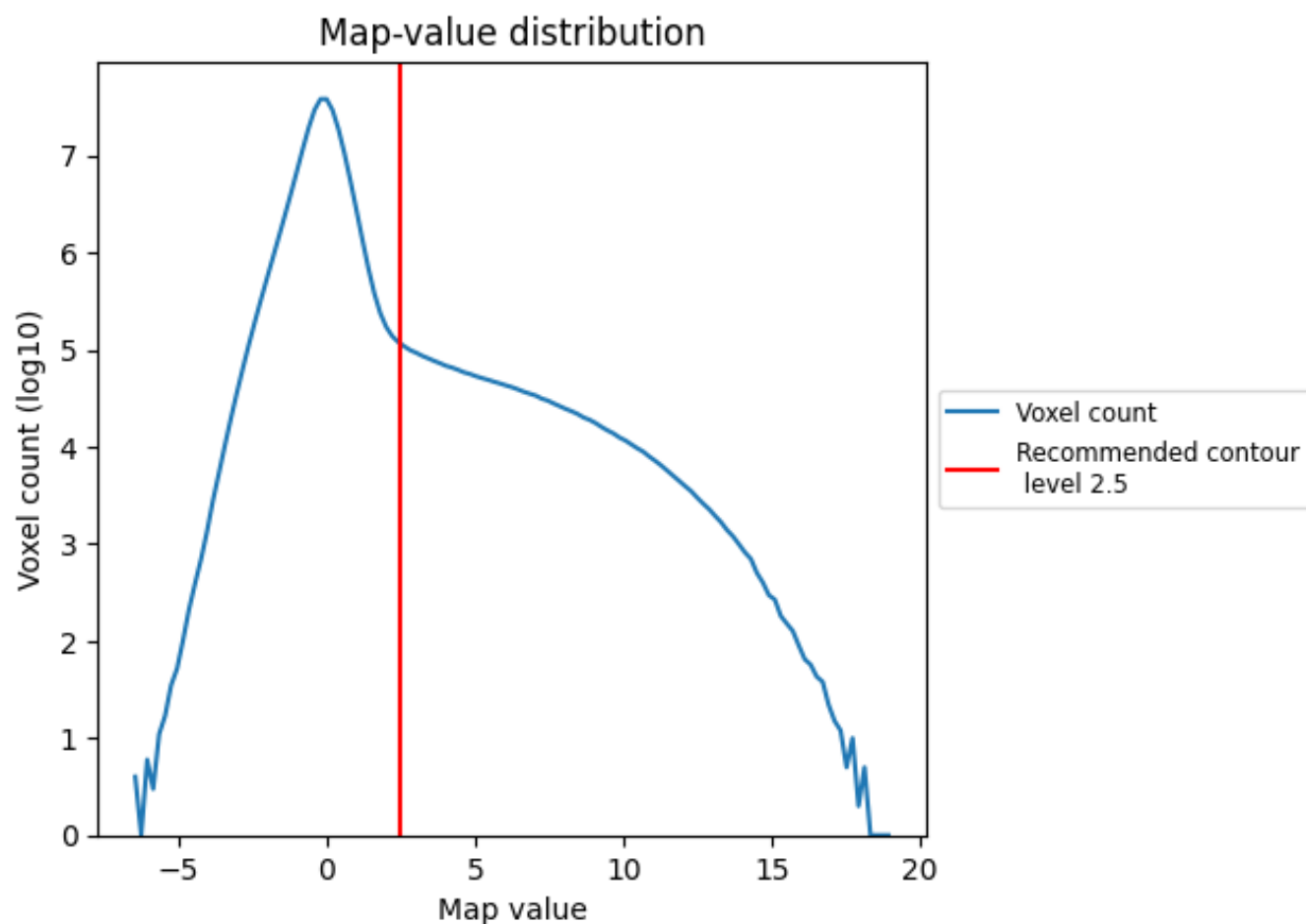
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

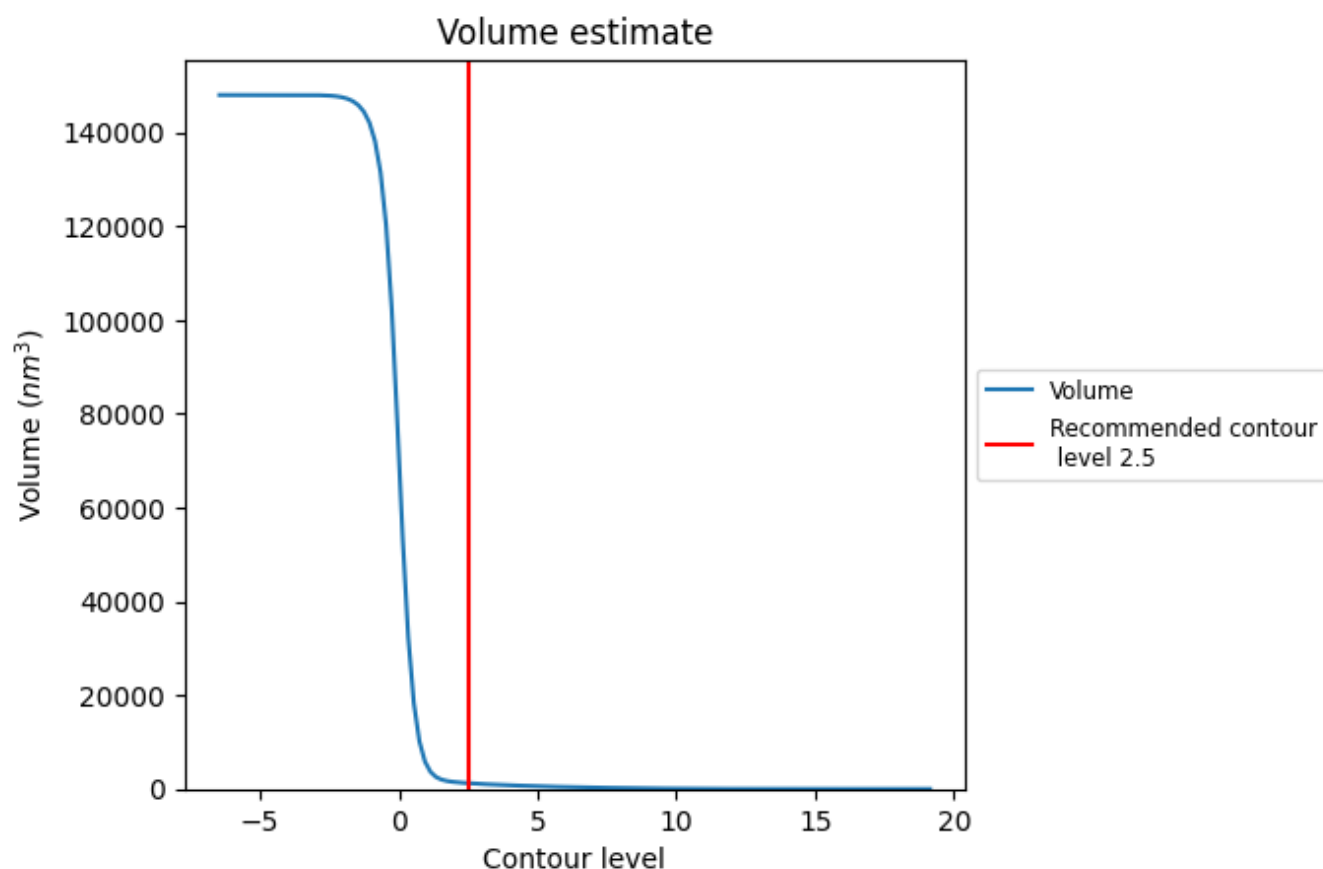
This section contains the results of statistical analysis of the map.

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.

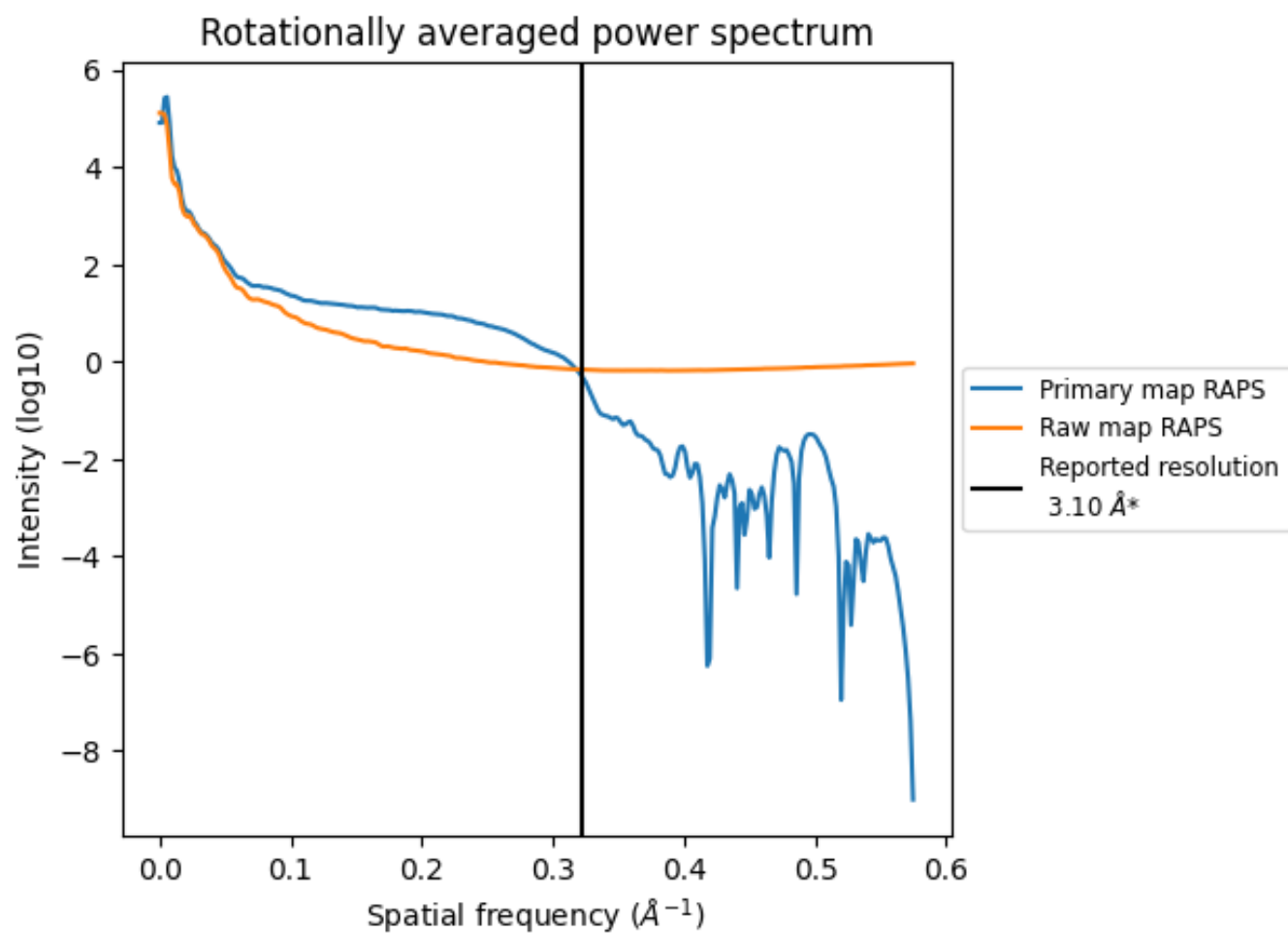
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1232 nm^3 ; this corresponds to an approximate mass of 1112 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 ⓘ

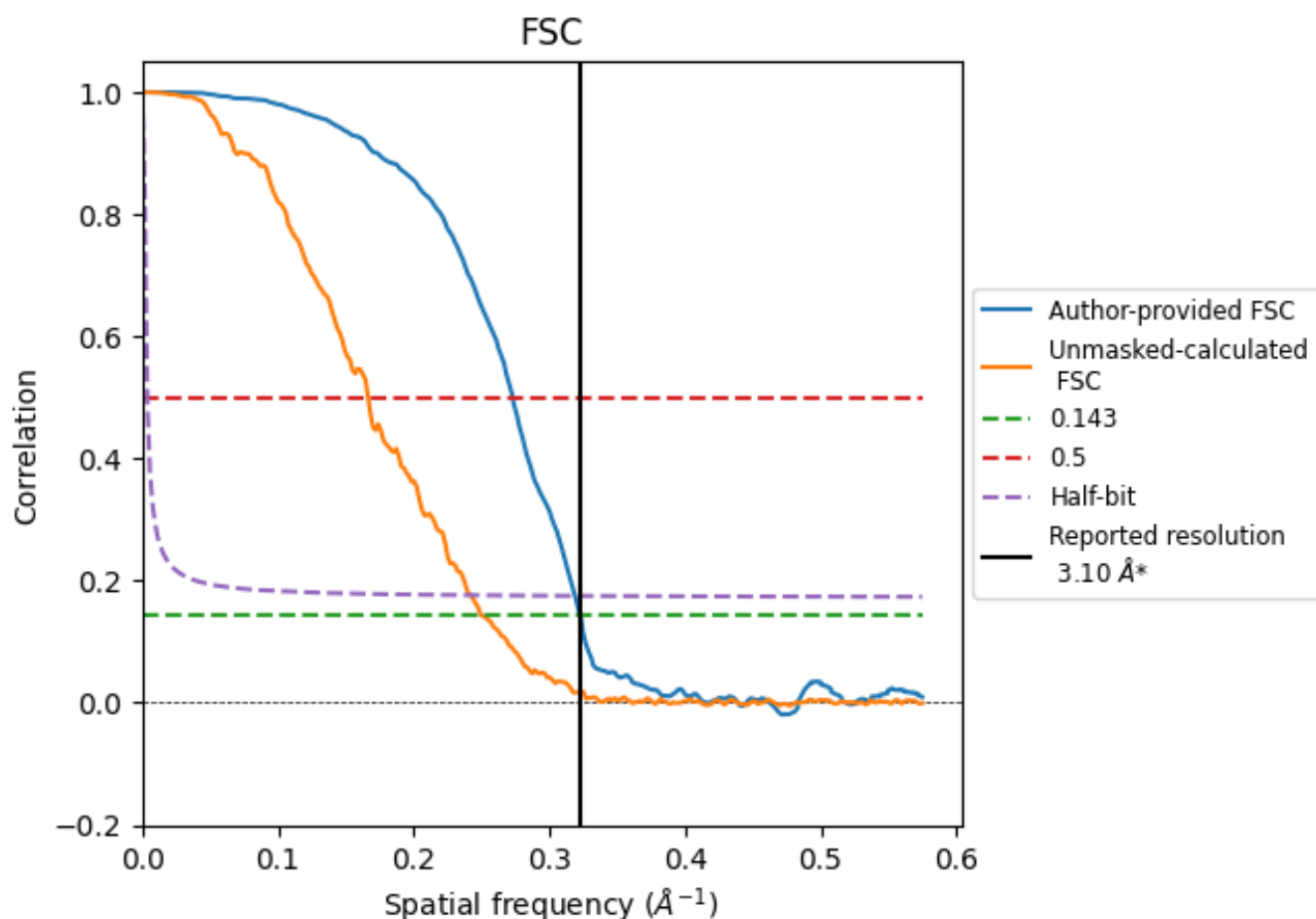


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

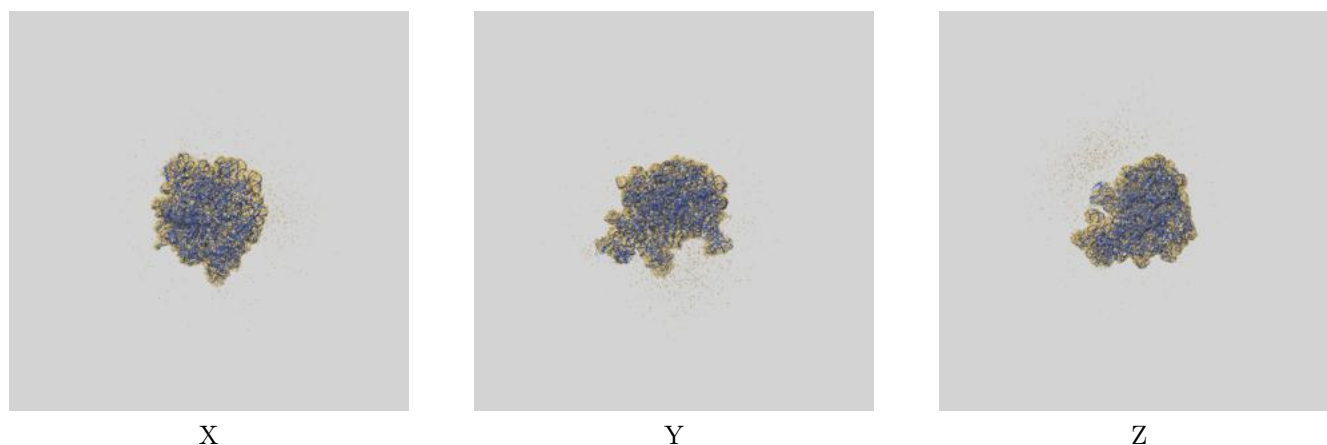
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.66	3.14
Unmasked-calculated*	4.00	6.01	4.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

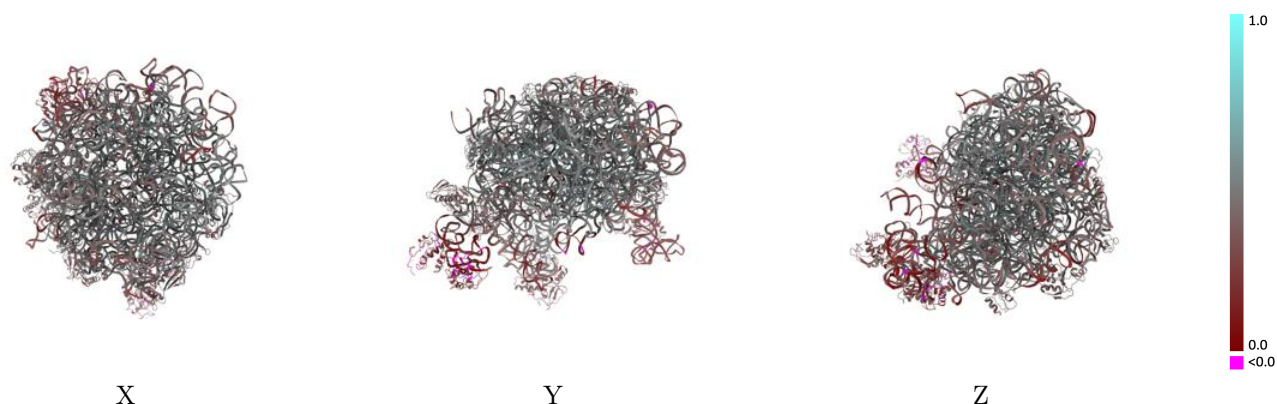
This section contains information regarding the fit between EMDB map EMD-21856 and PDB model 6WNT. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



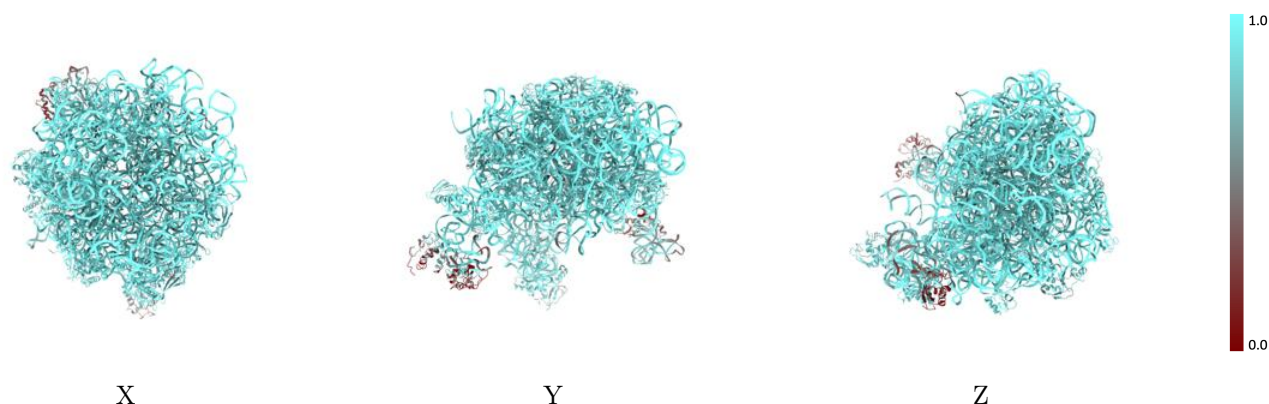
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



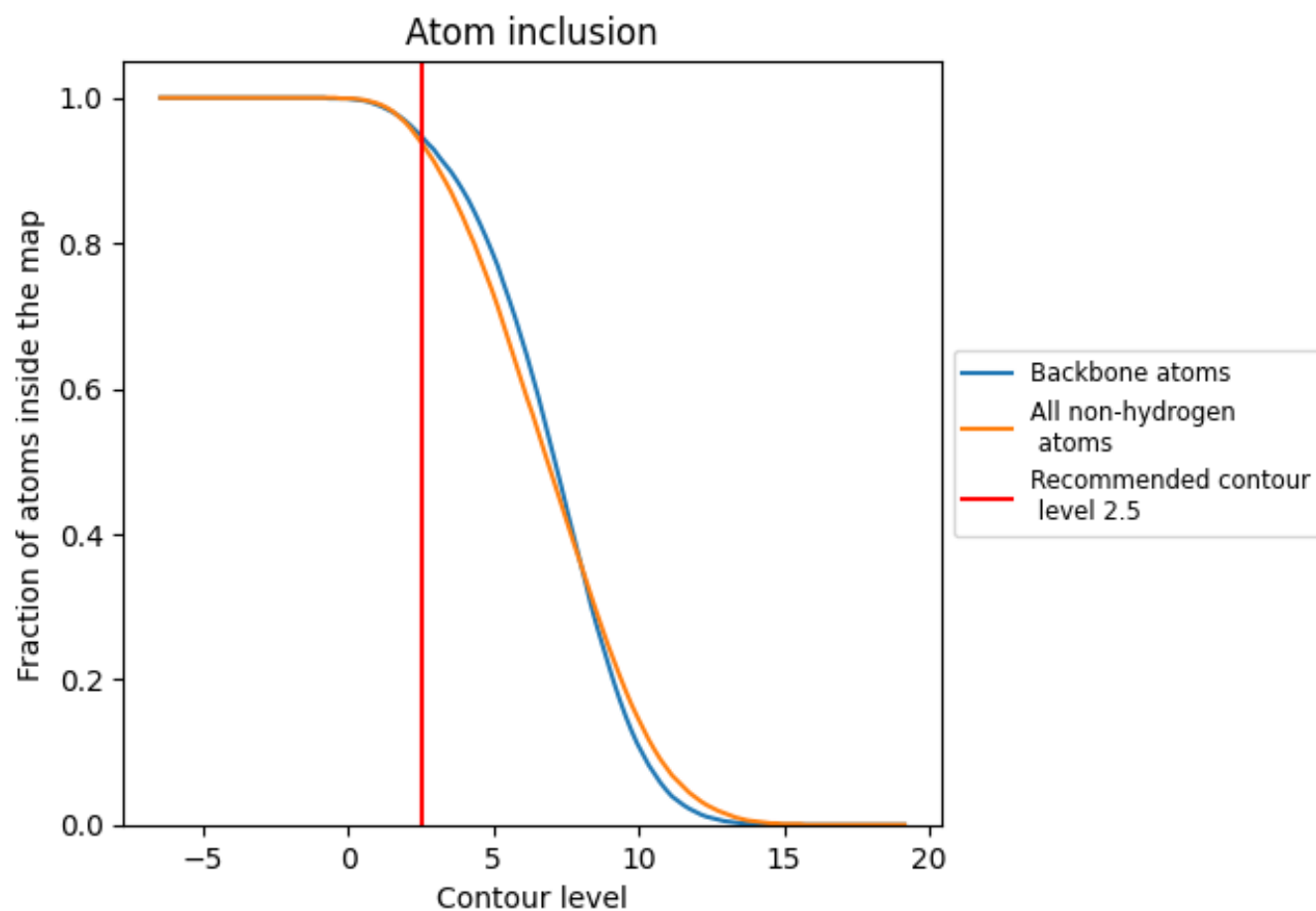
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.4250
4	 0.9750	 0.4290
A	 0.7180	 0.3310
B	 0.9370	 0.4790
D	 0.9320	 0.4950
E	 0.9410	 0.4870
F	 0.9070	 0.4740
a	 0.3100	 0.2300
b	 0.9490	 0.4840
c	 0.9240	 0.4780
d	 0.8480	 0.4180
e	 0.8670	 0.3130
f	 0.9170	 0.3960
g	 0.8580	 0.3650
h	 0.4980	 0.2020
i	 0.3240	 0.2000
j	 0.9220	 0.4760
k	 0.9280	 0.4640
l	 0.9300	 0.4590
n	 0.9350	 0.4830
o	 0.9410	 0.3960
p	 0.9060	 0.4570
q	 0.9340	 0.4740
r	 0.9070	 0.4540
s	 0.9040	 0.4740
t	 0.9100	 0.4550
u	 0.9240	 0.4210
v	 0.8370	 0.3310
w	 0.9140	 0.4760
x	 0.9520	 0.4720
y	 0.8970	 0.3890
z	 0.9220	 0.4780

