



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:45 AM UTC

PDB ID : 8EUG / pdb_00008eug
EMDB ID : EMD-24412
Title : Ytm1 associated nascent 60S ribosome State 3
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-18
Resolution : 2.80 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:

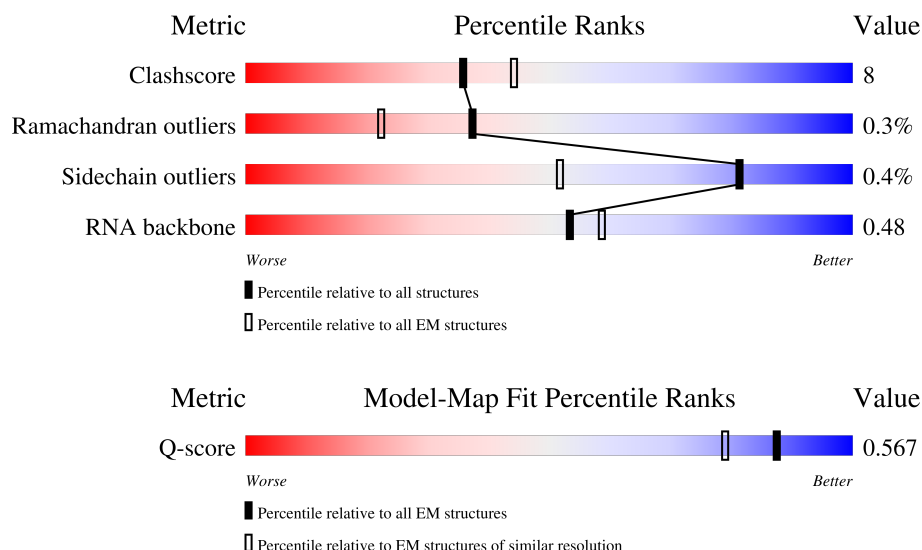
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.80 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.



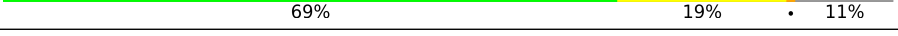
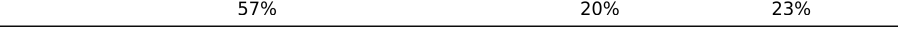
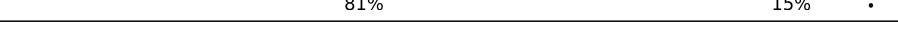
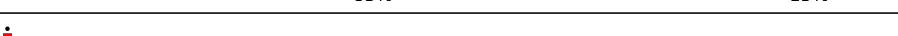
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	1	3498	
2	2	165	
3	3	302	

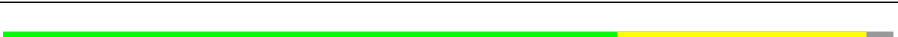
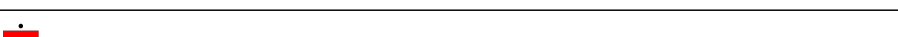
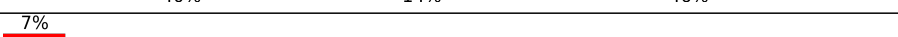
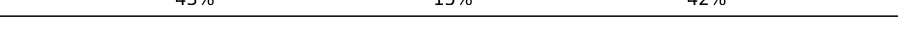
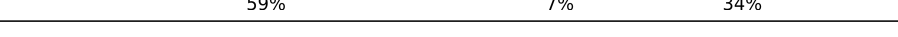
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Mol	Chain	Length	Quality of chain
4	8	51	
5	9	229	
6	A	253	
7	B	388	
8	C	363	
9	D	294	
10	E	195	
11	F	250	
12	G	259	
13	H	190	
14	I	221	
15	J	174	
16	K	94	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	R	193	
24	S	176	
25	T	160	
26	U	117	
27	V	139	
28	X	141	

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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	136	
31	a	148	
32	b	61	
33	c	117	
34	d	113	
35	e	127	
36	f	108	
37	g	112	
38	h	122	
39	i	99	
40	j	91	
41	k	74	
42	m	740	
43	n	607	
44	o	106	
45	p	440	
46	u	192	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 123162 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (2863-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2869	Total	C	N	O	P	0	0
			61386	27430	11112	19975	2869		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483
1	2185	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	151	Total	C	N	O	P	0	0
			3211	1437	569	1054	151		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	119	Total	C	N	O	S	0	0
			1006	637	188	175	6		

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	50	Total	C	N	O	S	0	0
			437	273	98	65	1		

- Molecule 5 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	118	Total	C	N	O	P	0	0
			2519	1124	452	825	118		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	244	Total	C	N	O	S	0	0
			1847	1152	370	320	5		

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	377	Total	C	N	O	S	0	0
			3003	1901	567	525	10		

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 9 is a protein called 60S ribosomal protein L5-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	287	Total	C	N	O	S	0	0
			2305	1457	409	435	4		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	172	Total	C	N	O	S	0	0
			1338	860	245	230	3		

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	214	Total	C	N	O	S	0	0
			1745	1124	320	298	3		

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	1	0
			1817	1161	334	319	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	178	Total	C	N	O	S	0	0
			1415	892	260	257	6		

- Molecule 14 is a protein called 60S ribosomal protein L10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	170	Total	C	N	O	S	0	0
			1372	869	256	242	5		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	157	Total	C	N	O	S	0	0
			1276	806	242	223	5		

- Molecule 16 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	90	Total	C	N	O	S	0	0
			695	428	144	117	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	202	Total	C	N	O	S	0	0
			1612	1008	321	282	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	171	Total	C	N	O	S	0	0
			1357	857	262	235	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	186	Total	C	N	O	S	0	0
			1486	933	300	252	1		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	148	Total	C	N	O	S	0	0
			1220	759	259	197	5		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	167	Total	C	N	O	S	0	0
			1388	896	259	228	5		

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	158	Total	C	N	O	S	0	0
			1282	807	247	225	3		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	98	Total	C	N	O	0	0
			791	513	137	141		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	137	Total	C	N	O	S	0	0
			1026	644	193	181	8		

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	120	Total	C	N	O	S	0	0
			962	614	178	169	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	134	Total	C	N	O	S	0	0
			1072	693	199	178	2		

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	147	Total	C	N	O	S	0	0
			1169	740	235	192	2		

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	54	Total	C	N	O	0	0
			463	281	106	76		

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	95	Total	C	N	O	S	0	0
			714	454	124	132	4		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	102	Total	C	N	O	S	0	0
			849	534	165	147	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	117	Total	C	N	O	S	0	0
			939	588	190	156	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	121	Total	C	N	O		0	0
			999	629	194	176			

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	96	Total	C	N	O	S	0	0
			767	478	160	128	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	83	Total	C	N	O	S	0	0
			657	402	141	107	7		

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	398	Total	C	N	O	S	0	0
			3127	2001	557	558	11		

- Molecule 43 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	354	Total	C	N	O	S	0	0
			2903	1892	496	503	12		

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	97	Total	C	N	O	S	0	0
			789	498	158	128	5		

- Molecule 45 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	p	290	Total	C	N	O	0	0
			1431	851	290	290		

- Molecule 46 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	59	Total	C	N	O	S	0	0
			493	315	100	72	6		

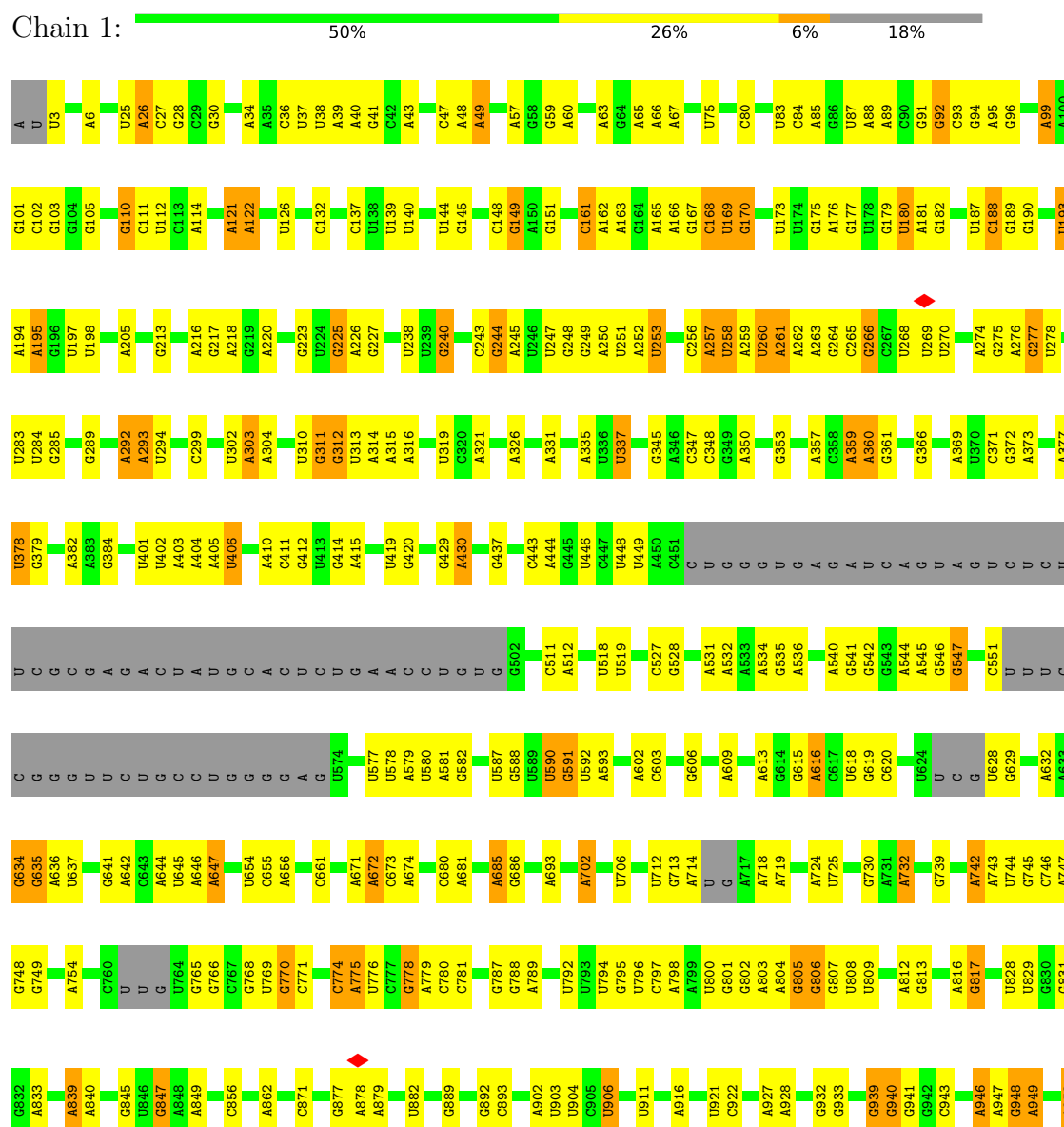
- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

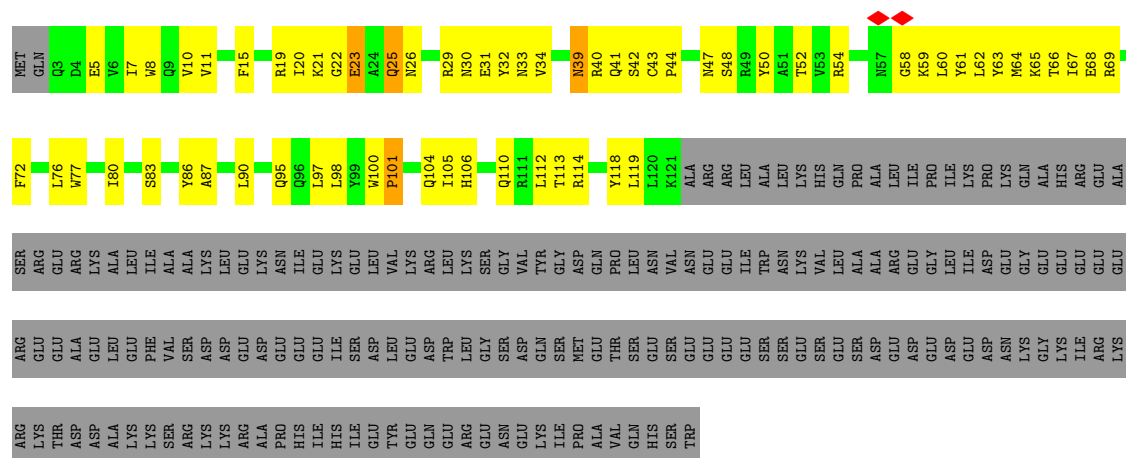
• Molecule 1: RNA (2863-MER)



G2298	G2202	G	A1919	C1834	U	A1638	C1531	G1401	A	G	A1164	U	G954
G2303	G2203	C	A1920	U1835	U	U1639	A1532	U1402	A	C	G1165	G	C955
G2304	G2204	U	C1921	U1836	G	A1640	G1536	U1412	U	A	A1166	G	G956
A2208	G2209	C	A1929	G1837	A	C1644	A1537	G1413	G1320	G	A1174	G	A957
G2210	G2210	C	A1933	A1838	C	G1645	C1542	G1421	A1322	A	U1175	A	G966
A2214	G2215	A	G1934	A1839	A	A1647	G1646	U1422	C1323	C	G1176	A	U967
A2312	G2216	C	U1936	A1748	C	A1648	A1549	A1424	G1326	G	C1177	G	A968
U2217	G2217	C	A1940	U1751	U	C1649	A1550	A1433	C1327	U	A1184	A	G969
G2218	G2218	C	A1941	G1752	C	C1650	A1551	A1441	G1332	G	A1185	A	U971
A2219	G2219	A	A1944	A1753	U	A1651	G1559	U1433	A1333	C	C1186	U	G972
G2224	G2224	G	G1944	G1852	A	A1653	C1565	G1438	A1333	C	G1188	U	U975
U2225	G2225	C	A1948	A1755	U	A1654	A1571	A1441	A1334	A	A1189	C	C976
U2228	G2228	U	G1952	U1757	G	A1660	A1571	U1445	U1335	U	A1190	C	C977
U2229	G2229	A	G1953	G1758	G	A1661	G1581	G1446	U1336	G	C1187	U	U978
A2230	G2230	C	G1954	U1761	U	A1664	U	U1459	G1338	A	G1188	U	G979
A2231	G2231	C	G1960	U1762	C	A1665	A1588	A1452	A1339	A	A1189	C	A984
A2232	G2232	U	G1961	A1763	U	C1666	U1589	A1453	U1340	G	G1207	A	G985
G2233	G2233	C	C1962	U1764	U	G1670	G1590	U1460	A1453	U	G1208	A	C989
G2234	G2234	U	A1963	C1765	C	G1673	U	U1459	G1344	C	A1211	U	G990
G2235	G2235	U	G1969	G1767	G	A1674	U	G1463	A1348	G	U1212	G	C991
G2236	G2236	C	G1975	U1777	U	C1674	G1597	G1468	A1349	A	G1217	A	U992
G2244	G2244	C	U1976	U1777	U	A1677	C1600	G1469	A1357	U	C1218	U	C993
G2245	G2245	C	C1981	G1780	C	A1678	G1601	U1470	C1359	C	U1219	U	A994
U2246	G2246	U	G1982	U1781	C	A1679	G1602	C1471	C1360	C	A1221	A	G995
G2248	G2248	C	U1987	G1786	U	G1693	U1604	G1484	A1361	C	C1223	A	A997
G2257	G2257	C	G1990	U1786	U	U1694	U1605	G1487	U1362	U	A1224	U	G1000
U2264	G2264	C	G1995	U1790	C	C1695	U1606	A1488	C1367	A	C1227	U	A1006
G2265	G2265	C	U1999	G1791	U	G1696	U1607	U1489	A1368	G	A1228	U	A1010
U2272	G2272	C	A2000	A1792	C	C1697	C1608	U1490	C1370	A	A1231	U	G1011
G2273	G2273	U	G2001	U1796	C	G1698	G1609	U1491	G1371	U	G1232	U	A1012
U2274	G2274	C	G2002	C1799	U	G1699	U	U1492	U1379	U	A1233	U	U1013
U2277	G2277	A	G2003	G1800	C	G1702	C1613	U1504	A1390	G	A1234	U	C1014
U2280	G2280	C	U2005	U	U	G1703	U	A1515	G	U	G1238	U	A1015
U2281	G2281	C	G1901	C1807	A	C1704	C	A1516	C	U	U1239	U	G1016
G2282	G2282	U	C1904	U1723	U	A1710	A1622	G1500	U	A	G1240	U	U1017
G2283	G2283	C	A1905	U1724	C	A1711	A1623	A1501	U	U	U1241	U	U1018
G2284	G2284	C	G1906	U1728	C	G1712	A1624	C1502	U	U	U1242	C	G1023
G2285	G2285	C	G1907	U1729	U	A1713	G1625	U1504	A1397	A	A1243	A	A1024
A2286	G2286	C	A1913	U1730	A	U1723	A1628	A1515	G1368	C	G1244	U	G1025
G2290	G2290	C	A1916	U1731	U	U1724	A1629	G1517	A1389	U	C1247	U	G1026
U2291	G2291	C	G1918	U1738	C	C1738	U1636	U1528	G1391	C	A	A	G1033
G2292	G2292	U	U1917	G1819	C	A1739	U1637	U1528	A1391	C	U	U	A1034
G2294	G2294	G	G1918	G1821	U	A1739	U1637	U1528	A1391	C	U	U	A1035
A2303	G2303	C	U1835	U1836	A	C1644	A1537	G1413	A1322	A	U1175	A	G966
G2304	G2304	C	A1838	A1839	C	G1645	C1542	G1421	C1323	C	G1176	A	U967
G2309	G2309	C	A1933	A1936	C	A1647	A1549	A1424	G1326	G	C1177	G	A968
A2310	G2310	C	G1934	A1748	C	A1648	A1550	A1433	C1327	U	A1184	A	G969
A2312	G2312	C	U1936	U1751	U	C1649	A1551	U1433	A1332	G	A1185	A	U971
U2313	G2313	C	A1940	G1752	C	C1650	A1559	G1438	A1333	C	C1186	U	G972
A2320	G2320	A	A1941	A1753	U	A1651	G1559	U1445	A1334	A	G1188	U	U975
G2323	G2323	G	G1944	G1852	A	A1653	C1565	A1441	A1335	U	A1189	C	C976
G2324	G2324	C	A1948	U1757	U	A1654	A1571	U1445	U1336	G	A1190	C	C977
G2325	G2325	U	G1952	G1758	G	A1660	A1571	G1446	U1336	G	C1187	U	U978
G2328	G2328	U	G1953	U1761	U	A1661	G1581	U1459	G1338	A	G1188	U	G979
U2329	G2329	A	G1954	U1762	C	A1664	U	A1452	A1339	A	A1189	C	A984
A2330	G2330	C	G1960	A1763	U	A1665	A1588	A1453	U1340	G	G1207	A	G985
A2331	G2331	U	G1961	U1764	U	C1666	U1589	U1460	A1453	U	G1208	A	C989
A2332	G2332	C	C1962	C1765	C	G1670	G1590	U1459	G1344	C	A1211	U	G990
G2333	G2333	U	A1963	G1767	G	A1673	U	G1463	A1348	G	U1212	G	C991
G2334	G2334	U	G1969	U1777	U	C1674	G1597	G1468	A1349	A	G1217	A	U992
G2335	G2335	U	U1975	U1777	U	A1677	C1600	U1470	A1357	U	C1218	U	C993
G2336	G2336	C	C1981	G1780	C	A1678	G1601	C1471	C1359	C	U1219	U	A994
G	G	C	G1982	U1781	C	A1679	G1602	G1484	C1360	C	A1221	A	G995
G	G	C	U1987	G1786	U	G1693	U1604	G1487	A1361	C	C1223	A	A997
G	G	C	G1990	U1786	U	U1694	U1605	U1489	U1362	U	A1224	U	G1000
G	G	C	G1995	U1790	C	C1695	U1606	A1488	C1367	A	C1227	U	A1006
G	G	C	U1999	G1791	U	G1696	U1607	U1489	A1368	G	A1228	U	A1010
G	G	C	A2000	A1792	C	C1697	C1608	U1490	C1370	A	A1231	U	G1011
G	G	C	G2001	U1796	C	G1698	G1609	U1491	G1371	U	G1232	U	A1012
G	G	C	G2002	C1799	U	G1699	U	U1492	U1379	U	A1233	U	U1013
G	G	C	G2003	G1800	C	G1702	C1613	U1504	A1390	G	A1234	U	C1014
G	G	C	G2004	U	U	A1703	U	A1515	G	U	G1238	U	A1015
G	G	C	U2005	U	U	C1704	C	A1516	C	U	U1239	U	G1016
G	G	C	U	C	C	A1710	A1622	G1500	U	A	G1240	U	U1017
G	G	C	G	C	C	A1711	A1623	A1501	U	U	U1241	U	U1018
G	G	C	G	C	C	G1712	A1624	C1502	U	U	U1242	C	G1023
G	G	C	G	C	C	U1723	A1628	U1504	A1397	A	A1243	A	A1024
G	G	C	G	C	C	U1724	A1629	A1515	G1368	C	G1244	U	G1025
G	G	C	G	C	C	U1728	U1630	A1516	A1389	U	C1247	U	G1026
G	G	C	G	C	C	U1729	U1631	G1517	A1391	C	A	A	G1033
G	G	C	G	C	C	A1731	C1632	G1521	A1391	C	U	U	A1034
G	G	C	G	C	C	C1738	U1636	A1524	A1396	U	A	A	G1042
G	G	C	G	C	C	A1739	U1637	U1528	A1397	U	G	G	U1046
G	G	C	G	C	C	A1739	U1637	U1528	C1398	C	A	A	C
G	G	C	G	C	C	A1739	U1637	U1528	G1399	C	A	A	U



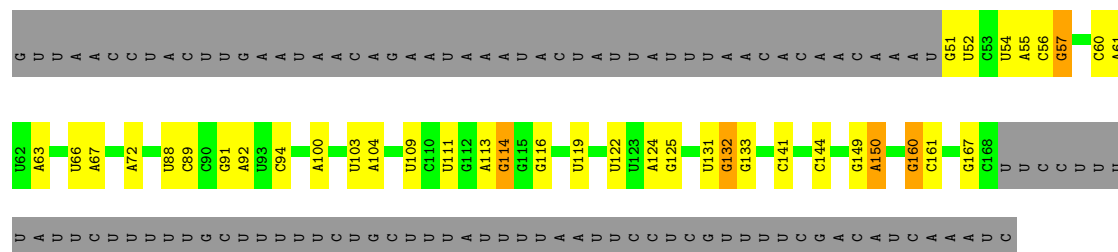
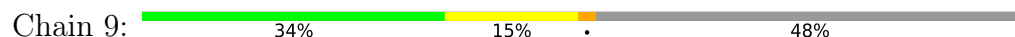
- Molecule 3: Protein mak16



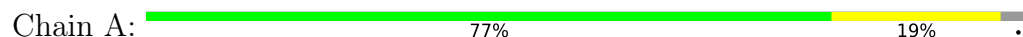
- Molecule 4: 60S ribosomal protein L39



- Molecule 5: RNA (118-MER)



- Molecule 6: 60S ribosomal protein L2-A





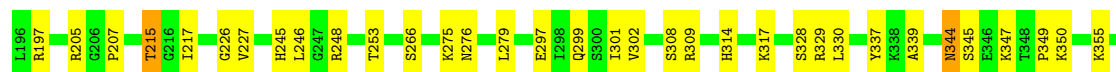
• Molecule 7: 60S ribosomal protein L3-A

Chain B: 73% 24% •



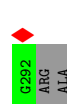
• Molecule 8: 60S ribosomal protein L4-B

Chain C: 81% 17% ••



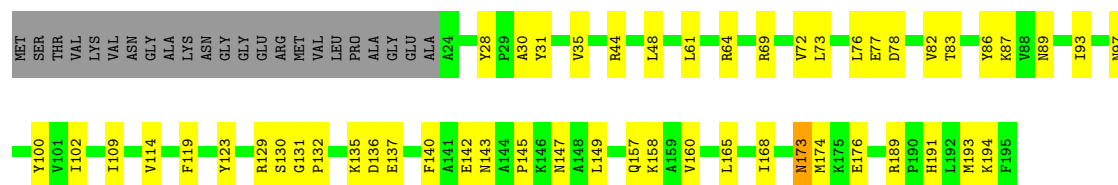
• Molecule 9: 60S ribosomal protein L5-A

Chain D: 78% 20% •



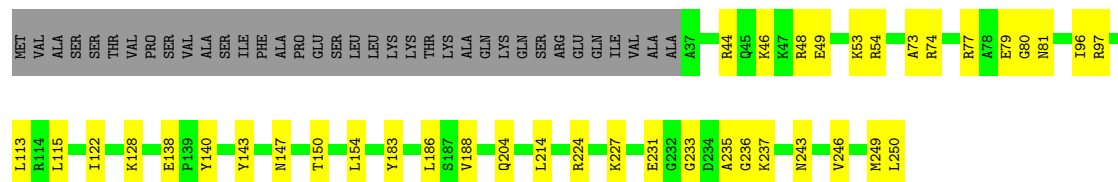
• Molecule 10: 60S ribosomal protein L6

Chain E: 62% 26% 12% •



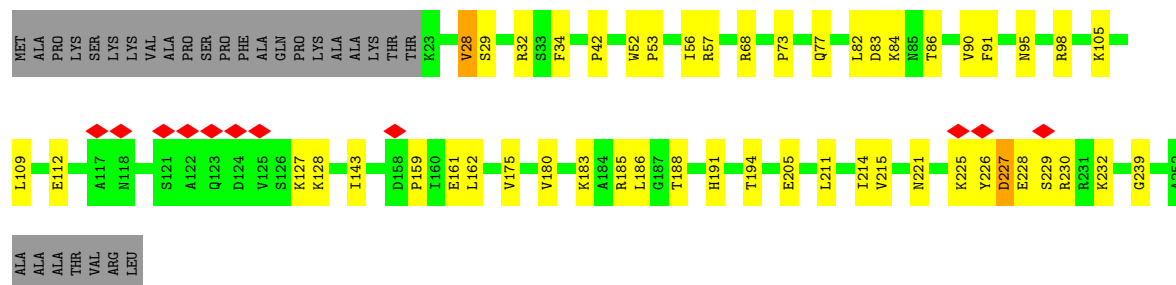
- Molecule 11: 60S ribosomal protein L7-B

Chain F:



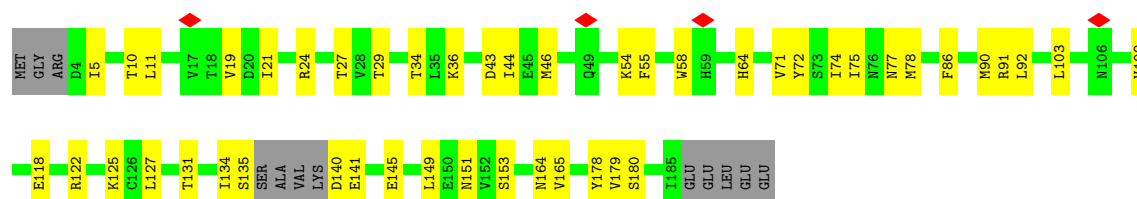
- Molecule 12: 60S ribosomal protein L8

Chain G:



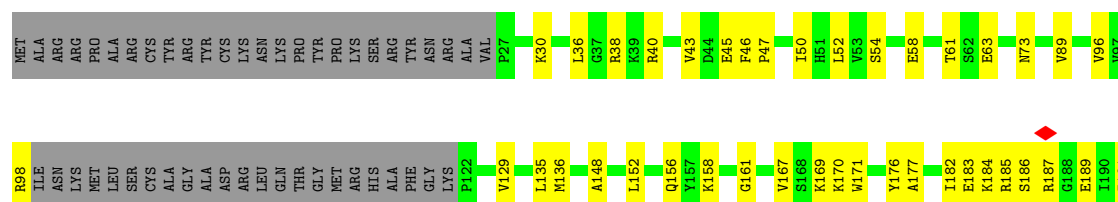
- Molecule 13: 60S ribosomal protein L9-A

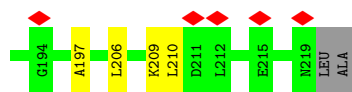
Chain H:



- Molecule 14: 60S ribosomal protein L10-A

Chain I:





- Molecule 15: 60S ribosomal protein L11-A

Chain J: 67% 22% 10%



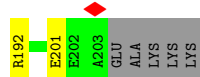
- Molecule 16: 60S ribosomal protein L43-A

Chain K: 80% 16%



- Molecule 17: 60S ribosomal protein L13

Chain L: 81% 15%



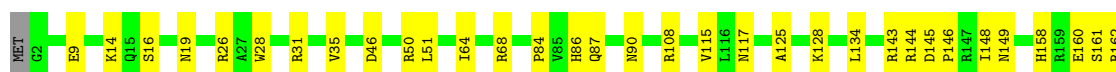
- Molecule 18: 60S ribosomal protein L14

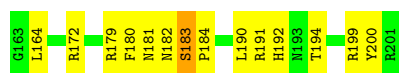
Chain M: 70% 22% 7%



- Molecule 19: 60S ribosomal protein L15-A

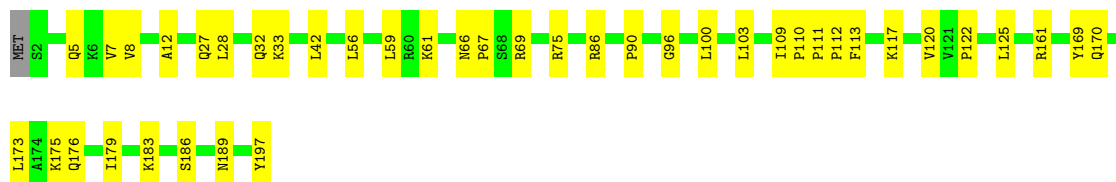
Chain N: 76% 23%





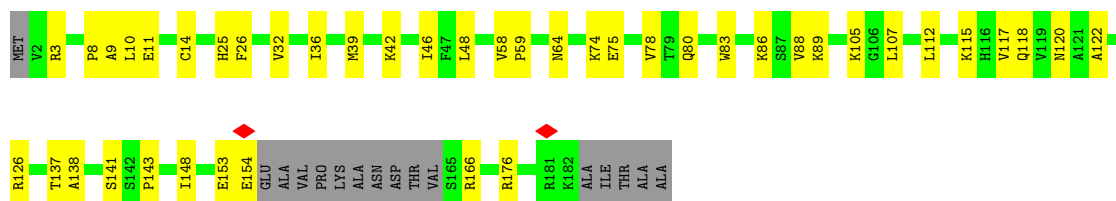
- Molecule 20: 60S ribosomal protein L16-B

Chain O: 79% 21%



- Molecule 21: 60S ribosomal protein L17-A

Chain P: 68% 23% 9%



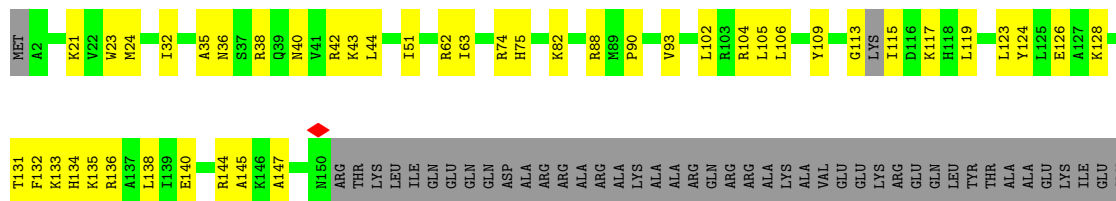
- Molecule 22: 60S ribosomal protein L18-A

Chain Q: 83% 15%



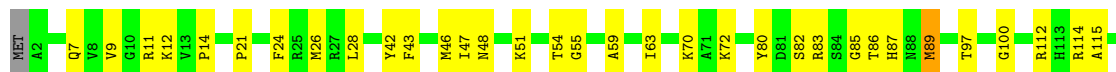
- Molecule 23: 60S ribosomal protein L19-A

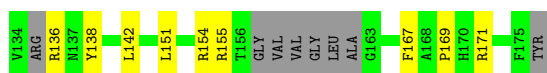
Chain R: 54% 23% 23%



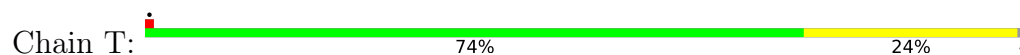
- Molecule 24: 60S ribosomal protein L20-A

Chain S: 71% 23% 5%

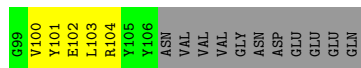
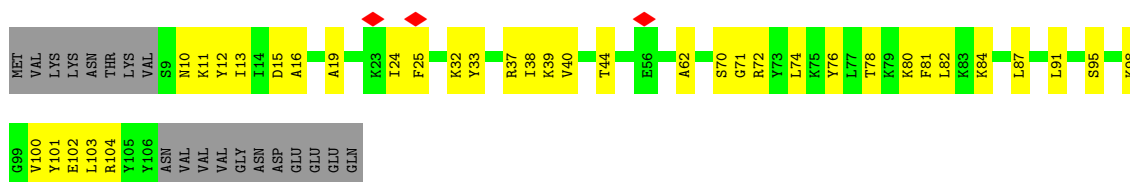




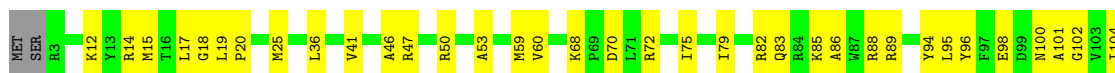
- Molecule 25: 60S ribosomal protein L21-A



- Molecule 26: 60S ribosomal protein L22



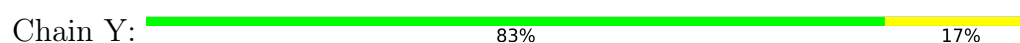
- Molecule 27: 60S ribosomal protein L23-A

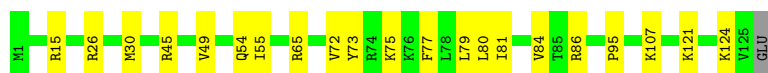


- Molecule 28: 60S ribosomal protein L25-A



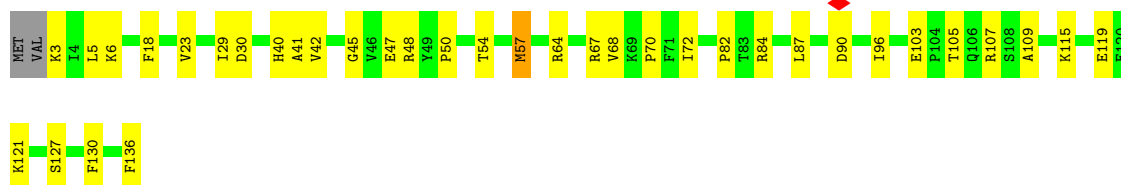
- Molecule 29: 60S ribosomal protein L26





- Molecule 30: 60S ribosomal protein L27-A

Chain Z: 72% 26% ..



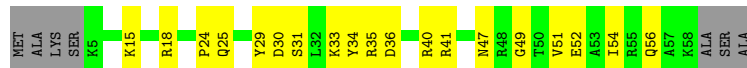
- Molecule 31: 60S ribosomal protein L28-A

Chain a: 78% 22% .



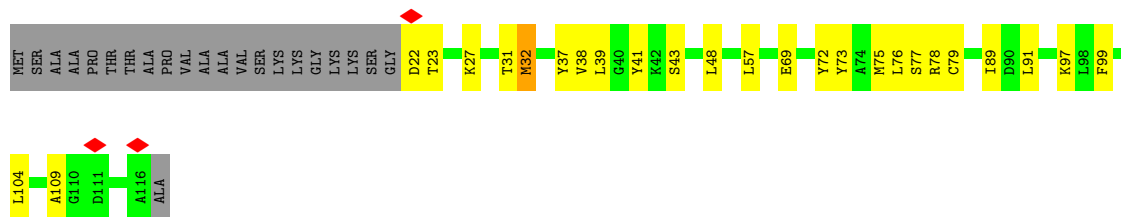
- Molecule 32: 60S ribosomal protein L29

Chain b: 57% 31% 11%



- Molecule 33: 60S ribosomal protein L30-2

Chain c: 59% 21% 19%



- Molecule 34: 60S ribosomal protein L31

Chain d: 72% 19% 10%

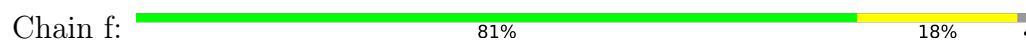


- Molecule 35: 60S ribosomal protein L32-A

Chain e: 72% 20% 8%



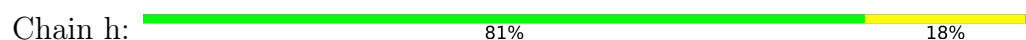
- Molecule 36: 60S ribosomal protein L33-B



- Molecule 37: 60S ribosomal protein L34-A



- Molecule 38: 60S ribosomal protein L35



- Molecule 39: 60S ribosomal protein L36-B



- Molecule 40: 60S ribosomal protein L37-B

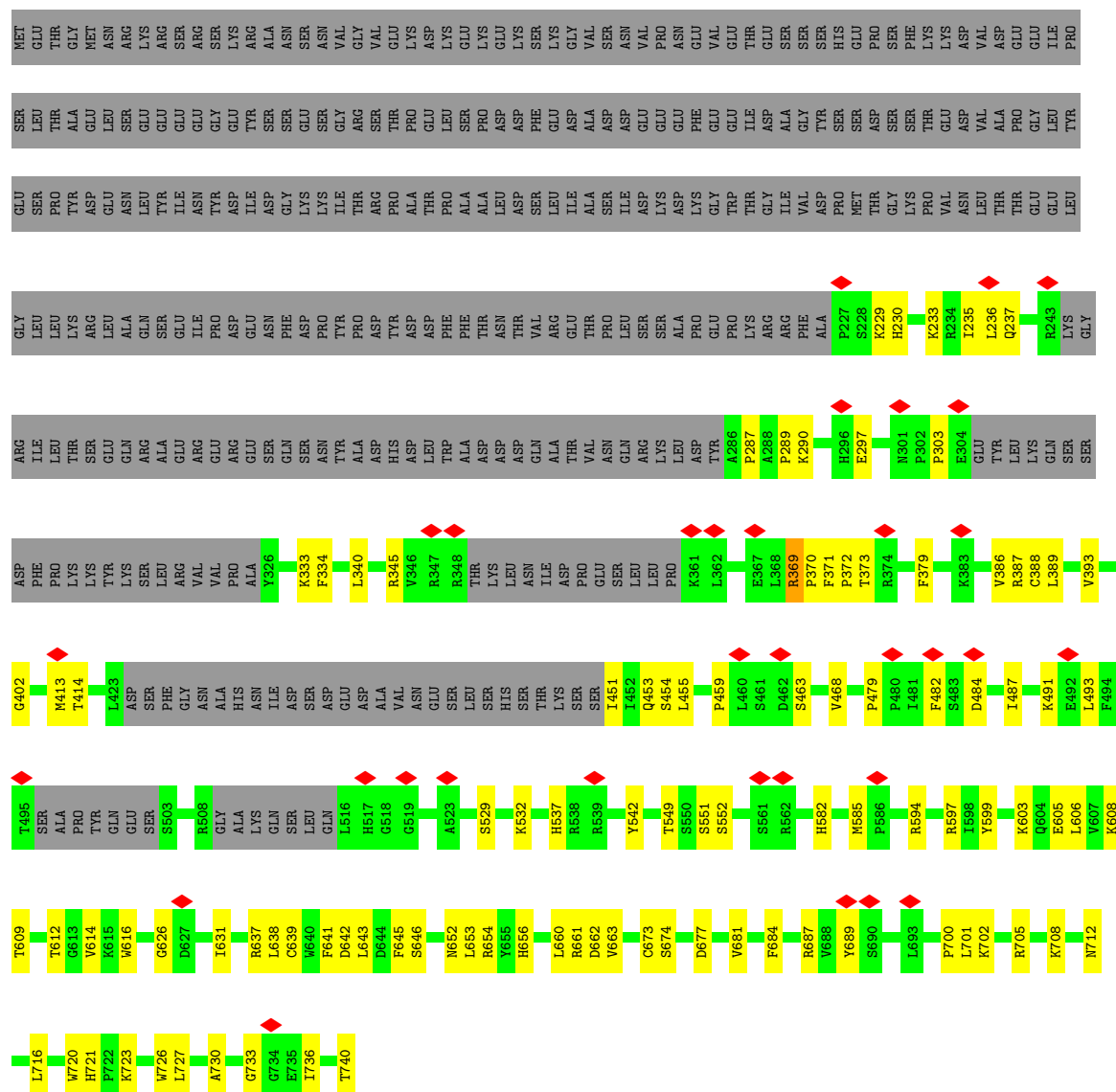


- Molecule 41: 60S ribosomal protein L38-1

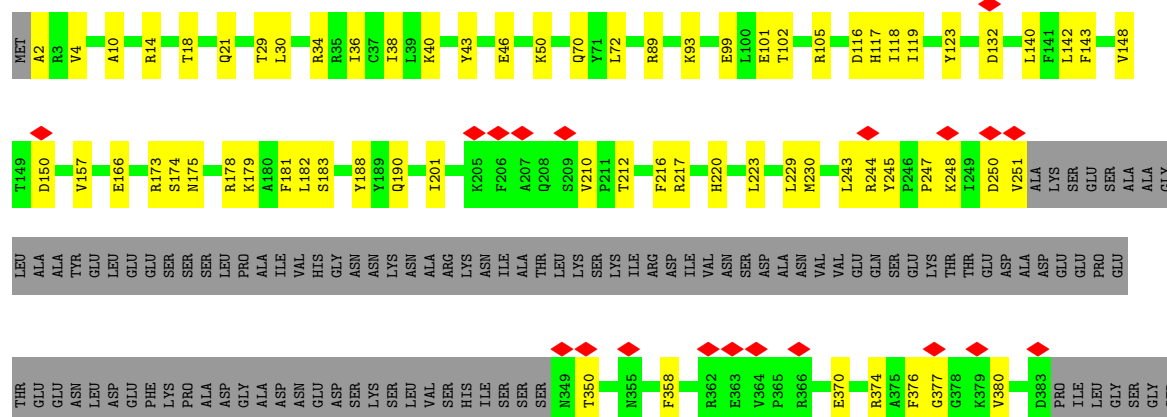


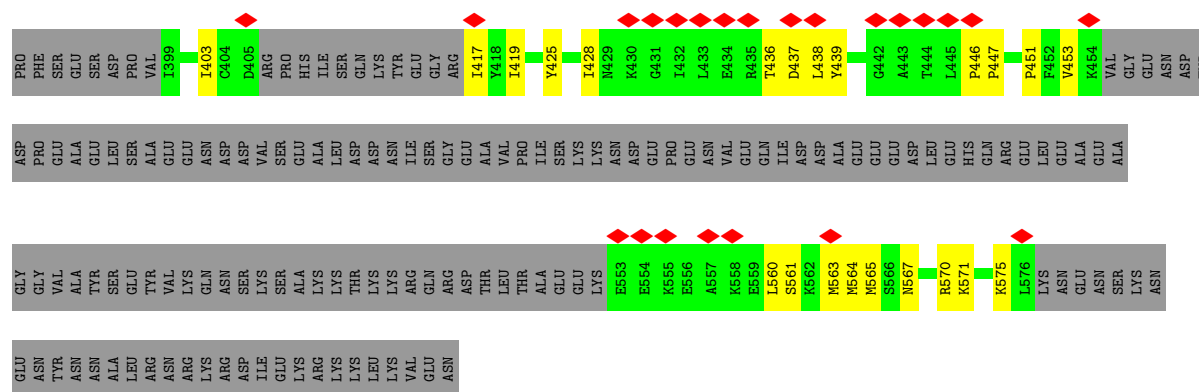
- Molecule 42: Ribosome biogenesis protein erb1





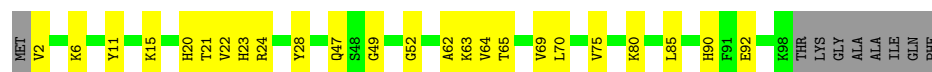
• Molecule 43: Pescadillo homolog





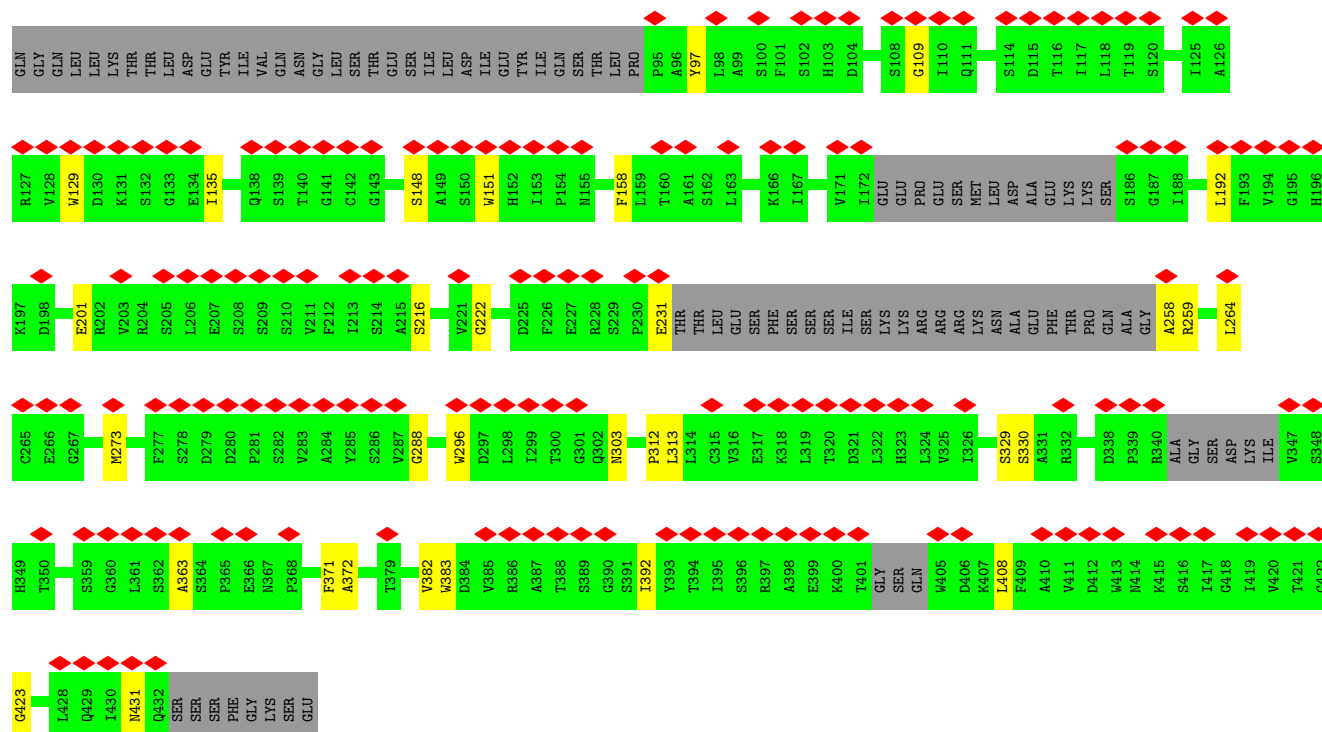
- Molecule 44: 60S ribosomal protein L42

Chain o: 69% 23% 8%

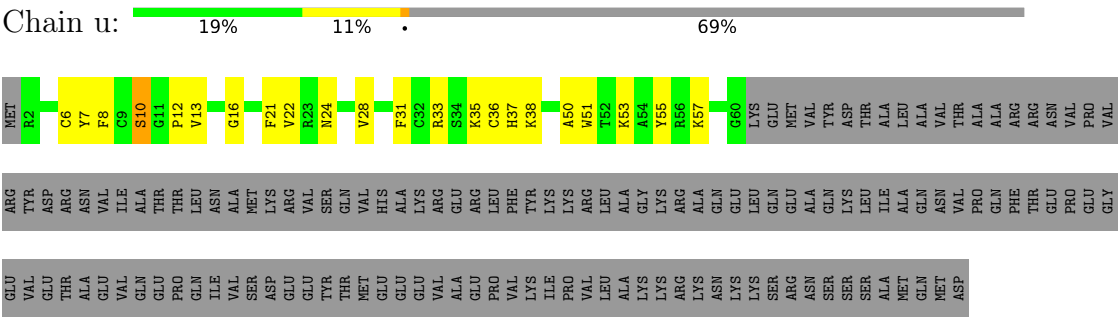


- Molecule 45: Ribosome biogenesis protein ytm1

Chain p: 36% 59% 7% 34%



- Molecule 46: Ribosome biogenesis protein rlp24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.870	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.11	0/68700	0.25	2/107035 (0.0%)
2	2	0.13	0/3589	0.25	0/5586
3	3	0.25	0/1028	0.57	0/1384
4	8	0.13	0/448	0.32	0/597
5	9	0.09	0/2816	0.18	0/4388
6	A	0.13	0/1885	0.32	0/2542
7	B	0.12	0/3069	0.30	0/4130
8	C	0.14	0/2848	0.32	0/3842
9	D	0.10	0/2354	0.26	0/3166
10	E	0.12	0/1366	0.34	0/1843
11	F	0.11	0/1781	0.29	0/2389
12	G	0.13	0/1846	0.35	0/2485
13	H	0.11	0/1433	0.33	0/1931
14	I	0.11	0/1398	0.33	0/1873
15	J	0.14	0/1296	0.38	0/1732
16	K	0.11	0/704	0.30	0/941
17	L	0.14	0/1644	0.32	0/2215
18	M	0.10	0/1024	0.28	0/1375
19	N	0.14	0/1717	0.33	0/2304
20	O	0.13	0/1588	0.32	0/2128
21	P	0.13	0/1381	0.32	0/1849
22	Q	0.12	0/1510	0.34	0/2017
23	R	0.13	0/1238	0.33	0/1647
24	S	0.12	0/1422	0.31	0/1909
25	T	0.12	0/1309	0.29	0/1761
26	U	0.14	0/805	0.40	0/1080
27	V	0.13	0/1042	0.32	0/1402
28	X	0.14	0/978	0.32	0/1314
29	Y	0.12	0/1008	0.33	0/1341
30	Z	0.14	0/1095	0.32	0/1467
31	a	0.13	0/1198	0.35	0/1608
32	b	0.15	0/471	0.37	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.13	0/723	0.32	0/973
34	d	0.11	0/864	0.27	0/1161
35	e	0.10	0/953	0.26	0/1271
36	f	0.11	0/859	0.27	0/1152
37	g	0.13	0/873	0.32	0/1170
38	h	0.11	0/1008	0.30	0/1340
39	i	0.11	0/774	0.29	0/1028
40	j	0.13	0/671	0.35	0/888
41	k	0.17	0/566	0.43	0/757
42	m	0.13	0/3209	0.38	1/4357 (0.0%)
43	n	0.11	0/2971	0.30	0/3997
44	o	0.10	0/803	0.34	0/1064
45	p	0.07	0/1426	0.21	0/1977
46	u	0.17	0/509	0.38	0/678
All	All	0.12	0/132200	0.28	3/193717 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	m	370	PRO	N-CA-C	-12.72	101.45	114.68
1	1	1388	G	C2'-C3'-O3'	-5.68	105.17	113.70
1	1	2657	A	C4'-C3'-O3'	5.55	117.73	109.40

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	1	61386	0	30879	602	0
2	2	3211	0	1623	26	0
3	3	1006	0	1007	66	0
4	8	437	0	463	5	0
5	9	2519	0	1273	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1847	0	1891	50	0
7	B	3003	0	3086	73	0
8	C	2795	0	2918	53	0
9	D	2305	0	2266	53	0
10	E	1338	0	1418	41	0
11	F	1745	0	1818	27	0
12	G	1817	0	1937	29	0
13	H	1415	0	1472	33	0
14	I	1372	0	1397	35	0
15	J	1276	0	1316	28	0
16	K	695	0	733	14	0
17	L	1612	0	1655	27	0
18	M	1007	0	1072	26	0
19	N	1676	0	1712	38	0
20	O	1557	0	1652	30	0
21	P	1357	0	1400	32	0
22	Q	1486	0	1588	22	0
23	R	1220	0	1300	36	0
24	S	1388	0	1442	37	0
25	T	1282	0	1308	33	0
26	U	791	0	825	29	0
27	V	1026	0	1076	31	0
28	X	962	0	1030	20	0
29	Y	998	0	1090	18	0
30	Z	1072	0	1145	26	0
31	a	1169	0	1215	28	0
32	b	463	0	471	17	0
33	c	714	0	753	17	0
34	d	849	0	885	16	0
35	e	939	0	1000	23	0
36	f	839	0	866	13	0
37	g	861	0	930	22	0
38	h	999	0	1092	18	0
39	i	767	0	851	19	0
40	j	657	0	668	14	0
41	k	560	0	608	15	0
42	m	3127	0	3104	81	0
43	n	2903	0	2972	64	0
44	o	789	0	853	17	0
45	p	1431	0	633	16	0
46	u	493	0	497	19	0
47	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	123162	0	91190	1577	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 8.

The worst 5 of 1577 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)
14:I:183:GLU:HG3	14:I:187:ARG:HH21	1.25	0.99
17:L:47:ALA:HB1	17:L:48:PRO:HD2	1.46	0.97
1:1:188:C:H41	1:1:244:G:H21	1.16	0.93
3:3:90:LEU:HD21	10:E:28:TYR:HE1	1.32	0.93
1:1:3369:A:H5''	1:1:3370:U:H3'	1.56	0.88

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	
3	3	117/302 (39%)	102 (87%)	13 (11%)	2 (2%)	7	25
4	8	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
6	A	242/253 (96%)	235 (97%)	7 (3%)	0	100	100
7	B	375/388 (97%)	365 (97%)	10 (3%)	0	100	100
8	C	357/363 (98%)	336 (94%)	20 (6%)	1 (0%)	36	66
9	D	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
10	E	170/195 (87%)	160 (94%)	9 (5%)	1 (1%)	21	51
11	F	212/250 (85%)	209 (99%)	3 (1%)	0	100	100
12	G	229/259 (88%)	219 (96%)	7 (3%)	3 (1%)	9	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	H	174/190 (92%)	168 (97%)	6 (3%)	0	100	100
14	I	166/221 (75%)	162 (98%)	4 (2%)	0	100	100
15	J	153/174 (88%)	151 (99%)	2 (1%)	0	100	100
16	K	88/94 (94%)	85 (97%)	3 (3%)	0	100	100
17	L	200/208 (96%)	194 (97%)	4 (2%)	2 (1%)	12	38
18	M	123/134 (92%)	118 (96%)	4 (3%)	1 (1%)	16	44
19	N	198/201 (98%)	184 (93%)	12 (6%)	2 (1%)	12	38
20	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
21	P	167/187 (89%)	161 (96%)	5 (3%)	1 (1%)	21	51
22	Q	184/187 (98%)	173 (94%)	8 (4%)	3 (2%)	7	27
23	R	144/193 (75%)	139 (96%)	4 (3%)	1 (1%)	18	47
24	S	161/176 (92%)	157 (98%)	4 (2%)	0	100	100
25	T	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
26	U	96/117 (82%)	91 (95%)	5 (5%)	0	100	100
27	V	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
28	X	118/141 (84%)	116 (98%)	2 (2%)	0	100	100
29	Y	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
30	Z	132/136 (97%)	123 (93%)	8 (6%)	1 (1%)	16	44
31	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
32	b	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
33	c	93/117 (80%)	91 (98%)	2 (2%)	0	100	100
34	d	100/113 (88%)	95 (95%)	5 (5%)	0	100	100
35	e	115/127 (91%)	114 (99%)	1 (1%)	0	100	100
36	f	104/108 (96%)	97 (93%)	7 (7%)	0	100	100
37	g	104/112 (93%)	99 (95%)	5 (5%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	94/99 (95%)	88 (94%)	6 (6%)	0	100	100
40	j	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
41	k	67/74 (90%)	67 (100%)	0	0	100	100
42	m	384/740 (52%)	361 (94%)	21 (6%)	2 (0%)	24	55
43	n	344/607 (57%)	329 (96%)	15 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	o	95/106 (90%)	92 (97%)	3 (3%)	0	100	100
45	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
46	u	57/192 (30%)	55 (96%)	2 (4%)	0	100	100
All	All	6981/8593 (81%)	6717 (96%)	244 (4%)	20 (0%)	37	66

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	G	28	VAL
12	G	227[A]	ASP
12	G	227[B]	ASP
42	m	369	ARG
17	L	47	ALA

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	
3	3	108/271 (40%)	106 (98%)	2 (2%)	50	81
4	8	46/47 (98%)	46 (100%)	0	100	100
6	A	187/192 (97%)	186 (100%)	1 (0%)	81	93
7	B	316/326 (97%)	316 (100%)	0	100	100
8	C	296/297 (100%)	294 (99%)	2 (1%)	76	91
9	D	235/241 (98%)	234 (100%)	1 (0%)	84	94
10	E	139/155 (90%)	137 (99%)	2 (1%)	59	85
11	F	180/210 (86%)	180 (100%)	0	100	100
12	G	192/212 (91%)	192 (100%)	0	100	100
13	H	160/170 (94%)	160 (100%)	0	100	100
14	I	146/187 (78%)	146 (100%)	0	100	100
15	J	134/146 (92%)	133 (99%)	1 (1%)	76	91
16	K	71/75 (95%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	L	162/167 (97%)	162 (100%)	0	100	100
18	M	108/113 (96%)	107 (99%)	1 (1%)	70	89
19	N	175/176 (99%)	175 (100%)	0	100	100
20	O	161/162 (99%)	161 (100%)	0	100	100
21	P	138/149 (93%)	138 (100%)	0	100	100
22	Q	158/159 (99%)	156 (99%)	2 (1%)	61	86
23	R	126/162 (78%)	126 (100%)	0	100	100
24	S	148/154 (96%)	146 (99%)	2 (1%)	59	85
25	T	137/139 (99%)	137 (100%)	0	100	100
26	U	85/103 (82%)	85 (100%)	0	100	100
27	V	105/107 (98%)	105 (100%)	0	100	100
28	X	106/122 (87%)	104 (98%)	2 (2%)	50	81
29	Y	110/111 (99%)	110 (100%)	0	100	100
30	Z	113/115 (98%)	113 (100%)	0	100	100
31	a	121/122 (99%)	120 (99%)	1 (1%)	73	90
32	b	47/51 (92%)	46 (98%)	1 (2%)	47	79
33	c	77/91 (85%)	76 (99%)	1 (1%)	61	86
34	d	93/102 (91%)	92 (99%)	1 (1%)	65	87
35	e	100/107 (94%)	99 (99%)	1 (1%)	68	88
36	f	89/91 (98%)	89 (100%)	0	100	100
37	g	92/97 (95%)	91 (99%)	1 (1%)	65	87
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	82/84 (98%)	82 (100%)	0	100	100
40	j	68/71 (96%)	68 (100%)	0	100	100
41	k	63/66 (96%)	63 (100%)	0	100	100
42	m	344/659 (52%)	344 (100%)	0	100	100
43	n	312/532 (59%)	312 (100%)	0	100	100
44	o	87/93 (94%)	86 (99%)	1 (1%)	65	87
46	u	52/168 (31%)	50 (96%)	2 (4%)	29	64
All	All	5775/6909 (84%)	5750 (100%)	25 (0%)	81	94

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	X	133	ASP
32	b	54	ILE
46	u	13	VAL
31	a	120	THR
33	c	32	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
19	N	153	ASN
28	X	67	ASN
20	O	190	GLN
25	T	24	GLN
30	Z	31	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2837/3498 (81%)	600 (21%)	19 (0%)
2	2	150/165 (90%)	24 (16%)	2 (1%)
5	9	117/229 (51%)	14 (11%)	0
All	All	3104/3892 (79%)	638 (20%)	21 (0%)

5 of 638 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	26	A
1	1	28	G
1	1	30	G
1	1	40	A
1	1	43	A

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2657	A
1	1	3358	U
2	2	131	G
1	1	3441	G
1	1	3174	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

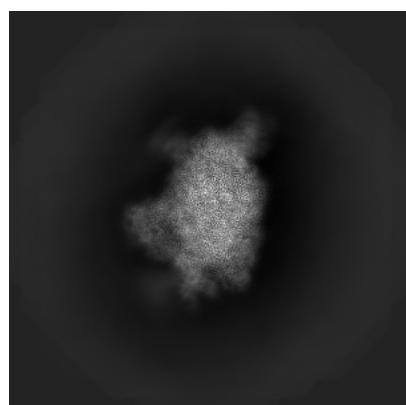
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24412. These allow visual inspection of the internal detail of the map and identification of artifacts.

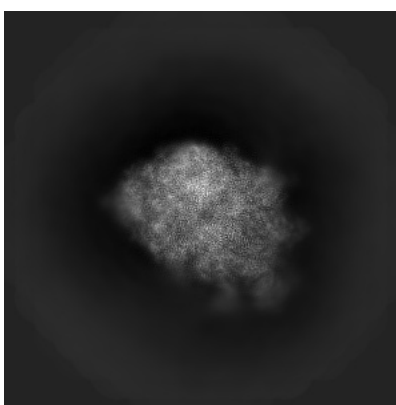
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

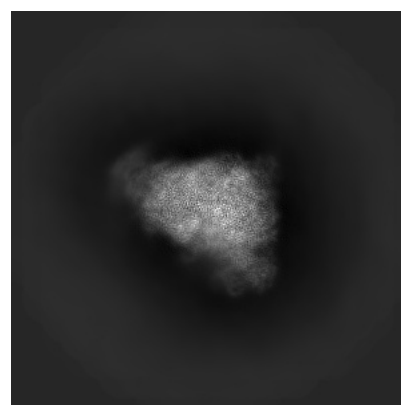
6.1.1 Primary map



X



Y



Z

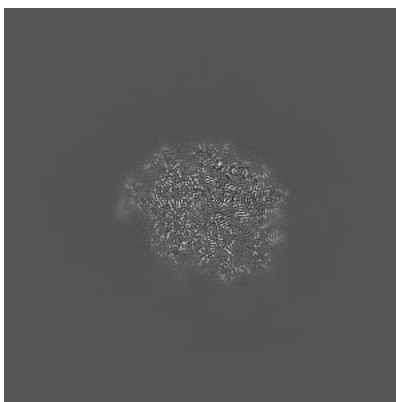
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

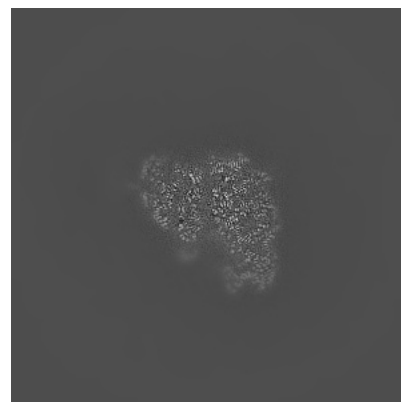
6.2.1 Primary map



X Index: 256



Y Index: 256

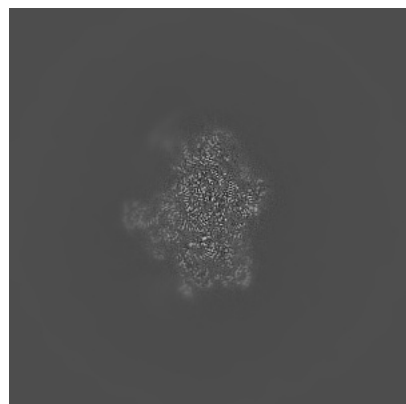


Z Index: 256

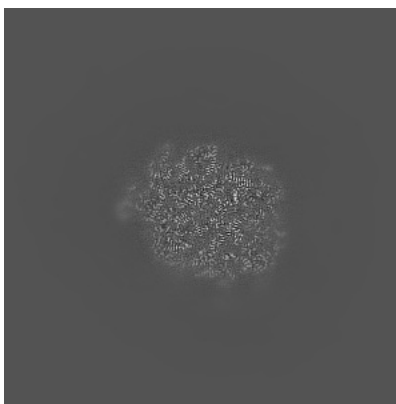
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

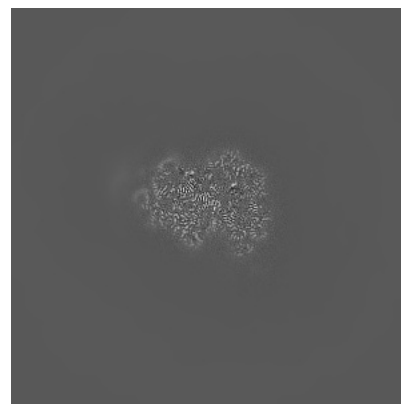
6.3.1 Primary map



X Index: 283



Y Index: 263

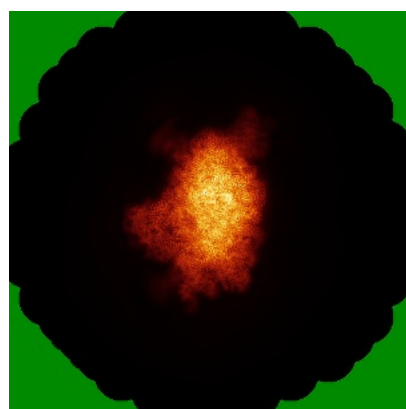


Z Index: 276

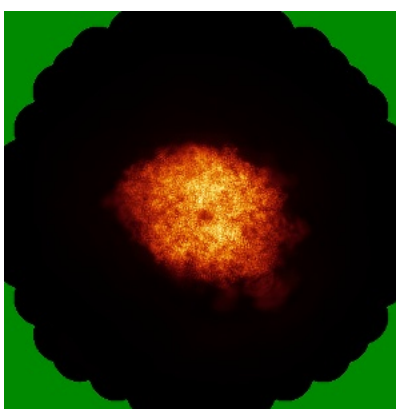
The images above show the largest variance slices of the map in three orthogonal directions.

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

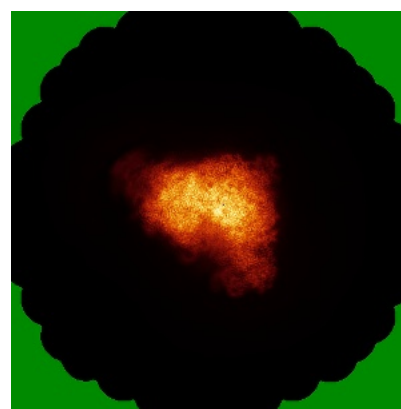
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

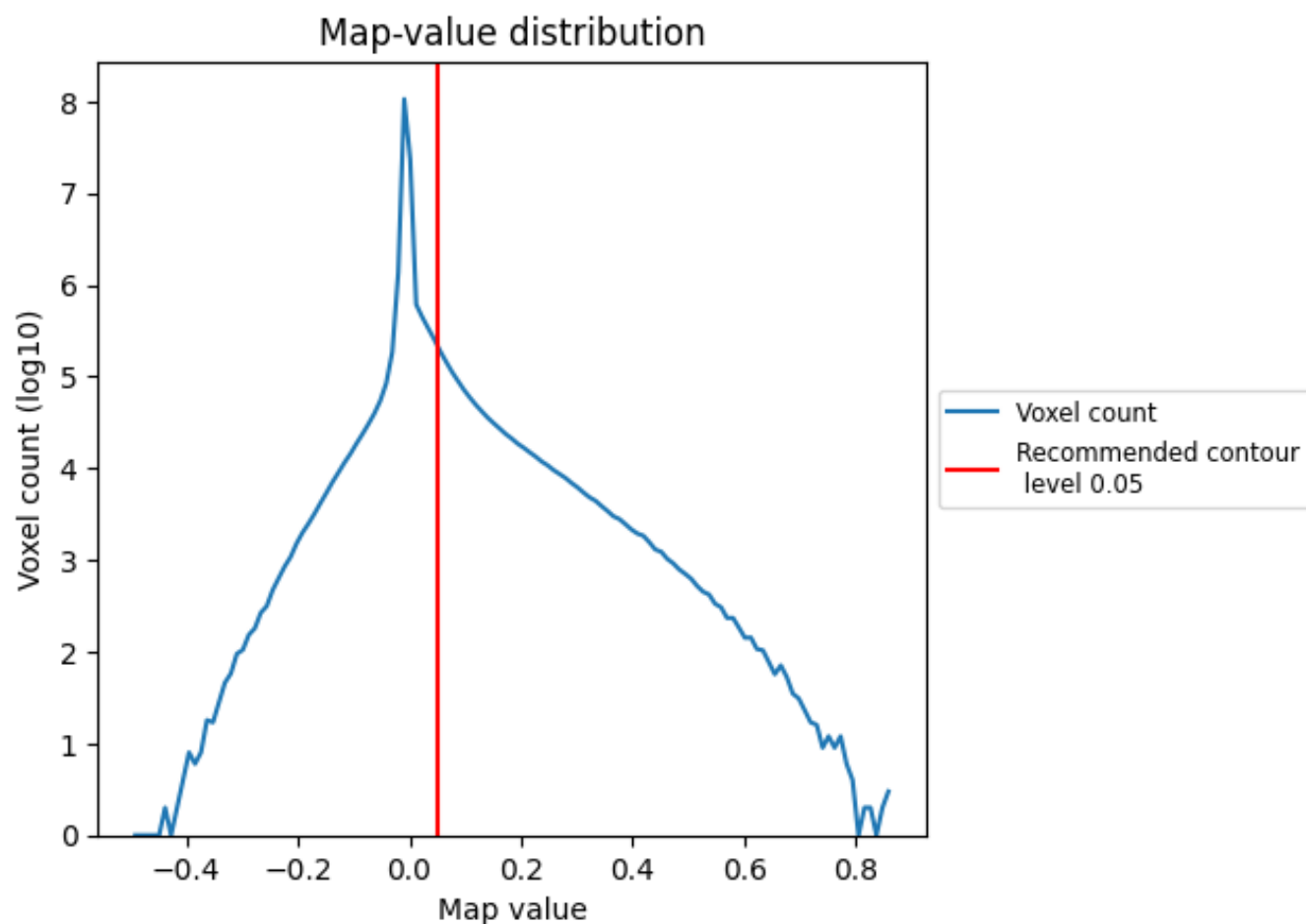
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

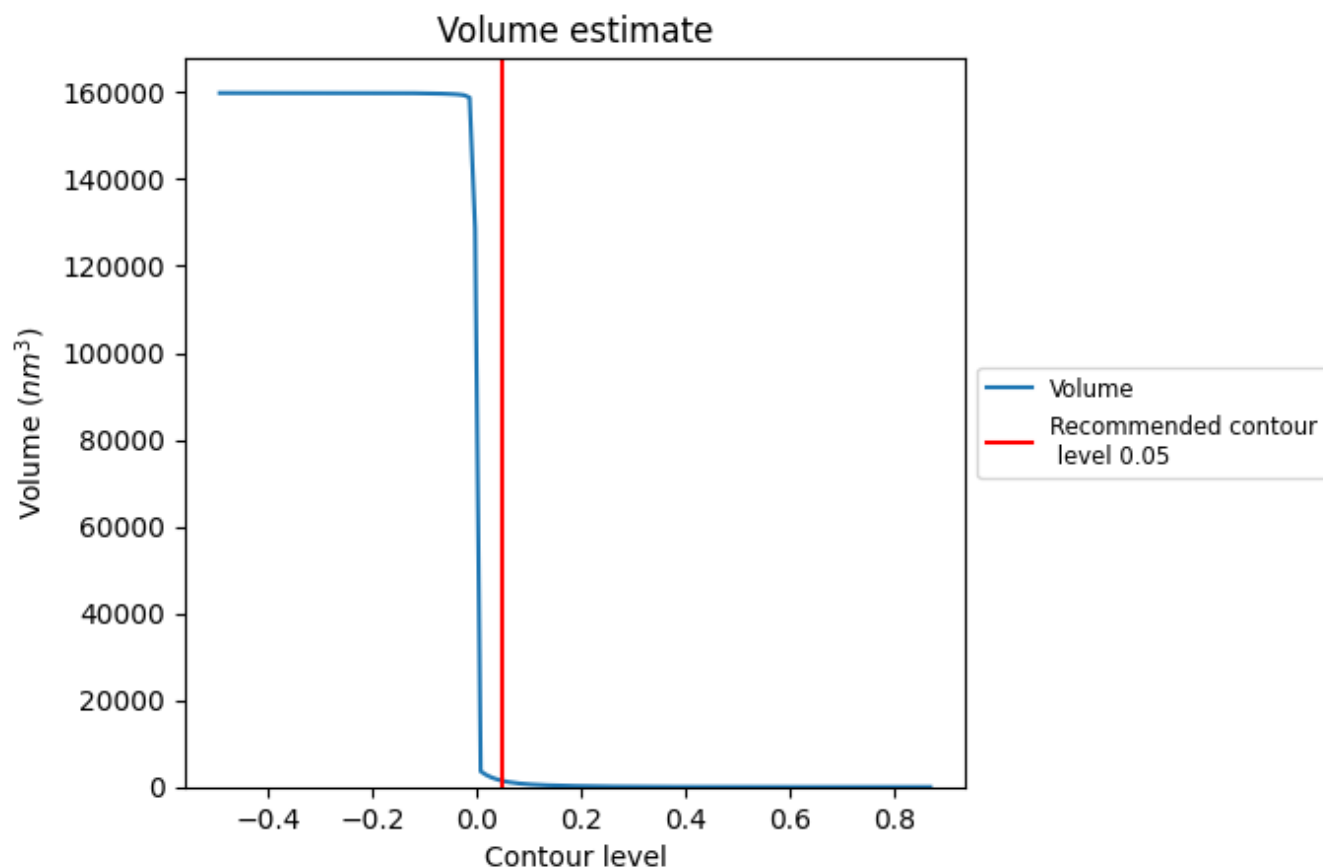
This section contains the results of statistical analysis of the map.

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.

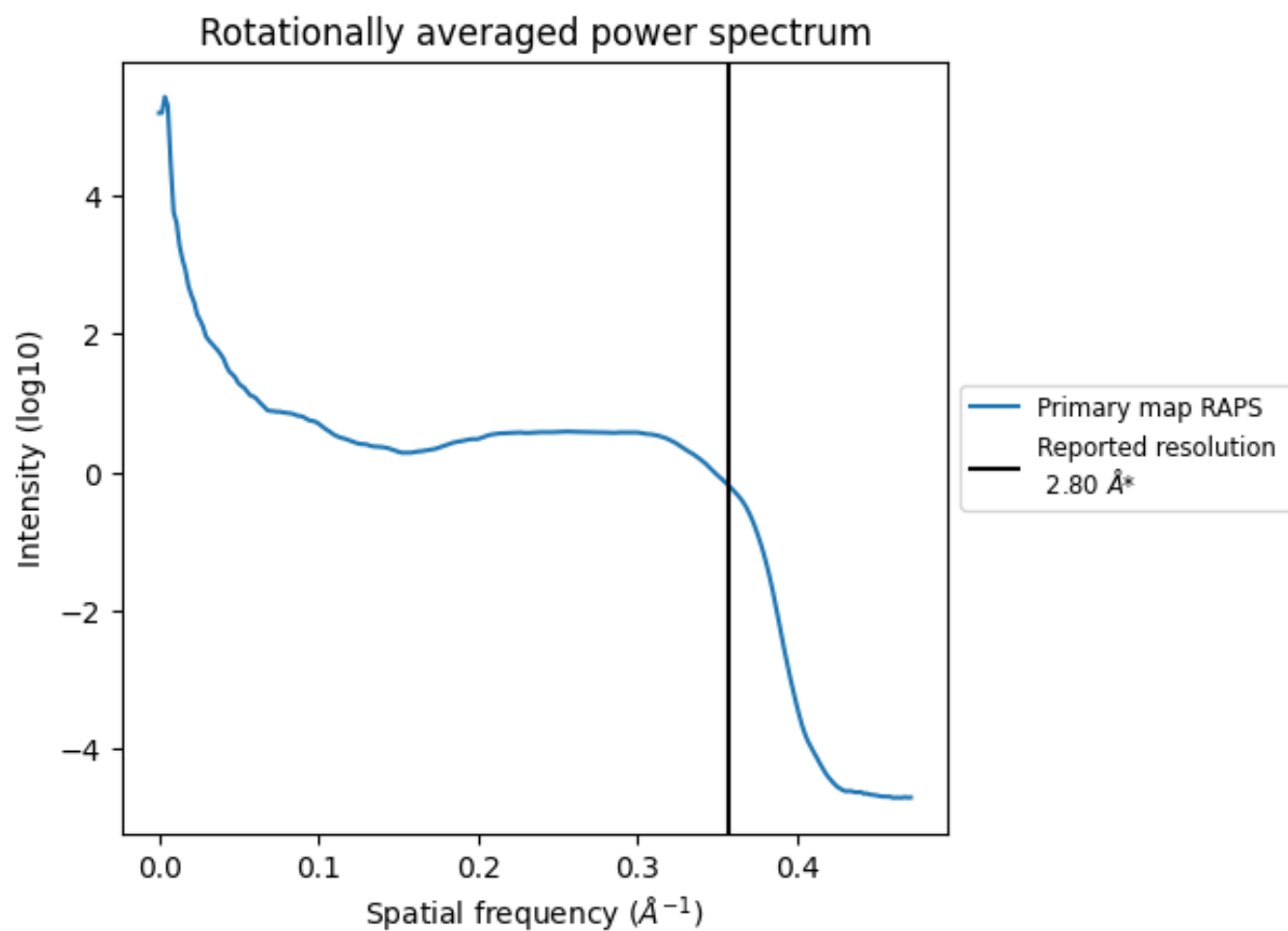
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1408 nm^3 ; this corresponds to an approximate mass of 1272 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 0.357 Å⁻¹

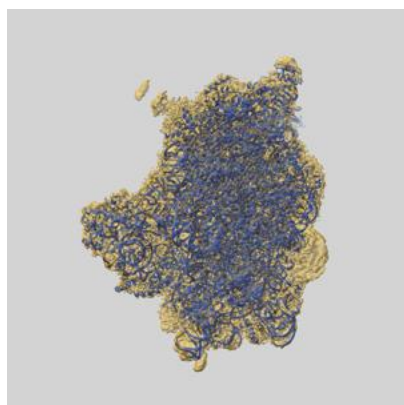
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

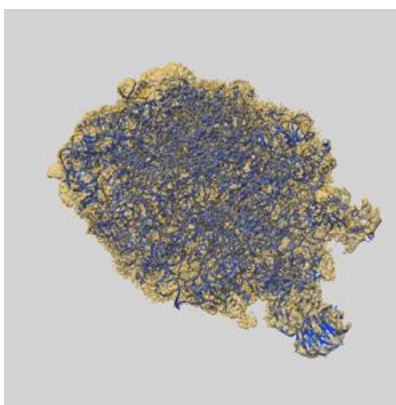
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24412 and PDB model 8EUG. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

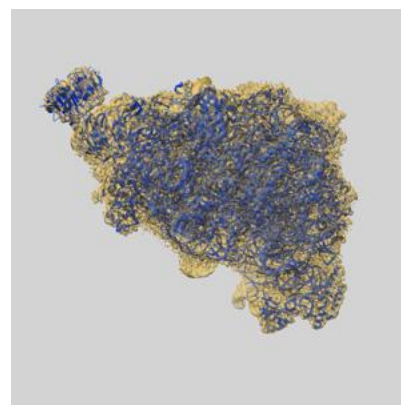
9.1 Map-model overlay [i](#)



X



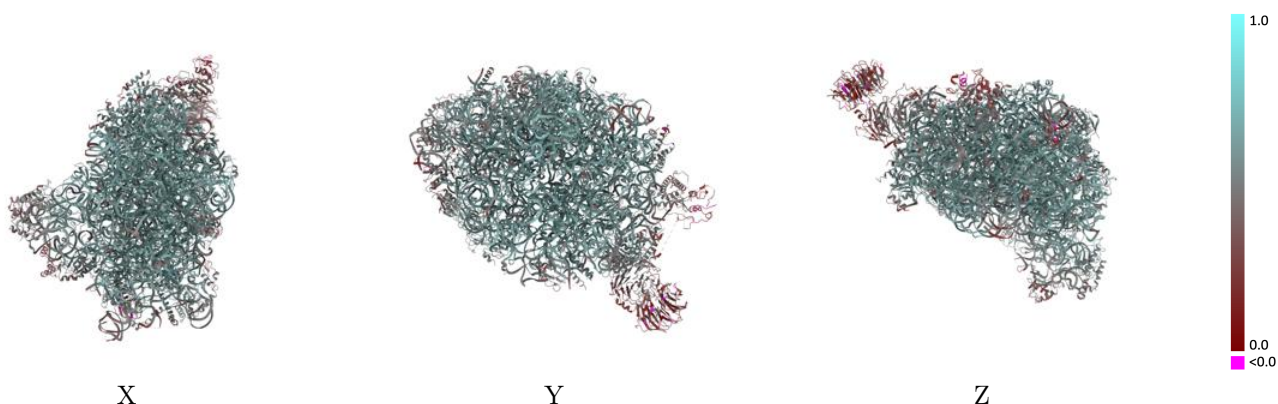
Y



Z

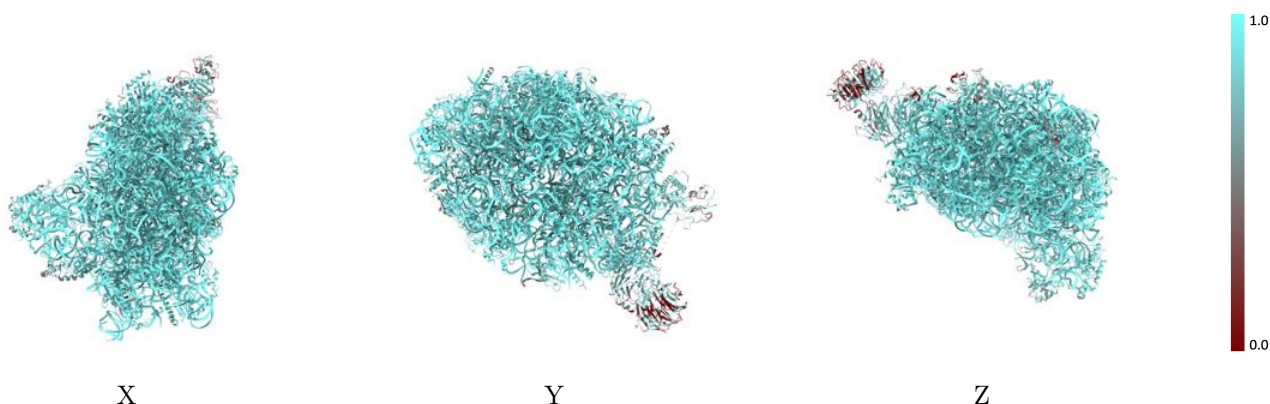
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



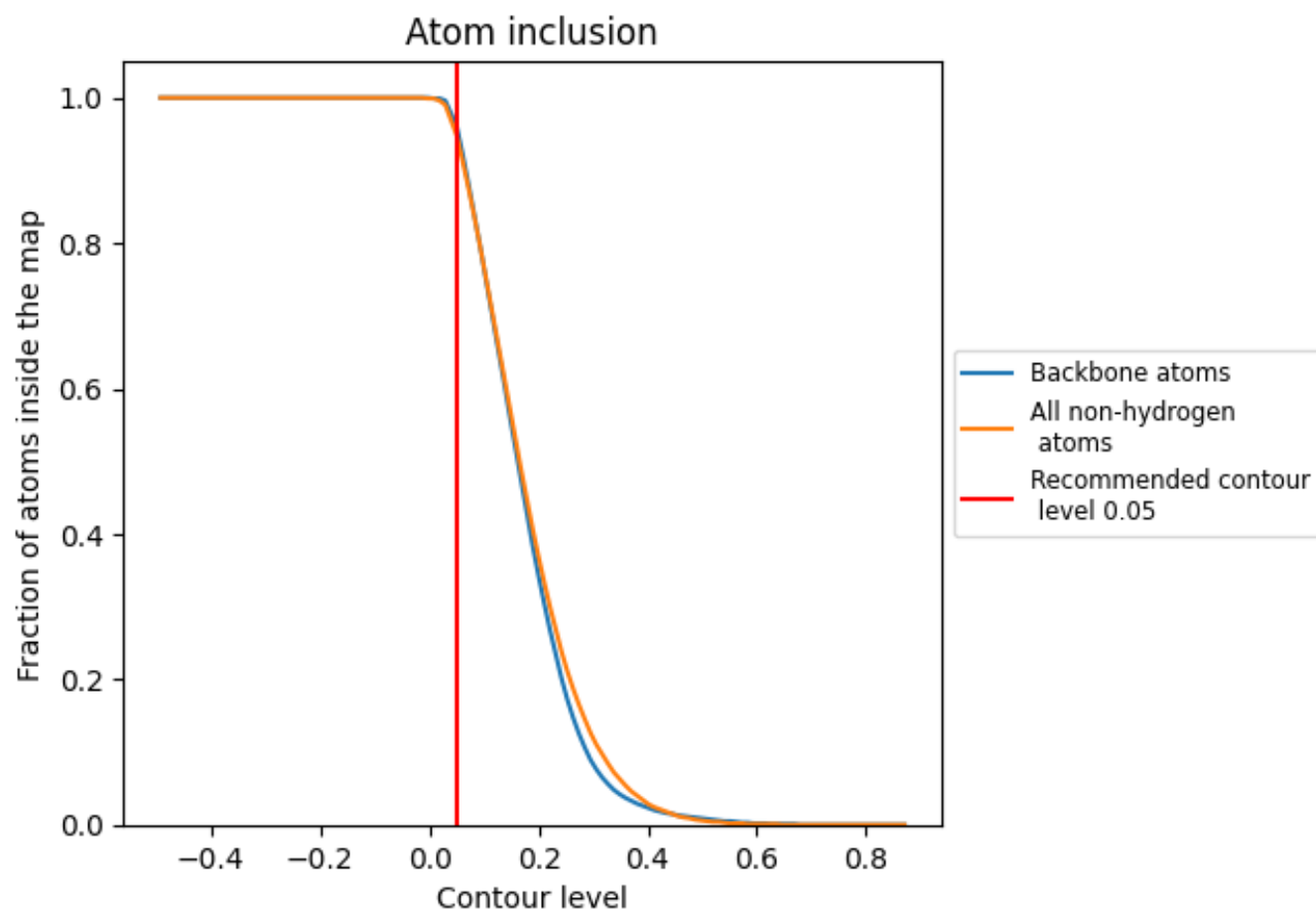
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.5670
1	 0.9860	 0.5950
2	 0.9910	 0.6210
3	 0.8360	 0.4530
8	 0.9900	 0.6190
9	 0.9920	 0.5370
A	 0.9820	 0.6130
B	 0.9730	 0.5920
C	 0.9740	 0.6030
D	 0.8880	 0.4980
E	 0.9280	 0.5250
F	 0.9620	 0.5920
G	 0.8950	 0.5310
H	 0.7750	 0.3480
I	 0.8450	 0.4870
J	 0.7800	 0.3820
K	 0.9580	 0.6010
L	 0.9580	 0.6030
M	 0.9490	 0.5140
N	 0.9890	 0.6350
O	 0.9620	 0.5810
P	 0.9500	 0.5850
Q	 0.9800	 0.6020
R	 0.9610	 0.5850
S	 0.9580	 0.5600
T	 0.9530	 0.5770
U	 0.7950	 0.4340
V	 0.9660	 0.5790
X	 0.9690	 0.6000
Y	 0.9710	 0.5930
Z	 0.9320	 0.5370
a	 0.9660	 0.6130
b	 0.9480	 0.5460
c	 0.8940	 0.5330
d	 0.9300	 0.5790



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Chain	Atom inclusion	Q-score
e	 0.9820	 0.6130
f	 0.9820	 0.6060
g	 0.9660	 0.6040
h	 0.9590	 0.5880
i	 0.9540	 0.5710
j	 0.9910	 0.6440
k	 0.8850	 0.5210
m	 0.7330	 0.3910
n	 0.7600	 0.4050
o	 0.9390	 0.5650
p	 0.4400	 0.2640
u	 0.9470	 0.5350