



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:50 PM UTC

PDB ID : 5JCS / pdb_00005jcs
EMDB ID : EMD-3199
Title : CRYO-EM STRUCTURE OF THE RIX1-REA1 PRE-60S PARTICLE
Authors : Barrio-Garcia, C.; Thoms, M.; Flemming, D.; Kater, L.; Berninghausen, O.;
Bassler, J.; Beckmann, R.; Hurt, E.
Deposited on : 2016-04-15
Resolution : 9.50 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:

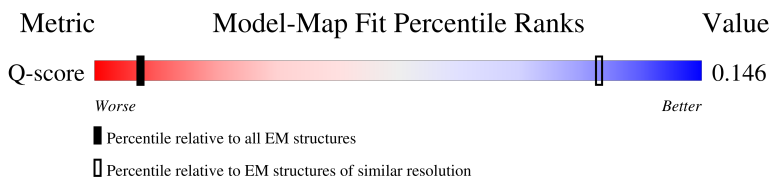
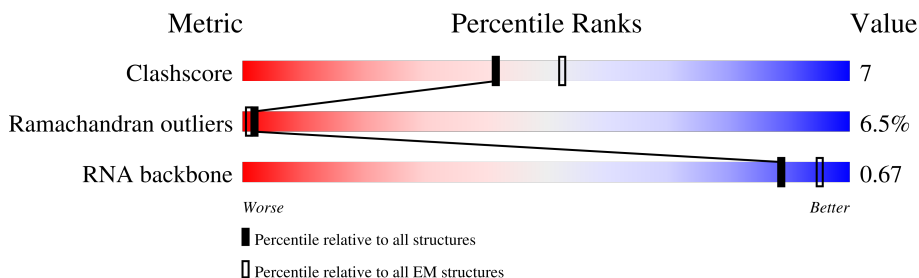
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.50 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	234 (9.00 - 10.00)

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	A	254	<p>39% (red), 81% (green), 15% (yellow), .. (grey)</p>
2	c	105	<p>12% (red), 88% (green), 5% (yellow), 8% (grey)</p>
3	B	387	<p>18% (red), 90% (green), 9% (yellow), . (grey)</p>
4	d	113	<p>15% (red), 89% (green), 6% (yellow), .. (grey)</p>

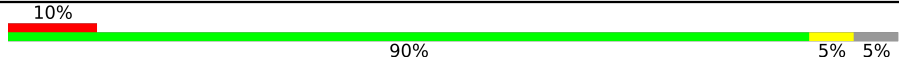
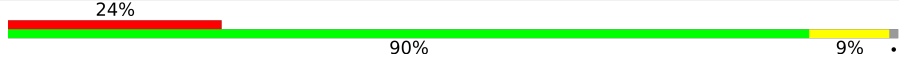

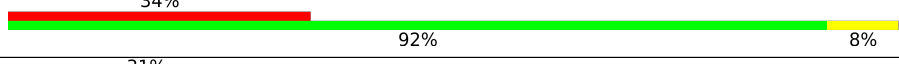
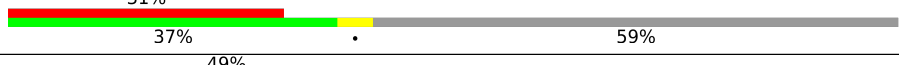
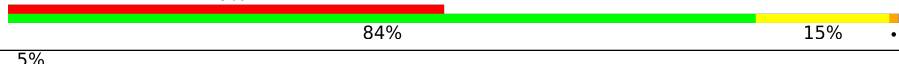
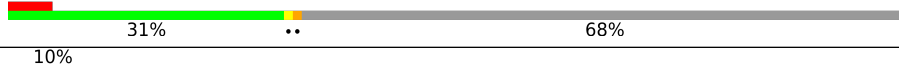
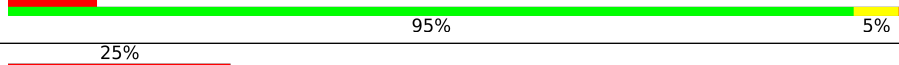


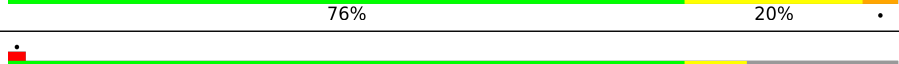
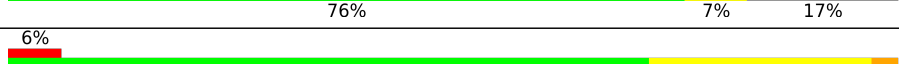
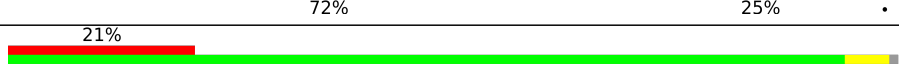
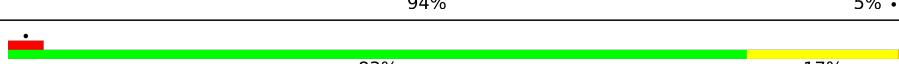

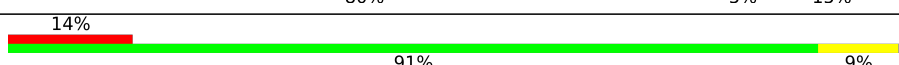
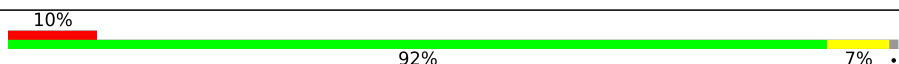
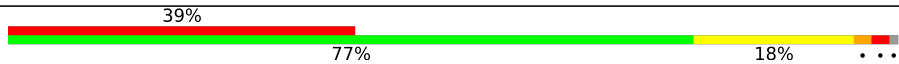

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Mol	Chain	Length	Quality of chain
5	C	362	25% 88% 10%
6	e	130	22% 95%
7	D	297	13% 95%
8	f	107	15% 87% 9%
9	E	176	12% 81% 7% 11%
10	g	121	39% 88% 7%
11	F	244	6% 84% 7% 9%
12	h	120	8% 95%
13	G	256	16% 87% 9%
14	i	100	20% 93% 6%
15	H	191	9% 95% 5%
16	j	88	40% 83% 13%
17	I	217	84% 94% 6%
18	k	78	9% 95%
19	J	174	66% 28%
20	l	51	27% 90% 8%
21	K	165	15% 64% 11% 23%
22	m	245	88% 9%
23	L	199	15% 86% 10%
24	n	236	86% 10%
25	M	138	10% 93% 6%
26	o	647	5% 41% 7% 5% 46%
27	N	204	21% 89% 10%
28	p	92	29% 95%
29	O	199	23% 84% 12%

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Mol	Chain	Length	Quality of chain
30	q	515	
31	P	184	
32	r	767	
33	Q	186	
34	s	4910	
35	R	189	
36	t	199	
37	S	172	
38	u	593	
39	T	160	
40	x	3396	
41	U	121	
42	y	158	
43	V	137	
44	z	121	
45	X	142	
46	Y	127	
47	Z	136	
48	a	149	

2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 118855 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 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	252	1007	504	252	251	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	c	97	387	194	97	96	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	B	386	1543	772	386	385	0	0

- Molecule 4 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	d	109	435	218	109	108	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	C	361	1443	722	361	360	0	0

- Molecule 6 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	e	127	507	254	127	126	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	D	296	1183	592	296	295	0	0

- Molecule 8 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	f	106	423	212	106	105	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	E	156	622	312	156	154	0	0

- Molecule 10 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	g	112	447	224	112	111	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	F	222	887	444	222	221	0	0

- Molecule 12 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	h	119	475	238	119	118	0	0

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	G	233	931	466	233	232	0	0

- Molecule 14 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	i	99	395	198	99	98	0	0

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	H	191	763	382	191	190	0	0

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	j	87	347	174	87	86	0	0

- Molecule 17 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	I	217	867	434	217	216	0	0

- Molecule 18 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	k	77	307	154	77	76	0	0

- Molecule 19 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	J	169	675	338	169	168	0	0

- Molecule 20 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	l	50	199	100	50	49	0	0

- Molecule 21 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
21	K	127	Total	C	N	O	0	0
			507	254	127	126		

- Molecule 22 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms			AltConf	Trace	
22	m	224	Total	C	N	O	0	0
			895	448	224	223		

- Molecule 23 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
23	L	193	Total	C	N	O	0	0
			771	386	193	192		

- Molecule 24 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms			AltConf	Trace	
24	n	212	Total	C	N	O	0	0
			847	424	212	211		

- Molecule 25 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
25	M	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 26 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
26	o	347	Total	C	N	O	0	0
			1387	694	347	346		

- Molecule 27 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
27	N	203	Total	C	N	O	0	0
			811	406	203	202		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	p	91	363	182	91	90	0	0

- Molecule 29 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	O	197	787	394	197	196	0	0

- Molecule 30 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	q	488	1951	976	488	487	0	0

- Molecule 31 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	P	183	731	366	183	182	0	0

- Molecule 32 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	r	333	1304	666	333	305	0	0

- Molecule 33 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	Q	185	739	370	185	184	0	0

- Molecule 34 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	s	2003	8007	4006	2003	1998	0	0

- Molecule 35 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	R	188	751	376	188	187	0	0

- Molecule 36 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	t	63	251	126	63	62	0	0

- Molecule 37 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	S	172	687	344	172	171	0	0

- Molecule 38 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	u	373	1491	746	373	372	0	0

- Molecule 39 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	T	159	635	318	159	158	0	0

- Molecule 40 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
40	x	3394	72570	32410	13042	23725	3393	0	0

- Molecule 41 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	U	100	399	200	100	99	0	0

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
42	y	158	3350	1500	586	1107	157	0	0

- Molecule 43 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	V	136	543	272	136	135	0	0

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
44	z	121	2576	1152	461	843	120	0	0

- Molecule 45 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	X	121	483	242	121	120	0	0

- Molecule 46 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	Y	126	503	252	126	125	0	0

- Molecule 47 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	Z	135	539	270	135	134	0	0

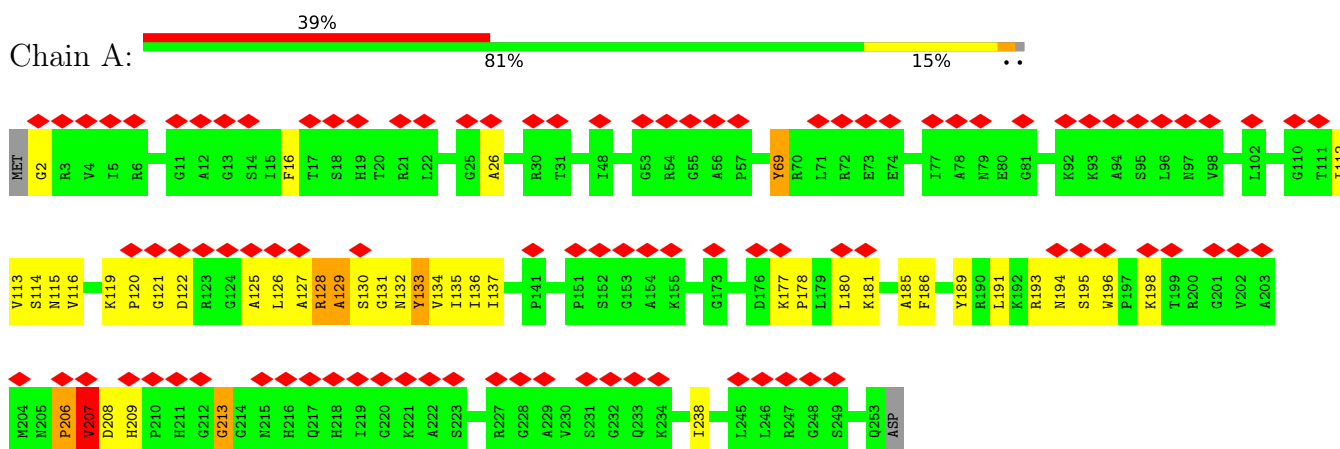
- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	a	148	591	296	148	147	0	0

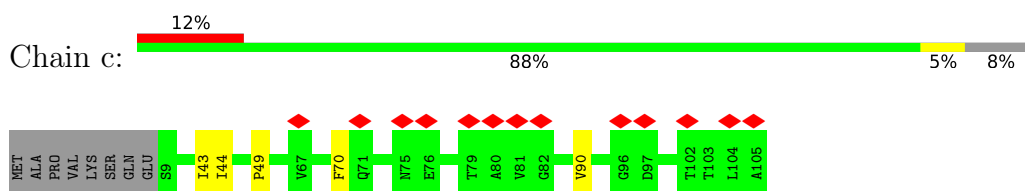
3 Residue-property plots [i](#)

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.

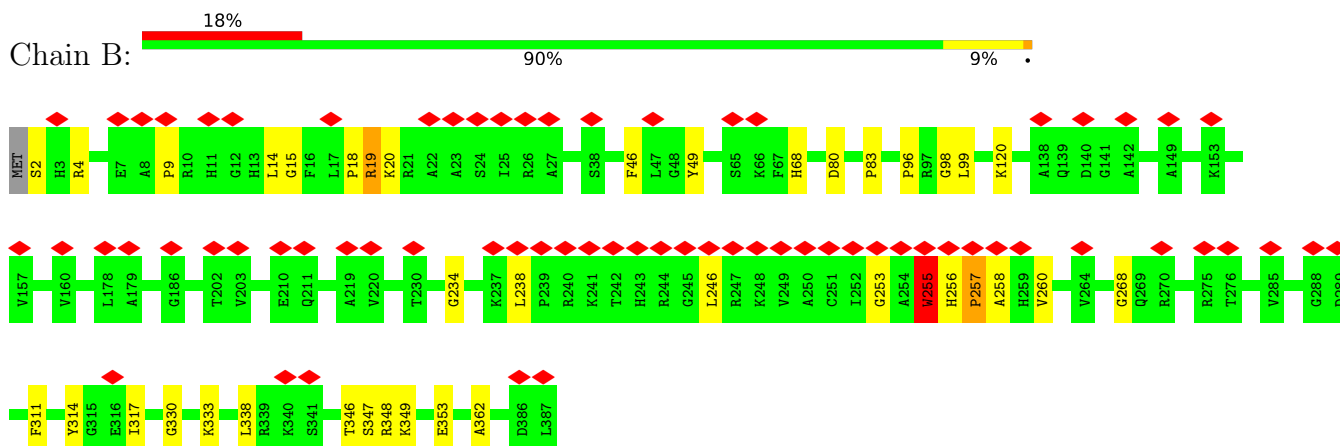
- Molecule 1: 60S ribosomal protein L2-A



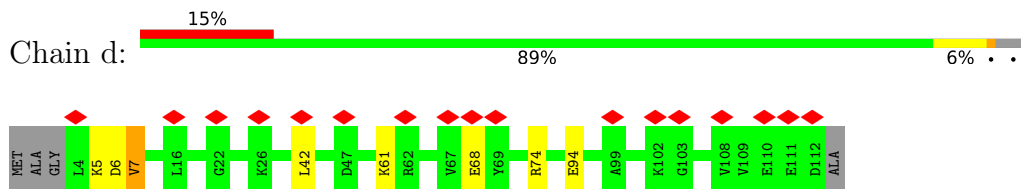
- Molecule 2: 60S ribosomal protein L30



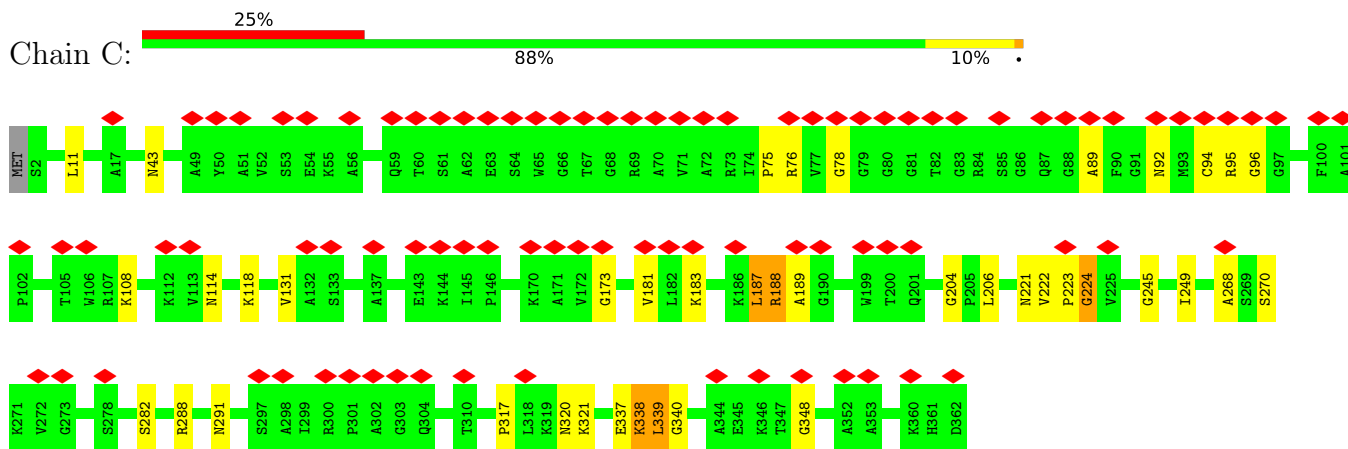
- Molecule 3: 60S ribosomal protein L3



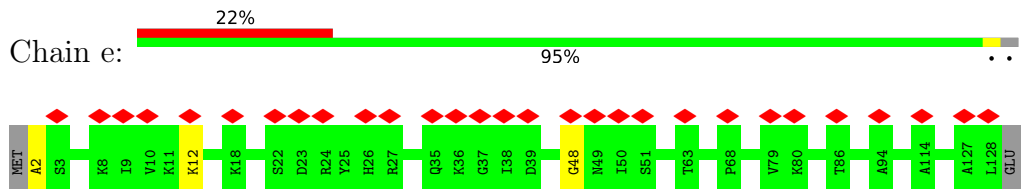
• Molecule 4: 60S ribosomal protein L31-A



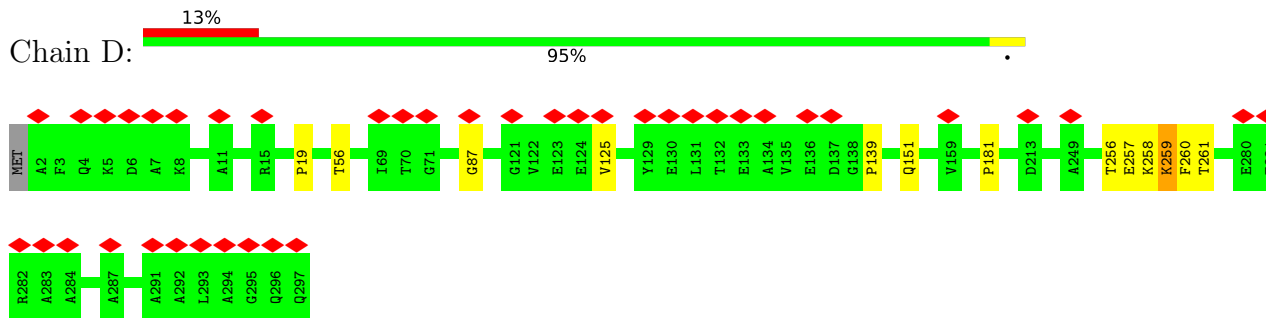
• Molecule 5: 60S ribosomal protein L4-A



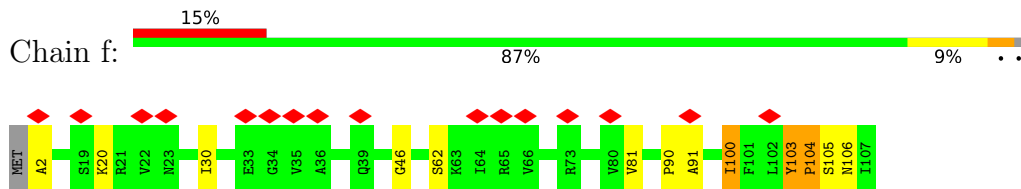
• Molecule 6: 60S ribosomal protein L32



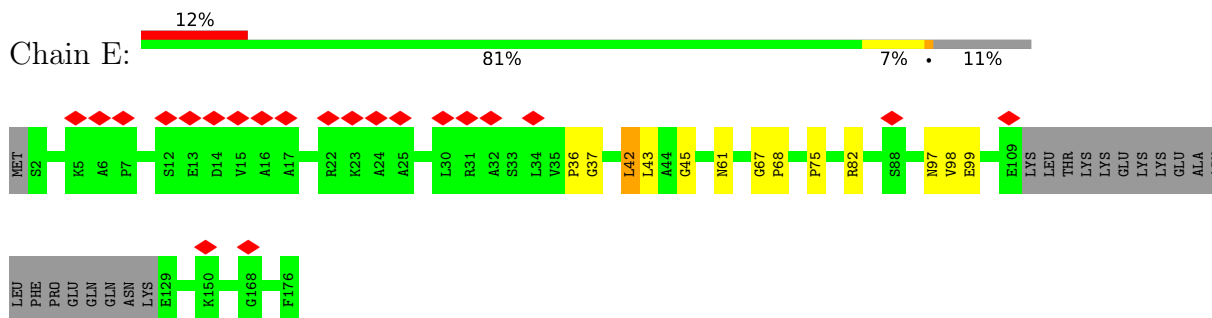
• Molecule 7: 60S ribosomal protein L5



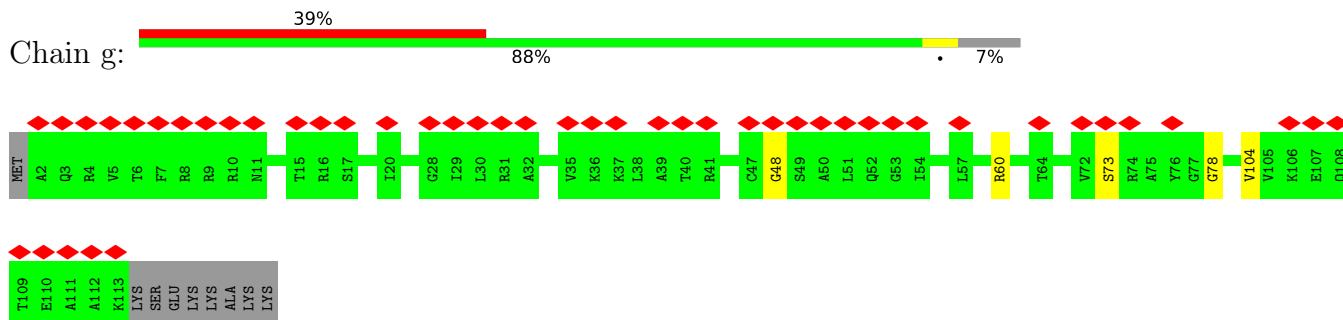
• Molecule 8: 60S ribosomal protein L33-A



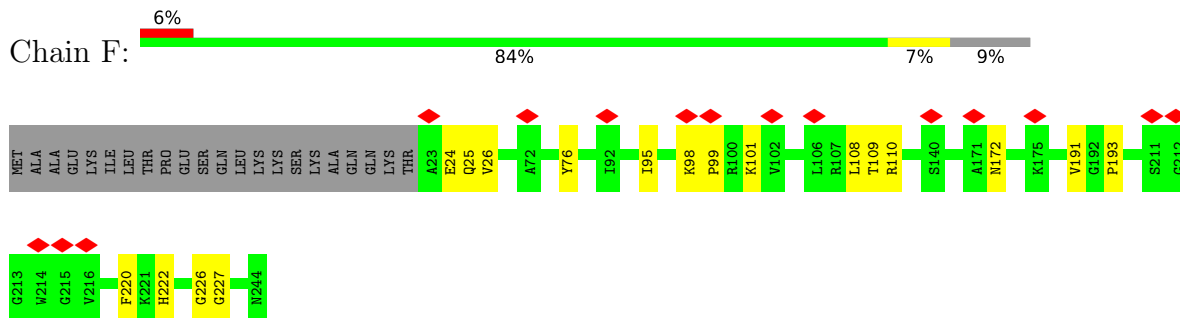
• Molecule 9: 60S ribosomal protein L6-A



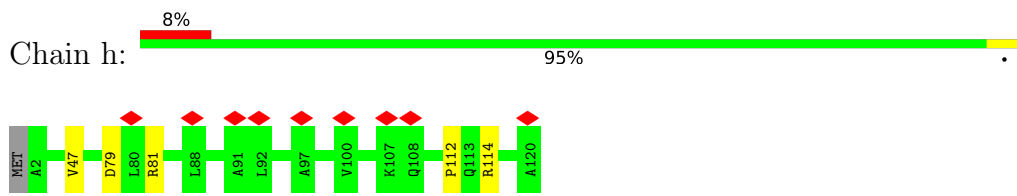
• Molecule 10: 60S ribosomal protein L34-A



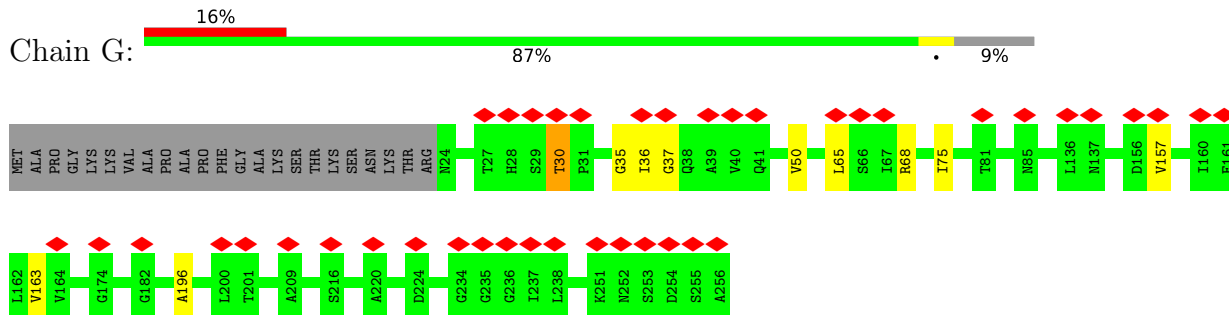
• Molecule 11: 60S ribosomal protein L7-A



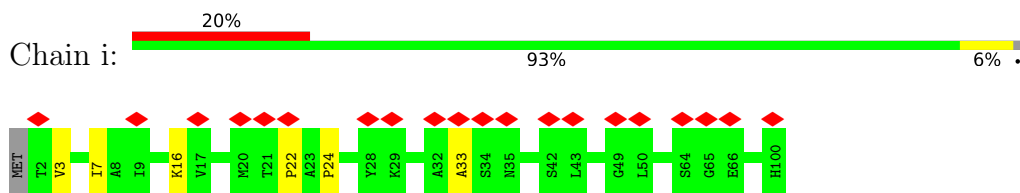
• Molecule 12: 60S ribosomal protein L35-A



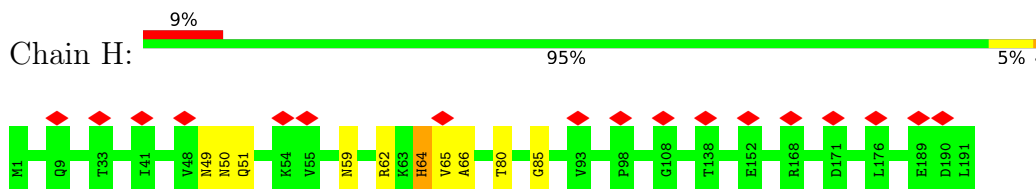
• Molecule 13: 60S ribosomal protein L8-A



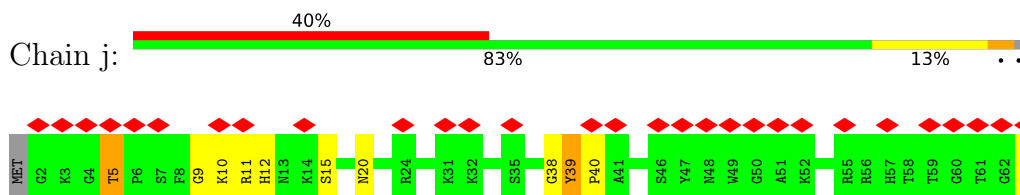
- Molecule 14: 60S ribosomal protein L36-A



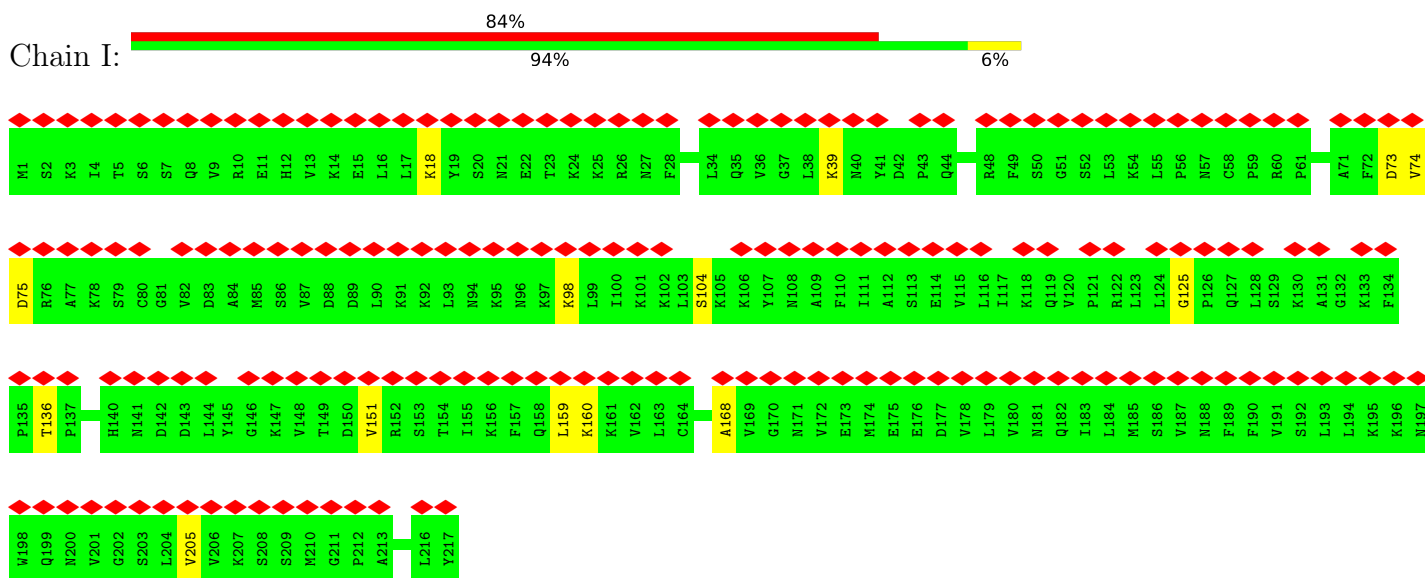
- Molecule 15: 60S ribosomal protein L9-A



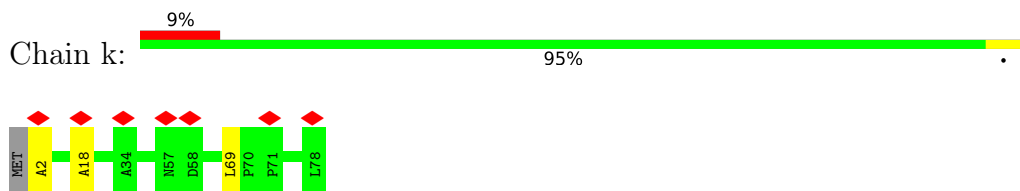
- Molecule 16: 60S ribosomal protein L37-A



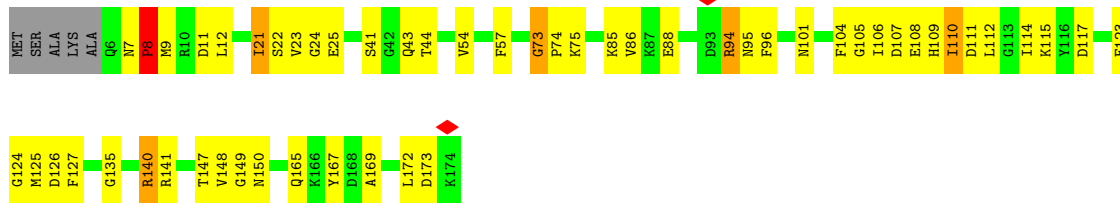
- Molecule 17: 60S ribosomal protein L1-A



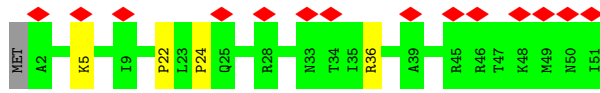
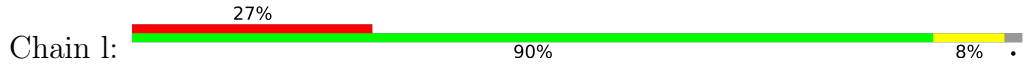
- Molecule 18: 60S ribosomal protein L38



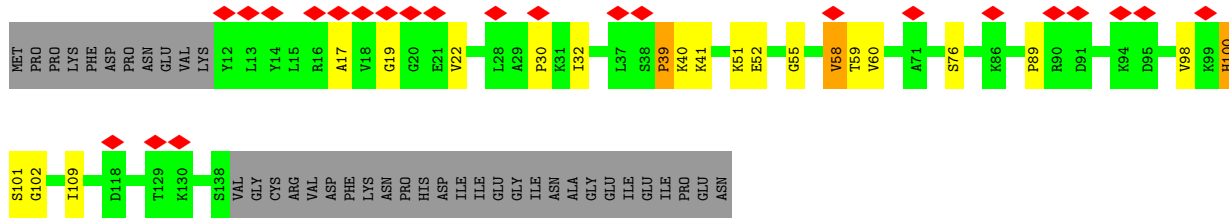
- Molecule 19: 60S ribosomal protein L11-A



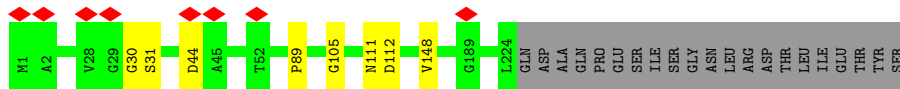
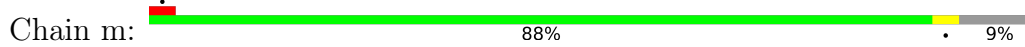
- Molecule 20: 60S ribosomal protein L39



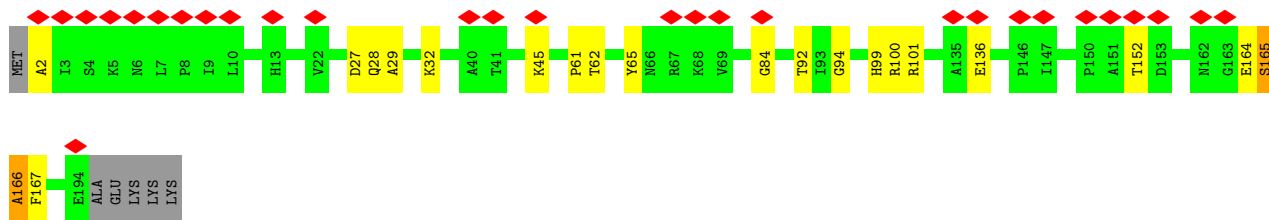
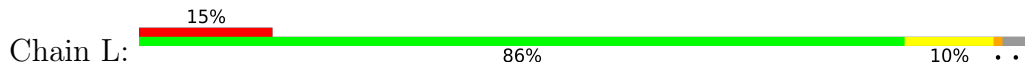
- Molecule 21: 60S ribosomal protein L12-A



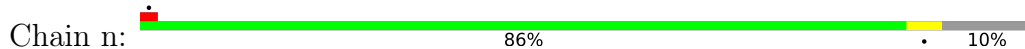
- Molecule 22: Eukaryotic translation initiation factor 6

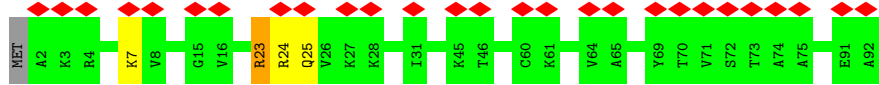
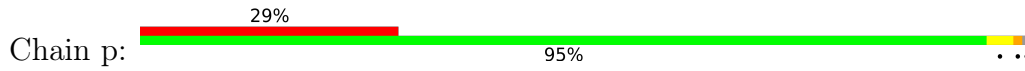


- Molecule 23: 60S ribosomal protein L13-A

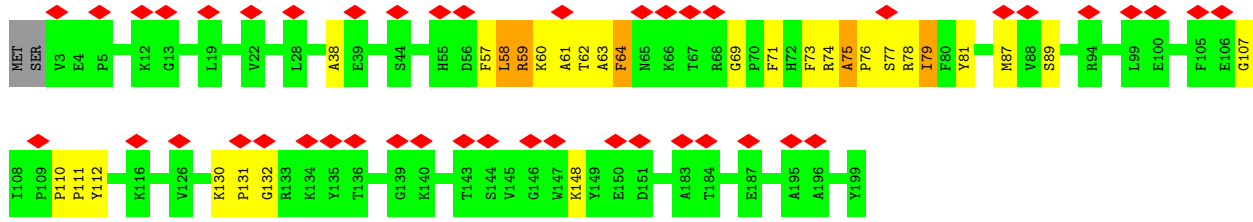
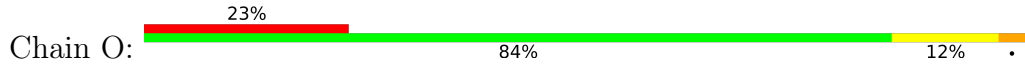


- Molecule 24: Ribosome assembly factor MRT4

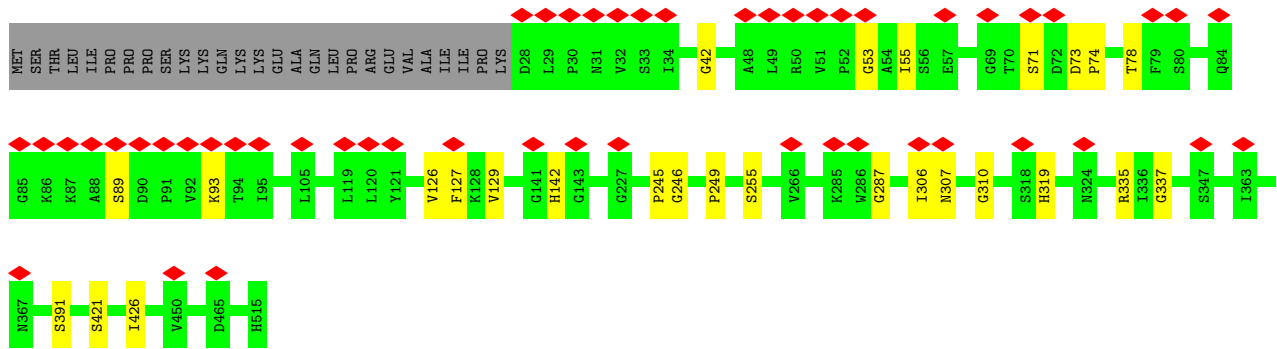
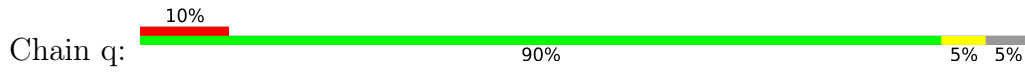




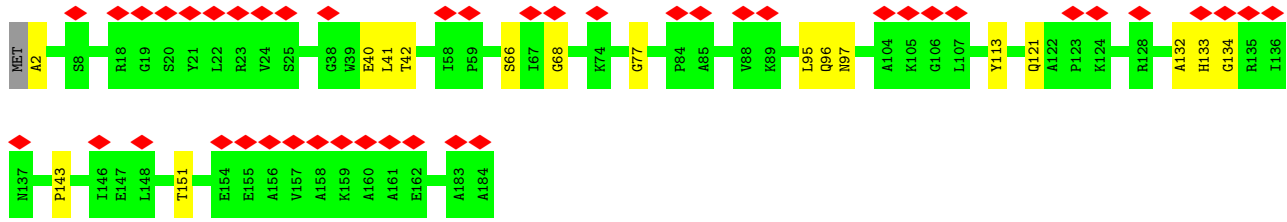
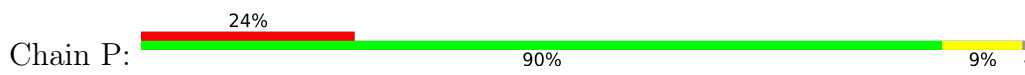
• Molecule 29: 60S ribosomal protein L16-A



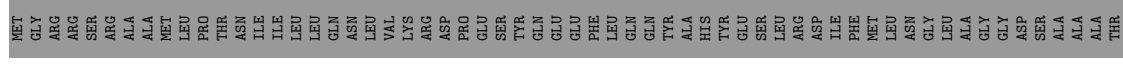
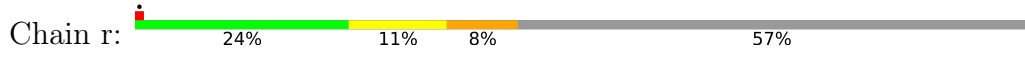
• Molecule 30: Ribosome assembly protein 4



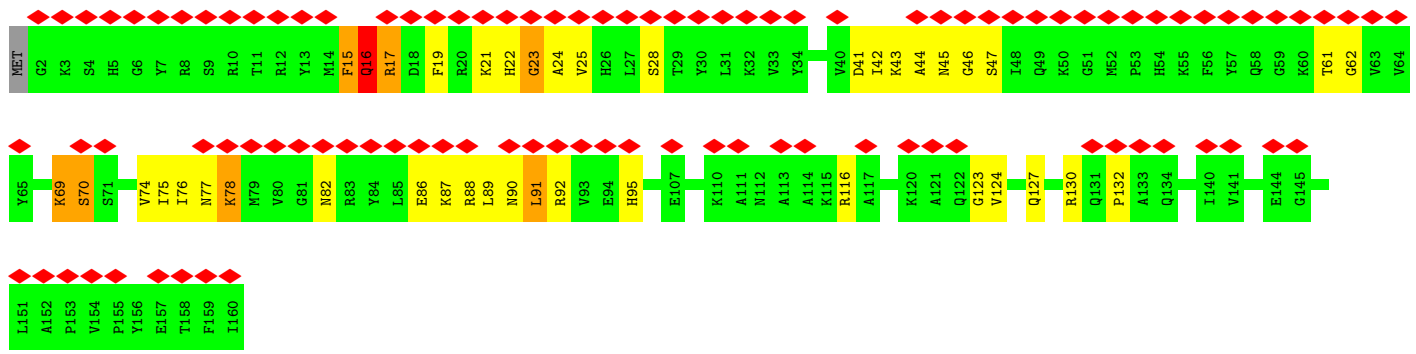
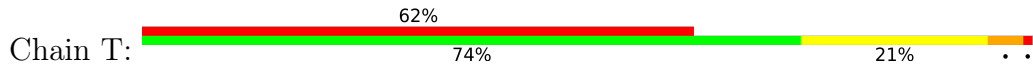
• Molecule 31: 60S ribosomal protein L17-A



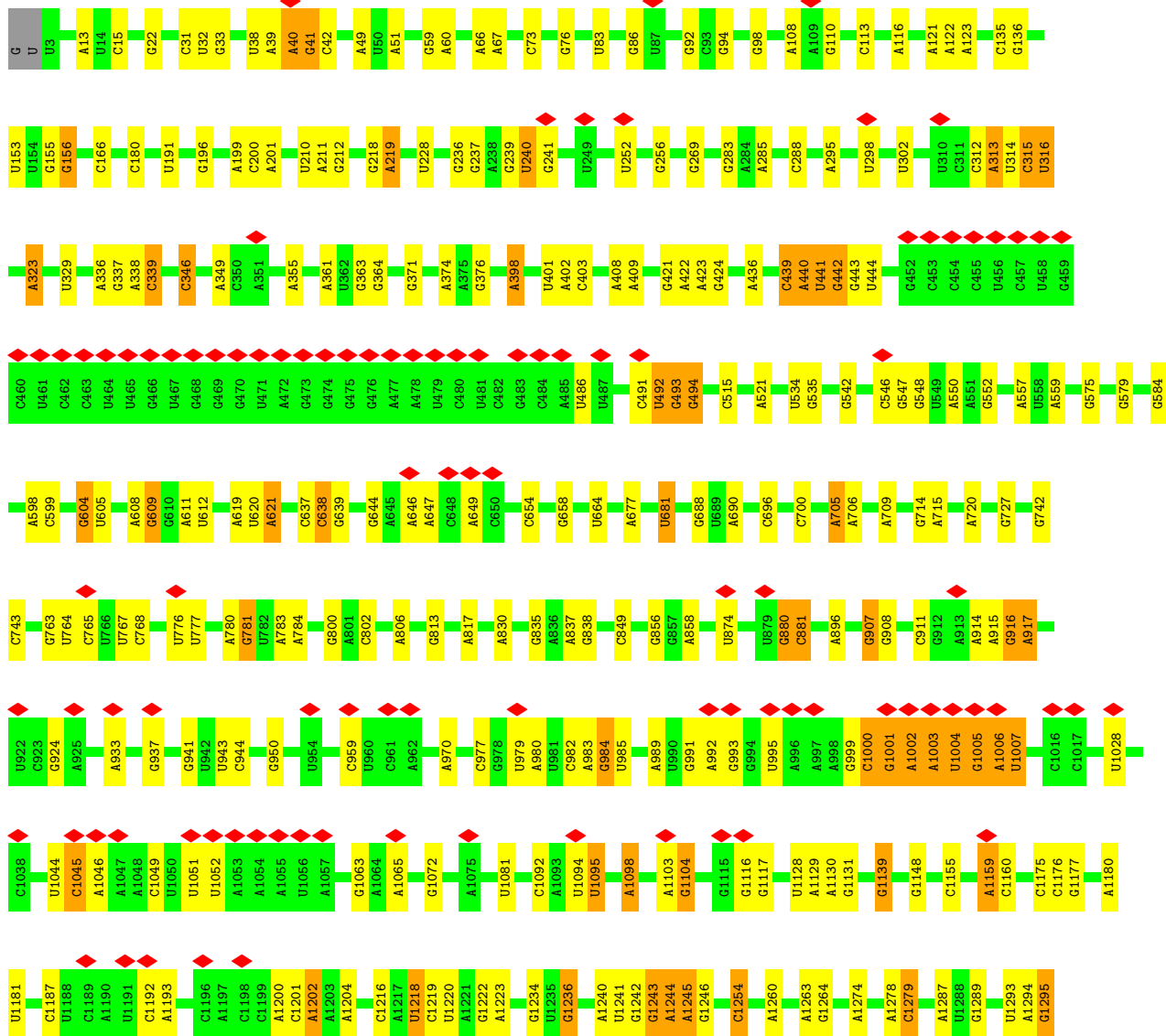
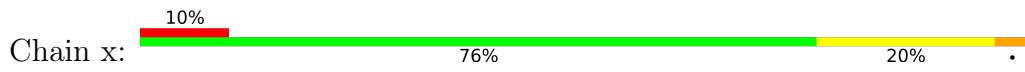
• Molecule 32: Protein SDA1

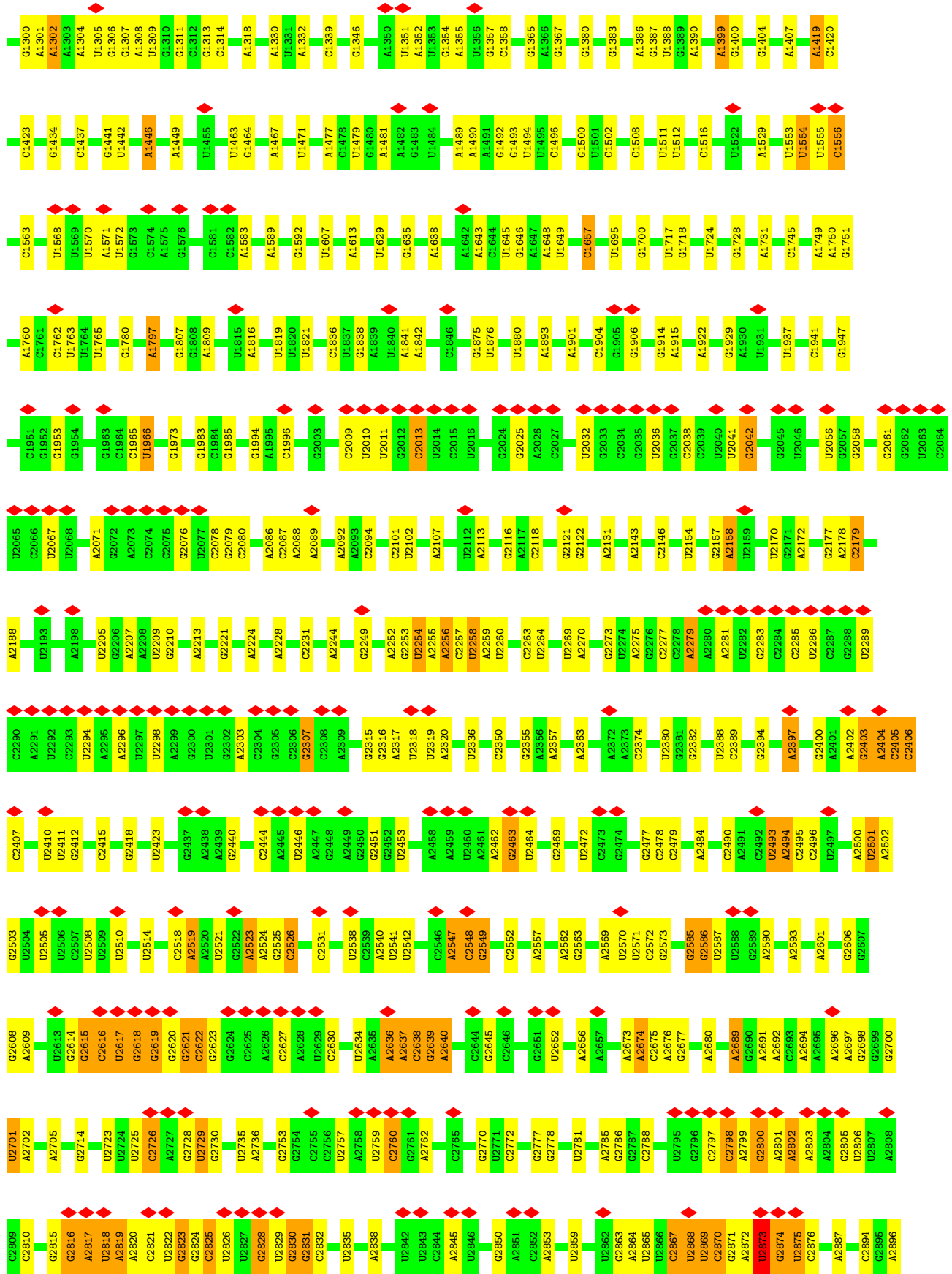


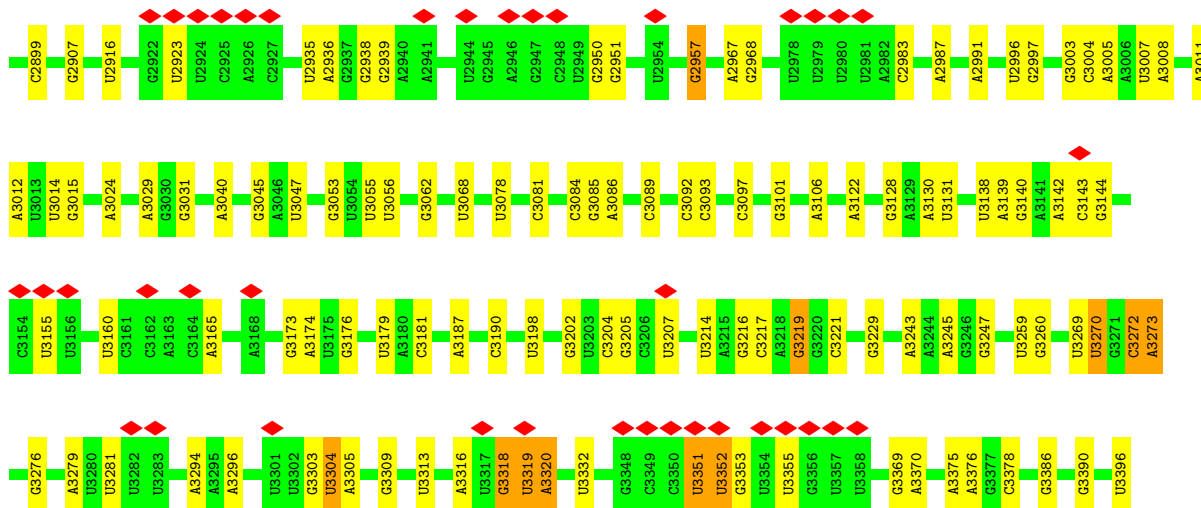
E927	W928	W929	G930	H931	D932	A934	K942	S953	K956	P957	S960	T965	L969	Y970	Y971	T972	D973	Y974	R977	Y978	S991	F992	L995	K999	I1003	L1004	K1005	F1006	K1010	L1013	G1014	R1015	L1016	K1017	M1018	V1019	K1020	S1021	I1022	M1023	S1024	GLN	THR	PRO	PRO														
Y1118	L1119	G1120	T1121	L1122	V1123	T1124	D1125	D1126	T1127	G1128	L1129	L1130	S1131	F1132	K1133	E1134	G1135	V1136	L1137	V1138	E1139	A1140	L1141	L1142	K1143	D1150	L1154	A1155	L1156	T1157	D1158	V1159	L1160	E1161	A1162	L1163	M1164	L1165	L1166	L1167	D1168	D1169	M1170	R1171	E1172	L1173	F1174	I1175	P1176	E1177	T1178	Q1179	E1180	V1181	V1182	H1183	P1184		
H1185	P1186	D1187	F1188	L1189	L1190	Q1194	M1195	P1196	P1197	G1198	I1199	Y1200	G1201	G1202	R1203	K1204	I1205	L1206	S1207	A1208	A1209	R1213	I1222	D1225	E1233	K1234	C1235	A1238	Y1241	V1248	Y1249	L1252	S1253	I1254	E1255	R1256	S1257	A1258	S1259	R1260	L1261	F1262	E1263	Q1264	K1265	M1266	N1267	F1268	A1269	V1270									
L1271	A1282	V1283	G1284	Y1285	L1295	L1296	A1297	E1298	R1299	C1300	R1301	T1302	E1305	K1306	L1313	V1319	K1320	L1321	D1322	M1323	ASP	GLN	TYR	TYR	ALA	SER	LEU	GLU	ASP	LYS	SER	LEU	LEU	ALA	ILE	GLY	SER	VAL	THR	T1344	K1361	Y1362	G1371	R1387	E1388	L1389	I1390	T1391	L1392	M1393									
A1394	H1395	Q1396	M1397	T1398	L1399	T1400	G1401	D1402	I1403	L1404	G1405	A1406	Q1407	R1408	P1409	V1410	M1411	M1412	R1413	S1414	E1415	I1416	Q1417	V1418	K1419	L1420	I1421	I1422	S1423	K1424	K1425	T1426	A1427	L1428	M1429	I1430	A1431	M1432	D1433	Q1434	D1435	V1436	D1437	L1438	K1439	E1440	L1441	L1442	Q1443	L1444	Y1445	S1446	K1447	S1448	L1449	M1450	K1451	M1452	I1453
A1454	E1455	D1456	V1457	Q1458	L1459	E1460	I1461	K1463	L1464	R1465	D1466	L1468	M1469	V1470	L1471	F1472	E1473	W1474	S1475	D1476	G1477	P1478	L1479	I1480	R1484	F1489	L1490	E1493	I1494	S1495	L1496	A1497	D1498	D1499	S1500	V1501	R1504	L1505	M1506	S1507	E1510	P1511	E1512	R1513	S1514	L1515	L1516	L1517	A1518	E1519	Q1520	G1521							
S1522	D1524	S1525	L1526	V1527	T1528	M1529	S1530	F1533	Q1534	F1535	F1536	A1537	T1538	M1539	G1542	G1543	D1544	Y1545	G1546	K1547	K1548	E1549	L1550	S1551	P1552	A1553	P1564	M1566	E1567	D1568	V1572	M1573	M1574	I1575	V1576	S1577	S1578	R1579	L1580	L1581	E1582	D1583	L1584	K1585	D1586	V1592	K1593	F1594	S1595	E1596	W1597	F1598							
G1599	K1600	K1601	L1602	G1603	G1604	G1605	M1606	A1607	T1608	S1609	G1610	V1611	I1612	S1613	L1614	L1618	A1619	M1625	K1626	V1627	F1628	P1629	Q1640	G1641	A1642	S1643	A1649	L1650	G1651	T1652	M1653	M1654	T1655	A1656	L1658	A1659	E1660	M1661	E1662	M1663	L1664	L1665	K1666	S1667	L1668	R1669	T1670	E1671	I1673	I1674	Q1675	G1680							
G1681	D1682	D1683	L1684	GLU	LEU	GLN	GLN	ILE	THR	ASN	GLU	ILE	ILE	VAL	THR	GLN	ASP	GLU	GLN	VAL	GLY	MET	PHE	LYS	ILE	PRO	ARG	PHE	PRO	ASP	ALA	GLN	SER	SER	SER	PHE	M1720	L1721	T1722	A1723	T1726	V1734	R1735	A1736	M1737	Q1738	Q1739	H1740	L1743	S1748	V1751	G1752							
K1753	T1754	S1755	L1756	I1757	A1761	M1762	I1763	T1764	G1765	M1766	K1767	L1768	T1769	I1770	I1771	M1772	L1773	S1774	E1775	Q1776	T1777	L1778	L1779	V1780	D1781	L1782	F1783	G1784	A1785	L1786	A1787	P1788	G1789	E1790	R1791	S1792	G1793	E1794	F1795	L1796	L1797	Q1798	H1798	D1799	A1800	P1801	F1802	L1803	K1807	K1808	G1809	V1812	L1813	L1814	D1815	E1816			
L1819	A1820	S1823	E1826	G1827	C1831	R1835	G1836	E1837	A1838	Y1839	I1840	P1841	E1842	L1843	D1844	I1845	S1846	F1847	S1848	C1849	H1850	P1851	M1852	F1853	L1854	V1855	F1856	A1857	P1861	Q1862	L1863	Q1864	G1865	G1866	G1867	R1868	P1872	K1873	S1874	M1877	F1883	I1884	T1888	S1889	D1890	D1891	L1892	L1893	D1894	L1895									
A1896	K1897	H1898	L1899	V1900	P1901	S1902	I1903	E1904	P1905	D1906	I1907	I1908	A1909	K1913	L1914	M1915	S1916	T1917	D1920	Q1921	V1922	C1923	K1924	R1925	K1926	L1927	W1928	G1929	M1930	S1933	P1934	R1940	L1943	L1946	K1947	L1948	L1949	M1950	Q1951	V1952	S1953	I1954	C1955	E1956	D1957	V1958	D1959	V1960	F1961	D1962	F1963	V1964	D1965						



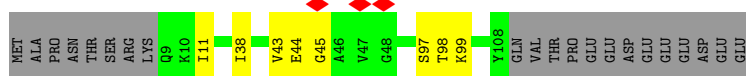
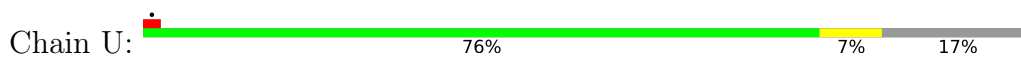
• Molecule 40: 25S ribosomal RNA



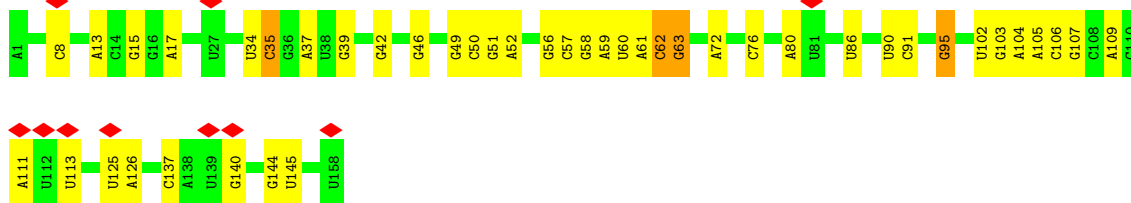




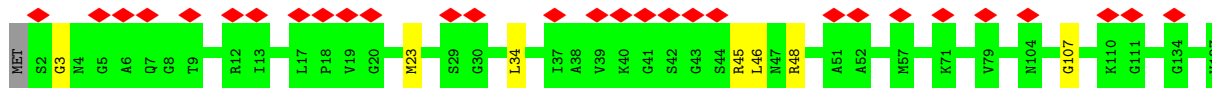
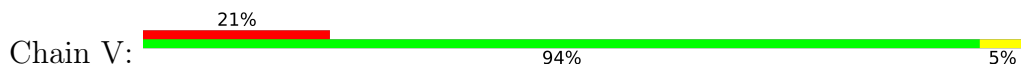
• Molecule 41: 60S ribosomal protein L22-A



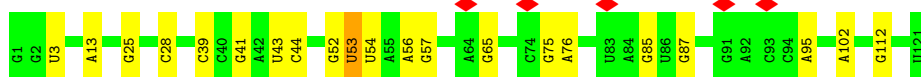
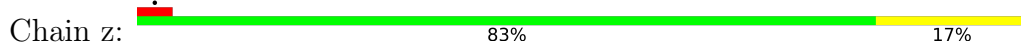
• Molecule 42: 5.8S ribosomal RNA



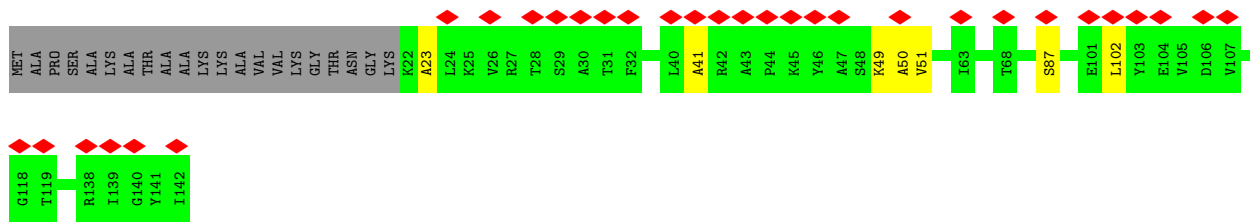
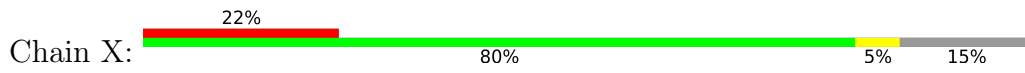
• Molecule 43: 60S ribosomal protein L23-A



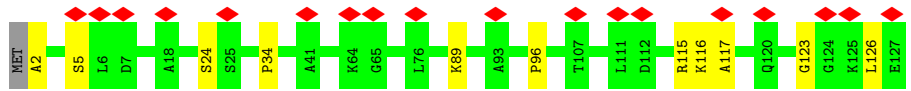
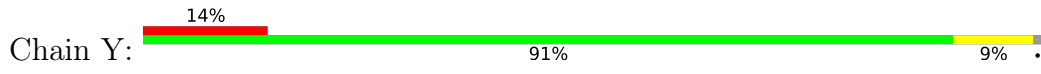
• Molecule 44: 5S ribosomal RNA



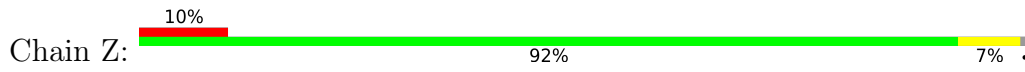
• Molecule 45: 60S ribosomal protein L25



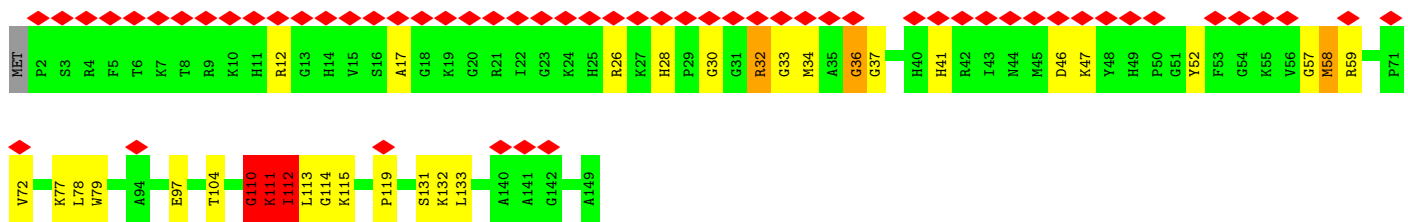
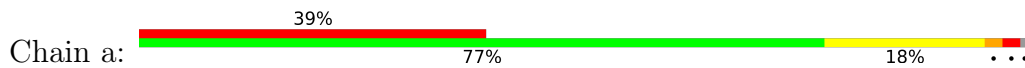
- Molecule 46: 60S ribosomal protein L26-A



- Molecule 47: 60S ribosomal protein L27-A



- Molecule 48: 60S ribosomal protein L28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15749	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor
Maximum map value	1.479	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	827.6, 827.6, 827.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.069, 2.069, 2.069	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	A	0.61	2/1006 (0.2%)	1.01	3/1256 (0.2%)
2	c	0.29	0/386	0.81	0/481
3	B	0.33	0/1542	0.94	3/1926 (0.2%)
4	d	0.31	0/434	0.91	0/541
5	C	0.34	0/1442	0.91	1/1801 (0.1%)
6	e	0.29	0/506	0.85	0/631
7	D	0.31	0/1182	0.86	0/1476
8	f	0.86	1/422 (0.2%)	1.33	4/526 (0.8%)
9	E	0.80	5/620 (0.8%)	1.59	8/772 (1.0%)
10	g	0.28	0/446	0.86	0/556
11	F	0.34	0/886	0.94	2/1106 (0.2%)
12	h	0.30	0/474	0.91	0/591
13	G	0.32	0/930	0.86	0/1161
14	i	0.29	0/394	0.83	0/491
15	H	0.28	0/762	0.86	0/951
16	j	0.89	1/346 (0.3%)	1.07	4/431 (0.9%)
17	I	0.33	0/866	0.89	0/1081
18	k	0.35	0/306	0.94	2/381 (0.5%)
19	J	0.91	0/674	1.55	6/841 (0.7%)
20	l	0.30	0/198	0.90	0/246
21	K	0.35	0/506	0.94	0/631
22	m	0.30	0/894	0.86	0/1116
23	L	0.33	0/770	0.92	0/961
24	n	0.31	0/846	0.91	0/1056
25	M	0.29	0/542	0.86	0/676
26	o	0.97	11/1386 (0.8%)	1.42	25/1731 (1.4%)
27	N	0.35	0/810	0.97	1/1011 (0.1%)
28	p	0.28	0/362	0.81	0/451
29	O	0.36	0/786	1.10	2/981 (0.2%)
30	q	1.54	0/1950	1.62	25/2436 (1.0%)
31	P	0.30	0/730	0.88	0/911
32	r	0.90	1/1276 (0.1%)	1.68	31/1553 (2.0%)
33	Q	0.31	0/738	0.85	0/921
34	s	0.50	14/8001 (0.2%)	0.99	28/9992 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.36	0/750	0.98	1/936 (0.1%)
36	t	0.53	0/250	1.01	0/311
37	S	0.30	0/686	0.91	0/856
38	u	1.56	0/1483	1.57	12/1840 (0.7%)
39	T	0.77	4/634 (0.6%)	1.17	5/791 (0.6%)
40	x	0.15	2/81221 (0.0%)	0.40	170/126638 (0.1%)
41	U	0.32	0/398	0.95	0/496
42	y	0.06	0/3743	0.06	0/5828
43	V	0.37	0/542	0.92	0/676
44	z	0.06	0/2880	0.05	0/4487
45	X	0.30	0/482	0.85	0/601
46	Y	0.30	0/502	0.87	0/626
47	Z	0.31	0/538	0.89	0/671
48	a	1.27	5/590 (0.8%)	1.12	6/736 (0.8%)
All	All	0.39	46/128118 (0.0%)	0.65	339/187166 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	B	0	2
8	f	0	2
9	E	0	1
19	J	0	1
26	o	0	1
32	r	0	3
34	s	0	11
36	t	0	1
39	T	0	3
48	a	0	1
All	All	0	27

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	a	111	LYS	N-CA	22.03	1.74	1.46
48	a	110	GLY	C-N	16.68	1.57	1.33
16	j	39	TYR	C-O	-13.49	1.06	1.24
8	f	100	ILE	C-N	12.64	1.50	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	o	44	ALA	CA-C	11.40	1.68	1.52

The worst 5 of 339 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	s	858	GLU	O-C-N	-25.52	88.65	122.59
9	E	67	GLY	CA-C-N	-20.95	96.46	120.13
9	E	67	GLY	C-N-CA	-20.95	96.46	120.13
40	x	494	G	C4'-C3'-O3'	17.76	136.04	109.40
40	x	2870	C	C4'-C3'-O3'	17.26	135.28	109.40

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	LYS	Peptide
3	B	255	TRP	Peptide
3	B	256	HIS	Peptide
8	f	100	ILE	Mainchain
8	f	103	TYR	Peptide

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	A	1007	0	310	59	0
2	c	387	0	113	2	0
3	B	1543	0	433	32	0
4	d	435	0	114	3	0
5	C	1443	0	399	24	0
6	e	507	0	135	1	0
7	D	1183	0	325	1	0
8	f	423	0	117	3	0
9	E	622	0	160	3	0
10	g	447	0	121	0	0
11	F	887	0	241	6	0
12	h	475	0	118	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	931	0	242	2	0
14	i	395	0	109	0	0
15	H	763	0	215	3	0
16	j	347	0	104	6	0
17	I	867	0	230	8	0
18	k	307	0	79	1	0
19	J	675	0	191	68	0
20	l	199	0	47	0	0
21	K	507	0	140	19	0
22	m	895	0	257	0	0
23	L	771	0	199	21	0
24	n	847	0	224	2	0
25	M	543	0	145	2	0
26	o	1387	0	358	58	0
27	N	811	0	221	11	0
28	p	363	0	108	1	0
29	O	787	0	214	30	0
30	q	1951	0	540	16	0
31	P	731	0	197	8	0
32	r	1304	0	332	114	0
33	Q	739	0	205	4	0
34	s	8007	0	2136	1	0
35	R	751	0	203	32	0
36	t	251	0	68	0	0
37	S	687	0	175	3	0
38	u	1491	0	399	8	0
39	T	635	0	174	58	0
40	x	72570	0	36462	692	0
41	U	399	0	109	2	0
42	y	3350	0	1696	21	0
43	V	543	0	162	3	0
44	z	2576	0	1304	28	0
45	X	483	0	121	1	0
46	Y	503	0	134	3	0
47	Z	539	0	144	3	0
48	a	591	0	176	89	0
All	All	118855	0	50406	1065	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 7.

The worst 5 of 1065 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)
21:K:100:HIS:C	30:q:246:GLY:CA	1.79	1.54
40:x:705:A:H2	48:a:110:GLY:C	1.03	1.52
48:a:111:LYS:N	48:a:111:LYS:CA	1.74	1.50
23:L:2:ALA:CA	48:a:33:GLY:N	1.74	1.49
40:x:705:A:C2	48:a:110:GLY:C	1.89	1.47

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	A	250/254 (98%)	156 (62%)	70 (28%)	24 (10%)	0	7
2	c	95/105 (90%)	84 (88%)	10 (10%)	1 (1%)	11	46
3	B	384/387 (99%)	294 (77%)	70 (18%)	20 (5%)	1	15
4	d	107/113 (95%)	88 (82%)	15 (14%)	4 (4%)	2	20
5	C	359/362 (99%)	254 (71%)	80 (22%)	25 (7%)	1	11
6	e	125/130 (96%)	99 (79%)	24 (19%)	2 (2%)	7	38
7	D	294/297 (99%)	229 (78%)	53 (18%)	12 (4%)	2	18
8	f	104/107 (97%)	78 (75%)	19 (18%)	7 (7%)	1	12
9	E	152/176 (86%)	113 (74%)	35 (23%)	4 (3%)	4	25
10	g	110/121 (91%)	78 (71%)	27 (24%)	5 (4%)	2	17
11	F	220/244 (90%)	181 (82%)	30 (14%)	9 (4%)	2	18
12	h	117/120 (98%)	92 (79%)	21 (18%)	4 (3%)	3	21
13	G	231/256 (90%)	180 (78%)	42 (18%)	9 (4%)	2	19
14	i	97/100 (97%)	78 (80%)	13 (13%)	6 (6%)	1	13
15	H	189/191 (99%)	147 (78%)	37 (20%)	5 (3%)	4	25
16	j	85/88 (97%)	53 (62%)	26 (31%)	6 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	I	215/217 (99%)	159 (74%)	48 (22%)	8 (4%)	2	20
18	k	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	9	42
19	J	167/174 (96%)	116 (70%)	29 (17%)	22 (13%)	0	4
20	l	48/51 (94%)	33 (69%)	11 (23%)	4 (8%)	0	9
21	K	125/165 (76%)	81 (65%)	27 (22%)	17 (14%)	0	4
22	m	222/245 (91%)	170 (77%)	44 (20%)	8 (4%)	2	20
23	L	191/199 (96%)	141 (74%)	39 (20%)	11 (6%)	1	14
24	n	210/236 (89%)	156 (74%)	48 (23%)	6 (3%)	3	23
25	M	134/138 (97%)	106 (79%)	22 (16%)	6 (4%)	2	17
26	o	345/647 (53%)	223 (65%)	72 (21%)	50 (14%)	0	3
27	N	201/204 (98%)	147 (73%)	44 (22%)	10 (5%)	1	16
28	p	89/92 (97%)	72 (81%)	14 (16%)	3 (3%)	3	21
29	O	195/199 (98%)	143 (73%)	39 (20%)	13 (7%)	1	12
30	q	486/515 (94%)	458 (94%)	22 (4%)	6 (1%)	10	44
31	P	181/184 (98%)	141 (78%)	35 (19%)	5 (3%)	4	24
32	r	277/767 (36%)	155 (56%)	57 (21%)	65 (24%)	0	1
33	Q	183/186 (98%)	143 (78%)	30 (16%)	10 (6%)	1	15
34	s	1991/4910 (40%)	1585 (80%)	229 (12%)	177 (9%)	0	8
35	R	186/189 (98%)	136 (73%)	44 (24%)	6 (3%)	3	21
36	t	61/199 (31%)	52 (85%)	7 (12%)	2 (3%)	3	21
37	S	170/172 (99%)	133 (78%)	31 (18%)	6 (4%)	3	20
38	u	357/593 (60%)	342 (96%)	6 (2%)	9 (2%)	4	26
39	T	157/160 (98%)	90 (57%)	46 (29%)	21 (13%)	0	4
41	U	98/121 (81%)	77 (79%)	17 (17%)	4 (4%)	2	18
43	V	134/137 (98%)	95 (71%)	37 (28%)	2 (2%)	8	40
45	X	119/142 (84%)	91 (76%)	23 (19%)	5 (4%)	2	17
46	Y	124/127 (98%)	91 (73%)	26 (21%)	7 (6%)	1	14
47	Z	133/136 (98%)	97 (73%)	30 (23%)	6 (4%)	2	17
48	a	146/149 (98%)	89 (61%)	40 (27%)	17 (12%)	0	5
All	All	9939/14383 (69%)	7592 (76%)	1697 (17%)	650 (6%)	2	12

5 of 650 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ASP
1	A	128	ARG
1	A	133	TYR
1	A	135	ILE
1	A	137	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
40	x	3393/3396 (99%)	376 (11%)	0
42	y	157/158 (99%)	20 (12%)	0
44	z	120/121 (99%)	7 (5%)	0
All	All	3670/3675 (99%)	403 (10%)	0

5 of 403 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
40	x	22	G
40	x	40	A
40	x	41	G
40	x	49	A
40	x	60	A

There are no RNA pucker outliers to report.

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.

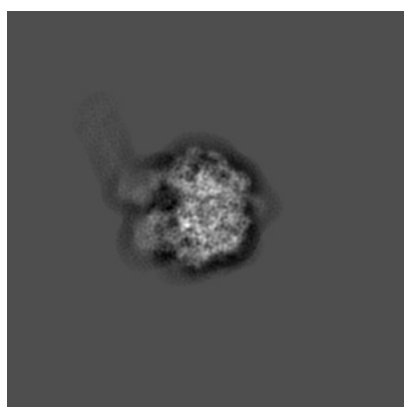
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3199. These allow visual inspection of the internal detail of the map and identification of artifacts.

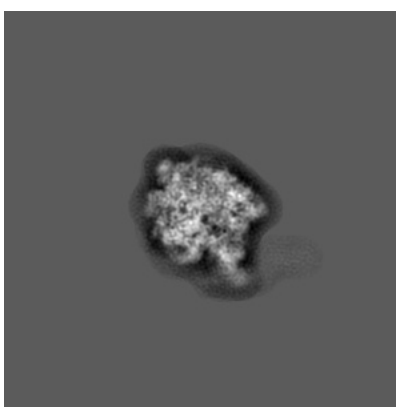
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

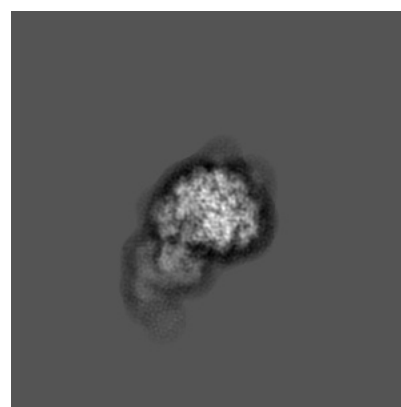
6.1.1 Primary map



X



Y

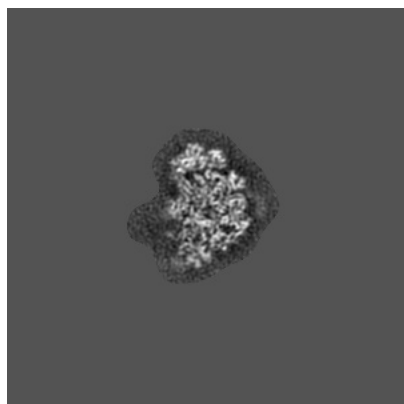


Z

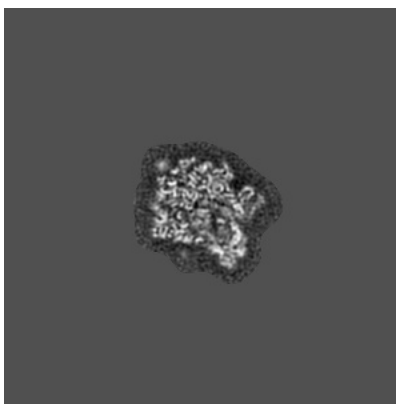
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

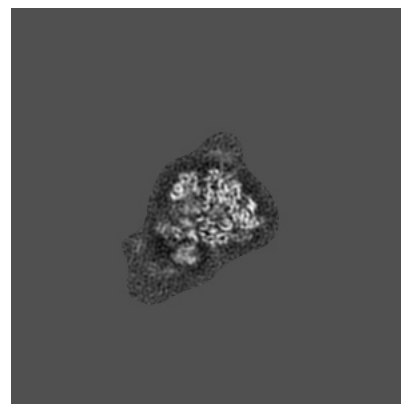
6.2.1 Primary map



X Index: 200



Y Index: 200

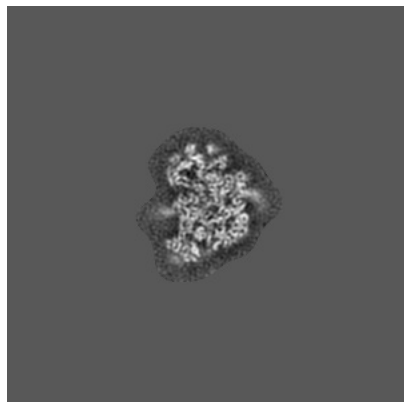


Z Index: 200

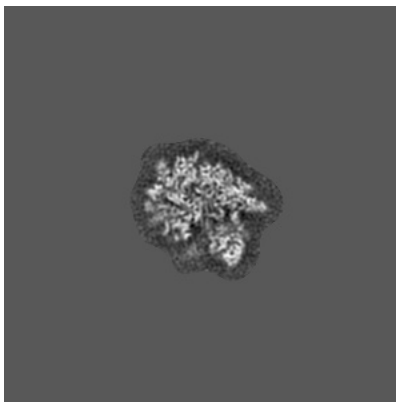
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

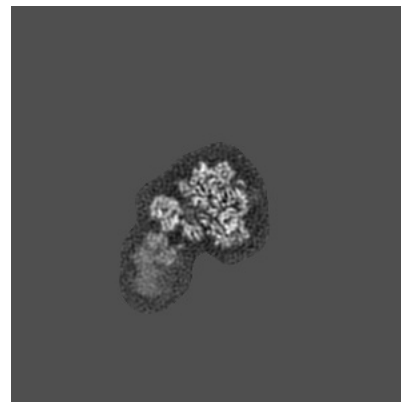
6.3.1 Primary map



X Index: 206



Y Index: 192

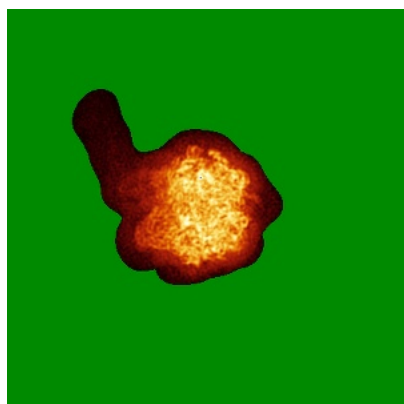


Z Index: 226

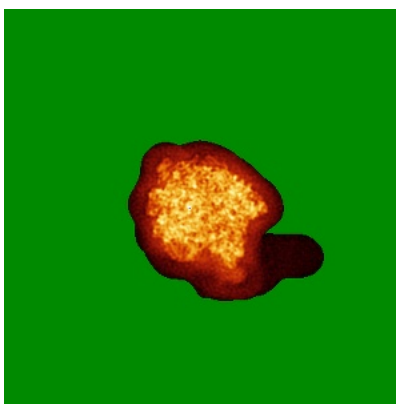
The images above show the largest variance slices of the map in three orthogonal directions.

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

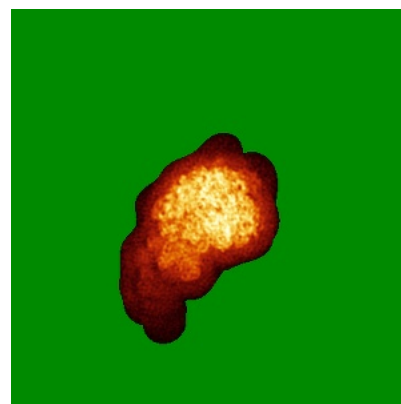
6.4.1 Primary map



X



Y

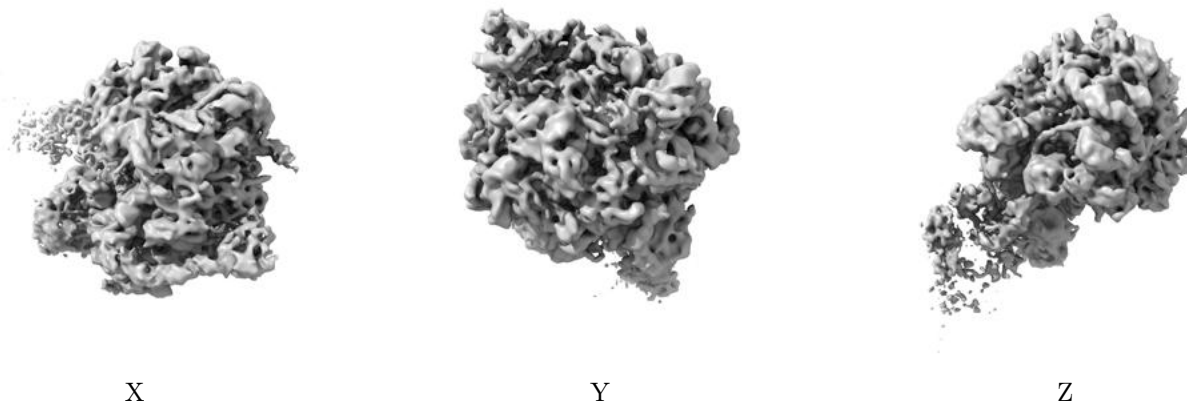


Z

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 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

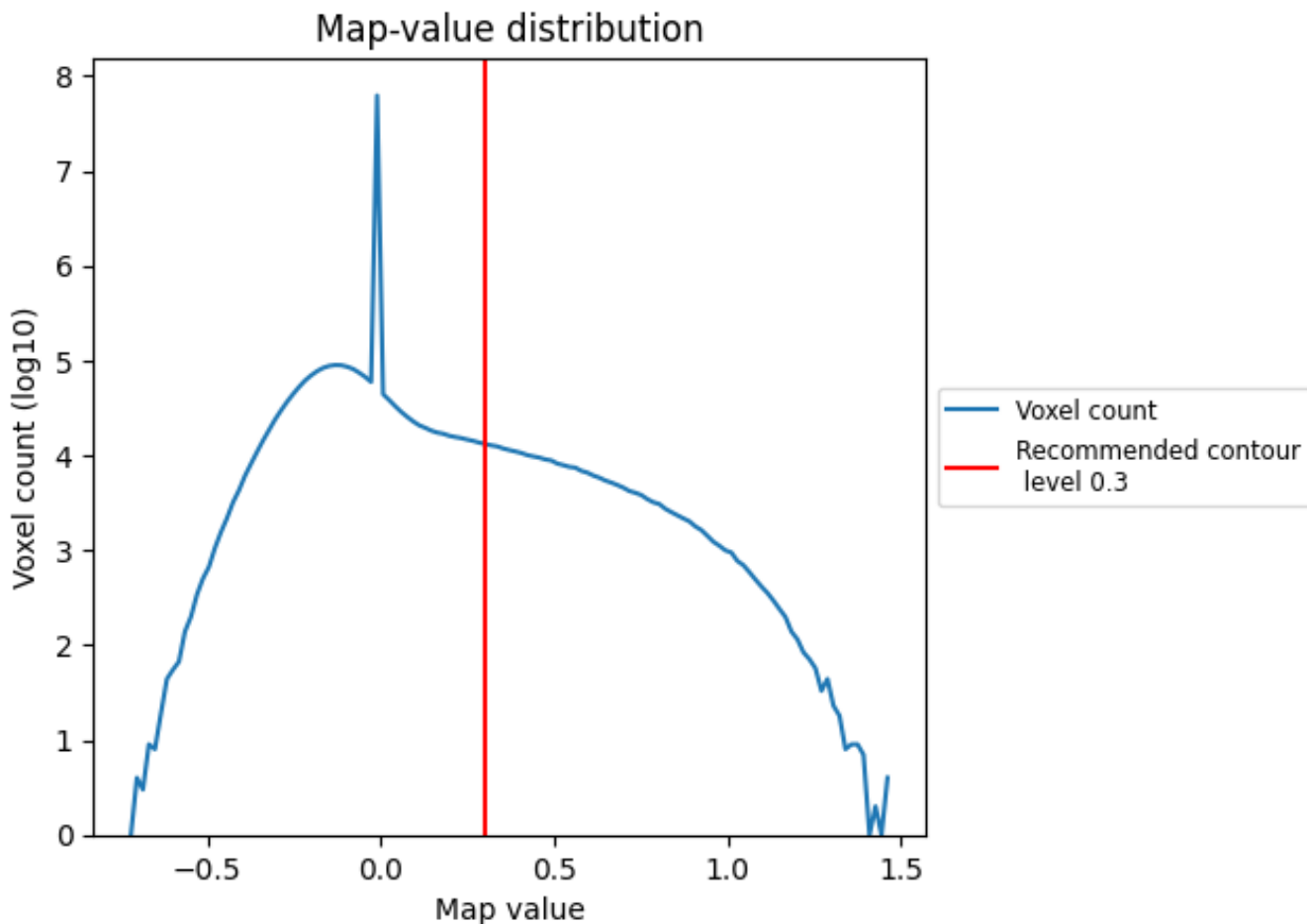
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

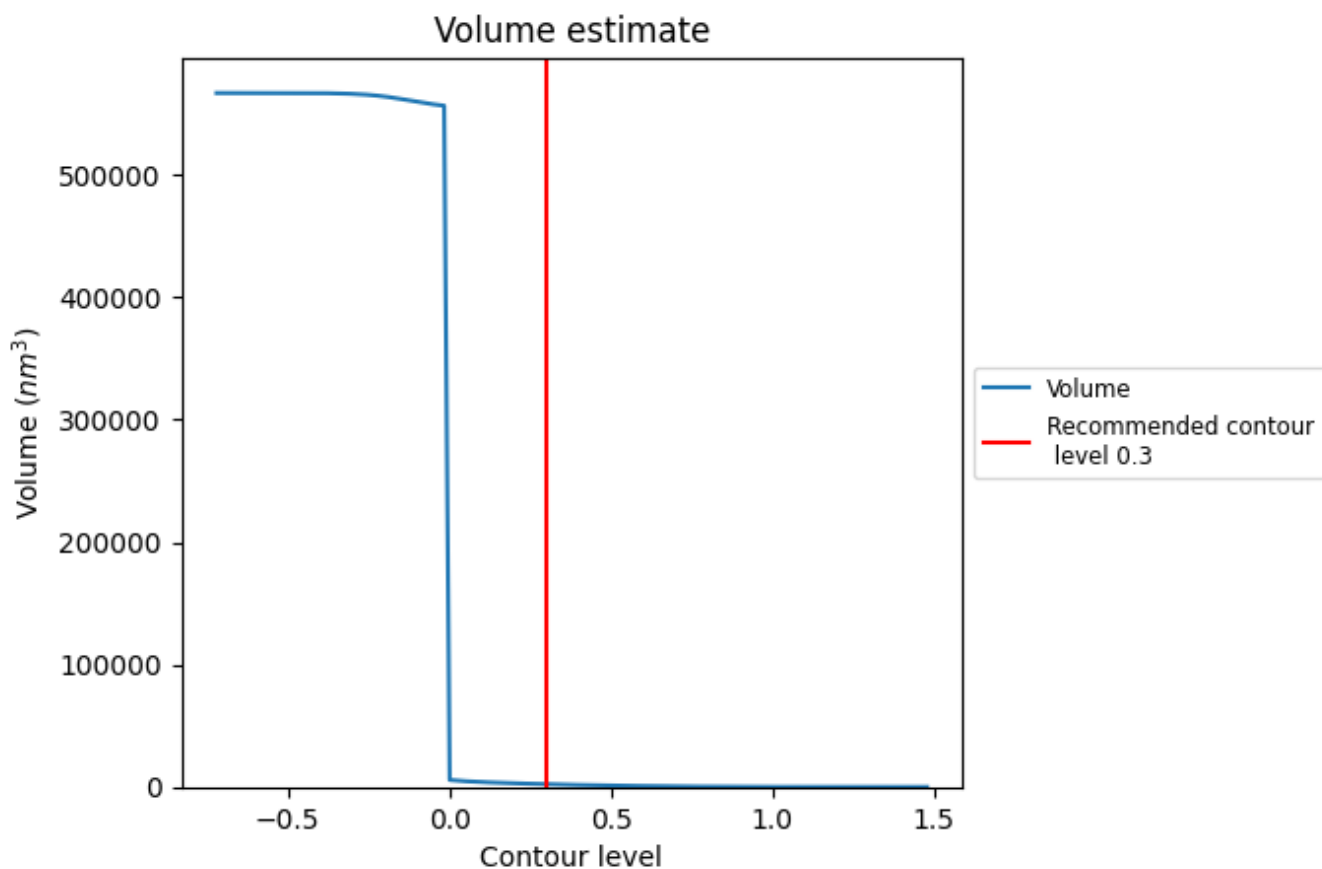
This section contains the results of statistical analysis of the map.

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.

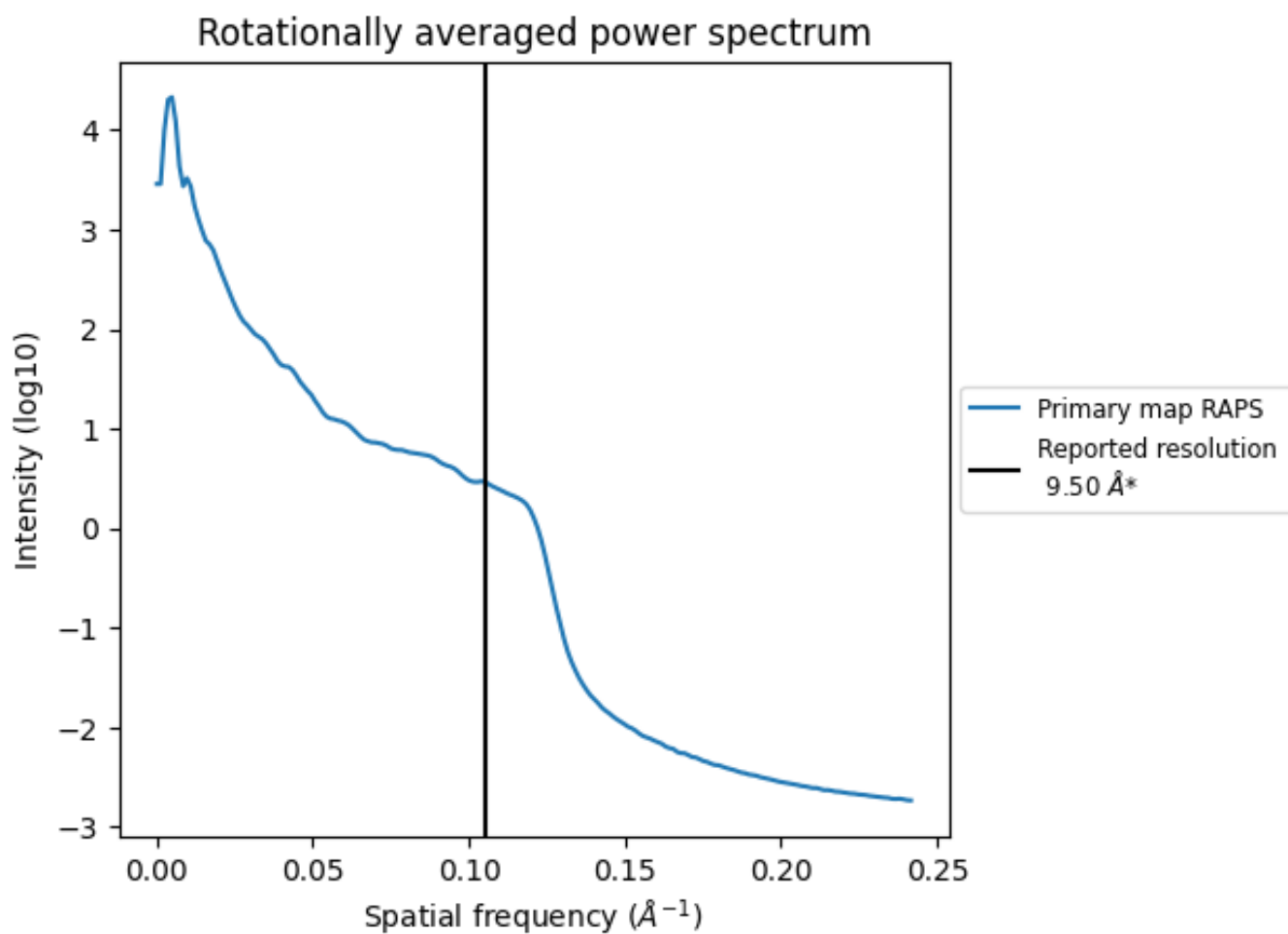
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2263 nm³; this corresponds to an approximate mass of 2044 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.105\AA^{-1}

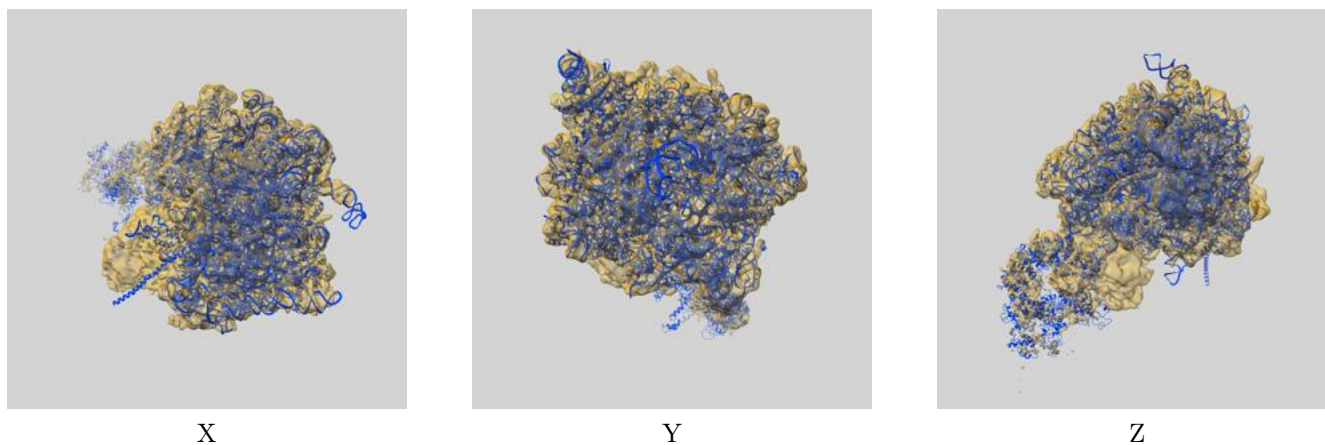
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

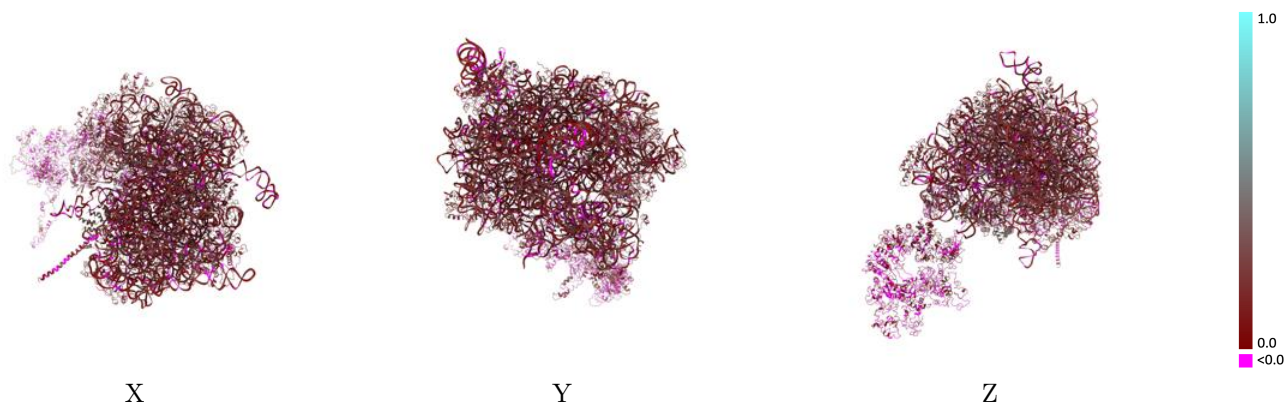
This section contains information regarding the fit between EMDB map EMD-3199 and PDB model 5JCS. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



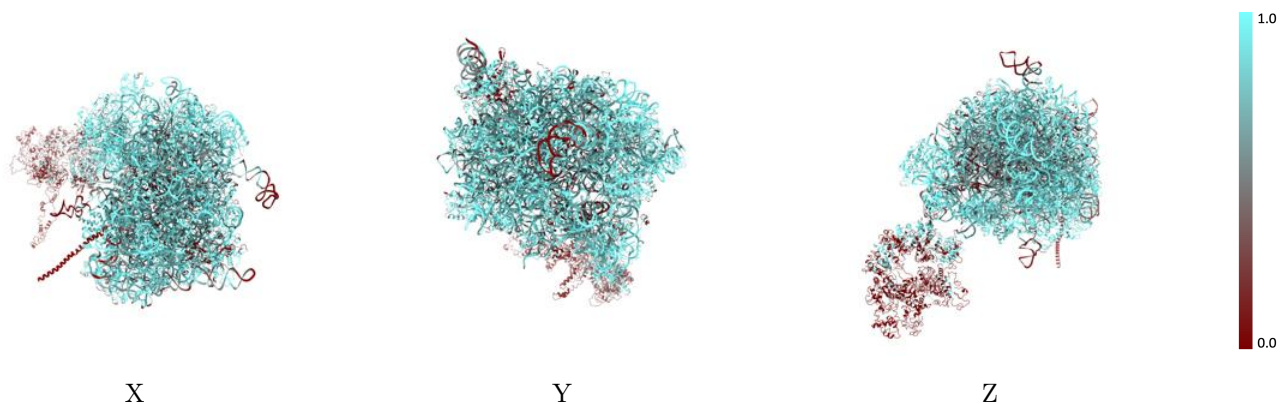
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



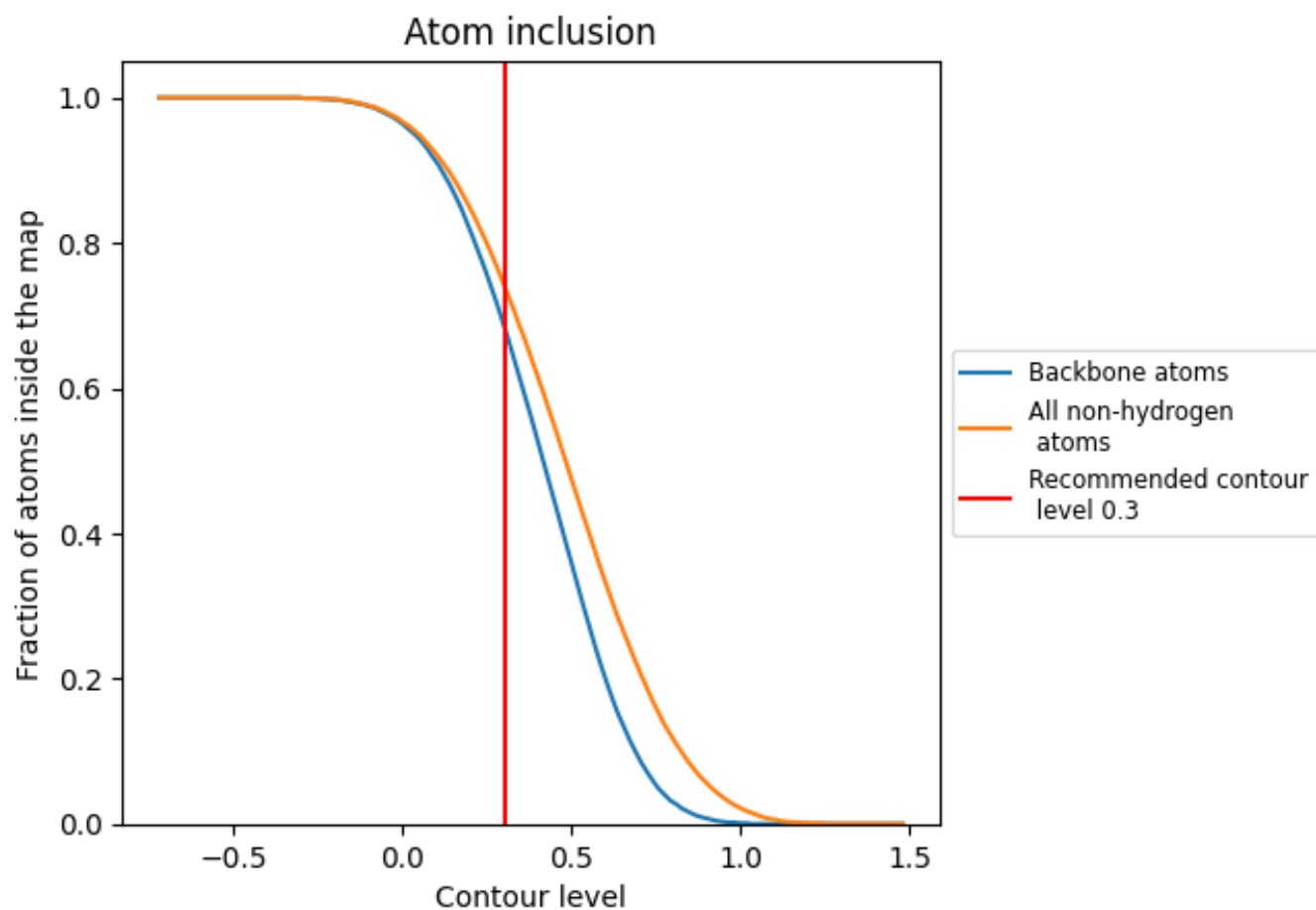
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 74% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7410	 0.1460
A	 0.5510	 0.1300
B	 0.7680	 0.1560
C	 0.6970	 0.1620
D	 0.8290	 0.1880
E	 0.8120	 0.1930
F	 0.8750	 0.2170
G	 0.7940	 0.1700
H	 0.8720	 0.2110
I	 0.1440	 0.0270
J	 0.9730	 0.2200
K	 0.7730	 0.1550
L	 0.8150	 0.2240
M	 0.8550	 0.2100
N	 0.7160	 0.1600
O	 0.7520	 0.1850
P	 0.7000	 0.1780
Q	 0.6290	 0.1620
R	 0.4970	 0.1260
S	 0.8600	 0.2170
T	 0.3450	 0.0350
U	 0.9220	 0.2360
V	 0.7270	 0.1850
X	 0.6830	 0.1650
Y	 0.8090	 0.1760
Z	 0.8530	 0.1750
a	 0.5790	 0.1180
c	 0.8350	 0.2030
d	 0.7770	 0.1850
e	 0.7100	 0.1950
f	 0.7710	 0.1620
g	 0.5350	 0.1170
h	 0.8700	 0.2310
i	 0.7520	 0.1900
j	 0.5590	 0.1000



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Chain	Atom inclusion	Q-score
k	 0.8830	 0.2150
l	 0.6430	 0.1760
m	 0.9350	 0.1940
n	 0.9520	 0.2070
o	 0.8750	 0.2300
p	 0.6420	 0.1540
q	 0.8610	 0.1840
r	 0.9720	 0.3470
s	 0.2120	 0.0620
t	 0.8130	 0.1450
u	 0.5510	 0.1670
x	 0.7880	 0.1400
y	 0.8110	 0.1410
z	 0.8850	 0.1520