



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 01:57 pm BST

PDB ID : 9SKD / pdb_00009skd
EMDB ID : EMD-53630
Title : Model of M. pneumoniae 50S membrane complex
Authors : Dobbs, J.M.; Mahamid, J.
Deposited on : 2025-09-02
Resolution : 7.70 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:

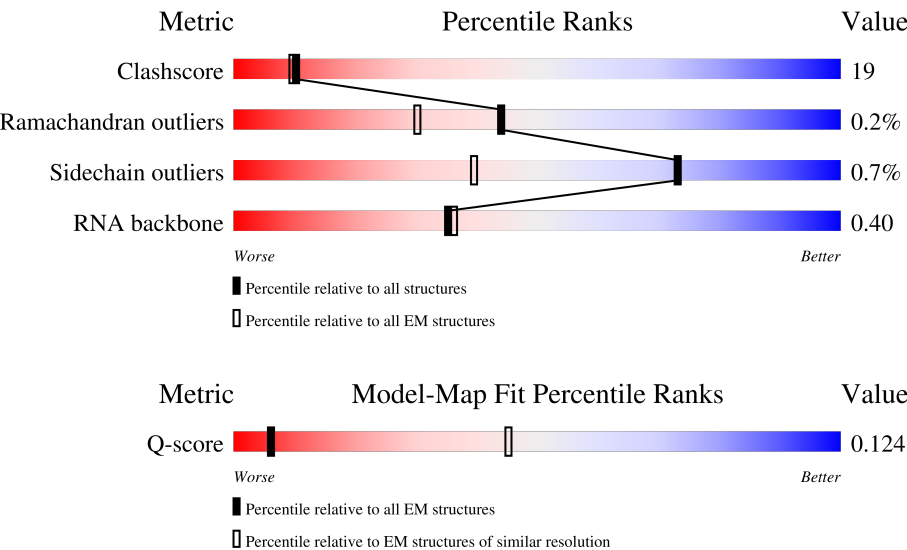
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.70 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.



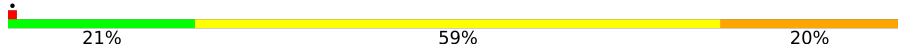
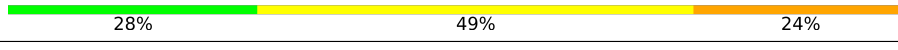
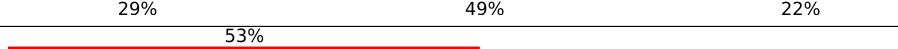
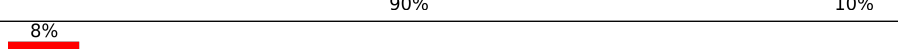
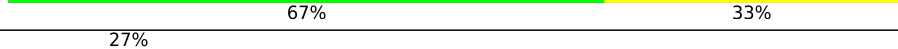
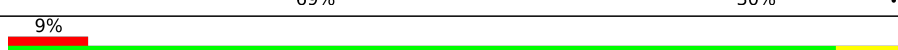
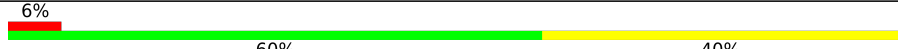
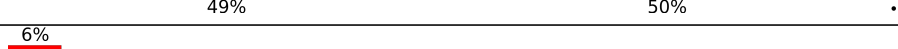
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	384 (7.20 - 8.20)

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	0	47	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	3	2878	
5	4	105	
6	8	51	
7	9	944	
8	A	161	
9	B	29	
9	C	29	
9	D	29	
9	E	29	
10	a	285	
11	b	229	
12	c	210	
13	d	175	
14	e	176	
15	f	145	
16	h	128	
17	i	144	
18	j	122	
19	k	148	
20	l	136	
21	m	119	
22	n	116	
23	o	115	
24	p	114	
25	q	99	

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Mol	Chain	Length	Quality of chain
26	r	139	
27	s	92	
28	t	111	
29	u	86	
30	v	63	
31	w	108	
32	x	44	
33	y	56	
34	z	50	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 100646 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 Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 6 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	51	Total	C	N	O	P	0	0
			1083	484	190	359	50		

- Molecule 7 is a protein called SecDF.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	9	899	Total	C	N	O	S	0	0
			7063	4595	1165	1293	10		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	161	Total	C	N	O	S	0	0
			1239	796	213	225	5		

- Molecule 9 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
9	C	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
9	D	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
9	E	29	Total	C	N	O	S	0	0
			232	146	34	50	2		

- Molecule 10 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	e	176	Total	C	N	O		0	0
			1396	899	247	250			

- Molecule 15 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	k	148	Total	C	N	O		0	0
			1153	731	226	196			

- Molecule 20 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 21 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 22 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 23 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 24 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 25 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 29 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 30 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	w	100	Total	C	N	O	S	0	0
			818	517	153	148			

- Molecule 32 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 33 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

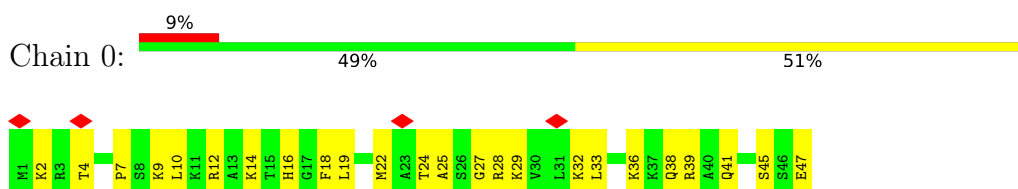
- Molecule 34 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	z	50	Total 408	C 255	N 81	O 68	S 4	0	0

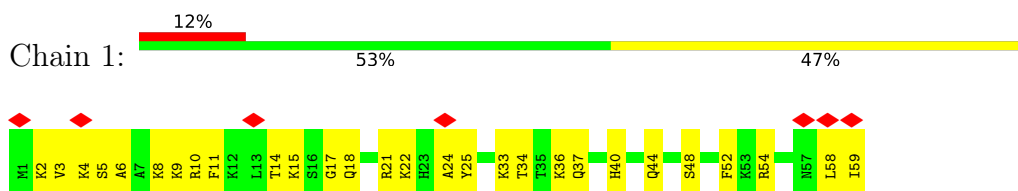
3 Residue-property plots

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.

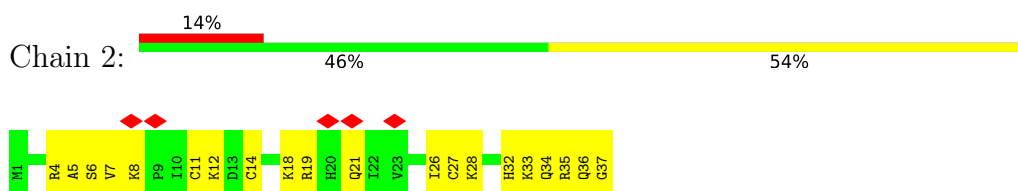
- Molecule 1: Large ribosomal subunit protein bL34



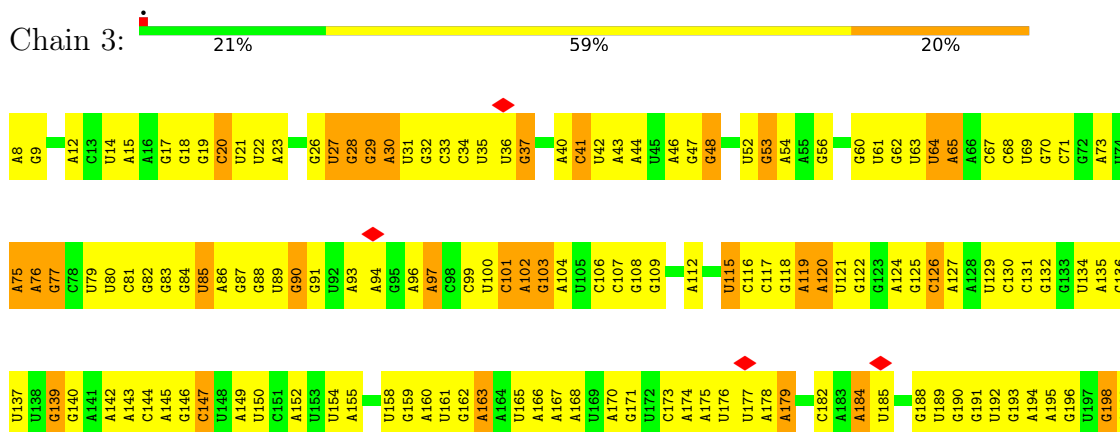
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

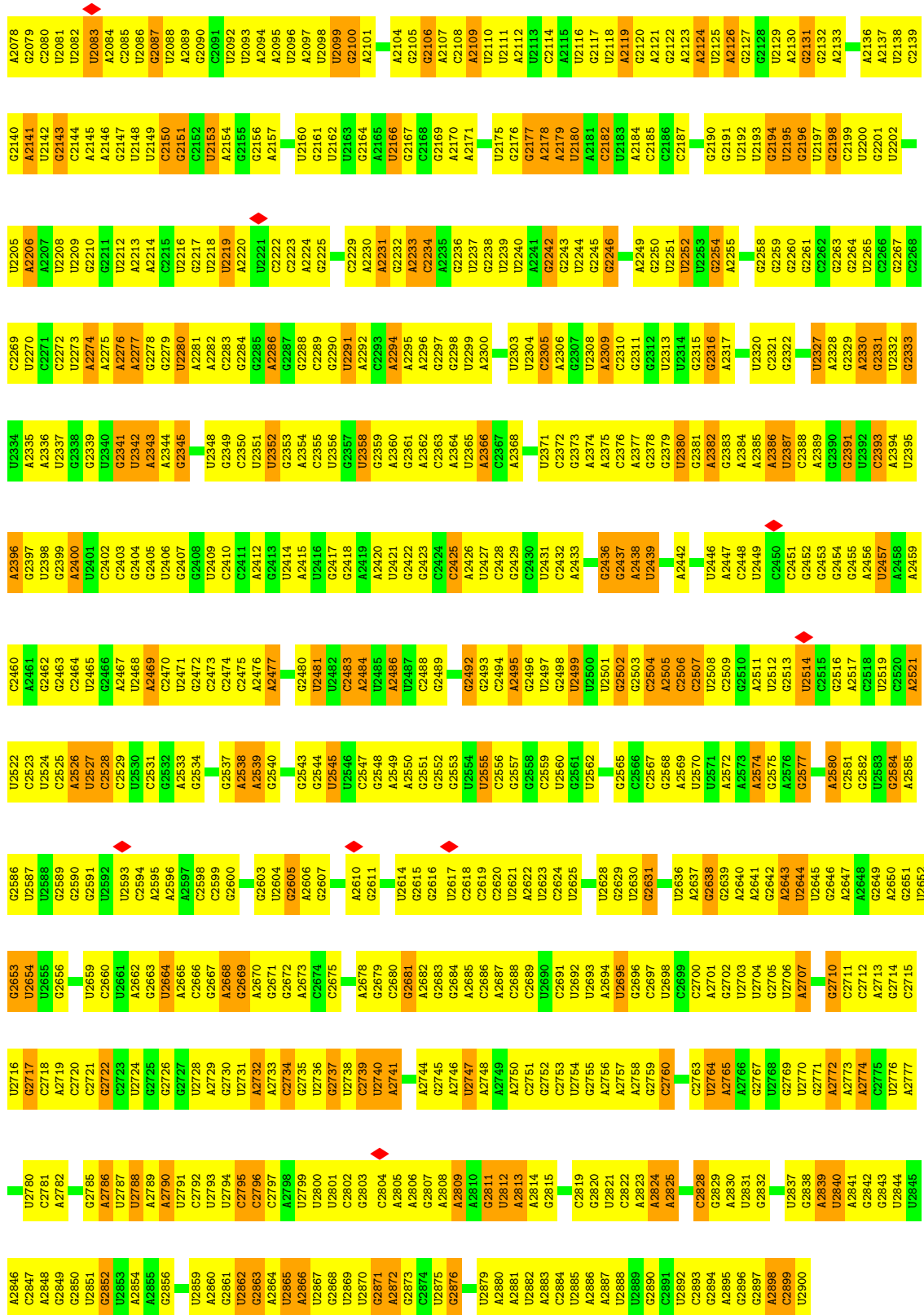


- Molecule 4: 23S ribosomal RNA

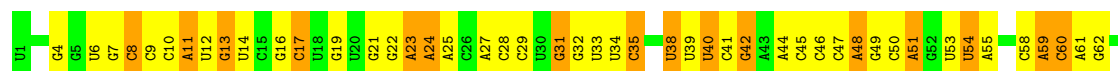




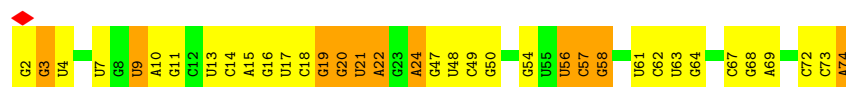
G2017	G1814	C1881	G1814	G1623	G1550	U1488	U1425	U1360	A1298	A1238	G1172
U2018	U1815	G1882	U1815	A1624	U1551	G1489	C1426	U1361	A1299	G1239	G1173
G2019	A1816	G1883	G1887	G1625	C1552	G1490	C1427	C1362	C1300	U1240	G1174
A2020	A1817	A1884	A1887	G1626	G1553	G1491	G1553	C1363	G1301	U1241	C1175
A2021	G1818	G1885	A1889	U1627	A1554	G1492	A1554	A1364	C1302	G1242	U1176
A2022	G1819	G1886	G1890	G1628	G1555	A1493	A1431	A1303	U1303	A1243	A1177
U2023	U1820	U1887	G1757	U1629	U1556	U1494	C1432	G1367	U1304	A1244	A1178
C2024	G1821	U1888	C1758	A1630	G1557	A1495	U1433	U1368	G1305	A1179	
C2025	A1822	C1759	A1631	A1631	U1558	A1496	U1434	U1369	G1306		
A2026	U1823	G1760	A1694	C1632	A1559	A1497	A1435	U1370	G1307	U1246	U1182
G2027	G1824	C1761	G1695	C1633	A1570	C1436	A1436	G1371	A1308	C1247	
G2028	U1825	G1696	C1697	A1634	G1571		A1437	U1372	A1309	A1248	
G2029	U1826	G1763	G1697	G1635	U1572	U1501	U1440	C1373	U1310	U1184	U1185
A2030	U1827	U1764	A1698	U1636	A1573	A1502	U1441	U1374	G1311	A1250	U1186
C2031	A1828	G1765	A1699	A1637	G1574	A1503	G1442	G1375	A1312	G1251	A1187
G2032	U1829	A1766	G1700	C1638	C1575	G1504	G1444		G1313	G1252	C1187
G2033	G1830	A1767	G1639	G1639	G1576	G1505	A1443	C1378	A1314	G1253	C1188
G2034	G1831	G1768	A1702	G1640	A1577	U1506	A1444	C1379	A1315	U1254	A1189
U2035	G1832	A1769	A1703	A1641	A1578	G1507	U1445	U1380	U1316	A1255	A1190
G2036		A1770	C1704	G1642	G1579	U1508	G1446	A1381	C1317	A1256	A1191
A2037	G1835	C1771	U1705	A1643	G1580	G1509	A1447	A1382	U1318	G1257	U1192
A2038	A1836	G1772	C1706	A1644	U1581	A1510	U1448	G1383	C1319	U1258	
G2039	C1837		U1707	A1645	G1582	C1511	G1449	A1384	U1320	A1259	U1194
A2040	A1838	G1776	G1708	G1646	U1584	A1512	G1450	U1385	C1321	U1260	A1195
A2041	C1839	G1777	G1709	A1647	U1584	A1513	G1451	G1386	A1322	G1261	U1196
A2042	C1840	G1778	A1710	A1648	A1585	U1514	G1452	A1387	A1323	G1262	G1197
C2043	U1841	G1779		C1649	U1586				A1324	G1263	G1198
C2044	G1842	A1780	U1713	A1650	G1587	A1515	A1455	G1388	C1325	U1264	A1199
C2045	C1843	G1781	U1714	C1651	A1588		C1456	G1389	C1326	G1265	U1200
G2046	C1844	U1782	A1715	A1652	U1590	A1519	A1457	G1392	A1327	A1267	A1201
	C1845	U1783	A1716	G1653	G1591	A1520	A1458	A1393	A1328	U1268	U1206
A2049		U1784	U1717	G1654	C1592	A1521	U1459	A1394	U1329	U1269	U1207
G2050	G1846	U1785	C1717	U1655	U1593	U1522	G1460	A1395	U1330	C1270	A1208
G2051	U1847	U1786	G1718	A1656	G1594	C1524	A1461			A1271	U1209
C2052	G1848					G1525	A1462	C1398	U1334	A1272	A1210
G2053	C1850	U1787	G1721			U1526	G1463	G1399	A1335	U1273	U1211
C2054	U1851	A1788	U1722	C1659	U1597	G1526	G1464	U1400	A1336	A1274	C1212
A2055	G1852	G1789	A1723	A1660	U1598	U1527	U1465	A1401	G1337	C1275	U1213
A2056	G1853	U1790	G1725	A1661	C1599	G1528	U1466	G1402	G1338	U1276	U1214
C2057	A1854	A1791	G1726	G1662	A1600	U1529	U1467	G1403	U1339	A1277	G1215
G2058	G1855	A1792	U1727	G1663	A1601	G1530	U1468	C1404	U1340	G1278	U1216
G2059	A1856	A1793	U1728	G1665	G1602	C1531	C1469	G1405	U1341	U1279	U1217
G2060	G1857	A1794	A1728	G1666	A1603	A1532	C1470	A1406	C1342	G1280	G1218
A2061	U1858	G1795		A1667	A1604	U1533	A1471	U1407	C1343	U1219	U1219
C2062	U1859	C1797	A1731	G1668	A1534	U1534	C1472	G1408	U1344	A1220	A1220
G2063	A1860	A1798	G1732	A1669	A1605	A1535	C1473	G1409	G1345	G1282	G1282
G2064	A1861	G1799	A1733	U1670	C1536	C1536	C1474	A1284	A1346	A1283	G1221
A2065	A1862	C1800	A1735	C1671	U1509	A1537	C1475	U1285	A1347	U1285	
A2066	G1863	U1801		C1672	U1610	U1538	C1476		C1348	G1286	G1226
A2067	A1864	C1802	G1738	U1673	C1611	U1539	U1477	A1413	C1349	C1287	C1227
G2068	A1865	U1803	G1739		U1612	G1540	U1478	A1414		C1288	
A2069	G1866	A1804		G1676	A1613	A1541	U1479	A1415	G1350	G1289	G1228
C2070	G1867	U1805		G1677	G1614	G1542	U1480	G1416	G1351	U1229	U1229
C2071	A1868	G1806	U1744	U1678	G1615	U1543	U1481	G1417	G1352	G1290	U1230
G2072	G1869	C1807	U1745	A1679	G1616	G1544	U1482	U1418	G1353	C1291	G1231
C2073	G1870	A1745	U1746	U1680	U1618	G1545	U1483	U1419	U1292	U1232	U1232
G2074	U1871	C1808	U1747	G1681	A1619	A1546	G1484	A1420	U1293	A1233	A1233
C2075	U1872	A1809	G1747	G1682	U1620	U1547	G1485	A1421	G1355	G1294	U1234
G2076	A1873		U1748	G1683	A1621	A1548	U1486	A1422	C1356	U1295	U1235
A2077		C1812	A1749	A1684	G1622	G1549	U1487	A1424	C1357	G1296	G1236
		C1813	A1750	A1684		U1549			C1358	U1297	G1237



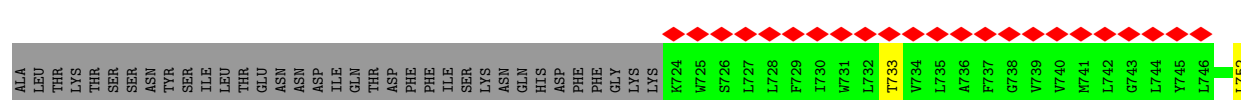
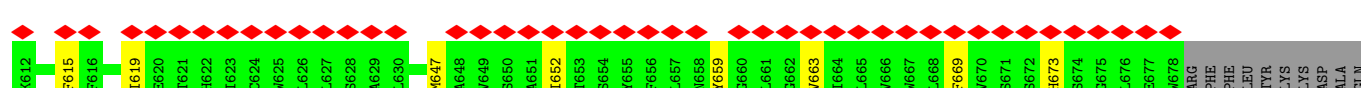
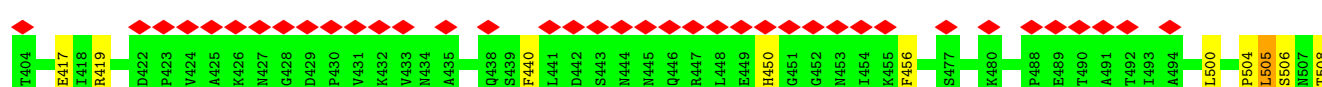
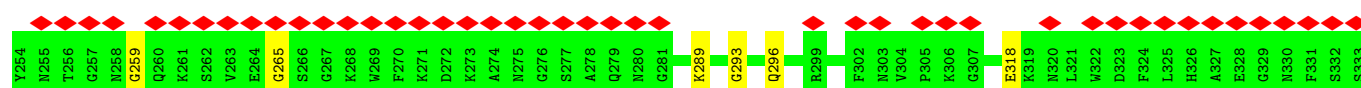
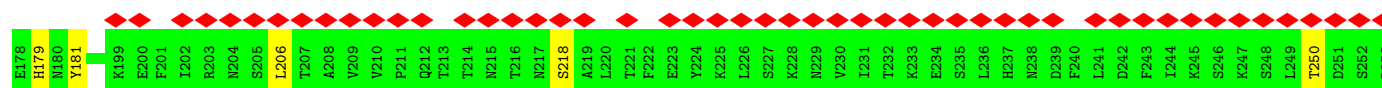
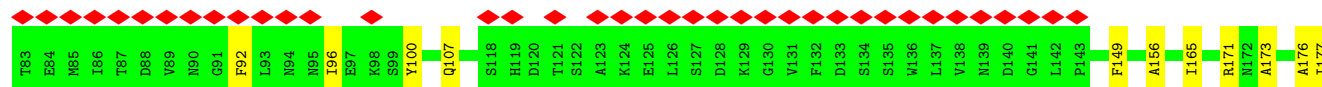
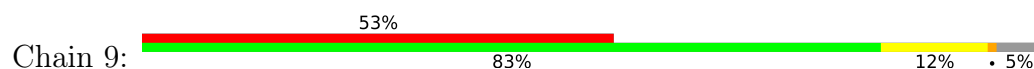
Molecule 5: 5S ribosomal RNA

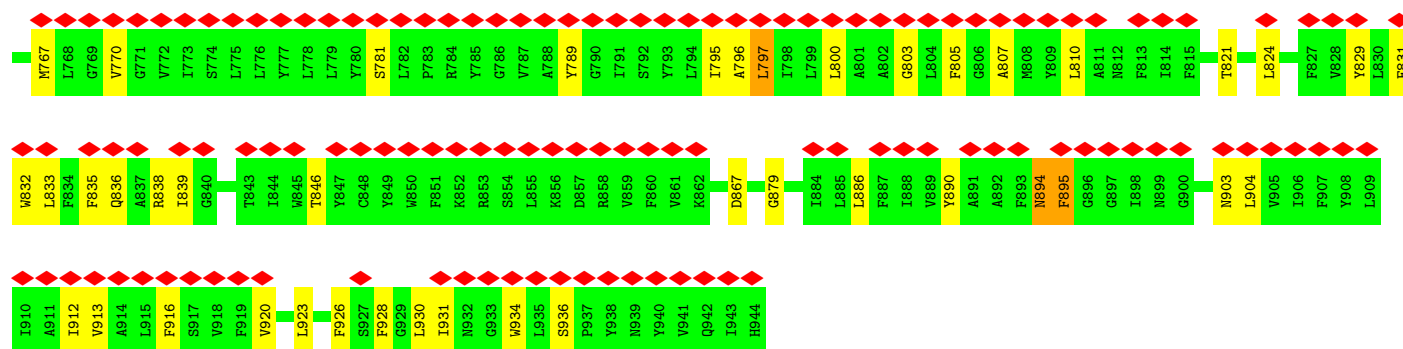


• Molecule 6: tRNA-Phe

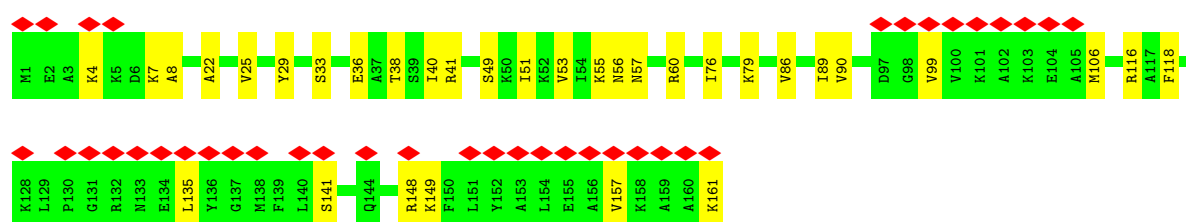
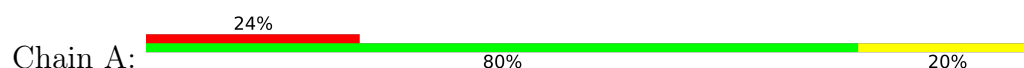


• Molecule 7: SecDF

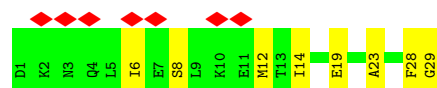
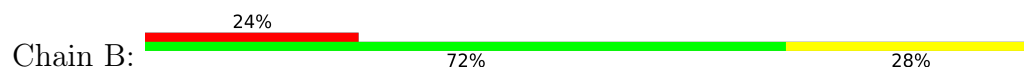




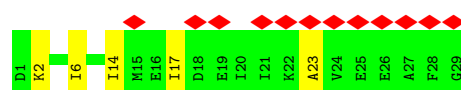
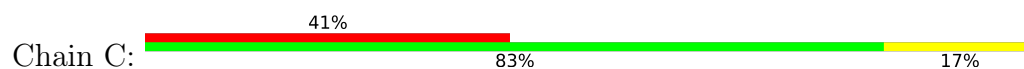
• Molecule 8: 50S ribosomal protein L10



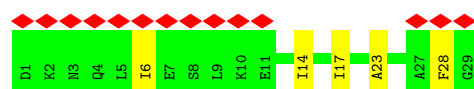
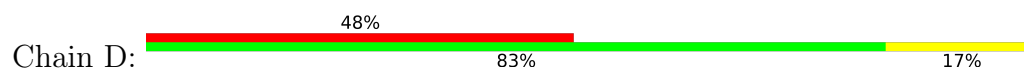
• Molecule 9: Large ribosomal subunit protein bL12



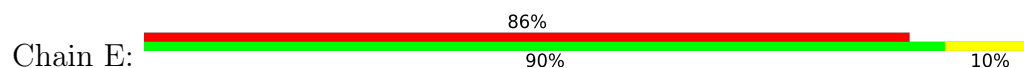
• Molecule 9: Large ribosomal subunit protein bL12



• Molecule 9: Large ribosomal subunit protein bL12

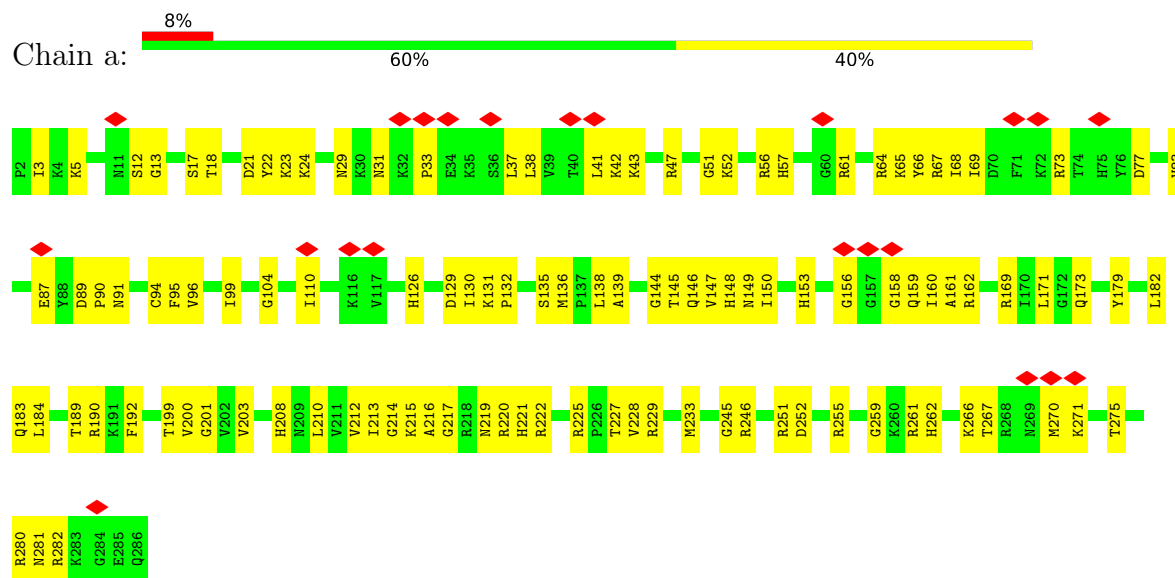


• Molecule 9: Large ribosomal subunit protein bL12

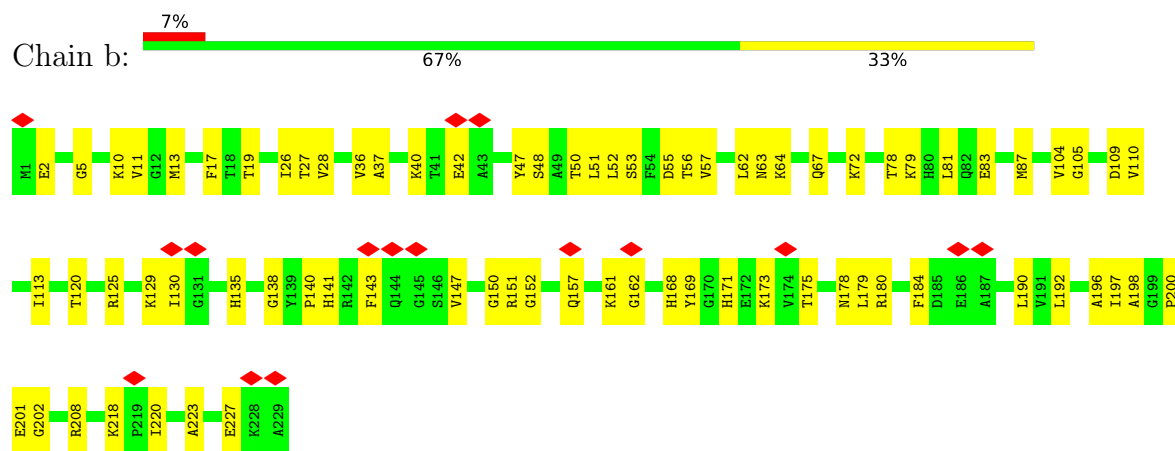




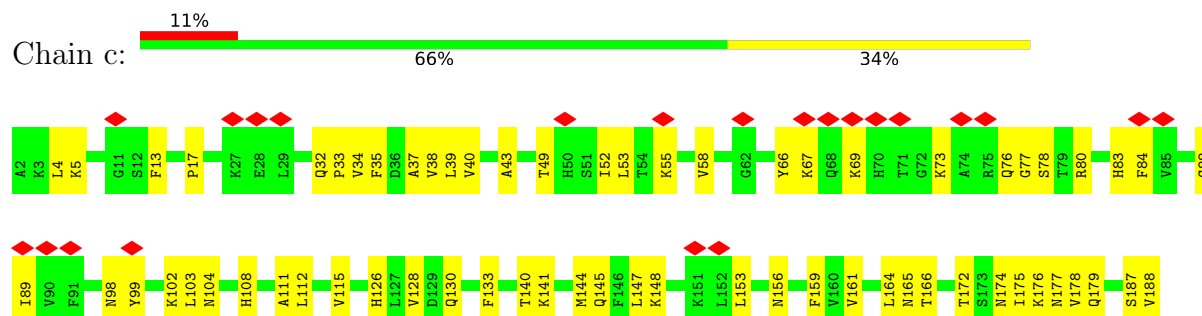
• Molecule 10: Large ribosomal subunit protein uL2

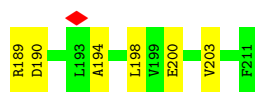


• Molecule 11: Large ribosomal subunit protein uL3



• Molecule 12: Large ribosomal subunit protein uL4

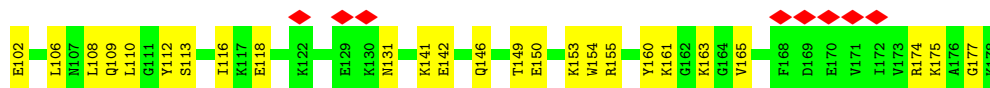




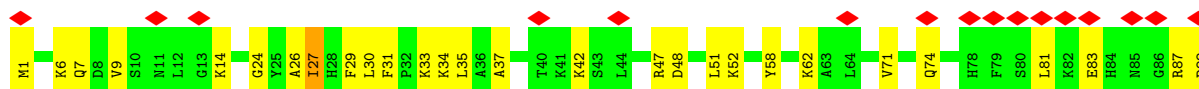
- Molecule 13: Large ribosomal subunit protein uL5



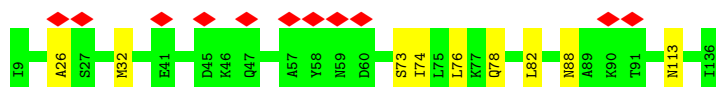
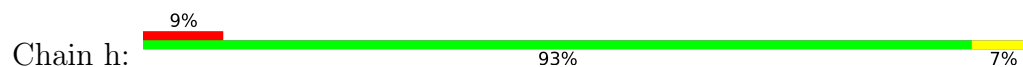
- Molecule 14: Large ribosomal subunit protein uL6



- Molecule 15: Large ribosomal subunit protein bL9

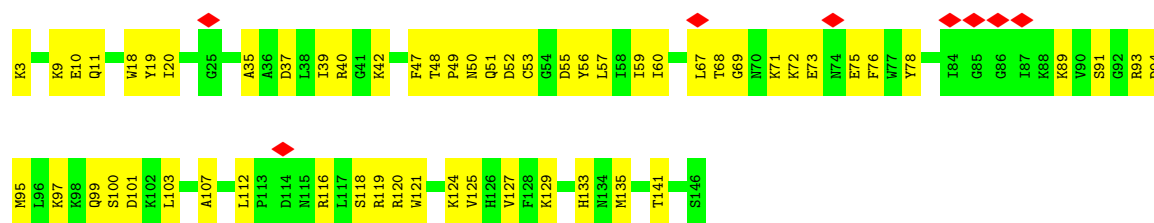


- Molecule 16: Large ribosomal subunit protein uL11

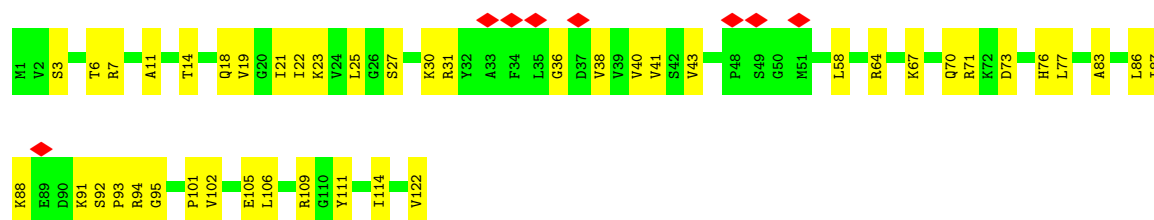


- Molecule 17: Large ribosomal subunit protein uL13

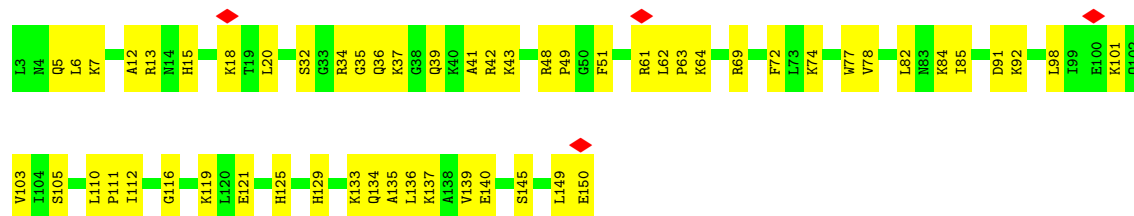




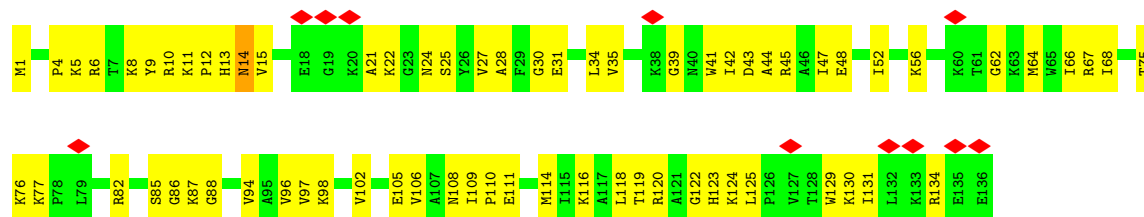
• Molecule 18: 50S ribosomal protein L14



• Molecule 19: Large ribosomal subunit protein uL15

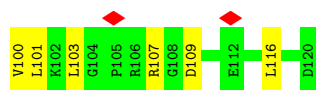


• Molecule 20: Large ribosomal subunit protein uL16



• Molecule 21: Large ribosomal subunit protein bL17





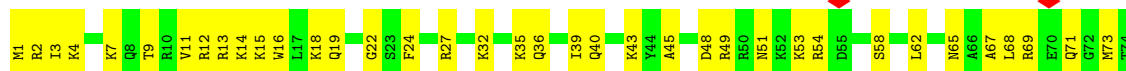
- Molecule 22: Large ribosomal subunit protein uL18



- Molecule 23: Large ribosomal subunit protein bL19



- Molecule 24: Large ribosomal subunit protein bL20

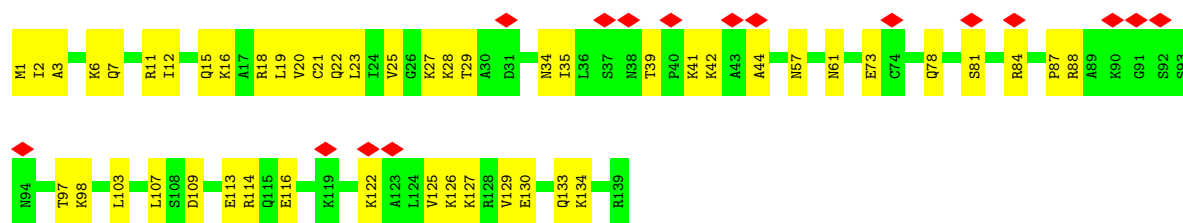


- Molecule 25: Large ribosomal subunit protein bL21

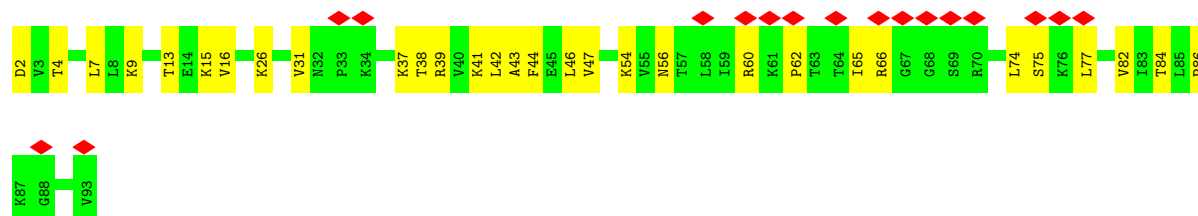


- Molecule 26: Large ribosomal subunit protein uL22

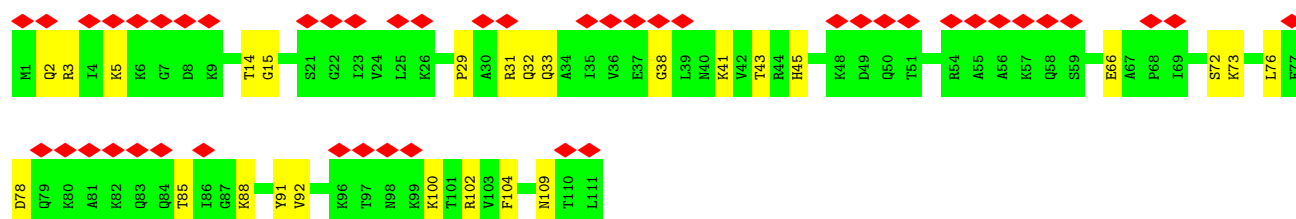
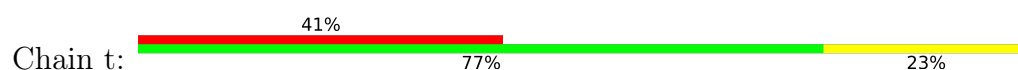




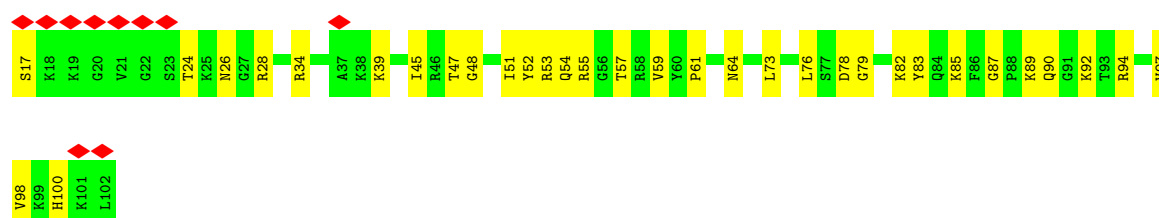
- Molecule 27: Large ribosomal subunit protein uL23



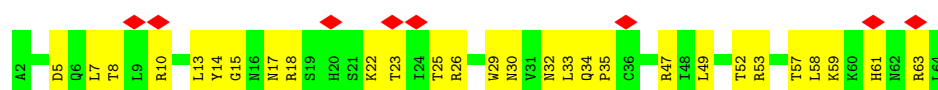
- Molecule 28: 50S ribosomal protein L24



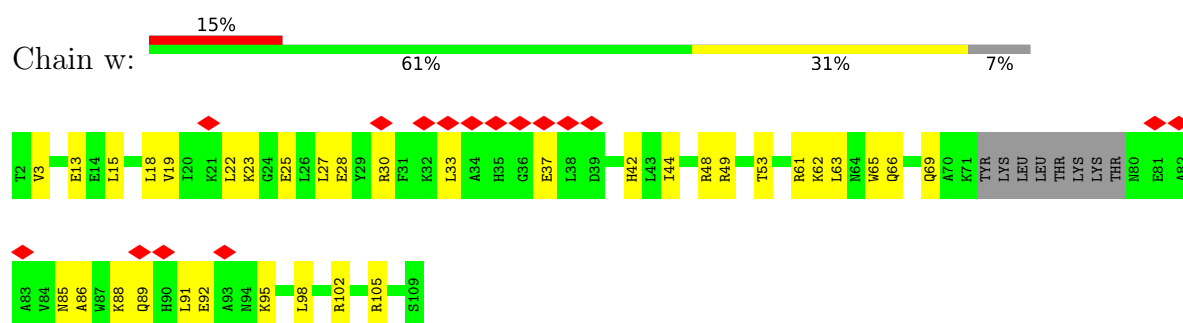
- Molecule 29: Large ribosomal subunit protein bL27



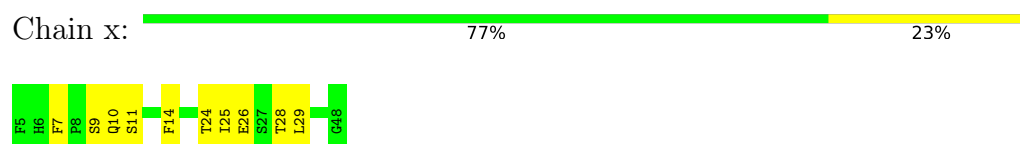
- Molecule 30: Large ribosomal subunit protein bL28



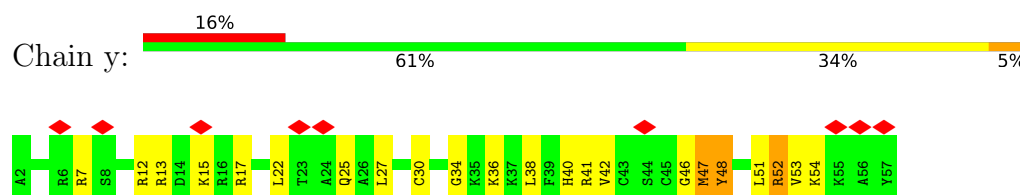
- Molecule 31: Large ribosomal subunit protein uL29



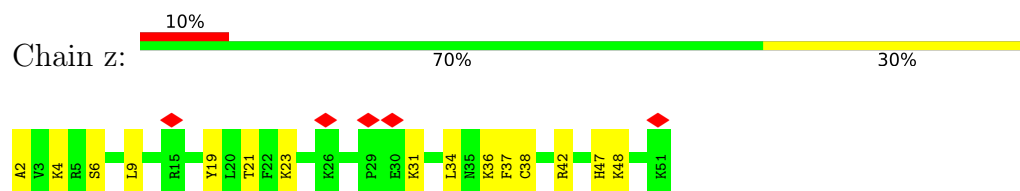
- Molecule 32: Large ribosomal subunit protein bL31



- Molecule 33: Large ribosomal subunit protein bL32



- Molecule 34: Large ribosomal subunit protein bL33A



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2877	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 ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.015	Depositor
Minimum map value	-0.006	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00147	Depositor
Map size (Å)	600.0, 600.0, 600.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0, 2.0, 2.0	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	0	0.13	0/383	0.40	0/504
2	1	0.12	0/484	0.39	0/637
3	2	0.12	0/306	0.42	0/401
4	3	0.10	0/69073	0.25	0/107710
5	4	0.10	0/2505	0.27	0/3902
6	8	0.12	0/1208	0.31	0/1879
7	9	0.75	0/7216	1.28	12/9795 (0.1%)
8	A	0.68	0/1254	1.10	0/1677
9	B	0.64	0/232	1.16	2/307 (0.7%)
9	C	0.61	0/232	1.09	0/307
9	D	0.64	0/232	1.04	0/307
9	E	0.63	0/232	1.07	0/307
10	a	0.15	0/2267	0.41	0/3044
11	b	0.14	0/1795	0.42	0/2412
12	c	0.13	0/1671	0.38	0/2246
13	d	0.15	0/1409	0.43	0/1894
14	e	0.15	0/1420	0.39	0/1912
15	f	0.15	0/1183	0.47	1/1587 (0.1%)
16	h	0.14	0/968	0.43	1/1298 (0.1%)
17	i	0.12	0/1186	0.40	0/1592
18	j	0.13	0/953	0.39	0/1275
19	k	0.15	0/1170	0.42	0/1559
20	l	0.15	0/1104	0.42	0/1481
21	m	0.13	0/973	0.40	0/1309
22	n	0.13	0/897	0.44	0/1198
23	o	0.15	0/948	0.42	0/1262
24	p	0.16	0/961	0.41	0/1278
25	q	0.15	0/828	0.42	0/1111
26	r	0.13	0/1077	0.37	0/1441
27	s	0.13	0/732	0.41	0/988
28	t	0.14	0/879	0.39	0/1165
29	u	0.15	0/665	0.47	0/884
30	v	0.14	0/519	0.41	0/695
31	w	0.14	0/826	0.40	0/1104

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	x	0.12	0/353	0.37	0/474
33	y	0.32	0/457	0.68	1/601 (0.2%)
34	z	0.14	0/412	0.38	0/547
All	All	0.24	0/109010	0.45	17/162090 (0.0%)

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
7	9	0	4
20	1	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	9	42	LEU	CA-C-N	8.33	137.74	121.41
7	9	42	LEU	C-N-CA	8.33	137.74	121.41
7	9	509	LEU	N-CA-C	6.26	119.09	111.82
7	9	402	ASP	CA-CB-CG	6.23	118.83	112.60
7	9	43	GLY	N-CA-C	6.20	127.87	113.18

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	9	362	TYR	Sidechain
7	9	399	ARG	Peptide
7	9	419	ARG	Sidechain
7	9	450	HIS	Peptide
20	1	14	ASN	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	0	380	0	429	23	0
2	1	477	0	530	25	0
3	2	304	0	350	21	0
4	3	61664	0	30953	2241	0
5	4	2239	0	1137	52	0
6	8	1083	0	550	57	0
7	9	7063	0	7119	56	0
8	A	1239	0	1309	101	0
9	B	232	0	237	10	0
9	C	232	0	237	7	0
9	D	232	0	237	9	0
9	E	232	0	237	7	0
10	a	2225	0	2301	106	0
11	b	1762	0	1808	65	0
12	c	1644	0	1731	57	0
13	d	1388	0	1469	41	0
14	e	1396	0	1481	39	0
15	f	1160	0	1172	32	0
16	h	959	0	1039	7	0
17	i	1164	0	1192	45	0
18	j	944	0	1019	37	0
19	k	1153	0	1256	54	0
20	l	1079	0	1134	52	0
21	m	958	0	1011	35	0
22	n	889	0	952	29	0
23	o	938	0	1008	47	0
24	p	947	0	1028	45	0
25	q	811	0	858	30	0
26	r	1068	0	1150	45	0
27	s	720	0	803	25	0
28	t	872	0	972	19	0
29	u	657	0	695	29	0
30	v	513	0	560	24	0
31	w	818	0	870	26	0
32	x	344	0	333	7	0
33	y	452	0	472	22	0
34	z	408	0	440	14	0
All	All	100646	0	70079	3053	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 19.

The worst 5 of 3053 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)
4:3:1081:A:C8	8:A:7:LYS:CD	2.00	1.42
4:3:1081:A:N7	8:A:7:LYS:HD2	1.19	1.42
4:3:1081:A:C8	8:A:7:LYS:HD2	1.58	1.37
4:3:1119:A:N1	8:A:29:TYR:CE2	1.96	1.32
4:3:2120:G:C1'	6:8:57:C:N4	1.90	1.32

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	0	45/47 (96%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
7	9	895/944 (95%)	849 (95%)	37 (4%)	9 (1%)	12	48
8	A	159/161 (99%)	154 (97%)	4 (2%)	1 (1%)	21	59
9	B	27/29 (93%)	27 (100%)	0	0	100	100
9	C	27/29 (93%)	27 (100%)	0	0	100	100
9	D	27/29 (93%)	27 (100%)	0	0	100	100
9	E	27/29 (93%)	27 (100%)	0	0	100	100
10	a	283/285 (99%)	260 (92%)	23 (8%)	0	100	100
11	b	227/229 (99%)	213 (94%)	14 (6%)	0	100	100
12	c	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
13	d	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
14	e	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
15	f	143/145 (99%)	130 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	h	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
17	i	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
18	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
19	k	146/148 (99%)	137 (94%)	9 (6%)	0	100	100
20	l	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
21	m	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
22	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
23	o	113/115 (98%)	104 (92%)	9 (8%)	0	100	100
24	p	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
25	q	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
26	r	137/139 (99%)	128 (93%)	9 (7%)	0	100	100
27	s	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
28	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
29	u	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
30	v	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
31	w	96/108 (89%)	88 (92%)	8 (8%)	0	100	100
32	x	42/44 (96%)	38 (90%)	4 (10%)	0	100	100
33	y	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
34	z	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
All	All	4443/4574 (97%)	4179 (94%)	254 (6%)	10 (0%)	44	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	9	398	LEU
7	9	43	GLY
7	9	265	GLY
7	9	376	LYS
7	9	400	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/40 (100%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
7	9	766/808 (95%)	741 (97%)	25 (3%)	33	55
8	A	129/129 (100%)	129 (100%)	0	100	100
9	B	26/26 (100%)	26 (100%)	0	100	100
9	C	26/26 (100%)	26 (100%)	0	100	100
9	D	26/26 (100%)	26 (100%)	0	100	100
9	E	26/26 (100%)	26 (100%)	0	100	100
10	a	241/241 (100%)	241 (100%)	0	100	100
11	b	186/186 (100%)	186 (100%)	0	100	100
12	c	182/182 (100%)	182 (100%)	0	100	100
13	d	150/150 (100%)	150 (100%)	0	100	100
14	e	153/153 (100%)	153 (100%)	0	100	100
15	f	123/131 (94%)	123 (100%)	0	100	100
16	h	102/102 (100%)	102 (100%)	0	100	100
17	i	126/126 (100%)	126 (100%)	0	100	100
18	j	103/103 (100%)	103 (100%)	0	100	100
19	k	123/123 (100%)	123 (100%)	0	100	100
20	l	113/113 (100%)	113 (100%)	0	100	100
21	m	105/105 (100%)	105 (100%)	0	100	100
22	n	96/99 (97%)	96 (100%)	0	100	100
23	o	101/101 (100%)	101 (100%)	0	100	100
24	p	100/100 (100%)	100 (100%)	0	100	100
25	q	90/90 (100%)	90 (100%)	0	100	100
26	r	116/116 (100%)	116 (100%)	0	100	100
27	s	82/82 (100%)	82 (100%)	0	100	100
28	t	96/96 (100%)	96 (100%)	0	100	100
29	u	69/69 (100%)	69 (100%)	0	100	100
30	v	58/58 (100%)	58 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	w	87/95 (92%)	87 (100%)	0	100	100
32	x	41/41 (100%)	41 (100%)	0	100	100
33	y	48/48 (100%)	45 (94%)	3 (6%)	16	37
34	z	47/47 (100%)	47 (100%)	0	100	100
All	All	3863/3924 (98%)	3835 (99%)	28 (1%)	73	81

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	9	509	LEU
33	y	52	ARG
7	9	752	LEU
7	9	936	SER
7	9	733	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
15	f	100	GLN
23	o	80	GLN
17	i	17	GLN
22	n	38	HIS
26	r	102	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	3	2875/2878 (99%)	844 (29%)	34 (1%)
5	4	103/105 (98%)	42 (40%)	3 (2%)
6	8	49/51 (96%)	22 (44%)	1 (2%)
All	All	3027/3034 (99%)	908 (29%)	38 (1%)

5 of 908 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	12	A
4	3	14	U
4	3	15	A

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Mol	Chain	Res	Type
4	3	20	C
4	3	27	U

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	3	2506	C
5	4	54	U
4	3	2668	A
4	3	2862	U
6	8	57	C

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	8	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	24:A	O3'	47:G	P	15.45

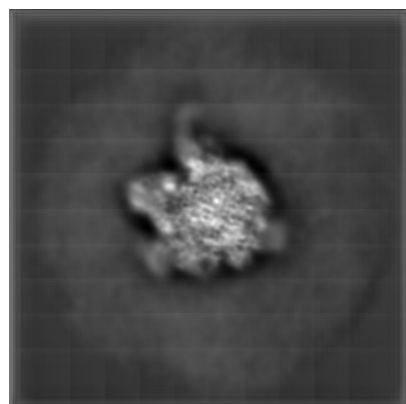
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53630. These allow visual inspection of the internal detail of the map and identification of artifacts.

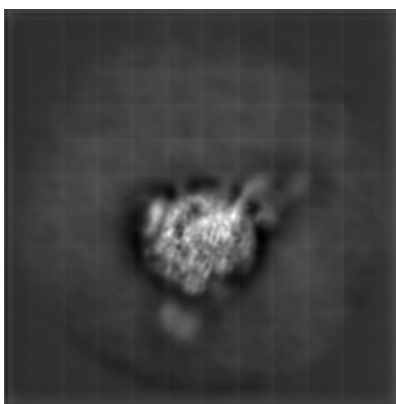
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

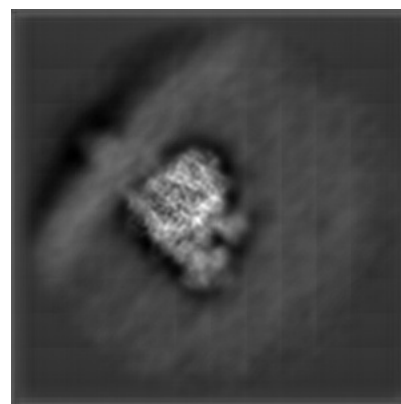
6.1.1 Primary map



X

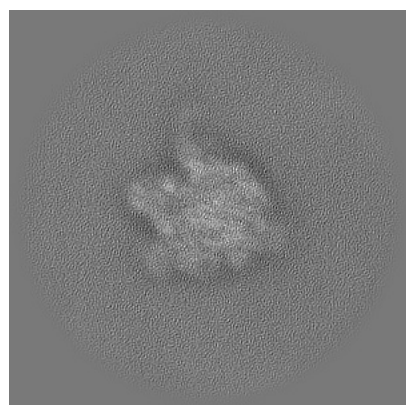


Y

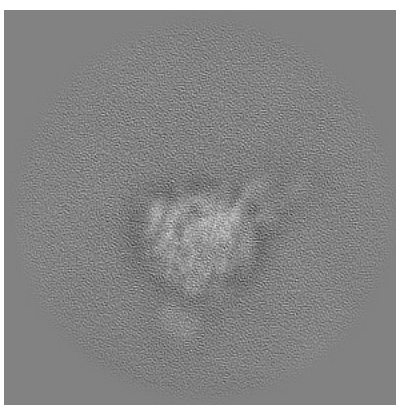


Z

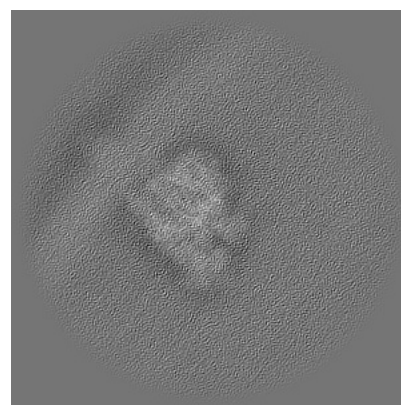
6.1.2 Raw map



X



Y

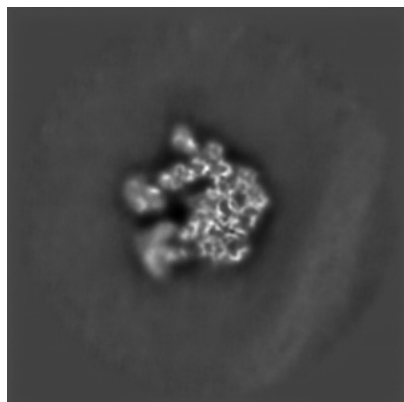


Z

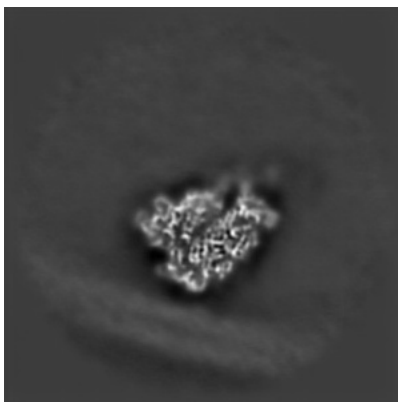
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

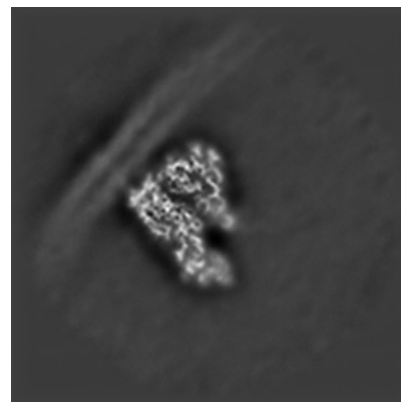
6.2.1 Primary map



X Index: 150

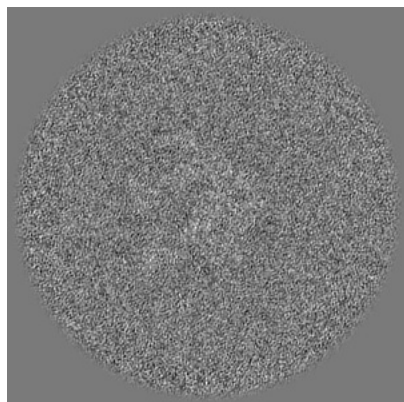


Y Index: 150

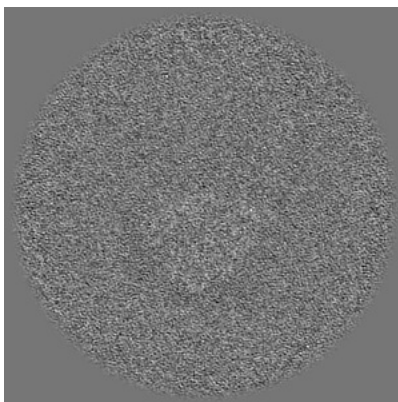


Z Index: 150

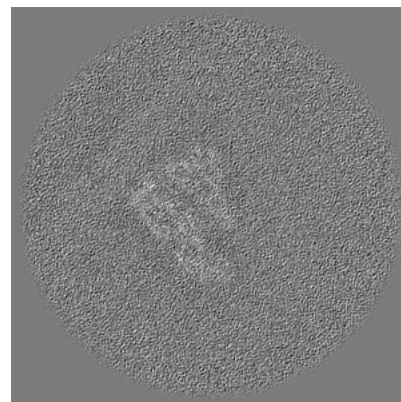
6.2.2 Raw map



X Index: 150



Y Index: 150

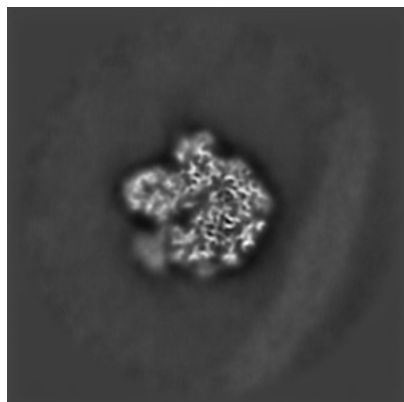


Z Index: 150

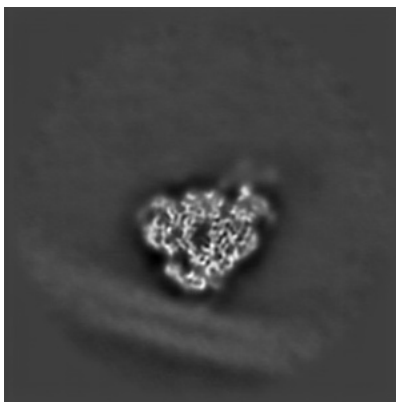
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

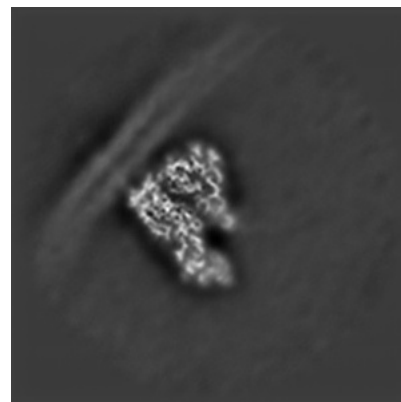
6.3.1 Primary map



X Index: 142

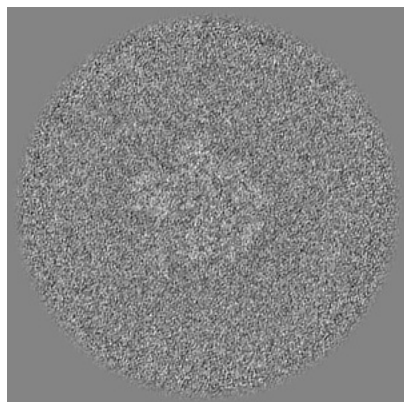


Y Index: 154

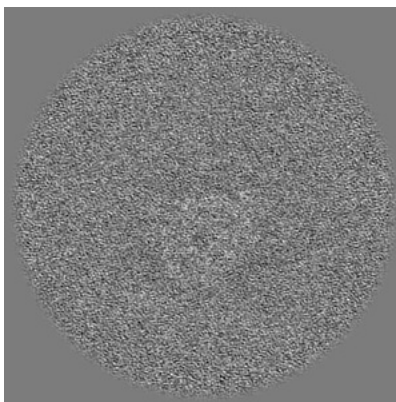


Z Index: 150

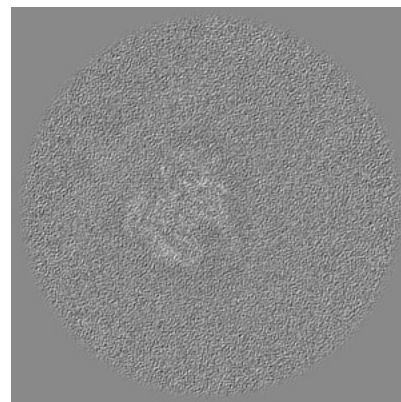
6.3.2 Raw map



X Index: 142



Y Index: 157

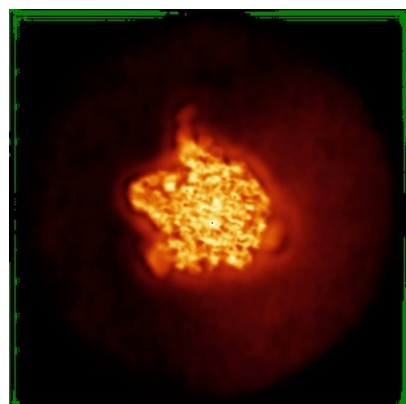


Z Index: 141

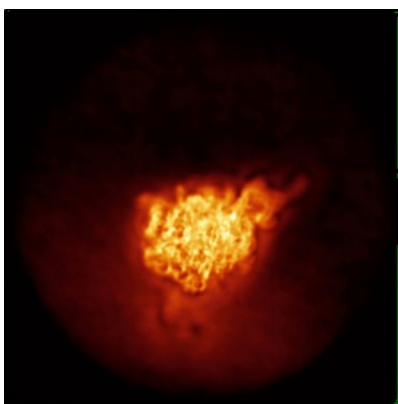
The images above show the largest variance slices of the map in three orthogonal directions.

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

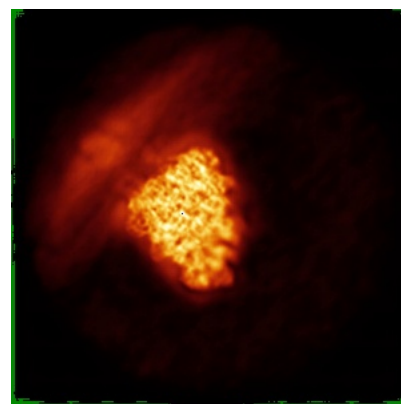
6.4.1 Primary map



X

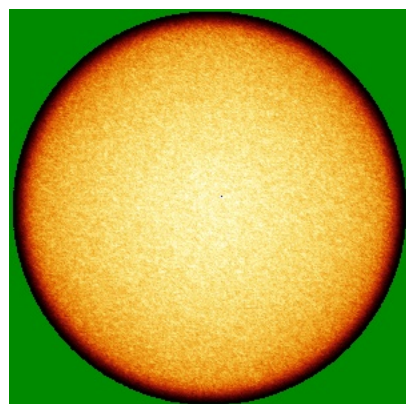


Y

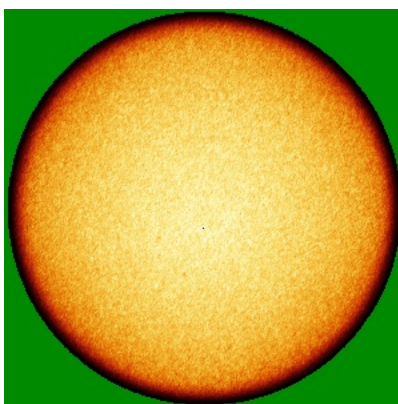


Z

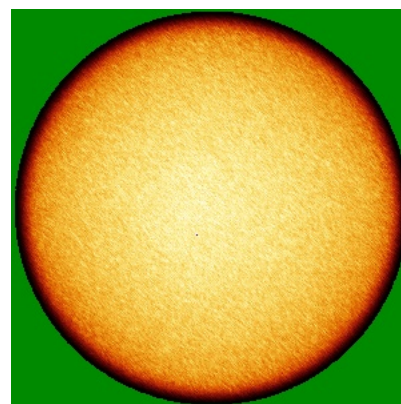
6.4.2 Raw map



X



Y

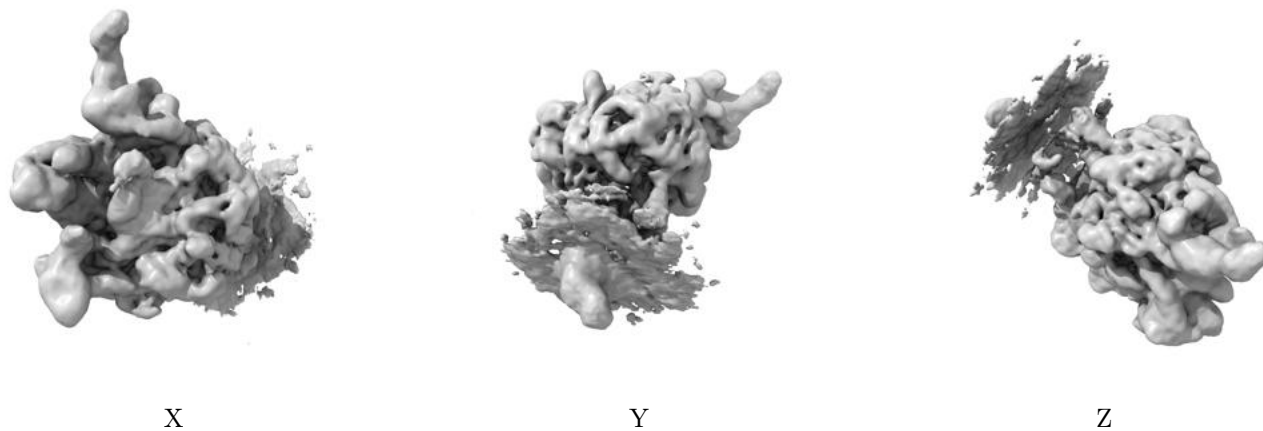


Z

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

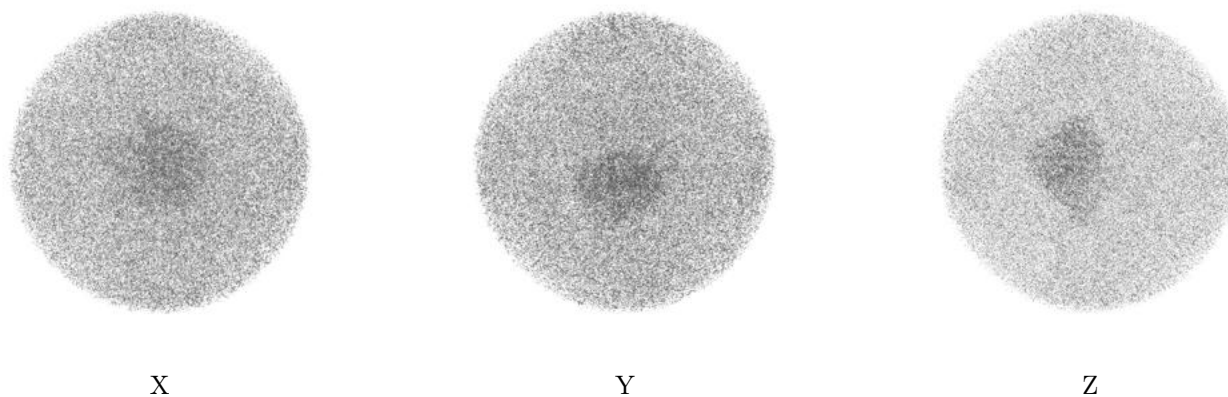
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

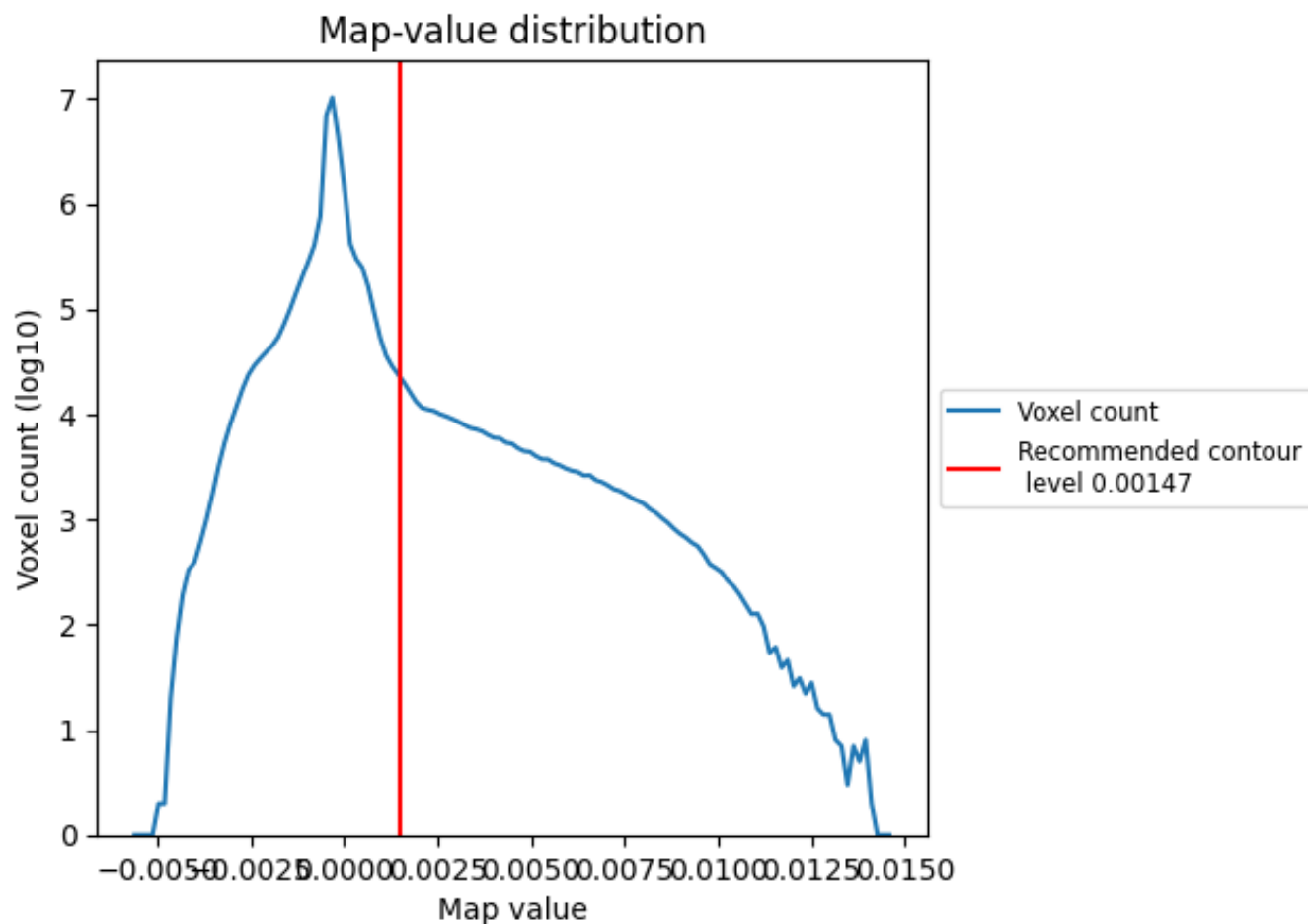
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

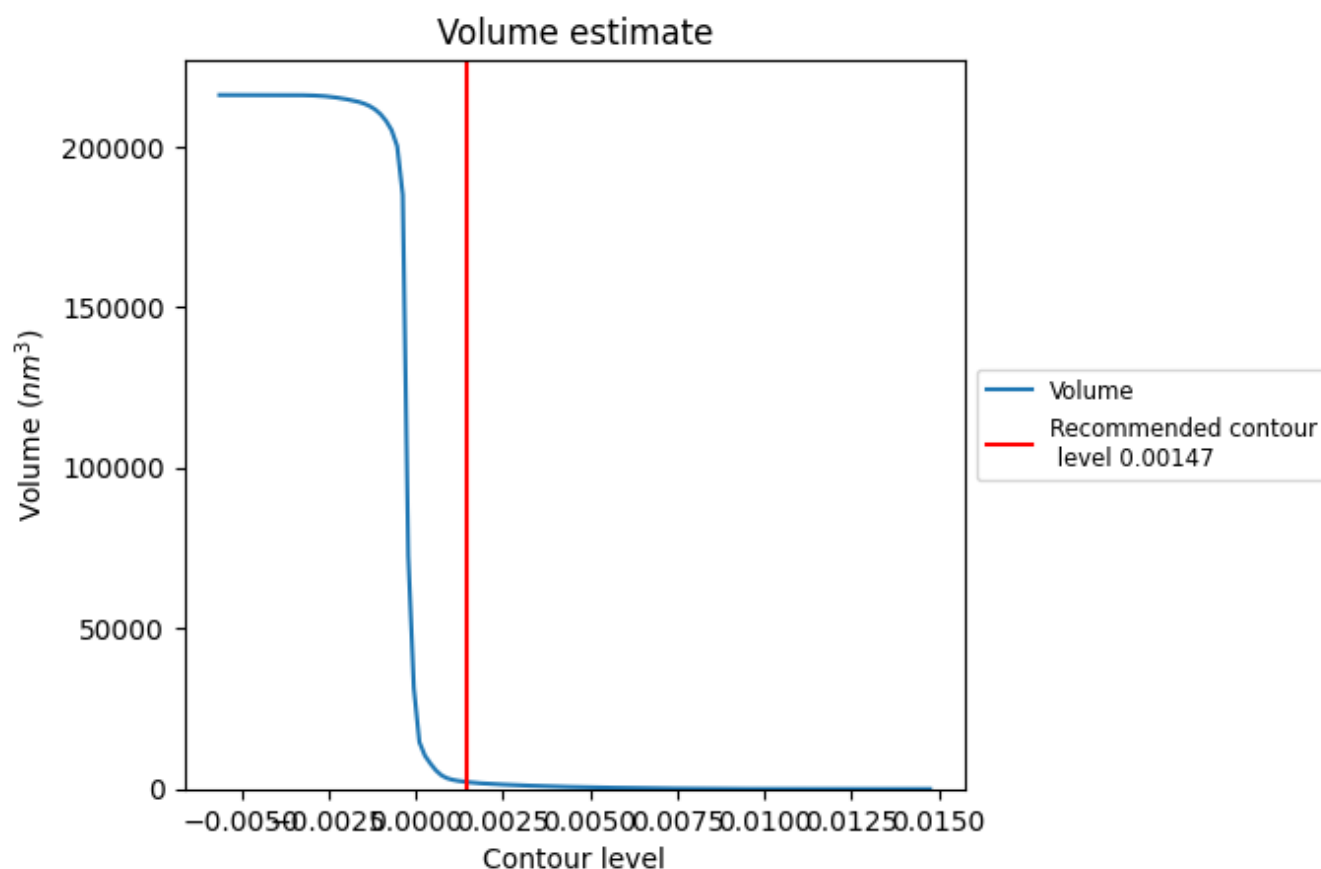
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

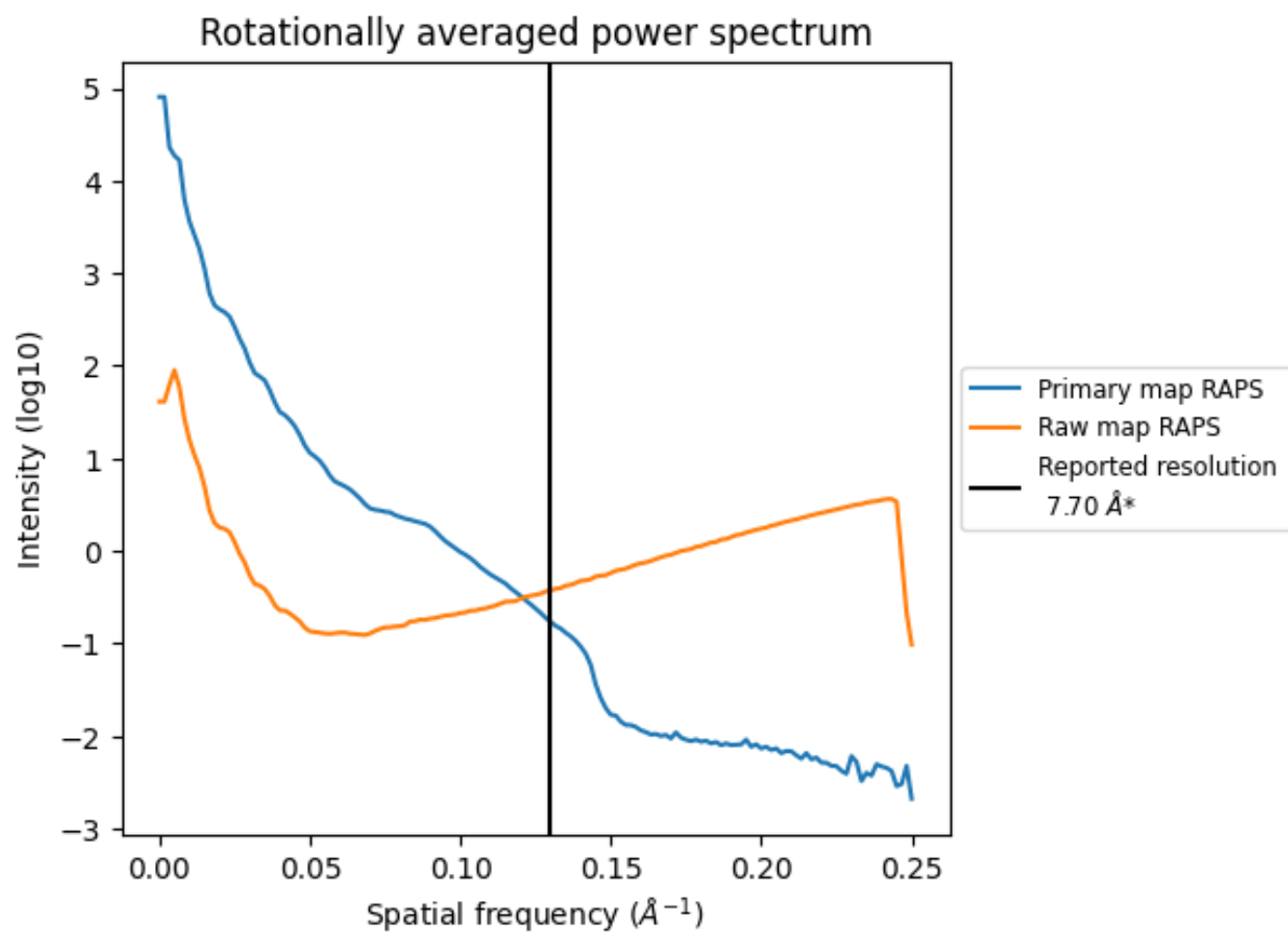
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2169 nm^3 ; this corresponds to an approximate mass of 1959 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 ⓘ

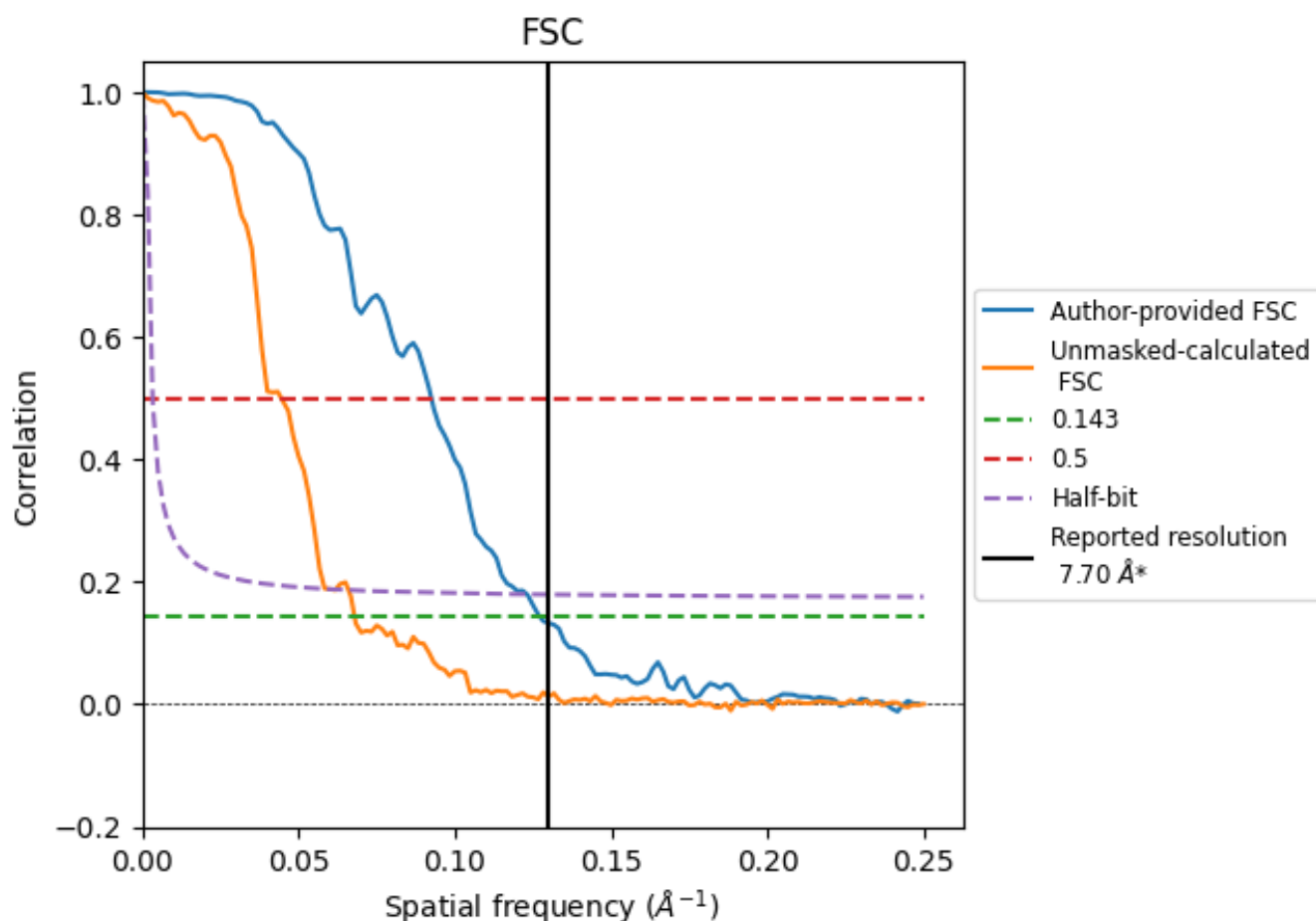


*Reported resolution corresponds to spatial frequency of 0.130 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.130 Å⁻¹

8.2 Resolution estimates [i](#)

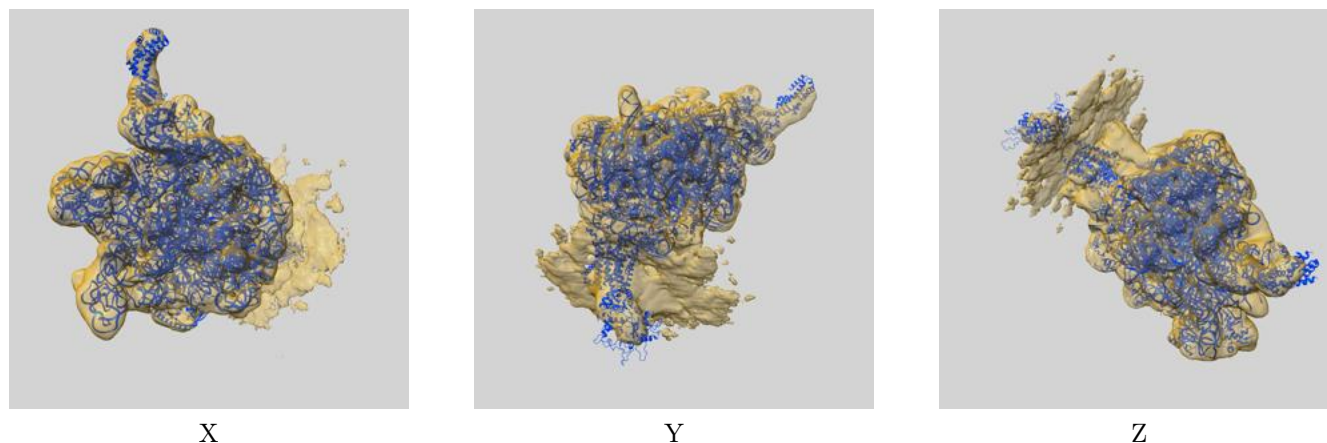
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.70	-	-
Author-provided FSC curve	7.86	10.81	8.12
Unmasked-calculated*	14.73	22.52	16.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 14.73 differs from the reported value 7.7 by more than 10 %

9 Map-model fit [i](#)

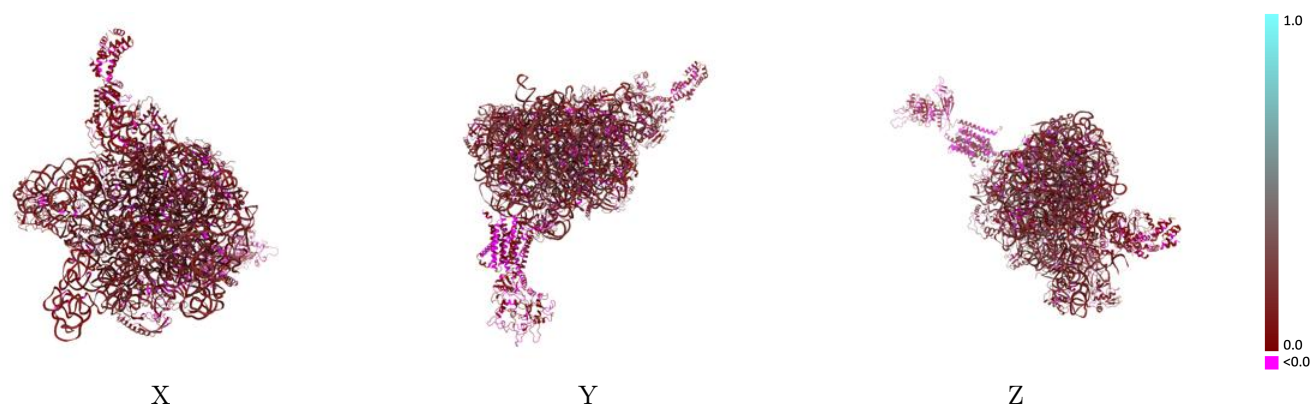
This section contains information regarding the fit between EMDB map EMD-53630 and PDB model 9SKD. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



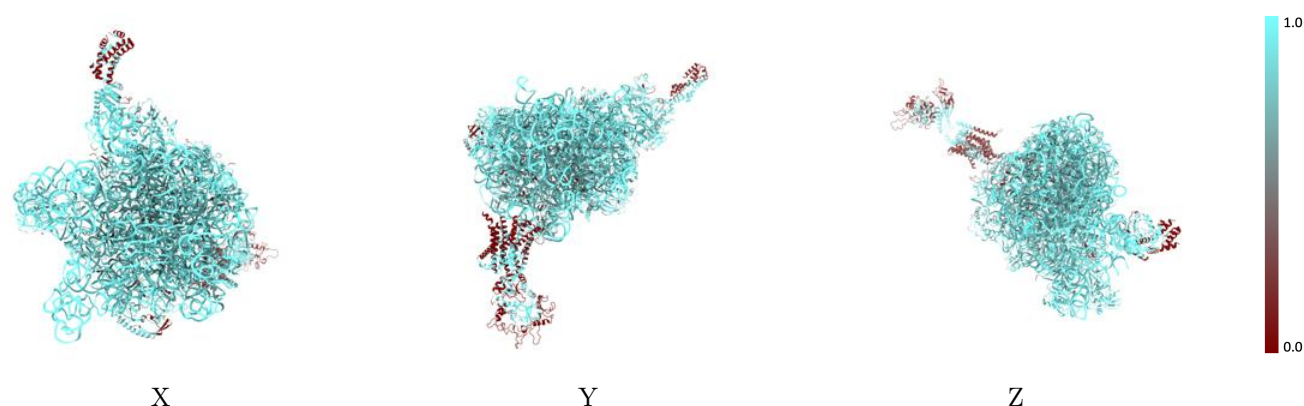
The images above show the 3D surface view of the map at the recommended contour level 0.00147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



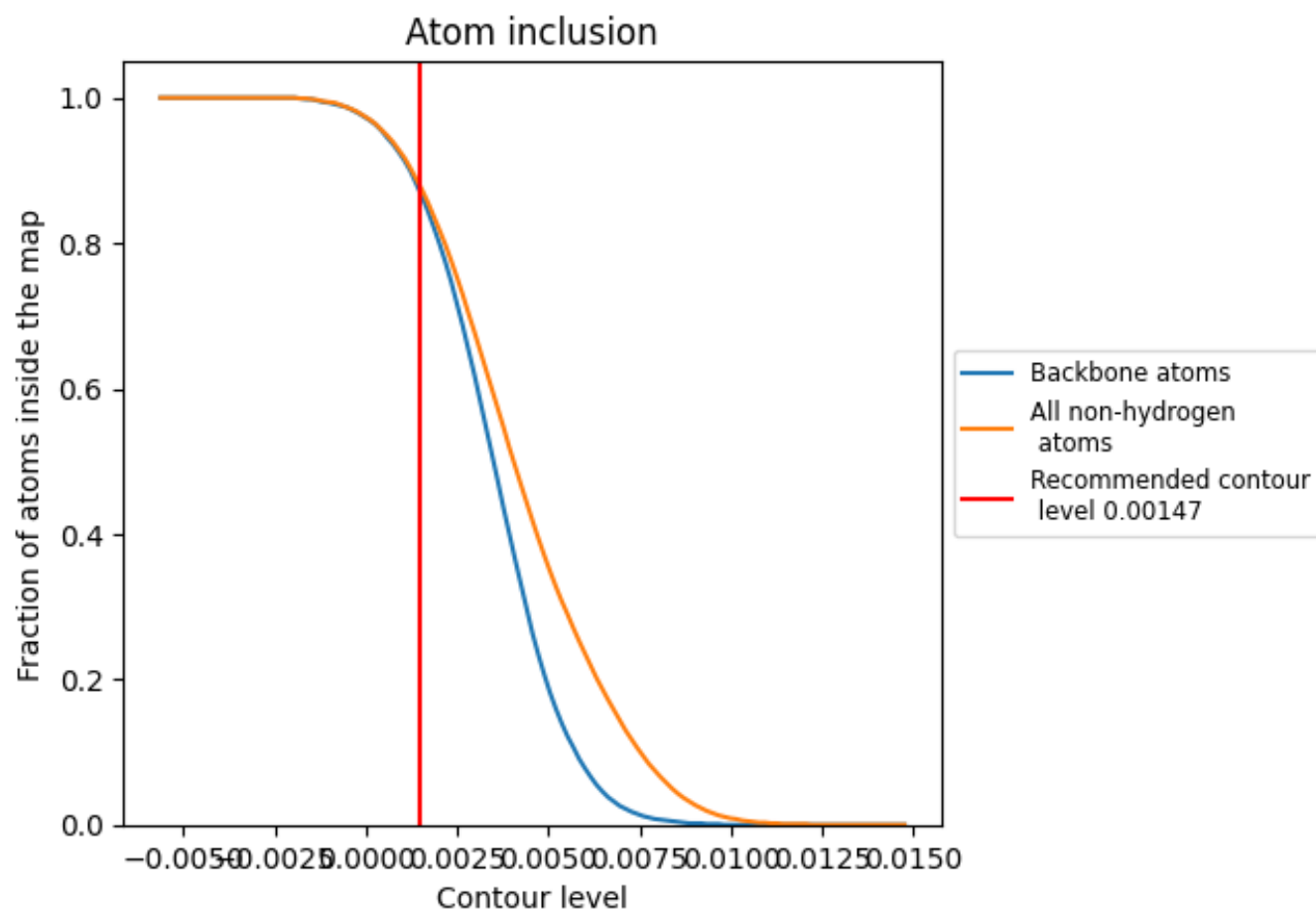
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00147).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.1240
0	 0.7560	 0.0980
1	 0.7920	 0.1070
2	 0.8350	 0.0350
3	 0.9580	 0.1490
4	 0.9950	 0.1440
8	 0.9220	 0.0960
9	 0.4160	 0.0280
A	 0.7300	 0.0610
B	 0.7240	 0.0540
C	 0.5520	 0.0650
D	 0.4960	 0.0840
E	 0.1290	 0.0570
a	 0.8660	 0.0820
b	 0.8560	 0.0840
c	 0.7990	 0.1040
d	 0.9550	 0.0900
e	 0.8740	 0.1050
f	 0.6850	 0.0930
h	 0.8810	 0.0740
i	 0.8650	 0.1140
j	 0.8550	 0.0920
k	 0.8820	 0.0960
l	 0.8530	 0.1070
m	 0.8010	 0.1040
n	 0.9330	 0.1040
o	 0.8800	 0.0960
p	 0.8720	 0.1080
q	 0.8750	 0.1060
r	 0.7460	 0.1160
s	 0.6800	 0.1030
t	 0.5320	 0.0520
u	 0.8300	 0.0500
v	 0.7560	 0.0700
w	 0.7650	 0.1280



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Chain	Atom inclusion	Q-score
x	 0.9560	 0.1160
y	 0.7700	 0.0780
z	 0.8940	 0.0680