



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2022 – 03:41 am BST

PDB ID : 7PIR
EMDB ID : EMD-13448
Title : 70S ribosome with A*- and P/E-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 12.10 Å (reported)
Based on initial models : 7OOD, 7OOC, 4V7C

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:

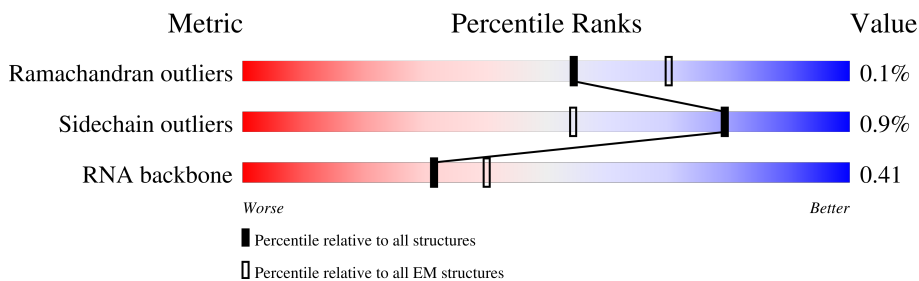
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 12.10 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	

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Mol	Chain	Length	Quality of chain
9	F	155	11% 97%
10	G	142	5% 96%
11	H	132	12% 95%
12	I	108	17% 93% 6%
13	J	121	17% 94% 6%
14	K	139	94%
15	L	124	10% 95% 5%
16	M	61	10% 97%
17	N	86	6% 95%
18	O	94	85% 15%
19	P	85	8% 98%
20	Q	104	62% 38%
21	R	87	9% 95%
22	S	87	89% 11%
23	T	60	10% 88% 12%
24	a	287	99%
25	b	287	5% 79% 20%
26	c	212	9% 99%
27	d	180	10% 97%
28	e	184	26% 96%
29	f	149	57% 97%
30	g	161	27% 68% 7% 24%
31	h	137	29% 93% 7%
32	i	146	99%
33	j	122	15% 100%

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Mol	Chain	Length	Quality of chain
34	k	151	11% 98%
35	l	139	5% 98%
36	m	124	94%
37	n	116	9% 97%
38	o	119	8% 97%
39	p	127	89% 10%
40	q	100	8% 98%
41	r	159	87% 13%
42	s	237	39% 61%
43	t	111	13% 100%
44	u	104	83% 17%
45	v	65	95%
46	w	111	5% 90% 10%
47	x	97	16% 45% 55%
48	y	57	5% 93% 5%
49	z	53	94% 6%
50	3	2907	62% 36%
51	4	108	61% 35%
52	5	1520	64% 34%
53	6	76	59% 39%
53	8	76	59% 39%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146081 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

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

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

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

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

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

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	240	1921	1226	334	352	9	0	0

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	215	1698	1073	313	307	5	0	0

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	203	1660	1051	314	290	5	0	0

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	153	1173	742	226	202	3	0	0

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	167	1362	857	240	263	2	0	0

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	154	1246	785	239	216	6	0	0

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	141	1110	723	193	192	2	0	0

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	128	1028	655	191	181	1	0	0

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	I	101	809	523	142	143	1	0	0

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	114	829	514	153	156	6	0	0

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O	S	0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O	S	0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O	S	0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O	S	0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

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

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

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

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	122	Total	C	N	O	S	0	0
			921	586	162	170	3		

- Molecule 31 is a protein called 50S ribosomal protein L11.

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

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

- Molecule 33 is a protein called 50S ribosomal protein L14.

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

- Molecule 34 is a protein called 50S ribosomal protein L15.

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

- Molecule 35 is a protein called 50S ribosomal protein L16.

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

- Molecule 36 is a protein called 50S ribosomal protein L17.

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

- Molecule 37 is a protein called 50S ribosomal protein L18.

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

- Molecule 38 is a protein called 50S ribosomal protein L19.

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

- Molecule 39 is a protein called 50S ribosomal protein L20.

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

- Molecule 40 is a protein called 50S ribosomal protein L21.

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

- Molecule 41 is a protein called 50S ribosomal protein L22.

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

- Molecule 42 is a protein called 50S ribosomal protein L23.

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

- Molecule 43 is a protein called 50S ribosomal protein L24.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

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

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L34

Chain 0:  98%



- Molecule 2: 50S ribosomal protein L35

Chain 1:  97%




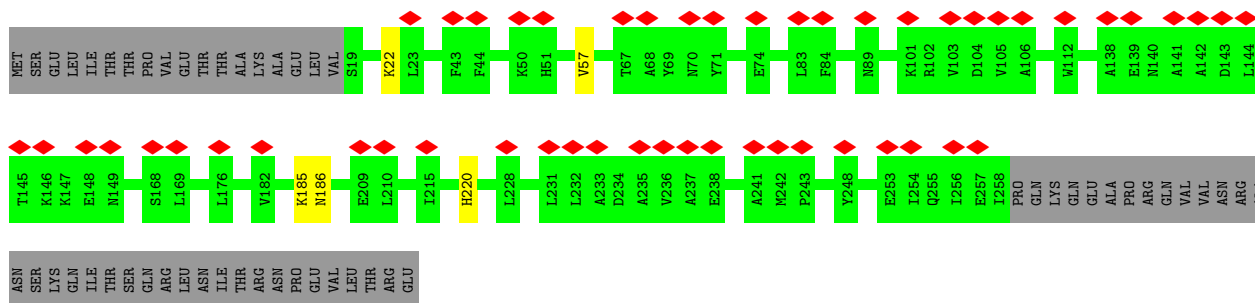
- Molecule 3: 50S ribosomal protein L36

Chain 2:  100%


There are no outlier residues recorded for this chain.

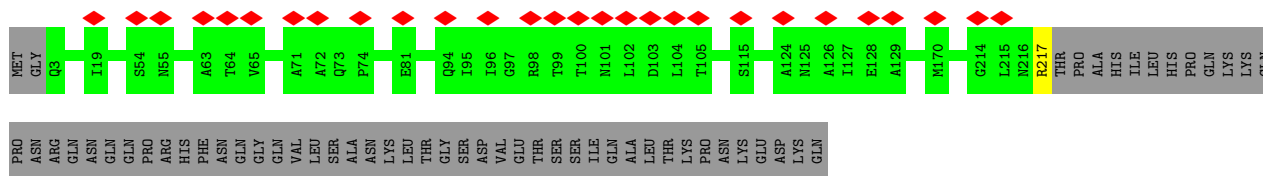
- Molecule 4: 30S ribosomal protein S2

Chain A:  18% 80% 18%

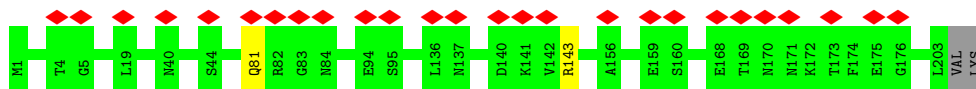


- Molecule 5: 30S ribosomal protein S3

Chain B:  10% 78% 21%



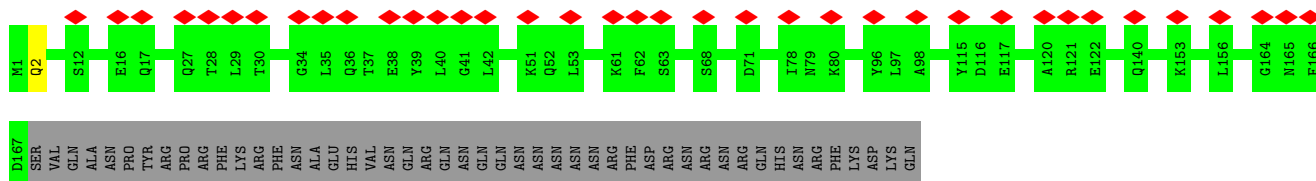
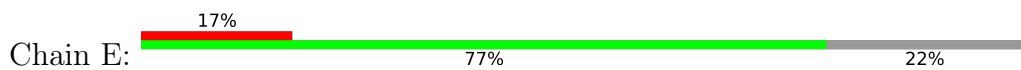
• Molecule 6: 30S ribosomal protein S4



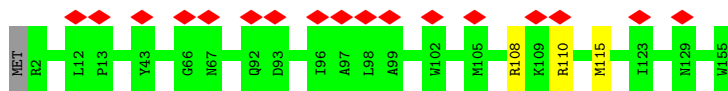
• Molecule 7: 30S ribosomal protein S5



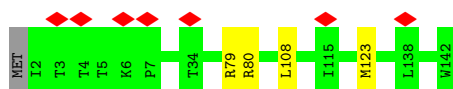
• Molecule 8: 30S ribosomal protein S6



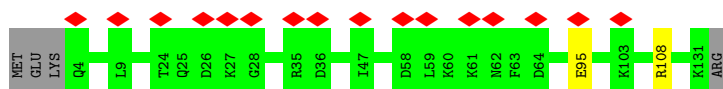
• Molecule 9: 30S ribosomal protein S7



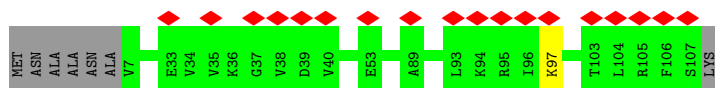
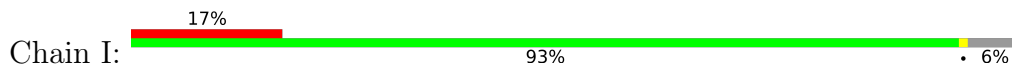
• Molecule 10: 30S ribosomal protein S8



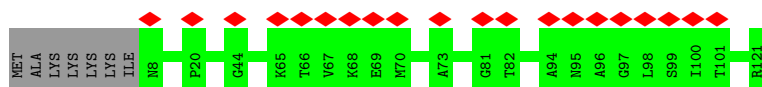
• Molecule 11: 30S ribosomal protein S9



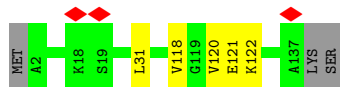
- Molecule 12: 30S ribosomal protein S10



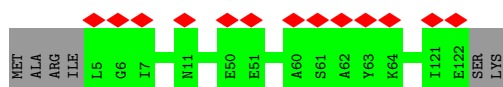
- Molecule 13: 30S ribosomal protein S11



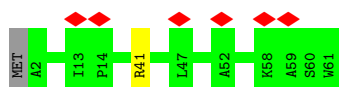
- Molecule 14: 30S ribosomal protein S12



- Molecule 15: 30S ribosomal protein S13




- Molecule 16: 30S ribosomal protein S14 type Z



- Molecule 17: 30S ribosomal protein S15



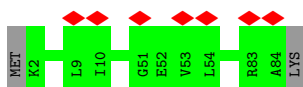
- Molecule 18: 30S ribosomal protein S16

Chain O:  85% 15%



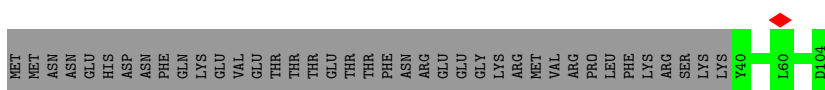
- Molecule 19: 30S ribosomal protein S17

Chain P:  8% 98%



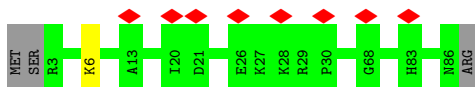
- Molecule 20: 30S ribosomal protein S18

Chain Q:  62% 38%




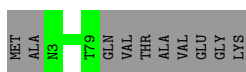
- Molecule 21: 30S ribosomal protein S19

Chain R:  9% 95%




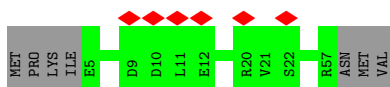
- Molecule 22: 30S ribosomal protein S20

Chain S:  89% 11%



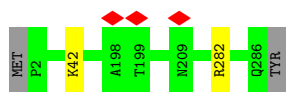
- Molecule 23: 30S ribosomal protein S21

Chain T:  10% 88% 12%

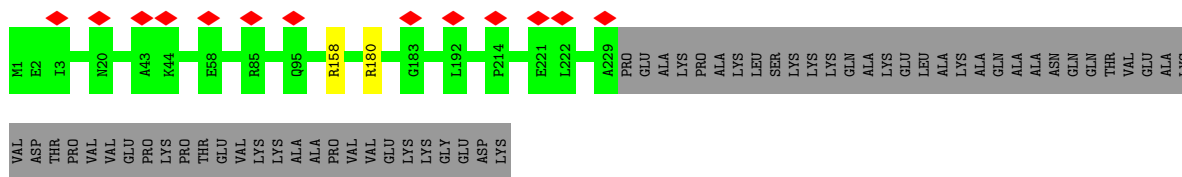
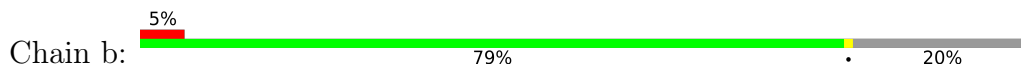


- Molecule 24: 50S ribosomal protein L2

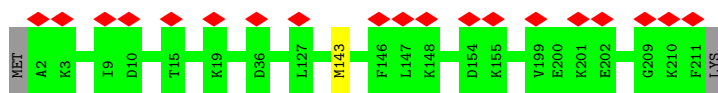
Chain a:  99%



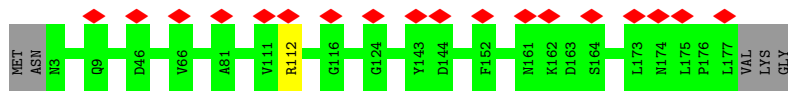
• Molecule 25: 50S ribosomal protein L3



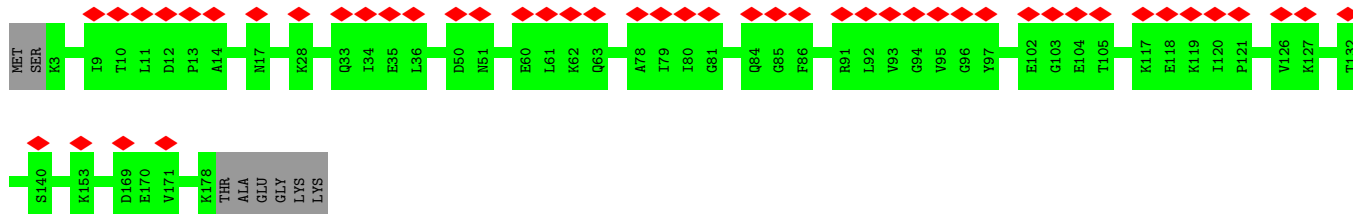
• Molecule 26: 50S ribosomal protein L4



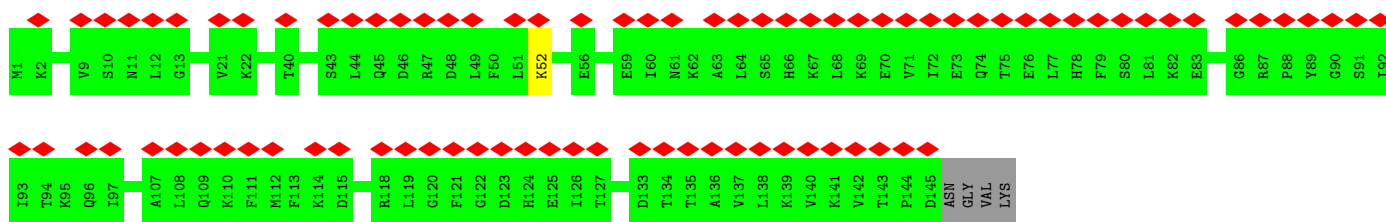
• Molecule 27: 50S ribosomal protein L5



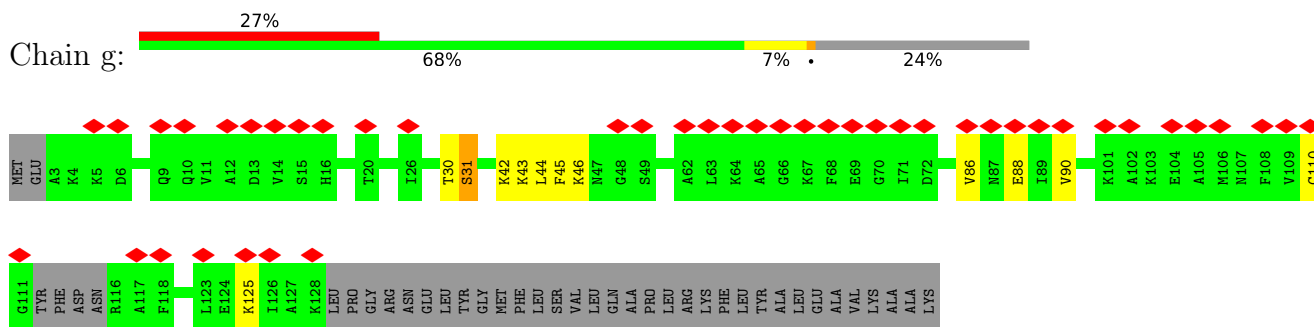
• Molecule 28: 50S ribosomal protein L6



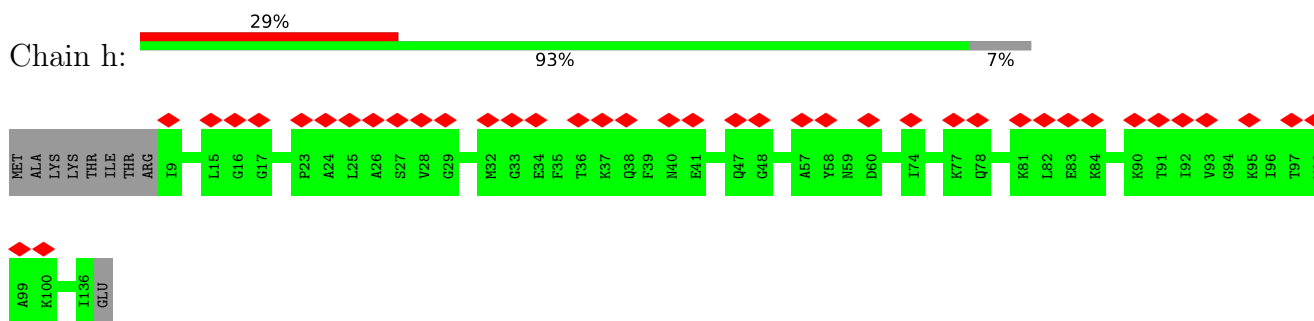
• Molecule 29: 50S ribosomal protein L9



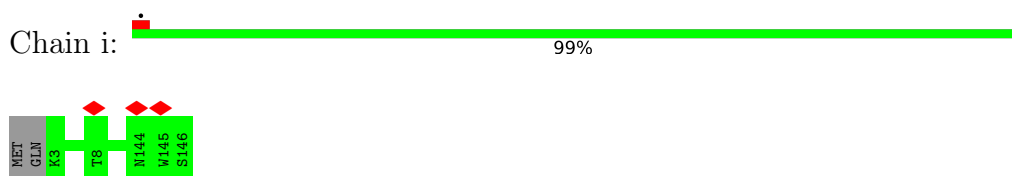
- Molecule 30: 50S ribosomal protein L10



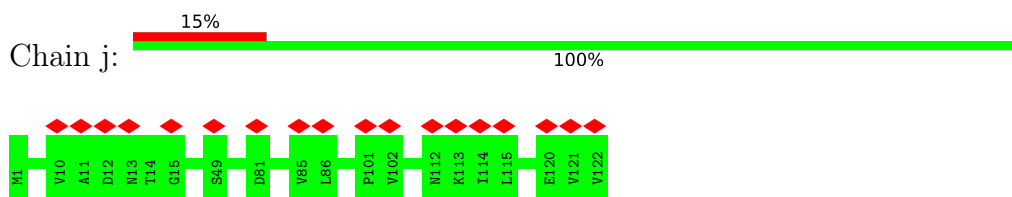
- Molecule 31: 50S ribosomal protein L11



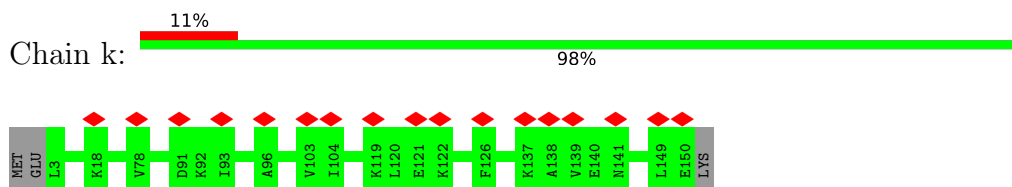
- Molecule 32: 50S ribosomal protein L13



- Molecule 33: 50S ribosomal protein L14

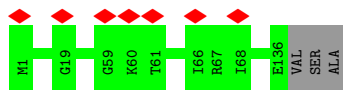


- Molecule 34: 50S ribosomal protein L15

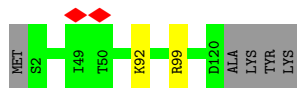


- Molecule 35: 50S ribosomal protein L16





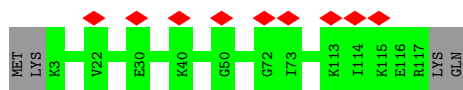
- Molecule 36: 50S ribosomal protein L17



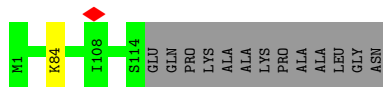
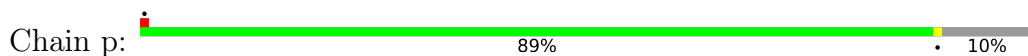
- Molecule 37: 50S ribosomal protein L18



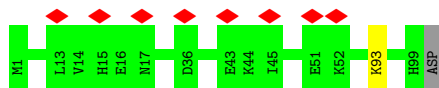
- Molecule 38: 50S ribosomal protein L19



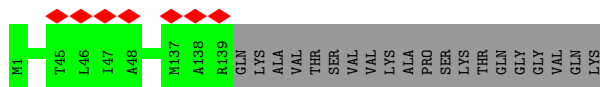
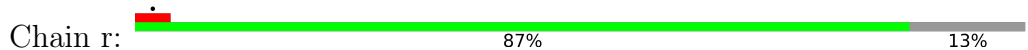
- Molecule 39: 50S ribosomal protein L20



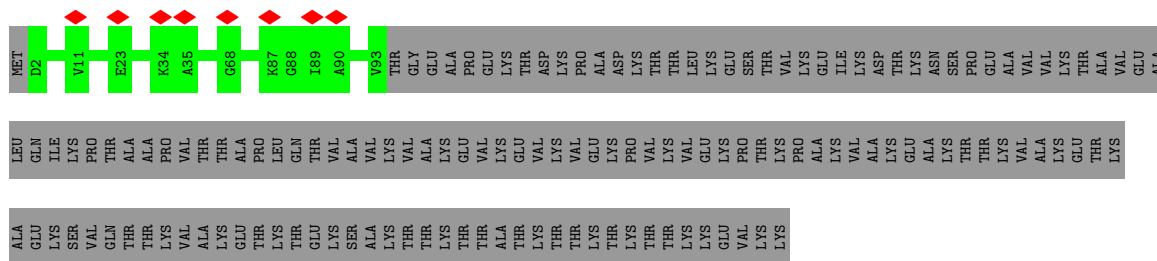
- Molecule 40: 50S ribosomal protein L21



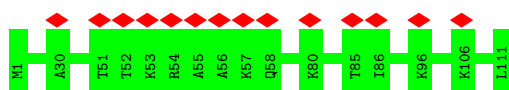
- Molecule 41: 50S ribosomal protein L22



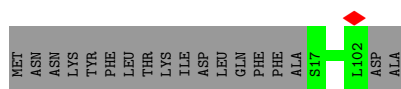
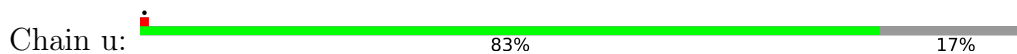
- Molecule 42: 50S ribosomal protein L23



• Molecule 43: 50S ribosomal protein L24



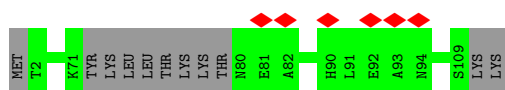
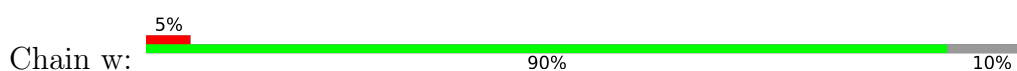
• Molecule 44: 50S ribosomal protein L27



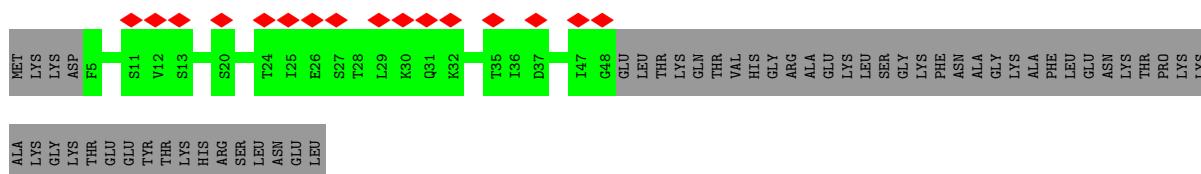
• Molecule 45: 50S ribosomal protein L28



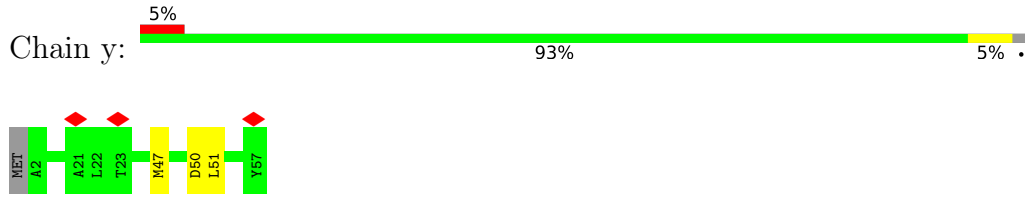
• Molecule 46: 50S ribosomal protein L29



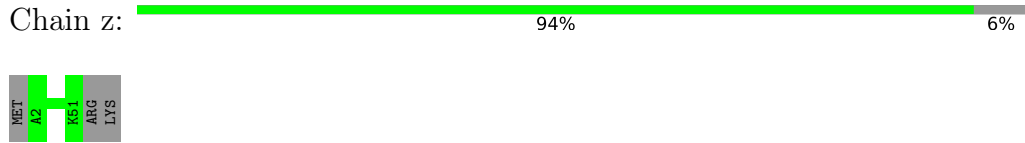
• Molecule 47: 50S ribosomal protein L31



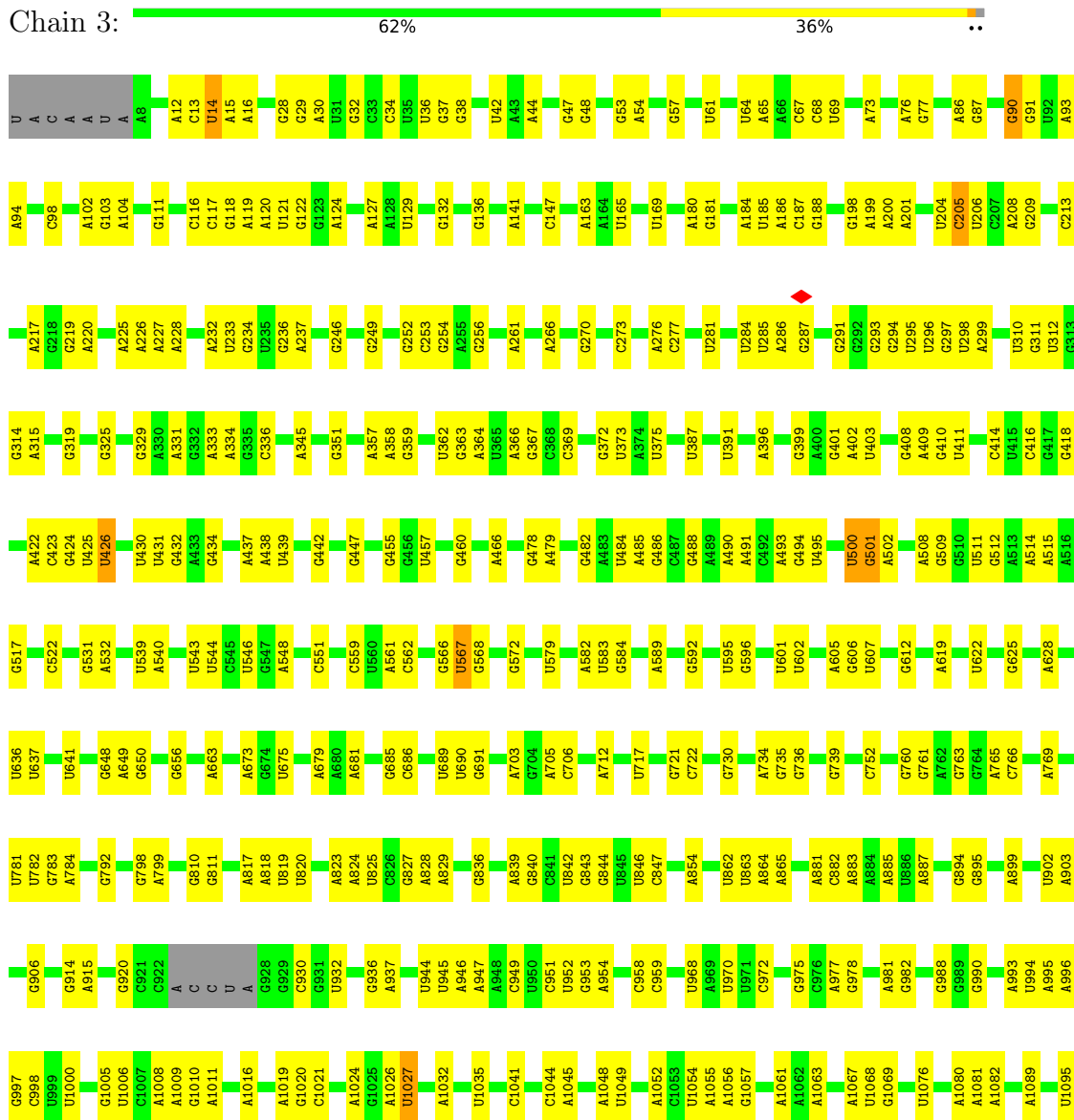
• Molecule 48: 50S ribosomal protein L32



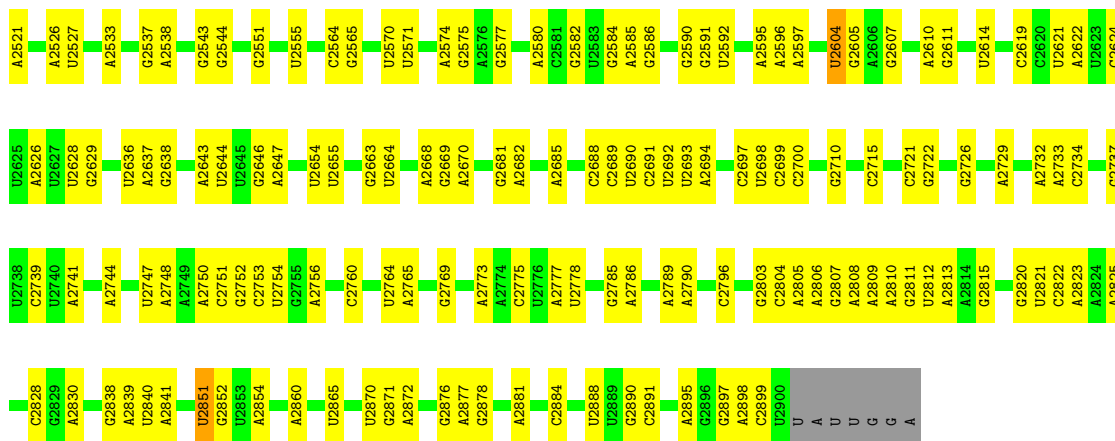
• Molecule 49: 50S ribosomal protein L33 1



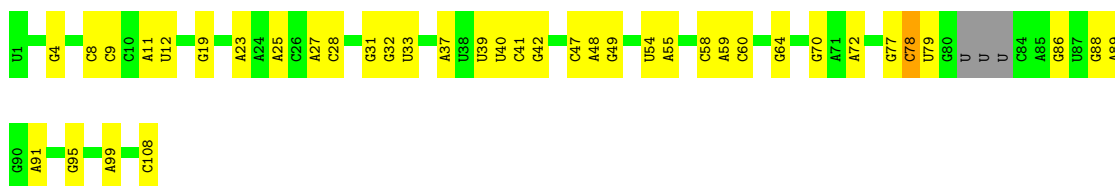
• Molecule 50: 23S ribosomal RNA



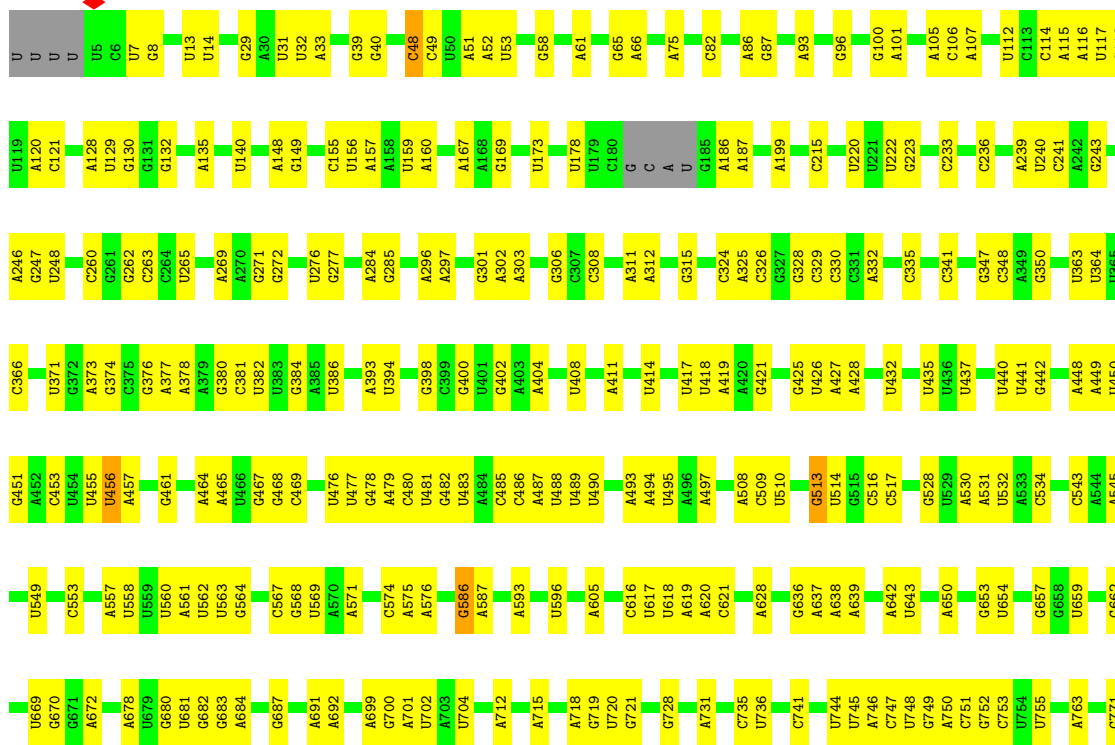
U1096	U1180	A1274	U1374	A1485	A1592	A1689	A1788	G1895	A2010	G2168	C2199	C2305	U2416
G1097	A1181	G1280	G1375	U1486	U1893	A1692	C1789	C1900	G2011	A2109	U2200	A2309	G2417
G1098	A1186	A1281	C1378	U1487	G1594	A1695	U1790	C1901	A2012	U2110	G2202	A2310	G2418
A1102	A1187	G1282	C1379	A1503	C1599	G1695	A1791	C1696	A2020	A2111	U2212	A2311	G2422
A1105	C1188	A1283	G1388	G1504	A1601	C1697	A1792	C1697	A2021	A2112	U2213	A2312	G2423
G1106	G1189	A1284	G1389	G1505	A1602	A1698	A1793	G1904	A2022	A2115	U2218	U2313	G2424
A1107	A1190	U1285	C1390	U1506	G1602	A1699	A1794	G1904	C2025	A2116	U2219	U2314	G2424
A1108	U1192	U1286	C1399	G1507	G1607	A1699	A1794	G1904	C2025	G2117	U2220	U2315	G2424
C1111	A1195	A1295	A1393	U1509	G1607	G1701	U1805	A1907	G2028	U2118	U2221	U2316	G2430
A1112	U1200	G1296	A1401	U1514	U1612	C1704	C1807	A1908	U2029	A2123	U2222	A2317	A2433
U1113	A1201	U1297	A1406	A1515	G1615	C1708	A1808	A1908	A2030	A2124	U2223	U2320	A2434
C1114	U1202	A1298	U1407	C1518	G1616	U1707	U1815	A1919	G2038	U2125	U2227	U2321	A2435
U1116	A1202	G1301	U1407	C1518	G1618	G1708	A1816	A1920	A2039	A2126	U2227	U2322	G2437
U1119	G1203	C1302	U1412	C1523	A1619	A1711	A1817	C1921	A2040	A2127	U2228	U2323	A2438
A1122	A1204	U1304	A1415	C1524	A1619	A1714	U1820	C1927	C2041	U2132	A2231	U2332	A2440
A1123	A1208	G1305	A1421	A1532	U1636	U1714	G1821	A1934	C2043	A2133	A2233	G2333	A2447
G1124	U1209	A1315	U1421	U1533	A1637	A1715	A1822	A1935	C2044	U2138	A2233	A2336	G2448
U1125	A1210	U1316	U1422	U1533	A1641	A1716	U1823	G1936	C2045	C2139	A2235	G2341	G2449
G1126	U1211	C1317	A1423	A1535	A1643	G1720	G1824	G1937	A2048	G2140	A2235	U2342	U2449
G1127	U1213	U1318	U1424	A1539	A1644	G1722	U1825	U1938	A2049	A2145	G2243	A2343	G2453
U1128	U1216	A1322	U1425	G1540	A1644	U1722	A1826	A1945	G2050	U2153	U2244	A2344	A2456
G1129	G1217	A1328	C1426	A1541	G1645	U1727	U1827	U1946	A2056	U2153	G2245	A2344	U2457
A1130	G1217	U1328	A1431	A1541	G1646	U1728	A1828	U1947	C2057	A2154	G2246	A2345	A2458
A1131	G1221	U1329	U1431	U1546	A1648	G1729	A1836	U1947	G2058	C2158	G2247	G2346	G2466
C1132	U1232	U1338	U1436	G1560	G1648	C1730	C1837	U1950	G2059	C2158	U2251	U2350	G2466
A1138	U1236	U1339	A1437	A1568	A1650	G1733	C1840	A1951	C2062	U2162	G2254	U2352	G2475
U1141	G1242	U1340	U1440	A1568	A1652	A1734	G1842	G1952	G2063	A2165	U2257	C2355	C2483
A1146	A1243	U1341	U1440	A1569	A1656	A1735	G1842	U1953	G2064	U2166	G2258	U2358	A2484
G1147	A1244	C1343	U1444	U	A1656	G1737	G1845	U1958	A2065	G2169	G2259	U2358	A2485
U1148	A1244	C1343	U1445	A	A1661	G1741	G1850	A1959	A2067	A2170	G2267	A2362	U2487
U1151	C1247	A1349	G1446	G	G1662	U1747	C1850	U1962	G2068	A2171	U2273	A2368	C2488
G1157	G1251	A1350	U1448	U	G1663	U1748	G1863	U1963	C2070	A2172	A2274	G2369	G2492
A1161	C1252	G1352	G1449	G	A1664	U1752	A1864	U1973	U2075	U2175	A2275	U2380	G2502
A1162	G1253	U1353	U1454	U	A1668	A1752	A1865	U1974	G2076	G2176	A2276	G2381	G2503
U1165	A1256	C1355	A1455	A	U1670	C1758	G1867	A1977	A2077	A2178	A2277	U2387	C2504
A1168	G1257	U1357	A1456	G1570	C1671	U1764	A1868	U1978	A2084	U2180	U2280	U2391	A2505
A1169	U1260	U1360	U1465	G1571	C1672	U1764	A1873	G1981	U2085	A2184	C2283	U2392	C2506
G1171	U1261	U1361	U1466	A1577	U1673	A1766	G1876	G1982	G2087	A2184	C2283	U2392	C2507
G1174	G1262	A1364	U1467	U1581	G1676	A1766	A1877	A1988	A2094	C2187	G2290	U2392	C2508
C1175	G1263	U1366	U1477	G1582	U1678	A1767	A1878	U1988	A2094	U2188	U2291	U2392	C2509
U1176	U1265	G1366	A1477	G1583	U1679	A1768	A1879	U1989	A2099	U2189	A2292	U2393	G2510
U1177	G1266	U1369	U1480	U1585	G1681	A1769	G1880	U1996	G2100	U2193	A2293	A2400	G2511
A1178	U1268	A1370	U1481	U1586	G1682	A1770	G1881	C1997	C2103	U2194	A2295	U2409	G2512
G1179	A1268	U1372	G1483	U1587	G1683	C1771	G1882	U1998	A2104	G2194	A2296	C2410	G2513
		C1373	G1484	A1589	A1688	A1780	U1887	G1999	A2107	U2197	G2297	A2415	G2514
						U1784	U1888	U2000		U2197	G2297	A2415	G2515
							U1889			U2197	G2297	A2415	G2516
										U2197	G2297	A2415	G2517
										U2197	G2297	A2415	G2520

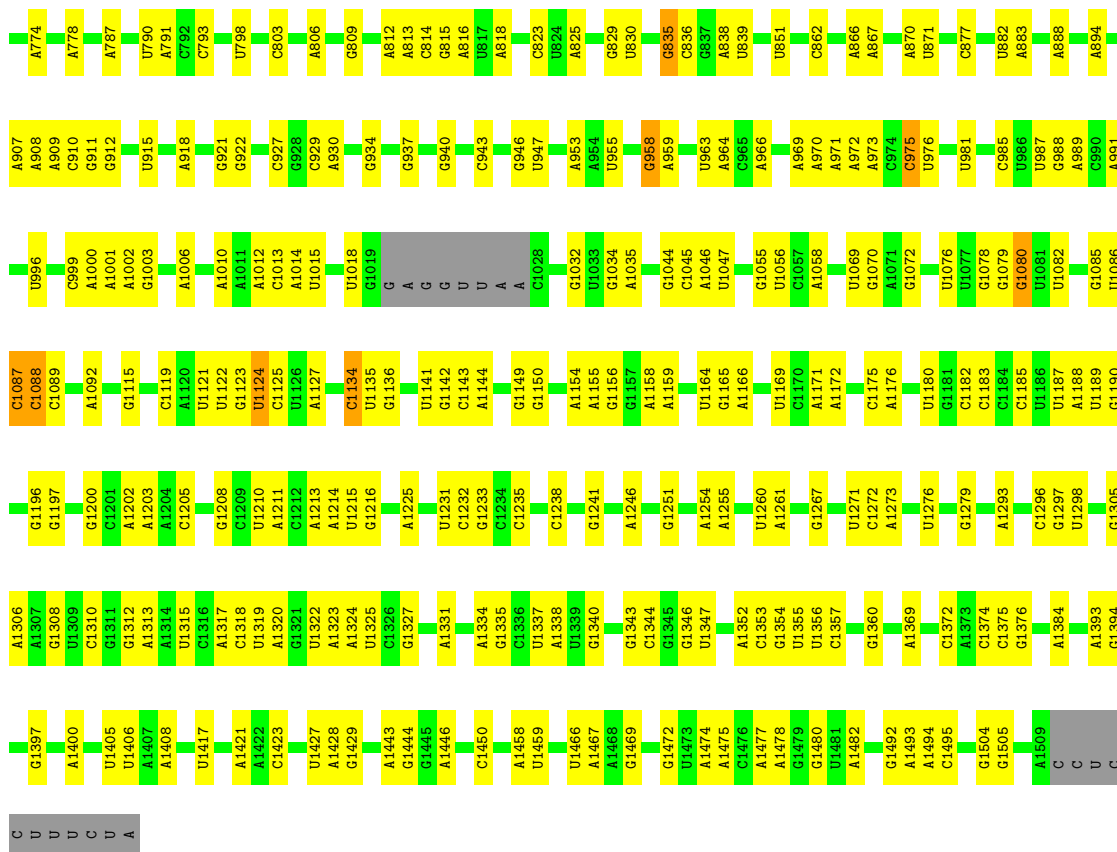


• Molecule 51: 5S ribosomal RNA

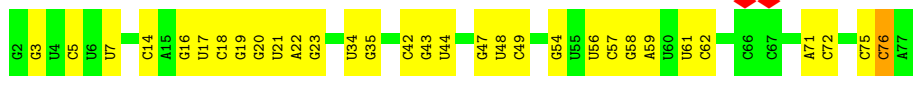


• Molecule 52: 16S ribosomal RNA





• Molecule 53: tRNA-Phe



• Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	940	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.996	Depositor
Minimum map value	-0.271	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.29	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.23	0/383	0.38	0/504
2	1	0.32	0/484	0.64	0/637
3	2	0.22	0/306	0.45	0/401
4	A	0.26	0/1954	0.49	1/2642 (0.0%)
5	B	0.25	0/1721	0.46	0/2323
6	C	0.31	0/1691	0.55	1/2267 (0.0%)
7	D	0.27	0/1188	0.56	0/1593
8	E	0.25	0/1384	0.47	0/1867
9	F	0.29	0/1266	0.70	3/1700 (0.2%)
10	G	0.28	0/1126	0.54	1/1517 (0.1%)
11	H	0.27	0/1044	0.49	0/1395
12	I	0.29	0/820	0.54	0/1103
13	J	0.26	0/844	0.47	0/1136
14	K	0.27	0/1094	0.53	1/1468 (0.1%)
15	L	0.23	0/962	0.45	0/1289
16	M	0.26	0/483	0.51	0/643
17	N	0.28	0/679	0.55	1/907 (0.1%)
18	O	0.23	0/659	0.41	0/885
19	P	0.23	0/684	0.47	0/913
20	Q	0.25	0/545	0.46	0/730
21	R	0.26	0/698	0.49	0/936
22	S	0.24	0/631	0.41	0/838
23	T	0.22	0/475	0.45	0/621
24	a	0.25	0/2267	0.48	0/3044
25	b	0.27	0/1795	0.52	0/2412
26	c	0.29	0/1671	0.50	1/2246 (0.0%)
27	d	0.30	0/1409	0.55	0/1894
28	e	0.26	0/1420	0.50	0/1912
29	f	0.26	0/1183	0.52	0/1587
30	g	0.36	0/927	0.58	0/1236
31	h	0.26	0/968	0.52	0/1298
32	i	0.24	0/1186	0.46	0/1592
33	j	0.24	0/953	0.49	0/1275
34	k	0.24	0/1170	0.47	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.28	0/1104	0.50	0/1481
36	m	0.26	0/973	0.50	0/1309
37	n	0.24	0/897	0.46	0/1198
38	o	0.24	0/948	0.49	0/1262
39	p	0.24	0/961	0.42	0/1278
40	q	0.28	0/828	0.53	0/1111
41	r	0.25	0/1077	0.49	0/1441
42	s	0.26	0/732	0.48	0/988
43	t	0.26	0/879	0.53	0/1165
44	u	0.25	0/665	0.47	0/884
45	v	0.23	0/519	0.49	0/695
46	w	0.23	0/826	0.46	0/1104
47	x	0.29	0/353	0.47	0/474
48	y	0.30	0/457	0.50	0/601
49	z	0.25	0/412	0.44	0/547
50	3	0.66	6/69073 (0.0%)	0.89	108/107710 (0.1%)
51	4	0.24	0/2505	0.87	3/3902 (0.1%)
52	5	0.24	1/35768 (0.0%)	0.86	43/55764 (0.1%)
53	6	1.04	5/1808 (0.3%)	2.54	14/2817 (0.5%)
53	8	1.04	5/1808 (0.3%)	2.54	14/2817 (0.5%)
All	All	0.50	17/158663 (0.0%)	0.88	191/236918 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	3	2440	A	N3-C4	84.54	1.85	1.34
50	3	2440	A	C6-N1	73.80	1.87	1.35
50	3	2440	A	C5-C6	61.45	1.96	1.41
50	3	2440	A	C5-C4	59.03	1.80	1.38
50	3	2440	A	C2-N3	56.92	1.84	1.33

The worst 5 of 191 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	6	76	C	C6-N1-C2	-96.08	81.87	120.30
53	8	76	C	C6-N1-C2	-95.94	81.93	120.30
53	6	76	C	C5-C6-N1	57.88	149.94	121.00
53	8	76	C	C5-C6-N1	57.74	149.87	121.00
53	8	76	C	N3-C2-O2	-34.59	97.69	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	45/48 (94%)	42 (93%)	3 (7%)	0	100	100
2	1	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	8	40
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	217 (91%)	21 (9%)	0	100	100
5	B	213/273 (78%)	191 (90%)	22 (10%)	0	100	100
6	C	201/205 (98%)	186 (92%)	15 (8%)	0	100	100
7	D	151/219 (69%)	144 (95%)	7 (5%)	0	100	100
8	E	165/215 (77%)	149 (90%)	16 (10%)	0	100	100
9	F	152/155 (98%)	144 (95%)	8 (5%)	0	100	100
10	G	139/142 (98%)	120 (86%)	19 (14%)	0	100	100
11	H	126/132 (96%)	113 (90%)	13 (10%)	0	100	100
12	I	99/108 (92%)	92 (93%)	7 (7%)	0	100	100
13	J	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
14	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
15	L	116/124 (94%)	106 (91%)	10 (9%)	0	100	100
16	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
17	N	81/86 (94%)	72 (89%)	9 (11%)	0	100	100
18	O	78/94 (83%)	71 (91%)	7 (9%)	0	100	100
19	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
20	Q	63/104 (61%)	51 (81%)	12 (19%)	0	100	100
21	R	82/87 (94%)	71 (87%)	11 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	51 (100%)	0	0	100	100
24	a	283/287 (99%)	252 (89%)	30 (11%)	1 (0%)	34	72
25	b	227/287 (79%)	210 (92%)	17 (8%)	0	100	100
26	c	208/212 (98%)	194 (93%)	14 (7%)	0	100	100
27	d	173/180 (96%)	149 (86%)	24 (14%)	0	100	100
28	e	174/184 (95%)	159 (91%)	15 (9%)	0	100	100
29	f	143/149 (96%)	132 (92%)	11 (8%)	0	100	100
30	g	118/161 (73%)	108 (92%)	9 (8%)	1 (1%)	19	60
31	h	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
32	i	142/146 (97%)	136 (96%)	6 (4%)	0	100	100
33	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	k	146/151 (97%)	136 (93%)	10 (7%)	0	100	100
35	l	134/139 (96%)	122 (91%)	12 (9%)	0	100	100
36	m	117/124 (94%)	110 (94%)	7 (6%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	105 (93%)	8 (7%)	0	100	100
39	p	112/127 (88%)	108 (96%)	4 (4%)	0	100	100
40	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
41	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
42	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
43	t	109/111 (98%)	100 (92%)	9 (8%)	0	100	100
44	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
45	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
46	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
47	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
48	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5814/6670 (87%)	5329 (92%)	482 (8%)	3 (0%)	54	86

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	26	THR
30	g	31	SER
24	a	282	ARG

5.3.2 Protein sidechains [i](#)

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	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	50 (98%)	1 (2%)	55	74
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	208 (98%)	4 (2%)	57	75
5	B	180/232 (78%)	179 (99%)	1 (1%)	86	92
6	C	181/183 (99%)	180 (99%)	1 (1%)	86	92
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	149 (99%)	1 (1%)	84	90
9	F	131/132 (99%)	130 (99%)	1 (1%)	81	89
10	G	123/124 (99%)	120 (98%)	3 (2%)	49	69
11	H	111/115 (96%)	109 (98%)	2 (2%)	59	77
12	I	95/99 (96%)	94 (99%)	1 (1%)	73	84
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	113 (97%)	4 (3%)	37	60
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	46 (98%)	1 (2%)	53	72
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	73 (99%)	1 (1%)	67	80
22	S	70/77 (91%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	240 (100%)	1 (0%)	91	94
25	b	186/233 (80%)	184 (99%)	2 (1%)	73	84
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	149 (99%)	1 (1%)	84	90
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	122 (99%)	1 (1%)	81	89
30	g	97/129 (75%)	85 (88%)	12 (12%)	4	19
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	103 (98%)	2 (2%)	57	75
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	99 (99%)	1 (1%)	76	86
40	q	90/91 (99%)	89 (99%)	1 (1%)	73	84
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	57 (98%)	1 (2%)	60	78
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	45 (94%)	3 (6%)	18	43
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5089/5751 (88%)	5043 (99%)	46 (1%)	79	87

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	42	LYS

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Mol	Chain	Res	Type
30	g	90	VAL
30	g	43	LYS
30	g	46	LYS
30	g	125	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
38	o	85	ASN
39	p	36	GLN
23	T	35	HIS
19	P	25	GLN
49	z	24	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	1032 (35%)	34 (1%)
51	4	103/108 (95%)	38 (36%)	2 (1%)
52	5	1490/1520 (98%)	509 (34%)	13 (0%)
53	6	75/76 (98%)	30 (40%)	6 (8%)
53	8	75/76 (98%)	30 (40%)	6 (8%)
All	All	4618/4687 (98%)	1639 (35%)	61 (1%)

5 of 1639 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	13	C
50	3	14	U
50	3	15	A
50	3	16	A

5 of 61 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2504	C
53	8	16	G
51	4	59	A
53	6	58	G

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Mol	Chain	Res	Type
53	8	56	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

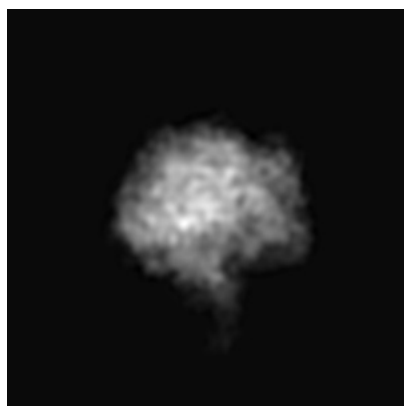
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13448. These allow visual inspection of the internal detail of the map and identification of artifacts.

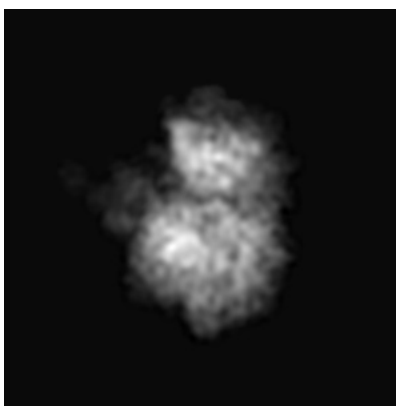
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

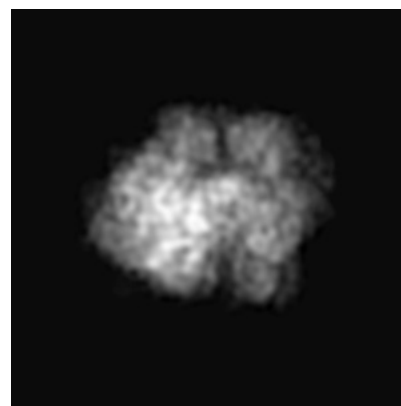
6.1.1 Primary map



X

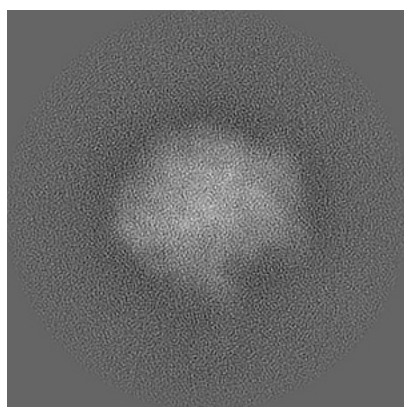


Y

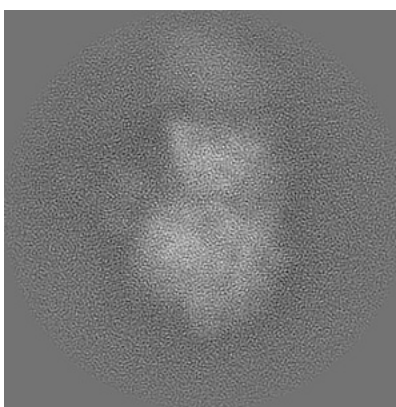


Z

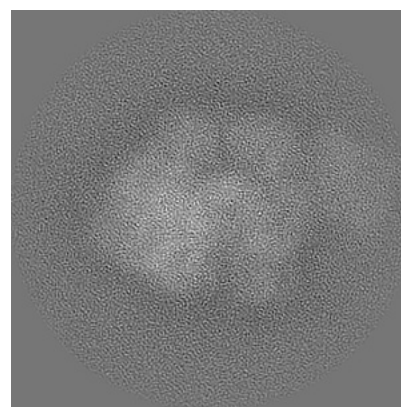
6.1.2 Raw map



X



Y

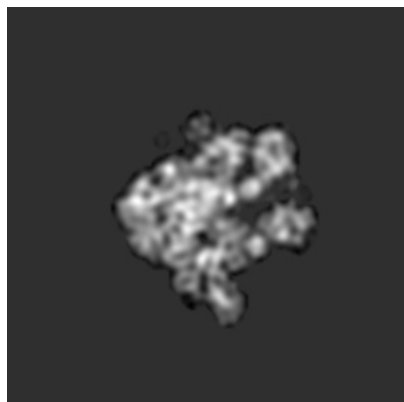


Z

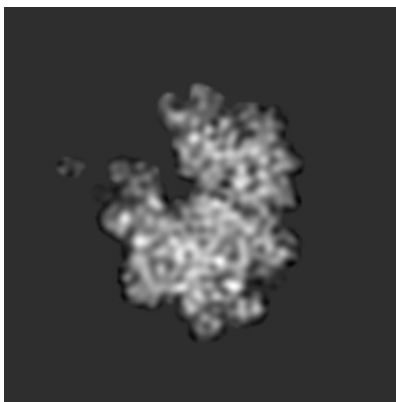
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

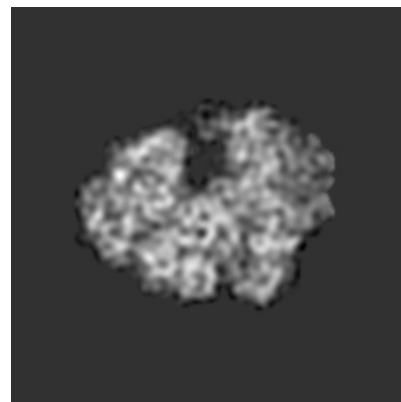
6.2.1 Primary map



X Index: 128

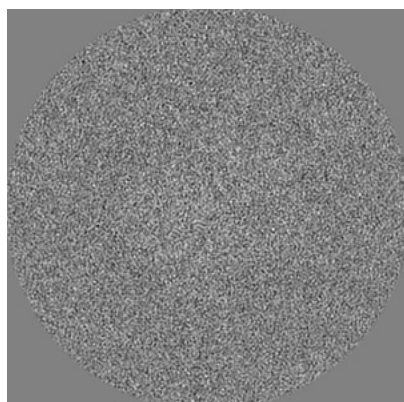


Y Index: 128

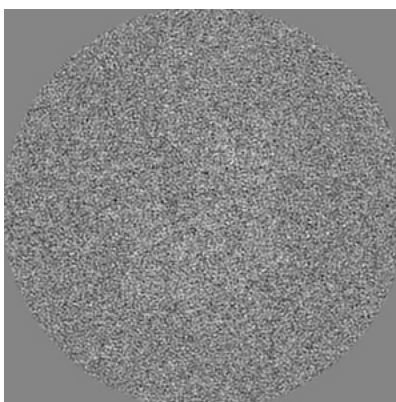


Z Index: 128

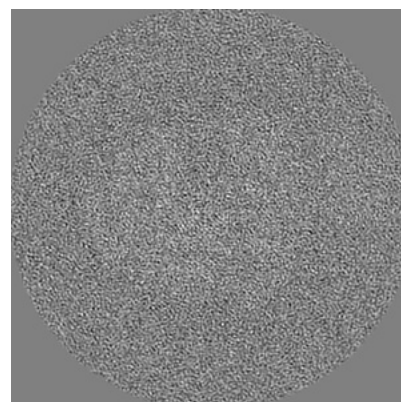
6.2.2 Raw map



X Index: 128



Y Index: 128

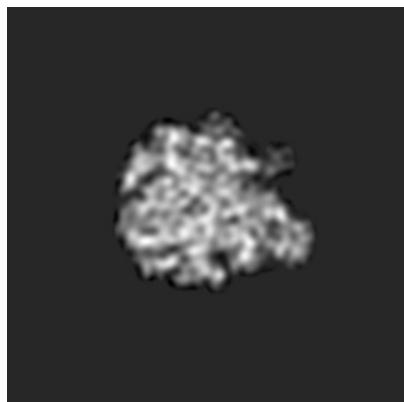


Z Index: 128

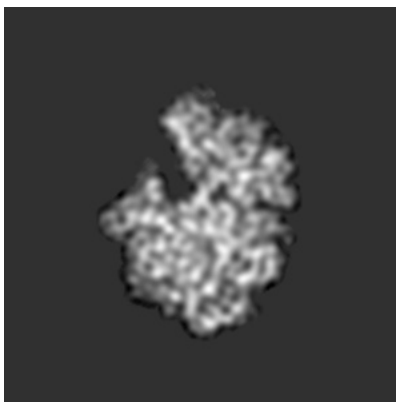
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

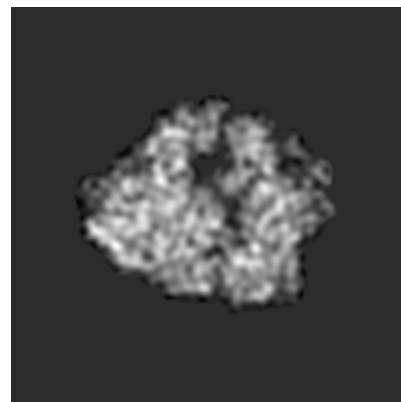
6.3.1 Primary map



X Index: 102

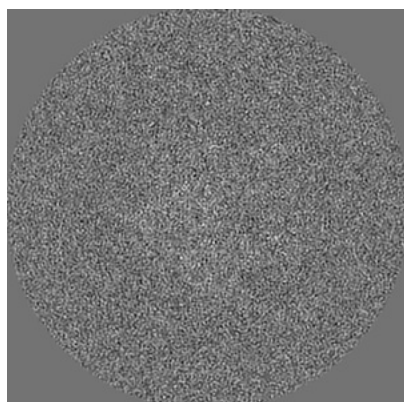


Y Index: 120

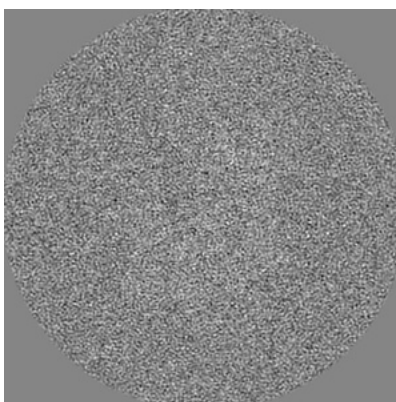


Z Index: 121

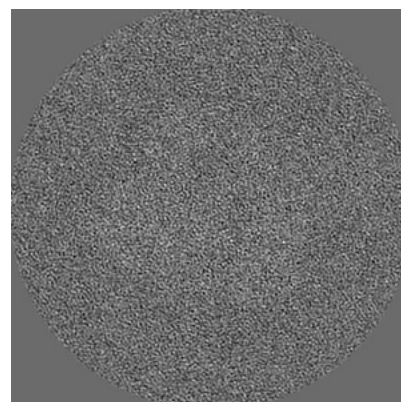
6.3.2 Raw map



X Index: 119



Y Index: 128

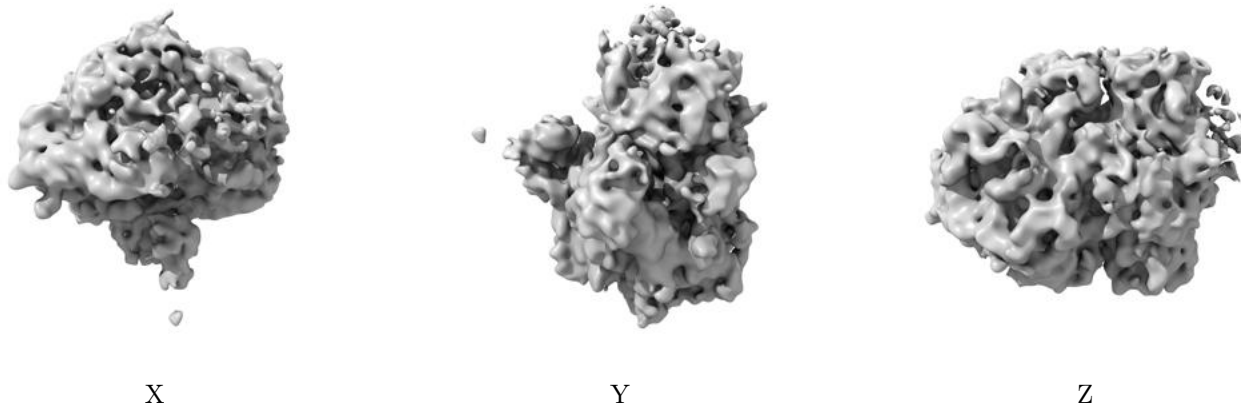


Z Index: 119

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

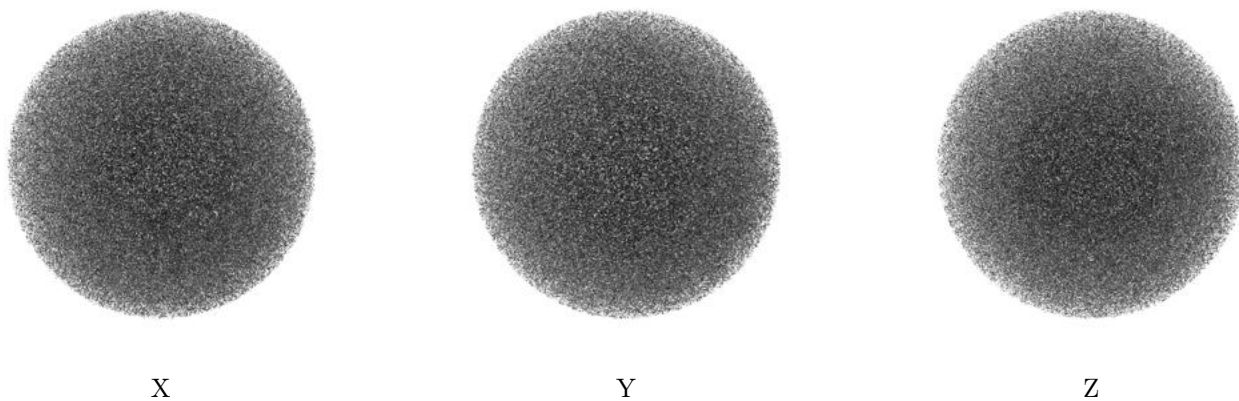
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.29. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

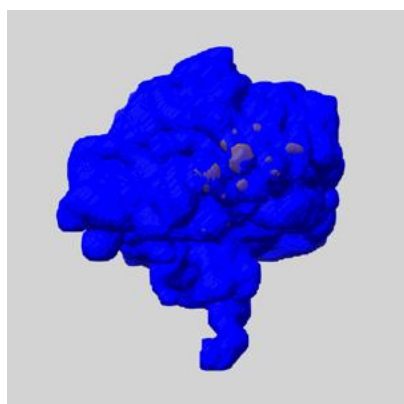
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

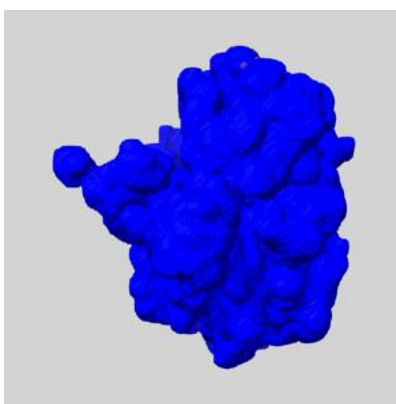
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

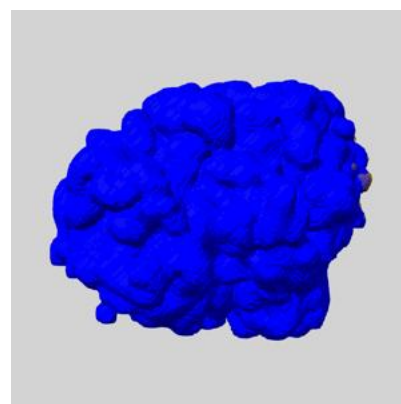
6.5.1 emd_13448_msk_1.map [i](#)



X



Y

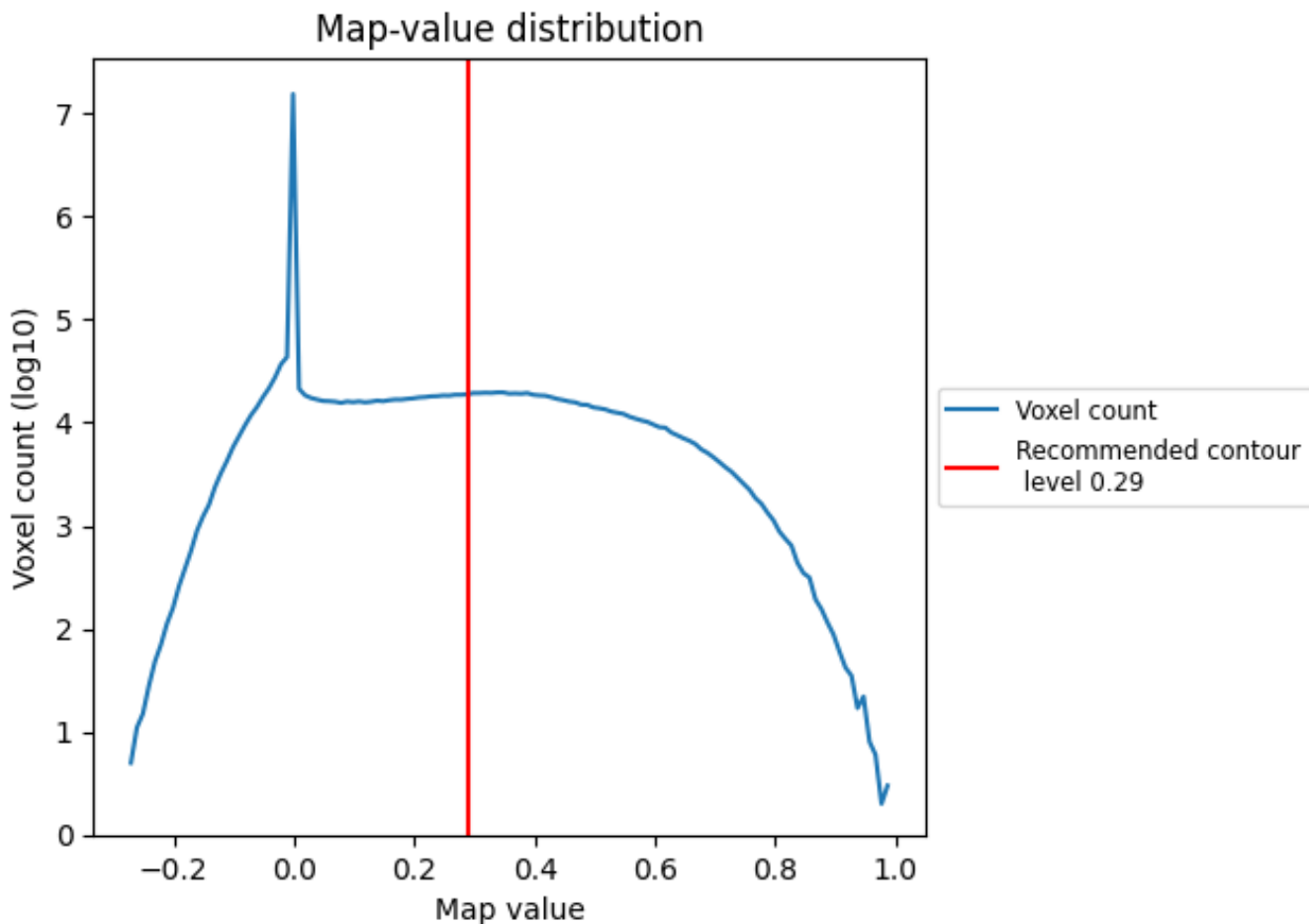


Z

7 Map analysis [i](#)

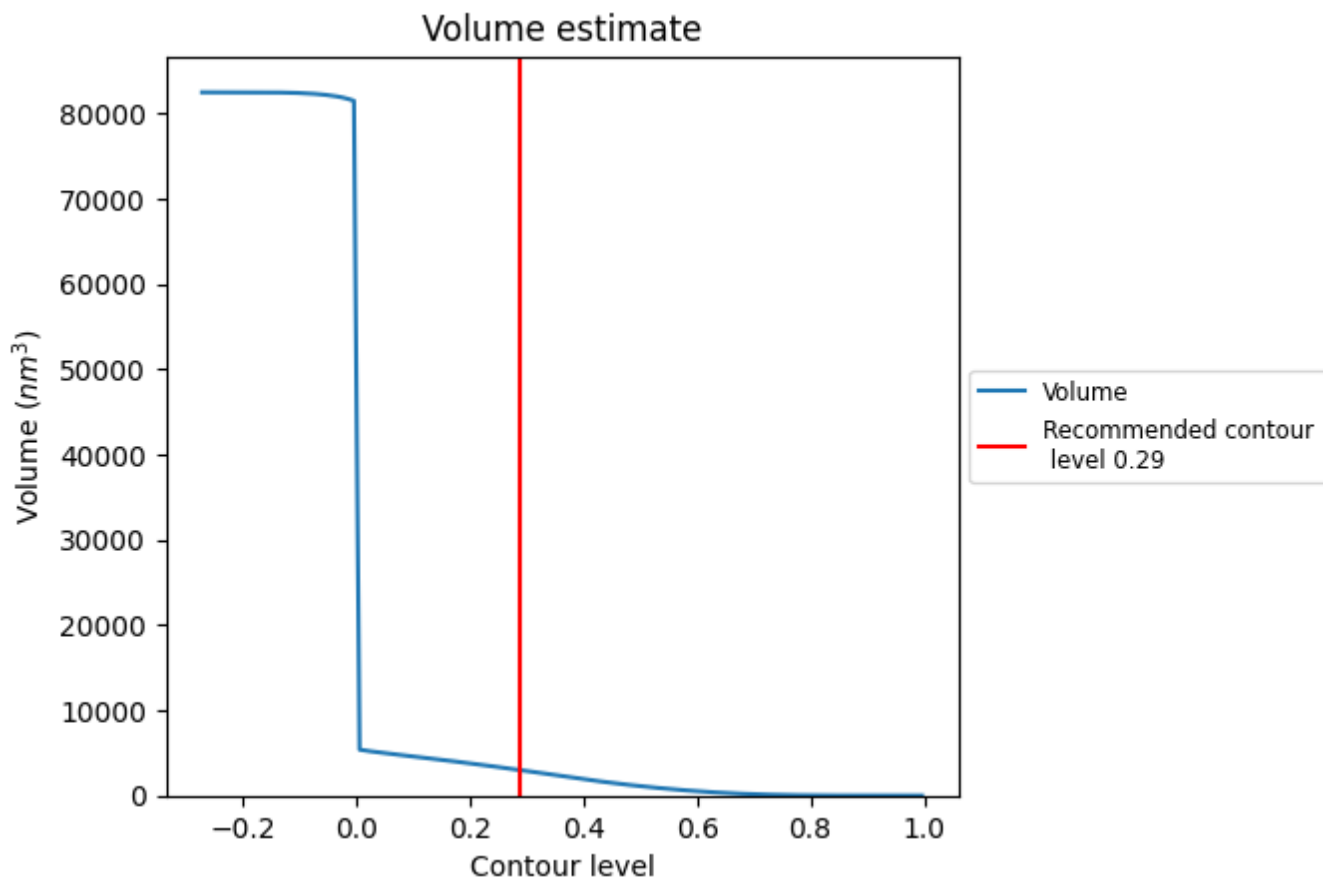
This section contains the results of statistical analysis of the map.

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.

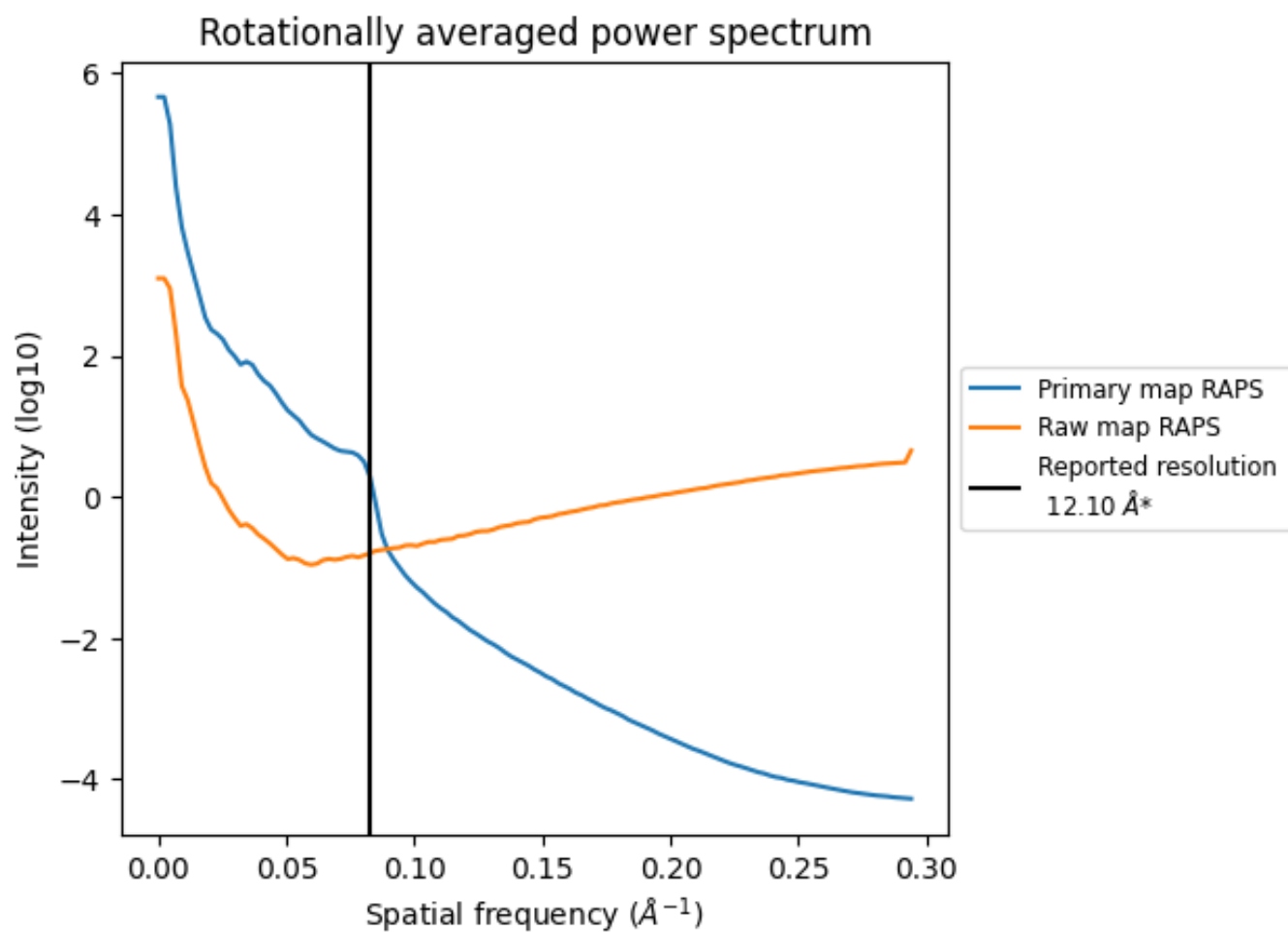
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2982 nm³; this corresponds to an approximate mass of 2693 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](#)

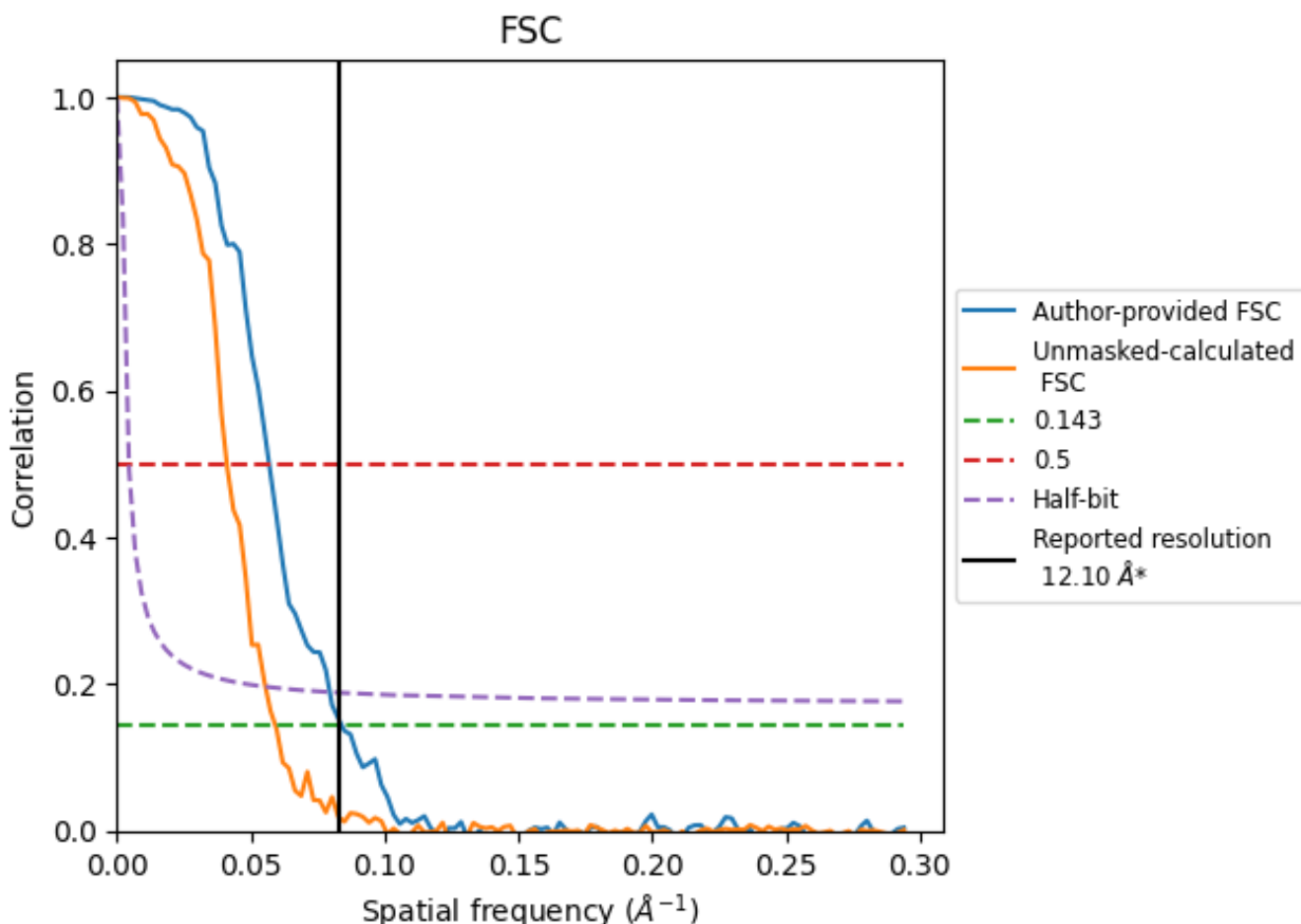


*Reported resolution corresponds to spatial frequency of 0.083 Å⁻¹

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 0.083 Å⁻¹

8.2 Resolution estimates [i](#)

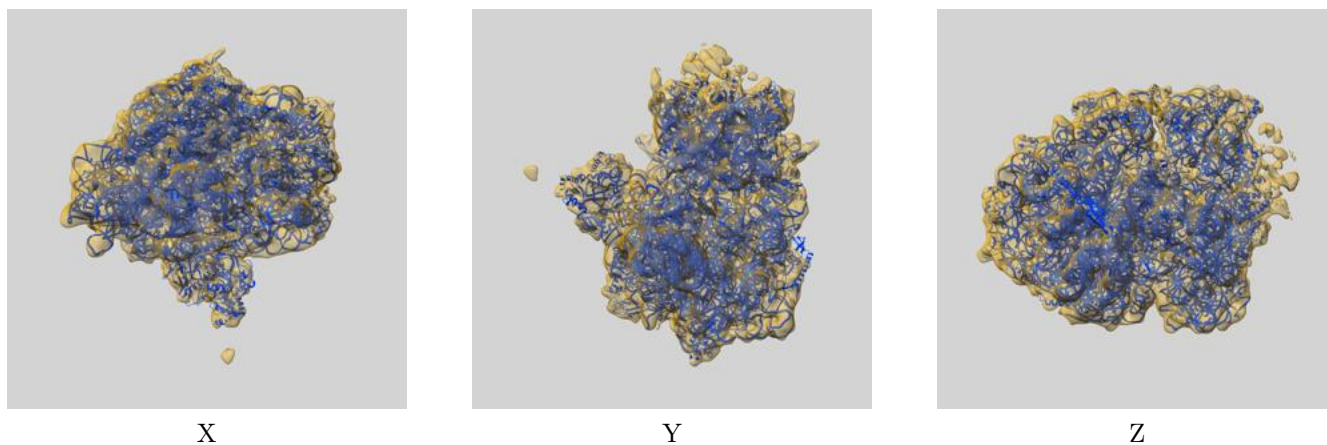
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	12.10	-	-
Author-provided FSC curve	11.90	17.57	12.56
Unmasked-calculated*	16.86	24.33	17.99

*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 16.86 differs from the reported value 12.1 by more than 10 %

9 Map-model fit [i](#)

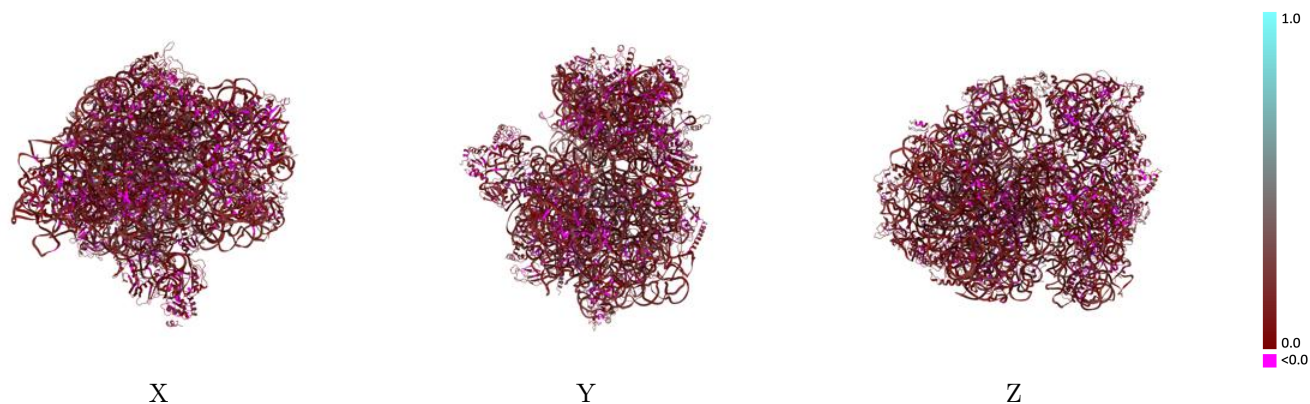
This section contains information regarding the fit between EMDB map EMD-13448 and PDB model 7PIR. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



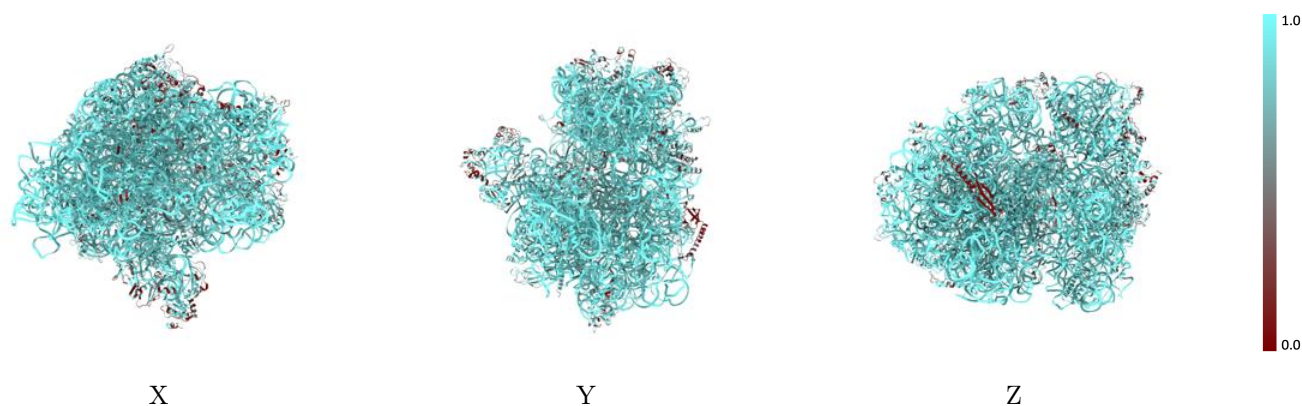
The images above show the 3D surface view of the map at the recommended contour level 0.29 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



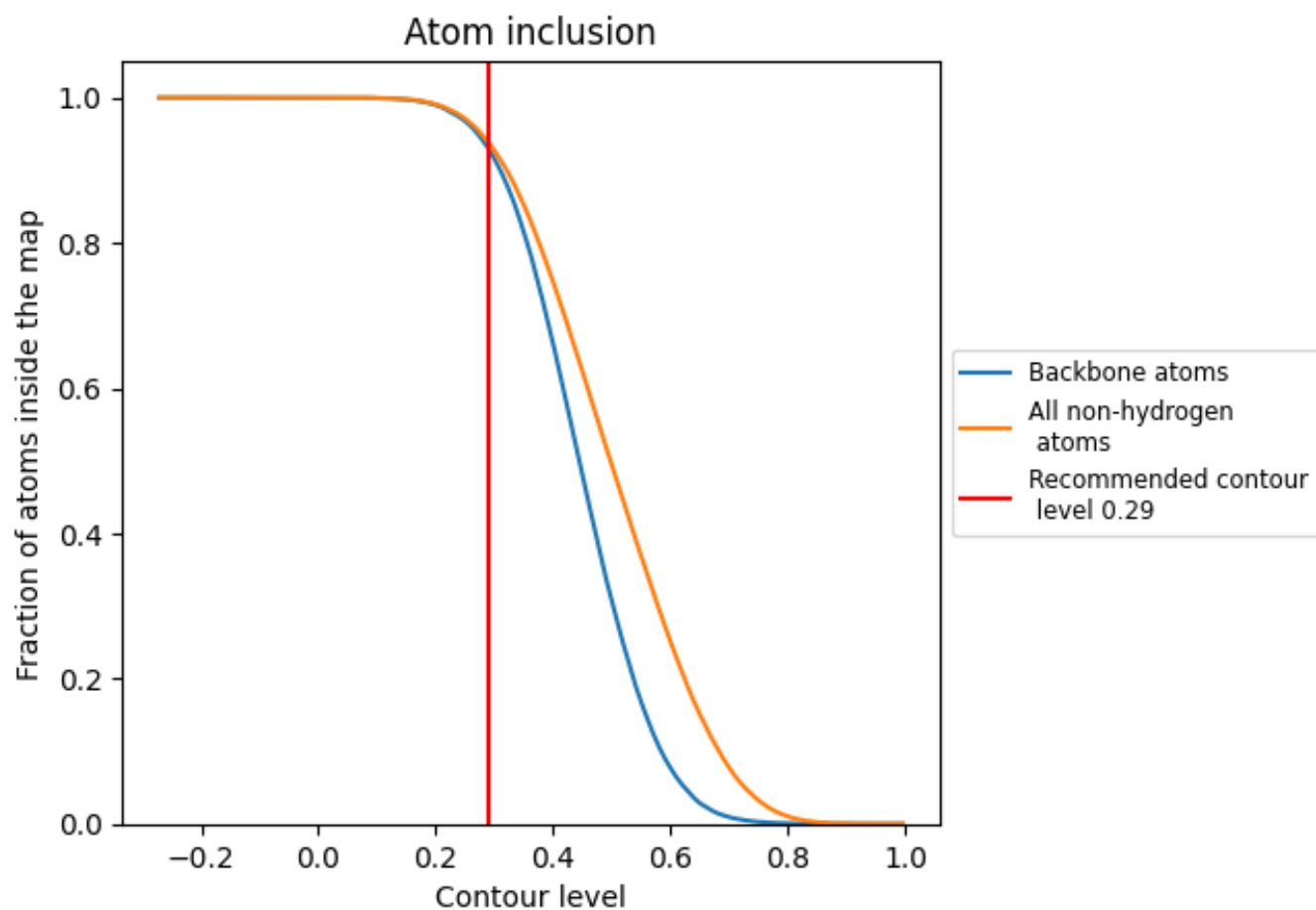
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.29).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary









































The table lists the average atom inclusion at the recommended contour level (0.29) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9385	 0.1040
0	 0.9973	 0.0760
1	 0.9936	 0.0650
2	 0.9730	 0.0330
3	 0.9882	 0.1150
4	 0.9929	 0.1240
5	 0.9872	 0.1150
6	 0.8282	 0.0820
8	 0.9728	 0.1300
A	 0.7068	 0.0950
B	 0.7874	 0.1110
C	 0.8426	 0.0710
D	 0.8192	 0.0700
E	 0.7081	 0.1080
F	 0.8140	 0.0850
G	 0.8854	 0.0850
H	 0.8292	 0.0670
I	 0.7509	 0.0790
J	 0.7772	 0.0670
K	 0.9492	 0.0650
L	 0.8192	 0.1010
M	 0.8659	 0.0000
N	 0.8852	 0.0830
O	 0.9523	 0.0750
P	 0.8721	 0.0900
Q	 0.9477	 0.0820
R	 0.8731	 0.0450
S	 0.9672	 0.0810
T	 0.8326	 0.1340
a	 0.9640	 0.0590
b	 0.9055	 0.0570
c	 0.8679	 0.0860
d	 0.8181	 0.0980
e	 0.6751	 0.0810
f	 0.3768	 0.0870



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Chain	Atom inclusion	Q-score
g	 0.5866	 0.0770
h	 0.6364	 0.0830
i	 0.9518	 0.0890
j	 0.8163	 0.0710
k	 0.8473	 0.0660
l	 0.9308	 0.0650
m	 0.9744	 0.0550
n	 0.8639	 0.0760
o	 0.8672	 0.0860
p	 0.9650	 0.0720
q	 0.8561	 0.0730
r	 0.9323	 0.0880
s	 0.8773	 0.0840
t	 0.8211	 0.0900
u	 0.9656	 0.0550
v	 0.9899	 0.0910
w	 0.8926	 0.1320
x	 0.5598	 0.1150
y	 0.9078	 0.0450
z	 0.9849	 0.0550