



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:27 PM UTC

PDB ID : 7PIA / pdb_00007pia
EMDB ID : EMD-13434
Title : 70S ribosome with A/P- and P/E-site tRNAs in spectinomycin-treated
Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 13.60 Å (reported)
Based on initial models : 4V7C, 7OOC, 7OOD

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

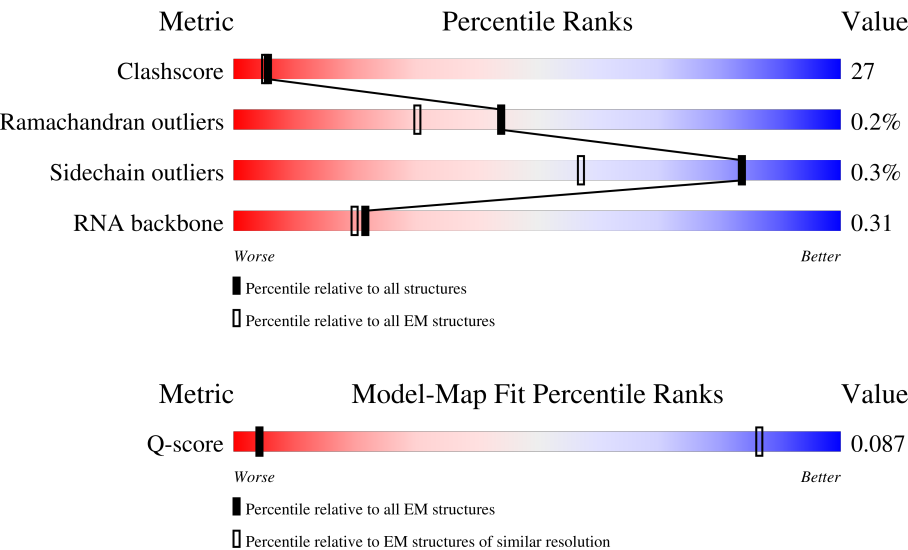
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 13.60 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	66 (13.10 - 14.10)

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	

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Mol	Chain	Length	Quality of chain
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	

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Mol	Chain	Length	Quality of chain
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	7	76	

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Mol	Chain	Length	Quality of chain
53	8	76	28% 51% 21%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146142 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
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 protein called 30S ribosomal protein S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		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		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		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
			1182	763	206	210	3	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	126	Total	C	N	O	S	0
			960	612	167	178	3	0

- 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
			959	616	160	177	6	0

- 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
			1164	737	213	209	5	0

- 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
			944	595	178	167	4	0

- 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
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

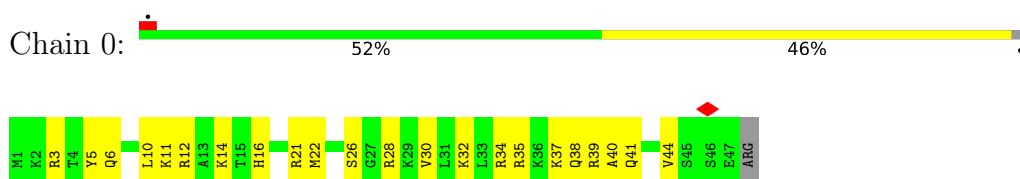
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	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		

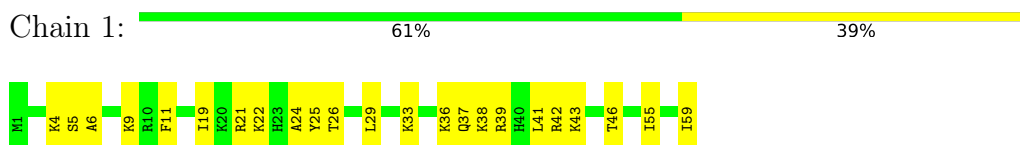
3 Residue-property plots [i](#)

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.

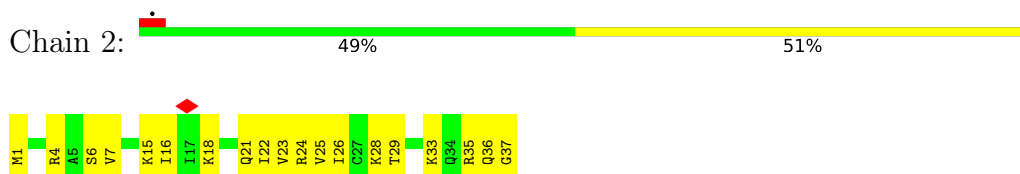
- Molecule 1: 50S ribosomal protein L34



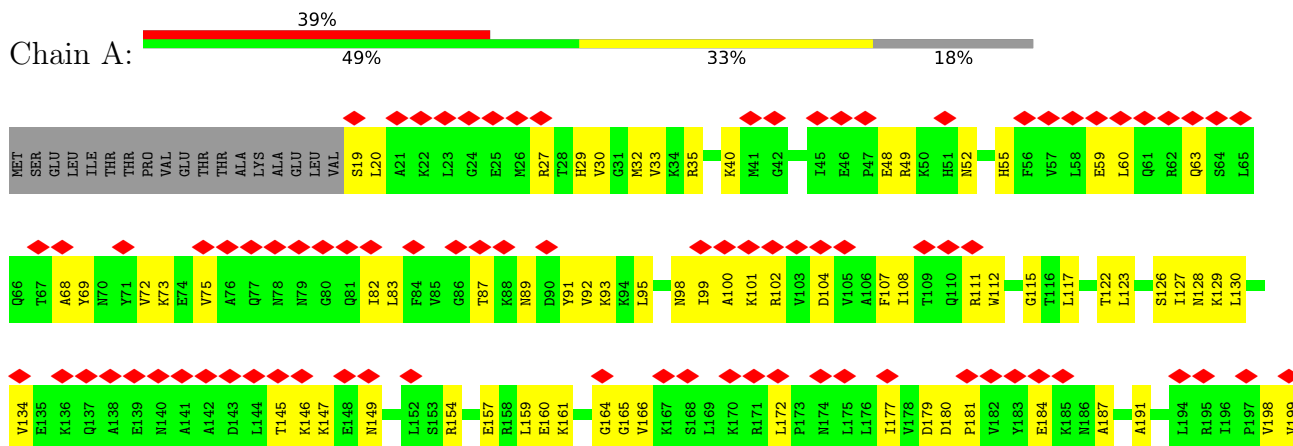
- Molecule 2: 50S ribosomal protein L35

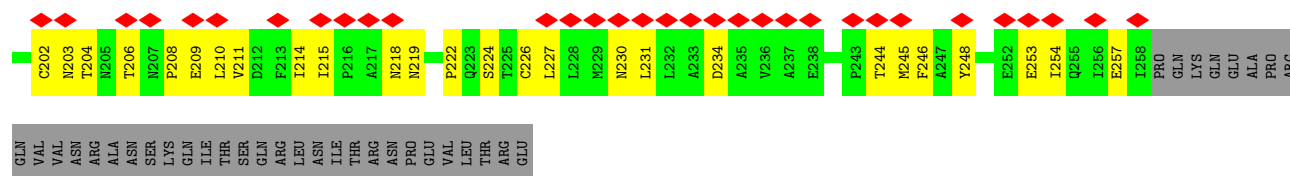


- Molecule 3: 50S ribosomal protein L36

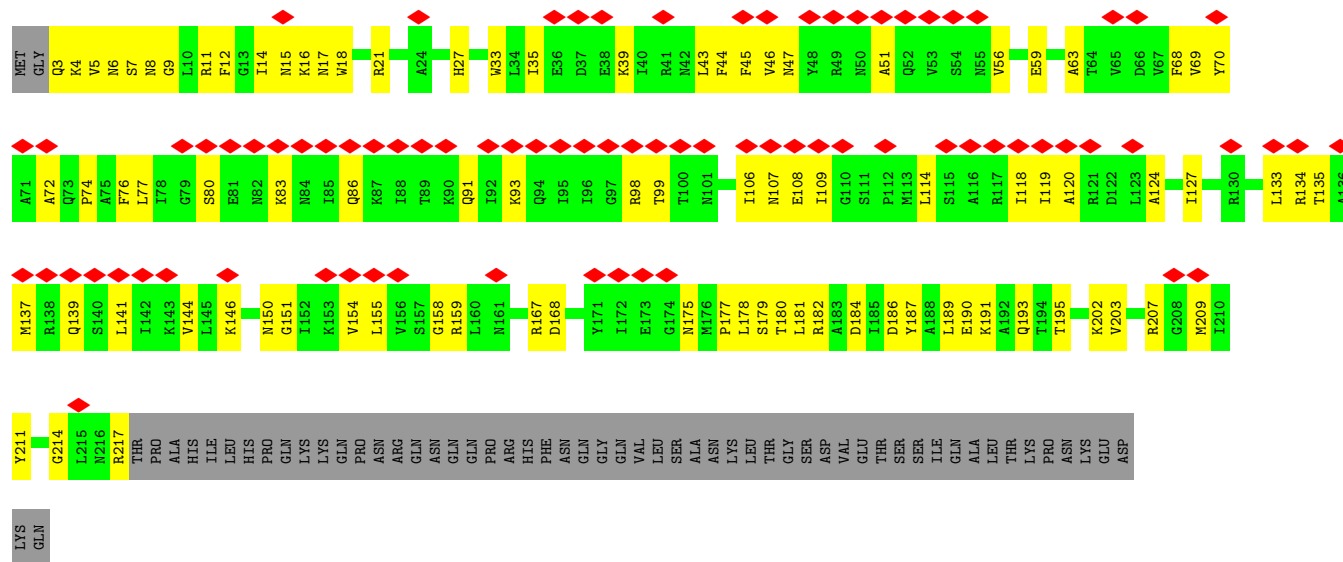


- Molecule 4: 30S ribosomal protein S2

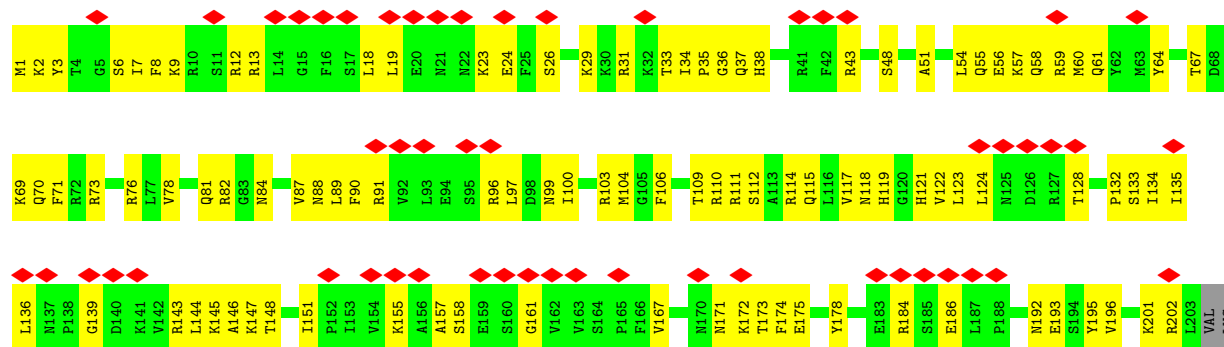




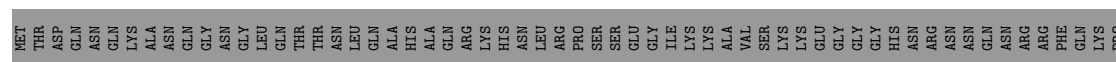
• Molecule 5: 30S ribosomal protein S3

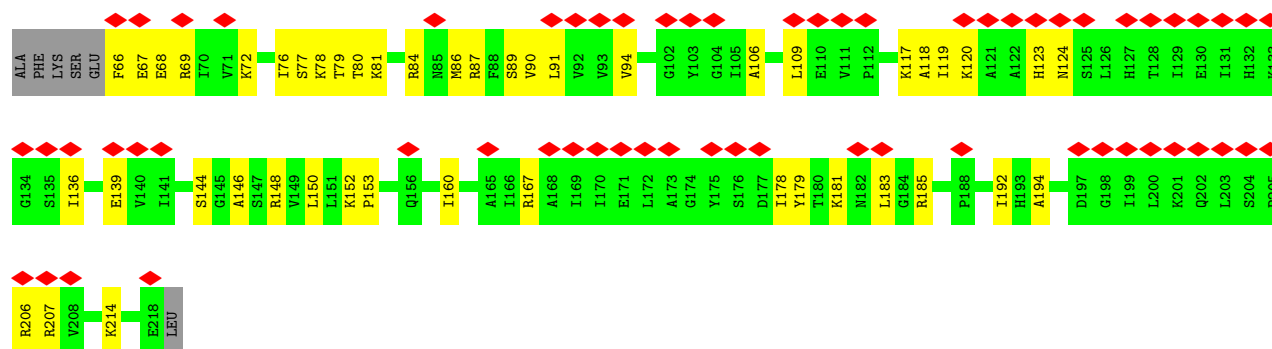


• Molecule 6: 30S ribosomal protein S4

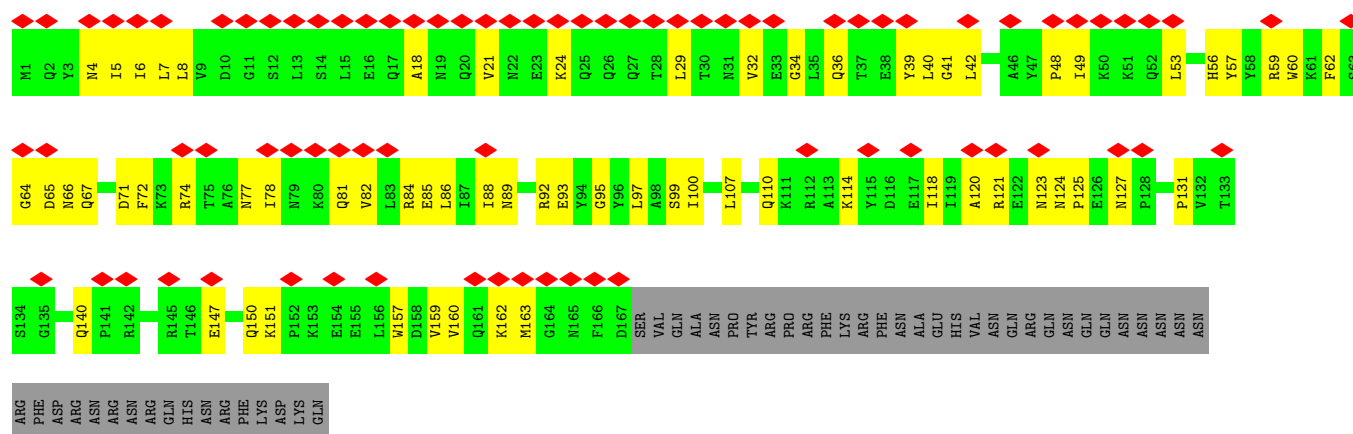


• Molecule 7: 30S ribosomal protein S5

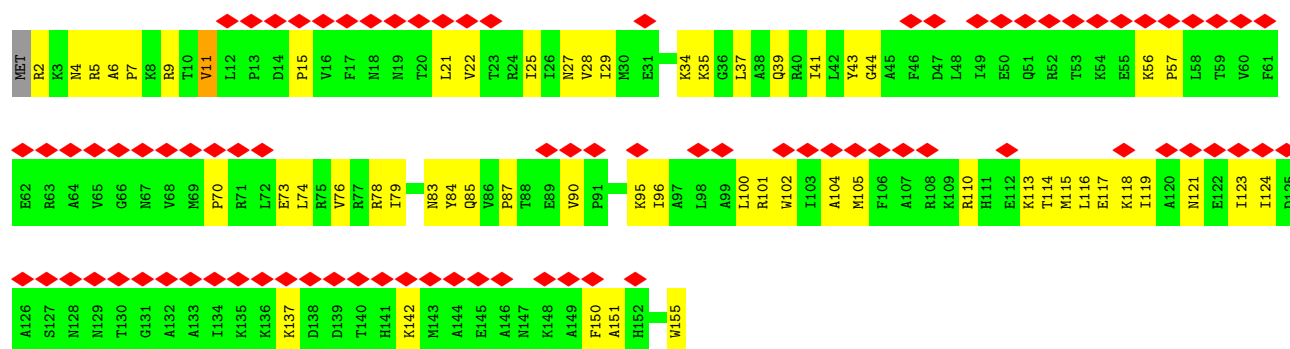




• Molecule 8: 30S ribosomal protein S6

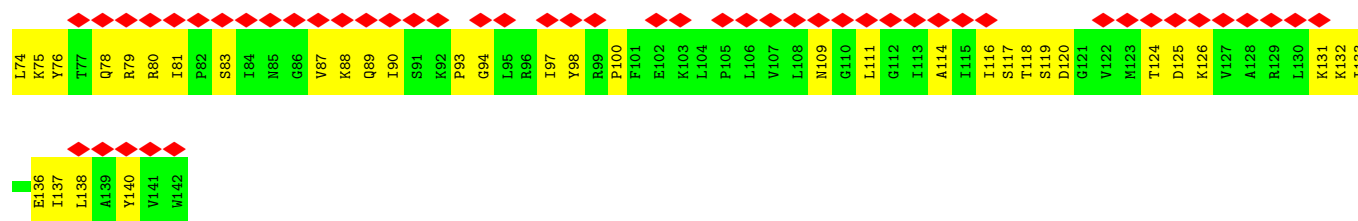


• Molecule 9: 30S ribosomal protein S7

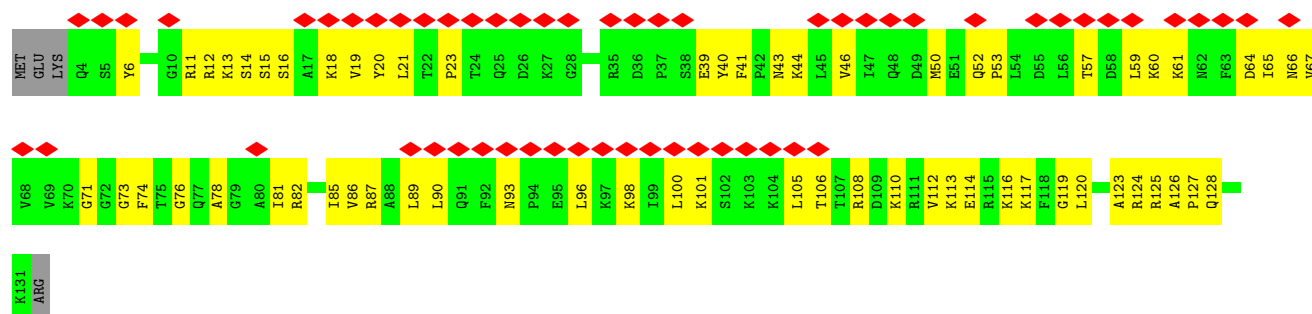
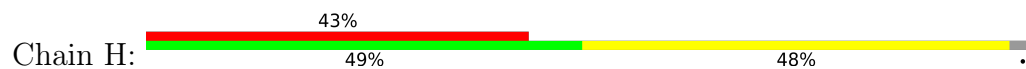


• Molecule 10: 30S ribosomal protein S8

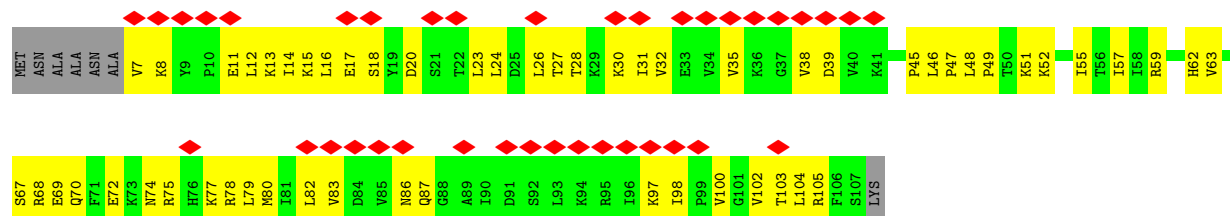




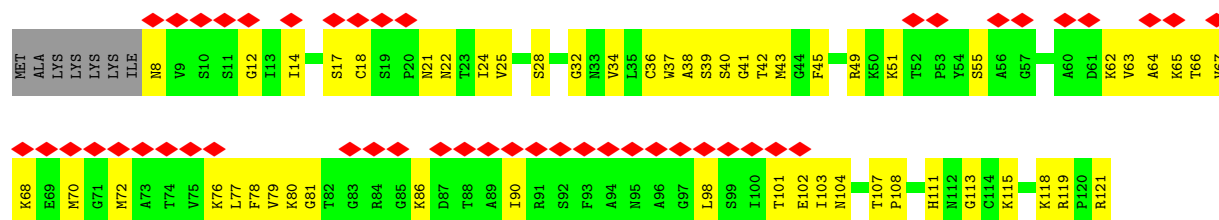
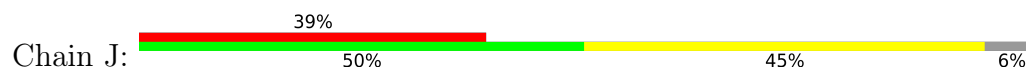
• Molecule 11: 30S ribosomal protein S9



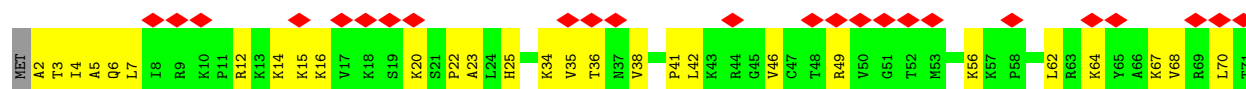
• Molecule 12: 30S ribosomal protein S10

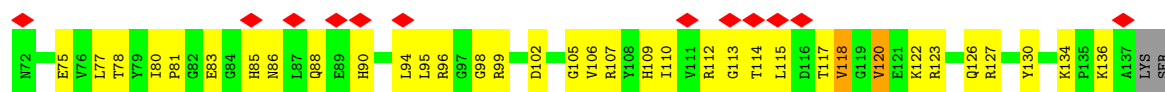


• Molecule 13: 30S ribosomal protein S11

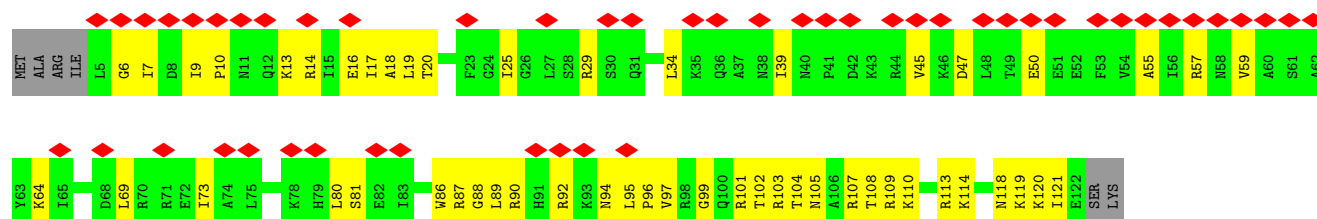


• Molecule 14: 30S ribosomal protein S12





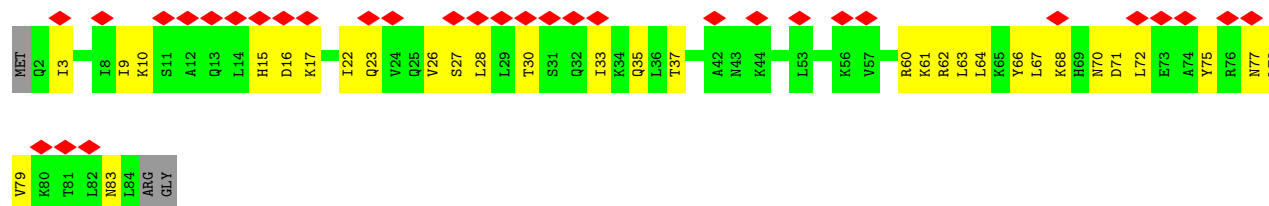
- Molecule 15: 30S ribosomal protein S13



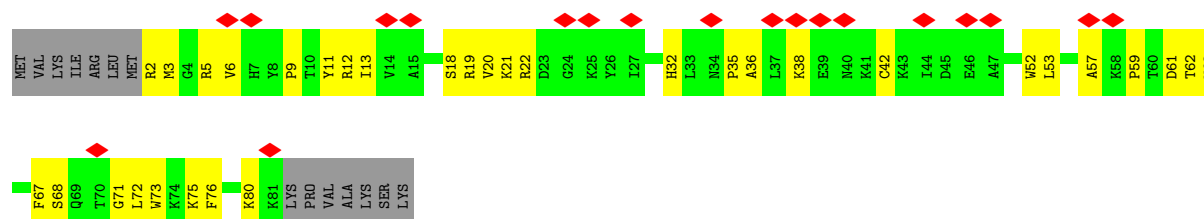
- Molecule 16: 30S ribosomal protein S14 type Z



- Molecule 17: 30S ribosomal protein S15

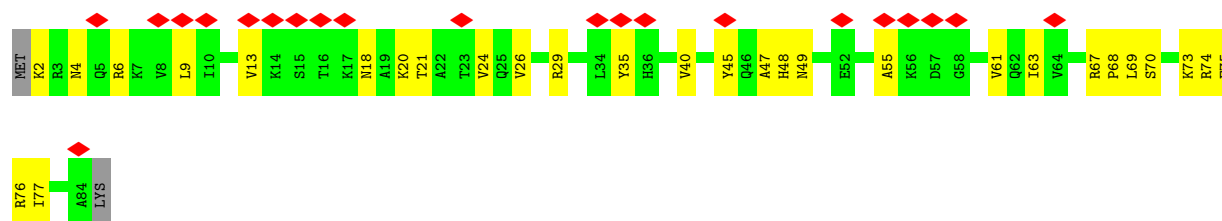


- Molecule 18: 30S ribosomal protein S16

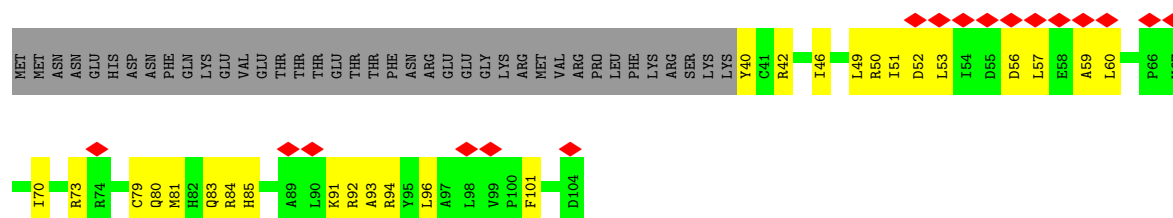


- Molecule 19: 30S ribosomal protein S17

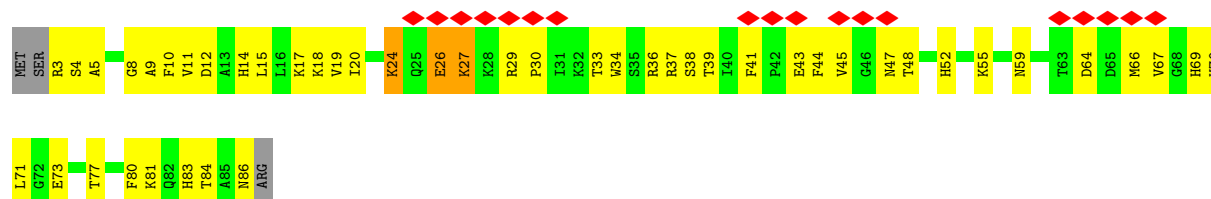
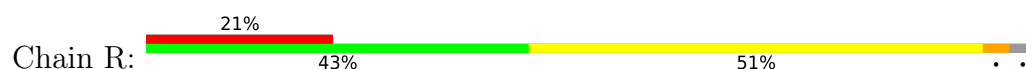




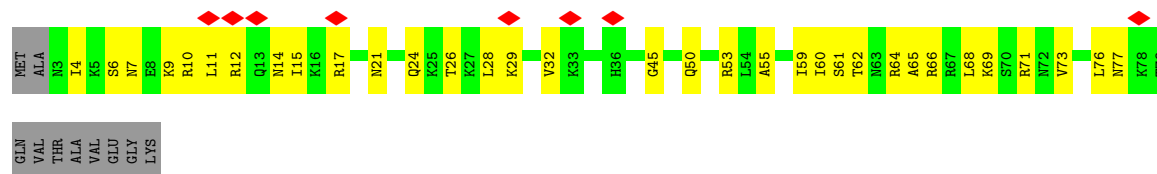
- Molecule 20: 30S ribosomal protein S18



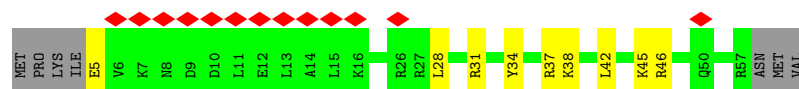
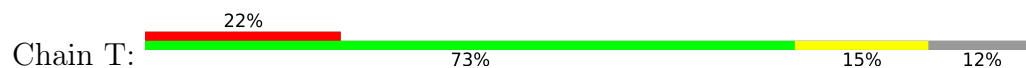
- Molecule 21: 30S ribosomal protein S19



- Molecule 22: 30S ribosomal protein S20

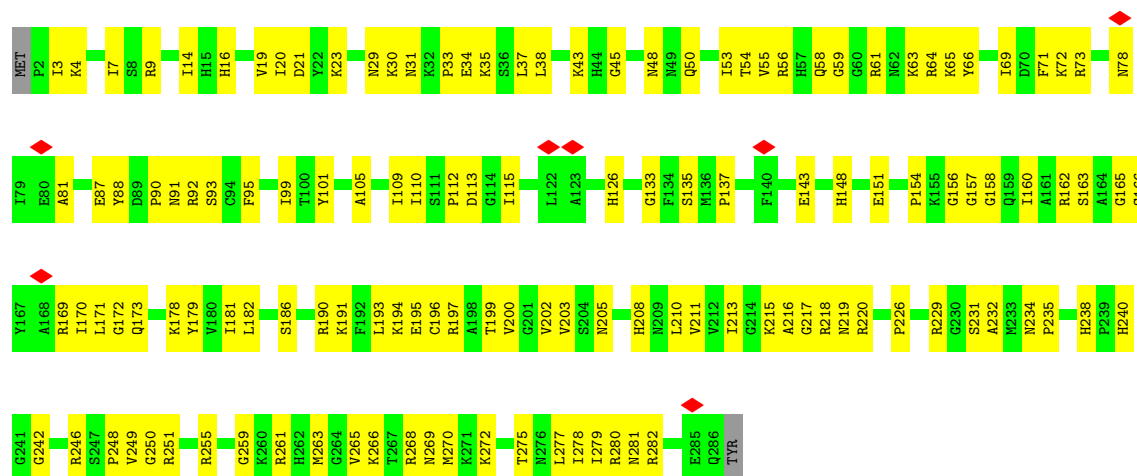


- Molecule 23: 30S ribosomal protein S21

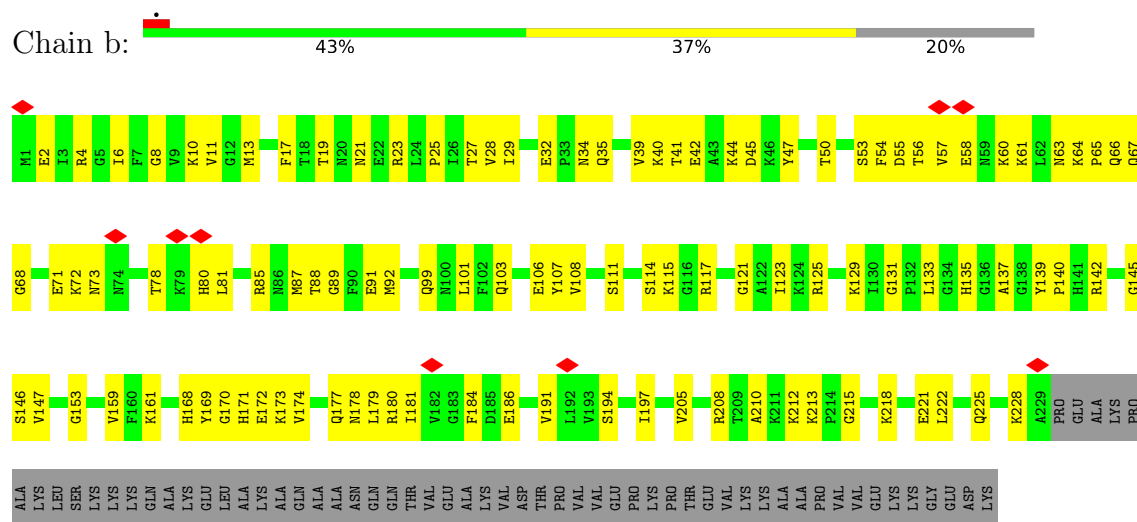


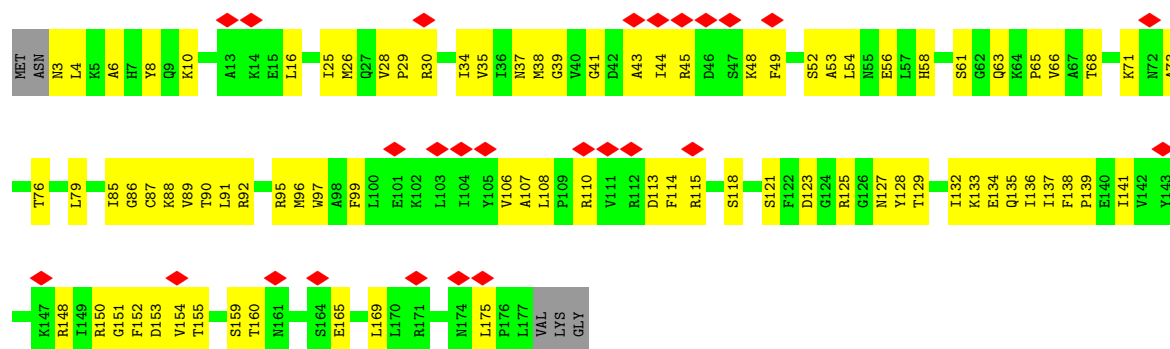
- Molecule 24: 50S ribosomal protein L2



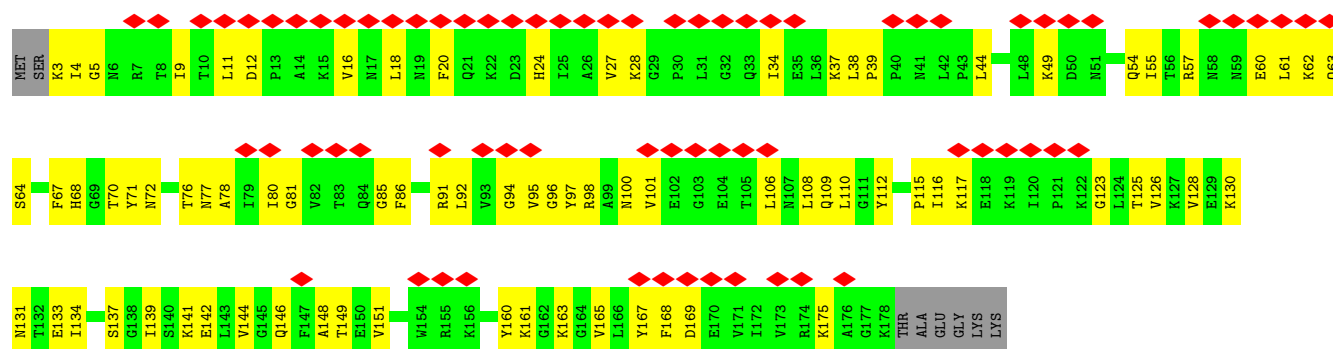
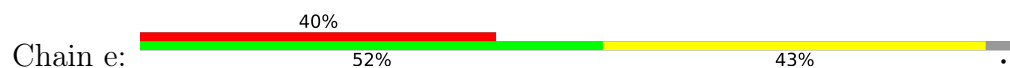


• Molecule 25: 50S ribosomal protein L3

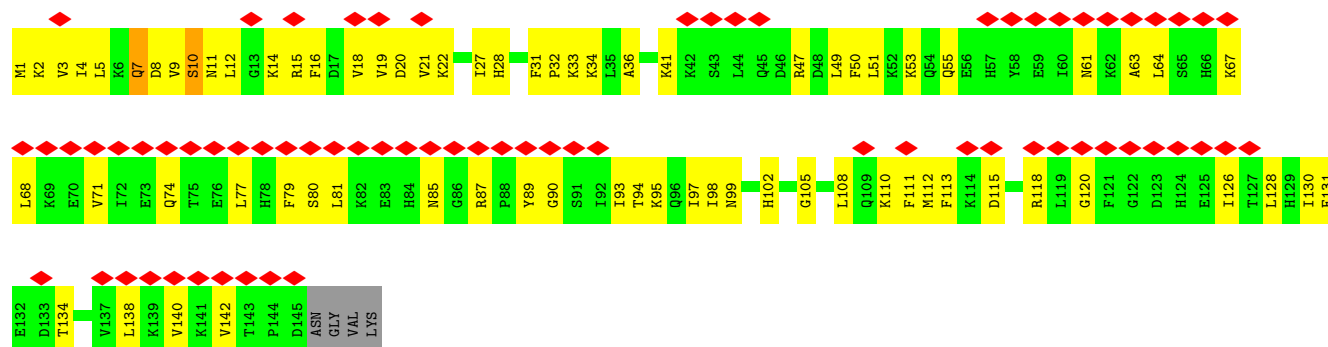




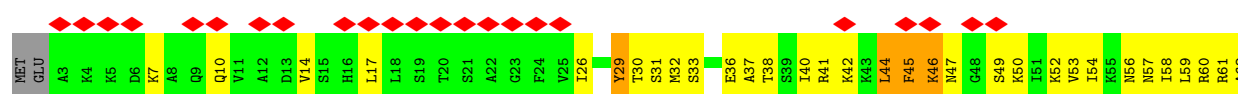
• Molecule 28: 50S ribosomal protein L6

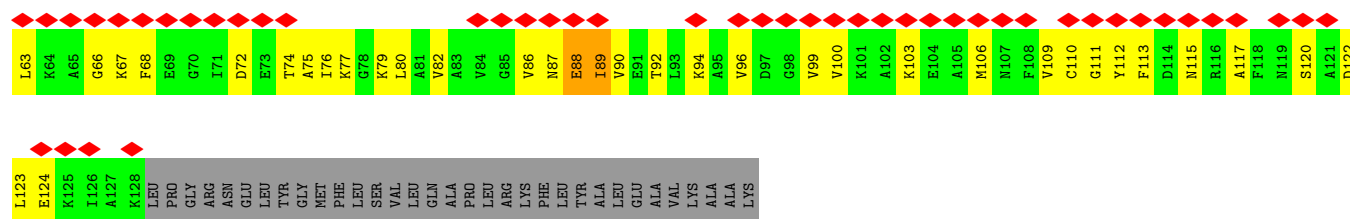


• Molecule 29: 50S ribosomal protein L9

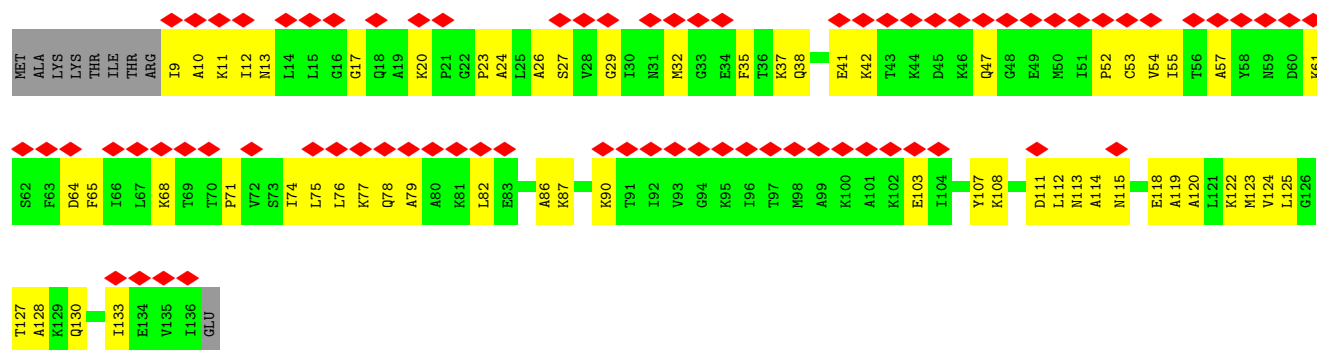


• Molecule 30: 50S ribosomal protein L10

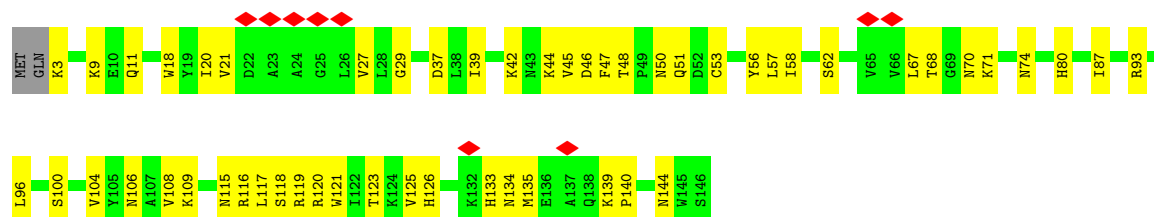




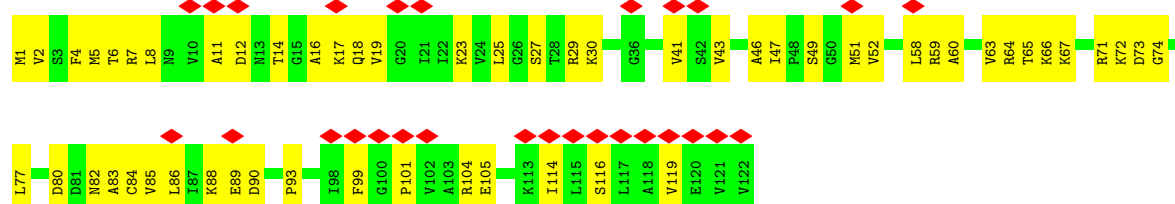
• Molecule 31: 50S ribosomal protein L11



• Molecule 32: 50S ribosomal protein L13

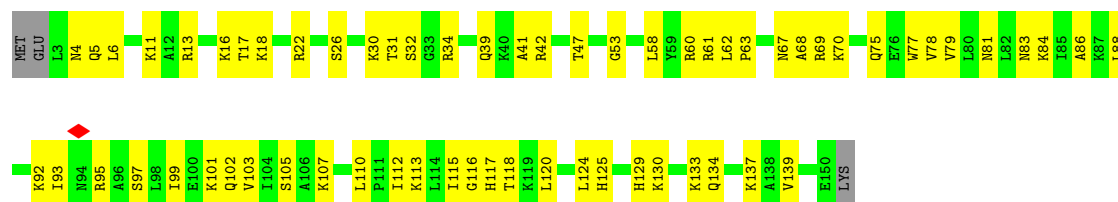


• Molecule 33: 50S ribosomal protein L14

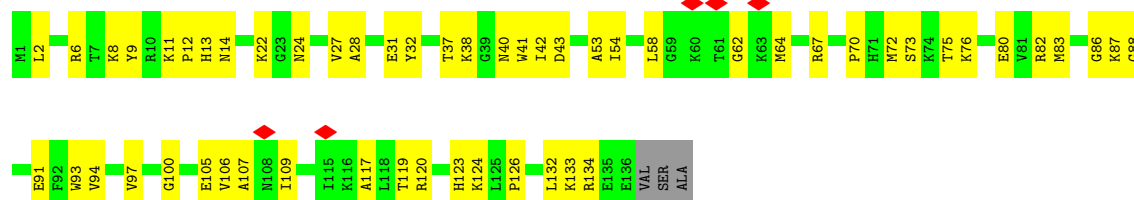


• Molecule 34: 50S ribosomal protein L15

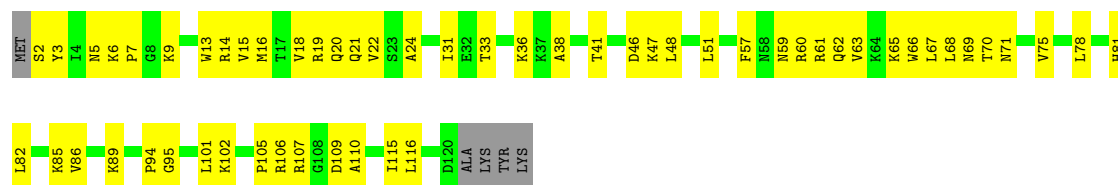




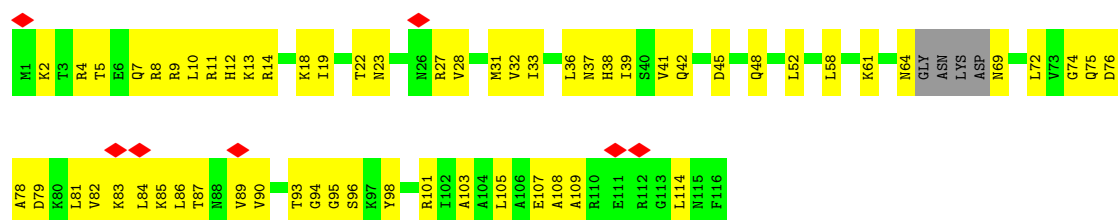
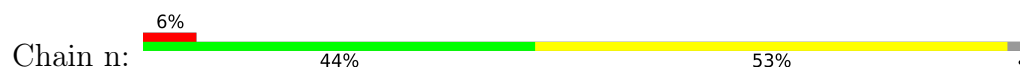
• Molecule 35: 50S ribosomal protein L16



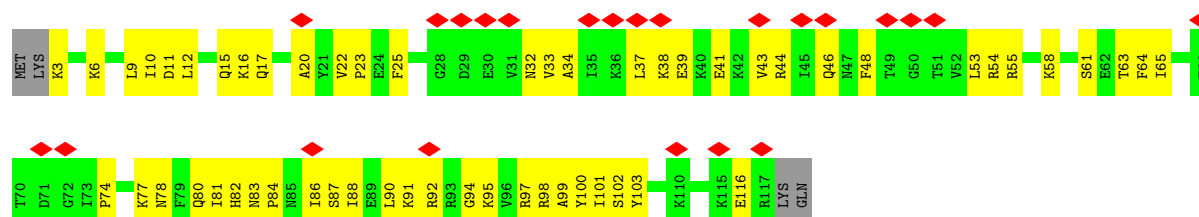
• Molecule 36: 50S ribosomal protein L17



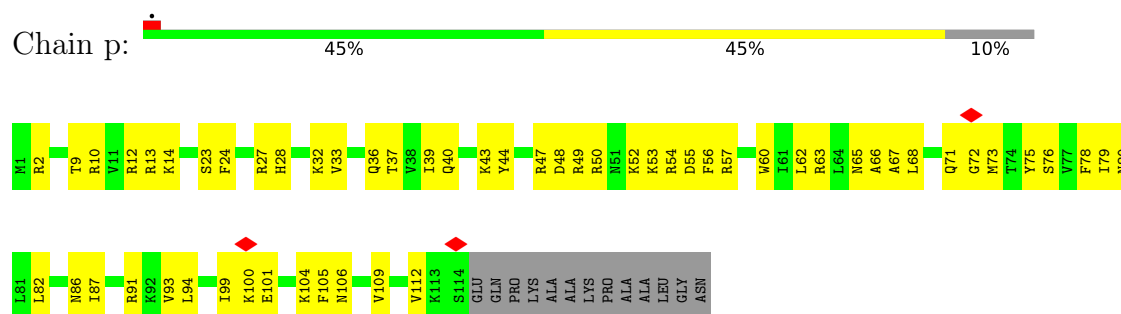
• Molecule 37: 50S ribosomal protein L18



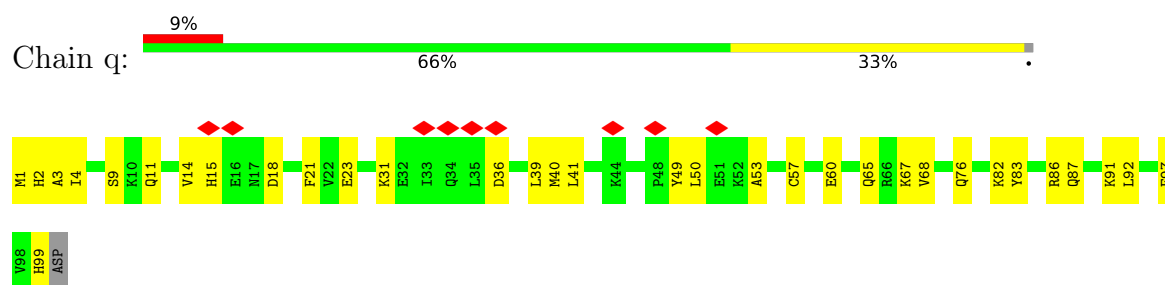
• Molecule 38: 50S ribosomal protein L19



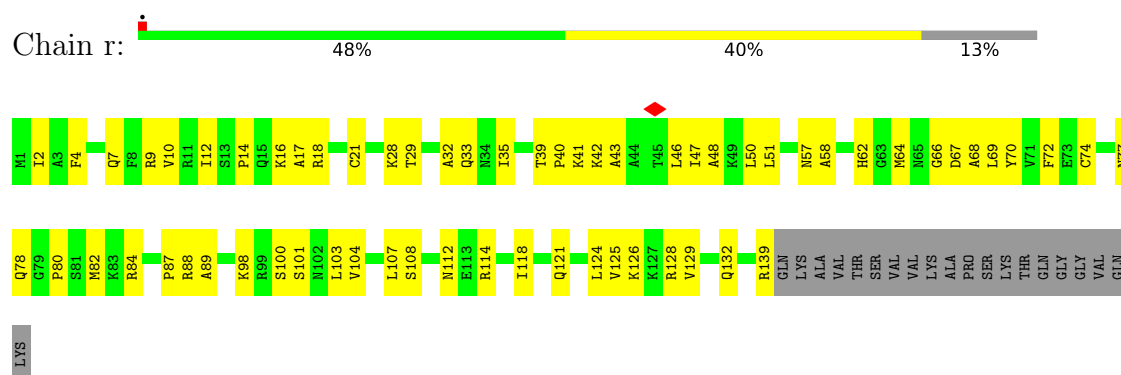
- Molecule 39: 50S ribosomal protein L20



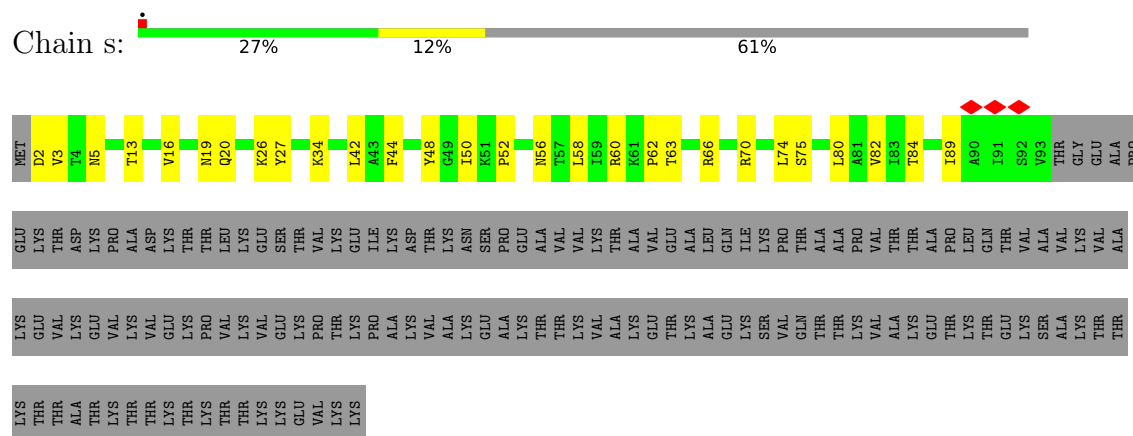
- Molecule 40: 50S ribosomal protein L21



- Molecule 41: 50S ribosomal protein L22

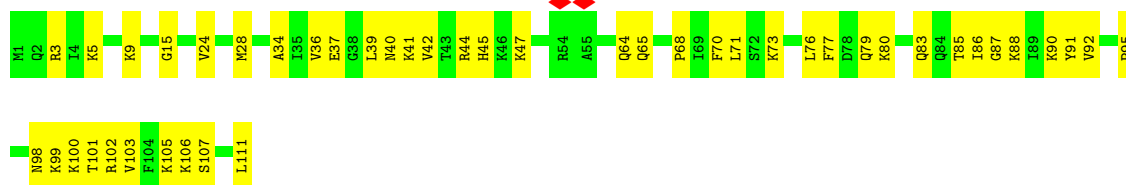


- Molecule 42: 50S ribosomal protein L23



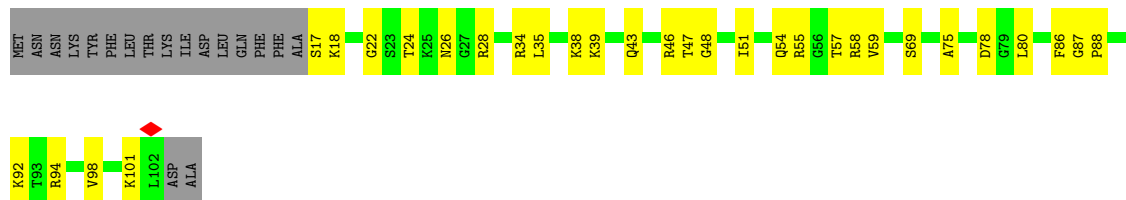
- Molecule 43: 50S ribosomal protein L24

Chain t: 



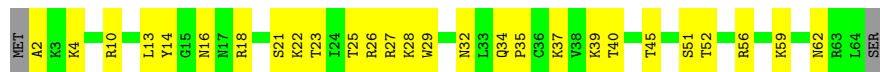
- Molecule 44: 50S ribosomal protein L27

Chain u: 

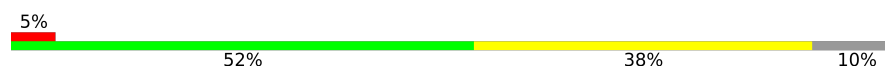


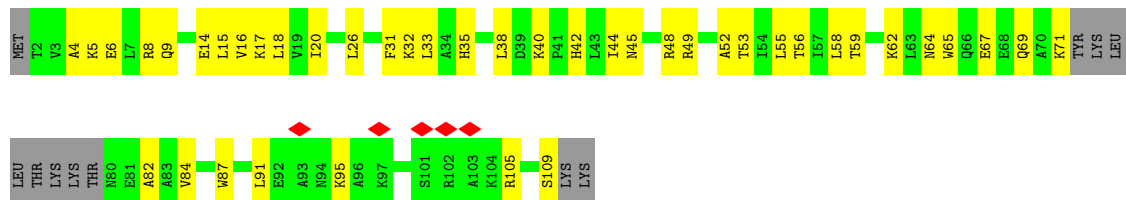
- Molecule 45: 50S ribosomal protein L28

Chain v: 



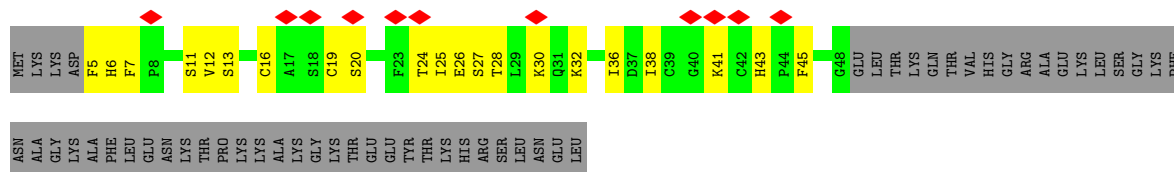
- Molecule 46: 50S ribosomal protein L29

Chain w: 



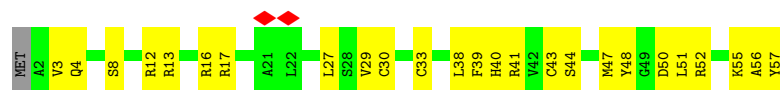
- Molecule 47: 50S ribosomal protein L31

Chain x: 

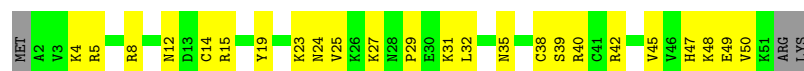


- Molecule 48: 50S ribosomal protein L32

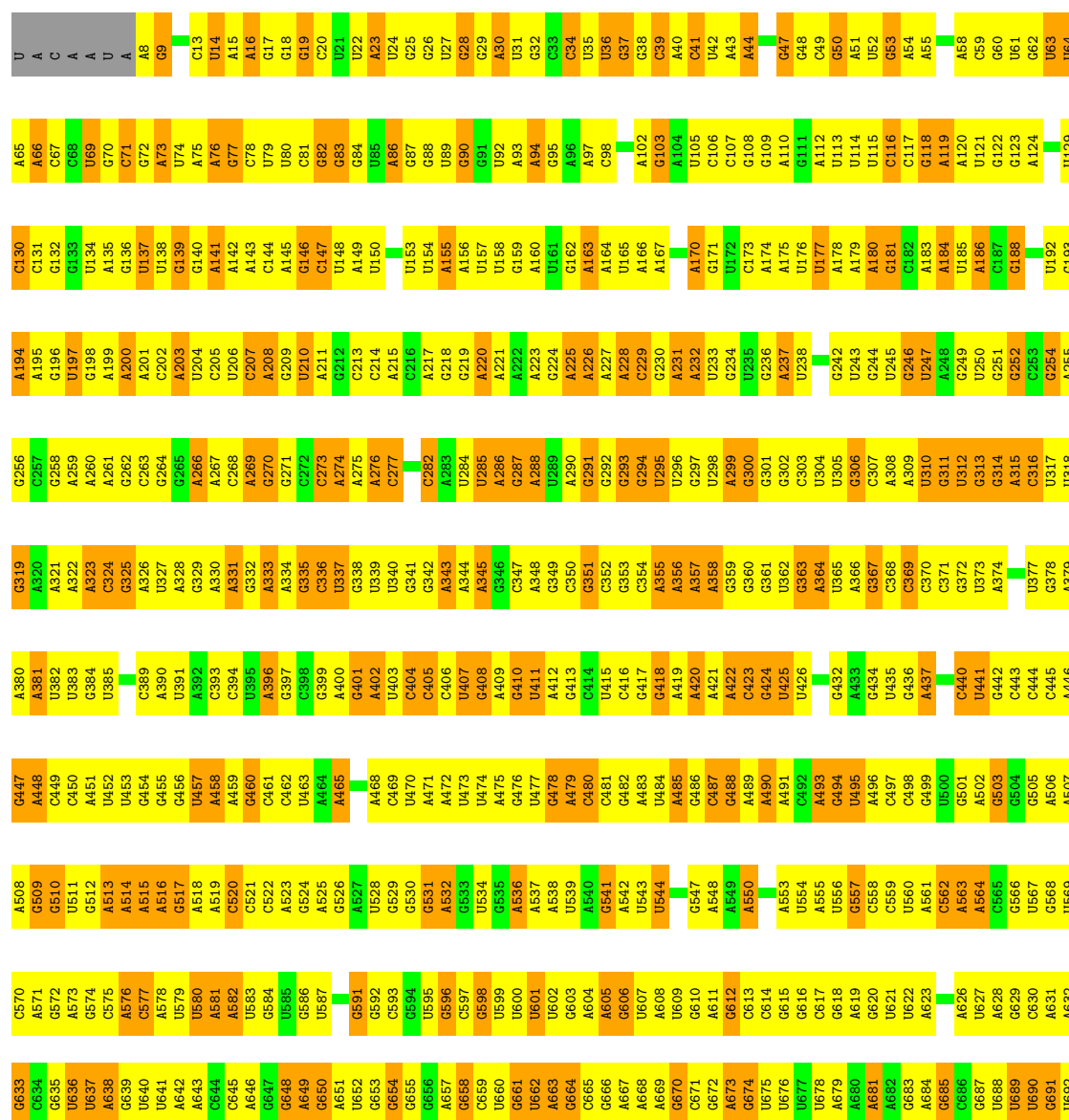
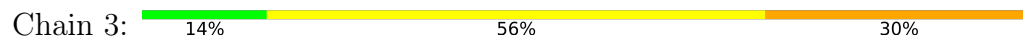
Chain y: 



- Molecule 49: 50S ribosomal protein L33 1



- Molecule 50: 23S ribosomal RNA

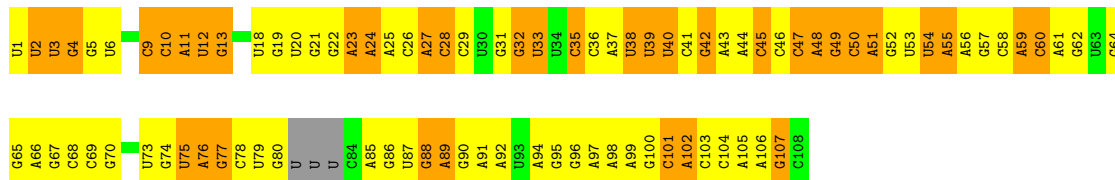


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C2518	C2518	U2212	U2212	A2272	G2151	C2090	G2029	U1967	G1904	A1836	A1773	A1652
U2519	U2519	A2213	A2213	C2273	C2152	G2091	A2030	C1968	U1905	C1837	U1774	C1653
C2520	C2520	U2214	U2214	G2274	U2153	U2092	C2031	C1969	G1906	A1838	G1775	A1654
U2521	U2521	C2215	C2215	A2275	U2154	U2093	G2032	G1970	A1907	U1841	G1776	U1655
C2522	C2522	U2216	U2216	G2276	G2155	A2094	G2033	G1971	C1908	G1842	G1777	A1656
U2523	U2523	G2217	G2217	C2277	C2156	A2095	G2034	C1972	C1909	C1843	G1778	G1657
C2524	C2524	U2218	U2218	U2278	G2157	U2096	U2035	U1973	G1910	C1844	G1779	U1658
U2525	U2525	A2219	A2219	A2279	C2158	A2097	G2036	U1974	C1911	C1845	C1781	C1659
C2526	C2526	U2220	U2220	G2280	G2159	U2098	A2037	G1975	C1912	U1846	U1784	A1660
U2527	U2527	U2221	U2221	C2281	U2159	U2099	A2038	A1976	G1913	A1847	G1785	A1661
C2528	C2528	C2222	C2222	G2282	U2160	G2100	G2039	A1977	G1914	G1847	U1786	G1662
U2529	U2529	G2223	G2223	U2283	G2161	U2101	A2040	U1978	C1915	U1848	A1787	G1663
C2530	C2530	A2224	A2224	A2284	U2162	U2102	C2041	G1979	C1916	G1849	A1788	A1664
U2531	U2531	G2225	G2225	G2285	U2163	C2103	A2042	G1980	G1917	C1850	C1789	G1665
C2532	C2532	U2226	U2226	C2286	G2164	A2105	C2043	U1981	U1918	U1851	U1790	A1666
U2533	U2533	U2227	U2227	G2287	A2165	G2106	C2044	G1982	A1791	G1852	U1727	G1667
C2534	C2534	G2228	G2228	U2288	U2166	A2107	G2045	U1983	A1920	A1855	U1728	G1668
U2535	U2535	C2229	C2229	A2289	G2167	C2108	G2046	U1984	C1921	G1856	G1729	A1669
C2536	C2536	A2230	A2230	G2290	C2168	U2109	U2047	C1987	U1922	C1857	U1730	U1670
U2537	U2537	U2231	U2231	U2291	G2169	A2110	U2048	A1988	A1923	G1857	C1731	C1671
C2538	C2538	G2232	G2232	C2292	A2170	U2111	G2050	U1989	U1924	U1858	G1732	C1672
U2539	U2539	A2233	A2233	U2293	G2171	U2112	C2051	U1990	C1925	A1860	U1733	U1673
C2540	C2540	C2234	C2234	G2294	A2172	A2113	C2052	C1991	U1926	A1797	A1734	A1674
U2541	U2541	U2235	U2235	U2295	U2173	U2114	G2053	U1991	G1927	A1861	A1735	A1675
C2542	C2542	G2236	G2236	A2296	G2174	C2054	C2054	U1992	G1928	A1862	G1736	G1676
U2543	U2543	U2237	U2237	U2297	U2175	A2055	C2055	U1994	C1929	A1863	U1737	G1677
C2544	C2544	G2238	G2238	G2298	G2176	U2116	A2056	G1995	U1930	A1864	C1800	U1678
U2545	U2545	U2239	U2239	U2299	G2177	C2057	C2057	U1996	A1934	A1865	G1738	U1679
C2546	C2546	U2240	U2240	C2302	A2178	U2118	G2058	C1997	A1935	G1866	U1740	A1680

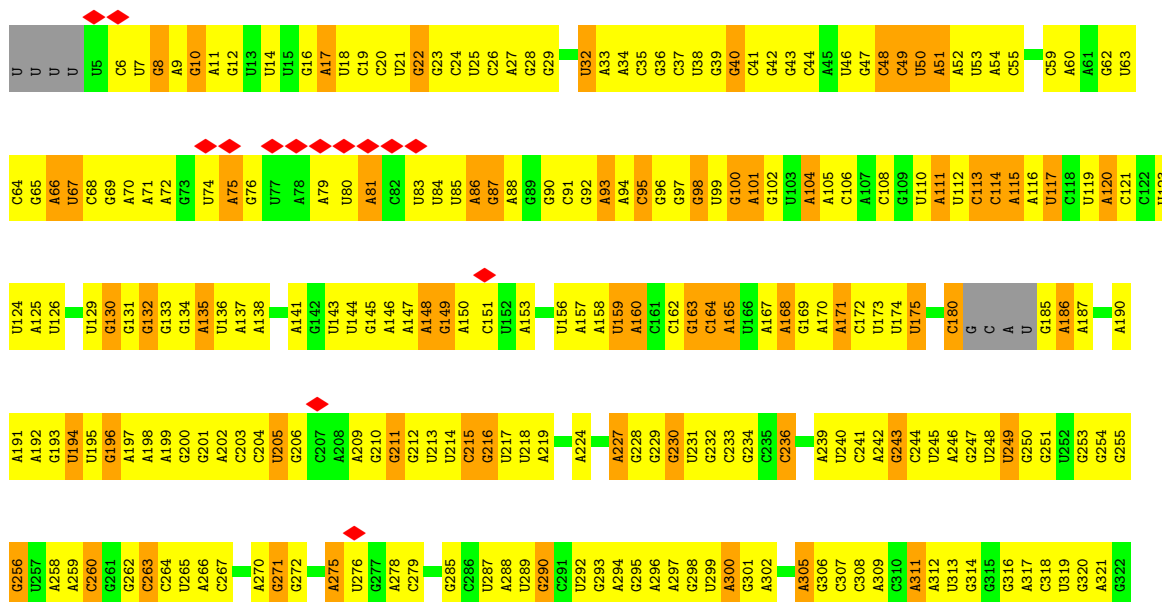
- Molecule 51: 5S ribosomal RNA

Chain 4: 13% 50% 34% .

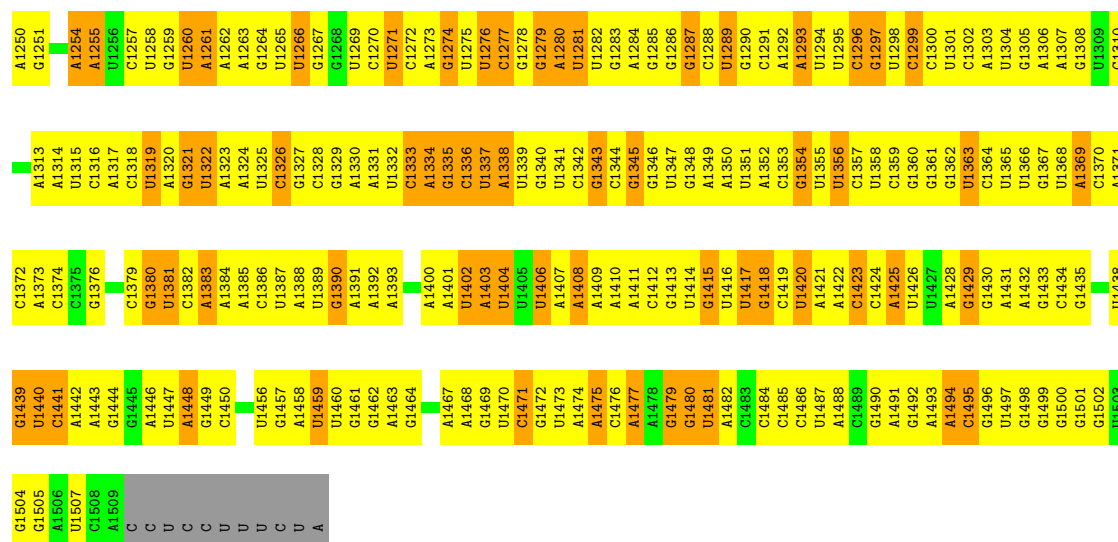


- Molecule 52: 16S ribosomal RNA

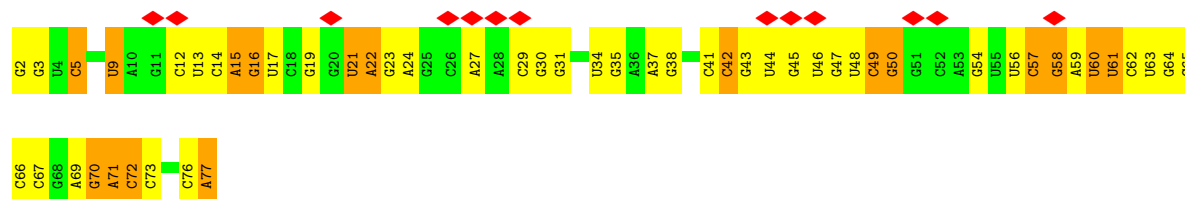
Chain 5: 14% 59% 26%



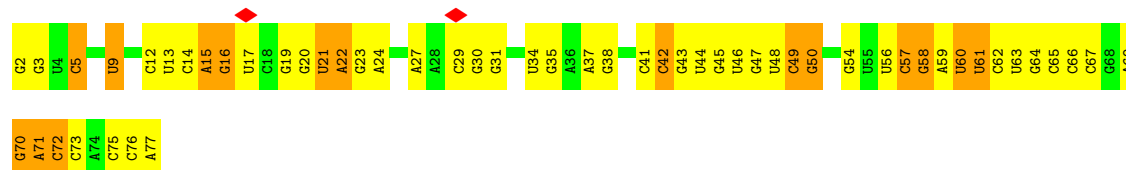
G1190	A1127	G1064	U1004	G942	G880	G819	U755	G630	U569	A508	A448	A385	A323
U1191	G1128	G1065	U1005	C943	G881	A820	A756	C631	A570	C509	A449	U386	C324
C1192	C1129	U1066	A1006	A944	U882	U821	U761	A632	A571	U510	U450	G387	A325
U1193	C1130	C1067	U1007	U945	A883	A822	G762	U633	A572	A511	C451	G388	C326
A1194	A1131	G1068	G1008	G946	G884	C823	A763	G634	C574	U512	U452	G327	G328
G1195	G1132	U1069	G1009	U947	U885	U824	A764	G635	C575	G513	C453	G329	G329
G1196	A1133	G1070	A1010	U948	A886	A825	A765	G636	A575	U514	U454	U394	C329
C1197	C1134	A1071	A1011	G949	C887	G826	G766	A637	A576	G515	U455	G395	C330
G1198	U1072	G1072	A1012	C950	A888	C827	U702	A638	G577	C516	U456	C396	C331
U1199	G1136	A953	A1013	A953	U889	U828	A703	C639	C578	C517	A457	C397	U332
C1200	C1137	U1073	A1014	U954	U890	G829	U704	G640	C579	G518	C458	G398	U333
C1201	U1138	G1075	A1015	A955	C891	U830	A705	U641	C580	G519	C459	C399	A334
A1202	A1139	U1076	A1016	U956	G892	C831	U706	A642	C581	C520	A460	G400	C335
A1203	A1140	U1077	A1017	U956	C893	G832	G771	U643	G882	A521	G461	U401	
C1204	U1141	G1082	U1018	C957	A894	G833	G772	U644	G583	G522	C462	G402	C338
C1205	G1142	G958	G1019	A894	A894	G834	A709	A645	C584	A403	U463	A403	U339
C1206	C1143	A959	G835	A959	G835	G835	G710	A646	G585	A404	A464	A404	A340
U1207	A1144	C960	A897	A957	C836	C836	G775	U647	G586	C405	A465	C405	C341
G1208	A1145	G961	G898	A898	G837	U837	C776	C648	A587	G406	U466	G406	G342
C1209	A1146	G962	G838	A898	G838	U838	A777	U649	G590	A407	G467	A407	G343
U1210	U1147	U1087	U839	A901	A839	U839	A778	A650	U596	U408	G468	U408	G344
A1211	U1148	A1088	A902	A902	G847	G847	A779	A651	A591	G409	C469	A409	A345
C1212	G1149	C1089	A903	A903	C841	C841	A780	A652	A592	A410	U470	A410	G346
A1213	G1150	A966	C904	C904	C842	C842	A781	G653	A593	U532	A471	A411	G347
A1214	A1151	C967	U905	U905	C843	C843	A782	U654	A594	A533	G472	G412	C348
U1215	G1152	G968	C906	C906	U844	U844	G783	G655	G595	C534	A473	G413	A349
G1216	G1153	A969	A907	A907	G847	U847	A784	U656	U596	A535	U414	U414	G350
C1217	A1154	U970	U908	U908	U848	U848	A785	G657	C597	U536	U475	C415	C351
C1218	G1155	A971	A909	A909	U849	U849	A786	G658	U598	A537	U476	U416	A352
A1219	A1156	A972	C910	C910	G849	G849	A787	U659	G599	G538	U477	U417	G353
G1220	G1157	A973	G911	G911	U850	U850	A788	A660	G600	G539	G478	U418	U354
A1221	A1158	C974	G912	G912	U851	U851	A789	G661	U601	U540	A479	A419	A355
U1222	U1099	C975	U915	U915	G852	G852	A790	G662	G602	C541	A480	A420	G356
C1223	C1100	U976	U916	U916	A853	A853	A791	G663	U603	C542	U481	G421	G357
C1224	A1101	U977	G917	G917	A854	A854	A792	U664	U604	C543	G482	A422	G358
A1225	A1102	A978	A918	A918	G855	G855	C793	G665	A605	A544	U483	U423	A359
A1226	C1103	C979	C919	C919	U856	U856	A793	U668	A606	G546	A484	U424	A360
A1227	C1104	C980	G920	G920	U857	U857	A794	U669	A607	C547	C485	G425	U361
C1228	U1106	U981	G921	G921	A858	A858	A795	G670	G608	C548	A486	U426	U362
A1229	C1107	A982	G922	G922	U859	U859	A796	U671	G609	U549	A487	A427	U363
G1230	U1107	G983	G923	G923	C860	C860	A797	G672	C610	U550	U488	A428	U364
U1231	A1108	A984	A924	A924	C861	C861	A798	A673	G611	A551	U489	A429	U365
C1232	U1109	C985	C925	C925	C862	C862	U801	U674	G612	U552	U490	G430	A367
G1233	C1170	U986	U986	U986	U863	U863	A802	U675	U614	C553	C492	U432	C368
C1234	A1171	U987	U987	U987	U864	U864	A803	U676	G615	C554	A493	C433	A369
C1235	A1172	G988	G988	G988	U865	U865	A804	C677	C616	G555	A494	U434	A370
A1236	U1173	A989	U996	U996	A866	A866	A805	C678	U617	G556	U495	U435	U371
C1237	C1174	C990	C990	C990	A867	A867	C742	A678	U618	A557	A496	U436	G372
C1238	A1175	G991	A991	A991	C868	C868	A806	U679	U619	U558	A497	U437	A373
U1239	U1176	U1115	G1052	G1052	U868	U868	C807	U680	A619	U559	C498	A438	G374
U1240	U1177	U1116	U1053	U1053	C869	C869	U744	U681	A620	U560	U499	U439	C375
G1241	C1178	U1117	C1054	C1054	A870	A870	U745	U682	C621	U561	U500	G376	G376
C1242	A1179	A1118	G1055	G1055	U871	U871	A746	G683	A622	A561	U440	U441	A377
U1243	U1180	C1119	U1056	U1056	C872	C872	C747	A684	G623	U562	A501	A377	U441
A1244	G1181	A1120	C1057	C1057	U873	U873	U748	U685	U624	G564	C502	G442	A378
C1245	U1121	U998	G937	G937	C874	C874	A749	G686	U626	G565	G503	G443	A379
A1245	U1122	C999	C937	C937	G875	G875	A813	G687	G626	G566	A504	G444	A379
A1246	G1123	U1000	U938	U938	C876	C876	C814	G688	A627	C567	C505	A445	A382
U1247	U1187	A1001	G939	G939	C877	C877	C751	G689	A628	U506	U506	A446	U383
A1248	A1188	C1062	G940	G940	U878	U878	U817	C752	U629	G568	A507	A447	G384
G1249	U1189	U1126	A941	A941	G879	G879	A818	U754					



• 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	1119	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 K3 (6k x 4k)	Depositor
Maximum map value	0.743	Depositor
Minimum map value	-0.278	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.22	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 ⓘ

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	0.16	0/383	0.47	0/504
2	1	0.15	0/484	0.43	0/637
3	2	0.15	0/306	0.48	0/401
4	A	0.17	0/1954	0.43	0/2642
5	B	0.15	0/1721	0.44	0/2323
6	C	0.16	0/1691	0.44	0/2267
7	D	0.17	0/1188	0.40	0/1593
8	E	0.20	0/1384	0.44	0/1867
9	F	0.17	0/1266	0.53	2/1700 (0.1%)
10	G	0.16	0/1126	0.46	0/1517
11	H	0.18	0/1044	0.55	0/1395
12	I	0.17	0/820	0.43	0/1103
13	J	0.17	0/844	0.44	0/1136
14	K	0.25	0/1094	0.54	0/1468
15	L	0.16	0/962	0.44	0/1289
16	M	0.17	0/483	0.45	0/643
17	N	0.16	0/679	0.42	0/907
18	O	0.16	0/659	0.45	0/885
19	P	0.14	0/684	0.40	0/913
20	Q	0.17	0/545	0.44	0/730
21	R	0.27	0/698	0.59	0/936
22	S	0.16	0/631	0.42	0/838
23	T	0.14	0/475	0.38	0/621
24	a	0.18	0/2267	0.46	0/3044
25	b	0.16	0/1795	0.45	1/2412 (0.0%)
26	c	0.16	0/1671	0.42	0/2246
27	d	0.16	0/1409	0.43	0/1894
28	e	0.17	0/1420	0.45	0/1912
29	f	0.25	0/1205	0.59	2/1616 (0.1%)
30	g	0.36	0/969	0.75	0/1295
31	h	0.19	0/968	0.49	1/1298 (0.1%)
32	i	0.16	0/1186	0.41	0/1592
33	j	0.15	0/953	0.44	0/1275
34	k	0.17	0/1170	0.48	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.15	0/1104	0.38	0/1481
36	m	0.16	0/973	0.44	0/1309
37	n	0.16	0/897	0.47	0/1198
38	o	0.15	0/948	0.47	0/1262
39	p	0.18	0/961	0.44	0/1278
40	q	0.18	0/828	0.48	0/1111
41	r	0.17	0/1077	0.46	0/1441
42	s	0.15	0/732	0.46	0/988
43	t	0.18	0/879	0.51	1/1165 (0.1%)
44	u	0.15	0/665	0.42	0/884
45	v	0.27	0/519	0.54	0/695
46	w	0.15	0/826	0.42	0/1104
47	x	0.15	0/353	0.52	1/474 (0.2%)
48	y	0.29	0/457	0.63	0/601
49	z	0.14	0/412	0.48	0/547
50	3	0.13	0/69073	0.32	0/107710
51	4	0.13	0/2505	0.35	0/3902
52	5	0.12	0/35768	0.30	0/55764
53	7	0.14	0/1808	0.33	0/2817
53	8	0.14	0/1808	0.33	0/2817
All	All	0.15	0/158727	0.36	8/237006 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	F	11	VAL	CA-C-N	8.77	132.94	120.49
9	F	11	VAL	C-N-CA	8.77	132.94	120.49
25	b	147	VAL	N-CA-C	-6.33	106.96	113.10
43	t	87	GLY	N-CA-C	6.26	118.47	110.20
29	f	10	SER	N-CA-C	-5.84	105.93	114.39

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	20	0
2	1	477	0	530	25	0
3	2	304	0	350	30	0
4	A	1921	0	1973	78	0
5	B	1698	0	1768	76	0
6	C	1660	0	1719	116	0
7	D	1173	0	1267	37	0
8	E	1362	0	1377	66	0
9	F	1246	0	1308	55	0
10	G	1110	0	1226	59	0
11	H	1028	0	1094	61	0
12	I	809	0	894	59	0
13	J	829	0	855	55	0
14	K	1076	0	1170	63	0
15	L	951	0	1014	57	0
16	M	474	0	509	34	0
17	N	673	0	730	25	0
18	O	646	0	677	38	0
19	P	675	0	728	34	0
20	Q	535	0	562	33	0
21	R	682	0	691	52	0
22	S	629	0	681	41	0
23	T	471	0	522	9	0
24	a	2225	0	2301	134	0
25	b	1762	0	1808	98	0
26	c	1644	0	1731	102	0
27	d	1388	0	1469	78	0
28	e	1396	0	1481	62	0
29	f	1182	0	1228	150	0
30	g	960	0	1014	66	0
31	h	959	0	1039	51	0
32	i	1164	0	1192	50	0
33	j	944	0	1019	51	0
34	k	1153	0	1256	81	0
35	l	1079	0	1134	60	0
36	m	958	0	1011	66	0
37	n	889	0	952	58	0
38	o	938	0	1008	46	0
39	p	947	0	1028	62	0
40	q	811	0	858	31	0
41	r	1068	0	1150	60	0
42	s	720	0	803	23	0
43	t	872	0	972	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	u	657	0	695	33	0
45	v	513	0	560	48	0
46	w	818	0	870	36	0
47	x	344	0	333	16	0
48	y	452	0	472	27	0
49	z	408	0	440	29	0
50	3	61664	0	30954	2986	0
51	4	2239	0	1137	100	0
52	5	31943	0	16058	1607	0
53	7	1618	0	821	37	0
53	8	1618	0	821	43	0
All	All	146142	0	99689	6419	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 27.

The worst 5 of 6419 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)
29:f:2:LYS:CE	29:f:5:LEU:HA	1.16	1.62
29:f:4:ILE:HG21	29:f:16:PHE:CE1	1.52	1.44
29:f:3:VAL:CG2	45:v:62:ASN:CG	1.93	1.40
29:f:4:ILE:CG2	29:f:16:PHE:CD1	2.08	1.37
29:f:4:ILE:CG2	29:f:16:PHE:CE1	2.08	1.36

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	45/48 (94%)	43 (96%)	2 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	218 (92%)	20 (8%)	0	100	100
5	B	213/273 (78%)	195 (92%)	18 (8%)	0	100	100
6	C	201/205 (98%)	187 (93%)	13 (6%)	1 (0%)	24	63
7	D	151/219 (69%)	137 (91%)	14 (9%)	0	100	100
8	E	165/215 (77%)	142 (86%)	23 (14%)	0	100	100
9	F	152/155 (98%)	142 (93%)	10 (7%)	0	100	100
10	G	139/142 (98%)	120 (86%)	19 (14%)	0	100	100
11	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
12	I	99/108 (92%)	88 (89%)	11 (11%)	0	100	100
13	J	112/121 (93%)	104 (93%)	8 (7%)	0	100	100
14	K	134/139 (96%)	116 (87%)	17 (13%)	1 (1%)	18	56
15	L	116/124 (94%)	104 (90%)	12 (10%)	0	100	100
16	M	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
17	N	81/86 (94%)	71 (88%)	10 (12%)	0	100	100
18	O	78/94 (83%)	68 (87%)	10 (13%)	0	100	100
19	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
20	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
21	R	82/87 (94%)	73 (89%)	7 (8%)	2 (2%)	4	27
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
24	a	283/287 (99%)	252 (89%)	31 (11%)	0	100	100
25	b	227/287 (79%)	212 (93%)	15 (7%)	0	100	100
26	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
27	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
28	e	174/184 (95%)	161 (92%)	13 (8%)	0	100	100
29	f	143/149 (96%)	132 (92%)	9 (6%)	2 (1%)	9	40
30	g	124/161 (77%)	106 (86%)	16 (13%)	2 (2%)	7	38
31	h	126/137 (92%)	116 (92%)	10 (8%)	0	100	100
32	i	142/146 (97%)	131 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	k	146/151 (97%)	127 (87%)	19 (13%)	0	100	100
35	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
36	m	117/124 (94%)	106 (91%)	11 (9%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	103 (91%)	10 (9%)	0	100	100
39	p	112/127 (88%)	107 (96%)	5 (4%)	0	100	100
40	q	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
41	r	137/159 (86%)	132 (96%)	5 (4%)	0	100	100
42	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
43	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
44	u	84/104 (81%)	75 (89%)	9 (11%)	0	100	100
45	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
46	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
47	x	42/97 (43%)	34 (81%)	8 (19%)	0	100	100
48	y	54/57 (95%)	46 (85%)	7 (13%)	1 (2%)	6	32
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5820/6670 (87%)	5310 (91%)	501 (9%)	9 (0%)	44	78

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	f	9	VAL
30	g	89	ILE
48	y	50	ASP
21	R	27	LYS
30	g	45	PHE

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	40/41 (98%)	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
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	115 (98%)	2 (2%)	53	69
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	46 (98%)	1 (2%)	47	65
17	N	76/78 (97%)	75 (99%)	1 (1%)	61	74
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%)	72 (97%)	2 (3%)	39	61
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	131/134 (98%)	130 (99%)	1 (1%)	73	80
30	g	101/129 (78%)	95 (94%)	6 (6%)	18	39
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	105 (100%)	0	100	100
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%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
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%)	58 (100%)	0	100	100
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%)	46 (96%)	2 (4%)	26	48
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5101/5751 (89%)	5086 (100%)	15 (0%)	84	86

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	29	TYR
48	y	47	MET
30	g	30	THR
48	y	51	LEU
30	g	47	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
32	i	11	GLN
37	n	42	GLN
32	i	70	ASN
34	k	141	ASN

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Mol	Chain	Res	Type
41	r	110	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	1078 (37%)	34 (1%)
51	4	103/108 (95%)	44 (42%)	5 (4%)
52	5	1490/1520 (98%)	496 (33%)	19 (1%)
53	7	75/76 (98%)	30 (40%)	3 (4%)
53	8	75/76 (98%)	30 (40%)	3 (4%)
All	All	4618/4687 (98%)	1678 (36%)	64 (1%)

5 of 1678 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	13	C
50	3	14	U
50	3	15	A
50	3	16	A

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	5	1480	G
53	7	57	C
50	3	1749	A
50	3	1703	A
53	7	71	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

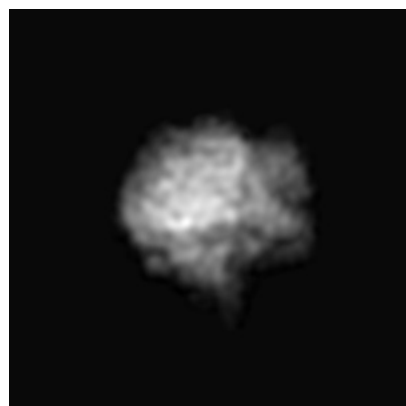
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13434. These allow visual inspection of the internal detail of the map and identification of artifacts.

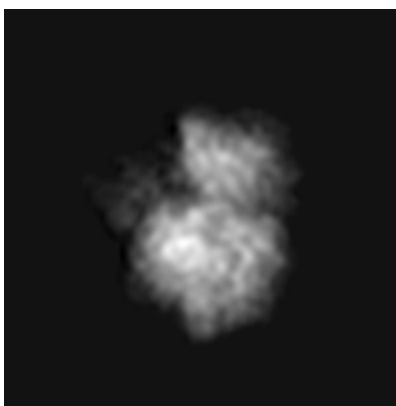
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

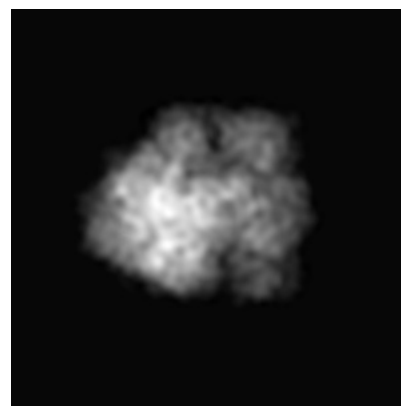
6.1.1 Primary map



X

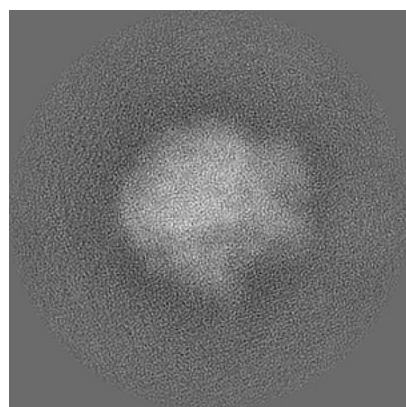


Y

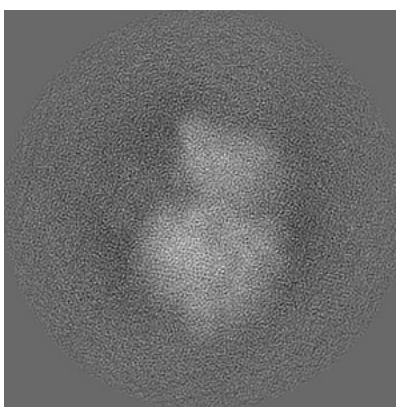


Z

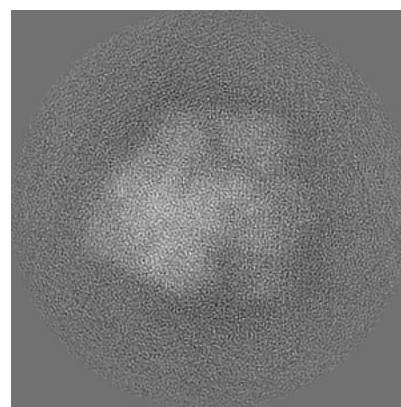
6.1.2 Raw map



X



Y

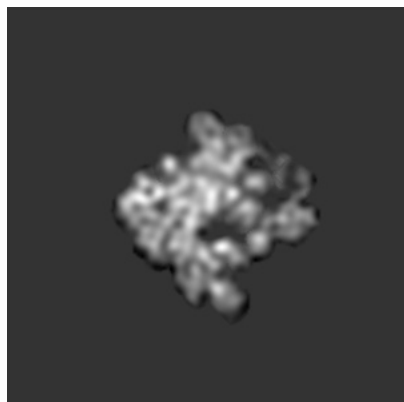


Z

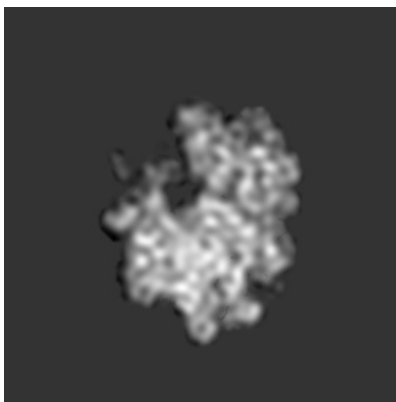
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

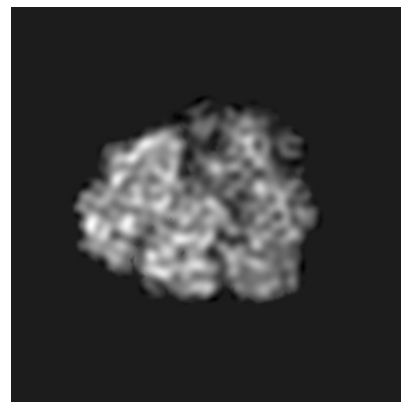
6.2.1 Primary map



X Index: 128

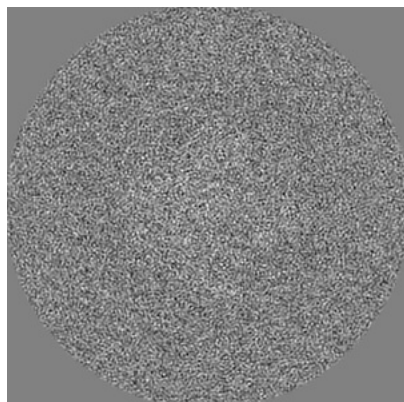


Y Index: 128

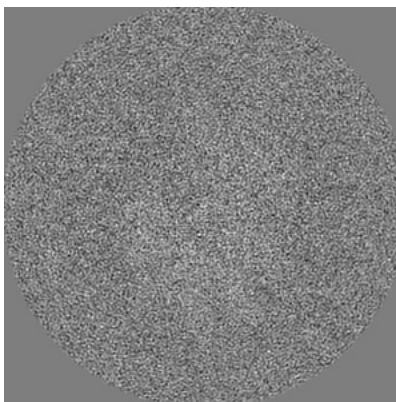


Z Index: 128

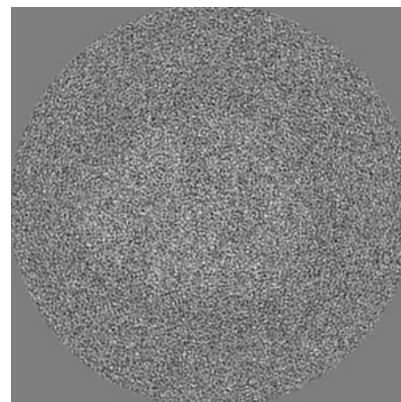
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

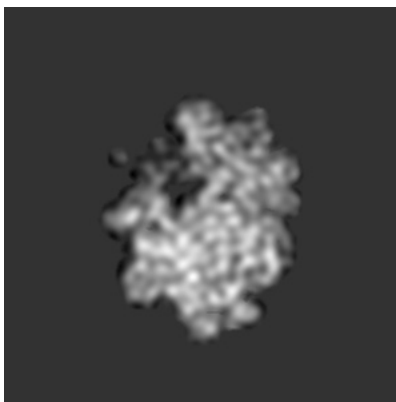
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

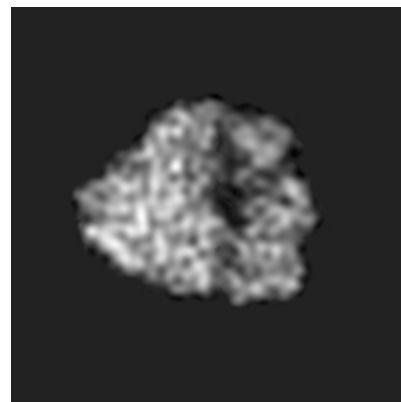
6.3.1 Primary map



X Index: 102

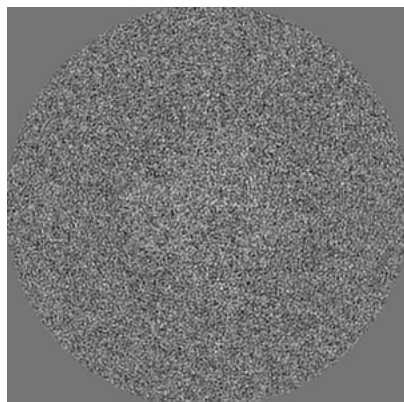


Y Index: 124

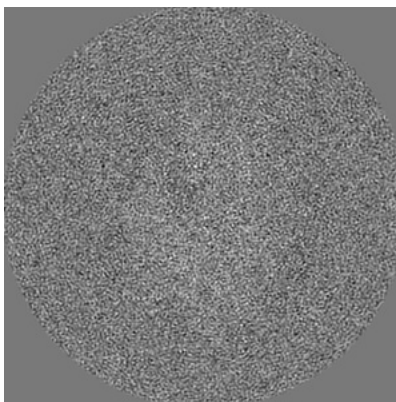


Z Index: 121

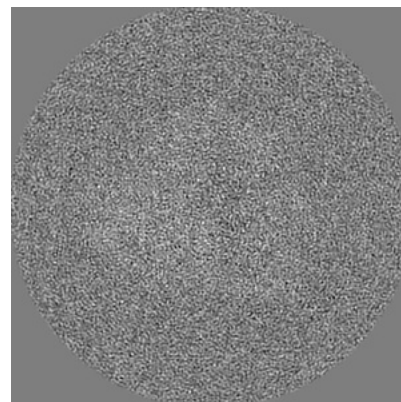
6.3.2 Raw map



X Index: 130



Y Index: 124



Z Index: 120

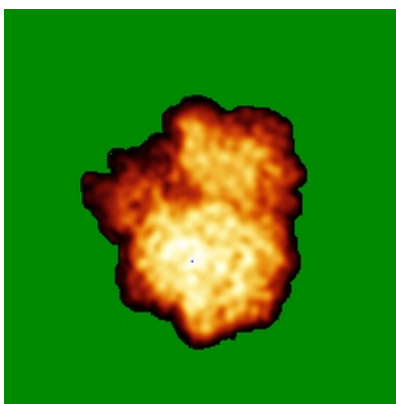
The images above show the largest variance slices of the map in three orthogonal directions.

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

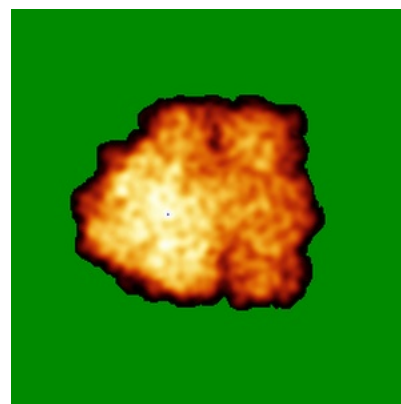
6.4.1 Primary map



X

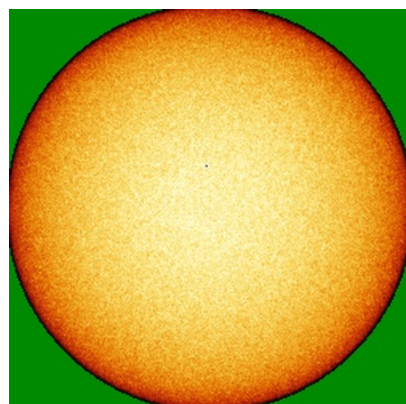


Y

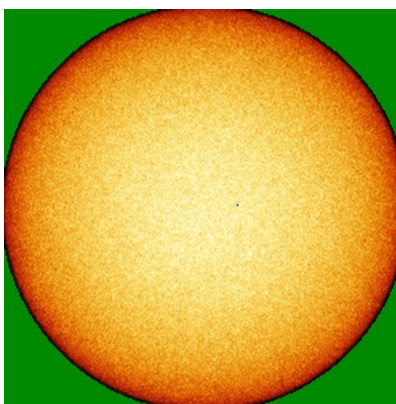


Z

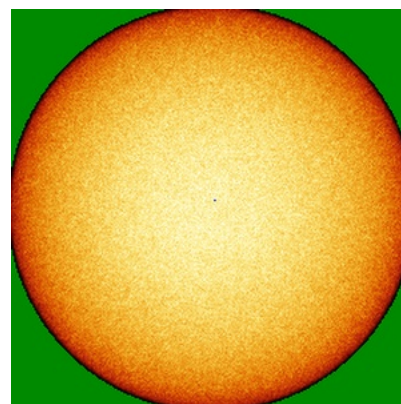
6.4.2 Raw map



X



Y

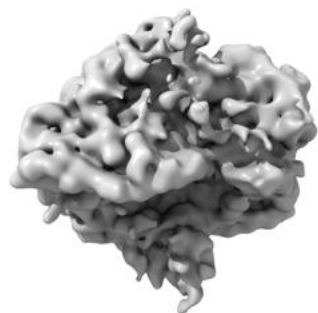


Z

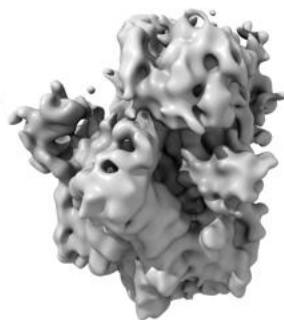
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

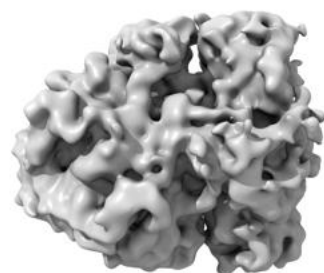
6.5.1 Primary map



X



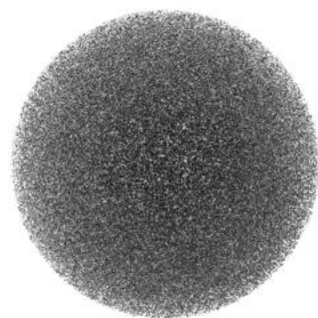
Y



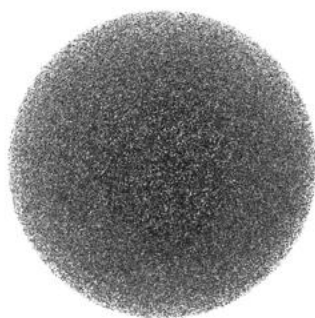
Z

The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

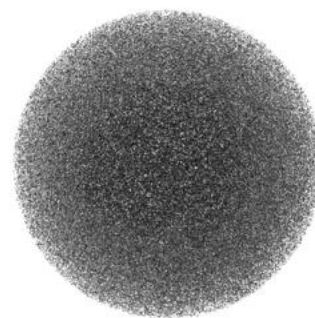
6.5.2 Raw map



X



Y



Z

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.

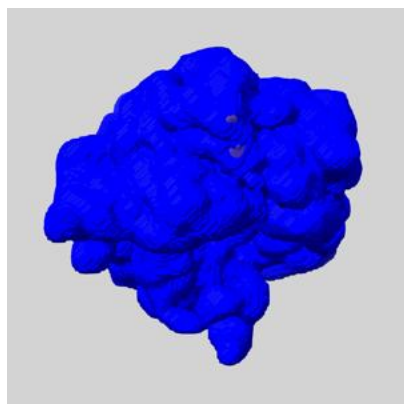
6.6 Mask visualisation [i](#)

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

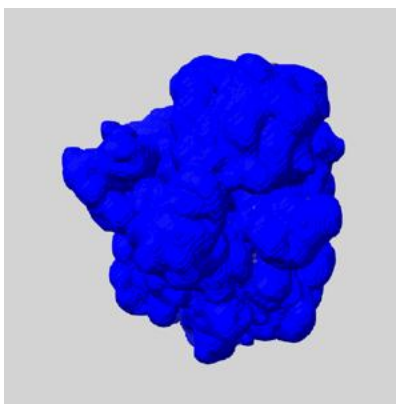
A mask typically either:

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

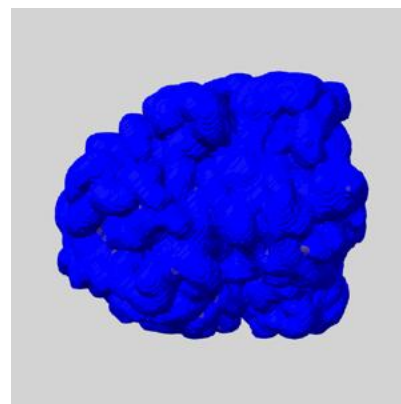
6.6.1 emd_13434_msk_1.map [i](#)



X



Y

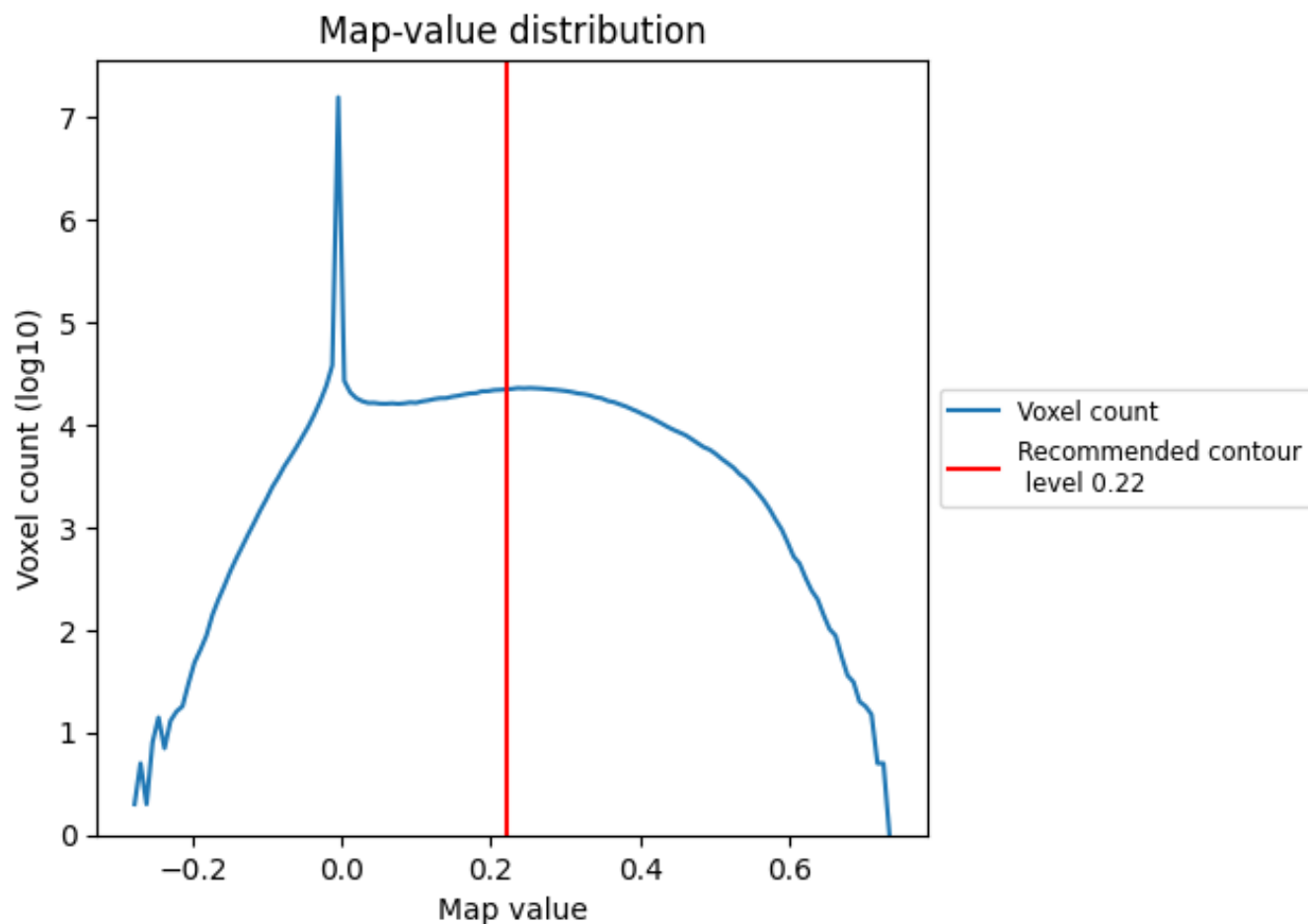


Z

7 Map analysis [i](#)

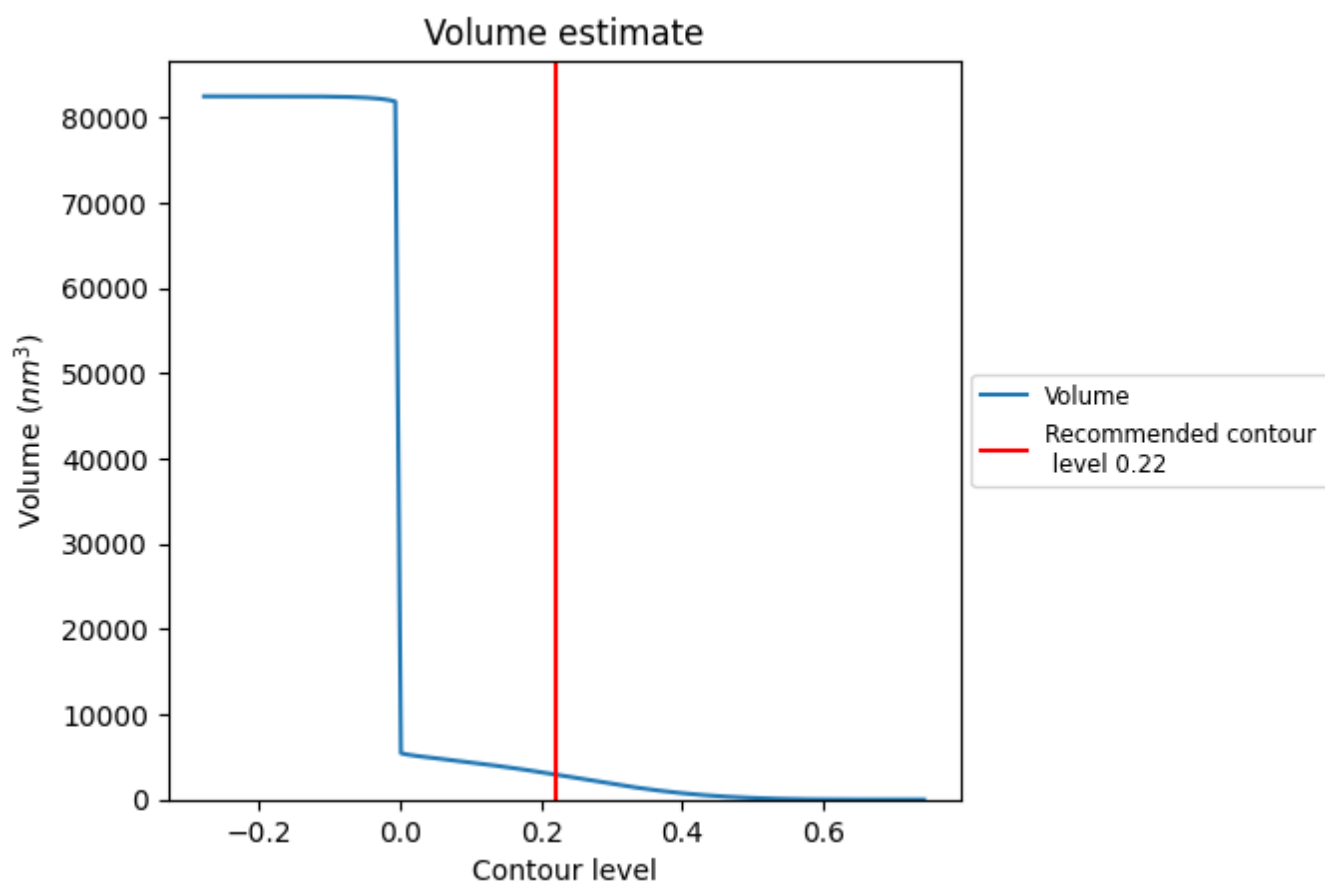
This section contains the results of statistical analysis of the map.

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.

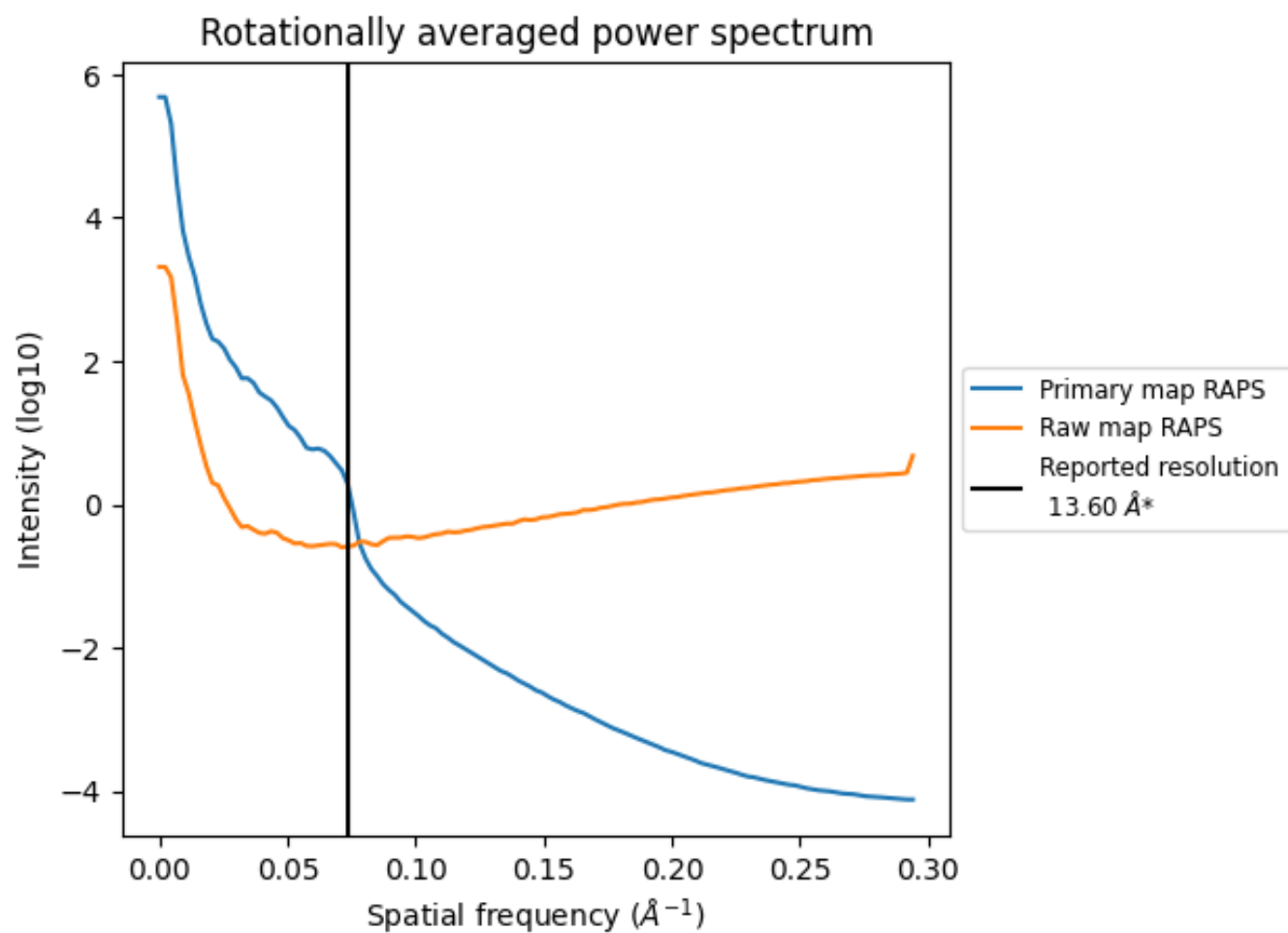
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2941 nm³; this corresponds to an approximate mass of 2657 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 ⓘ

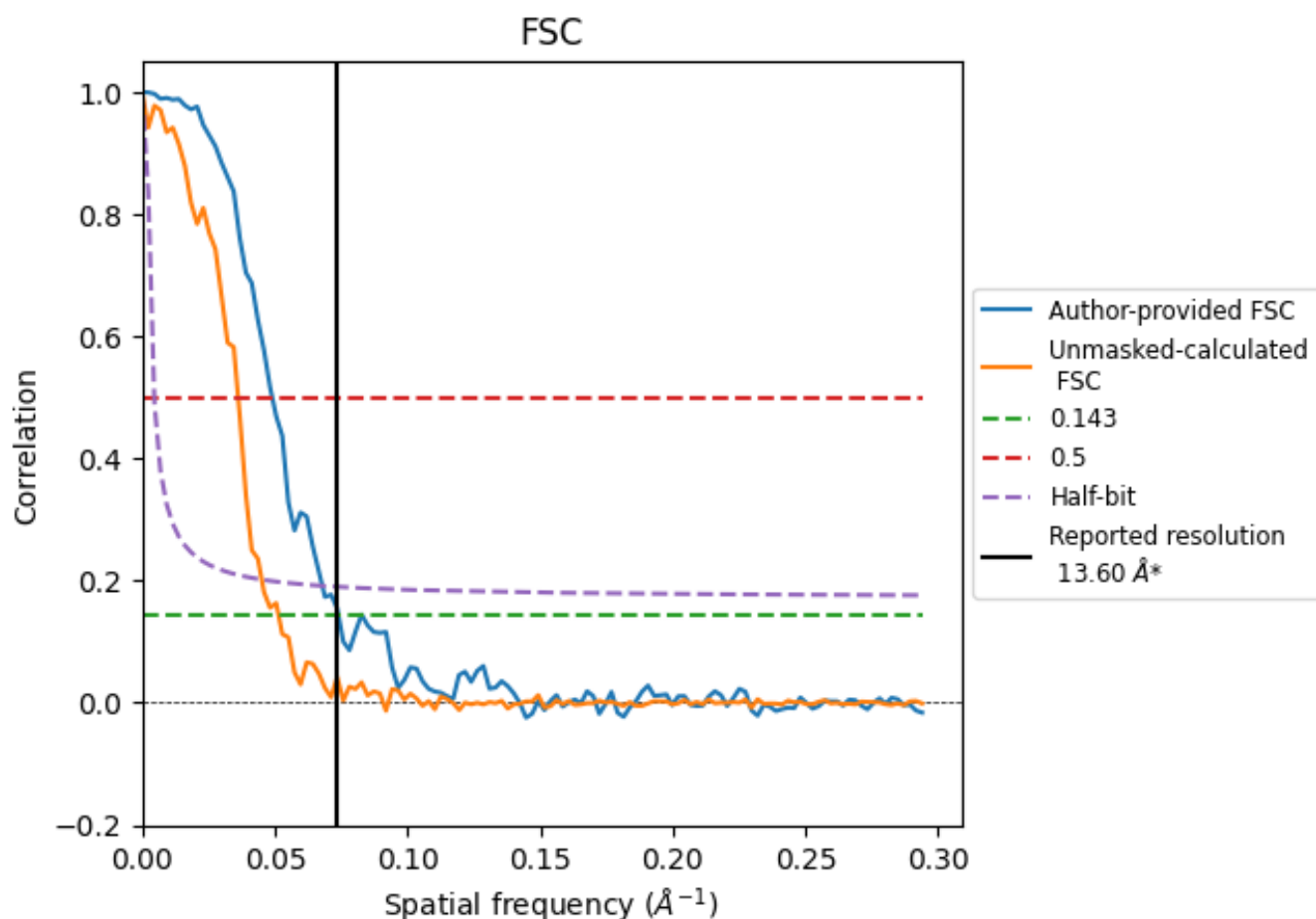


*Reported resolution corresponds to spatial frequency of 0.074 $\text{\AA}^{-1}$

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 0.074 Å⁻¹

8.2 Resolution estimates [i](#)

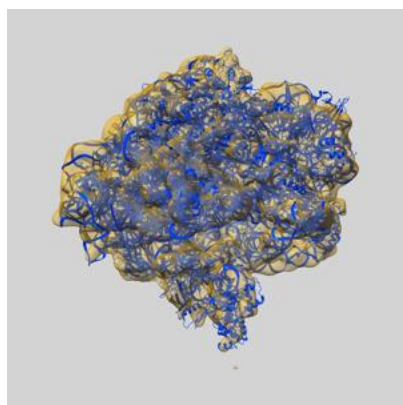
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	13.60	-	-
Author-provided FSC curve	13.51	20.37	14.73
Unmasked-calculated*	19.46	27.70	22.17

*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 19.46 differs from the reported value 13.6 by more than 10 %

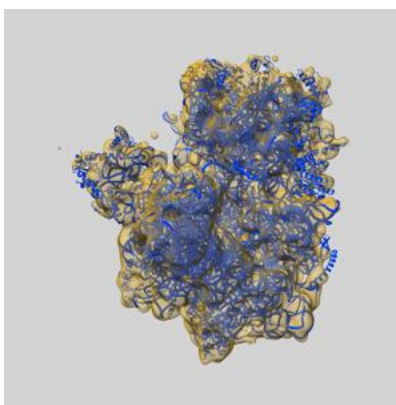
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13434 and PDB model 7PIA. Per-residue inclusion information can be found in section [3](#) on page [14](#).

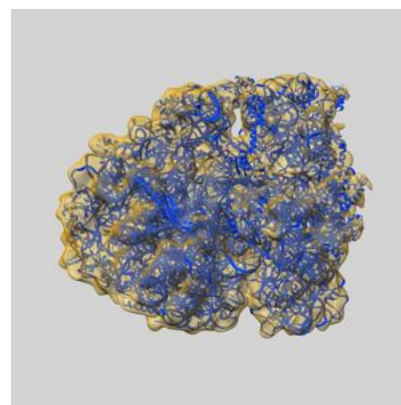
9.1 Map-model overlay [i](#)



X



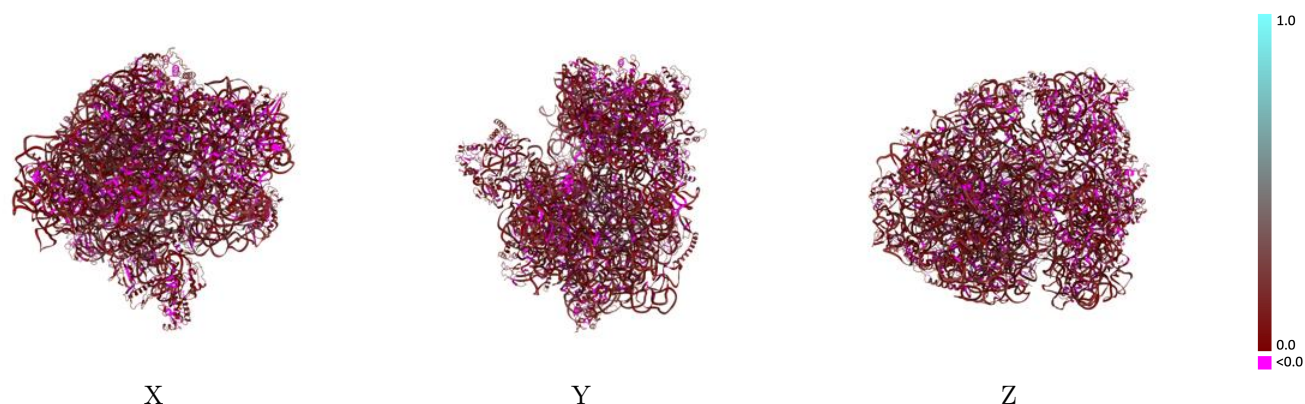
Y



Z

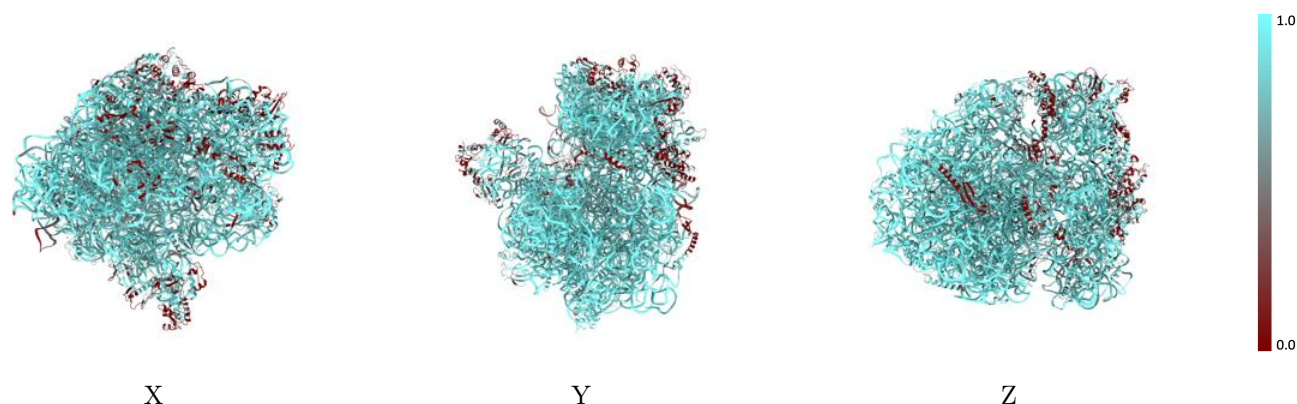
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



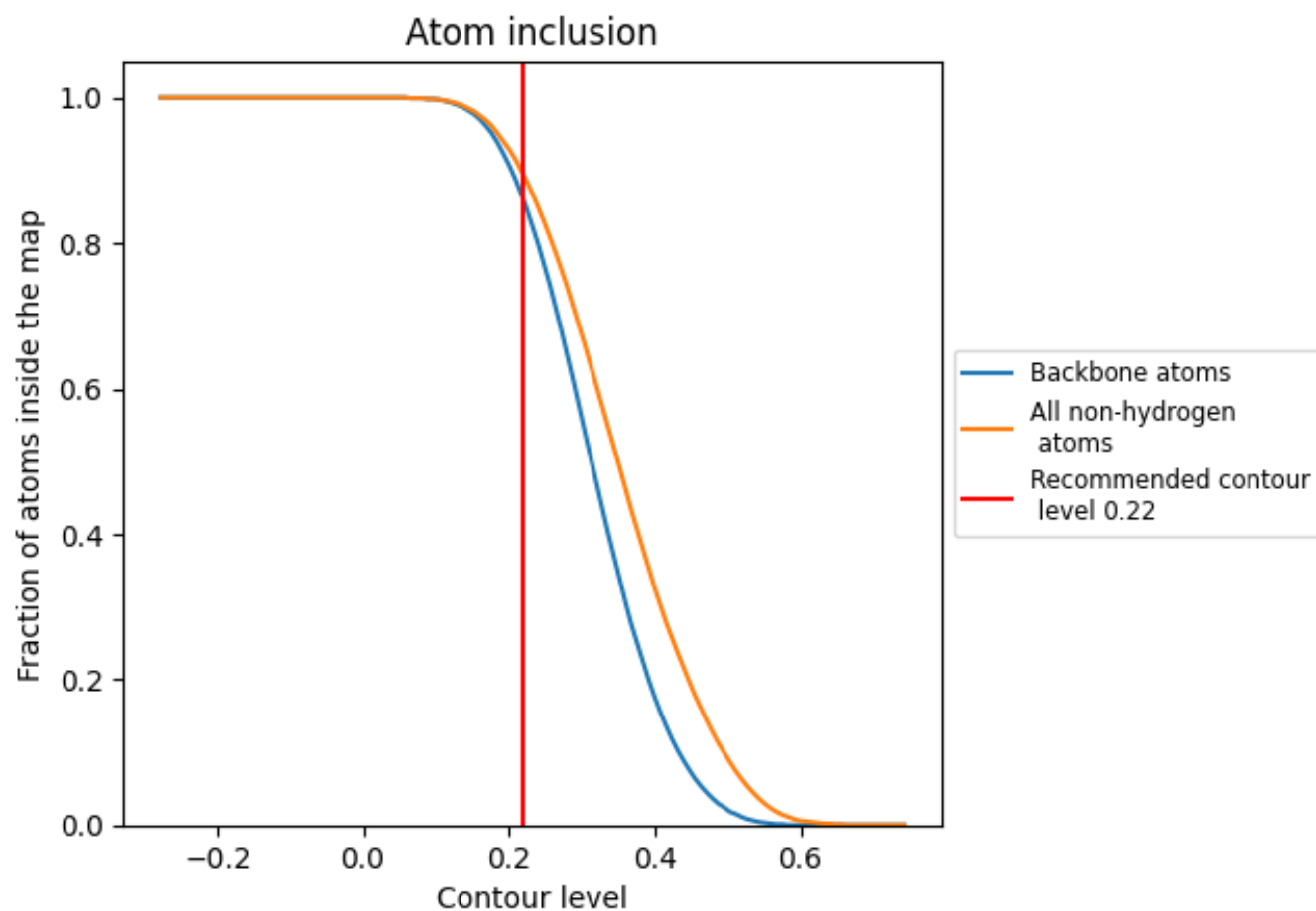
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 89% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8940	 0.0870
0	 0.9810	 0.0300
1	 1.0000	 0.0060
2	 0.9430	 0.0510
3	 0.9820	 0.1010
4	 0.9670	 0.1070
5	 0.9460	 0.0960
7	 0.7850	 0.0600
8	 0.9130	 0.1020
A	 0.4830	 0.0800
B	 0.5680	 0.0600
C	 0.6780	 0.0520
D	 0.5400	 0.0560
E	 0.4790	 0.1070
F	 0.4200	 0.0660
G	 0.5100	 0.0510
H	 0.5350	 0.0430
I	 0.6350	 0.0390
J	 0.5470	 0.0530
K	 0.7070	 0.0370
L	 0.5180	 0.0550
M	 0.9670	 0.0460
N	 0.5790	 0.0620
O	 0.7200	 0.0290
P	 0.6560	 0.0700
Q	 0.7040	 0.0290
R	 0.7520	 0.0580
S	 0.8340	 0.0550
T	 0.6790	 0.1220
a	 0.9600	 0.0510
b	 0.9290	 0.0500
c	 0.9750	 0.0580
d	 0.7950	 0.0780
e	 0.5140	 0.0830
f	 0.4870	 0.0920



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Chain	Atom inclusion	Q-score
g	 0.4190	 0.0810
h	 0.3630	 0.0820
i	 0.9300	 0.0490
j	 0.7150	 0.0640
k	 0.9760	 0.0540
l	 0.9330	 0.0530
m	 0.9850	 0.0500
n	 0.9110	 0.0630
o	 0.7270	 0.0480
p	 0.9490	 0.0590
q	 0.8950	 0.0780
r	 0.9940	 0.0750
s	 0.9650	 0.0740
t	 0.9610	 0.0770
u	 0.9830	 0.0480
v	 0.9960	 0.0550
w	 0.9180	 0.0840
x	 0.7170	 0.1250
y	 0.9540	 0.0400
z	 0.9980	 0.0340