



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 08:10 AM UTC

PDB ID : 3JBU / pdb_00003jbu
EMDB ID : EMD-6483
Title : Mechanisms of Ribosome Stalling by SecM at Multiple Elongation Steps
Authors : Zhang, J.; Pan, X.J.; Yan, K.G.; Sun, S.; Gao, N.; Sui, S.F.
Deposited on : 2015-10-16
Resolution : 3.64 Å(reported)
Based on initial model : 4V7T

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:

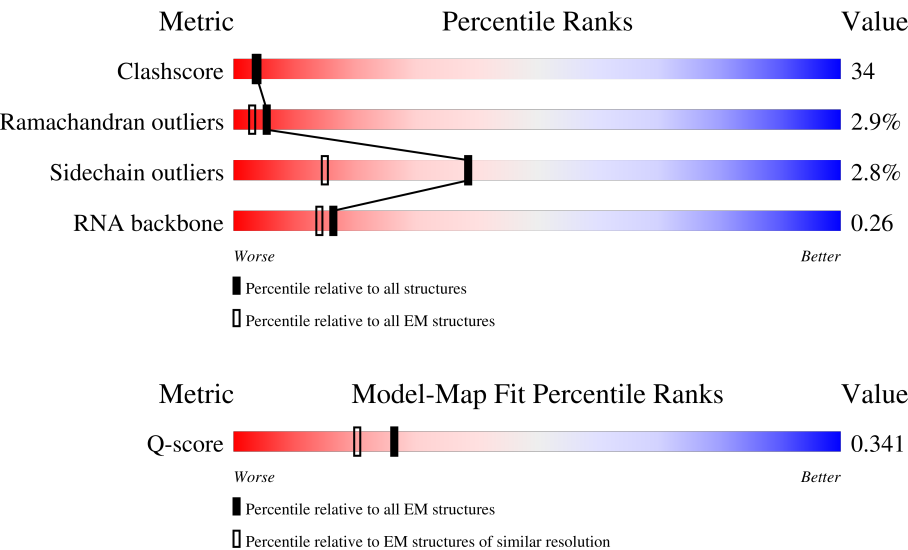
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.64 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	11633 (3.14 - 4.14)

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	B	241	85% 56% 33% 10%
2	C	233	81% 59% 27% 12%
3	D	206	87% 54% 43%

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Mol	Chain	Length	Quality of chain
4	E	167	
5	F	131	
6	G	156	
7	H	130	
8	I	130	
9	J	103	
10	K	129	
11	L	124	
12	M	118	
13	N	101	
14	O	89	
15	P	82	
16	Q	84	
17	R	75	
18	S	92	
19	T	87	
20	U	71	
21	0	78	
22	1	63	
23	2	59	
24	3	57	
25	4	55	
26	6	46	
27	7	65	
28	8	38	

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Mol	Chain	Length	Quality of chain
29	c	273	
30	d	209	
31	e	201	
32	f	179	
33	g	177	
34	h	149	
35	j	142	
36	k	123	
37	l	144	
38	m	136	
39	n	127	
40	o	117	
41	p	115	
42	q	118	
43	r	103	
44	s	110	
45	t	100	
46	u	104	
47	w	94	
48	y	85	
49	z	87	
50	A	1542	
51	X	11	
52	a	120	
53	b	2904	

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Mol	Chain	Length	Quality of chain
54	v	76	22% 51% 33% 14%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 143334 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	113	Total	C	N	O	S	0	0
			876	541	177	155	3		

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	79	ARG	GLN	conflict	UNP P0ADZ4

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	R	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 31 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 32 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 34 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	135	Total	C	N	O	S	0	0
			1063	680	201	176	6		

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 49 is a protein called SecM-glycine.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	26	Total	C	N	O	0	0
			203	129	33	41		

- Molecule 50 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	A	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

- Molecule 51 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	X	11	Total	C	N	O	P	0	0
			232	103	39	79	11		

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	118	Total	C	N	O	P	0	0
			2528	1126	464	821	117		

- Molecule 53 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

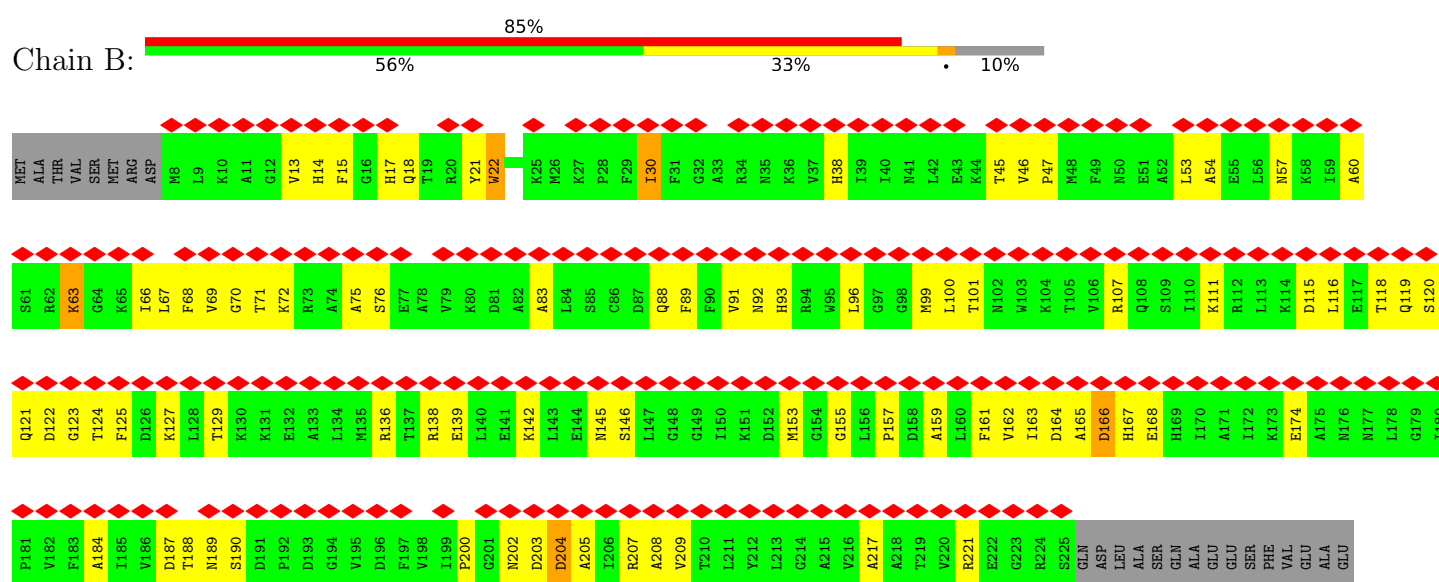
- Molecule 54 is a RNA chain called glycine-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	76	Total	C	N	O	P	0	0
			1623	722	291	534	76		

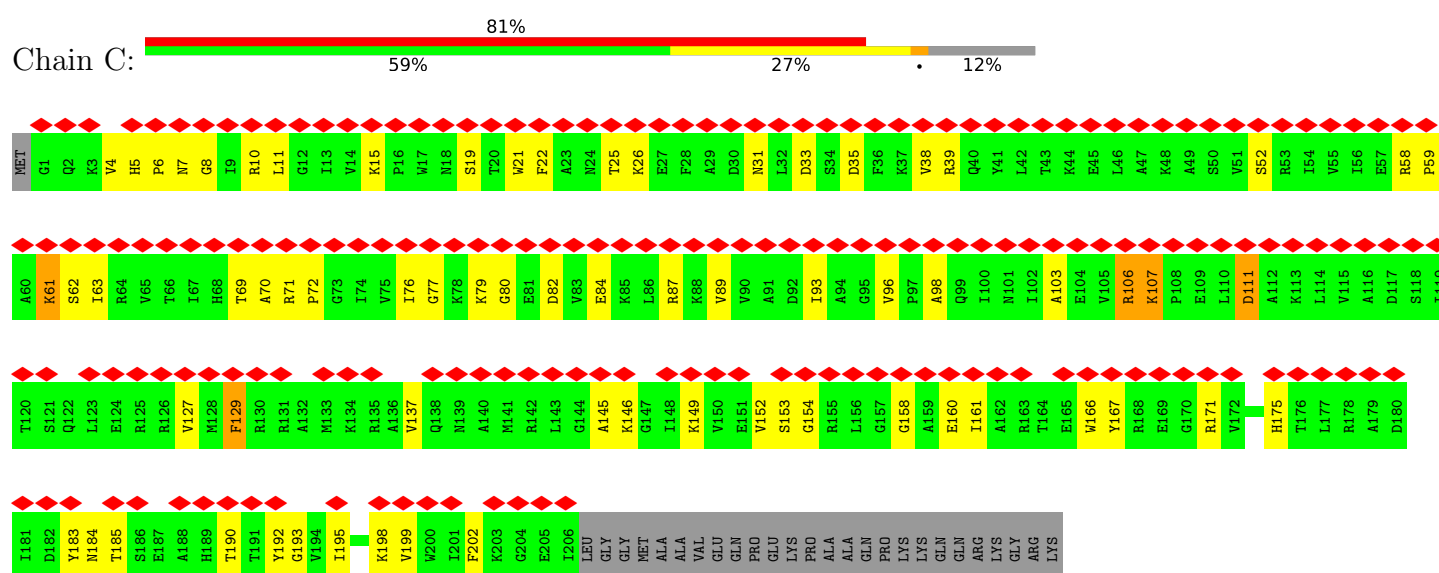
3 Residue-property plots

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

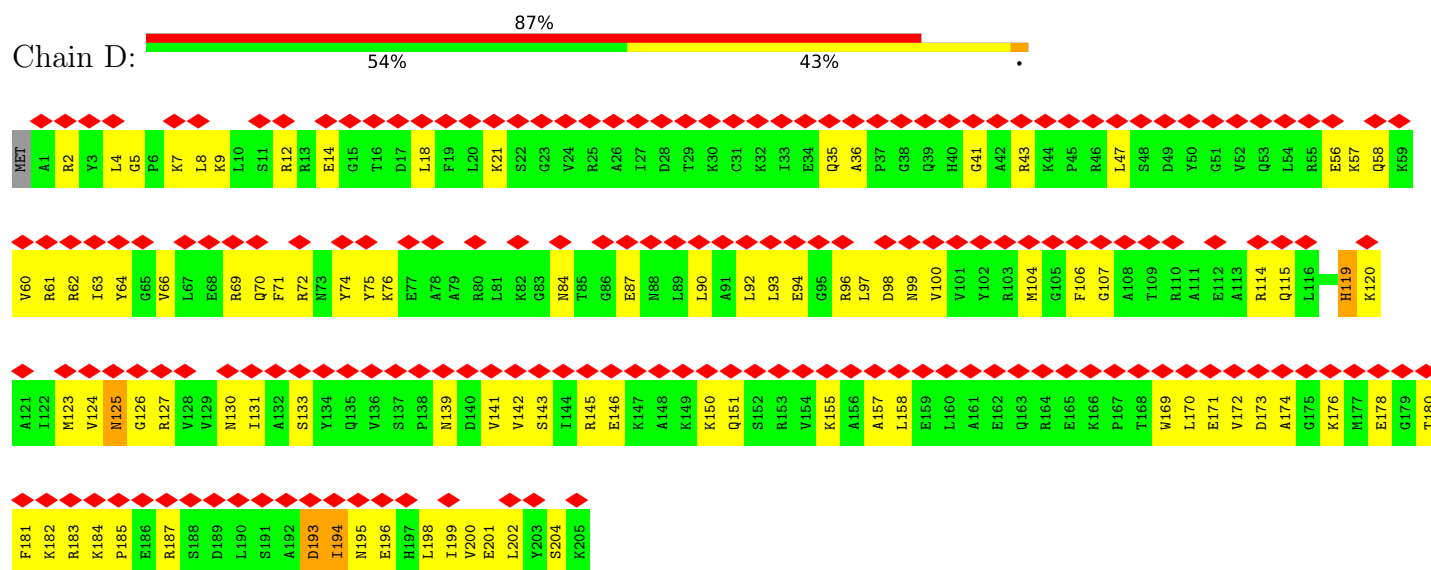
• Molecule 1: 30S ribosomal protein S2



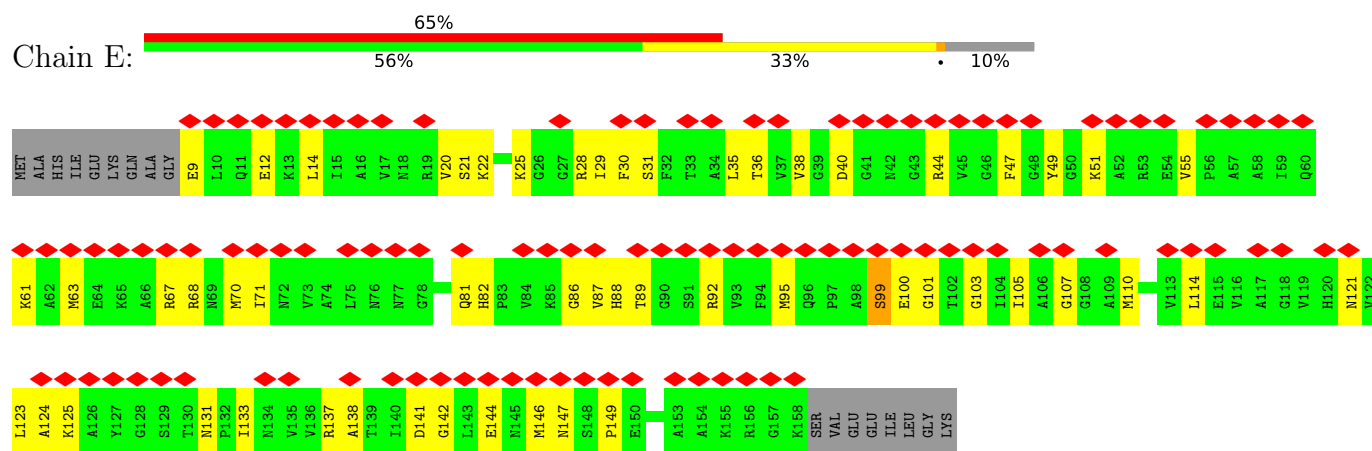
• Molecule 2: 30S ribosomal protein S3



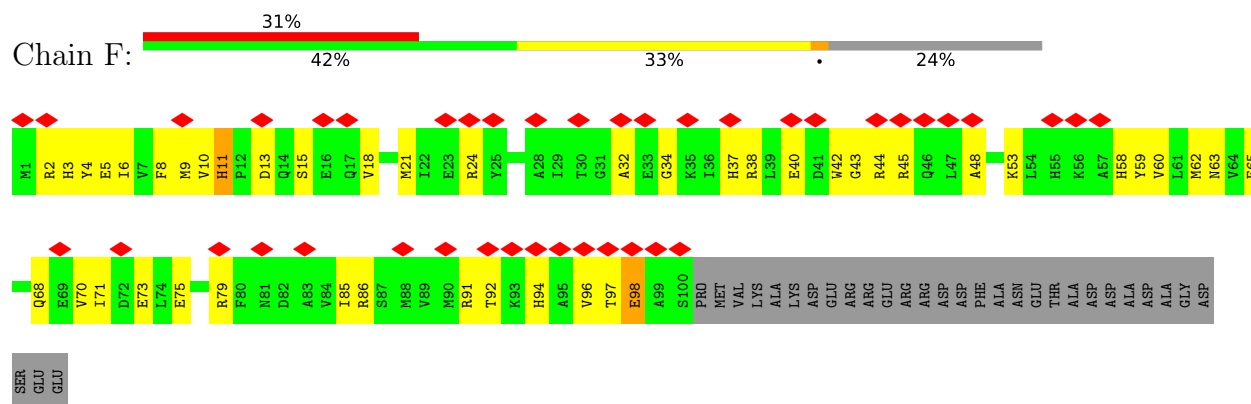
• Molecule 3: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S5

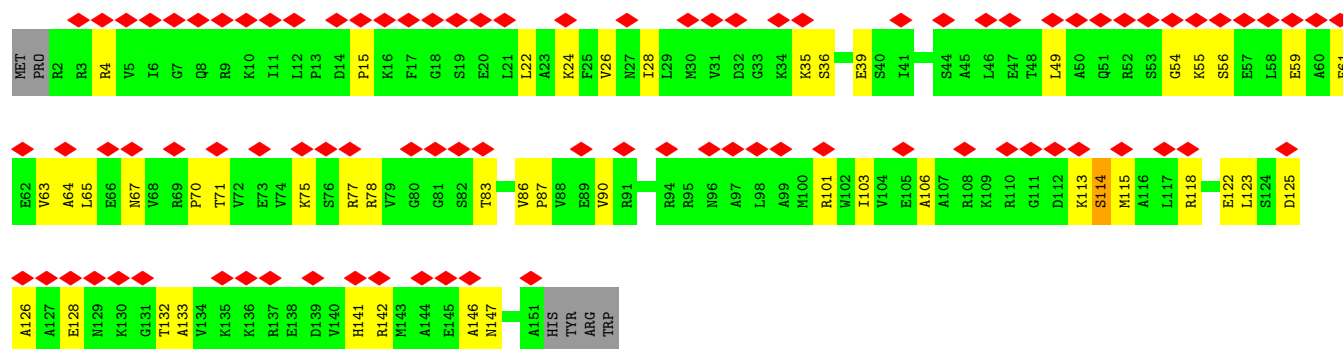


• Molecule 5: 30S ribosomal protein S6

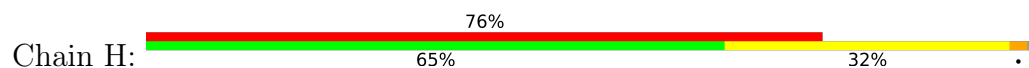


• Molecule 6: 30S ribosomal protein S7

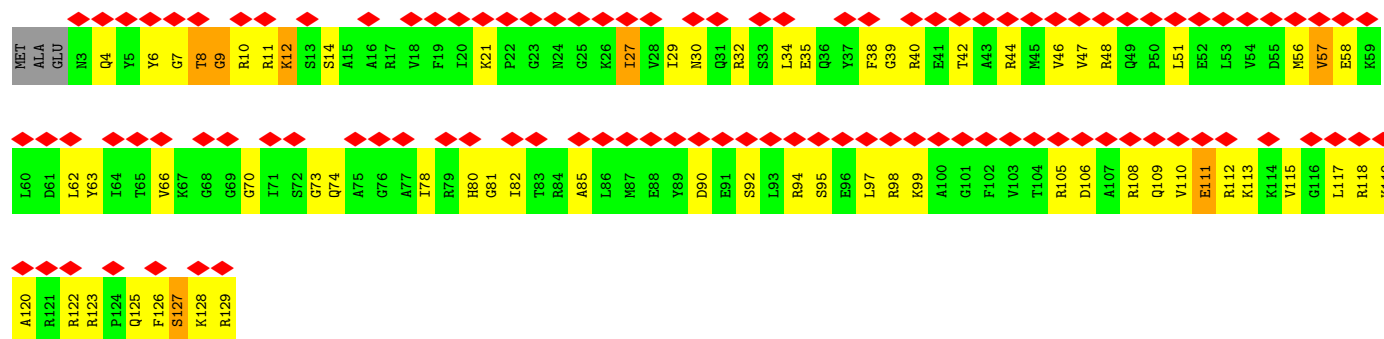
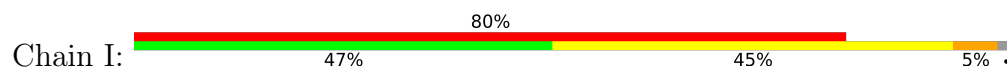




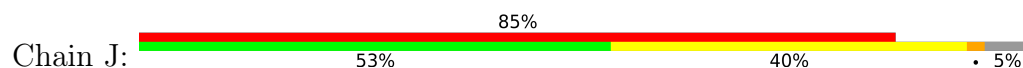
• Molecule 7: 30S ribosomal protein S8



• Molecule 8: 30S ribosomal protein S9

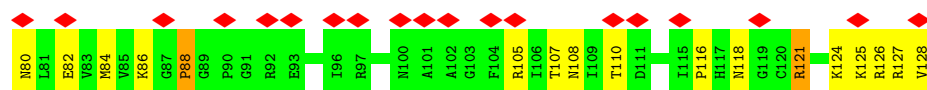
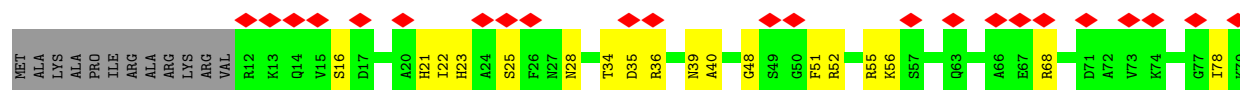


• Molecule 9: 30S ribosomal protein S10

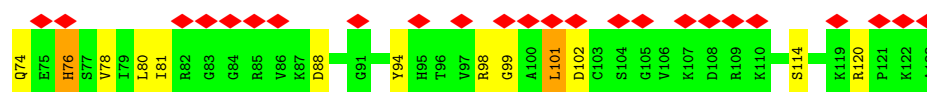
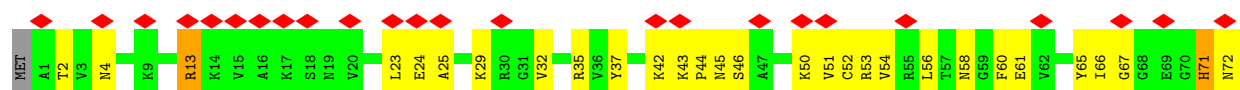




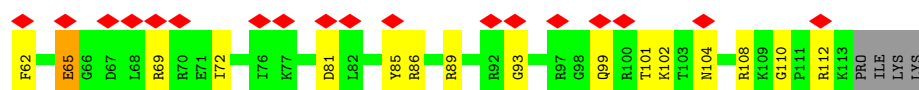
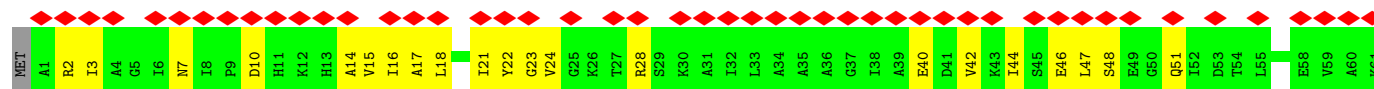
• Molecule 10: 30S ribosomal protein S11



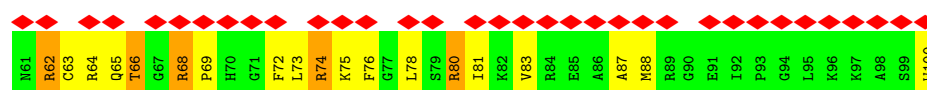
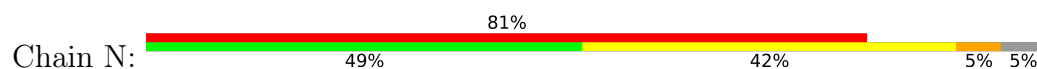
• Molecule 11: 30S ribosomal protein S12



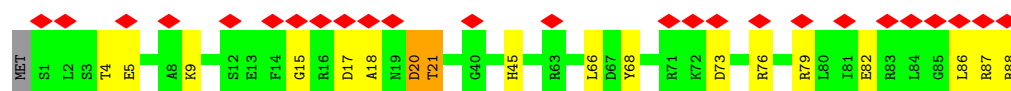
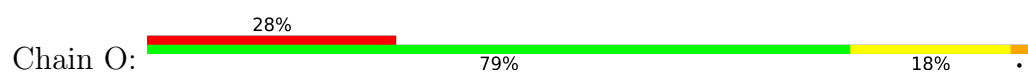
• Molecule 12: 30S ribosomal protein S13



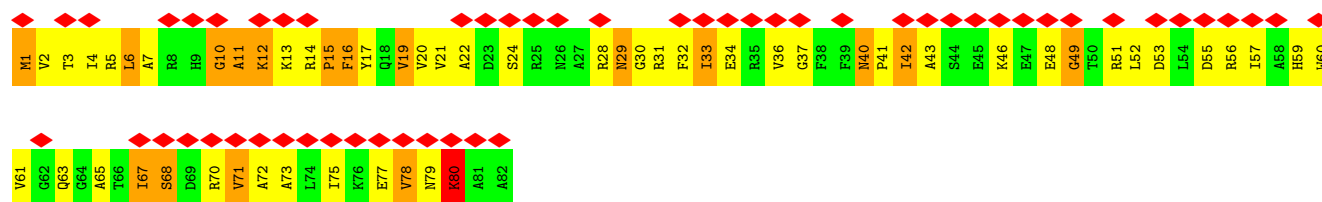
• Molecule 13: 30S ribosomal protein S14



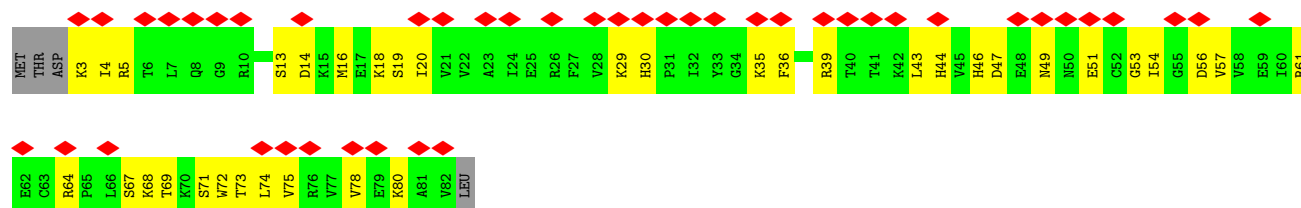
• Molecule 14: 30S ribosomal protein S15



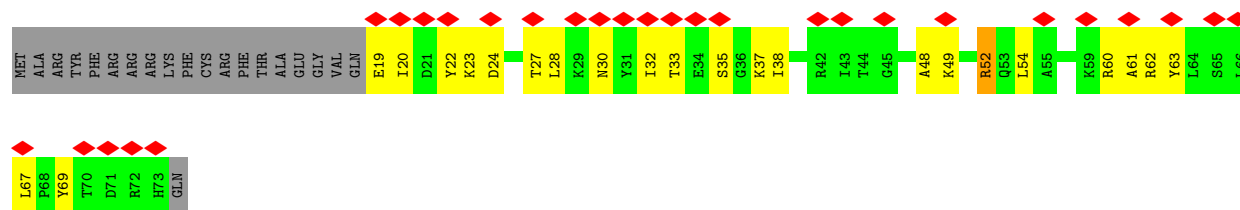
• Molecule 15: 30S ribosomal protein S16



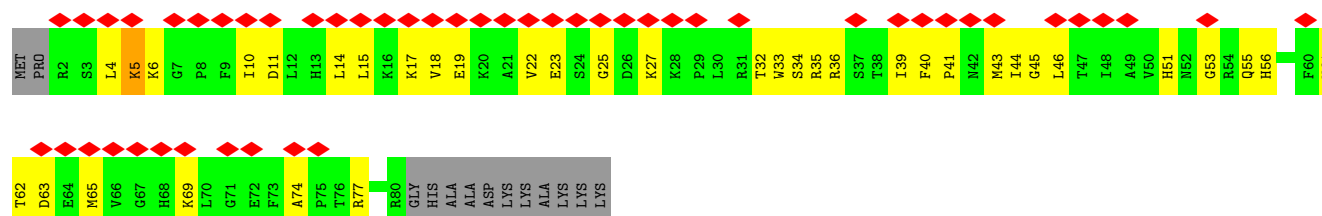
• Molecule 16: 30S ribosomal protein S17



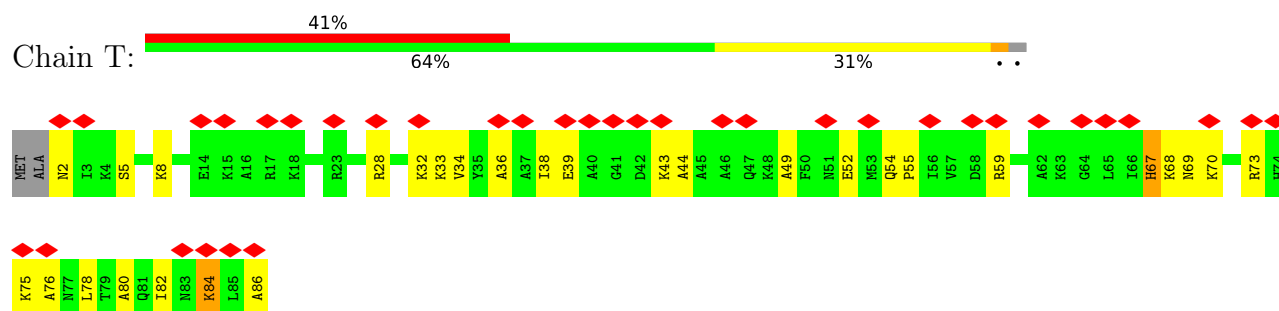
• Molecule 17: 30S ribosomal protein S18



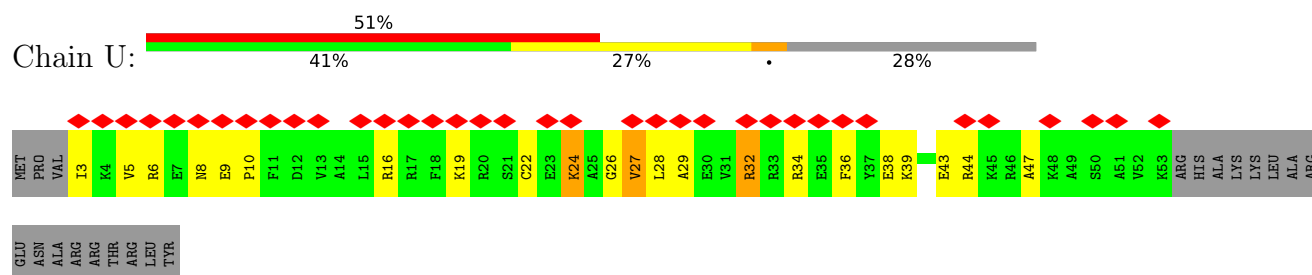
• Molecule 18: 30S ribosomal protein S19



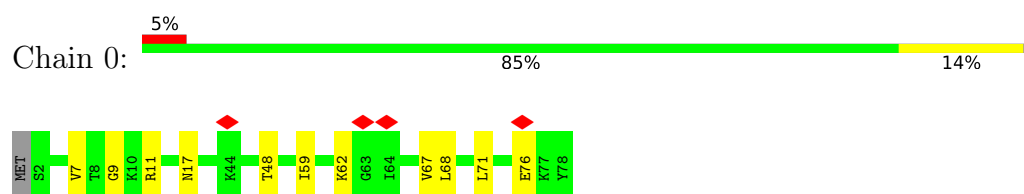
- Molecule 19: 30S ribosomal protein S20



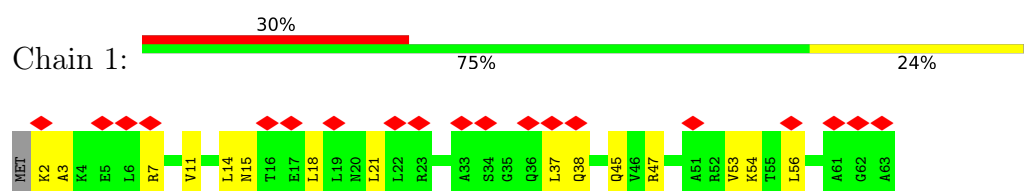
- Molecule 20: 30S ribosomal protein S21



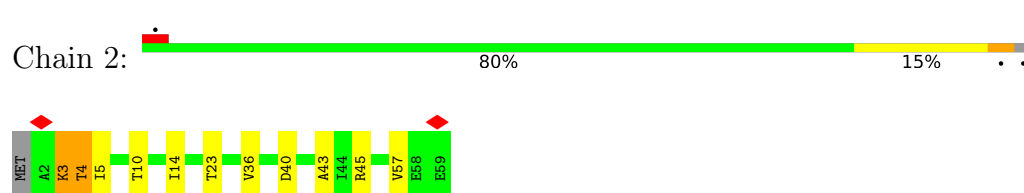
- Molecule 21: 50S ribosomal protein L28



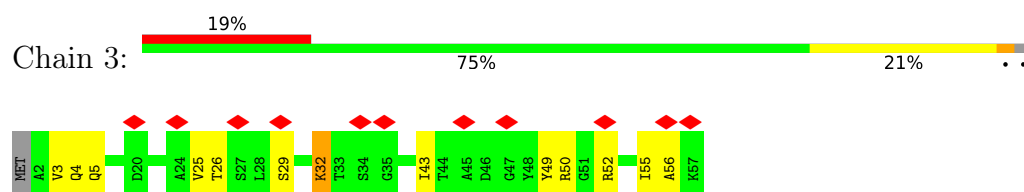
- Molecule 22: 50S ribosomal protein L29



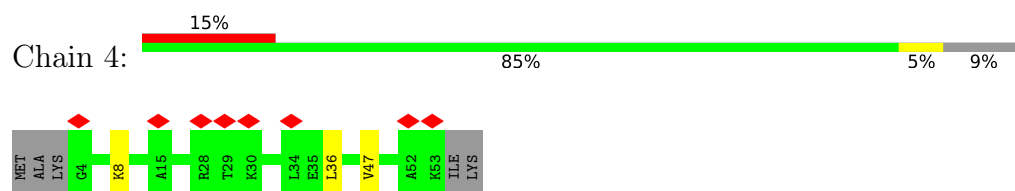
- Molecule 23: 50S ribosomal protein L30



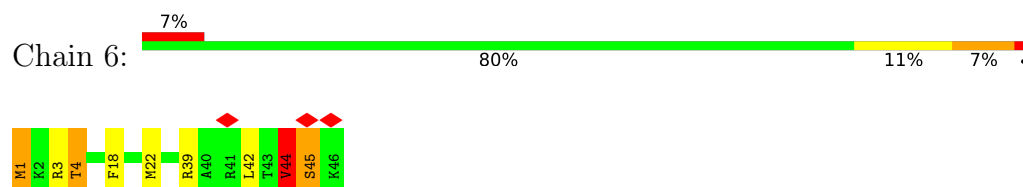
- Molecule 24: 50S ribosomal protein L32



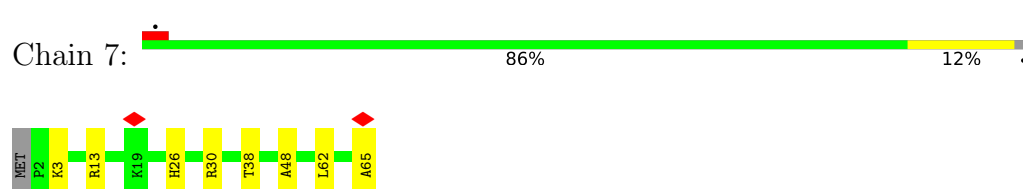
- Molecule 25: 50S ribosomal protein L33



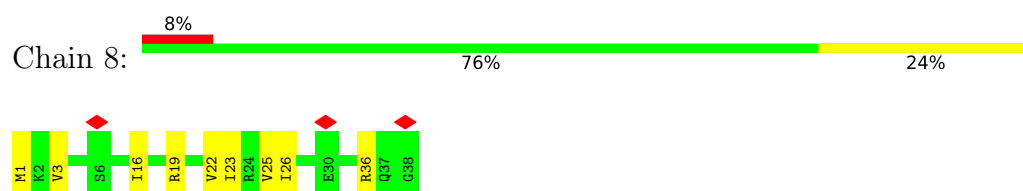
- Molecule 26: 50S ribosomal protein L34



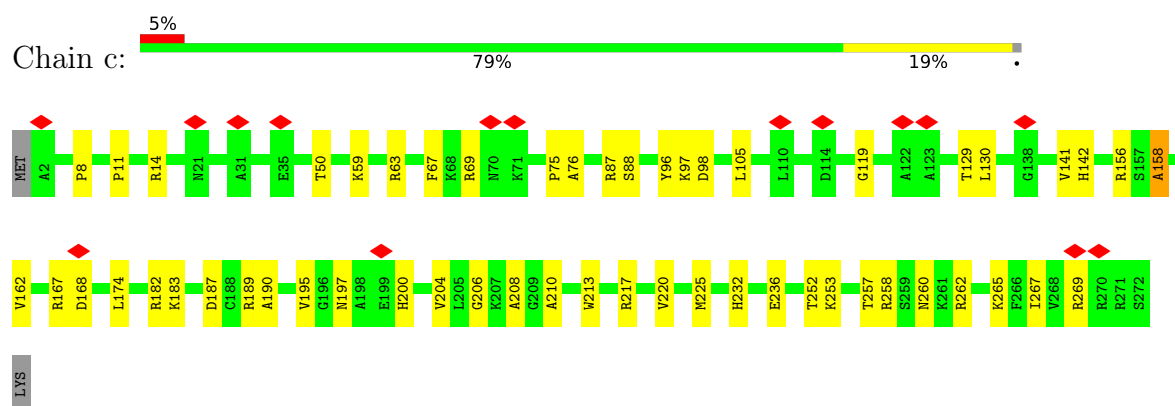
- Molecule 27: 50S ribosomal protein L35



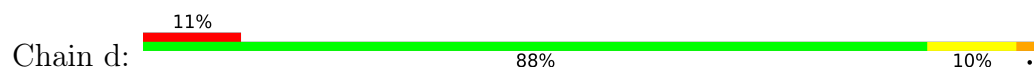
- Molecule 28: 50S ribosomal protein L36

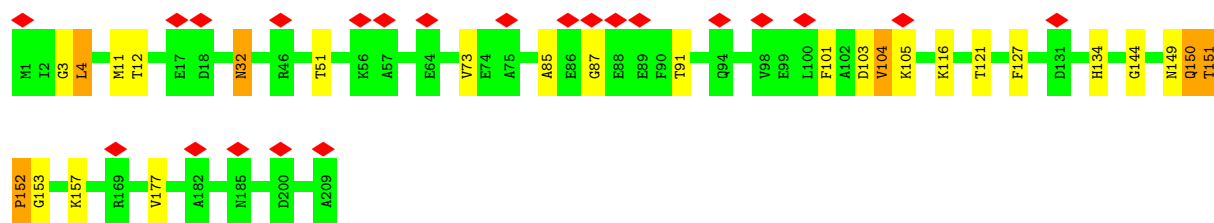


- Molecule 29: 50S ribosomal protein L2

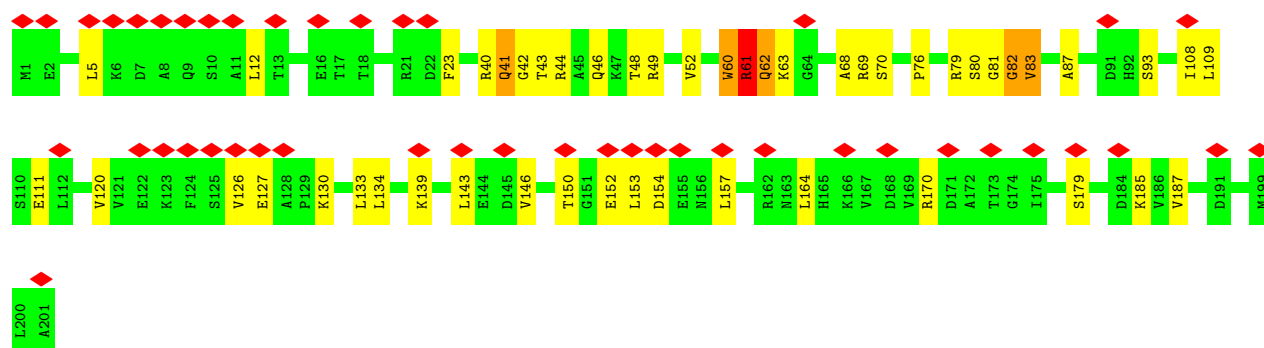
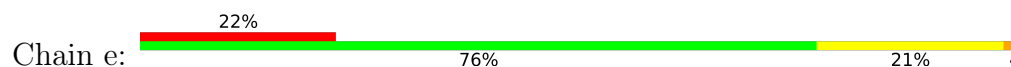


- Molecule 30: 50S ribosomal protein L3

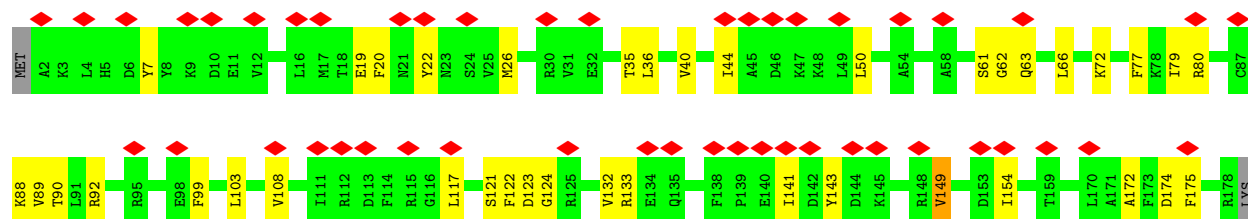
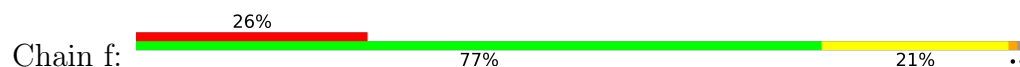




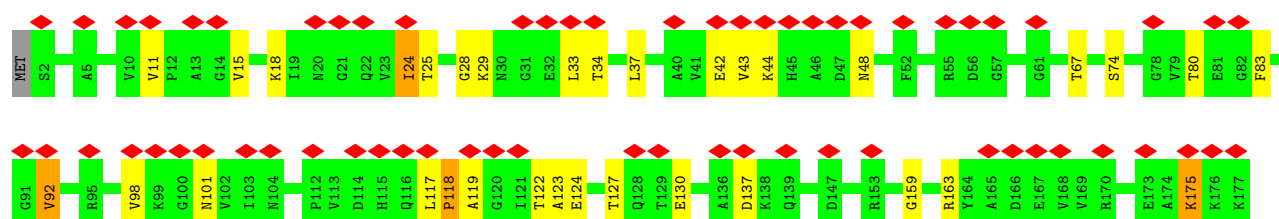
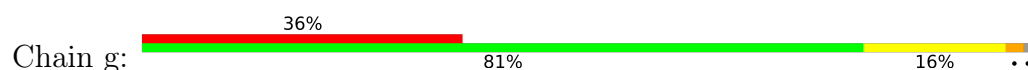
• Molecule 31: 50S ribosomal protein L4



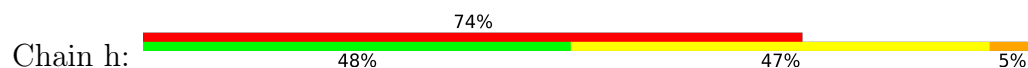
• Molecule 32: 50S ribosomal protein L5

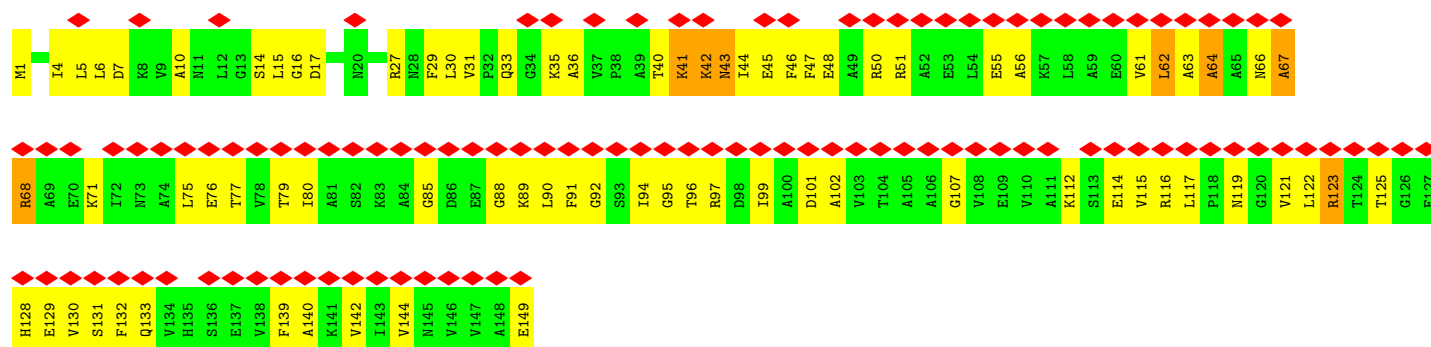


• Molecule 33: 50S ribosomal protein L6

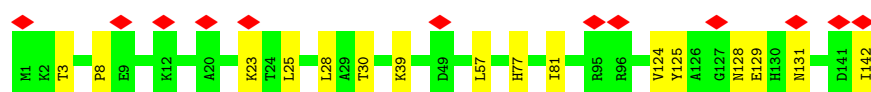
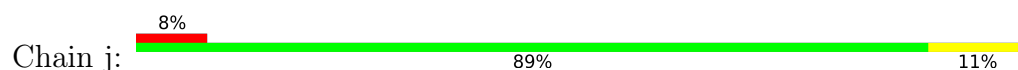


• Molecule 34: 50S ribosomal protein L9

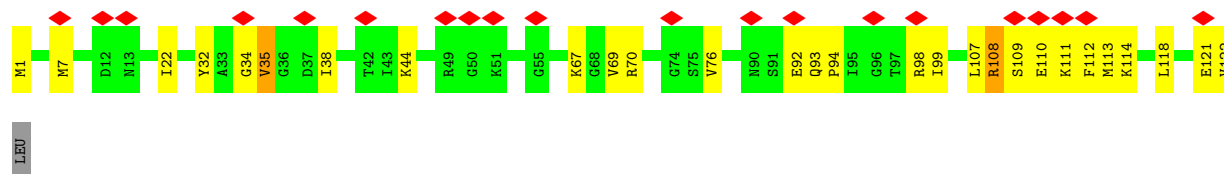
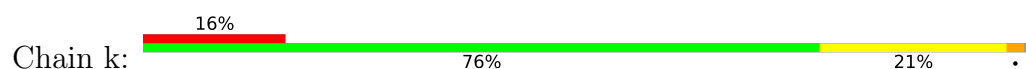




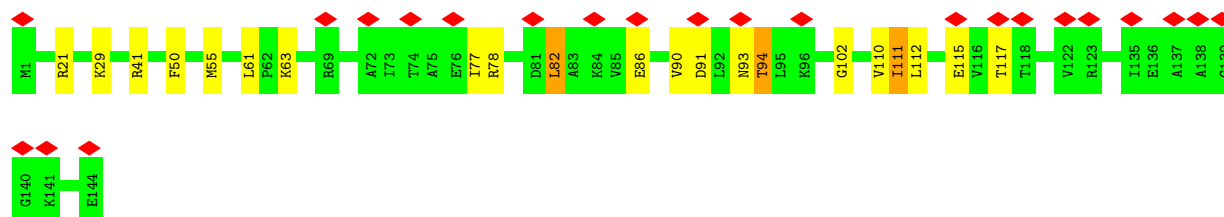
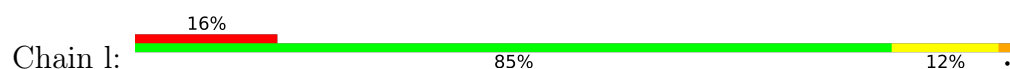
- Molecule 35: 50S ribosomal protein L13



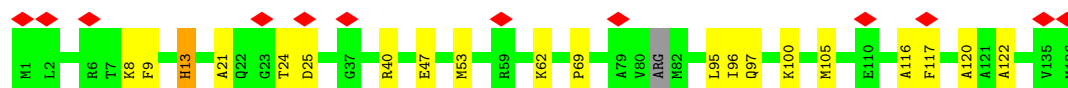
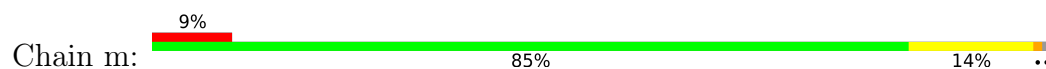
- Molecule 36: 50S ribosomal protein L14



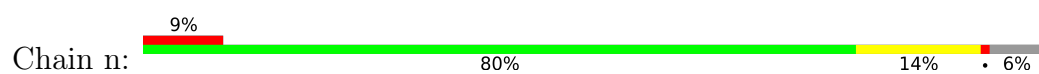
- Molecule 37: 50S ribosomal protein L15



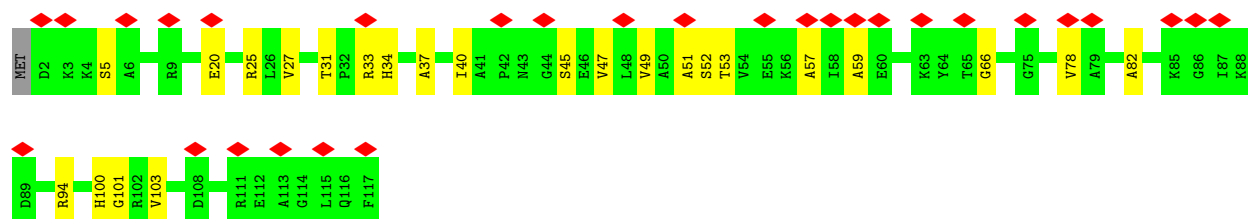
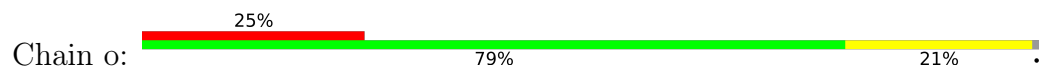
- Molecule 38: 50S ribosomal protein L16



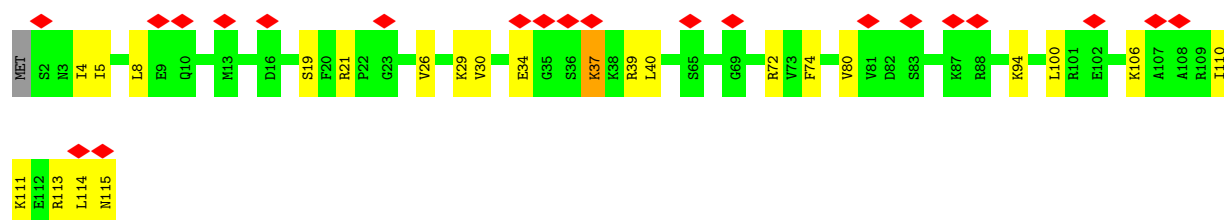
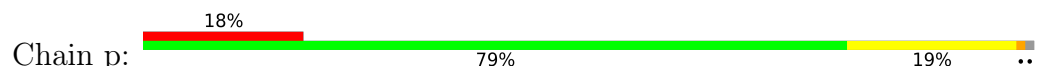
- Molecule 39: 50S ribosomal protein L17



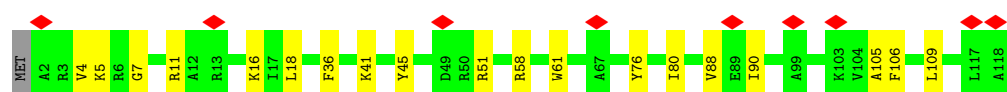
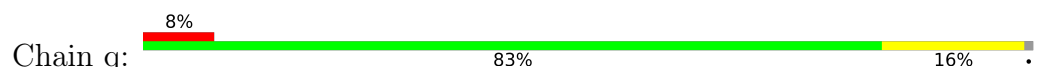
- Molecule 40: 50S ribosomal protein L18



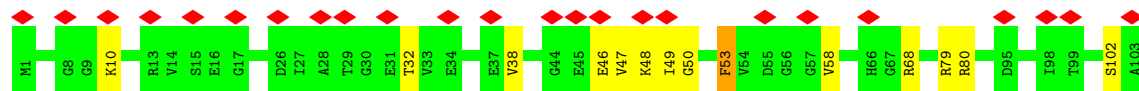
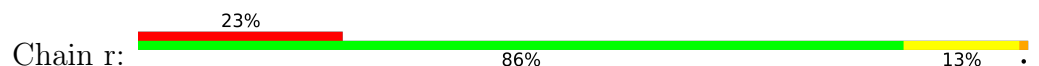
- Molecule 41: 50S ribosomal protein L19



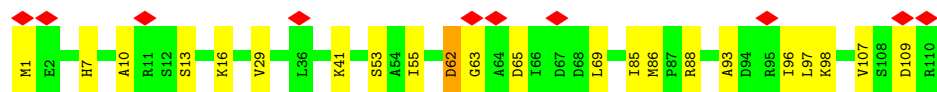
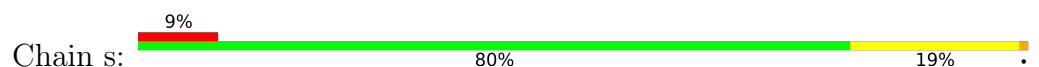
- Molecule 42: 50S ribosomal protein L20



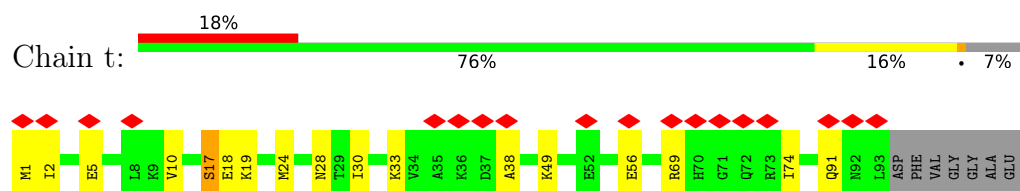
- Molecule 43: 50S ribosomal protein L21



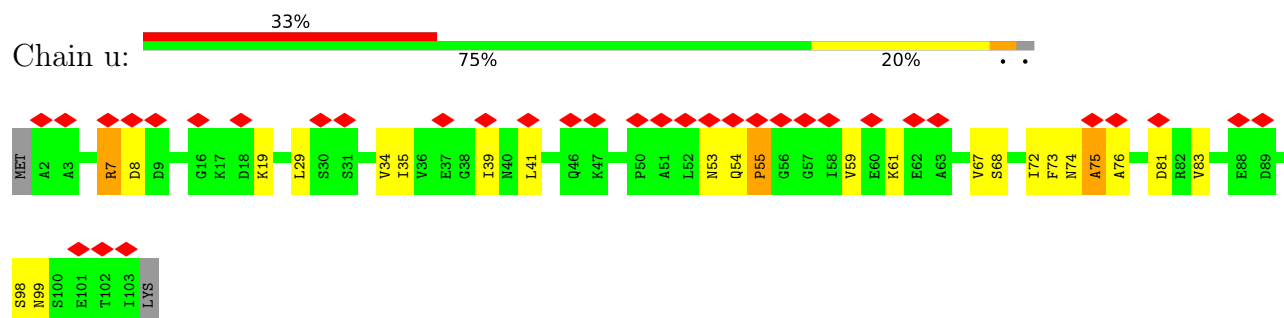
- Molecule 44: 50S ribosomal protein L22



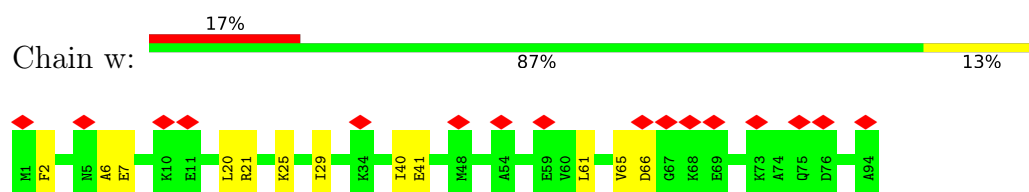
- Molecule 45: 50S ribosomal protein L23



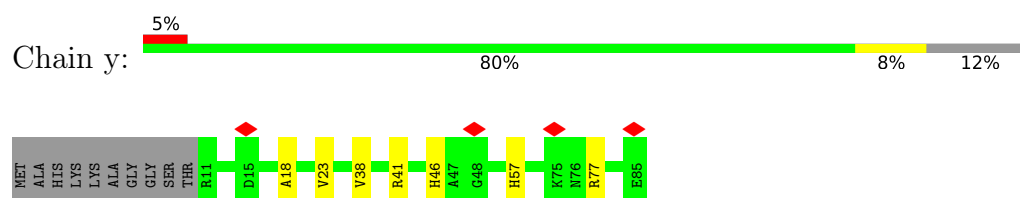
- Molecule 46: 50S ribosomal protein L24



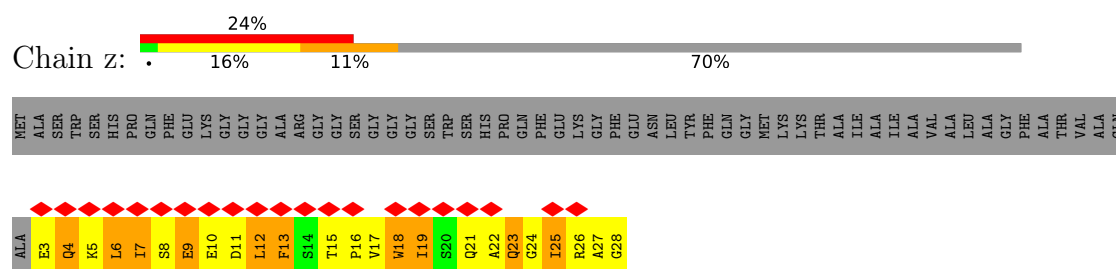
- Molecule 47: 50S ribosomal protein L25



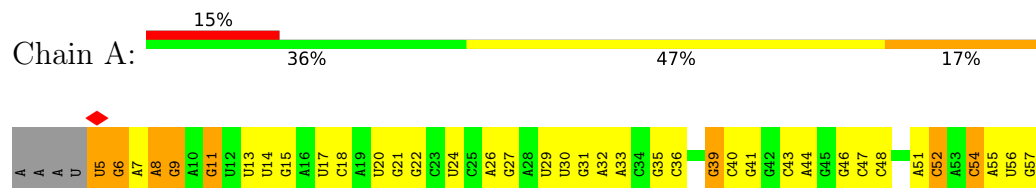
- Molecule 48: 50S ribosomal protein L27

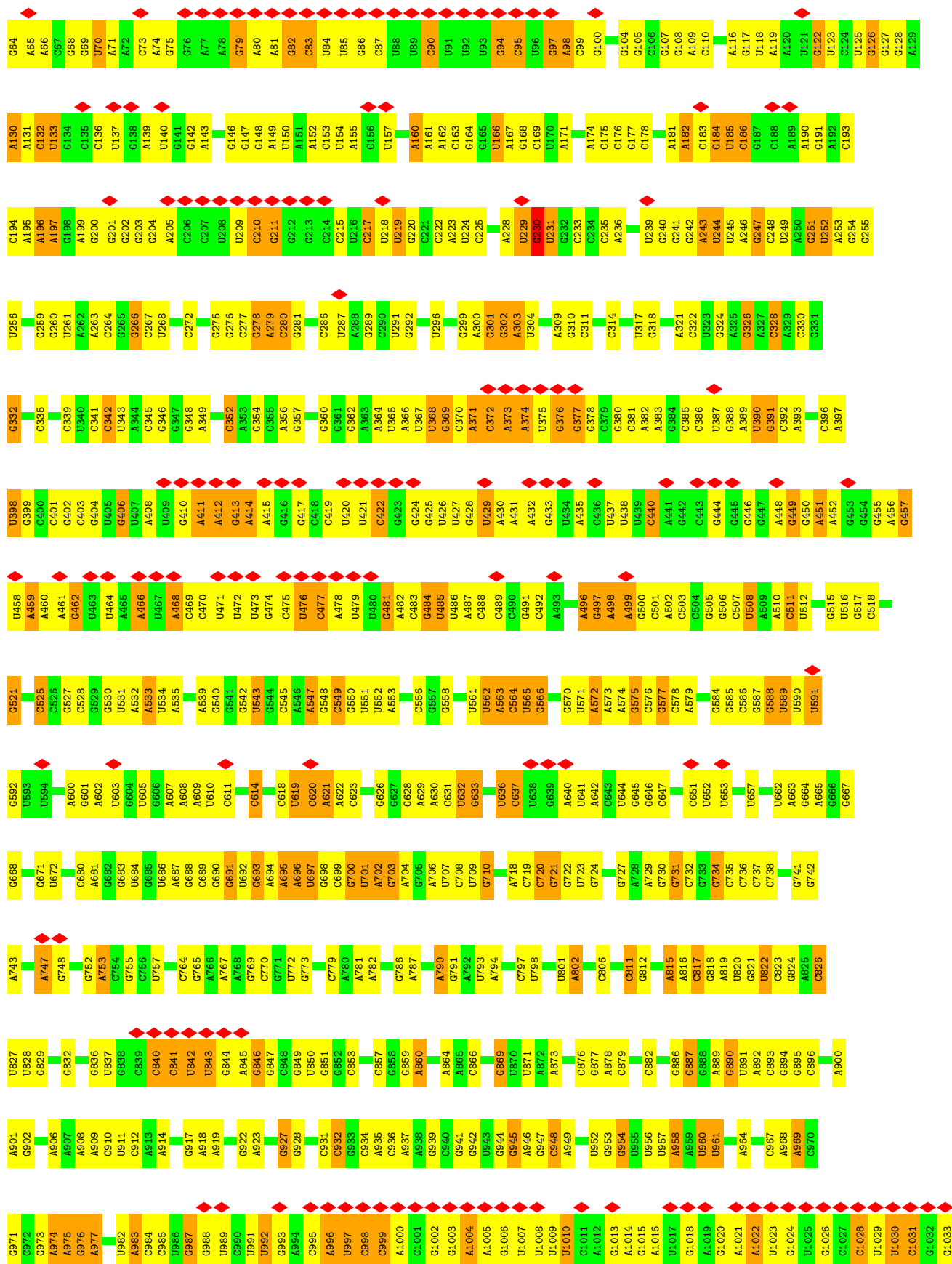


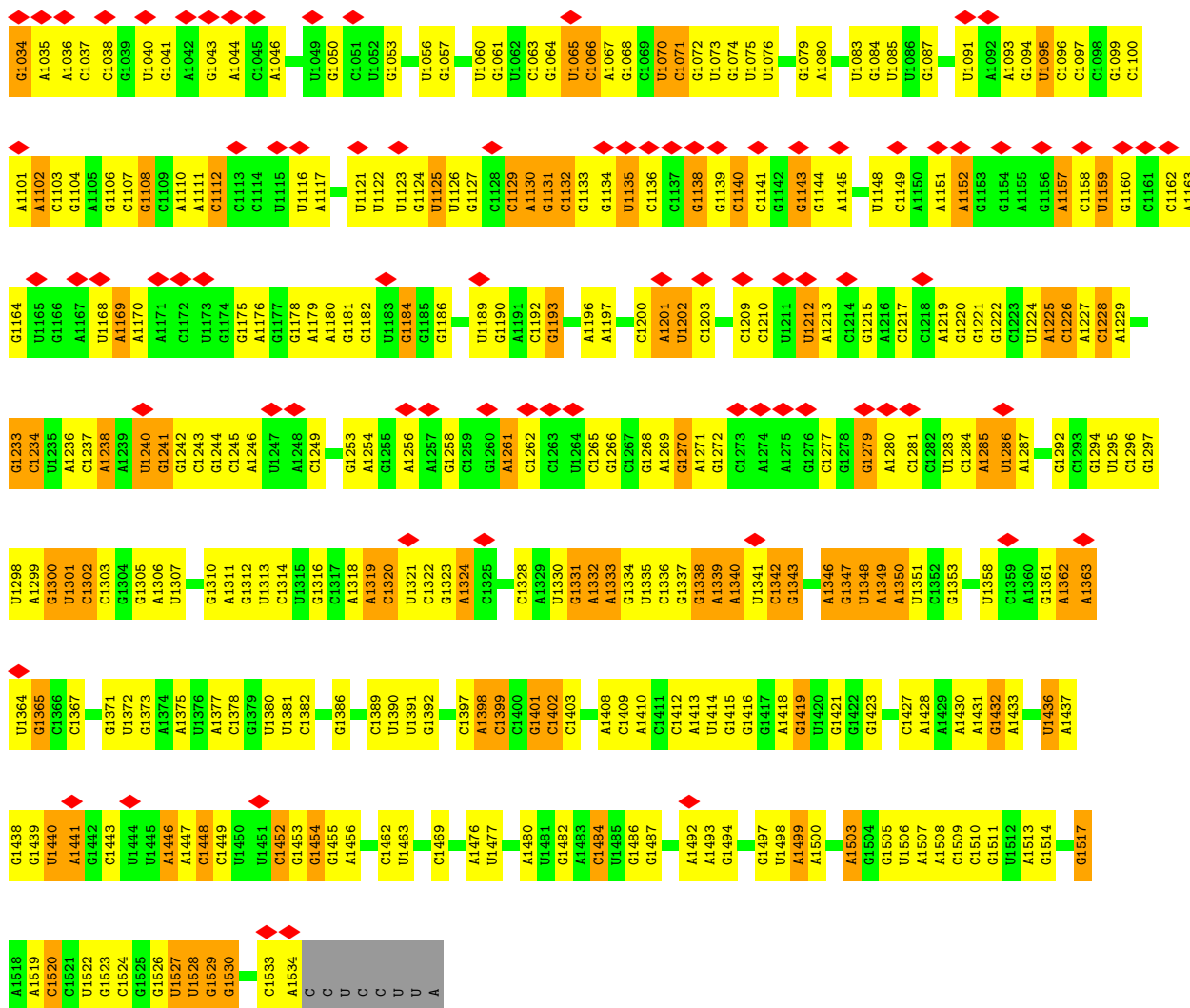
- Molecule 49: SecM-glycine

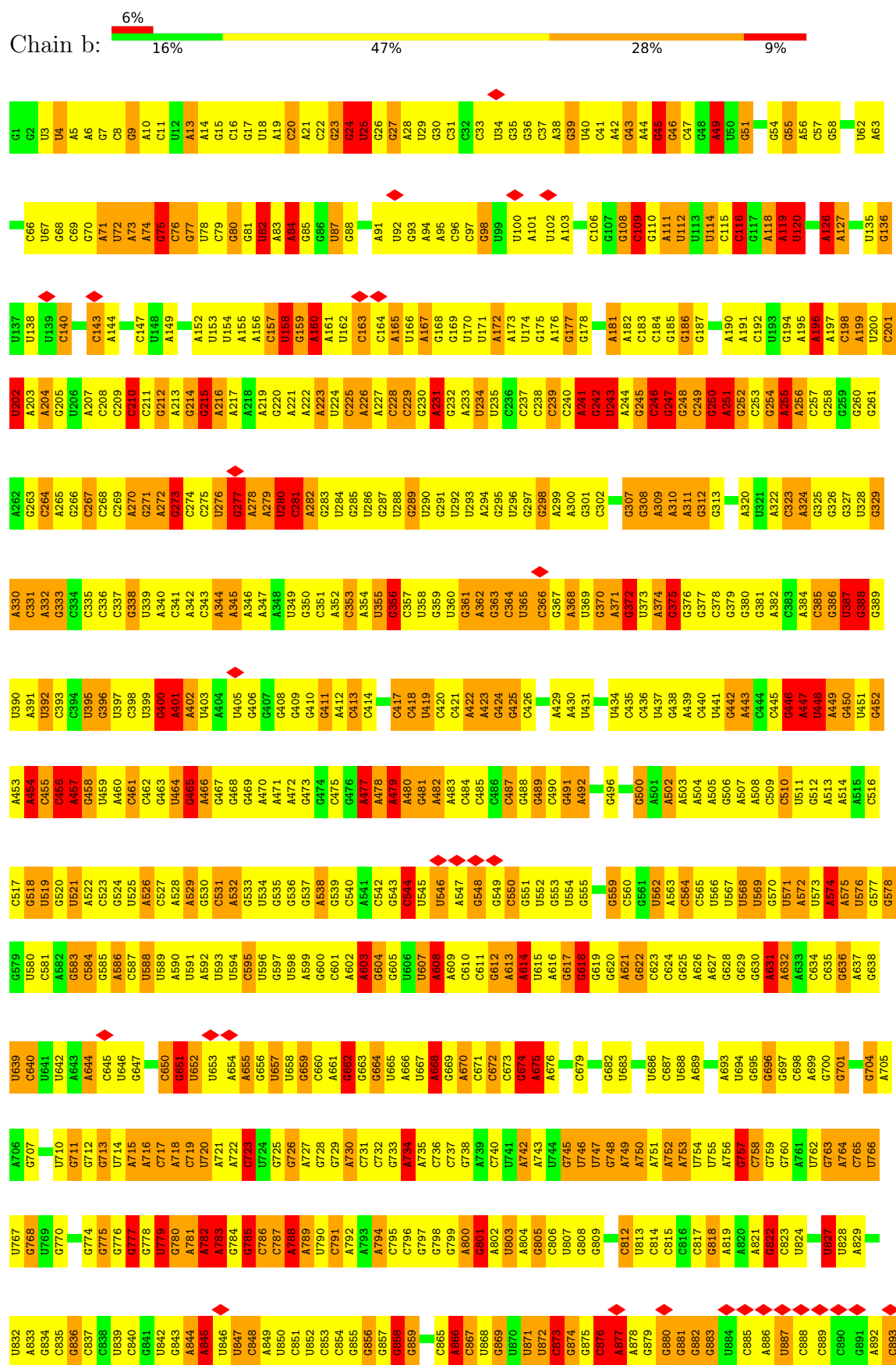


- Molecule 50: 16S rRNA



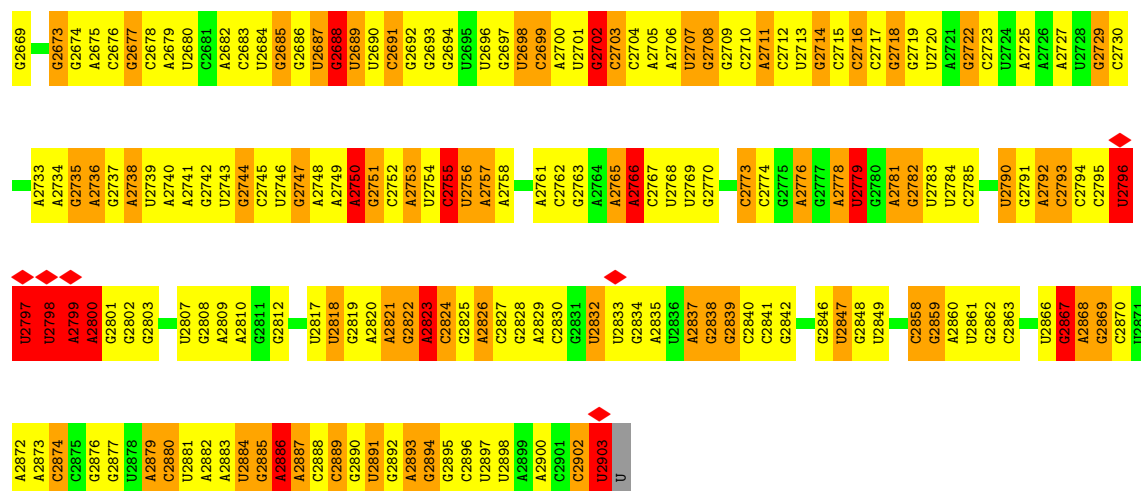




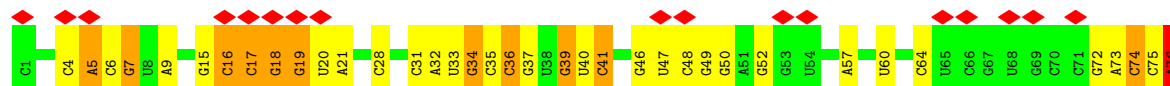


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									U1141			

U2604	U2605	U2606	U2607	U2608	U2609	U2610	U2611	U2612	U2613	U2614	U2615	U2616	U2617	U2618	U2619	U2620	U2621	U2622	U2623	U2624	U2625	U2626	U2627	U2628	U2629	U2630	U2631	U2632	U2633	U2634	U2635	U2636	U2637	U2638	U2639	U2640	U2641	U2642	U2643	U2644	U2645	U2646	U2647	U2648	U2649	U2650	U2651	U2652	U2653	U2654	U2655	U2656	U2657	U2658	U2659	U2660	U2661	U2662	U2663	U2664	U2665	U2666	U2667	U2668																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
G1770	G1771	G1772	G1773	G1774	G1775	G1776	G1777	G1778	G1779	G1780	G1781	G1782	G1783	G1784	G1785	G1786	G1787	G1788	G1789	G1790	G1791	G1792	G1793	G1794	G1795	G1796	G1797	G1798	G1799	G1800	G1801	G1802	G1803	G1804	G1805	G1806	G1807	G1808	G1809	G1810	G1811	G1812	G1813	G1814	G1815	G1816	G1817	G1818	G1819	G1820	G1821	G1822	G1823	G1824	G1825	G1826	G1827	G1828	G1829	G1830	G1831																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	G1840	U1841	G1842	C1843	U1844	G1845	C1846	U1847	G1848	C1849	G1850	C1851	G1852	C1853	G1854	C1855	G1856	C1857	G1858	C1859	G1860	C1861	G1862	U1863	C1864	U1865	C1866	U1867	C1868	U1869	C1870	U1871	C1872	U1873	C1874	U1875	C1876	U1877	C1878	U1879	C1880	U1881	C1882	U1883	C1884	U1885	C1886	U1887	C1888	U1889	C1890	U1891	C1892	U1893	C1894	U1895	C1896	U1897	C1898	U1899	C1900	U1901	C1902																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G1905	G1906	G1907	C1908	C1909	G1910	U1911	G1912	C1913	G1914	U1915	G1916	U1917	C1918	U1919	G1920	C1921	G1922	C1923	U1924	C1925	G1926	U1927	C1928	U1929	C1930	U1931	C1932	U1933	C1934	U1935	C1936	U1937	C1938	U1939	U1940	C1941	G1942	U1943	U1944	C1945	U1946	C1947	U1948	G1949	C1950	U1951	C1952	U1953	C1954	U1955	C1956	U1957	C1958	U1959	C1960	U1961	C1962	U1963	C1964	U1965	C1966	U1967	C1968	U1969	C1970	U1971	C1972	U1973	C1974	U1975	C1976	U1977	C1978	U1979	C1980	U1981	C1982	U1983	C1984	U1985	C1986	U1987	C1988	U1989	C1990	U1991	C1992	U1993	C1994	U1995	C1996	U1997	C1998	U1999	C2000	U2001	C2002	U2003	C2004	U2005	C2006	U2007	C2008	U2009	C2010	U2011	C2012	U2013	C2014	U2015	C2016	U2017	C2018	U2019	C2020	U2021	C2022	U2023	C2024	U2025	C2026	U2027	C2028	U2029	C2030	U2031	C2032	U2033	C2034	U2035	C2036	U2037	C2038	U2039	C2040	U2041	C2042	U2043	C2044	U2045	C2046	U2047	C2048	U2049	C2050	U2051	C2052	U2053	C2054	U2055	C2056	U2057	C2058	U2059	C2060	U2061	C2062	U2063	C2064	U2065	C2066	U2067	C2068	U2069	C2070	U2071	C2072	U2073	C2074	U2075	C2076	U2077	C2078	U2079	C2080	U2081	C2082	U2083	C2084	U2085	C2086	U2087	C2088	U2089	C2090	U2091	C2092	U2093	C2094	U2095	C2096	U2097	C2098	U2099	C2100	U2101	C2102	U2103	C2104	U2105	C2106	U2107	C2108	U2109	C2110	U2111	C2112	U2113	C2114	U2115	C2116	U2117	C2118	U2119	C2120	U2121	C2122	U2123	C2124	U2125	C2126	U2127	C2128	U2129	C2130	U2131	C2132	U2133	C2134	U2135	C2136	U2137	C2138	U2139	C2140	U2141	C2142	U2143	C2144	U2145	C2146	U2147	C2148	U2149	C2150	U2151	C2152	U2153	C2154	U2155	C2156	U2157	C2158	U2159	C2160	U2161	C2162	U2163	C2164	U2165	C2166	U2167	C2168	U2169	C2170	U2171	C2172	U2173	C2174	U2175	C2176	U2177	C2178	U2179	C2180	U2181	C2182	U2183	C2184	U2185	C2186	U2187	C2188	U2189	C2190	U2191	C2192	U2193	C2194	U2195	C2196	U2197	C2198	U2199	C2200	U2201	C2202	U2203	C2204	U2205	C2206	U2207	C2208	U2209	C2210	U2211	C2212	U2213	C2214	U2215	C2216	U2217	C2218	U2219	C2220	U2221	C2222	U2223	C2224	U2225	C2226	U2227	C2228	U2229	C2230	U2231	C2232	U2233	C2234	U2235	C2236	U2237	C2238	U2239	C2240	U2241	C2242	U2243	C2244	U2245	C2246	U2247	C2248	U2249	C2250	U2251	C2252	U2253	C2254	U2255	C2256	U2257	C2258	U2259	C2260	U2261	C2262	U2263	C2264	U2265	C2266	U2267	C2268	U2269	C2270	U2271	C2272	U2273	C2274	U2275	C2276	U2277	C2278	U2279	C2280	U2281	C2282	U2283	C2284	U2285	C2286	U2287	C2288	U2289	C2290	U2291	C2292	U2293	C2294	U2295	C2296	U2297	C2298	U2299	C2300	U2301	C2302	U2303	C2304	U2305	C2306	U2307	C2308	U2309	C2310	U2311	C2312	U2313	C2314	U2315	C2316	U2317	C2318	U2319	C2320	U2321	C2322	U2323	C2324	U2325	C2326	U2327	C2328	U2329	C2330	U2331	C2332	U2333	C2334	U2335	C2336	U2337	C2338	U2339	C2340	U2341	C2342	U2343	C2344	U2345	C2346	U2347	C2348	U2349	C2350	U2351	C2352	U2353	C2354	U2355	C2356	U2357	C2358	U2359	C2360	U2361	C2362	U2363	C2364	U2365	C2366	U2367	C2368	U2369	C2370	U2371	C2372	U2373	C2374	U2375	C2376	U2377	C2378	U2379	C2380	U2381	C2382	U2383	C2384	U2385	C2386	U2387	C2388	U2389	C2390	U2391	C2392	U2393	C2394	U2395	C2396	U2397	C2398	U2399	C2400	U2401	C2402	U2403	C2404	U2405	C2406	U2407	C2408	U2409	C2410	U2411	C2412	U2413	C2414	U2415	C2416	U2417	C2418	U2419	C2420	U2421	C2422	U2423	C2424	U2425	C2426	U2427	C2428	U2429	C2430	U2431	C2432	U2433	C2434	U2435	C2436	U2437	C2438	U2439	C2440	U2441	C2442	U2443	C2444	U2445	C2446	U2447	C2448	U2449	C2450	U2451	C2452	U2453	C2454	U2455	C2456	U2457	C2458	U2459	C2460	U2461	C2462	U2463	C2464	U2465	C2466	U2467	C2468	U2469	C2470	U2471	C2472	U2473	C2474	U2475	C2476	U2477	C2478	U2479	C2480	U2481	C2482	U2483	C2484	U2485	C2486	U2487	C2488	U2489	C2490	U2491	C2492	U2493	C2494	U2495	C2496	U2497	C2498	U2499	C2500	U2501	C2502	U2503	C2504	U2505	C2506	U2507	C2508	U2509	C2510	U2511	C2512	U2513	C2514	U2515	C2516	U2517	C2518	U2519	C2520	U2521	C2522	U2523	C2524	U2525	C2526	U2527	C2528	U2529	C2530	U2531	C2532	U2533	C2534	U2535	C2536	U2537	C2538	U2539	C2540	U2541	C2542	U2543	C2544	U2545	C2546	U2547	C2548	U2549	C2550	U2551	C2552	U2553	C2554	U2555	C2556	U2557	C2558	U2559	C2560	U2561	C2562	U2563	C2564	U2565	C2566	U2567	C2568	U2569	C2570	U2571	C2572	U2573	C2574	U2575	C2576	U2577	C2578	U2579	C2580	U2581	C2582	U2583	C2584	U2585	C2586	U2587	C2588	U2589	C2590	U2591	C2592	U2593	C2594	U2595	C2596	U2597	C2598	U2599	C2600	U2601	C2602	U2603	C2604	U2605	C2606	U2607	C2608	U2609	C2610	U2611	C2612	U2613	C2614	U2615	C2616	U2617	C2618	U2619	C2620	U2621	C2622	U2623	C2624	U2625	C2626	U2627	C2628	U2629	C2630	U2631	C2632	U2633	C2634	U2635	C2636	U2637	C2638	U2639	C2640	U2641	C2642	U2643	C2644	U2645	C2646	U2647	C2648	U2649	C2650	U2651	C2652	U2653	C2654	U2655	C2656	U2657	C2658	U2659	C2660	U2661	C2662	U2663	C2664	U2665	C2666	U2667	C2668	U2669	C2670	U2671	C2672	U2673	C2674	U2675	C2676	U2677	C2678	U2679	C2680	U2681	C2682	U2683	C2684	U2685	C2686	U2687	C2688	U2689	C2690	U2691	C2692	U2693	C2694	U2695	C2696	U2697	C2698	U2699	C2700	U2701	C2702	U2703	C2704	U2705	C2706	U2707	C2708	U2709	C2710	U2711	C2712	U2713	C2714	U2715	C2716	U2717	C2718	U2719	C2720	U2721	C2722	U2723	C2724	U2725	C2726	U2727	C2728	U2729	C2730	U2731	C2732	U2733	C2734	U2735	C2736	U2737	C2738	U2739	C2740	U2741	C2742	U2743	C2744	U2745	C2746	U2747	C2748	U2749	C2750	U2751	C2752	U2753	C2754	U2755	C2756	U2757	C2758	U2759	C2760	U2761	C2762	U2763	C2764	U2765	C2766	U2767	C2768	U2769	C2770	U2771	C2772	U2773	C2774	U2775	C2776	U2777	C2778	U2779	C2780	U2781	C2782	U2783	C2784	U2785	C2786	U2787	C2788	U2789	C2790	U2791	C2792	U2793	C2794	U2795	C2796	U2797	C2798	U2799	C2800	U2801	C2802	U2803	C2804	U2805	C2806	U2807	C2808	U2809	C2810	U2811	C2812	U2813	C2814	U2815	C2816	U2817	C2818	U2819	C2820	U2821	C2822	U2823	C2824	U2825	C2826	U2827	C2828	U2829	C2830	U2831	C2832	U2833	C2834	U2835	C2836	U2837	C2838	U2839	C2840	U2841	C2842	U2843	C2844	U2845	C2846	U2847	C2848	U2849	C2850	U2851	C2852	U2853	C2854	U2855	C2856	U2857	C2858	U2859	C2860	U2861	C2862	U2863	C2864	U2865	C2866	U2867	C2868	U2869	C2870	U2871	C2872	U2873	C2874	U2875	C2876	U2877	C2878	U2879	C2880	U2881	C2882	U2883	C2884	U2885	C2886	U2887	C2888	U2889	C2890	U2891	C2892	U2893	C2894	U2895	C2896	U2897	C2898	U2899	C2900	U2901	C2902	U2903	C2904	U2905	C2906	U2907	C2908	U2909	C2910	U2911	C2912	U2913	C2914	U2915	C2916	U2917	C2918	U2919	C2920	U2921	C2922	U2923	C2924	U2925	C2926	U2927	C2928	U2929	C2930	U2931	C2932	U2933	C2934	U2935	C2936	U2937	C2938	U2939	C2940	U2941	C2942	U2943	C2944	U2945	C2946	U2947	C2948	U2949	C2950	U2951	C2952	U2953	C2954	U2955	C2956	U2957	C2958	U2959	C2960	U2961	C2962	U2963	C2964	U2965	C2966	U2967	C2968	U2969	C2970	U2971	C2972	U2973	C2974	U2975	C2976	U2977	C2978	U2979	C2980	U2981	C2982	U2983	C2984	U2985	C2986	U2987	C2988	U2989	C2990	U2991	C2992	U2993	C2994	U2995	C2996	U2997	C2998	U2999	C3000	U3001	C3002	U3003	C3004	U3005	C3006	U3007	C3008	U3009	C3010



• Molecule 54: glycine-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60354	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	37878	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.180	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	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	B	0.42	0/1735	0.86	0/2338
2	C	0.45	0/1651	0.94	7/2225 (0.3%)
3	D	0.44	0/1665	0.89	4/2227 (0.2%)
4	E	0.49	0/1118	0.93	1/1504 (0.1%)
5	F	0.42	0/835	0.96	2/1128 (0.2%)
6	G	0.42	0/1187	0.86	3/1591 (0.2%)
7	H	0.47	0/989	0.89	0/1326
8	I	0.43	0/1034	0.97	4/1375 (0.3%)
9	J	0.44	0/796	0.88	0/1077
10	K	0.42	0/893	0.98	2/1205 (0.2%)
11	L	0.47	0/969	1.00	5/1300 (0.4%)
12	M	0.43	0/884	0.89	3/1181 (0.3%)
13	N	0.46	0/785	0.92	3/1043 (0.3%)
14	O	0.41	0/724	0.77	0/966
15	P	0.38	0/659	0.87	4/884 (0.5%)
16	Q	0.42	0/657	0.86	3/881 (0.3%)
17	R	0.47	0/462	0.92	1/621 (0.2%)
18	S	0.43	0/652	0.88	0/877
19	T	0.49	0/671	0.85	1/888 (0.1%)
20	U	0.42	0/430	0.97	0/570
21	0	0.50	0/635	0.79	0/848
22	1	0.49	0/502	0.88	0/667
23	2	0.54	0/453	0.80	0/605
24	3	0.56	0/450	0.89	1/599 (0.2%)
25	4	0.50	0/416	0.68	0/554
26	6	0.55	0/380	0.89	0/498
27	7	0.54	0/513	0.83	0/676
28	8	0.57	0/303	0.75	0/397
29	c	0.55	0/2121	0.80	3/2852 (0.1%)
30	d	0.53	0/1586	0.76	0/2134
31	e	0.56	0/1571	0.88	2/2113 (0.1%)
32	f	0.55	0/1434	0.84	0/1926
33	g	0.55	0/1343	0.73	0/1816
34	h	0.58	4/1122 (0.4%)	1.24	9/1515 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.50	0/1152	0.76	0/1551
36	k	0.52	0/947	0.71	0/1268
37	l	0.58	0/1062	0.85	0/1413
38	m	0.52	0/1081	0.76	0/1443
39	n	0.52	0/973	0.84	0/1301
40	o	0.53	0/902	0.91	0/1209
41	p	0.47	0/929	0.70	0/1242
42	q	0.50	0/960	0.84	0/1278
43	r	0.51	0/829	0.76	0/1107
44	s	0.49	0/864	0.82	0/1156
45	t	0.58	0/744	0.82	0/994
46	u	0.56	0/787	0.81	0/1051
47	w	0.49	0/766	0.71	0/1025
48	y	0.48	0/576	0.66	0/762
49	z	0.66	1/206 (0.5%)	1.38	6/277 (2.2%)
50	A	0.36	6/36762 (0.0%)	0.32	0/57350
51	X	0.78	3/257 (1.2%)	0.60	0/396
52	a	0.50	2/2824 (0.1%)	1.02	15/4402 (0.3%)
53	b	0.56	25/69800 (0.0%)	1.09	617/108892 (0.6%)
54	v	0.40	0/1812	0.87	4/2822 (0.1%)
All	All	0.50	41/155858 (0.0%)	0.89	700/233346 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	L	0	1
23	2	0	1
29	c	0	1
30	d	0	1
36	k	0	1
37	l	0	1
43	r	0	1
52	a	0	1
53	b	0	72
All	All	0	80

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	A	230	G	C2-N3	22.08	1.76	1.32
50	A	230	G	N1-C2	21.53	1.80	1.37
50	A	230	G	C6-N1	21.29	1.82	1.39
50	A	230	G	N3-C4	20.50	1.76	1.35
50	A	230	G	C5-C6	19.93	1.82	1.42

The worst 5 of 700 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	v	74	C	O3'-P-O5'	-19.87	74.20	104.00
34	h	62	LEU	N-CA-C	18.87	131.26	111.07
34	h	61	VAL	N-CA-C	18.55	129.45	110.72
53	b	1102	C	N1-C1'-C2'	15.64	135.47	112.00
53	b	1509	A	N9-C1'-C2'	15.55	137.32	114.00

There are no chirality outliers.

5 of 80 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	2	3	LYS	Peptide
11	L	71	HIS	Peptide
29	c	232	HIS	Peptide
30	d	151	THR	Peptide
36	k	34	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1704	0	1732	61	0
2	C	1624	0	1699	50	0
3	D	1643	0	1710	83	0
4	E	1105	0	1148	44	0
5	F	817	0	808	33	0
6	G	1174	0	1230	27	0
7	H	979	0	1034	32	0
8	I	1022	0	1067	134	0
9	J	786	0	828	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	K	877	0	887	34	0
11	L	955	0	1019	35	0
12	M	876	0	935	29	0
13	N	774	0	827	39	0
14	O	716	0	742	16	0
15	P	649	0	663	121	0
16	Q	648	0	691	32	0
17	R	455	0	478	23	0
18	S	637	0	665	37	0
19	T	665	0	714	26	0
20	U	425	0	449	31	0
21	0	625	0	652	7	0
22	1	501	0	531	13	0
23	2	449	0	488	18	0
24	3	444	0	457	13	0
25	4	409	0	440	1	0
26	6	377	0	418	11	0
27	7	504	0	572	7	0
28	8	302	0	343	13	0
29	c	2082	0	2154	58	0
30	d	1565	0	1616	20	0
31	e	1552	0	1619	65	0
32	f	1410	0	1444	31	0
33	g	1323	0	1371	31	0
34	h	1111	0	1148	90	0
35	j	1129	0	1162	27	0
36	k	938	0	1012	17	0
37	l	1053	0	1129	16	0
38	m	1063	0	1143	53	0
39	n	960	0	1000	40	0
40	o	892	0	923	10	0
41	p	917	0	960	40	0
42	q	947	0	1019	21	0
43	r	816	0	839	17	0
44	s	857	0	922	36	0
45	t	738	0	807	8	0
46	u	779	0	831	15	0
47	w	753	0	780	12	0
48	y	569	0	581	7	0
49	z	203	0	198	91	0
50	A	32831	0	16518	916	0
51	X	232	0	118	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	a	2528	0	1283	206	0
53	b	62321	0	31336	5597	0
54	v	1623	0	823	52	0
All	All	143334	0	95963	7984	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 34.

The worst 5 of 7984 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)
50:A:230:G:C5	50:A:230:G:C6	1.82	1.68
53:b:2798:U:H2'	53:b:2799:A:C2	1.19	1.67
8:I:111:GLU:CB	50:A:1348:U:C4'	1.75	1.65
50:A:702:A:C2	53:b:1848:A:C8	1.90	1.58
15:P:70:ARG:HG2	50:A:375:U:C5'	1.15	1.57

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	B	216/241 (90%)	186 (86%)	22 (10%)	8 (4%)	2	18
2	C	204/233 (88%)	173 (85%)	22 (11%)	9 (4%)	2	15
3	D	203/206 (98%)	179 (88%)	19 (9%)	5 (2%)	4	24
4	E	148/167 (89%)	125 (84%)	18 (12%)	5 (3%)	3	20
5	F	98/131 (75%)	82 (84%)	12 (12%)	4 (4%)	2	17
6	G	148/156 (95%)	128 (86%)	15 (10%)	5 (3%)	3	20
7	H	127/130 (98%)	111 (87%)	12 (9%)	4 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	I	125/130 (96%)	99 (79%)	20 (16%)	6 (5%)	2	14
9	J	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	0	6
10	K	115/129 (89%)	101 (88%)	13 (11%)	1 (1%)	14	43
11	L	121/124 (98%)	100 (83%)	16 (13%)	5 (4%)	2	17
12	M	111/118 (94%)	100 (90%)	9 (8%)	2 (2%)	6	30
13	N	92/101 (91%)	78 (85%)	7 (8%)	7 (8%)	1	7
14	O	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5	26
15	P	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	3
16	Q	78/84 (93%)	67 (86%)	9 (12%)	2 (3%)	4	23
17	R	53/75 (71%)	49 (92%)	4 (8%)	0	100	100
18	S	77/92 (84%)	66 (86%)	9 (12%)	2 (3%)	4	23
19	T	83/87 (95%)	78 (94%)	3 (4%)	2 (2%)	4	25
20	U	49/71 (69%)	39 (80%)	6 (12%)	4 (8%)	0	6
21	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
22	1	60/63 (95%)	51 (85%)	7 (12%)	2 (3%)	3	20
23	2	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	30
24	3	54/57 (95%)	49 (91%)	3 (6%)	2 (4%)	2	18
25	4	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
26	6	44/46 (96%)	41 (93%)	1 (2%)	2 (4%)	2	15
27	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
28	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
29	c	269/273 (98%)	252 (94%)	16 (6%)	1 (0%)	30	59
30	d	207/209 (99%)	195 (94%)	10 (5%)	2 (1%)	12	41
31	e	199/201 (99%)	186 (94%)	5 (2%)	8 (4%)	2	17
32	f	175/179 (98%)	154 (88%)	15 (9%)	6 (3%)	3	20
33	g	174/177 (98%)	139 (80%)	30 (17%)	5 (3%)	3	22
34	h	147/149 (99%)	120 (82%)	19 (13%)	8 (5%)	1	13
35	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	34
36	k	120/123 (98%)	112 (93%)	6 (5%)	2 (2%)	7	31
37	l	142/144 (99%)	128 (90%)	9 (6%)	5 (4%)	3	20
38	m	131/136 (96%)	125 (95%)	5 (4%)	1 (1%)	16	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	n	118/127 (93%)	111 (94%)	4 (3%)	3 (2%)	4	24
40	o	114/117 (97%)	107 (94%)	2 (2%)	5 (4%)	2	15
41	p	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	14	43
42	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
43	r	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	12	41
44	s	108/110 (98%)	103 (95%)	2 (2%)	3 (3%)	4	22
45	t	91/100 (91%)	82 (90%)	6 (7%)	3 (3%)	3	20
46	u	100/104 (96%)	82 (82%)	12 (12%)	6 (6%)	1	11
47	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
48	y	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
49	z	24/87 (28%)	21 (88%)	3 (12%)	0	100	100
All	All	5497/5903 (93%)	4898 (89%)	440 (8%)	159 (3%)	5	22

5 of 159 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	76	SER
2	C	7	ASN
2	C	61	LYS
4	E	99	SER
4	E	146	MET

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	B	180/199 (90%)	180 (100%)	0	100	100
2	C	170/190 (90%)	170 (100%)	0	100	100
3	D	172/173 (99%)	172 (100%)	0	100	100
4	E	113/126 (90%)	113 (100%)	0	100	100
5	F	87/112 (78%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G	123/129 (95%)	123 (100%)	0	100	100
7	H	104/105 (99%)	104 (100%)	0	100	100
8	I	105/107 (98%)	105 (100%)	0	100	100
9	J	86/90 (96%)	86 (100%)	0	100	100
10	K	90/99 (91%)	90 (100%)	0	100	100
11	L	103/104 (99%)	103 (100%)	0	100	100
12	M	91/96 (95%)	91 (100%)	0	100	100
13	N	79/84 (94%)	79 (100%)	0	100	100
14	O	76/77 (99%)	76 (100%)	0	100	100
15	P	65/65 (100%)	53 (82%)	12 (18%)	1	10
16	Q	74/78 (95%)	74 (100%)	0	100	100
17	R	48/65 (74%)	48 (100%)	0	100	100
18	S	70/79 (89%)	70 (100%)	0	100	100
19	T	65/66 (98%)	65 (100%)	0	100	100
20	U	44/61 (72%)	44 (100%)	0	100	100
21	0	67/68 (98%)	64 (96%)	3 (4%)	24	48
22	1	54/55 (98%)	51 (94%)	3 (6%)	19	43
23	2	48/49 (98%)	46 (96%)	2 (4%)	26	49
24	3	47/48 (98%)	45 (96%)	2 (4%)	26	49
25	4	45/49 (92%)	43 (96%)	2 (4%)	25	48
26	6	38/38 (100%)	33 (87%)	5 (13%)	4	18
27	7	51/52 (98%)	51 (100%)	0	100	100
28	8	34/34 (100%)	34 (100%)	0	100	100
29	c	216/218 (99%)	210 (97%)	6 (3%)	38	57
30	d	164/164 (100%)	155 (94%)	9 (6%)	19	44
31	e	165/165 (100%)	157 (95%)	8 (5%)	23	46
32	f	148/150 (99%)	140 (95%)	8 (5%)	20	44
33	g	137/138 (99%)	132 (96%)	5 (4%)	31	52
34	h	114/114 (100%)	112 (98%)	2 (2%)	51	64
35	j	116/116 (100%)	111 (96%)	5 (4%)	26	49
36	k	103/104 (99%)	99 (96%)	4 (4%)	28	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	l	103/103 (100%)	100 (97%)	3 (3%)	37	56
38	m	108/109 (99%)	106 (98%)	2 (2%)	50	64
39	n	100/103 (97%)	97 (97%)	3 (3%)	36	55
40	o	86/87 (99%)	81 (94%)	5 (6%)	18	43
41	p	99/100 (99%)	95 (96%)	4 (4%)	28	50
42	q	89/90 (99%)	87 (98%)	2 (2%)	45	61
43	r	84/84 (100%)	78 (93%)	6 (7%)	13	38
44	s	93/93 (100%)	91 (98%)	2 (2%)	45	61
45	t	80/84 (95%)	75 (94%)	5 (6%)	16	41
46	u	83/85 (98%)	78 (94%)	5 (6%)	17	42
47	w	78/78 (100%)	73 (94%)	5 (6%)	16	40
48	y	56/63 (89%)	56 (100%)	0	100	100
49	z	21/62 (34%)	9 (43%)	12 (57%)	0	0
All	All	4572/4808 (95%)	4442 (97%)	130 (3%)	38	57

5 of 130 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	w	29	ILE
49	z	6	LEU
31	e	109	LEU
31	e	108	ILE
49	z	8	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
28	8	37	GLN
36	k	88	ASN
30	d	49	GLN
34	h	28	ASN
39	n	73	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	A	1530/1542 (99%)	427 (27%)	36 (2%)
51	X	11/11 (100%)	7 (63%)	2 (18%)
52	a	116/120 (96%)	40 (34%)	0
53	b	2902/2904 (99%)	1245 (42%)	0
54	v	75/76 (98%)	27 (36%)	0
All	All	4634/4653 (99%)	1746 (37%)	38 (0%)

5 of 1746 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	A	6	G
50	A	7	A
50	A	8	A
50	A	9	G
50	A	11	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	A	1302	C
50	A	1527	U
50	A	1332	A
50	A	1348	U
51	X	14	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 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	b	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	1087:G	O3'	1088:A	P	1.81
1	b	2055:C	O3'	2056:G	P	1.80

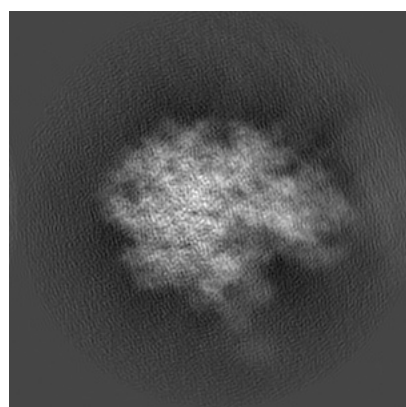
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6483. These allow visual inspection of the internal detail of the map and identification of artifacts.

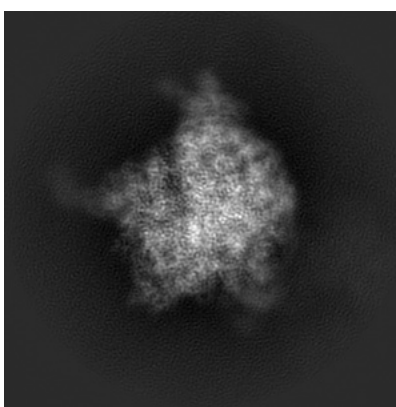
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

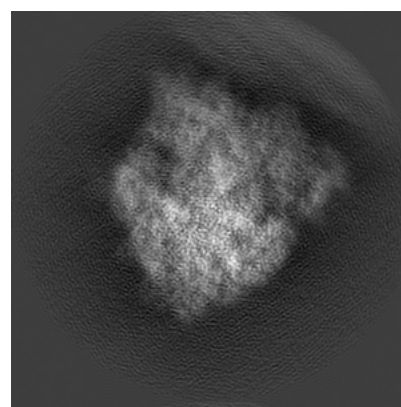
6.1.1 Primary map



X



Y

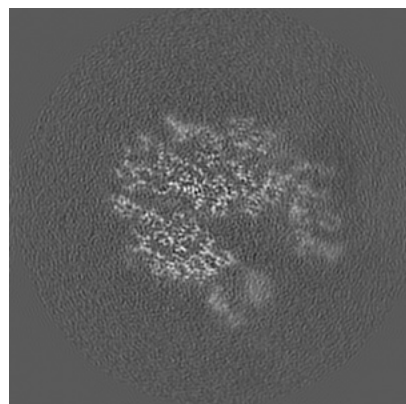


Z

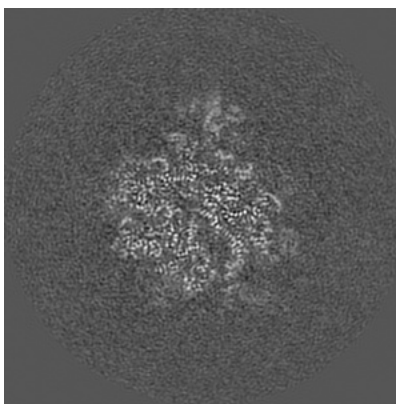
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

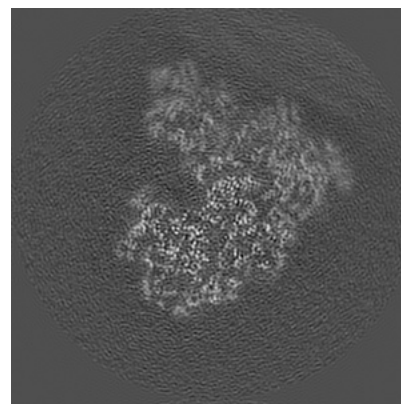
6.2.1 Primary map



X Index: 160



Y Index: 160

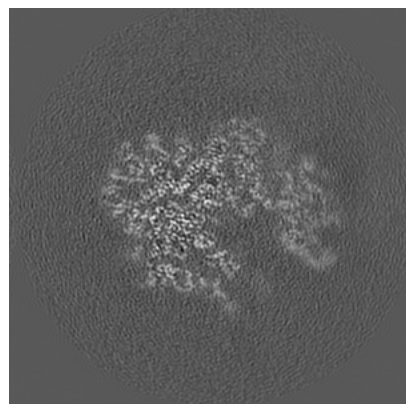


Z Index: 160

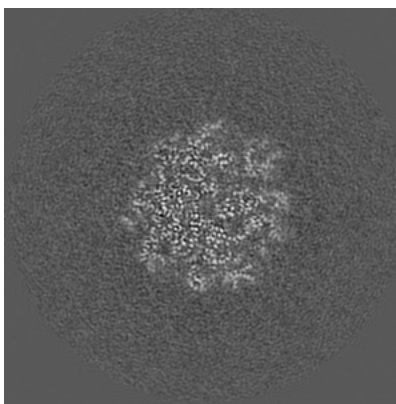
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

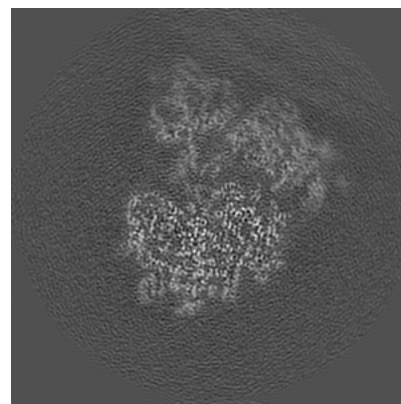
6.3.1 Primary map



X Index: 153



Y Index: 138

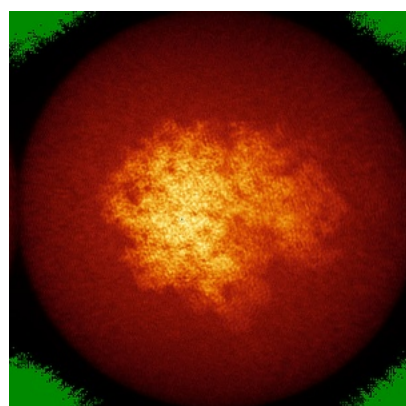


Z Index: 153

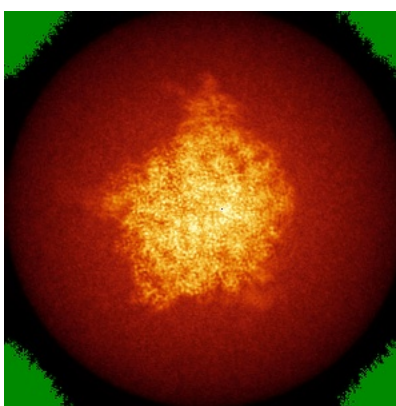
The images above show the largest variance slices of the map in three orthogonal directions.

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

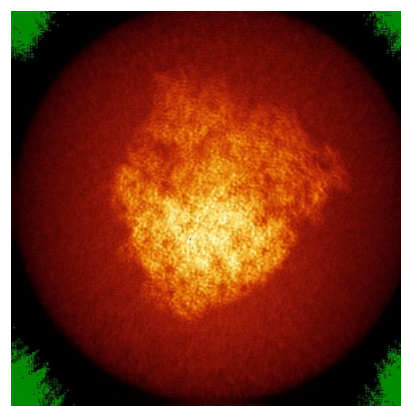
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

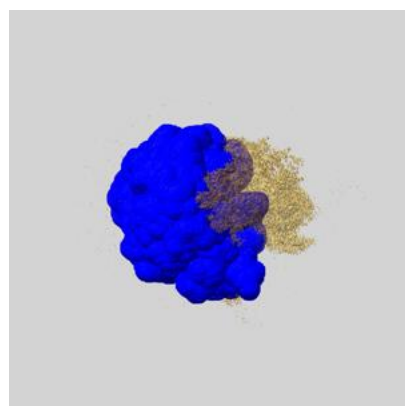
6.6 Mask visualisation [i](#)

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

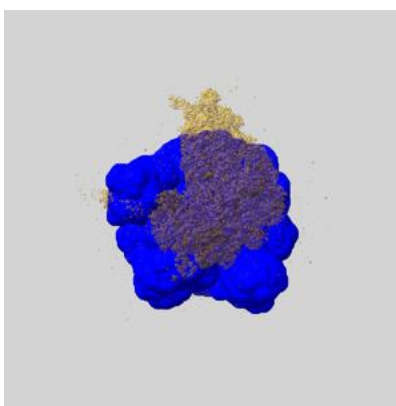
A mask typically either:

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

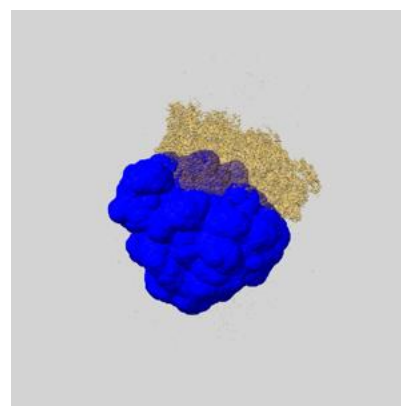
6.6.1 emd_6483_msk_1.map [i](#)



X



Y

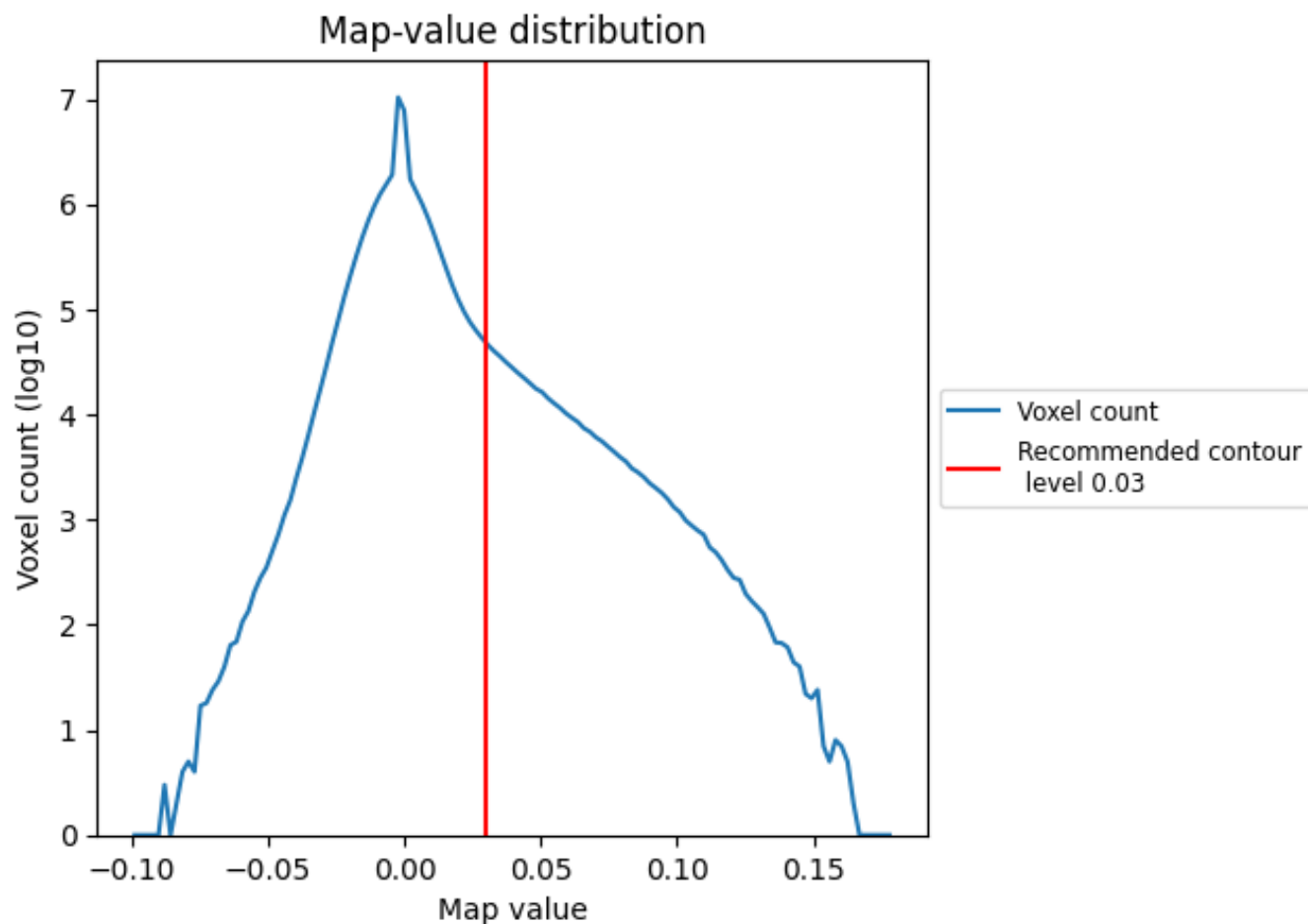


Z

7 Map analysis [i](#)

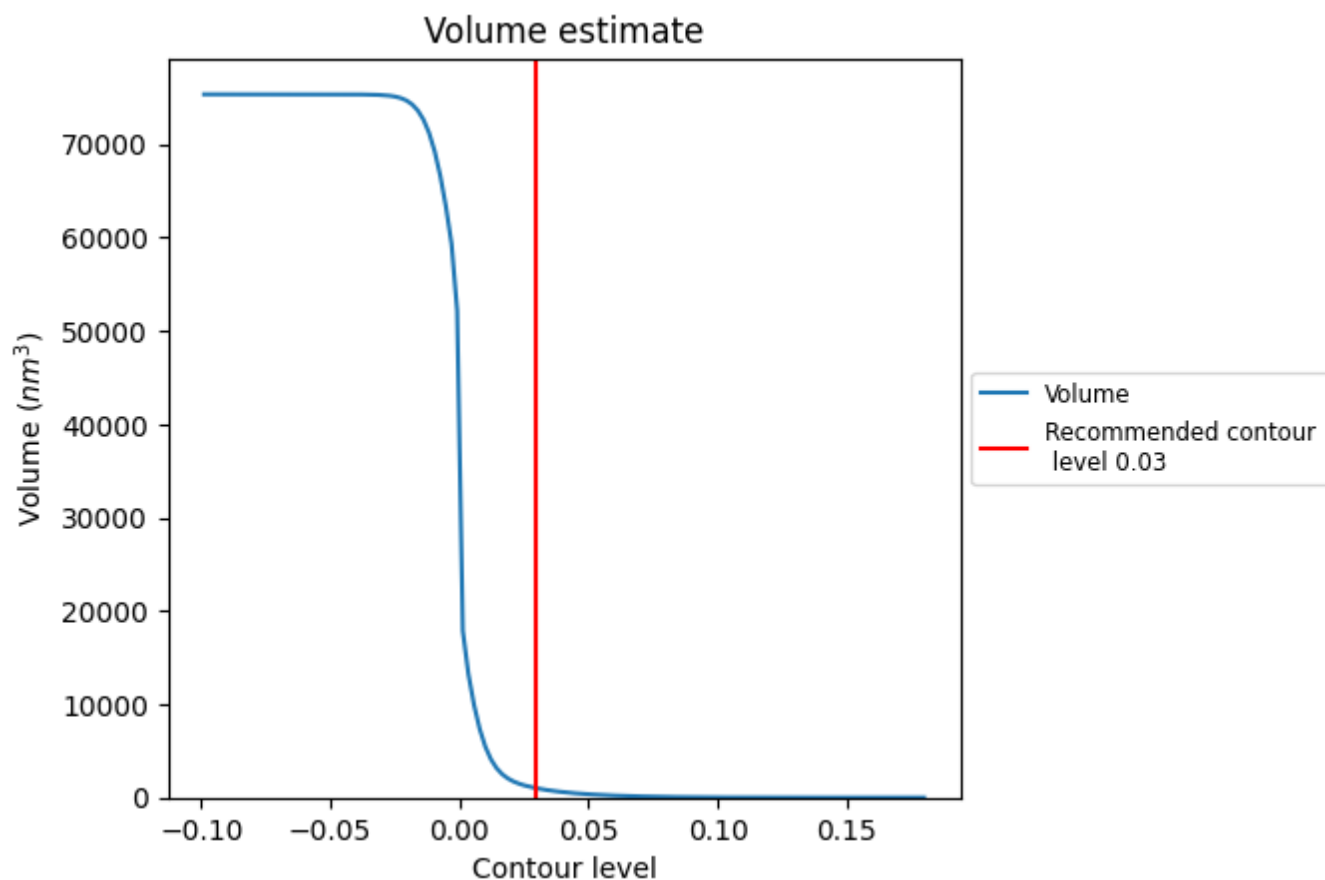
This section contains the results of statistical analysis of the map.

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.

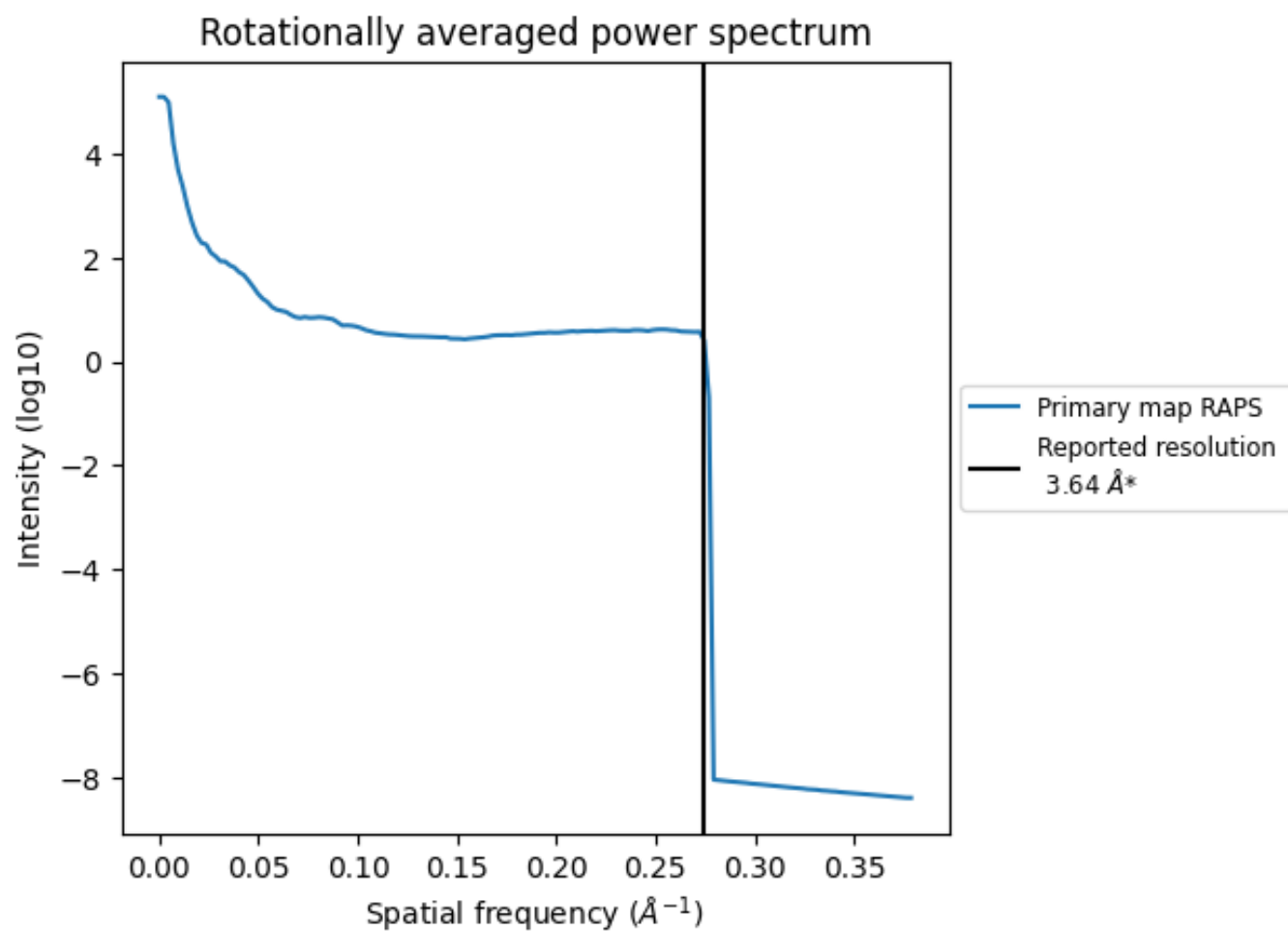
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 995 nm³; this corresponds to an approximate mass of 899 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 ⓘ

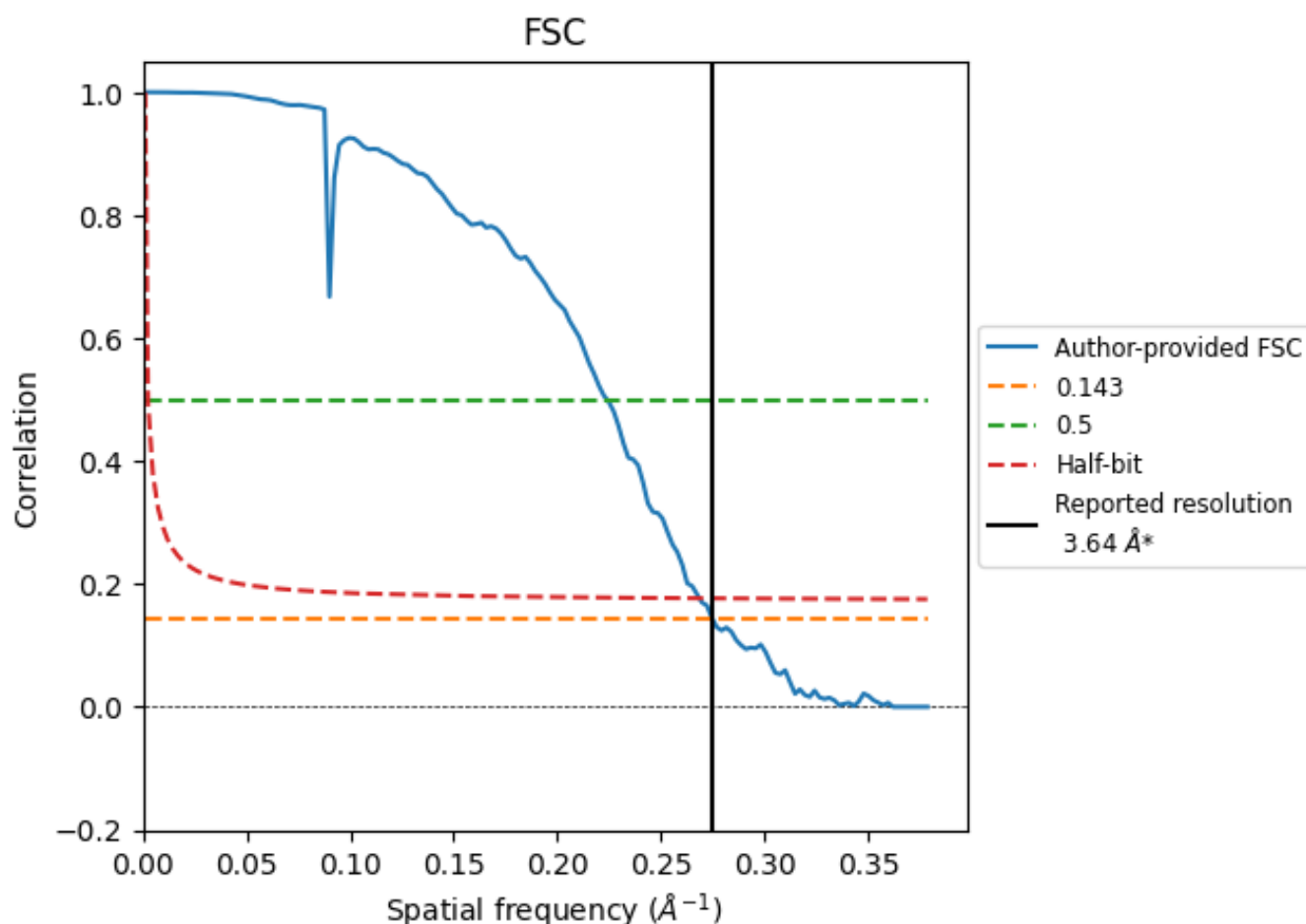


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

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 0.275 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.64	4.46	3.72
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

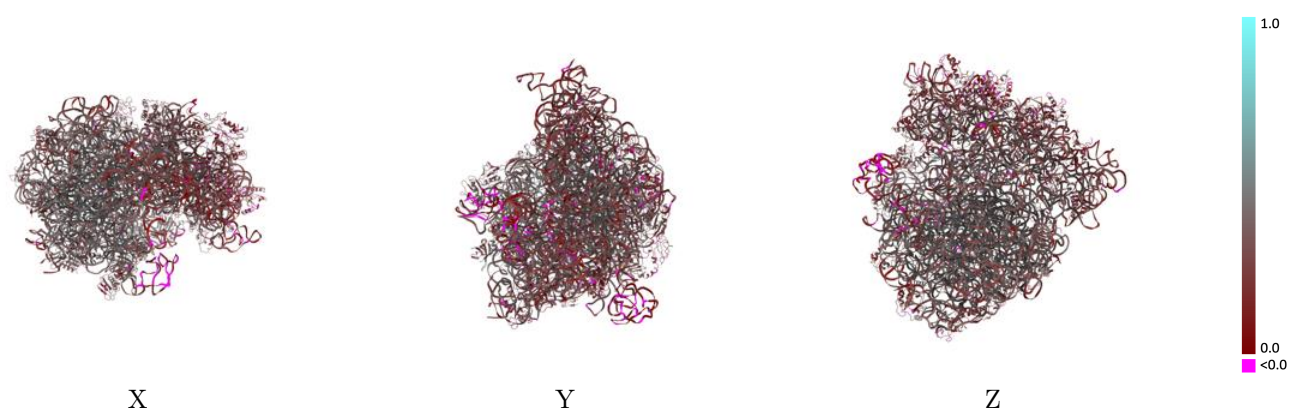
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-6483 and PDB model 3JBU. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay ⓘ

This section was not generated.

9.2 Q-score mapped to coordinate model ⓘ

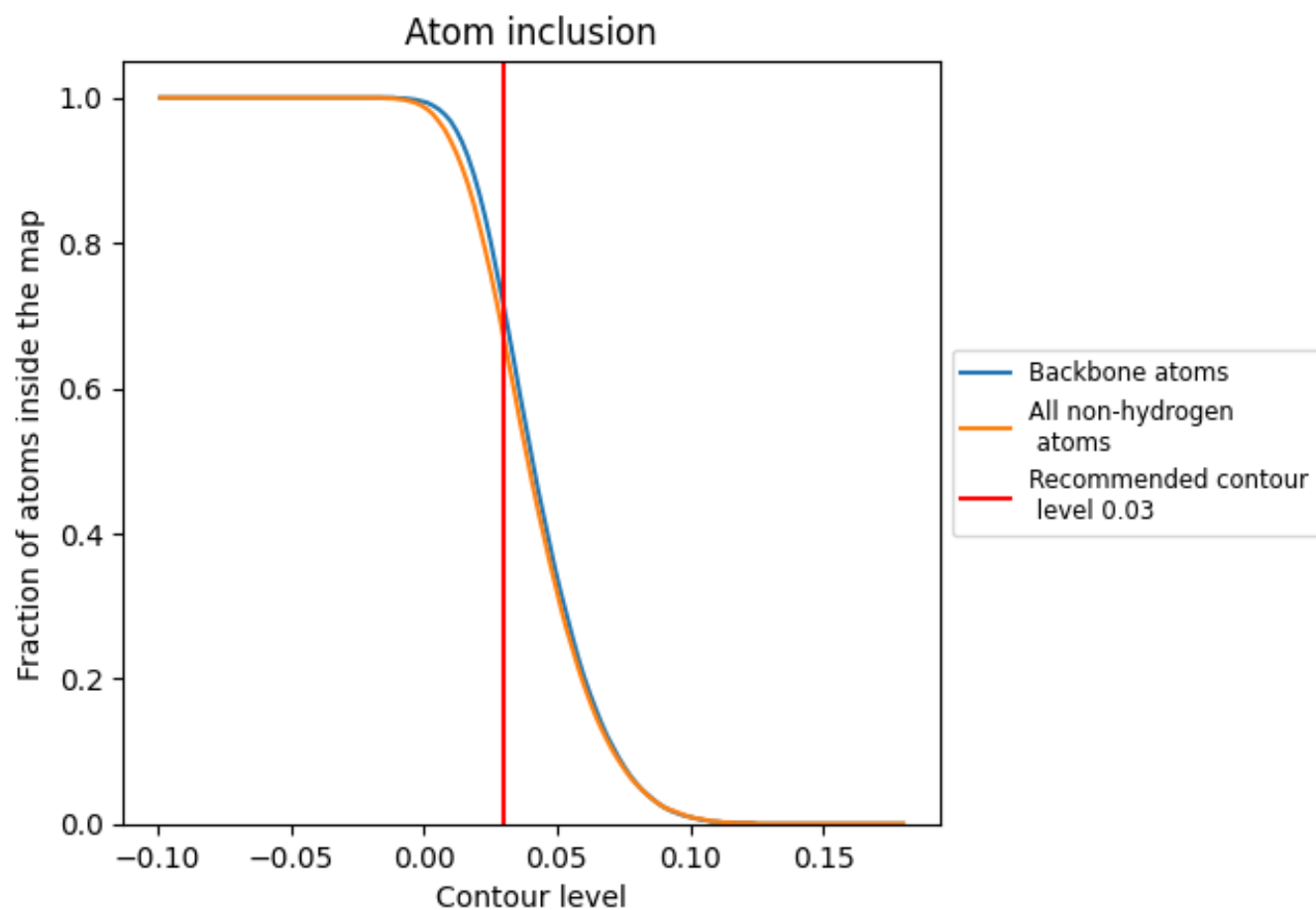


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 67% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6710	 0.3410
0	 0.6670	 0.3850
1	 0.4720	 0.2700
2	 0.6660	 0.3800
3	 0.6280	 0.3380
4	 0.6230	 0.3710
6	 0.7470	 0.4140
7	 0.7350	 0.4340
8	 0.6880	 0.4020
A	 0.6530	 0.3220
B	 0.1160	 0.2000
C	 0.1570	 0.1960
D	 0.1660	 0.1960
E	 0.2730	 0.2450
F	 0.4640	 0.3230
G	 0.3450	 0.2520
H	 0.2660	 0.2590
I	 0.2180	 0.1810
J	 0.1410	 0.1890
K	 0.4950	 0.3390
L	 0.4650	 0.3250
M	 0.3820	 0.2680
N	 0.2220	 0.2110
O	 0.5200	 0.2980
P	 0.3000	 0.2170
Q	 0.4000	 0.2910
R	 0.4380	 0.3410
S	 0.3240	 0.2680
T	 0.4570	 0.2500
U	 0.3130	 0.2140
X	 0.4480	 0.2590
a	 0.8220	 0.3620
b	 0.8130	 0.3760
c	 0.7110	 0.3900
d	 0.6570	 0.3880



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Chain	Atom inclusion	Q-score
e	 0.5800	 0.3340
f	 0.5290	 0.2630
g	 0.4890	 0.3040
h	 0.2420	 0.1940
j	 0.6860	 0.3860
k	 0.6070	 0.3850
l	 0.6440	 0.3720
m	 0.6620	 0.3920
n	 0.6630	 0.3710
o	 0.5840	 0.2880
p	 0.5890	 0.3400
q	 0.7090	 0.3910
r	 0.6050	 0.3710
s	 0.6590	 0.3890
t	 0.5650	 0.3130
u	 0.5060	 0.2760
v	 0.5580	 0.2800
w	 0.6060	 0.3440
y	 0.7050	 0.4020
z	 0.1850	 0.3150