



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 07:50 AM UTC

PDB ID : 6T59 / pdb_00006t59
EMDB ID : EMD-10380
Title : Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 and nascent chain-associated complex
Authors : Lin, Z.; Gasic, I.; Chandrasekaran, V.; Peters, N.; Shao, S.; Ramakrishnan, V.; Mitchison, T.J.; Hegde, R.S.
Deposited on : 2019-10-15
Resolution : 3.11 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

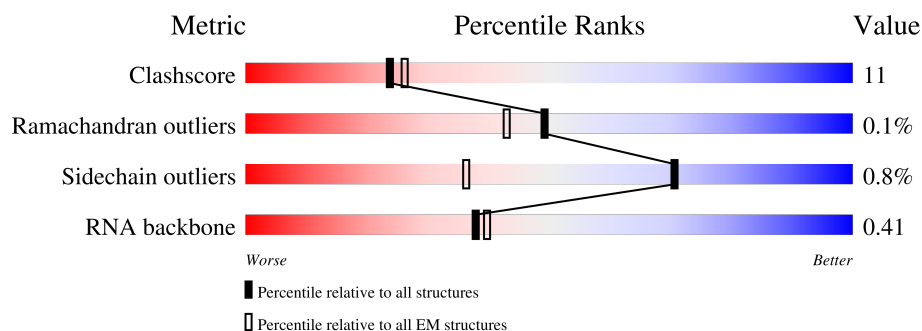
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	A3	257	85% 67% 30% .
2	B3	403	79% 68% 29% .
3	C3	425	68% 62% 23% 15%
4	D3	297	70% 75% 24% .
5	E3	291	62% 53% 21% 26%
6	F3	247	75% 68% 23% 9%
7	G3	319	57% 54% 19% 27%

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Mol	Chain	Length	Quality of chain
8	H3	192	
9	I3	214	
10	J3	178	
11	L3	211	
12	M3	218	
13	N3	204	
14	O3	203	
15	P3	184	
16	Q3	188	
17	R3	196	
18	S3	176	
19	T3	160	
20	U3	128	
21	V3	140	
22	W3	157	
23	X3	156	
24	Y3	145	
25	Z3	136	
26	a3	148	
27	b3	226	
28	c3	115	
29	d3	125	
30	e3	135	
31	f3	110	
32	g3	116	

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Mol	Chain	Length	Quality of chain
33	h3	123	
34	i3	105	
35	j3	97	
36	k3	70	
37	l3	51	
38	m3	102	
39	n3	25	
40	o3	106	
41	p3	92	
42	r3	137	
43	s3	318	
44	t3	165	
45	23	76	
46	54	3543	
47	74	120	
48	84	156	
49	NI	29	
50	NA	215	
51	NB	206	
52	TT	440	
53	1	64	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 143047 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B3	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D3	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D3	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E3	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called Ul30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F3	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	61	ARG	GLY	conflict	UNP G1TUB1
F3	93	ARG	GLY	conflict	UNP G1TUB1
F3	131	MET	VAL	conflict	UNP G1TUB1
F3	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J3	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M3	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N3	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O3	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P3	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q3	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R3	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S3	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T3	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U3	102	Total	C	N	O	S	0	0
			834	534	146	152	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V3	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W3	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X3	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y3	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z3	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a3	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a3	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b3	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c3	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d3	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e3	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f3	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g3	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h3	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i3	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j3	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k3	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k3	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l3	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m3	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n3	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o3	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p3	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r3	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s3	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t3	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	23	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 46 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	54	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	74	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	84	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	NI	29	Total	C	N	O	0	0
			150	92	29	29		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	54	Total	C	N	O	S	0	0
			420	270	71	78	1		

- Molecule 51 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	58	Total	C	N	O	S	0	0
			444	278	76	88	2		

- Molecule 52 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	TT	426	Total	C	N	O	S	0	0
			3337	2097	580	647	13		

- Molecule 53 is a protein called Tubulin Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	36	Total	C	N	O	S	0	0
			292	184	51	55	2		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	P3	2	Total	Mg	0
			2	2	
54	V3	1	Total	Mg	0
			1	1	
54	a3	1	Total	Mg	0
			1	1	
54	g3	1	Total	Mg	0
			1	1	
54	j3	1	Total	Mg	0
			1	1	
54	54	201	Total	Mg	0
			201	201	
54	74	7	Total	Mg	0
			7	7	
54	84	6	Total	Mg	0
			6	6	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	g3	1	Total	Zn	0
			1	1	
55	j3	1	Total	Zn	0
			1	1	

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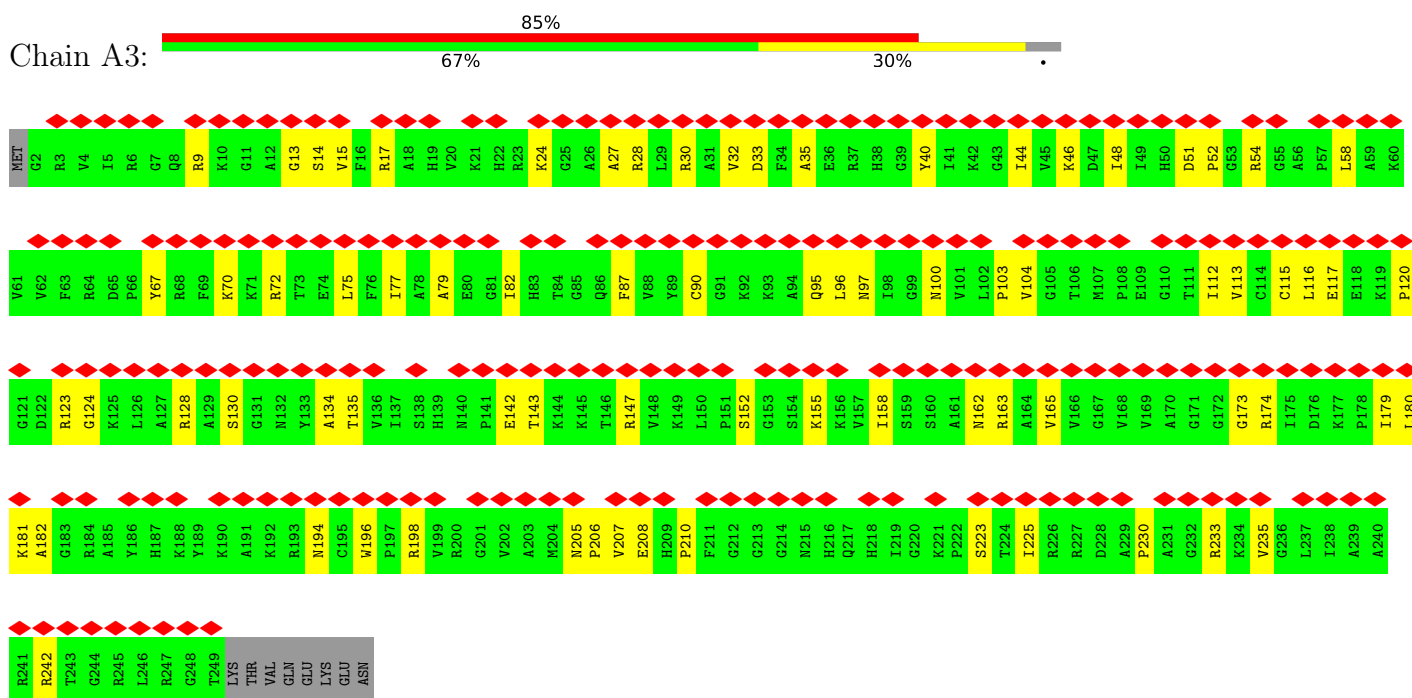
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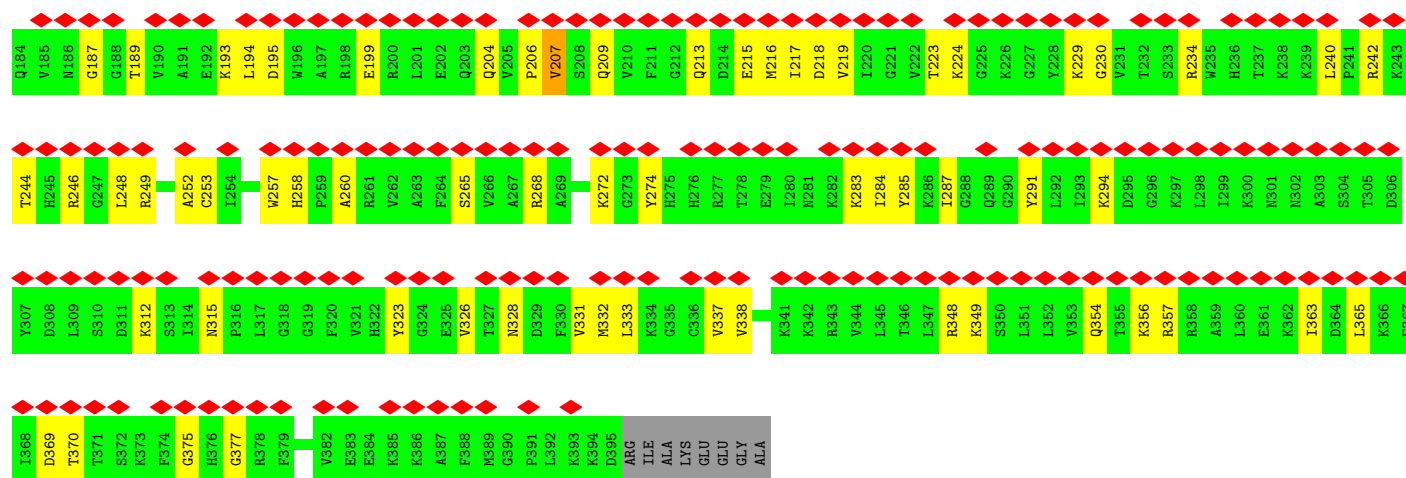
Mol	Chain	Residues	Atoms		AltConf
55	m3	1	Total 1	Zn 1	0
55	o3	1	Total 1	Zn 1	0
55	p3	1	Total 1	Zn 1	0

3 Residue-property plots

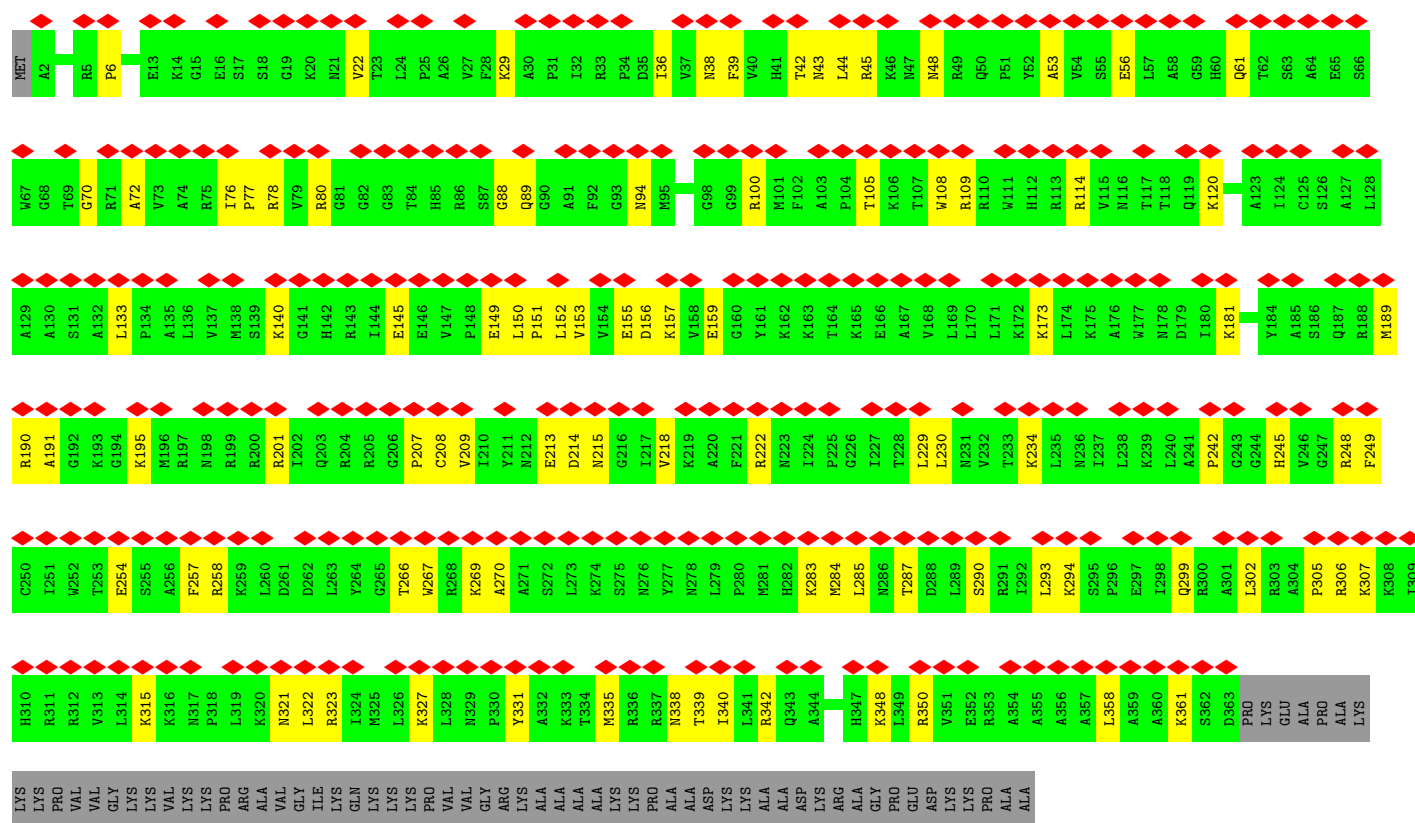
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Ribosomal protein L8

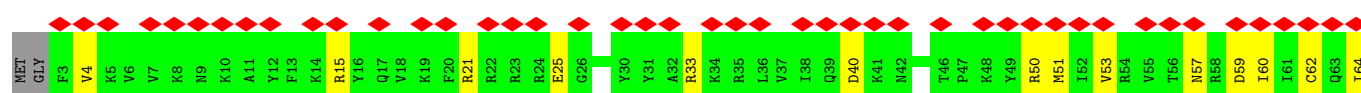
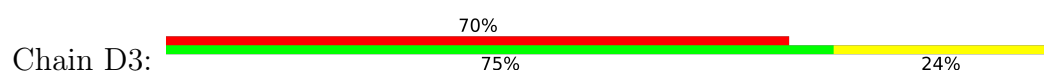


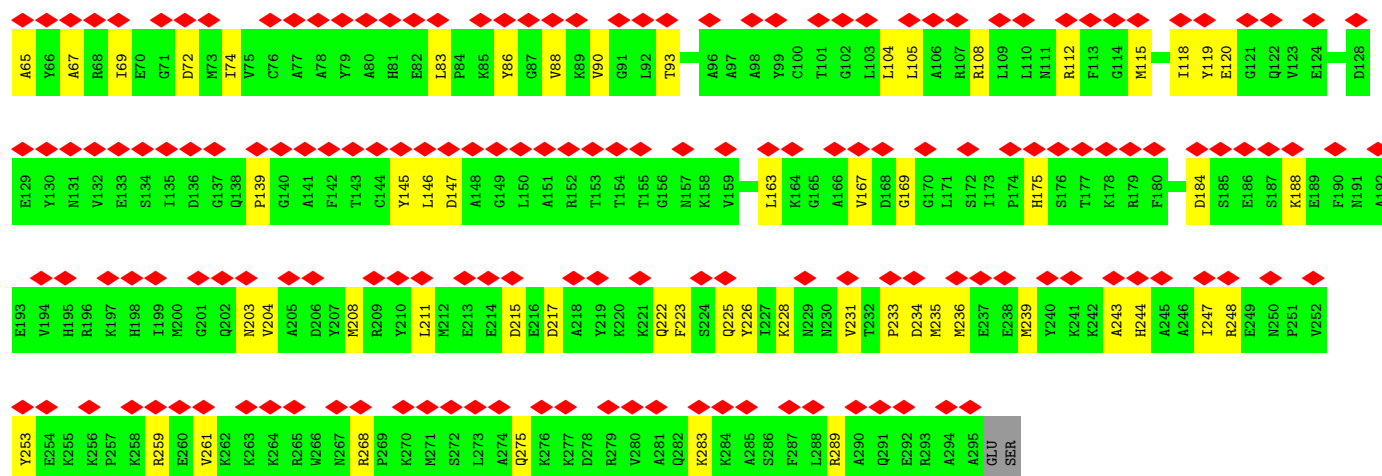


• Molecule 3: uL4

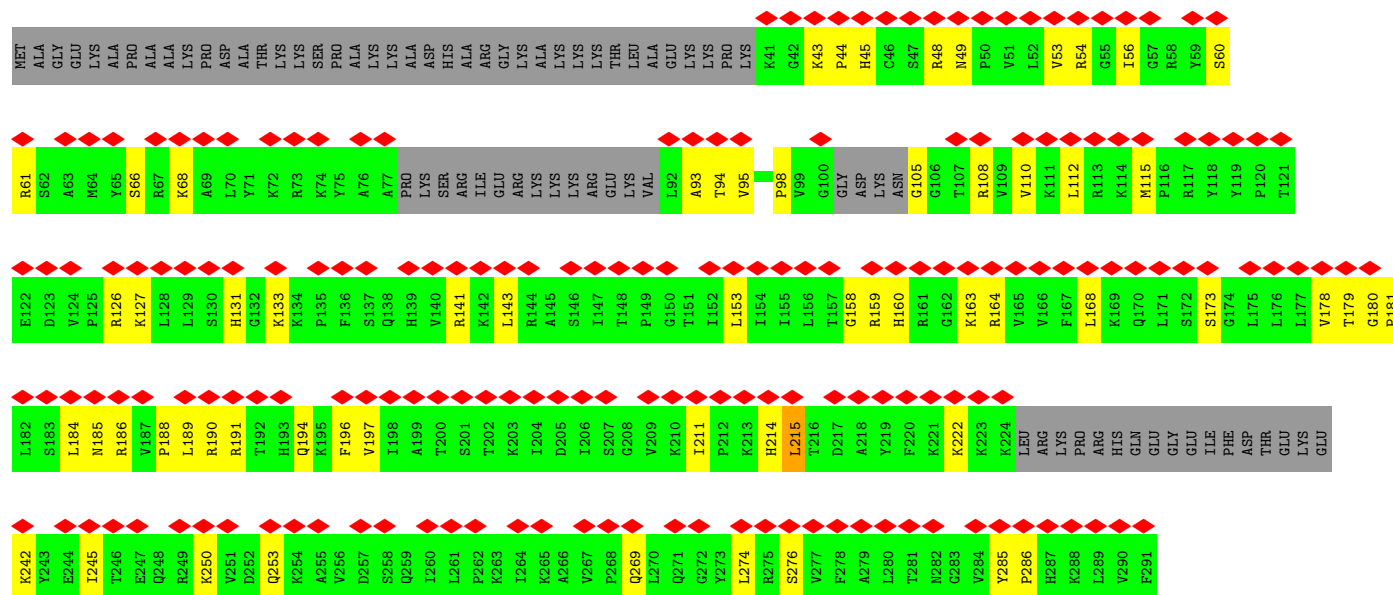


• Molecule 4: 60S ribosomal protein L5

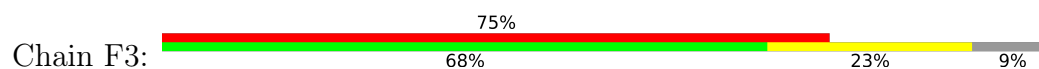


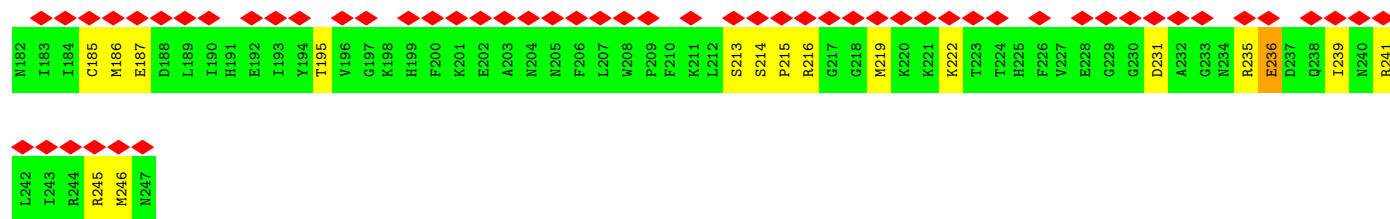


• Molecule 5: 60S ribosomal protein L6

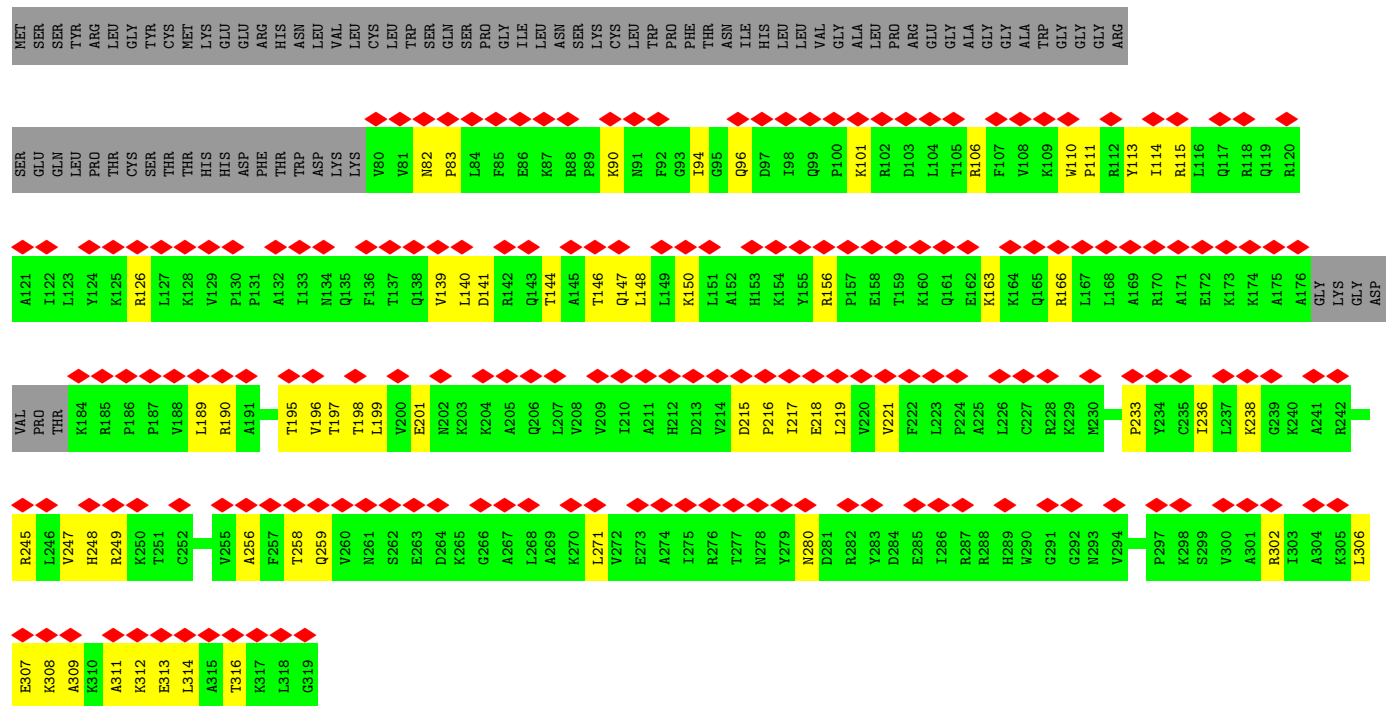


• Molecule 6: U130

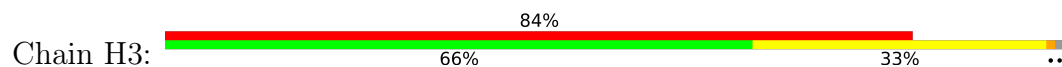




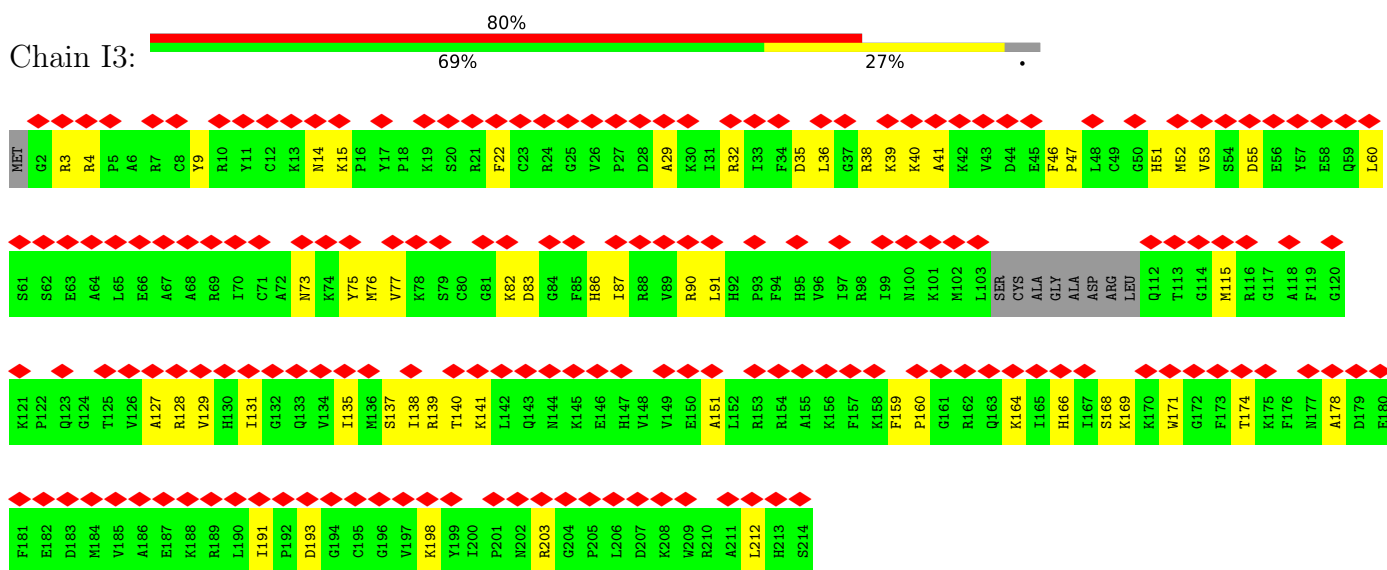
• Molecule 7: eL8



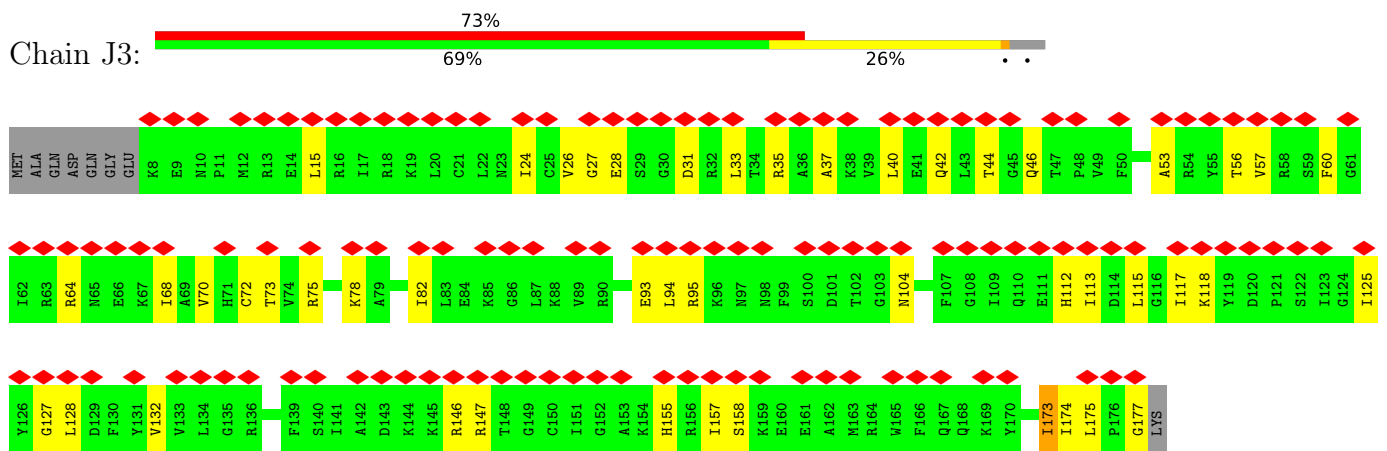
• Molecule 8: uL6



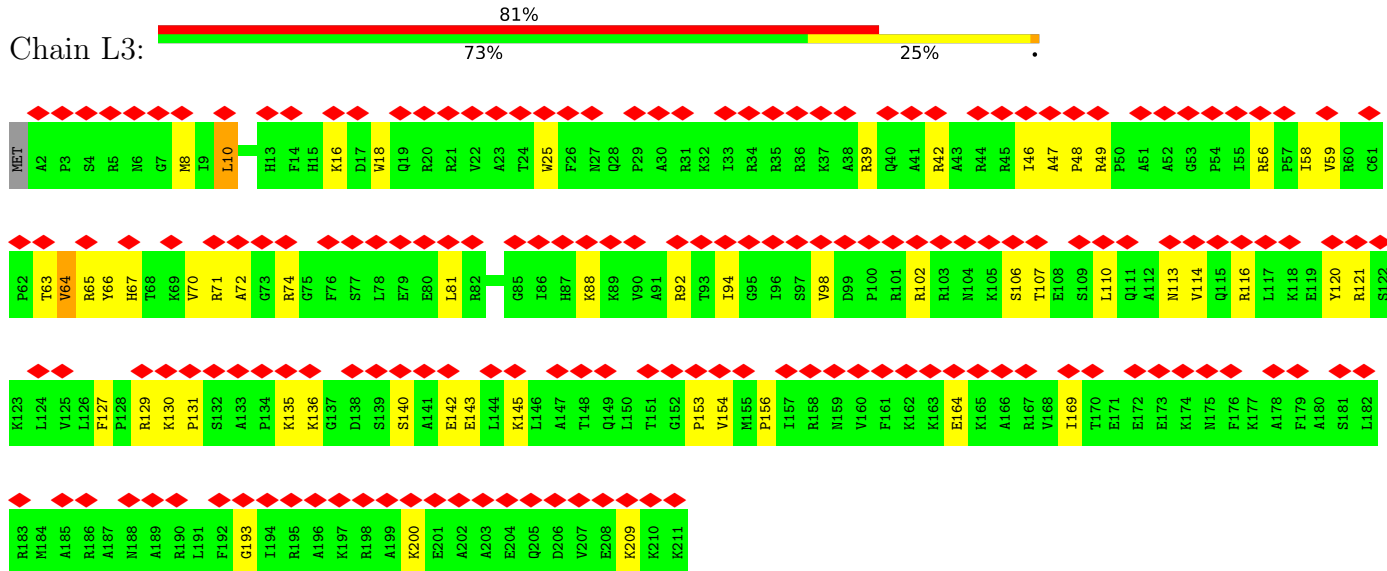
• Molecule 9: 60S ribosomal protein L10



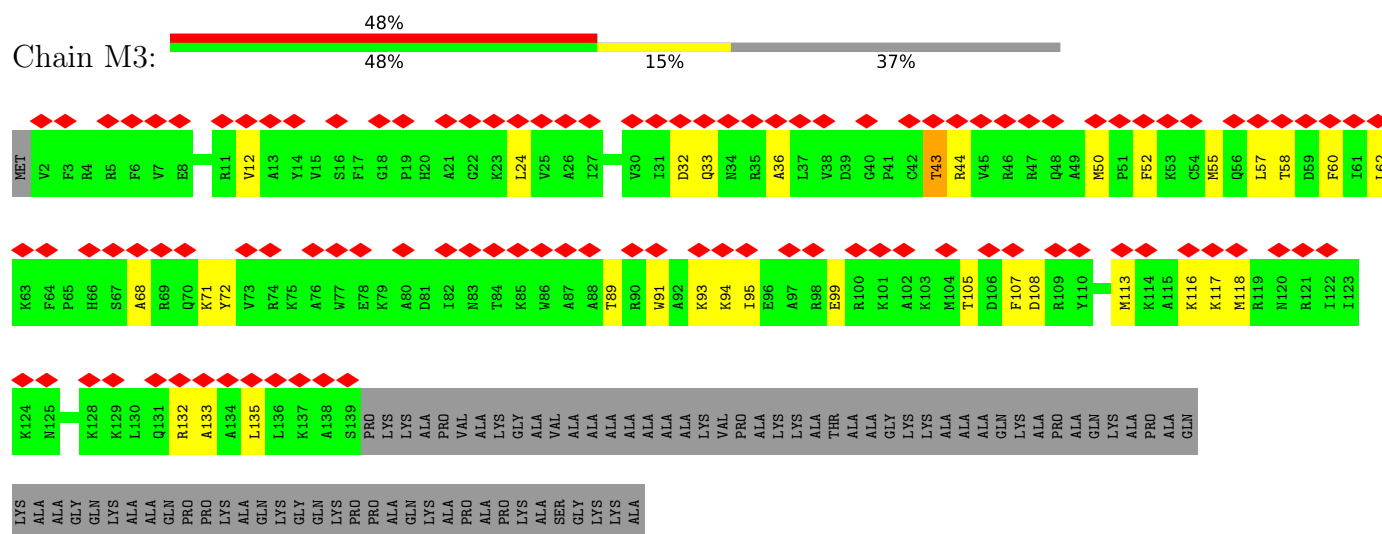
• Molecule 10: Ribosomal protein L11



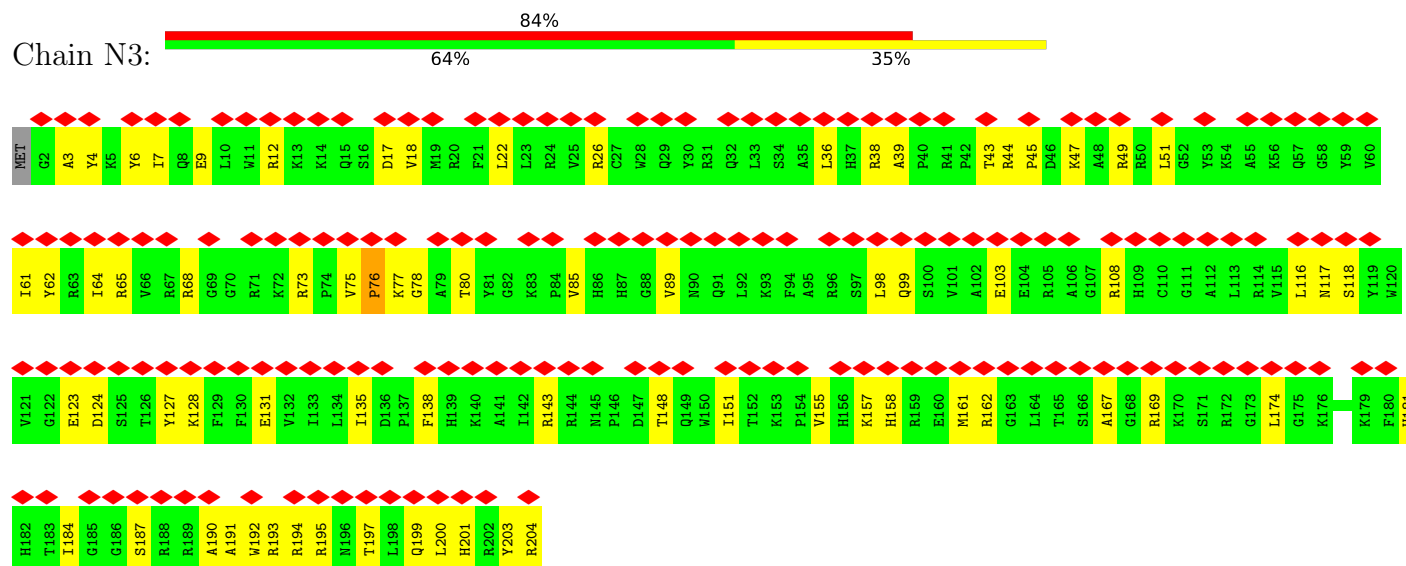
• Molecule 11: eL13



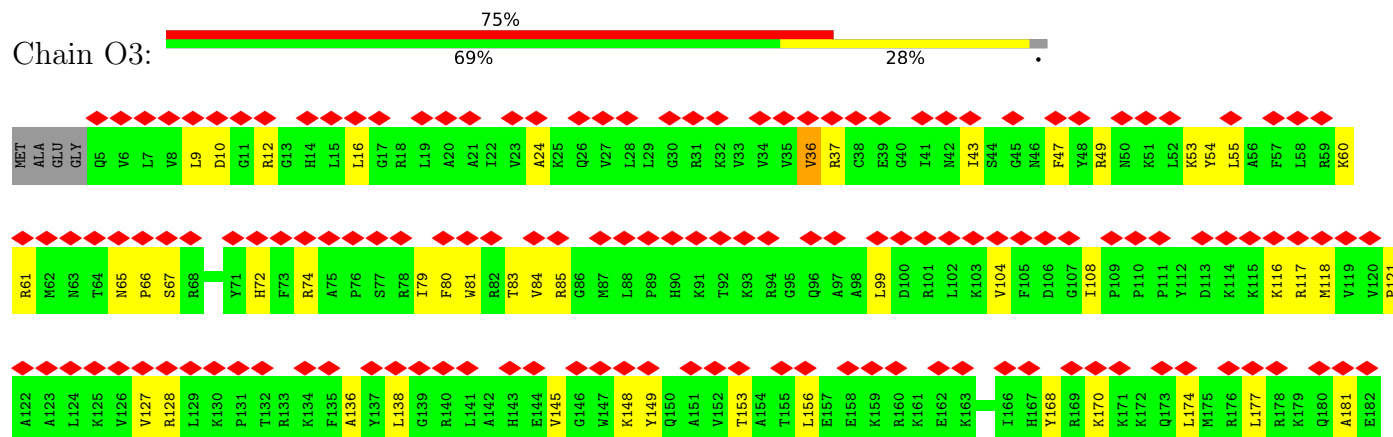
• Molecule 12: Ribosomal protein L14

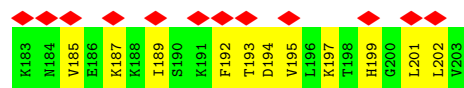


- Molecule 13: Ribosomal protein L15

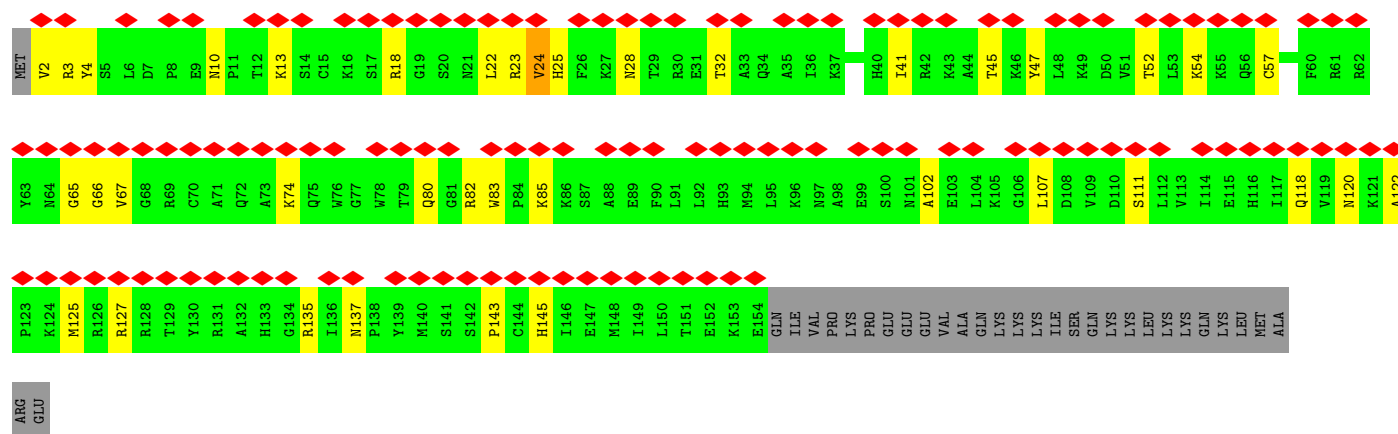


- Molecule 14: uL13

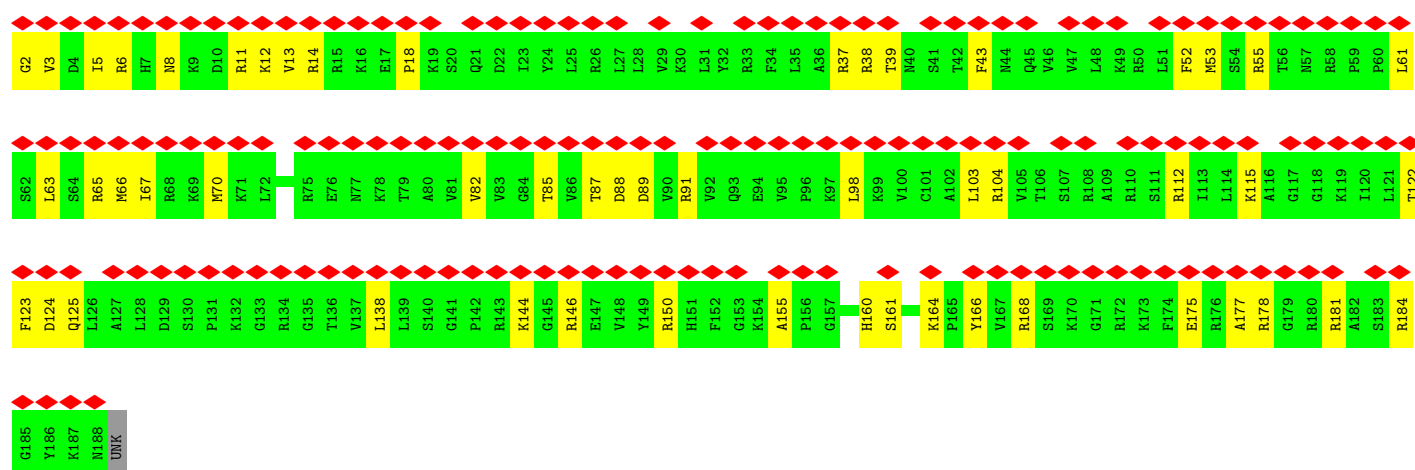
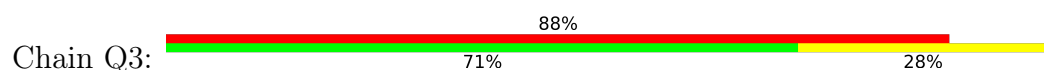




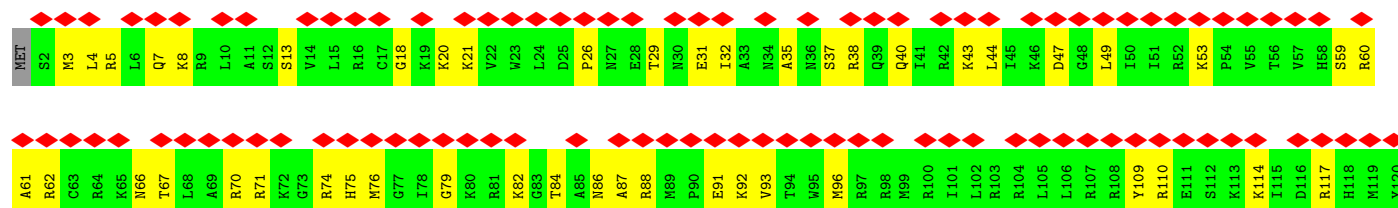
• Molecule 15: uL22



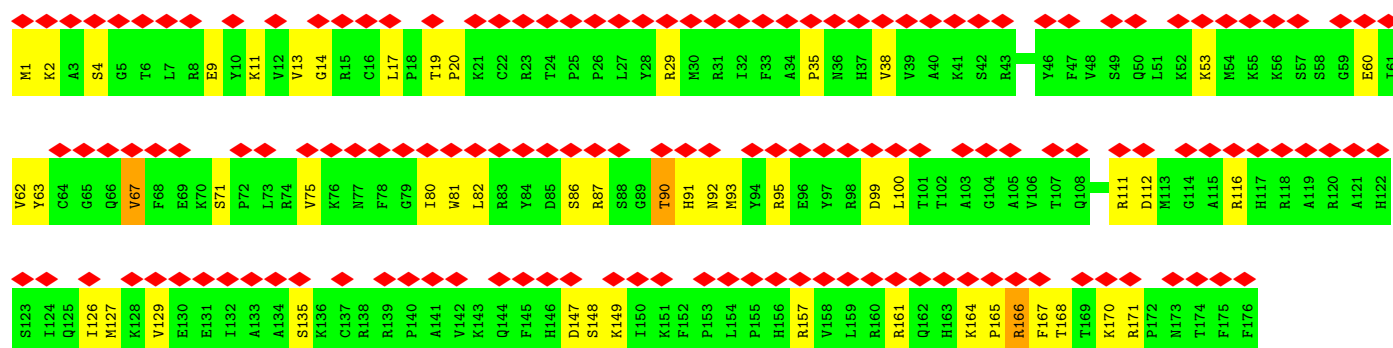
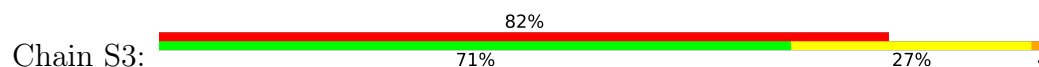
• Molecule 16: eL18



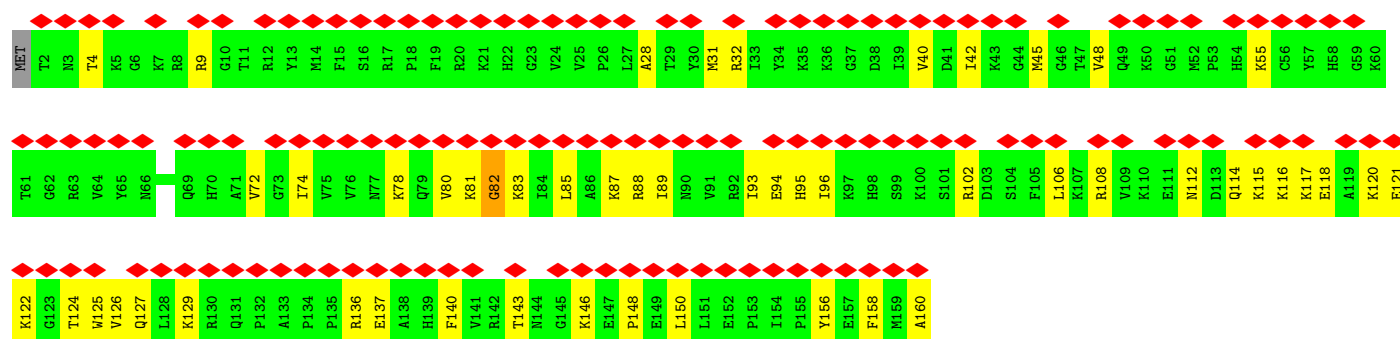
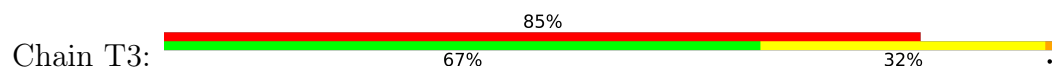
• Molecule 17: eL19



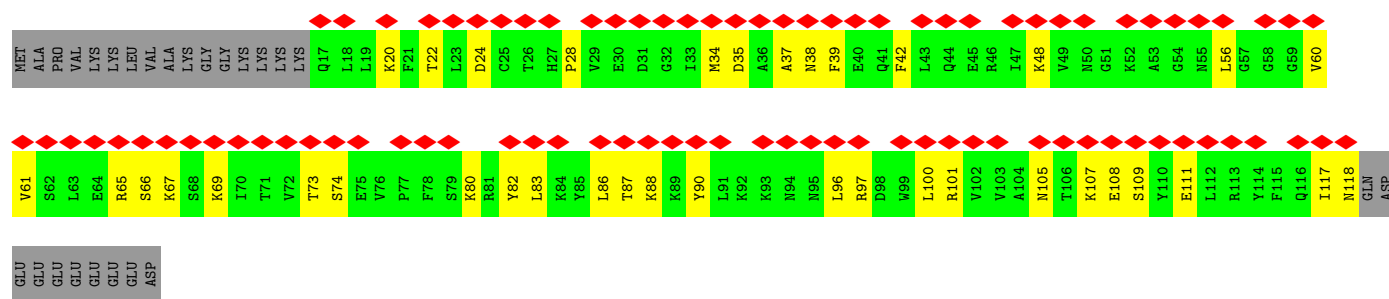
- Molecule 18: eL20



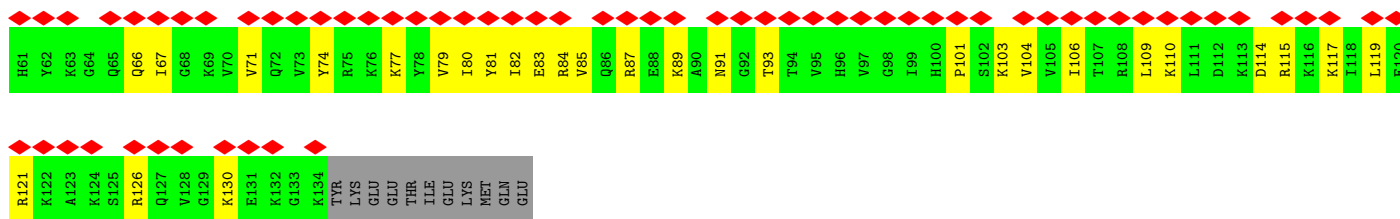
- Molecule 19: eL21



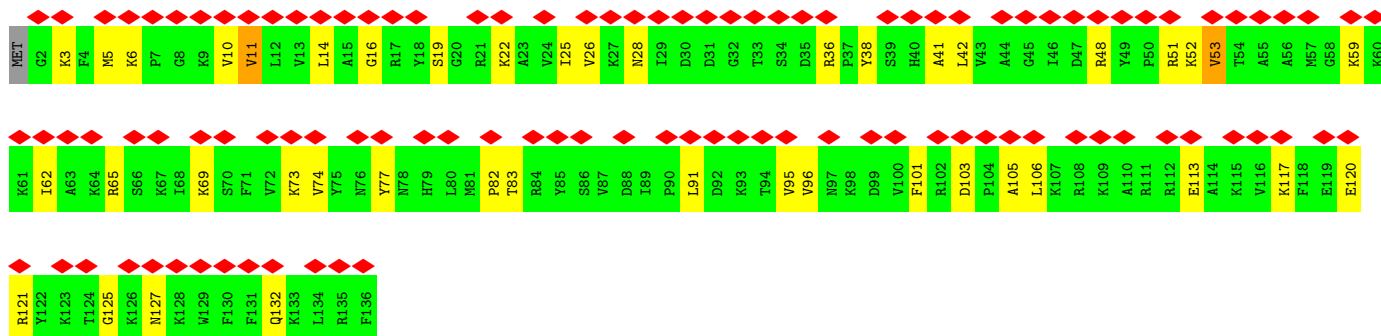
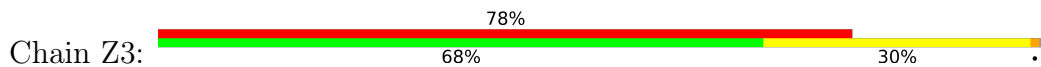
- Molecule 20: eL22



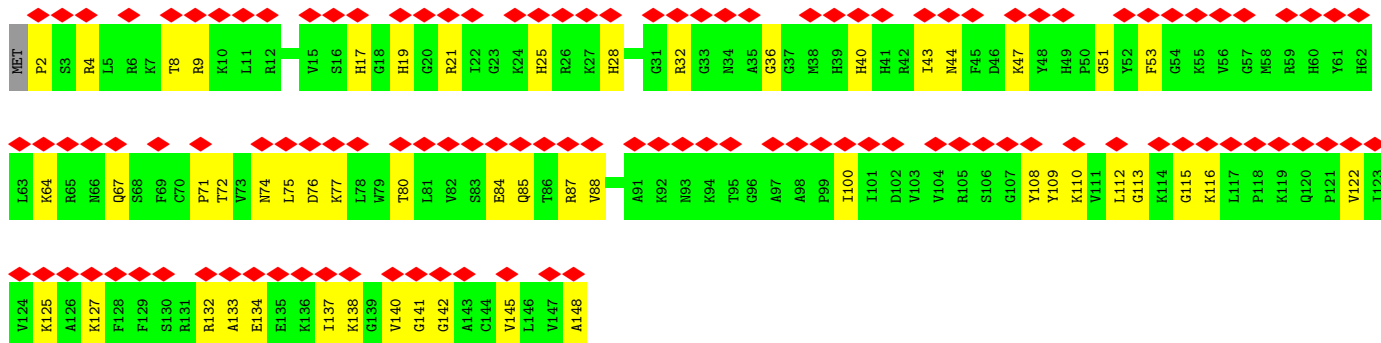
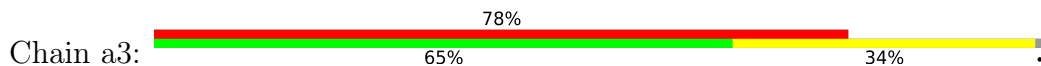
- Molecule 21: Ribosomal protein L23



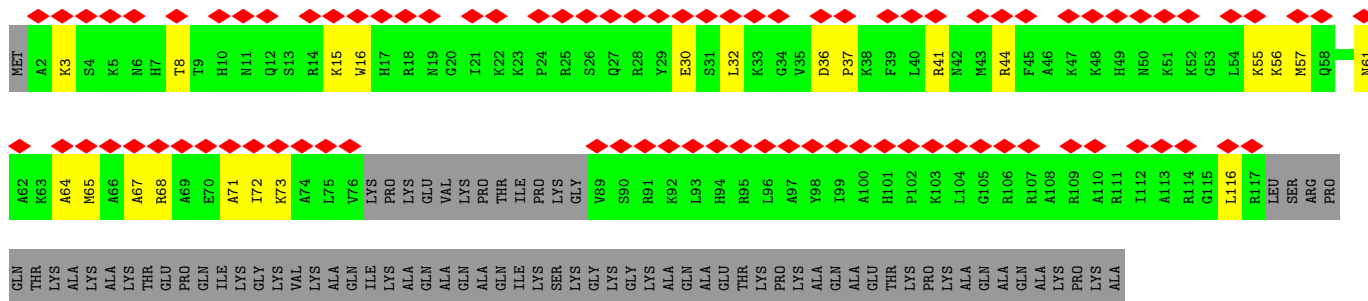
• Molecule 25: 60S ribosomal protein L27

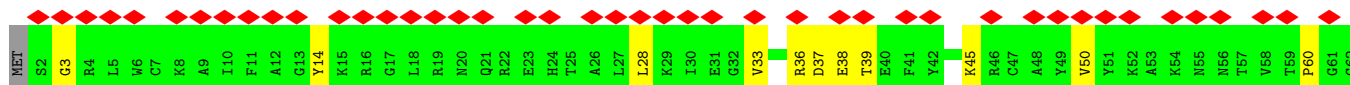
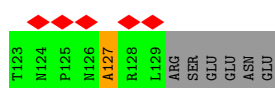
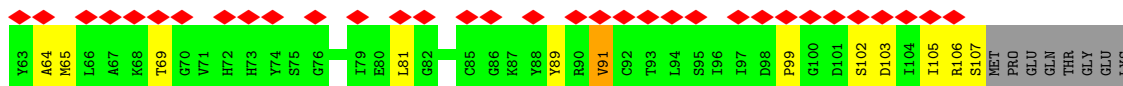


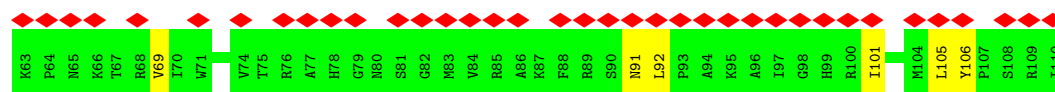
• Molecule 26: uL15



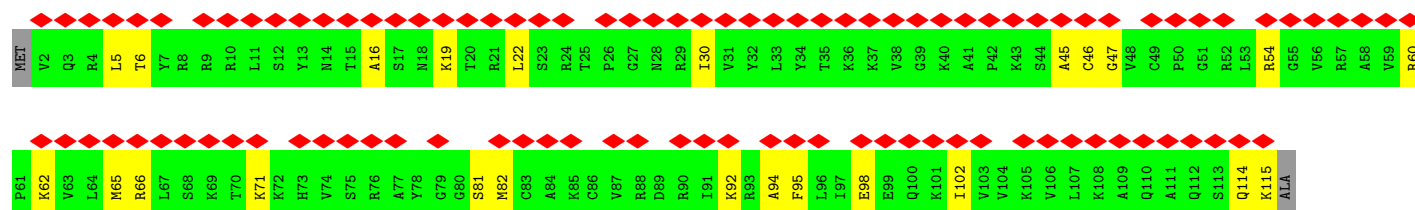
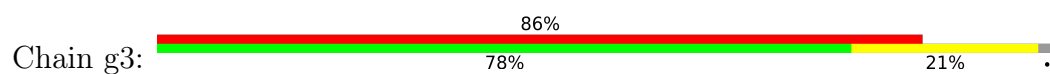
• Molecule 27: eL29



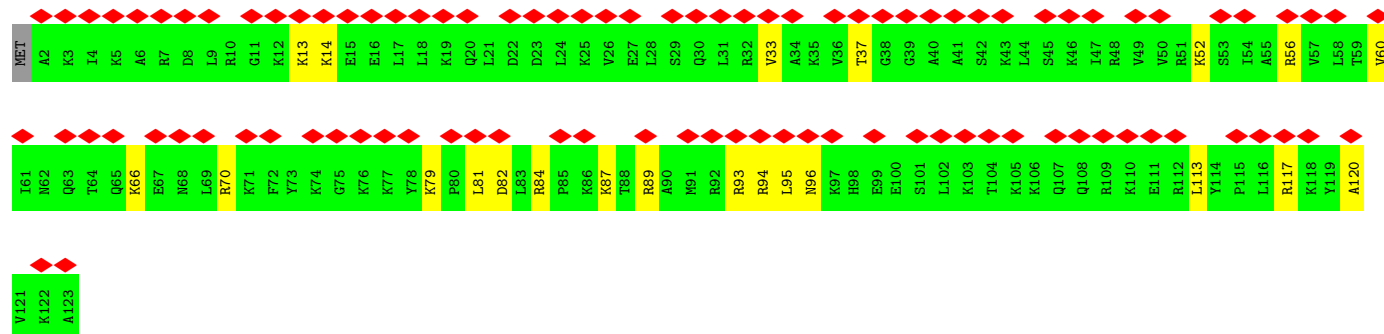
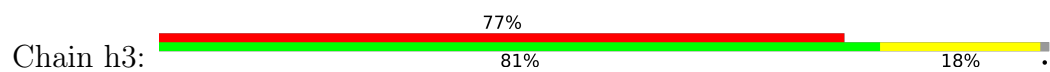




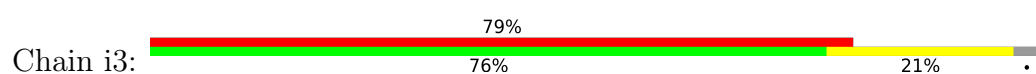
- Molecule 32: eL34



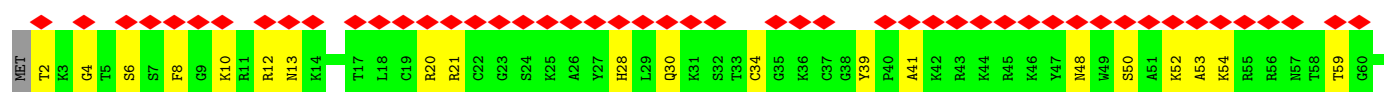
- Molecule 33: uL29



- Molecule 34: 60S ribosomal protein L36

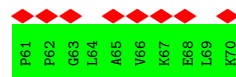
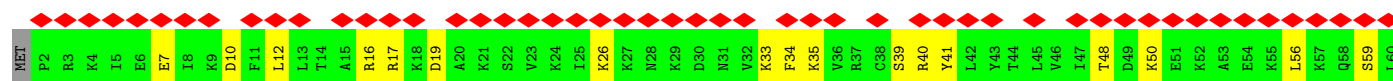
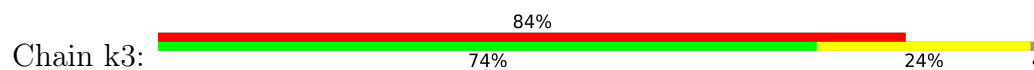


- Molecule 35: Ribosomal protein L37





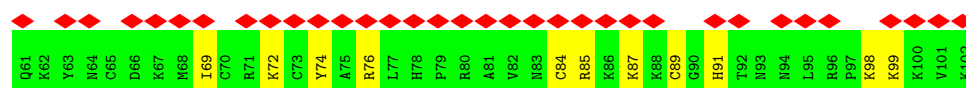
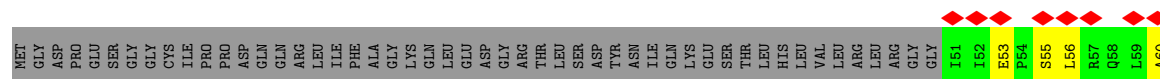
• Molecule 36: eL38



• Molecule 37: eL39



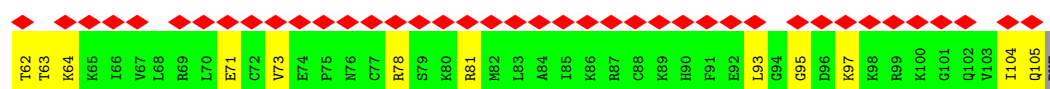
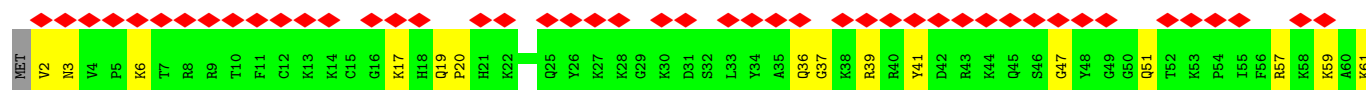
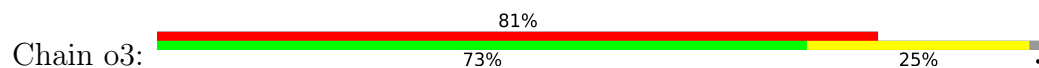
• Molecule 38: eL40

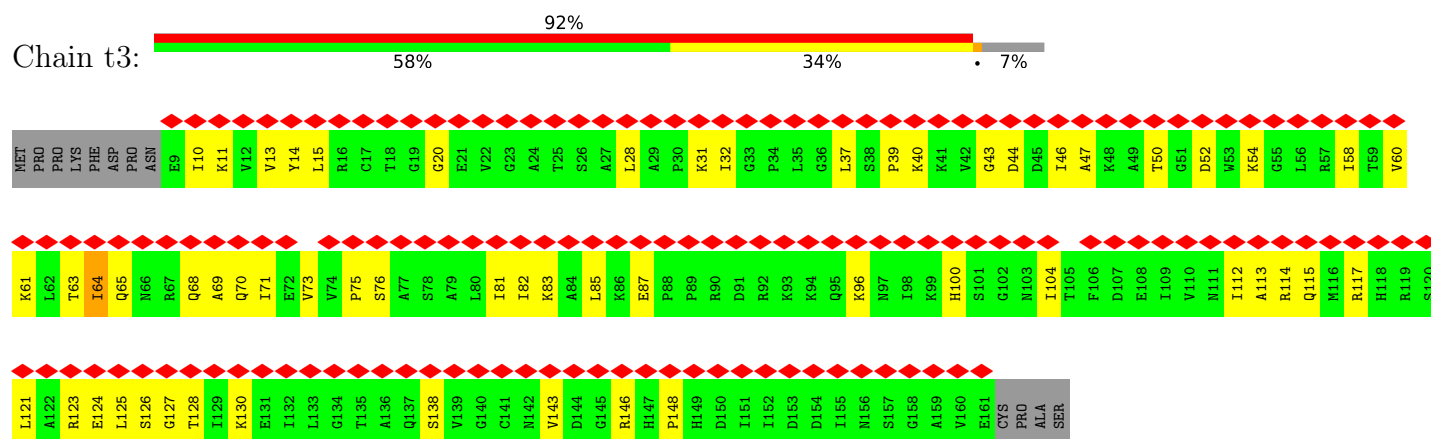


• Molecule 39: 60s ribosomal protein l41

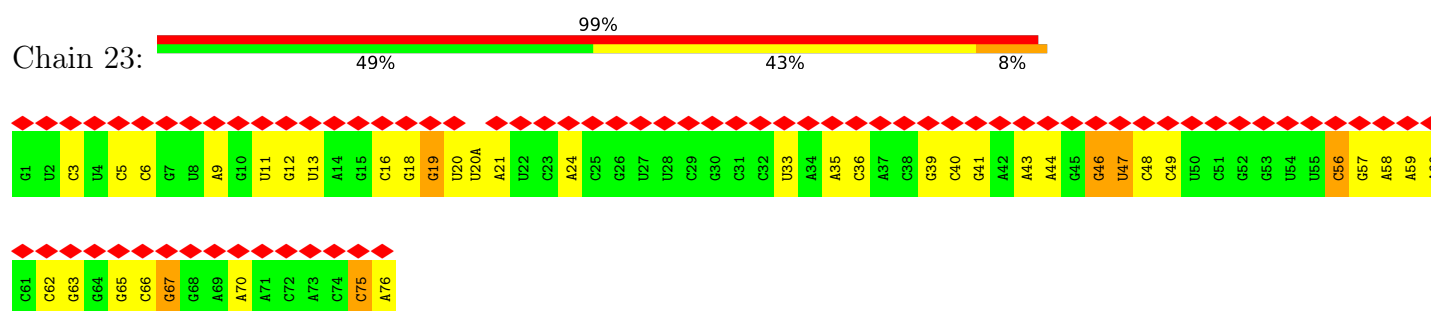


• Molecule 40: eL42

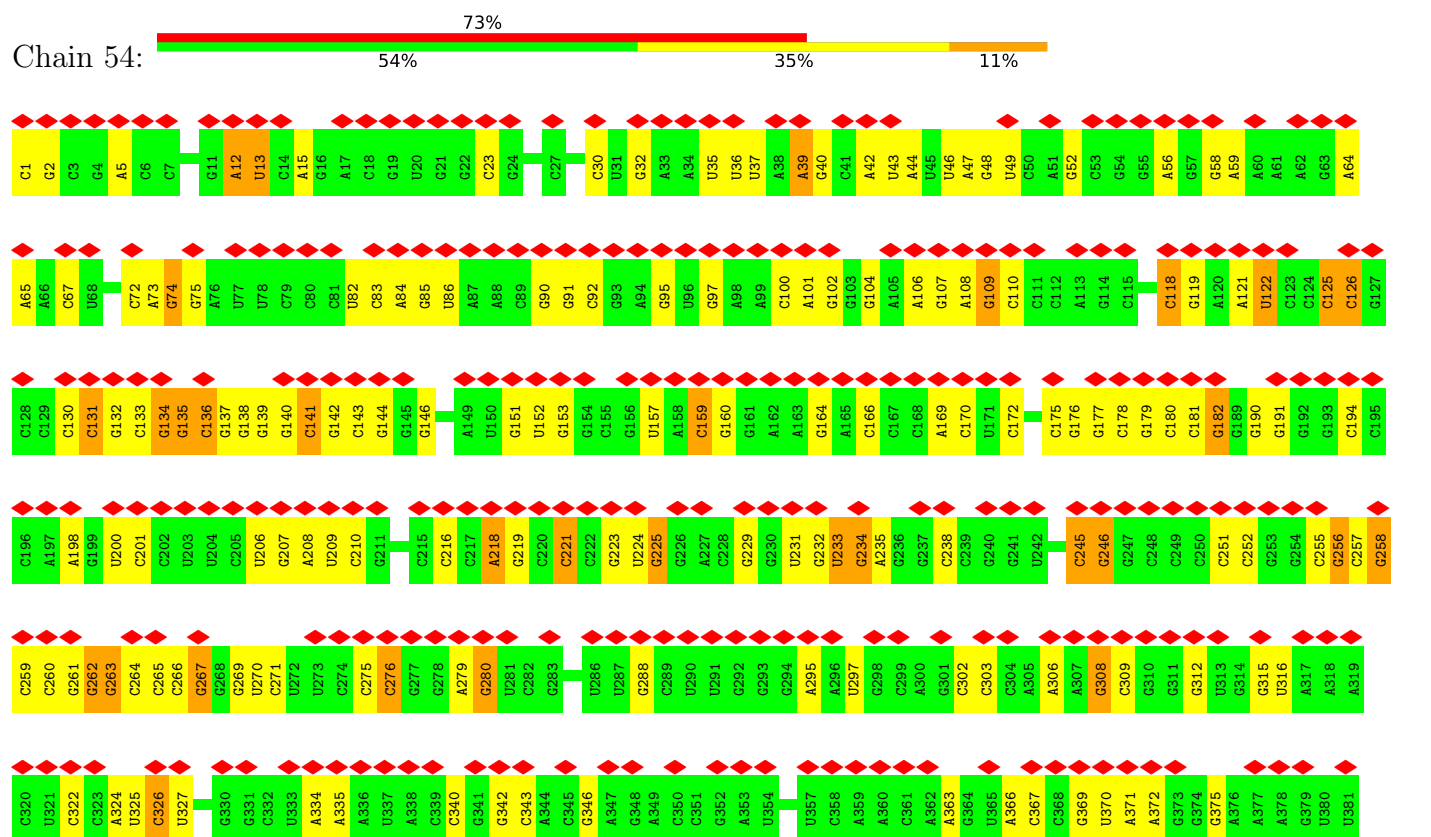


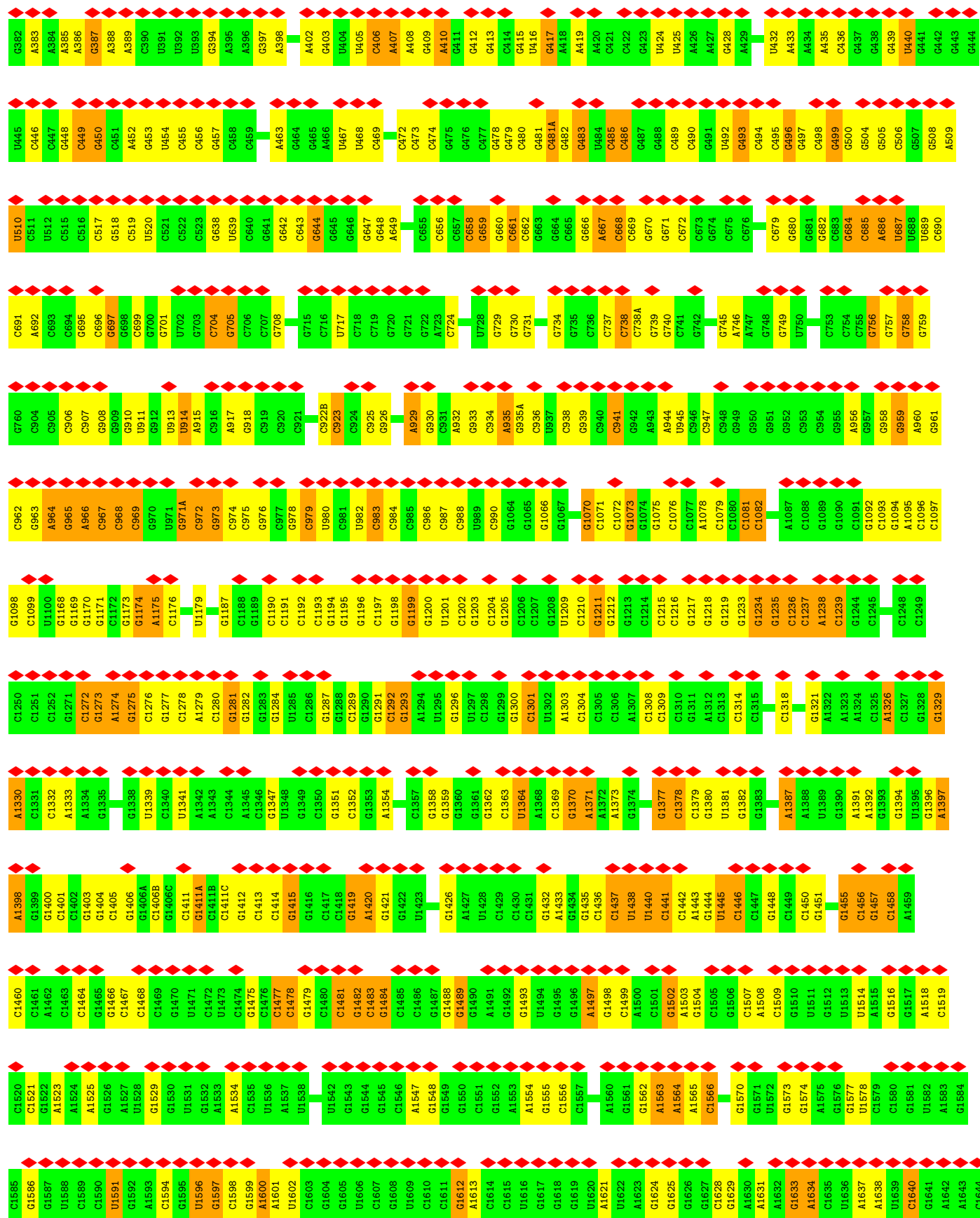


• Molecule 45: P-site tRNA



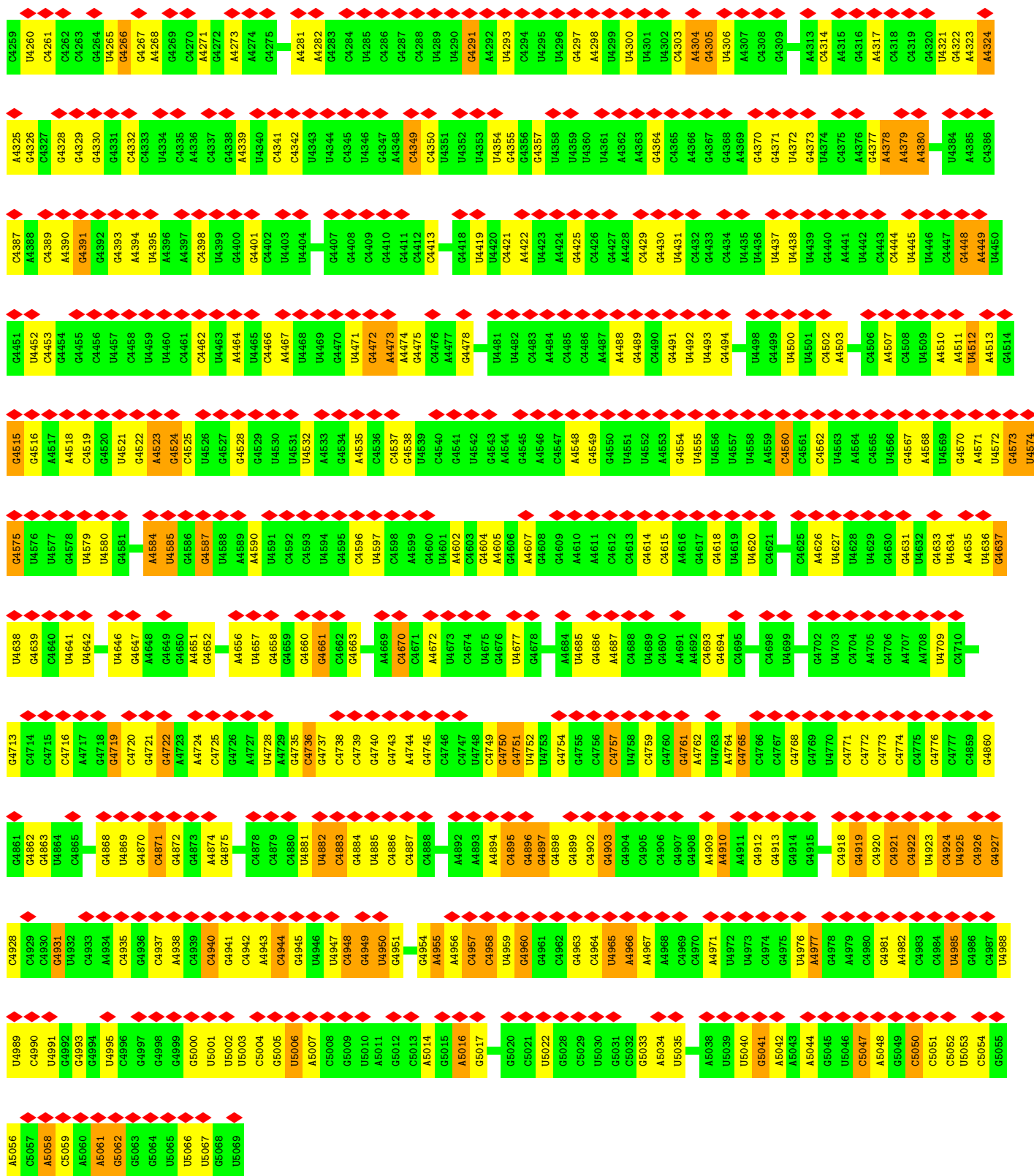
• Molecule 46: 28S ribosomal RNA





G2562	G2563	G2564	G2565	G2566	G2567	G2568	G2569	G2570	G2571	U2575	U2576	G2577	G2578	G2579	U2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2594	G2595	G2596	G2597	G2598	G2599	A2600	A2601	G2602	G2603	G2604	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2660	G2661																																																																																																																																																																																																																																																																																																																																																																																																											
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U2044	G2045	G2046	A2047	U2048	G2049	G2050	G2051	G2052	G2053	G2054	G2055	G2056	A2057	G2058	G2059	G2060	U2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	A2069	U2070	A2071	G2072	G2073	G2076	G2077	G2078	G2079	U2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	A2088	G2089	U2090	G2091	G2092	G2093	G2094	A2095	G2096	A2097	G2098	G2099	U2100	A2101	G2102	A2103	A2104	G2105	G2106	A2107	G2108	A2109	G2110	U2111	G2112	G2113	G2114	G2115	G2116	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	A2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	A2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	A2341	G2342	G2343	U2344	G2345	G2346	A2347	G2348	A2349	U2350	G2351	U2352	U2353	G2354	G2355	U2356	G2357	G2358	U2359	A2360	G2361	U2362	A2363	G2364	G2365	A2366	A2367	A2368	U2369	A2370	U2371	U2372	G2373	G2374	A2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465																																		

C2627	U2628	C2629	U2630	U2631	U2632	U2633	C2634	U2637	C2638	U2639	C2640	A2641	U2642	C2643	U2644	C2645	A2647	U2648	C2649	U2650	C2651	C2652	C2653	C2654	C2655	U2656	C2657	C2658	A2660	U2661	C2662	C2663	C2664	U2665	U2666	C2667	C2668	C2669	C2670	C2671	C2672	C2673	A2674	U2675	A2676	C2677	U2678	C2679	C2680	C2681	C2682	C2683	C2684	C2685	U2687				
C2688	C2689	C2690	U2691	U2692	C2693	C2694	A2695	C2696	A2697	C2698	C2702	C2703	U2704	C2705	C2706	U2707	U2708	C2709	C2710	C2711	C2712	C2713	C2714	C2715	C2716	C2717	U2718	C2719	C2720	C2721	C2722	A2725	C2726	C2727	U2728	C2729	U2730	C2731	C2732	C2733	U2734	C2738	C2739	U2740	U2741	C2742	U2743	A2744	U2745	C2746	U2747	C2748	C2749	C2750	C2751	C2752			
C2753	C2754	A2755	C2759	C2760	U2761	C2762	U2763	A2764	A2765	C2768	U2769	C2770	C2771	C2772	C2773	C2774	C2775	C2776	C2777	C2778	C2779	C2780	C2781	C2782	U2783	C2784	C2785	C2786	C2787	U2788	C2789	U2790	C2791	C2792	C2793	C2794	A2795	C2796	C2797	A2798	C2799	C2800	U2801	C2802	U2803	C2804	C2805	A2806	C2807	C2808	C2809	U2810	C2811	C2812	A2813	C2814	A2815		
C2816	C2817	C2818	U2819	C2820	U2821	C2822	C2823	C2824	A2825	U2826	C2827	U2828	U2829	C2830	C2831	A2832	C2833	C2834	U2837	A2840	C2841	C2842	U2843	A2844	A2845	C2846	C2847	C2848	A2849	C2850	C2851	U2852	C2853	C2854	C2855	C2856	C2859	C2860	C2861	C2862	C2863	A2864	C2865	C2866	C2867	C2868	U2869	A2870	A2871	C2872	U2873	U2874	C2875	C2876	C2877	C2878			
A2879	U2880	A2881	A2882	C2883	U2884	A2885	U2886	C2890	U2891	C2892	U2893	A2894	A2895	C2896	C2899	U2900	C2901	C3597	C3598	A3599	C3600	C3601	C3602	C3603	A3604	C3605	U3606	U3607	A3608	C3609	A3610	A3611	C3612	U3613	C3614	C3615	U3616	C3617	C3618	C3619	C3620	A3621	C3622	C3623	A3624	C3625	C3626	C3627	C3628	A3629	A3630	U3631	C3632	C3633	C3634	A3635	C3636		
U3637	C3638	U3639	U3640	U3641	C3642	A3643	U3644	U3645	U3646	A3647	A3648	A3649	C3650	A3651	A3652	A3653	C3654	C3655	A3656	U3657	C3658	C3659	C3660	C3661	A3662	C3663	C3664	C3665	C3666	C3667	C3668	C3669	C3670	C3671	C3672	C3673	C3674	C3675	C3676	U3677	C3678	U3679	C3680	C3681	C3682	C3683	U3684	C3685	C3686	C3687	U3688	U3689	C3690	C3691	A3692	U3693	U3694	C3696	
U3697	C3698	C3699	C3700	C3701	C3702	C3703	U3704	C3705	C3706	U3707	C3708	U3709	C3710	A3711	A3712	U3713	C3714	U3715	C3716	A3717	A3718	C3719	C3720	U3721	C3722	A3723	A3724	C3725	A3726	A3727	A3728	U3729	U3730	C3731	U3734	C3735	C3736	A3737	C3738	C3739	C3740	C3741	C3742	C3743	C3744	U3745	A3746	A3747	C3748	C3749	C3750	C3751	C3752	C3753	C3754	C3755	A3756	C3757	
U3758	A3759	A3760	C3761	U3762	C3763	U3764	C3765	A3766	C3767	U3768	C3769	U3770	C3771	U3772	U3773	A3774	A3775	C3776	C3777	U3778	A3779	C3780	C3781	C3782	A3783	A3784	A3785	U3786	C3787	C3788	C3789	U3790	C3791	C3792	U3793	C3794	A3795	U3796	C3797	U3798	A3799	A3800	U3801	U3802	A3803	C3804	U3805	C3806	A3807	C3808	C3809	C3810	C3811	C3812	A3813	U3814	C3815	A3816	A3817
U3818	C3819	C3820	A3821	U3822	C3823	A3824	A3825	C3826	C3827	A3828	C3829	U3830	U3831	U3832	C3833	C3834	C3835	A3836	C3837	U3838	C3839	A3901	A3902	A3903	C3904	A3905	A3906	C3907	A3908	C3909	C3910	C3911	U3914	U3915	C3916	A3917	C3918	C3919	U3920	U3921	C3922	A3923	C3924	U3925	C3926	U3927	A3928	C3929	U3930	C3931	U3932	C3933	C3934	C3937	C3938	C3939	U3940	C3941	
A3942	A3943	G3946	A3947	C3948	G3949	U4005	U4006	U4007	U4008	U4009	A4070	U4071	C4072	A4073	C4074	U4075	U4076	A4077	C4078	C4079	C4080	G4081	G4082	U4083	G4084	A4085	G4086	G4087	C4088	G4089	G4090	G4091	C4092	G4093	G4094	G4095	C4096	G4097	A4098	C4099	C4100	C4101	G4107	G4108	G4109	C4110	U4111	C4112	U4113	C4114	C4115	C4116	U4117	U4118	C4119	U4120	G4121	G4122	C4123
C4124	C4125	C4126	A4127	A4128	C4129	C4130	C4131	C4132	C4133	C4134	C4135	C4136	C4137	C4138	G4146	C4147	C4148	C4149	C4150	C4151	C4152	C4153	C4154	C4155	C4156	A4157	C4158	C4159	C4160	C4161	C4162	U4163	C4164	C4165	C4166	C4167	C4168	C4169	A4170	C4171	C4172	C4173	U4174	C4175	C4176	C4177	A4178	C4182	C4183	C4184	C4185	C4186	C4187	U4188	U4189	U4190	C4191	C4192	
C4193	U4194	C4195	C4196	C4197	C4198	C4199	C4200	C4201	U4202	A4203	C4204	A4205	C4206	C4207	U4208	C4211	A4212	C4215	C4216	C4217	U4218	A4219	C4220	A4221	C4222	C4223	A4224	C4225	C4226	U4227	C4228	C4229	C4230	C4231	U4232	A4233	A4234	C4235	C4236	C4237	U4242	C4243	A4244	C4245	C4246	C4247	C4250	A4251	C4252	A4253	C4254	A4255	A4256	C4257	C4258				





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49626	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 ($e^-/\text{\AA}^2$)	48.36	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.694	Depositor
Minimum map value	-0.371	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	A3	0.56	0/1936	0.52	0/2596
2	B3	0.57	0/3240	0.50	0/4339
3	C3	0.59	1/2937 (0.0%)	0.54	0/3946
4	D3	0.49	0/2437	0.45	0/3264
5	E3	0.48	0/1762	0.49	0/2362
6	F3	0.61	0/1911	0.49	0/2549
7	G3	0.45	0/1910	0.45	0/2569
8	H3	0.49	0/1535	0.48	0/2063
9	I3	0.53	0/1702	0.47	0/2272
10	J3	0.39	0/1385	0.46	0/1852
11	L3	0.50	0/1733	0.49	0/2316
12	M3	0.54	0/1158	0.45	0/1547
13	N3	0.63	0/1746	0.54	0/2338
14	O3	0.60	0/1662	0.53	0/2222
15	P3	0.58	0/1268	0.53	0/1700
16	Q3	0.60	0/1538	0.57	0/2054
17	R3	0.50	0/1310	0.51	0/1734
18	S3	0.60	0/1501	0.52	0/2012
19	T3	0.55	0/1326	0.49	0/1770
20	U3	0.42	0/848	0.48	0/1138
21	V3	0.54	0/993	0.48	0/1332
22	W3	0.52	0/541	0.48	0/720
23	X3	0.49	0/984	0.45	0/1323
24	Y3	0.53	0/1132	0.52	0/1504
25	Z3	0.45	0/1130	0.46	0/1507
26	a3	0.62	0/1191	0.49	0/1590
27	b3	0.42	0/861	0.47	0/1138
28	c3	0.47	0/771	0.43	0/1034
29	d3	0.53	0/903	0.48	0/1216
30	e3	0.61	0/1071	0.53	0/1429
31	f3	0.64	0/895	0.61	0/1198
32	g3	0.51	0/916	0.48	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h3	0.48	0/1021	0.46	0/1348
34	i3	0.43	0/841	0.47	0/1112
35	j3	0.61	0/720	0.53	0/952
36	k3	0.41	0/575	0.43	0/761
37	l3	0.59	0/459	0.58	0/608
38	m3	0.52	0/435	0.50	0/575
39	n3	0.25	0/240	0.48	0/305
40	o3	0.50	0/864	0.49	0/1140
41	p3	0.50	0/718	0.52	0/953
42	r3	0.57	0/1010	0.53	0/1354
43	s3	0.20	0/1530	0.42	0/2064
44	t3	0.18	0/1174	0.46	0/1582
45	23	0.20	0/1805	0.32	0/2809
46	54	0.58	0/84976	0.41	0/132520
47	74	0.57	0/2858	0.36	0/4455
48	84	0.57	0/3581	0.37	0/5577
49	NI	0.30	0/150	0.76	1/209 (0.5%)
50	NA	0.20	0/425	0.45	0/572
51	NB	0.20	0/450	0.46	0/612
52	TT	0.20	0/3402	0.41	0/4603
53	1	0.53	0/295	0.79	0/394
All	All	0.55	1/153762 (0.0%)	0.44	1/226359 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	N3	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C3	61	GLN	CA-C	-5.17	1.45	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	NI	17	ALA	N-CA-C	5.21	114.72	107.73

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	N3	76	PRO	Peptide
13	N3	78	GLY	Peptide

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	A3	1898	0	1993	65	0
2	B3	3172	0	3310	91	0
3	C3	2883	0	3053	82	0
4	D3	2391	0	2424	58	0
5	E3	1729	0	1887	49	0
6	F3	1875	0	1995	44	0
7	G3	1879	0	2027	47	0
8	H3	1516	0	1597	46	0
9	I3	1664	0	1712	41	0
10	J3	1362	0	1399	33	0
11	L3	1702	0	1820	47	0
12	M3	1137	0	1211	28	0
13	N3	1701	0	1749	54	0
14	O3	1630	0	1778	46	0
15	P3	1242	0	1274	31	0
16	Q3	1514	0	1634	53	0
17	R3	1294	0	1434	46	0
18	S3	1462	0	1508	43	0
19	T3	1298	0	1366	53	0
20	U3	834	0	858	24	0
21	V3	979	0	1039	25	0
22	W3	528	0	541	13	0
23	X3	967	0	1040	24	0
24	Y3	1115	0	1205	41	0
25	Z3	1107	0	1182	33	0
26	a3	1162	0	1209	43	0
27	b3	848	0	920	19	0
28	c3	761	0	794	13	0
29	d3	888	0	930	21	0
30	e3	1053	0	1147	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	f3	876	0	912	13	0
32	g3	906	0	999	23	0
33	h3	1013	0	1147	20	0
34	i3	830	0	916	18	0
35	j3	705	0	737	22	0
36	k3	569	0	637	14	0
37	l3	447	0	480	18	0
38	m3	429	0	465	12	0
39	n3	239	0	289	10	0
40	o3	851	0	920	20	0
41	p3	708	0	757	26	0
42	r3	994	0	1051	32	0
43	s3	1507	0	1564	60	0
44	t3	1160	0	1218	43	0
45	23	1616	0	823	20	0
46	54	75972	0	38385	1073	0
47	74	2558	0	1296	23	0
48	84	3208	0	1629	40	0
49	NI	150	0	152	1	0
50	NA	420	0	450	30	0
51	NB	444	0	441	25	0
52	TT	3337	0	3318	153	0
53	1	292	0	291	28	0
54	54	201	0	0	0	0
54	74	7	0	0	0	0
54	84	6	0	0	0	0
54	P3	2	0	0	0	0
54	V3	1	0	0	0	0
54	a3	1	0	0	0	0
54	g3	1	0	0	0	0
54	j3	1	0	0	0	0
55	g3	1	0	0	0	0
55	j3	1	0	0	0	0
55	m3	1	0	0	0	0
55	o3	1	0	0	0	0
55	p3	1	0	0	0	0
All	All	143047	0	104913	2477	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 11.

The worst 5 of 2477 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)
46:54:973:G:N2	46:54:1282:G:N7	2.03	1.07
46:54:2638:G:N2	46:54:2697:A:N1	2.11	0.98
46:54:2486:G:H1	46:54:2492:C:H42	1.16	0.92
46:54:4751:G:H1	46:54:4948:C:H5	1.14	0.91
46:54:496:G:N1	46:54:658:C:N3	2.17	0.91

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	A3	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	B3	392/403 (97%)	358 (91%)	34 (9%)	0	100	100
3	C3	360/425 (85%)	331 (92%)	29 (8%)	0	100	100
4	D3	291/297 (98%)	265 (91%)	26 (9%)	0	100	100
5	E3	208/291 (72%)	185 (89%)	23 (11%)	0	100	100
6	F3	223/247 (90%)	206 (92%)	17 (8%)	0	100	100
7	G3	229/319 (72%)	212 (93%)	17 (7%)	0	100	100
8	H3	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I3	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J3	168/178 (94%)	155 (92%)	13 (8%)	0	100	100
11	L3	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	24	55
12	M3	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N3	201/204 (98%)	185 (92%)	16 (8%)	0	100	100
14	O3	197/203 (97%)	185 (94%)	12 (6%)	0	100	100
15	P3	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
16	Q3	185/188 (98%)	170 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R3	153/196 (78%)	142 (93%)	11 (7%)	0	100	100
18	S3	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	21	50
19	T3	157/160 (98%)	138 (88%)	18 (12%)	1 (1%)	21	50
20	U3	100/128 (78%)	89 (89%)	11 (11%)	0	100	100
21	V3	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
22	W3	61/157 (39%)	54 (88%)	7 (12%)	0	100	100
23	X3	116/156 (74%)	104 (90%)	12 (10%)	0	100	100
24	Y3	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z3	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a3	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	b3	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
28	c3	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d3	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e3	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	16	45
31	f3	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g3	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h3	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
34	i3	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j3	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
36	k3	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l3	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m3	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
39	n3	23/25 (92%)	23 (100%)	0	0	100	100
40	o3	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p3	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	r3	122/137 (89%)	111 (91%)	11 (9%)	0	100	100
43	s3	194/318 (61%)	167 (86%)	27 (14%)	0	100	100
44	t3	151/165 (92%)	121 (80%)	30 (20%)	0	100	100
49	NI	27/29 (93%)	15 (56%)	11 (41%)	1 (4%)	2	14
50	NA	52/215 (24%)	42 (81%)	10 (19%)	0	100	100
51	NB	56/206 (27%)	50 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	TT	424/440 (96%)	395 (93%)	29 (7%)	0	100	100
53	1	32/64 (50%)	17 (53%)	13 (41%)	2 (6%)	1	6
All	All	7271/8745 (83%)	6614 (91%)	650 (9%)	7 (0%)	49	77

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	1	4	ILE
11	L3	64	VAL
18	S3	166	ARG
30	e3	127	ALA
49	NI	20	ALA

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	A3	190/199 (96%)	188 (99%)	2 (1%)	65	76
2	B3	342/348 (98%)	340 (99%)	2 (1%)	78	81
3	C3	302/347 (87%)	302 (100%)	0	100	100
4	D3	247/250 (99%)	247 (100%)	0	100	100
5	E3	190/251 (76%)	188 (99%)	2 (1%)	65	76
6	F3	196/215 (91%)	195 (100%)	1 (0%)	81	83
7	G3	200/272 (74%)	200 (100%)	0	100	100
8	H3	169/171 (99%)	168 (99%)	1 (1%)	78	81
9	I3	175/181 (97%)	175 (100%)	0	100	100
10	J3	143/149 (96%)	141 (99%)	2 (1%)	59	74
11	L3	175/176 (99%)	172 (98%)	3 (2%)	53	72
12	M3	117/161 (73%)	116 (99%)	1 (1%)	70	78
13	N3	171/172 (99%)	169 (99%)	2 (1%)	63	76
14	O3	171/173 (99%)	169 (99%)	2 (1%)	63	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P3	134/163 (82%)	133 (99%)	1 (1%)	76	80
16	Q3	164/164 (100%)	164 (100%)	0	100	100
17	R3	138/175 (79%)	138 (100%)	0	100	100
18	S3	157/157 (100%)	155 (99%)	2 (1%)	61	75
19	T3	139/140 (99%)	139 (100%)	0	100	100
20	U3	92/114 (81%)	92 (100%)	0	100	100
21	V3	101/107 (94%)	100 (99%)	1 (1%)	68	77
22	W3	55/126 (44%)	55 (100%)	0	100	100
23	X3	106/134 (79%)	105 (99%)	1 (1%)	70	78
24	Y3	124/135 (92%)	123 (99%)	1 (1%)	73	80
25	Z3	117/118 (99%)	115 (98%)	2 (2%)	53	72
26	a3	119/120 (99%)	118 (99%)	1 (1%)	73	80
27	b3	84/172 (49%)	83 (99%)	1 (1%)	63	76
28	c3	84/98 (86%)	83 (99%)	1 (1%)	63	76
29	d3	98/110 (89%)	96 (98%)	2 (2%)	48	70
30	e3	114/121 (94%)	114 (100%)	0	100	100
31	f3	88/89 (99%)	88 (100%)	0	100	100
32	g3	98/99 (99%)	98 (100%)	0	100	100
33	h3	109/110 (99%)	108 (99%)	1 (1%)	70	78
34	i3	86/89 (97%)	86 (100%)	0	100	100
35	j3	73/80 (91%)	71 (97%)	2 (3%)	39	65
36	k3	64/65 (98%)	63 (98%)	1 (2%)	55	73
37	l3	47/48 (98%)	47 (100%)	0	100	100
38	m3	48/90 (53%)	48 (100%)	0	100	100
39	n3	24/24 (100%)	24 (100%)	0	100	100
40	o3	92/94 (98%)	92 (100%)	0	100	100
41	p3	74/75 (99%)	72 (97%)	2 (3%)	39	65
42	r3	108/121 (89%)	108 (100%)	0	100	100
43	s3	164/258 (64%)	164 (100%)	0	100	100
44	t3	126/137 (92%)	125 (99%)	1 (1%)	73	80
49	NI	2/2 (100%)	2 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	NA	48/183 (26%)	47 (98%)	1 (2%)	47	69
51	NB	51/165 (31%)	51 (100%)	0	100	100
52	TT	370/381 (97%)	368 (100%)	2 (0%)	81	83
53	1	32/53 (60%)	25 (78%)	7 (22%)	1	4
All	All	6318/7382 (86%)	6270 (99%)	48 (1%)	70	80

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	c3	91	VAL
41	p3	16	THR
29	d3	22	THR
35	j3	67	LEU
44	t3	64	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 131 such sidechains are listed below:

Mol	Chain	Res	Type
43	s3	105	ASN
52	TT	93	GLN
53	1	8	GLN
13	N3	196	ASN
13	N3	156	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	23	74/76 (97%)	13 (17%)	0
46	54	3518/3543 (99%)	823 (23%)	58 (1%)
47	74	119/120 (99%)	14 (11%)	0
48	84	149/156 (95%)	32 (21%)	1 (0%)
All	All	3860/3895 (99%)	882 (22%)	59 (1%)

5 of 882 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	23	9	A
45	23	13	U

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Mol	Chain	Res	Type
45	23	16	C
45	23	19	G
45	23	20(A)	U

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	54	1455	G
46	54	4925	U
46	54	2266	C
46	54	4921	C
46	54	4354	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](#)

Of 225 ligands modelled in this entry, 225 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
46	54	27
45	23	1

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	54	2113:G	O3'	2258:C	P	40.63
1	54	1252:C	O3'	1271:G	P	37.10
1	54	1219:G	O3'	1233:G	P	19.39
1	54	3948:C	O3'	4065:G	P	18.92
1	54	4138:C	O3'	4146:G	P	18.16

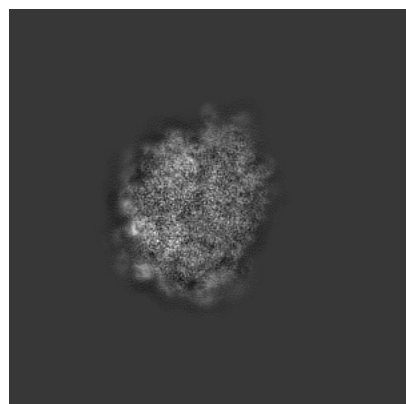
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10380. These allow visual inspection of the internal detail of the map and identification of artifacts.

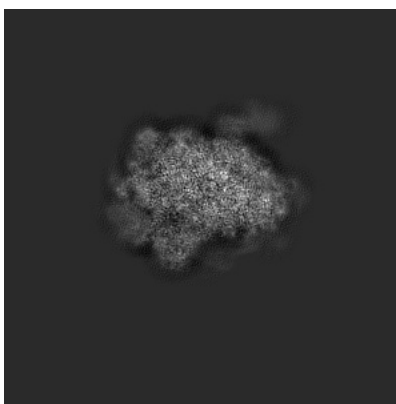
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

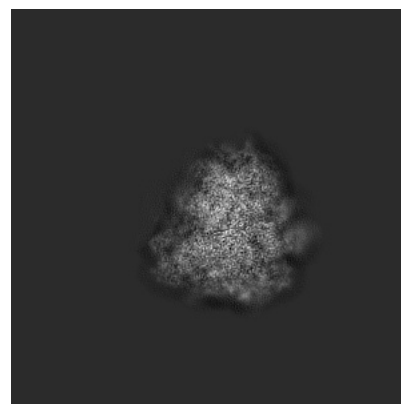
6.1.1 Primary map



X

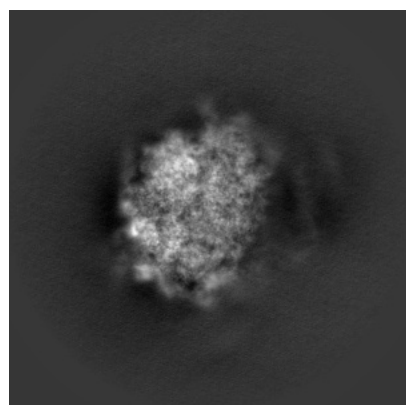


Y

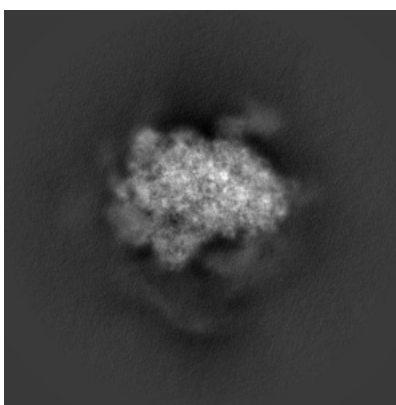


Z

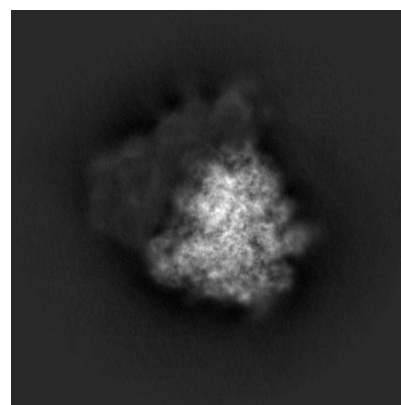
6.1.2 Raw map



X



Y

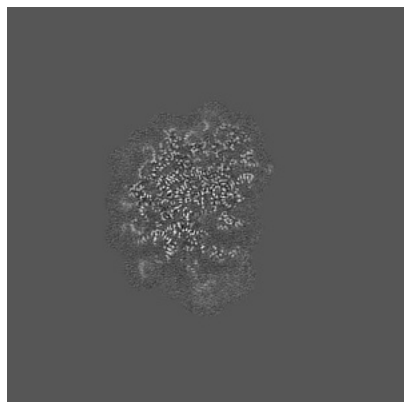


Z

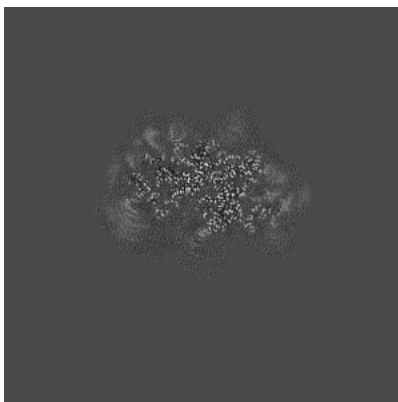
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

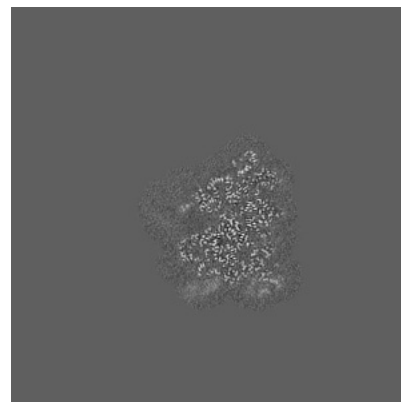
6.2.1 Primary map



X Index: 200

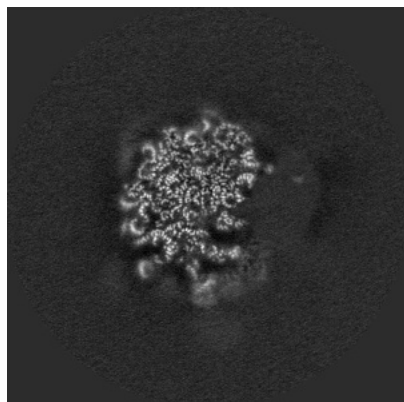


Y Index: 200

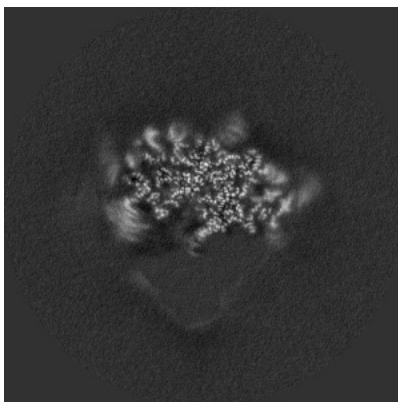


Z Index: 200

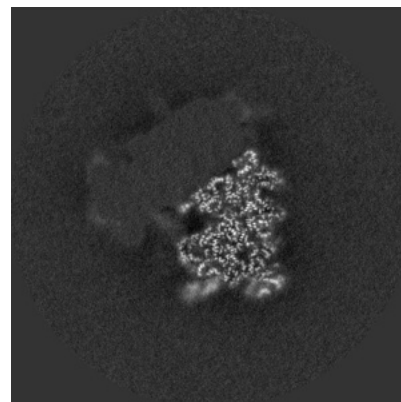
6.2.2 Raw map



X Index: 200



Y Index: 200

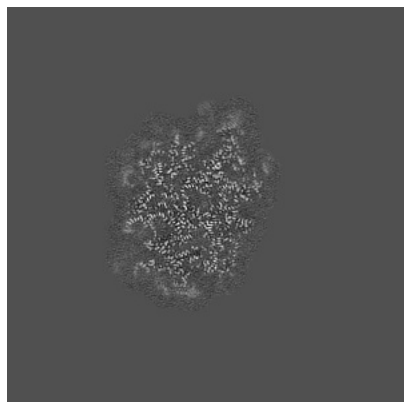


Z Index: 200

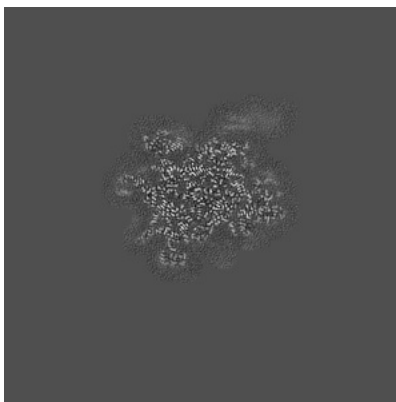
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

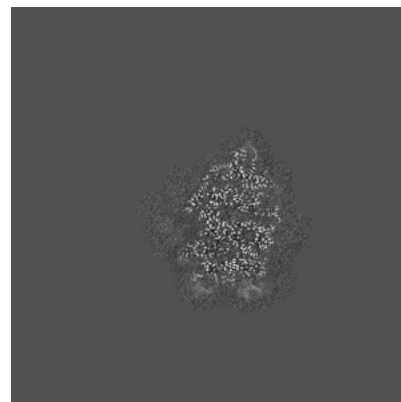
6.3.1 Primary map



X Index: 218

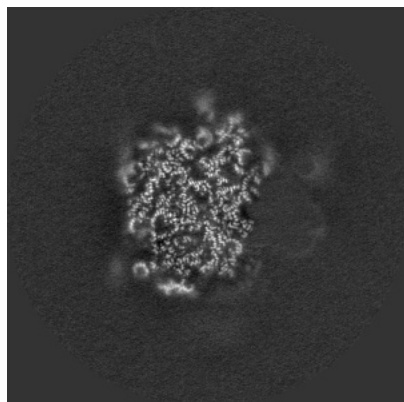


Y Index: 161

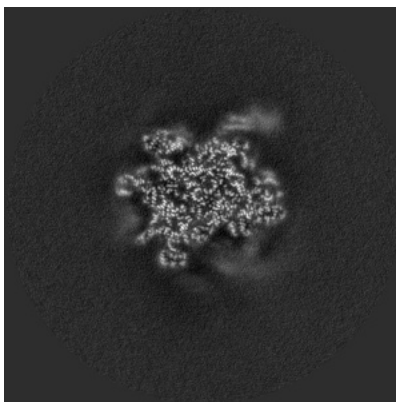


Z Index: 208

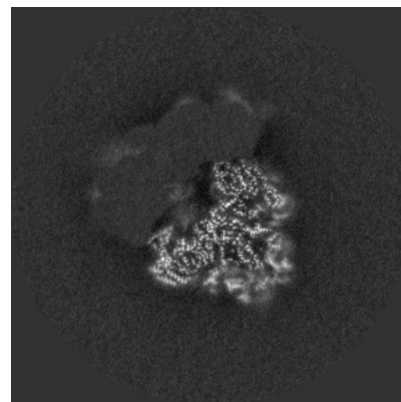
6.3.2 Raw map



X Index: 215



Y Index: 161

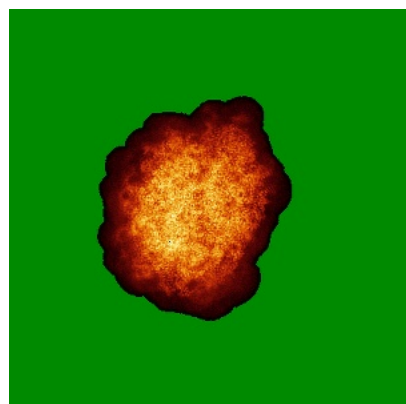


Z Index: 176

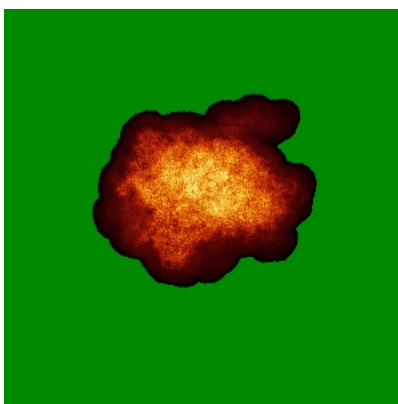
The images above show the largest variance slices of the map in three orthogonal directions.

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

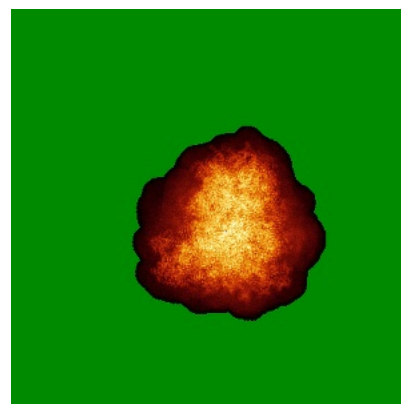
6.4.1 Primary map



X

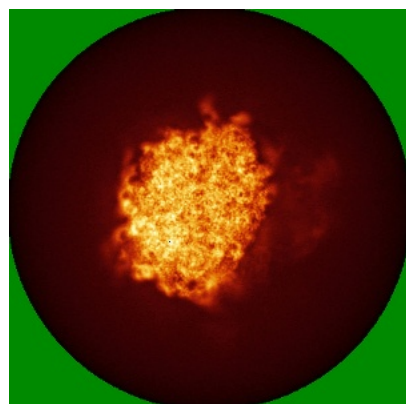


Y

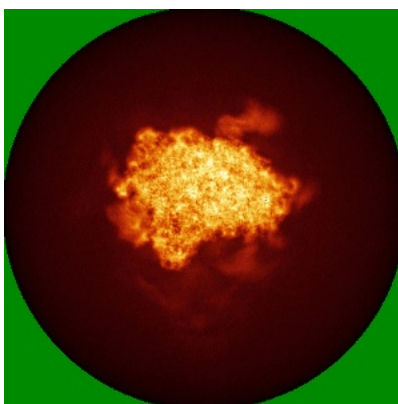


Z

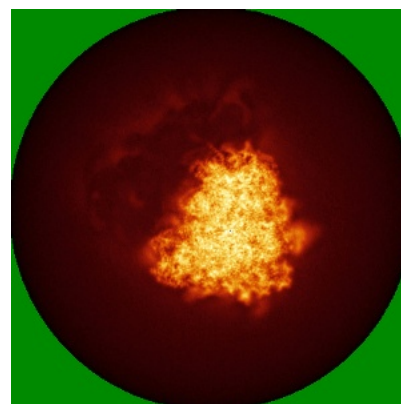
6.4.2 Raw map



X



Y

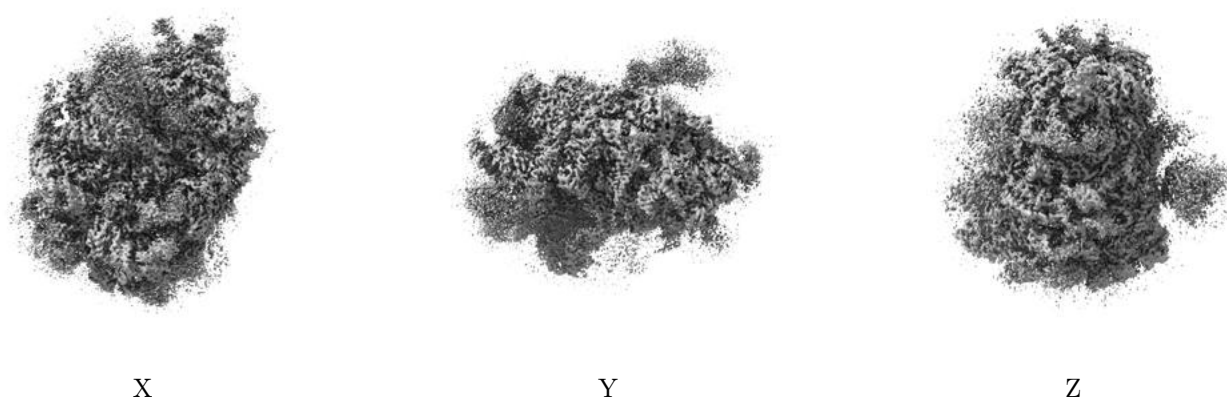


Z

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

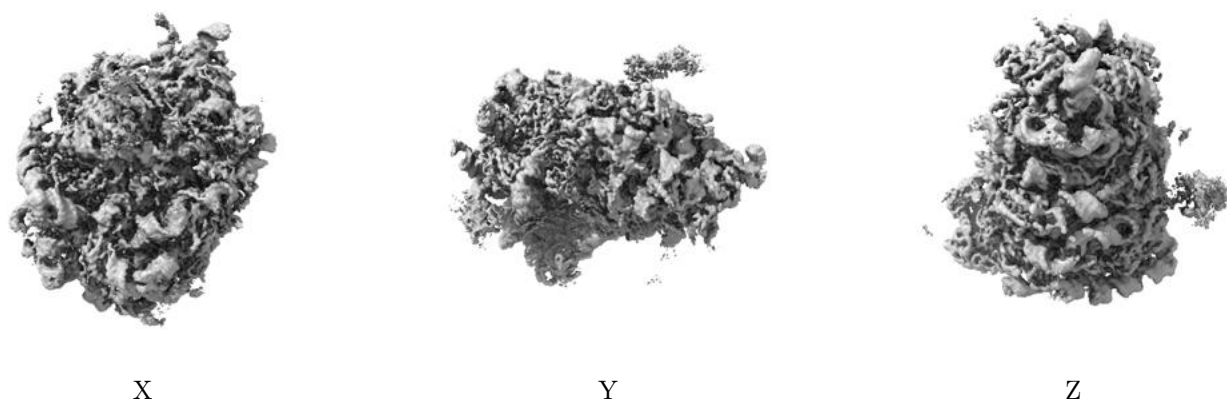
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

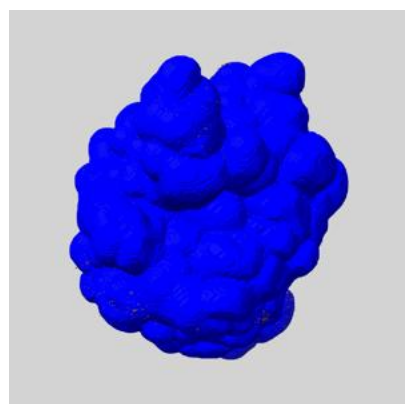
6.6 Mask visualisation [i](#)

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

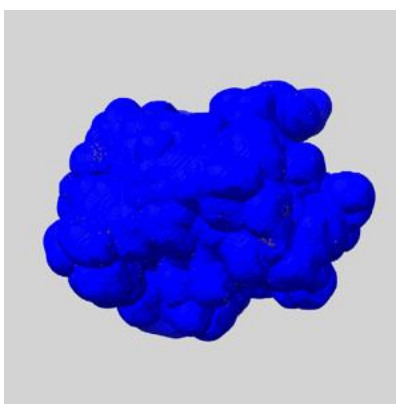
A mask typically either:

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

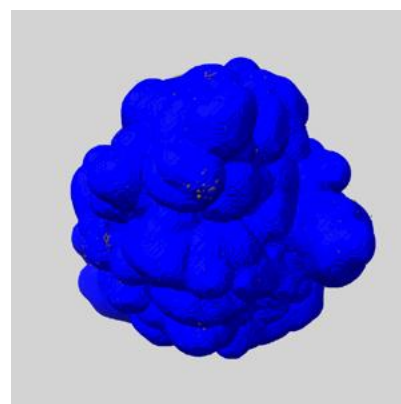
6.6.1 emd_10380_msk_1.map [i](#)



X



Y

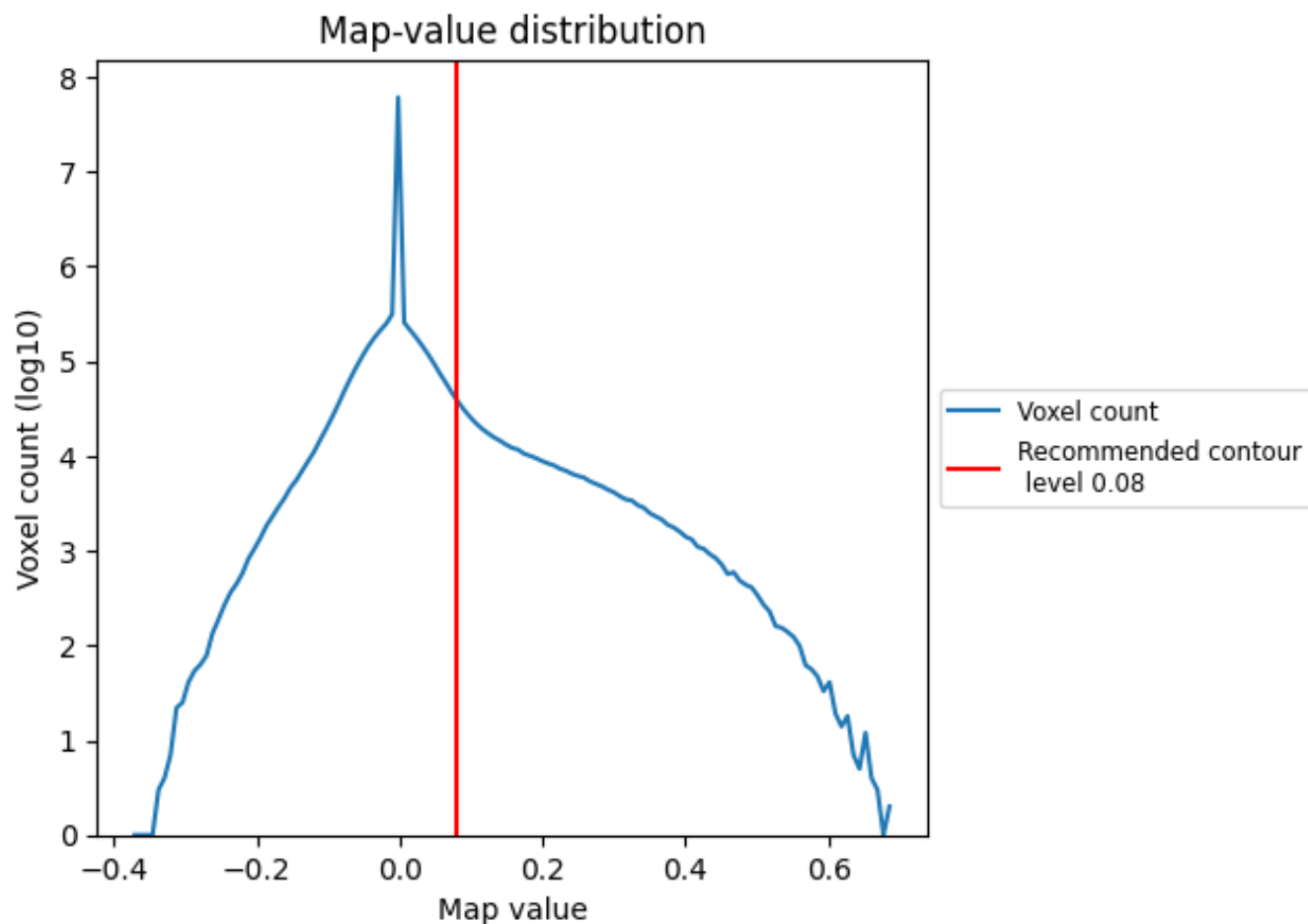


Z

7 Map analysis [i](#)

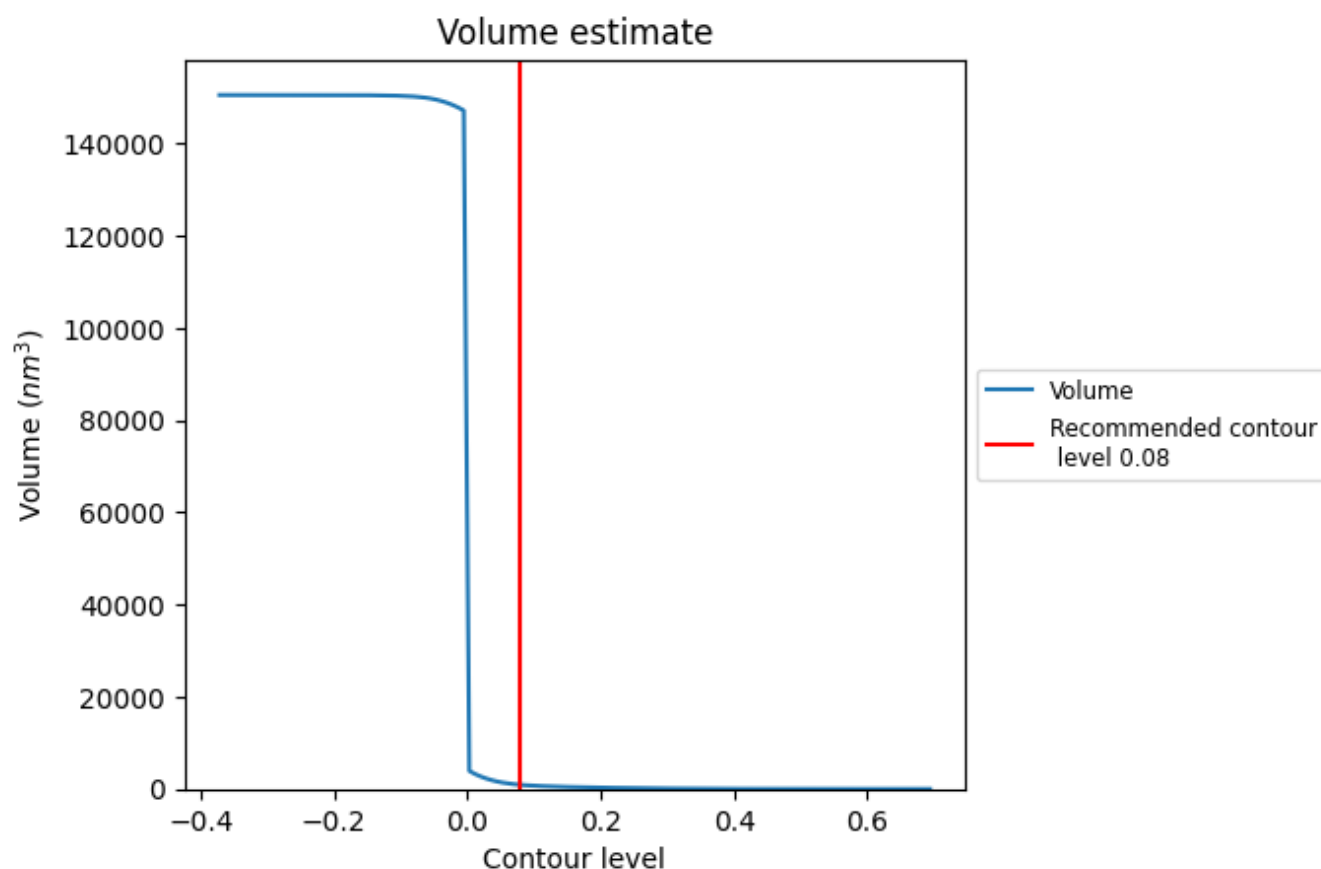
This section contains the results of statistical analysis of the map.

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.

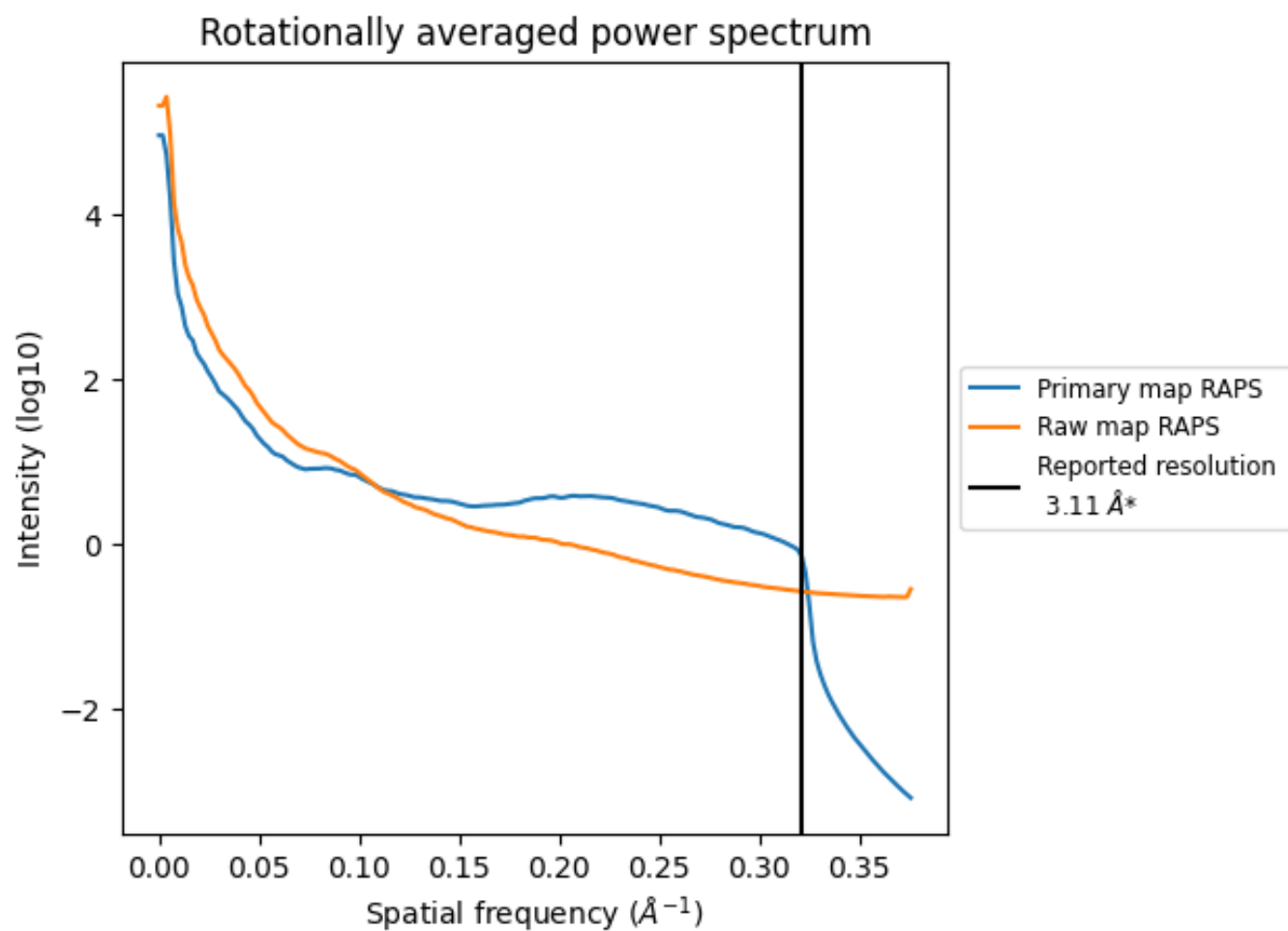
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 897 nm^3 ; this corresponds to an approximate mass of 810 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 ⓘ

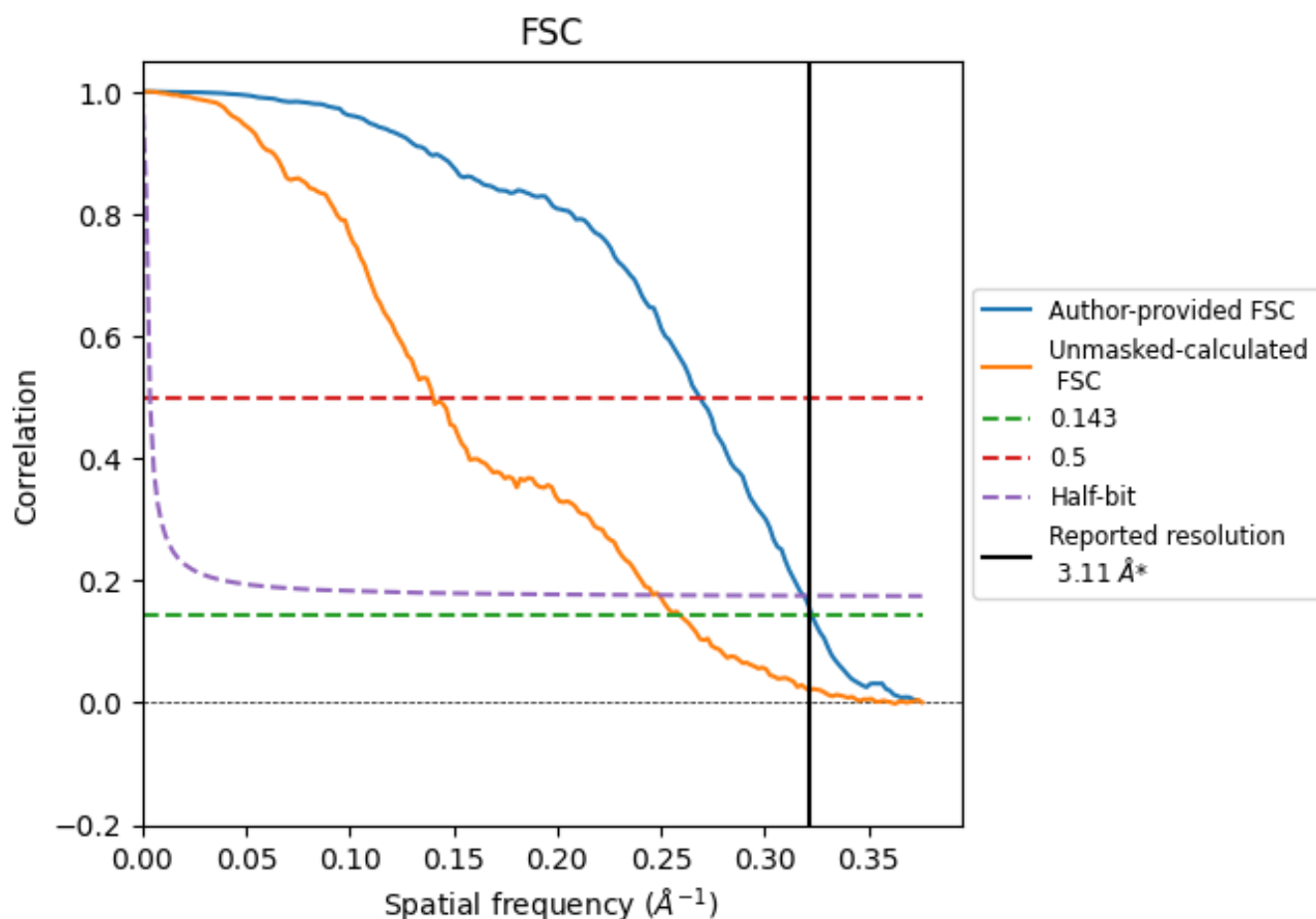


*Reported resolution corresponds to spatial frequency of $0.322 \text{ \AA}^{-1}$

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 0.322 Å⁻¹

8.2 Resolution estimates [i](#)

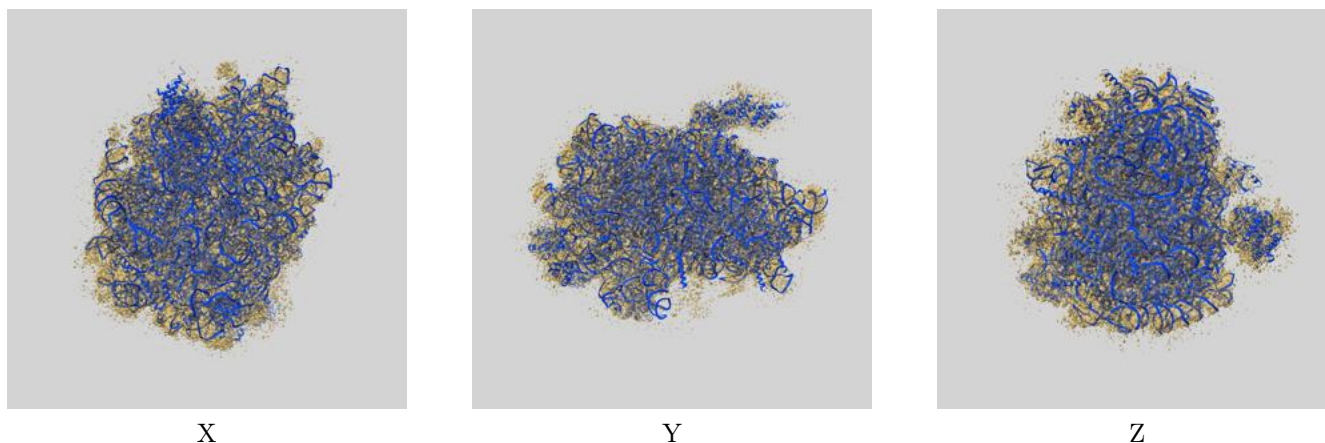
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.11	-	-
Author-provided FSC curve	3.10	3.72	3.14
Unmasked-calculated*	3.86	7.14	4.02

*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 3.86 differs from the reported value 3.11 by more than 10 %

9 Map-model fit [i](#)

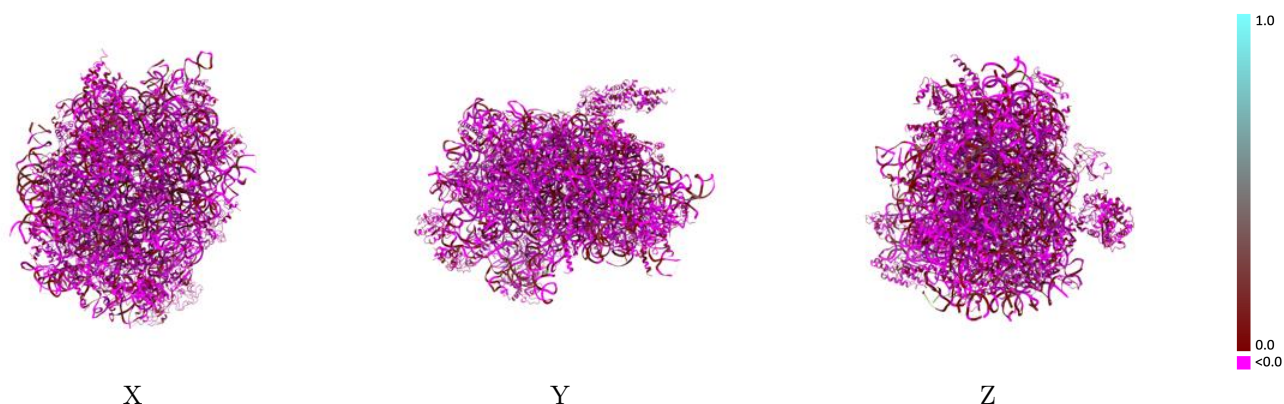
This section contains information regarding the fit between EMDB map EMD-10380 and PDB model 6T59. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



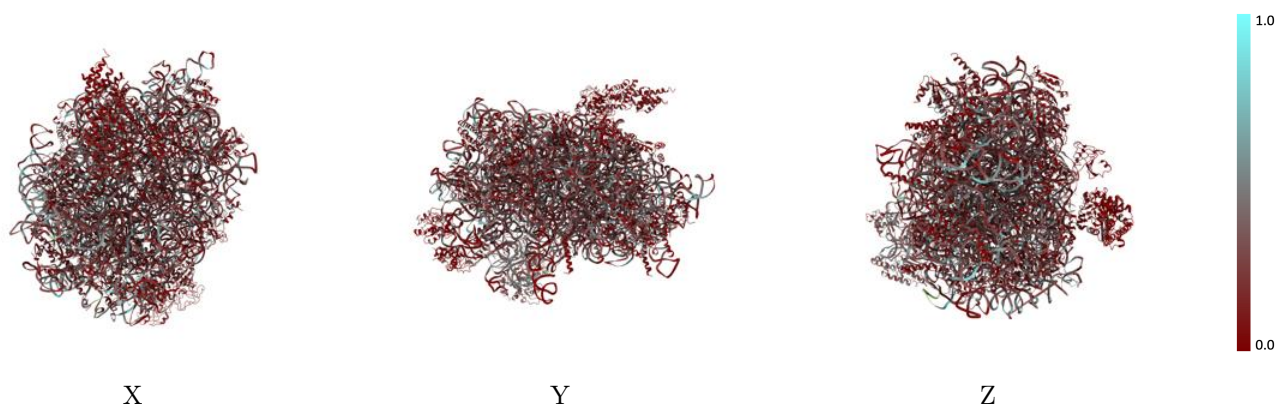
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



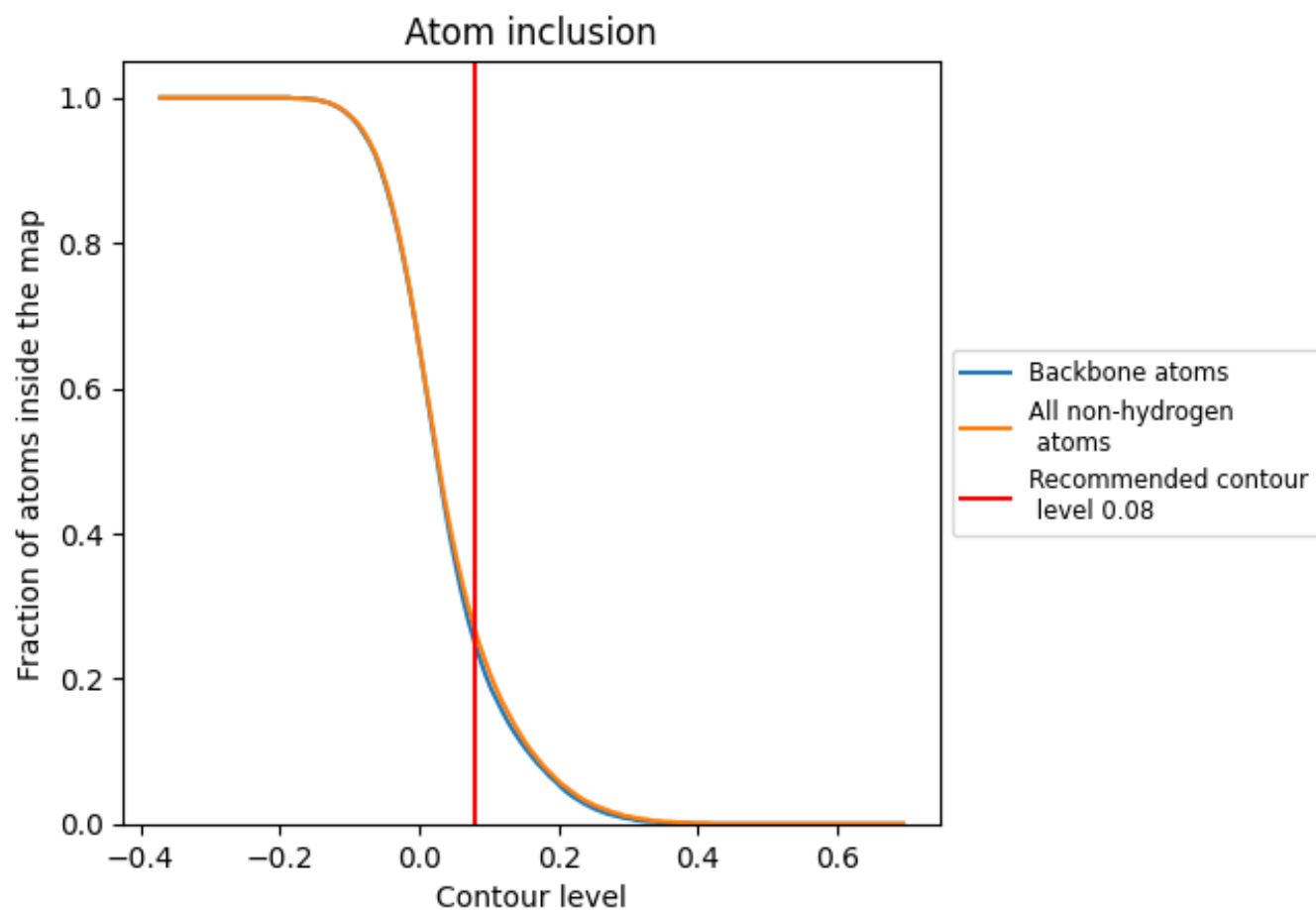
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 25% of all backbone atoms, 27% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2670	 -0.0680
1	 0.0460	 0.0020
23	 0.0730	 -0.0110
54	 0.3170	 -0.0600
74	 0.3820	 -0.1130
84	 0.3300	 -0.0320
A3	 0.1850	 -0.1380
B3	 0.2070	 -0.0910
C3	 0.2270	 -0.0980
D3	 0.2970	 -0.0630
E3	 0.2210	 -0.0940
F3	 0.2230	 -0.1080
G3	 0.2170	 -0.0680
H3	 0.1930	 -0.0940
I3	 0.2320	 -0.0920
J3	 0.2410	 -0.0470
L3	 0.2320	 -0.0770
M3	 0.2550	 -0.1010
N3	 0.2200	 -0.1120
NA	 0.0560	 0.0400
NB	 0.0220	 0.0230
NI	 0.1530	 -0.1020
O3	 0.2320	 -0.0910
P3	 0.1900	 -0.1070
Q3	 0.1930	 -0.1340
R3	 0.2200	 -0.0660
S3	 0.2570	 -0.0880
T3	 0.2250	 -0.1000
TT	 0.0900	 -0.0270
U3	 0.1740	 -0.0630
V3	 0.1680	 -0.1160
W3	 0.1850	 -0.0880
X3	 0.1820	 -0.0520
Y3	 0.1860	 -0.0900
Z3	 0.2130	 -0.0630



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Chain	Atom inclusion	Q-score
a3	 0.2390	 -0.1140
b3	 0.1890	 -0.0920
c3	 0.2510	 -0.0690
d3	 0.1770	 -0.0770
e3	 0.1940	 -0.1160
f3	 0.2200	 -0.1000
g3	 0.1850	 -0.0740
h3	 0.2060	 -0.0630
i3	 0.2410	 -0.0720
j3	 0.2370	 -0.0720
k3	 0.1690	 -0.0380
l3	 0.2180	 -0.0780
m3	 0.2020	 -0.1270
n3	 0.0320	 -0.0910
o3	 0.1900	 -0.1030
p3	 0.2470	 -0.0540
r3	 0.1910	 -0.1180
s3	 0.0700	 -0.0170
t3	 0.0580	 0.0140