



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:55 PM UTC

PDB ID : 6OIG / pdb_00006oig
EMDB ID : EMD-20077
Title : Subunit joining exposes nascent pre-40S rRNA for processing and quality control
Authors : Rai, J.; Parker, M.D.; Ghalei, H.; Johnson, M.C.; Karbstein, K.; Stroupe, M.E.
Deposited on : 2019-04-09
Resolution : 3.80 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:

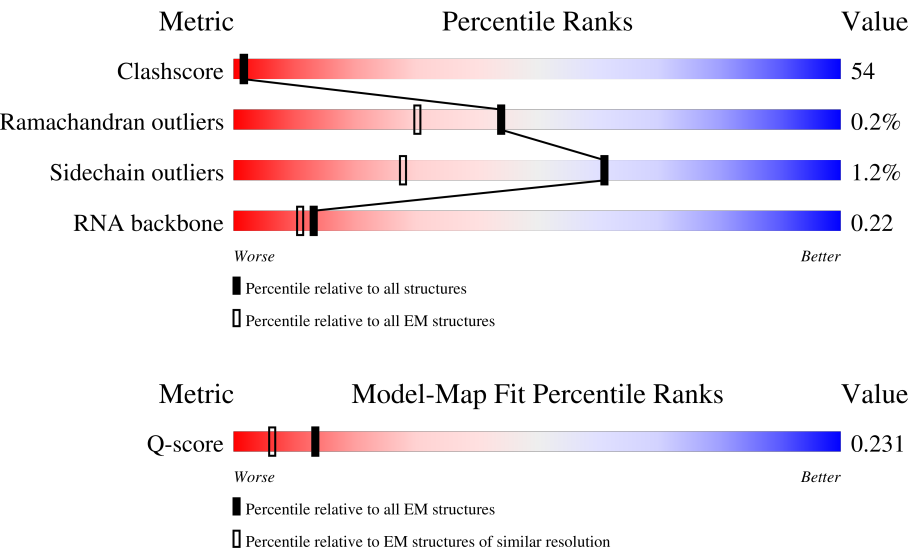
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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.



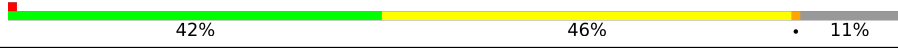
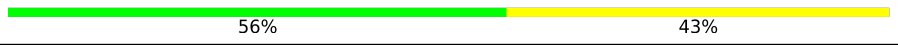
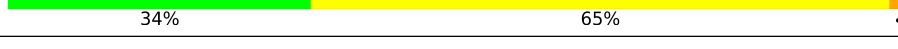
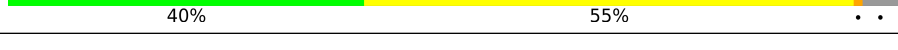
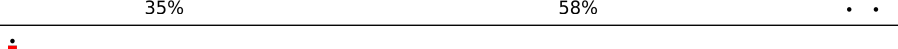
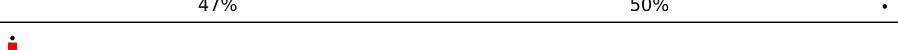
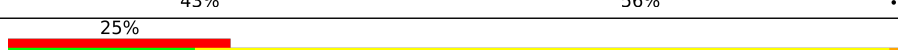
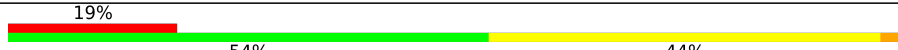
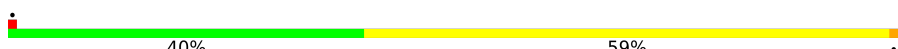
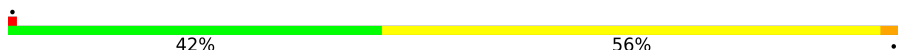
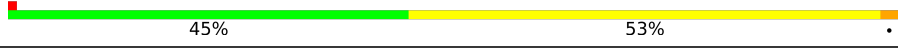
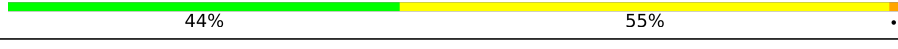
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	z	204	28% 37% 56% 6%
2	A	252	47% 52% .
3	B	386	50% 49% .

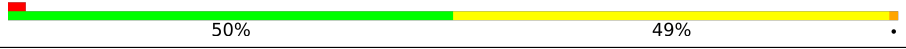
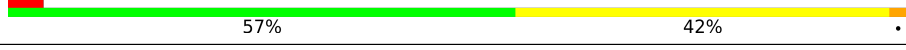
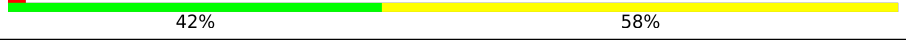
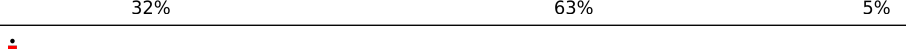
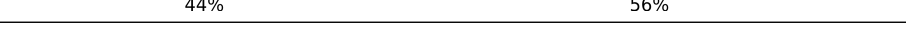
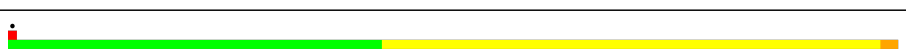
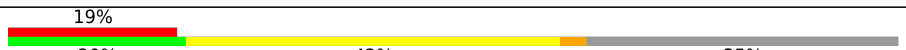
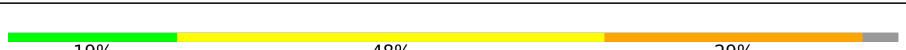
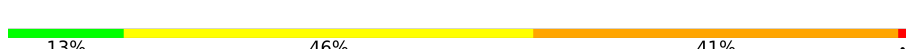
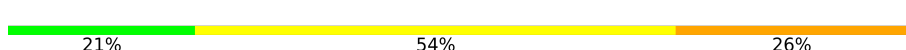
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Mol	Chain	Length	Quality of chain
4	C	361	
5	D	296	
6	E	175	
7	F	222	
8	G	233	
9	H	191	
10	I	220	
11	J	169	
12	s	155	
13	L	193	
14	M	136	
15	N	203	
16	O	197	
17	P	183	
18	Q	185	
19	R	188	
20	S	172	
21	T	159	
22	U	100	
23	V	136	
24	W	135	
25	X	121	
26	Y	126	
27	Z	135	
28	a	148	

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Mol	Chain	Length	Quality of chain
29	b	58	
30	c	97	
31	d	109	
32	e	127	
33	f	106	
34	g	112	
35	h	119	
36	i	99	
37	j	87	
38	k	77	
39	l	50	
40	m	52	
41	o	105	
42	p	91	
43	q	219	
44	5	3394	
45	8	158	
46	7	121	
47	x	47	
48	y	46	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 129140 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 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	z	204	Total	C	N	O	S	0	0
			1602	1026	277	290	9		

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 6 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 7 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 11 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 12 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	s	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	183	Total	C	N	O	S	0	0
			1443	896	287	260			

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	188	Total	C	N	O	S	0	0
			1522	935	326	261			

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1446	930	267	245	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1277	805	246	222	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	135	Total	C	N	O	S	0	0
			1089	682	219	187	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			969	623	170	174	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	126	Total	C	N	O		0	0
			994	625	192	177			

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	135	Total	C	N	O		0	0
			1093	710	202	181			

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1174	749	231	191	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	58	Total	C	N	O		0	0
			463	289	100	74			

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	77	Total	C	N	O		0	0
			613	391	115	107			

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 41 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0,60S acidic ribosomal protein P0,AO, L1OE.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	143	Total	C	N	O	S	0	0
			1077	687	192	195	3		

- Molecule 44 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5	3243	Total	C	N	O	P	0	0
			69359	30981	12493	22643	3242		

- Molecule 45 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 47 is a protein called P1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	x	47	Total	C	N	O	0	0
			235	141	47	47		

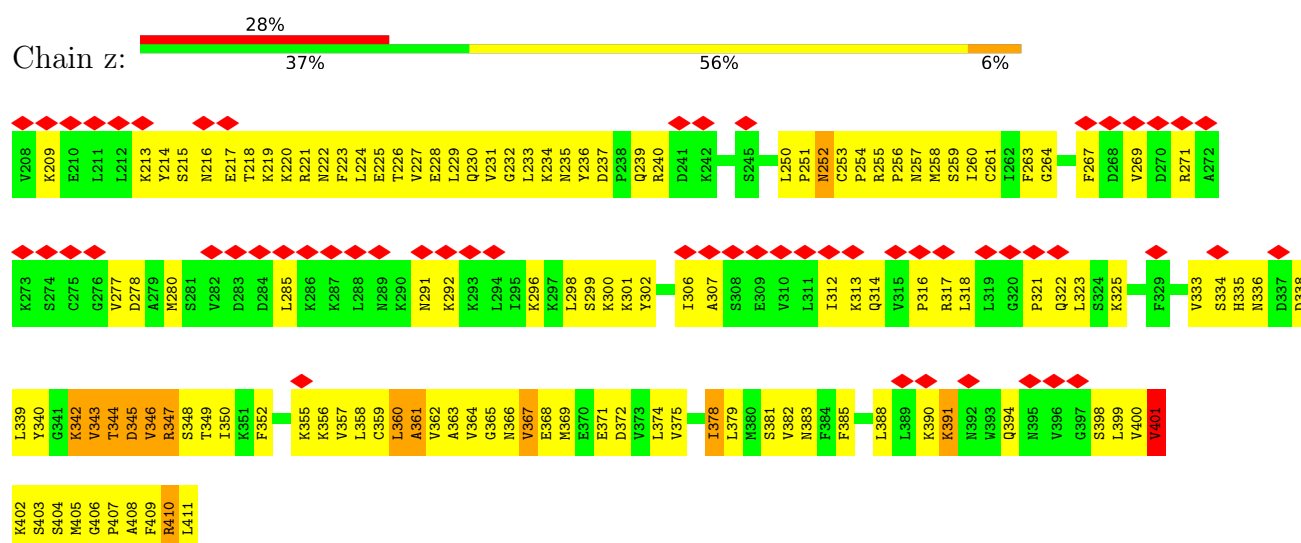
- Molecule 48 is a protein called P2.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	y	46	Total	C	N	O	0	0
			230	138	46	46		

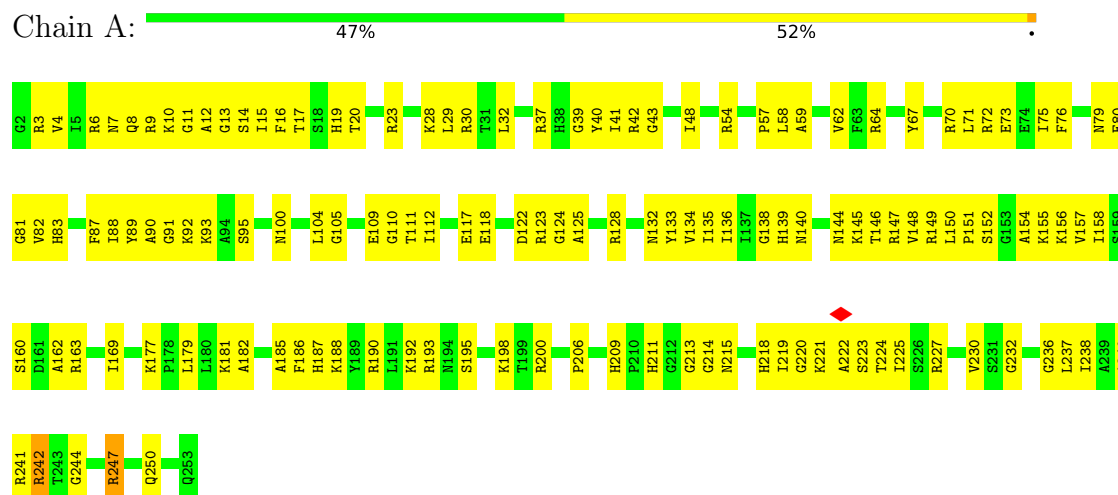
3 Residue-property plots

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: 60S ribosomal protein L1-A

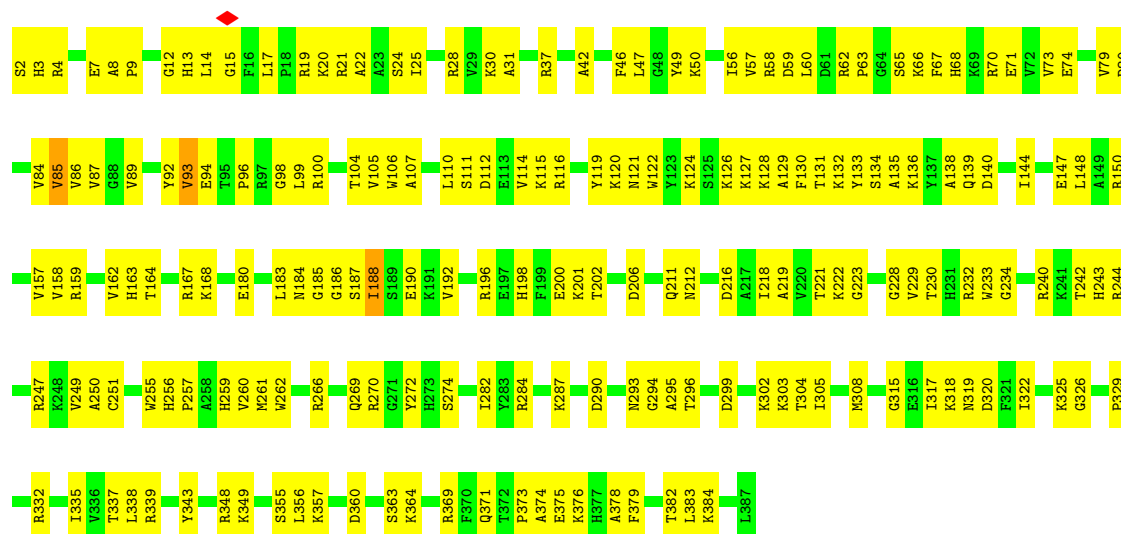


• Molecule 2: 60S ribosomal protein L2-A

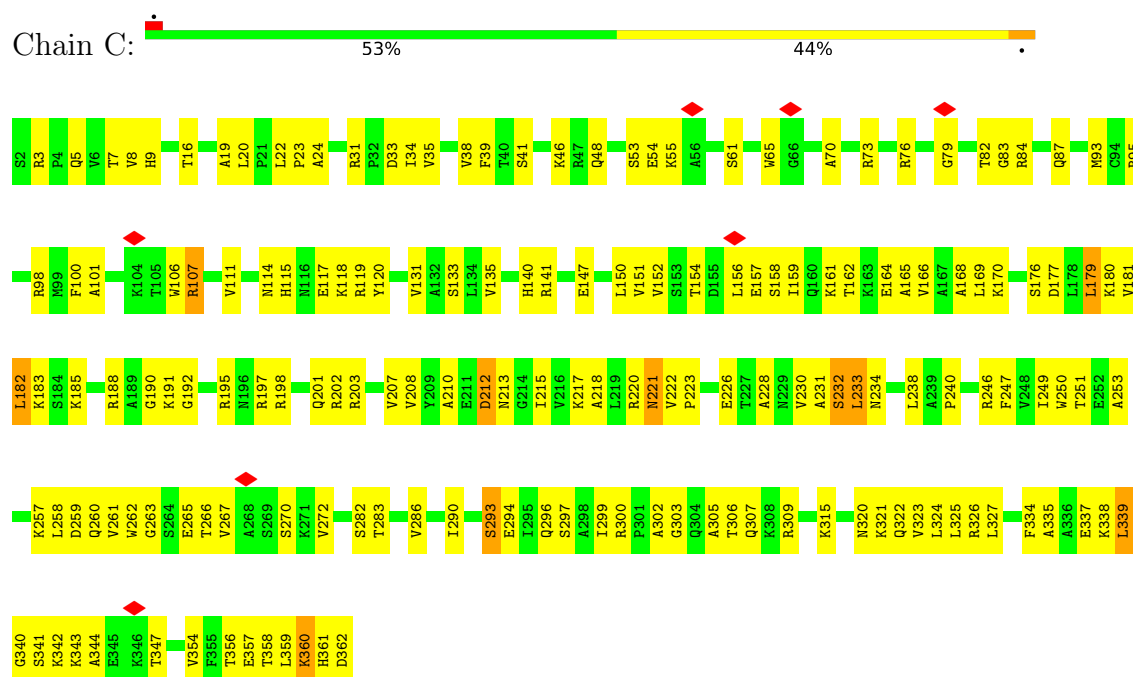


• Molecule 3: 60S ribosomal protein L3

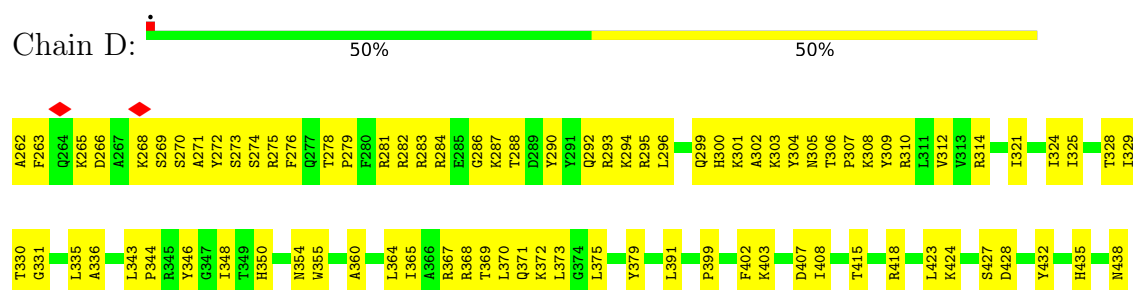




• Molecule 4: 60S ribosomal protein L4-A

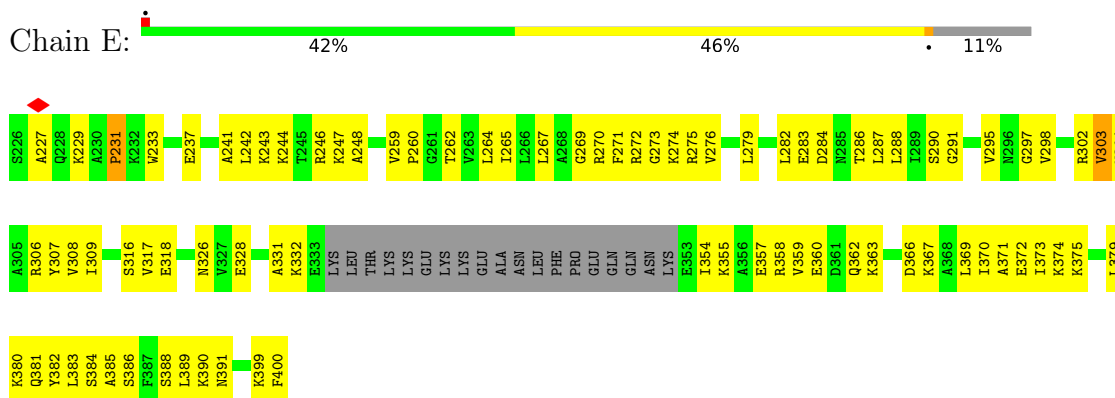


• Molecule 5: 60S ribosomal protein L5

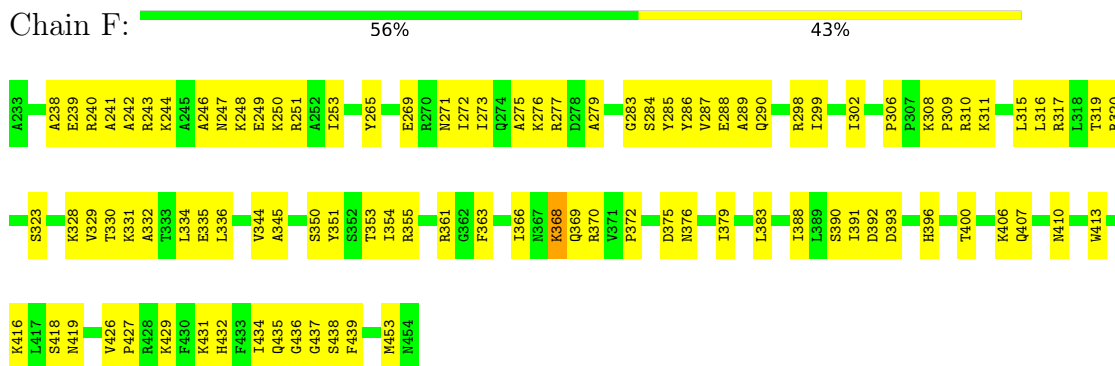




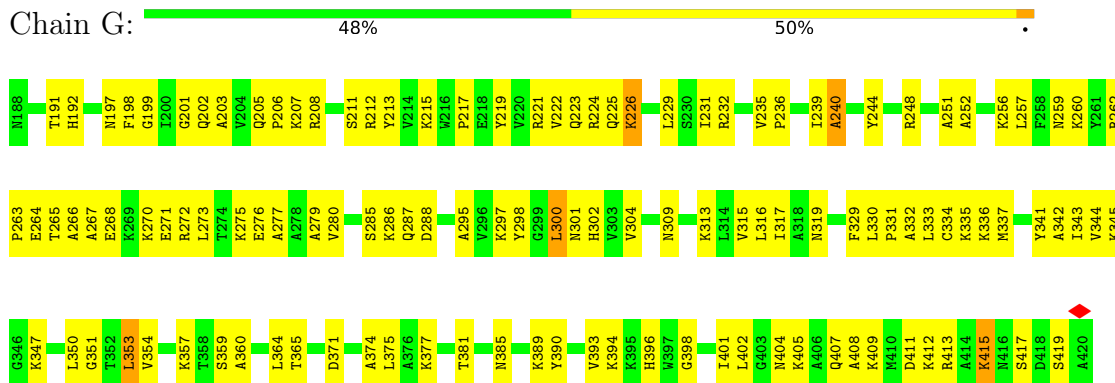
• Molecule 6: 60S ribosomal protein L6-A



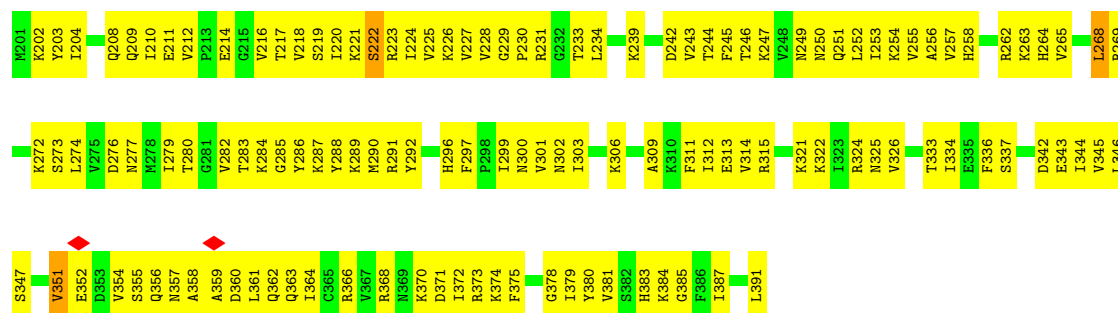
• Molecule 7: 60S ribosomal protein L7-A



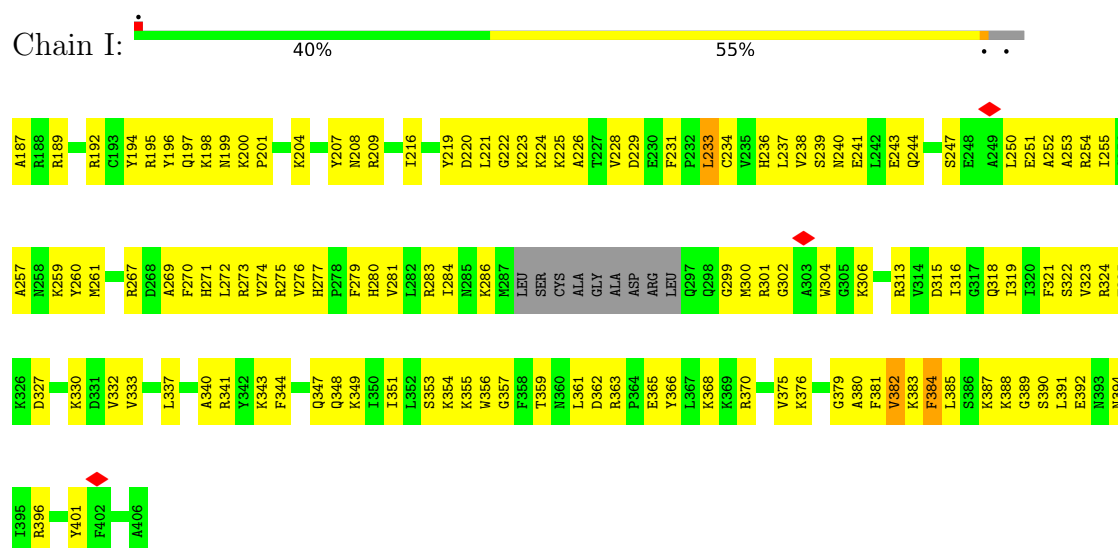
• Molecule 8: 60S ribosomal protein L8-A



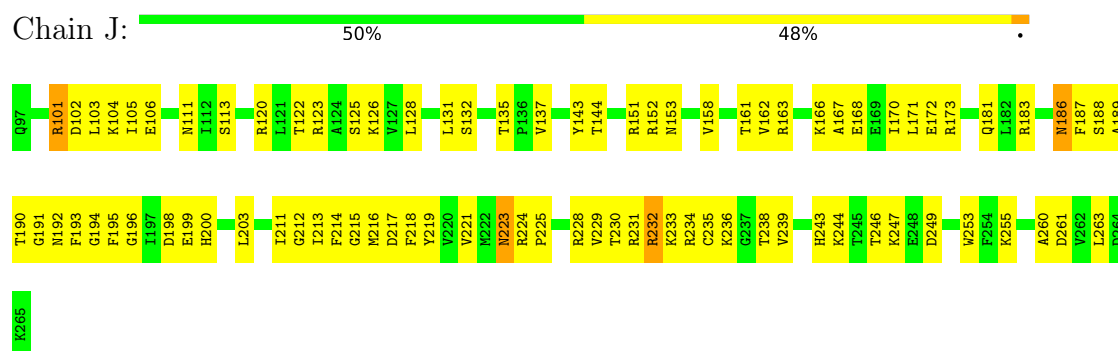
• Molecule 9: 60S ribosomal protein L9-A



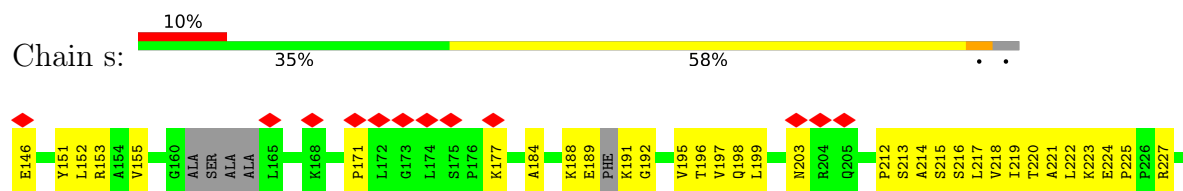
• Molecule 10: 60S ribosomal protein L10

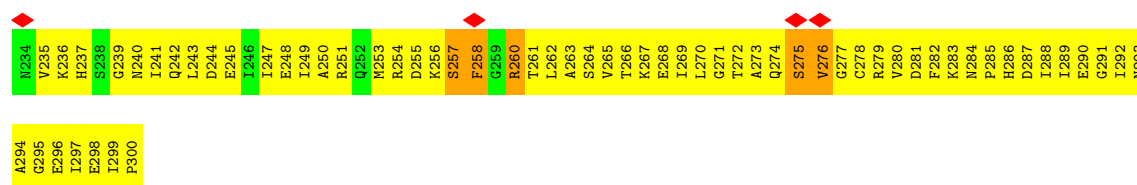


• Molecule 11: 60S ribosomal protein L11-B



• Molecule 12: 60S ribosomal protein L12-A





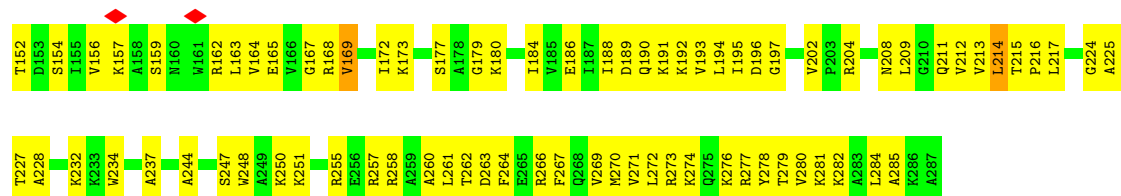
• Molecule 13: 60S ribosomal protein L13-A

Chain L: 47% 50%



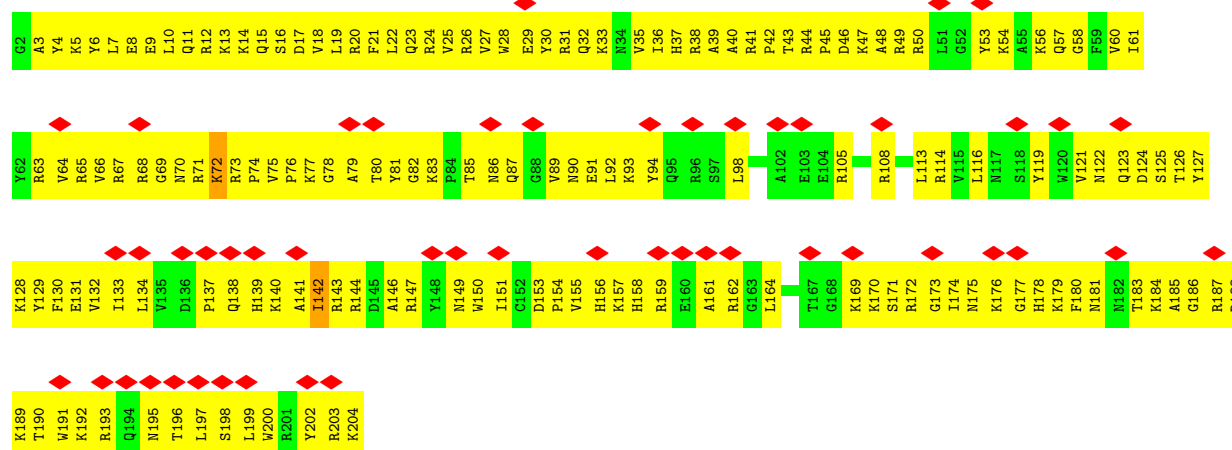
• Molecule 14: 60S ribosomal protein L14-A

Chain M: 43% 56%



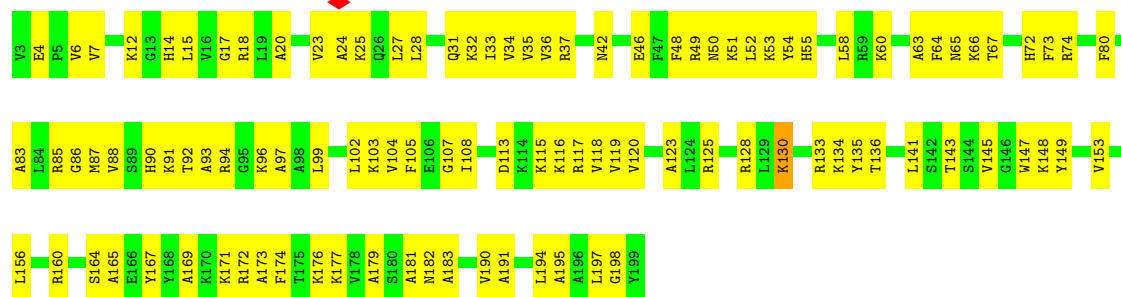
• Molecule 15: 60S ribosomal protein L15-A

Chain N: 25% 21% 78%



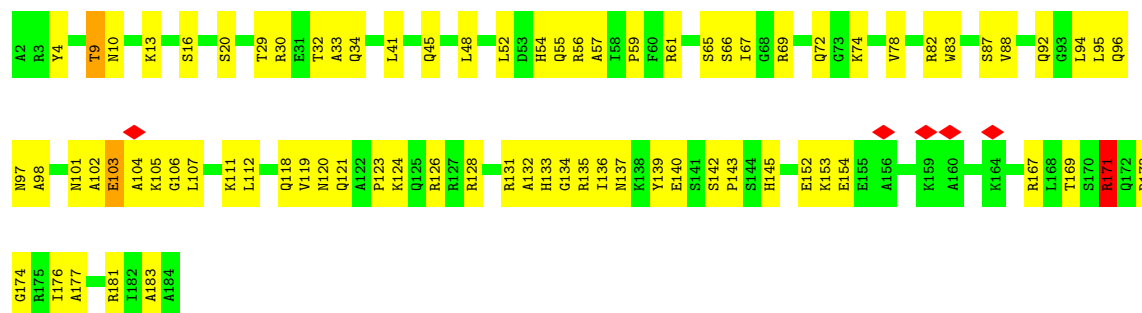
• Molecule 16: 60S ribosomal protein L16-A

Chain O:  47% 53%



• Molecule 17: 60S ribosomal protein L17-A

Chain P:  57% 42%



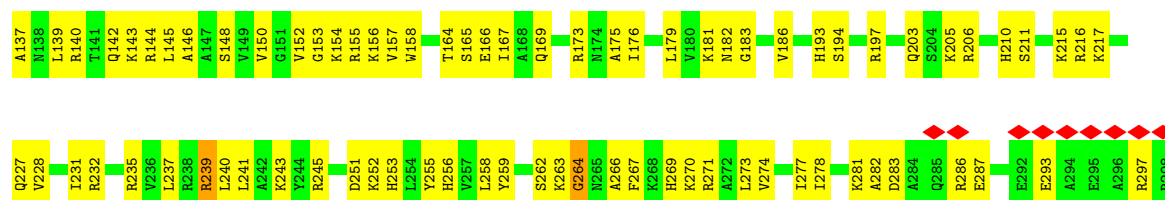
• Molecule 18: 60S ribosomal protein L18-A

Chain Q:  53% 45%



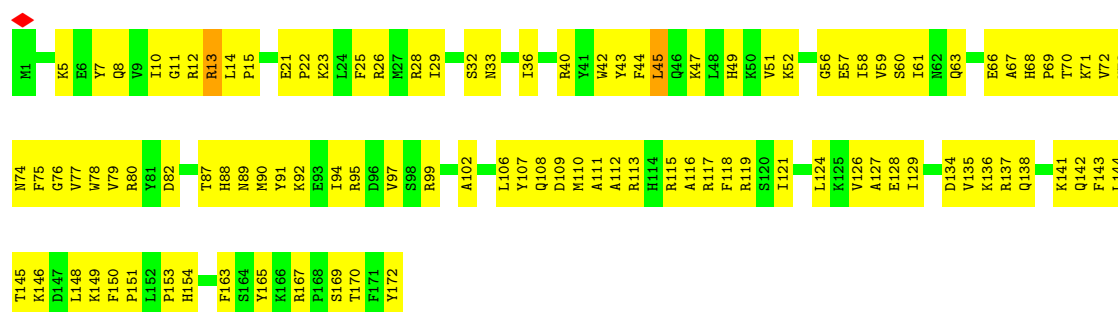
• Molecule 19: 60S ribosomal protein L19-A

Chain R:  19% 54% 44%

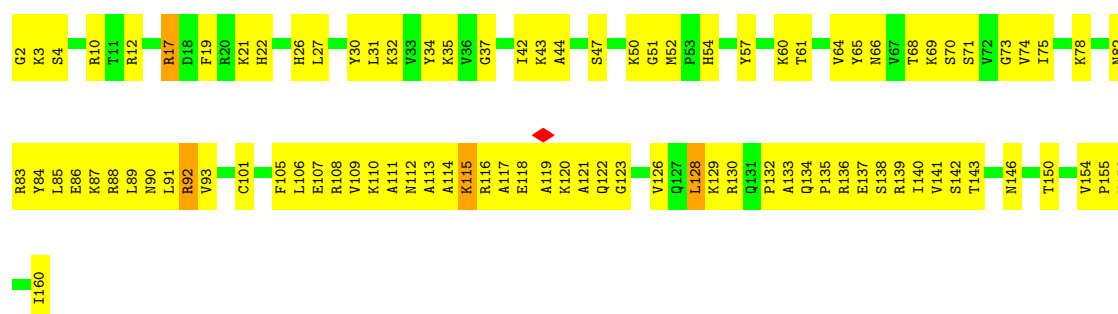




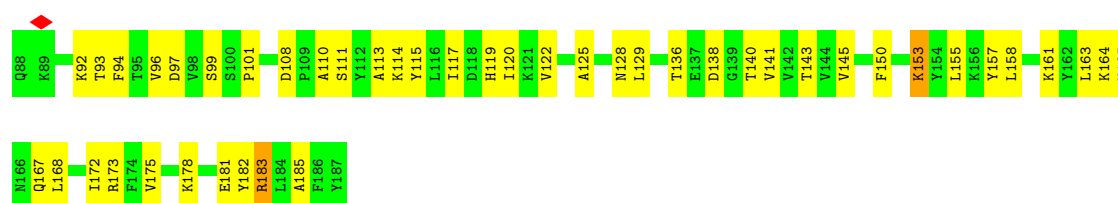
• Molecule 20: 60S ribosomal protein L20-A



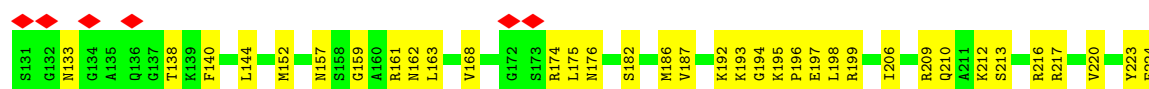
• Molecule 21: 60S ribosomal protein L21-A



• Molecule 22: 60S ribosomal protein L22-A

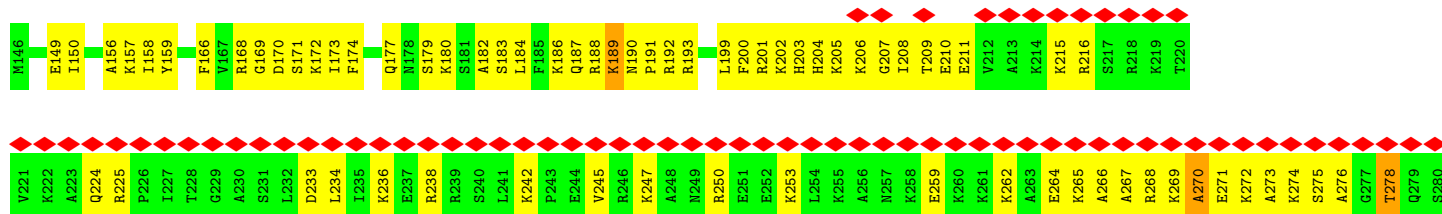


• Molecule 23: 60S ribosomal protein L23-A

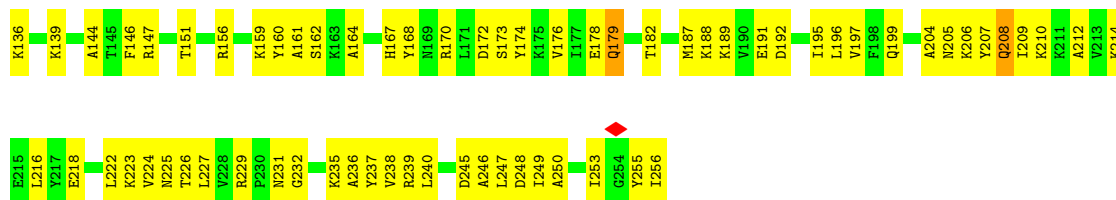




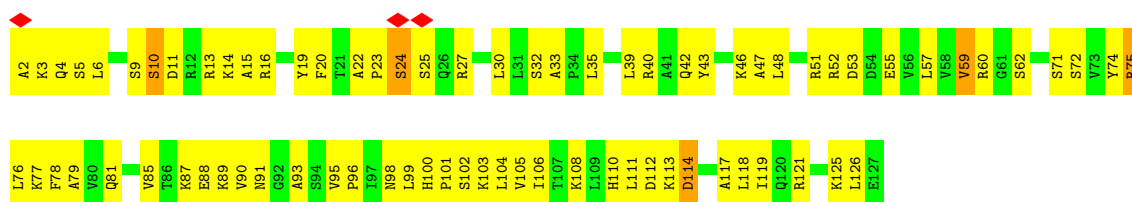
• Molecule 24: 60S ribosomal protein L24-A



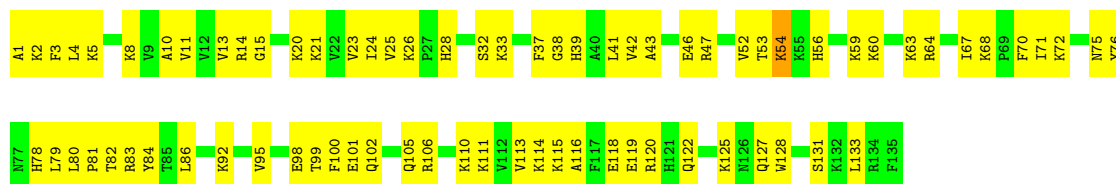
• Molecule 25: 60S ribosomal protein L25



• Molecule 26: 60S ribosomal protein L26-A

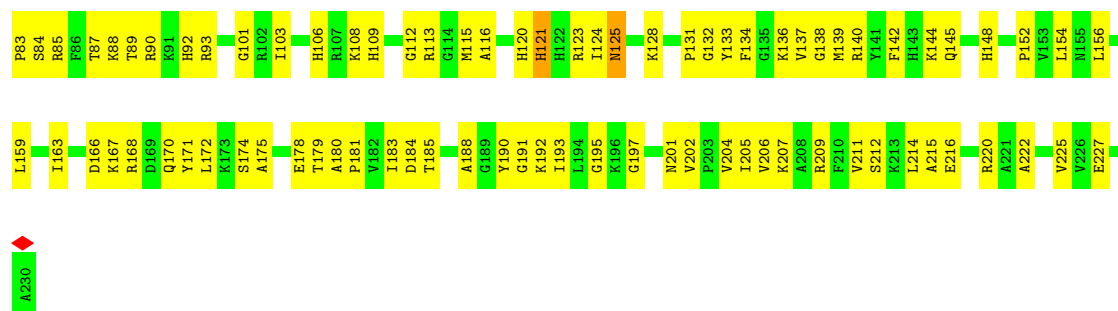


• Molecule 27: 60S ribosomal protein L27-A

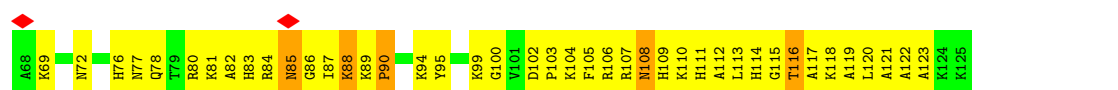


• Molecule 28: 60S ribosomal protein L28

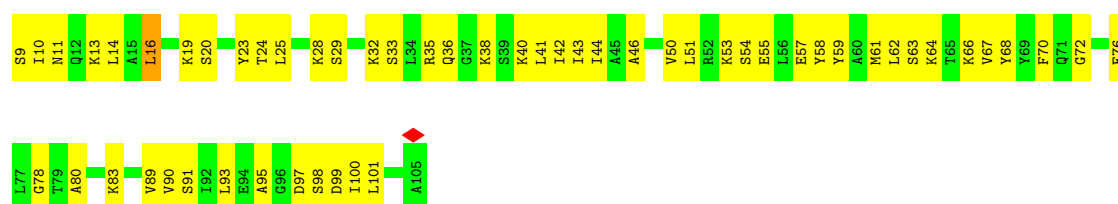




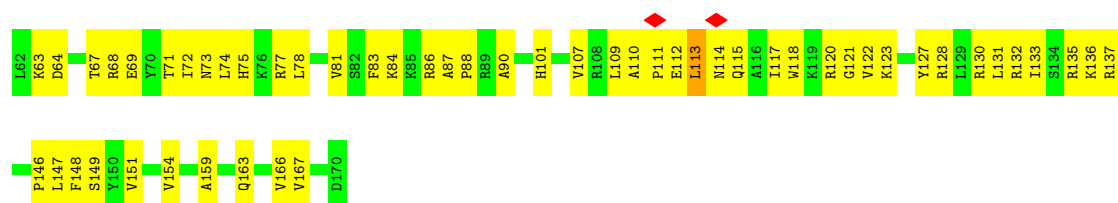
- Molecule 29: 60S ribosomal protein L29



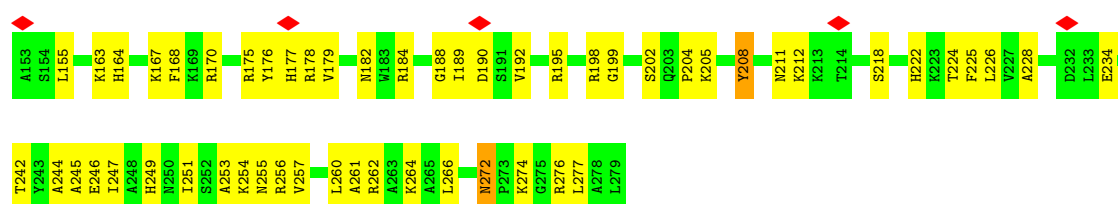
- Molecule 30: 60S ribosomal protein L30



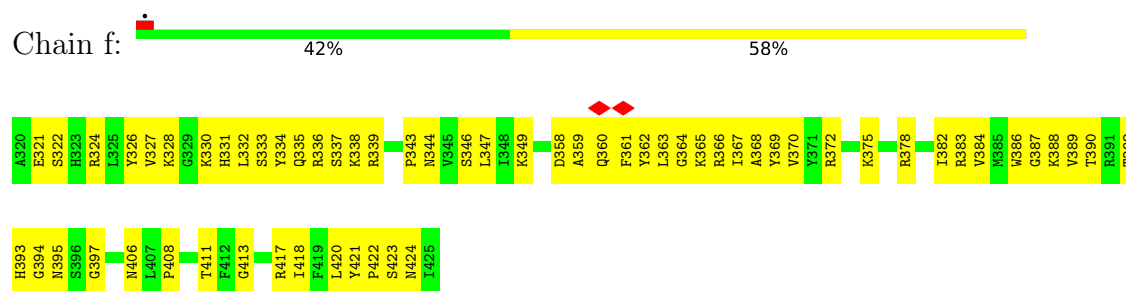
- Molecule 31: 60S ribosomal protein L31-A



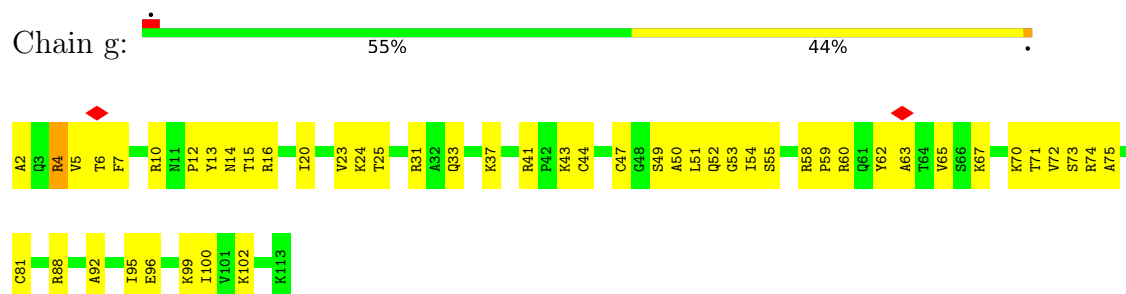
- Molecule 32: 60S ribosomal protein L32



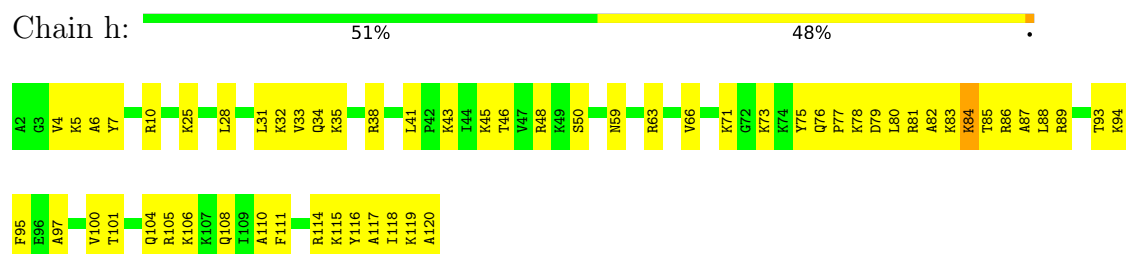
- Molecule 33: 60S ribosomal protein L33-A



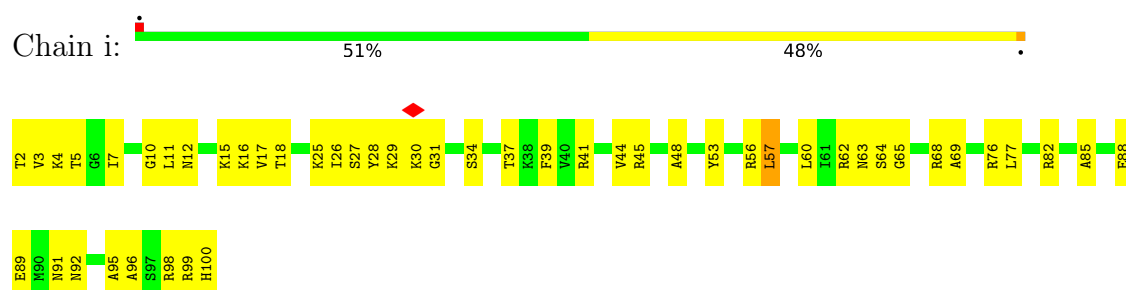
- Molecule 34: 60S ribosomal protein L34-A



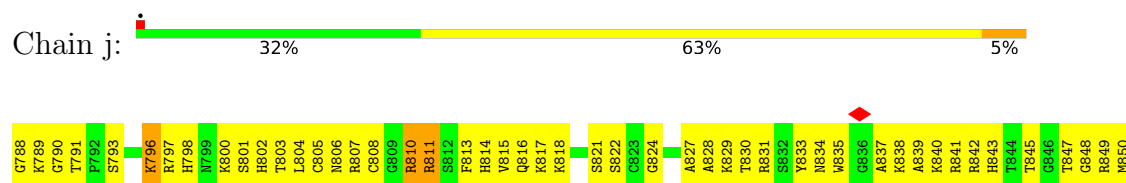
- Molecule 35: 60S ribosomal protein L35-A



- Molecule 36: 60S ribosomal protein L36-A

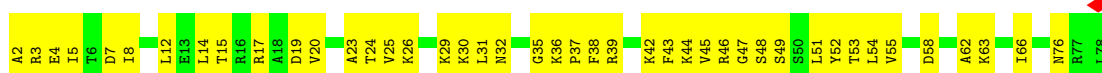


- Molecule 37: 60S ribosomal protein L37-A

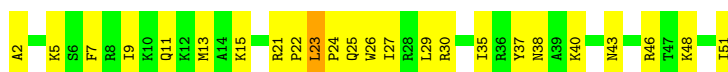




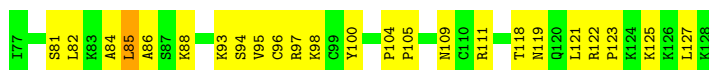
- Molecule 38: 60S ribosomal protein L38



- Molecule 39: 60S ribosomal protein L39



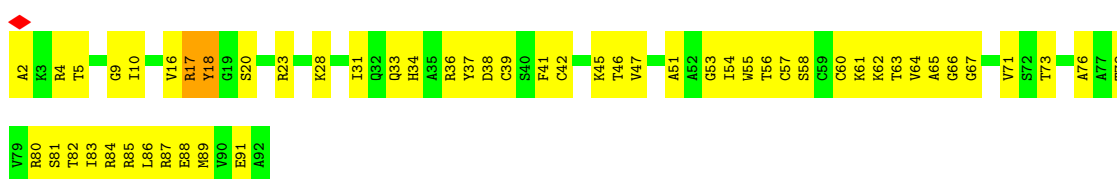
- Molecule 40: Ubiquitin-60S ribosomal protein L40



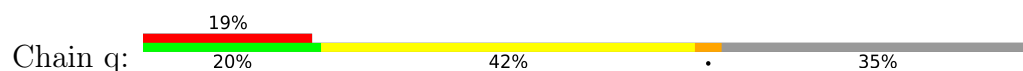
- Molecule 41: 60S ribosomal protein L42-A

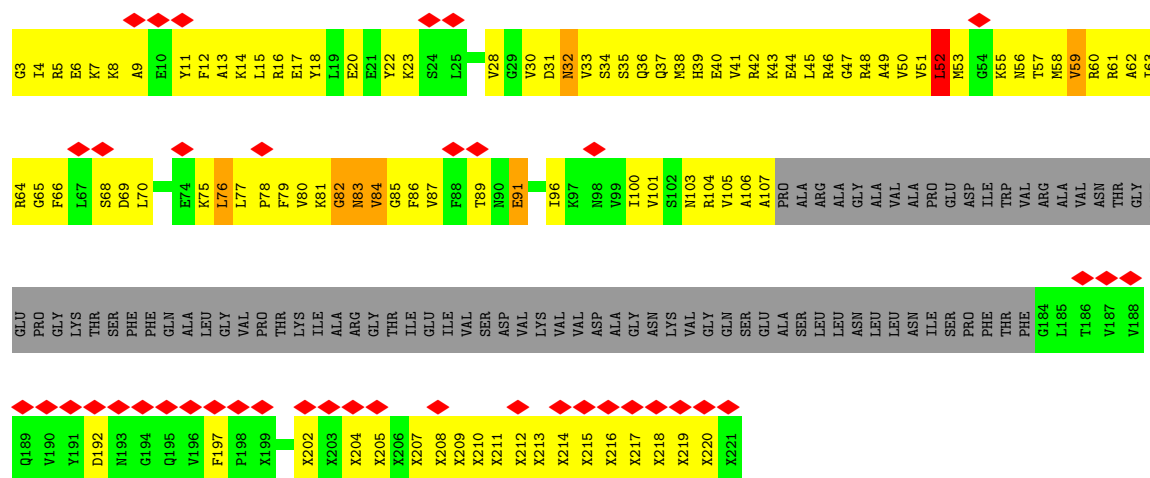


- Molecule 42: 60S ribosomal protein L43-A



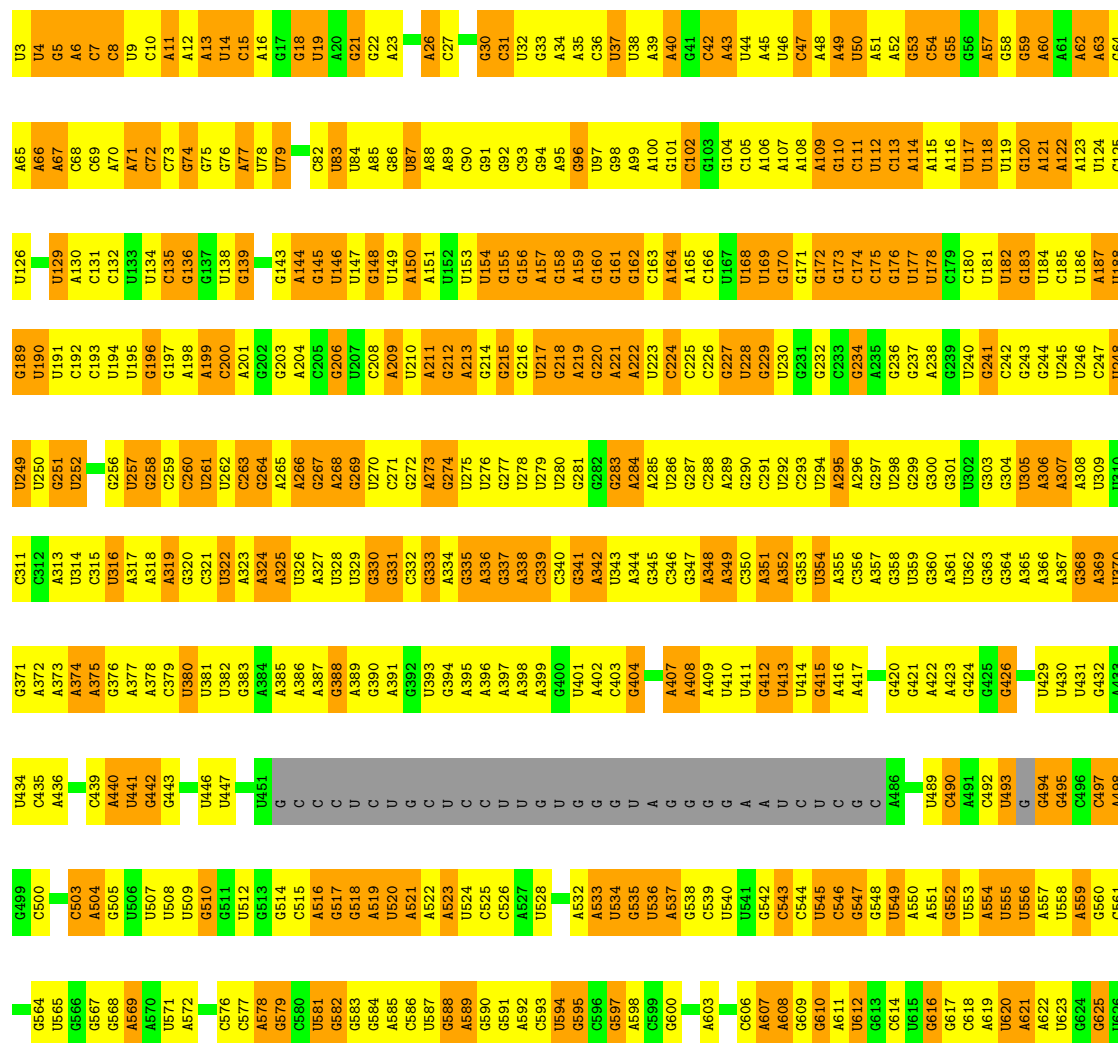
- Molecule 43: 60S acidic ribosomal protein P0,60S acidic ribosomal protein P0,AO, L1OE





• Molecule 44: 25S ribosomal RNA

Chain 5: 19% 48% 29% .



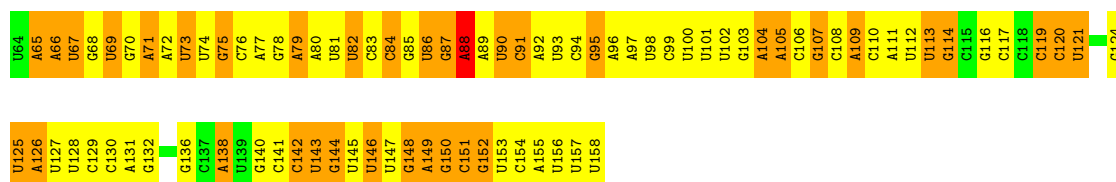
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A1534	A1471	A1406	C1339	A1273	G1213	U1151	U1081	G1019	C959	U893	G826	G763	G632
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G1536	G1473	G1408	U1341	C1275	C1215	G1153	G1083	A962	C961	A896	U829	C765	C634
A1537	A1474	C1411	U1342	U1276	C1216	A1154	A1084	G1021	G962	U897	U829	U766	G701
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G1542	A1481	G1416	C1349	C1281	A1221	A1159	G1089	U1027	U967	G902	U834	U772	U707
G1543	A1482	C1417	A1350	G1282	C1222	A1160	U1090	U1028	G968	U903	G835	G773	G708
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U2530	A2404	A2275	U2340	A2275	A2139	A1884	C1953	A1884	U1821	G1758	G1634
U2531	C2405	G2276	A2341	G2276	A2140	U1885	U1954	U1885	C1822	C1759	G1635
U2532	U2406	C2277	U2342	C2277	A2141	A1886	A1955	A1886	A1823	A1760	U1636
U2533	C2407	C2278	U2343	C2278	A2142	A1887	A1956	A1887	U1824	C1761	A1637
U2534	U2408	A2279	A2344	A2279	A2143	G1888	C1957	G1888	G1825	C1762	A1638
U2535	U2409	A2280	C2345	A2280	U2144	U1889	U1958	U1889	C1826	U1763	C1639
U2536	U2410	A2281	U2346	A2281	A2145	G1890	C1959	G1890	G1829	U1764	G1640
U2537	U2411	U2282	A2347	U2282	A2146	A1893	A1960	A1893	G1830	U1765	U1641
U2538	G2412	G2283	A2348	G2283	C2151	U1894	G1961	U1894	U1831	G1768	A1642
U2539	U2413	C2284	C2350	C2284	A2152	A1895	G1962	A1895	C1832	U1769	A1643
U2540	U2414	C2285	U2351	C2285	U2153	G1896	C	G1896	C1833	C1770	C1644
U2541	U2415	U2286	A2352	U2286	U2154	G1897	C	G1897	A1835	G1770	U1645
U2542	U2416	C2287	G2353	C2287	G2155	G1898	C	G1898	C1836	C1771	G1646
U2543	A2417	C2288	C2354	C2288	C2156	G1899	U	G1899	U1837	C1772	A1647
U2544	A2418	U2289	A2355	U2289	G2157	U1900	U	U1900	G1773	C1773	A1648
U2545	A2419	C2290	G2356	C2290	A2158	A1901	G	A1901	C1774	U1774	U1649
U2546	A2420	A2291	U2357	A2291	U2159	G1902	U	G1902	G1775	G1775	G1650
U2547	U2423	U2292	A2358	U2292	G2160	U1903	C	U1903	U1776	U1776	U1651
U2548	A2424	C2293	A2359	C2293	G2161	G1904	C	G1904	U1777	U1777	G1652
U2549	G2425	U2294	A2361	U2294	U2162	G1905	U	G1905	G1778	U1717	G1653
U2550	U2426	U2295	C2362	U2295	C2163	U1906	C	U1906	C1842	G1718	A1654
U2551	U2427	A2296	A2363	A2296	A2164	C1907	G	C1907	G1843	G1719	G1655
U2552	U2428	A2297	U2364	A2297	C2094	C1907	C	C1907	C1844	G1780	A1656
U2553	U2429	U2297	C2365	U2297	G2165	A1908	C	A1908	G1845		
U2554	U2430	U2298	C2366	U2298	G2166						
U2555	U2431	U2299	C2367	U2299	G2167						
U2556	U2432	U2300	A2368	U2300	G2168						
U2557	U2433	U2301	A2369	U2301	G2169						
U2558	U2434	U2302	G2370	U2302	G2170						
U2559	U2435	U2303	G2371	U2303	G2171						
U2560	U2436	U2304	A2372	U2304	A2172						
U2561	U2437	U2305	A2373	U2305	U2173						
U2562	U2438	U2306	C2374	U2306	G2174						
U2563	U2439	U2307	G2375	U2307	U2175						
U2564	U2440	U2308	G2376	U2308	U2176						
U2565	U2441	U2309	G2377	U2309	G2177						
U2566	U2442	U2310	A2378	U2310	A2178						
U2567	U2443	U2311	C2379	U2311	C2179						
U2568	U2444	U2312	U2380	U2312	G2180						
U2569	U2445	U2313	U2381	U2313	G2181						
U2570	U2446	U2314	U2382	U2314	A2182						
U2571	U2447	U2315	U2383	U2315	U2183						
U2572	U2448	U2316	U2384	U2316	U2184						
U2573	U2449	U2317	U2385	U2317	G2185						
U2574	U2450	U2318	U2386	U2318	U2186						
U2575	U2451	U2319	A2387	U2319	G2187						
U2576	U2452	U2320	U2388	U2320	A2188						
U2577	U2453	U2321	U2389	U2321	U2189						
U2578	U2454	U2322	U2390	U2322	G2190						
U2579	U2455	U2323	U2391	U2323	G2191						
U2580	U2456	U2324	U2392	U2324	G2192						
U2581	U2457	U2325	U2393	U2325	U2193						
U2582	U2458	U2326	U2394	U2326	G2194						
U2583	U2459	U2327	U2395	U2327	C2195						
U2584	U2460	U2328	U2396	U2328	C2196						
U2585	U2461	U2329	U2397	U2329	C2197						
U2586	U2462	U2330	U2398	U2330	A2198						
U2587	U2463	U2331	U2399	U2331	U2199						
U2588	U2464	U2332	U2400	U2332	G2192						
U2589	U2465	U2333	A2401	U2333	U2193						
U2590	U2466	U2334	G2402	U2334	G2194						
U2591	U2467	U2335	A2403	U2335	C2195						
U2592	U2468	U2336	G2404	U2336	C2196						
U2593	U2469	U2337	A2405	U2337	C2197						
U2594	U2470	U2338	C2406	U2338	C2198						
U2595	U2471	U2339	C2407	U2339	A2198						
U2596	U2472	U2340	U2408	U2340	G2199						
U2597	U2473	U2341	U2409	U2341	G2200						
U2598	U2474	U2342	U2410	U2342	G2201						
U2599	U2475	U2343	U2411	U2343	G2202						
U2600	U2476	U2344	U2412	U2344	G2203						
U2601	U2477	U2345	U2413	U2345	G2204						
U2602	U2478	U2346	U2414	U2346	G2205						
U2603	U2479	U2347	U2415	U2347	G2206						
U2604	U2480	U2348	U2416	U2348	G2207						
U2605	U2481	U2349	U2417	U2349	A2207						
U2606	U2482	U2350	U2418	U2350	A2208						
U2607	U2483	U2351	U2419	U2351	U2209						
U2608	U2484	U2352	U2420	U2352	G2210						
U2609	U2485	U2353	U2421	U2353	G2211						
U2610	U2486	U2354	U2422	U2354	C2212						
U2611	U2487	U2355	U2423	U2355	A2213						
U2612	U2488	U2356	U2424	U2356	G2214						
U2613	U2489	U2357	U2425	U2357	A2215						
U2614	U2490	U2358	U2426	U2358	G2216						
U2615	U2491	U2359	U2427</								

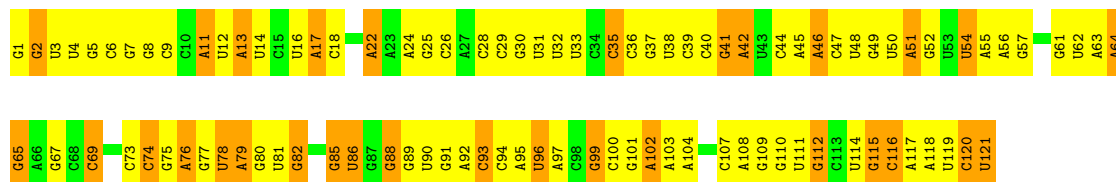
- Molecule 45: 5.8S ribosomal RNA

Chain 8: 13% 46% 41%

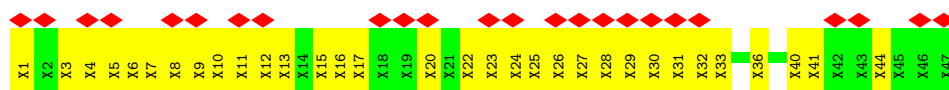
[illegible]



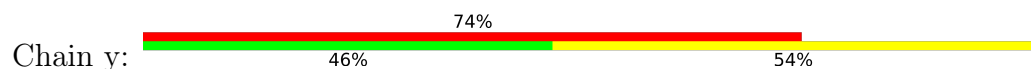
• Molecule 46: 5S ribosomal RNA



• Molecule 47: P1



• Molecule 48: P2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83558	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	0.232	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	476.16, 476.16, 476.16	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.24, 1.24, 1.24	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	z	0.46	0/1620	1.05	5/2164 (0.2%)
2	A	0.40	0/1952	0.78	0/2622
3	B	0.39	0/3153	0.77	2/4239 (0.0%)
4	C	0.41	0/2802	0.83	2/3792 (0.1%)
5	D	0.42	0/2426	0.74	0/3271
6	E	0.44	0/1261	0.83	2/1694 (0.1%)
7	F	0.49	0/1822	0.84	0/2451
8	G	0.42	0/1850	0.79	0/2495
9	H	0.48	0/1540	0.82	1/2073 (0.0%)
10	I	0.47	0/1754	0.82	1/2350 (0.0%)
11	J	0.45	0/1375	0.88	1/1842 (0.1%)
12	s	0.41	0/734	0.97	2/1015 (0.2%)
13	L	0.44	0/1568	0.87	0/2106
14	M	0.47	0/1069	0.80	0/1438
15	N	0.38	0/1758	0.80	0/2354
16	O	0.41	0/1586	0.72	0/2128
17	P	0.44	0/1466	0.81	2/1968 (0.1%)
18	Q	0.42	0/1466	0.84	0/1965
19	R	1.85	3/1539 (0.2%)	1.22	10/2050 (0.5%)
20	S	0.43	0/1482	0.80	0/1990
21	T	0.41	0/1301	0.79	0/1743
22	U	0.44	0/812	0.81	0/1099
23	V	0.39	0/1019	0.74	0/1369
24	W	0.47	0/1099	0.91	2/1446 (0.1%)
25	X	0.41	0/984	0.78	1/1325 (0.1%)
26	Y	0.44	0/1005	0.89	0/1341
27	Z	0.46	0/1119	0.84	0/1497
28	a	0.38	0/1205	0.82	1/1612 (0.1%)
29	b	0.50	0/474	1.08	4/629 (0.6%)
30	c	0.48	0/751	0.82	0/1008
31	d	0.43	0/904	0.75	0/1213
32	e	0.43	0/1041	0.88	0/1394
33	f	0.39	0/869	0.74	0/1168
34	g	0.40	0/891	0.79	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.46	0/979	0.81	2/1301 (0.2%)
36	i	0.47	0/779	0.83	0/1034
37	j	0.45	0/697	0.86	1/923 (0.1%)
38	k	0.41	0/619	0.81	0/826
39	l	0.43	0/444	0.86	0/588
40	m	0.40	0/424	0.79	0/562
41	o	0.59	1/861 (0.1%)	0.86	0/1136
42	p	0.47	0/702	0.81	0/934
43	q	0.50	0/977	1.01	3/1313 (0.2%)
44	5	0.60	3/77625 (0.0%)	0.70	16/121004 (0.0%)
45	8	0.58	0/3747	0.69	1/5832 (0.0%)
46	7	0.59	0/2884	0.67	0/4491
All	All	0.57	7/138435 (0.0%)	0.75	59/203986 (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
1	z	0	8
2	A	0	2
4	C	0	11
5	D	0	2
6	E	0	4
7	F	0	4
8	G	0	1
9	H	0	2
10	I	0	1
11	J	0	2
12	s	0	4
13	L	0	3
14	M	0	1
15	N	0	1
17	P	0	2
18	Q	0	2
19	R	0	3
20	S	0	3
21	T	0	4
24	W	0	3
25	X	0	2
26	Y	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	Z	0	1
28	a	0	1
29	b	0	2
32	e	0	2
33	f	0	1
34	g	0	1
37	j	0	2
42	p	0	1
43	q	0	3
All	All	0	85

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	312	VAL	CA-C	68.87	2.35	1.52
44	5	2263	C	O3'-P	-66.41	0.61	1.61
44	5	2279	A	O3'-P	23.70	1.96	1.61
41	o	12	CYS	CA-CB	-12.40	1.36	1.52
19	R	312	VAL	C-N	12.15	1.50	1.33

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	5	2279	A	O3'-P-O5'	-39.18	45.23	104.00
44	5	2279	A	P-O3'-C3'	28.41	162.82	120.20
19	R	312	VAL	CB-CA-C	25.93	138.62	110.62
44	5	2263	C	P-O3'-C3'	25.66	158.69	120.20
44	5	2263	C	OP2-P-O3'	-17.15	56.55	108.00

There are no chirality outliers.

5 of 85 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	z	345	ASP	Peptide
1	z	347	ARG	Peptide
1	z	355	LYS	Peptide
1	z	361	ALA	Peptide
1	z	367	VAL	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	z	1602	0	1622	801	0
2	A	1918	0	1987	170	0
3	B	3082	0	3164	344	0
4	C	2750	0	2863	216	0
5	D	2376	0	2324	252	0
6	E	1240	0	1325	217	0
7	F	1785	0	1860	229	0
8	G	1818	0	1908	146	0
9	H	1519	0	1584	211	0
10	I	1718	0	1753	255	0
11	J	1354	0	1383	119	0
12	s	737	0	293	736	0
13	L	1543	0	1608	237	0
14	M	1054	0	1149	176	0
15	N	1721	0	1679	1806	0
16	O	1556	0	1659	167	0
17	P	1443	0	1485	101	0
18	Q	1442	0	1543	108	0
19	R	1522	0	1617	125	0
20	S	1446	0	1487	146	0
21	T	1277	0	1321	319	0
22	U	796	0	812	40	0
23	V	1004	0	1048	75	0
24	W	1089	0	1176	65	0
25	X	969	0	1036	82	0
26	Y	994	0	1081	150	0
27	Z	1093	0	1158	76	0
28	a	1174	0	1215	97	0
29	b	463	0	491	112	0
30	c	743	0	797	66	0
31	d	890	0	938	69	0
32	e	1020	0	1090	88	0
33	f	851	0	880	105	0
34	g	881	0	949	160	0
35	h	970	0	1078	150	0
36	i	772	0	847	110	0
37	j	682	0	680	192	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	613	0	682	31	0
39	l	437	0	474	88	0
40	m	418	0	459	33	0
41	o	848	0	918	87	0
42	p	695	0	738	95	0
43	q	1077	0	954	789	0
44	5	69359	0	34686	7895	0
45	8	3354	0	1689	368	0
46	7	2580	0	1302	208	0
47	x	235	0	41	135	0
48	y	230	0	42	140	0
All	All	129140	0	92875	11329	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 54.

The worst 5 of 11329 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)
1:z:363:ALA:CB	44:5:2466:G:C6	1.75	1.70
15:N:81:TYR:HA	44:5:2427:U:C6	1.25	1.66
15:N:81:TYR:CE1	44:5:2428:U:H6	0.99	1.65
43:q:28:VAL:CG2	44:5:1281:G:H4'	1.23	1.65
15:N:7:LEU:HD21	44:5:111:C:C4	1.24	1.64

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	z	199/204 (98%)	138 (69%)	61 (31%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	250/252 (99%)	204 (82%)	46 (18%)	0	100	100
3	B	384/386 (100%)	315 (82%)	67 (17%)	2 (0%)	24	57
4	C	359/361 (99%)	292 (81%)	65 (18%)	2 (1%)	21	54
5	D	294/296 (99%)	263 (90%)	31 (10%)	0	100	100
6	E	152/175 (87%)	133 (88%)	19 (12%)	0	100	100
7	F	220/222 (99%)	188 (86%)	31 (14%)	1 (0%)	24	57
8	G	231/233 (99%)	199 (86%)	32 (14%)	0	100	100
9	H	189/191 (99%)	159 (84%)	30 (16%)	0	100	100
10	I	207/220 (94%)	173 (84%)	34 (16%)	0	100	100
11	J	167/169 (99%)	140 (84%)	27 (16%)	0	100	100
12	s	144/155 (93%)	93 (65%)	51 (35%)	0	100	100
13	L	191/193 (99%)	161 (84%)	27 (14%)	3 (2%)	7	35
14	M	134/136 (98%)	117 (87%)	17 (13%)	0	100	100
15	N	201/203 (99%)	171 (85%)	29 (14%)	1 (0%)	24	57
16	O	195/197 (99%)	171 (88%)	24 (12%)	0	100	100
17	P	181/183 (99%)	156 (86%)	25 (14%)	0	100	100
18	Q	183/185 (99%)	157 (86%)	26 (14%)	0	100	100
19	R	186/188 (99%)	159 (86%)	26 (14%)	1 (0%)	24	57
20	S	170/172 (99%)	143 (84%)	27 (16%)	0	100	100
21	T	157/159 (99%)	136 (87%)	21 (13%)	0	100	100
22	U	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
23	V	134/136 (98%)	113 (84%)	21 (16%)	0	100	100
24	W	126/135 (93%)	101 (80%)	24 (19%)	1 (1%)	16	48
25	X	119/121 (98%)	102 (86%)	17 (14%)	0	100	100
26	Y	124/126 (98%)	105 (85%)	19 (15%)	0	100	100
27	Z	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	16	48
28	a	146/148 (99%)	124 (85%)	21 (14%)	1 (1%)	18	51
29	b	56/58 (97%)	47 (84%)	8 (14%)	1 (2%)	6	33
30	c	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
31	d	107/109 (98%)	88 (82%)	19 (18%)	0	100	100
32	e	125/127 (98%)	105 (84%)	20 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	f	104/106 (98%)	86 (83%)	18 (17%)	0	100	100
34	g	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
35	h	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
36	i	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
37	j	85/87 (98%)	70 (82%)	15 (18%)	0	100	100
38	k	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
39	l	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	31
40	m	50/52 (96%)	37 (74%)	13 (26%)	0	100	100
41	o	103/105 (98%)	83 (81%)	20 (19%)	0	100	100
42	p	89/91 (98%)	75 (84%)	13 (15%)	1 (1%)	11	41
43	q	117/219 (53%)	91 (78%)	26 (22%)	0	100	100
All	All	6652/6889 (97%)	5580 (84%)	1056 (16%)	16 (0%)	44	73

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	F	369	GLN
13	L	62	THR
27	Z	33	LYS
13	L	61	PRO
15	N	146	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	z	179/185 (97%)	173 (97%)	6 (3%)	32	55
2	A	194/194 (100%)	193 (100%)	1 (0%)	81	81
3	B	322/322 (100%)	320 (99%)	2 (1%)	78	79
4	C	288/288 (100%)	287 (100%)	1 (0%)	86	84
5	D	244/244 (100%)	244 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	E	134/152 (88%)	130 (97%)	4 (3%)	36	57
7	F	186/186 (100%)	185 (100%)	1 (0%)	81	81
8	G	191/191 (100%)	185 (97%)	6 (3%)	35	57
9	H	171/171 (100%)	168 (98%)	3 (2%)	51	67
10	I	180/186 (97%)	178 (99%)	2 (1%)	65	73
11	J	147/147 (100%)	143 (97%)	4 (3%)	39	59
13	L	154/154 (100%)	151 (98%)	3 (2%)	50	66
14	M	107/107 (100%)	106 (99%)	1 (1%)	70	74
15	N	175/175 (100%)	174 (99%)	1 (1%)	78	79
16	O	160/160 (100%)	159 (99%)	1 (1%)	78	79
17	P	145/145 (100%)	143 (99%)	2 (1%)	59	70
18	Q	150/150 (100%)	148 (99%)	2 (1%)	61	71
19	R	153/153 (100%)	152 (99%)	1 (1%)	76	77
20	S	156/156 (100%)	155 (99%)	1 (1%)	78	79
21	T	136/136 (100%)	135 (99%)	1 (1%)	76	77
22	U	87/87 (100%)	85 (98%)	2 (2%)	44	63
23	V	104/104 (100%)	104 (100%)	0	100	100
24	W	114/114 (100%)	114 (100%)	0	100	100
25	X	105/105 (100%)	105 (100%)	0	100	100
26	Y	109/109 (100%)	107 (98%)	2 (2%)	51	67
27	Z	115/115 (100%)	112 (97%)	3 (3%)	40	60
28	a	118/118 (100%)	116 (98%)	2 (2%)	53	67
29	b	46/46 (100%)	45 (98%)	1 (2%)	45	63
30	c	81/81 (100%)	80 (99%)	1 (1%)	63	72
31	d	96/96 (100%)	95 (99%)	1 (1%)	68	74
32	e	109/109 (100%)	109 (100%)	0	100	100
33	f	90/90 (100%)	90 (100%)	0	100	100
34	g	95/95 (100%)	94 (99%)	1 (1%)	65	73
35	h	104/104 (100%)	103 (99%)	1 (1%)	68	74
36	i	81/81 (100%)	79 (98%)	2 (2%)	42	61
37	j	70/70 (100%)	69 (99%)	1 (1%)	59	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	k	68/68 (100%)	68 (100%)	0	100	100
39	l	45/45 (100%)	43 (96%)	2 (4%)	25	49
40	m	47/47 (100%)	46 (98%)	1 (2%)	47	64
41	o	90/90 (100%)	90 (100%)	0	100	100
42	p	71/71 (100%)	71 (100%)	0	100	100
43	q	105/165 (64%)	102 (97%)	3 (3%)	37	58
All	All	5522/5612 (98%)	5456 (99%)	66 (1%)	61	72

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	i	18	THR
37	j	861	LYS
43	q	84	VAL
10	I	233	LEU
9	H	354	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
18	Q	170	ASN
37	j	814	HIS
21	T	45	ASN
37	j	798	HIS
43	q	56	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	5	3232/3394 (95%)	1470 (45%)	32 (0%)
45	8	157/158 (99%)	85 (54%)	0
46	7	120/121 (99%)	41 (34%)	0
All	All	3509/3673 (95%)	1596 (45%)	32 (0%)

5 of 1596 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	5	4	U

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Mol	Chain	Res	Type
44	5	5	G
44	5	6	A
44	5	7	C
44	5	8	C

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	5	2541	U
44	5	3121	U
44	5	705	A
44	5	637	C
44	5	3228	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	5	9
24	W	4

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2083:G	O3'	2084:C	P	19.95
1	W	217:SER	C	218:ARG	N	12.39
1	W	219:LYS	C	220:THR	N	9.79
1	W	229:GLY	C	230:ALA	N	9.10
1	5	2513:U	O3'	2514:U	P	8.49

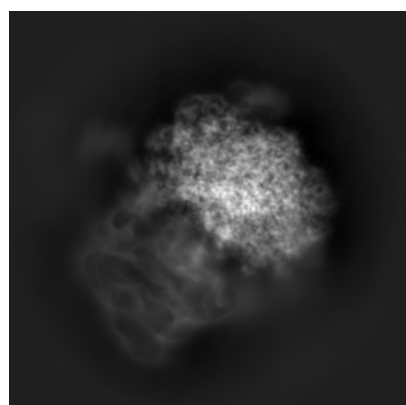
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20077. These allow visual inspection of the internal detail of the map and identification of artifacts.

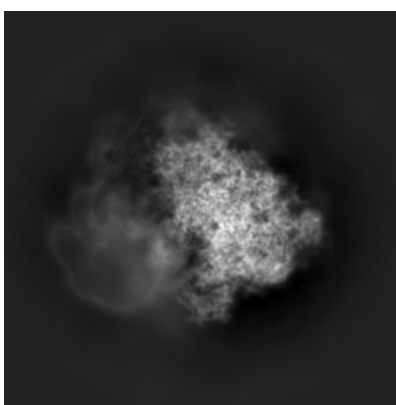
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

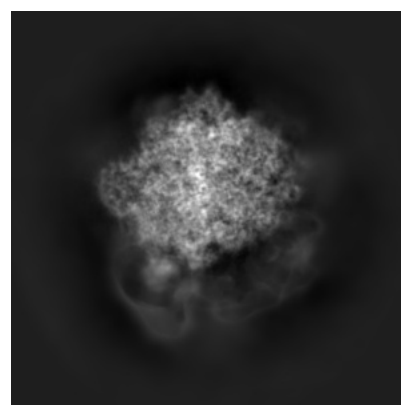
6.1.1 Primary map



X



Y

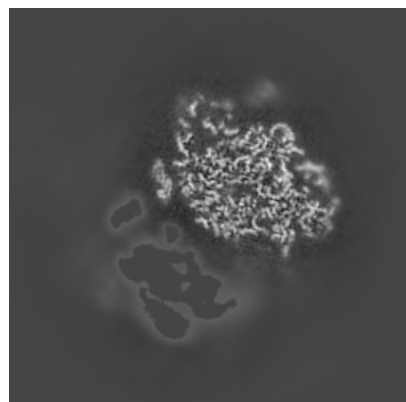


Z

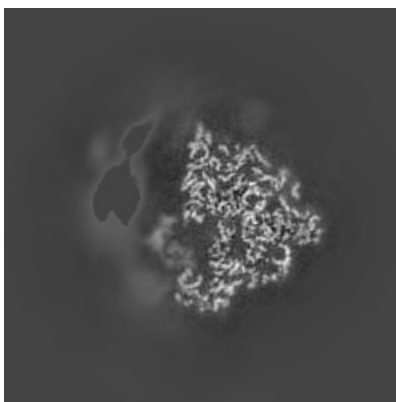
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

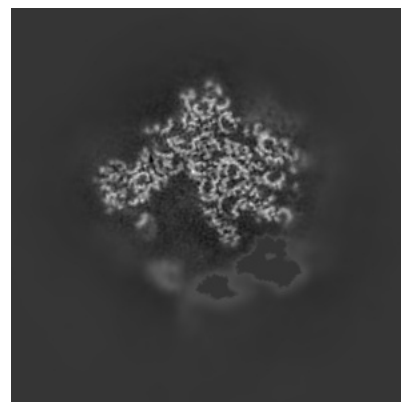
6.2.1 Primary map



X Index: 192



Y Index: 192

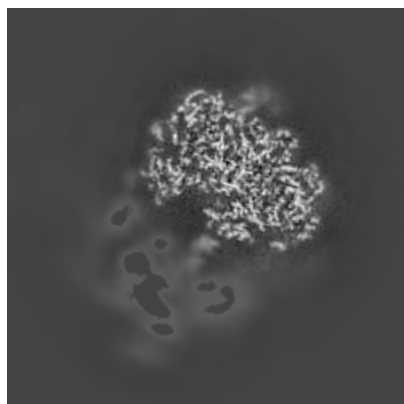


Z Index: 192

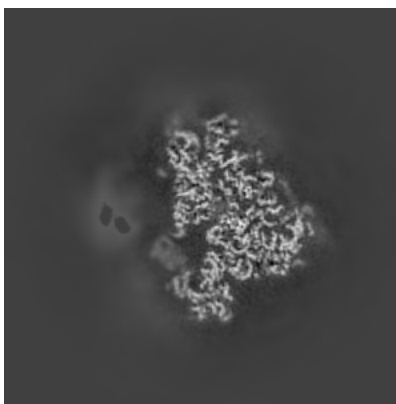
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

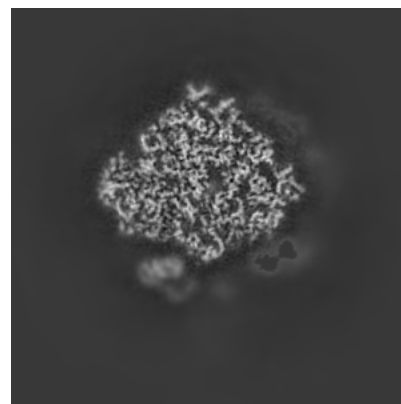
6.3.1 Primary map



X Index: 179



Y Index: 209

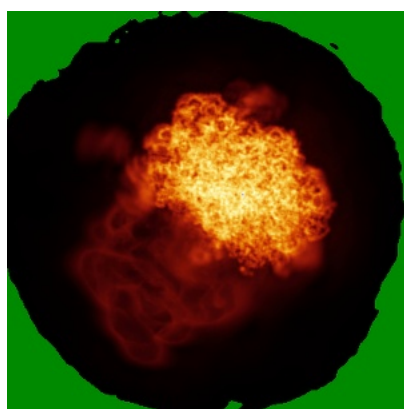


Z Index: 209

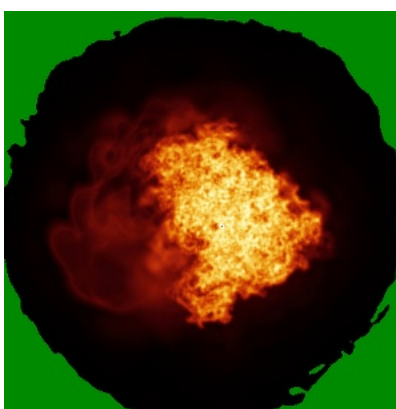
The images above show the largest variance slices of the map in three orthogonal directions.

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

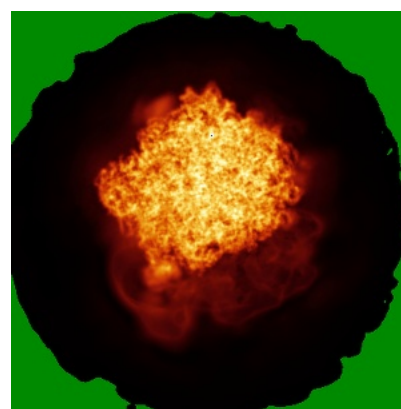
6.4.1 Primary map



X



Y

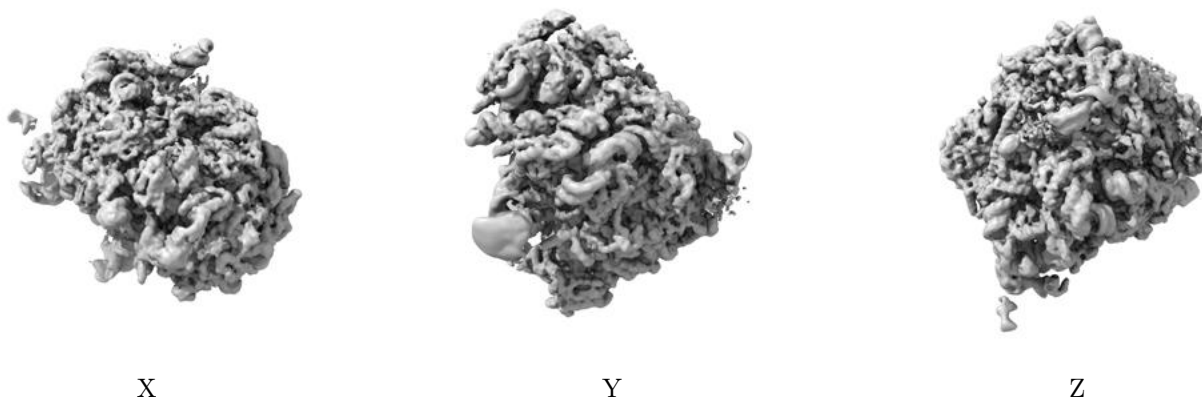


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

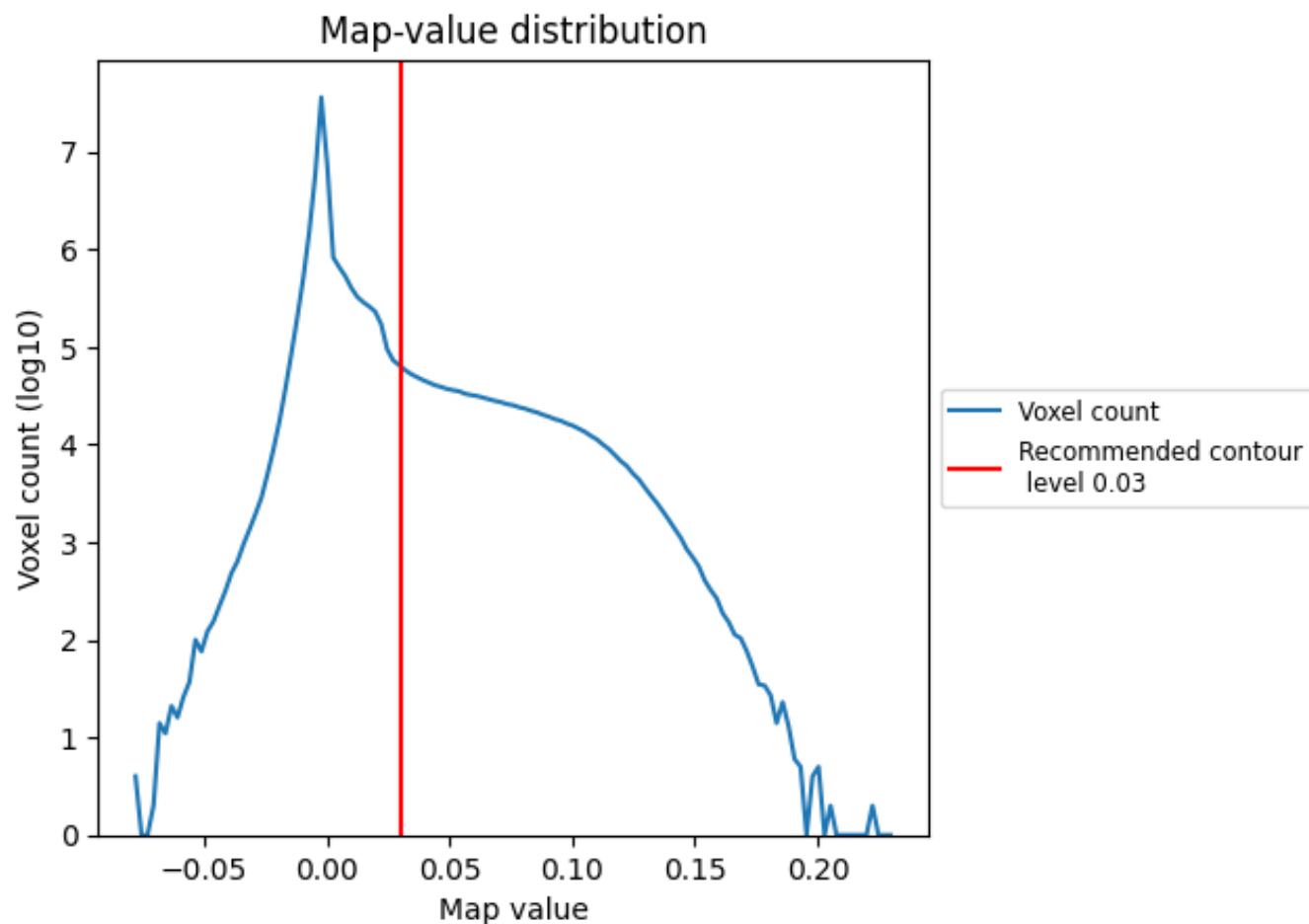
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

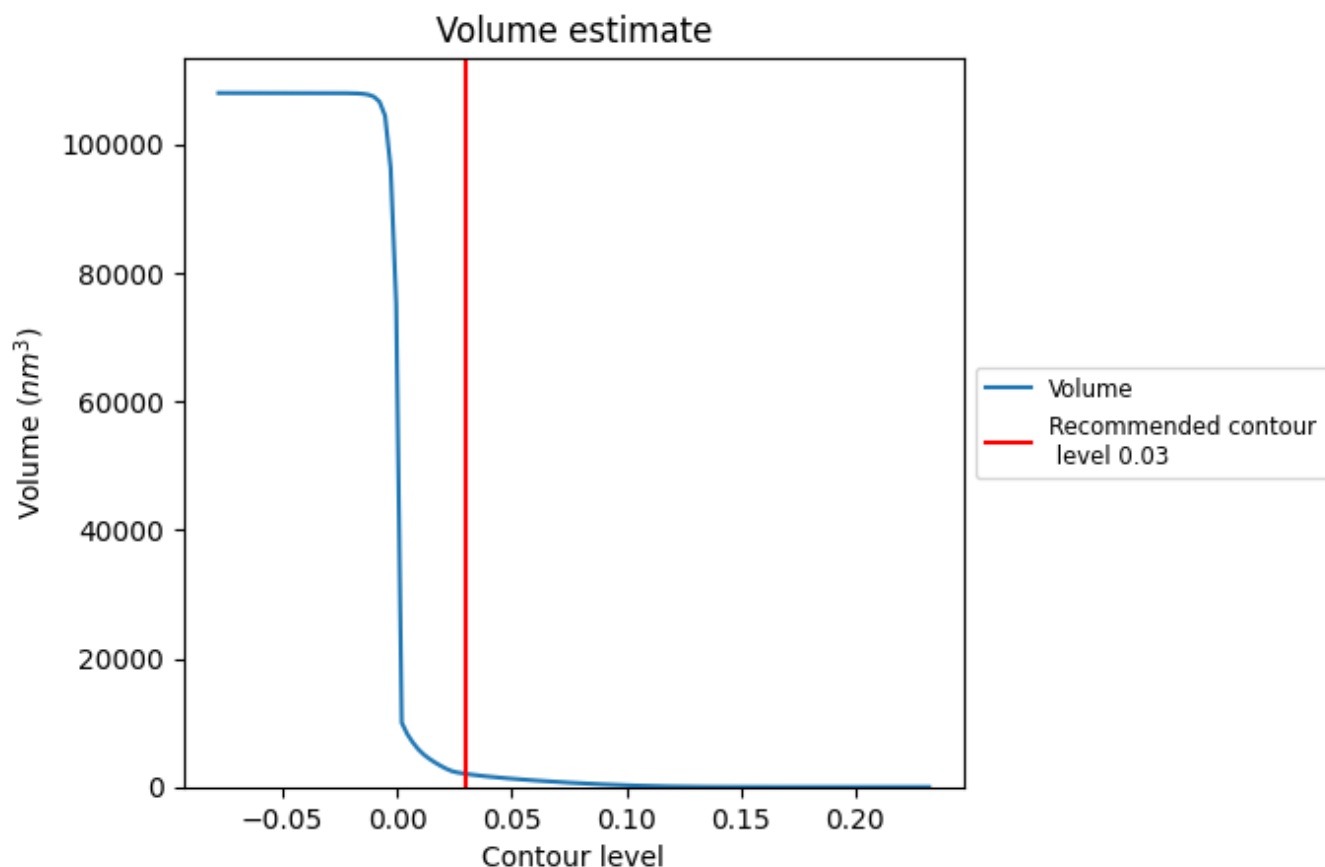
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

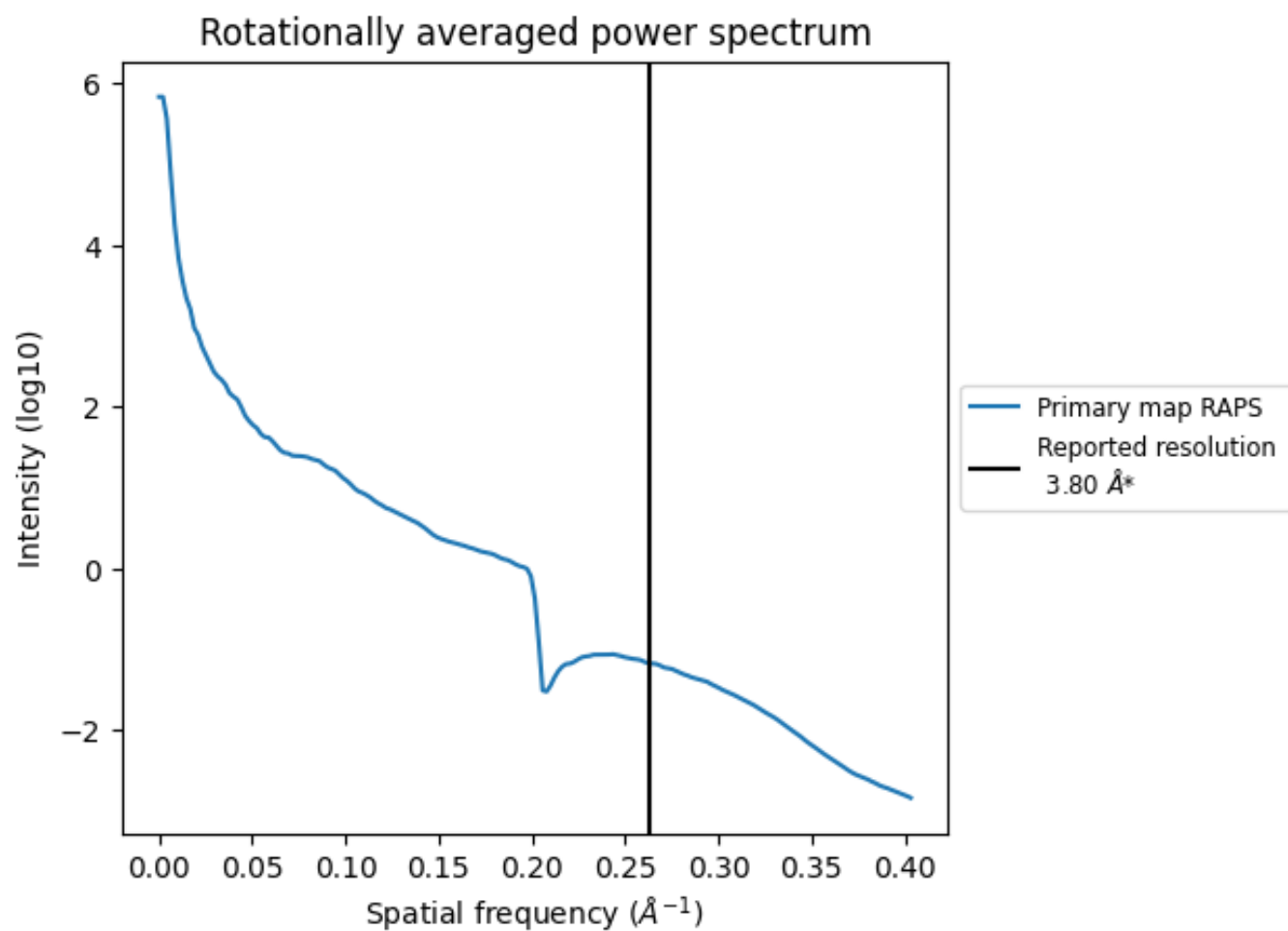
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2037 nm^3 ; this corresponds to an approximate mass of 1840 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 0.263 Å⁻¹

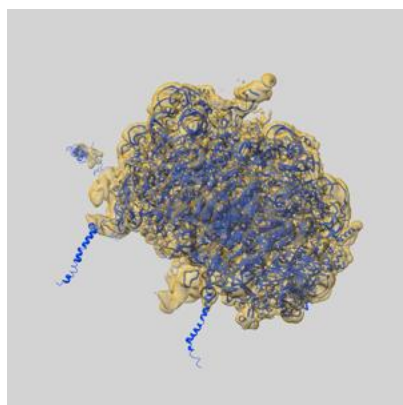
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

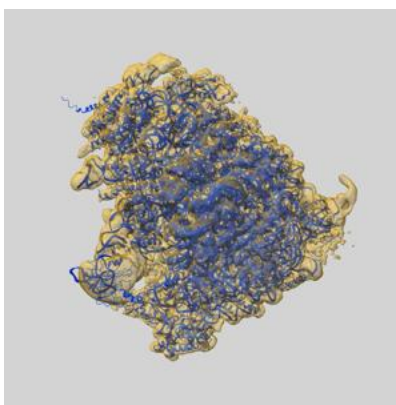
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20077 and PDB model 6OIG. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

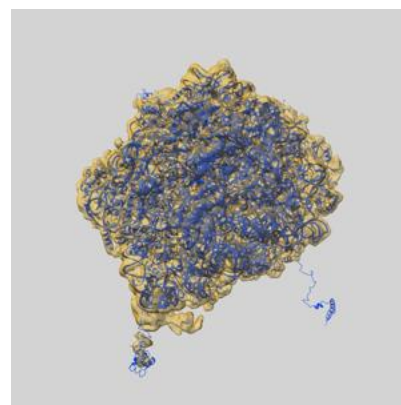
9.1 Map-model overlay [i](#)



X



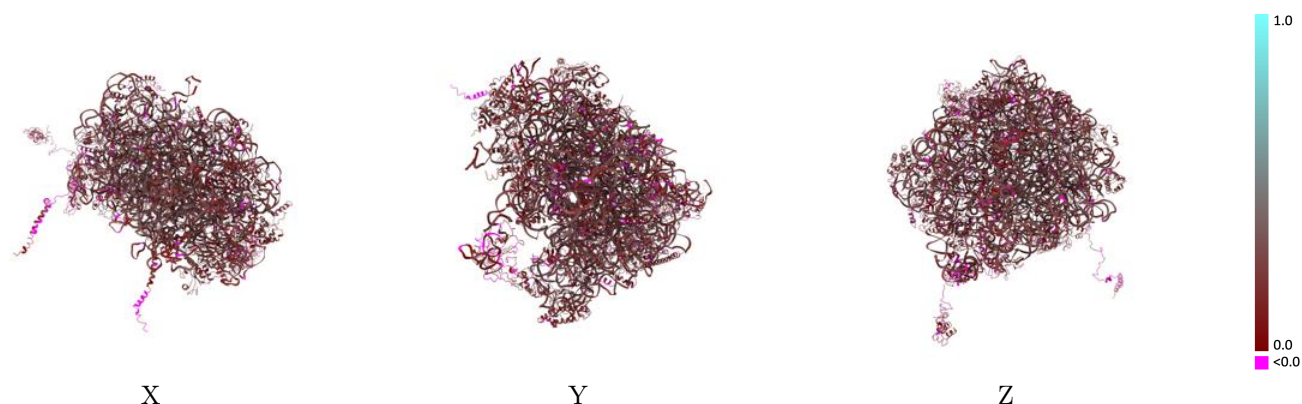
Y



Z

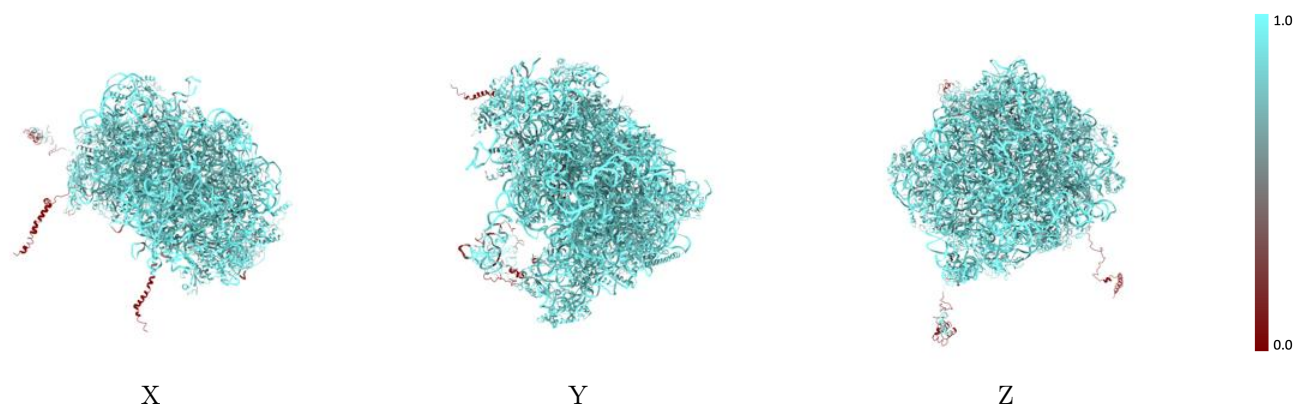
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



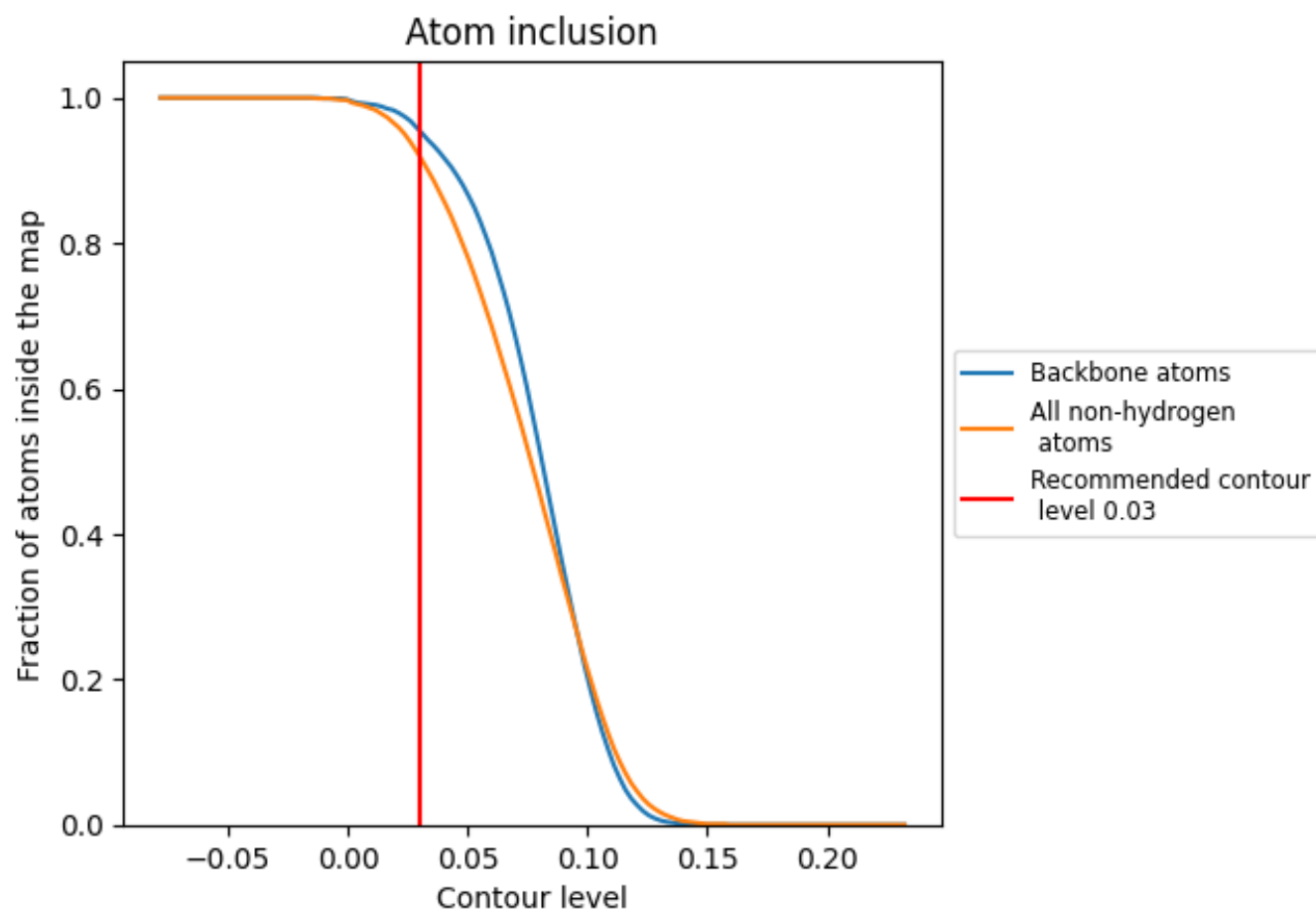
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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	 0.9200	 0.2310
5	 0.9800	 0.2690
7	 0.9960	 0.2860
8	 0.9810	 0.2620
A	 0.8420	 0.2020
B	 0.8840	 0.2050
C	 0.8760	 0.1820
D	 0.8790	 0.1900
E	 0.8750	 0.1800
F	 0.8720	 0.2000
G	 0.8760	 0.2030
H	 0.8720	 0.1790
I	 0.8260	 0.1350
J	 0.8600	 0.1810
L	 0.8950	 0.1870
M	 0.8800	 0.1810
N	 0.6720	 0.0710
O	 0.8790	 0.2020
P	 0.8680	 0.1890
Q	 0.8710	 0.2090
R	 0.7120	 0.1660
S	 0.8790	 0.2100
T	 0.9010	 0.2100
U	 0.8750	 0.2240
V	 0.7970	 0.2140
W	 0.3950	 0.0920
X	 0.8300	 0.1850
Y	 0.8830	 0.1610
Z	 0.8780	 0.2180
a	 0.8790	 0.2060
b	 0.8210	 0.1460
c	 0.8660	 0.2460
d	 0.8480	 0.1830
e	 0.8290	 0.1620
f	 0.8670	 0.1840



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Chain	Atom inclusion	Q-score
g	 0.8580	 0.1910
h	 0.8750	 0.1740
i	 0.8740	 0.2150
j	 0.8810	 0.1430
k	 0.8570	 0.2030
l	 0.8370	 0.1750
m	 0.8740	 0.2340
o	 0.8350	 0.1790
p	 0.8600	 0.2020
q	 0.7010	 0.0560
s	 0.9010	 0.0890
x	 0.4720	 0.1690
y	 0.2520	 0.1190
z	 0.6650	 0.0620