



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:03 PM UTC

PDB ID : 3J7Q / pdb_00003j7q
EMDB ID : EMD-2650
Title : Structure of the idle mammalian ribosome-Sec61 complex
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.40 Å(reported)
Based on initial models : 3J3B, 3J3F

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

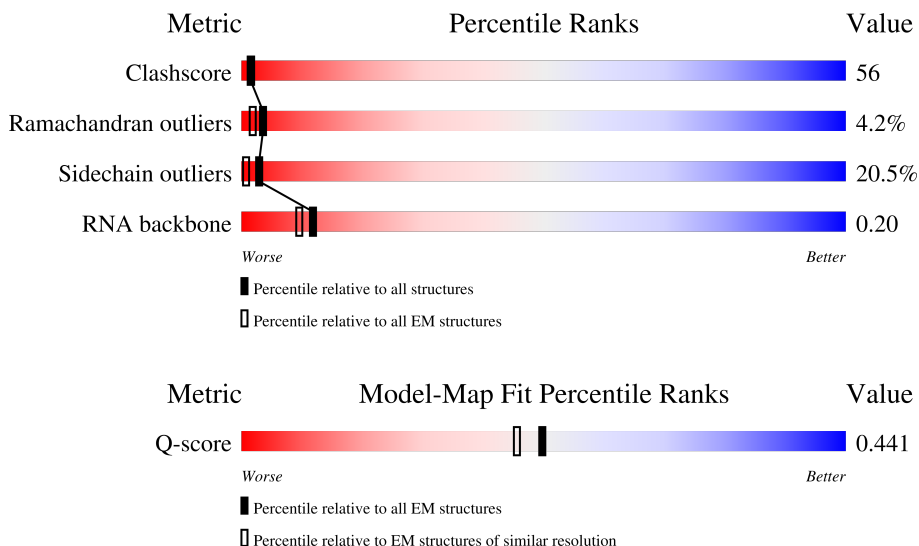
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



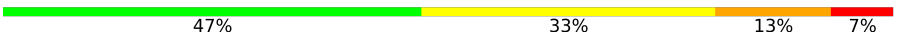
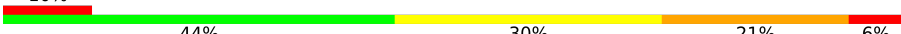
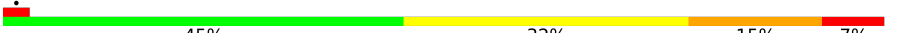
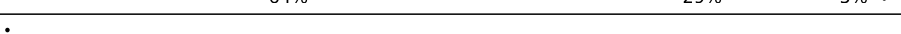
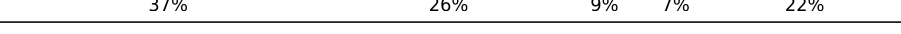
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	5	3722	
2	7	120	
3	8	156	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	257	
5	B	394	
6	C	367	
7	D	297	
8	E	236	
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	201	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	
34	f	110	
35	g	117	
36	h	123	
37	i	105	
38	j	86	
39	k	70	
40	l	51	
41	m	128	
42	n	25	
43	o	106	
44	p	91	
45	r	125	
46	1	476	
47	2	68	
48	3	36	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
50	ZN	m	201	-	-	X	-

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140540 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ILE	VAL	conflict	UNP A0A480L253
B	86	VAL	ILE	conflict	UNP A0A480L253
B	140	ALA	GLU	conflict	UNP A0A480L253

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	141	ALA	ASP	conflict	UNP A0A480L253
B	143	ALA	LYS	conflict	UNP A0A480L253
B	144	ALA	LYS	conflict	UNP A0A480L253
B	145	ALA	GLN	conflict	UNP A0A480L253
B	147	ALA	GLU	conflict	UNP A0A480L253
B	148	ALA	ARG	conflict	UNP A0A480L253
B	155	ALA	LYS	conflict	UNP A0A480L253

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	354	ALA	-	insertion	UNP A0A287AE76
C	355	ALA	-	insertion	UNP A0A287AE76
C	356	ALA	-	insertion	UNP A0A287AE76

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	62	MET	LYS	conflict	UNP Q2YGT9
E	64	MET	LEU	conflict	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	SER	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	GLU	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	ARG	deletion	UNP Q2YGT9
E	176	VAL	SER	conflict	UNP Q2YGT9
E	206	LYS	GLU	conflict	UNP Q2YGT9

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	31	LYS	ARG	conflict	UNP A0A480W0U3

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	53	ARG	CYS	conflict	UNP A0A4X1W808
G	172	ALA	SER	conflict	UNP A0A4X1W808
G	185	LYS	ASN	conflict	UNP A0A4X1W808
G	231	ASN	ASP	conflict	UNP A0A4X1W808

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	49	GLY	CYS	conflict	UNP Q29195
I	82	ARG	LYS	conflict	UNP Q29195
I	87	MET	ILE	conflict	UNP Q29195
I	145	GLU	LYS	conflict	UNP Q29195
I	187	LYS	GLU	conflict	UNP Q29195
I	189	CYS	ARG	conflict	UNP Q29195
I	200	VAL	ILE	conflict	UNP Q29195
I	203	HIS	ARG	conflict	UNP Q29195
I	211	VAL	ALA	conflict	UNP Q29195

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

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

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	3	GLU	-	variant	UNP A0A481CAM4
O	4	GLY	-	variant	UNP A0A481CAM4

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	TYR	-	variant	UNP A0A480VXS3

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

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

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

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

- Molecule 25 is a protein called Ribosomal protein eL24.

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

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

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

- Molecule 28 is a protein called Ribosomal protein eL27.

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

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

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

- Molecule 33 is a protein called Ribosomal protein eL32.

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

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

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

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	82	ILE	THR	conflict	UNP A0A480UVT3

- Molecule 39 is a protein called Ribosomal protein eL38.

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

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

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

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	64	ILE	MET	conflict	UNP A0A480YX24

- Molecule 46 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	392	Total	C	N	O	S	0	0
			3051	2007	493	532	19		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	343	HIS	TYR	conflict	UNP A0A480EHF8

- Molecule 47 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 48 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	5	119	Total	Mg	0
			119	119	
49	7	5	Total	Mg	0
			5	5	
49	8	4	Total	Mg	0
			4	4	
49	P	1	Total	Mg	0
			1	1	
49	V	1	Total	Mg	0
			1	1	

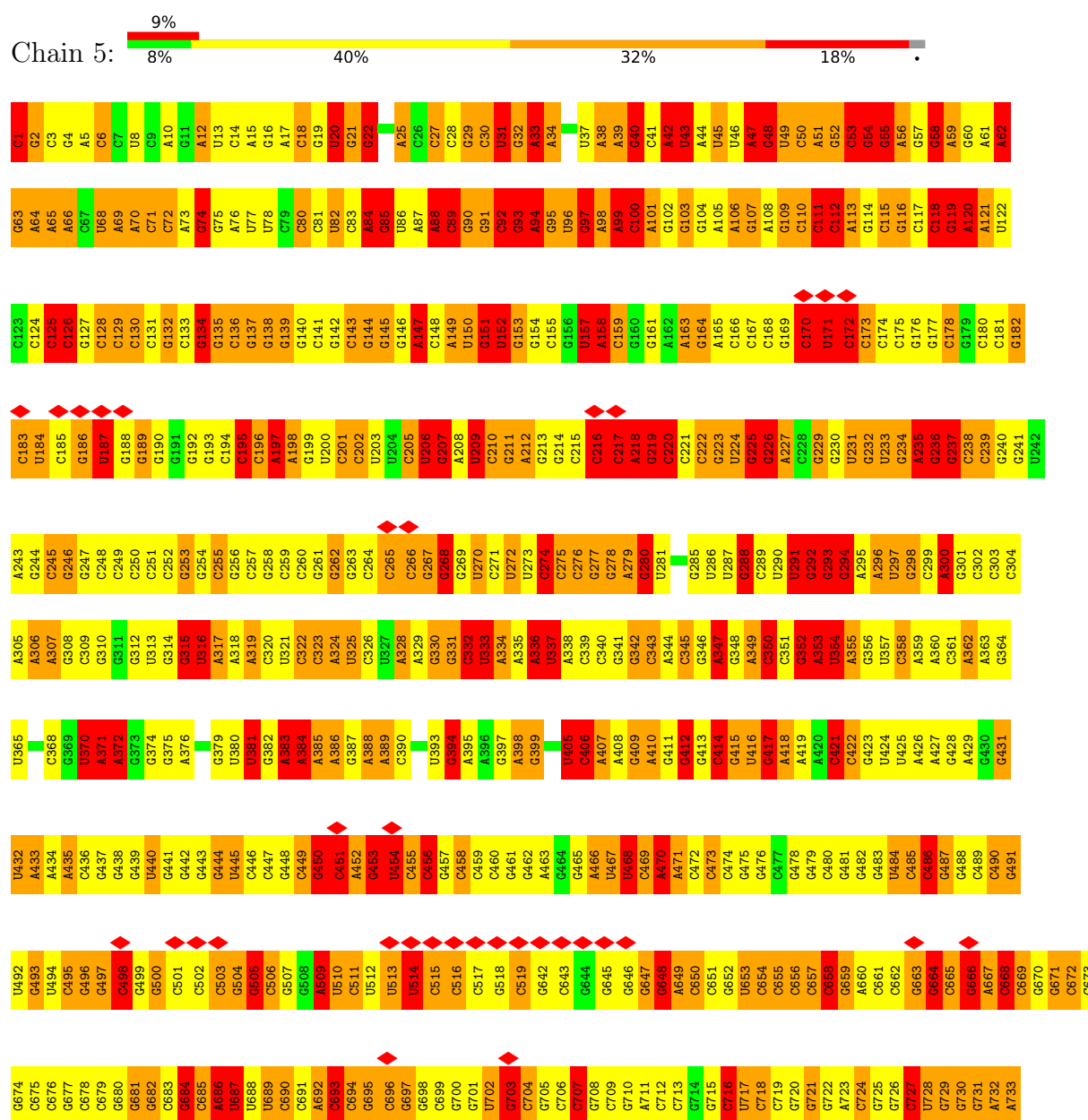
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

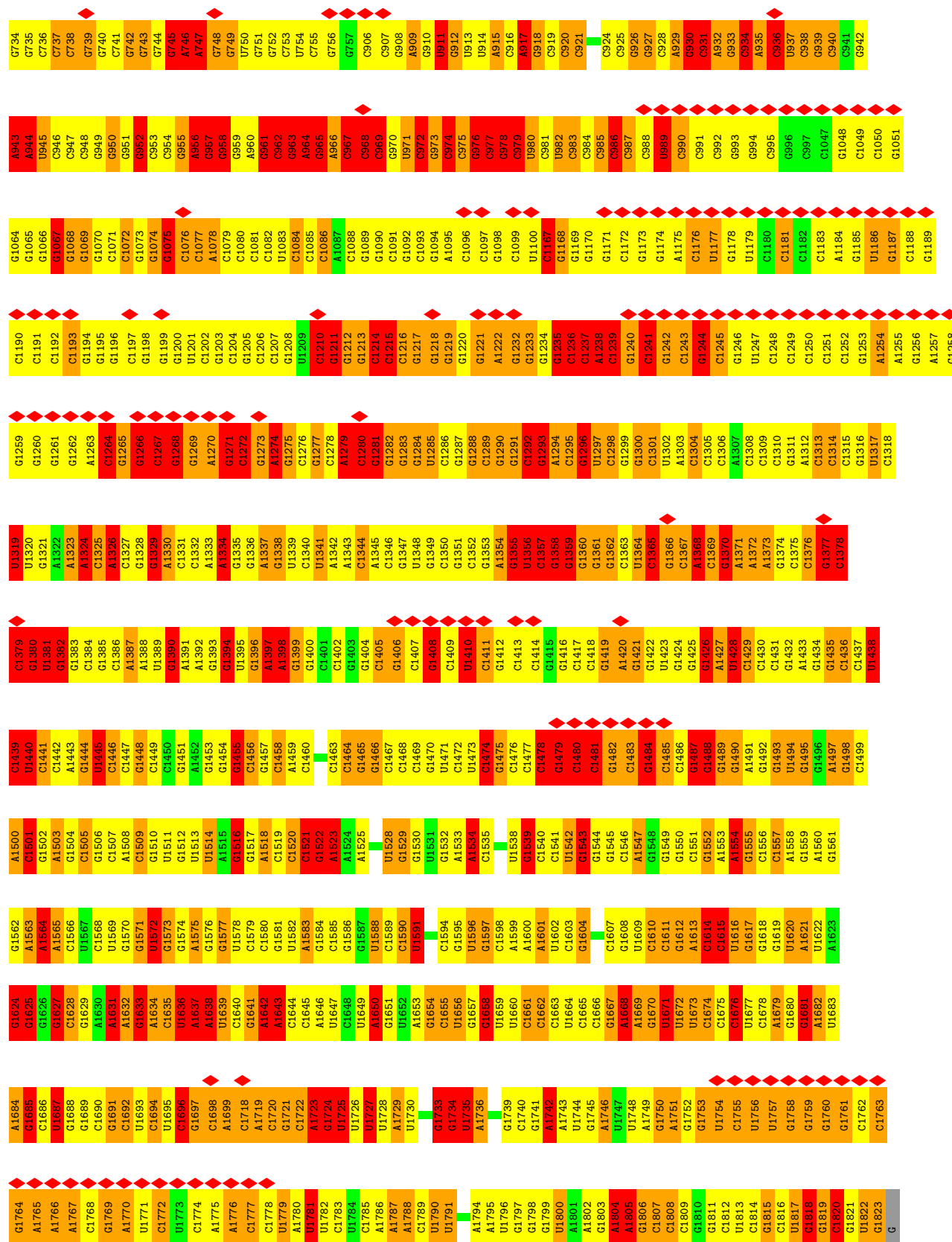
Mol	Chain	Residues	Atoms		AltConf
50	j	1	Total	Zn	0
			1	1	
50	m	1	Total	Zn	0
			1	1	
50	o	1	Total	Zn	0
			1	1	

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.

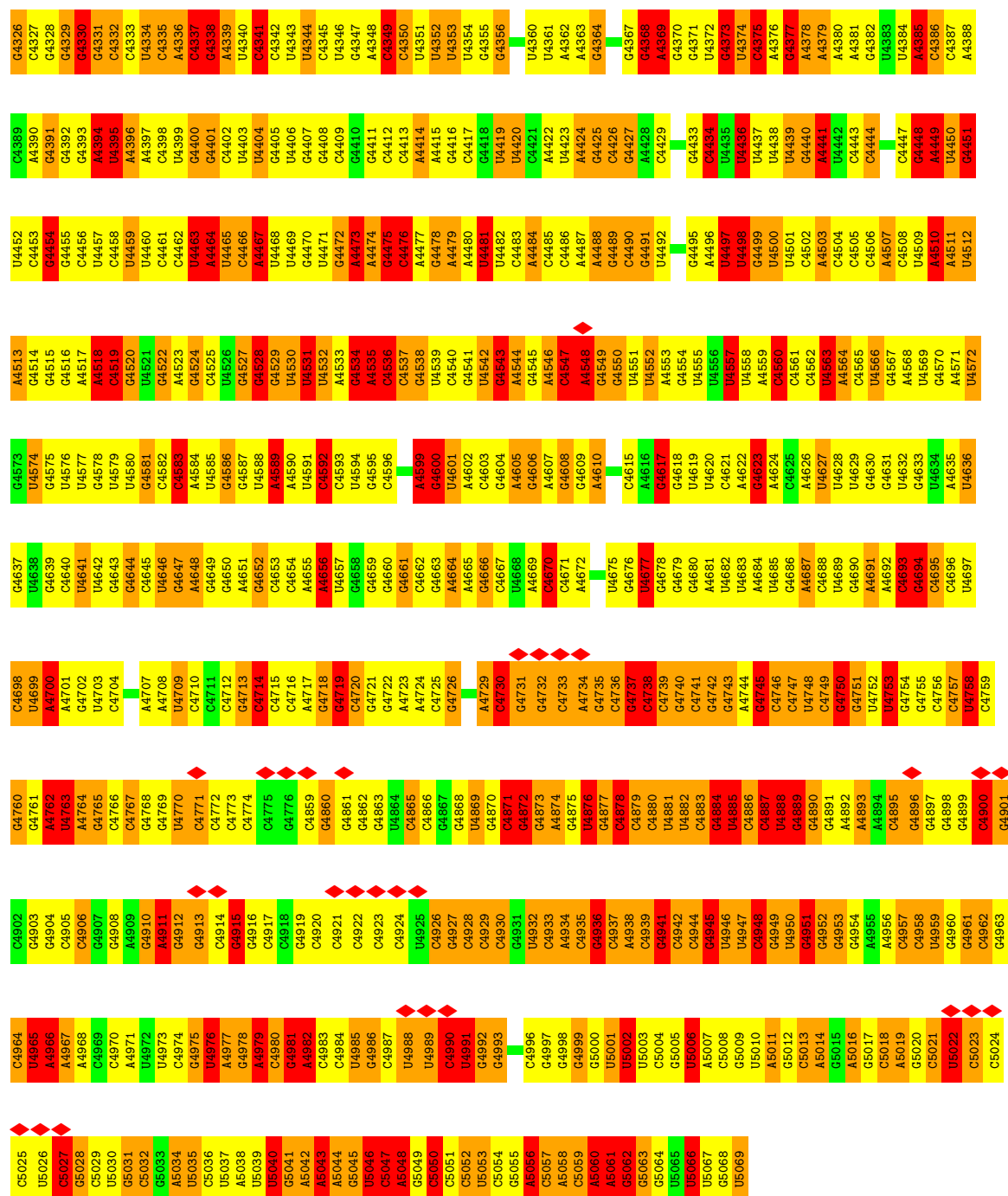
• Molecule 1: 28S ribosomal RNA





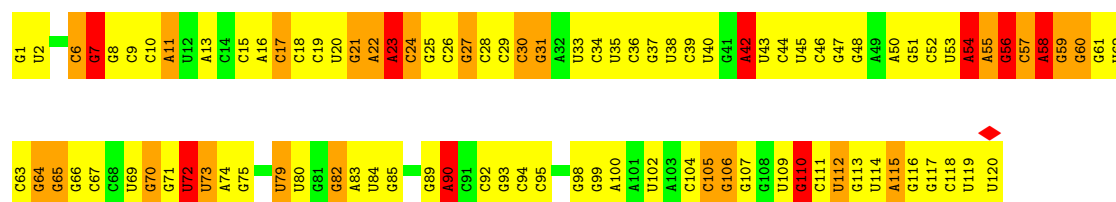
C2671	A2611	G2549	C2488	C2428	C3865	U2304	C2243	C2072	U1948	G1886	A1825
C2672	G2612	G2650	C2489	A2429	A2366	U2305	C2244	C2073	U1949	G1887	G1826
A2674	G2613	A2651	U2490	C2430	A2367	G2306	G2245	G2074	U1950	A1888	C1827
G2675	C2614	G2563	C2491	A2431	A2368	A2307	C2246	G2075	U1951	U1889	C1828
A2676	C2615	U2564	C2492	G2432	U2369	A2308	C2247	G2076	U1952	G1890	G1829
G2677	G2616	G2565	C2493	G2433	U2370	G2309	C2248	G2077	U1953	A1891	G1830
A2678	G2617	G2566	G2494	G2434	U2371	C2310	C2249	G2078	U1954	A1892	G1831
G2679	G2618	G2567	U2494	G2435	U2372	C2311	C2250	G2079	U1955	G1893	C1832
	G2619	G2568	U2495	U2436	C2373	C2312	C2251	U2080	A1956	G1894	G1833
G2682	G2620	G2569	U2496	A2437	A2375	A2314	G2252	C2081		G1895	G1834
C2683	G2621	C2560	C2497	A2438	A2376	G2315	G2253	G2082	U1959	A1896	G1835
G2684	A2622	C2561	C2498	G2439	A2377	G2316	G2254	C2083	A1960	A1897	G1836
C2685	A2623	G2562	C2499	C2441	G2378	C2317	G2255	G2084	G1961	A1898	A1837
G2686	G2624			G2442	G2379	G2318	G2256	G2085	A1962	G1899	A1838
U2687	C2627	C2563	G2602	G2443	A2382	G2319	G2257	G2086	C1963	G1900	U1839
C2688	G2628	G2564	G2503	U2444	C2383	G2320	C2258	U2087	C1964	G1901	G1840
C2689	U2628	A2665	C2504	C2445	U2384	G2321	C2259	G2098	G1965	G1902	C
G2690	C2629	G2566	C2505	G2446	U2385	G2322	C2260	G2099	A1966	G1903	
U2691	U2630	G2567	C2506	U2447	U2386	C2323	C2261	C2091	A1967	U1906	
G2692	U2631	C2568	A2507	U2448		C2324	C2262	G2092	G1968	A1907	
G2693	U2632	G2569	C2508	A2449	G2389	G2325	C2263	G2093	G1969	A1908	
G2694	U2633	U2570	U2509	G2450	G2390	G2326	C2264	A2094	C1970	G1909	
A2695	C2634	C2571	G2510	A2451	G2391	G2327	C2265	G2095	C1963	U1910	
C2696	U2635	C2572	A2511	G2452	C2392	G2328	C2266	A2096	C1964	G1911	
A2697	U2636	A2573	A2512	A2453	C2393	G2329	C2267	U2032	G1972	G1912	
G2698	U2637	G2574	A2513	U2454	C2394	U2330	C2268	A2033	G1973	C1913	
C2699	U2638	U2575	G2514	G2455	A2395	G2331	C2269	C2036	U1974		
G2700	C2629	G2566	C2505	G2456	A2396	A2332	G2270	G2037	G1975	U1916	
U2691	U2630	G2567	C2506	U2447	U2386	G2333	C2271	U2038	G1976	U1917	
G2692	U2631	C2568	A2507	U2448		G2334	C2272	G2039	G1977	U1918	
G2693	U2632	G2569	C2508	A2449	G2389	C2335	C2273	A2040	C1978	U1919	
G2694	U2633	U2570	U2509	G2450	G2390	C2336	C2274	A2041	A1979	G1920	
A2695	C2634	C2571	G2510	A2451	G2391	G2337	C2275	A2042	U1980	G1921	
C2696	U2635	C2572	A2511	G2452	C2392	C2338	C2276	G2101	G1981	G1922	
A2697	U2636	A2573	A2512	A2453	C2393	G2339	C2277	G2102	G1982	A1923	
G2698	U2637	G2574	A2513	U2454	C2394	C2340	C2278	G2103	A1983	G1924	
C2699	U2638	U2575	G2514	G2455	A2395	A2341	C2279	G2104	A1984	G1925	
G2700	C2629	G2566	C2505	G2456	A2396	G2342	C2280	G2105	U1985	C1926	
U2701	U2630	G2567	C2506	U2447	U2386	U2343	C2281	G2106	U1986	U1927	
G2702	U2631	C2568	A2507	U2448		U2344	C2282	G2107	C1987	C1928	
G2703	U2632	G2569	C2508	A2449	G2389	G2345	C2283	G2108	G1988	A1929	
G2704	U2633	U2570	U2509	G2450	G2390	G2346	C2284	G2109	G1989	U1930	
A2695	C2634	C2571	G2510	A2451	G2391	A2347	C2285	G2110	U1990	C1931	
C2696	U2635	C2572	A2511	G2452	C2392	C2348	C2286	G2111	A1991	A1932	
A2697	U2636	A2573	A2512	A2453	C2393	G2349	C2287	G2112	U1992	C1933	
G2698	U2637	G2574	A2513	U2454	C2394	A2350	C2288	G2113	G1993	G1934	
C2699	U2638	U2575	G2514	G2455	A2395	U2351	C2289	G2114	A1994	A1935	
G2700	C2629	G2566	C2505	G2456	A2396	U2352	C2290	G2115	G1995	G1877	
U2701	U2630	G2567	C2506	U2447	U2386	U2353	C2291	G2116	C1996	G1878	
G2702	U2631	C2568	A2507	U2448		U2354	C2292	G2117	U1997	C1879	
G2703	U2632	G2569	C2508	A2449	G2389	U2355	C2293	G2118	A1998	G1880	
G2704	U2633	U2570	U2509	G2450	G2390	U2356	C2294	G2119	G1999	A1942	
A2695	C2634	C2571	G2510	A2451	G2391	U2357	C2295	G2120	A1999	A1943	
C2696	U2635	C2572	A2511	G2452	C2392	G2358	C2296	G2121	G2000	A1944	
A2697	U2636	A2573	A2512	A2453	C2393	G2359	C2297	G2122	G2001	G1945	
G2698	U2637	G2574	A2513	U2454	C2394	G2360	C2298	G2123	A2002	C1884	
C2699	U2638	U2575	G2514	G2455	A2395	U2361	C2299	G2124	G2002	G1946	
G2700	C2629	G2566	C2505	G2456	A2396	U2362	C2300	G2125	A2003	U1947	
U2701	U2630	G2567	C2506	U2447	U2386	U2363	C2301	G2126	U2004		
G2702	U2631	C2568	A2507	U2448		U2364	C2302	G2127	G2005		
G2703	U2632	G2569	C2508	A2449	G2389		C2303	G2128	U2006		
G2704	U2633	U2570	U2509	G2450	G2390			G2129	G2007		
A2695	C2634	C2571	G2510	A2451	G2391			G2130	U2008		
C2696	U2635	C2572	A2511	G2452	C2392			C2131			
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396						
U2701	U2630	G2567	C2506	U2447	U2386						
G2702	U2631	C2568	A2507	U2448							
G2703	U2632	G2569	C2508	A2449	G2389						
G2704	U2633	U2570	U2509	G2450	G2390						
A2695	C2634	C2571	G2510	A2451	G2391						
C2696	U2635	C2572	A2511	G2452	C2392						
A2697	U2636	A2573	A2512	A2453	C2393						
G2698	U2637	G2574	A2513	U2454	C2394						
C2699	U2638	U2575	G2514	G2455	A2395						
G2700	C2629	G2566	C2505	G2456	A2396		</				



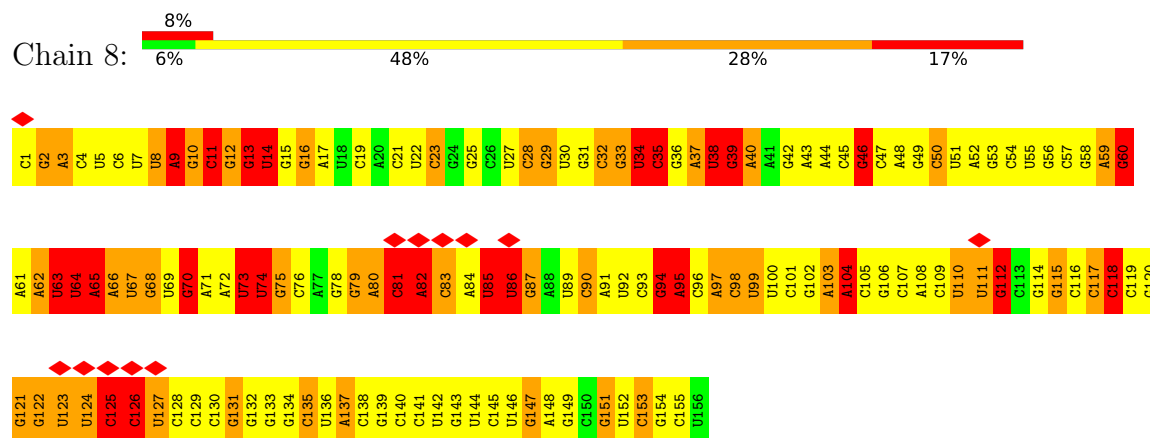


• Molecule 2: 5S ribosomal RNA

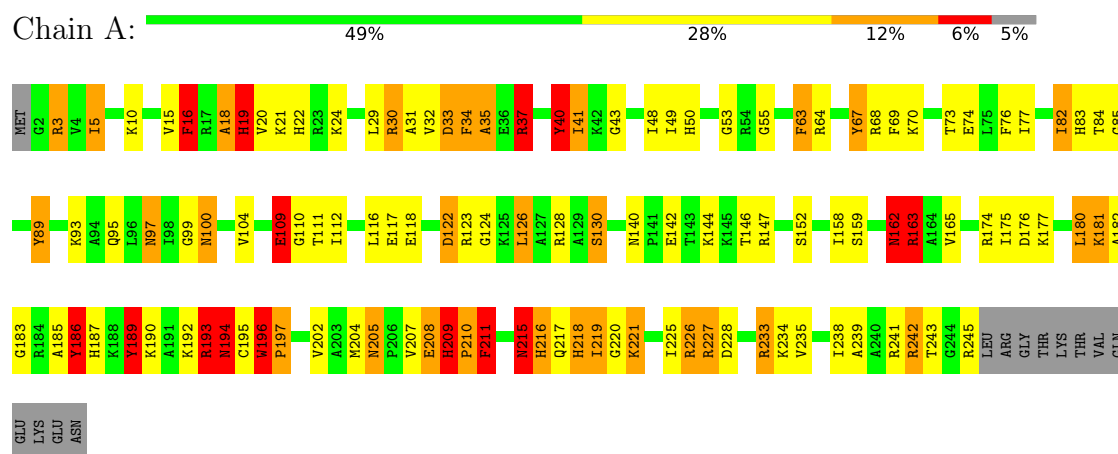
Chain 7: 18% 55% 19% 8%



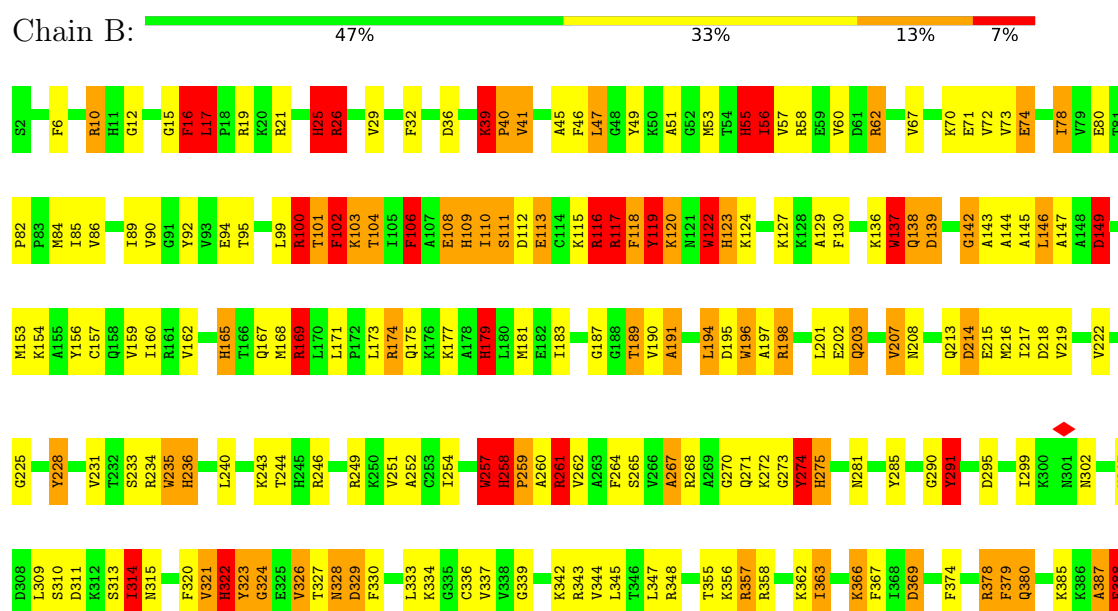
- Molecule 3: 5.8S ribosomal RNA



- Molecule 4: Ribosomal protein uL2

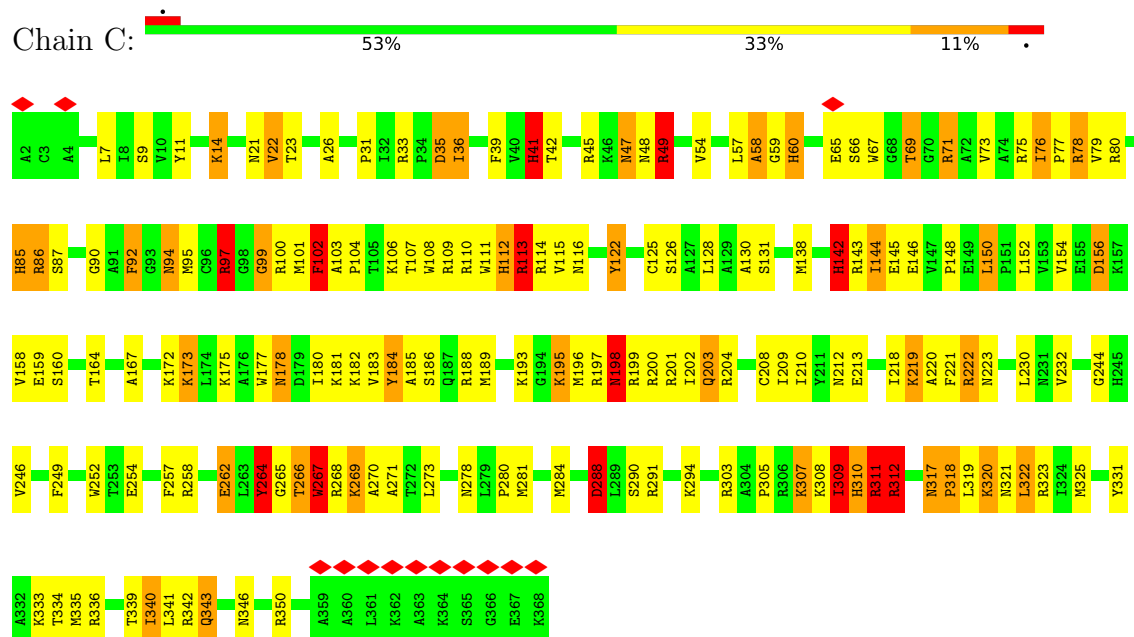


- Molecule 5: Ribosomal protein uL3

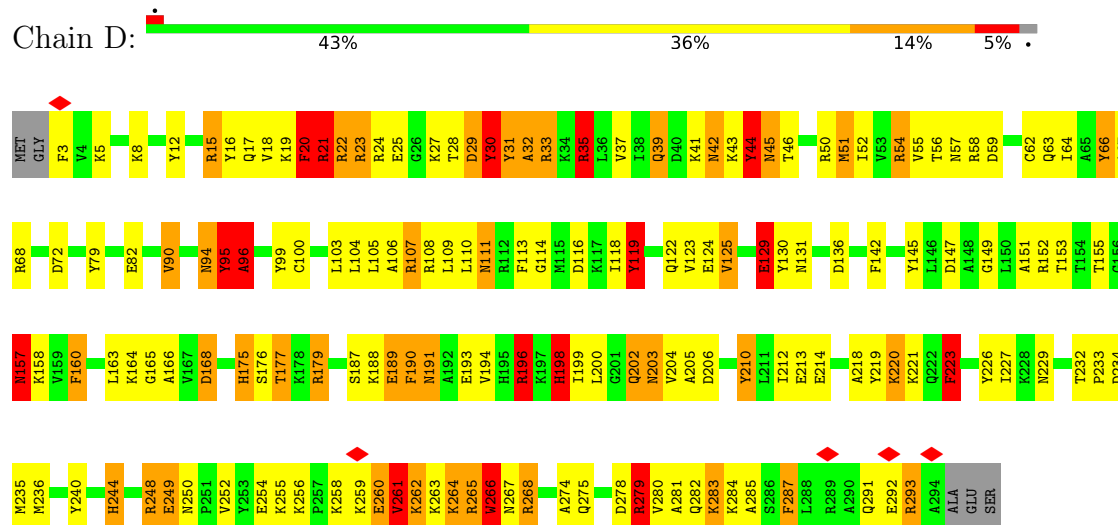


M389
G390
K393
K394
D395

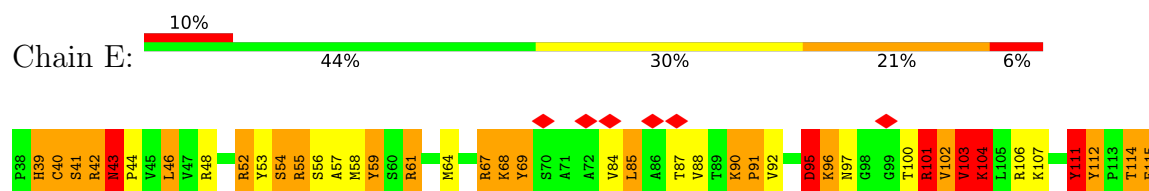
• Molecule 6: Ribosomal protein uL4

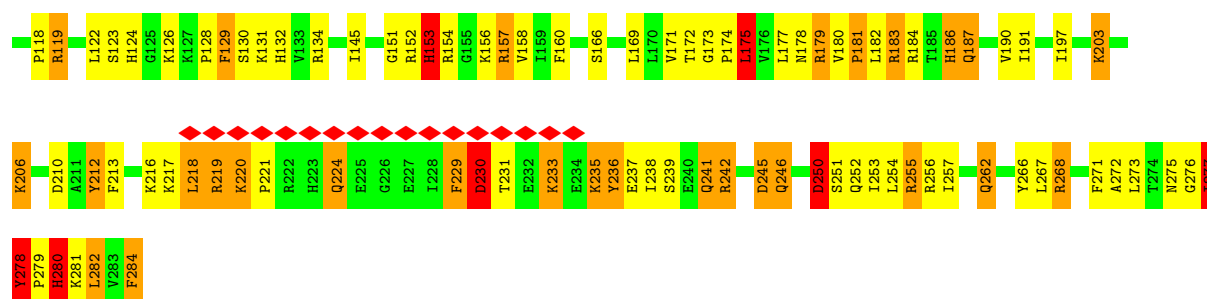


• Molecule 7: Ribosomal protein uL18

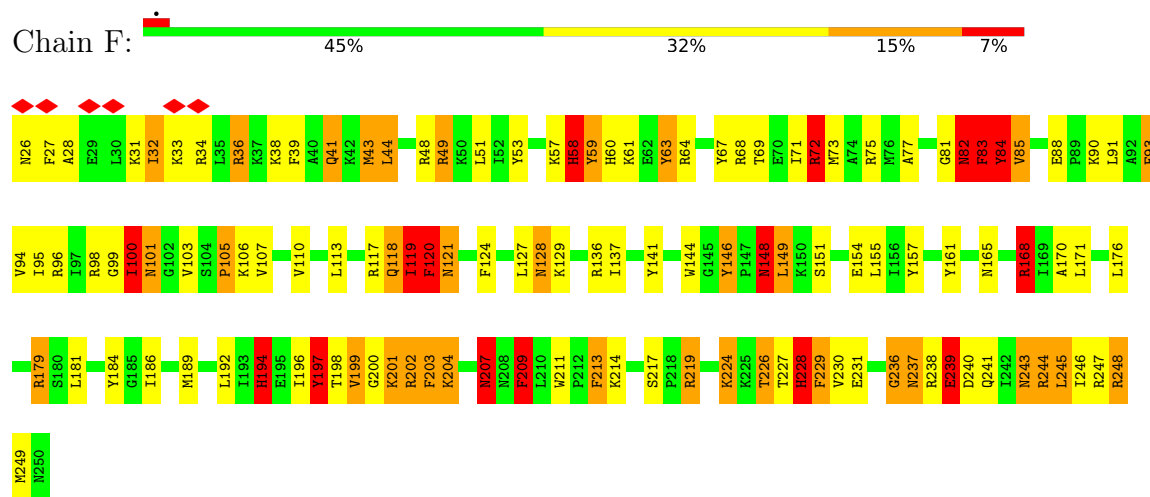


• Molecule 8: Ribosomal protein eL6

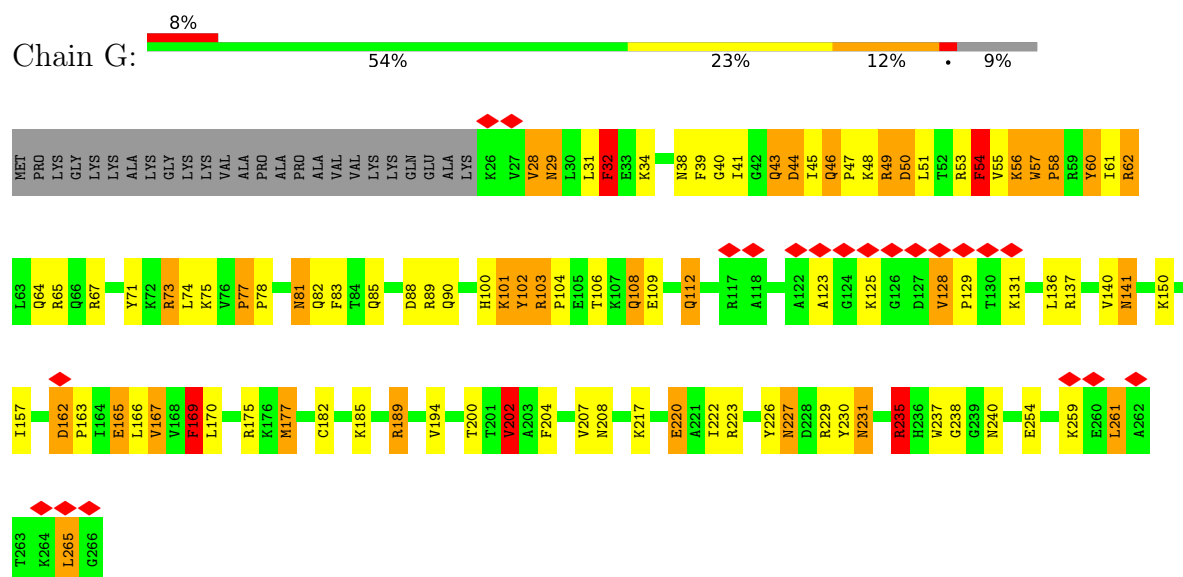




• Molecule 9: Ribosomal protein uL30

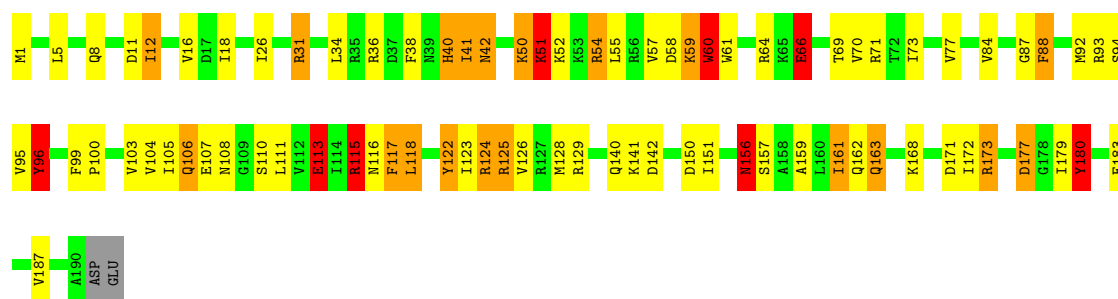


• Molecule 10: Ribosomal protein eL8

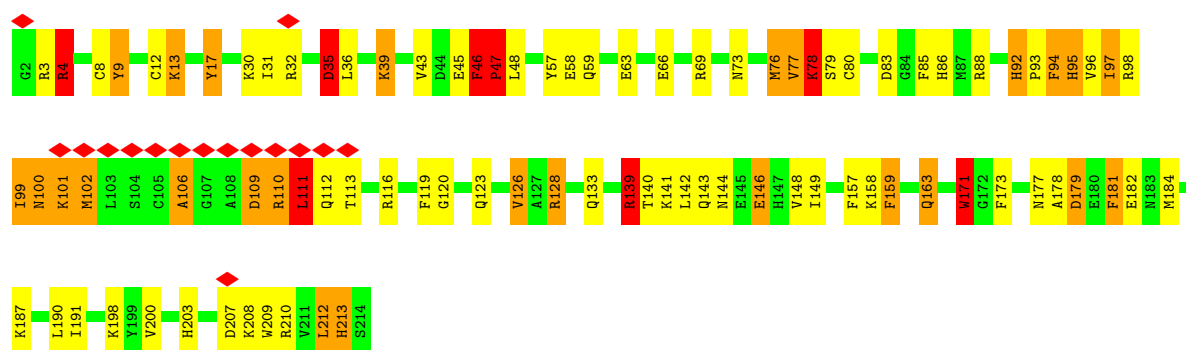


• Molecule 11: Ribosomal protein uL6

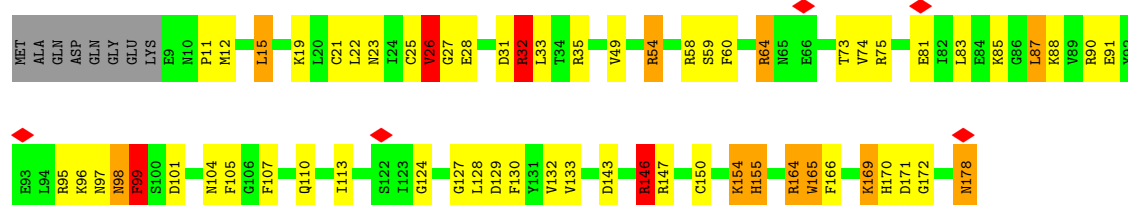




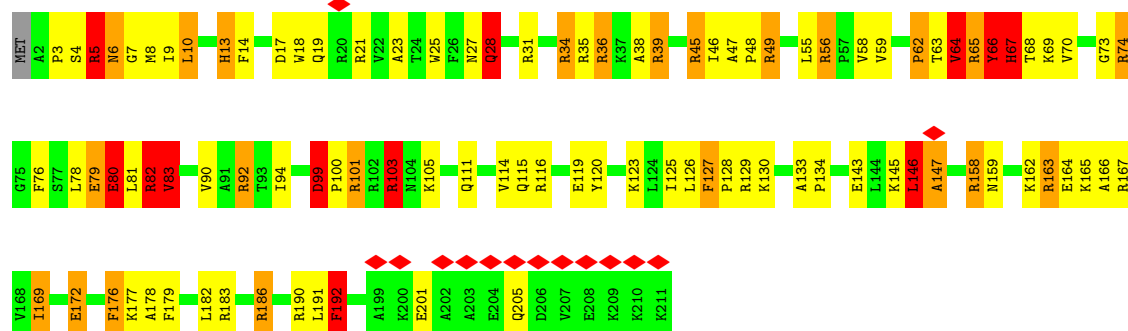
• Molecule 12: Ribosomal protein uL16



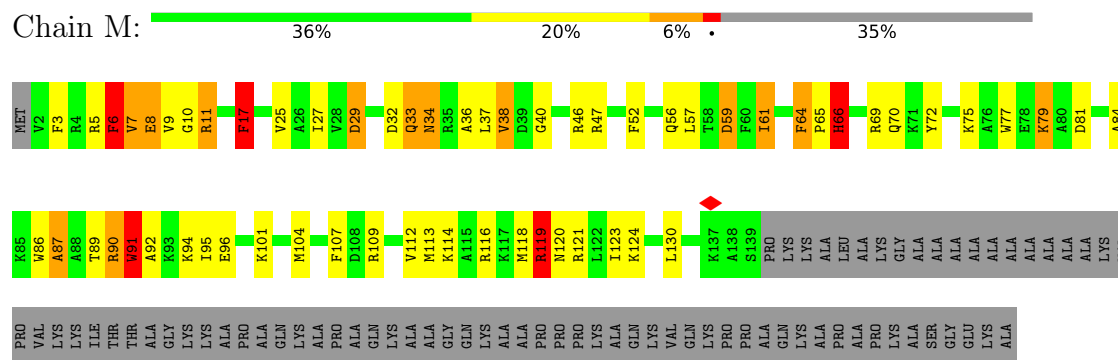
• Molecule 13: Ribosomal protein uL5



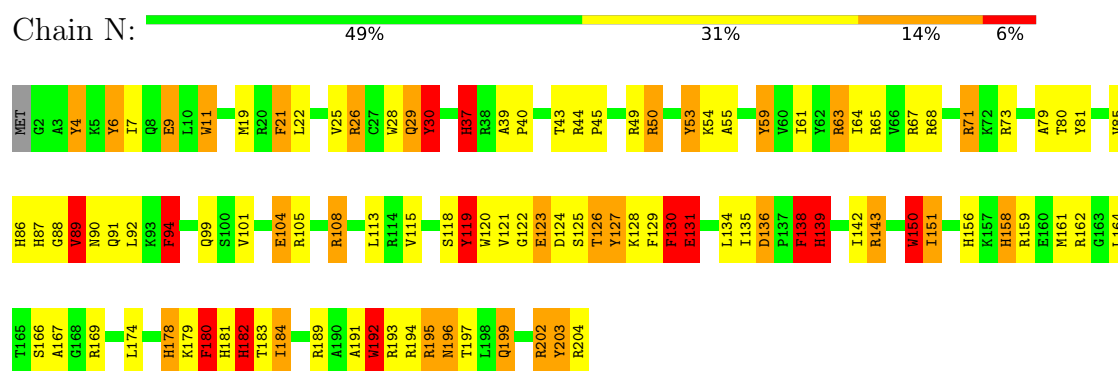
• Molecule 14: Ribosomal protein eL13



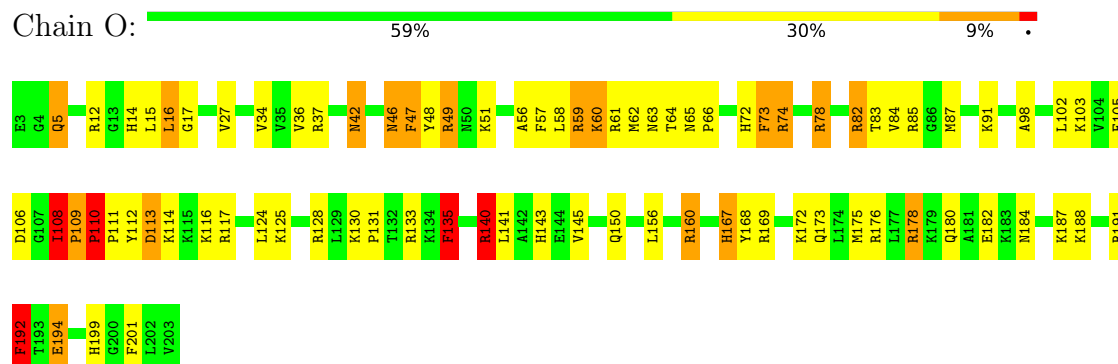
- Molecule 15: Ribosomal protein eL14



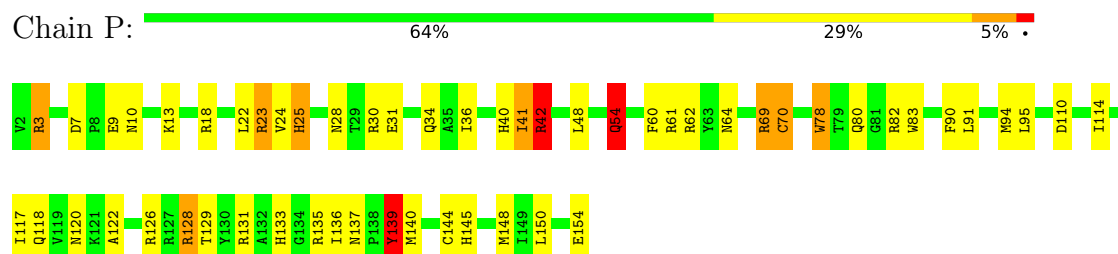
- Molecule 16: Ribosomal protein eL15



- Molecule 17: Ribosomal protein uL13

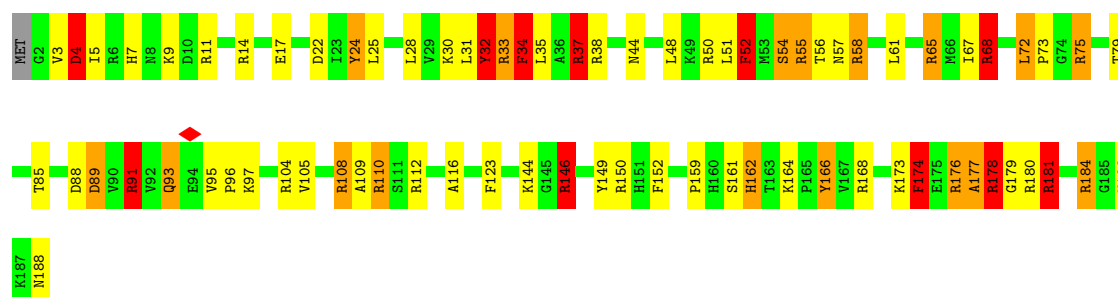


- Molecule 18: Ribosomal protein uL22



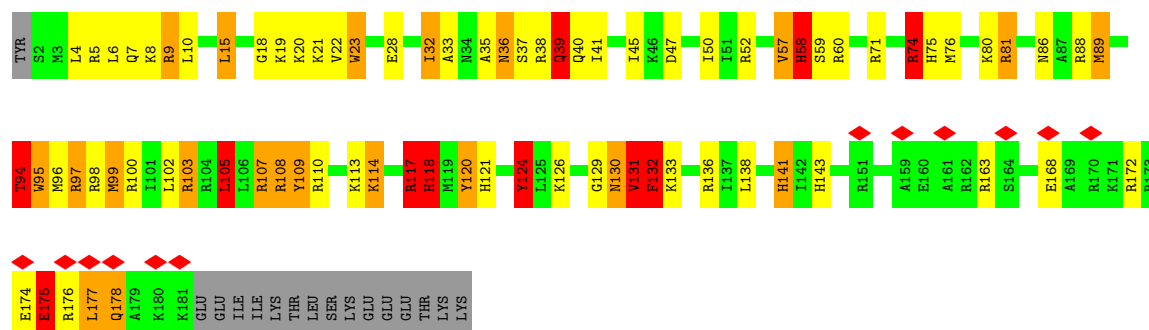
- Molecule 19: Ribosomal protein eL18

Chain Q: 

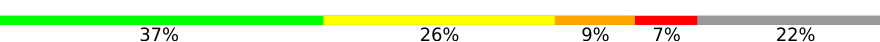


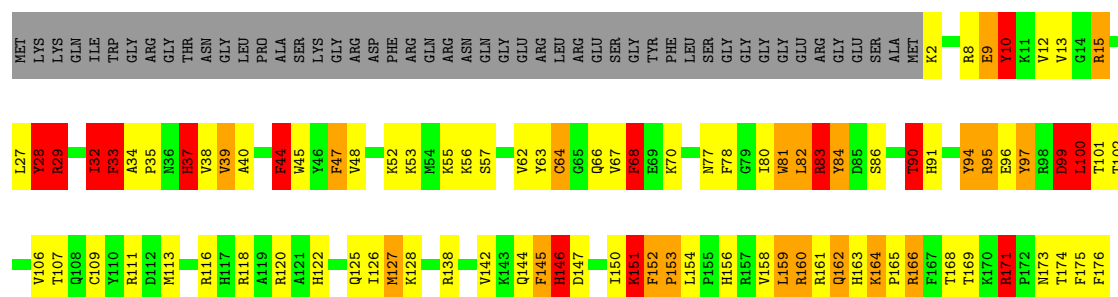
- Molecule 20: Ribosomal protein eL19

Chain R: 



- Molecule 21: Ribosomal protein eL20

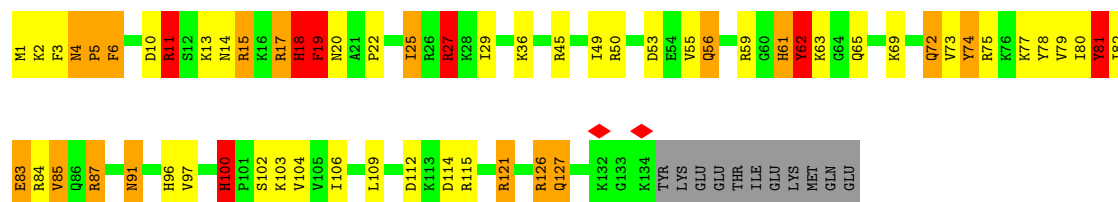
Chain S: 



- Molecule 22: Ribosomal protein eL21

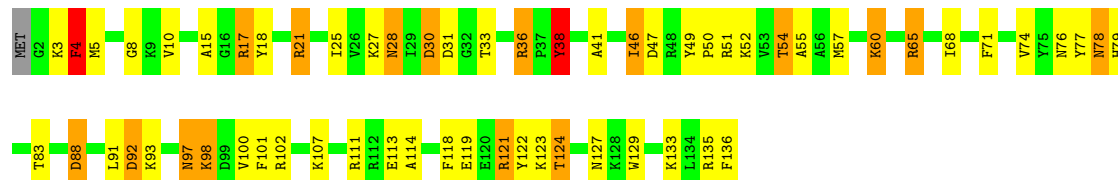
Chain T: 





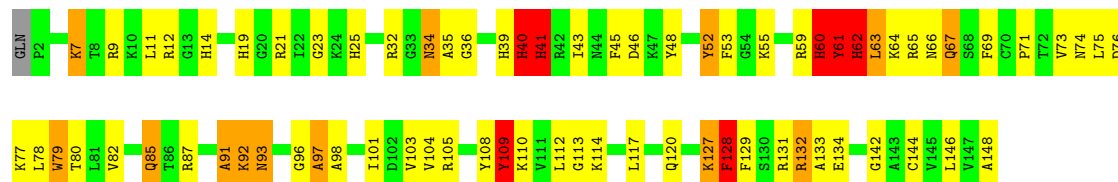
• Molecule 28: Ribosomal protein eL27

Chain Z: 54% 32% 12% ..



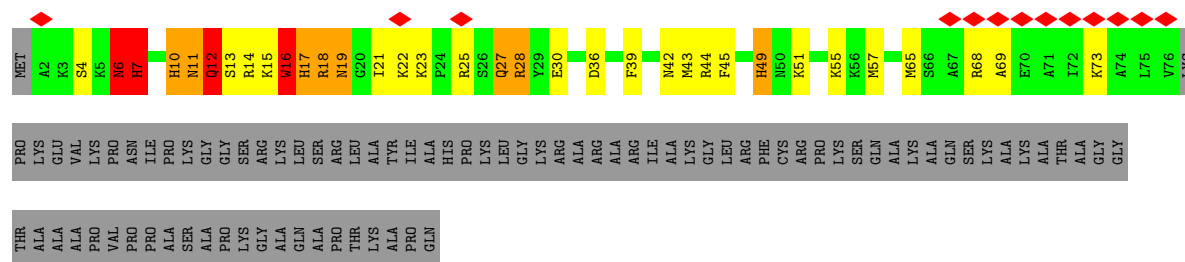
• Molecule 29: Ribosomal protein uL15

Chain a: 49% 36% 9% 5% .



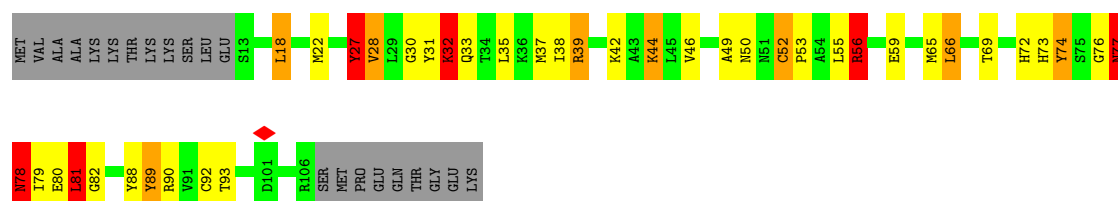
• Molecule 30: Ribosomal protein eL29

Chain b: 8% 26% 14% 5% 53%

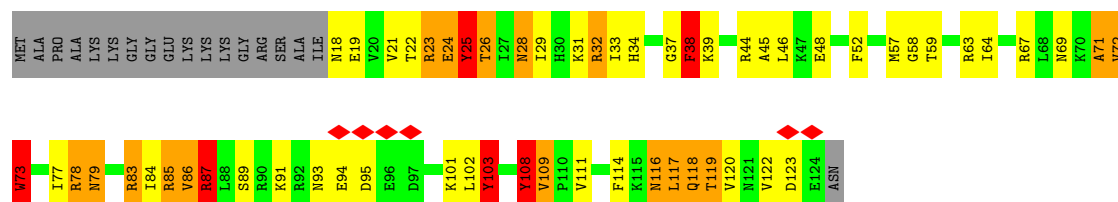


• Molecule 31: Ribosomal protein eL30

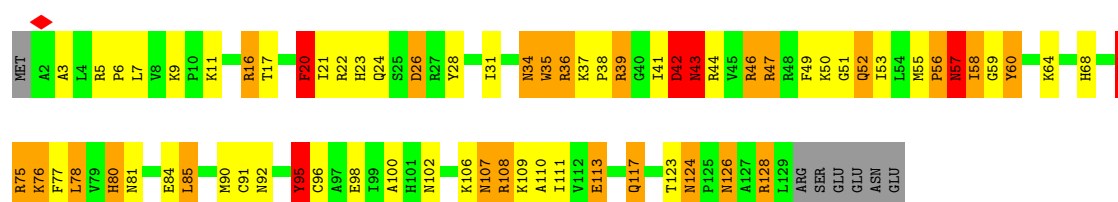
Chain c: 47% 23% 7% 5% 18%



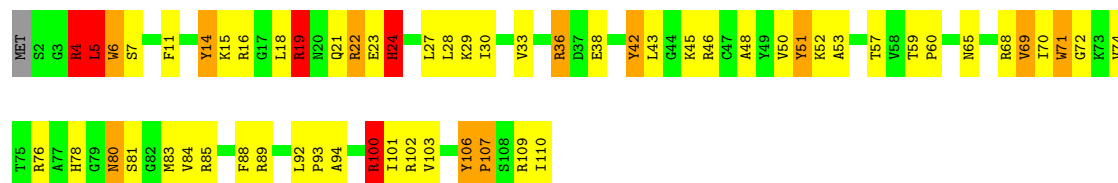
Chain d:



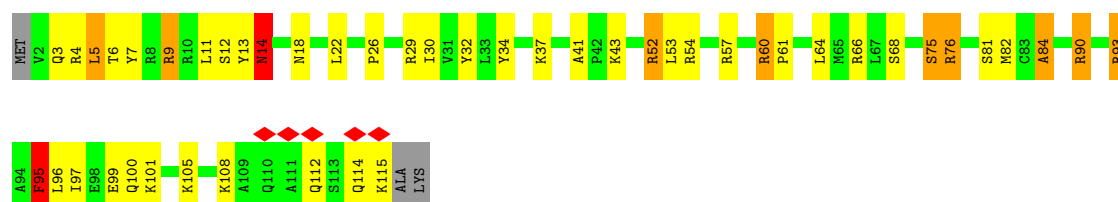
Chain e: 43% 30% 18% 5%



Chain f: 45% 40% 10% 5%



Chain g: 57% 31% 8%



Chain h: 60% 26% 11%



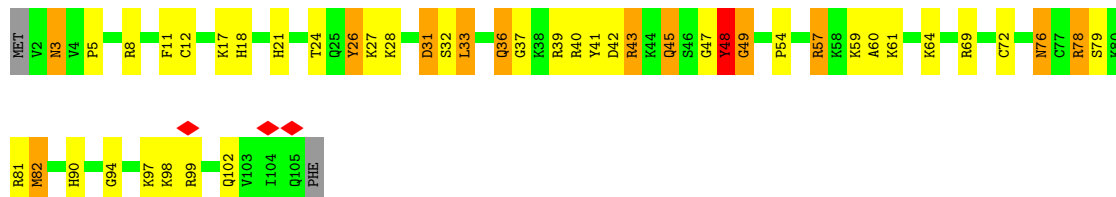
- Molecule 42: Ribosomal protein eL41

Chain n: 



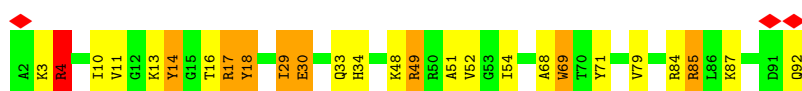
- Molecule 43: Ribosomal protein eL42

Chain o: 



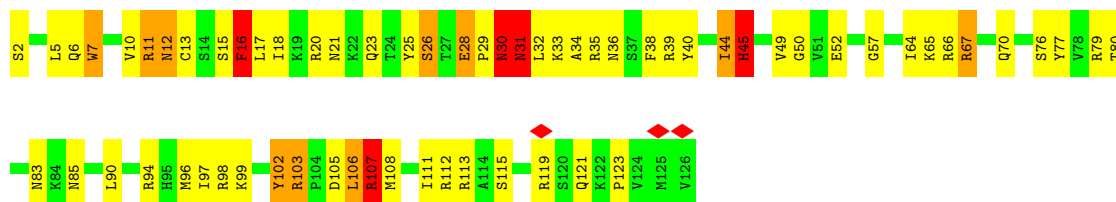
- Molecule 44: Ribosomal protein eL43

Chain p: 



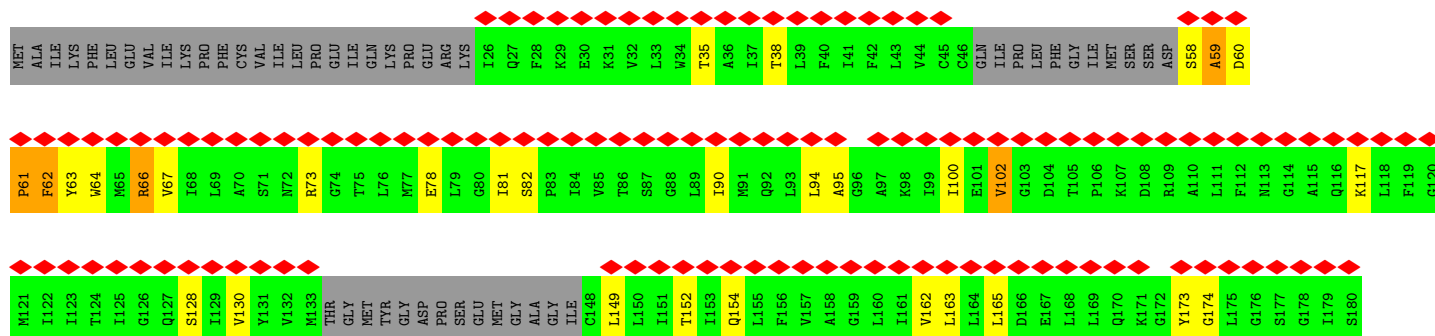
- Molecule 45: Ribosomal protein eL28

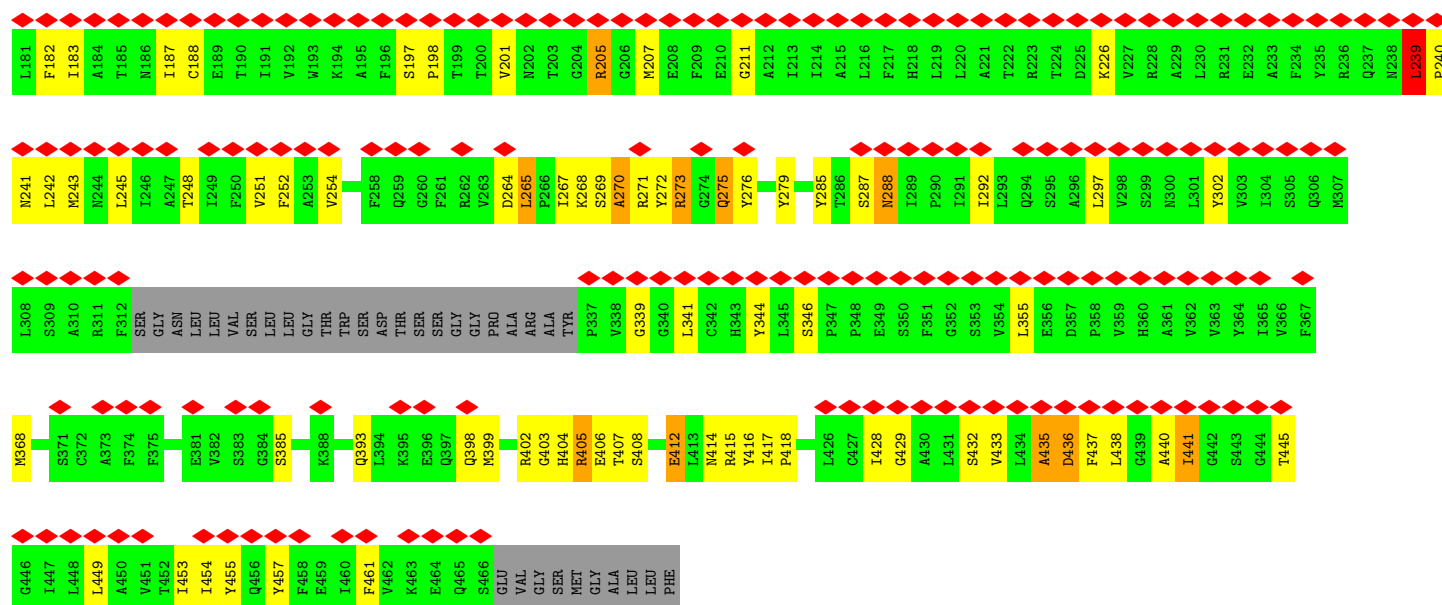
Chain r: 



- Molecule 46: Sec61 alpha subunit

Chain 1: 

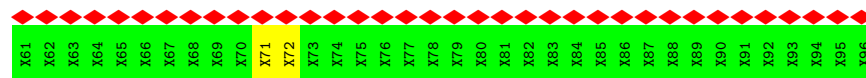




• Molecule 47: Sec61 gamma subunit



• Molecule 48: Sec61 beta subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.043	Depositor
Minimum map value	-0.599	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.09	Depositor
Map size ($\text{\AA}$)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	5	0.59	24/87792 (0.0%)	1.26	1287/136945 (0.9%)
2	7	0.51	1/2858 (0.0%)	1.11	16/4455 (0.4%)
3	8	0.62	0/3701	1.30	63/5766 (1.1%)
4	A	1.06	8/1906 (0.4%)	1.40	32/2556 (1.3%)
5	B	1.02	11/3214 (0.3%)	1.30	32/4308 (0.7%)
6	C	0.95	3/2973 (0.1%)	1.24	19/3990 (0.5%)
7	D	0.95	9/2426 (0.4%)	1.39	30/3252 (0.9%)
8	E	0.99	7/1941 (0.4%)	1.39	19/2601 (0.7%)
9	F	1.03	2/1905 (0.1%)	1.51	35/2539 (1.4%)
10	G	0.90	4/1966 (0.2%)	1.25	15/2645 (0.6%)
11	H	0.90	2/1537 (0.1%)	1.29	11/2066 (0.5%)
12	I	0.84	2/1753 (0.1%)	1.28	21/2343 (0.9%)
13	J	0.76	1/1382 (0.1%)	1.10	8/1849 (0.4%)
14	L	0.93	3/1734 (0.2%)	1.26	15/2318 (0.6%)
15	M	0.92	2/1152 (0.2%)	1.27	12/1539 (0.8%)
16	N	1.01	5/1746 (0.3%)	1.49	30/2338 (1.3%)
17	O	0.93	2/1684 (0.1%)	1.30	14/2251 (0.6%)
18	P	0.96	1/1268 (0.1%)	1.21	8/1701 (0.5%)
19	Q	0.89	1/1530 (0.1%)	1.41	24/2041 (1.2%)
20	R	0.97	7/1524 (0.5%)	1.42	21/2013 (1.0%)
21	S	1.20	8/1493 (0.5%)	1.45	28/2002 (1.4%)
22	T	0.88	1/1326 (0.1%)	1.21	12/1770 (0.7%)
23	U	0.83	3/822 (0.4%)	1.12	3/1103 (0.3%)
24	V	1.08	5/993 (0.5%)	1.26	6/1332 (0.5%)
25	W	0.91	1/541 (0.2%)	1.28	0/720
26	X	0.85	3/993 (0.3%)	1.26	7/1334 (0.5%)
27	Y	0.94	3/1132 (0.3%)	1.32	15/1504 (1.0%)
28	Z	0.84	0/1130	1.21	6/1507 (0.4%)
29	a	1.20	7/1192 (0.6%)	1.57	20/1591 (1.3%)
30	b	0.99	3/620 (0.5%)	1.45	11/819 (1.3%)
31	c	0.94	3/742 (0.4%)	1.31	8/996 (0.8%)
32	d	1.08	6/903 (0.7%)	1.46	14/1216 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	1.05	5/1071 (0.5%)	1.39	20/1429 (1.4%)
34	f	1.16	4/895 (0.4%)	1.37	16/1198 (1.3%)
35	g	0.87	0/916	1.22	8/1220 (0.7%)
36	h	0.82	2/1023 (0.2%)	1.26	9/1350 (0.7%)
37	i	0.85	2/843 (0.2%)	1.29	8/1115 (0.7%)
38	j	1.13	4/721 (0.6%)	1.57	16/953 (1.7%)
39	k	0.74	1/575 (0.2%)	1.16	3/761 (0.4%)
40	l	0.81	0/454	1.15	4/599 (0.7%)
41	m	0.77	0/435	1.14	1/575 (0.2%)
42	n	0.63	0/223	1.10	0/284
43	o	0.83	1/864 (0.1%)	1.34	8/1140 (0.7%)
44	p	0.80	0/718	1.22	7/953 (0.7%)
45	r	0.89	1/1017 (0.1%)	1.31	13/1365 (1.0%)
46	1	0.64	0/3114	0.94	3/4218 (0.1%)
47	2	0.75	0/504	1.14	5/673 (0.7%)
All	All	0.74	158/151252 (0.1%)	1.28	1963/223243 (0.9%)

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	5	1	158
2	7	0	2
3	8	0	11
4	A	0	6
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
43	o	0	6
44	p	0	1
45	r	0	5
46	1	0	1
47	2	0	1
All	All	1	340

The worst 5 of 158 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	33.19	2.10	1.61
21	S	81	TRP	CA-CB	14.99	1.71	1.53
29	a	109	TYR	CA-CB	14.19	1.72	1.53
8	E	278	TYR	CA-CB	14.02	1.72	1.53
24	V	97	TYR	CA-CB	12.45	1.73	1.53

The worst 5 of 1963 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	E	278	TYR	CB-CA-C	21.50	129.79	110.44
17	O	135	PHE	N-CA-C	17.84	134.65	108.60
11	H	156	ASN	N-CA-C	-17.41	92.44	111.07
3	8	34	U	C4'-C3'-O3'	-16.89	87.67	113.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	5	383	A	C1'-C2'-O2'	-15.03	89.26	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 340 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

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	5	78486	0	39661	10410	0
2	7	2558	0	1296	308	0
3	8	3314	0	1683	501	0
4	A	1868	0	1959	163	0
5	B	3147	0	3280	224	0
6	C	2919	0	3100	179	0
7	D	2380	0	2412	182	0
8	E	1904	0	2055	148	0
9	F	1870	0	1996	180	0
10	G	1934	0	2086	102	0
11	H	1518	0	1601	84	0
12	I	1713	0	1752	90	0
13	J	1359	0	1390	62	0
14	L	1703	0	1818	102	0
15	M	1131	0	1209	74	0
16	N	1701	0	1749	128	0
17	O	1651	0	1786	89	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	P	1242	0	1269	57	0
19	Q	1506	0	1623	78	0
20	R	1508	0	1664	94	0
21	S	1454	0	1496	127	0
22	T	1298	0	1366	84	0
23	U	808	0	831	26	0
24	V	979	0	1039	52	0
25	W	528	0	541	52	0
26	X	976	0	1053	64	0
27	Y	1115	0	1205	62	0
28	Z	1107	0	1182	56	0
29	a	1163	0	1211	108	0
30	b	610	0	650	48	0
31	c	732	0	769	41	0
32	d	888	0	930	66	0
33	e	1053	0	1147	91	0
34	f	876	0	912	58	0
35	g	906	0	1002	54	0
36	h	1015	0	1149	56	0
37	i	832	0	917	29	0
38	j	706	0	743	53	0
39	k	569	0	637	21	0
40	l	444	0	483	36	0
41	m	429	0	466	28	0
42	n	222	0	264	0	0
43	o	851	0	922	43	0
44	p	708	0	760	26	0
45	r	1001	0	1062	74	0
46	1	3051	0	3158	177	0
47	2	494	0	527	23	0
48	3	180	0	40	1	0
49	5	119	0	0	0	0
49	7	5	0	0	0	0
49	8	4	0	0	0	0
49	P	1	0	0	0	0
49	V	1	0	0	0	0
50	j	1	0	0	1	0
50	m	1	0	0	2	0
50	o	1	0	0	1	0
All	All	140540	0	101851	13543	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 56.

The worst 5 of 13543 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)
1:5:100:C:C5	1:5:101:A:C8	2.00	1.49
40:1:21:ARG:NH2	40:1:24:PRO:HG3	1.28	1.43
1:5:1174:G:N2	1:5:1175:A:N7	1.67	1.41
1:5:2526:C:C5	46:1:405:ARG:CZ	2.04	1.41
1:5:1266:G:N2	1:5:2111:G:N3	1.67	1.39

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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2	16
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	4
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	15
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	5
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	1
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	2	12
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	19
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	24
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	1	7
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	11
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	1	10
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	30
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	18
17	O	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	8	30

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	9	33
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	20
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	24
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	28
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	26
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	24
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	23
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	7	29
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	28
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	12
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	2	15
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	9
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	9
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	13
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	15
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	44
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	12
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	6	26
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	21
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	25
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	11
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	5
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	14
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	8
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	11	38
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	1	11
46	1	384/476 (81%)	325 (85%)	42 (11%)	17 (4%)	2	13
47	2	60/68 (88%)	51 (85%)	6 (10%)	3 (5%)	1	10
All	All	6815/7601 (90%)	5717 (84%)	811 (12%)	287 (4%)	3	14

5 of 287 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

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	
4	A	187/199 (94%)	141 (75%)	46 (25%)	1	2
5	B	335/335 (100%)	267 (80%)	68 (20%)	1	4
6	C	305/305 (100%)	242 (79%)	63 (21%)	1	4
7	D	246/250 (98%)	179 (73%)	67 (27%)	0	1
8	E	209/209 (100%)	162 (78%)	47 (22%)	1	3
9	F	194/194 (100%)	143 (74%)	51 (26%)	0	1
10	G	206/226 (91%)	156 (76%)	50 (24%)	1	2
11	H	169/171 (99%)	126 (75%)	43 (25%)	0	1
12	I	180/180 (100%)	140 (78%)	40 (22%)	1	3
13	J	143/149 (96%)	111 (78%)	32 (22%)	1	3
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	2
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	7
16	N	171/172 (99%)	132 (77%)	39 (23%)	1	3
17	O	172/172 (100%)	144 (84%)	28 (16%)	2	10
18	P	134/134 (100%)	113 (84%)	21 (16%)	2	10
19	Q	163/164 (99%)	132 (81%)	31 (19%)	1	6
20	R	159/175 (91%)	119 (75%)	40 (25%)	0	1
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	3
22	T	139/140 (99%)	117 (84%)	22 (16%)	2	10

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	89/114 (78%)	70 (79%)	19 (21%)	1	3
24	V	101/107 (94%)	79 (78%)	22 (22%)	1	3
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	2
26	X	107/133 (80%)	87 (81%)	20 (19%)	1	6
27	Y	124/135 (92%)	92 (74%)	32 (26%)	0	1
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	5
29	a	119/120 (99%)	104 (87%)	15 (13%)	4	18
30	b	63/123 (51%)	46 (73%)	17 (27%)	0	1
31	c	79/97 (81%)	61 (77%)	18 (23%)	1	3
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	0
33	e	114/121 (94%)	87 (76%)	27 (24%)	1	2
34	f	88/89 (99%)	69 (78%)	19 (22%)	1	3
35	g	98/100 (98%)	80 (82%)	18 (18%)	1	7
36	h	109/110 (99%)	91 (84%)	18 (16%)	2	10
37	i	86/89 (97%)	69 (80%)	17 (20%)	1	5
38	j	73/73 (100%)	61 (84%)	12 (16%)	2	10
39	k	64/65 (98%)	54 (84%)	10 (16%)	2	10
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	9
41	m	48/116 (41%)	35 (73%)	13 (27%)	0	1
42	n	22/24 (92%)	19 (86%)	3 (14%)	3	15
43	o	92/94 (98%)	71 (77%)	21 (23%)	1	3
44	p	74/74 (100%)	62 (84%)	12 (16%)	2	10
45	r	109/109 (100%)	92 (84%)	17 (16%)	2	10
46	1	330/398 (83%)	310 (94%)	20 (6%)	17	43
47	2	53/59 (90%)	49 (92%)	4 (8%)	12	38
All	All	5919/6456 (92%)	4704 (80%)	1215 (20%)	3	4

5 of 1215 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	a	85	GLN
43	o	33	LEU
31	c	56	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	a	77	LYS
34	f	103	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 197 such sidechains are listed below:

Mol	Chain	Res	Type
21	S	37	HIS
29	a	41	HIS
21	S	125	GLN
26	X	57	GLN
31	c	19	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3652/3722 (98%)	1667 (45%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3926/3998 (98%)	1759 (44%)	660 (16%)

5 of 1759 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3860	A
1	5	4645	C
1	5	4084	G
1	5	3856	A
1	5	4287	G

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 133 ligands modelled in this entry, 133 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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	12
8	E	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	23.51
1	5	4776:G	O3'	4859:C	P	17.87
1	5	757:G	O3'	906:C	P	16.89
1	5	519:C	O3'	642:G	P	16.61
1	5	2910:G	O3'	3583:U	P	16.04

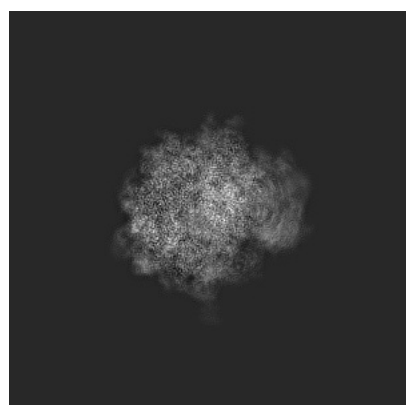
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2650. These allow visual inspection of the internal detail of the map and identification of artifacts.

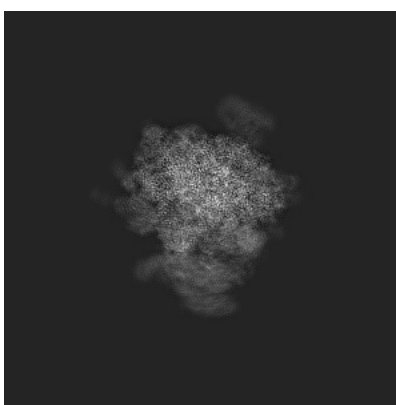
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

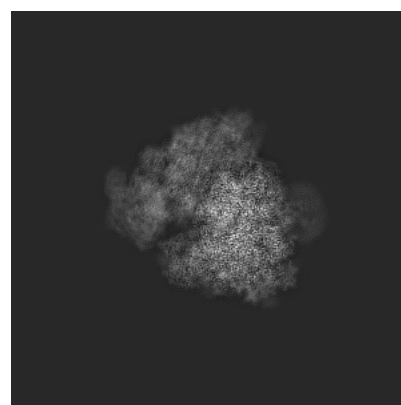
6.1.1 Primary map



X



Y

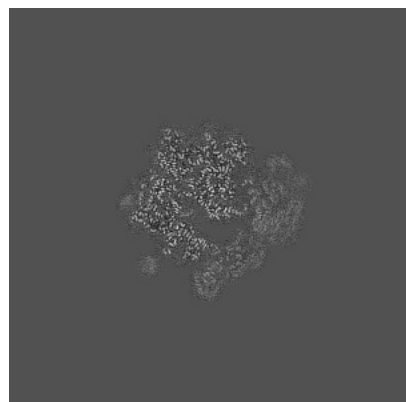


Z

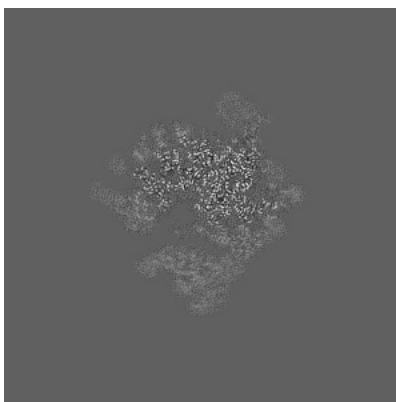
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 210



Y Index: 210

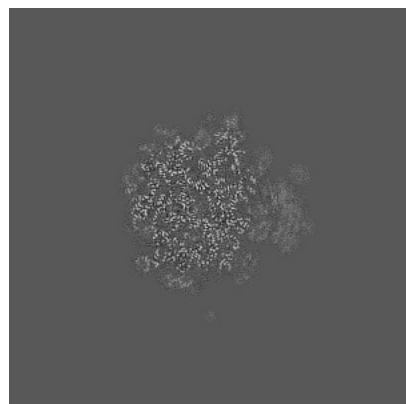


Z Index: 210

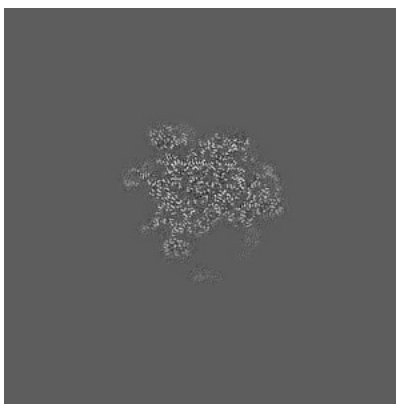
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

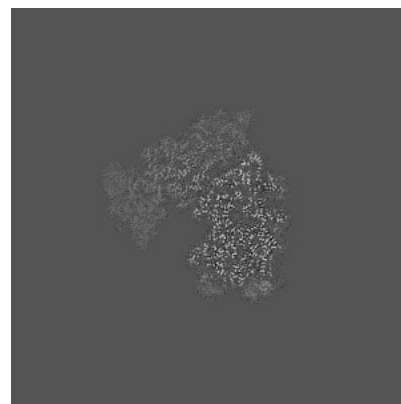
6.3.1 Primary map



X Index: 233



Y Index: 168

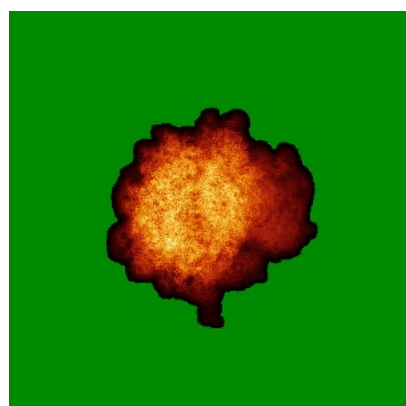


Z Index: 219

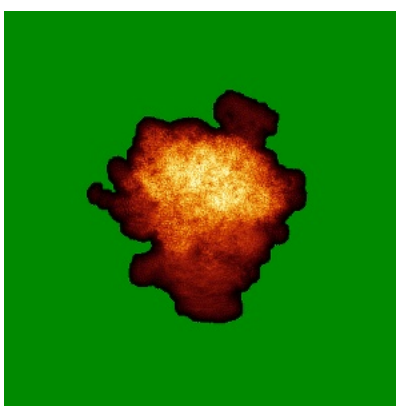
The images above show the largest variance slices of the map in three orthogonal directions.

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

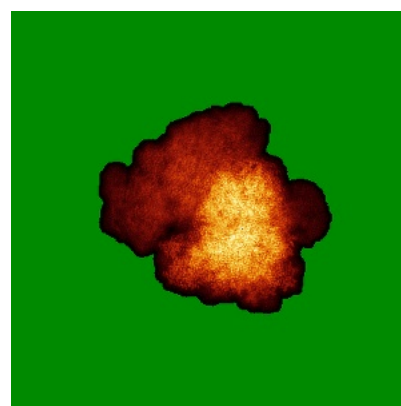
6.4.1 Primary map



X



Y

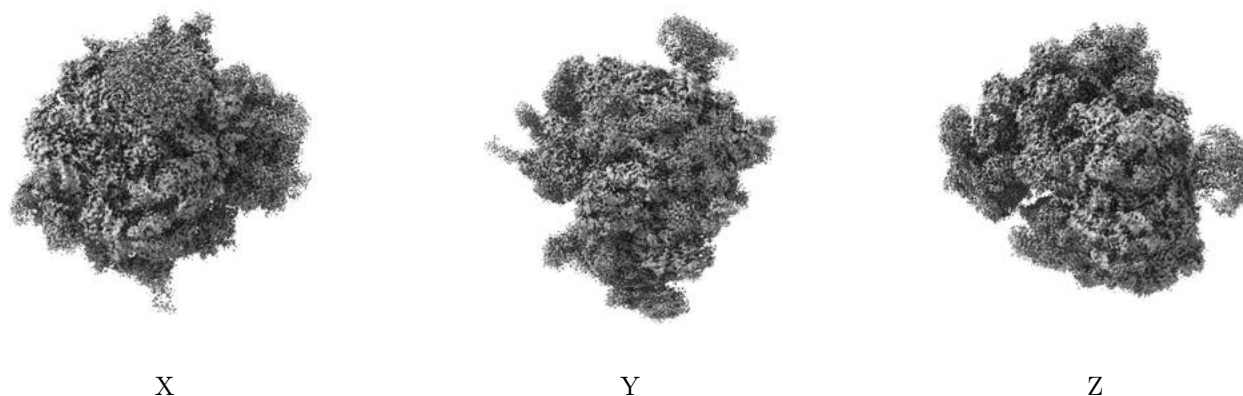


Z

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 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

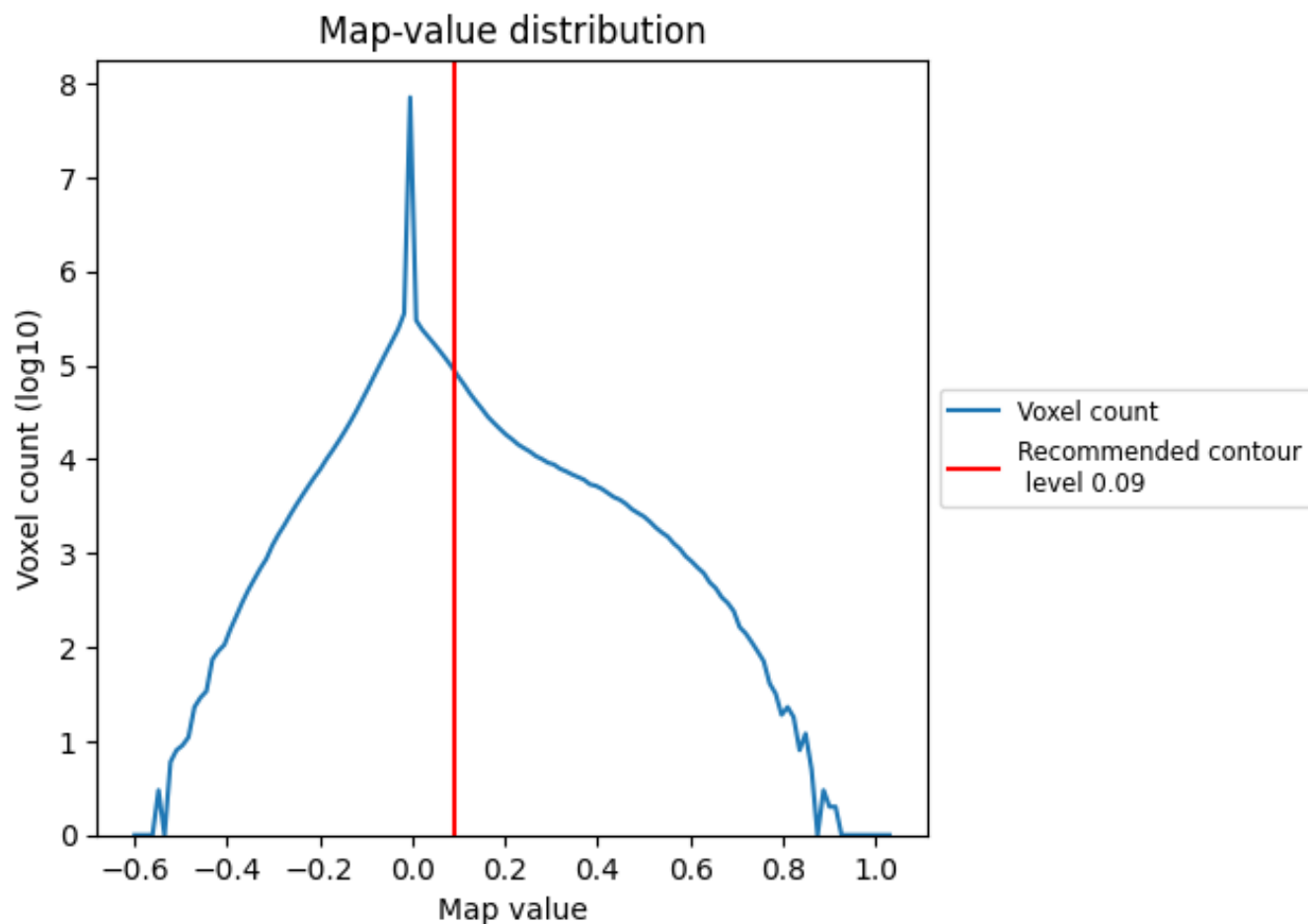
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

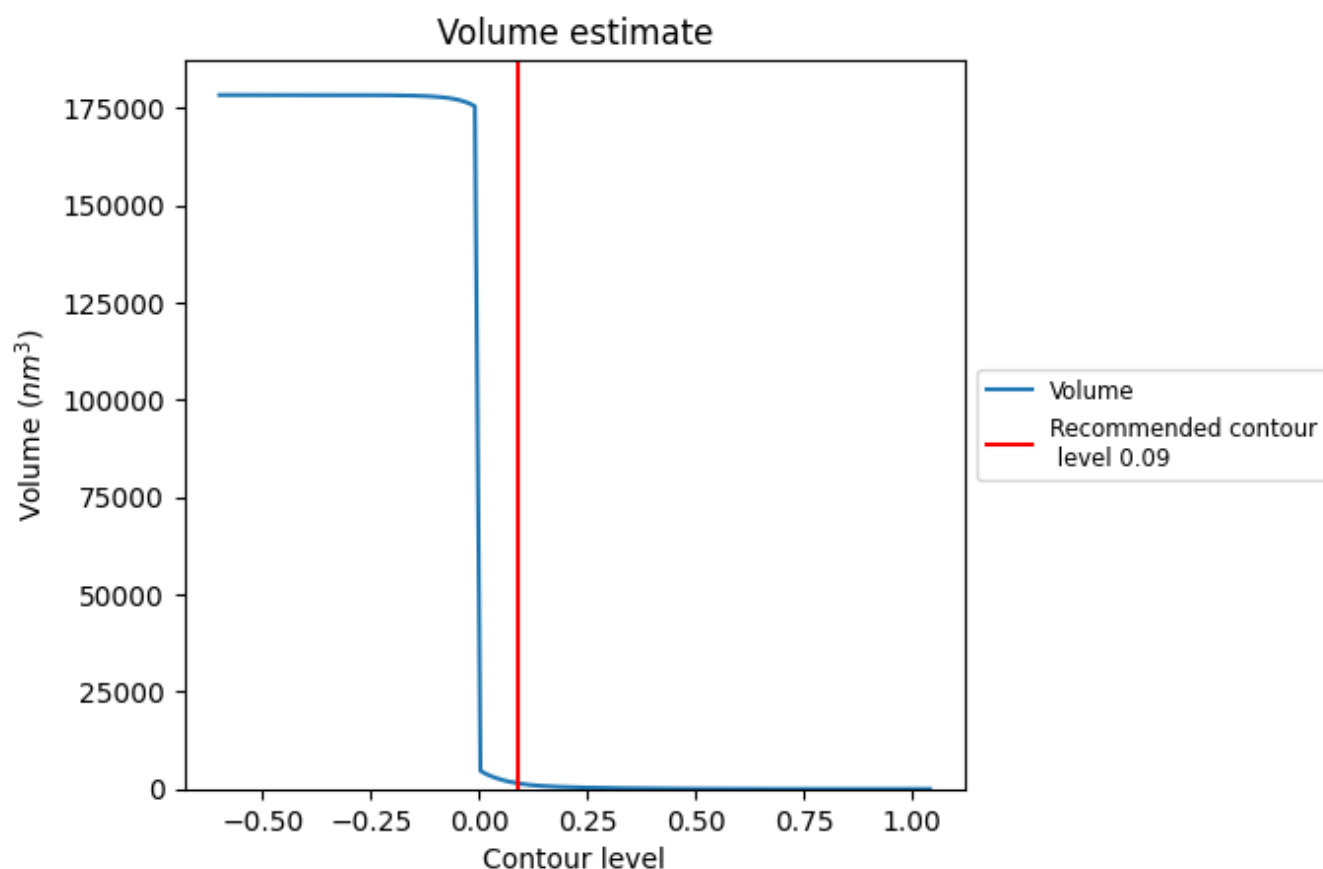
This section contains the results of statistical analysis of the map.

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.

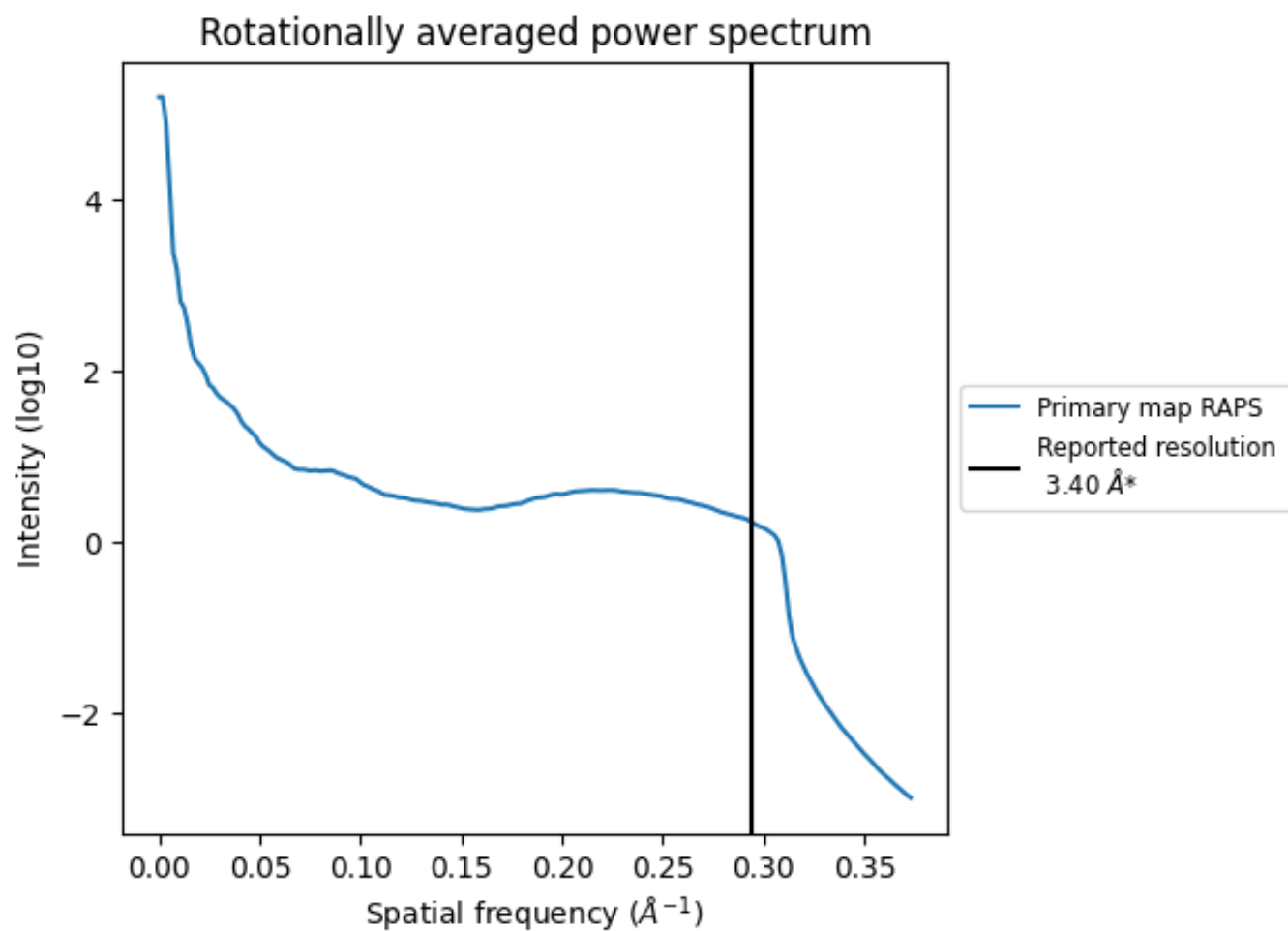
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1453 nm^3 ; this corresponds to an approximate mass of 1312 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 0.294 Å⁻¹

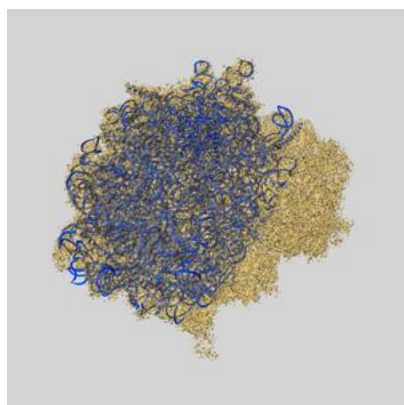
8 Fourier-Shell correlation

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

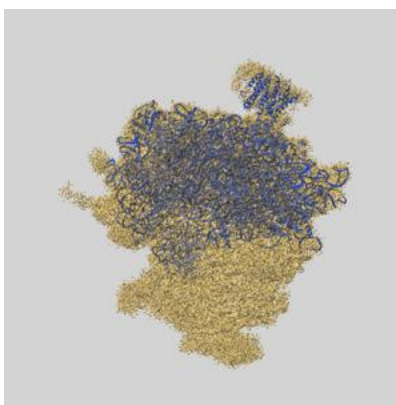
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2650 and PDB model 3J7Q. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

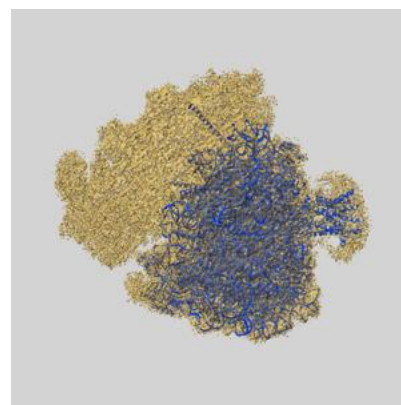
9.1 Map-model overlay [i](#)



X



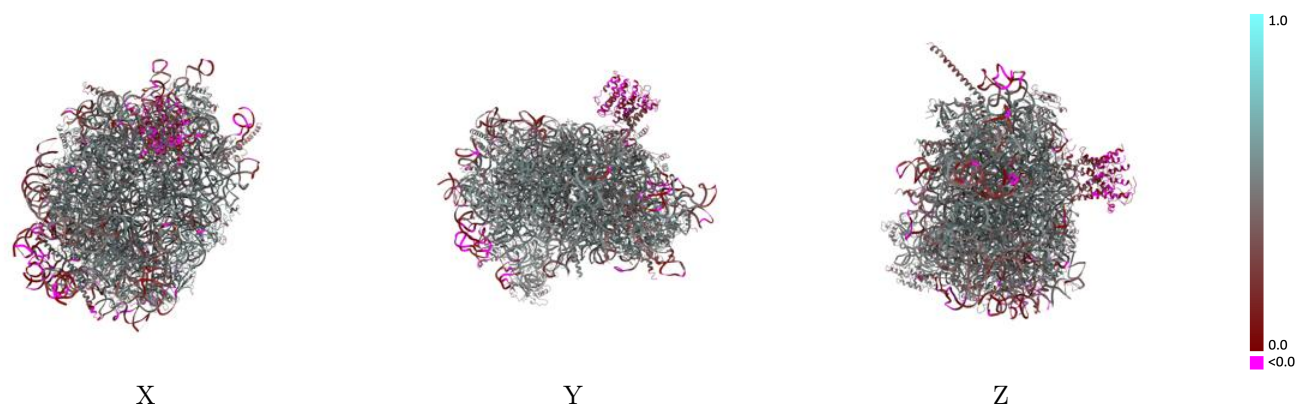
Y



Z

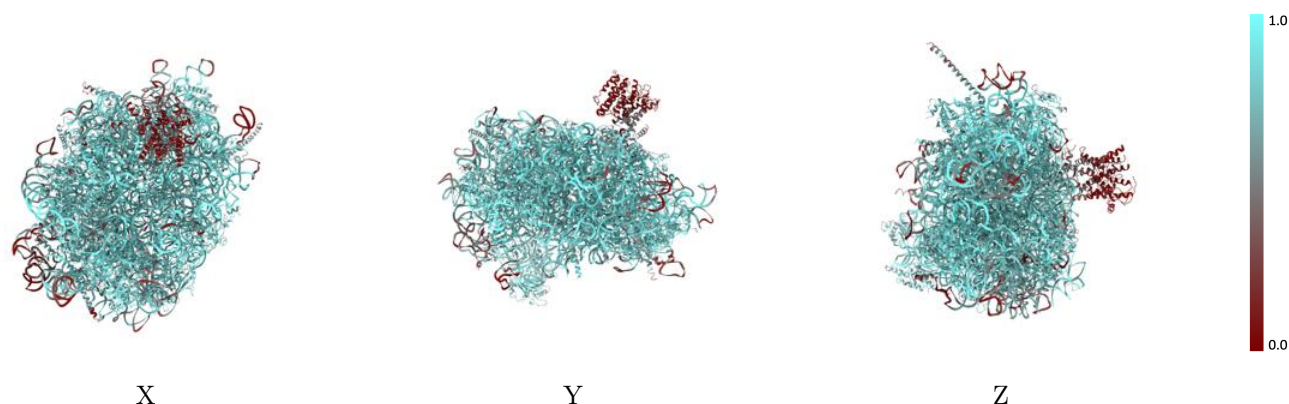
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



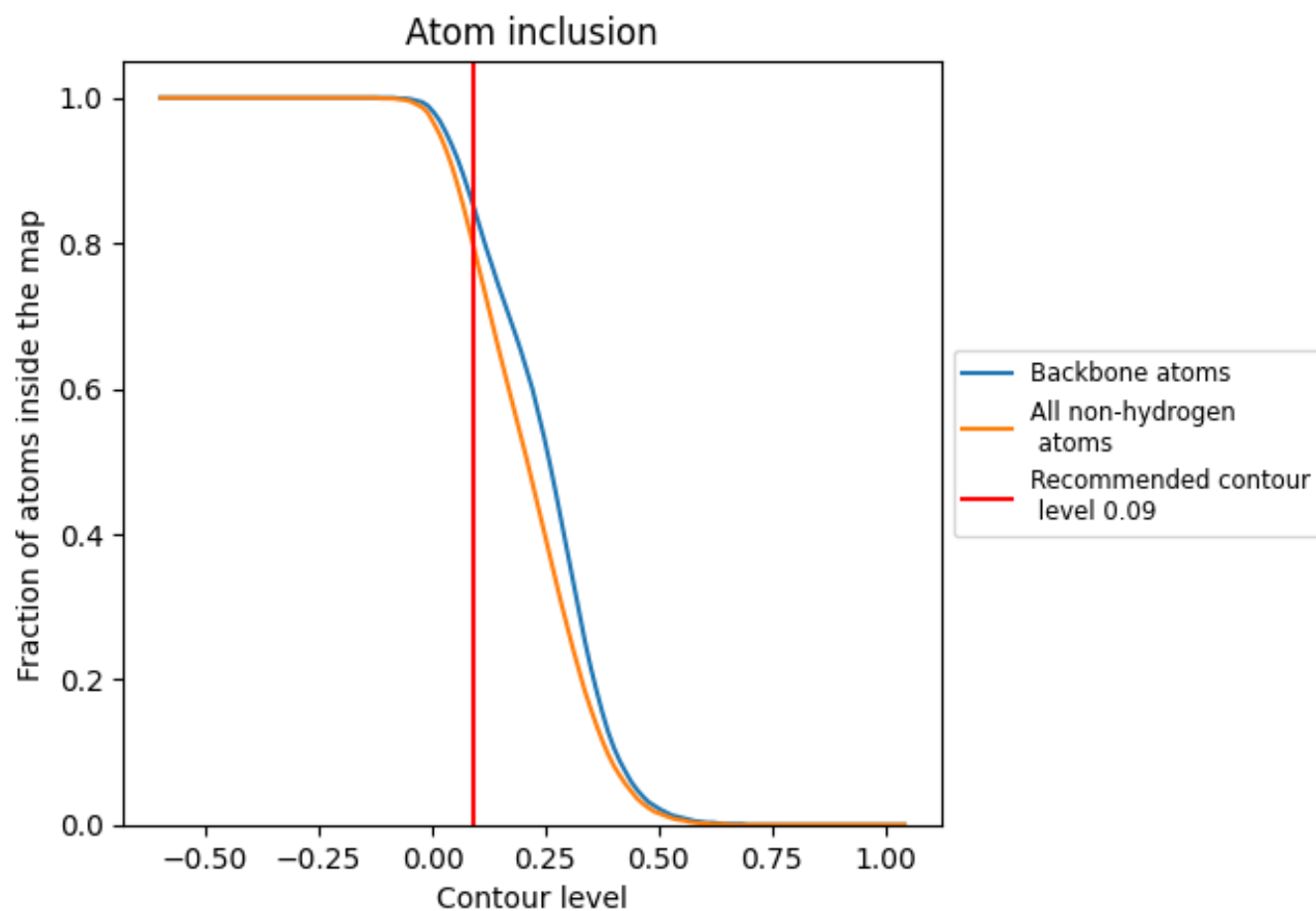
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.4410
1	 0.2230	 0.1560
2	 0.2590	 0.1820
3	 0.0280	 0.0620
5	 0.8090	 0.4170
7	 0.9290	 0.4920
8	 0.8500	 0.4530
A	 0.8620	 0.5200
B	 0.8600	 0.5130
C	 0.8300	 0.5000
D	 0.8060	 0.4580
E	 0.7580	 0.4480
F	 0.8320	 0.5010
G	 0.7680	 0.4560
H	 0.8280	 0.5050
I	 0.8010	 0.4800
J	 0.7620	 0.4510
L	 0.7750	 0.4650
M	 0.8310	 0.5010
N	 0.8720	 0.5200
O	 0.8570	 0.5230
P	 0.8350	 0.5160
Q	 0.8610	 0.5230
R	 0.7790	 0.4670
S	 0.8610	 0.5190
T	 0.8250	 0.5020
U	 0.7200	 0.4240
V	 0.8430	 0.5190
W	 0.8210	 0.5040
X	 0.7870	 0.4910
Y	 0.8100	 0.4990
Z	 0.8310	 0.4950
a	 0.8630	 0.5160
b	 0.6780	 0.4120
c	 0.8080	 0.4850



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
d	 0.7990	 0.4790
e	 0.8470	 0.5210
f	 0.8780	 0.5260
g	 0.8150	 0.5080
h	 0.7890	 0.4880
i	 0.8040	 0.4890
j	 0.8470	 0.5010
k	 0.7540	 0.4600
l	 0.8350	 0.5180
m	 0.8490	 0.5220
n	 0.7710	 0.4760
o	 0.8010	 0.5020
p	 0.8200	 0.5160
r	 0.8390	 0.5060