



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 05:23 PM UTC

PDB ID : 3JBV / pdb_00003jbv
EMDB ID : EMD-6486
Title : Mechanisms of Ribosome Stalling by SecM at Multiple Elongation Steps
Authors : Zhang, J.; Pan, X.J.; Yan, K.G.; Sun, S.; Gao, N.; Sui, S.F.
Deposited on : 2015-10-16
Resolution : 3.32 Å(reported)
Based on initial model : 4V7T

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

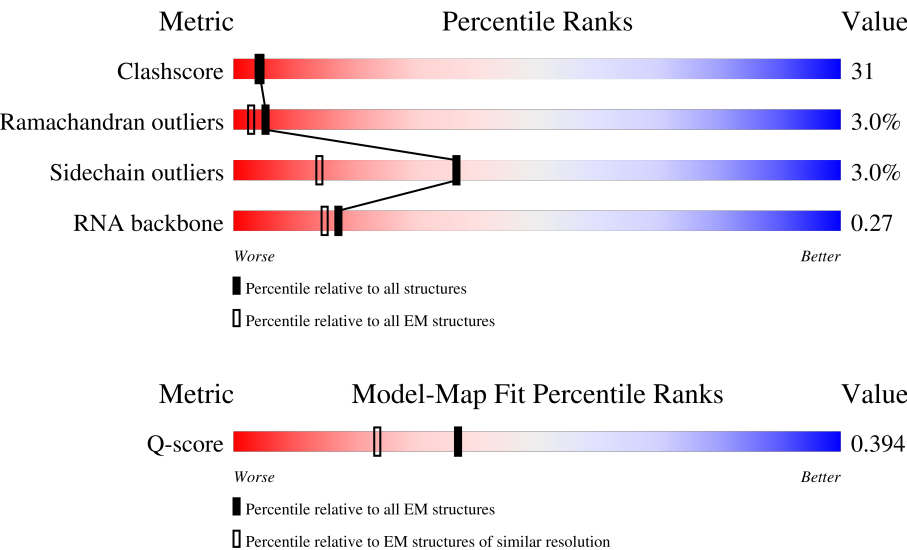
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.32 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	14518 (2.82 - 3.82)

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	A	1542	13% 42% 40% 17% .
2	B	241	83% 56% 32% . 10%
3	C	233	67% 53% 33% . 12%

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Mol	Chain	Length	Quality of chain
4	D	206	88% 56% 42% .
5	E	167	57% 54% 30% 5% 10%
6	F	131	46% 48% 28% 24%
7	G	156	74% 63% 31% . .
8	H	130	56% 65% 34% .
9	I	130	73% 43% 51% . .
10	J	103	81% 50% 43% . 5%
11	K	129	36% 56% 33% . 9%
12	L	124	40% 64% 34% . .
13	M	118	64% 52% 44% .
14	N	101	61% 50% 43% . 5%
15	O	89	35% 64% 35% .
16	P	82	84% 30% 48% 21% .
17	Q	84	67% 61% 33% . 5%
18	R	75	33% 48% 25% 27%
19	S	92	52% 50% 35% . 14%
20	T	87	63% 69% 29% .
21	U	71	51% 35% 30% 7% 28%
22	V	76	75% 14% 38% 46% .
23	W	75	16% 31% 44% 24% .
24	X	11	36% 27% 64% 9%
25	0	78	19% 86% 13% .
26	1	63	46% 84% 13% . .
27	2	59	14% 78% 17% . .
28	3	57	18% 67% 30% . .

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Mol	Chain	Length	Quality of chain
29	4	55	
30	6	46	
31	7	65	
32	8	38	
33	a	120	
34	b	2904	
35	c	273	
36	i	142	
37	d	209	
38	e	201	
39	f	179	
40	g	177	
41	h	149	
42	j	142	
43	k	123	
44	l	144	
45	m	136	
46	n	127	
47	o	117	
48	p	115	
49	q	118	
50	r	103	
51	s	110	
52	t	100	
53	u	104	

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Mol	Chain	Length	Quality of chain
54	w	94	
55	y	85	
56	z	27	

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
57	CLM	b	9000	-	-	X	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145911 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 RNA (1530-MER).

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

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	125	ASP	GLU	conflict	UNP P02358

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

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

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

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

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	76	Total	C	N	O	P	0	0
			1620	723	290	532	75		

- Molecule 23 is a RNA chain called RNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	75	Total	C	N	O	P	0	0
			1599	713	287	525	74		

- Molecule 24 is a RNA chain called RNA (5'-R(P*CP*UP*GP*GP*CP*CP*CP*UP*CP*A P*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	11	Total	C	N	O	P	0	0
			231	103	39	78	11		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 33 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	117	Total	C	N	O	P	0	0
			2506	1116	459	814	117		

- Molecule 34 is a RNA chain called RNA (2903-MER).

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

- Molecule 35 is a protein called 50S ribosomal protein L2.

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

- Molecule 36 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	134	Total	C	N	O	S	0	0
			976	614	169	187	6		

- Molecule 37 is a protein called 50S ribosomal protein L3.

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

- Molecule 38 is a protein called 50S ribosomal protein L4.

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

- Molecule 39 is a protein called 50S ribosomal protein L5.

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

- Molecule 40 is a protein called 50S ribosomal protein L6.

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

- Molecule 41 is a protein called 50S ribosomal protein L9.

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

- Molecule 42 is a protein called 50S ribosomal protein L13.

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

- Molecule 43 is a protein called 50S ribosomal protein L14.

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

- Molecule 44 is a protein called 50S ribosomal protein L15.

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

- Molecule 45 is a protein called 50S ribosomal protein L16.

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

- Molecule 46 is a protein called 50S ribosomal protein L17.

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

- Molecule 47 is a protein called 50S ribosomal protein L18.

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

- Molecule 48 is a protein called 50S ribosomal protein L19.

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

- Molecule 49 is a protein called 50S ribosomal protein L20.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L22.

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

- Molecule 52 is a protein called 50S ribosomal protein L23.

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

- Molecule 53 is a protein called 50S ribosomal protein L24.

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

- Molecule 54 is a protein called 50S ribosomal protein L25.

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

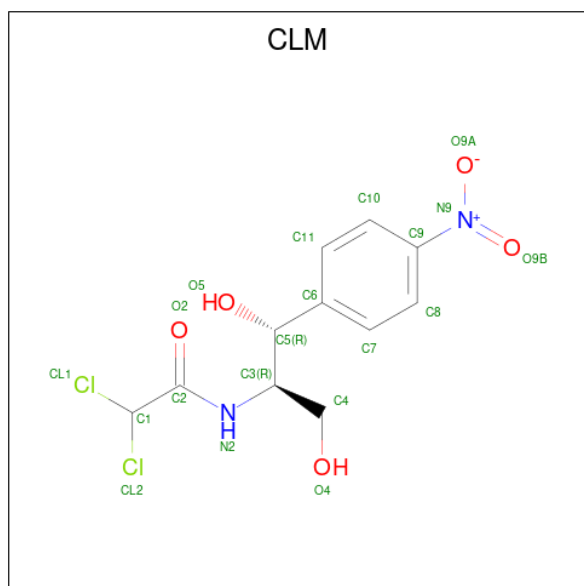
- Molecule 55 is a protein called 50S ribosomal protein L27.

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

- Molecule 56 is a protein called Secretion monitor.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	z	27	Total	C	N	O	0	0
			211	134	35	42		

- Molecule 57 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$).



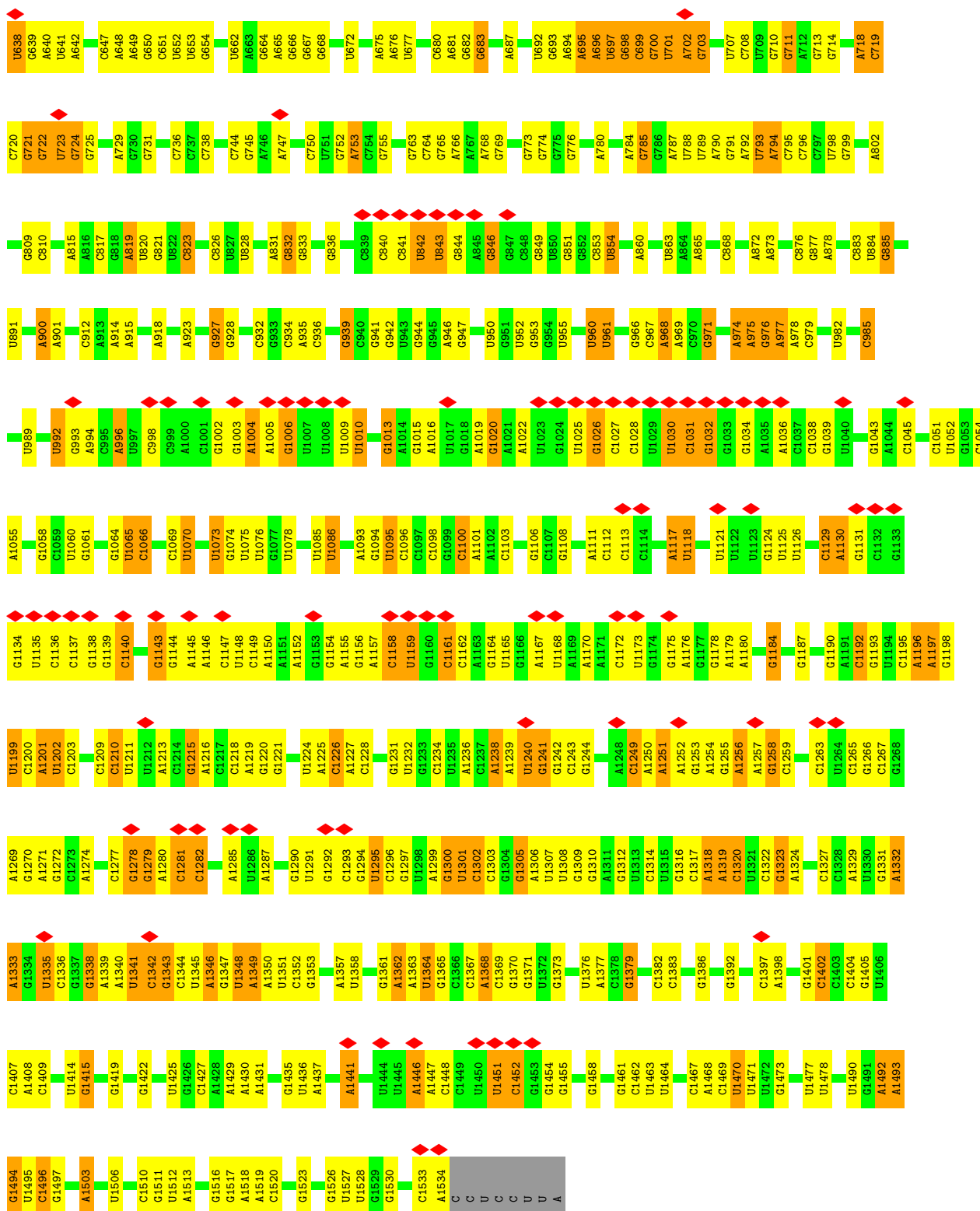
Mol	Chain	Residues	Atoms					AltConf
57	b	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

3 Residue-property plots

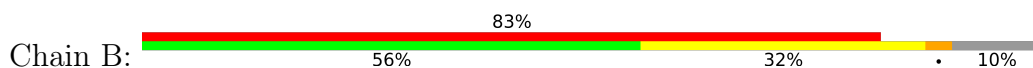
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

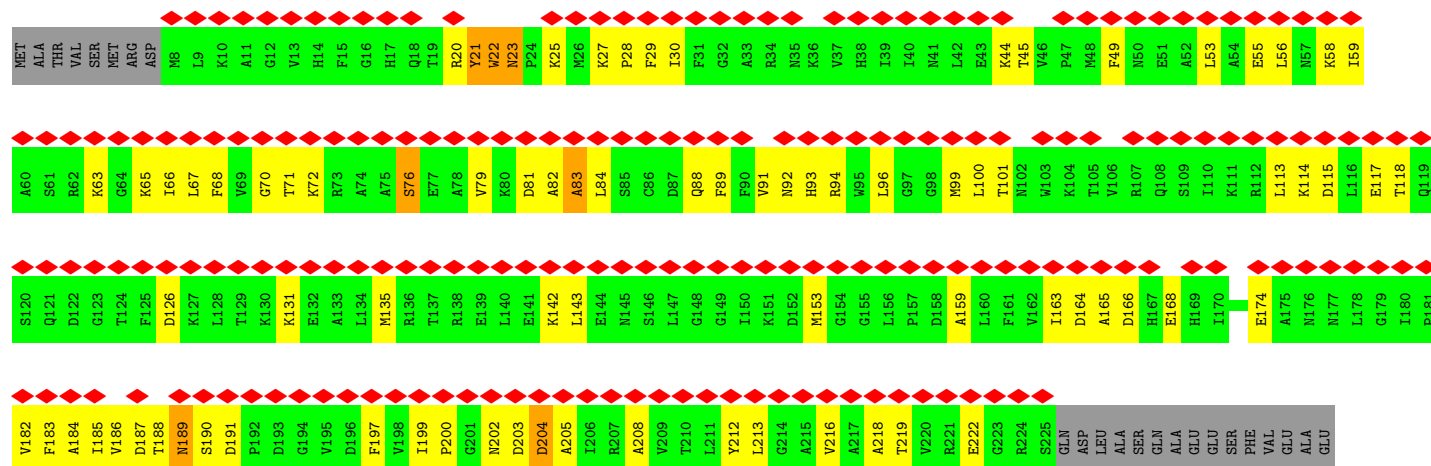
• Molecule 1: RNA (1530-MER)



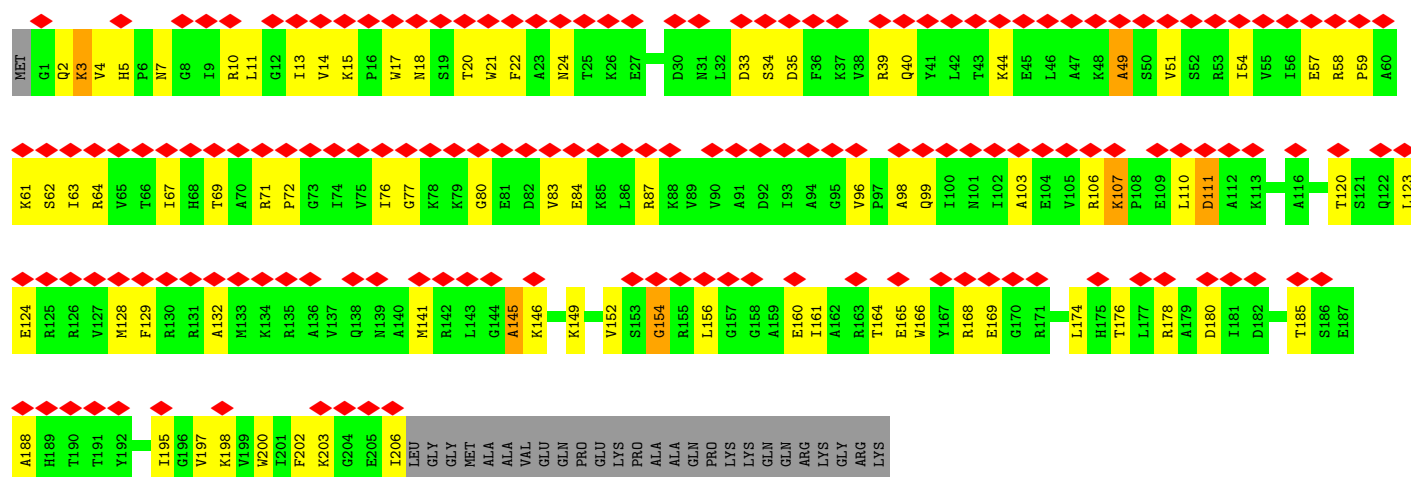


• Molecule 2: 30S ribosomal protein S2

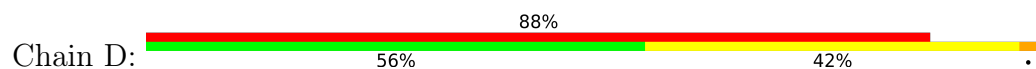




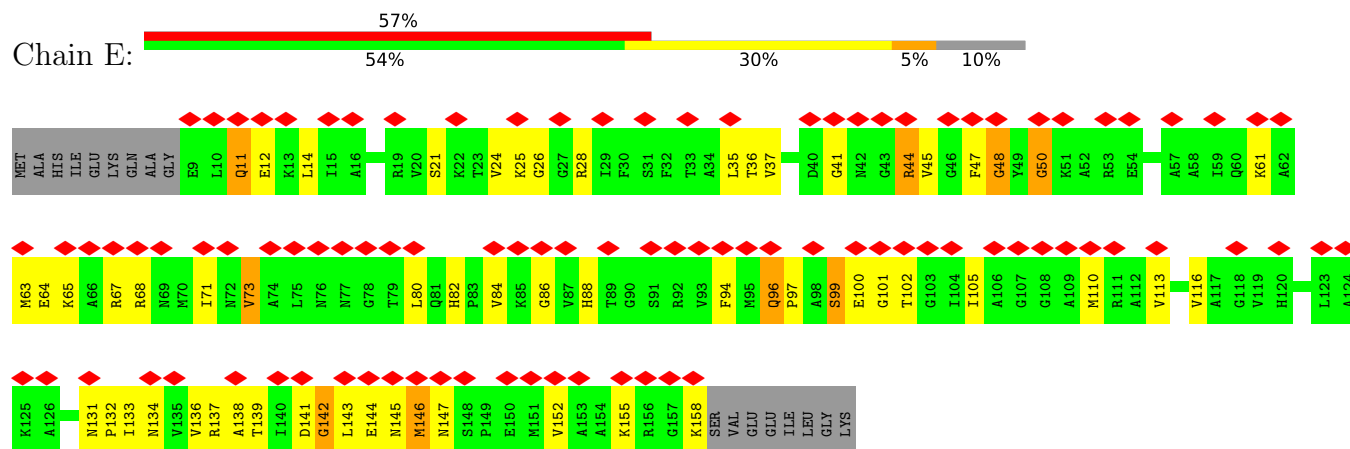
• Molecule 3: 30S ribosomal protein S3



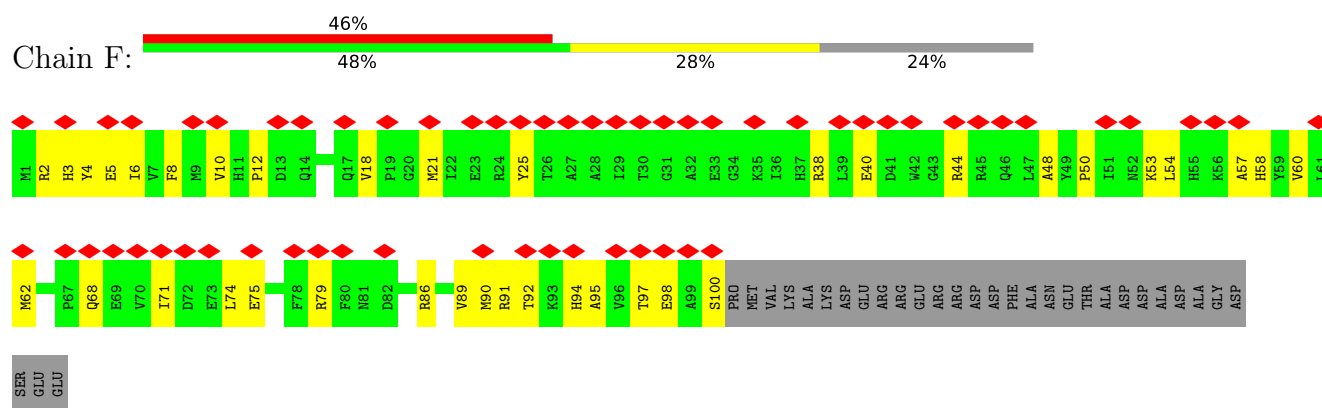
• Molecule 4: 30S ribosomal protein S4



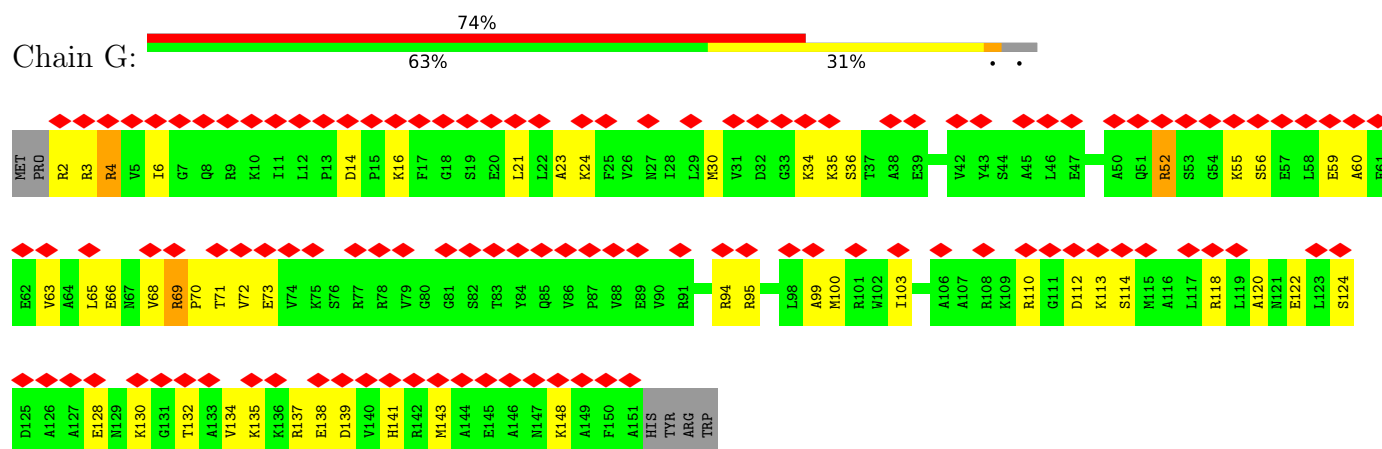
- Molecule 5: 30S ribosomal protein S5



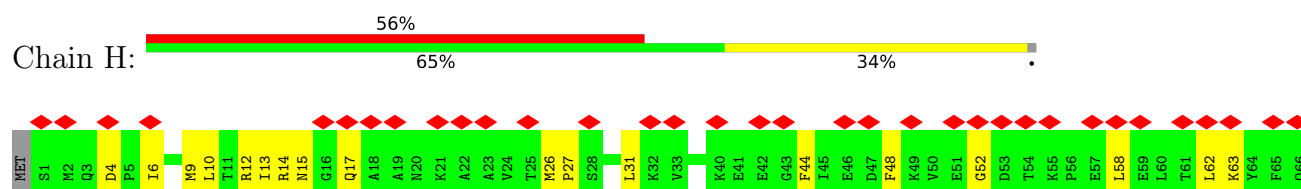
- Molecule 6: 30S ribosomal protein S6

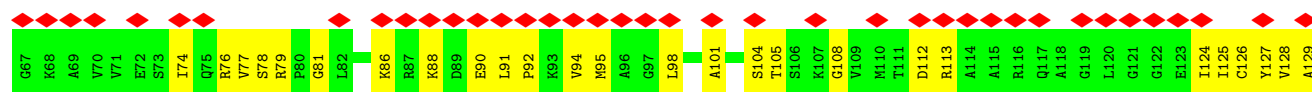


- Molecule 7: 30S ribosomal protein S7

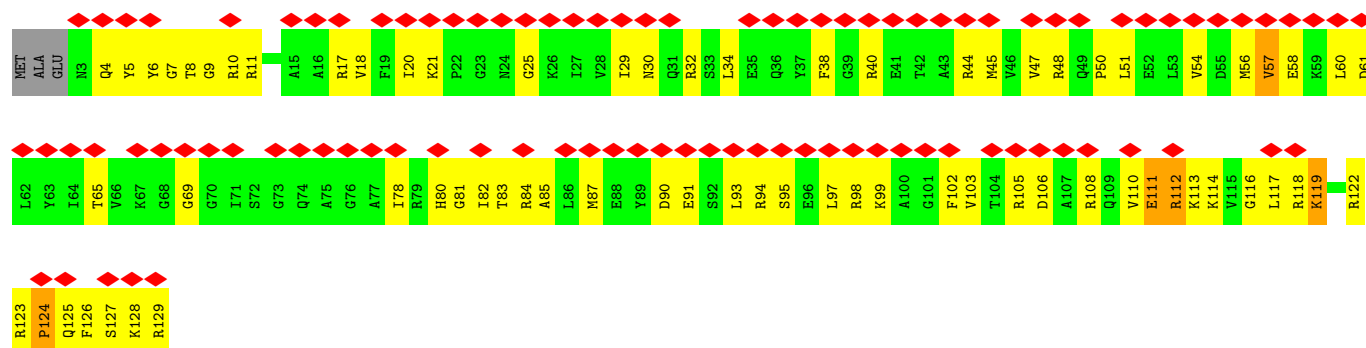
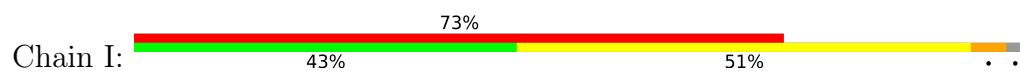


- Molecule 8: 30S ribosomal protein S8

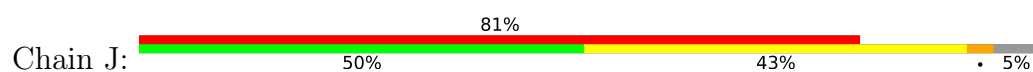




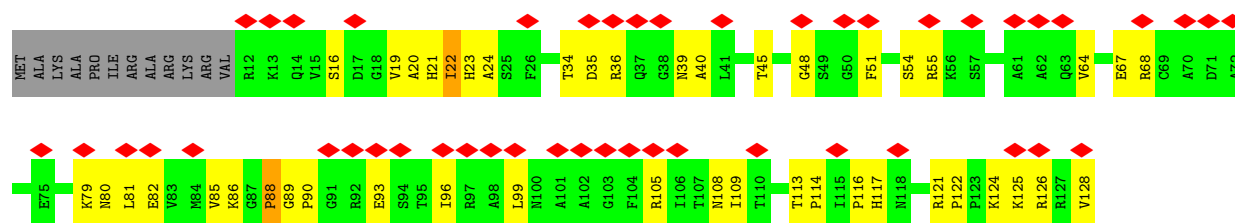
• Molecule 9: 30S ribosomal protein S9



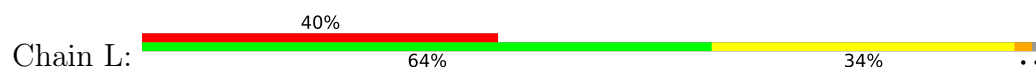
• Molecule 10: 30S ribosomal protein S10

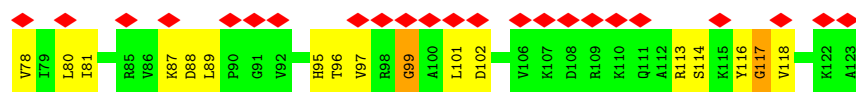


• Molecule 11: 30S ribosomal protein S11

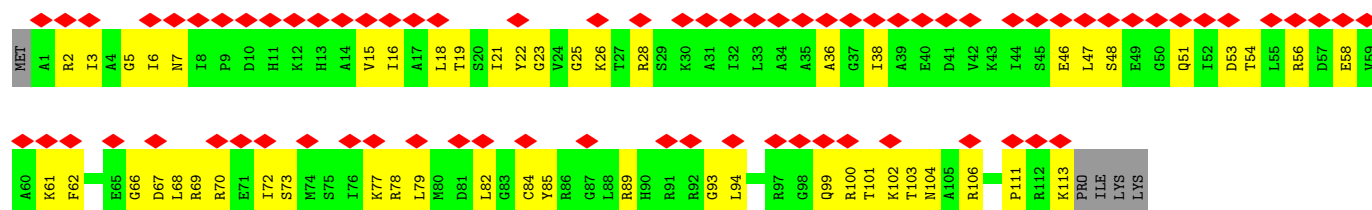


• Molecule 12: 30S ribosomal protein S12

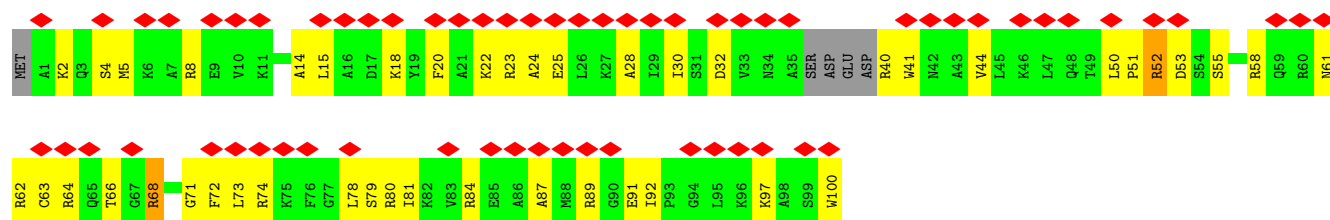




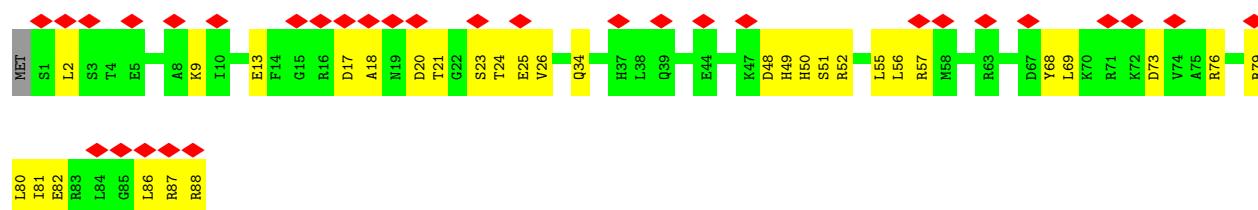
- Molecule 13: 30S ribosomal protein S13



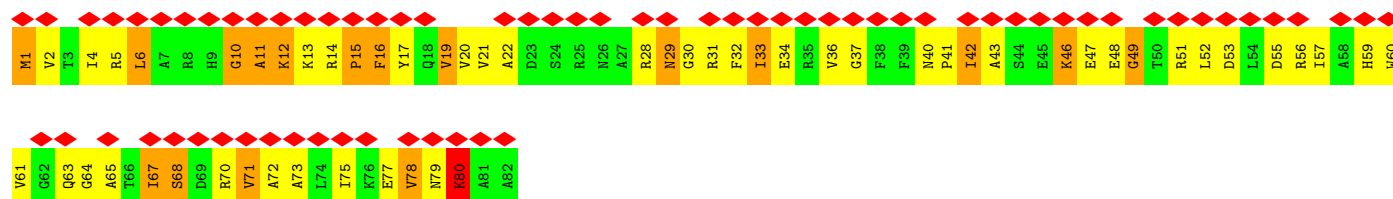
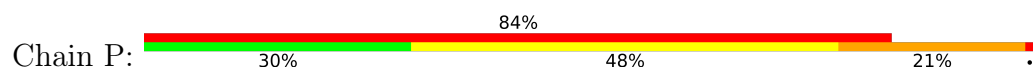
- Molecule 14: 30S ribosomal protein S14



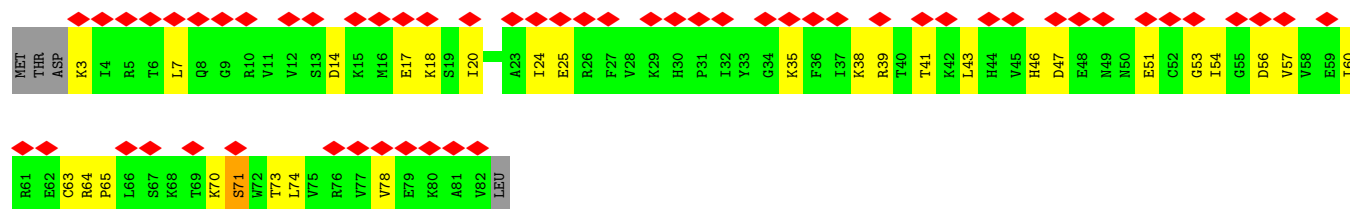
- Molecule 15: 30S ribosomal protein S15



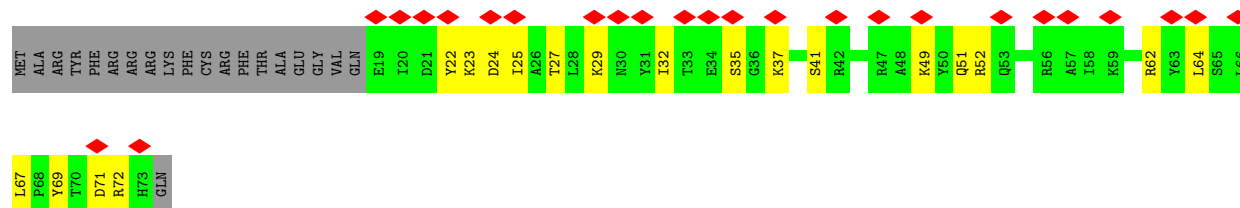
- Molecule 16: 30S ribosomal protein S16



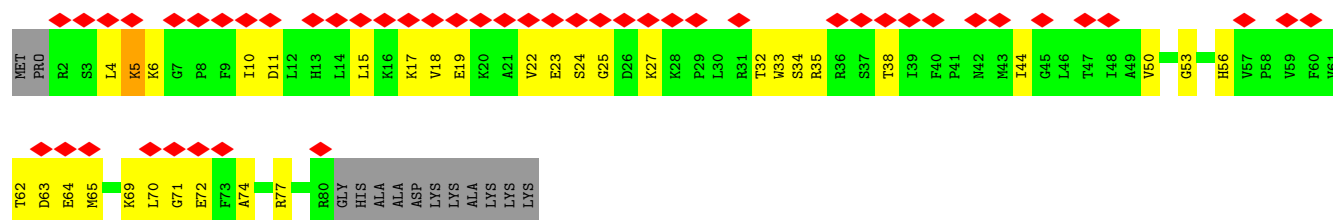
- Molecule 17: 30S ribosomal protein S17



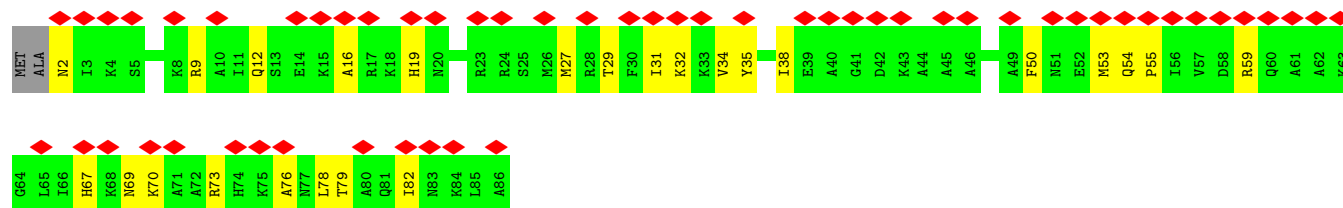
- Molecule 18: 30S ribosomal protein S18



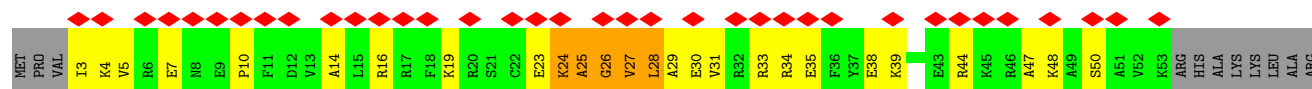
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20

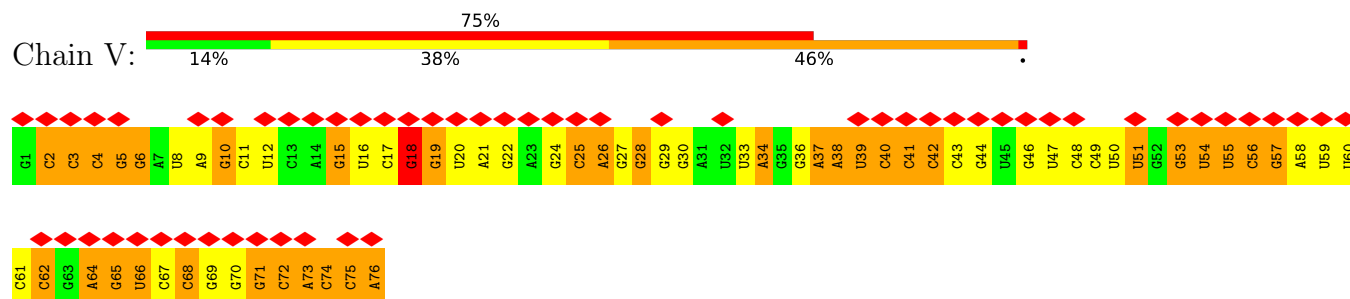


- Molecule 21: 30S ribosomal protein S21

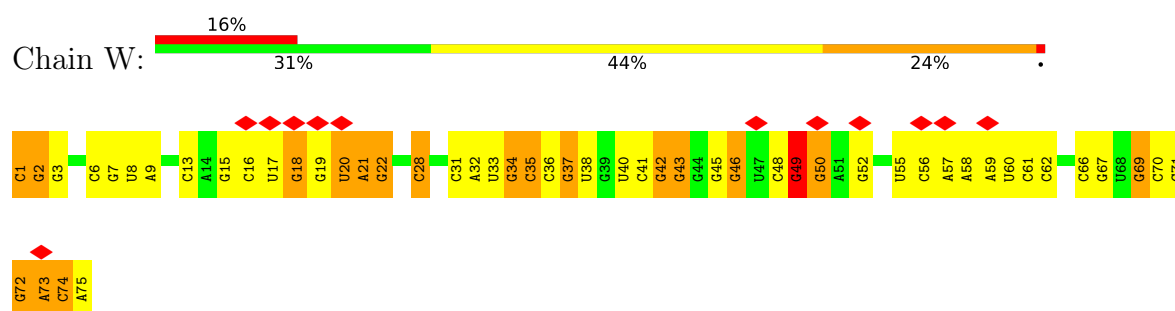


GLU
ASN
ALA
ARG
THR
ARG
LEU
TYR

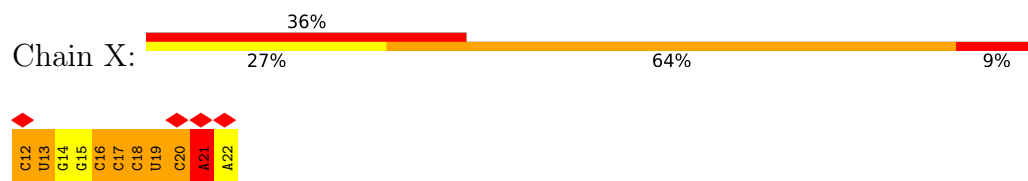
• Molecule 22: RNA (76-MER)



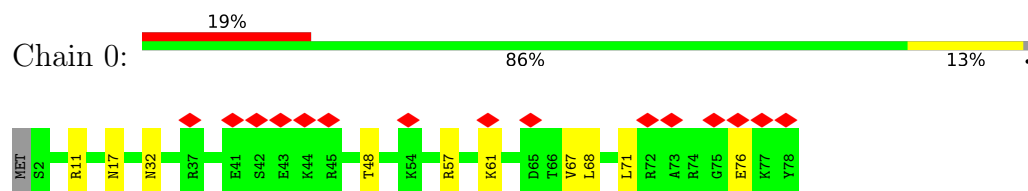
• Molecule 23: RNA (75-MER)



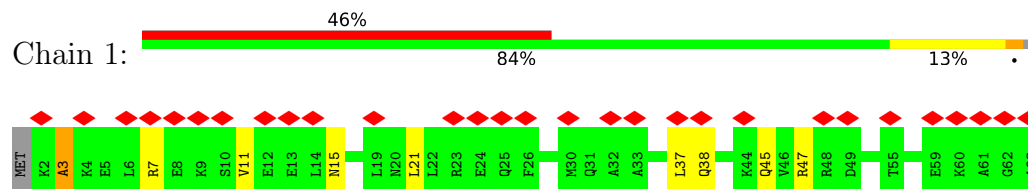
• Molecule 24: RNA (5'-R(P*CP*UP*GP*GP*CP*CP*CP*UP*CP*AP*A)-3')



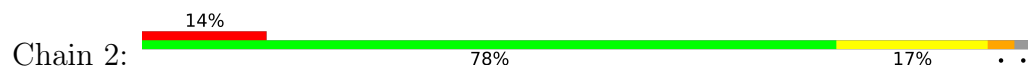
• Molecule 25: 50S ribosomal protein L28

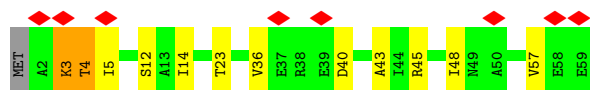


• Molecule 26: 50S ribosomal protein L29

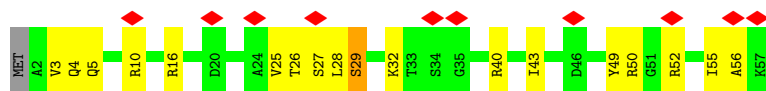


• Molecule 27: 50S ribosomal protein L30

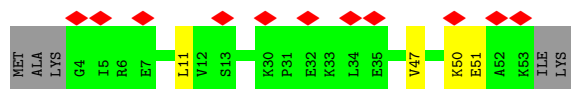
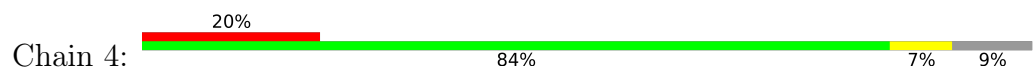




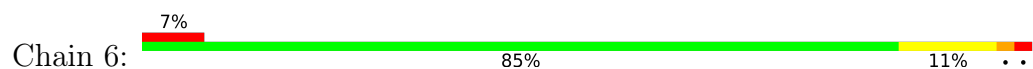
- Molecule 28: 50S ribosomal protein L32



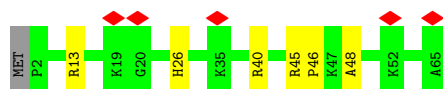
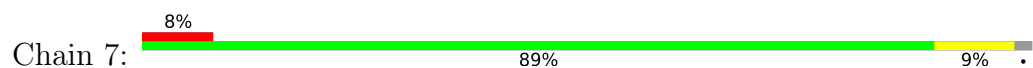
- Molecule 29: 50S ribosomal protein L33



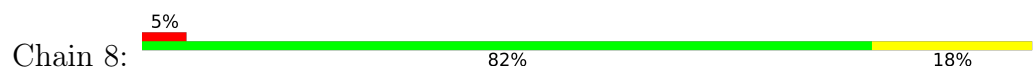
- Molecule 30: 50S ribosomal protein L34



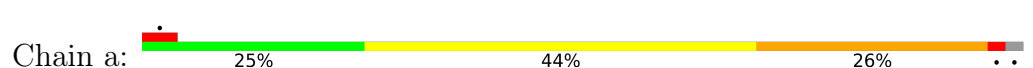
- Molecule 31: 50S ribosomal protein L35



- Molecule 32: 50S ribosomal protein L36



- Molecule 33: RNA (118-MER)

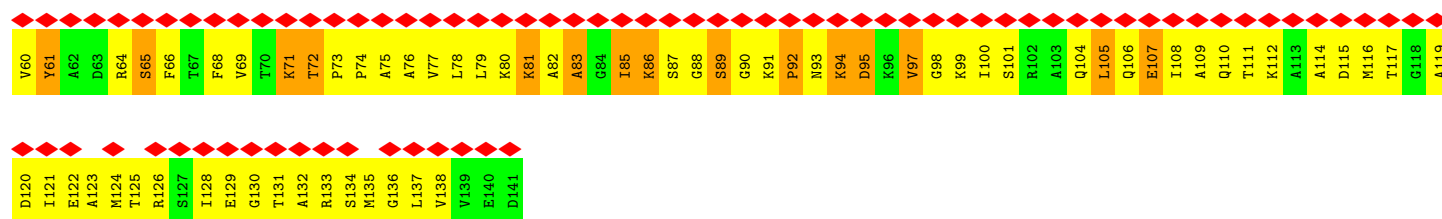


Chain b:

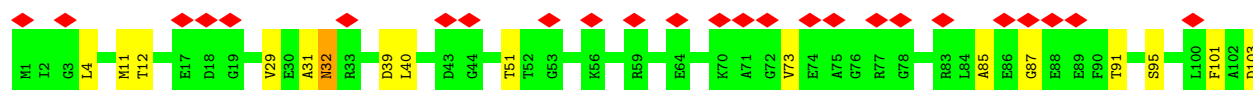
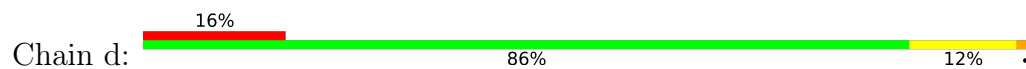




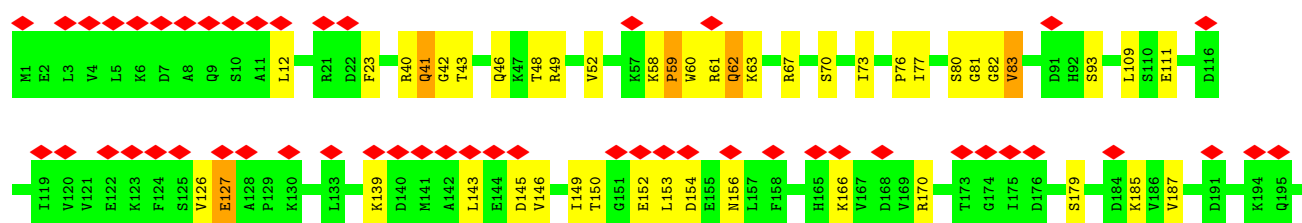
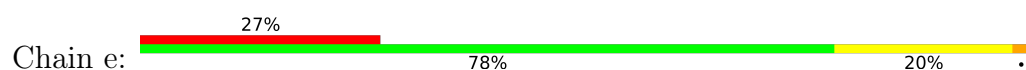
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G2286	A2287	A2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	A2299	G2299	G2300	G2301	G2302	G2303	G2304	U2305	G2306	G2307	G2308	A2309	G2310	A2311	G2312	G2313	A2314	G2315	G2316	A2317	G2318	G2319	G2320	G2321	A2322	G2323	G2324	G2325	G2326	A2327	A2328	U2329	G2330	G2331	G2332	A2333	U2334	A2335	A2336	G2337	G2338	G2339	A2340	G2341	G2342	G2343	G2344	G2345		
A2346	C2347	U2348	G2349	C2350	G2351	A2352	C2353	C2354	G2357	A2358	C2359	G2360	G2361	G2362	G2363	G2364	G2365	A2366	C2367	C2368	G2371	U2372	G2373	C2374	G2375	A2376	A2377	A2378	G2379	G2380	A2381	G2382	G2383	G2384	C2385	A2386	U2387	A2388	G2389	U2390	G2391	C2395	G2396	G2397	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	G2410	A2411	A2412							
G2221	G2222	G2223	G2224	A2225	C2226	A2227	G2228	G2229	G2230	U2231	G2232	U2233	G2234	G2235	U2236	G2237	G2238	G2239	U2242	U2243	A2247	C2248	U2249	G2250	G2251	G2252	G2255	G2256	U2257	G2258	U2259	C2260	C2261	U2262	G2263	C2264	U2265	A2266	A2267	A2268	G2269	A2270	G2271	U2272	A2273	A2274	G2275	G2276	G2279	G2280	G2281	G2282	G2283	A2284	C2285							
A2158	G2159	C2160	G2161	G2162	A2163	A2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2197	A2198	A2199	C2200	U2203	G2204	A2205	G2206	G2207	G2208	G2209	U2210	A2211	A2212	U2213	C2214	G2215	G2216	G2217	G2218	U2219	U2220					
A2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	C2044	C2045	G2046	G2047	G2048	G2049	C2050	A2051	A2052	G2053	A2054	G2055	G2056	G2057	A2060	A2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075	U2076	A2077	C2078	U2079	A2080	A2081	A2082	G2083	G2087	A2088	C2089	A2090	C2091	U2092	G2093	A2094	A2095	C2096					
A1970	U1971	G1972	G1973	G1974	C1975	U1976	A1977	A1978	U1979	G1980	A1981	U1982	G1983	G1984	G1985	C1986	G1989	C1990	U1991	G1992	U1993	G1994	U1995	C1996	A1997	A1998	C1999	C2000	C2001	A2005	G2006	U2007	C2008	A2009	G2010	U2011	G2012	A2013	A2014	A2015	U2016	U2017	A2020	C2021	U2022	G2023	G2024	C2025	U2026	U2027	U2028	G2029	A2030	G2031	G2032	A2033						
C1909	G1910	U1911	A1912	A1913	G1914	U1915	A1916	U1917	A1918	A1919	C1920	G1921	U1922	G1923	U1924	C1925	U1926	A1927	U1928	C1929	G1930	U1931	A1932	G1933	A1936	A1937	A1938	U1939	U1940	C1941	G1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	U1950	A1951	A1952	C1953	G1954	U1955	U1956	C1957	C1958	G1959	A1960	C1961	G1962	U1963	G1964	C1965	A1966	A1967	A1969					
C1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	A1851	U1852	A1853	A1854	U1855	G1856	A1857	U1858	U1859	G1860	G1861	G1862	G1863	U1864	U1865	A1866	G1867	C1868	G1869	C1870	A1871	A1872	C1873	A1874	G1875	A1876	A1877	U1880	C1881	U1882	U1883	C1884	A1885	A1889	A1890	G1891	C1892	C1893	C1894	C1895	G1896	A1900	A1901	C1902	C1905	G1906	G1907	C1908							
U1777	U1778	U1779	A1780	U1781	U1782	A1783	A1784	A1785	A1786	A1787	C1790	A1791	G1792	C1793	A1794	C1795	U1796	G1797	C1800	A1801	A1802	A1803	C1804	A1805	C1806	G1807	A1808	A1809	A1810	G1811	C1812	G1813	G1814	A1815	C1816	G1817	U1818	A1819	U1820	A1821	G1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	G1839	U1840	U1841	G1842							
U1714	G1715	U1716	A1717	G1718	G1719	U1720	A1721	A1722	C1727	C1728	U1729	C1730	G1731	C1732	G1733	G1734	A1735	U1736	G1737	G1738	A1739	G1740	C1741	U1742	G1743	A1744	A1745	A1746	C1747	C1748	A1749	G1750	U1751	G1752	C1753	U1754	A1755	G1756	C1757	A1758	U1759	C1760	A1761	G1762	G1763	C1764	U1765	G1766	G1767	C1768	U1769	G1770	C1771	A1772	A1773	C1774	U1775	G1776				
U1648	G1649	A1650	G1651	A1652	G1653	A1654	A1655	C1656	U1657	C1658	G1659	G1660	G1661	U1662	G1663	G1666	G1667	A1668	A1669	C1670	U1671	A1672	G1673	G1674	C1675	A1676	A1677	U1680	A1681	G1682	U1683	C1684	C1685	C1686	G1687	U1688	A1689	A1690	G1691	U1692	U1693	A1694	A1698	G1699	A1700	A1701	G1702	G1703	C1704	A1705	C1706	G1707	G1710	A1713								



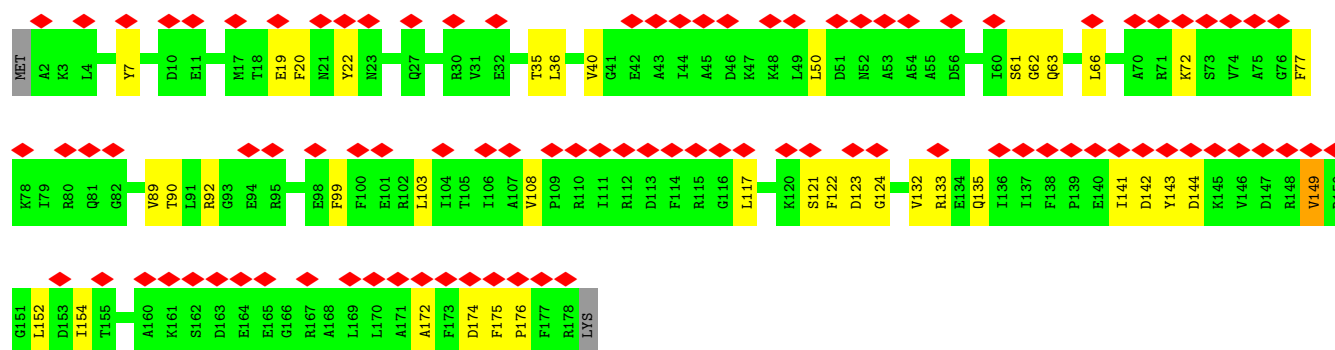
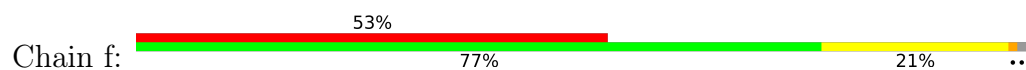
• Molecule 37: 50S ribosomal protein L3



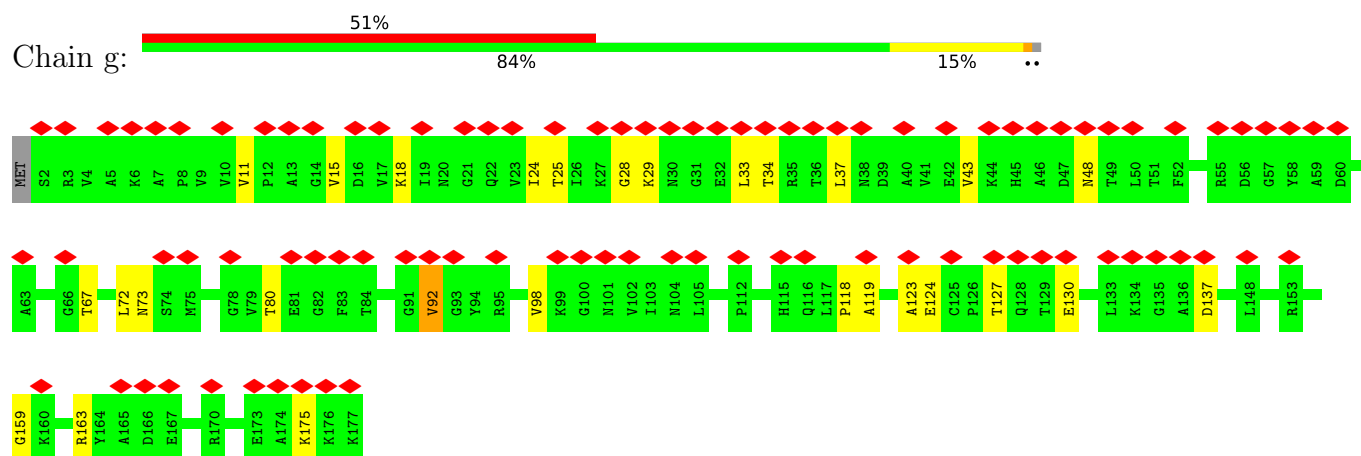
• Molecule 38: 50S ribosomal protein L4



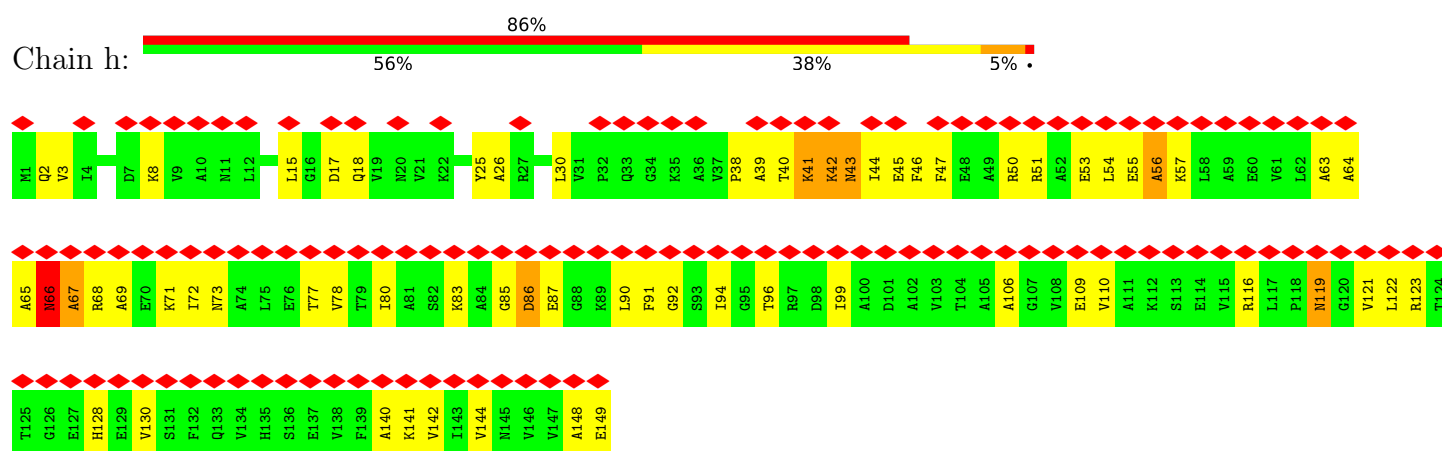
• Molecule 39: 50S ribosomal protein L5



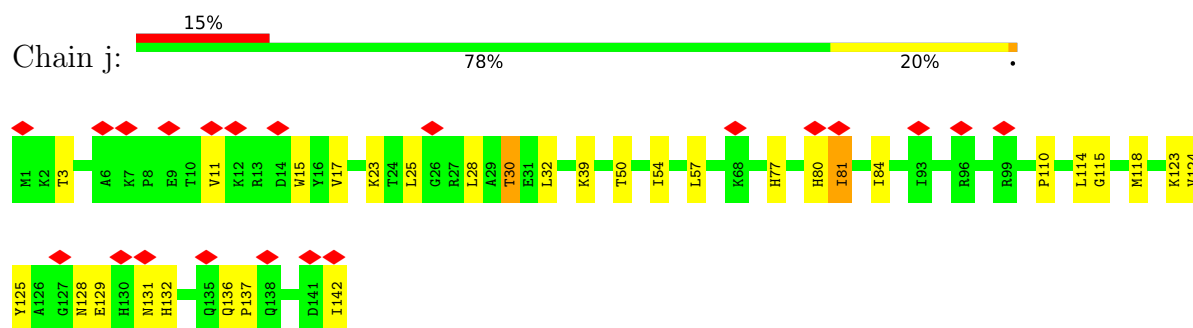
• Molecule 40: 50S ribosomal protein L6



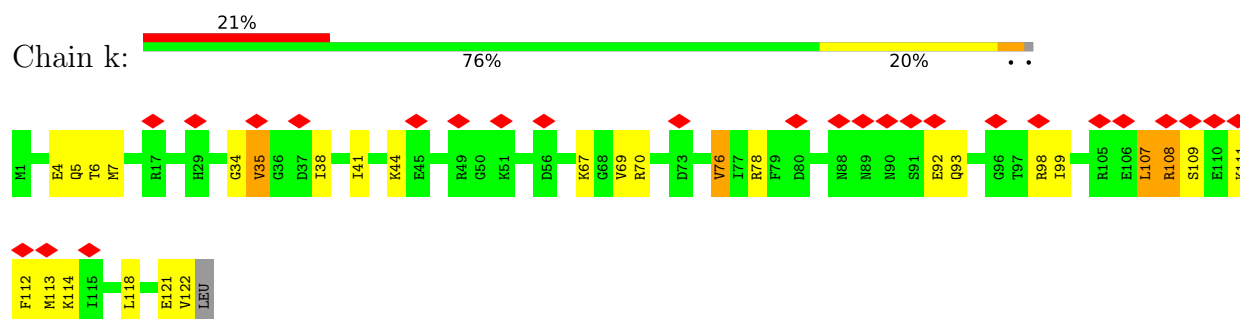
• Molecule 41: 50S ribosomal protein L9



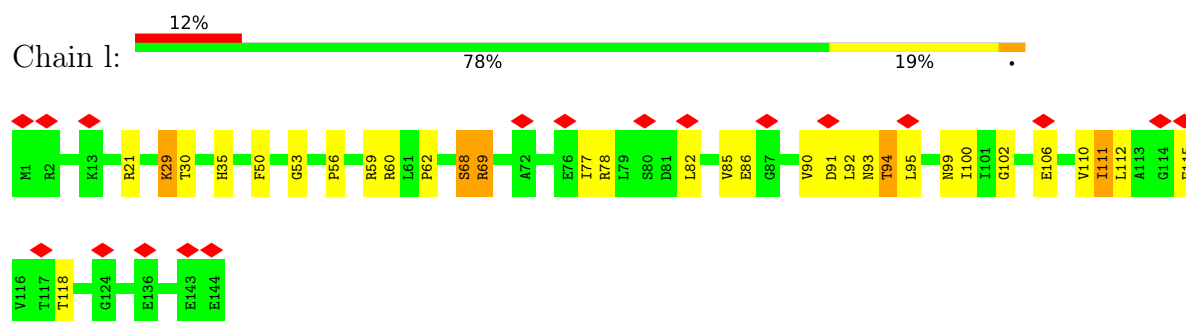
• Molecule 42: 50S ribosomal protein L13



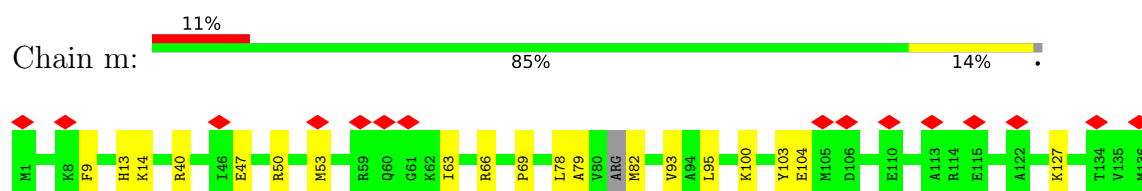
• Molecule 43: 50S ribosomal protein L14



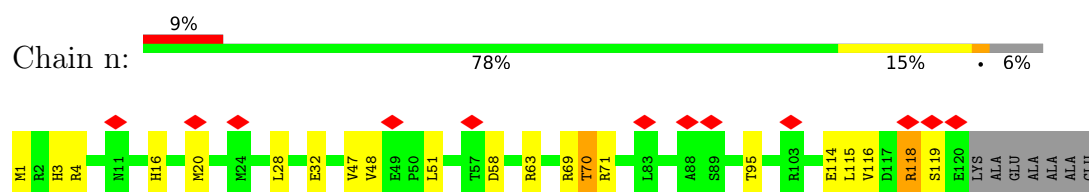
- Molecule 44: 50S ribosomal protein L15



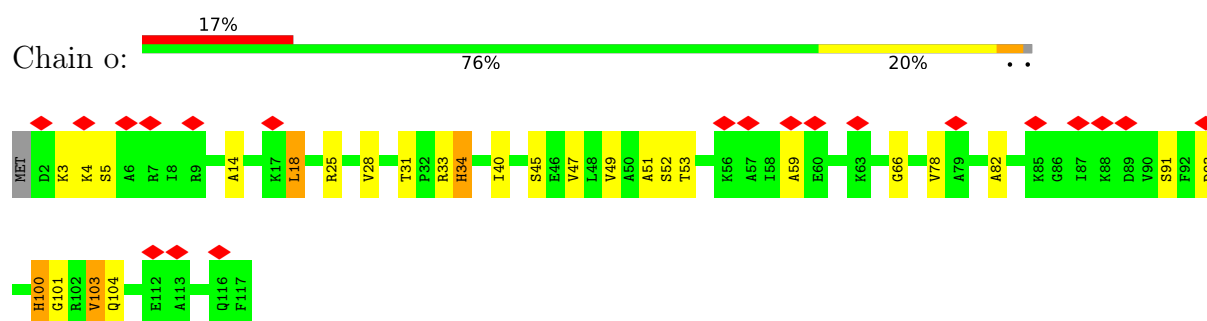
- Molecule 45: 50S ribosomal protein L16



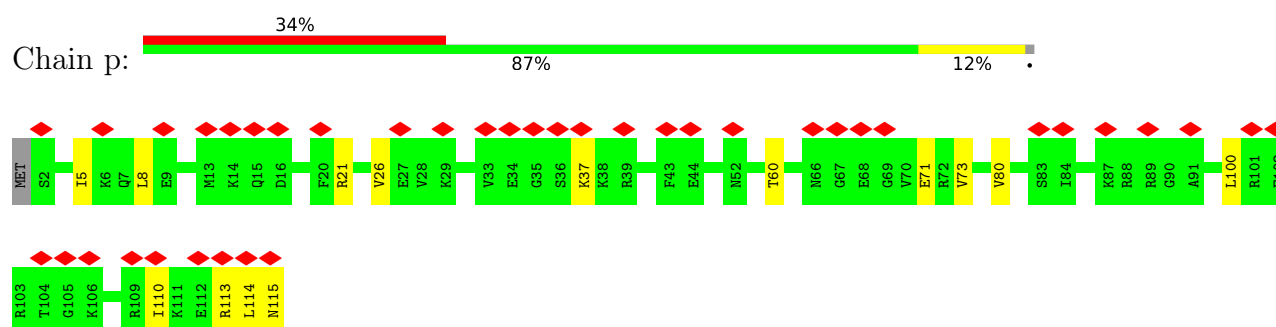
- Molecule 46: 50S ribosomal protein L17



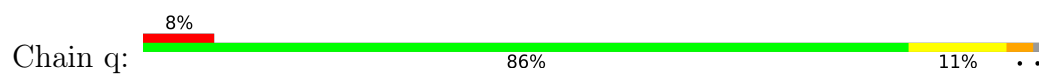
- Molecule 47: 50S ribosomal protein L18



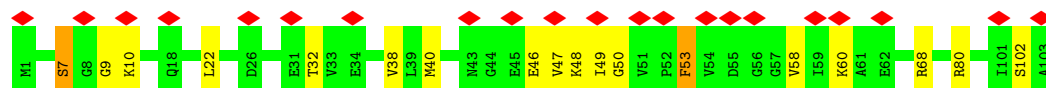
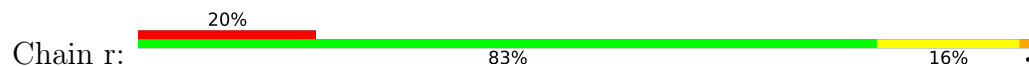
- Molecule 48: 50S ribosomal protein L19



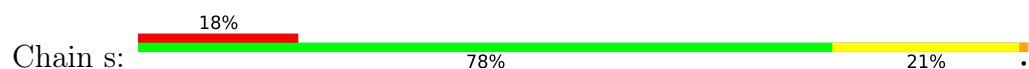
- Molecule 49: 50S ribosomal protein L20



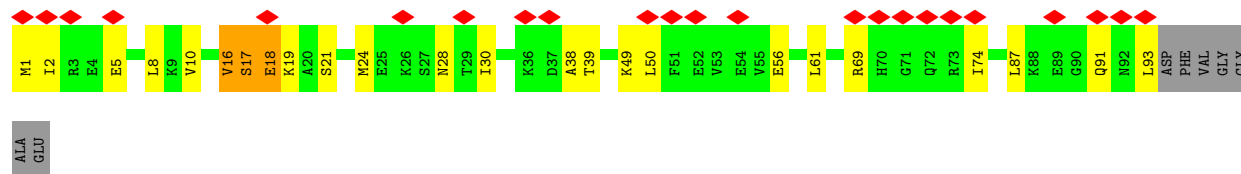
- Molecule 50: 50S ribosomal protein L21



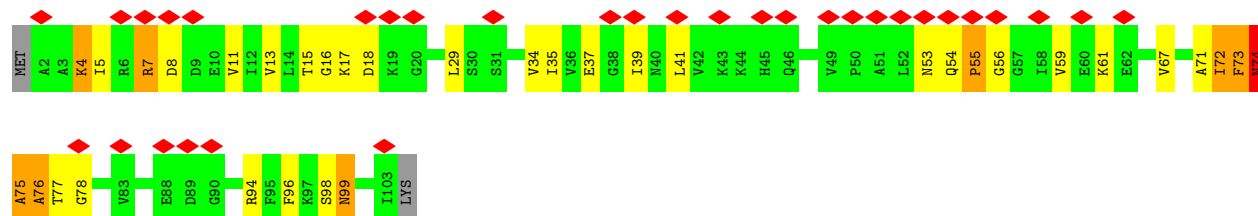
- Molecule 51: 50S ribosomal protein L22



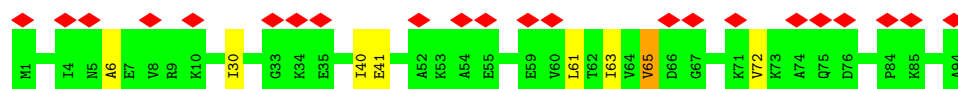
- Molecule 52: 50S ribosomal protein L23



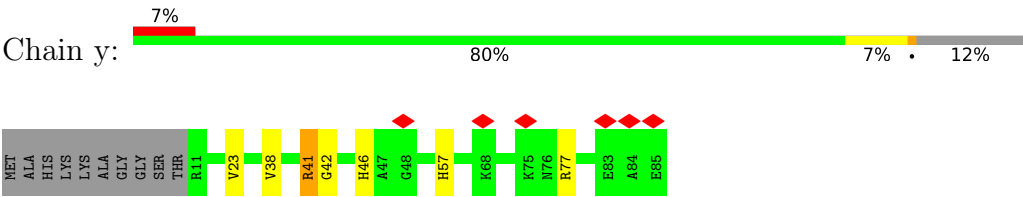
- Molecule 53: 50S ribosomal protein L24



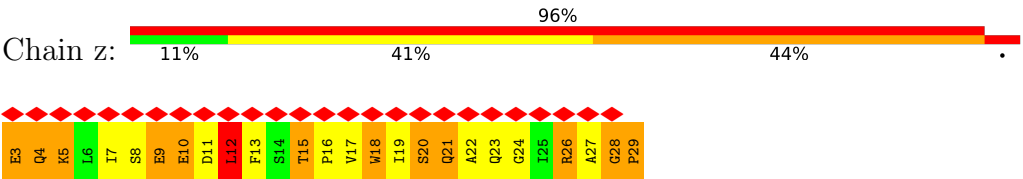
- Molecule 54: 50S ribosomal protein L25



• Molecule 55: 50S ribosomal protein L27



• Molecule 56: Secretion monitor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60354	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	37878	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.22	0/36762	0.29	0/57350
2	B	0.38	0/1735	0.83	2/2338 (0.1%)
3	C	0.42	0/1651	0.90	4/2225 (0.2%)
4	D	0.39	0/1665	0.85	6/2227 (0.3%)
5	E	0.43	0/1118	0.93	4/1504 (0.3%)
6	F	0.37	0/835	0.89	0/1128
7	G	0.37	0/1187	0.86	3/1591 (0.2%)
8	H	0.43	0/989	0.88	0/1326
9	I	0.43	0/1034	0.90	2/1375 (0.1%)
10	J	0.43	0/796	0.89	0/1077
11	K	0.40	0/893	0.91	1/1205 (0.1%)
12	L	0.42	0/969	0.93	2/1300 (0.2%)
13	M	0.37	0/884	0.79	0/1181
14	N	0.44	0/785	0.90	2/1043 (0.2%)
15	O	0.37	0/724	0.70	0/966
16	P	0.37	0/659	0.87	4/884 (0.5%)
17	Q	0.37	0/657	0.74	0/881
18	R	0.41	0/462	0.78	0/621
19	S	0.37	0/652	0.83	1/877 (0.1%)
20	T	0.43	0/671	0.81	0/888
21	U	0.40	0/430	1.02	2/570 (0.4%)
22	V	0.43	0/1810	0.87	7/2821 (0.2%)
23	W	0.44	0/1786	1.04	10/2784 (0.4%)
24	X	0.56	1/256 (0.4%)	0.71	0/394
25	0	0.55	0/635	0.86	0/848
26	1	0.46	0/502	0.85	0/667
27	2	0.53	0/453	0.81	0/605
28	3	0.55	0/450	0.84	0/599
29	4	0.50	0/416	0.71	0/554
30	6	0.59	0/380	0.98	0/498
31	7	0.56	0/513	0.84	0/676
32	8	0.57	0/303	0.78	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.48	0/2802	0.98	12/4369 (0.3%)
34	b	0.57	32/69800 (0.0%)	1.10	675/108892 (0.6%)
35	c	0.57	0/2121	0.82	3/2852 (0.1%)
36	i	0.36	0/989	0.89	3/1334 (0.2%)
37	d	0.54	0/1586	0.80	0/2134
38	e	0.53	0/1571	0.88	3/2113 (0.1%)
39	f	0.54	0/1434	0.84	0/1926
40	g	0.52	0/1343	0.73	0/1816
41	h	0.38	0/1122	0.93	4/1515 (0.3%)
42	j	0.52	0/1152	0.79	0/1551
43	k	0.52	0/947	0.76	0/1268
44	l	0.58	0/1062	0.90	1/1413 (0.1%)
45	m	0.55	0/1081	0.81	0/1443
46	n	0.56	0/973	0.88	0/1301
47	o	0.53	0/902	0.93	1/1209 (0.1%)
48	p	0.49	0/929	0.72	0/1242
49	q	0.54	0/960	0.87	1/1278 (0.1%)
50	r	0.54	0/829	0.75	0/1107
51	s	0.53	0/864	0.84	0/1156
52	t	0.59	0/744	0.81	0/994
53	u	0.52	0/787	0.83	1/1051 (0.1%)
54	w	0.48	0/766	0.72	0/1025
55	y	0.51	0/576	0.68	0/762
56	z	0.53	1/215 (0.5%)	1.12	3/291 (1.0%)
All	All	0.48	34/158617 (0.0%)	0.89	757/237442 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	I	0	1
27	2	0	1
34	b	0	64
35	c	0	1
37	d	0	1
43	k	0	1
44	l	0	1
50	r	0	1
All	All	0	71

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	b	2610	C	O3'-P	14.61	1.83	1.61
34	b	2504	U	O3'-P	13.56	1.81	1.61
34	b	2248	C	O3'-P	11.44	1.78	1.61
34	b	399	U	C5'-C4'	10.96	1.67	1.51
34	b	1323	C	O3'-P	10.59	1.77	1.61

The worst 5 of 757 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	36	C	O3'-P-O5'	28.29	146.43	104.00
34	b	400	G	N9-C1'-C2'	13.93	132.89	112.00
34	b	2123	G	N9-C1'-C2'	13.19	131.78	112.00
34	b	1275	A	N9-C1'-C2'	13.07	133.61	114.00
34	b	1930	G	C2'-C3'-O3'	12.71	128.57	109.50

There are no chirality outliers.

5 of 71 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	2	3	LYS	Peptide
9	I	124	PRO	Peptide
34	b	119	A	Sidechain
34	b	195	A	Sidechain
34	b	25	U	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32831	0	16518	811	0
2	B	1704	0	1732	56	0
3	C	1624	0	1699	64	0
4	D	1643	0	1710	92	0
5	E	1105	0	1148	44	0
6	F	817	0	808	29	0
7	G	1174	0	1230	40	0
8	H	979	0	1034	36	0
9	I	1022	0	1070	118	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	786	0	828	45	0
11	K	877	0	887	54	0
12	L	955	0	1019	30	0
13	M	876	0	936	63	0
14	N	774	0	827	41	0
15	O	716	0	742	36	0
16	P	649	0	664	123	0
17	Q	648	0	691	23	0
18	R	455	0	478	13	0
19	S	637	0	665	33	0
20	T	665	0	714	22	0
21	U	425	0	449	59	0
22	V	1620	0	817	150	0
23	W	1599	0	813	31	0
24	X	231	0	120	32	0
25	0	625	0	652	6	0
26	1	501	0	531	3	0
27	2	449	0	488	14	0
28	3	444	0	458	26	0
29	4	409	0	440	2	0
30	6	377	0	418	9	0
31	7	504	0	572	5	0
32	8	302	0	343	7	0
33	a	2506	0	1270	167	0
34	b	62321	0	31311	5000	0
35	c	2082	0	2154	61	0
36	i	976	0	1008	590	0
37	d	1565	0	1616	29	0
38	e	1552	0	1619	48	0
39	f	1410	0	1444	50	0
40	g	1323	0	1371	21	0
41	h	1111	0	1148	102	0
42	j	1129	0	1162	37	0
43	k	938	0	1012	27	0
44	l	1053	0	1129	34	0
45	m	1063	0	1143	27	0
46	n	960	0	1000	31	0
47	o	892	0	923	23	0
48	p	917	0	961	9	0
49	q	947	0	1019	17	0
50	r	816	0	839	11	0
51	s	857	0	922	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	t	738	0	807	14	0
53	u	779	0	831	50	0
54	w	753	0	780	15	0
55	y	569	0	581	6	0
56	z	211	0	206	95	0
57	b	20	0	11	22	0
All	All	145911	0	97768	7516	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 31.

The worst 5 of 7516 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)
34:b:1080:A:C6	36:i:109:ALA:CB	1.74	1.68
34:b:1063:G:C5	36:i:135:MET:CE	1.74	1.63
57:b:9000:CLM:CL2	56:z:28:GLY:HA3	1.33	1.63
34:b:1071:G:C6	34:b:1089:A:C8	1.82	1.61
34:b:1071:G:C2	34:b:1089:A:H3'	1.21	1.61

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	
2	B	216/241 (90%)	188 (87%)	19 (9%)	9 (4%)	2	15
3	C	204/233 (88%)	171 (84%)	23 (11%)	10 (5%)	1	12
4	D	203/206 (98%)	190 (94%)	9 (4%)	4 (2%)	6	28
5	E	148/167 (89%)	131 (88%)	7 (5%)	10 (7%)	1	7
6	F	98/131 (75%)	81 (83%)	14 (14%)	3 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	148/156 (95%)	135 (91%)	8 (5%)	5 (3%)	3	19
8	H	127/130 (98%)	110 (87%)	15 (12%)	2 (2%)	7	32
9	I	125/130 (96%)	106 (85%)	16 (13%)	3 (2%)	4	25
10	J	96/103 (93%)	84 (88%)	7 (7%)	5 (5%)	1	11
11	K	115/129 (89%)	104 (90%)	10 (9%)	1 (1%)	14	43
12	L	121/124 (98%)	94 (78%)	22 (18%)	5 (4%)	2	15
13	M	111/118 (94%)	99 (89%)	5 (4%)	7 (6%)	1	8
14	N	92/101 (91%)	80 (87%)	8 (9%)	4 (4%)	2	15
15	O	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10	37
16	P	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	2
17	Q	78/84 (93%)	66 (85%)	11 (14%)	1 (1%)	9	35
18	R	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
19	S	77/92 (84%)	69 (90%)	5 (6%)	3 (4%)	2	16
20	T	83/87 (95%)	77 (93%)	5 (6%)	1 (1%)	10	37
21	U	49/71 (69%)	40 (82%)	5 (10%)	4 (8%)	0	5
25	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
26	1	60/63 (95%)	53 (88%)	5 (8%)	2 (3%)	3	19
27	2	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	30
28	3	54/57 (95%)	49 (91%)	3 (6%)	2 (4%)	2	17
29	4	48/55 (87%)	39 (81%)	9 (19%)	0	100	100
30	6	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	14
31	7	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
32	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
35	c	269/273 (98%)	251 (93%)	17 (6%)	1 (0%)	30	60
36	i	132/142 (93%)	83 (63%)	38 (29%)	11 (8%)	0	5
37	d	207/209 (99%)	194 (94%)	11 (5%)	2 (1%)	12	41
38	e	199/201 (99%)	186 (94%)	7 (4%)	6 (3%)	3	21
39	f	175/179 (98%)	157 (90%)	12 (7%)	6 (3%)	3	19
40	g	174/177 (98%)	139 (80%)	31 (18%)	4 (2%)	5	26
41	h	147/149 (99%)	122 (83%)	20 (14%)	5 (3%)	3	19
42	j	140/142 (99%)	128 (91%)	10 (7%)	2 (1%)	9	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	k	120/123 (98%)	112 (93%)	6 (5%)	2 (2%)	7	31
44	l	142/144 (99%)	126 (89%)	10 (7%)	6 (4%)	2	15
45	m	131/136 (96%)	123 (94%)	7 (5%)	1 (1%)	16	45
46	n	118/127 (93%)	111 (94%)	4 (3%)	3 (2%)	4	24
47	o	114/117 (97%)	104 (91%)	5 (4%)	5 (4%)	2	14
48	p	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	14	43
49	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
50	r	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	3	21
51	s	108/110 (98%)	103 (95%)	2 (2%)	3 (3%)	4	22
52	t	91/100 (91%)	80 (88%)	8 (9%)	3 (3%)	3	19
53	u	100/104 (96%)	77 (77%)	12 (12%)	11 (11%)	0	2
54	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
55	y	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
56	z	25/27 (93%)	20 (80%)	5 (20%)	0	100	100
All	All	5630/5985 (94%)	5003 (89%)	458 (8%)	169 (3%)	5	21

5 of 169 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	7	ASN
5	E	99	SER
8	H	44	PHE
9	I	57	VAL
12	L	88	ASP

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	
2	B	180/199 (90%)	180 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	172/173 (99%)	172 (100%)	0	100	100
5	E	113/126 (90%)	113 (100%)	0	100	100
6	F	87/112 (78%)	87 (100%)	0	100	100
7	G	123/129 (95%)	123 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	90/99 (91%)	90 (100%)	0	100	100
12	L	103/104 (99%)	103 (100%)	0	100	100
13	M	91/96 (95%)	91 (100%)	0	100	100
14	N	79/84 (94%)	79 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	53 (82%)	12 (18%)	1	8
17	Q	74/78 (95%)	74 (100%)	0	100	100
18	R	48/65 (74%)	48 (100%)	0	100	100
19	S	70/79 (89%)	70 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	44/61 (72%)	44 (100%)	0	100	100
25	0	67/68 (98%)	62 (92%)	5 (8%)	12	38
26	1	54/55 (98%)	52 (96%)	2 (4%)	30	58
27	2	48/49 (98%)	47 (98%)	1 (2%)	47	66
28	3	47/48 (98%)	44 (94%)	3 (6%)	16	44
29	4	45/49 (92%)	44 (98%)	1 (2%)	45	66
30	6	38/38 (100%)	36 (95%)	2 (5%)	20	49
31	7	51/52 (98%)	51 (100%)	0	100	100
32	8	34/34 (100%)	33 (97%)	1 (3%)	37	62
35	c	216/218 (99%)	208 (96%)	8 (4%)	30	58
36	i	104/110 (94%)	90 (86%)	14 (14%)	4	16
37	d	164/164 (100%)	159 (97%)	5 (3%)	36	61
38	e	165/165 (100%)	156 (94%)	9 (6%)	19	47
39	f	148/150 (99%)	140 (95%)	8 (5%)	20	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	g	137/138 (99%)	132 (96%)	5 (4%)	31	58
41	h	114/114 (100%)	114 (100%)	0	100	100
42	j	116/116 (100%)	110 (95%)	6 (5%)	21	49
43	k	103/104 (99%)	98 (95%)	5 (5%)	22	51
44	l	103/103 (100%)	100 (97%)	3 (3%)	37	62
45	m	108/109 (99%)	105 (97%)	3 (3%)	38	63
46	n	100/103 (97%)	98 (98%)	2 (2%)	48	67
47	o	86/87 (99%)	82 (95%)	4 (5%)	23	52
48	p	99/100 (99%)	95 (96%)	4 (4%)	28	56
49	q	89/90 (99%)	85 (96%)	4 (4%)	24	53
50	r	84/84 (100%)	77 (92%)	7 (8%)	10	35
51	s	93/93 (100%)	90 (97%)	3 (3%)	34	60
52	t	80/84 (95%)	74 (92%)	6 (8%)	12	38
53	u	83/85 (98%)	77 (93%)	6 (7%)	13	40
54	w	78/78 (100%)	77 (99%)	1 (1%)	61	73
55	y	56/63 (89%)	55 (98%)	1 (2%)	51	69
56	z	23/23 (100%)	12 (52%)	11 (48%)	0	0
All	All	4678/4879 (96%)	4536 (97%)	142 (3%)	37	61

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	s	41	LYS
52	t	16	VAL
55	y	41	ARG
36	i	107	GLU
36	i	95	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
19	S	51	HIS
30	6	29	GLN
54	w	12	GLN
19	S	68	HIS

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Mol	Chain	Res	Type
20	T	77	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1530/1542 (99%)	422 (27%)	30 (1%)
22	V	75/76 (98%)	47 (62%)	9 (12%)
23	W	75/75 (100%)	40 (53%)	10 (13%)
24	X	11/11 (100%)	8 (72%)	3 (27%)
33	a	116/120 (96%)	43 (37%)	0
34	b	2902/2904 (99%)	1241 (42%)	0
All	All	4709/4728 (99%)	1801 (38%)	52 (1%)

5 of 1801 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	22	G

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1348	U
22	V	40	C
24	X	12	C
1	A	1492	A
22	V	18	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	CLM	b	9000	-	20,20,20	0.88	1 (5%)	23,27,27	0.81	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	CLM	b	9000	-	-	10/20/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	b	9000	CLM	C9-N9	-2.13	1.40	1.45

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

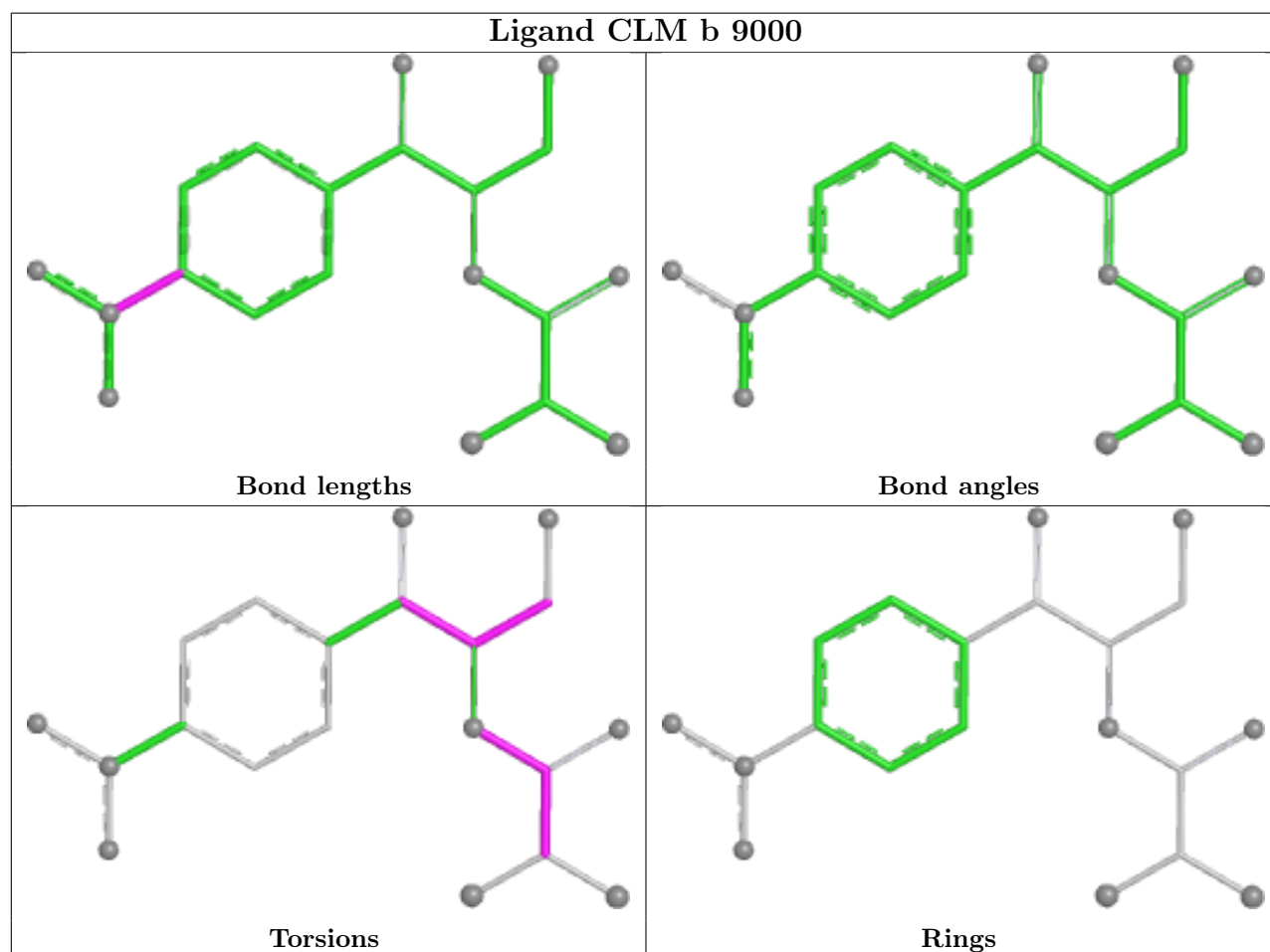
Mol	Chain	Res	Type	Atoms
57	b	9000	CLM	N2-C3-C5-O5
57	b	9000	CLM	N2-C3-C5-C6
57	b	9000	CLM	C4-C3-C5-O5
57	b	9000	CLM	O2-C2-N2-C3
57	b	9000	CLM	C1-C2-N2-C3

There are no ring outliers.

1 monomer is involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	b	9000	CLM	22	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	b	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	2610:C	O3'	2611:C	P	1.83
1	b	2504:U	O3'	2505:G	P	1.81
1	b	2248:C	O3'	2249:U	P	1.78
1	b	1323:C	O3'	1324:G	P	1.77

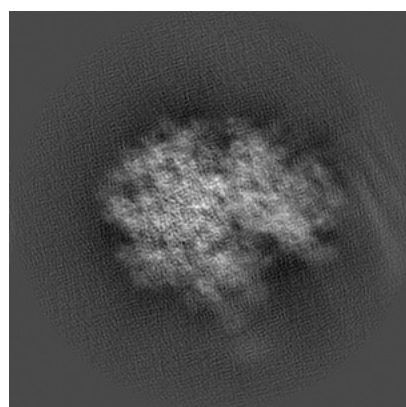
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6486. These allow visual inspection of the internal detail of the map and identification of artifacts.

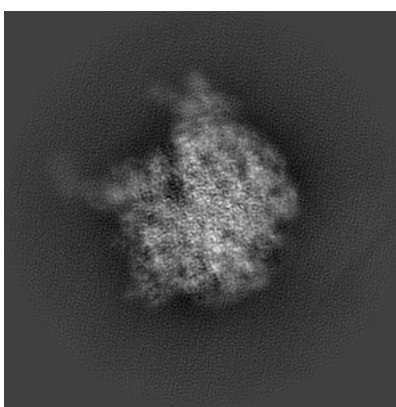
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

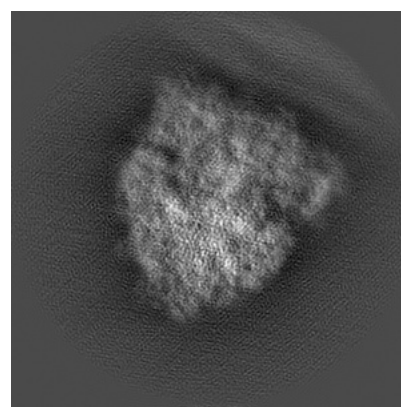
6.1.1 Primary map



X



Y

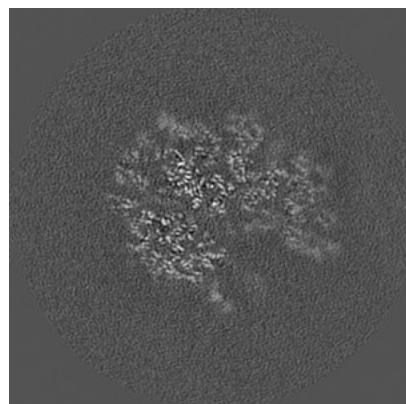


Z

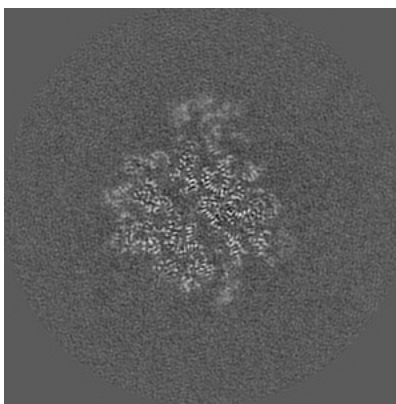
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

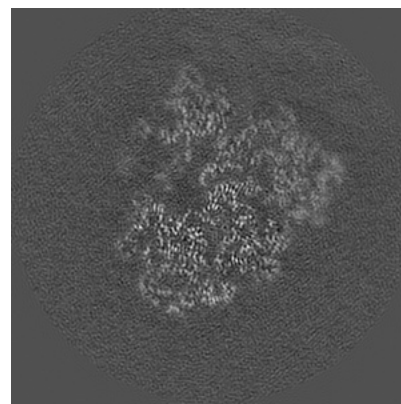
6.2.1 Primary map



X Index: 160



Y Index: 160

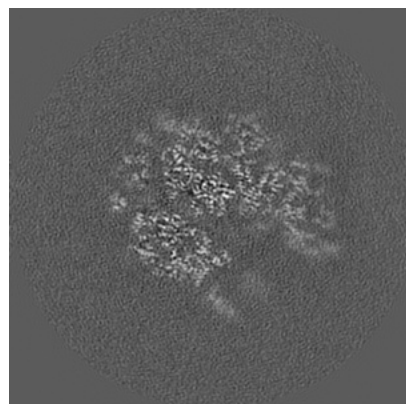


Z Index: 160

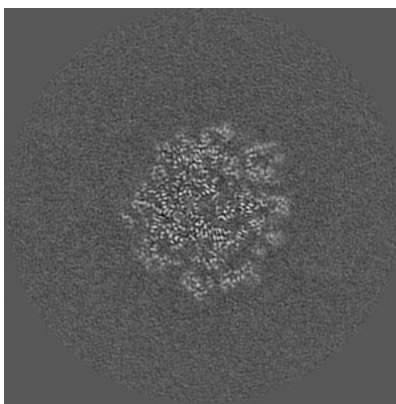
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

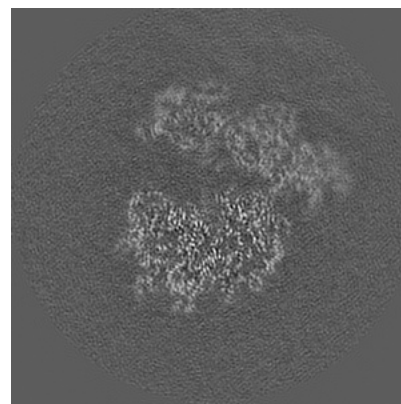
6.3.1 Primary map



X Index: 162



Y Index: 136

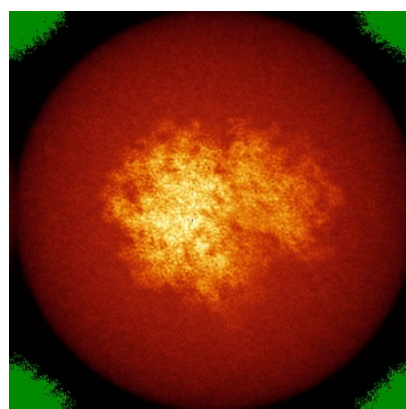


Z Index: 151

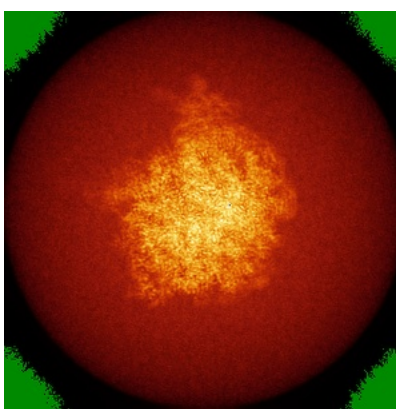
The images above show the largest variance slices of the map in three orthogonal directions.

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

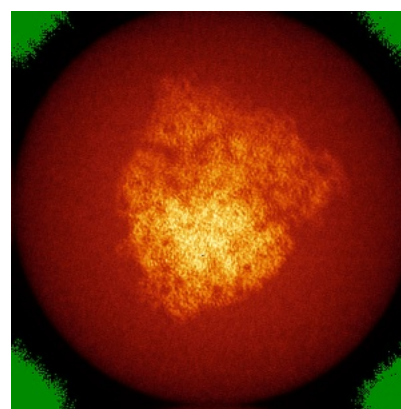
6.4.1 Primary map



X



Y

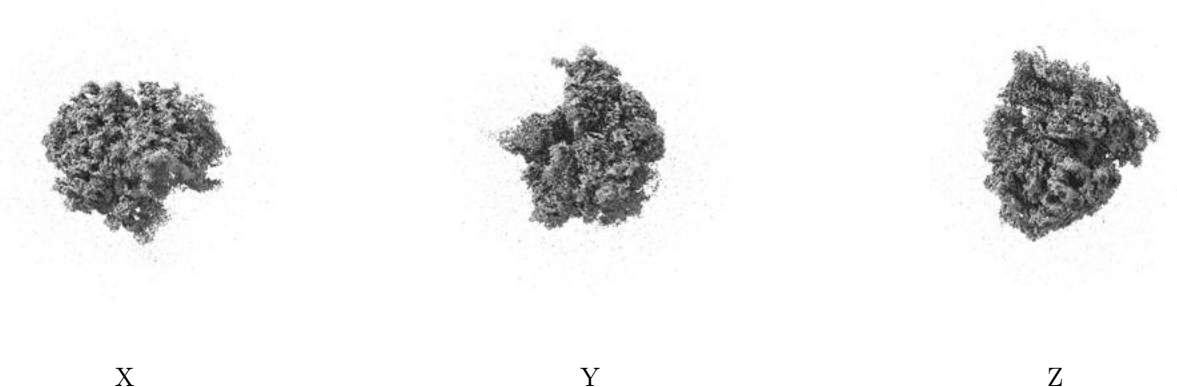


Z

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.

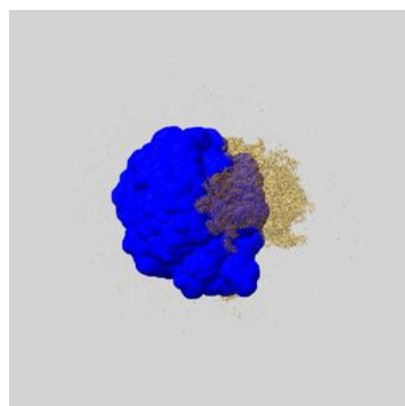
6.6 Mask visualisation [i](#)

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

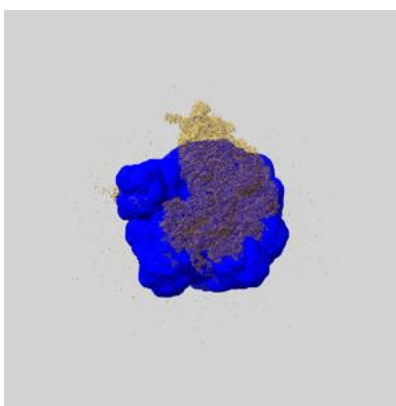
A mask typically either:

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

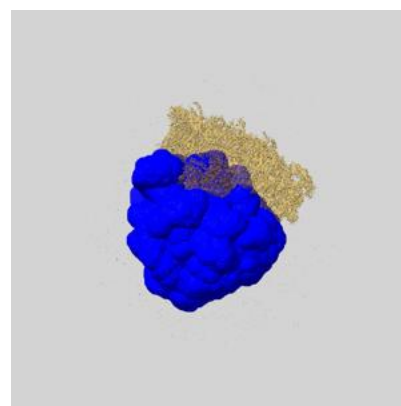
6.6.1 emd_6486_msk_1.map [i](#)



X



Y

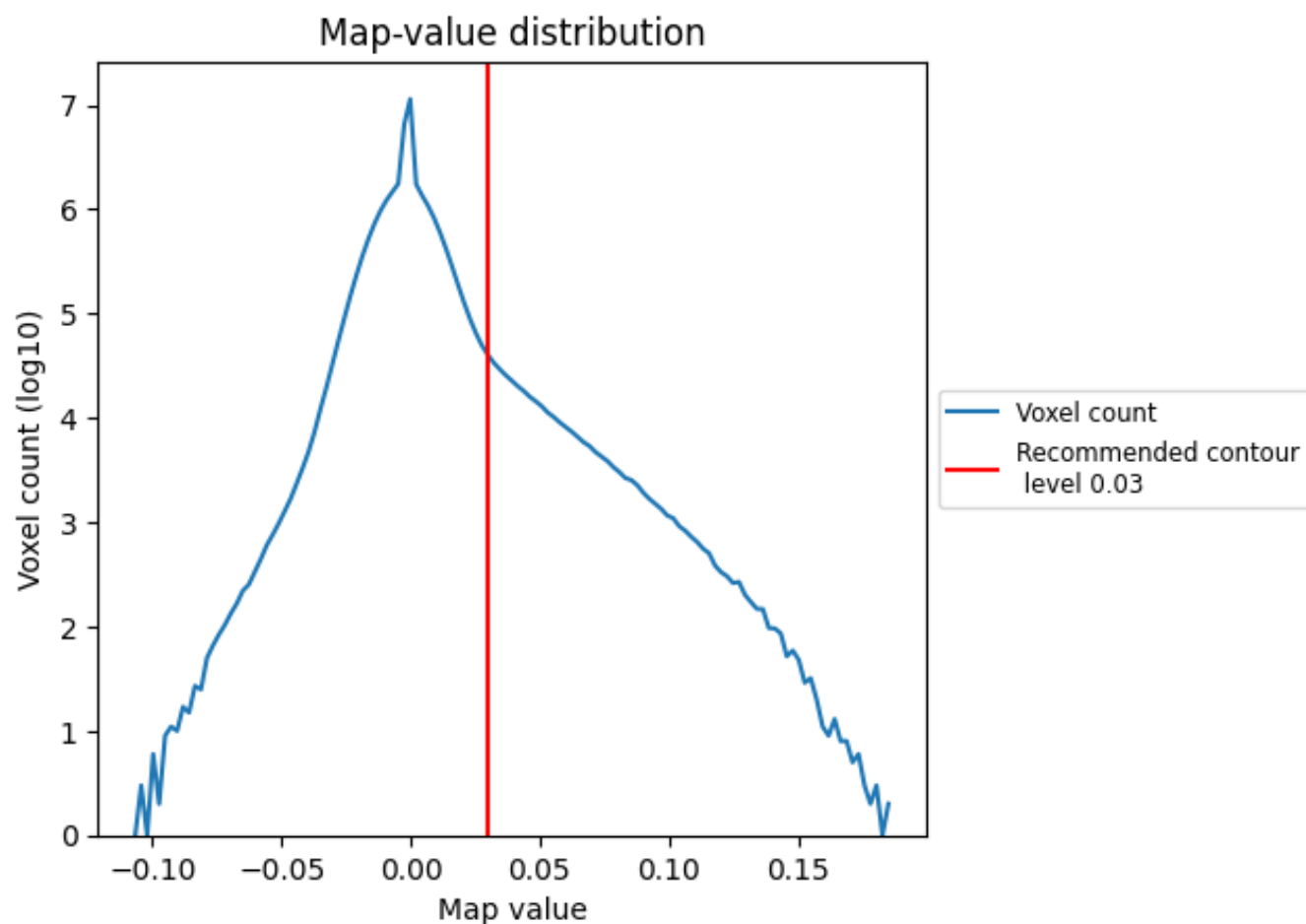


Z

7 Map analysis [i](#)

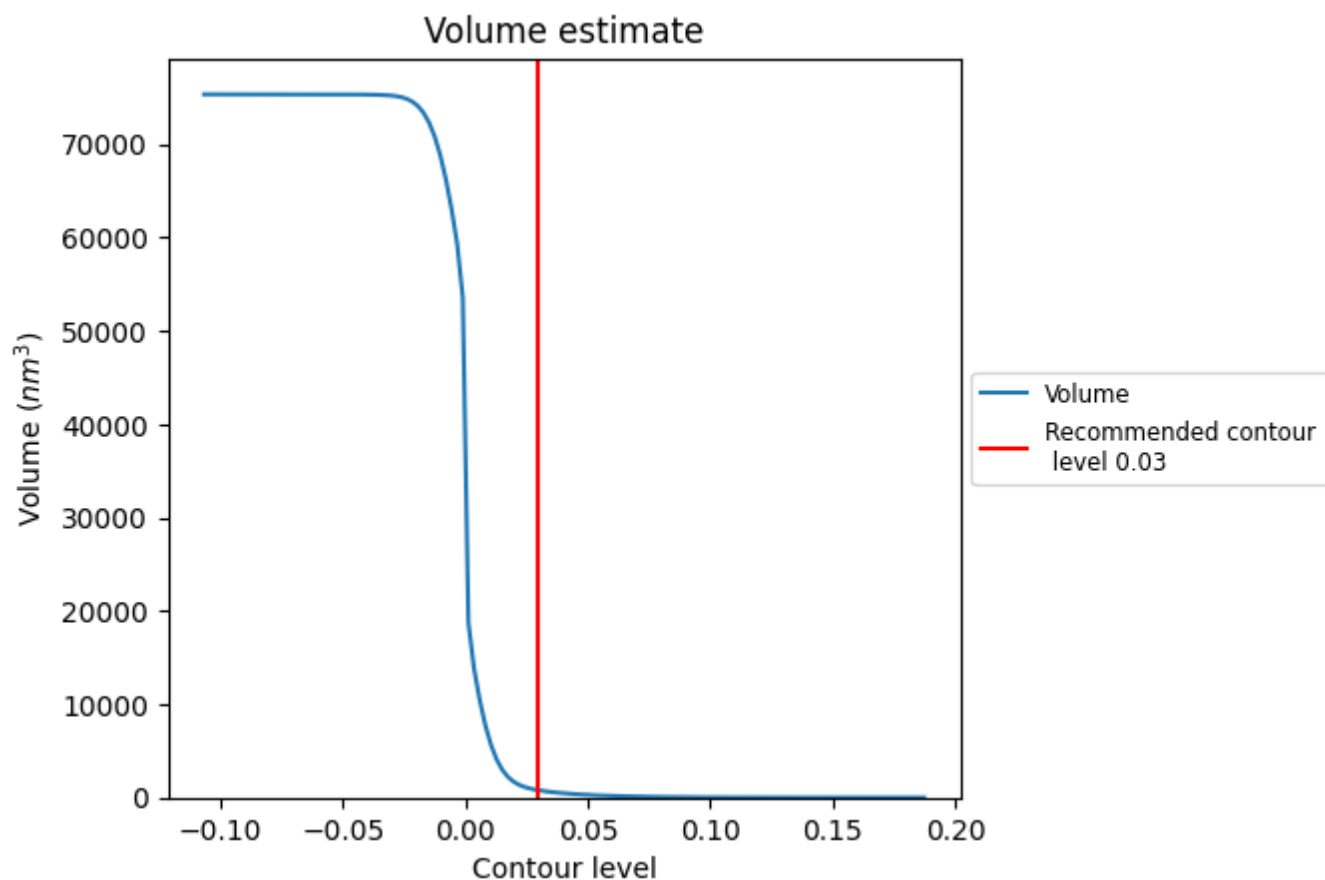
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

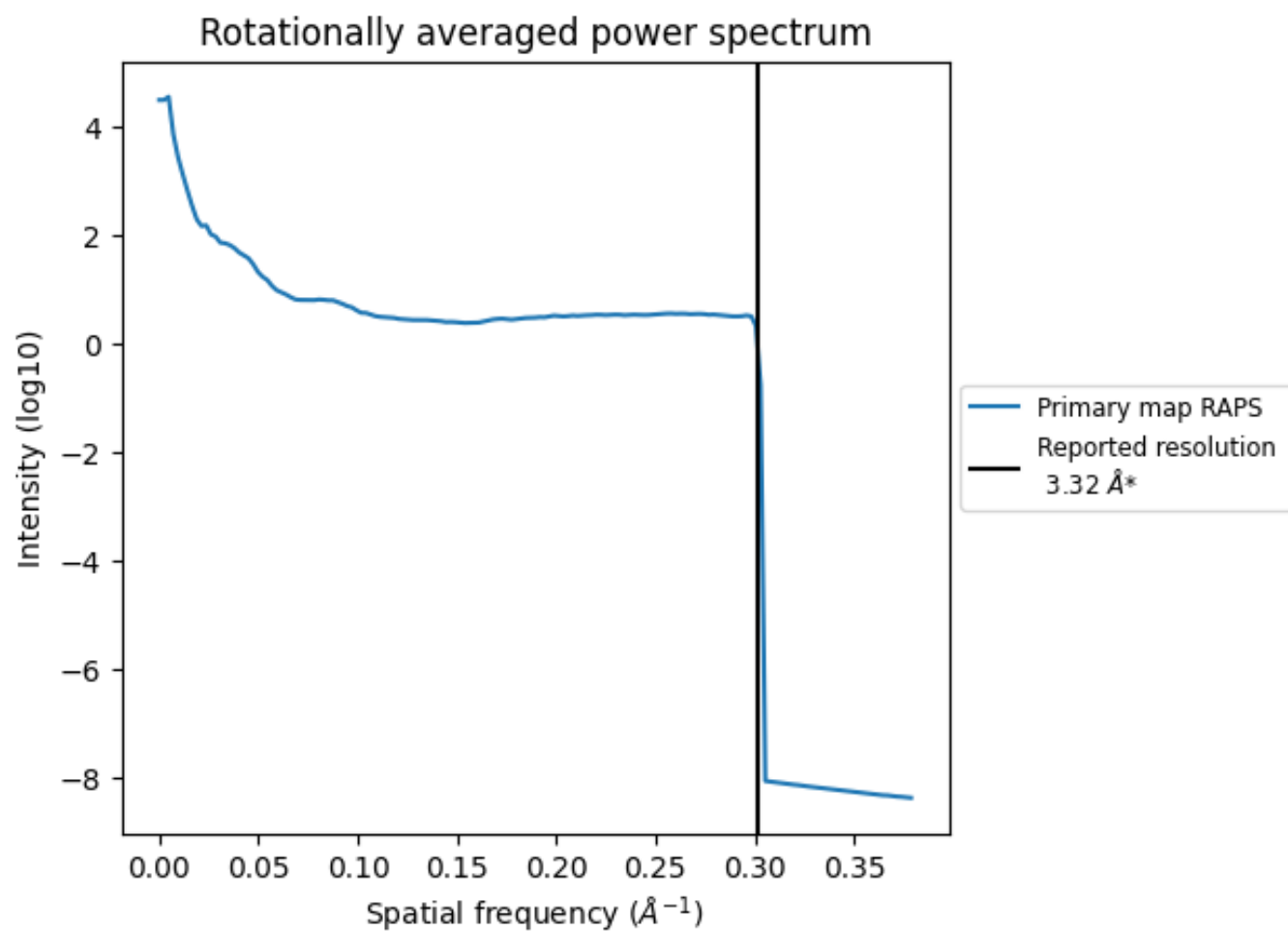
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 781 nm³; this corresponds to an approximate mass of 706 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 ⓘ

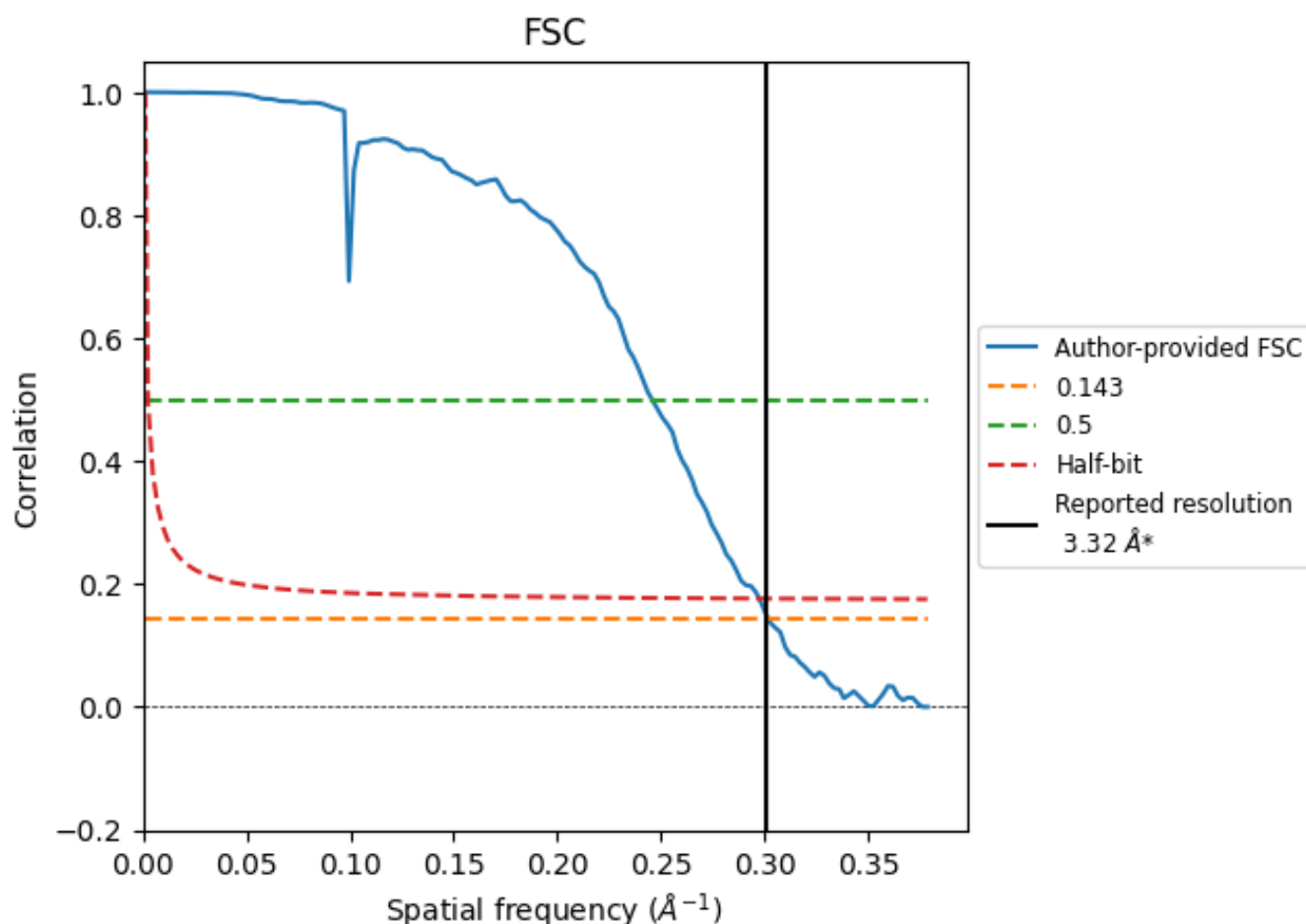


*Reported resolution corresponds to spatial frequency of 0.301 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.301 Å⁻¹

8.2 Resolution estimates [i](#)

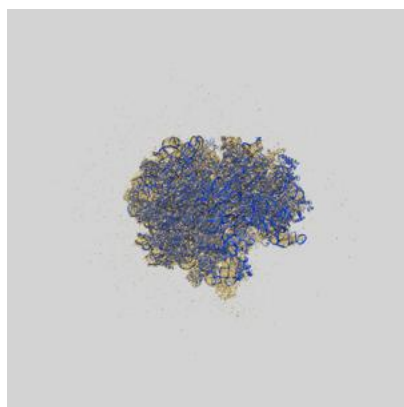
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.31	4.07	3.36
Unmasked-calculated*	-	-	-

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

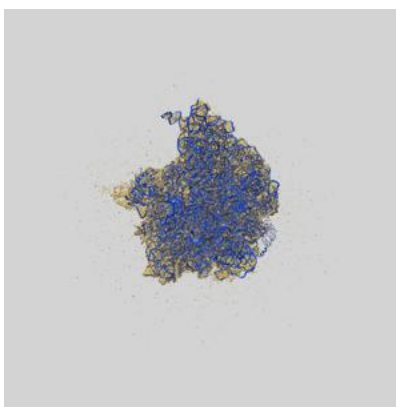
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6486 and PDB model 3JBV. Per-residue inclusion information can be found in section [3](#) on page [15](#).

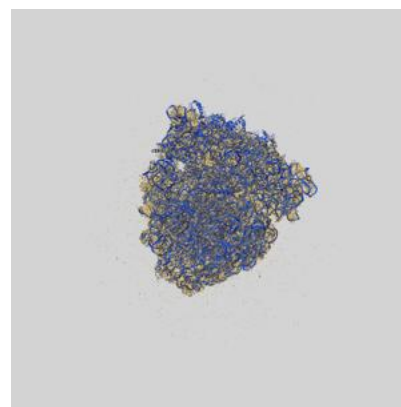
9.1 Map-model overlay [i](#)



X



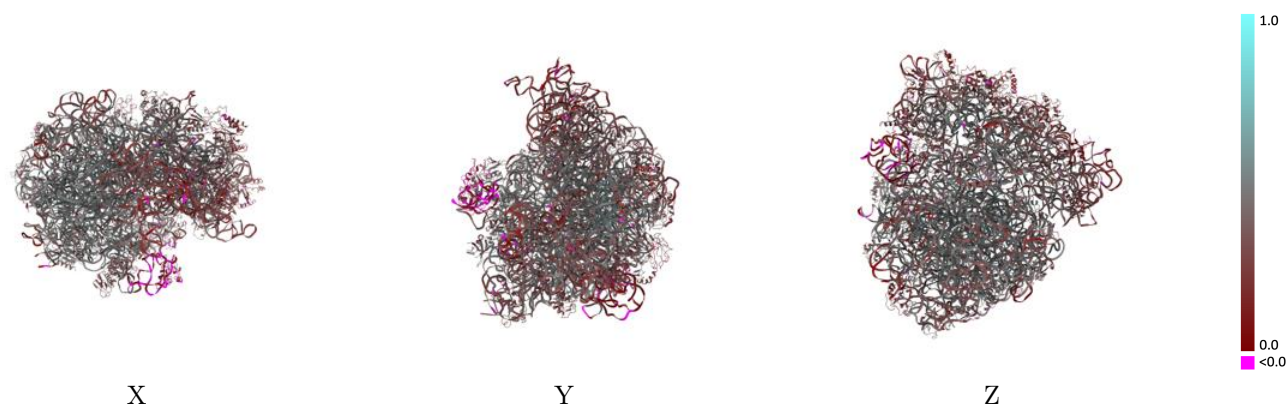
Y



Z

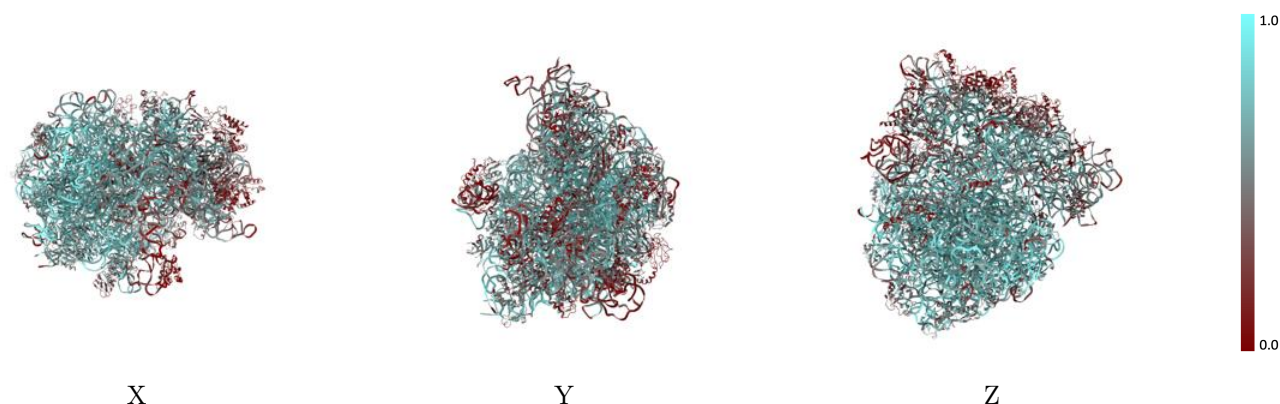
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



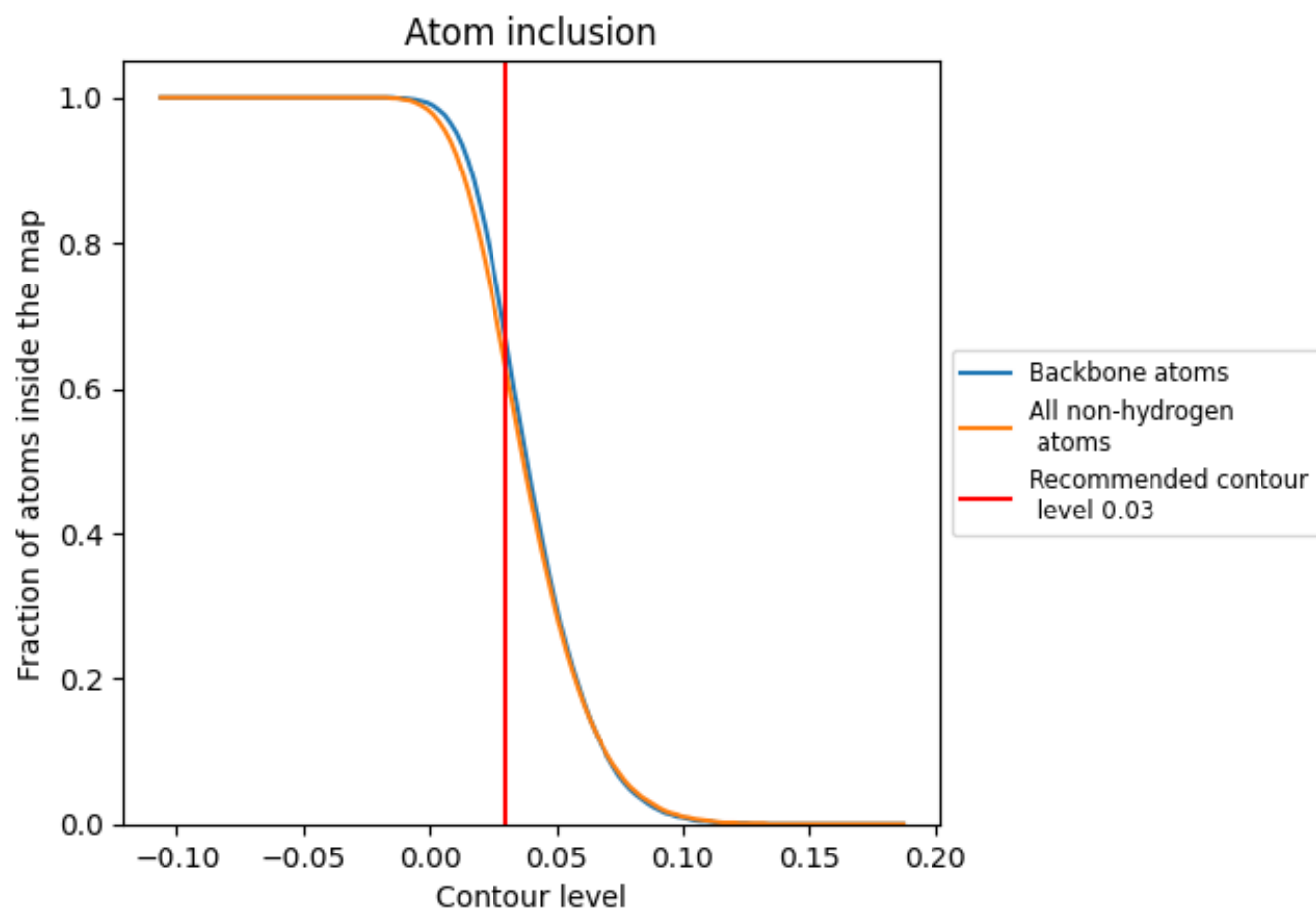
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 67% of all backbone atoms, 63% 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	 0.6300	 0.3940
0	 0.5870	 0.4320
1	 0.4560	 0.3300
2	 0.6020	 0.4520
3	 0.6400	 0.4360
4	 0.5540	 0.3990
6	 0.7210	 0.4850
7	 0.6990	 0.5070
8	 0.6540	 0.4600
A	 0.6510	 0.3950
B	 0.1570	 0.2650
C	 0.2480	 0.3040
D	 0.1840	 0.2520
E	 0.3200	 0.3460
F	 0.3680	 0.3420
G	 0.2420	 0.2950
H	 0.3740	 0.3520
I	 0.2720	 0.2630
J	 0.2100	 0.2600
K	 0.4710	 0.3920
L	 0.4360	 0.3790
M	 0.3160	 0.3130
N	 0.3260	 0.3420
O	 0.5000	 0.3860
P	 0.2060	 0.1160
Q	 0.3420	 0.3360
R	 0.4450	 0.3770
S	 0.3690	 0.3650
T	 0.3350	 0.2890
U	 0.3150	 0.3170
V	 0.2700	 0.2560
W	 0.6120	 0.3470
X	 0.5370	 0.3990
a	 0.7500	 0.3890
b	 0.7590	 0.4220



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Chain	Atom inclusion	Q-score
c	 0.6770	 0.4680
d	 0.6030	 0.4520
e	 0.5470	 0.3900
f	 0.3860	 0.2860
g	 0.4130	 0.3360
h	 0.1500	 0.2440
i	 0.0620	 0.0360
j	 0.6230	 0.4430
k	 0.5610	 0.4450
l	 0.6280	 0.4350
m	 0.6140	 0.4560
n	 0.6430	 0.4500
o	 0.5700	 0.3650
p	 0.5170	 0.4020
q	 0.6730	 0.4670
r	 0.5820	 0.4160
s	 0.5910	 0.4500
t	 0.5280	 0.3770
u	 0.5060	 0.3570
w	 0.5530	 0.4050
y	 0.6680	 0.4770
z	 0.0620	 0.3120