



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 03:01 pm BST

PDB ID : 7ASO
EMDB ID : EMD-11902
Title : Staphylococcus aureus 70S after 30 minutes incubation at 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 3.11 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

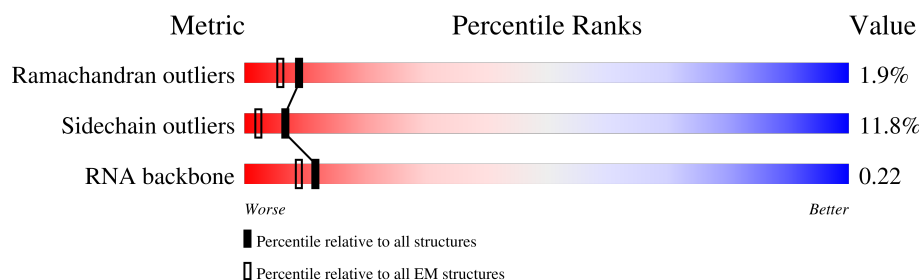
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	C	114	
2	B	202	
3	I	198	
4	D	156	
5	E	95	
6	G	155	
7	F	130	
8	H	127	

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Mol	Chain	Length	Quality of chain
9	1	80	<div> <div>91%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>
10	2	114	<div> <div>93%</div> <div>95%</div> <div>5%</div> </div>
11	3	136	<div> <div>89%</div> <div>95%</div> <div>5%</div> </div>
12	4	113	<div> <div>64%</div> <div>89%</div> <div>11%</div> </div>
13	5	60	<div> <div>87%</div> <div>83%</div> <div>17%</div> </div>
14	6	88	<div> <div>56%</div> <div>97%</div> <div>.</div> </div>
15	7	83	<div> <div>48%</div> <div>75%</div> <div>24%</div> <div>.</div> </div>
16	8	80	<div> <div>50%</div> <div>100%</div> </div>
17	9	56	<div> <div>66%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
18	I	78	<div> <div>82%</div> <div>96%</div> <div>..</div> </div>
19	A	78	<div> <div>71%</div> <div>97%</div> <div>.</div> </div>
20	X	1415	<div> <div>10%</div> <div>26%</div> <div>73%</div> <div>.</div> </div>
21	e	215	<div> <div>87%</div> <div>13%</div> </div>
22	J	205	<div> <div>86%</div> <div>14%</div> </div>
23	K	165	<div> <div>37%</div> <div>91%</div> <div>9%</div> </div>
24	L	174	<div> <div>80%</div> <div>98%</div> <div>.</div> </div>
25	M	145	<div> <div>.</div> <div>83%</div> <div>17%</div> </div>
26	N	122	<div> <div>87%</div> <div>13%</div> </div>
27	O	145	<div> <div>82%</div> <div>18%</div> </div>
28	P	136	<div> <div>.</div> <div>93%</div> <div>7%</div> </div>
29	Q	119	<div> <div>.</div> <div>85%</div> <div>14%</div> <div>.</div> </div>
30	R	113	<div> <div>.</div> <div>96%</div> <div>.</div> </div>
31	S	116	<div> <div>86%</div> <div>14%</div> </div>
32	U	102	<div> <div>78%</div> <div>22%</div> </div>
33	V	112	<div> <div>.</div> <div>84%</div> <div>16%</div> </div>

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Mol	Chain	Length	Quality of chain
34	W	89	
35	Z	103	
36	a	93	
37	b	82	
38	c	49	
39	d	62	
40	f	57	
41	g	47	
42	T	47	
43	i	43	
44	j	60	
45	k	37	
46	h	74	
47	Y	2720	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 125530 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 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	114	Total	C	N	O	P	0	0
			2430	1086	436	794	114		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	202	Total	C	N	O	S	0	0
			1551	979	293	278	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	1	198	Total	C	N	O	0	0
			1058	634	211	213		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	156	Total	C	N	O	S	0	0
			1153	727	211	213	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	155	Total	C	N	O	S	0	0
			1164	724	220	217	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	130	Total	C	N	O	S	0	0
			1007	639	180	184	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	127	Total	C	N	O	S	0	0
			975	605	194	175	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	1	80	Total	C	N	O	0	0
			626	394	116	116		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	2	114	Total	C	N	O	S	0	0
			826	507	158	159	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	3	136	Total	C	N	O	S	0	0
			976	611	190	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	4	113	Total	C	N	O	S	0	0
			828	510	168	149	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	5	60	Total	C	N	O	S	0	0
			497	314	99	79	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	6	88	Total	C	N	O	S	0	0
			713	441	148	123	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	7	83	Total	C	N	O	S	0	0
			537	335	105	96	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	8	80	Total	C	N	O	0	0
			520	327	97	96		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	9	56	Total	C	N	O	S	0	0
			458	292	88	76	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	78	Total	C	N	O	S	0	0
			541	340	104	96	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	A	78	Total	C	N	O	S	0	0
			503	303	100	99	1		

- Molecule 20 is a RNA chain called 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	1415	Total	C	N	O	P	0	0
			30328	13542	5559	9814	1413		

- Molecule 21 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	215	Total	C	N	O	S	0	0
			1570	987	295	283	5		

- Molecule 22 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	J	205	Total	C	N	O	S	0	0
			1514	953	282	277	2		

- Molecule 23 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	165	Total	C	N	O	S	0	0
			1021	632	184	203	2		

- Molecule 24 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	174	Total	C	N	O	S	0	0
			1062	660	205	195	2		

- Molecule 25 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	M	145	Total	C	N	O	S	0	0
			1124	703	205	213	3		

- Molecule 26 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	N	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 27 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	O	145	Total	C	N	O	0	0
			1020	631	207	182		

- Molecule 28 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	P	136	Total	C	N	O	S	0	0
			1043	672	202	165	4		

- Molecule 29 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Q	119	Total	C	N	O	S	0	0
			898	551	176	170	1		

- Molecule 30 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	R	113	Total	C	N	O	S	0	0
			765	474	145	146			

- Molecule 31 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 32 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	U	102	Total	C	N	O	S	0	0
			749	474	140	134	1		

- Molecule 33 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	V	112	Total	C	N	O	S	0	0
			837	526	163	146	2		

- Molecule 34 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	W	89	Total	C	N	O	S	0	0
			694	436	126	128	4		

- Molecule 35 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Z	103	Total	C	N	O	0	0
			734	462	137	135		

- Molecule 36 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	a	93	Total	C	N	O	0	0
			648	411	115	122		

- Molecule 37 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	b	82	Total	C	N	O	0	0
			615	382	122	111		

- Molecule 38 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	c	49	Total	C	N	O	0	0
			377	233	82	62		

- Molecule 39 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	d	62	Total	C	N	O	0	0
			493	304	93	96		

- Molecule 40 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	f	57	Total	C	N	O	0	0
			436	272	83	81		

- Molecule 41 is a protein called 50S ribosomalprotein L32p.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	47	Total	C	N	O	S	0	0
			356	218	77	59	2		

- Molecule 42 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	47	Total	C	N	O	S	0	0
			380	233	75	68	4		

- Molecule 43 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 44 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	60	Total	C	N	O	S	0	0
			446	277	92	75	2		

- Molecule 45 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	37	Total	C	N	O	S	0	0
			272	170	57	40	5		

- Molecule 46 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	h	74	Total	C	N	O	S	0	0
			447	269	86	91	1		

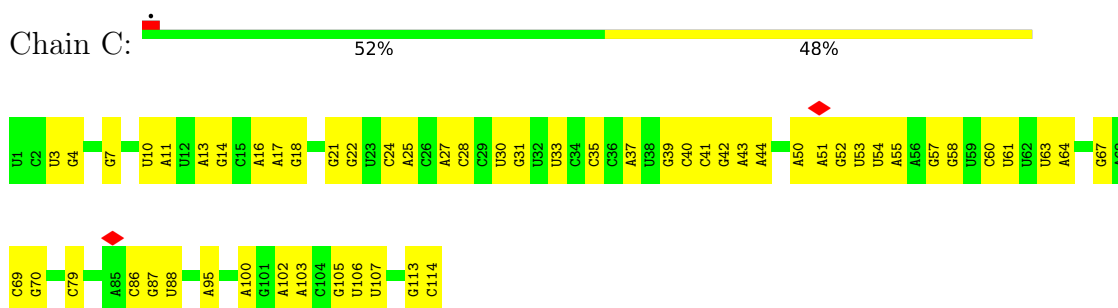
- Molecule 47 is a RNA chain called 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	2720	Total	C	N	O	P	0	0
			58326	26039	10694	18873	2720		

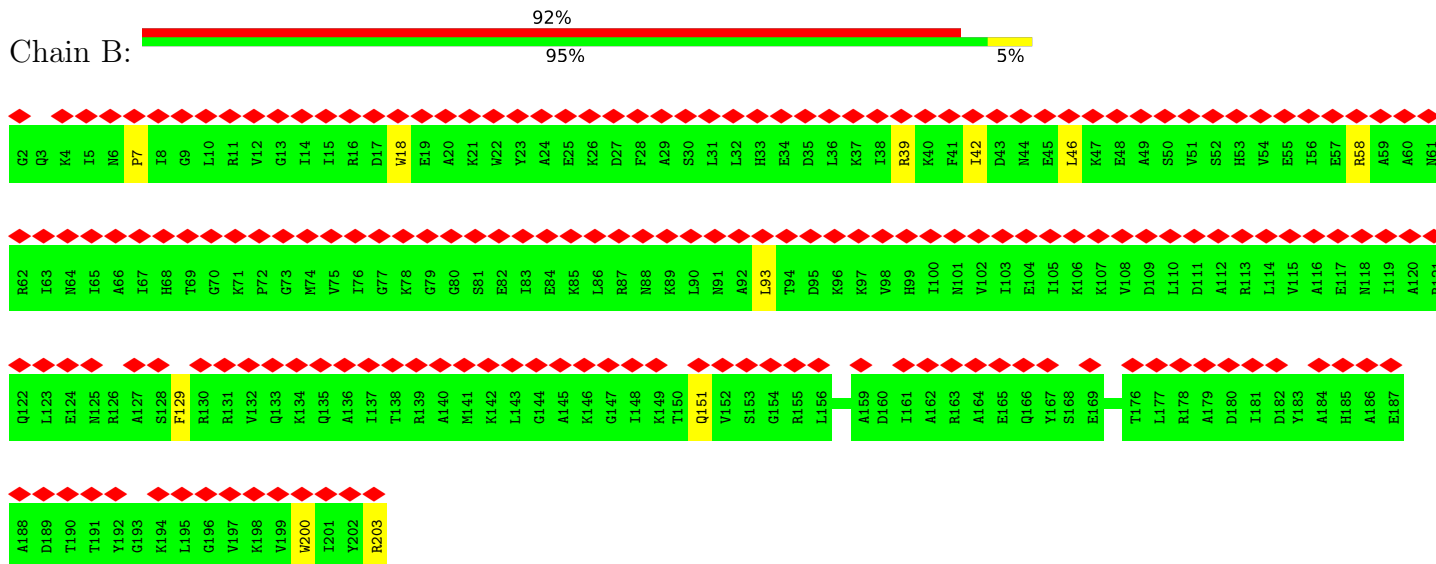
3 Residue-property plots

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.

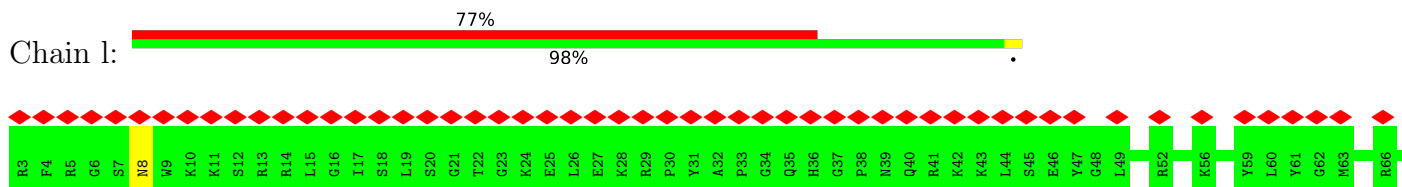
- Molecule 1: 5S

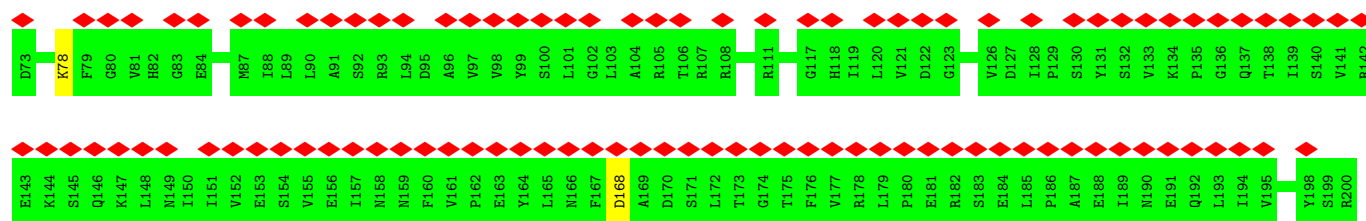


- Molecule 2: 30S ribosomal protein S3

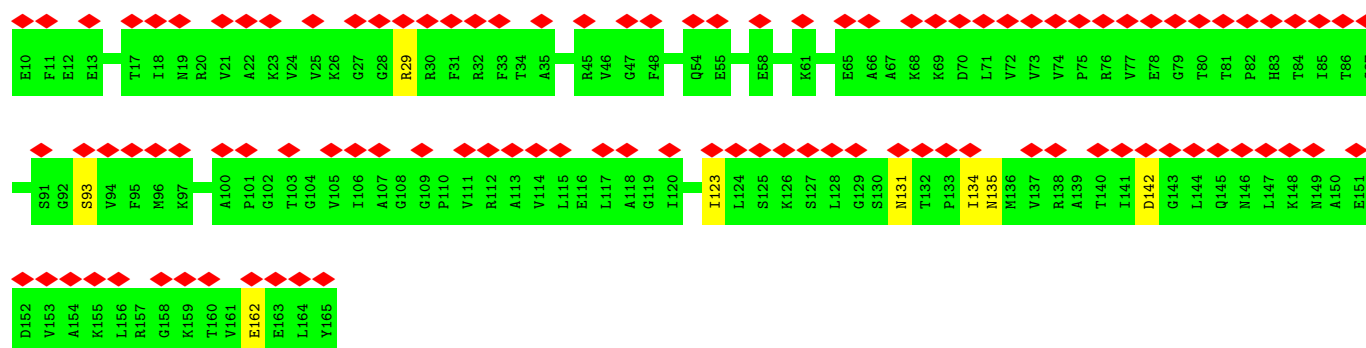


- Molecule 3: 30S ribosomal protein S4

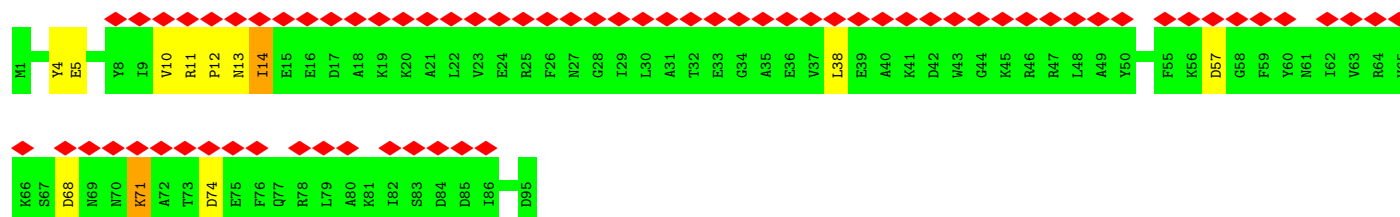
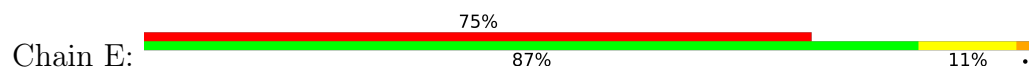




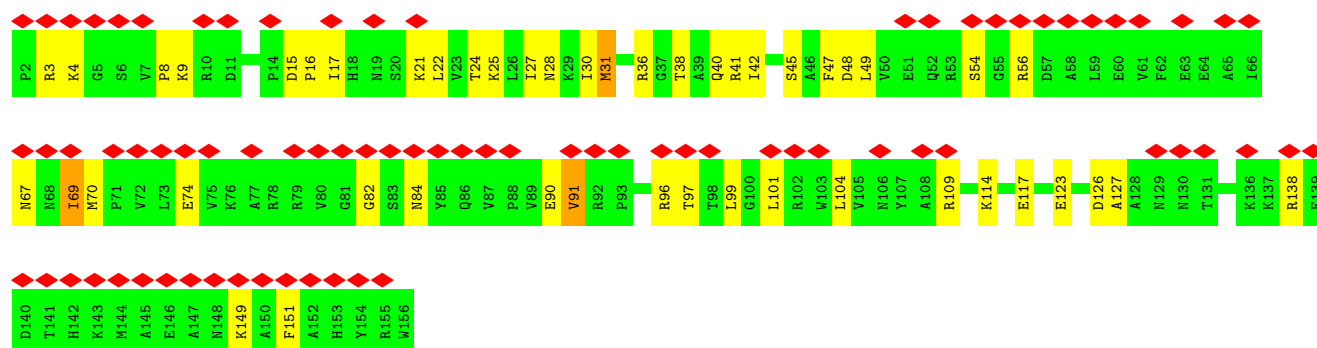
• Molecule 4: 30S ribosomal protein S5



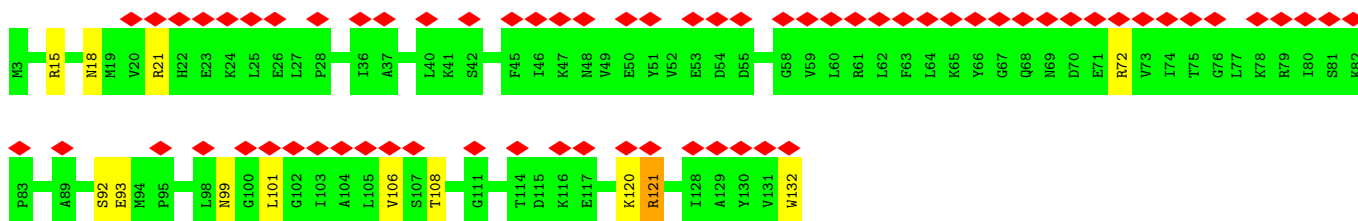
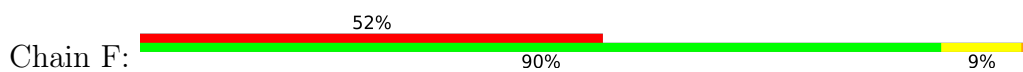
• Molecule 5: 30S ribosomal protein S6



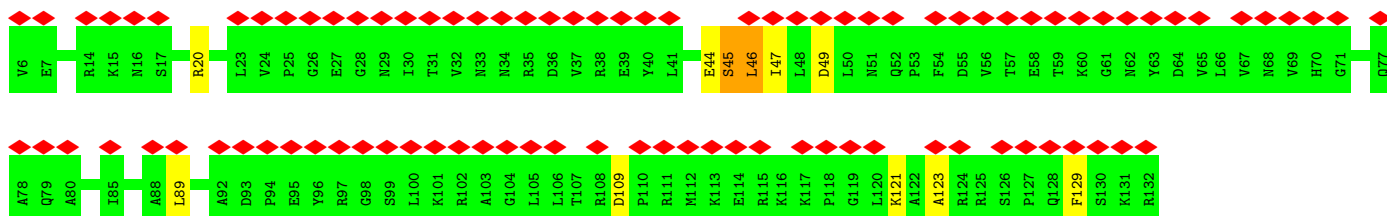
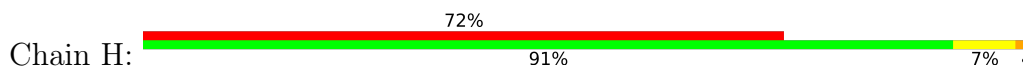
• Molecule 6: 30S ribosomal protein S7



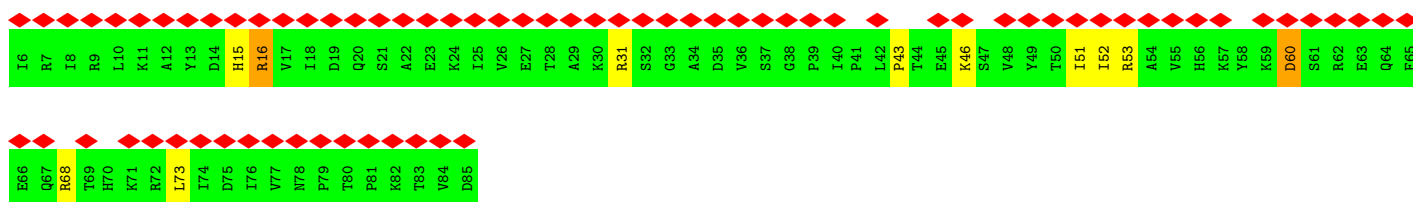
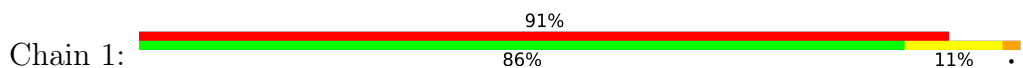
• Molecule 7: 30S ribosomal protein S8



• Molecule 8: 30S ribosomal protein S9



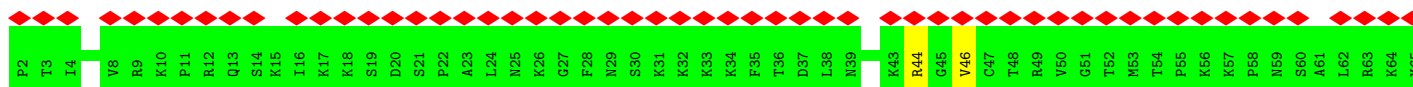
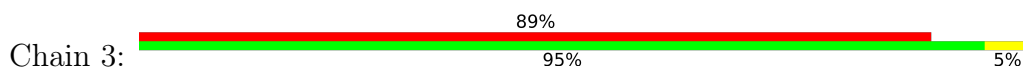
• Molecule 9: 30S ribosomal protein S10



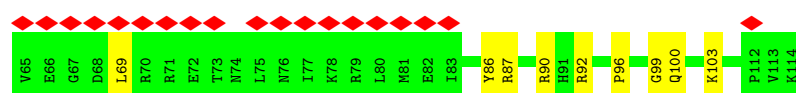
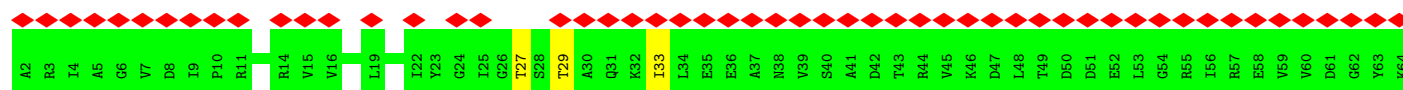
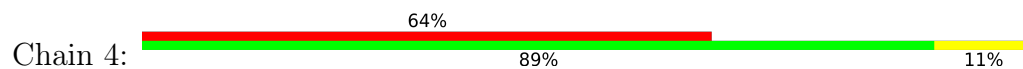
• Molecule 10: 30S ribosomal protein S11



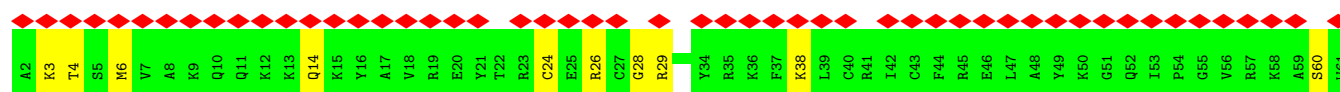
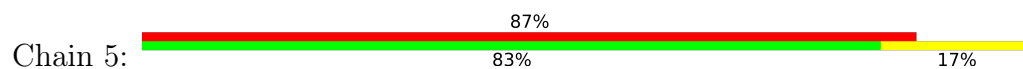
• Molecule 11: 30S ribosomal protein S12



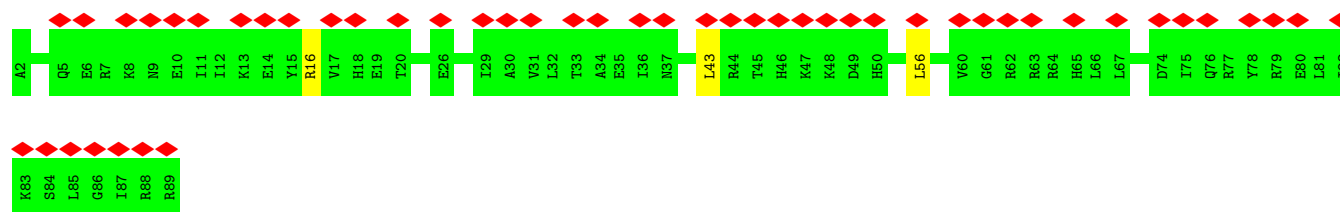
- Molecule 12: 30S ribosomal protein S13



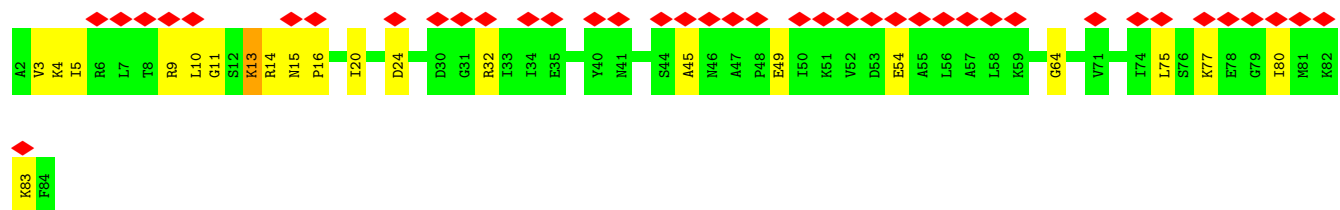
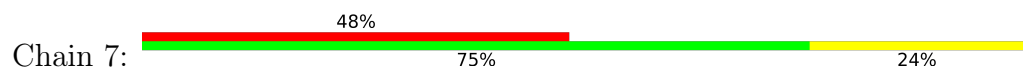
- Molecule 13: 30S ribosomal protein S14 type Z



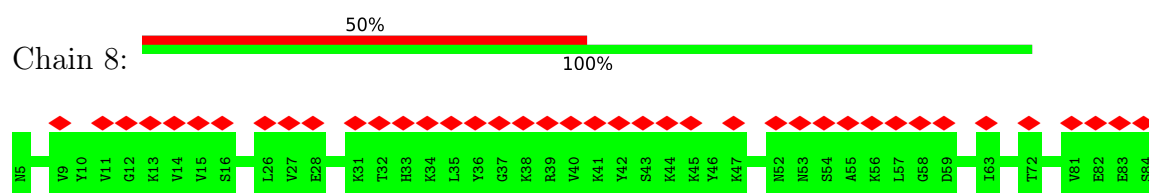
- Molecule 14: 30S ribosomal protein S15



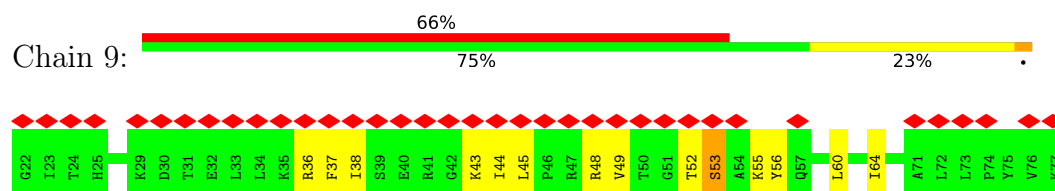
- Molecule 15: 30S ribosomal protein S16



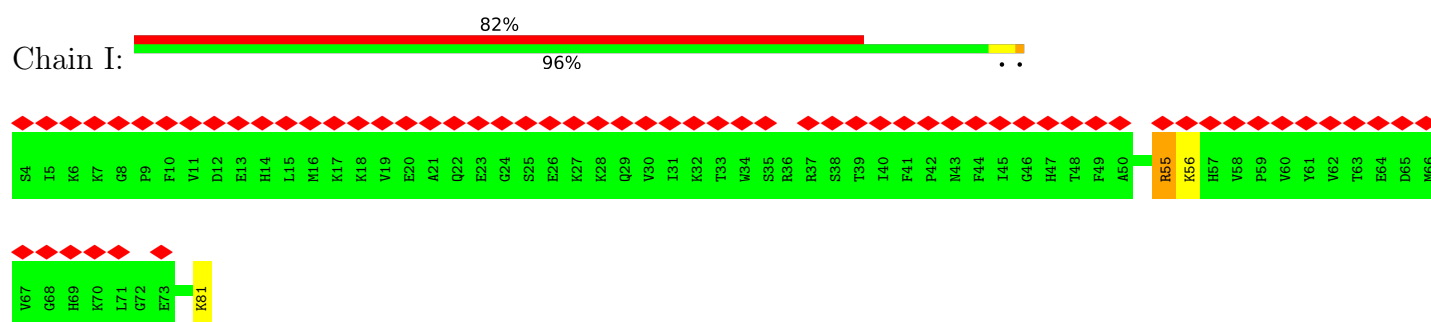
- Molecule 16: 30S ribosomal protein S17



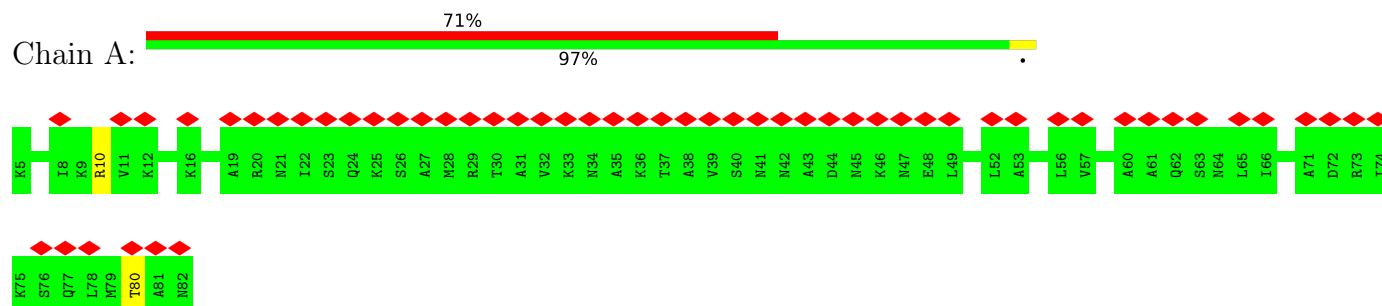
• Molecule 17: 30S ribosomal protein S18



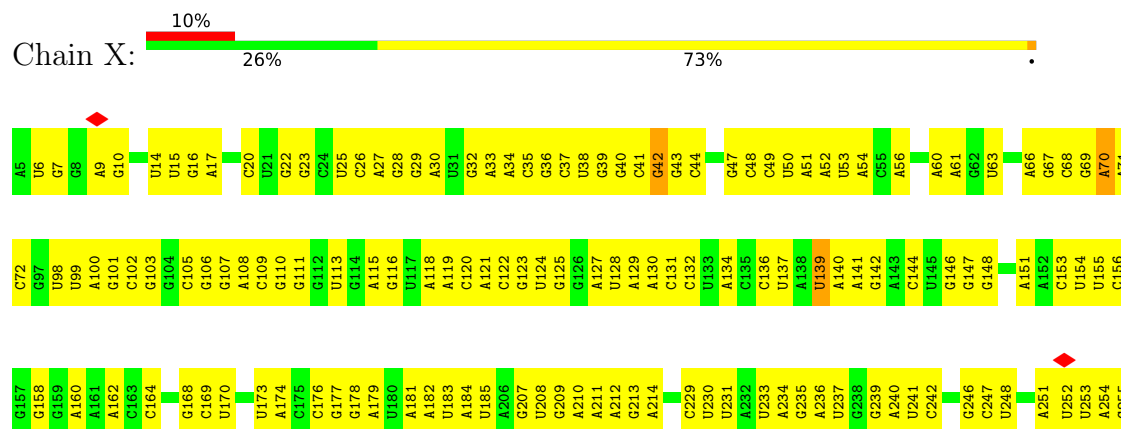
• Molecule 18: 30S ribosomal protein S19



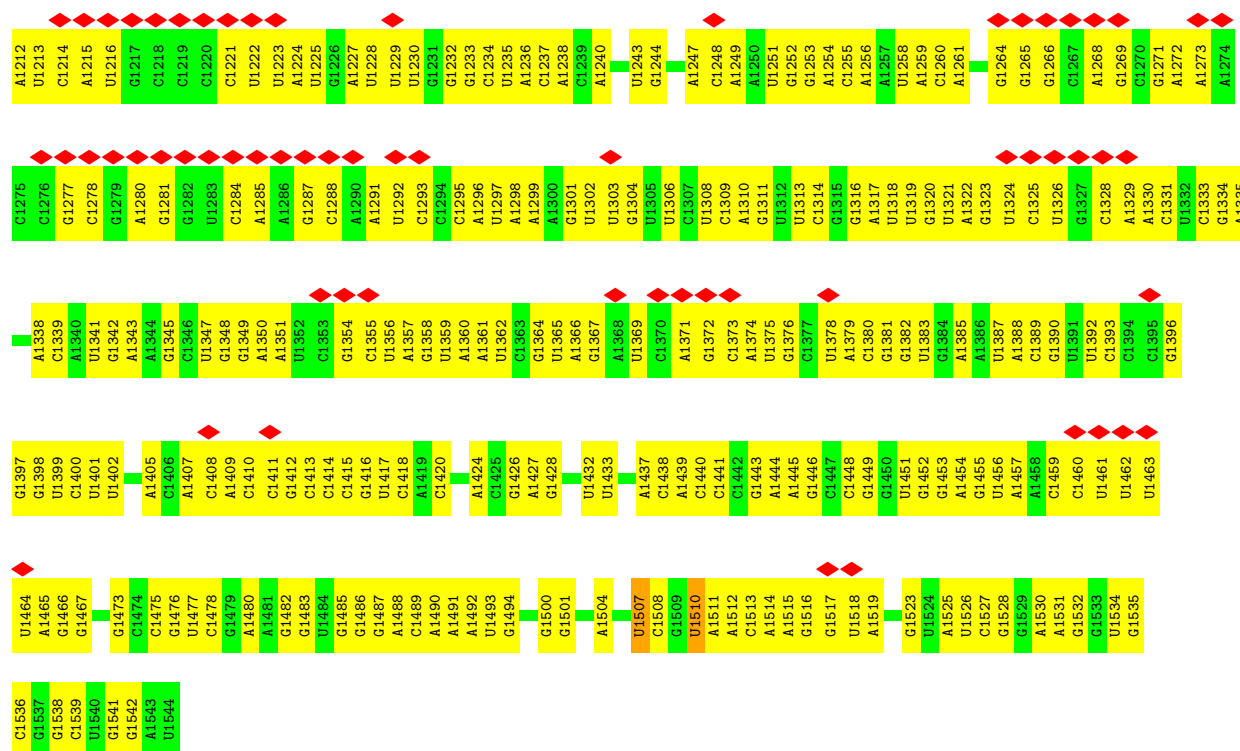
• Molecule 19: 30S ribosomal protein S20



• Molecule 20: 16S



A1148	A1149	A1150	U1151	U1152	G1153	G1154	G1155	G1156	C1157	C1158	U1159	G1160	U1161	A1162	A1163	G1164	U1165	G1166	A1167	A1168	C1169	U1170	G1171	C1172	C1173	G1174	U1175	U1176	G1177	U1178	C1179	A1180	A1181	A1182	C1183	G1184	G1185	G1186	A1187	C1188	G1189	A1190	C1191	G1192	G1193	G1194	G1195	G1196	G1201	A1202	C1203	G1204	A1207	A1208	A1209	U1210	C1211																																																																																																																																																																																																																																									
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G1086	U1087	C1088	G1089	G1090	G1091	G1092	G1093	A1094	U1095	U1098	G1099	G1100	G1101	U1102	U1103	A1104	G1105	U1106	C1107	C1108	C1109	C1110	G1111	C1112	A1113	A1114	C1115	G1116	A1117	G1118	C1119	G1120	C1121	A1122	A1123	C1124	C1125	C1126	U1127	A1130	G1131	C1132	U1133	U1134	A1135	G1136	U1137	U1138	G1139	C1140	C1141	A1142	U1143	C1144	A1145	A1146	U1147																																																																																																																																																																																																																																									
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C857	C858	C859	U860	U861	A862	C863	U864	C865	C866	C869	A870	G871	C872	U873	A874	A875	C876	G877	C878	A879	U880	U881	A882	A883	C884	C885	A886	C887	U888	C889	C890	C891	C892	C893	U894	C895	C896	C897	C8																																																																																																																																																																																																																																																											



- Molecule 21: 50S ribosomal protein L3

Chain e: 87% 13%



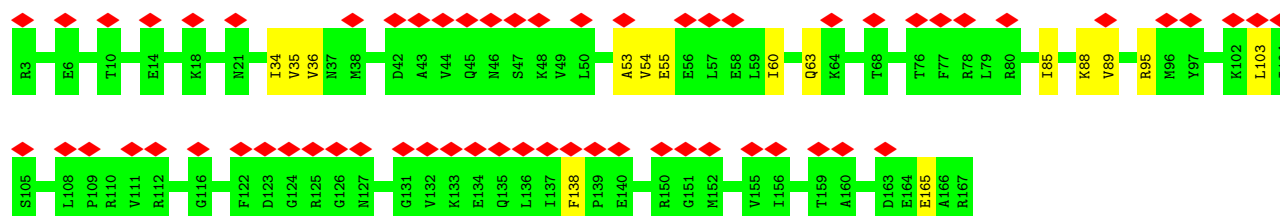
- Molecule 22: 50S ribosomal protein L4

Chain J: 86% 14%

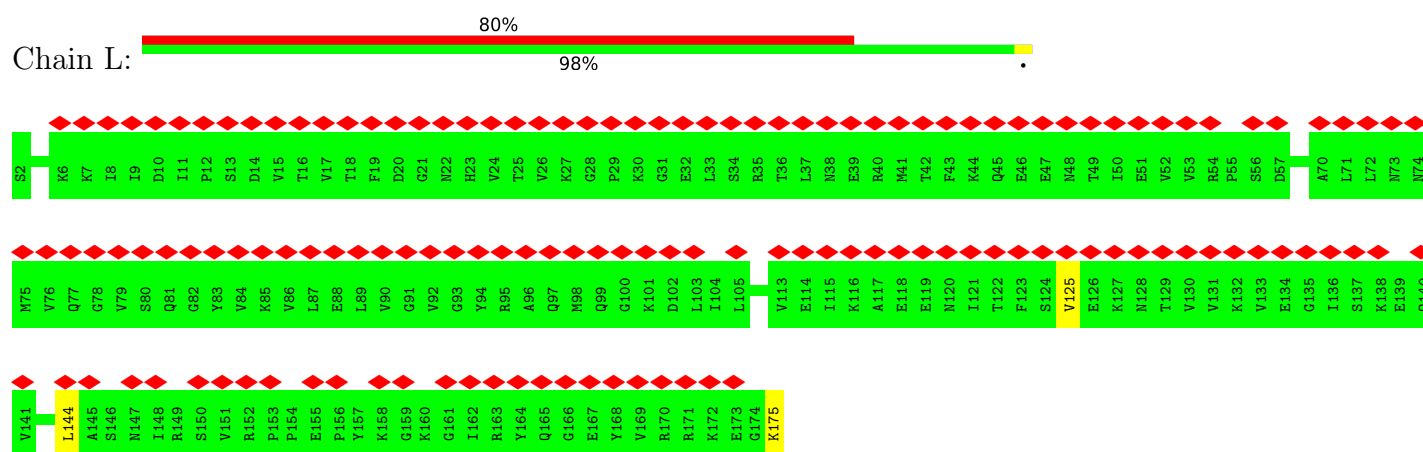


- Molecule 23: 50S ribosomal protein L5

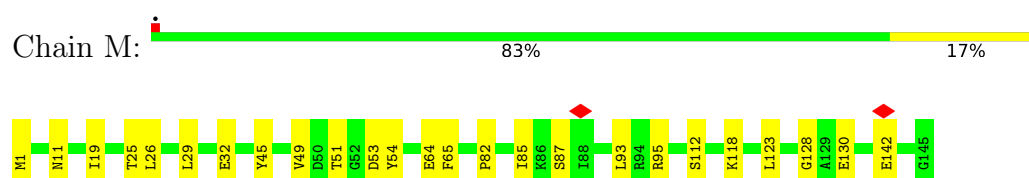
Chain K: 37% 91% 9%



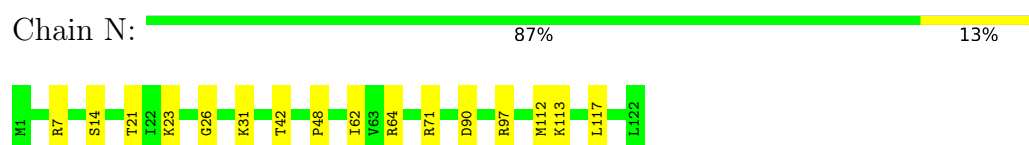
- Molecule 24: 50S ribosomal protein L6



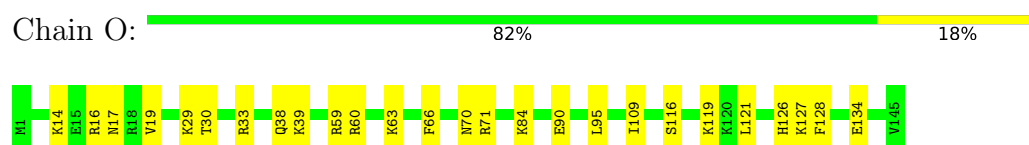
- Molecule 25: 50S ribosomal protein L13



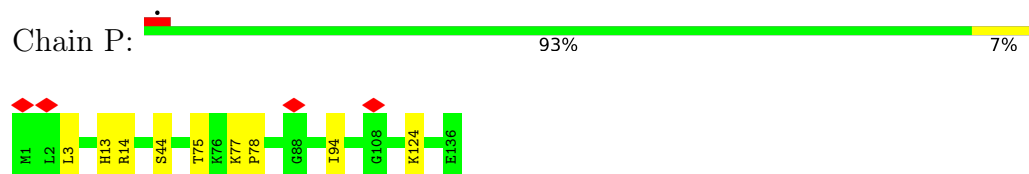
- Molecule 26: 50S ribosomal protein L14



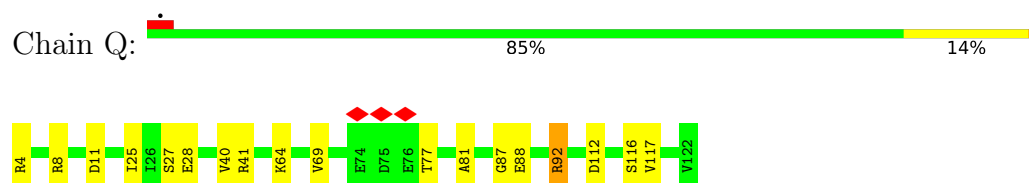
- Molecule 27: 50S ribosomal protein L15



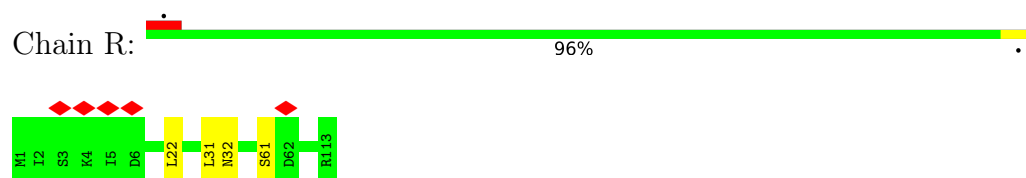
- Molecule 28: 50S ribosomal protein L16



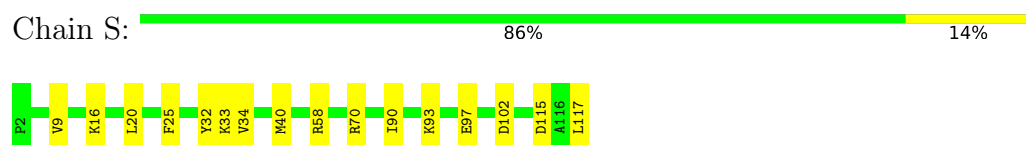
- Molecule 29: 50S ribosomal protein L17



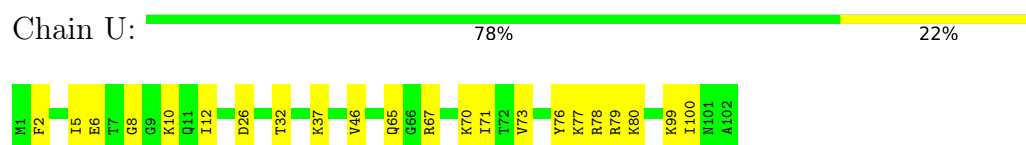
- Molecule 30: 50S ribosomal protein L18



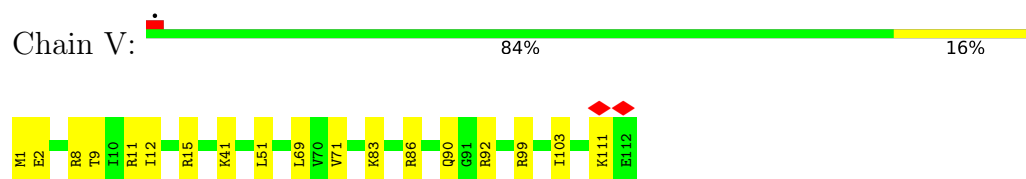
- Molecule 31: 50S ribosomal protein L20



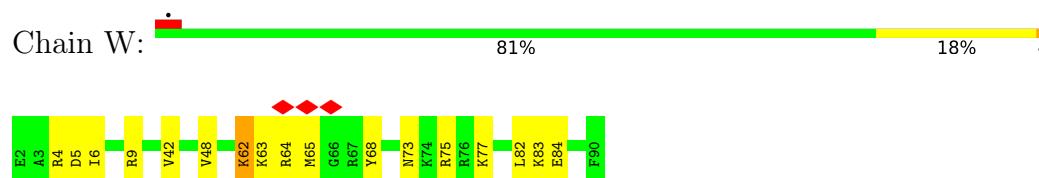
- Molecule 32: 50S ribosomal protein L21



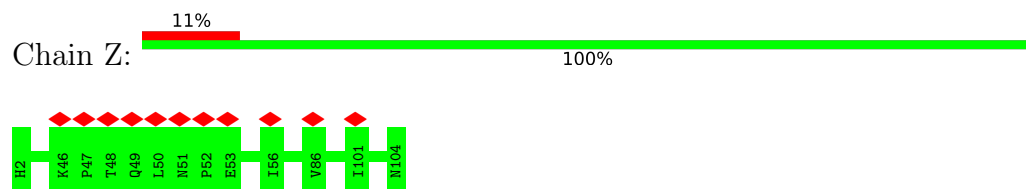
- Molecule 33: 50S ribosomal protein L22



- Molecule 34: 50S ribosomal protein L23

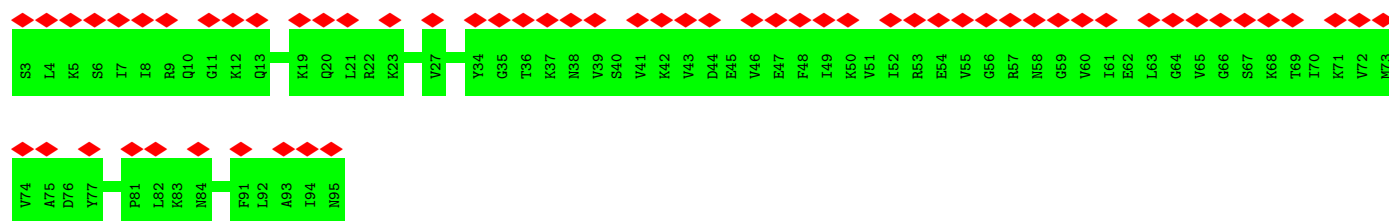


- Molecule 35: 50S ribosomal protein L24

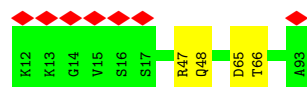


- Molecule 36: 50S ribosomal protein L25

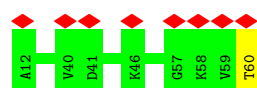




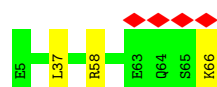
- Molecule 37: 50S ribosomal protein L27



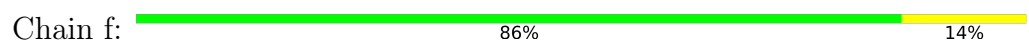
- Molecule 38: 50S ribosomal protein L28



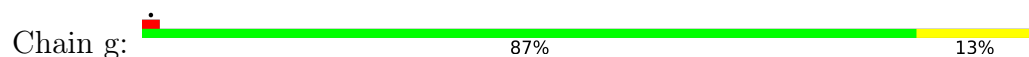
- Molecule 39: 50S ribosomal protein L29



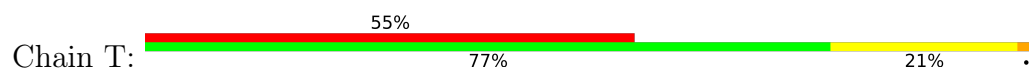
- Molecule 40: 50S ribosomal protein L30

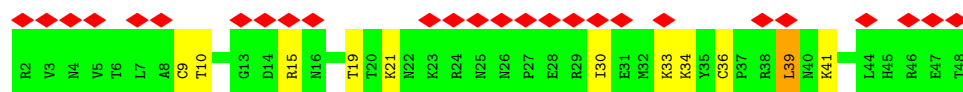


- Molecule 41: 50S ribosomal protein L32p



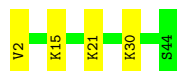
- Molecule 42: 50S ribosomal protein L33





- Molecule 43: 50S ribosomal protein L34

Chain i: 91% 9%



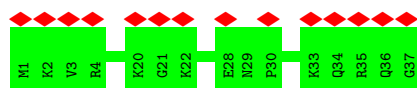
- Molecule 44: 50S ribosomal protein L35

Chain j: 93% 7%



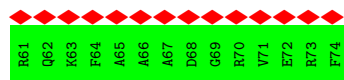
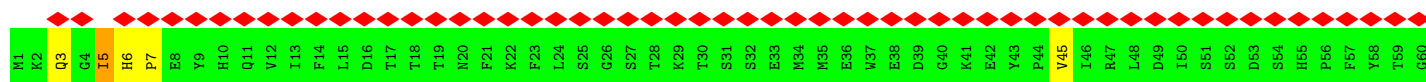
- Molecule 45: 50S ribosomal protein L36

Chain k: 38% 100%



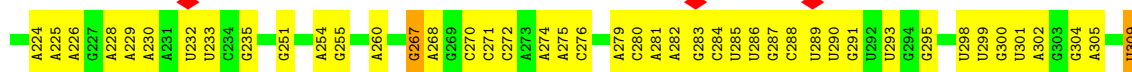
- Molecule 46: 50S ribosomal protein L31 type B

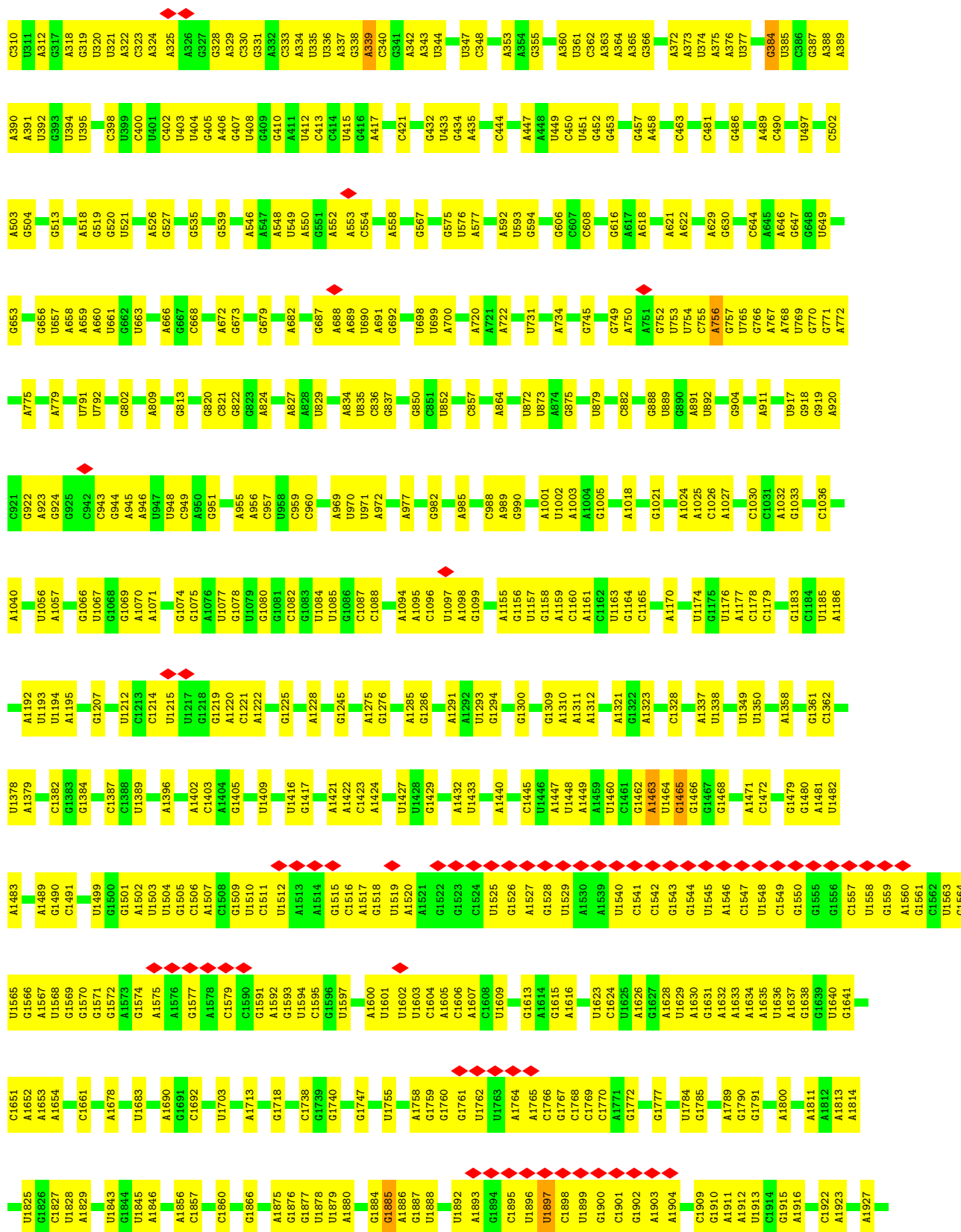
Chain h: 96% 93% 5%



- Molecule 47: 23S

Chain Y: 65% 35%





G2790	A2684	G2552	U2450	U2342	C2219	G2036	G1931
A2791	C2685	G2553	C2451	A2345	U2220	U2046	C1932
A2792	G2686	G2559	A2452	U2346	U2221	A2047	G1933
G2793	A2687	U2560	G2456	A2347	U2222	G2048	G1934
C2794	G2688	U2564	A2457	G2348	A2226	U2049	C1935
A2803	A2689	U2587	U2458	A2349	C2231	A2050	C1936
G2804	G2690	A2593	A2459	G2352	A2232	U2053	U1938
A2805	G2691	G2594	A2460	U2352	A2232	G2054	A1945
U2806	A2692	C2583	A2461	U2353	C2233	A2058	A1946
G2807	C2693	C2587	A2462	A2354	C2234	G2059	C1947
	C2694	A2596	A2466	U2361	U2237	A2060	G1948
	G2695	G2595	C2467	A2362	U2238		G1949
	G2696	C2594	C2468	U2370	A2239		
	G2700	G2596	G2472	U2371	C2241	U2068	A1954
	G2712	G2597	G2473	G2372	G2242	A2069	A1955
	U2716	U2598	G2474	A2373	U2243	C2070	G1956
	U2716	A2599	A2475	C2374	G2244	C2071	
	U2833	C2600	U2476	U2375	G2247	C2072	C1961
			A2477	G2376			
				C2377	A2252	G2079	
			U2487	A2388	G2255	C2082	A1964
						G2083	A1965
			C2492	G2394	C2263	G2084	
			A2495	G2399	G2264	A2087	U1970
			A2496	G2399	G2265	G2088	U1971
			G2497	U2400	G2266	A2089	G1972
			A2498	C2401	C2267		G1975
			G2499			G2096	G1976
				G2410	A2295		G1977
				A2411		U2103	U1982
				C2412	G2306	A2104	
				U2417	C2310		A1987
				G2418		G2120	C1988
				A2419	A2314	A2121	C1989
					A2315	A2122	C1990
				G2424	G2316		G1991
				U2425		G2127	C1992
				G2426	C2324	G2128	A1993
				U2427	A2325	C2129	C1994
				G2428	G2326		A1997
				U2429	A2327	C2131	A1998
				C2430	A2328	A2132	G1999
				G2431	U2329	G2133	
				G2432	G2330	C2134	A2004
				C2433	G2331	U2135	U2009
				A2434	U2332	U2336	
				U2435	U2333	A2208	G2013
					G2334	G2209	
				A2438	G2335	C2210	U2018
					A2336	U2211	G2019
				G2441	A2337	G2212	U2020
					U2339	U2213	A2024
				A2445	C2340	G2214	
				U2446	A2341	U2215	U2034
						U2216	G2035
						G2217	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	123520	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0052	Depositor
Map size (\AA)	361.2, 361.2, 361.2	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.86, 0.86, 0.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.20	0/2717	0.63	0/4232
2	B	0.42	0/1573	0.71	1/2121 (0.0%)
3	I	0.32	0/1062	0.62	0/1465
4	D	0.47	0/1167	0.75	0/1576
5	E	0.50	0/796	0.78	1/1069 (0.1%)
6	G	0.66	0/1180	0.60	0/1595
7	F	0.49	0/1019	0.80	0/1371
8	H	0.46	0/990	0.72	1/1332 (0.1%)
9	1	0.48	0/637	0.61	0/865
10	2	0.42	0/840	0.70	0/1137
11	3	0.47	0/991	0.77	0/1337
12	4	0.45	0/835	0.71	1/1123 (0.1%)
13	5	0.54	0/507	0.77	0/674
14	6	0.38	0/721	0.73	2/964 (0.2%)
15	7	0.72	0/541	0.70	0/733
16	8	0.36	0/527	0.70	0/721
17	9	0.54	0/465	0.66	0/620
18	I	0.43	0/551	0.72	0/747
19	A	0.44	0/502	0.60	0/679
20	X	0.21	0/33951	0.65	15/52921 (0.0%)
21	e	0.67	0/1593	0.59	0/2143
22	J	0.66	0/1536	0.57	0/2078
23	K	0.49	0/1028	0.68	1/1405 (0.1%)
24	L	0.33	0/1074	0.68	1/1467 (0.1%)
25	M	0.65	0/1146	0.56	0/1546
26	N	0.66	0/925	0.59	0/1242
27	O	0.68	0/1034	0.60	0/1388
28	P	0.60	1/1067 (0.1%)	0.68	0/1436
29	Q	0.66	0/900	0.57	0/1205
30	R	0.42	0/770	0.65	0/1044
31	S	0.63	0/954	0.55	0/1264
32	U	0.67	0/758	0.57	0/1014
33	V	0.66	0/845	0.59	0/1140
34	W	0.65	0/701	0.57	0/939

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Z	0.46	0/742	0.66	0/1001
36	a	0.41	0/655	0.77	0/888
37	b	0.72	0/621	0.71	0/824
38	c	0.57	0/382	0.65	0/512
39	d	0.47	0/494	0.69	0/660
40	f	0.66	0/438	0.58	0/591
41	g	0.65	0/361	0.58	0/481
42	T	0.63	0/385	0.57	0/518
43	i	0.62	0/371	0.57	0/484
44	j	0.70	0/450	0.83	1/597 (0.2%)
45	k	0.38	0/275	0.69	0/366
46	h	0.39	0/454	0.62	0/624
47	Y	0.21	1/65313 (0.0%)	0.63	9/101832 (0.0%)
All	All	0.33	2/136844 (0.0%)	0.64	33/205971 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2
3	l	0	3
4	D	0	1
7	F	0	1
8	H	0	1
10	2	0	2
11	3	0	3
12	4	0	2
13	5	0	1
19	A	0	1
23	K	0	1
24	L	0	1
30	R	0	3
39	d	0	1
44	j	0	2
46	h	0	1
All	All	0	26

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Y	765	U	O3'-P	7.60	1.70	1.61
28	P	124	LYS	C-N	-5.85	1.20	1.34

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	Y	1463	A	C2'-C3'-O3'	7.93	126.95	109.50
47	Y	756	A	C2'-C3'-O3'	7.61	126.24	109.50
47	Y	267	G	C2'-C3'-O3'	7.36	125.69	109.50
20	X	409	C	C2'-C3'-O3'	7.05	125.00	109.50
20	X	139	U	C2'-C3'-O3'	7.01	124.92	109.50

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	58	ARG	Peptide
2	B	7	PRO	Peptide
3	1	168	ASP	Peptide
3	1	78	LYS	Peptide
3	1	8	ASN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	200/202 (99%)	155 (78%)	43 (22%)	2 (1%)	13	40
3	1	196/198 (99%)	128 (65%)	68 (35%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	154/156 (99%)	118 (77%)	35 (23%)	1 (1%)	22	52
5	E	93/95 (98%)	66 (71%)	23 (25%)	4 (4%)	2	11
6	G	153/155 (99%)	105 (69%)	39 (26%)	9 (6%)	1	7
7	F	128/130 (98%)	89 (70%)	36 (28%)	3 (2%)	5	22
8	H	125/127 (98%)	88 (70%)	33 (26%)	4 (3%)	3	17
9	1	78/80 (98%)	63 (81%)	12 (15%)	3 (4%)	2	14
10	2	112/114 (98%)	78 (70%)	33 (30%)	1 (1%)	14	43
11	3	134/136 (98%)	92 (69%)	40 (30%)	2 (2%)	8	31
12	4	111/113 (98%)	79 (71%)	29 (26%)	3 (3%)	4	19
13	5	58/60 (97%)	39 (67%)	18 (31%)	1 (2%)	7	29
14	6	86/88 (98%)	64 (74%)	22 (26%)	0	100	100
15	7	81/83 (98%)	55 (68%)	18 (22%)	8 (10%)	0	2
16	8	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
17	9	54/56 (96%)	41 (76%)	12 (22%)	1 (2%)	6	26
18	I	76/78 (97%)	47 (62%)	27 (36%)	2 (3%)	4	20
19	A	76/78 (97%)	64 (84%)	12 (16%)	0	100	100
21	e	213/215 (99%)	173 (81%)	37 (17%)	3 (1%)	9	32
22	J	203/205 (99%)	175 (86%)	26 (13%)	2 (1%)	13	40
23	K	163/165 (99%)	112 (69%)	46 (28%)	5 (3%)	3	17
24	L	172/174 (99%)	115 (67%)	57 (33%)	0	100	100
25	M	143/145 (99%)	123 (86%)	15 (10%)	5 (4%)	3	15
26	N	120/122 (98%)	99 (82%)	18 (15%)	3 (2%)	4	20
27	O	143/145 (99%)	111 (78%)	30 (21%)	2 (1%)	9	32
28	P	134/136 (98%)	115 (86%)	17 (13%)	2 (2%)	8	31
29	Q	117/119 (98%)	97 (83%)	14 (12%)	6 (5%)	1	9
30	R	111/113 (98%)	80 (72%)	31 (28%)	0	100	100
31	S	114/116 (98%)	108 (95%)	4 (4%)	2 (2%)	7	27
32	U	100/102 (98%)	73 (73%)	24 (24%)	3 (3%)	3	18
33	V	110/112 (98%)	95 (86%)	15 (14%)	0	100	100
34	W	87/89 (98%)	70 (80%)	13 (15%)	4 (5%)	2	11
35	Z	101/103 (98%)	74 (73%)	27 (27%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	a	91/93 (98%)	69 (76%)	22 (24%)	0	100	100
37	b	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	20
38	c	47/49 (96%)	38 (81%)	9 (19%)	0	100	100
39	d	60/62 (97%)	49 (82%)	11 (18%)	0	100	100
40	f	55/57 (96%)	52 (94%)	3 (6%)	0	100	100
41	g	45/47 (96%)	38 (84%)	6 (13%)	1 (2%)	5	23
42	T	45/47 (96%)	41 (91%)	3 (7%)	1 (2%)	5	23
43	i	41/43 (95%)	36 (88%)	5 (12%)	0	100	100
44	j	58/60 (97%)	43 (74%)	15 (26%)	0	100	100
45	k	35/37 (95%)	24 (69%)	11 (31%)	0	100	100
46	h	72/74 (97%)	40 (56%)	30 (42%)	2 (3%)	4	19
All	All	4653/4741 (98%)	3540 (76%)	1026 (22%)	87 (2%)	9	26

5 of 87 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	12	PRO
15	7	13	LYS
21	e	19	ASN
23	K	95	ARG
28	P	78	PRO

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	151/164 (92%)	145 (96%)	6 (4%)	27	56
3	l	23/174 (13%)	23 (100%)	0	100	100
4	D	120/122 (98%)	114 (95%)	6 (5%)	20	48
5	E	82/83 (99%)	73 (89%)	9 (11%)	5	20
6	G	115/131 (88%)	73 (64%)	42 (36%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	F	107/111 (96%)	97 (91%)	10 (9%)	7	26
8	H	96/105 (91%)	89 (93%)	7 (7%)	11	35
9	1	67/73 (92%)	57 (85%)	10 (15%)	2	10
10	2	85/90 (94%)	82 (96%)	3 (4%)	31	59
11	3	95/118 (80%)	93 (98%)	2 (2%)	48	71
12	4	75/97 (77%)	69 (92%)	6 (8%)	10	32
13	5	51/52 (98%)	43 (84%)	8 (16%)	2	9
14	6	74/80 (92%)	73 (99%)	1 (1%)	62	79
15	7	36/70 (51%)	22 (61%)	14 (39%)	0	0
16	8	35/75 (47%)	35 (100%)	0	100	100
17	9	49/50 (98%)	35 (71%)	14 (29%)	0	1
18	I	45/69 (65%)	43 (96%)	2 (4%)	24	52
19	A	37/65 (57%)	36 (97%)	1 (3%)	40	65
21	e	158/173 (91%)	134 (85%)	24 (15%)	2	9
22	J	154/168 (92%)	127 (82%)	27 (18%)	1	7
23	K	67/146 (46%)	59 (88%)	8 (12%)	4	16
24	L	61/152 (40%)	60 (98%)	1 (2%)	58	77
25	M	117/123 (95%)	97 (83%)	20 (17%)	1	7
26	N	100/100 (100%)	87 (87%)	13 (13%)	3	14
27	O	91/111 (82%)	67 (74%)	24 (26%)	0	1
28	P	101/113 (89%)	95 (94%)	6 (6%)	16	42
29	Q	90/100 (90%)	77 (86%)	13 (14%)	2	11
30	R	63/90 (70%)	62 (98%)	1 (2%)	58	77
31	S	96/96 (100%)	82 (85%)	14 (15%)	2	11
32	U	68/86 (79%)	49 (72%)	19 (28%)	0	1
33	V	84/91 (92%)	66 (79%)	18 (21%)	1	4
34	W	72/80 (90%)	58 (81%)	14 (19%)	1	5
35	Z	71/88 (81%)	71 (100%)	0	100	100
36	a	58/82 (71%)	58 (100%)	0	100	100
37	b	61/64 (95%)	59 (97%)	2 (3%)	33	60
38	c	38/41 (93%)	37 (97%)	1 (3%)	41	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	d	52/57 (91%)	50 (96%)	2 (4%)	28	57
40	f	50/51 (98%)	42 (84%)	8 (16%)	2	8
41	g	35/43 (81%)	30 (86%)	5 (14%)	2	11
42	T	42/45 (93%)	31 (74%)	11 (26%)	0	1
43	i	39/39 (100%)	35 (90%)	4 (10%)	6	21
44	j	44/52 (85%)	43 (98%)	1 (2%)	45	68
45	k	29/35 (83%)	29 (100%)	0	100	100
46	h	23/66 (35%)	20 (87%)	3 (13%)	3	14
All	All	3207/4021 (80%)	2827 (88%)	380 (12%)	7	17

5 of 380 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	N	112	MET
31	S	70	ARG
27	O	30	THR
28	P	14	ARG
32	U	65	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
25	M	137	GLN
31	S	29	HIS
42	T	26	ASN
26	N	4	GLN
27	O	143	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	113/114 (99%)	55 (48%)	2 (1%)
20	X	1401/1415 (99%)	1035 (73%)	80 (5%)
47	Y	2703/2720 (99%)	954 (35%)	36 (1%)
All	All	4217/4249 (99%)	2044 (48%)	118 (2%)

5 of 2044 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	3	U
1	C	4	G
1	C	7	G
1	C	10	U
1	C	11	A

5 of 118 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	X	936	G
47	Y	1885	G
20	X	1298	A
47	Y	1845	U
47	Y	1463	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	Y	16
20	X	11

The worst 5 of 27 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	1492:G	O3'	1498:U	P	29.74
1	Y	2135:U	O3'	2208:A	P	19.22
1	Y	1530:A	O3'	1539:A	P	17.34
1	Y	1550:G	O3'	1555:G	P	16.75
1	X	215:C	O3'	228:A	P	16.72

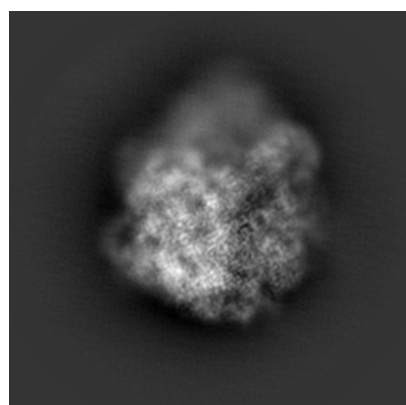
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11902. These allow visual inspection of the internal detail of the map and identification of artifacts.

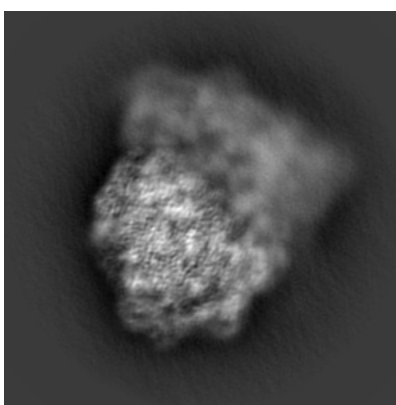
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

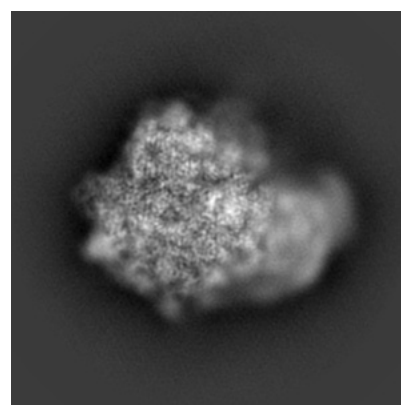
6.1.1 Primary map



X



Y

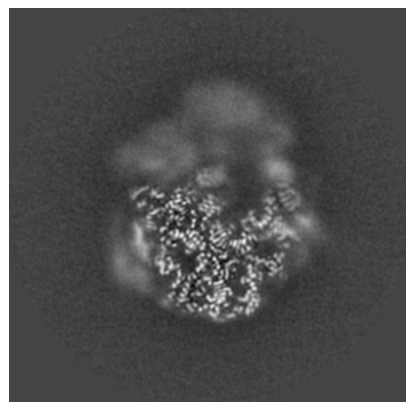


Z

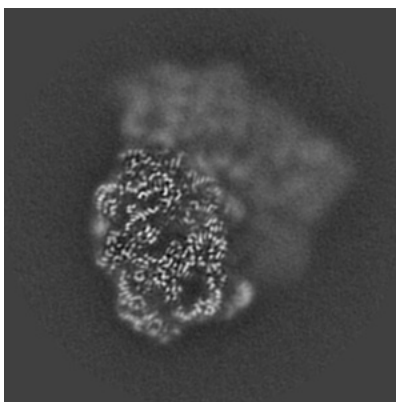
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

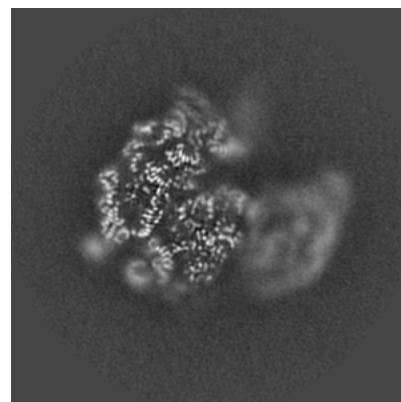
6.2.1 Primary map



X Index: 210



Y Index: 210

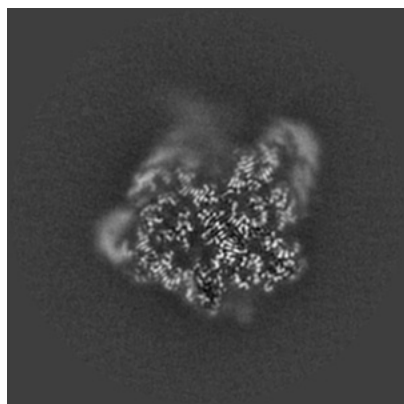


Z Index: 210

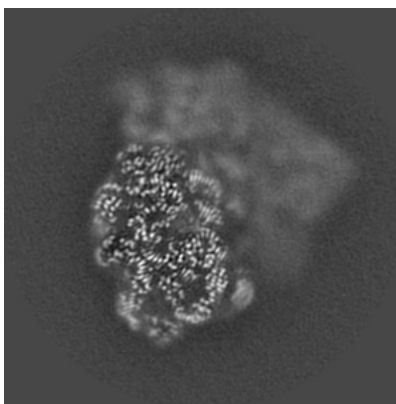
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

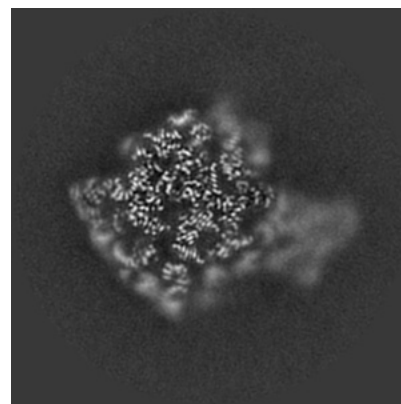
6.3.1 Primary map



X Index: 167



Y Index: 214

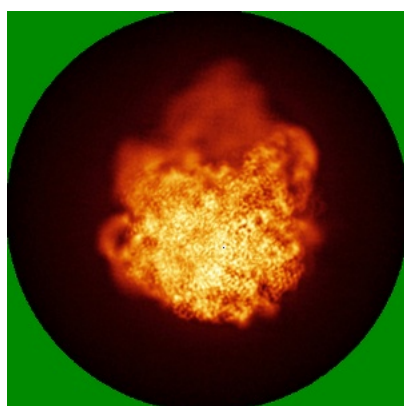


Z Index: 167

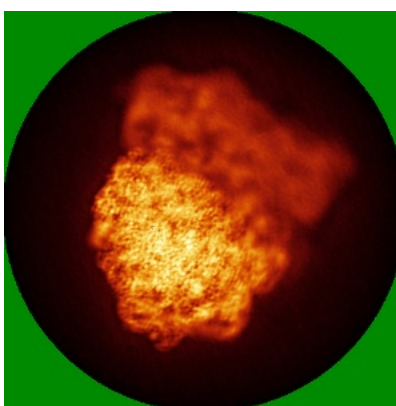
The images above show the largest variance slices of the map in three orthogonal directions.

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

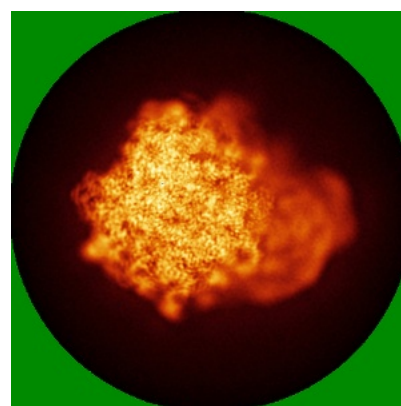
6.4.1 Primary map



X



Y

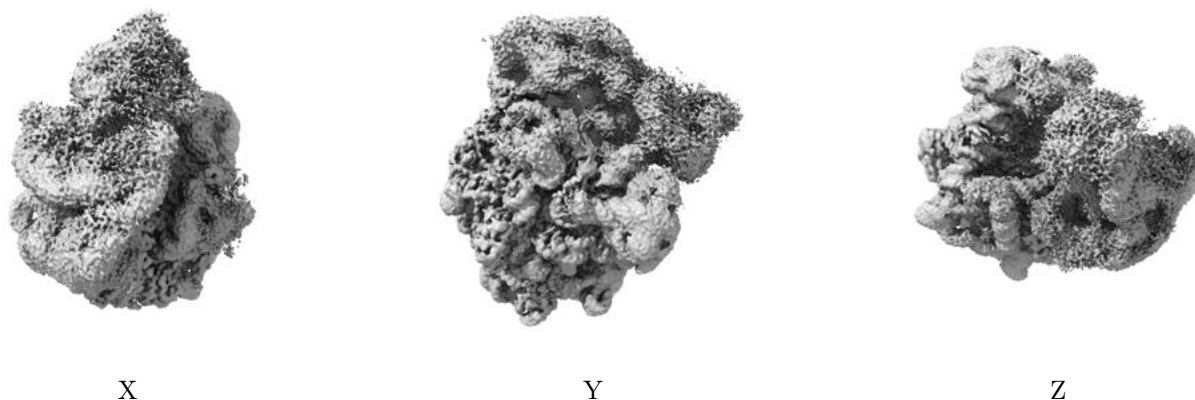


Z

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 0.0052. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

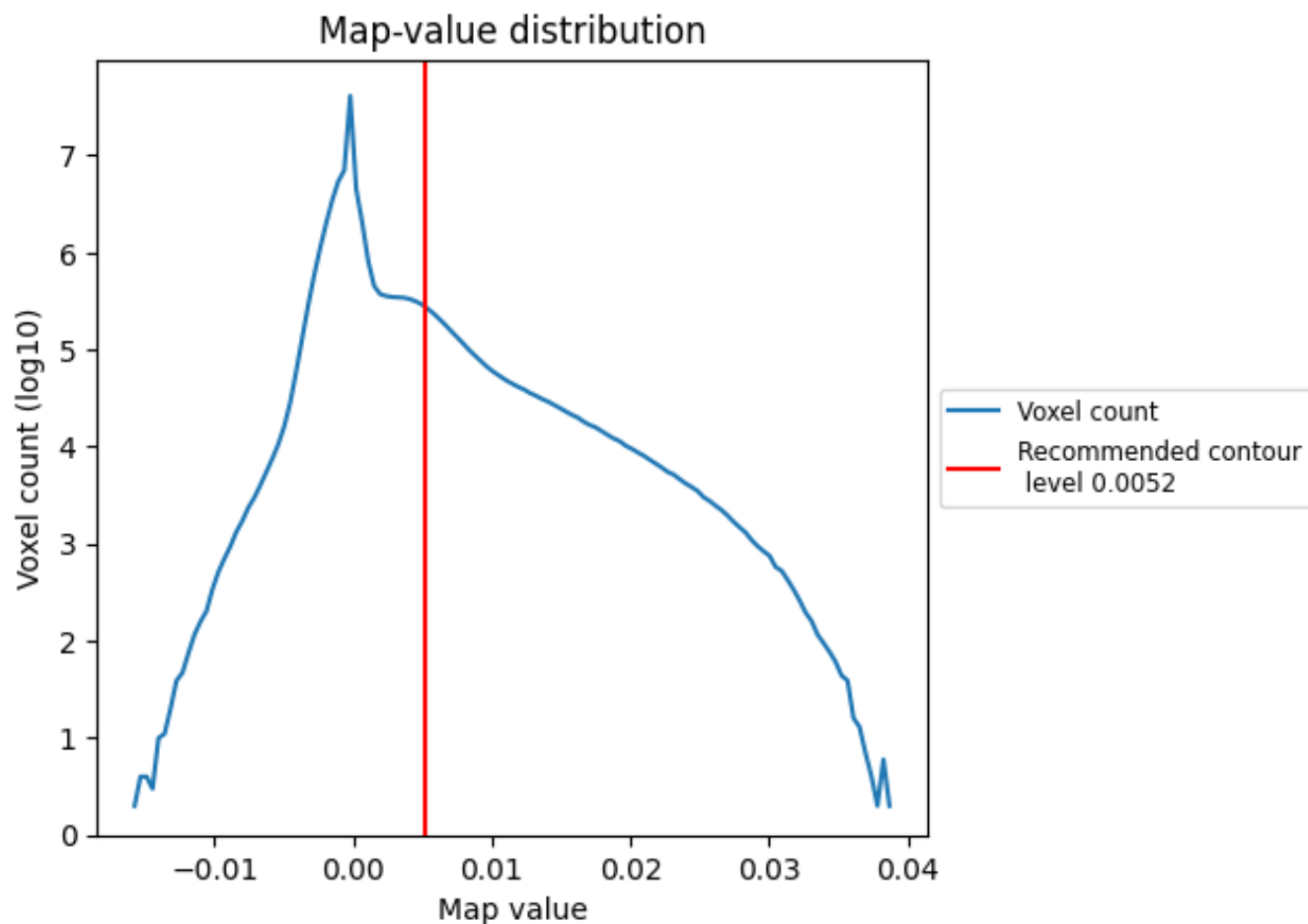
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

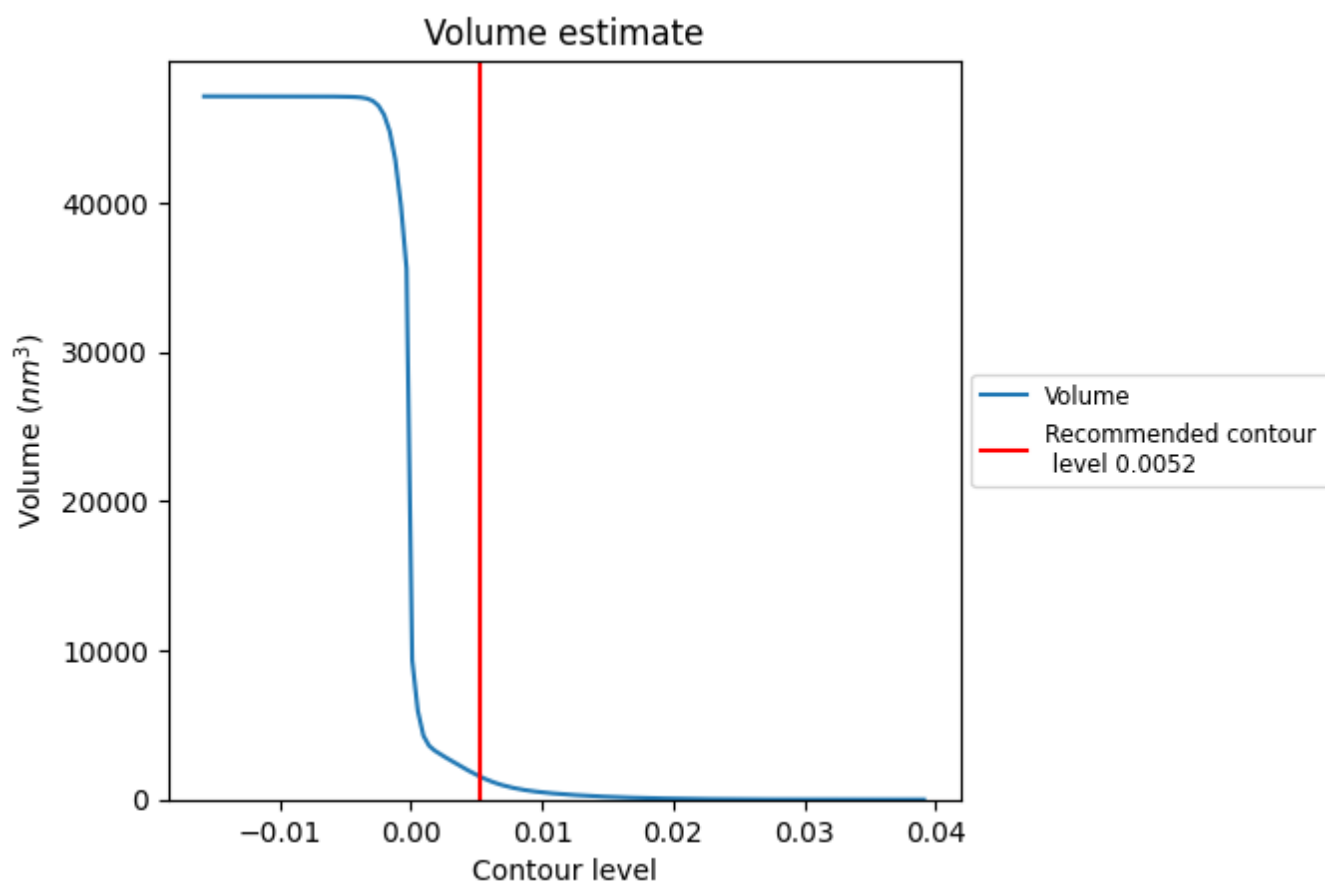
This section contains the results of statistical analysis of the map.

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.

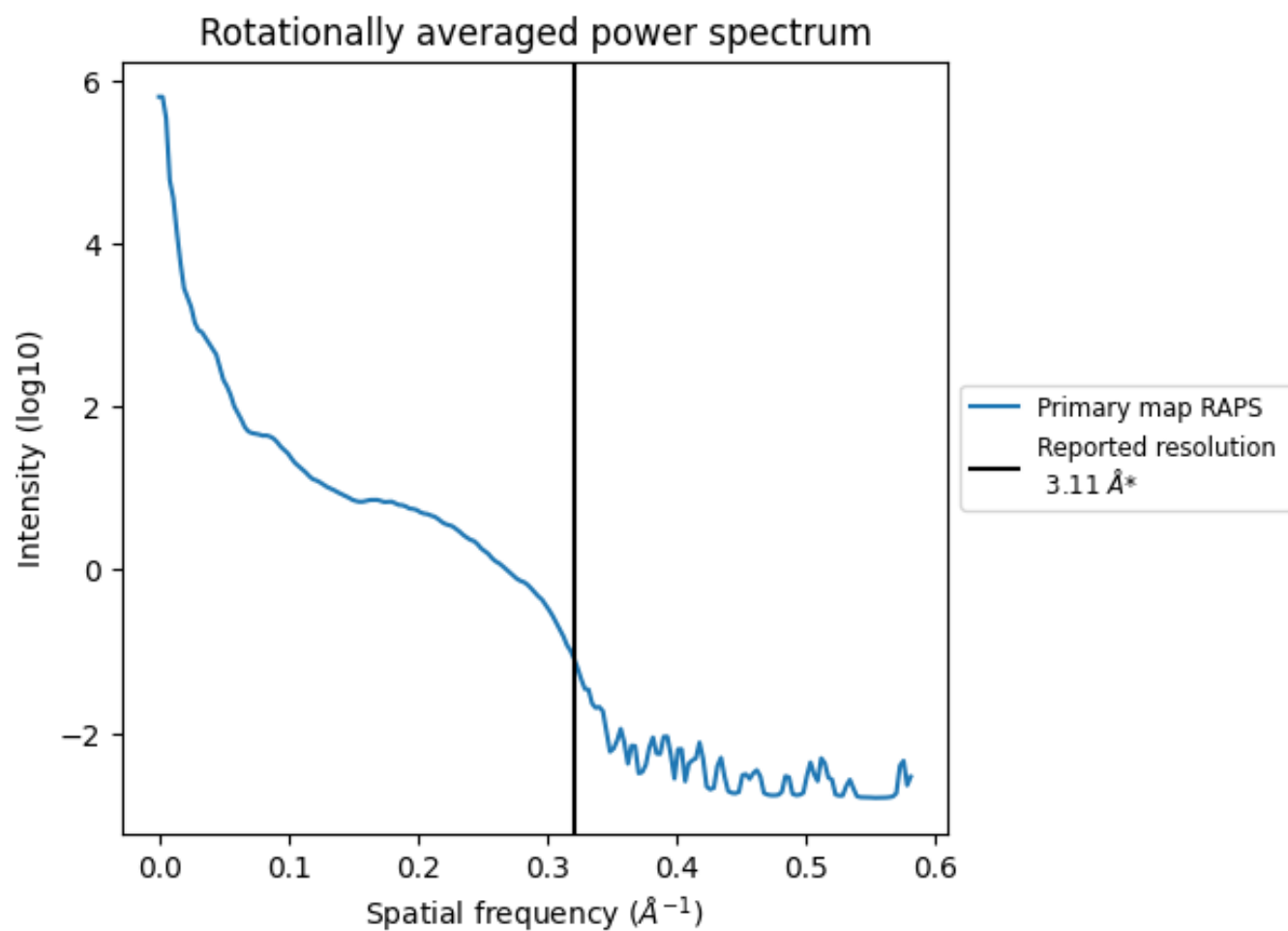
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1571 nm³; this corresponds to an approximate mass of 1419 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.322 Å⁻¹

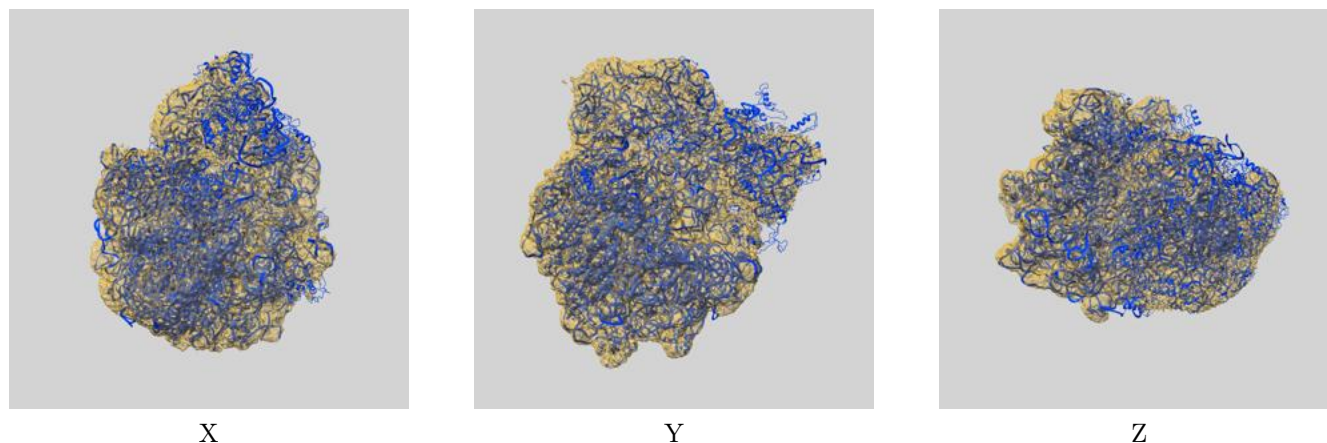
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

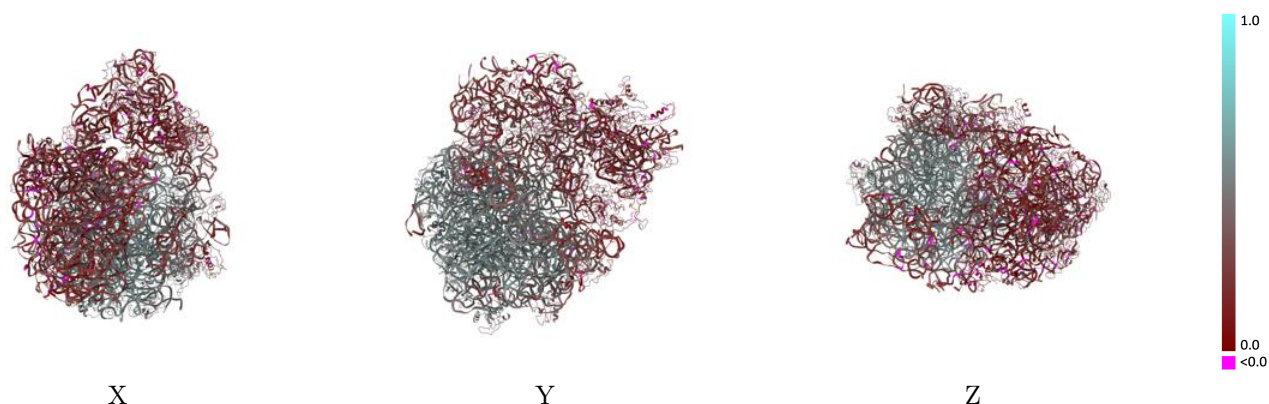
This section contains information regarding the fit between EMDB map EMD-11902 and PDB model 7ASO. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



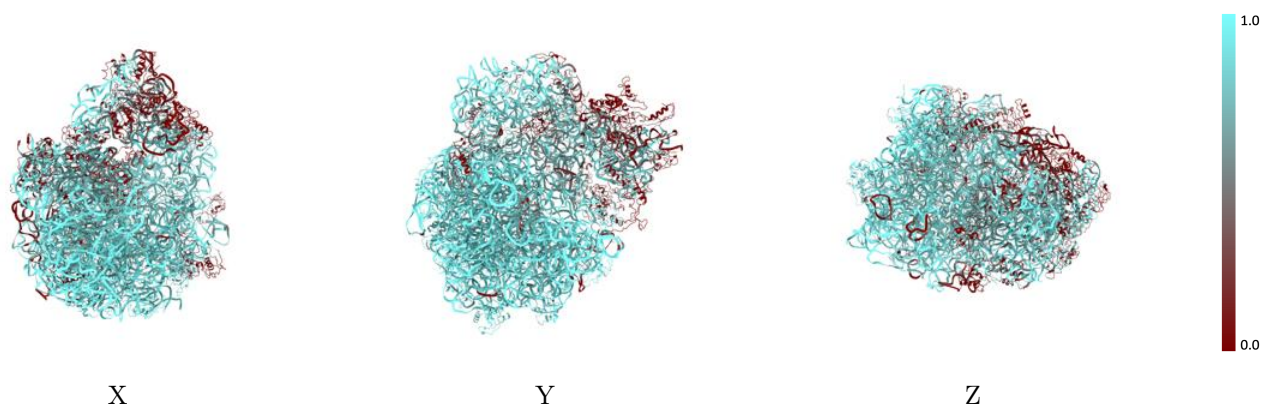
The images above show the 3D surface view of the map at the recommended contour level 0.0052 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



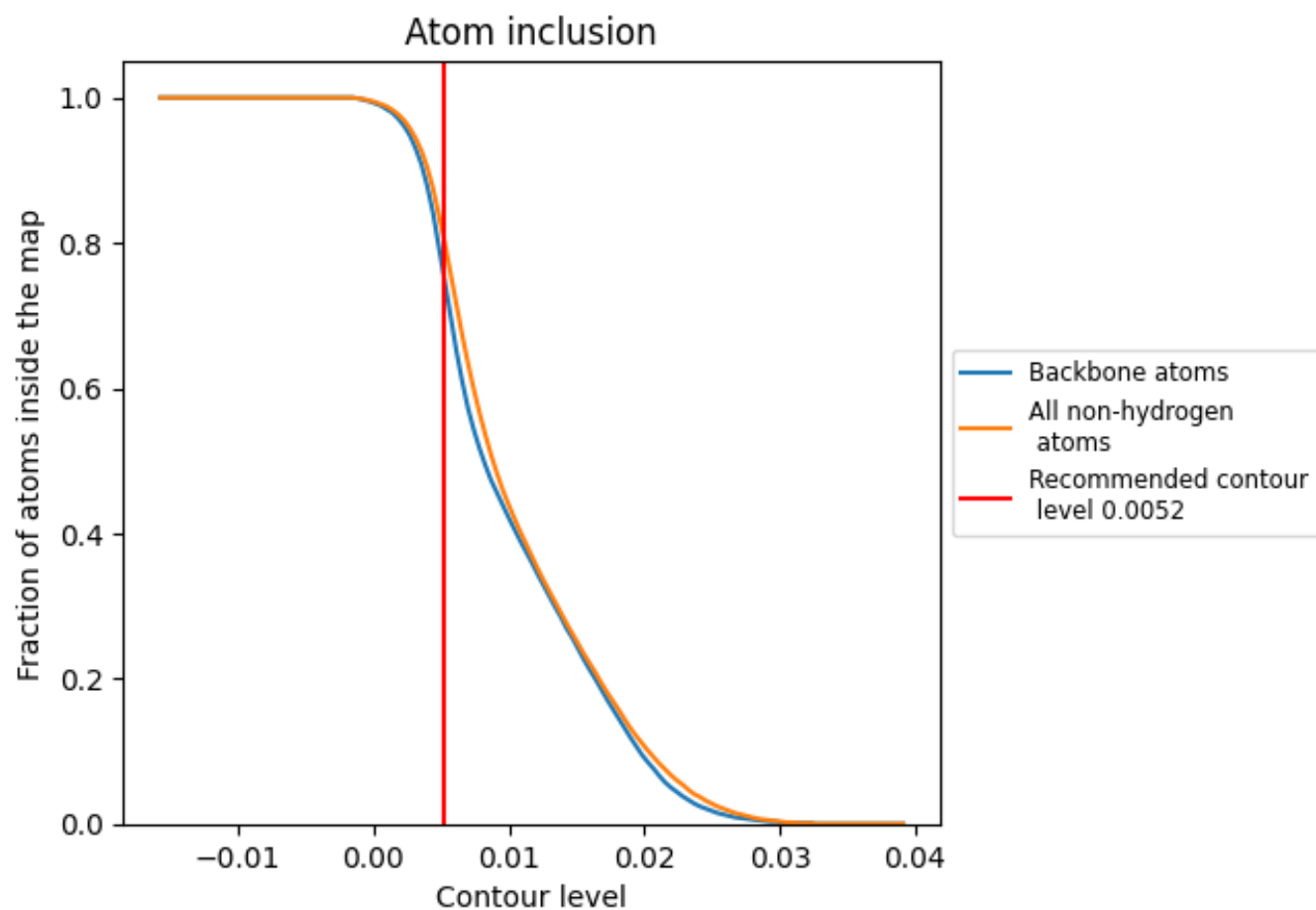
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0052).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% 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 (0.0052) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8050	 0.3580
1	 0.1170	 0.1950
2	 0.0890	 0.2510
3	 0.1020	 0.2140
4	 0.3150	 0.2170
5	 0.1370	 0.2110
6	 0.3920	 0.2180
7	 0.4750	 0.1430
8	 0.4380	 0.2580
9	 0.3450	 0.2210
A	 0.2720	 0.2000
B	 0.0890	 0.2520
C	 0.9440	 0.2810
D	 0.2920	 0.2540
E	 0.2540	 0.1940
F	 0.4140	 0.2310
G	 0.4520	 0.1910
H	 0.2700	 0.2470
I	 0.1680	 0.2250
J	 0.9080	 0.4850
K	 0.6090	 0.2410
L	 0.2190	 0.2550
M	 0.9100	 0.5130
N	 0.8490	 0.5230
O	 0.9040	 0.4810
P	 0.8370	 0.4750
Q	 0.9000	 0.5110
R	 0.8640	 0.3240
S	 0.9280	 0.5410
T	 0.4280	 0.3970
U	 0.9350	 0.5160
V	 0.8930	 0.5300
W	 0.8630	 0.4550
X	 0.8040	 0.1890
Y	 0.9410	 0.4510



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Chain	Atom inclusion	Q-score
Z	 0.7720	 0.4180
a	 0.3600	 0.3440
b	 0.8510	 0.5050
c	 0.7330	 0.4770
d	 0.8350	 0.3850
e	 0.9370	 0.5280
f	 0.9140	 0.5110
g	 0.8630	 0.4480
h	 0.0520	 0.2470
i	 0.9100	 0.5490
j	 0.8880	 0.5200
k	 0.5260	 0.3340
l	 0.2660	 0.2720