



wwPDB EM Validation Summary Report ⓘ

Sep 6, 2026 – 07:09 PM EDT

PDB ID : 11JJ / pdb_000011jj
EMDB ID : EMD-75740
Title : Rabbit 80S with eEF2,IFRD2 and LARP1,40S-head-swiveled
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-27
Resolution : 2.90 Å(reported)
Based on initial model : 7TOR

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:

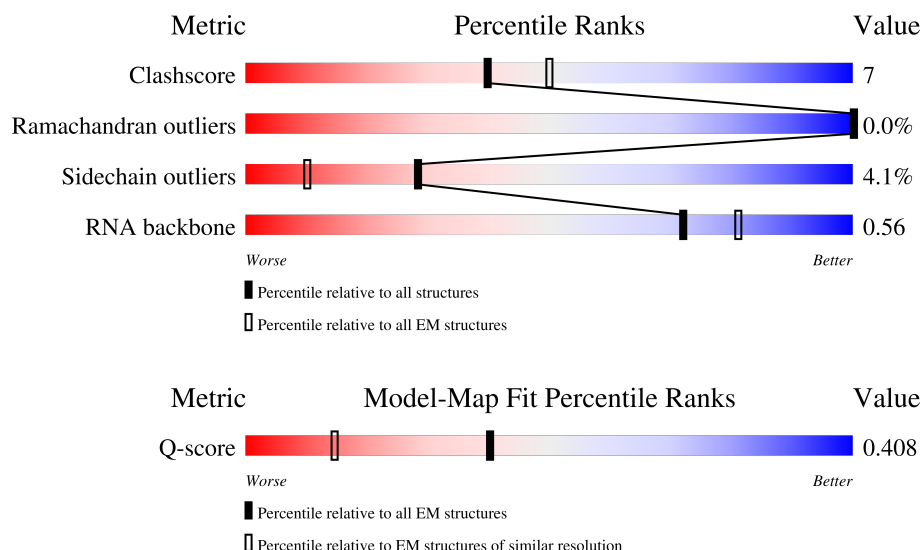
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.90 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	13054 (2.40 - 3.40)

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	IF	442	
2	BB	217	
3	S2	221	

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Mol	Chain	Length	Quality of chain
4	PP	83	
5	DD	151	
6	58	156	
7	6	120	
8	L8	248	
9	L3	394	
10	L4	362	
11	L5	293	
12	L6	291	
13	L7	225	
14	aa	240	
15	10	213	
16	13	210	
17	14	138	
18	15	203	
19	bb	199	
20	17	153	
21	19	180	
22	20	176	
23	21	159	
24	22	99	
25	cc	118	
26	26	134	
27	27	135	
28	dd	147	

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Mol	Chain	Length	Quality of chain
29	29	245	
30	30	98	
31	31	107	
32	32	128	
33	ee	109	
34	34	114	
35	35	122	
36	36	102	
37	37	86	
38	38	69	
39	39	50	
40	40	52	
41	41	25	
42	42	104	
43	ff	91	
44	gg	124	
45	AS	213	
46	FF	149	
47	VV	83	
48	s	196	
49	t	153	
50	F	358	
51	Q	188	
52	ZZ	68	
53	EE	132	

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Mol	Chain	Length	Quality of chain
54	TT	75	
55	S5	191	
56	WW	62	
57	II	142	
58	CC	96	
59	AA	313	
60	OO	100	
61	MM	141	
62	LL	144	
63	XX	55	
64	RR	141	
65	SS	124	
66	S6	237	
67	S4	262	
68	S9	185	
69	S7	189	
70	YY	55	
71	S3	214	
72	RS	132	
73	WX	129	
74	S8	206	
75	W	121	
76	GG	135	
77	UU	101	
78	11	170	

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Mol	Chain	Length	Quality of chain
79	L9	190	
80	18	1698	
81	v	857	
82	LA	1096	
83	A	121	
84	ES	5070	
85	28	4808	
86	23	139	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 224036 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called IFRD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	IF	346	Total	C	N	O	S	0	0
			2692	1702	484	493	13		

- Molecule 2 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 3 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S2	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 4 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	PP	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 5 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DD	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 7 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L4	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L5	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 13 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 14 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 15 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	17	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 22 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 24 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 28 is a protein called 60S ribosomal protein L27a.

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

- Molecule 29 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 32 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 33 is a protein called Large ribosomal subunit protein eL33.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 38 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 41 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 42 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	42	102	Total	C	N	O	S	0	0
			834	522	171	135	6		

- Molecule 43 is a protein called 60S ribosomal protein L37a.

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

- Molecule 44 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	gg	124	Total	C	N	O	S	0	0
			990	615	202	167	6		

- Molecule 45 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AS	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 46 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	FF	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 47 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	VV	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 49 is a protein called uL11.

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

- Molecule 50 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	358	Total	C	N	O	S	0	0
			2798	1762	482	537	17		

- Molecule 51 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 52 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	ZZ	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 53 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	EE	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 54 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	TT	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 55 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S5	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	WW	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 57 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	II	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 58 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CC	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 59 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AA	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 60 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	OO	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 61 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	MM	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 62 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LL	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 63 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	XX	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 64 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RR	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SS	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 66 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	S6	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 67 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	S4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 68 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S9	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 69 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	S7	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 70 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	YY	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 71 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	S3	214	Total	C	N	O	S	0	0
			1662	1060	302	292	8		

- Molecule 72 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	RS	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	WX	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S8	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 75 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 76 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	GG	135	Total	C	N	O	S	0	0
			1007	615	198	188	6		

- Molecule 77 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	UU	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 78 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 79 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	L9	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 80 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	18	1688	Total	C	N	O	P	0	0
			36043	16088	6476	11792	1687		

- Molecule 81 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	829	Total	C	N	O	S	0	0
			6470	4114	1108	1205	43		

- Molecule 82 is a protein called LARP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	LA	51	Total	C	N	O	S	0	0
			421	264	74	82	1		

- Molecule 83 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A	121	Total	C	N	O	S	0	0
			983	622	184	170	7		

- Molecule 84 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ES	35	Total	C	N	O	P	0	0
			756	335	142	244	35		

- Molecule 85 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	28	3502	Total	C	N	O	P	0	0
			75105	33448	13761	24394	3502		

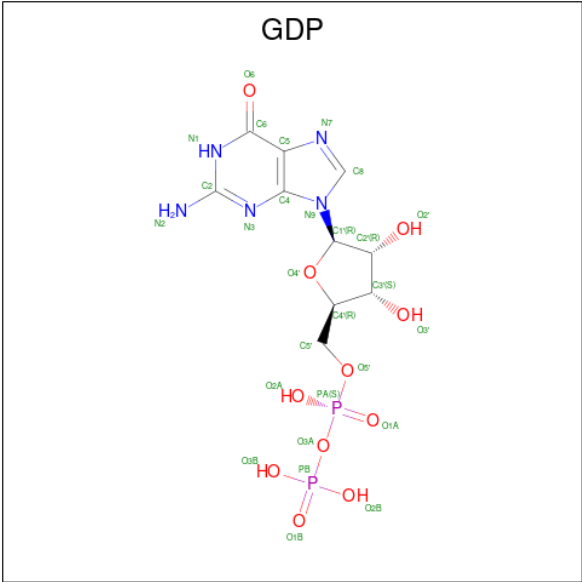
- Molecule 86 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	23	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	34	1	Total	Zn	0
			1	1	
87	37	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	
87	UU	1	Total	Zn	0
			1	1	

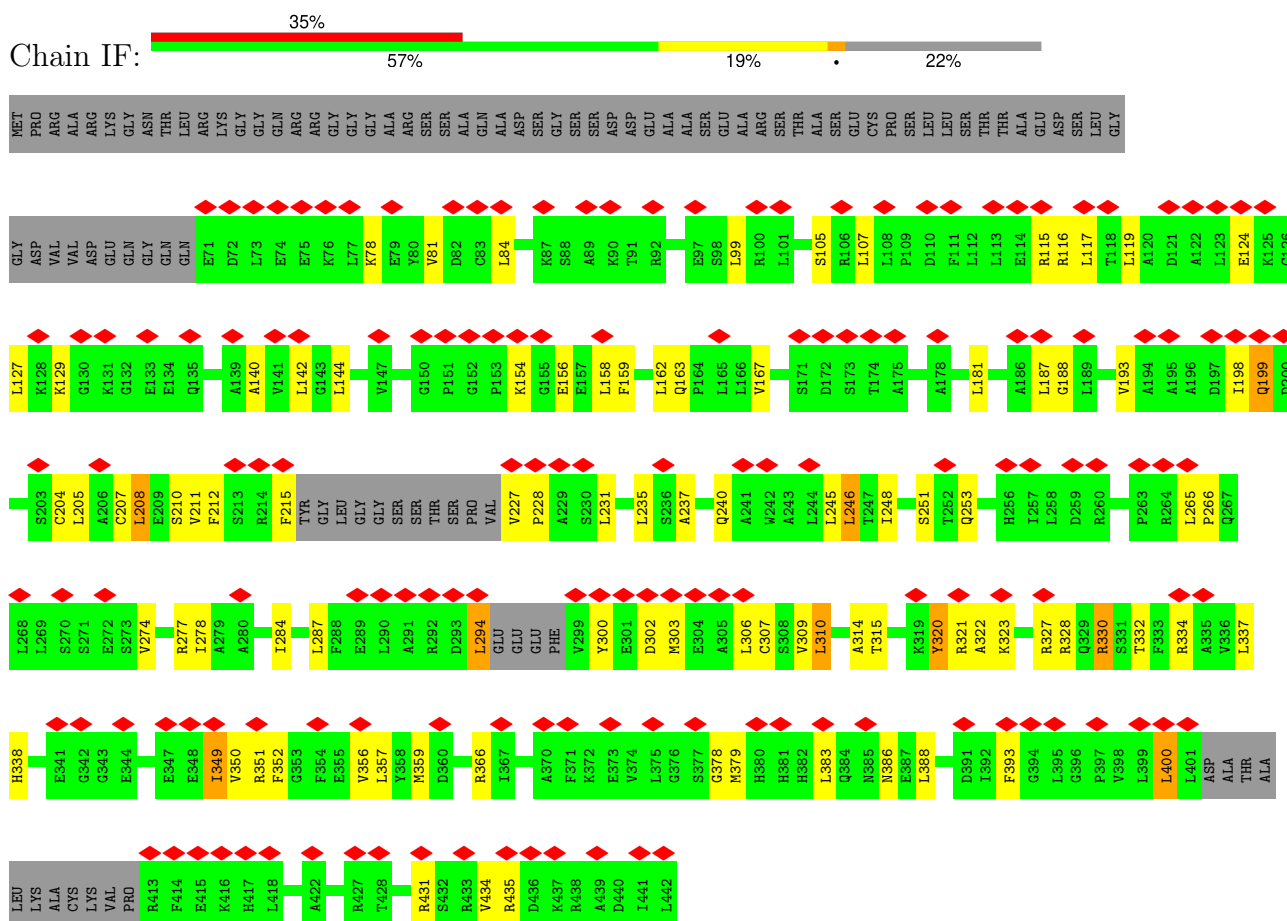
- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



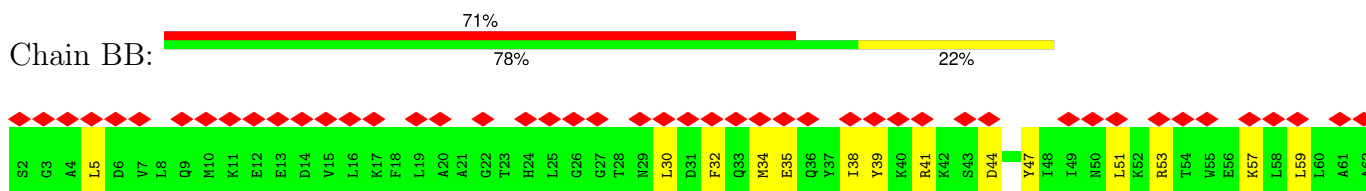
3 Residue-property plots

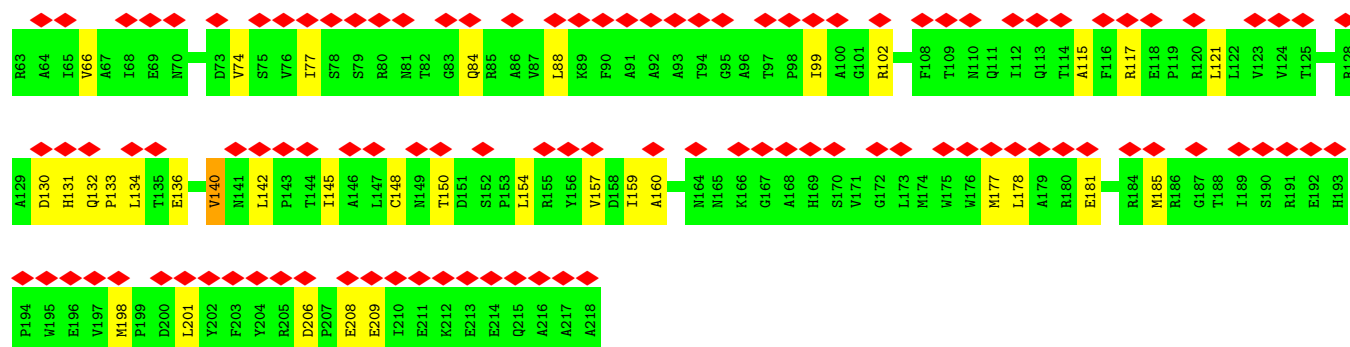
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: IFRD2

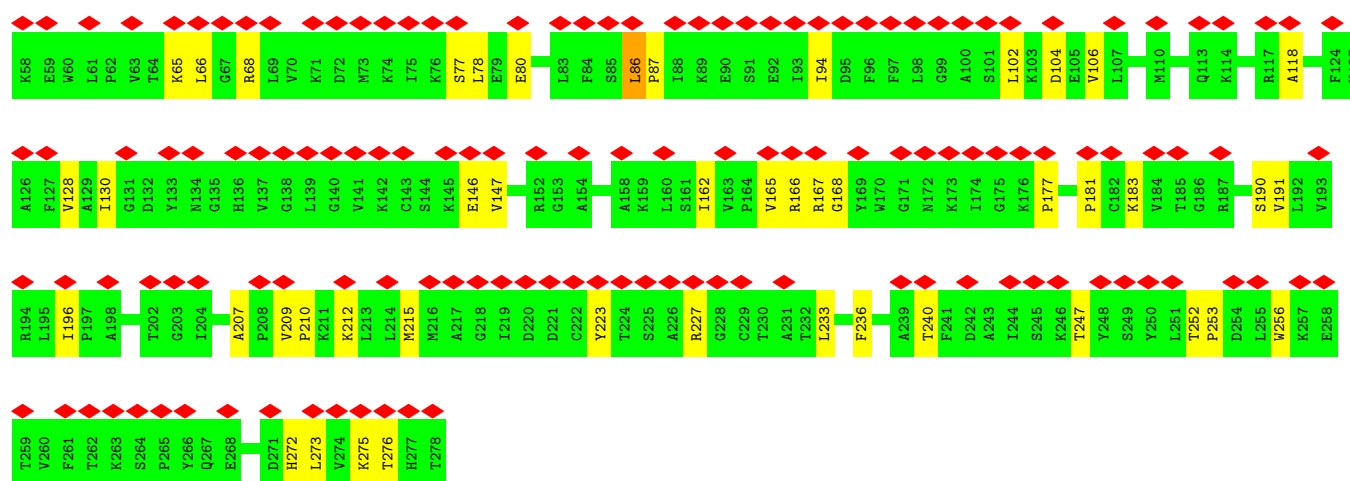
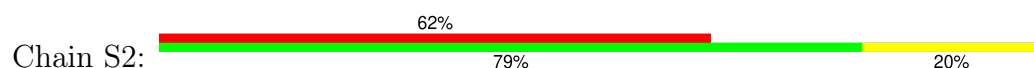


• Molecule 2: 40S_SA_C domain-containing protein

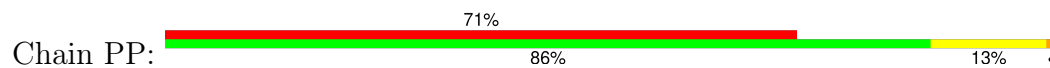




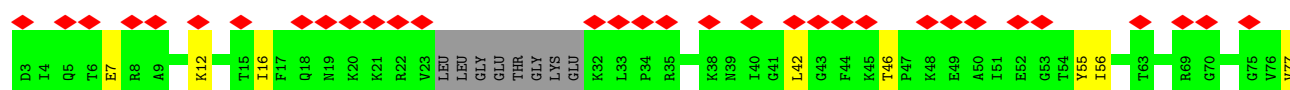
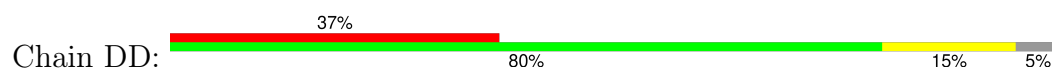
• Molecule 3: 40S ribosomal protein S2

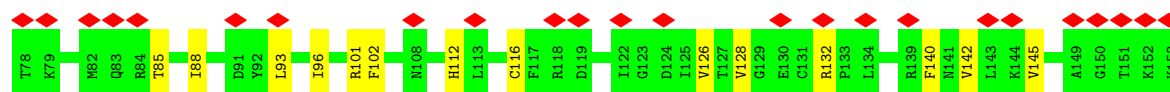


• Molecule 4: eS21

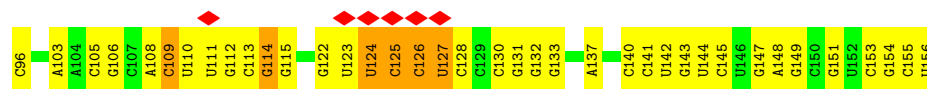


• Molecule 5: Small ribosomal subunit protein uS17





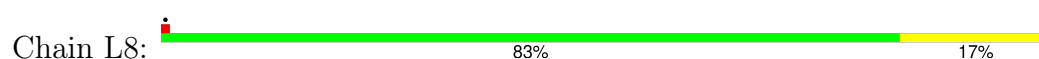
• Molecule 6: 5.8S rRNA



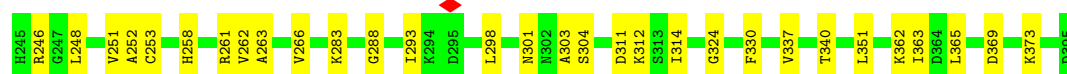
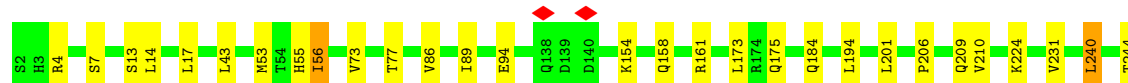
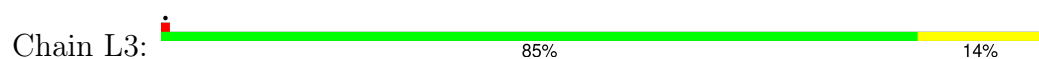
• Molecule 7: 5S rRNA



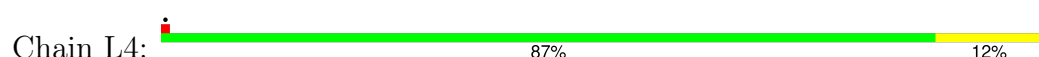
• Molecule 8: 60S ribosomal protein L8

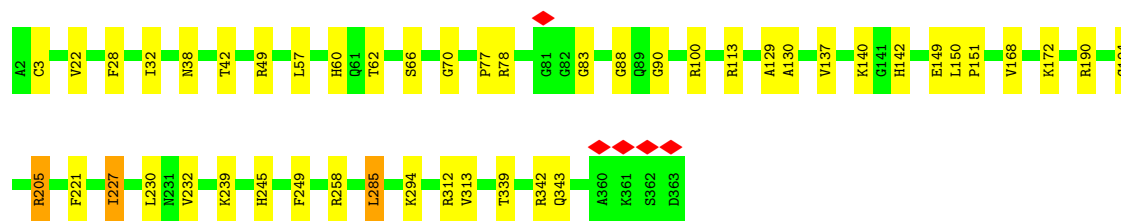


• Molecule 9: 60S ribosomal protein L3

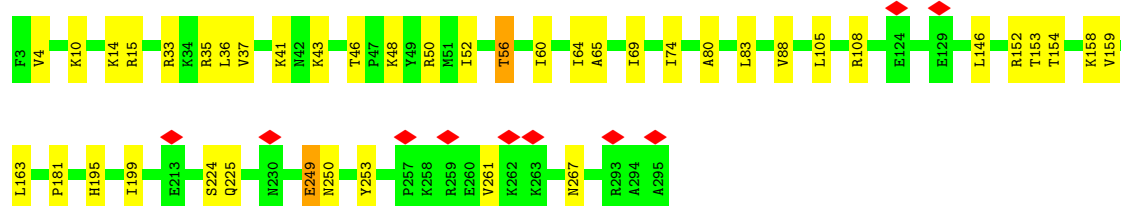
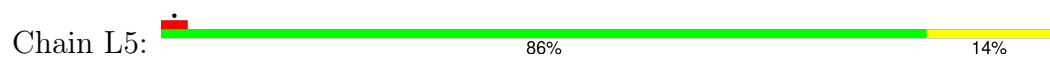


• Molecule 10: 60S ribosomal protein L4

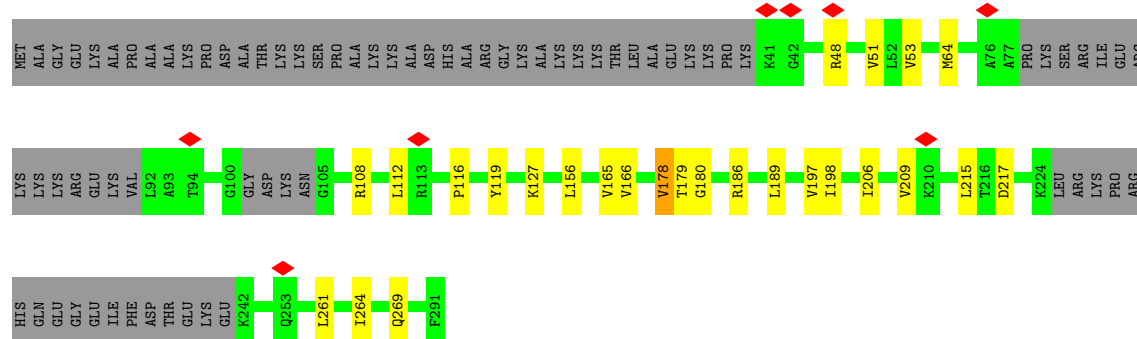




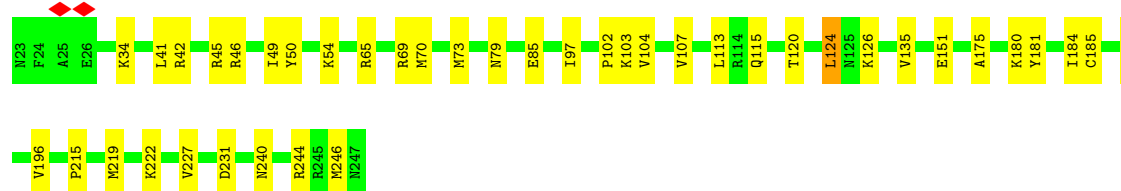
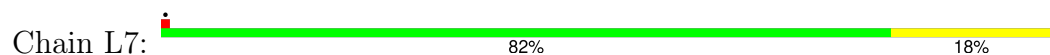
• Molecule 11: 60S ribosomal protein L5



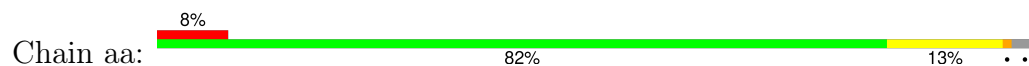
• Molecule 12: 60S ribosomal protein L6

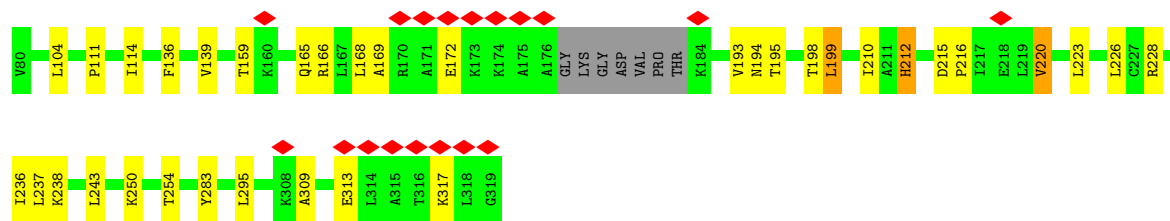


• Molecule 13: 60S ribosomal protein L7

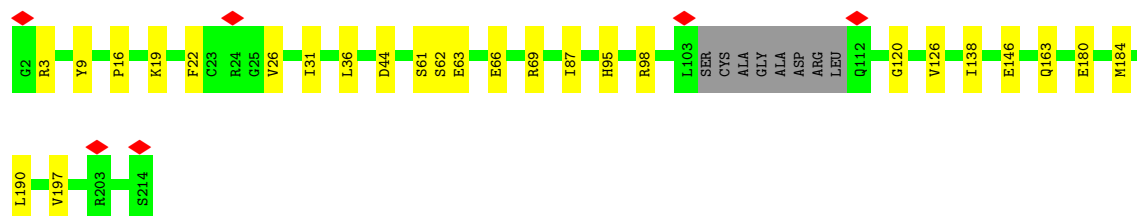
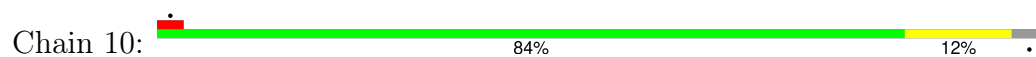


• Molecule 14: Large ribosomal subunit protein eL8

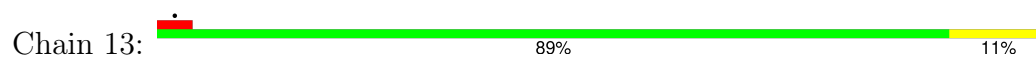




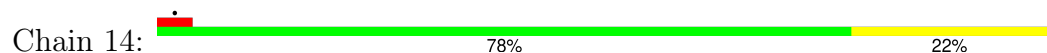
• Molecule 15: Ribosomal protein L10



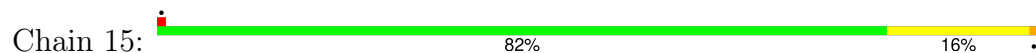
• Molecule 16: Large ribosomal subunit protein eL13



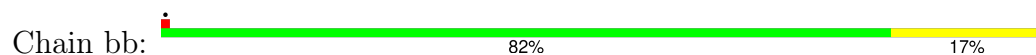
• Molecule 17: 60S ribosomal protein L14



• Molecule 18: 60S ribosomal protein L15



• Molecule 19: Large ribosomal subunit protein uL13





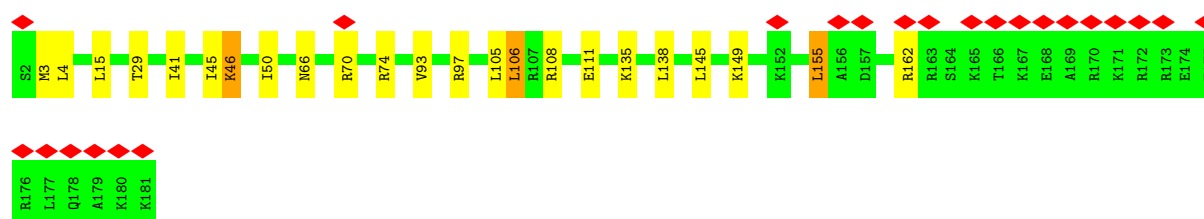
- Molecule 20: 60S ribosomal protein L17

Chain 17: 



- Molecule 21: 60S ribosomal protein L19

Chain 19: 



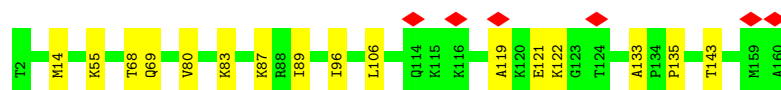
- Molecule 22: Large ribosomal subunit protein eL20

Chain 20: 



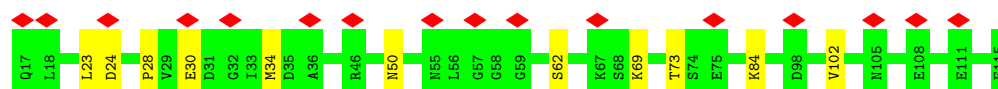
- Molecule 23: 60S ribosomal protein L21

Chain 21: 



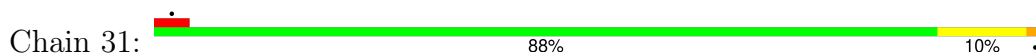
- Molecule 24: Large ribosomal subunit protein eL22

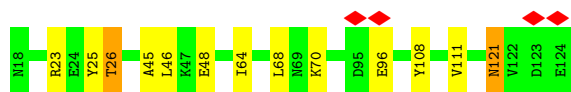
Chain 22: 



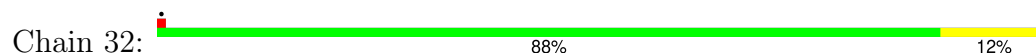
- Molecule 25: Large ribosomal subunit protein uL23

Chain cc: 

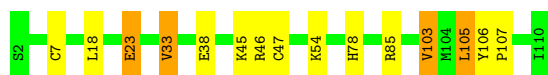




- Molecule 32: Large ribosomal subunit protein eL32



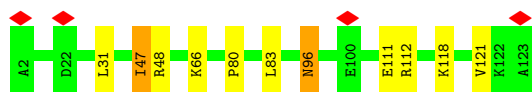
- Molecule 33: Large ribosomal subunit protein eL33



- Molecule 34: 60S ribosomal protein L34



- Molecule 35: 60S ribosomal protein L35



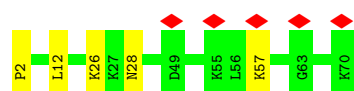
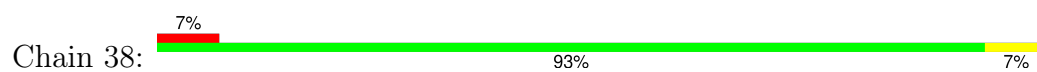
- Molecule 36: 60S ribosomal protein L36



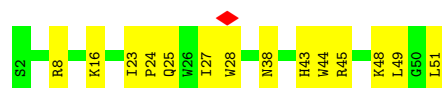
- Molecule 37: 60S ribosomal protein L37



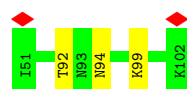
- Molecule 38: Large ribosomal subunit protein eL38



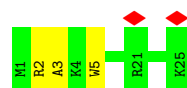
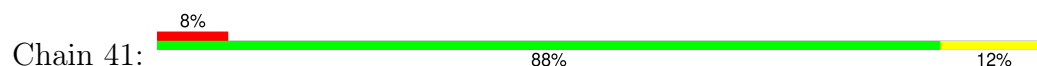
- Molecule 39: 60S ribosomal protein L39



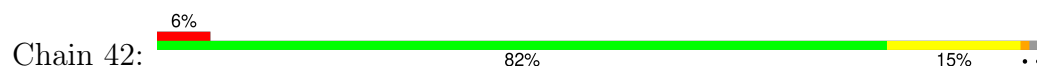
- Molecule 40: Large ribosomal subunit protein eL40



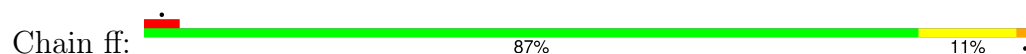
- Molecule 41: eL41



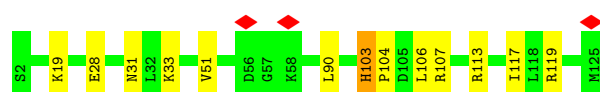
- Molecule 42: eL42



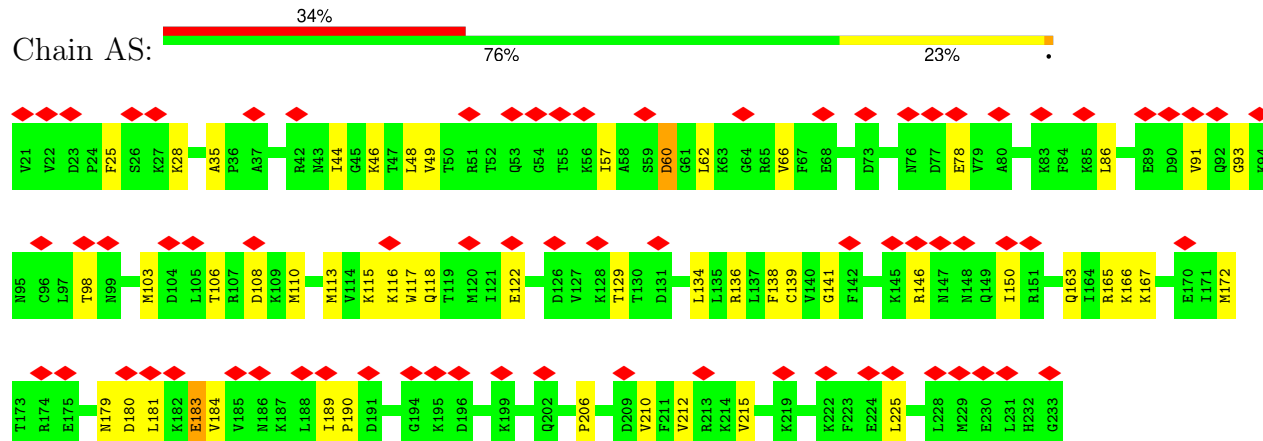
- Molecule 43: 60S ribosomal protein L37a



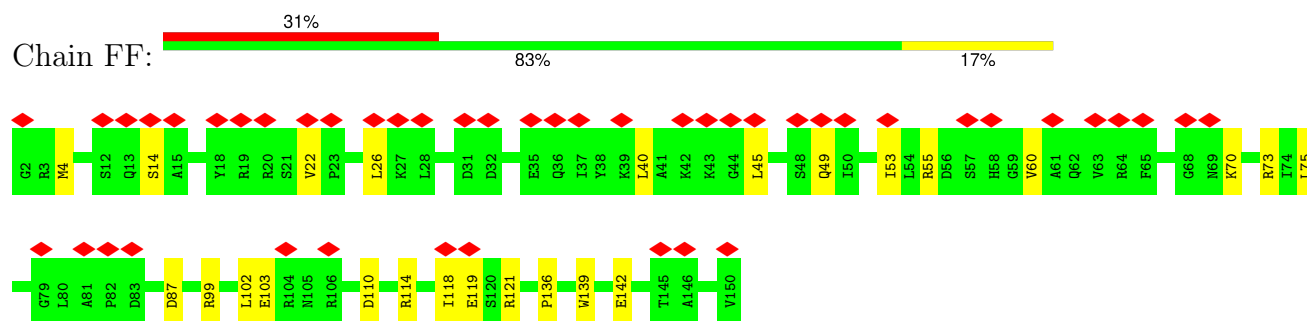
- Molecule 44: 60S ribosomal protein L28



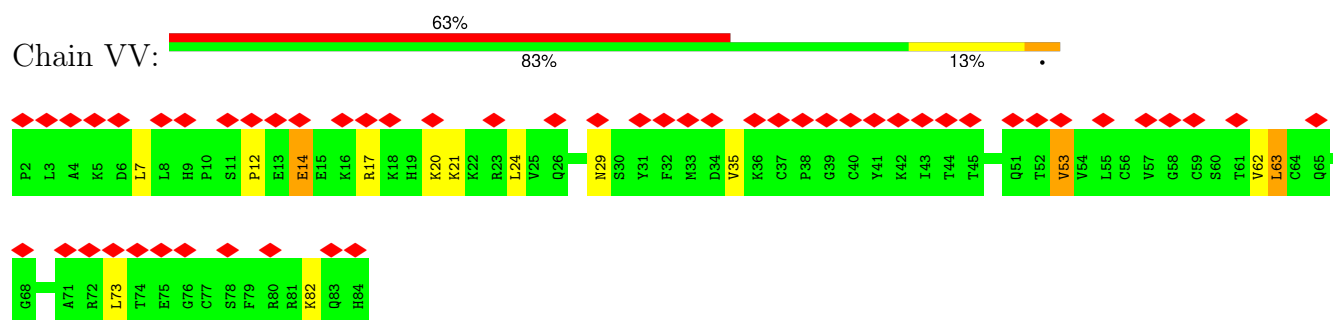
- Molecule 45: 40S ribosomal protein S3a



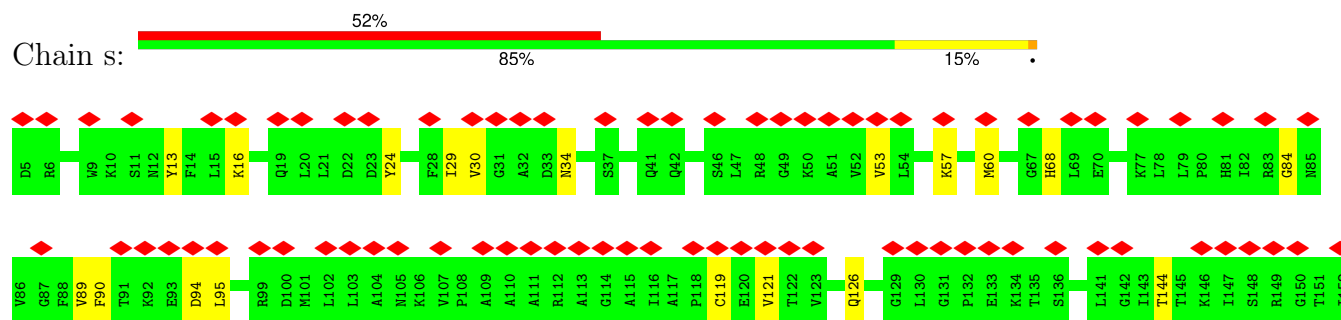
- Molecule 46: 40S ribosomal protein S13



- Molecule 47: 40S ribosomal protein S27

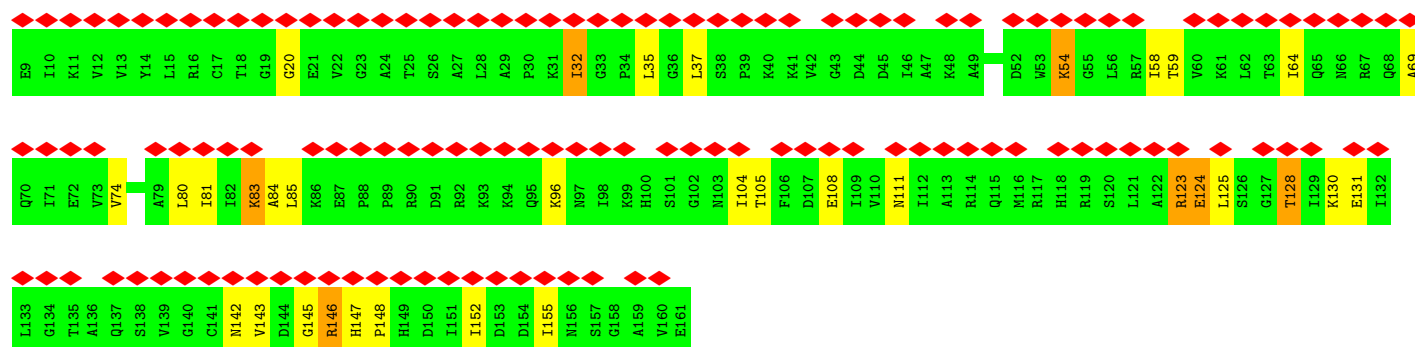
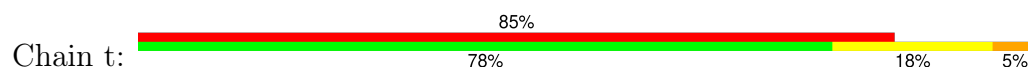


- Molecule 48: 60S acidic ribosomal protein P0

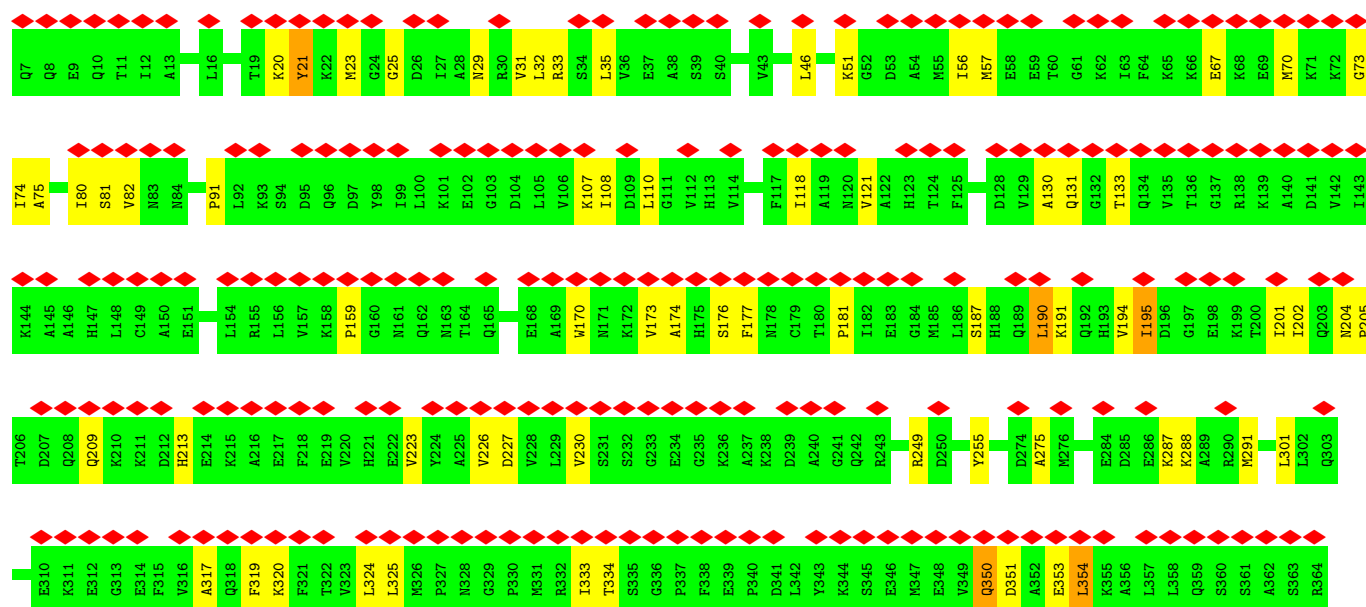
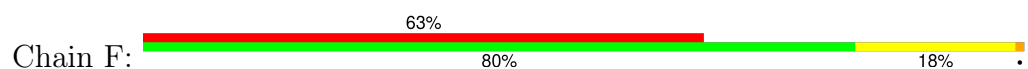




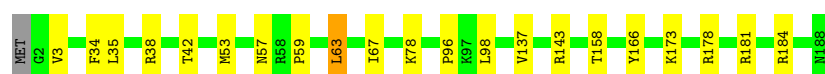
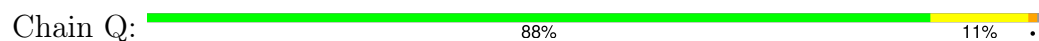
• Molecule 49: uL11



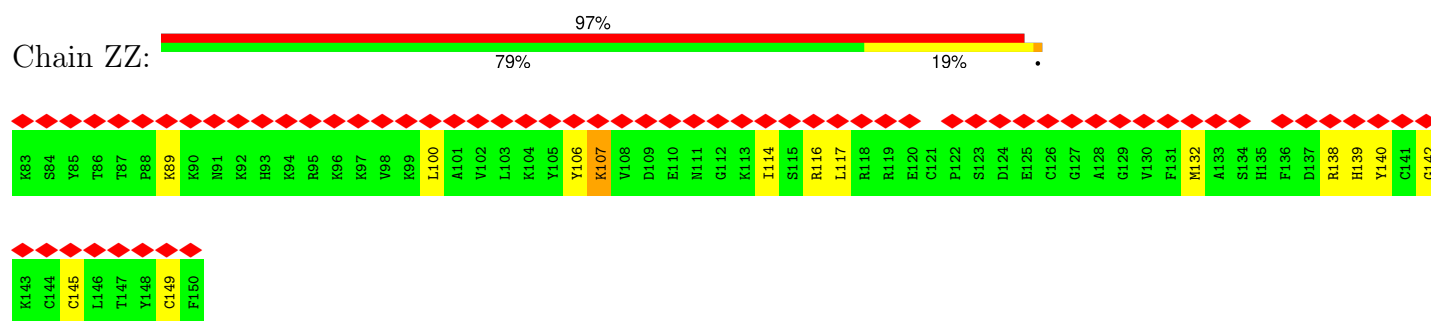
• Molecule 50: Proliferation-associated protein 2G4



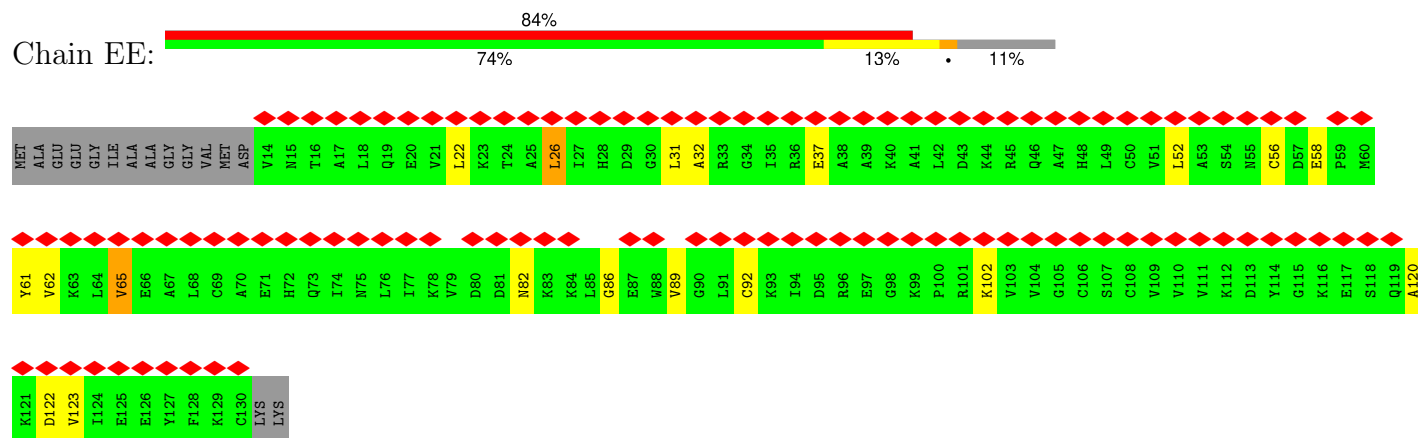
• Molecule 51: Large ribosomal subunit protein eL18



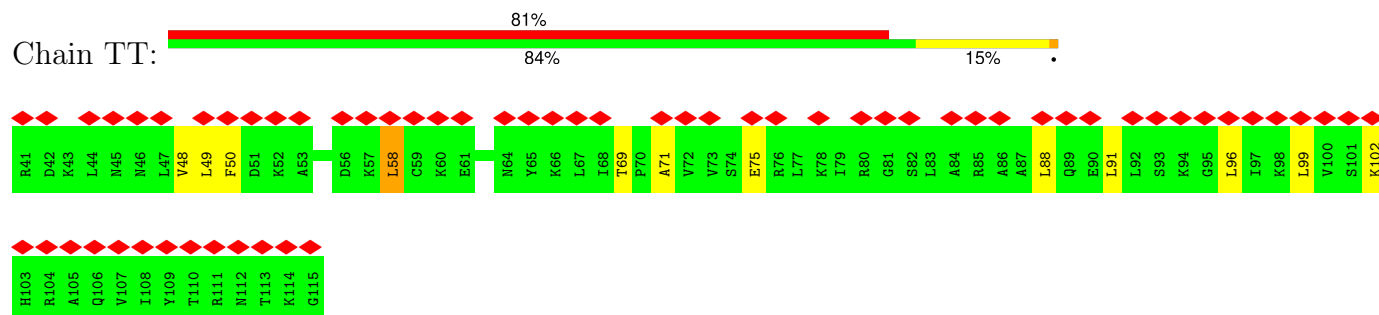
• Molecule 52: 40S ribosomal protein S27a



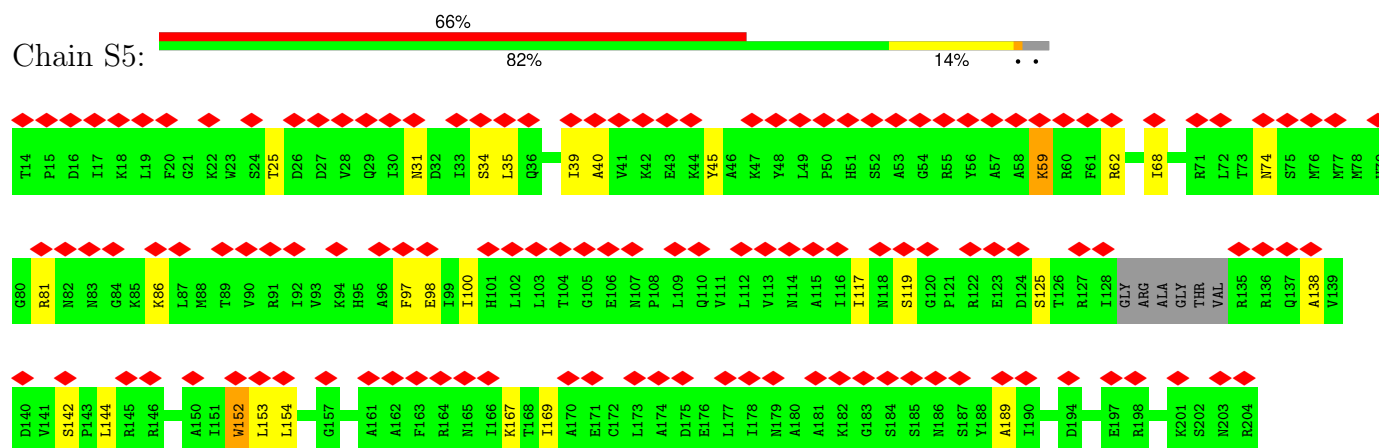
• Molecule 53: 40S ribosomal protein S12



• Molecule 54: 40S ribosomal protein S25

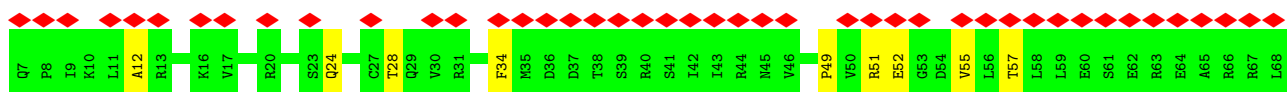


• Molecule 55: Small ribosomal subunit protein uS7



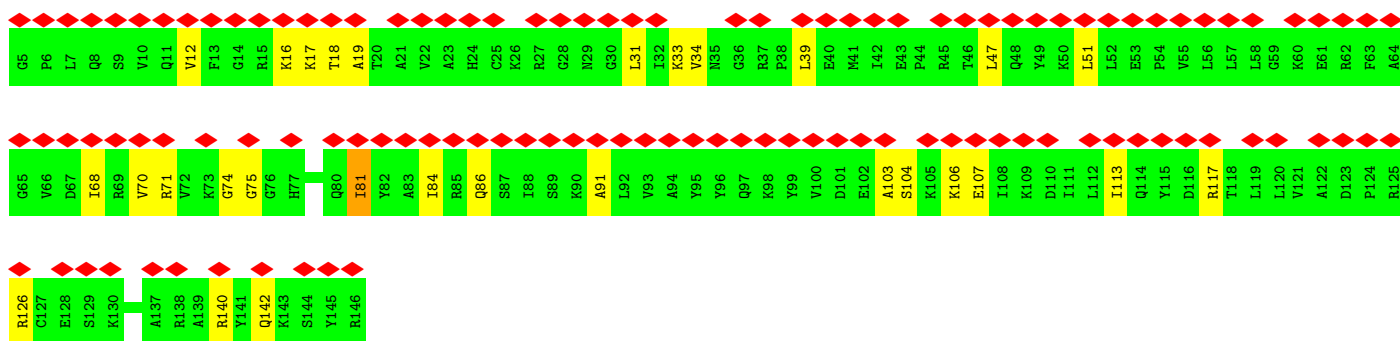
- Molecule 56: 40S ribosomal protein S28

Chain WW: 



- Molecule 57: Small ribosomal subunit protein uS9

Chain II: 

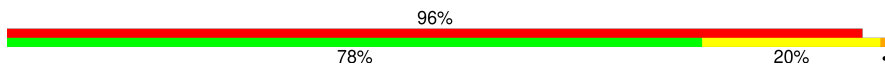


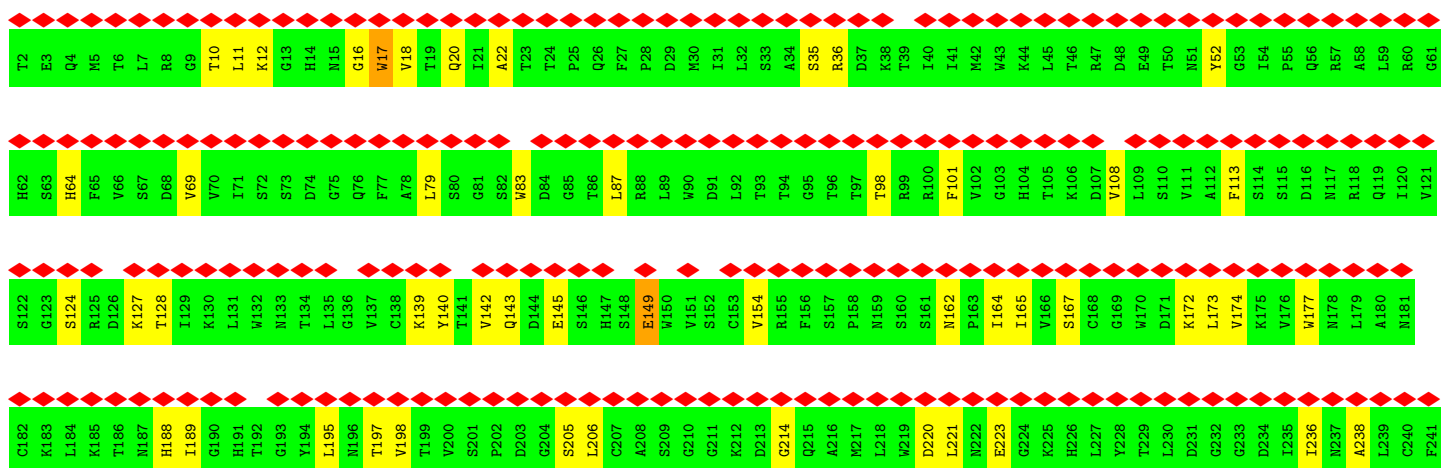
- Molecule 58: 40S ribosomal protein S10

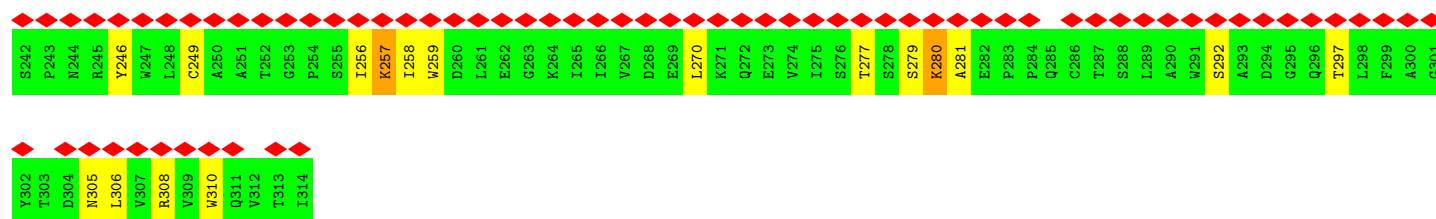
Chain CC: 



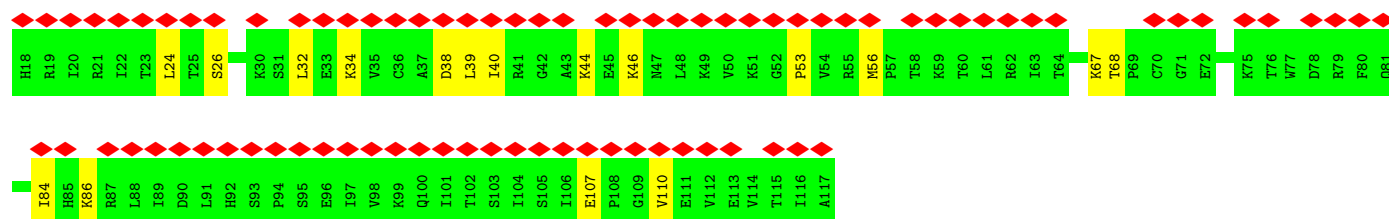
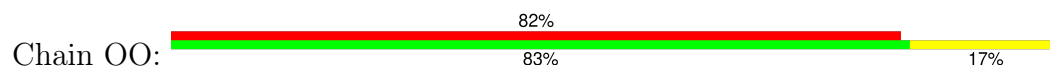
- Molecule 59: Receptor of activated protein C kinase 1

Chain AA: 

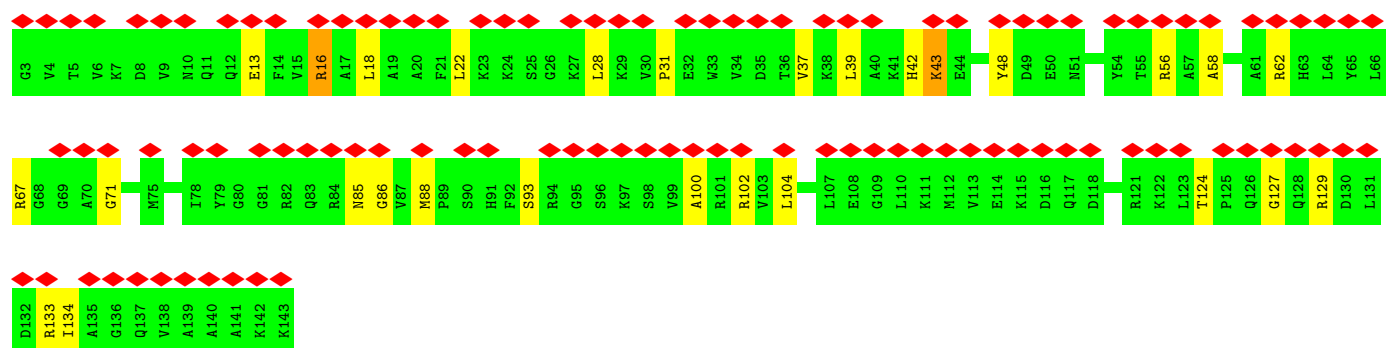
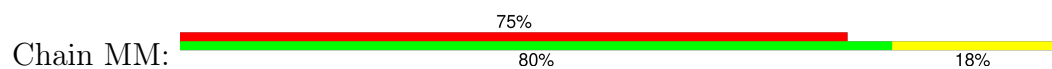




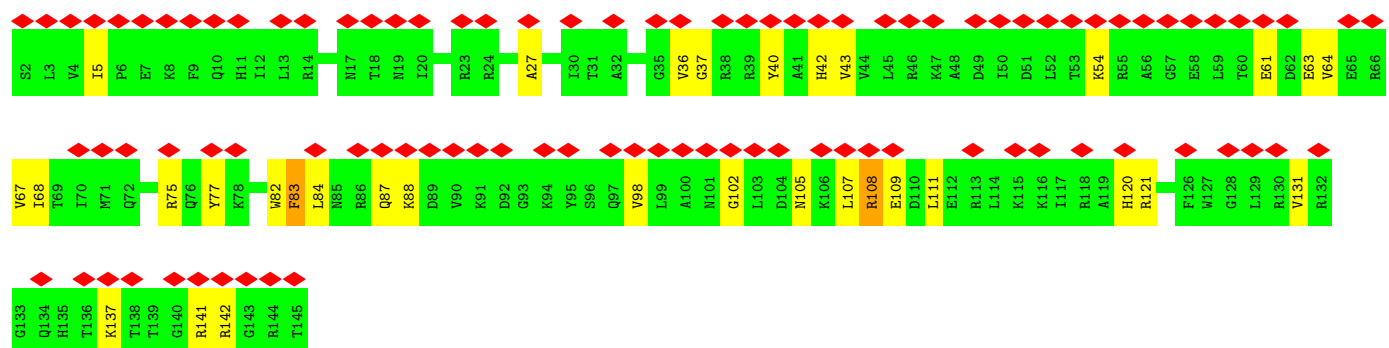
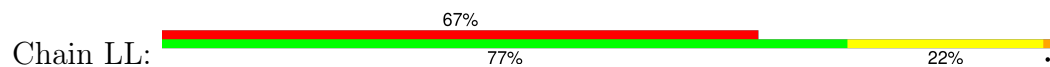
• Molecule 60: 40S ribosomal protein S20



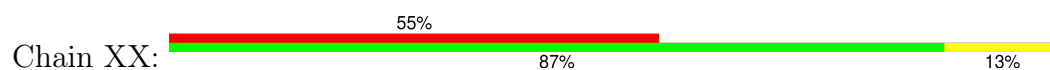
• Molecule 61: Small ribosomal subunit protein eS19



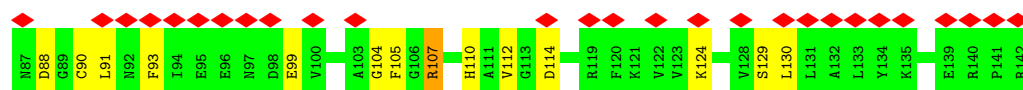
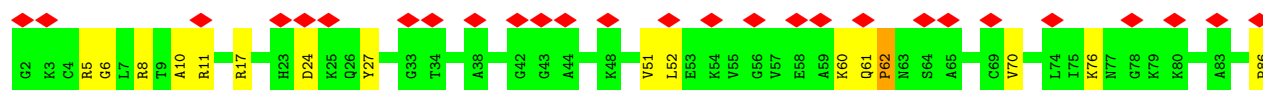
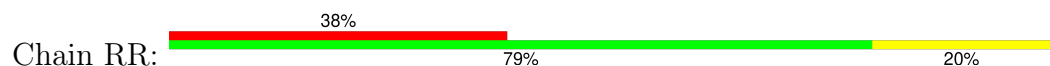
• Molecule 62: 40S ribosomal protein S18



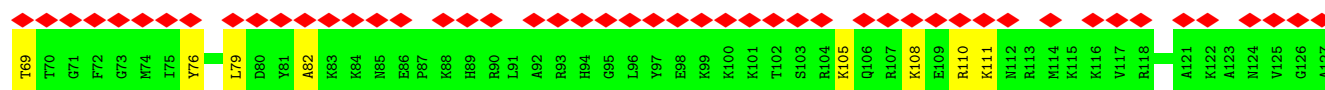
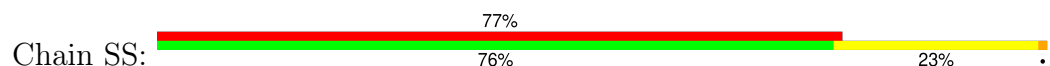
• Molecule 63: 40S ribosomal protein S29



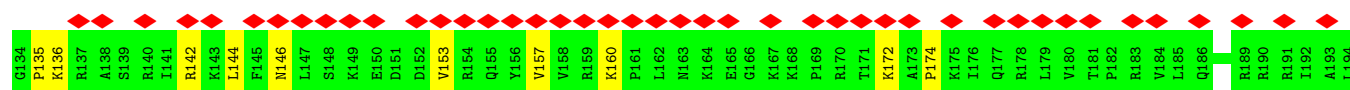
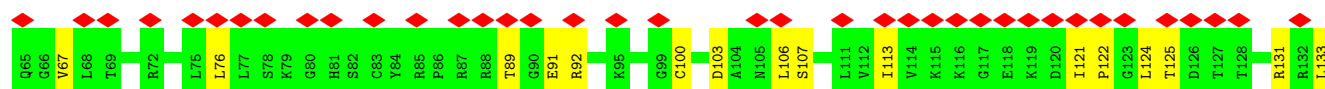
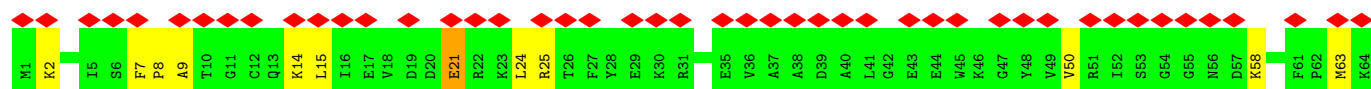
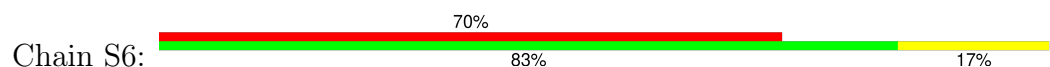
• Molecule 64: 40S ribosomal protein S23



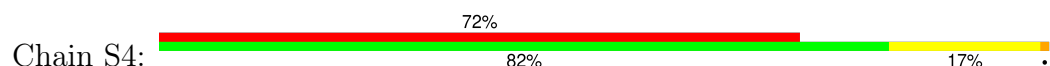
• Molecule 65: 40S ribosomal protein S24

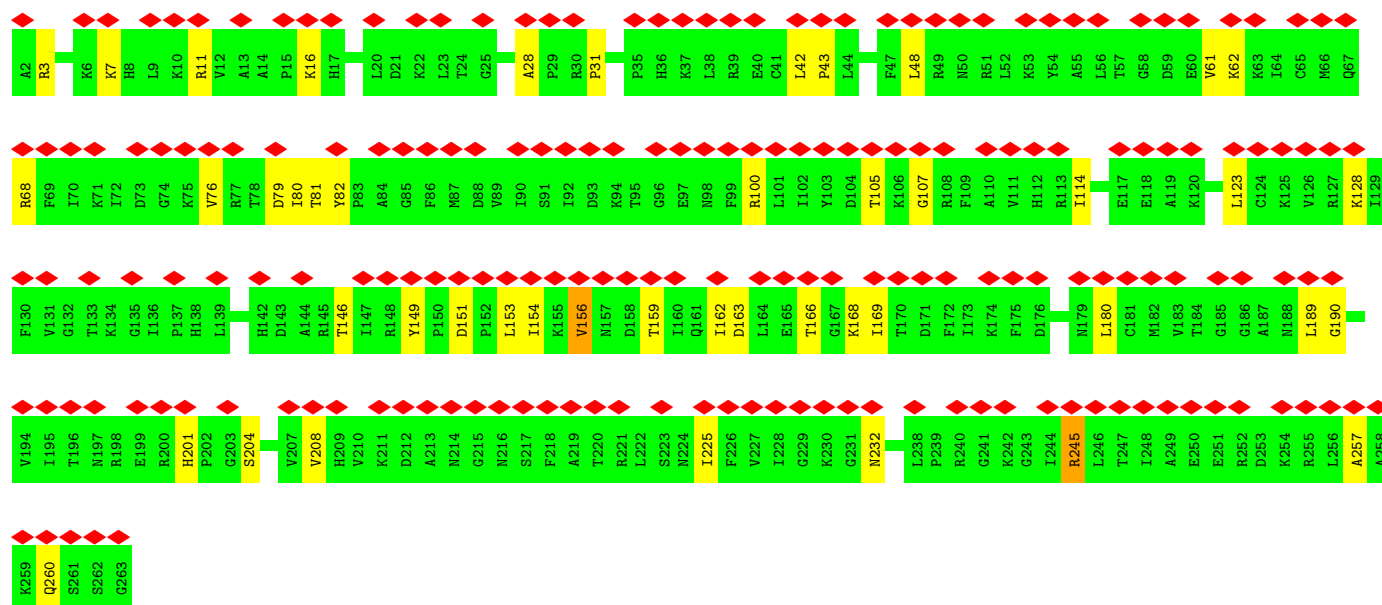


• Molecule 66: 40S ribosomal protein S6

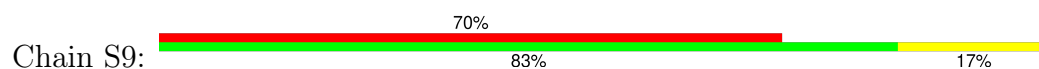


• Molecule 67: 40S ribosomal protein S4

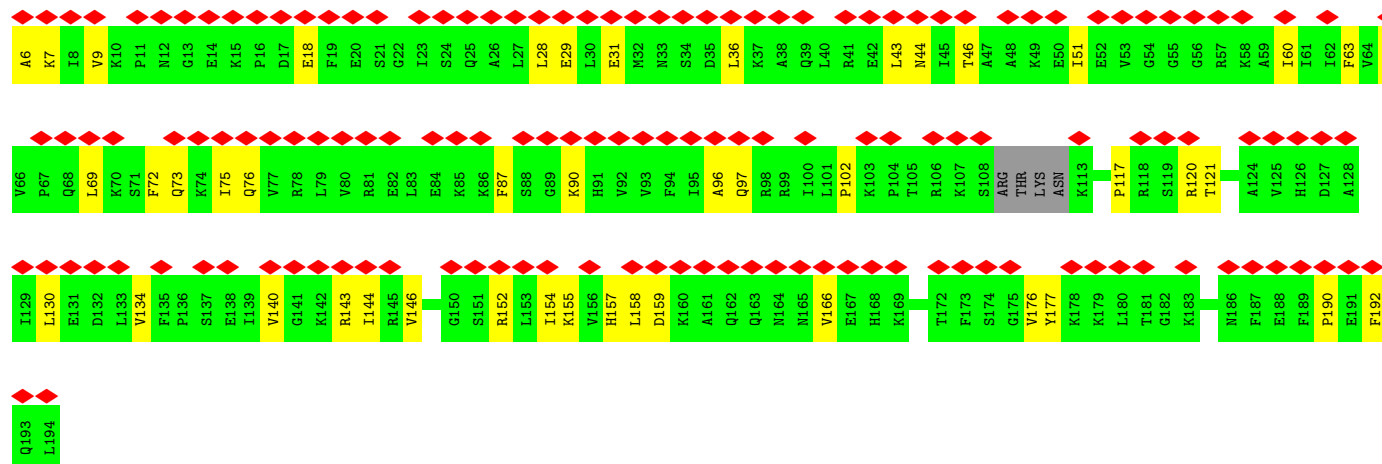
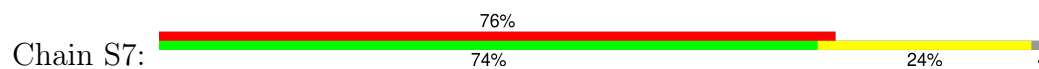




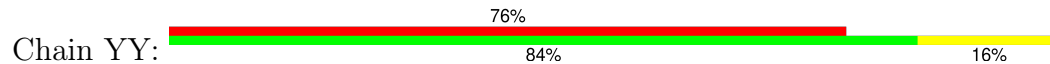
- Molecule 68: 40S ribosomal protein S9



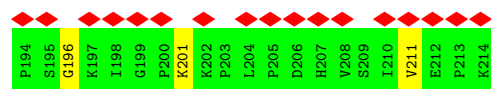
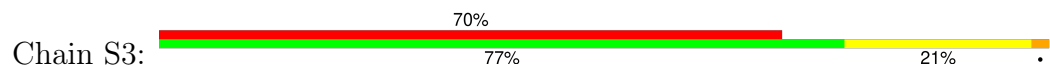
- Molecule 69: Small ribosomal subunit protein eS7



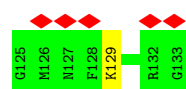
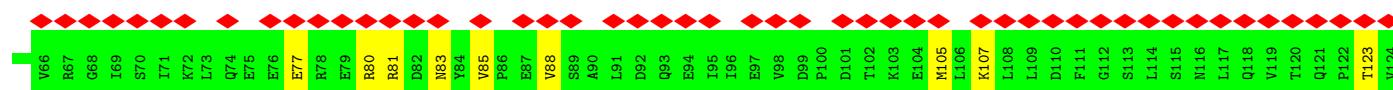
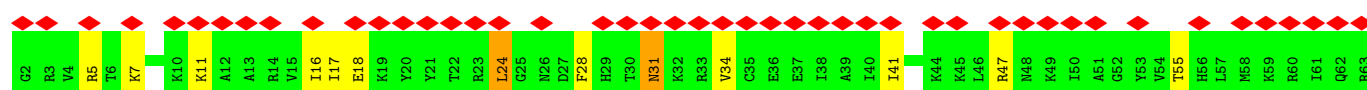
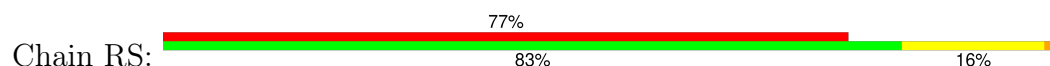
- Molecule 70: 40S ribosomal protein S30



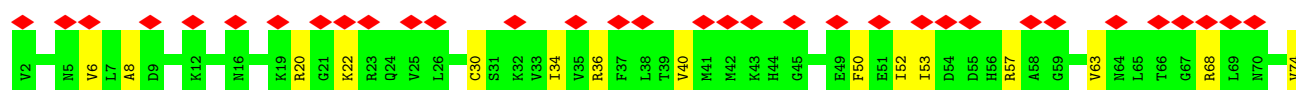
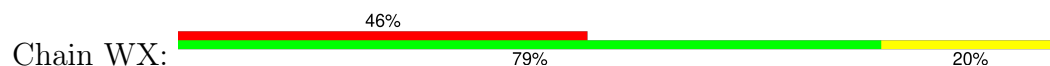
- Molecule 71: Small ribosomal subunit protein uS3

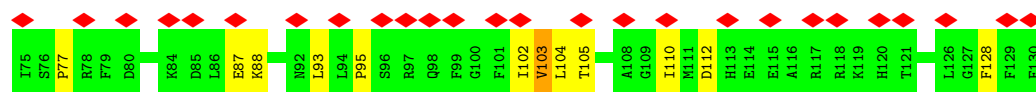


- Molecule 72: 40S ribosomal protein S17

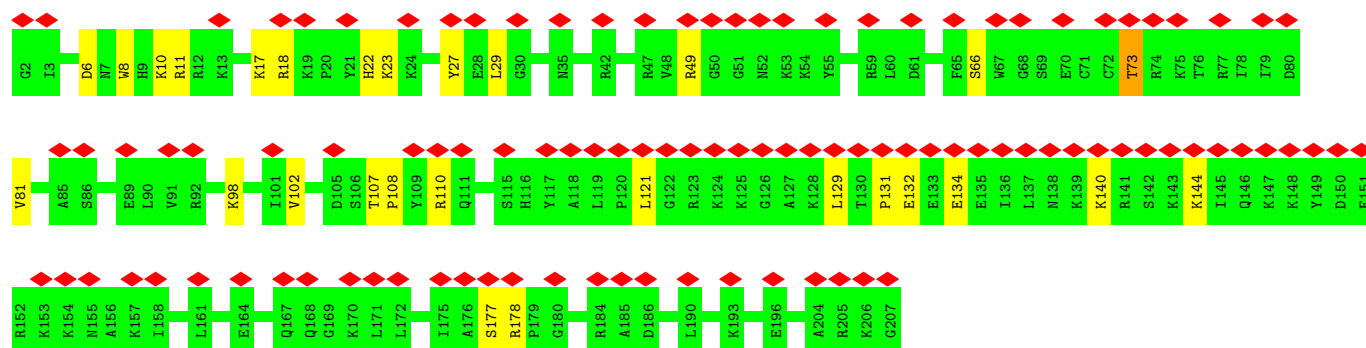
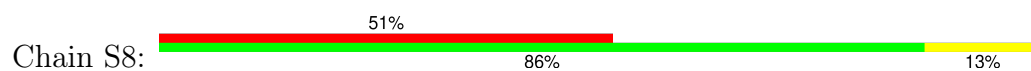


- Molecule 73: 40S ribosomal protein S15a

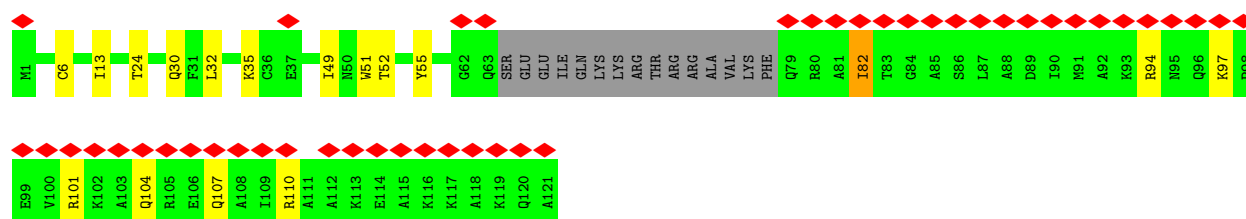
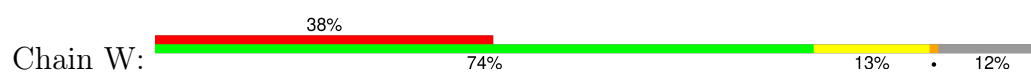




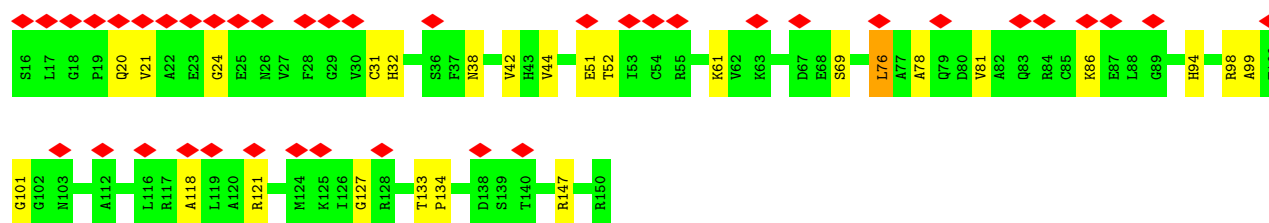
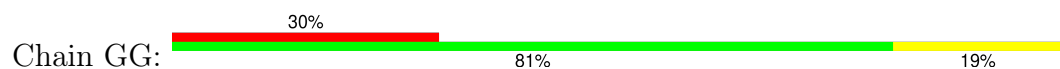
- Molecule 74: 40S ribosomal protein S8



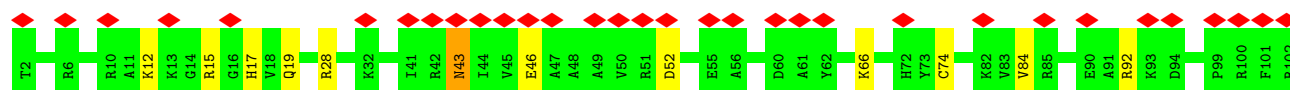
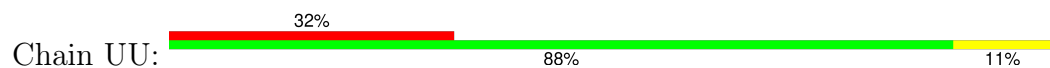
- Molecule 75: Ribosomal protein L24



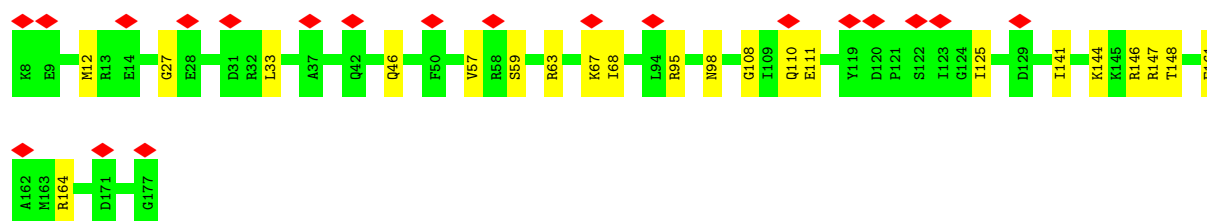
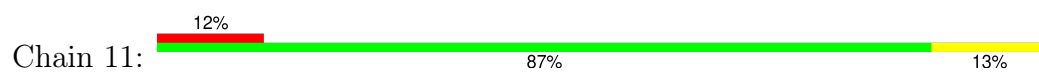
- Molecule 76: Small ribosomal subunit protein uS11



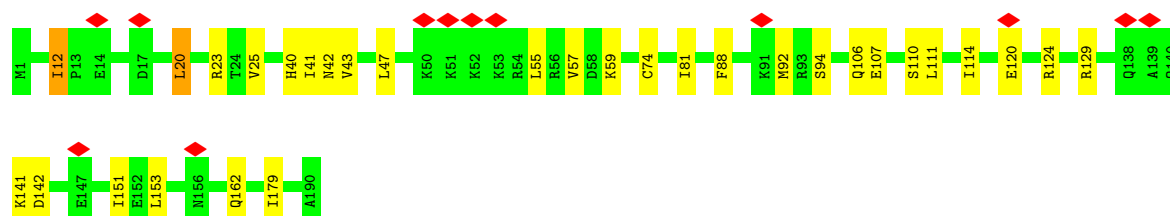
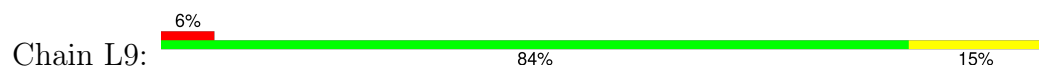
- Molecule 77: eS26



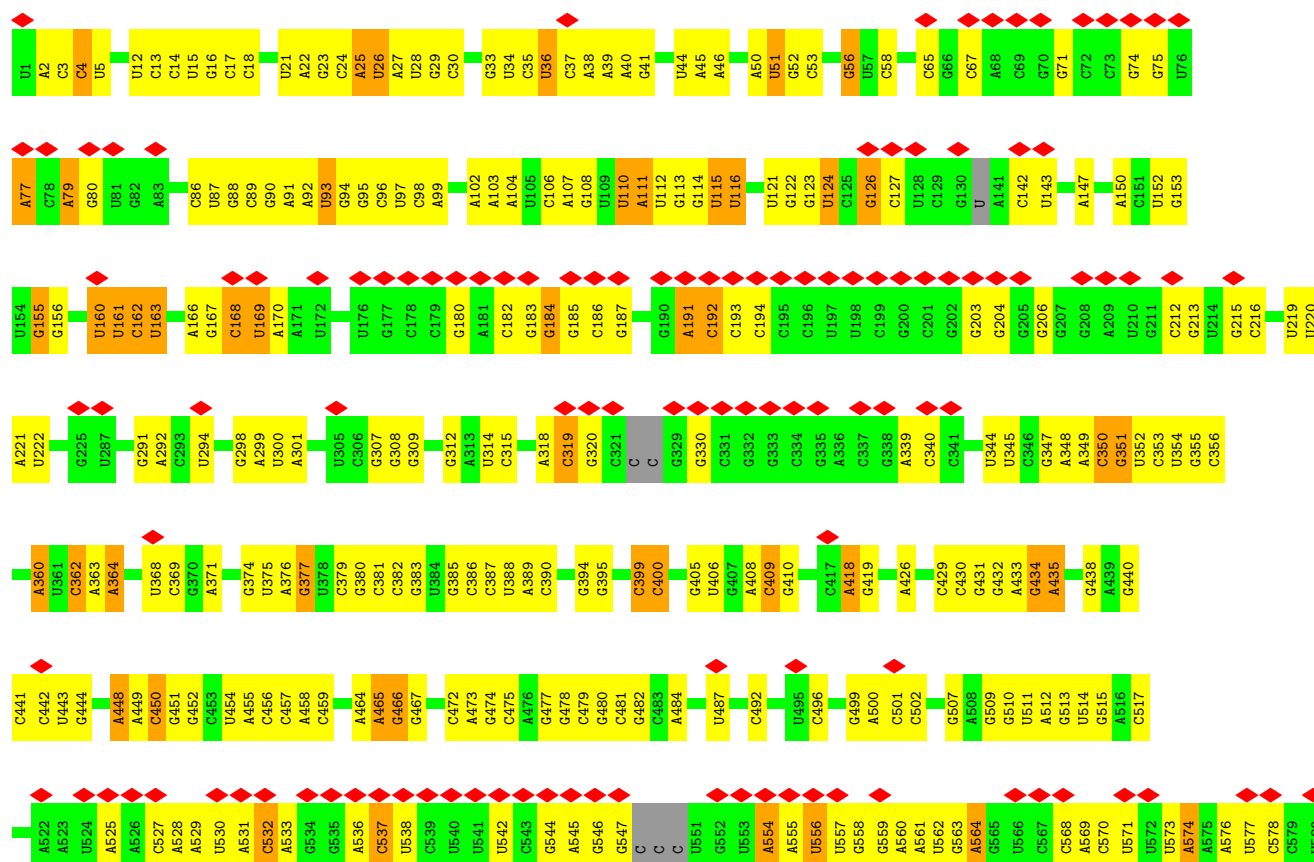
- Molecule 78: 60S ribosomal protein L11



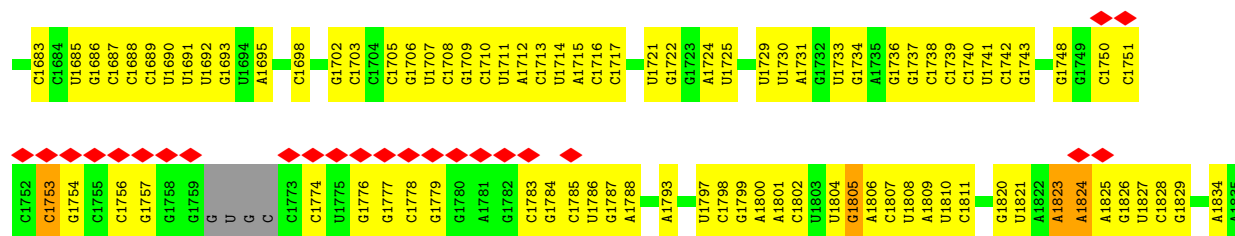
- Molecule 79: 60S ribosomal protein L9



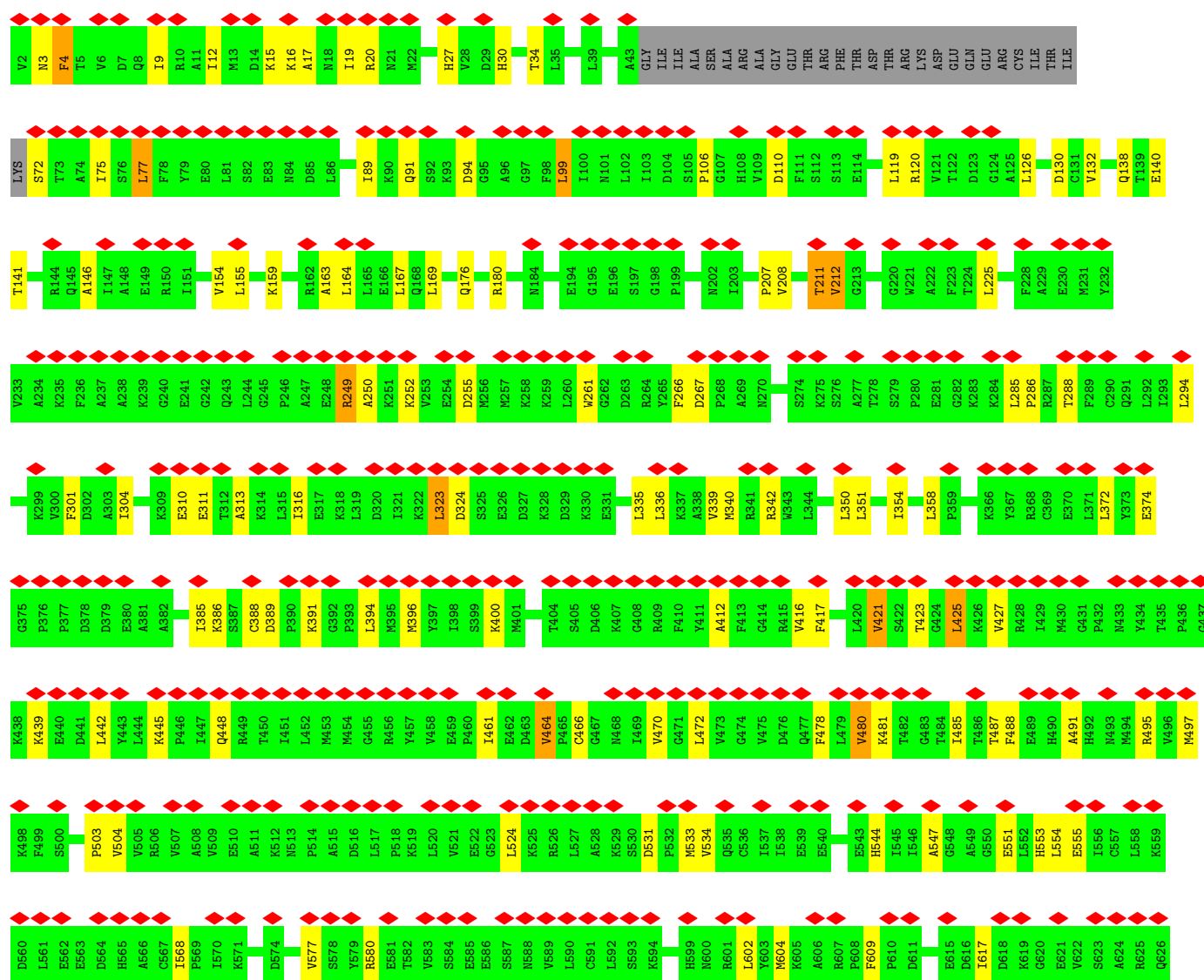
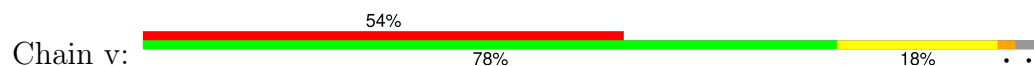
- Molecule 80: 18S rRNA

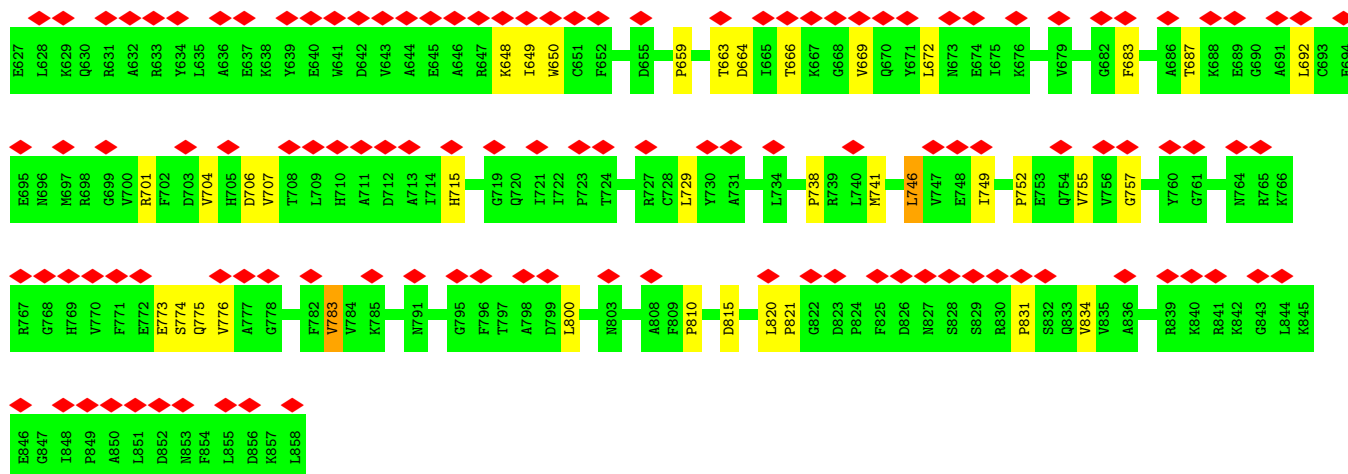






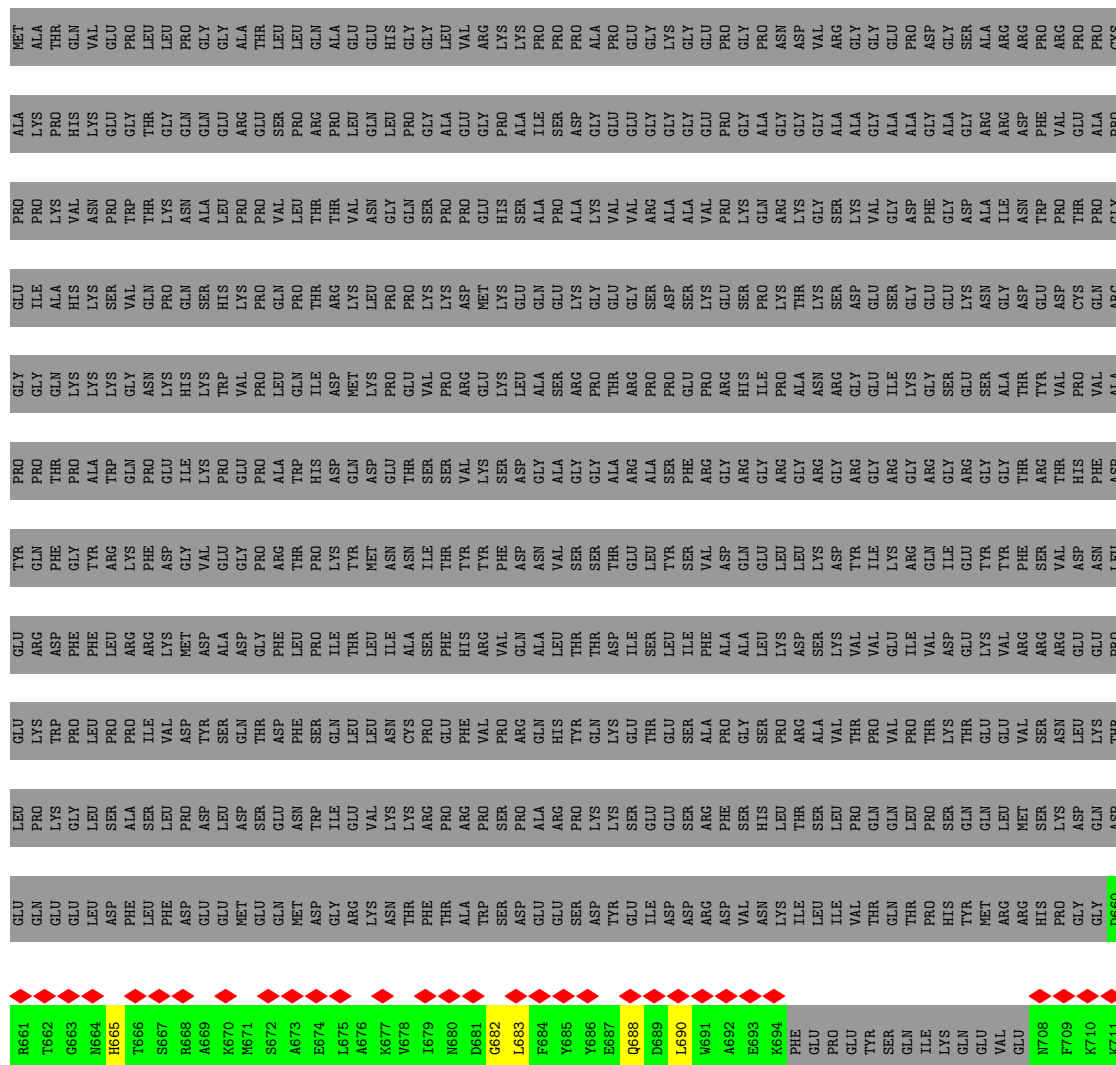
• Molecule 81: Elongation factor 2

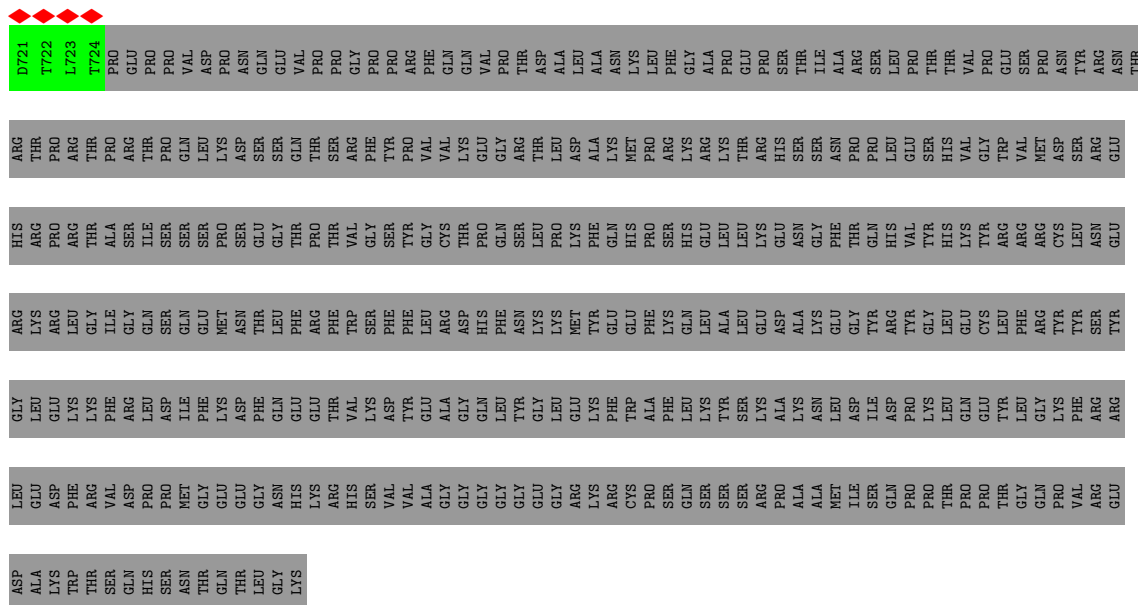




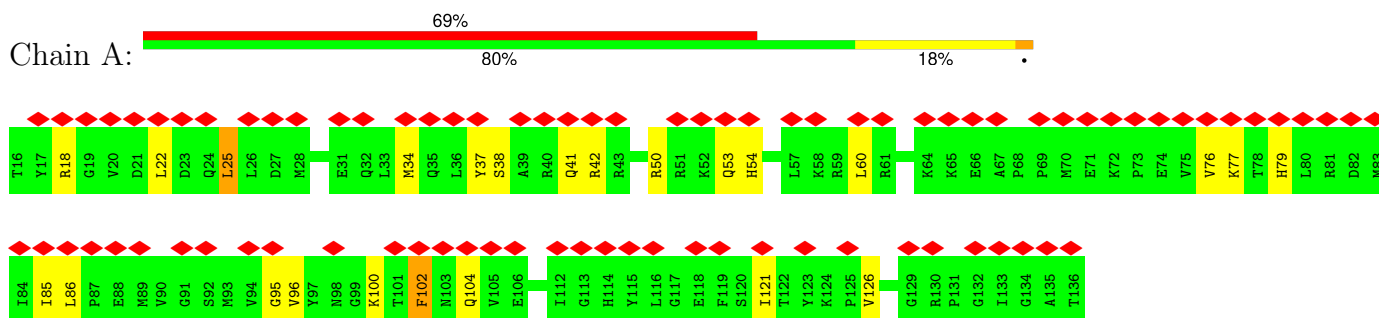
• Molecule 82: LARP1

Chain LA: 95%

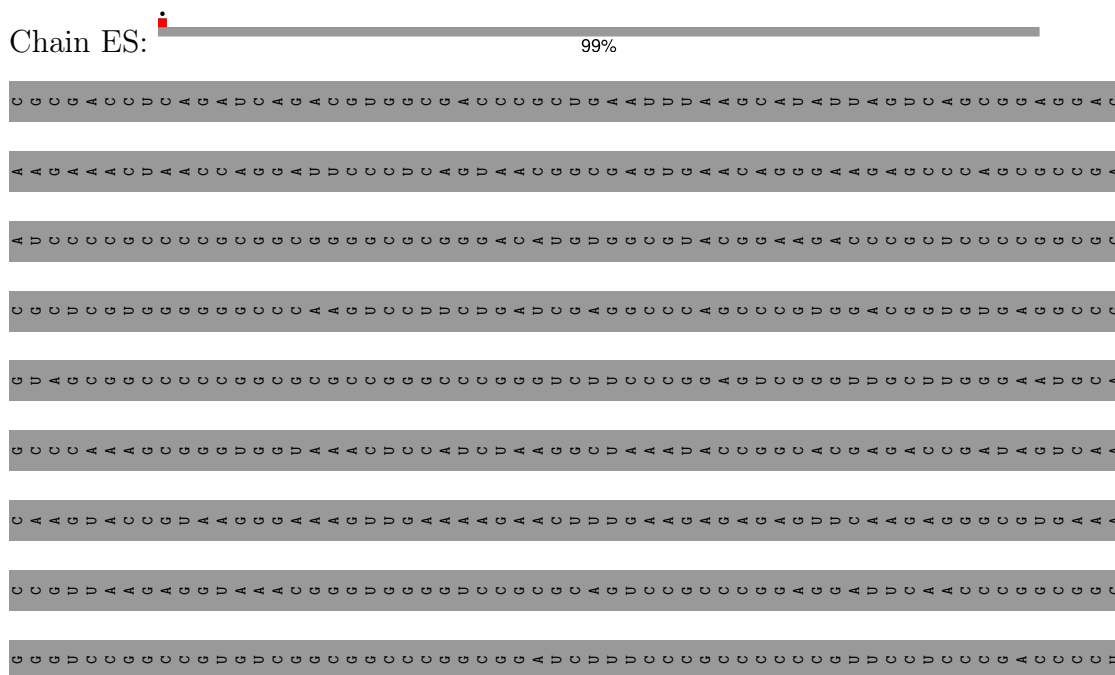




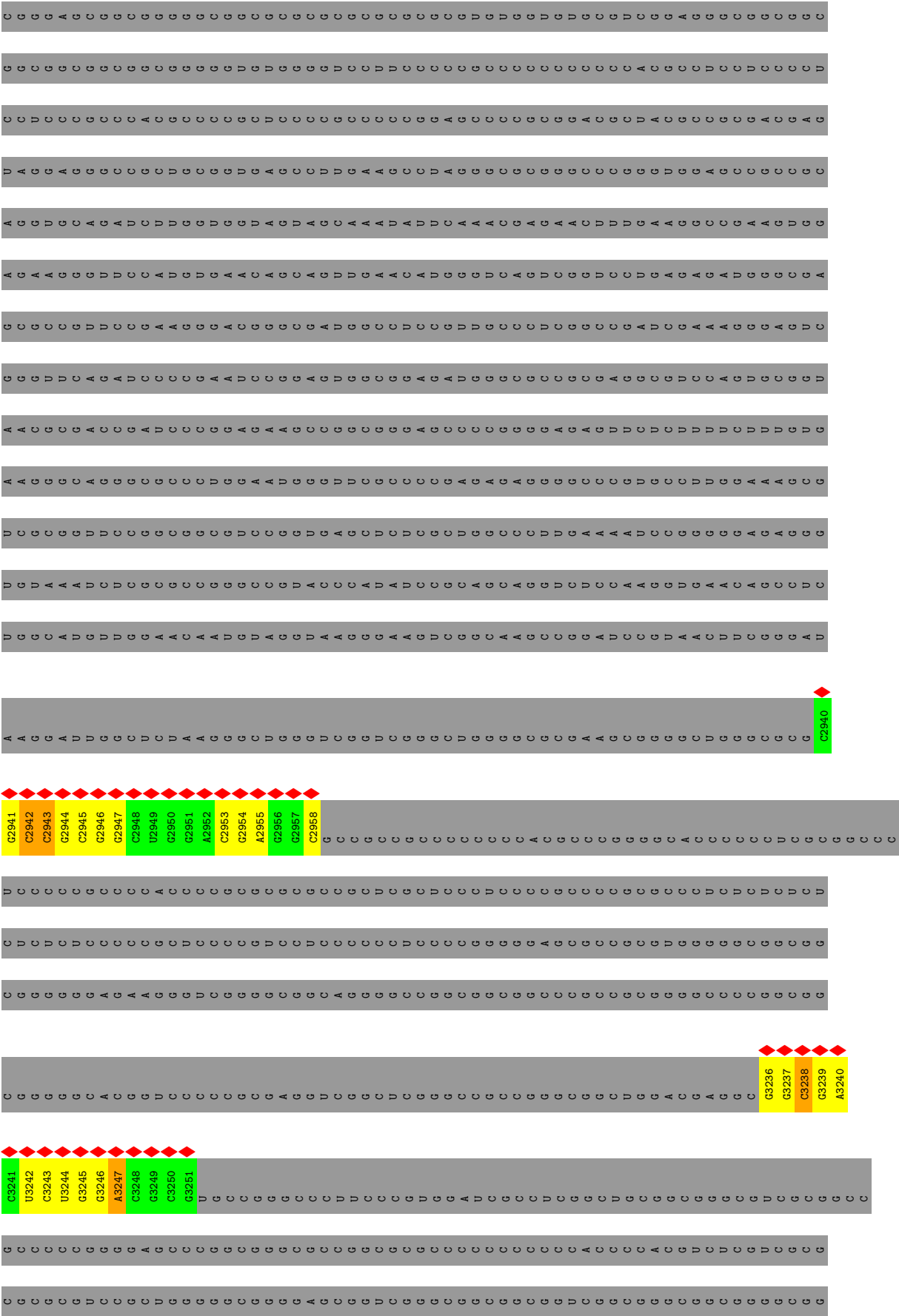
- Molecule 83: Small ribosomal subunit protein uS19



- Molecule 84: ES27L







G G C G G G U D C G G U C C C C C G C C C U A C C C C C C G G C C C G D C C G G C C C C C G G U C C C C C C U C U D C

C U C G G G C G C G G C C G C G G G G G G C G G C G G C A G G C C G C G G A G G G C C C G G C C C C C C C G G C

C G G G U C C G C C C C C G G G G G C C G C G G C C G U D C C G C C G C G G C

C C G A A C U U A G A A C U G G G U G C G G A C C A G G G A A C U C G A

G A A G G C C C G C C G G G G G U G U G A C C G C G A A U G U C

U G A A A A A A U U C C A A U A A A G C C G C C G G G U A A A C C G C C G G G A A G U A A C U A U G A A C C U C C U A A G G U A A G

C C A A A U G C C C U C G A U C A U C C A A U U A G U G A A C G C C G C A U G G A A U G A A A U G A A C C C C C C C C C C C C C C C C C C C

C C C U A C C U A C C U C C A G C C G A A A C C C A C C A G G G C C A A G G G C C A A C G G G C C U U G G C C G A A U C C A A G C C G G G G

A A A A A A G A C C C C U U U G A G C C U U C C A A G C C U U G G C C A C C G G G G A A G A G A A C C C C C C C C C C C C C C C C C C C

G A A A A A G U G G G G A G C C C C C G G G G C

C C G C C G G C C C C C G G G G C C C C C G G U A A A U C C C A C U C C U G G A U U C

G G U G A A G C C C G G G G G G G G G C C A A G C

G C G C C C G C C C G G G G C C G C

G U A C C A C C U G G U C A A C G G G U A A A C G C C A A G C C U U A A G G C

C C C G U G G A G C C A A G G G C C A A A A G C C U C C G C C U U G A U C C U U U U C C A G U U U C C C C C C C C C C C C C C C C C C C

U G A A A G C C G G G G C C U C A A C C G A U C C C U G G A C C C U U C C U U U G G C

A G U U A C C A C A G G A A G G A U A A C C U U G G C C C U U G U G G C

A U C C U U C G A U G A U C G G G C C U C C U C C A A U U U G U G A A A G C C A A U U C C A C C A A G C C G U U U G U G U

U C A C C C A C C U A A U A G G G A A C C U G U G A A G C C U U G G G G U U A G C

C C U A C C U G A U G A A U G U U G C C A A U G G G A A A U C C C U G C

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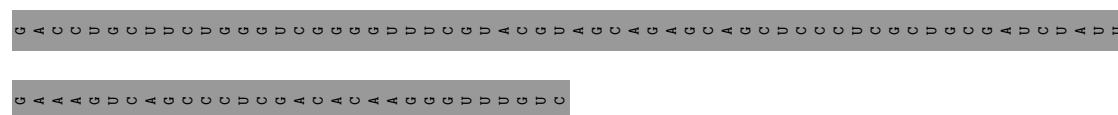
A U A A U G A C

G G G A G C C U C G G A A U G G C

C C

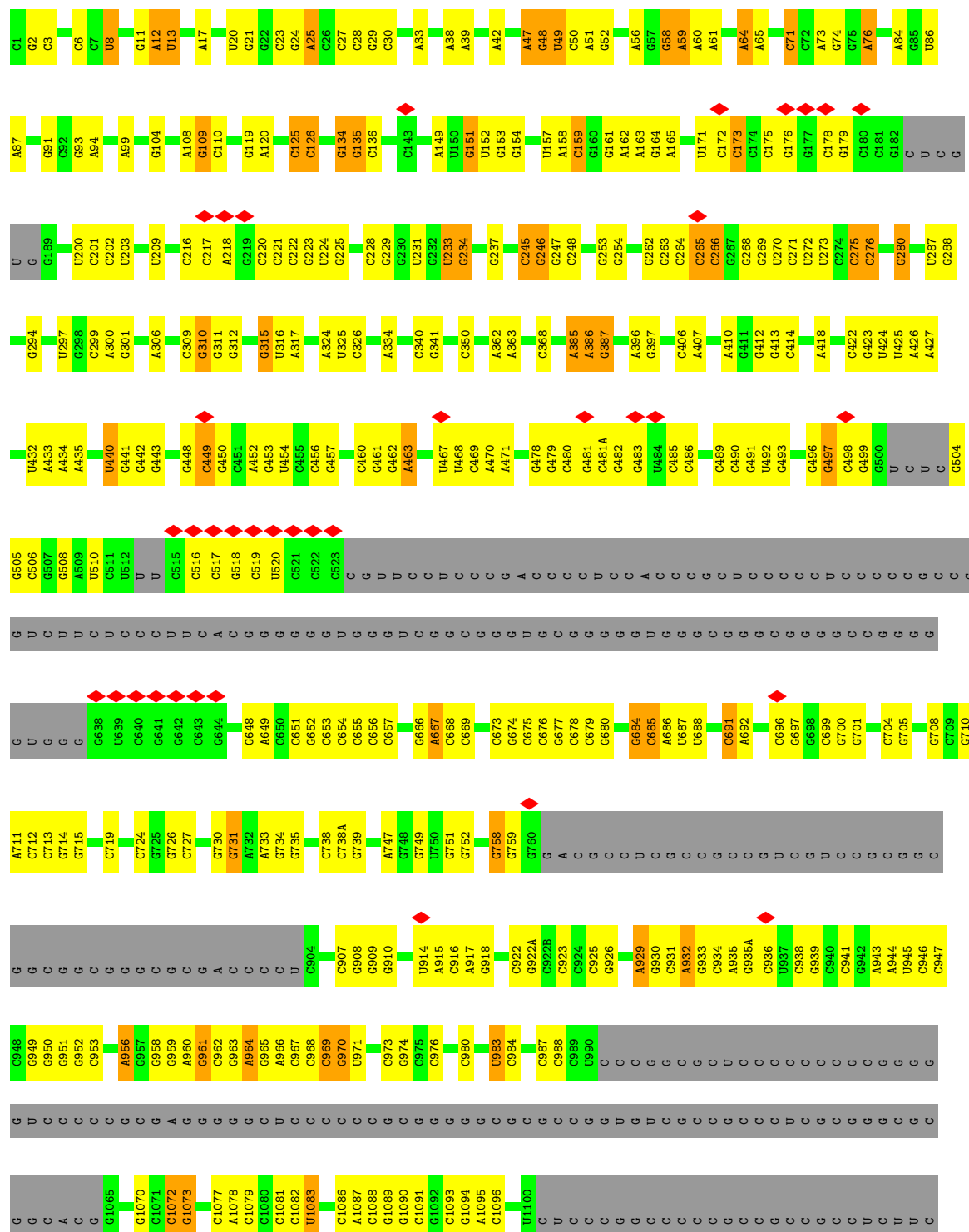
G G G U C C C G U G C C G A G U G C

C C



Molecule 85: 28S rRNA

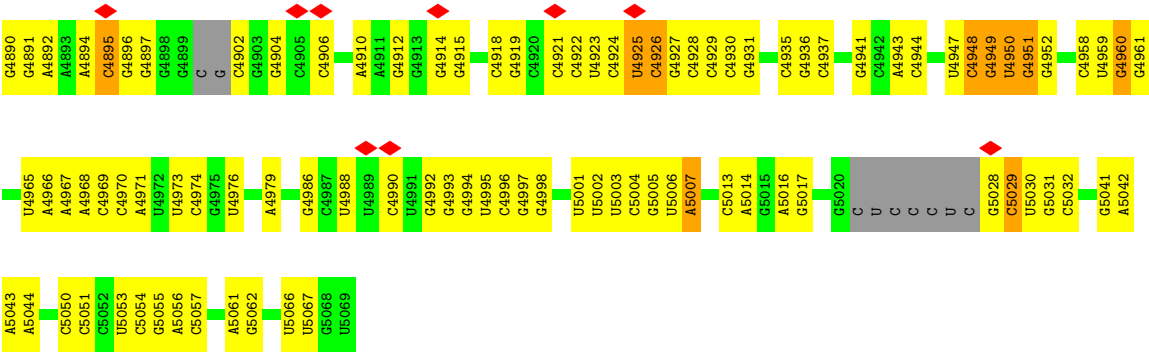
Chain 28:  39% 29% 27%



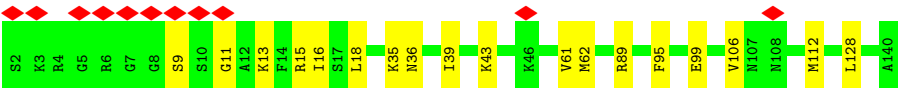
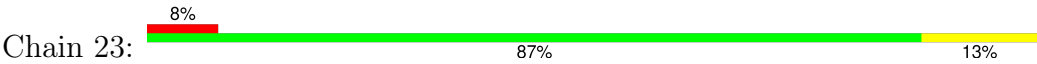


A3642	C2804	U2707	G2610	C2520	A2428	G2330	A
A3643	C2805	U2708	A2611	G2521	A2429	G2333	C
U3644	U2810	C2709	C2627	G2522	G2433	C2334	C
U3645	U2815	G2710	U2628	G2528	G2434	C2335	C
A3646	A2815	G2711	C2629	A2529	G2435	G2336	C
A3647	G2816	G2712	U2630	U2530	U2436	C2337	C
A3648	U2826	C2713	U2633	C2533	C2441	G2348	C
A3652	G2827	G2714	U2634	A2537	G2448	C2351	C
A3653	U2828	C2715	U2635	U2538	A2449	G2358	C
G3654	U2832	G2716	U2636	C2539	G2457	U2359	C
A3662	A2833	G2724	G2638	C2540	C2458	A2360	G
A3663	U2839	A2725	U2639	G2541	G2465	C2373	C
A3664	U2842	G2726	G2640	G2542	C2466	A2374	C
G3665	U2843	C2727	A2641	A2543	G2470	A2375	C
A3672	G2844	U2728	A2647	G2544	G2471	A2376	C
C3673	A2845	U2729	G2648	U2545	G2475	C2377	C
C3677	G2855	C2730	C2653	G2546	G2476	G2378	C
G3681	A2856	U2731	U2656	C2547	G2477	A2379	C
G3684	A2857	C2732	G2662	C2548	C2478	G2380	C
G3685	A2858	U2733	G2663	A2553	G2479	U2385	C
G3686	G2859	G2734	G2664	U2554	G2480	U2386	C
U3690	C2860	C2735	C2669	G2555	G2481	G2387	C
G3691	G2861	U2740	C2670	U2556	C2482	A2388	C
A3692	C2862	U2741	C2671	G2557	G2483	U2281	C
C3696	A2863	G2742	C2672	C2558	A2484	A2282	C
U3697	G2864	A2743	C2673	G2559	U2485	C2289	C
G3698	U2865	U2744	A2676	C2560	G2486	G2290	C
A3702	U2869	A2745	G2677	G2561	G2487	C2291	C
G3703	A2870	A2746	A2677	G2562	C2488	C2292	C
U3707	G2875	C2749	G2682	G2563	G2489	U2293	C
C3708	A2885	G2750	C2683	G2564	A2403	G2294	C
A3711	U2886	U2751	C2684	A2565	A2404	G2297	C
A3712	G2890	G2760	U2687	U2575	U2409	A2300	C
U3607	U2891	U2763	G2688	C2567	C2410	G2301	C
A3608	A2894	A2764	C2689	G2568	A2411	C2302	C
G3609	G2895	A2765	C2690	G2569	U2412	C2303	C
A3610	U2896	U2769	U2692	U2576	U2413	G2306	C
A3611	A2897	G2770	G2693	A2587	U2415	A2307	C
U3616	G2897	C2771	A2694	C2588	G2416	A2308	C
G3619	U2900	C2772	G2695	C2589	A2417	G2309	C
A3624	G	C2780	A2696	A2591	U2500	G2309	C
G3625	C	U2781	A2699	U2592	C2501	C2310	C
G3626	C	A2783	C2699	G2602	A2502	U2312	C
G3633	C	U2788	G2700	C2603	G2503	A2313	C
G3634	C	A2789	C2704	G2604	C2504	G2314	C
A3635	C	U2790	G2705	G2605	C2505	G2315	C
A3636	C	G2796	G2706	G2606	A2507	G2316	C
A3637	C			G2607	A2513	U2426	C
A3638	C			G2608	G2518	G2427	C
A3639	C			G2609	U2519		C





• Molecule 86: Large ribosomal subunit protein uL14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16727	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	20.804	Depositor
Minimum map value	-10.773	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.853	Depositor
Recommended contour level	3.2	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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

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	IF	0.31	0/2731	0.66	8/3681 (0.2%)
2	BB	0.13	0/1747	0.35	0/2374
3	S2	0.13	0/1753	0.31	0/2369
4	PP	0.12	0/643	0.29	0/860
5	DD	0.13	0/1195	0.31	0/1597
6	58	0.16	0/3581	0.29	0/5577
7	6	0.16	0/2858	0.26	0/4455
8	L8	0.16	0/1936	0.33	0/2596
9	L3	0.15	0/3240	0.34	0/4339
10	L4	0.15	0/2937	0.32	0/3946
11	L5	0.14	0/2437	0.33	0/3264
12	L6	0.14	0/1762	0.33	0/2362
13	L7	0.15	0/1911	0.29	0/2549
14	aa	0.15	0/1910	0.34	0/2569
15	10	0.14	0/1702	0.31	0/2272
16	13	0.14	0/1733	0.30	0/2316
17	14	0.15	0/1158	0.34	0/1547
18	15	0.16	0/1746	0.32	0/2338
19	bb	0.16	0/1662	0.32	0/2222
20	17	0.15	0/1268	0.33	0/1700
21	19	0.15	0/1524	0.30	0/2013
22	20	0.15	0/1501	0.29	0/2012
23	21	0.13	0/1326	0.28	0/1770
24	22	0.14	0/823	0.36	0/1104
25	cc	0.14	0/984	0.31	0/1323
26	26	0.13	0/1132	0.32	0/1504
27	27	0.13	0/1130	0.29	0/1507
28	dd	0.16	0/1191	0.35	0/1590
29	29	0.14	0/861	0.30	0/1138
30	30	0.13	0/771	0.28	0/1034
31	31	0.16	0/903	0.33	0/1216
32	32	0.15	0/1071	0.33	0/1429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	ee	0.15	0/895	0.33	0/1198
34	34	0.15	0/916	0.33	0/1220
35	35	0.14	0/1021	0.32	0/1348
36	36	0.13	0/841	0.29	0/1112
37	37	0.15	0/720	0.35	0/952
38	38	0.12	0/575	0.29	0/761
39	39	0.15	0/459	0.31	0/608
40	40	0.12	0/435	0.28	0/575
41	41	0.14	0/240	0.27	0/305
42	42	0.15	0/847	0.31	0/1117
43	ff	0.14	0/718	0.35	0/953
44	gg	0.14	0/1006	0.30	0/1349
45	AS	0.14	0/1756	0.35	0/2350
46	FF	0.14	0/1226	0.36	0/1649
47	VV	0.13	0/665	0.30	0/891
48	s	0.14	0/1530	0.38	0/2064
49	t	0.16	0/1174	0.41	0/1582
50	F	0.20	1/2845 (0.0%)	0.34	0/3828
51	Q	0.15	0/1539	0.37	0/2054
52	ZZ	0.13	0/567	0.35	0/753
53	EE	0.14	0/918	0.36	0/1233
54	TT	0.21	0/604	0.38	1/810 (0.1%)
55	S5	0.14	0/1492	0.37	0/2005
56	WW	0.12	0/490	0.29	0/656
57	II	0.15	0/1146	0.35	0/1534
58	CC	0.15	0/834	0.41	0/1125
59	AA	0.13	0/2493	0.34	0/3394
60	OO	0.13	0/805	0.33	0/1081
61	MM	0.14	0/1115	0.33	0/1493
62	LL	0.14	0/1208	0.39	0/1618
63	XX	0.13	0/470	0.33	0/623
64	RR	0.13	0/1116	0.35	0/1490
65	SS	0.13	0/1028	0.31	0/1366
66	S6	0.14	0/1946	0.36	1/2590 (0.0%)
67	S4	0.21	1/2118 (0.0%)	0.34	0/2849
68	S9	0.14	0/1550	0.33	0/2069
69	S7	0.14	0/1510	0.35	0/2022
70	YY	0.13	0/447	0.34	0/587
71	S3	0.15	0/1688	0.34	0/2269
72	RS	0.13	0/1082	0.34	0/1452
73	WX	0.14	0/1051	0.36	0/1406
74	S8	0.13	0/1715	0.33	0/2287
75	W	0.15	0/873	0.32	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	GG	0.13	0/1020	0.35	0/1369
77	UU	0.13	0/828	0.31	0/1109
78	11	0.14	0/1385	0.32	0/1852
79	L9	0.15	0/1535	0.33	0/2063
80	18	0.14	0/40302	0.30	0/62804
81	v	0.13	0/6577	0.33	0/8883
82	LA	0.13	0/426	0.32	0/568
83	A	0.14	0/1001	0.37	0/1339
84	ES	0.17	0/844	0.41	0/1314
85	28	0.17	0/84014	0.31	1/131028 (0.0%)
86	23	0.15	0/1048	0.32	0/1402
All	All	0.16	2/239781 (0.0%)	0.32	11/350090 (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
48	s	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	F	204	ASN	C-O	-7.68	1.20	1.23
67	S4	149	TYR	C-O	7.15	1.27	1.23

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	IF	337	LEU	O-C-N	15.62	140.49	122.22
1	IF	337	LEU	CA-C-N	-12.08	103.14	120.29
1	IF	337	LEU	C-N-CA	-12.08	103.14	120.29
1	IF	328	ARG	N-CA-C	8.86	123.19	112.38
1	IF	320	TYR	O-C-N	8.37	133.18	122.39

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	s	119	CYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IF	2692	0	2763	93	0
2	BB	1710	0	1708	22	0
3	S2	1716	0	1806	27	0
4	PP	636	0	637	5	0
5	DD	1175	0	1249	12	0
6	58	3208	0	1629	55	0
7	6	2558	0	1296	30	0
8	L8	1898	0	1993	25	0
9	L3	3172	0	3310	31	0
10	L4	2883	0	3053	28	0
11	L5	2391	0	2424	27	0
12	L6	1729	0	1887	16	0
13	L7	1875	0	1995	25	0
14	aa	1879	0	2027	20	0
15	10	1664	0	1712	13	0
16	13	1702	0	1820	15	0
17	14	1137	0	1211	14	0
18	15	1701	0	1749	22	0
19	bb	1630	0	1778	20	0
20	17	1242	0	1274	9	0
21	19	1508	0	1664	12	0
22	20	1462	0	1508	15	0
23	21	1298	0	1366	10	0
24	22	809	0	833	4	0
25	cc	967	0	1040	11	0
26	26	1115	0	1205	10	0
27	27	1107	0	1182	14	0
28	dd	1162	0	1209	18	0
29	29	848	0	920	5	0
30	30	761	0	794	10	0
31	31	888	0	930	8	0
32	32	1053	0	1147	7	0
33	ee	876	0	912	11	0
34	34	906	0	1000	5	0
35	35	1013	0	1147	8	0
36	36	830	0	916	5	0
37	37	705	0	738	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	38	569	0	637	2	0
39	39	447	0	480	10	0
40	40	429	0	469	2	0
41	41	239	0	289	2	0
42	42	834	0	905	10	0
43	ff	708	0	758	7	0
44	gg	990	0	1044	7	0
45	AS	1729	0	1803	31	0
46	FF	1202	0	1289	11	0
47	VV	651	0	672	7	0
48	s	1507	0	1564	11	0
49	t	1160	0	1218	24	0
50	F	2798	0	2809	37	0
51	Q	1515	0	1634	14	0
52	ZZ	555	0	567	9	0
53	EE	908	0	939	10	0
54	TT	598	0	656	6	0
55	S5	1471	0	1522	15	0
56	WW	488	0	514	4	0
57	II	1128	0	1195	17	0
58	CC	810	0	836	12	0
59	AA	2436	0	2393	36	0
60	OO	795	0	862	10	0
61	MM	1097	0	1132	18	0
62	LL	1190	0	1249	18	0
63	XX	459	0	452	4	0
64	RR	1098	0	1167	21	0
65	SS	1011	0	1083	18	0
66	S6	1923	0	2089	25	0
67	S4	2076	0	2177	25	0
68	S9	1525	0	1640	19	0
69	S7	1488	0	1582	23	0
70	YY	443	0	492	5	0
71	S3	1662	0	1760	27	0
72	RS	1068	0	1121	11	0
73	WX	1034	0	1080	17	0
74	S8	1686	0	1772	18	0
75	W	860	0	903	10	0
76	GG	1007	0	1028	16	0
77	UU	814	0	865	9	0
78	11	1362	0	1399	12	0
79	L9	1516	0	1597	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	18	36043	0	18202	636	0
81	v	6470	0	6548	77	0
82	LA	421	0	405	2	0
83	A	983	0	1030	10	0
84	ES	756	0	384	20	0
85	28	75105	0	37942	1058	0
86	23	1034	0	1097	10	0
87	34	1	0	0	0	0
87	37	1	0	0	0	0
87	UU	1	0	0	0	0
87	ff	1	0	0	0	0
88	v	28	0	12	1	0
All	All	224036	0	171095	2811	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 7.

The worst 5 of 2811 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IF:350:VAL:CG1	1:IF:357:LEU:HB3	1.67	1.25
1:IF:350:VAL:HG13	1:IF:357:LEU:HB3	1.31	1.12
1:IF:349:ILE:H	1:IF:349:ILE:HD13	1.23	1.03
1:IF:116:ARG:HG3	1:IF:117:LEU:N	1.72	1.03
1:IF:400:LEU:H	1:IF:400:LEU:HD13	1.28	0.99

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	IF	338/442 (76%)	336 (99%)	2 (1%)	0	100	100
2	BB	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
3	S2	219/221 (99%)	217 (99%)	2 (1%)	0	100	100
4	PP	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
5	DD	139/151 (92%)	133 (96%)	6 (4%)	0	100	100
8	L8	246/248 (99%)	237 (96%)	9 (4%)	0	100	100
9	L3	392/394 (100%)	380 (97%)	12 (3%)	0	100	100
10	L4	360/362 (99%)	355 (99%)	5 (1%)	0	100	100
11	L5	291/293 (99%)	285 (98%)	6 (2%)	0	100	100
12	L6	208/291 (72%)	197 (95%)	11 (5%)	0	100	100
13	L7	223/225 (99%)	214 (96%)	8 (4%)	1 (0%)	30	59
14	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
15	10	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
16	13	208/210 (99%)	203 (98%)	5 (2%)	0	100	100
17	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
18	15	201/203 (99%)	192 (96%)	9 (4%)	0	100	100
19	bb	197/199 (99%)	196 (100%)	1 (0%)	0	100	100
20	17	151/153 (99%)	151 (100%)	0	0	100	100
21	19	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
22	20	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
23	21	157/159 (99%)	155 (99%)	2 (1%)	0	100	100
24	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
25	cc	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
26	26	132/134 (98%)	132 (100%)	0	0	100	100
27	27	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
28	dd	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
29	29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
30	30	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
31	31	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
32	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
33	ee	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
34	34	112/114 (98%)	112 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	35	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
36	36	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
37	37	84/86 (98%)	84 (100%)	0	0	100	100
38	38	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
39	39	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
40	40	50/52 (96%)	50 (100%)	0	0	100	100
41	41	23/25 (92%)	23 (100%)	0	0	100	100
42	42	100/104 (96%)	99 (99%)	1 (1%)	0	100	100
43	ff	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
44	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
45	AS	211/213 (99%)	207 (98%)	4 (2%)	0	100	100
46	FF	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
47	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
48	s	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
49	t	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
50	F	356/358 (99%)	348 (98%)	8 (2%)	0	100	100
51	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
52	ZZ	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
53	EE	115/132 (87%)	109 (95%)	6 (5%)	0	100	100
54	TT	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
55	S5	181/191 (95%)	169 (93%)	12 (7%)	0	100	100
56	WW	60/62 (97%)	60 (100%)	0	0	100	100
57	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
58	CC	94/96 (98%)	86 (92%)	7 (7%)	1 (1%)	11	36
59	AA	311/313 (99%)	299 (96%)	12 (4%)	0	100	100
60	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
61	MM	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
62	LL	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
63	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
64	RR	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	48
65	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	S6	235/237 (99%)	233 (99%)	2 (1%)	0	100	100
67	S4	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
68	S9	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
69	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
70	YY	53/55 (96%)	53 (100%)	0	0	100	100
71	S3	212/214 (99%)	209 (99%)	3 (1%)	0	100	100
72	RS	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
73	WX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
74	S8	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
75	W	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
76	GG	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
77	UU	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
78	11	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
79	L9	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
81	v	824/857 (96%)	813 (99%)	11 (1%)	0	100	100
82	LA	45/1096 (4%)	45 (100%)	0	0	100	100
83	A	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
86	23	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
All	All	13074/14720 (89%)	12774 (98%)	297 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	CC	65	ARG
64	RR	62	PRO
13	L7	196	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IF	286/357 (80%)	273 (96%)	13 (4%)	24	58
2	BB	180/181 (99%)	167 (93%)	13 (7%)	13	39
3	S2	187/187 (100%)	180 (96%)	7 (4%)	30	64
4	PP	67/67 (100%)	63 (94%)	4 (6%)	17	47
5	DD	130/136 (96%)	124 (95%)	6 (5%)	24	57
8	L8	190/190 (100%)	182 (96%)	8 (4%)	26	60
9	L3	342/342 (100%)	329 (96%)	13 (4%)	29	64
10	L4	302/302 (100%)	292 (97%)	10 (3%)	33	67
11	L5	247/247 (100%)	241 (98%)	6 (2%)	43	75
12	L6	190/251 (76%)	183 (96%)	7 (4%)	30	64
13	L7	196/196 (100%)	189 (96%)	7 (4%)	31	65
14	aa	200/205 (98%)	191 (96%)	9 (4%)	24	58
15	10	175/180 (97%)	171 (98%)	4 (2%)	44	76
16	13	175/175 (100%)	167 (95%)	8 (5%)	24	57
17	14	117/117 (100%)	111 (95%)	6 (5%)	21	53
18	15	171/171 (100%)	164 (96%)	7 (4%)	27	61
19	bb	171/171 (100%)	163 (95%)	8 (5%)	23	56
20	17	134/134 (100%)	132 (98%)	2 (2%)	57	84
21	19	159/159 (100%)	151 (95%)	8 (5%)	22	53
22	20	157/157 (100%)	150 (96%)	7 (4%)	24	58
23	21	139/139 (100%)	136 (98%)	3 (2%)	45	77
24	22	89/89 (100%)	86 (97%)	3 (3%)	32	66
25	cc	106/106 (100%)	105 (99%)	1 (1%)	70	90
26	26	124/124 (100%)	117 (94%)	7 (6%)	19	50
27	27	117/117 (100%)	114 (97%)	3 (3%)	40	73
28	dd	119/119 (100%)	117 (98%)	2 (2%)	53	82
29	29	84/184 (46%)	81 (96%)	3 (4%)	31	65
30	30	84/84 (100%)	83 (99%)	1 (1%)	63	86
31	31	98/98 (100%)	93 (95%)	5 (5%)	21	53
32	32	114/114 (100%)	108 (95%)	6 (5%)	20	52
33	ee	88/88 (100%)	83 (94%)	5 (6%)	18	49
34	34	98/98 (100%)	97 (99%)	1 (1%)	68	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	35	109/109 (100%)	106 (97%)	3 (3%)	38	72
36	36	86/86 (100%)	82 (95%)	4 (5%)	23	56
37	37	73/73 (100%)	71 (97%)	2 (3%)	39	73
38	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
39	39	47/47 (100%)	46 (98%)	1 (2%)	47	77
40	40	48/48 (100%)	48 (100%)	0	100	100
41	41	24/24 (100%)	24 (100%)	0	100	100
42	42	90/92 (98%)	88 (98%)	2 (2%)	45	77
43	ff	74/74 (100%)	70 (95%)	4 (5%)	20	51
44	gg	107/108 (99%)	104 (97%)	3 (3%)	38	72
45	AS	194/194 (100%)	188 (97%)	6 (3%)	35	69
46	FF	130/130 (100%)	123 (95%)	7 (5%)	20	51
47	VV	75/75 (100%)	69 (92%)	6 (8%)	11	34
48	s	164/164 (100%)	152 (93%)	12 (7%)	13	38
49	t	126/126 (100%)	115 (91%)	11 (9%)	9	30
50	F	307/307 (100%)	293 (95%)	14 (5%)	24	57
51	Q	164/165 (99%)	162 (99%)	2 (1%)	63	86
52	ZZ	61/61 (100%)	59 (97%)	2 (3%)	33	67
53	EE	99/108 (92%)	96 (97%)	3 (3%)	36	70
54	TT	66/66 (100%)	63 (96%)	3 (4%)	24	58
55	S5	158/161 (98%)	151 (96%)	7 (4%)	25	59
56	WW	55/55 (100%)	52 (94%)	3 (6%)	19	50
57	II	117/117 (100%)	111 (95%)	6 (5%)	21	53
58	CC	87/87 (100%)	84 (97%)	3 (3%)	32	66
59	AA	272/272 (100%)	263 (97%)	9 (3%)	33	67
60	OO	92/92 (100%)	87 (95%)	5 (5%)	20	51
61	MM	111/111 (100%)	109 (98%)	2 (2%)	51	80
62	LL	125/125 (100%)	117 (94%)	8 (6%)	16	44
63	XX	48/48 (100%)	46 (96%)	2 (4%)	26	60
64	RR	113/113 (100%)	109 (96%)	4 (4%)	32	66
65	SS	107/107 (100%)	101 (94%)	6 (6%)	19	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	S6	207/207 (100%)	202 (98%)	5 (2%)	43	75
67	S4	224/224 (100%)	220 (98%)	4 (2%)	51	80
68	S9	161/161 (100%)	154 (96%)	7 (4%)	26	60
69	S7	165/169 (98%)	159 (96%)	6 (4%)	31	65
70	YY	46/46 (100%)	44 (96%)	2 (4%)	26	60
71	S3	177/177 (100%)	162 (92%)	15 (8%)	10	31
72	RS	119/119 (100%)	111 (93%)	8 (7%)	15	43
73	WX	112/112 (100%)	108 (96%)	4 (4%)	31	65
74	S8	178/178 (100%)	173 (97%)	5 (3%)	38	72
75	W	86/100 (86%)	82 (95%)	4 (5%)	23	56
76	GG	105/105 (100%)	100 (95%)	5 (5%)	23	55
77	UU	88/88 (100%)	85 (97%)	3 (3%)	32	66
78	11	143/143 (100%)	139 (97%)	4 (3%)	38	72
79	L9	169/169 (100%)	162 (96%)	7 (4%)	27	61
81	v	705/728 (97%)	667 (95%)	38 (5%)	20	51
82	LA	45/948 (5%)	41 (91%)	4 (9%)	9	28
83	A	107/107 (100%)	97 (91%)	10 (9%)	8	27
86	23	106/106 (100%)	103 (97%)	3 (3%)	38	72
All	All	11372/12581 (90%)	10903 (96%)	469 (4%)	28	61

5 of 469 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	VV	63	LEU
81	v	568	ILE
55	S5	154	LEU
81	v	442	LEU
76	GG	147	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 138 such sidechains are listed below:

Mol	Chain	Res	Type
72	RS	93	GLN
75	W	30	GLN
81	v	535	GLN

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Mol	Chain	Res	Type
24	22	38	ASN
24	22	17	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	58	149/156 (95%)	22 (14%)	1 (0%)
7	6	119/120 (99%)	9 (7%)	0
80	18	1675/1698 (98%)	299 (17%)	14 (0%)
84	ES	34/5070 (0%)	7 (20%)	1 (2%)
85	28	3479/4808 (72%)	579 (16%)	48 (1%)
All	All	5456/11852 (46%)	916 (16%)	64 (1%)

5 of 916 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	58	2	G
6	58	34	U
6	58	35	C
6	58	59	A
6	58	62	A

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	28	4232	U
85	28	4699	U
85	28	275	C
85	28	265	C
85	28	4884	G

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

1 non-standard protein/DNA/RNA residue 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
81	DDE	v	715	81	18,20,21	1.00	1 (5%)	17,28,30	0.95	1 (5%)

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
81	DDE	v	715	81	-	8/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	v	715	DDE	CD2-CG	2.29	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	v	715	DDE	CAU-CBW-CBI	-2.74	105.86	111.22

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	v	715	DDE	CAT-CAU-CBW-CBI
81	v	715	DDE	N-CA-CB-CG
81	v	715	DDE	CAT-CAU-CBW-NCB
81	v	715	DDE	C-CA-CB-CG
81	v	715	DDE	CA-CB-CG-CD2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
88	GDP	v	900	-	29,30,30	3.30	12 (41%)	45,47,47	1.89	13 (28%)

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
88	GDP	v	900	-	-	0/16/32/32	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	v	900	GDP	O6-C6	9.61	1.41	1.23
88	v	900	GDP	C2'-C3'	-8.57	1.30	1.53
88	v	900	GDP	O4'-C4'	-6.19	1.31	1.45
88	v	900	GDP	C2-N2	4.68	1.45	1.34
88	v	900	GDP	PA-O3A	4.18	1.64	1.59

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	v	900	GDP	C5-C4-N3	-5.88	119.03	128.39
88	v	900	GDP	C2-N3-C4	4.78	120.53	112.30
88	v	900	GDP	N9-C4-N3	4.01	133.97	125.95
88	v	900	GDP	C6-C5-N7	2.92	135.60	130.29
88	v	900	GDP	C4-C5-N7	-2.91	106.07	110.67

There are no chirality outliers.

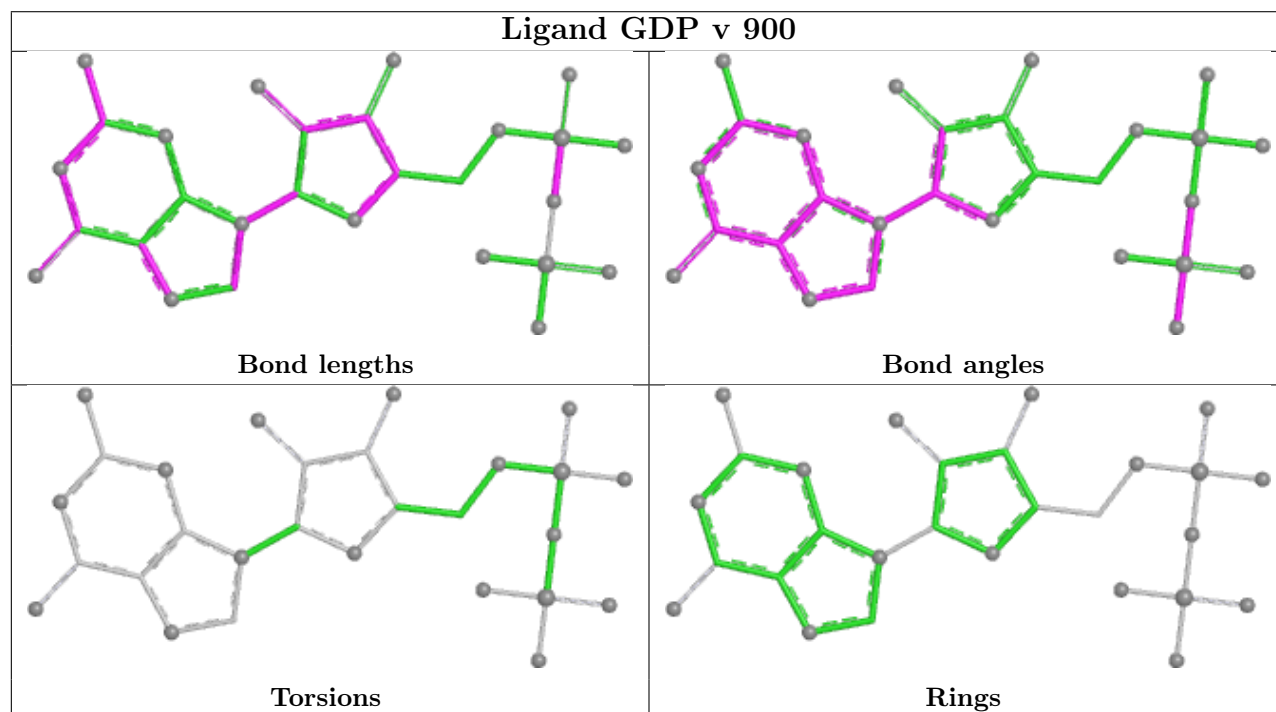
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	v	900	GDP	1	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
80	18	8

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	18	756:C	O3'	788:G	P	20.24
1	18	697:G	O3'	729:C	P	19.25
1	18	1417:C	O3'	1423:C	P	17.98
1	18	834:C	O3'	841:G	P	16.30
1	18	745:C	O3'	749:U	P	8.18

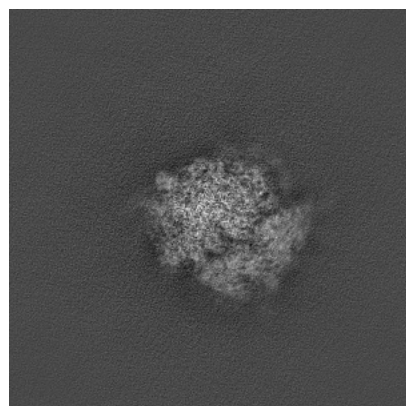
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75740. These allow visual inspection of the internal detail of the map and identification of artifacts.

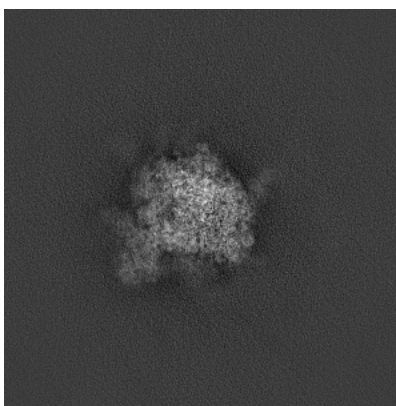
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

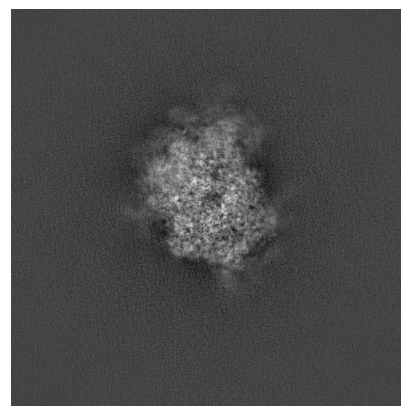
6.1.1 Primary map



X

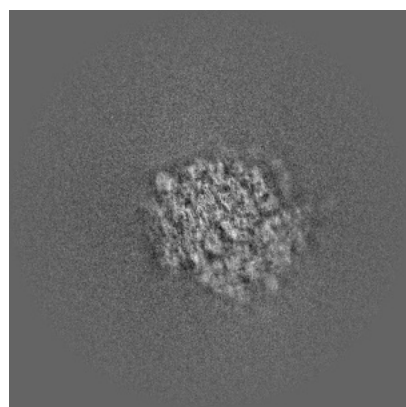


Y

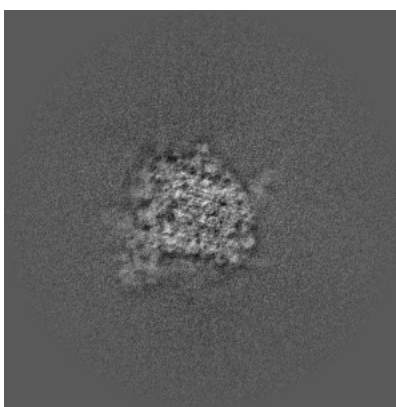


Z

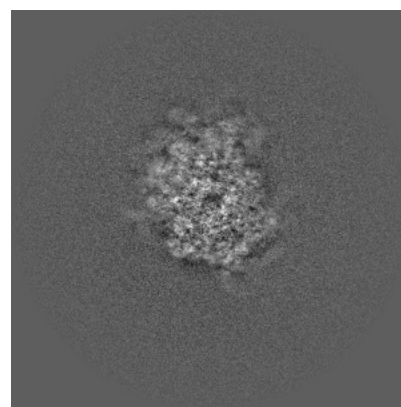
6.1.2 Raw map



X



Y

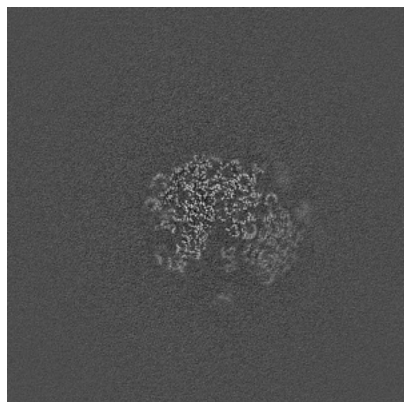


Z

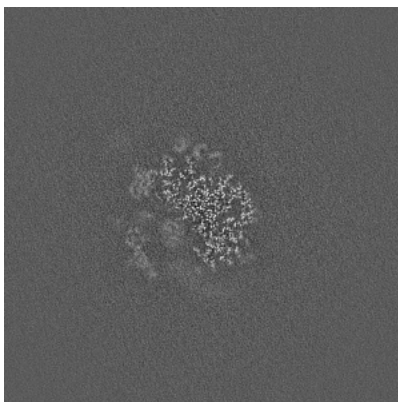
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

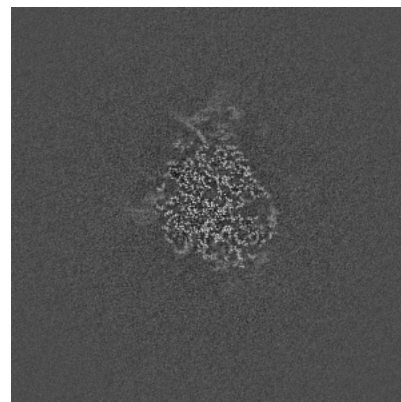
6.2.1 Primary map



X Index: 400

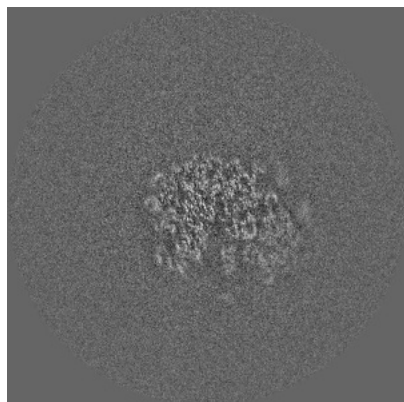


Y Index: 400

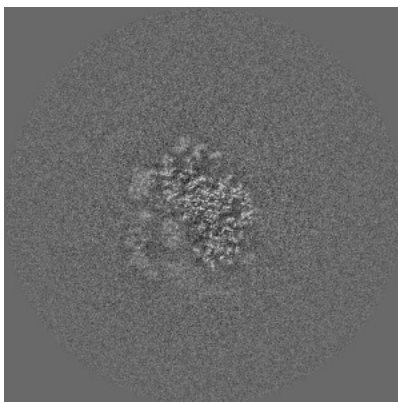


Z Index: 400

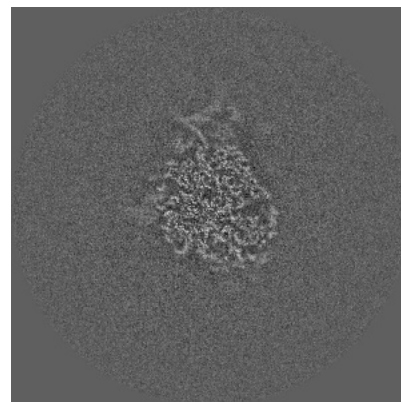
6.2.2 Raw map



X Index: 400



Y Index: 400

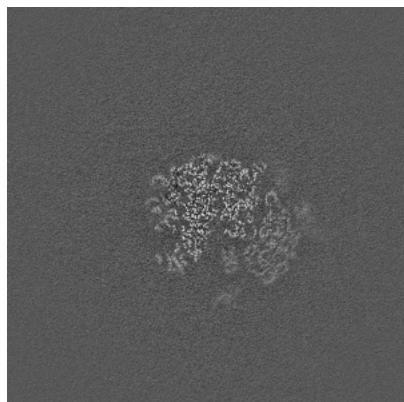


Z Index: 400

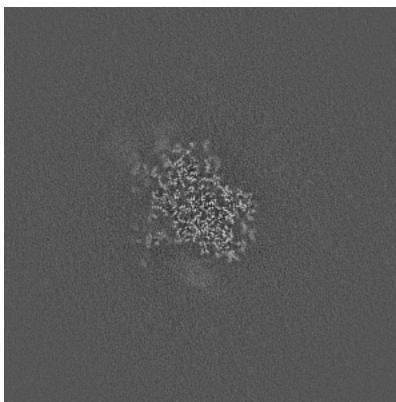
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

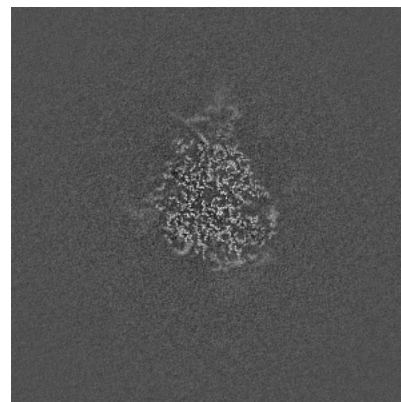
6.3.1 Primary map



X Index: 397

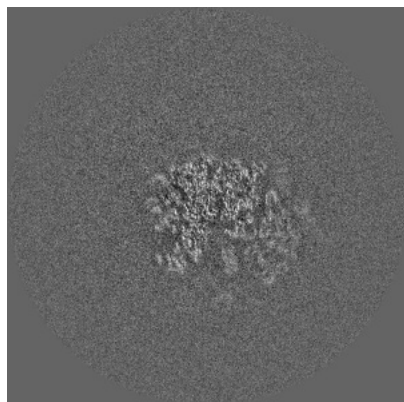


Y Index: 381

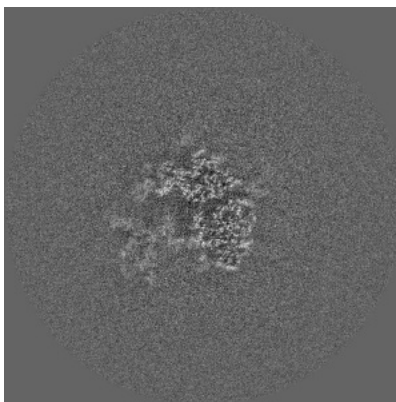


Z Index: 402

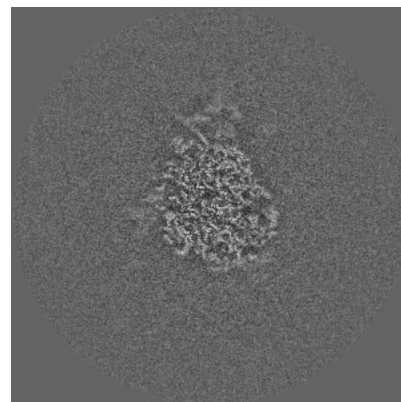
6.3.2 Raw map



X Index: 397



Y Index: 420

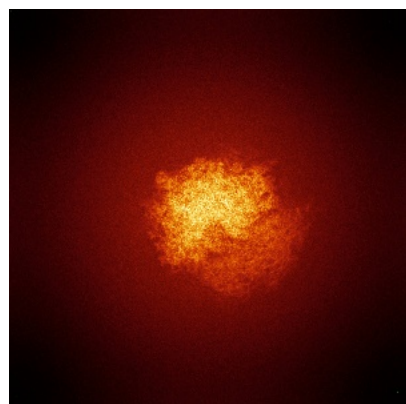


Z Index: 402

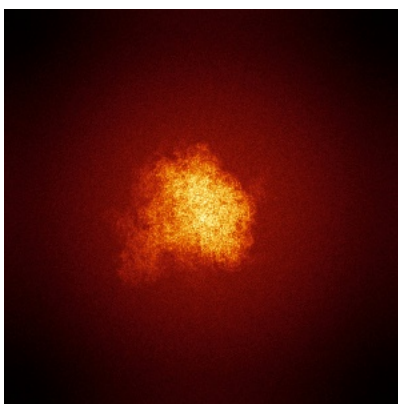
The images above show the largest variance slices of the map in three orthogonal directions.

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

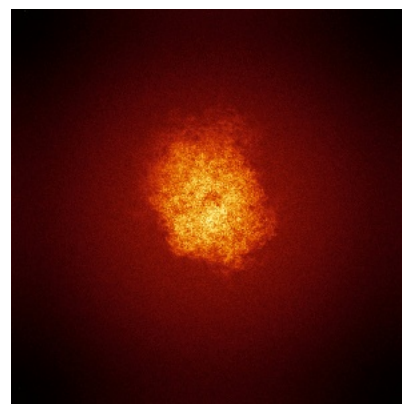
6.4.1 Primary map



X

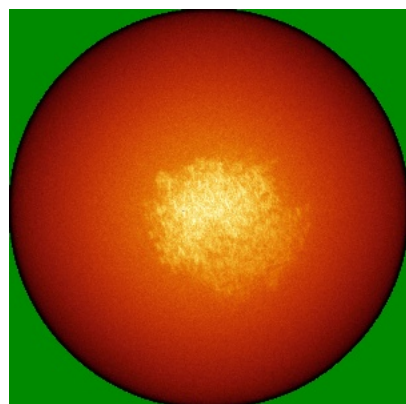


Y

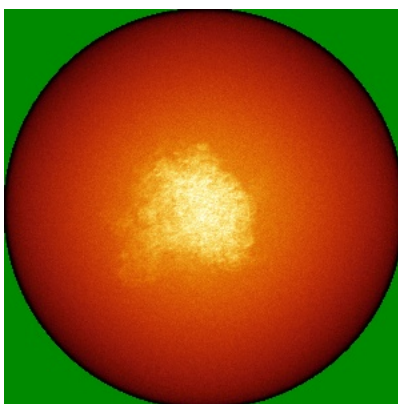


Z

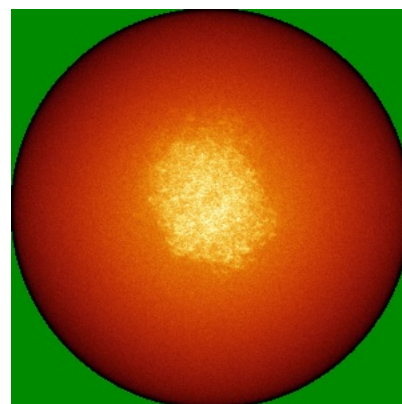
6.4.2 Raw map



X



Y

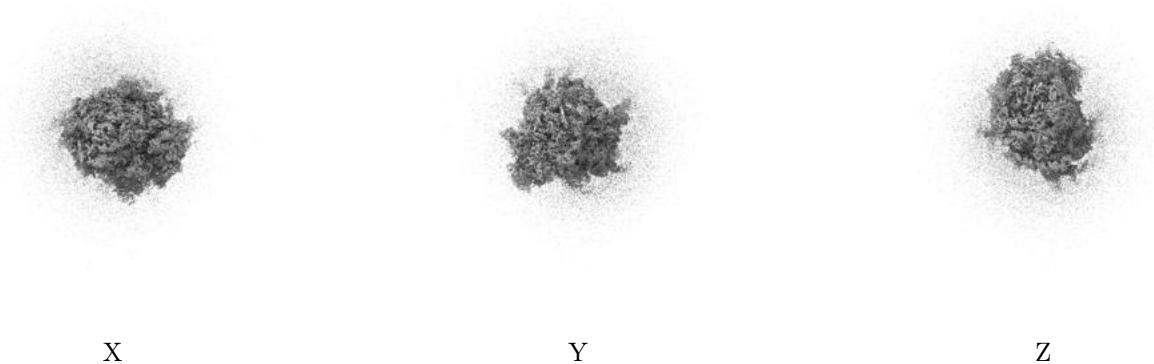


Z

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

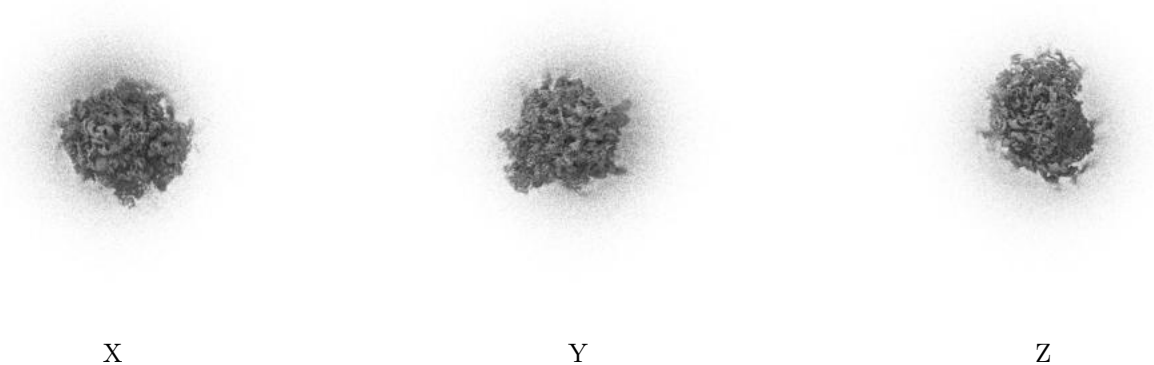
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

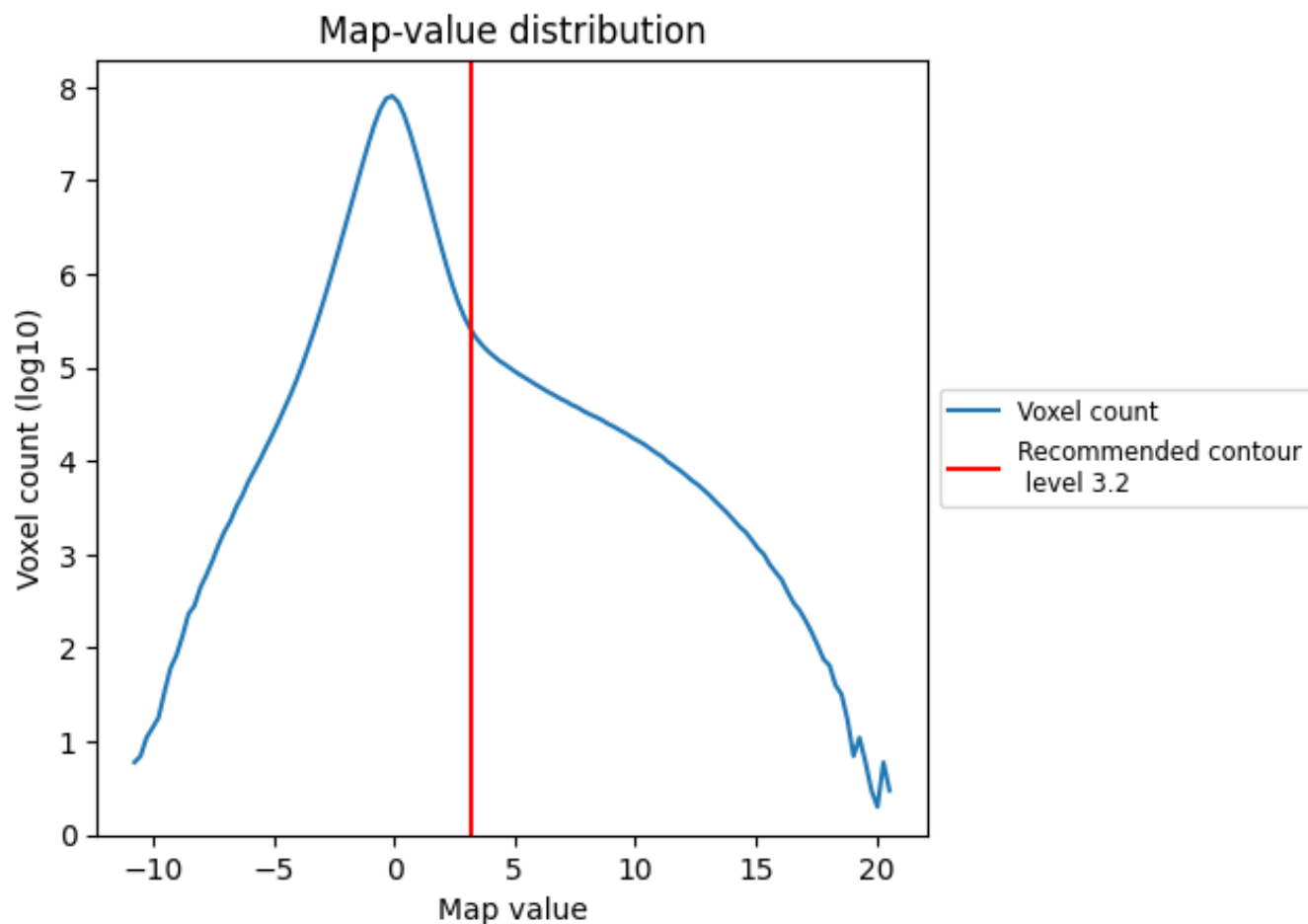
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

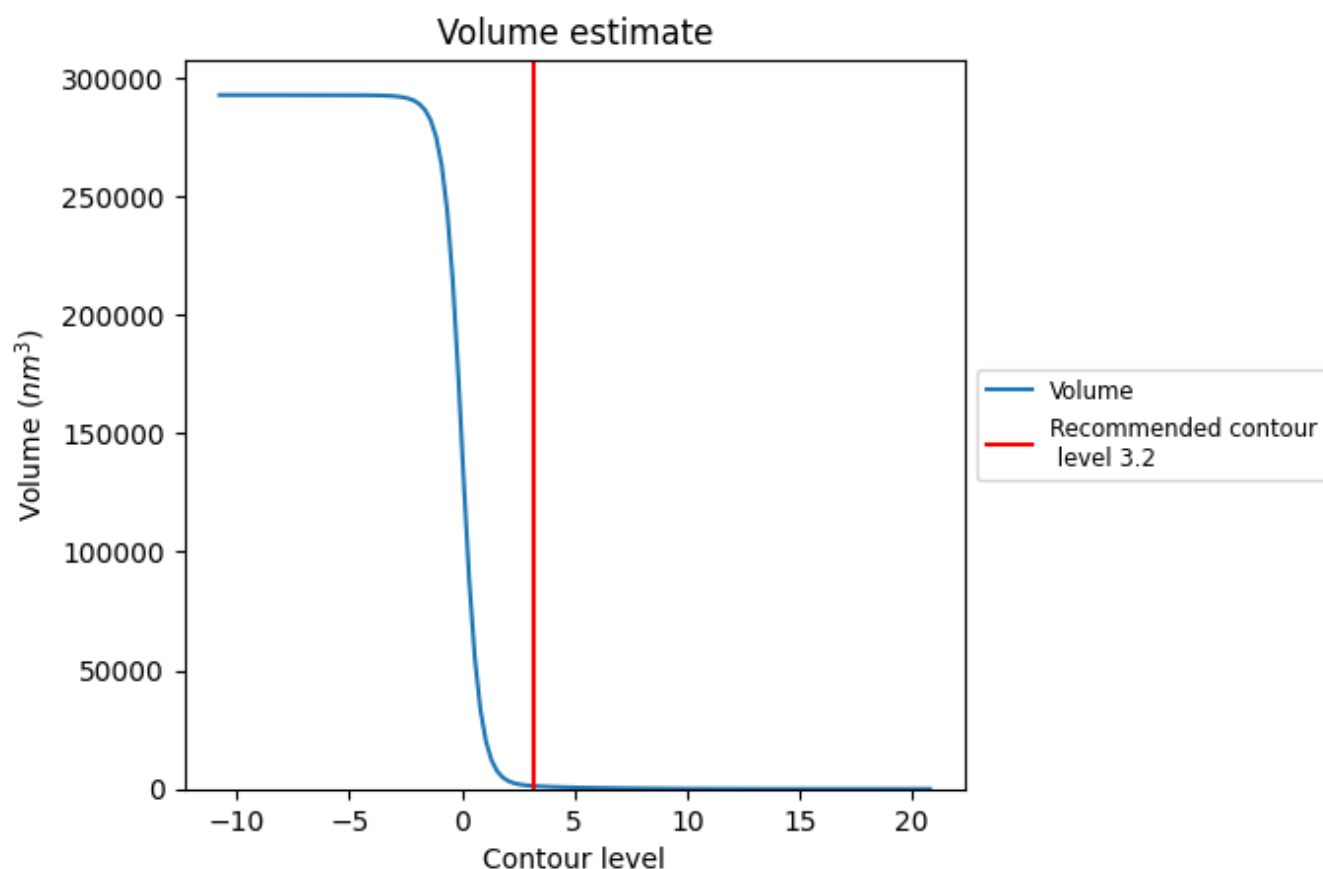
This section contains the results of statistical analysis of the map.

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.

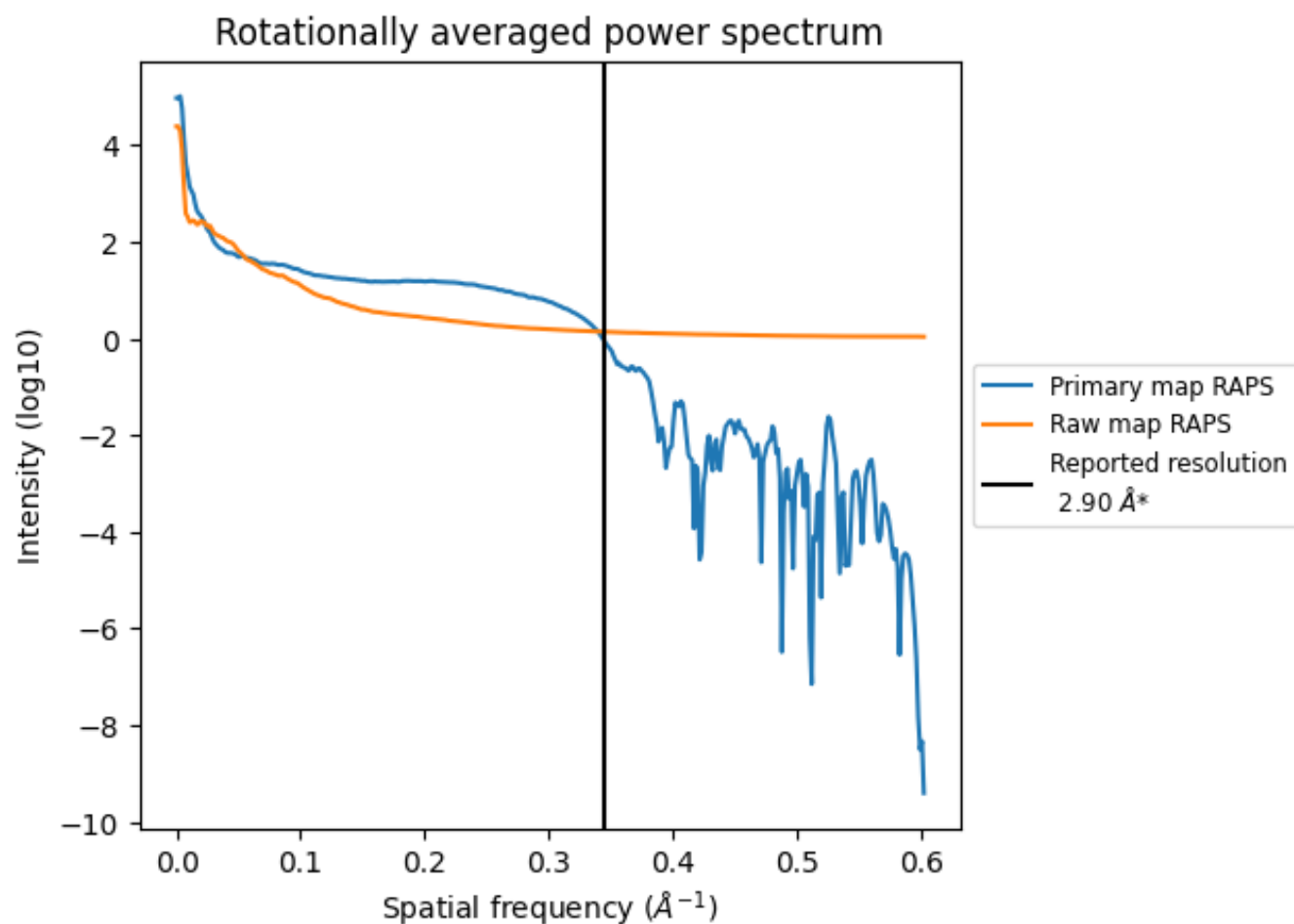
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1261 nm^3 ; this corresponds to an approximate mass of 1139 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 ⓘ

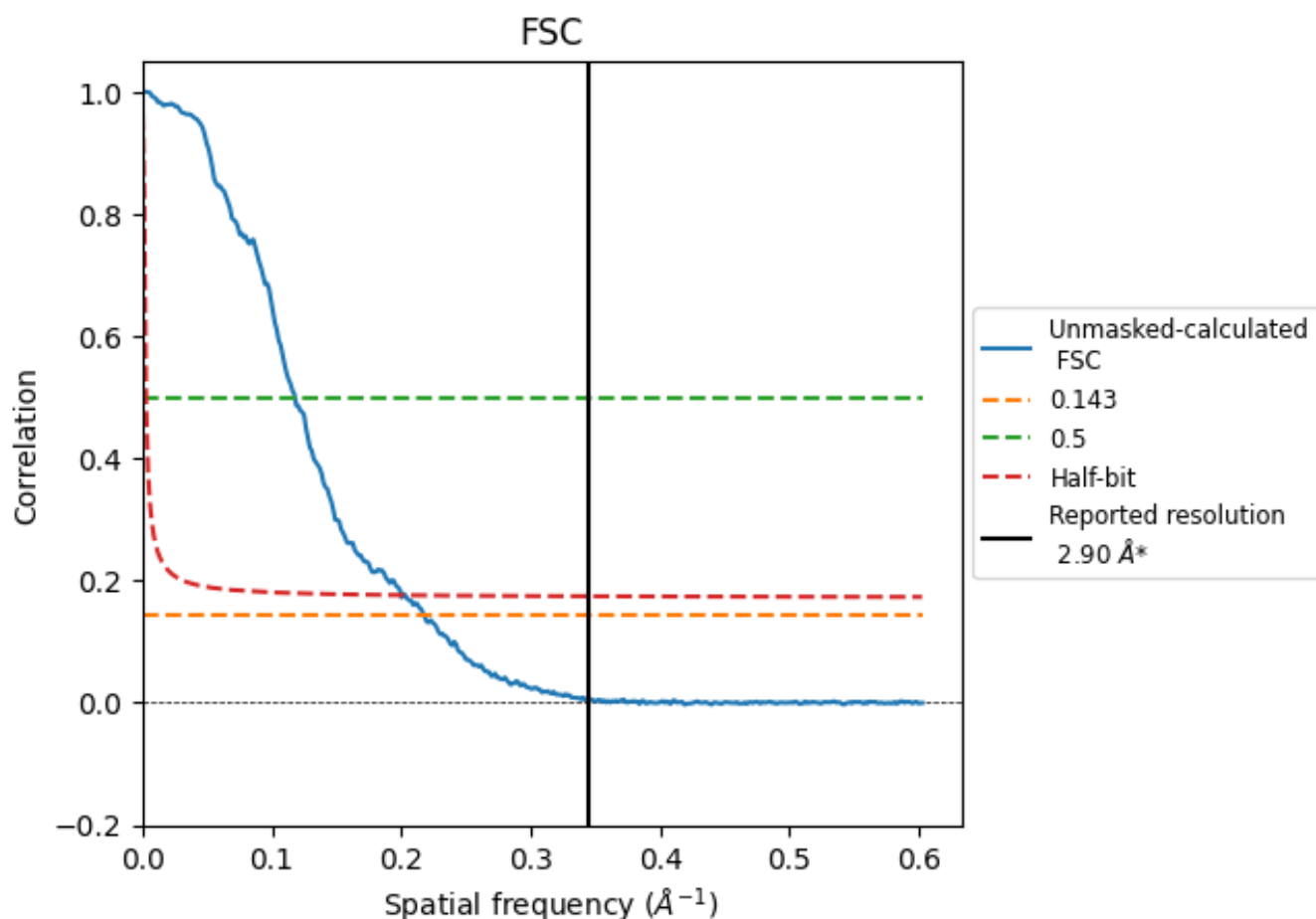


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

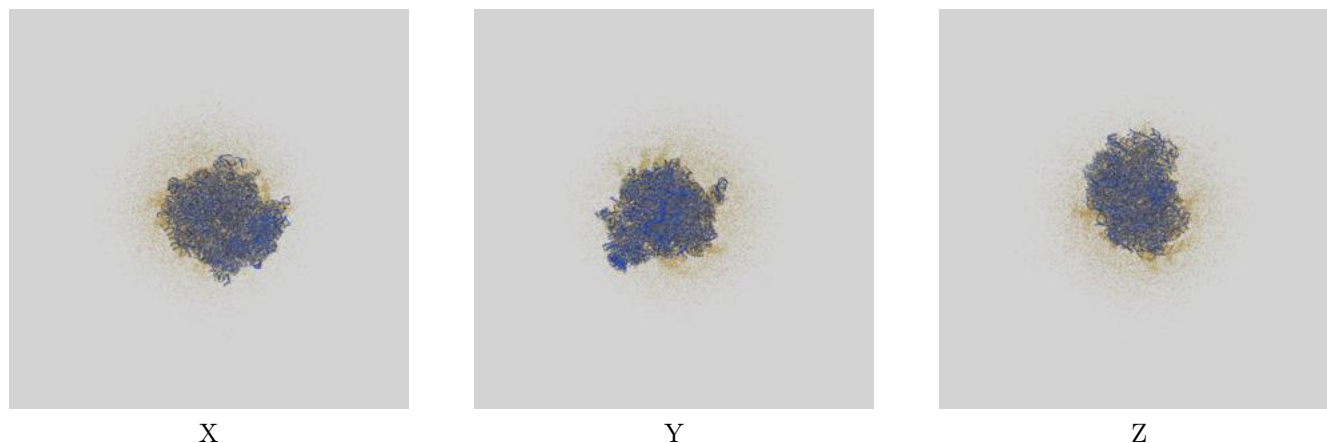
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.59	8.48	5.00

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.59 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

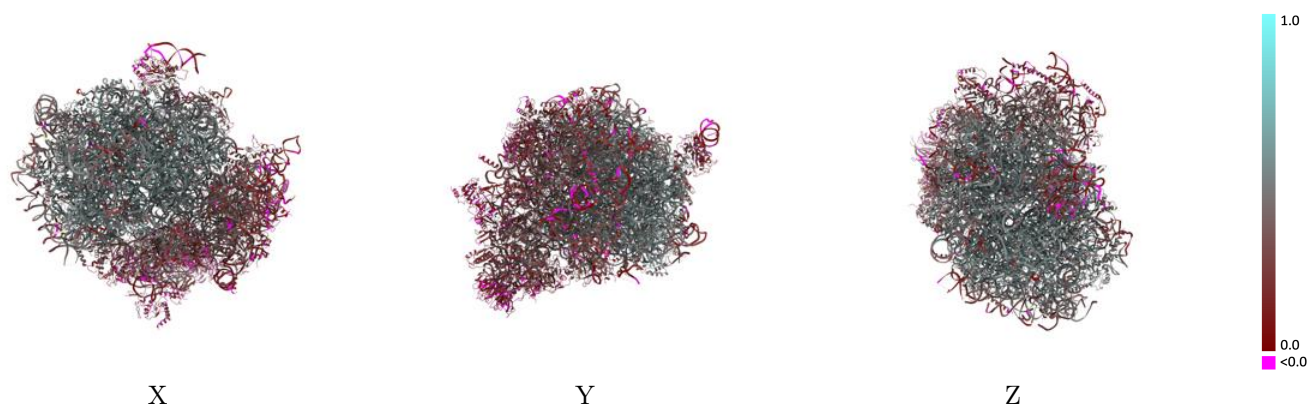
This section contains information regarding the fit between EMDB map EMD-75740 and PDB model 11JJ. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



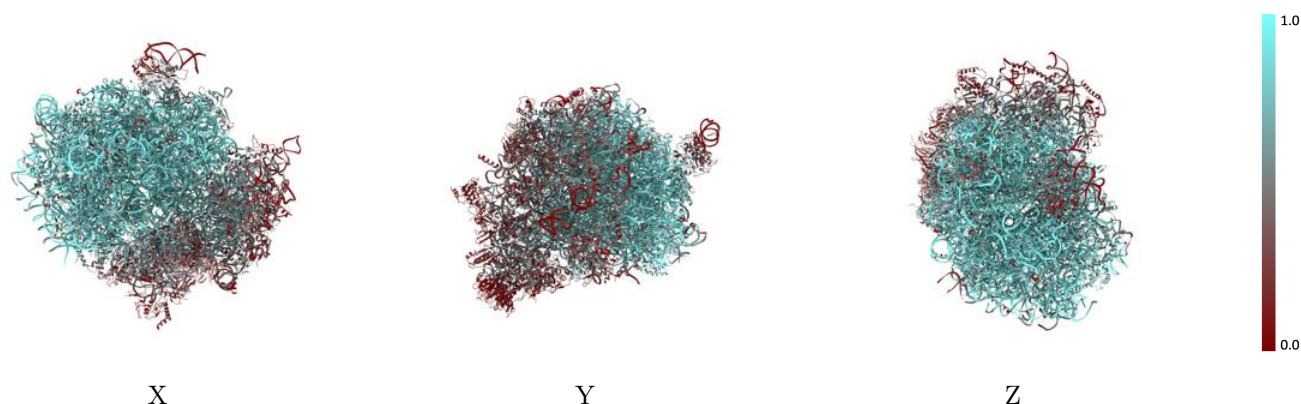
The images above show the 3D surface view of the map at the recommended contour level 3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



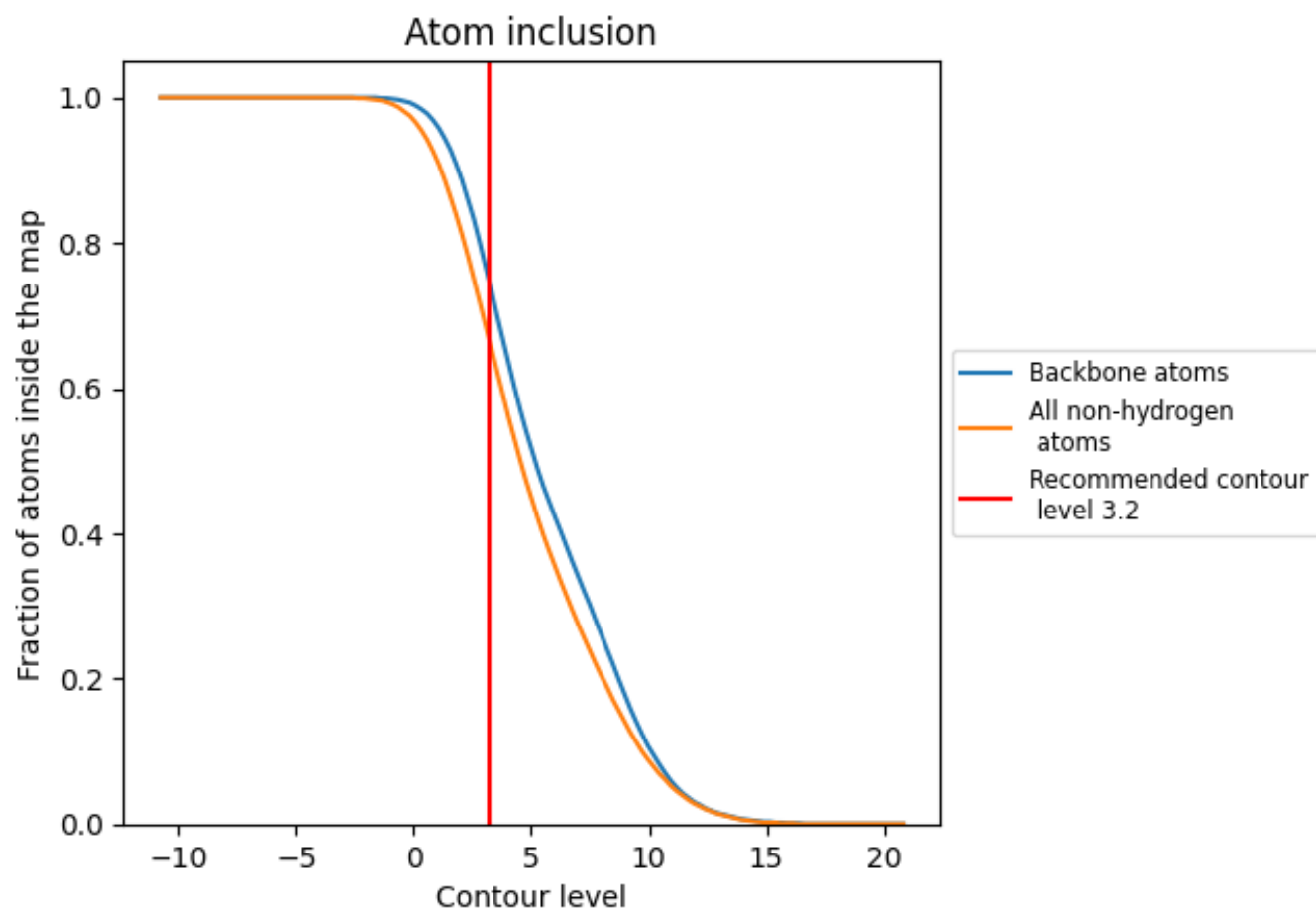
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6670	 0.4080
10	 0.7490	 0.4880
11	 0.6020	 0.3890
13	 0.7640	 0.4850
14	 0.7450	 0.4850
15	 0.8280	 0.5430
17	 0.7860	 0.5120
18	 0.6030	 0.3420
19	 0.6910	 0.4330
20	 0.8050	 0.5280
21	 0.7620	 0.4910
22	 0.5930	 0.3740
23	 0.7080	 0.5010
26	 0.7700	 0.4910
27	 0.7360	 0.4740
28	 0.8630	 0.4850
29	 0.6700	 0.4220
30	 0.6870	 0.4530
31	 0.7340	 0.4790
32	 0.7990	 0.5310
34	 0.7480	 0.5010
35	 0.7320	 0.4780
36	 0.7610	 0.4710
37	 0.8260	 0.5310
38	 0.6640	 0.3980
39	 0.7470	 0.4960
40	 0.7450	 0.4700
41	 0.6010	 0.4280
42	 0.7660	 0.4940
58	 0.8800	 0.5010
6	 0.9160	 0.5280
A	 0.3080	 0.2190
AA	 0.1050	 0.1450
AS	 0.4760	 0.3570
BB	 0.3090	 0.2870



Continued on next page...

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Chain	Atom inclusion	Q-score
CC	 0.2570	 0.1650
DD	 0.4560	 0.3680
EE	 0.0970	 0.1220
ES	 0.0520	 0.0560
F	 0.3330	 0.2280
FF	 0.5150	 0.3820
GG	 0.5140	 0.3690
IF	 0.4380	 0.3460
II	 0.2230	 0.2210
L3	 0.7740	 0.5130
L4	 0.7960	 0.5140
L5	 0.7250	 0.4560
L6	 0.7380	 0.4660
L7	 0.8050	 0.5220
L8	 0.8020	 0.5290
L9	 0.7210	 0.4690
LA	 0.1890	 0.2190
LL	 0.3280	 0.2330
MM	 0.2730	 0.2120
OO	 0.2130	 0.2300
PP	 0.3040	 0.2730
Q	 0.8080	 0.5280
RR	 0.4590	 0.3320
RS	 0.2560	 0.2360
S2	 0.3490	 0.3000
S3	 0.3040	 0.2600
S4	 0.2960	 0.2750
S5	 0.3190	 0.2380
S6	 0.3070	 0.2260
S7	 0.2480	 0.2370
S8	 0.4090	 0.3260
S9	 0.3250	 0.2760
SS	 0.2620	 0.2010
TT	 0.2500	 0.1950
UU	 0.5100	 0.3560
VV	 0.3410	 0.3030
W	 0.5030	 0.3490
WW	 0.2830	 0.2500
WX	 0.4140	 0.3510
XX	 0.4040	 0.2980
YY	 0.2490	 0.2060
ZZ	 0.1220	 0.1120

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Chain	Atom inclusion	Q-score
aa	 0.7120	 0.4390
bb	 0.8070	 0.5140
cc	 0.7490	 0.4890
dd	 0.8120	 0.5380
ee	 0.8230	 0.5340
ff	 0.7370	 0.4960
gg	 0.7990	 0.5110
s	 0.3910	 0.2590
t	 0.1840	 0.1360
v	 0.3680	 0.2590