



wwPDB EM Validation Summary Report ⓘ

Sep 6, 2026 – 06:27 PM EDT

PDB ID : 11KH / pdb_000011kh
EMDB ID : EMD-75768
Title : Rabbit 80S with 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 : 2026-02-28
Resolution : 3.10 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:

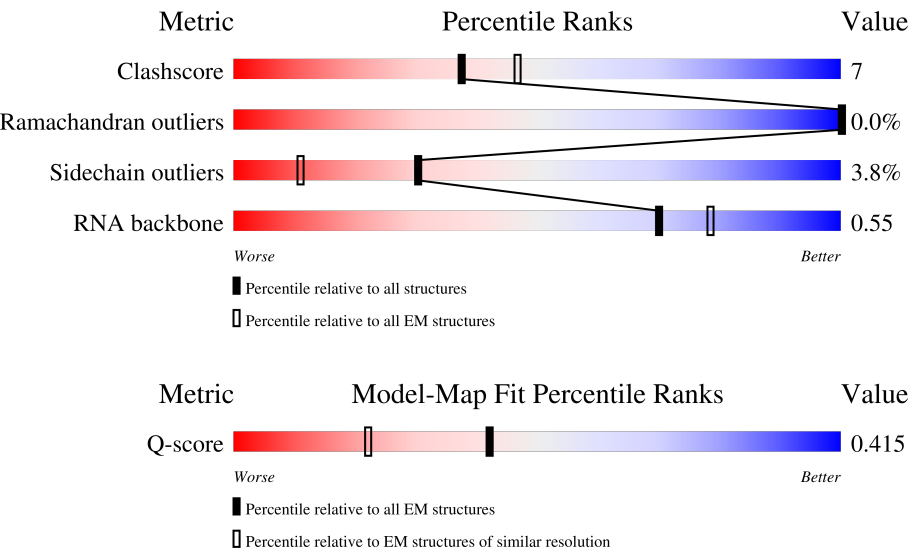
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.10 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.



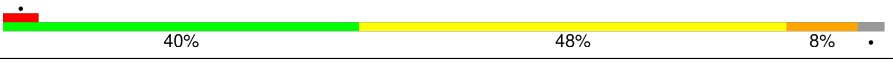
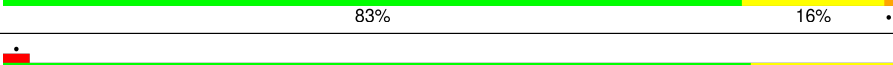
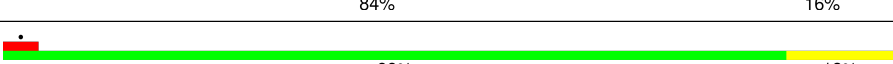
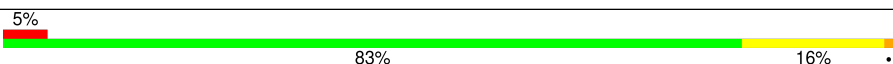
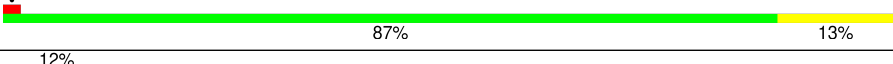
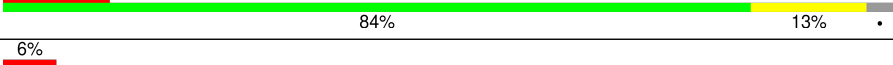
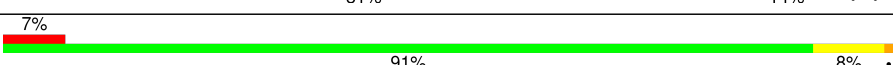
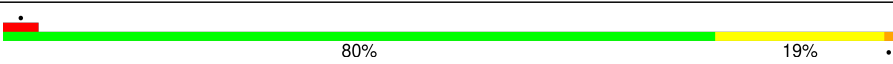
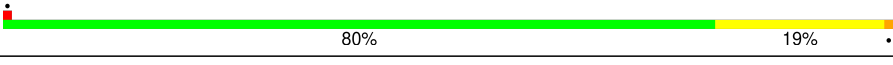
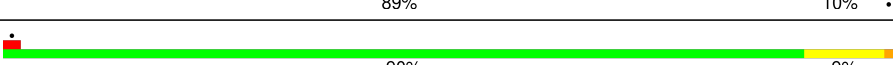
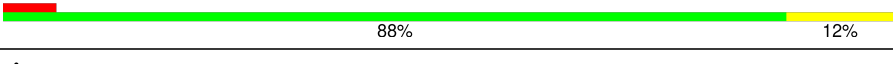
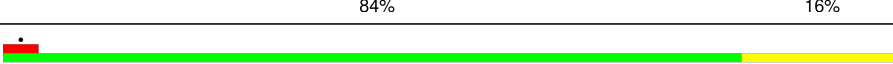
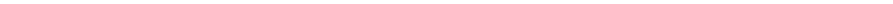
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	BB	295	60% 64%9%26%
2	S2	293	55% 62%13%25%
3	PP	83	84% 90%10%

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Mol	Chain	Length	Quality of chain
4	DD	151	
5	58	156	
6	5	120	
7	L8	248	
8	L3	394	
9	L4	362	
10	L5	293	
11	L6	347	
12	L7	225	
13	aa	240	
14	L9	190	
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	23	131	
26	cc	118	
27	26	134	
28	27	135	

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Mol	Chain	Length	Quality of chain
29	dd	147	
30	29	245	
31	30	98	
32	31	107	
33	32	128	
34	ee	109	
35	34	114	
36	35	122	
37	36	102	
38	37	86	
39	38	69	
40	39	50	
41	40	52	
42	41	25	
43	42	104	
44	ff	91	
45	gg	124	
46	AS	213	
47	FF	149	
48	VV	83	
49	s	196	
50	F	359	
51	Q	188	
52	ES	5070	
53	ZZ	68	

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Mol	Chain	Length	Quality of chain
54	EE	117	
55	TT	75	
56	S5	191	
57	WW	62	
58	II	142	
59	CC	96	
60	AA	313	
61	OO	100	
62	MM	141	
63	LL	144	
64	HH	120	
65	18	1698	
66	XX	55	
67	RR	141	
68	SS	124	
69	S6	237	
70	S4	262	
71	S9	185	
72	S7	189	
73	YY	55	
74	S3	214	
75	RS	132	
76	WX	129	
77	S8	206	
78	W	157	

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Mol	Chain	Length	Quality of chain
79	GG	135	
80	UU	115	
81	11	170	
82	IF	643	
83	LA	35	
84	t	153	
85	28	4805	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 218380 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 Small ribosomal subunit protein uS2.

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

- Molecule 2 is a protein called 40S ribosomal protein S2.

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

- Molecule 3 is a protein called eS21.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

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

- Molecule 9 is a protein called 60S ribosomal protein L4.

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

- Molecule 10 is a protein called 60S ribosomal protein L5.

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

- Molecule 11 is a protein called large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L6	216	Total	C	N	O	S	0	0
			1728	1115	329	281	3		

- Molecule 12 is a protein called 60S ribosomal protein L7.

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

- Molecule 13 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 14 is a protein called 60S ribosomal protein L9.

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

- 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 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	23	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a protein called 40S ribosomal protein S3a.

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

- Molecule 47 is a protein called 40S ribosomal protein S13.

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

- Molecule 48 is a protein called 40S ribosomal protein S27.

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

- Molecule 49 is a protein called 60S acidic ribosomal protein P0.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	359	Total	C	N	O	S	0	0
			2807	1768	484	538	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 RNA chain called ES27L.

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

- Molecule 53 is a protein called 40S ribosomal protein S27a.

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

- Molecule 54 is a protein called 40S ribosomal protein S12.

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

- Molecule 55 is a protein called 40S ribosomal protein S25.

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

- Molecule 56 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 57 is a protein called 40S ribosomal protein S28.

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

- Molecule 58 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 59 is a protein called 40S ribosomal protein S10.

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

- Molecule 60 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 61 is a protein called 40S ribosomal protein S20.

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

- Molecule 62 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 63 is a protein called 40S ribosomal protein S18.

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

- Molecule 64 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	HH	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 65 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	18	1691	Total	C	N	O	P	0	0
			36103	16115	6485	11813	1690		

- Molecule 66 is a protein called 40S ribosomal protein S29.

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

- Molecule 67 is a protein called 40S ribosomal protein S23.

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

- Molecule 68 is a protein called 40S ribosomal protein S24.

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

- Molecule 69 is a protein called 40S ribosomal protein S6.

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

- Molecule 70 is a protein called 40S ribosomal protein S4.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 73 is a protein called 40S ribosomal protein S30.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 75 is a protein called 40S ribosomal protein S17.

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

- Molecule 76 is a protein called 40S ribosomal protein S15a.

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

- Molecule 77 is a protein called 40S ribosomal protein S8.

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

- Molecule 78 is a protein called eL24.

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

- Molecule 79 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 80 is a protein called eS26.

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

- Molecule 81 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 82 is a protein called IFRD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	IF	357	Total	C	N	O	S	0	0
			2767	1750	497	506	14		

- Molecule 83 is a protein called La-related protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	LA	35	Total	C	N	O	S	0	0
			280	174	49	56	1		

- Molecule 84 is a protein called uL11.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
85	28	3542	Total	C	N	O	P	0	0
			75969	33835	13925	24667	3542		

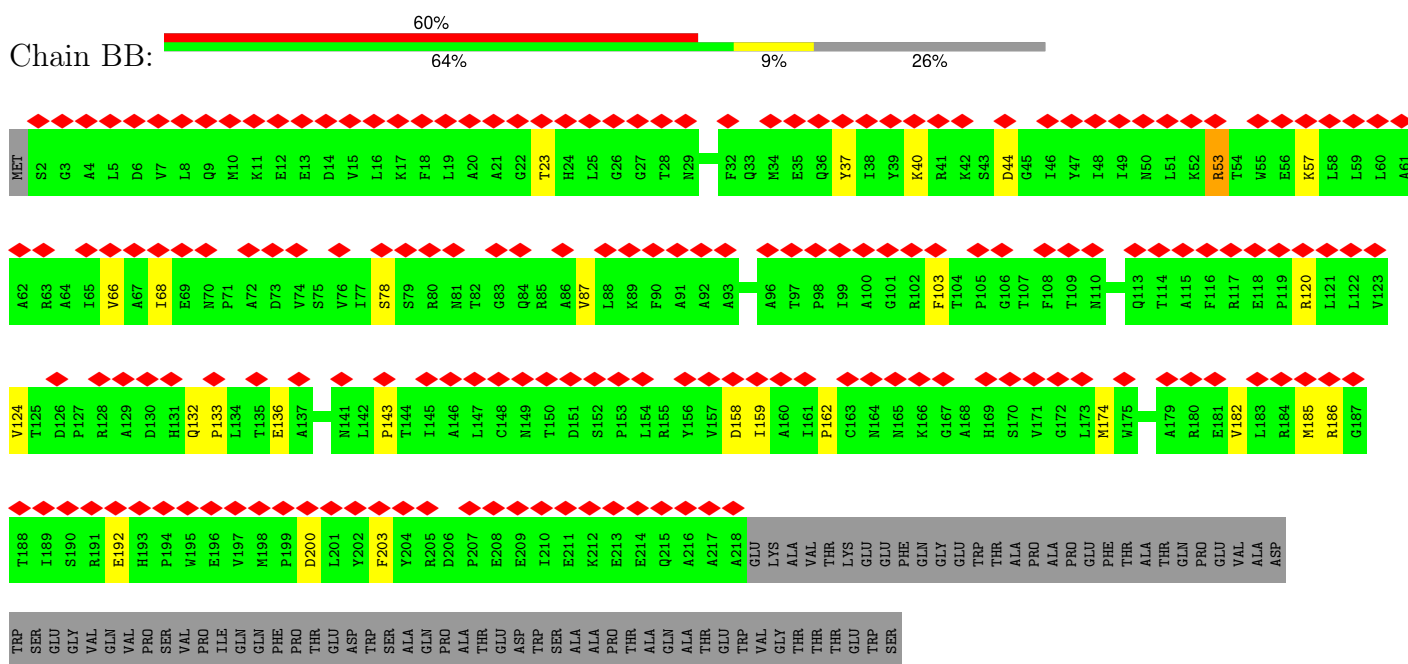
- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

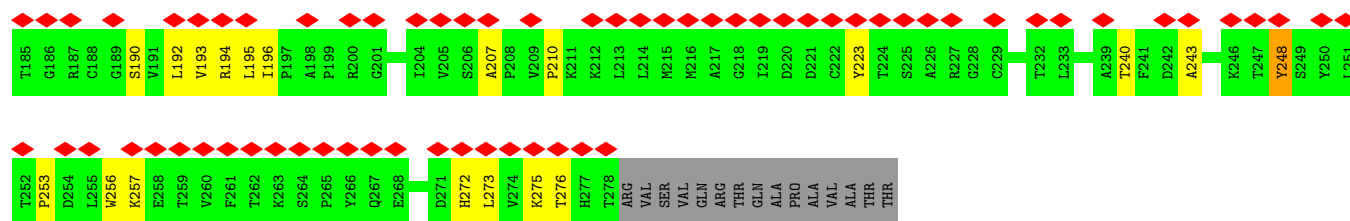
Mol	Chain	Residues	Atoms		AltConf
86	34	1	Total	Zn	0
			1	1	
86	37	1	Total	Zn	0
			1	1	
86	ff	1	Total	Zn	0
			1	1	
86	UU	1	Total	Zn	0
			1	1	

3 Residue-property plots

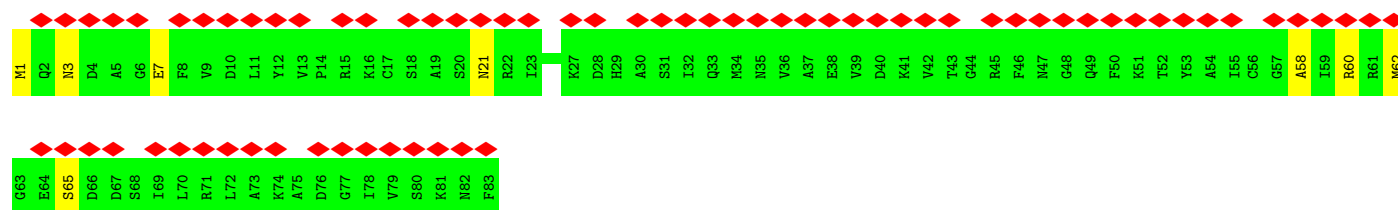
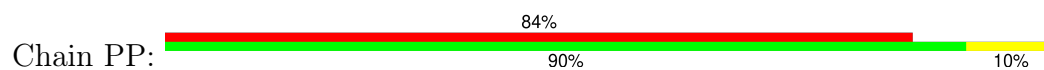
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Small ribosomal subunit protein uS2

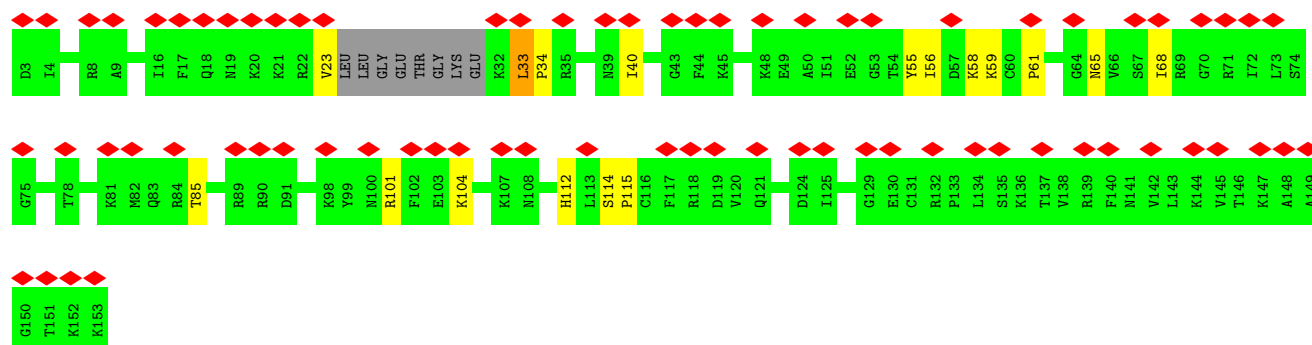
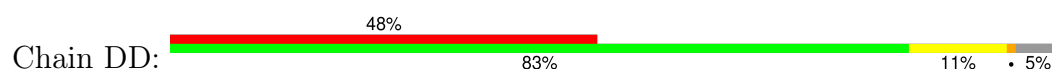




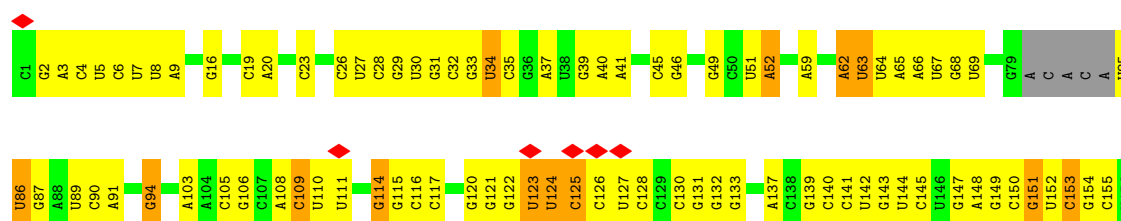
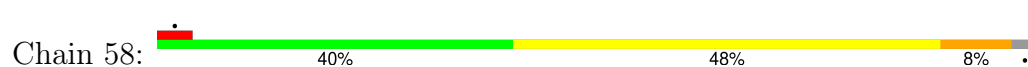
• Molecule 3: eS21



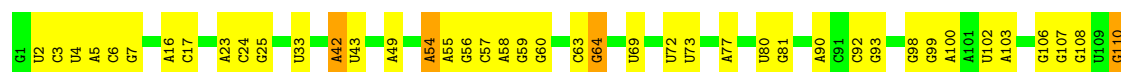
• Molecule 4: Small ribosomal subunit protein uS17

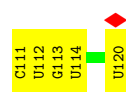


• Molecule 5: 5.8S rRNA

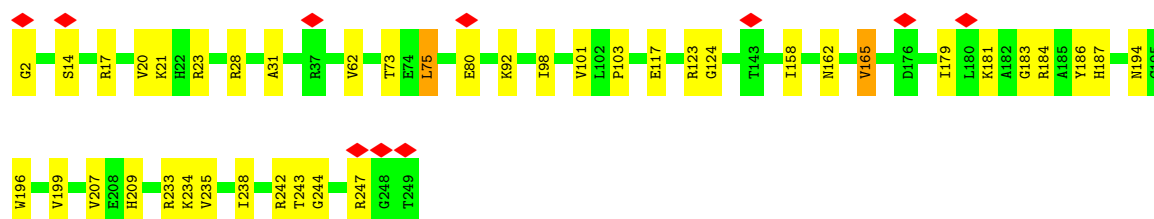
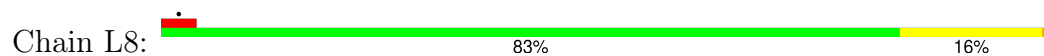


• Molecule 6: 5S rRNA

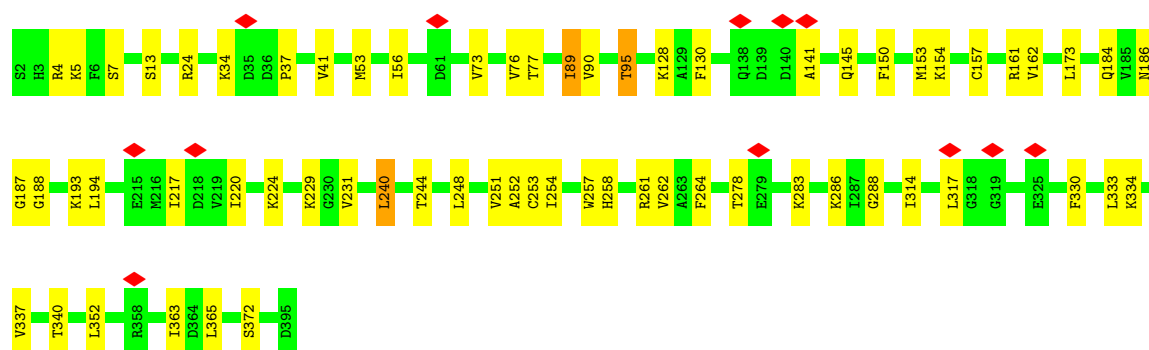
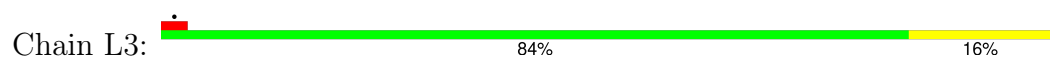




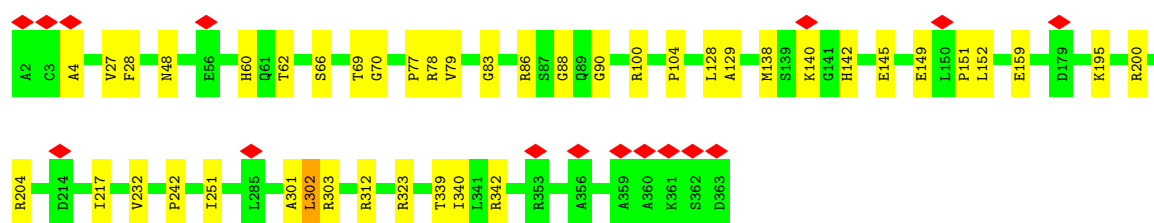
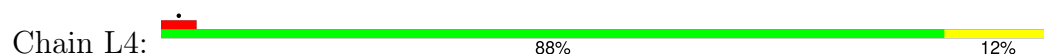
- Molecule 7: 60S ribosomal protein L8



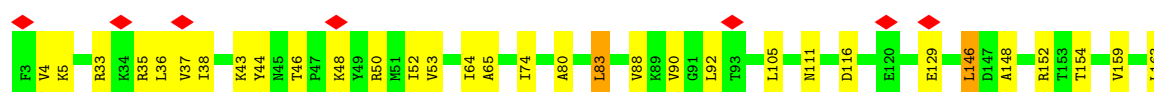
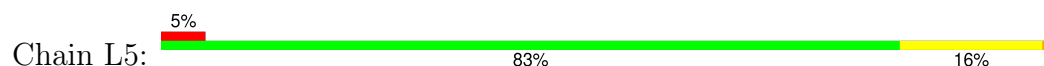
- Molecule 8: 60S ribosomal protein L3

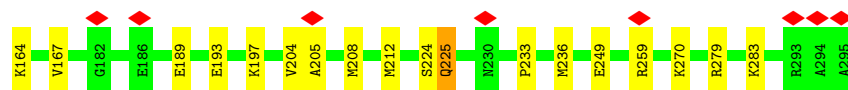


- Molecule 9: 60S ribosomal protein L4

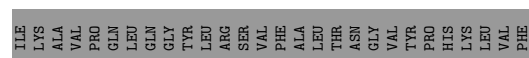
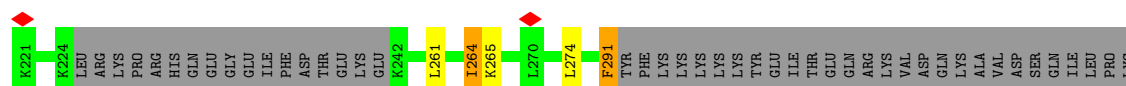
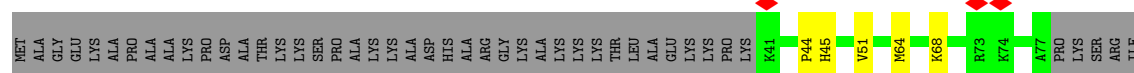


- Molecule 10: 60S ribosomal protein L5

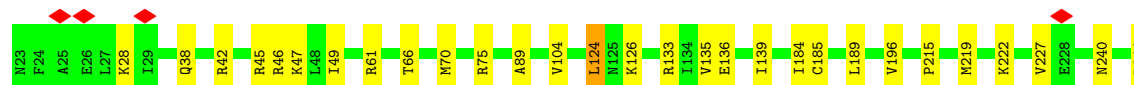




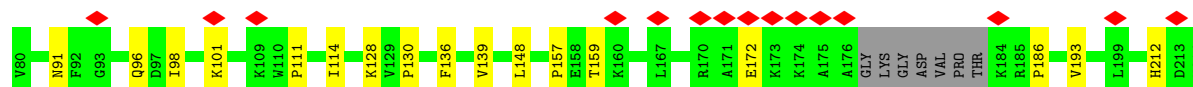
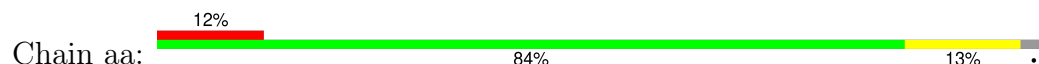
- Molecule 11: large ribosomal subunit protein eL6



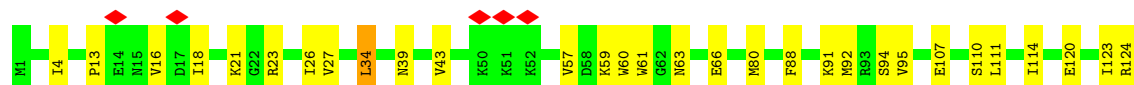
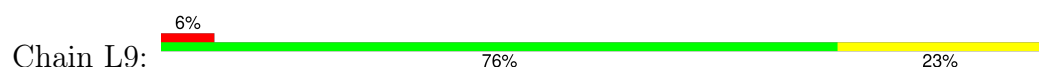
- Molecule 12: 60S ribosomal protein L7



- Molecule 13: Large ribosomal subunit protein eL8

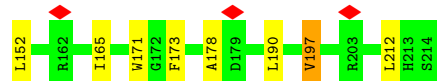
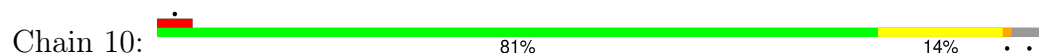


- Molecule 14: 60S ribosomal protein L9

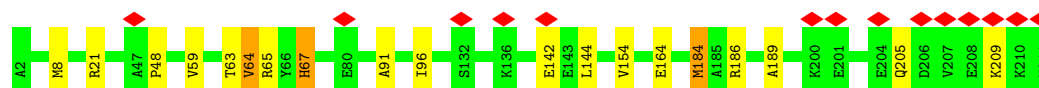
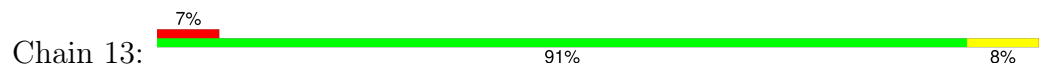




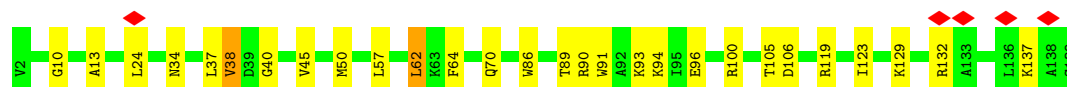
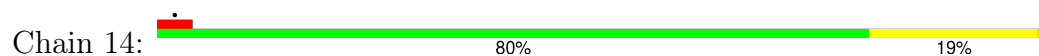
- Molecule 15: Ribosomal protein L10



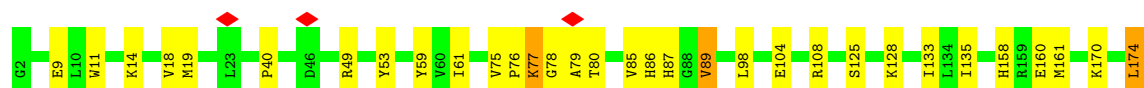
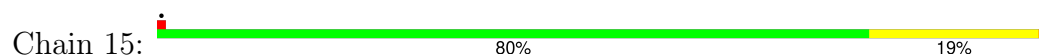
- Molecule 16: Large ribosomal subunit protein eL13



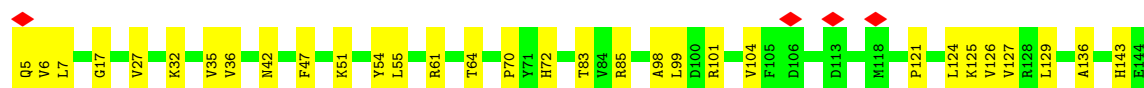
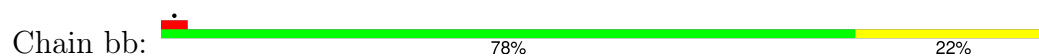
- Molecule 17: 60S ribosomal protein L14



- Molecule 18: 60S ribosomal protein L15

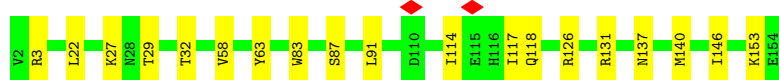
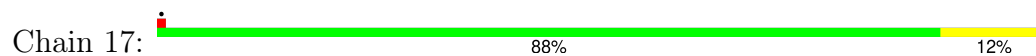


- Molecule 19: Large ribosomal subunit protein uL13

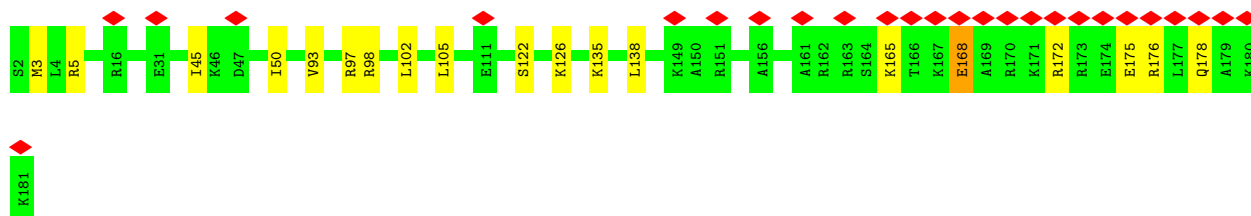




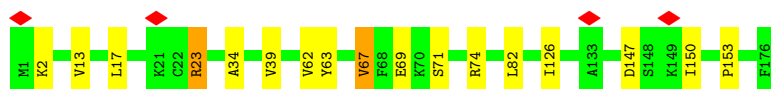
- Molecule 20: 60S ribosomal protein L17



- Molecule 21: 60S ribosomal protein L19



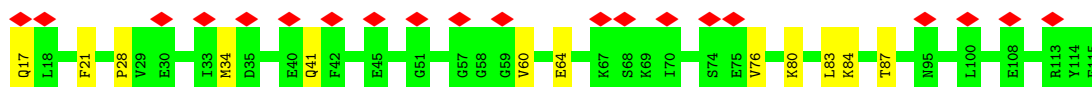
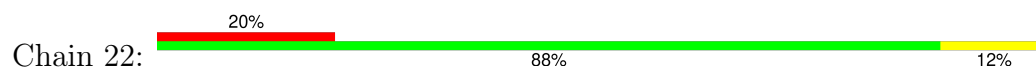
- Molecule 22: Large ribosomal subunit protein eL20



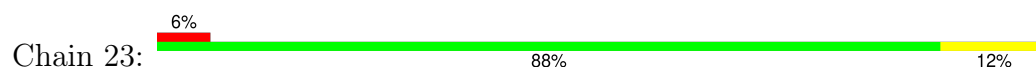
- Molecule 23: 60S ribosomal protein L21



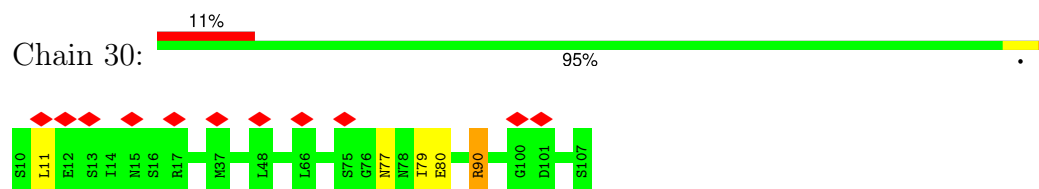
- Molecule 24: Large ribosomal subunit protein eL22



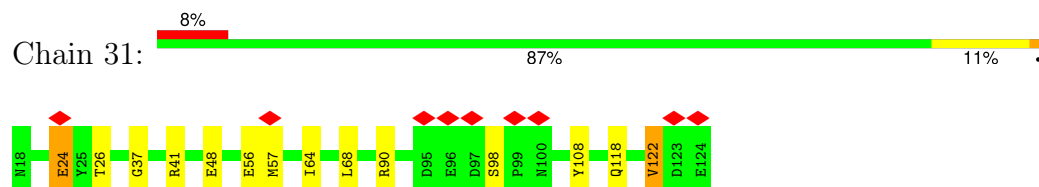
- Molecule 25: 60S ribosomal protein L23



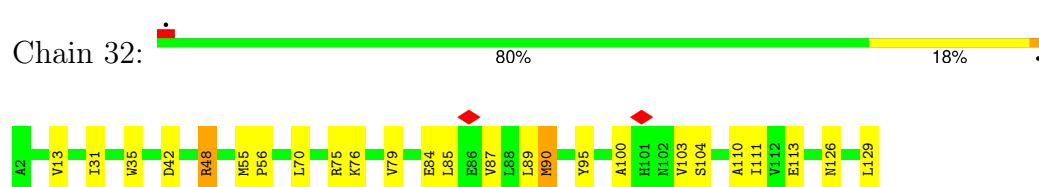
- Molecule 31: 60S ribosomal protein L30



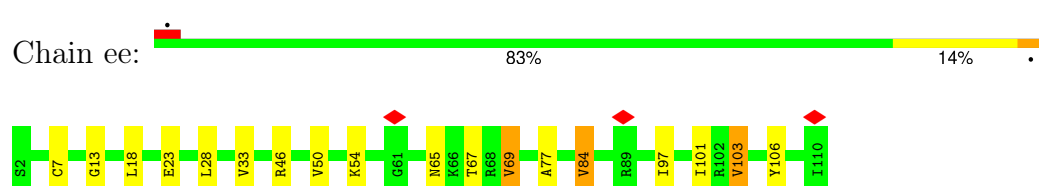
- Molecule 32: 60S ribosomal protein L31



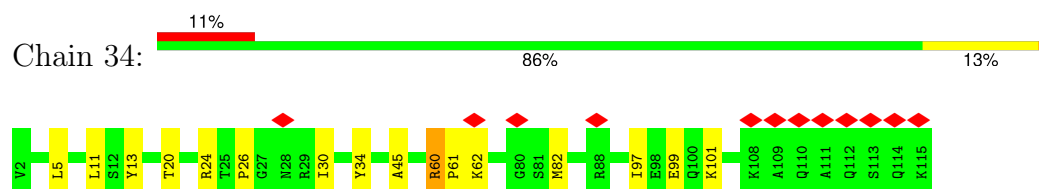
- Molecule 33: Large ribosomal subunit protein eL32



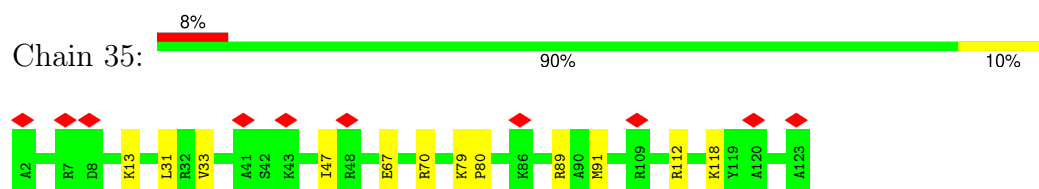
- Molecule 34: Large ribosomal subunit protein eL33



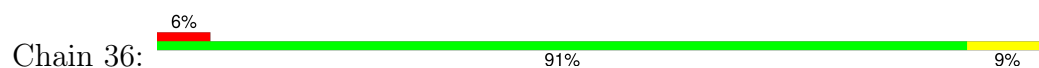
- Molecule 35: 60S ribosomal protein L34

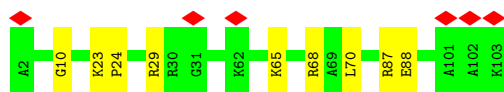


- Molecule 36: 60S ribosomal protein L35



- Molecule 37: 60S ribosomal protein L36

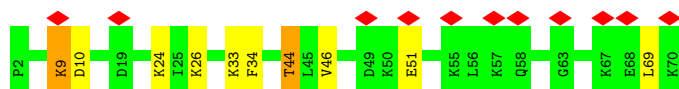
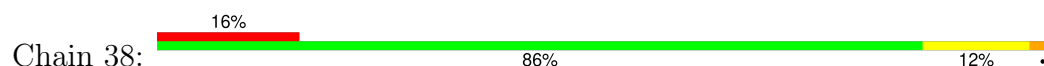




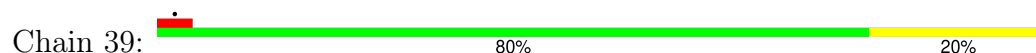
- Molecule 38: 60S ribosomal protein L37



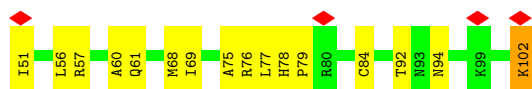
- Molecule 39: Large ribosomal subunit protein eL38



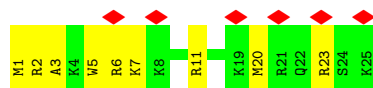
- Molecule 40: 60S ribosomal protein L39



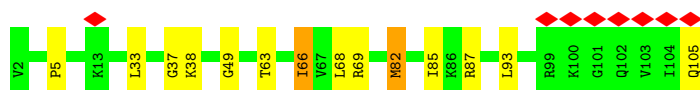
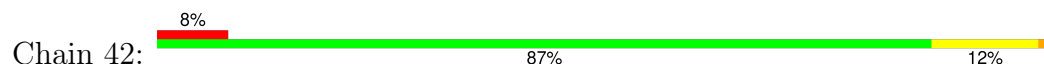
- Molecule 41: Large ribosomal subunit protein eL40



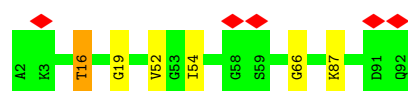
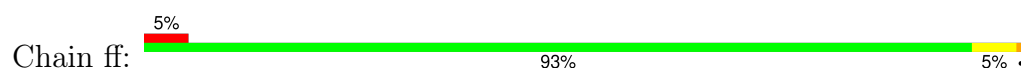
- Molecule 42: eL41



- Molecule 43: eL42



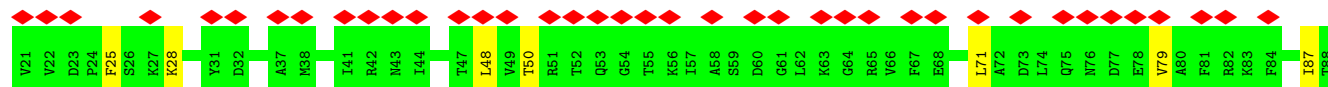
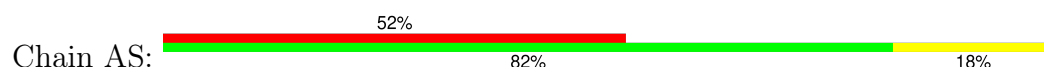
- Molecule 44: 60S ribosomal protein L37a



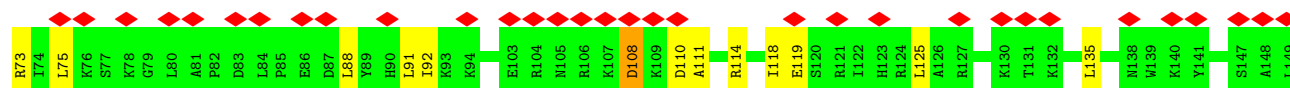
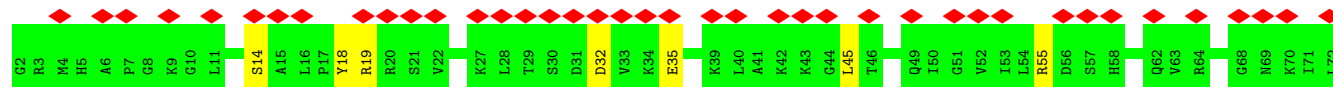
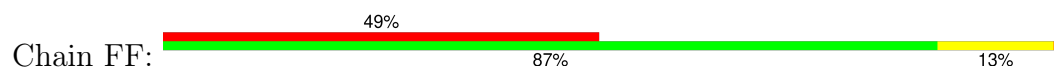
- Molecule 45: 60S ribosomal protein L28



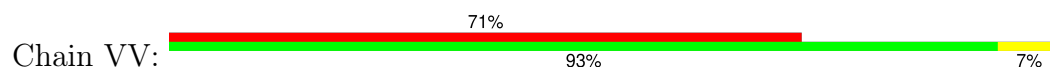
- Molecule 46: 40S ribosomal protein S3a

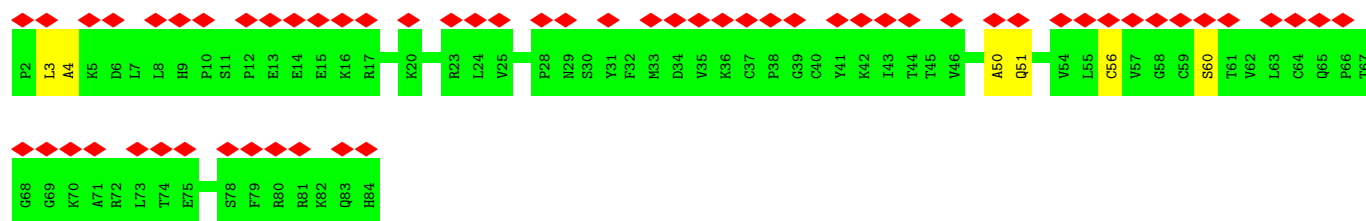


- Molecule 47: 40S ribosomal protein S13

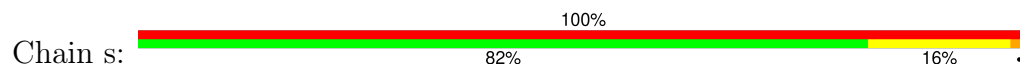


- Molecule 48: 40S ribosomal protein S27

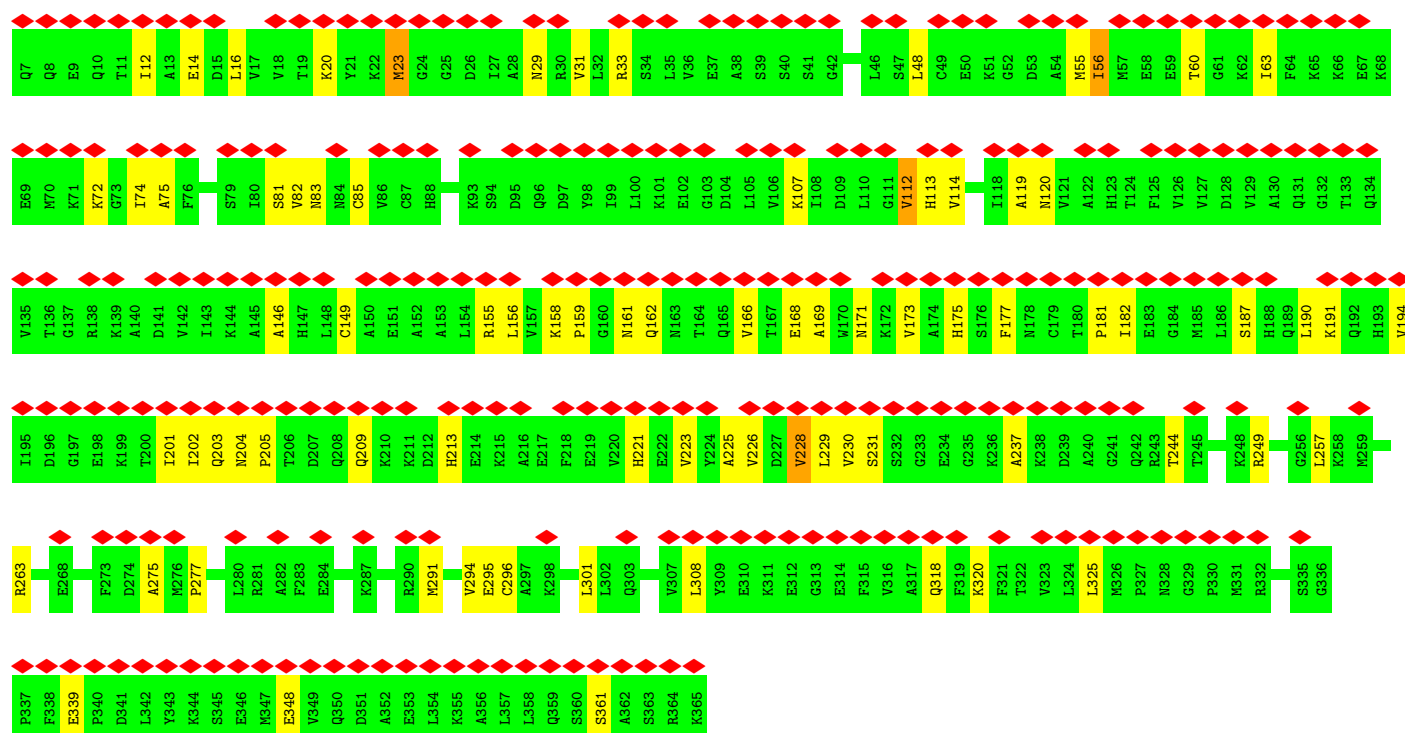
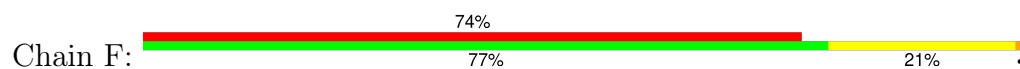


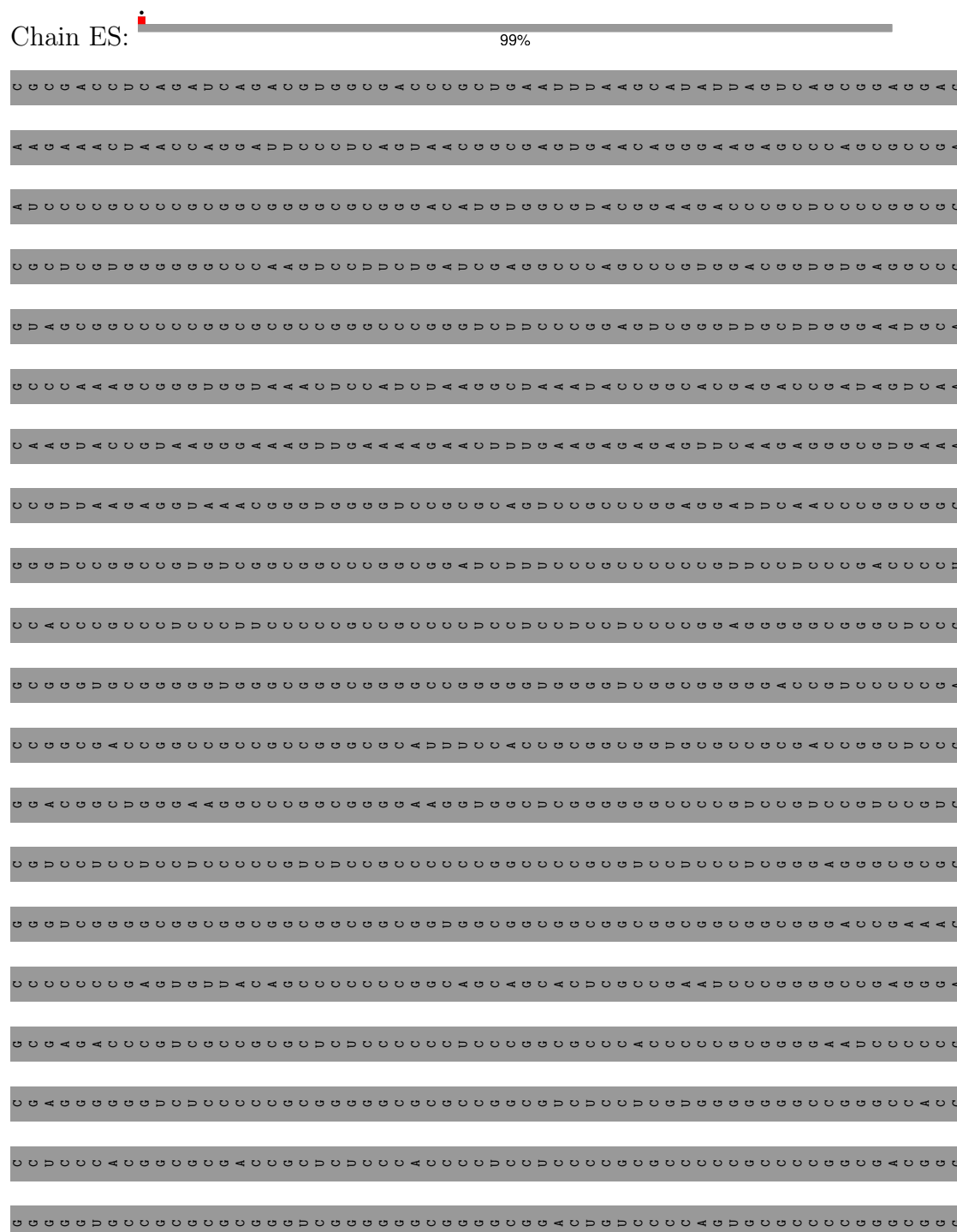


• Molecule 49: 60S acidic ribosomal protein P0



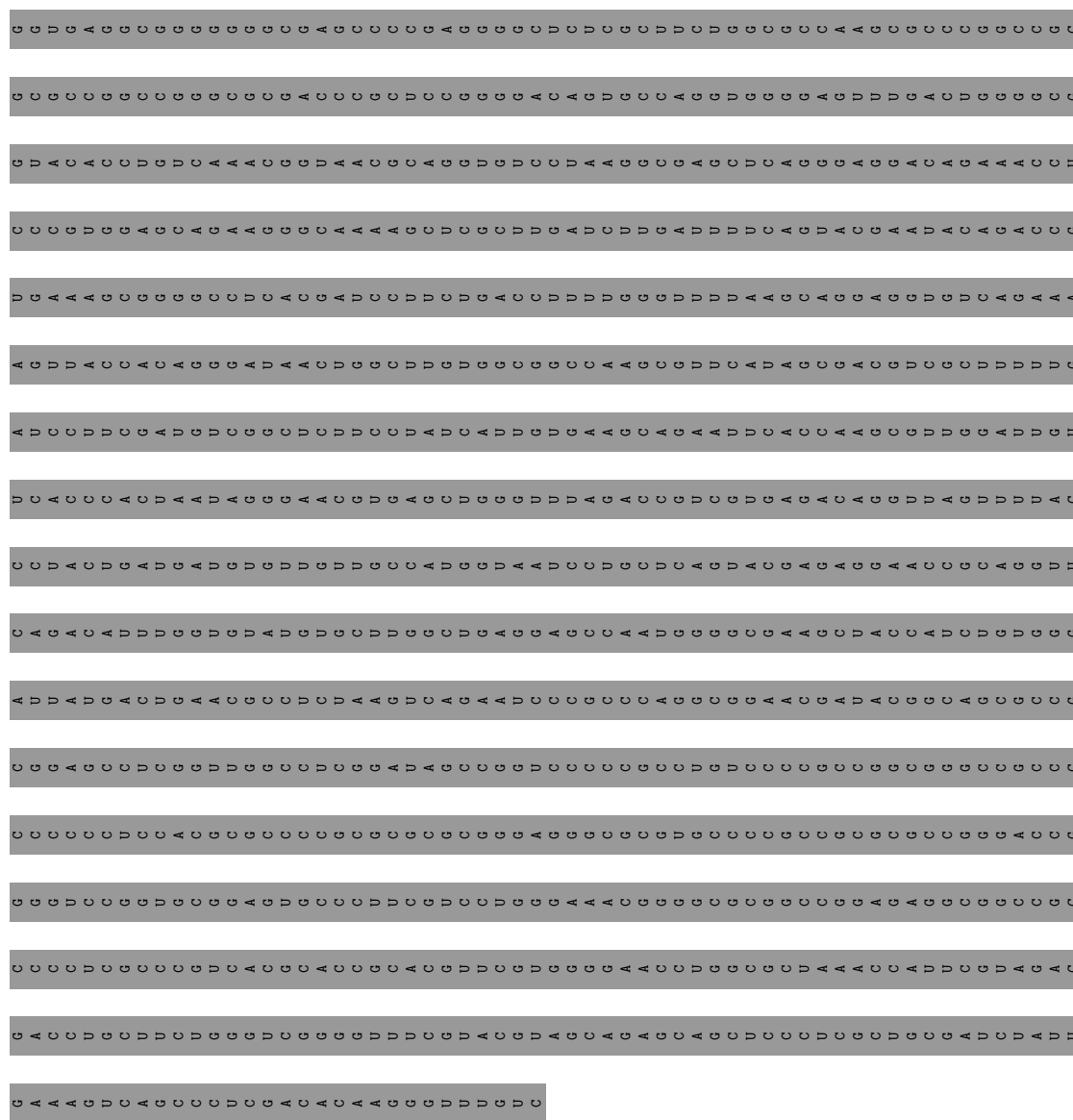
• Molecule 50: Proliferation-associated protein 2G4



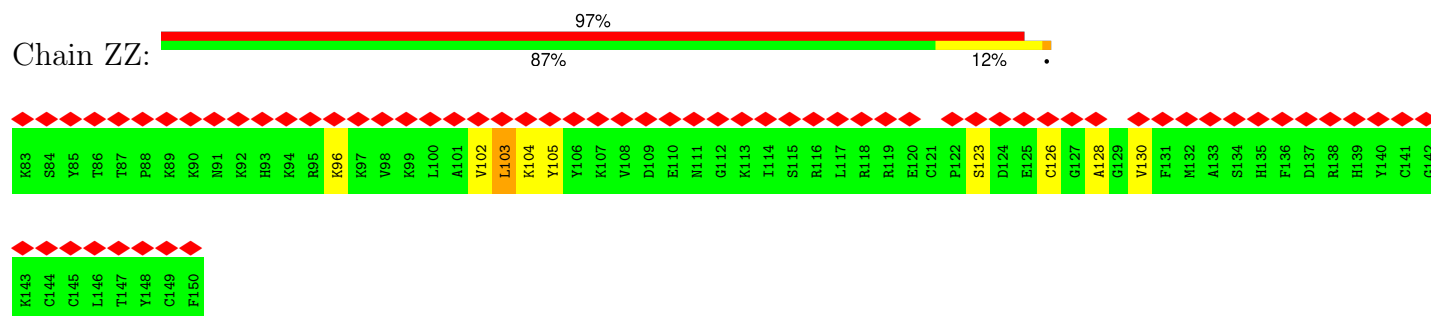




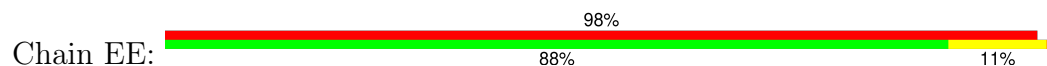


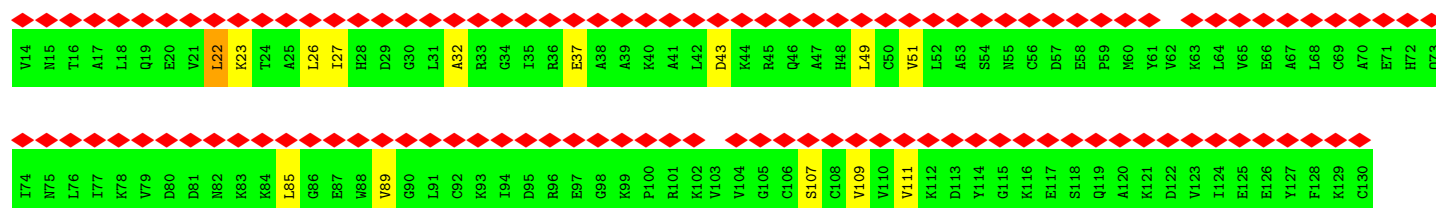


- Molecule 53: 40S ribosomal protein S27a

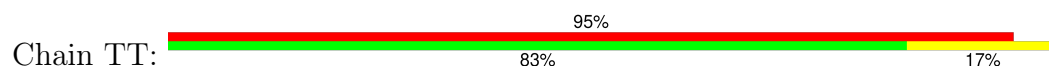


- Molecule 54: 40S ribosomal protein S12

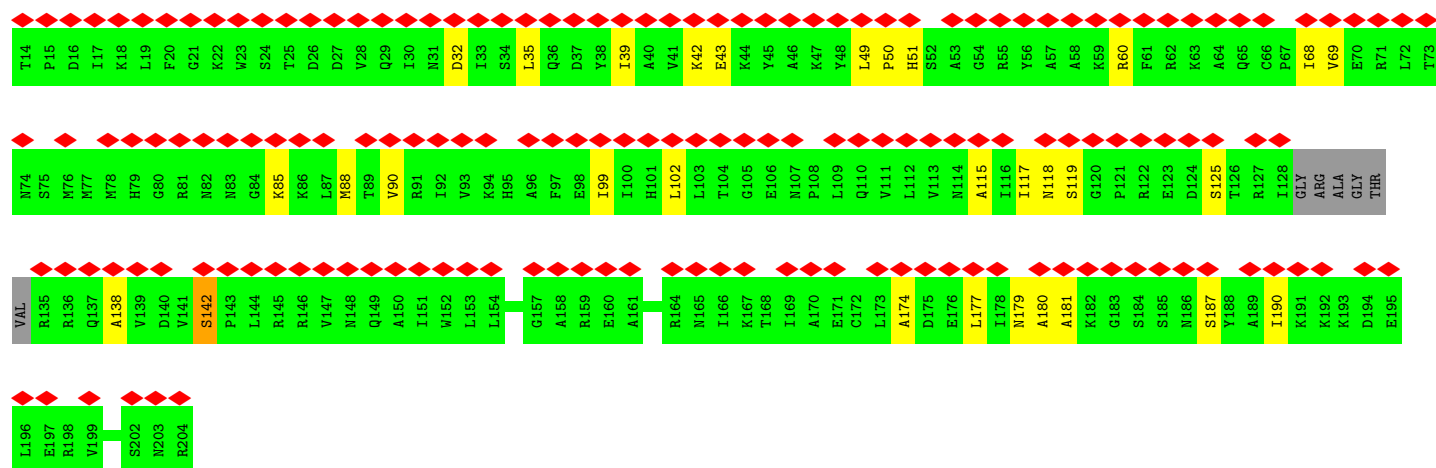
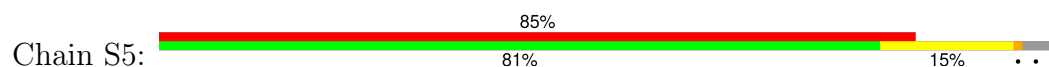




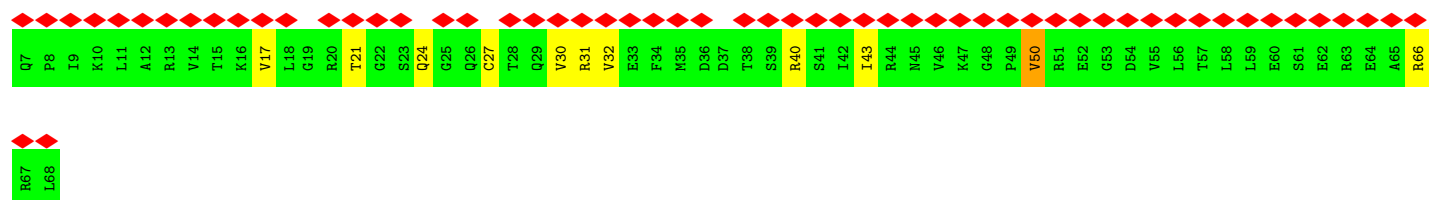
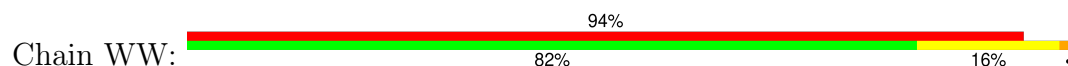
• Molecule 55: 40S ribosomal protein S25



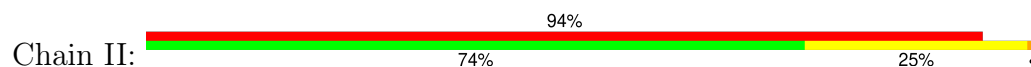
• Molecule 56: Small ribosomal subunit protein uS7

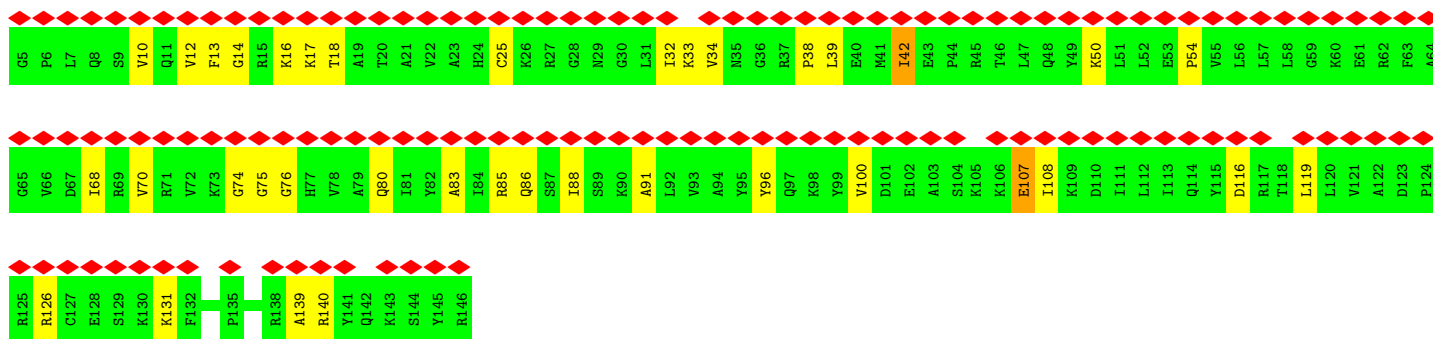


• Molecule 57: 40S ribosomal protein S28

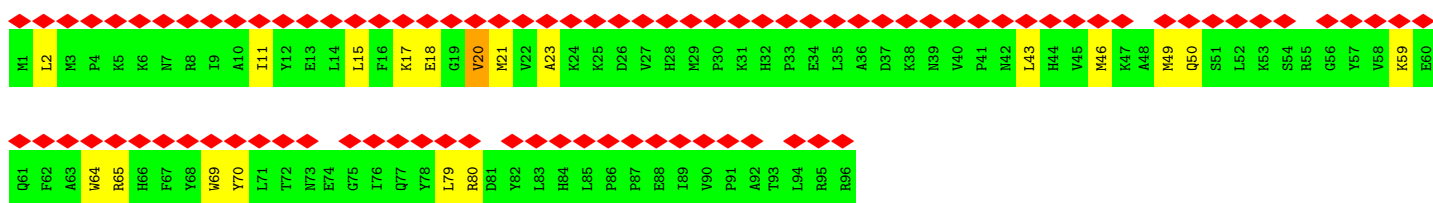
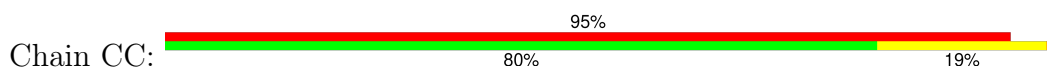


• Molecule 58: Small ribosomal subunit protein uS9

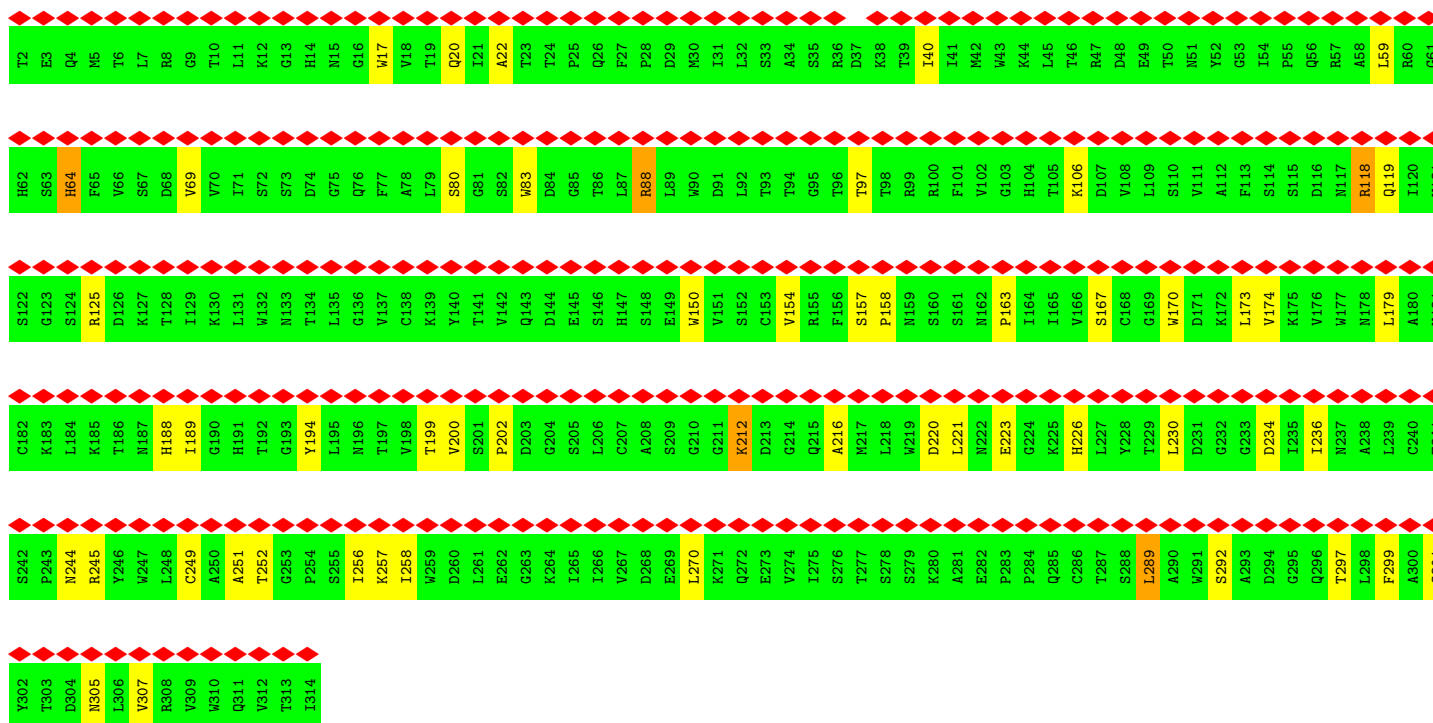
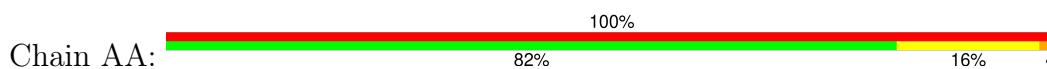




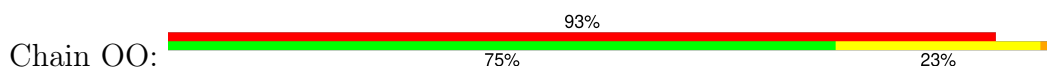
• Molecule 59: 40S ribosomal protein S10

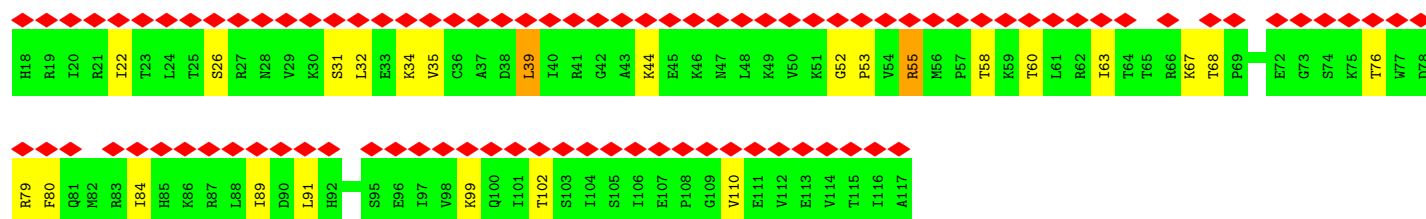


• Molecule 60: Receptor of activated protein C kinase 1

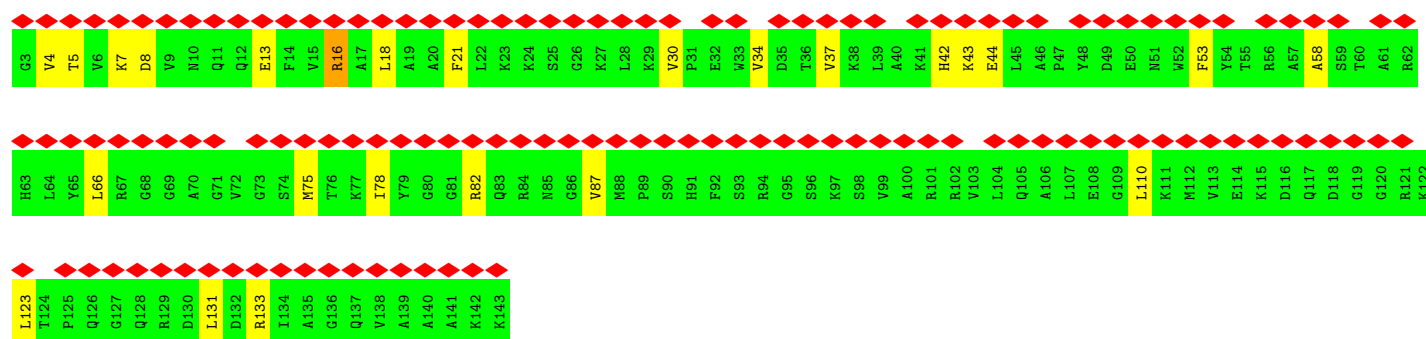
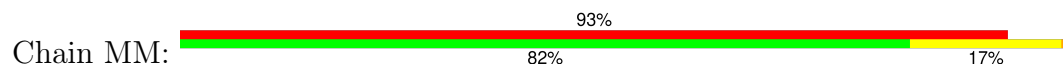


• Molecule 61: 40S ribosomal protein S20

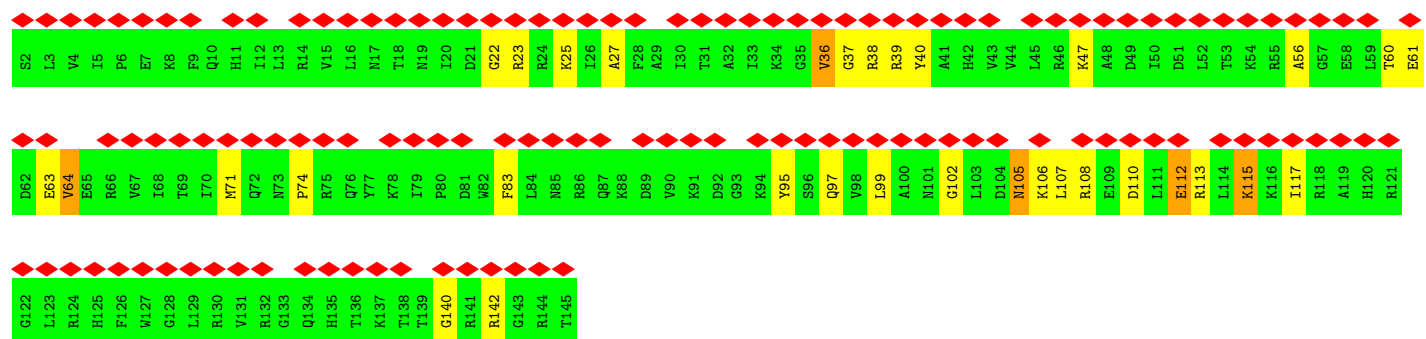
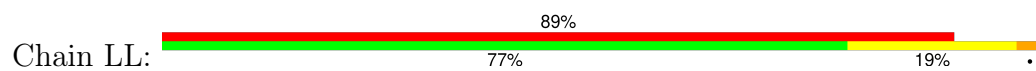




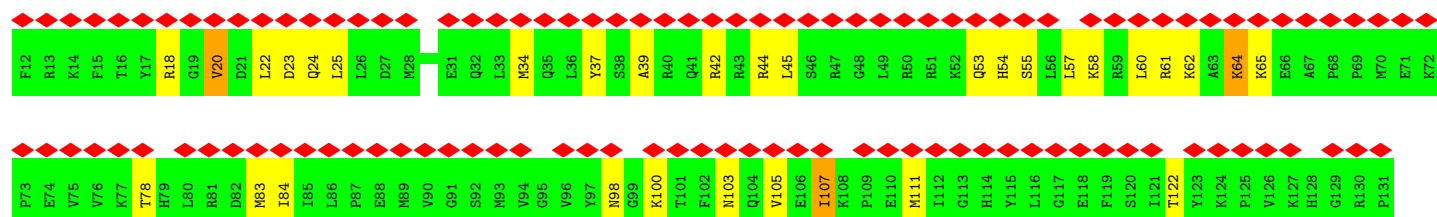
• Molecule 62: Small ribosomal subunit protein eS19



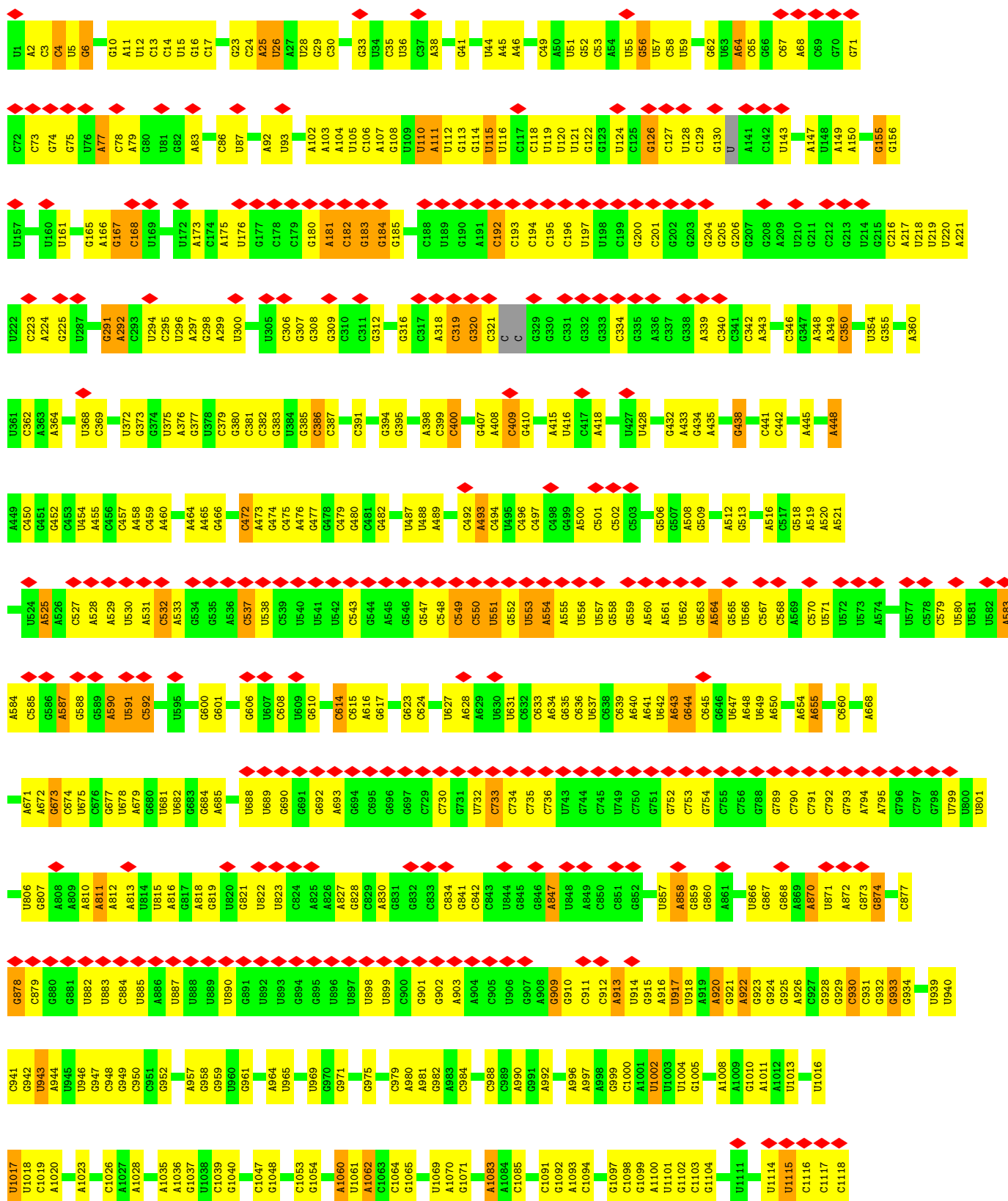
• Molecule 63: 40S ribosomal protein S18

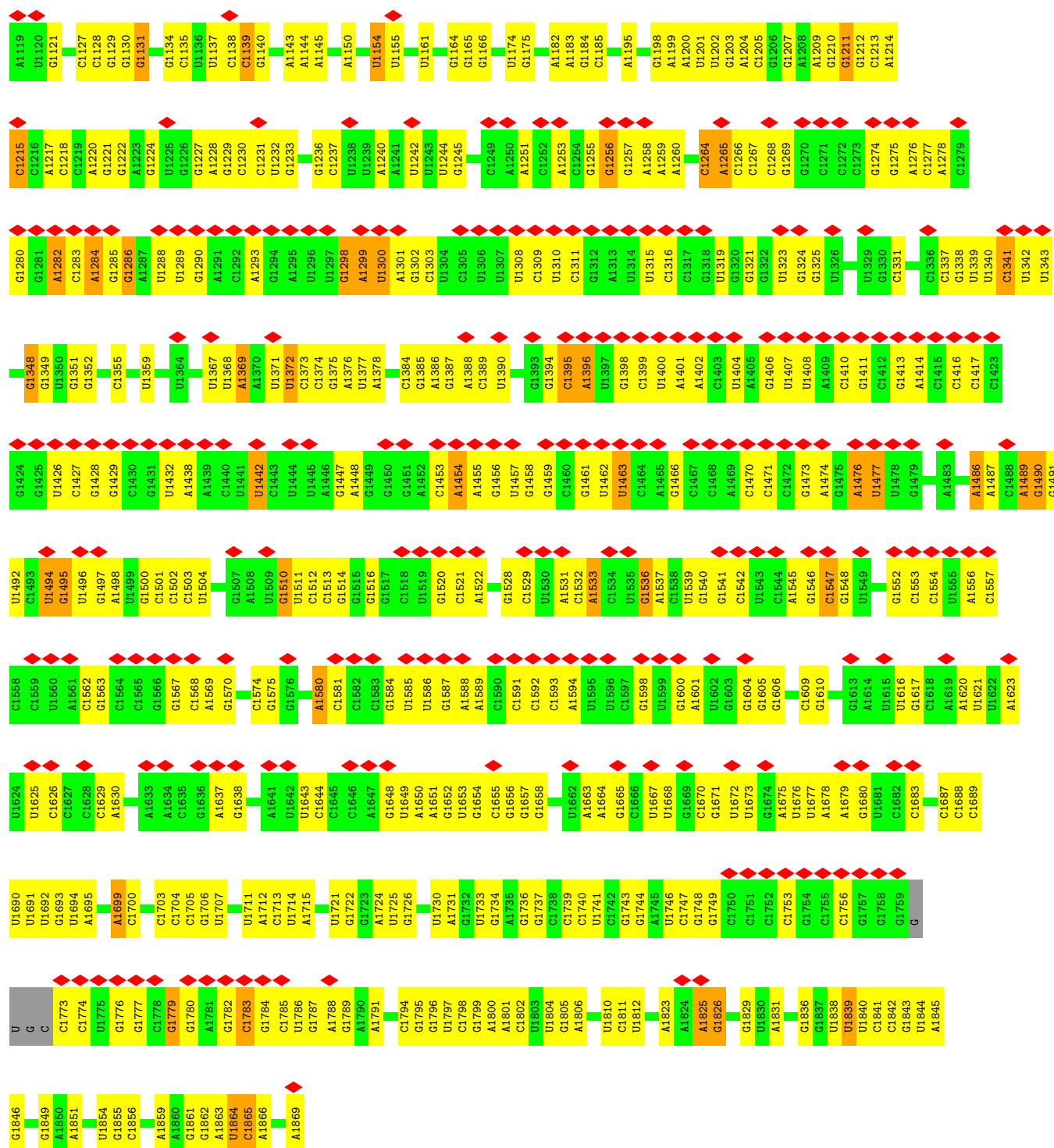


• Molecule 64: 40S ribosomal protein S15

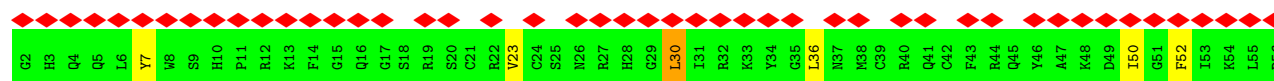
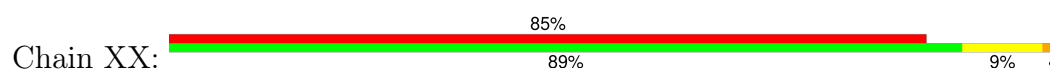


• Molecule 65: 18S rRNA





• Molecule 66: 40S ribosomal protein S29



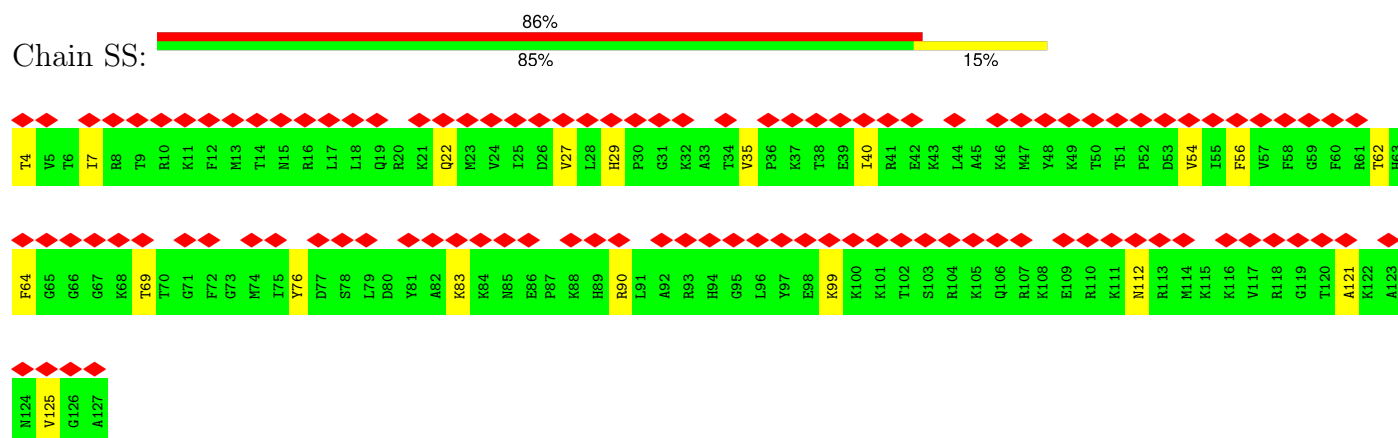
- Molecule 67: 40S ribosomal protein S23

Chain RR:



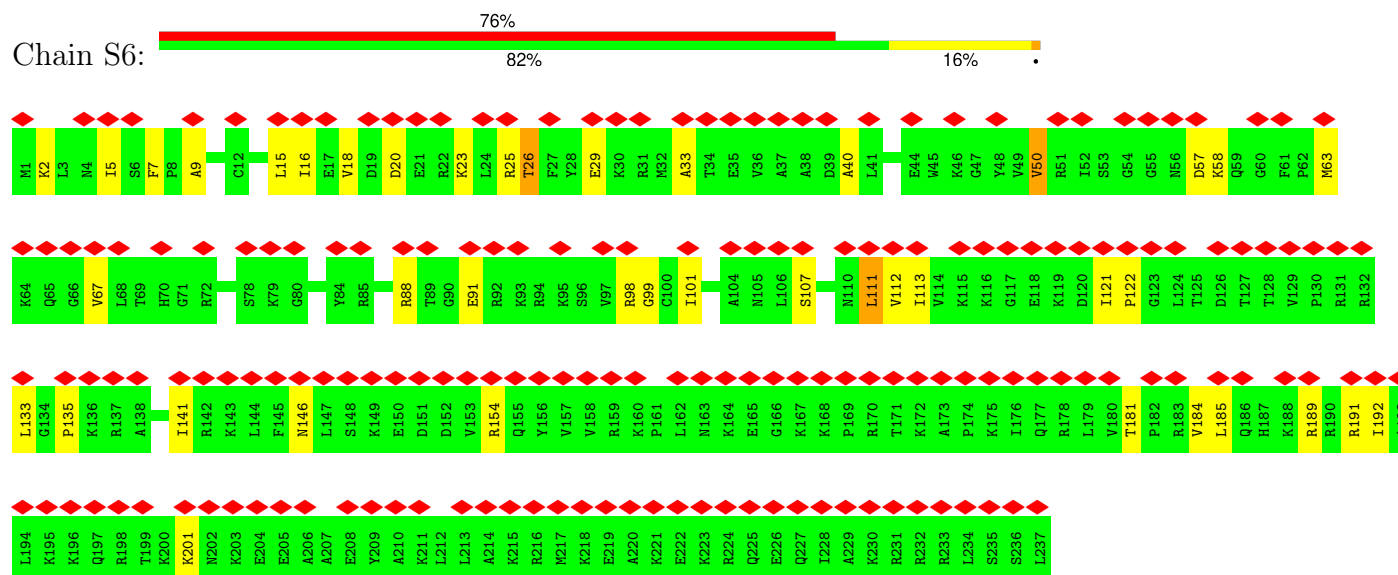
- Molecule 68: 40S ribosomal protein S24

Chain SS:



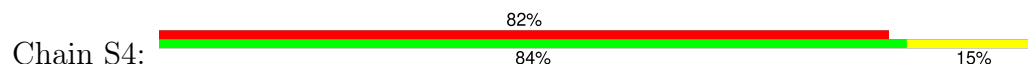
- Molecule 69: 40S ribosomal protein S6

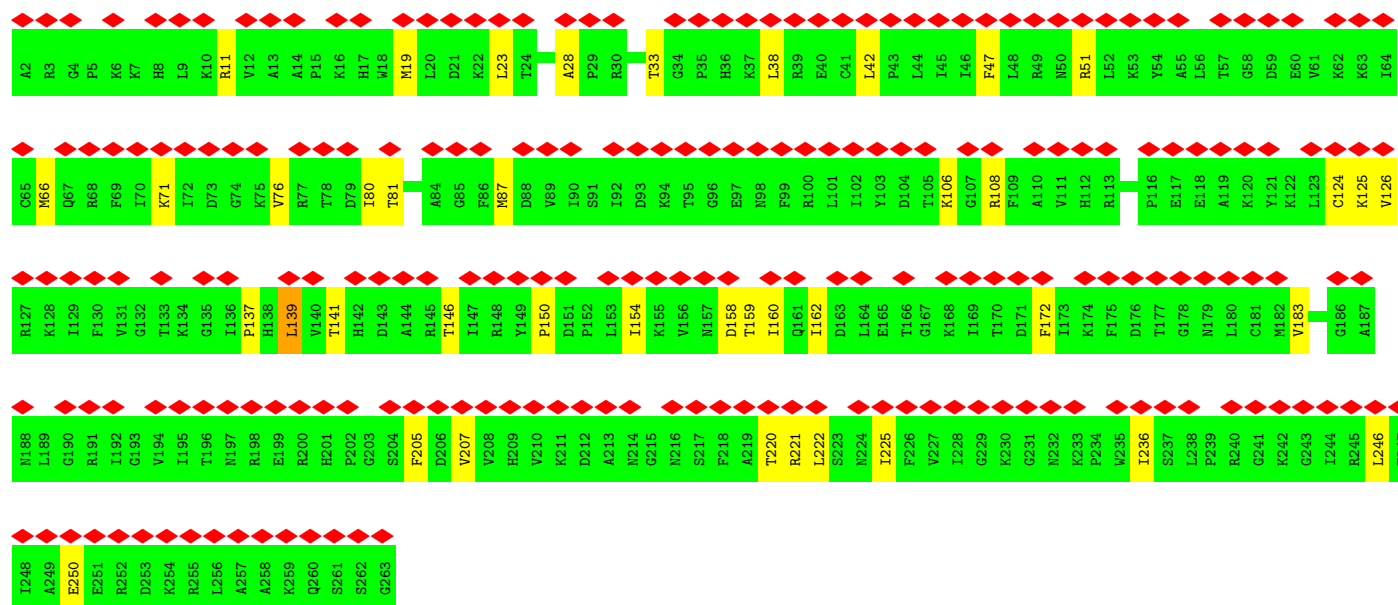
Chain S6:



- Molecule 70: 40S ribosomal protein S4

Chain S4:





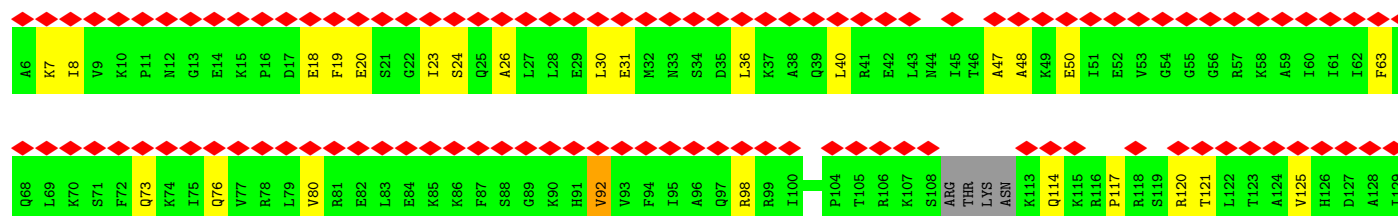
• Molecule 71: 40S ribosomal protein S9

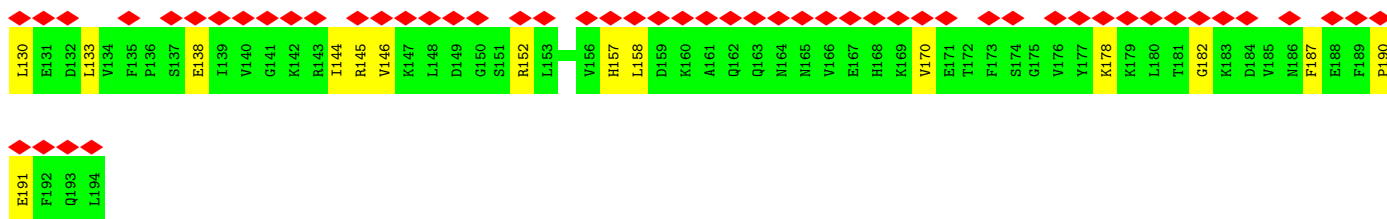
Chain S9: 80% 76% 23%



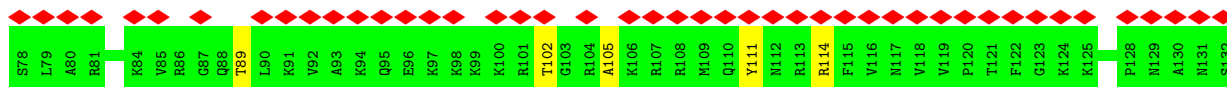
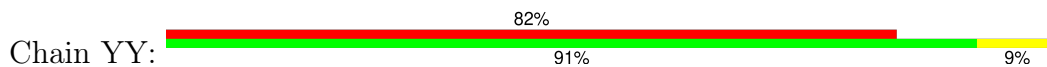
• Molecule 72: Small ribosomal subunit protein eS7

Chain S7: 86% 76% 21%

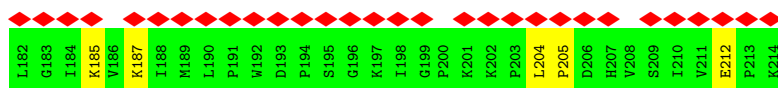
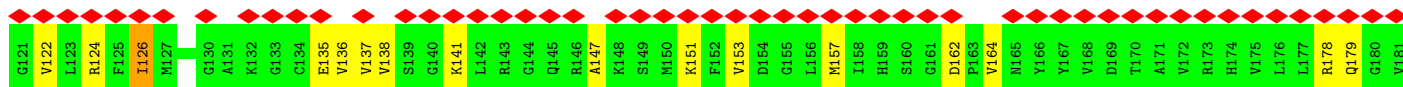
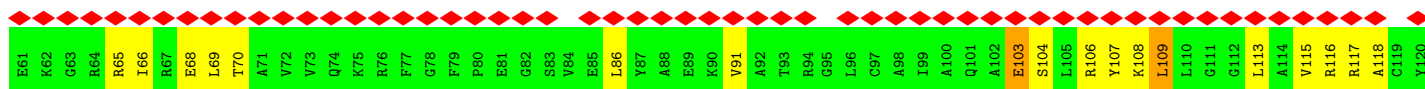
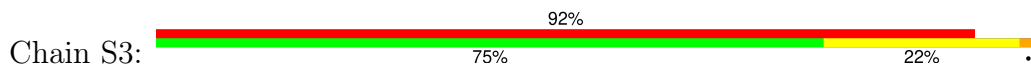




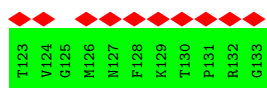
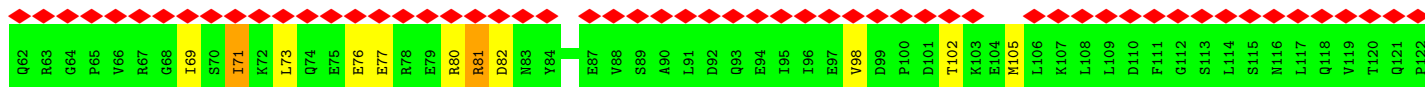
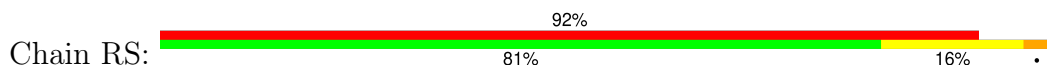
- Molecule 73: 40S ribosomal protein S30



- Molecule 74: Small ribosomal subunit protein uS3

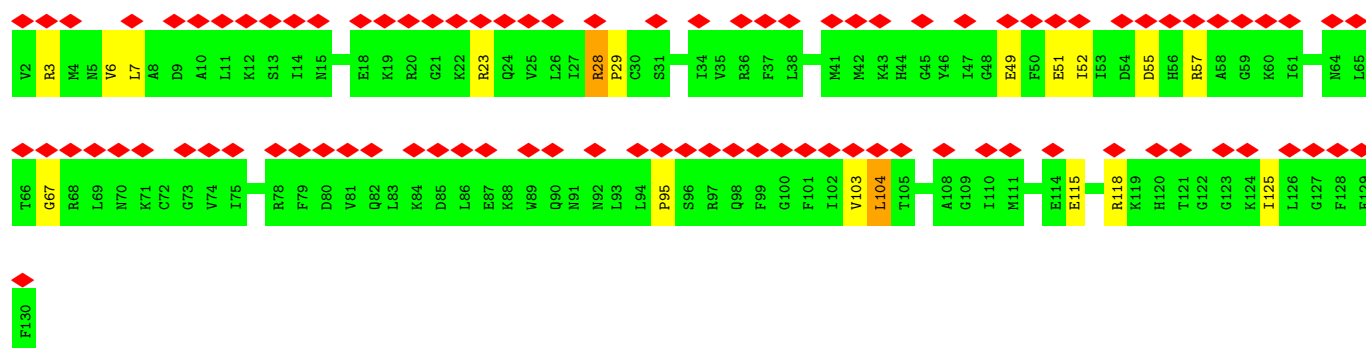


- Molecule 75: 40S ribosomal protein S17

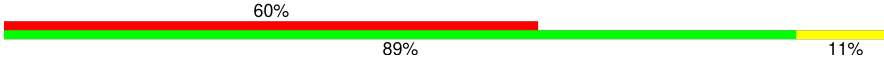


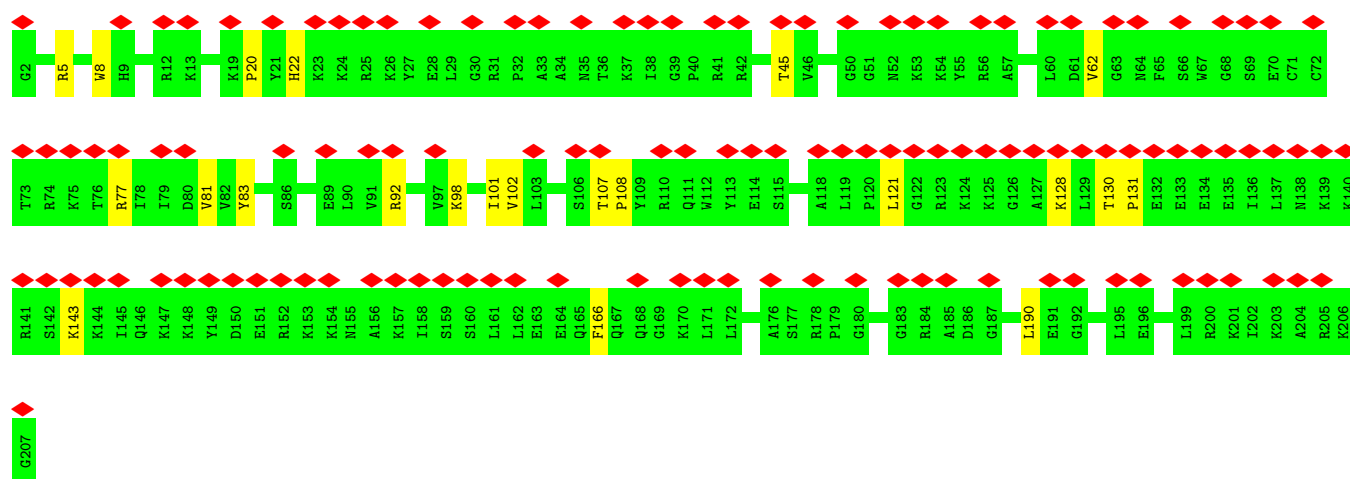
- Molecule 76: 40S ribosomal protein S15a

Chain WX: 



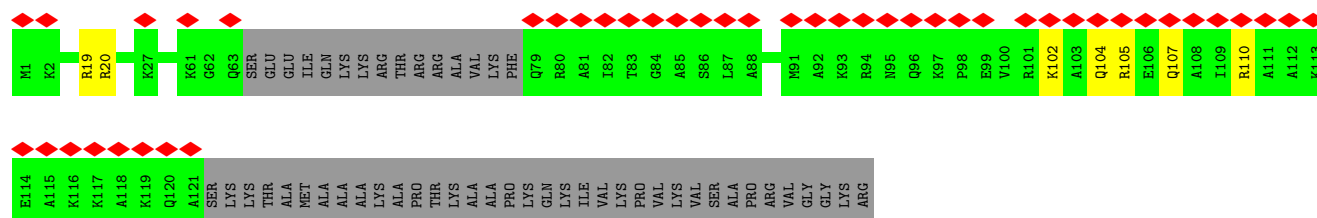
- Molecule 77: 40S ribosomal protein S8

Chain S8: 



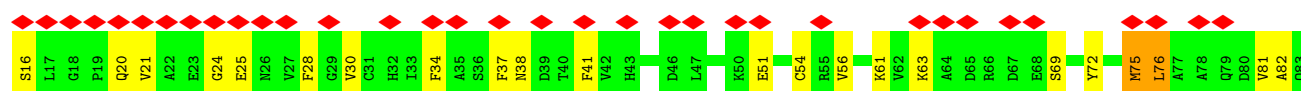
- Molecule 78: eL24

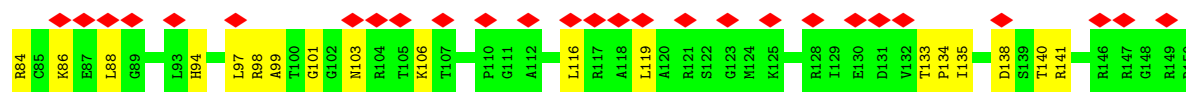
Chain W: 



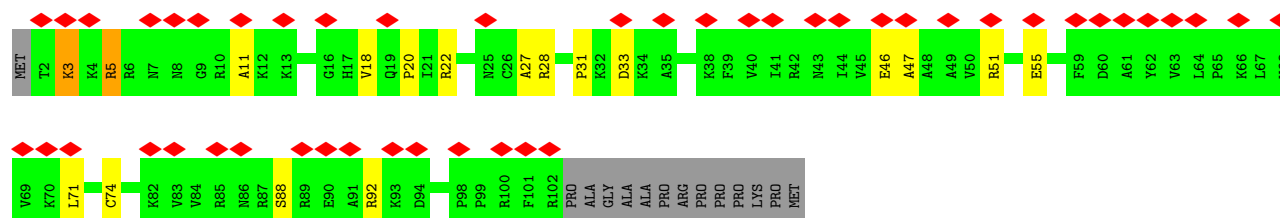
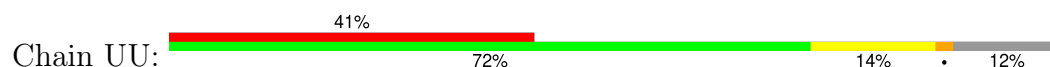
- Molecule 79: Small ribosomal subunit protein uS11

Chain GG: 

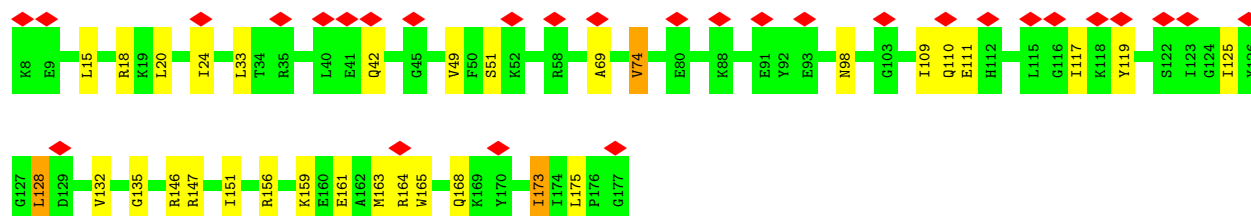
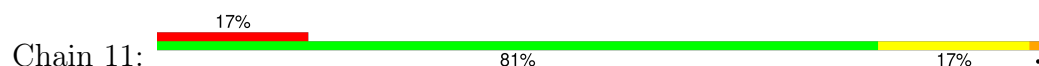




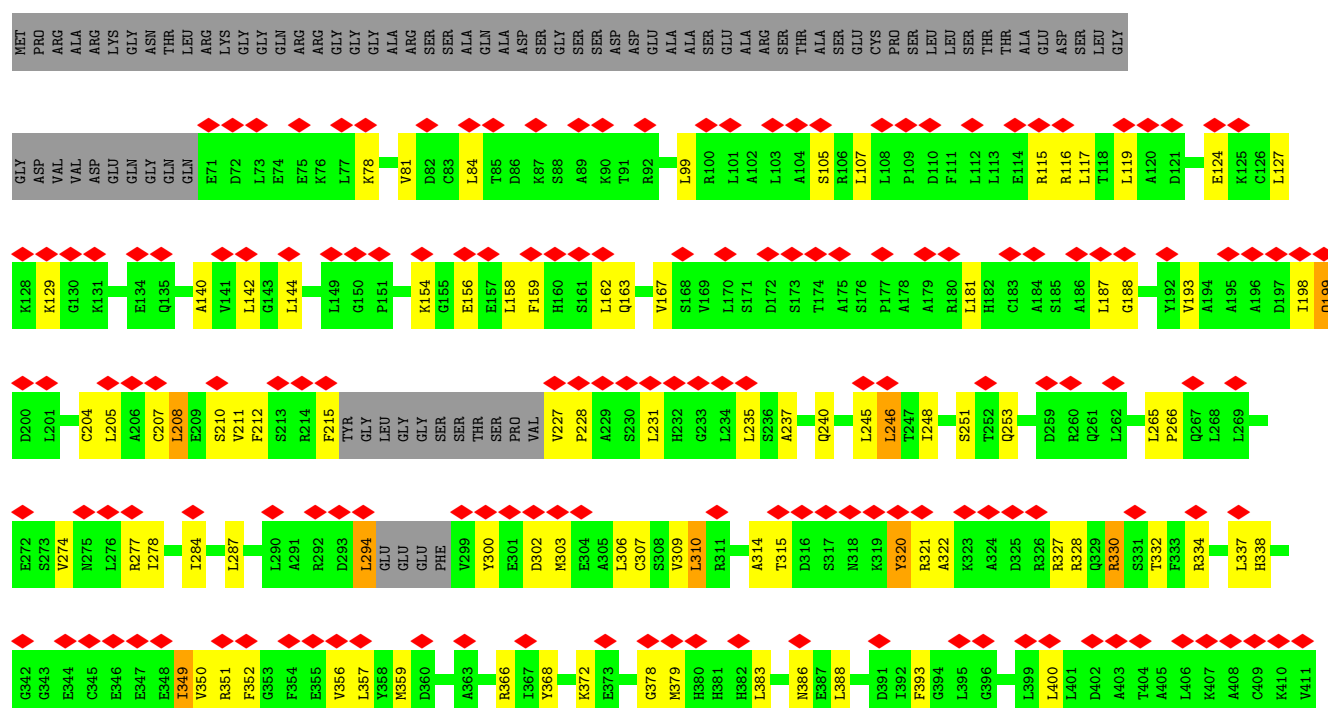
• Molecule 80: eS26

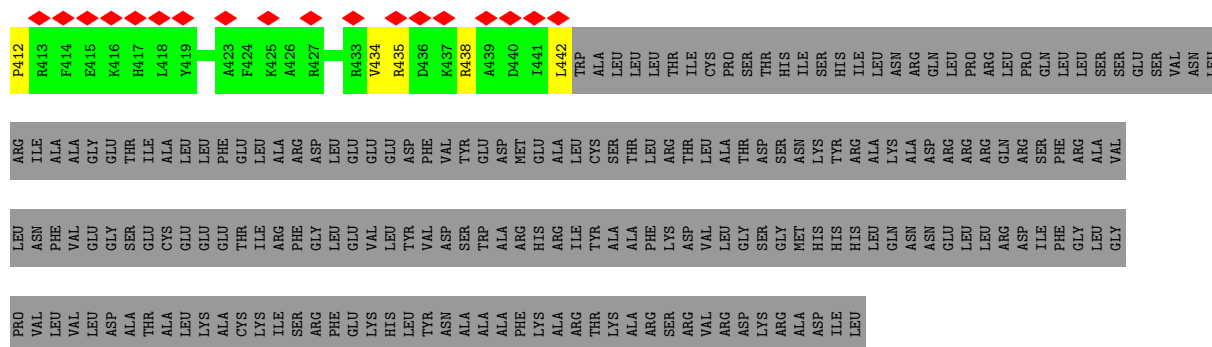


• Molecule 81: 60S ribosomal protein L11

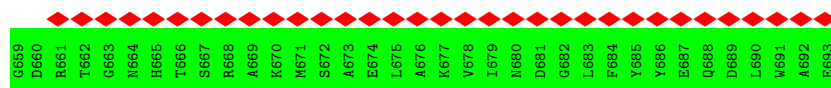


• Molecule 82: IFRD2

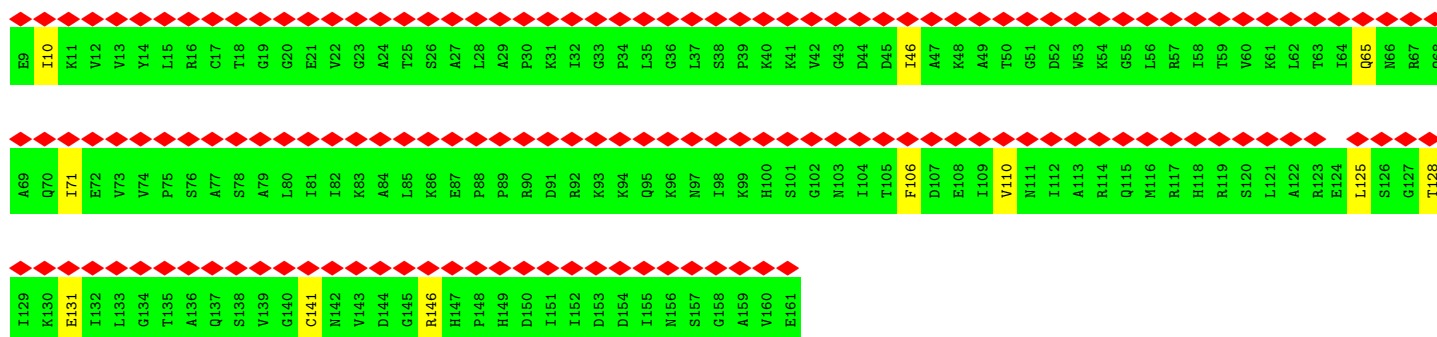




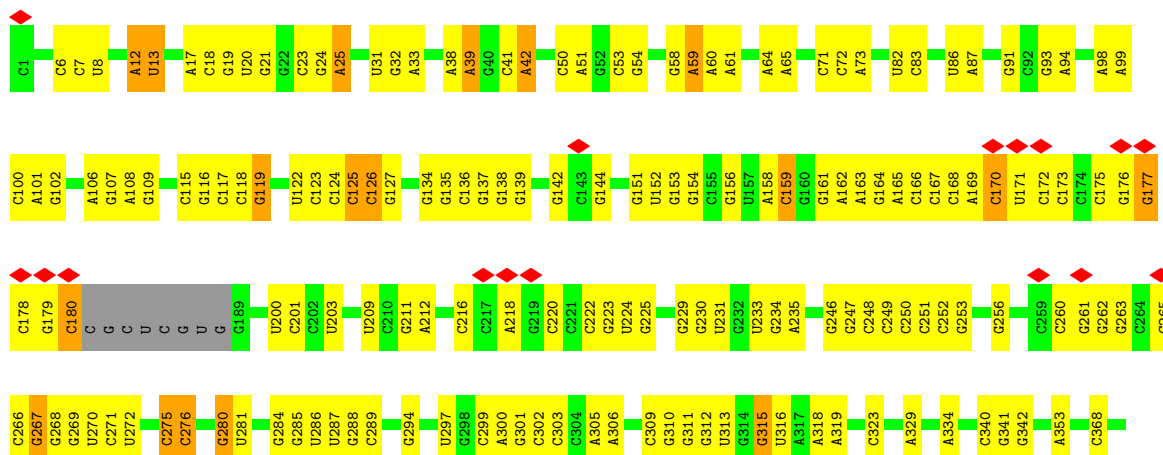
• Molecule 83: La-related protein 1



• Molecule 84: uL11



• Molecule 85: 28S rRNA

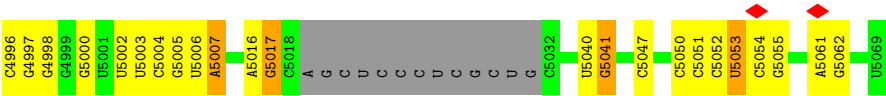












4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10932	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	18.967	Depositor
Minimum map value	-12.752	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.837	Depositor
Recommended contour level	3.5	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: PSU, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	BB	0.13	0/1747	0.33	0/2374
2	S2	0.13	0/1753	0.34	0/2369
3	PP	0.13	0/643	0.31	0/860
4	DD	0.13	0/1195	0.32	0/1597
5	58	0.13	0/3581	0.29	0/5577
6	5	0.13	0/2858	0.26	0/4455
7	L8	0.12	0/1936	0.31	0/2596
8	L3	0.13	0/3240	0.33	0/4339
9	L4	0.12	0/2937	0.30	0/3946
10	L5	0.13	0/2437	0.33	0/3264
11	L6	0.14	0/1761	0.33	0/2362
12	L7	0.13	0/1911	0.32	0/2549
13	aa	0.14	0/1910	0.33	0/2569
14	L9	0.13	0/1535	0.33	0/2063
15	10	0.12	0/1702	0.30	0/2272
16	13	0.14	0/1733	0.31	0/2316
17	14	0.14	0/1158	0.33	0/1547
18	15	0.13	0/1746	0.36	3/2338 (0.1%)
19	bb	0.14	0/1662	0.31	0/2222
20	17	0.12	0/1268	0.33	0/1700
21	19	0.13	0/1524	0.30	0/2013
22	20	0.13	0/1501	0.29	0/2012
23	21	0.12	0/1326	0.32	0/1770
24	22	0.12	0/823	0.32	0/1104
25	23	0.12	0/993	0.33	0/1332
26	cc	0.11	0/984	0.30	0/1323
27	26	0.12	0/1132	0.32	0/1504
28	27	0.13	0/1130	0.31	0/1507
29	dd	0.13	0/1191	0.34	0/1590
30	29	0.14	0/861	0.34	0/1138
31	30	0.12	0/771	0.26	0/1034
32	31	0.13	0/903	0.34	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	32	0.12	0/1071	0.30	0/1429
34	ee	0.12	0/895	0.32	0/1198
35	34	0.12	0/916	0.30	0/1220
36	35	0.12	0/1021	0.31	0/1348
37	36	0.13	0/841	0.31	0/1112
38	37	0.12	0/720	0.33	0/952
39	38	0.11	0/575	0.31	0/761
40	39	0.13	0/459	0.33	0/608
41	40	0.13	0/435	0.31	0/575
42	41	0.14	0/240	0.34	0/305
43	42	0.14	0/864	0.34	0/1140
44	ff	0.13	0/718	0.33	0/953
45	gg	0.12	0/1006	0.30	0/1349
46	AS	0.13	0/1756	0.35	0/2350
47	FF	0.13	0/1226	0.31	0/1649
48	VV	0.12	0/665	0.31	0/891
49	s	0.16	0/1530	0.39	0/2064
50	F	0.14	0/2854	0.34	0/3839
51	Q	0.13	0/1539	0.33	0/2054
52	ES	0.17	0/844	0.41	0/1314
53	ZZ	0.13	0/567	0.33	0/753
54	EE	0.15	0/918	0.36	0/1233
55	TT	0.15	0/604	0.33	0/810
56	S5	0.15	0/1492	0.40	0/2005
57	WW	0.13	0/490	0.34	0/656
58	II	0.16	0/1146	0.36	0/1534
59	CC	0.14	0/834	0.40	0/1125
60	AA	0.13	0/2493	0.32	0/3394
61	OO	0.15	0/805	0.35	0/1081
62	MM	0.15	0/1115	0.35	0/1493
63	LL	0.15	0/1208	0.40	0/1618
64	HH	0.14	0/1017	0.37	0/1358
65	18	0.13	0/40369	0.30	0/62910
66	XX	0.13	0/470	0.34	0/623
67	RR	0.15	0/1116	0.45	2/1490 (0.1%)
68	SS	0.12	0/1028	0.29	0/1366
69	S6	0.13	0/1946	0.33	0/2590
70	S4	0.13	0/2118	0.34	0/2849
71	S9	0.12	0/1550	0.31	0/2069
72	S7	0.15	0/1510	0.36	0/2022
73	YY	0.14	0/447	0.36	0/587
74	S3	0.16	0/1688	0.39	0/2269
75	RS	0.14	0/1082	0.34	0/1452

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	WX	0.14	0/1051	0.35	0/1406
77	S8	0.12	0/1715	0.35	0/2287
78	W	0.13	0/873	0.33	0/1158
79	GG	0.14	0/1020	0.37	0/1369
80	UU	0.16	0/828	0.33	0/1109
81	11	0.13	0/1385	0.32	0/1852
82	IF	0.36	0/2807	0.73	10/3786 (0.3%)
83	LA	0.16	0/285	0.29	0/383
84	t	0.19	0/1174	0.49	0/1582
85	28	0.14	0/84963	0.30	0/132509
All	All	0.14	0/234141	0.32	15/342697 (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
18	15	0	1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	IF	337	LEU	O-C-N	15.62	140.49	122.22
82	IF	337	LEU	CA-C-N	-12.08	103.14	120.29
82	IF	337	LEU	C-N-CA	-12.08	103.14	120.29
82	IF	328	ARG	N-CA-C	8.86	123.19	112.38
82	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
18	15	77	LYS	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	BB	1710	0	1708	12	0
2	S2	1716	0	1806	26	0
3	PP	636	0	637	6	0
4	DD	1175	0	1249	8	0
5	58	3208	0	1629	67	0
6	5	2558	0	1296	33	0
7	L8	1898	0	1993	28	0
8	L3	3172	0	3310	39	0
9	L4	2883	0	3053	29	0
10	L5	2391	0	2424	30	0
11	L6	1728	0	1887	17	0
12	L7	1875	0	1995	19	0
13	aa	1879	0	2027	19	0
14	L9	1516	0	1597	26	0
15	10	1664	0	1712	16	0
16	13	1702	0	1820	12	0
17	14	1137	0	1211	14	0
18	15	1701	0	1749	27	0
19	bb	1630	0	1778	23	0
20	17	1242	0	1274	11	0
21	19	1508	0	1664	12	0
22	20	1462	0	1508	10	0
23	21	1298	0	1366	9	0
24	22	809	0	833	4	0
25	23	979	0	1039	7	0
26	cc	967	0	1040	12	0
27	26	1115	0	1205	9	0
28	27	1107	0	1182	9	0
29	dd	1162	0	1209	9	0
30	29	848	0	920	6	0
31	30	761	0	794	3	0
32	31	888	0	930	6	0
33	32	1053	0	1147	12	0
34	ee	876	0	912	8	0
35	34	906	0	1001	9	0
36	35	1013	0	1147	10	0
37	36	830	0	916	3	0
38	37	705	0	738	5	0
39	38	569	0	637	7	0
40	39	447	0	480	7	0
41	40	429	0	469	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	41	239	0	289	6	0
43	42	851	0	924	17	0
44	ff	708	0	757	3	0
45	gg	990	0	1044	3	0
46	AS	1729	0	1803	20	0
47	FF	1202	0	1289	11	0
48	VV	651	0	672	3	0
49	s	1507	0	1564	16	0
50	F	2807	0	2822	36	0
51	Q	1515	0	1634	23	0
52	ES	756	0	384	20	0
53	ZZ	555	0	567	6	0
54	EE	908	0	939	9	0
55	TT	598	0	656	10	0
56	S5	1471	0	1522	19	0
57	WW	488	0	514	4	0
58	II	1128	0	1195	24	0
59	CC	810	0	836	12	0
60	AA	2436	0	2393	31	0
61	OO	795	0	862	13	0
62	MM	1097	0	1132	11	0
63	LL	1190	0	1249	22	0
64	HH	997	0	1045	18	0
65	18	36103	0	18234	611	0
66	XX	459	0	452	6	0
67	RR	1098	0	1167	15	0
68	SS	1011	0	1083	12	0
69	S6	1923	0	2089	27	0
70	S4	2076	0	2177	21	0
71	S9	1525	0	1640	27	0
72	S7	1488	0	1582	24	0
73	YY	443	0	492	3	0
74	S3	1662	0	1760	32	0
75	RS	1068	0	1121	18	0
76	WX	1034	0	1080	14	0
77	S8	1686	0	1772	13	0
78	W	860	0	903	5	0
79	GG	1007	0	1028	23	0
80	UU	814	0	864	13	0
81	11	1362	0	1399	15	0
82	IF	2767	0	2847	97	0
83	LA	280	0	260	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	t	1160	0	1218	5	0
85	28	75969	0	38372	1192	0
86	34	1	0	0	0	0
86	37	1	0	0	0	0
86	UU	1	0	0	0	0
86	ff	1	0	0	0	0
All	All	218380	0	164924	2867	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 2867 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)
43:42:105:GLN:HB2	82:IF:198:ILE:CD1	1.37	1.52
82:IF:350:VAL:CG1	82:IF:357:LEU:HB3	1.67	1.25
43:42:105:GLN:CB	82:IF:198:ILE:HD11	1.68	1.22
43:42:105:GLN:CB	82:IF:198:ILE:CD1	2.21	1.18
82:IF:350:VAL:HG13	82:IF:357:LEU:HB3	1.31	1.12

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	BB	215/295 (73%)	202 (94%)	13 (6%)	0	100	100
2	S2	219/293 (75%)	216 (99%)	3 (1%)	0	100	100
3	PP	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
4	DD	139/151 (92%)	134 (96%)	5 (4%)	0	100	100
7	L8	246/248 (99%)	239 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	L3	392/394 (100%)	377 (96%)	15 (4%)	0	100	100
9	L4	360/362 (99%)	354 (98%)	6 (2%)	0	100	100
10	L5	291/293 (99%)	283 (97%)	8 (3%)	0	100	100
11	L6	208/347 (60%)	203 (98%)	5 (2%)	0	100	100
12	L7	223/225 (99%)	215 (96%)	7 (3%)	1 (0%)	30	61
13	aa	229/240 (95%)	223 (97%)	6 (3%)	0	100	100
14	L9	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
15	10	201/213 (94%)	197 (98%)	4 (2%)	0	100	100
16	13	208/210 (99%)	201 (97%)	6 (3%)	1 (0%)	24	57
17	14	136/138 (99%)	135 (99%)	1 (1%)	0	100	100
18	15	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	24	57
19	bb	197/199 (99%)	197 (100%)	0	0	100	100
20	17	151/153 (99%)	150 (99%)	1 (1%)	0	100	100
21	19	178/180 (99%)	176 (99%)	2 (1%)	0	100	100
22	20	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
23	21	157/159 (99%)	155 (99%)	2 (1%)	0	100	100
24	22	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
25	23	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
26	cc	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
27	26	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
28	27	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
29	dd	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
30	29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
31	30	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
32	31	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
33	32	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
34	ee	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
35	34	112/114 (98%)	112 (100%)	0	0	100	100
36	35	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
37	36	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
38	37	84/86 (98%)	83 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	38	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
40	39	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
42	41	23/25 (92%)	23 (100%)	0	0	100	100
43	42	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
44	ff	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
45	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
46	AS	211/213 (99%)	206 (98%)	5 (2%)	0	100	100
47	FF	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
48	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
49	s	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
50	F	357/359 (99%)	349 (98%)	7 (2%)	1 (0%)	36	67
51	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
53	ZZ	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
54	EE	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
55	TT	73/75 (97%)	73 (100%)	0	0	100	100
56	S5	181/191 (95%)	170 (94%)	11 (6%)	0	100	100
57	WW	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
58	II	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
59	CC	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
60	AA	311/313 (99%)	300 (96%)	11 (4%)	0	100	100
61	OO	98/100 (98%)	98 (100%)	0	0	100	100
62	MM	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
63	LL	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
64	HH	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
66	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
67	RR	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	49
68	SS	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
69	S6	235/237 (99%)	235 (100%)	0	0	100	100
70	S4	260/262 (99%)	255 (98%)	5 (2%)	0	100	100
71	S9	183/185 (99%)	180 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
73	YY	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
74	S3	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
75	RS	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
76	WX	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
77	S8	204/206 (99%)	196 (96%)	8 (4%)	0	100	100
78	W	102/157 (65%)	100 (98%)	2 (2%)	0	100	100
79	GG	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
80	UU	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
81	11	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
82	IF	349/643 (54%)	345 (99%)	4 (1%)	0	100	100
83	LA	33/35 (94%)	33 (100%)	0	0	100	100
84	t	151/153 (99%)	136 (90%)	15 (10%)	0	100	100
All	All	12243/13236 (92%)	11920 (97%)	318 (3%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
50	F	83	ASN
67	RR	62	PRO
16	13	64	VAL
18	15	78	GLY
12	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	BB	180/245 (74%)	174 (97%)	6 (3%)	33	63
2	S2	187/224 (84%)	184 (98%)	3 (2%)	55	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	PP	67/67 (100%)	67 (100%)	0	100	100
4	DD	130/136 (96%)	126 (97%)	4 (3%)	35	64
7	L8	190/190 (100%)	186 (98%)	4 (2%)	47	71
8	L3	342/342 (100%)	329 (96%)	13 (4%)	29	60
9	L4	302/302 (100%)	297 (98%)	5 (2%)	53	74
10	L5	247/247 (100%)	237 (96%)	10 (4%)	28	60
11	L6	190/302 (63%)	180 (95%)	10 (5%)	20	51
12	L7	196/196 (100%)	192 (98%)	4 (2%)	48	72
13	aa	200/205 (98%)	196 (98%)	4 (2%)	48	72
14	L9	169/169 (100%)	161 (95%)	8 (5%)	23	55
15	10	175/180 (97%)	168 (96%)	7 (4%)	28	60
16	13	175/175 (100%)	167 (95%)	8 (5%)	24	55
17	14	117/117 (100%)	110 (94%)	7 (6%)	17	47
18	15	171/171 (100%)	167 (98%)	4 (2%)	44	70
19	bb	171/171 (100%)	165 (96%)	6 (4%)	32	62
20	17	134/134 (100%)	132 (98%)	2 (2%)	57	75
21	19	159/159 (100%)	155 (98%)	4 (2%)	42	69
22	20	157/157 (100%)	151 (96%)	6 (4%)	29	60
23	21	139/139 (100%)	134 (96%)	5 (4%)	31	62
24	22	89/89 (100%)	85 (96%)	4 (4%)	24	56
25	23	101/101 (100%)	97 (96%)	4 (4%)	28	60
26	cc	106/106 (100%)	103 (97%)	3 (3%)	38	66
27	26	124/124 (100%)	115 (93%)	9 (7%)	13	40
28	27	117/117 (100%)	111 (95%)	6 (5%)	21	52
29	dd	119/119 (100%)	118 (99%)	1 (1%)	73	81
30	29	84/184 (46%)	81 (96%)	3 (4%)	31	62
31	30	84/84 (100%)	82 (98%)	2 (2%)	43	69
32	31	98/98 (100%)	92 (94%)	6 (6%)	17	46
33	32	114/114 (100%)	109 (96%)	5 (4%)	25	56
34	ee	88/88 (100%)	82 (93%)	6 (7%)	14	42
35	34	98/98 (100%)	96 (98%)	2 (2%)	48	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	35	109/109 (100%)	108 (99%)	1 (1%)	70	80
37	36	86/86 (100%)	82 (95%)	4 (5%)	23	55
38	37	73/73 (100%)	71 (97%)	2 (3%)	39	67
39	38	64/64 (100%)	61 (95%)	3 (5%)	23	55
40	39	47/47 (100%)	47 (100%)	0	100	100
41	40	48/48 (100%)	46 (96%)	2 (4%)	26	58
42	41	24/24 (100%)	24 (100%)	0	100	100
43	42	92/92 (100%)	89 (97%)	3 (3%)	33	63
44	ff	74/74 (100%)	70 (95%)	4 (5%)	20	50
45	gg	107/108 (99%)	104 (97%)	3 (3%)	38	66
46	AS	194/194 (100%)	188 (97%)	6 (3%)	35	64
47	FF	130/130 (100%)	124 (95%)	6 (5%)	24	55
48	VV	75/75 (100%)	74 (99%)	1 (1%)	61	77
49	s	164/164 (100%)	152 (93%)	12 (7%)	13	40
50	F	308/308 (100%)	287 (93%)	21 (7%)	14	42
51	Q	164/165 (99%)	163 (99%)	1 (1%)	78	83
53	ZZ	61/61 (100%)	60 (98%)	1 (2%)	55	75
54	EE	99/99 (100%)	98 (99%)	1 (1%)	68	79
55	TT	66/66 (100%)	65 (98%)	1 (2%)	57	75
56	S5	158/161 (98%)	156 (99%)	2 (1%)	61	77
57	WW	55/55 (100%)	50 (91%)	5 (9%)	9	32
58	II	117/117 (100%)	115 (98%)	2 (2%)	53	74
59	CC	87/87 (100%)	82 (94%)	5 (6%)	18	49
60	AA	272/272 (100%)	263 (97%)	9 (3%)	33	63
61	OO	92/92 (100%)	82 (89%)	10 (11%)	6	24
62	MM	111/111 (100%)	103 (93%)	8 (7%)	13	40
63	LL	125/125 (100%)	114 (91%)	11 (9%)	9	33
64	HH	109/109 (100%)	101 (93%)	8 (7%)	13	40
66	XX	48/48 (100%)	46 (96%)	2 (4%)	26	58
67	RR	113/113 (100%)	108 (96%)	5 (4%)	25	56
68	SS	107/107 (100%)	103 (96%)	4 (4%)	30	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	S6	207/207 (100%)	200 (97%)	7 (3%)	32	63
70	S4	224/224 (100%)	216 (96%)	8 (4%)	31	62
71	S9	161/161 (100%)	157 (98%)	4 (2%)	42	69
72	S7	165/169 (98%)	160 (97%)	5 (3%)	36	65
73	YY	46/46 (100%)	44 (96%)	2 (4%)	26	57
74	S3	177/177 (100%)	163 (92%)	14 (8%)	11	37
75	RS	119/119 (100%)	112 (94%)	7 (6%)	18	48
76	WX	112/112 (100%)	108 (96%)	4 (4%)	31	62
77	S8	178/178 (100%)	176 (99%)	2 (1%)	65	78
78	W	86/126 (68%)	86 (100%)	0	100	100
79	GG	105/105 (100%)	98 (93%)	7 (7%)	15	43
80	UU	88/98 (90%)	84 (96%)	4 (4%)	24	56
81	11	143/143 (100%)	134 (94%)	9 (6%)	16	45
82	IF	294/529 (56%)	281 (96%)	13 (4%)	25	56
83	LA	28/28 (100%)	28 (100%)	0	100	100
84	t	126/126 (100%)	124 (98%)	2 (2%)	55	75
All	All	10658/11282 (94%)	10256 (96%)	402 (4%)	30	60

5 of 402 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	F	226	VAL
63	LL	47	LYS
82	IF	434	VAL
50	F	348	GLU
60	AA	199	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 155 such sidechains are listed below:

Mol	Chain	Res	Type
60	AA	311	GLN
75	RS	93	GLN
64	HH	41	GLN
70	S4	157	ASN
82	IF	253	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	58	149/156 (95%)	27 (18%)	1 (0%)
52	ES	34/5070 (0%)	7 (20%)	1 (2%)
6	5	119/120 (99%)	10 (8%)	0
65	18	1679/1698 (98%)	310 (18%)	15 (0%)
85	28	3518/4805 (73%)	601 (17%)	43 (1%)
All	All	5499/11849 (46%)	955 (17%)	60 (1%)

5 of 955 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	58	23	C
5	58	34	U
5	58	35	C
5	58	39	G
5	58	51	U

5 of 60 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	28	971(A)	G
85	28	4884	G
85	28	1445	U
85	28	4719	G
85	28	4947	U

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
85	PSU	28	3715	85	18,21,22	1.14	1 (5%)	21,30,33	1.83	4 (19%)

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
85	PSU	28	3715	85	-	0/7/25/26	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	28	3715	PSU	C6-C5	3.82	1.39	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	28	3715	PSU	C4-N3-C2	-4.62	120.01	126.37
85	28	3715	PSU	N1-C2-N3	4.49	119.90	115.17
85	28	3715	PSU	O2-C2-N1	-2.80	119.90	122.79
85	28	3715	PSU	C6-N1-C2	-2.26	120.59	122.69

There are no chirality outliers.

There are no torsion outliers.

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 [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
65	18	8
82	IF	1

The worst 5 of 9 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	19.23
1	18	697:G	O3'	729:C	P	18.69
1	18	834:C	O3'	841:G	P	17.90
1	18	1417:C	O3'	1423:C	P	16.77
1	18	736:C	O3'	743:U	P	8.07

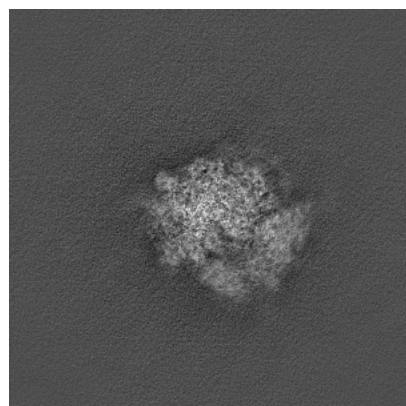
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75768. These allow visual inspection of the internal detail of the map and identification of artifacts.

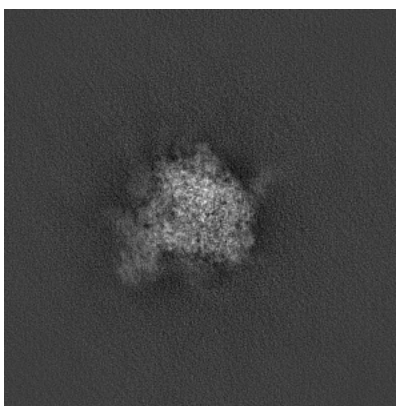
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

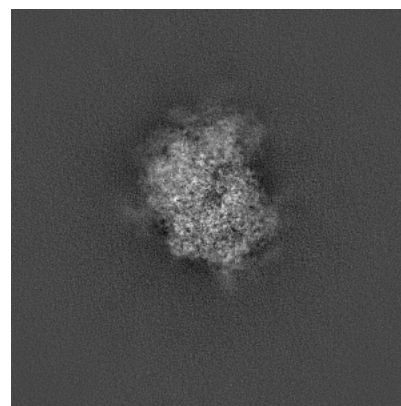
6.1.1 Primary map



X

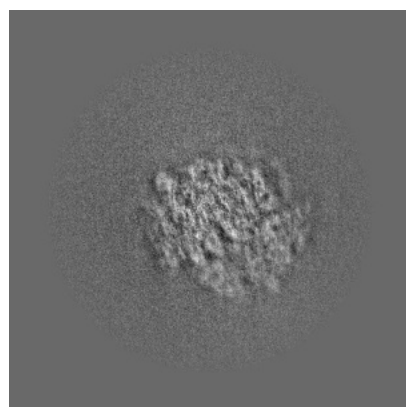


Y

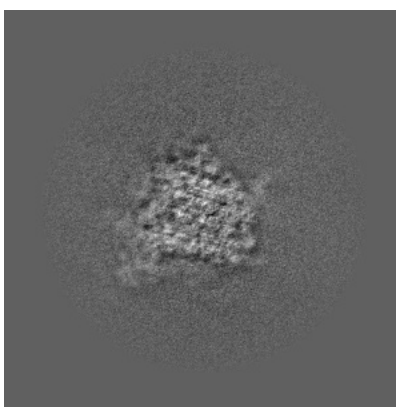


Z

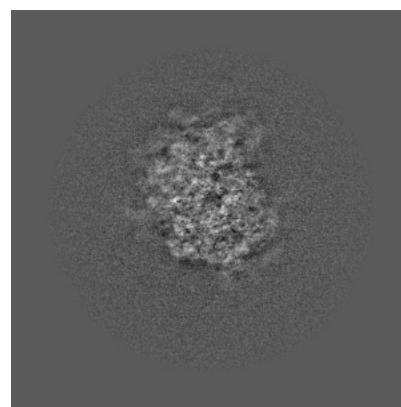
6.1.2 Raw map



X



Y

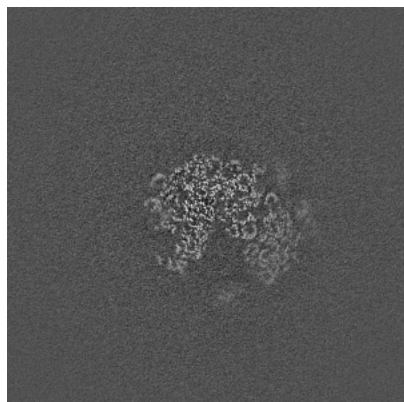


Z

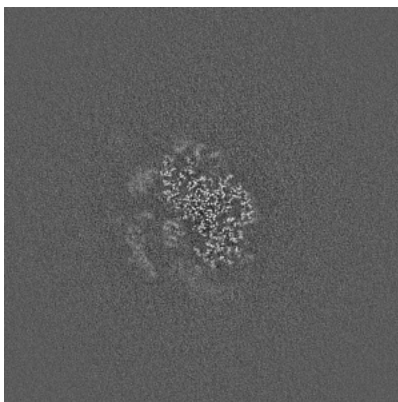
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

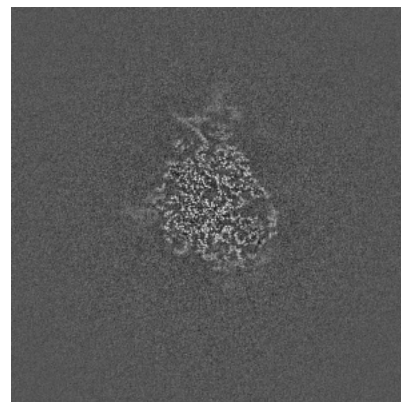
6.2.1 Primary map



X Index: 400

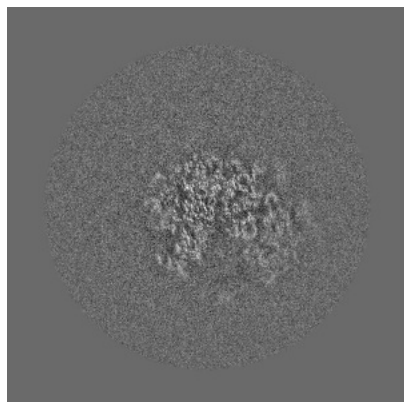


Y Index: 400

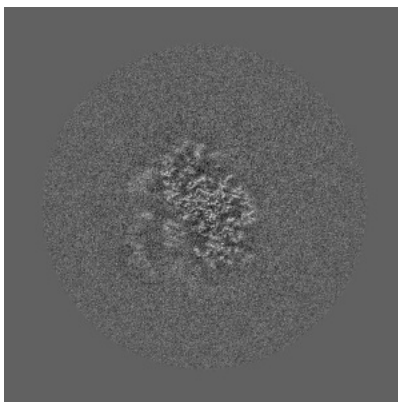


Z Index: 400

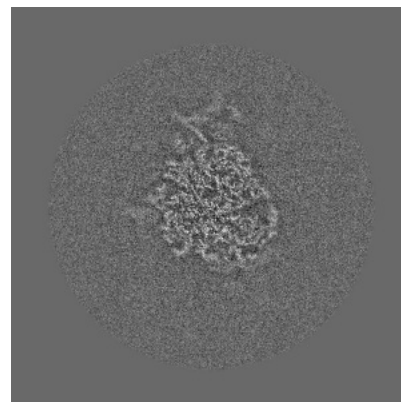
6.2.2 Raw map



X Index: 400



Y Index: 400

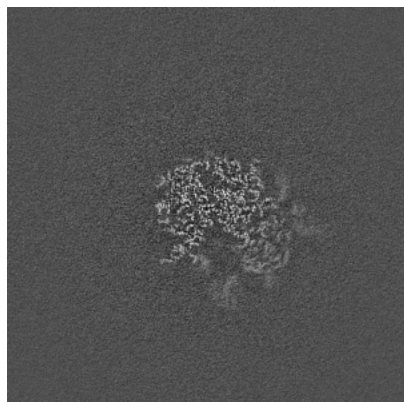


Z Index: 400

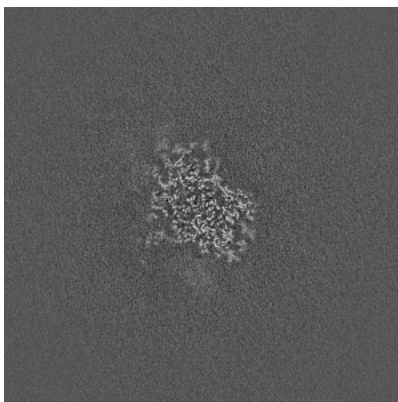
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

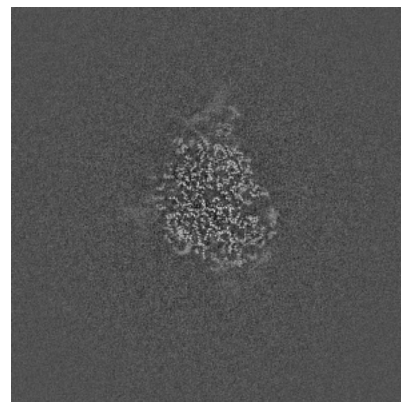
6.3.1 Primary map



X Index: 385

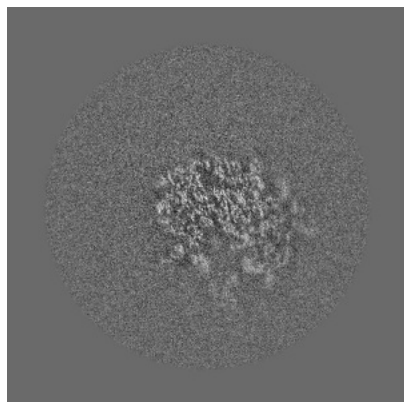


Y Index: 380

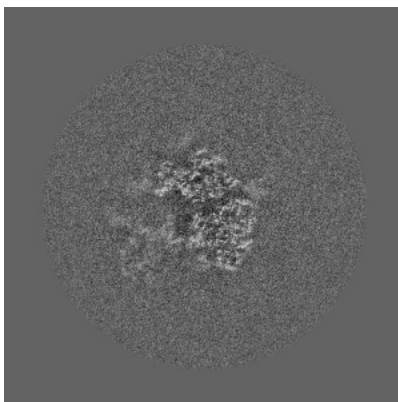


Z Index: 403

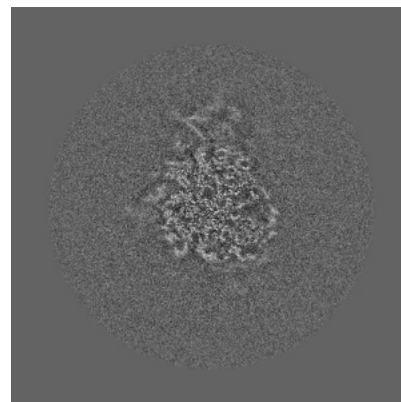
6.3.2 Raw map



X Index: 384



Y Index: 421

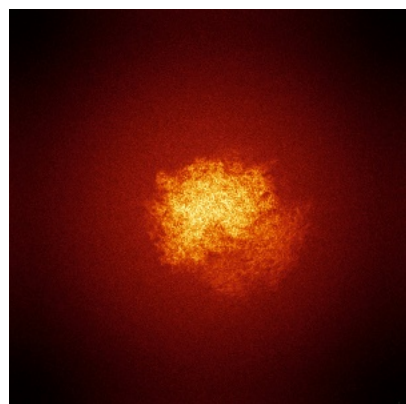


Z Index: 398

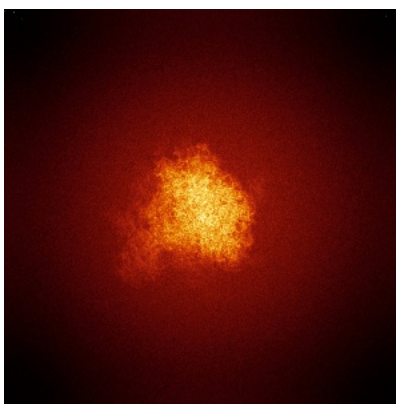
The images above show the largest variance slices of the map in three orthogonal directions.

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

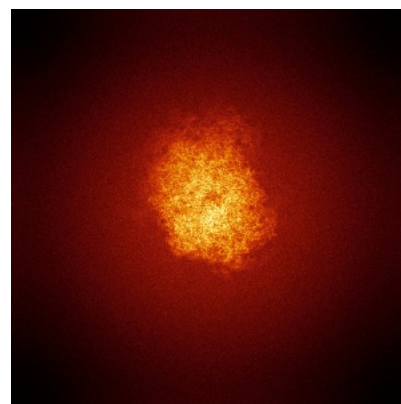
6.4.1 Primary map



X

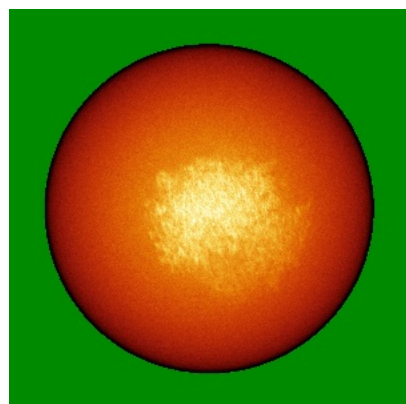


Y

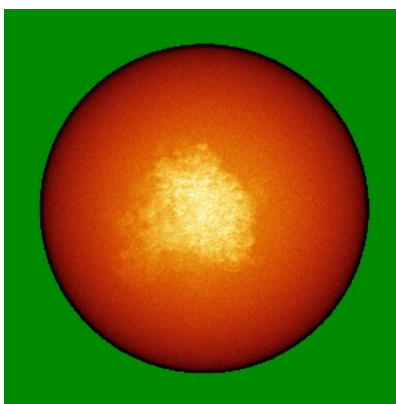


Z

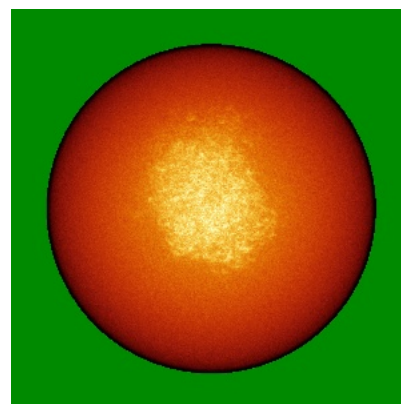
6.4.2 Raw map



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.

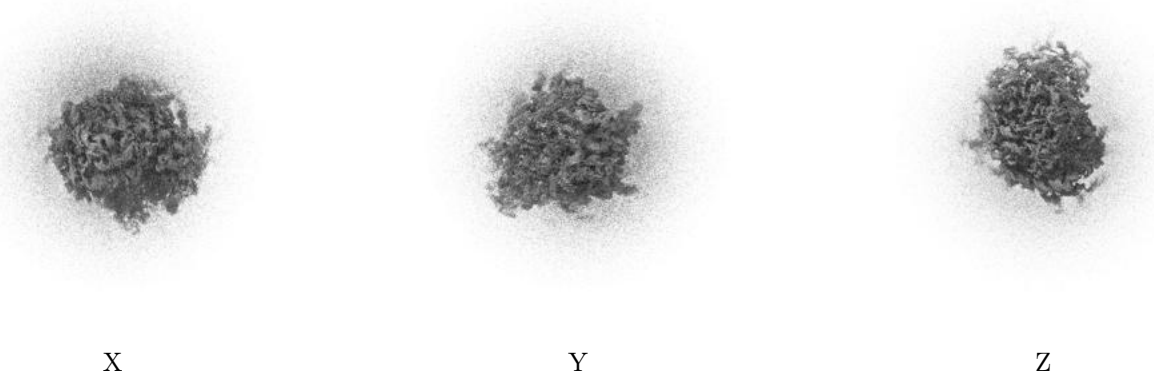
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. 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.

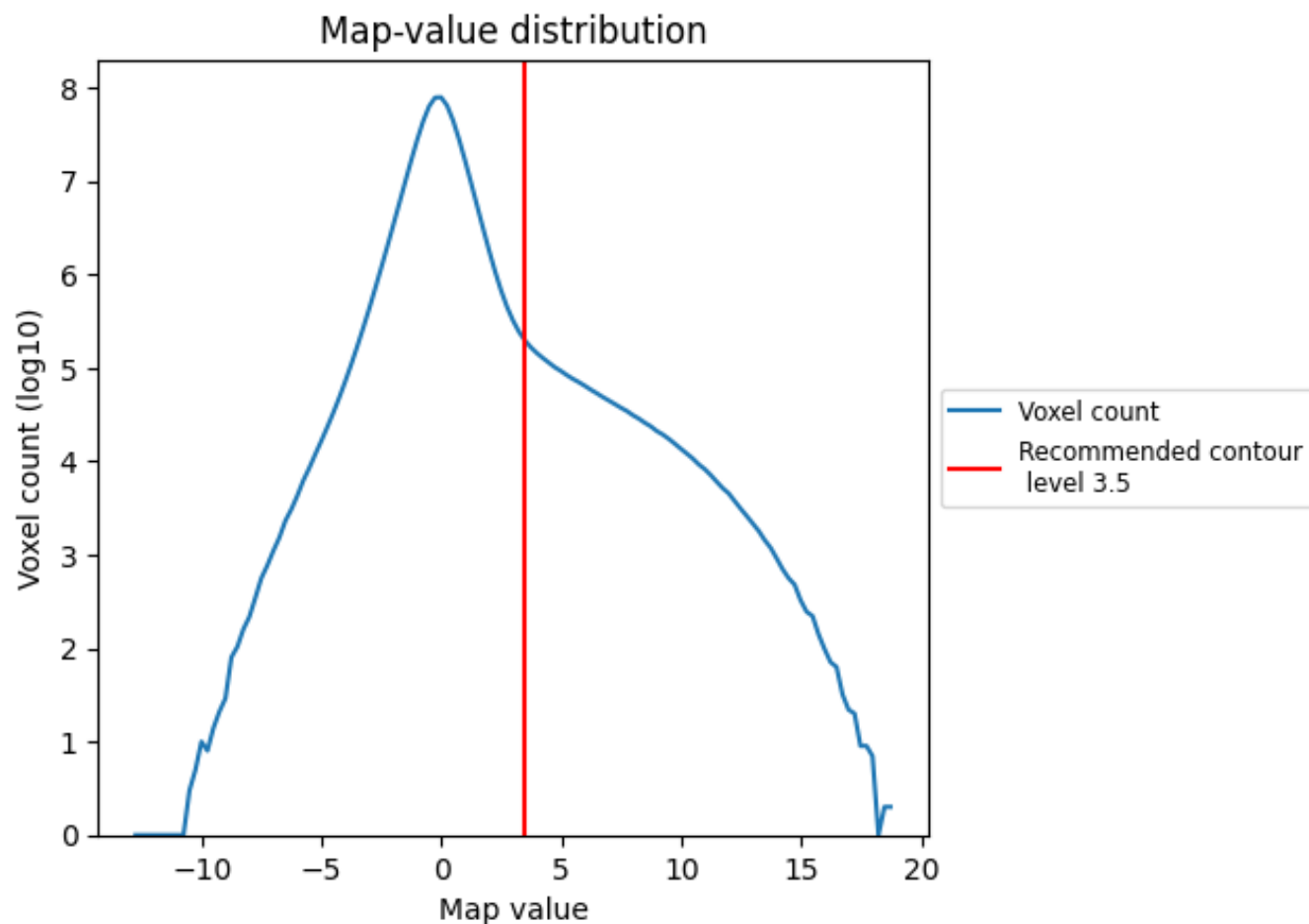
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

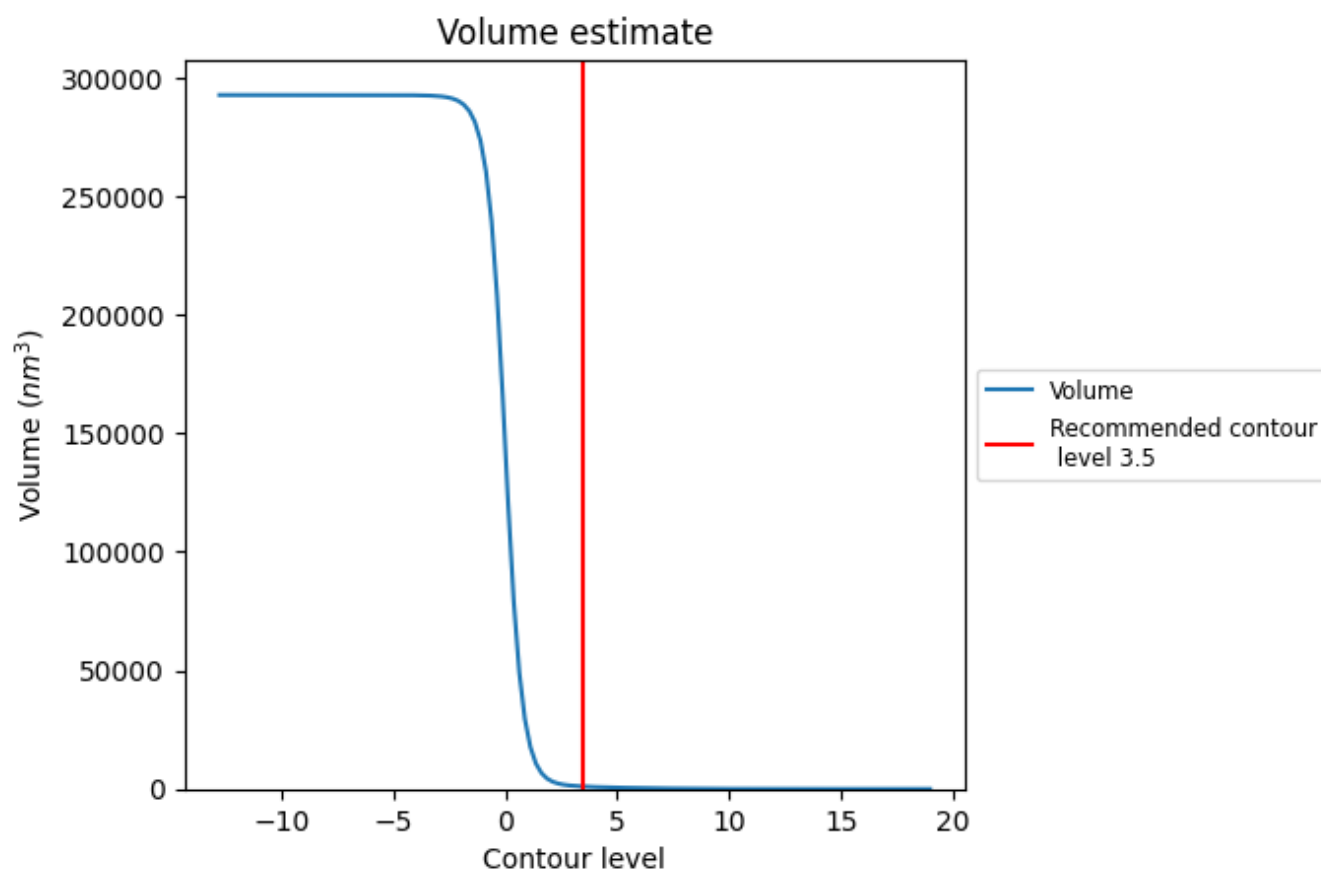
This section contains the results of statistical analysis of the map.

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.

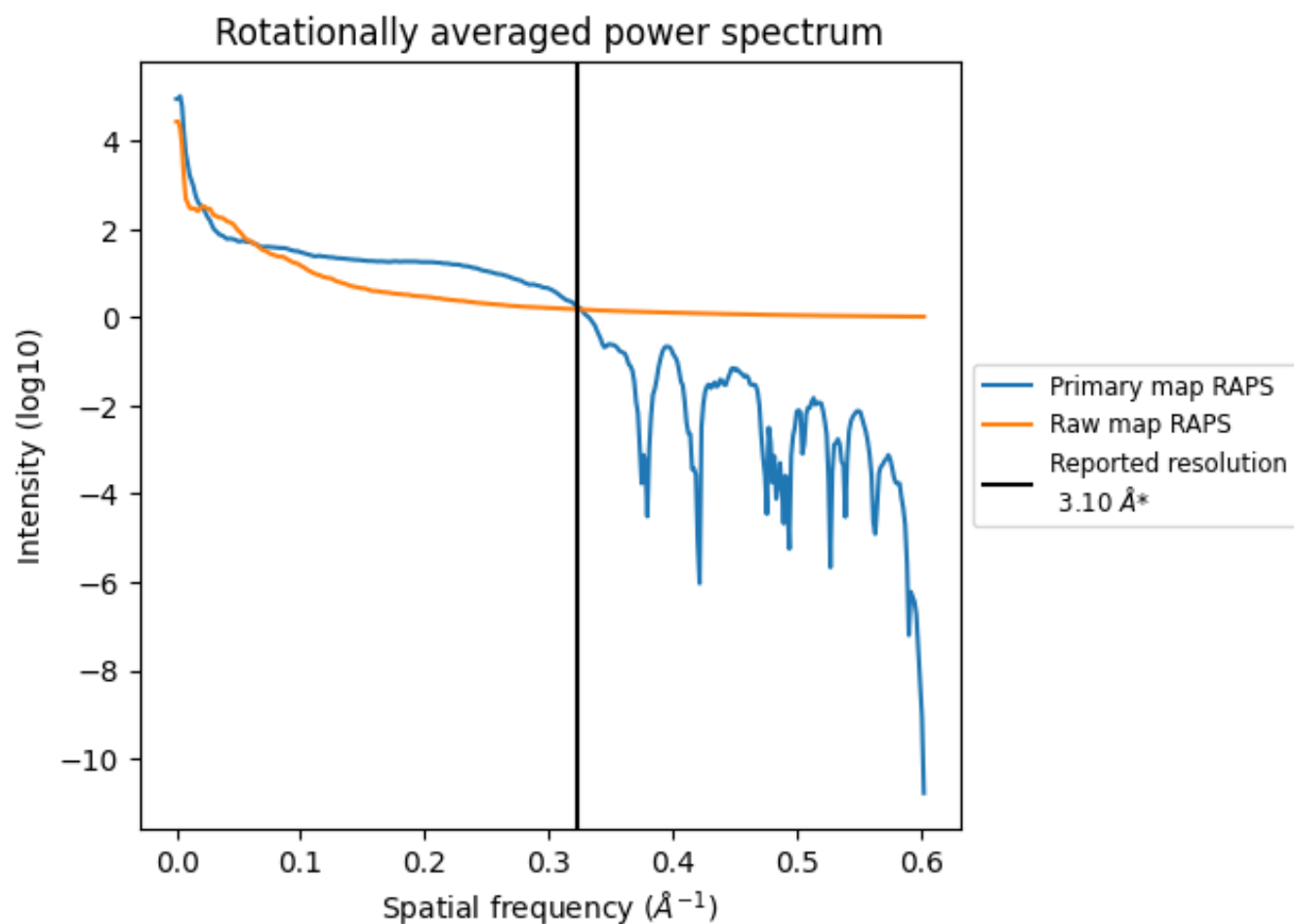
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1045 nm³; this corresponds to an approximate mass of 944 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 ⓘ

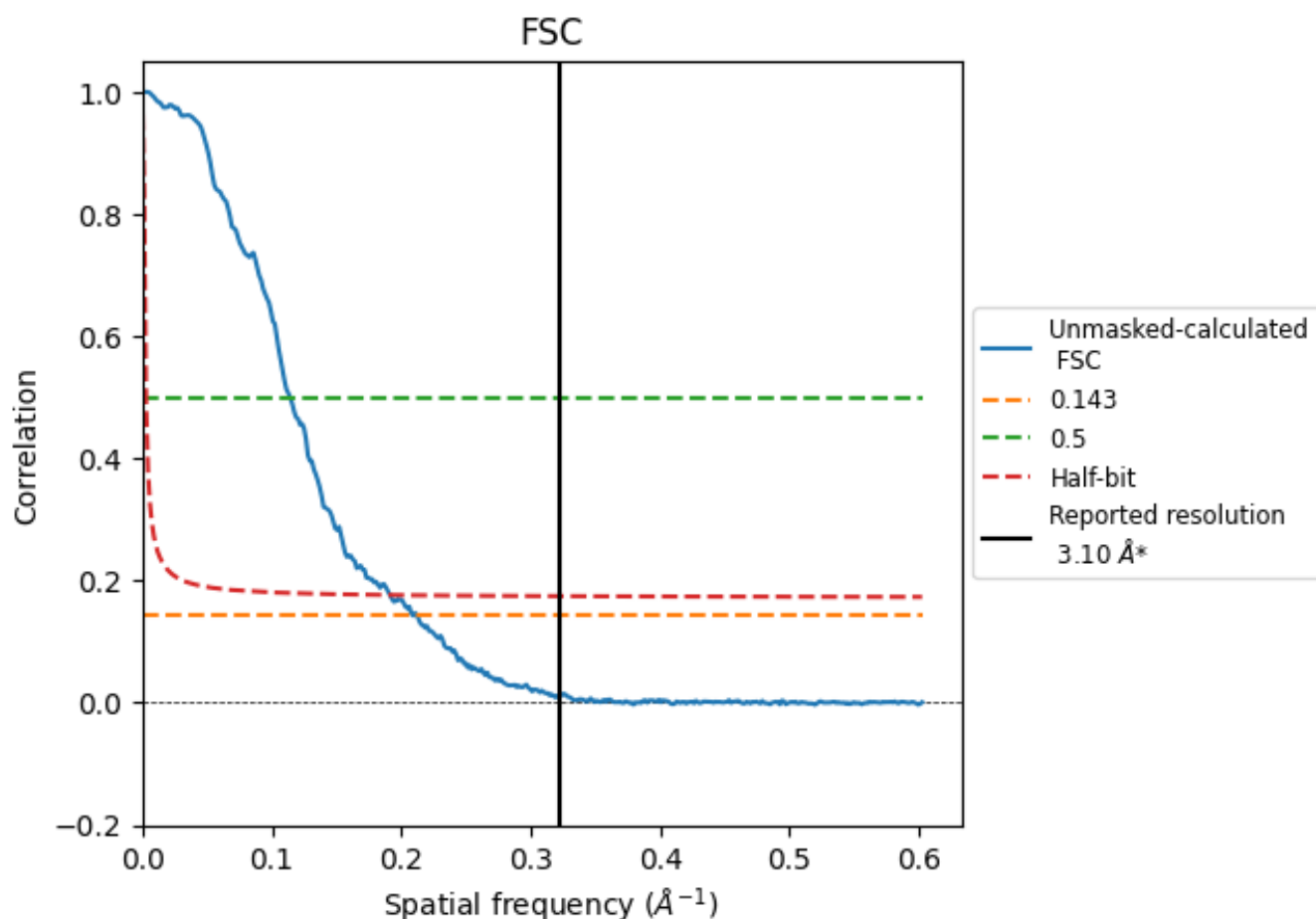


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

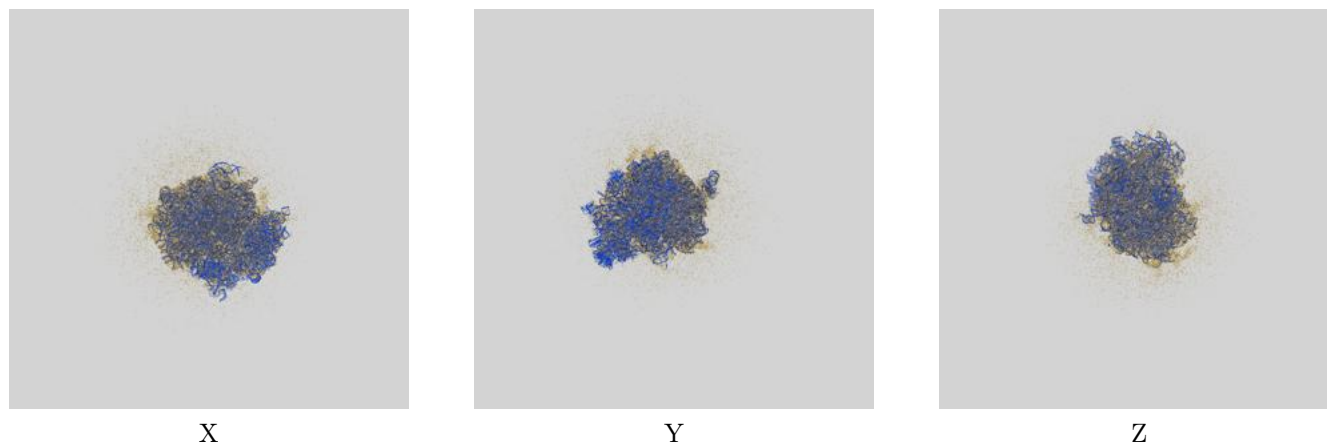
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.78	8.76	5.23

*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 4.78 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

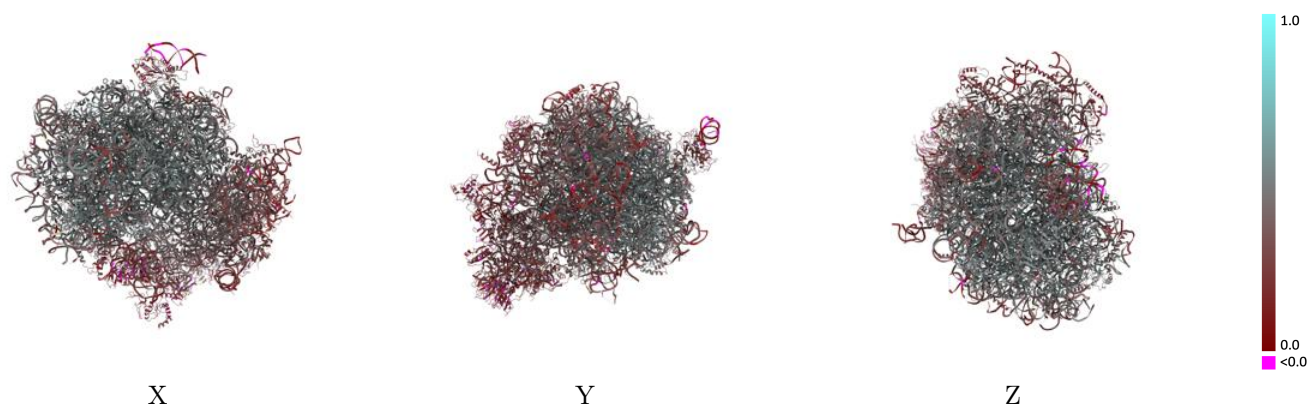
This section contains information regarding the fit between EMDB map EMD-75768 and PDB model 11KH. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



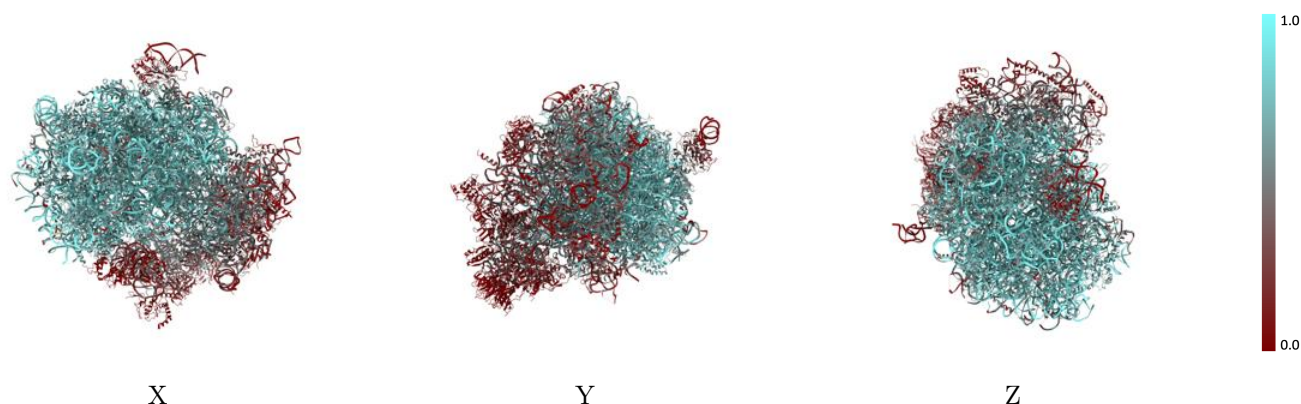
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



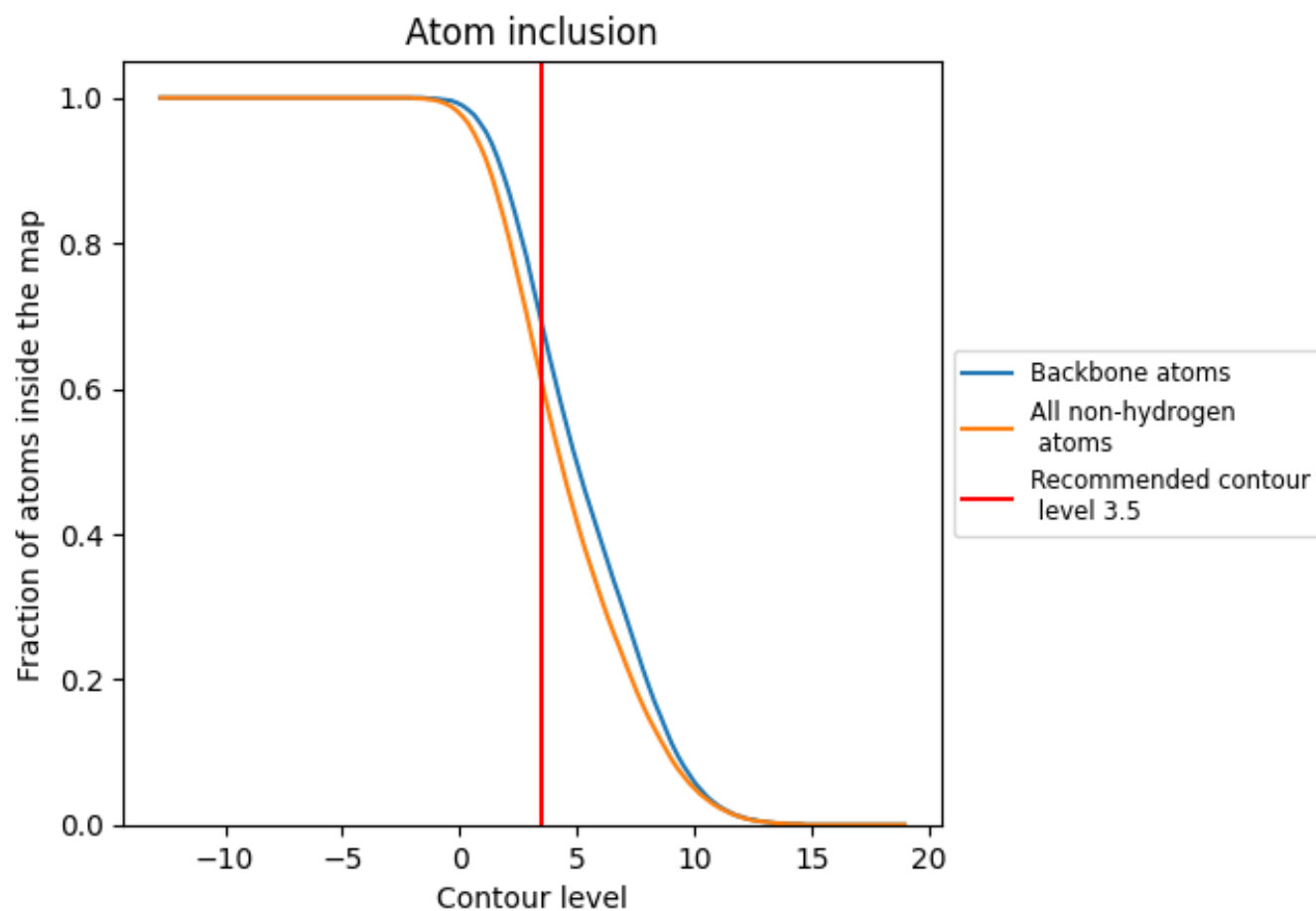
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 61% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6080	 0.4150
10	 0.6910	 0.4900
11	 0.5720	 0.4140
13	 0.6930	 0.4830
14	 0.7000	 0.4750
15	 0.7540	 0.5180
17	 0.7210	 0.5090
18	 0.5220	 0.3550
19	 0.6160	 0.4460
20	 0.7390	 0.4960
21	 0.7120	 0.4960
22	 0.5460	 0.4020
23	 0.6660	 0.4960
26	 0.7010	 0.4870
27	 0.6550	 0.4740
28	 0.8070	 0.4630
29	 0.6120	 0.4370
30	 0.6120	 0.4520
31	 0.6770	 0.4760
32	 0.7530	 0.5160
34	 0.6650	 0.4890
35	 0.6650	 0.4740
36	 0.7000	 0.4650
37	 0.7820	 0.5240
38	 0.5940	 0.4280
39	 0.6910	 0.4770
40	 0.6840	 0.4880
41	 0.5920	 0.4620
42	 0.6790	 0.4920
5	 0.8730	 0.5010
58	 0.8430	 0.4810
AA	 0.0430	 0.2100
AS	 0.3940	 0.3960
BB	 0.2170	 0.3350
CC	 0.1180	 0.2260



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Chain	Atom inclusion	Q-score
DD	0.4040	0.4150
EE	0.0530	0.2040
ES	0.0440	0.0400
F	0.2750	0.3100
FF	0.4180	0.4010
GG	0.4410	0.3960
HH	0.1710	0.2460
IF	0.4250	0.3000
II	0.1010	0.2470
L3	0.7110	0.4970
L4	0.7340	0.5050
L5	0.6810	0.4660
L6	0.6850	0.4630
L7	0.7270	0.4980
L8	0.7340	0.5130
L9	0.6850	0.4760
LA	0.1210	0.2660
LL	0.1830	0.2640
MM	0.1360	0.2610
OO	0.1050	0.2460
PP	0.2300	0.3160
Q	0.7580	0.5210
RR	0.4440	0.3880
RS	0.1650	0.3090
S2	0.2700	0.3510
S3	0.1530	0.2790
S4	0.2320	0.3310
S5	0.1860	0.2760
S6	0.2540	0.3110
S7	0.1860	0.3070
S8	0.3610	0.3810
S9	0.2510	0.3300
SS	0.2070	0.3130
TT	0.1170	0.2490
UU	0.4320	0.4060
VV	0.2960	0.3610
W	0.4440	0.3820
WW	0.1340	0.2750
WX	0.2900	0.3910
XX	0.2290	0.2720
YY	0.2680	0.3230
ZZ	0.0700	0.1990

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Chain	Atom inclusion	Q-score
aa	 0.6380	 0.4460
bb	 0.7380	 0.4980
cc	 0.6900	 0.4840
dd	 0.7510	 0.5200
ee	 0.7550	 0.5230
ff	 0.6690	 0.4940
gg	 0.7410	 0.5060
s	 0.0460	 0.1940
t	 0.0500	 0.2150