



wwPDB EM Validation Summary Report

Nov 19, 2022 – 02:10 pm GMT


PDB ID : 5MC6
EMDB ID : EMD-3461
Title : Cryo-EM structure of a native ribosome-Ski2-Ski3-Ski8 complex from *S. cerevisiae*
Authors : Schmidt, C.; Kowalinski, E.; Shanmuganathan, V.; Defenouillere, Q.; Braunger, K.; Heuer, A.; Pech, M.; Namane, A.; Berninghausen, O.; Fromont-Racine, M.; Jacquier, A.; Conti, E.; Becker, T.; Beckmann, R.
Deposited on : 2016-11-09
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the  symbol.

The types of validation reports are described at

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

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

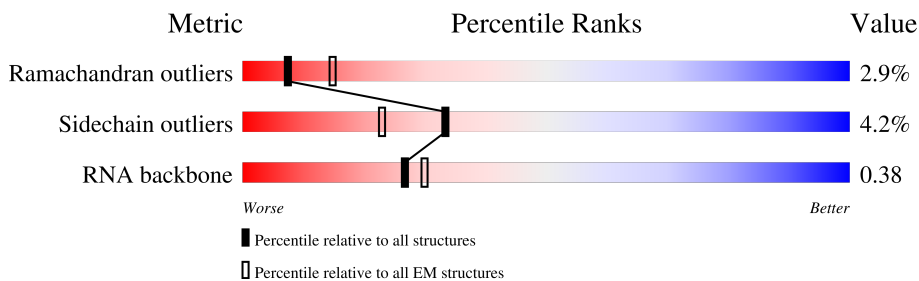
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	2	1800	
2	A	240	
3	B	225	
4	C	105	
5	D	143	
6	E	142	
7	F	143	
8	G	136	

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Mol	Chain	Length	Quality of chain
9	H	146	40% 89% 10%
10	I	144	42% 85% 13%
11	J	121	28% 83% 6% 12%
12	K	108	29% 57% 7% 35%
13	L	67	61% 91% 6%
14	M	56	12% 89% 5% 5%
15	N	152	24% 31% 66%
16	O	319	38% 95%
17	P	252	21% 76% 5% 18%
18	Q	255	41% 76% 7% 16%
19	R	254	15% 83% 13%
20	S	261	44% 95% 5%
21	T	236	43% 89% 6%
22	U	190	61% 89% 7%
23	V	200	37% 74% 16% 6%
24	W	197	32% 87% 10%
25	X	156	38% 93% 6%
26	Y	151	34% 93% 6%
27	Z	137	32% 85% 7% 7%
28	a	87	30% 94% 5%
29	b	130	23% 95%
30	c	145	30% 96%
31	d	135	42% 87% 9%
32	e	119	35% 68% 13% 18%
33	f	82	40% 93% 6%

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Mol	Chain	Length	Quality of chain
34	g	63	
35	l	34	
36	m	76	
37	n	77	
38	h	1287	
39	i	1432	
40	j	397	
40	k	397	
41	AA	256	
42	AB	137	
43	AC	100	
44	AD	191	
45	AE	155	
46	AF	88	
47	AG	174	
48	AH	142	
49	AI	78	
50	AJ	199	
51	AK	127	
52	AL	51	
53	AM	138	
54	AN	136	
55	AO	128	
56	AP	106	
57	AQ	204	



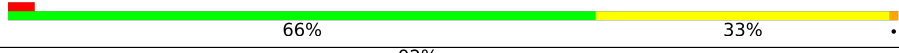

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Mol	Chain	Length	Quality of chain
58	AR	149	11% 90% 7% ..
59	AS	25	56% 92% 8%
60	AT	92	24% 96% ..
61	AU	199	13% 95% ..
62	AV	59	27% 97% ..
63	AW	254	15% 96% ..
64	AX	184	12% 93% 6% .
65	AY	105	29% 89% 8%
66	AZ	210	91% 100%
67	BA	387	15% 93% 7%
68	BB	186	11% 95% 5% .
69	BC	113	19% 88% 8% ..
70	BD	221	25% 89% 10% .
71	BE	362	12% 93% 7%
72	BF	189	21% 95% ..
73	BG	130	12% 94% ..
74	BH	172	19% 95% 5%
75	BI	297	19% 94% 5%
76	BJ	160	19% 91% 8% .
77	BK	107	12% 94% 5% .
78	BL	121	18% 79% 17%
79	BM	176	23% 83% 5% . 11%
80	BN	121	12% 89% 7%
81	BO	244	9% 87% 9%
82	BP	120	12% 96% ..

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Mol	Chain	Length	Quality of chain
83	BQ	3396	 <p>60% 32% 7%</p>
84	BR	121	 <p>69% 30%</p>
85	BS	158	 <p>66% 33%</p>
86	BT	157	 <p>92% 89% 8%</p>

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 229285 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1767	37645	16830	6656	12392	1767	0	0

- Molecule 2 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	223	1734	1101	313	314	6	0	0

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	206	1609	1007	300	299	3	0	0

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	96	813	527	133	151	2	0	0

- Molecule 5 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	121	877	552	153	170	2	0	0

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	124	977	622	182	166	7	0	0

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	F	141	1105	708	203	194	0	0

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	91	746	467	144	133	2	0	0

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	145	1192	743	237	210	2	0	0

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	143	1112	694	208	208	2	0	0

- Molecule 11 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	107	855	539	156	159	1	0	0

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	K	70	563	360	104	99	0	0

- Molecule 13 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	63	497	306	99	91	1	0	0

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 19 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	T	226	1799	1129	346	321	3	0	0

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	U	184	1481	951	265	265		0	0

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	V	188	1489	925	298	264	2	0	0

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	178	1434	905	276	252	1	0	0

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	X	155	1213	774	230	206	3	0	0

- Molecule 26 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	150	1192	759	224	207	2	0	0

- Molecule 27 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Z	127	891	545	182	163	1	0	0

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	d	132	Total	C	N	O	0	0
			1060	669	206	185		

- Molecule 32 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	34	Total	C	N	O	P	0	0
			692	311	84	263	34		

- Molecule 36 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 37 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 38 is a protein called Antiviral helicase SKI2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	1121	Total	C	N	O	S	0	0
			8814	5643	1504	1625	42		

- Molecule 39 is a protein called Superkiller protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	1365	Total	C	N	O	S	0	0
			9827	6302	1663	1825	37		

- Molecule 40 is a protein called Antiviral protein SKI8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	392	Total	C	N	O	S	0	0
			2933	1861	500	558	14		
40	k	388	Total	C	N	O	S	0	0
			2919	1851	502	552	14		

- Molecule 41 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 42 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	AB	136	1003	628	189	179	7	0	0

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AC	99	771	481	156	132	2	0	0

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	AD	191	1518	963	274	277	4	0	0

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	AE	98	699	443	137	118	1	0	0

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	AF	87	681	414	148	114	5	0	0

- Molecule 47 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	AG	169	1353	847	253	249	4	0	0

- Molecule 48 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	AH	121	964	620	169	173	2	0	0

- Molecule 49 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	AI	77	612	391	115	106	0	0

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	AJ	193	1543	962	315	266	0	0

- Molecule 51 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
51	AK	126	993	625	192	176	0	0

- Molecule 52 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AL	50	436	272	97	65	2	0	0

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	AM	136	1053	675	199	177	2	0	0

- Molecule 54 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	AN	135	1092	710	202	180	0	0

- Molecule 55 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	AO	52	417	259	86	67	5	0	0

- Molecule 56 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 57 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 58 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 59 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 60 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 61 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	AV	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 63 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	AW	252	1914	1191	388	334	1	0	0

- Molecule 64 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	AX	183	1420	882	281	257		0	0

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	AY	97	742	479	124	138	1	0	0

- Molecule 66 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	AZ	210	1050	630	210	210		0	0

- Molecule 67 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	BA	386	3075	1950	584	533	8	0	0

- Molecule 68 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	BB	185	1441	908	290	241	2	0	0

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	BC	109	876	556	167	152	1	0	0

- Molecule 70 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	BD	220	1770	1121	335	307	7	0	0

- Molecule 71 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	BE	361	2748	1729	522	494	3	0	0

- Molecule 72 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
72	BF	188	1521	935	326	260	0	0

- Molecule 73 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	BG	127	1020	647	205	167	1	0	0

- Molecule 74 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	BH	172	1445	930	267	244	4	0	0

- Molecule 75 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	BI	296	2375	1501	414	458	2	0	0

- Molecule 76 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	BJ	159	1276	805	246	221	4	0	0

- Molecule 77 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	BK	106	850	540	165	144	1	0	0

- Molecule 78 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
78	BL	100	796	516	131	149	0	0

- Molecule 79 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	BM	156	1239	800	222	216	1	0	0

- Molecule 80 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	BN	112	880	545	179	152	4	0	0

- Molecule 81 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	BO	222	1784	1151	324	308	1	0	0

- Molecule 82 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	BP	119	969	615	186	167	1	0	0

- Molecule 83 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	BQ	3165	67695	30238	12201	22091	3165	0	0

- Molecule 84 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
84	BR	121	2579	1152	461	845	121	0	0

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
85	BS	158	3352	1500	586	1108	158	0	0

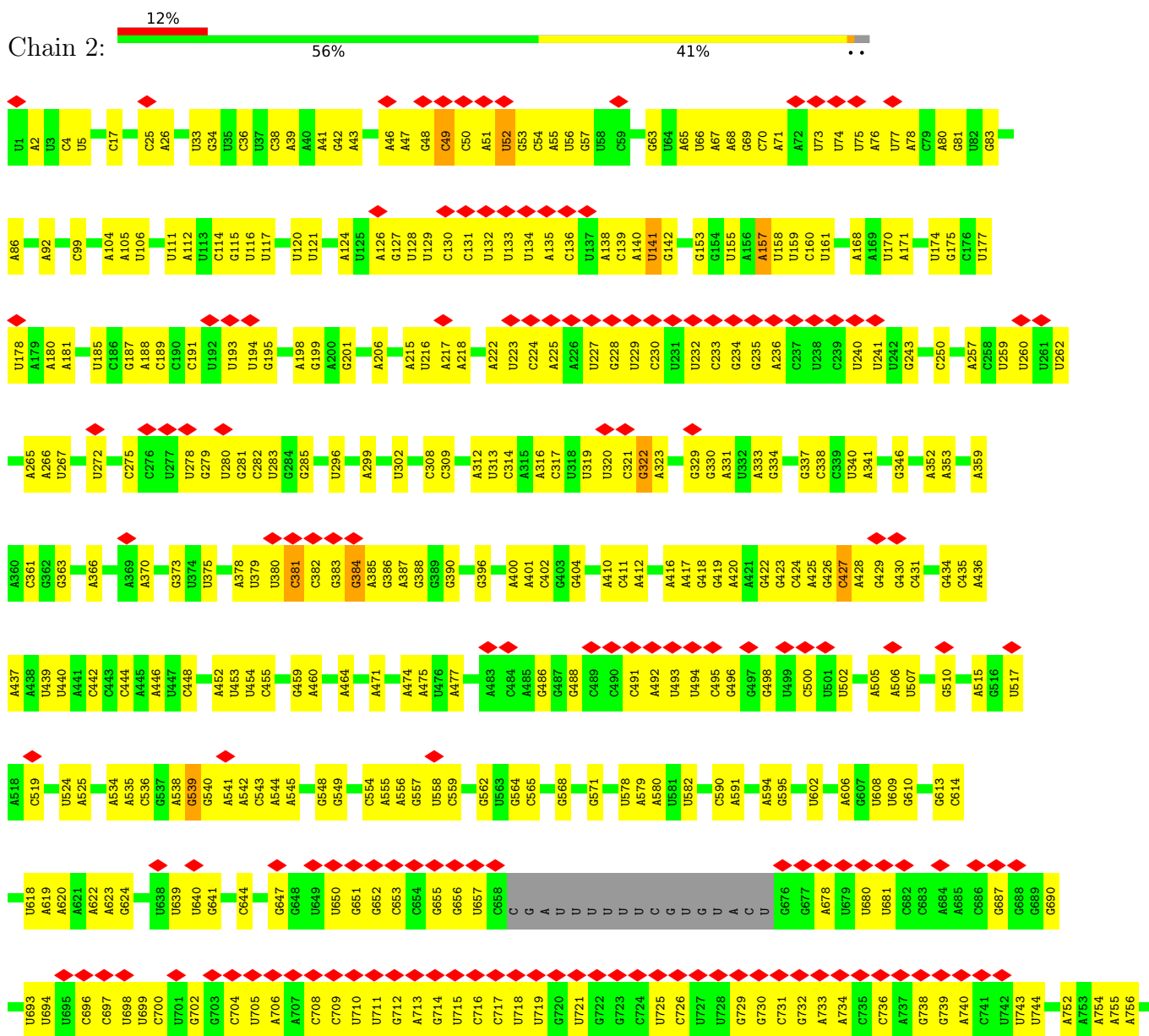
- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

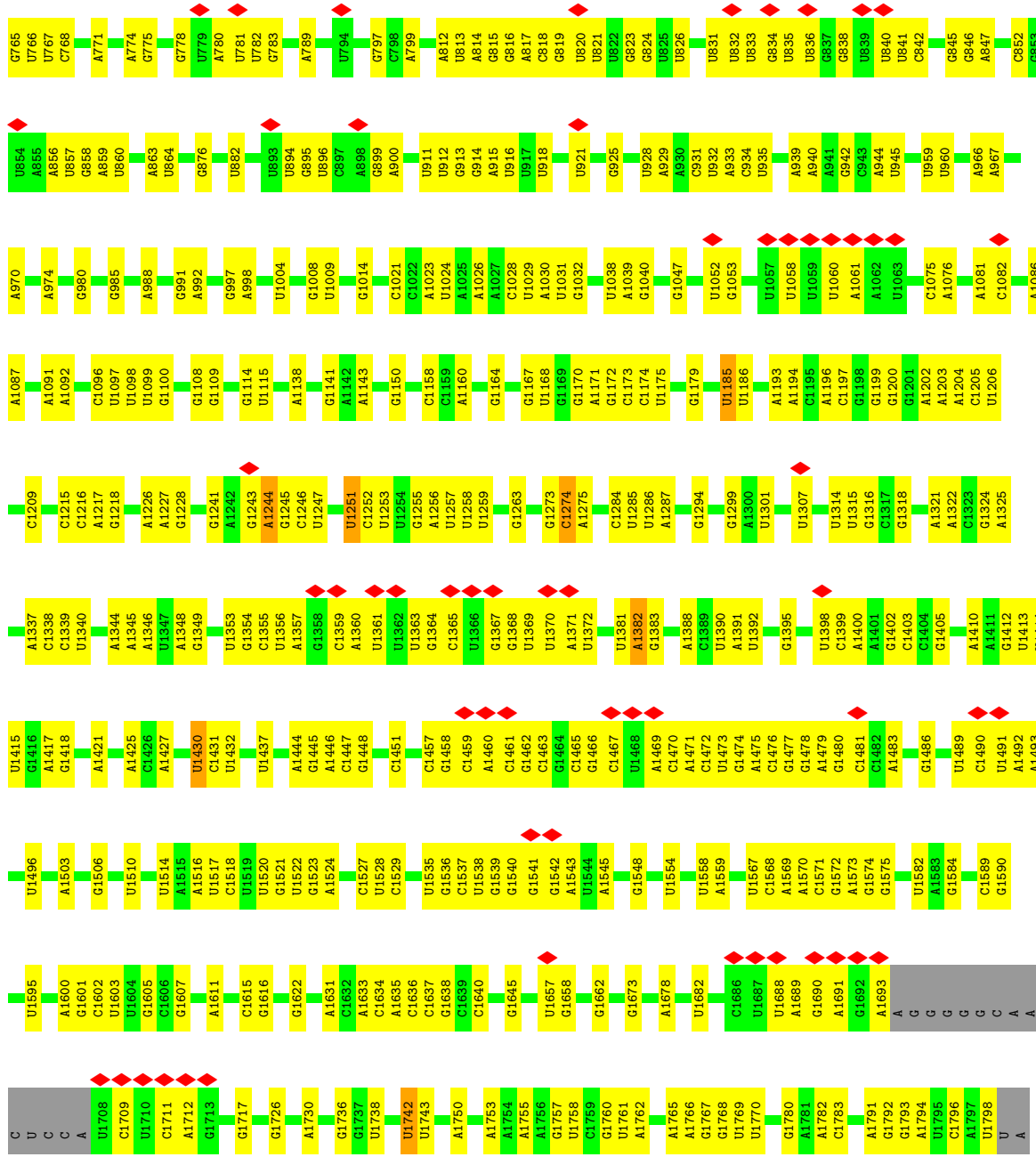
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	BT	154	1143	709	195	230	9	0	0

3 Residue-property plots

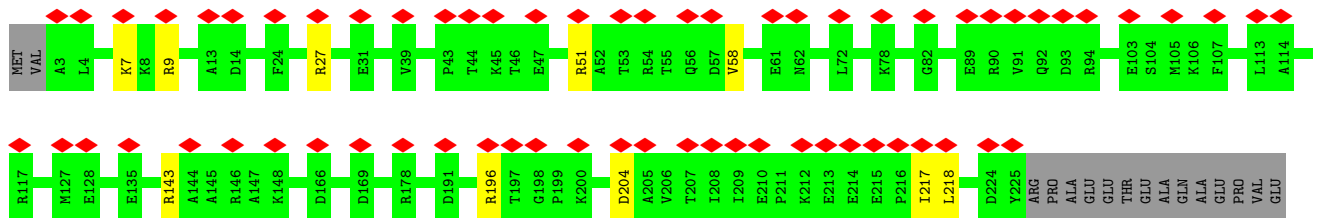
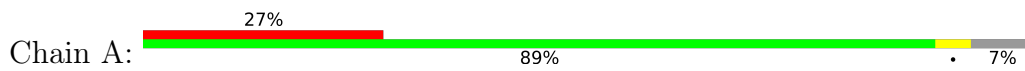
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S ribosomal RNA



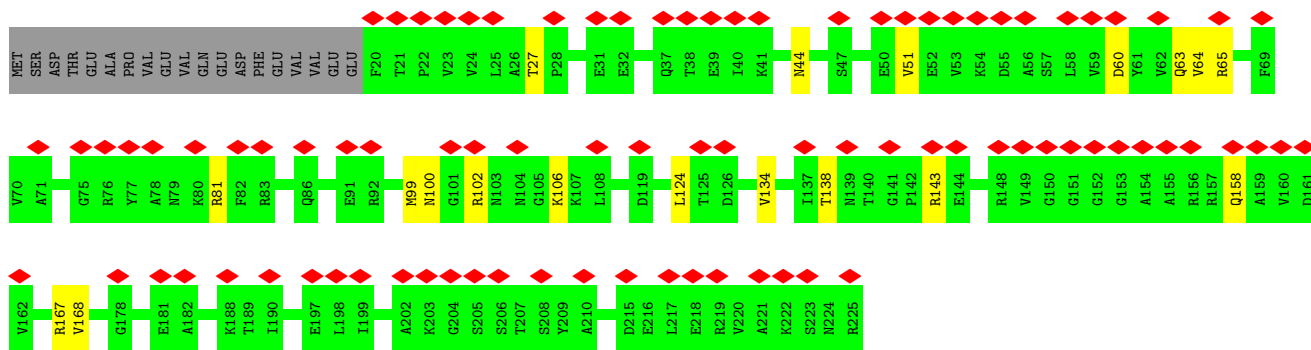
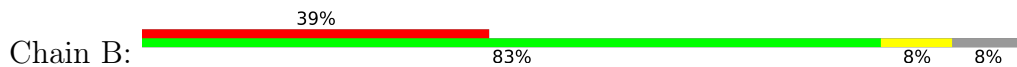


• Molecule 2: 40S ribosomal protein S3

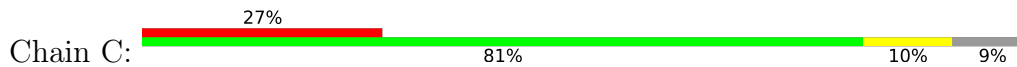


ALA

• Molecule 3: 40S ribosomal protein S5

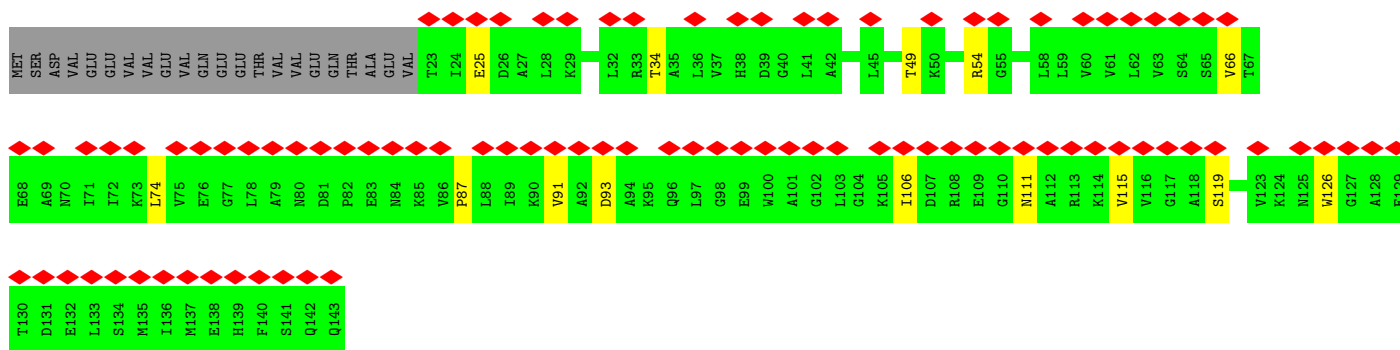
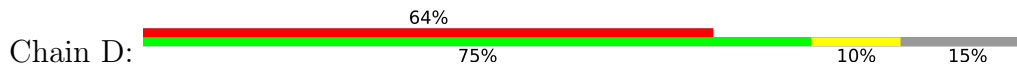


• Molecule 4: 40S ribosomal protein S10-A

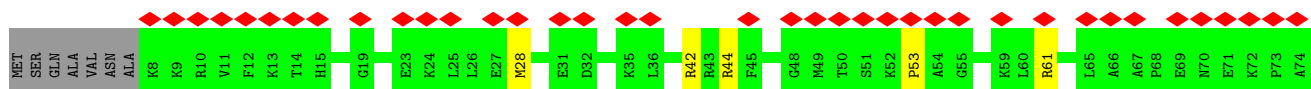
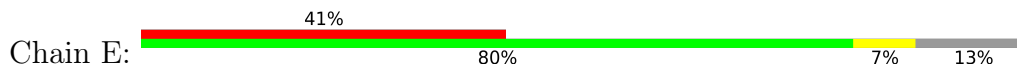


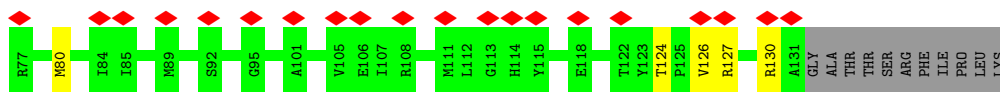
TYR

• Molecule 5: 40S ribosomal protein S12

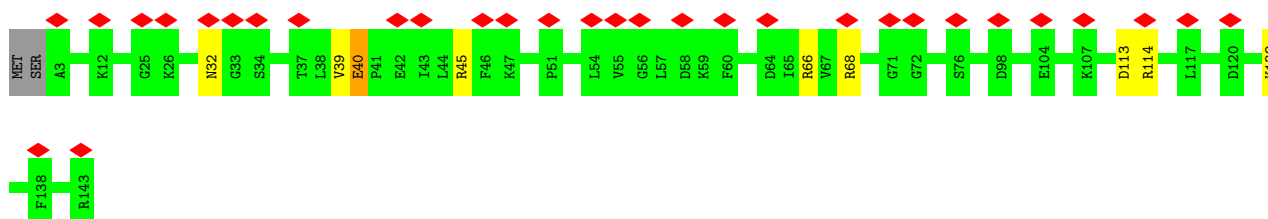
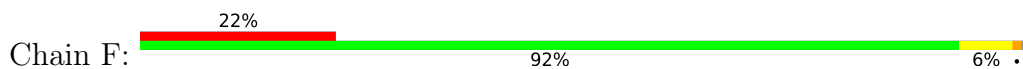


• Molecule 6: 40S ribosomal protein S15

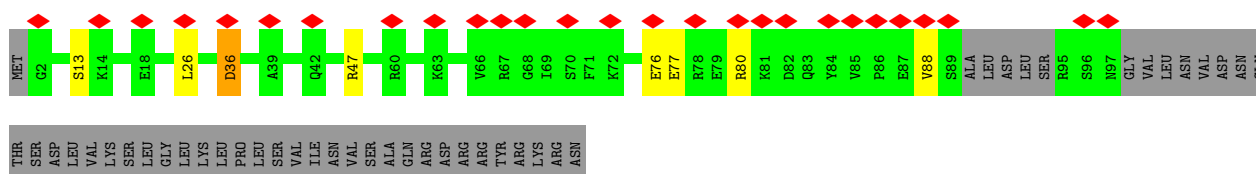




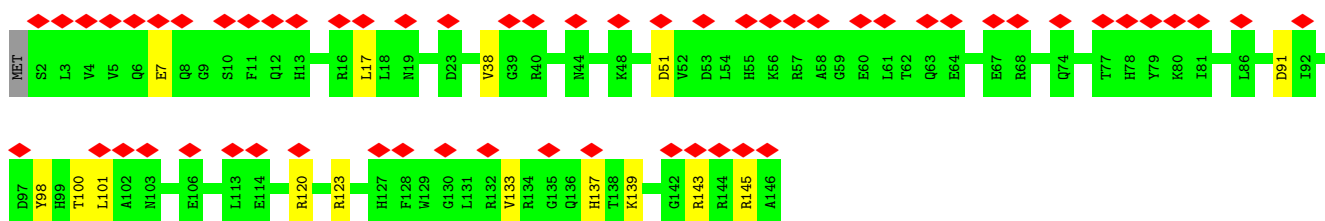
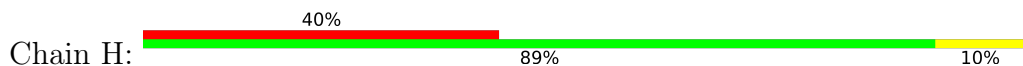
- Molecule 7: 40S ribosomal protein S16-A



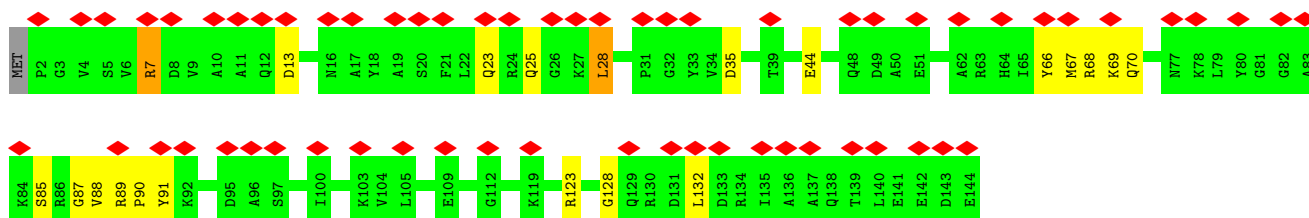
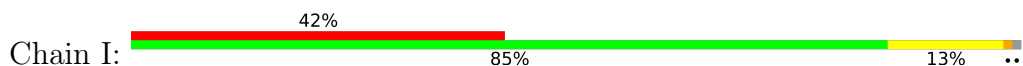
- Molecule 8: 40S ribosomal protein S17-B



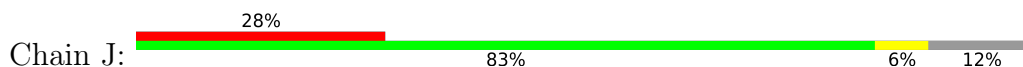
- Molecule 9: 40S ribosomal protein S18-A

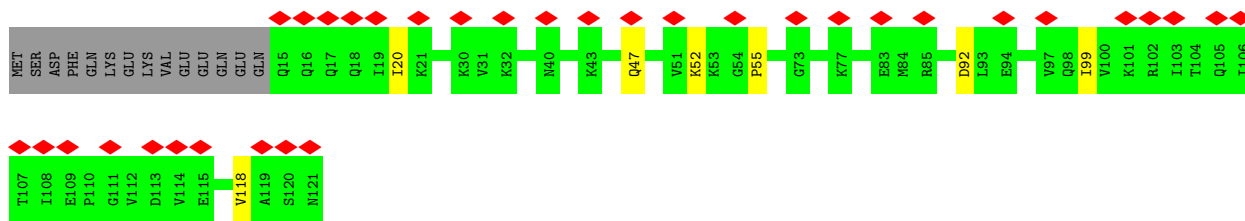


- Molecule 10: 40S ribosomal protein S19-A

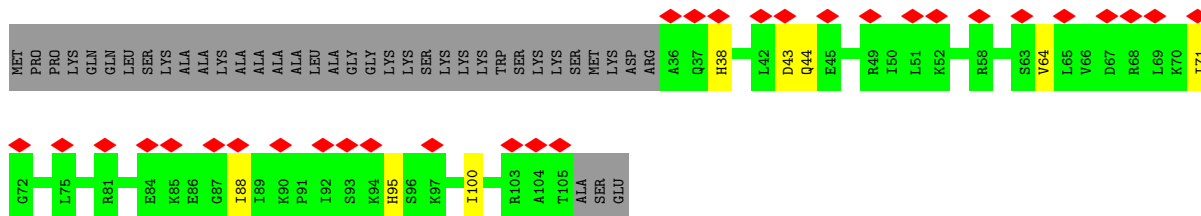


- Molecule 11: 40S ribosomal protein S20

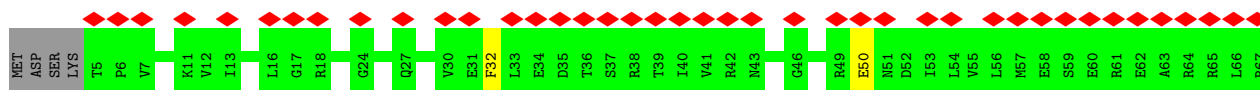
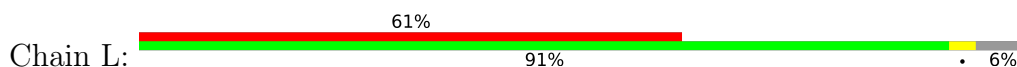




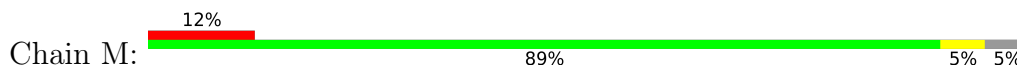
• Molecule 12: 40S ribosomal protein S25-A



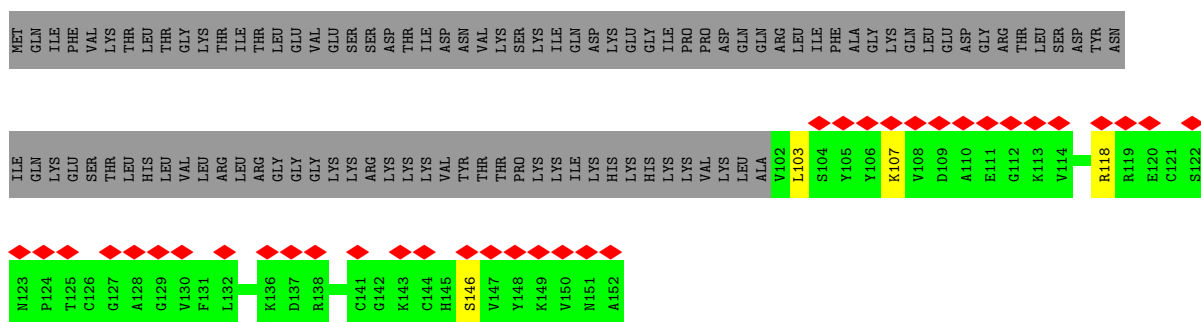
• Molecule 13: 40S ribosomal protein S28-B



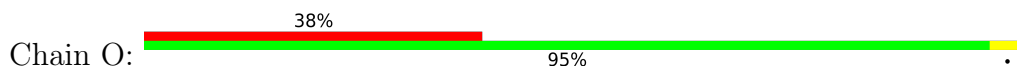
• Molecule 14: 40S ribosomal protein S29-A

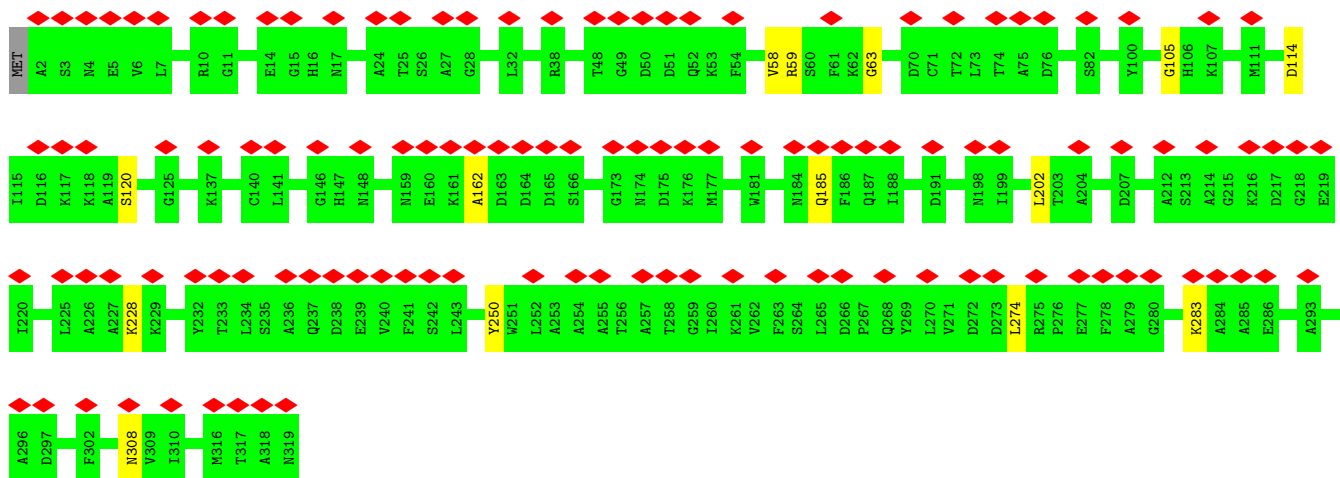


• Molecule 15: Ubiquitin-40S ribosomal protein S31

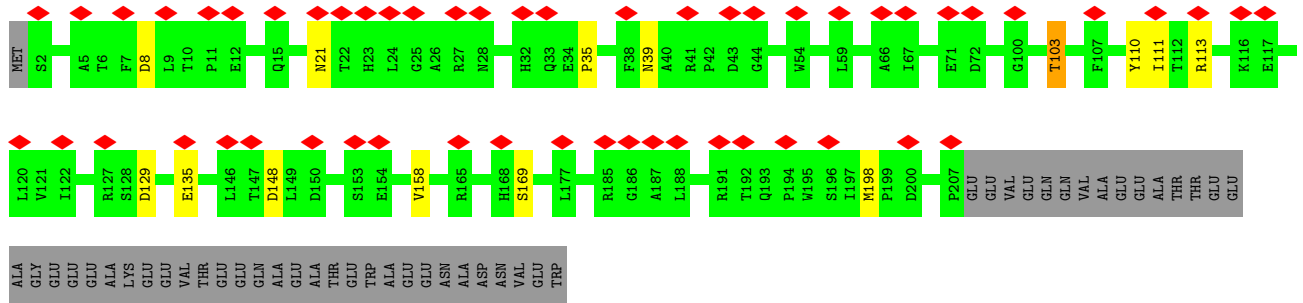
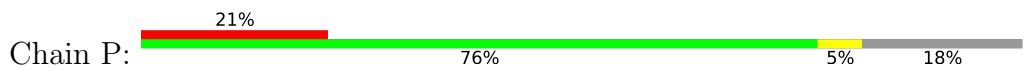


• Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein

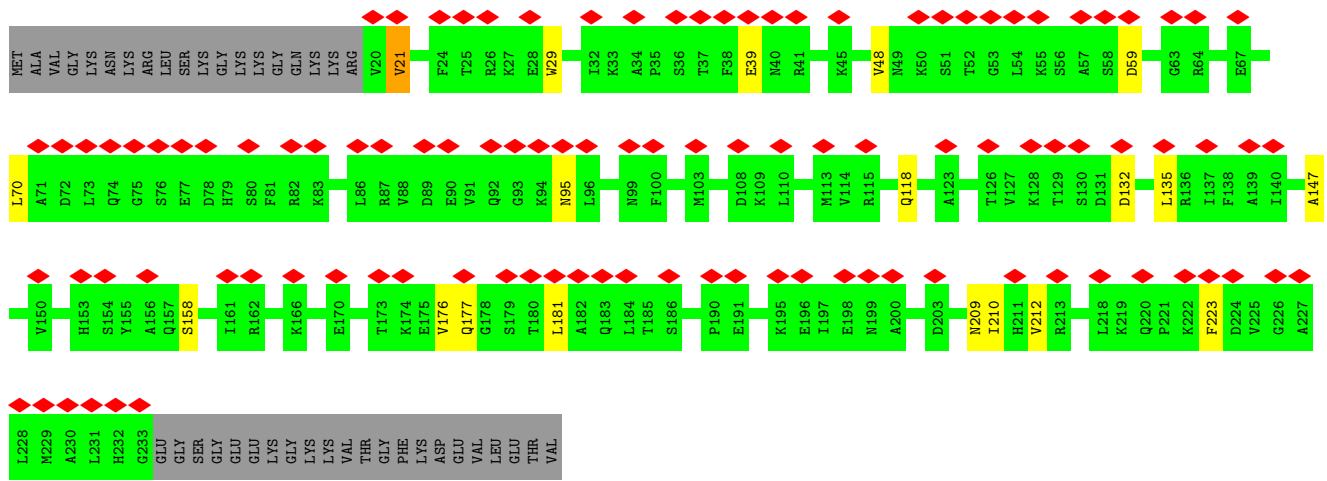
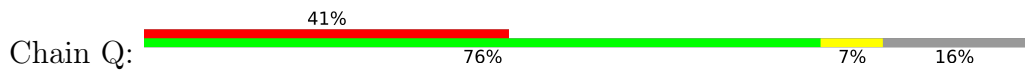




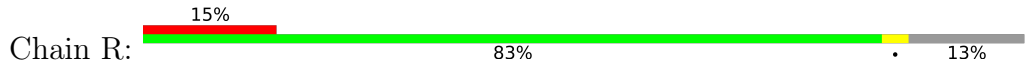
● Molecule 17: 40S ribosomal protein S0-A

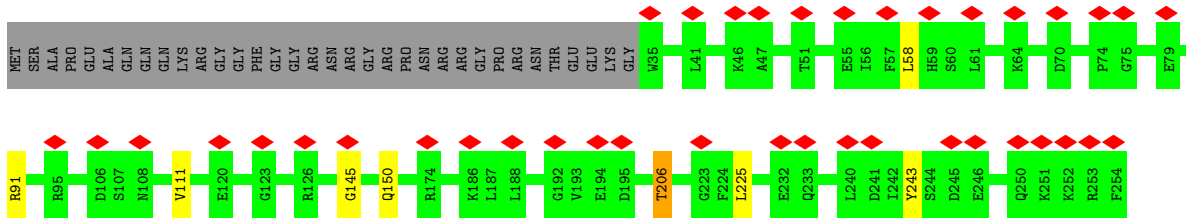


● Molecule 18: 40S ribosomal protein S1-A

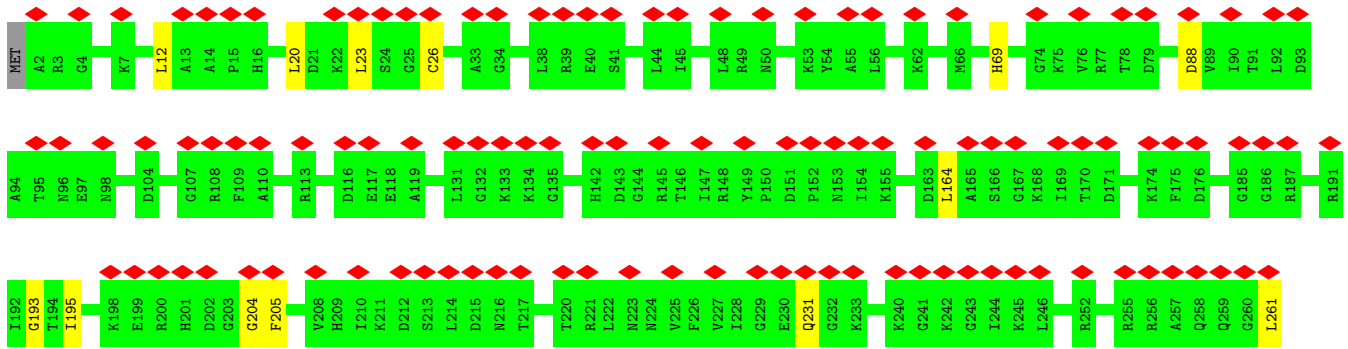


● Molecule 19: 40S ribosomal protein S2

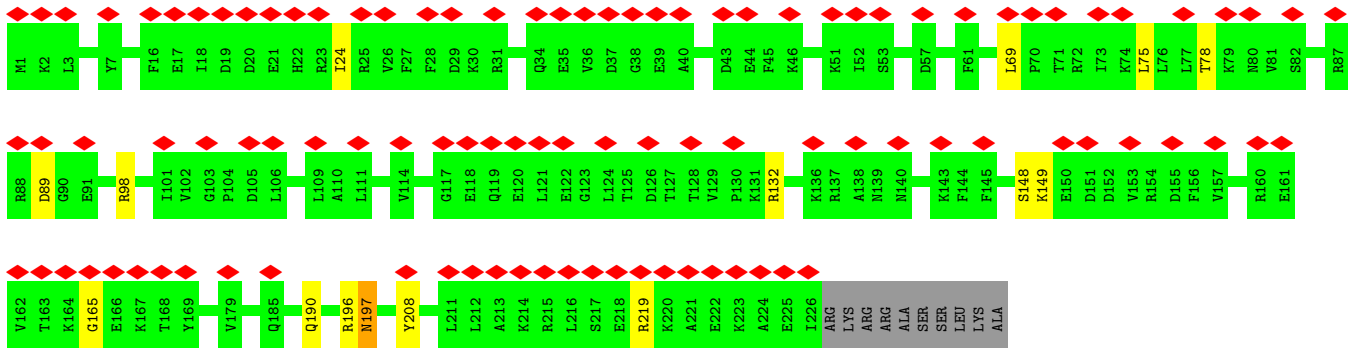
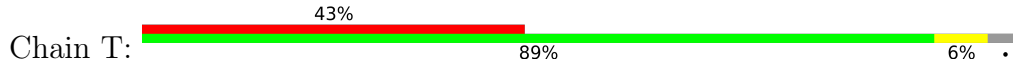




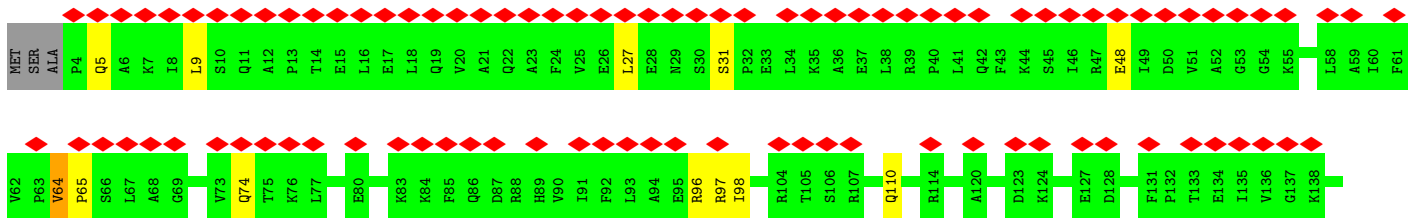
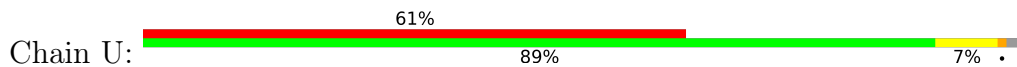
- Molecule 20: 40S ribosomal protein S4-A

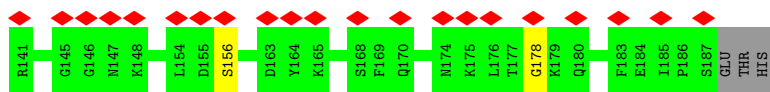


- Molecule 21: 40S ribosomal protein S6-A

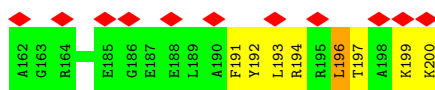
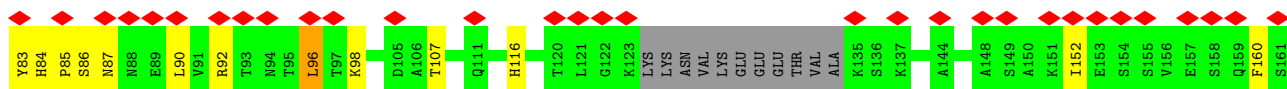
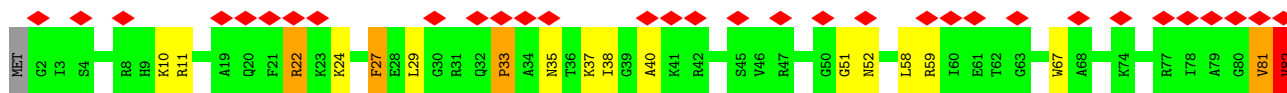
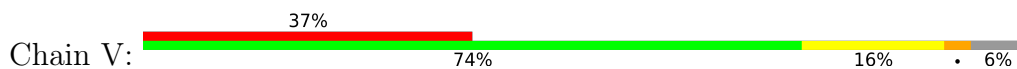


- Molecule 22: 40S ribosomal protein S7-A

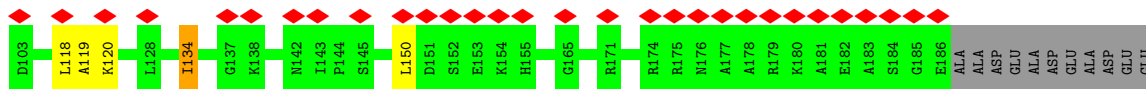
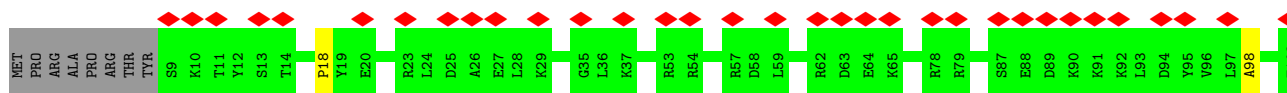
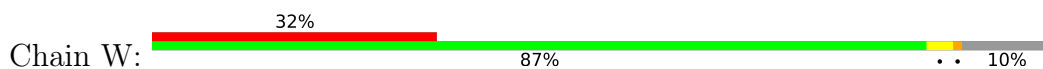




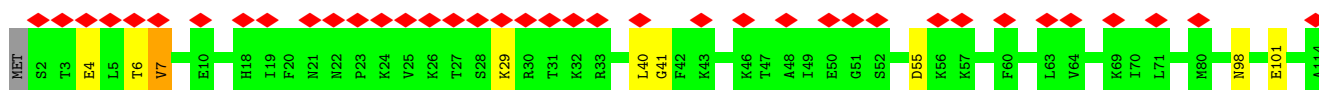
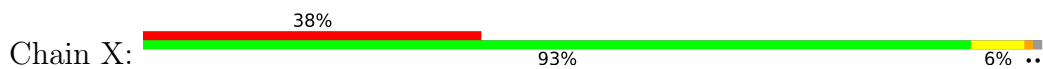
- Molecule 23: 40S ribosomal protein S8-A



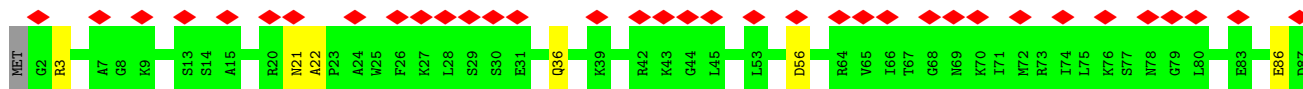
- Molecule 24: 40S ribosomal protein S9-A

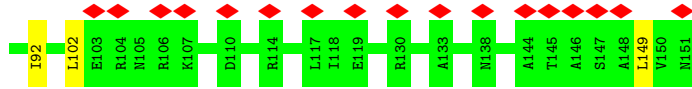


- Molecule 25: 40S ribosomal protein S11-A

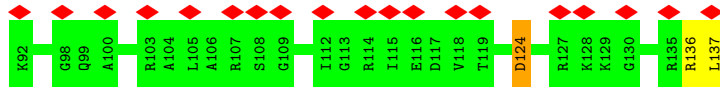
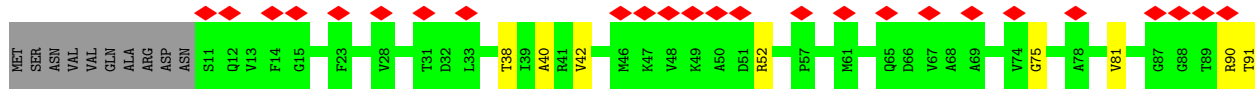
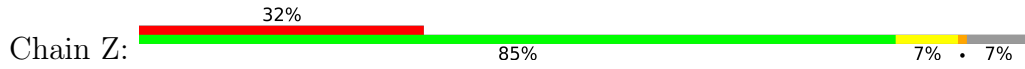


- Molecule 26: 40S ribosomal protein S13

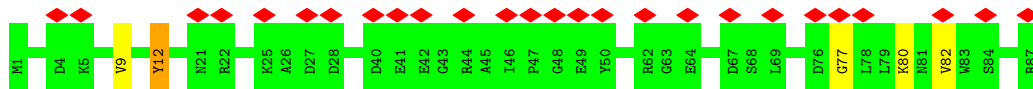
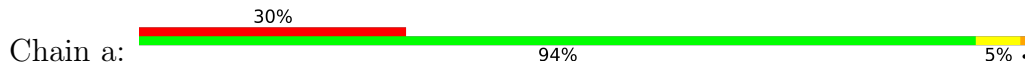




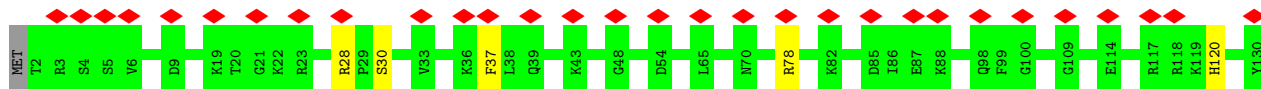
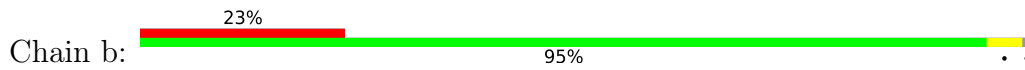
• Molecule 27: 40S ribosomal protein S14-A



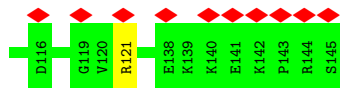
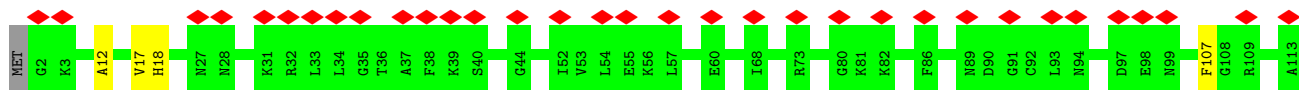
• Molecule 28: 40S ribosomal protein S21-A



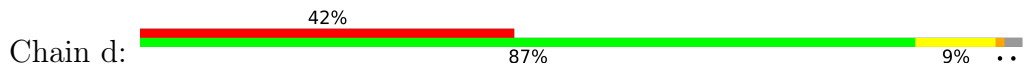
• Molecule 29: 40S ribosomal protein S22-A



• Molecule 30: 40S ribosomal protein S23-A

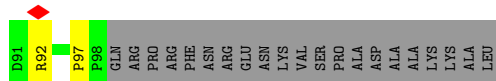
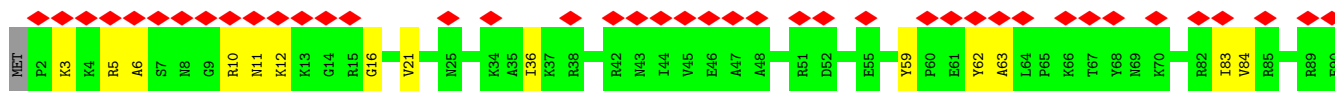


• Molecule 31: 40S ribosomal protein S24-A

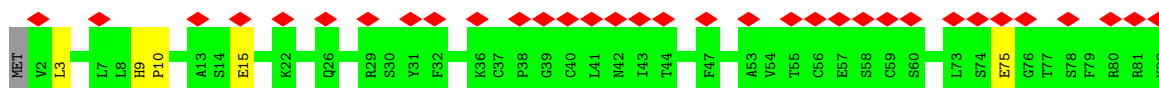
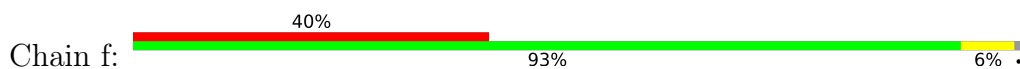




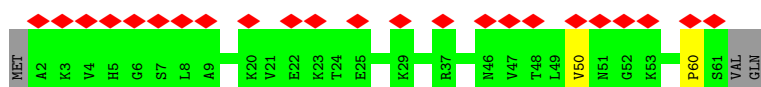
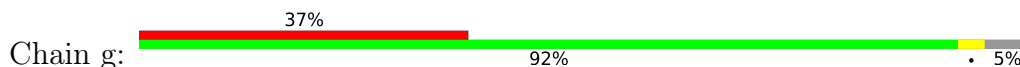
- Molecule 32: 40S ribosomal protein S26-A



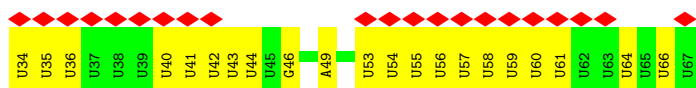
- Molecule 33: 40S ribosomal protein S27-A



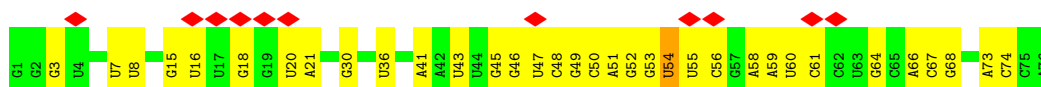
- Molecule 34: 40S ribosomal protein S30-A



- Molecule 35: mRNA

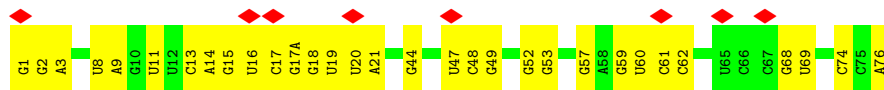


- Molecule 36: A-site tRNA

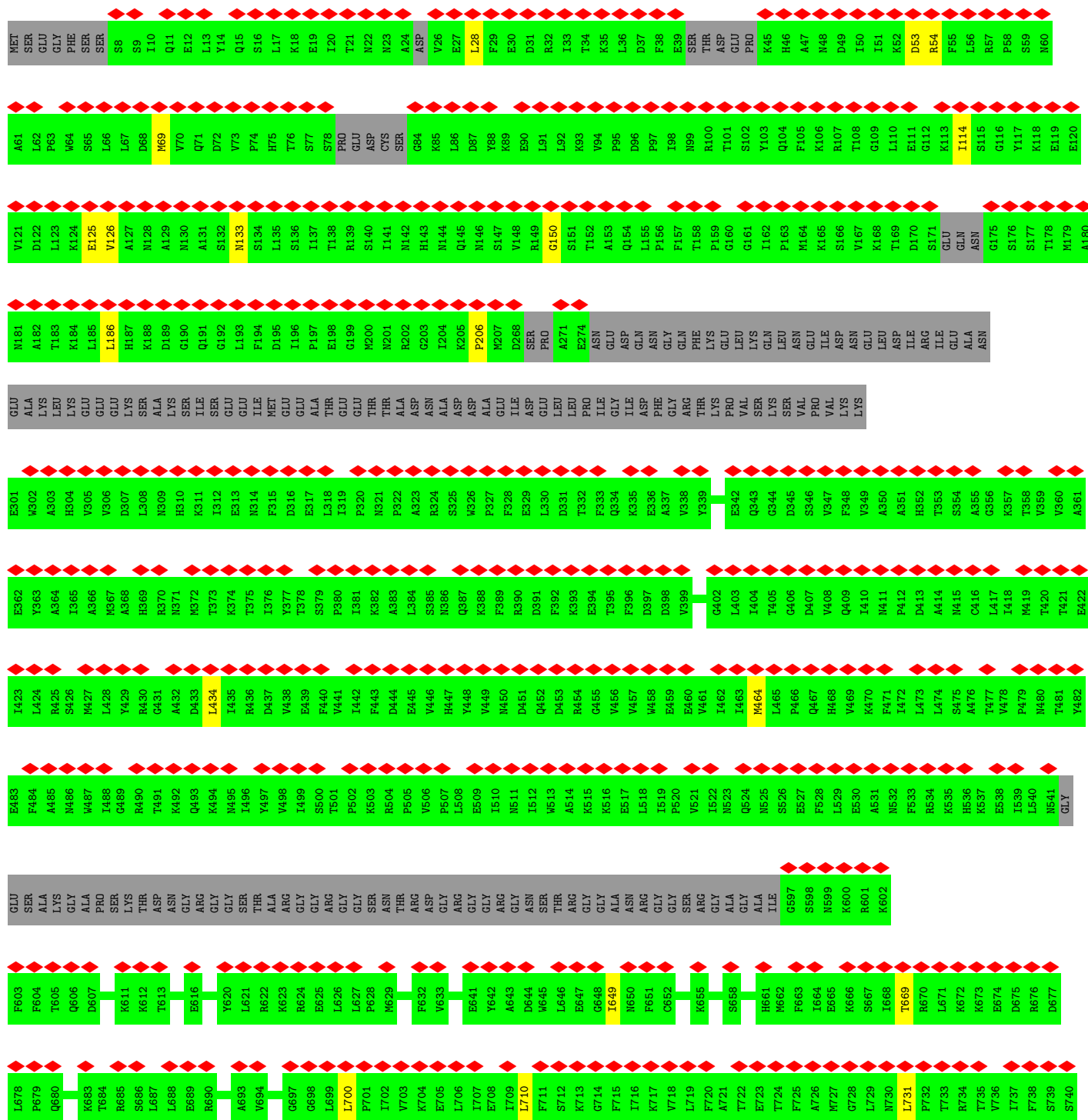
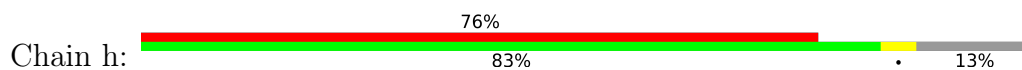


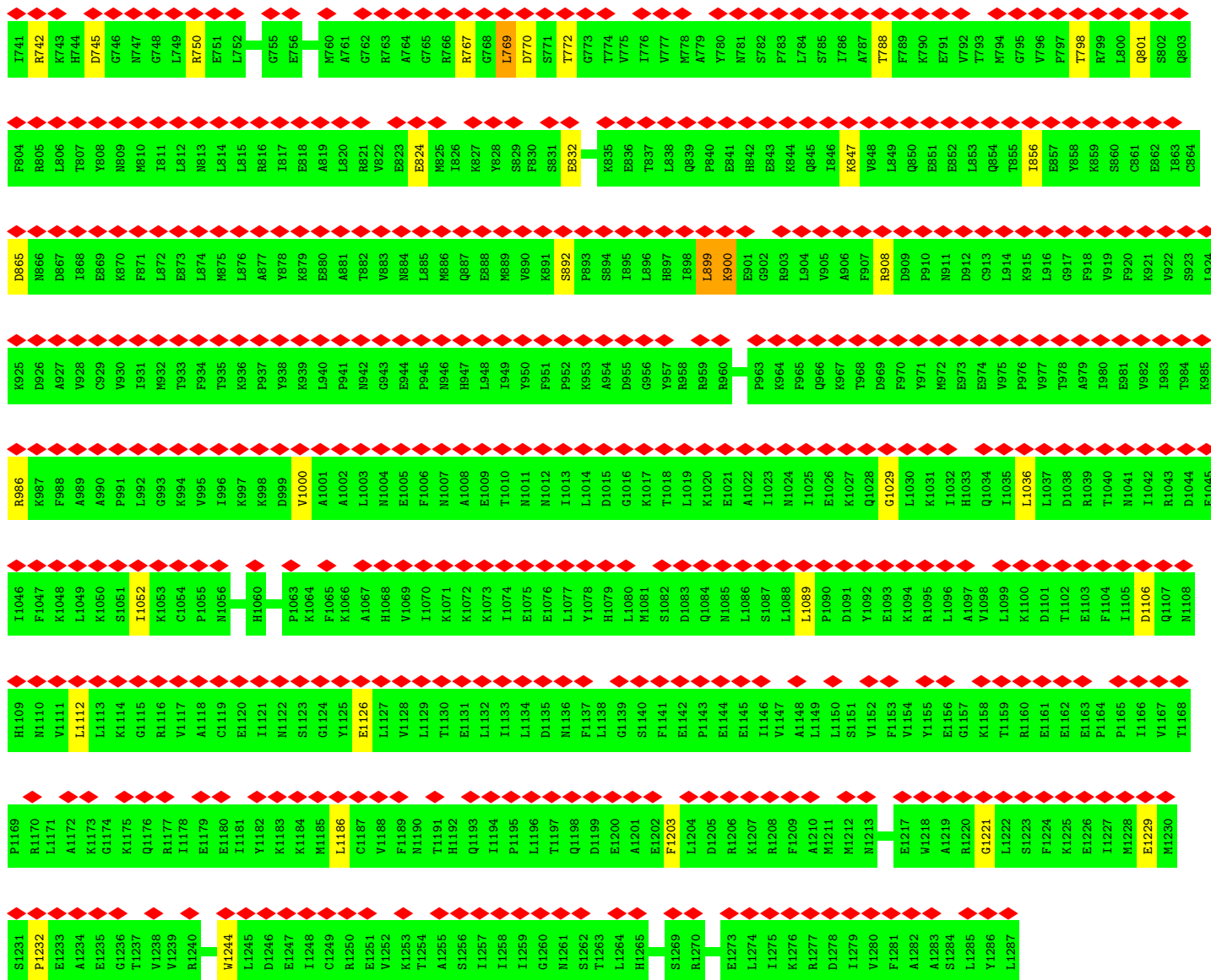
- Molecule 37: P-site tRNA



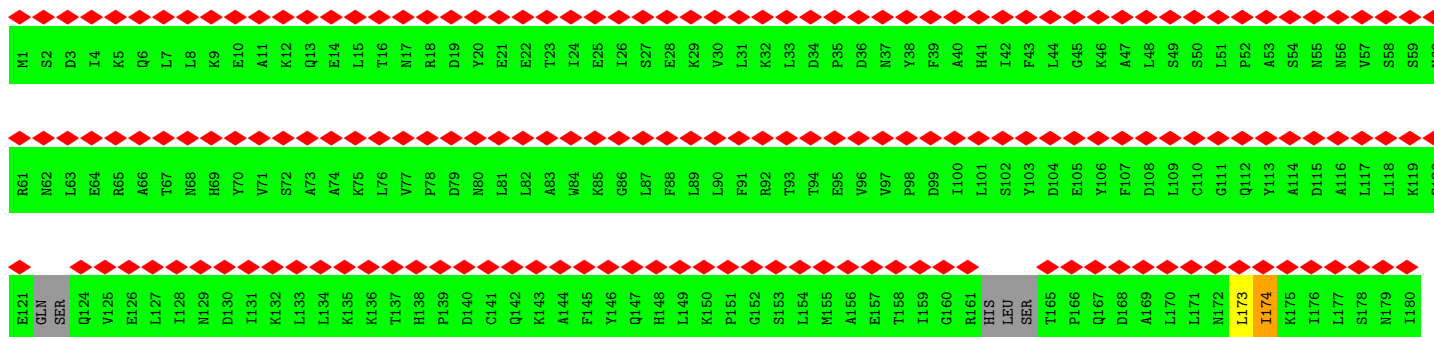
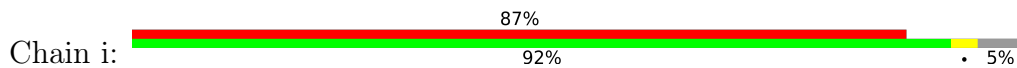


• Molecule 38: Antiviral helicase SKI2

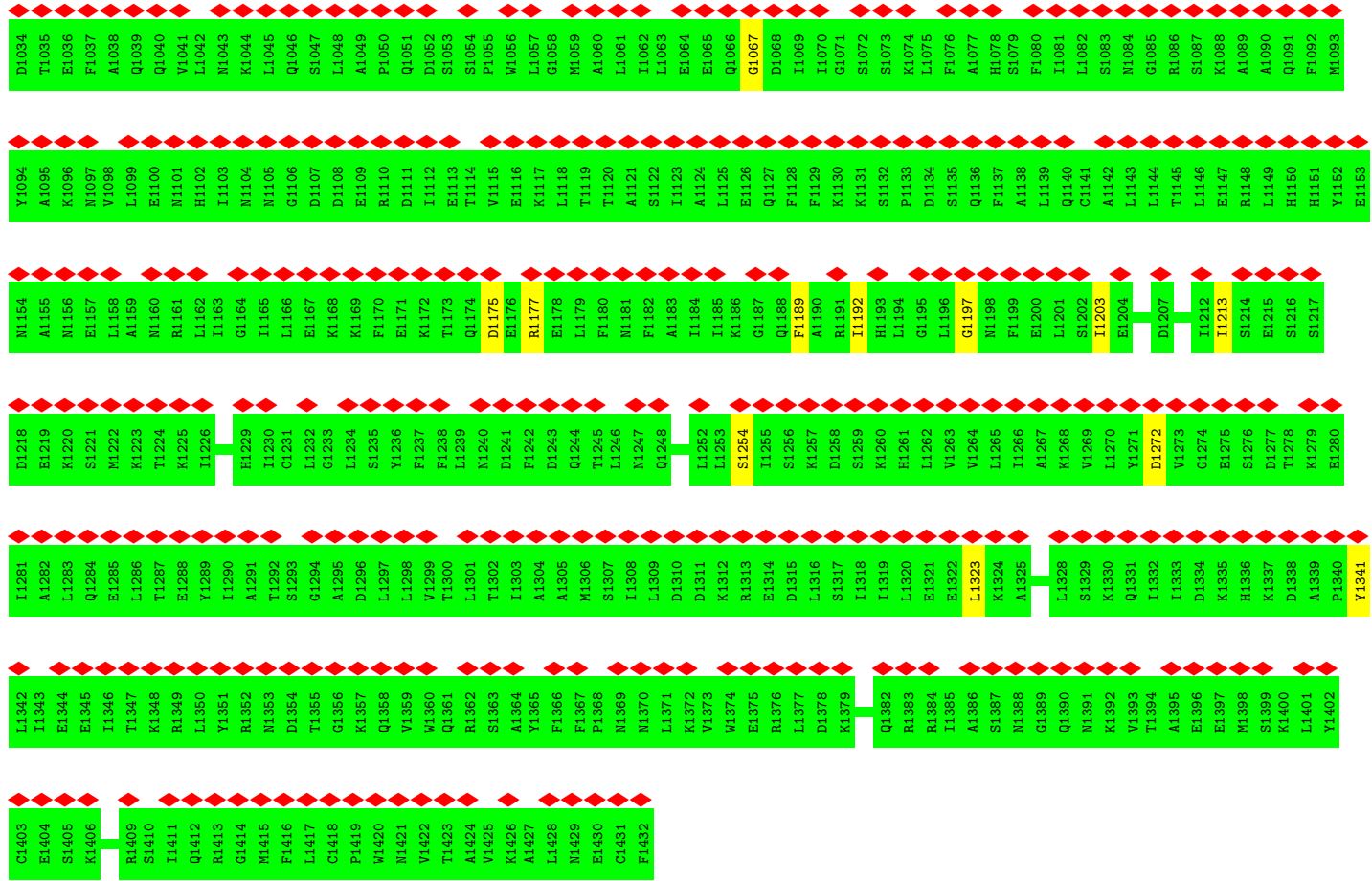




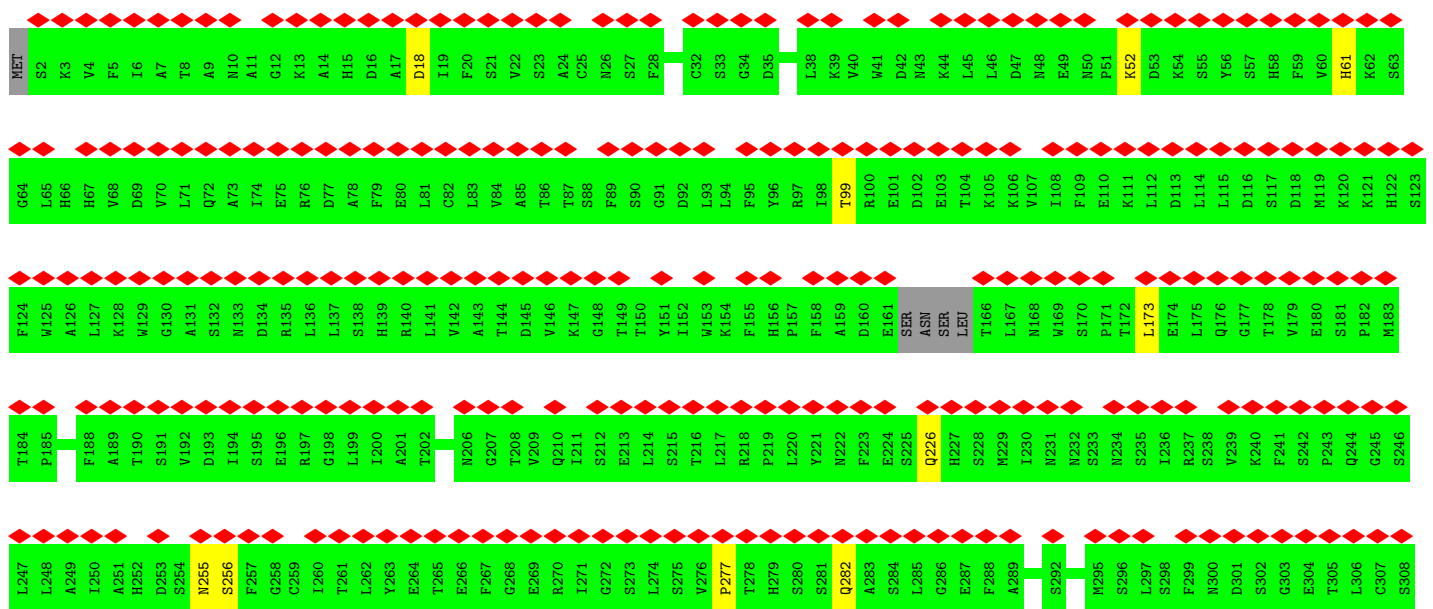
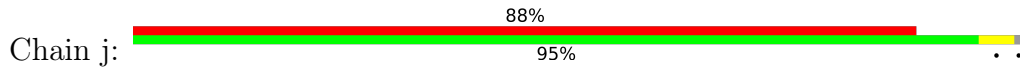
● Molecule 39: Supercollider protein 3

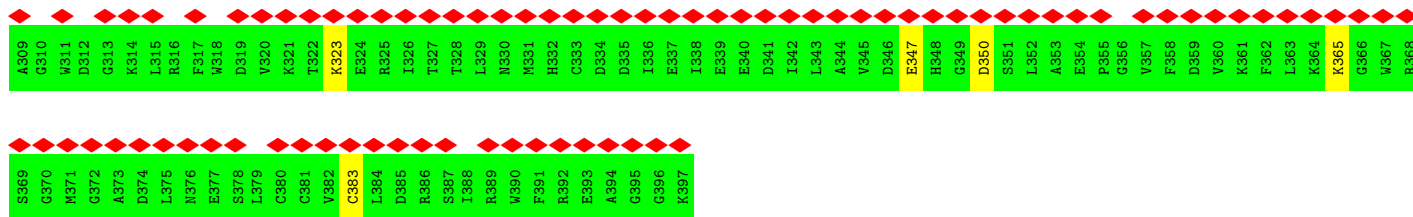


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E241	N242	Q243	W244	L245	E246	Y247	R248	I249	K250	V251	L252	K253	S254	M255	P256	L257	D258	A199	K260	K261	D262	F263	F264	T265	K266	V267	K268	E269	M270	V271	E272	D273	M274	V275	L276	V277	N278	H279	Q280	A281	L282	L283	A284	W285	Q286	K287	Y288	F289	E290	W291	L292	D293	Y294	E295	D296	L297	D298	N299	M300
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G481	THR	ASN	GLU	GLU	VAL	LYS	ARG	VAL	GLY	GLU	VAL	LYS	ARG	ARG	GLU	GLU	VAL	LYS	ASP	GLM	ASP	GLU	ALA	LYS	GLU	GLU	GLU	GLU	ASP	LEU	D399	D400	I401	E402	I403	G404	L405	L406	E407	E408	E409	V410	V411	T412	V413	L414	L415	E416	N417	I418	V419	K420							
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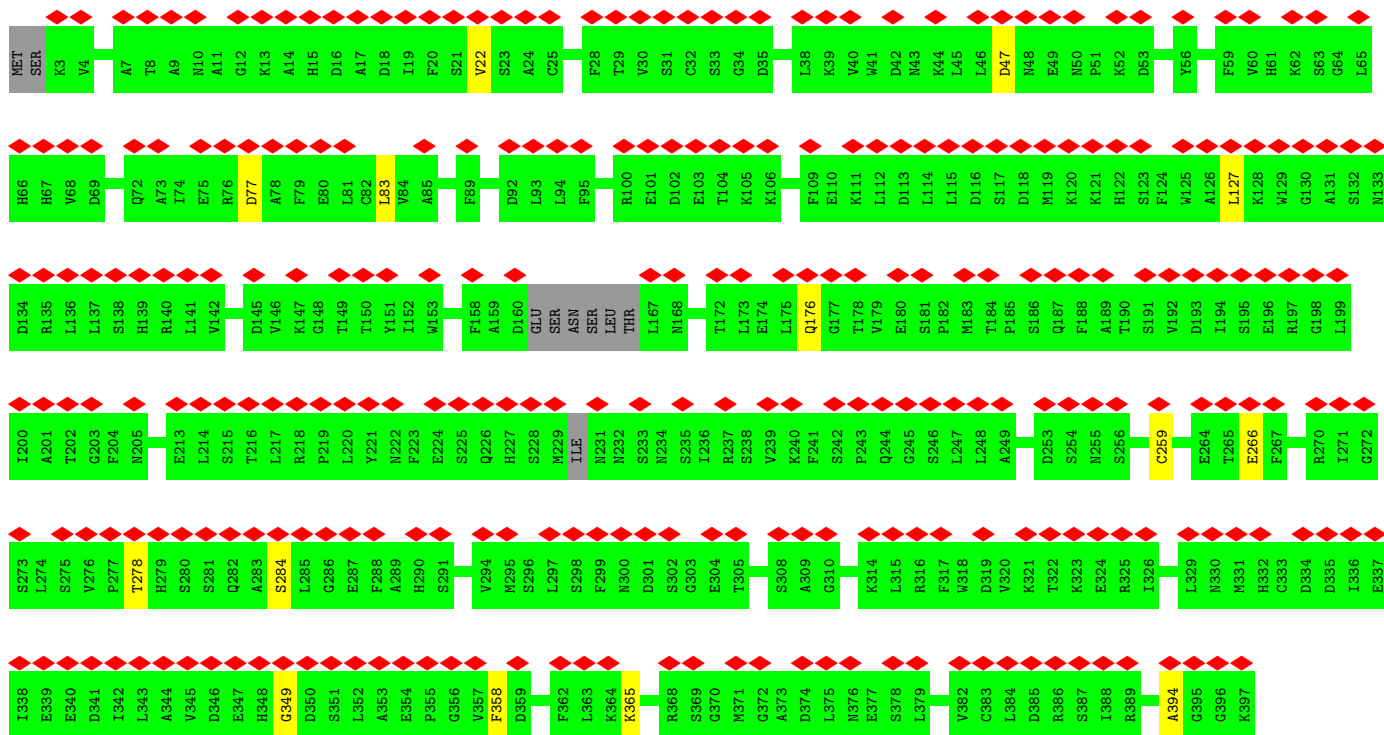
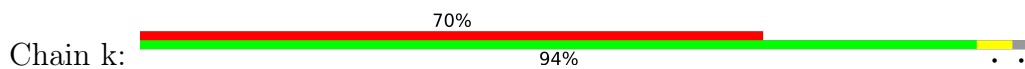


• Molecule 40: Antiviral protein SKI8

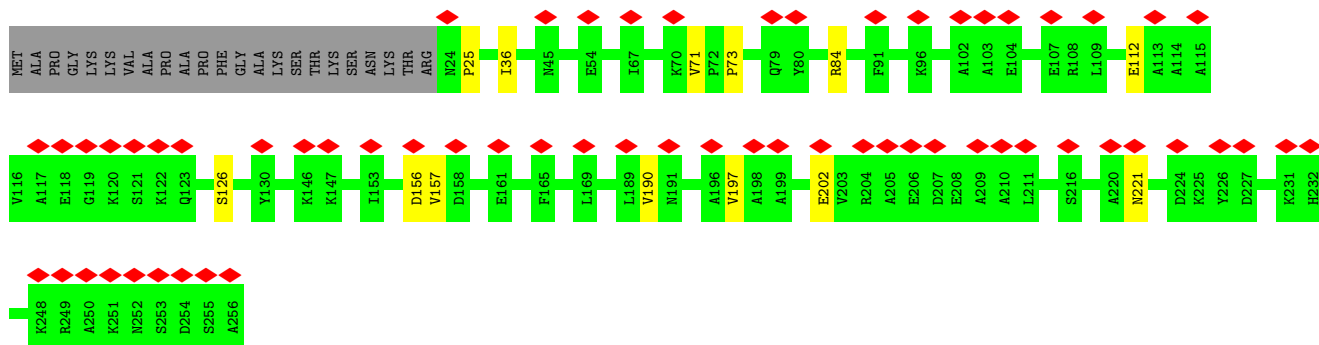
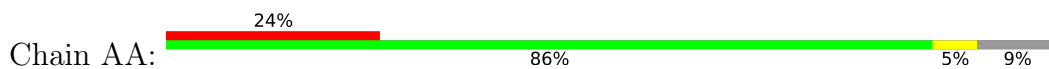




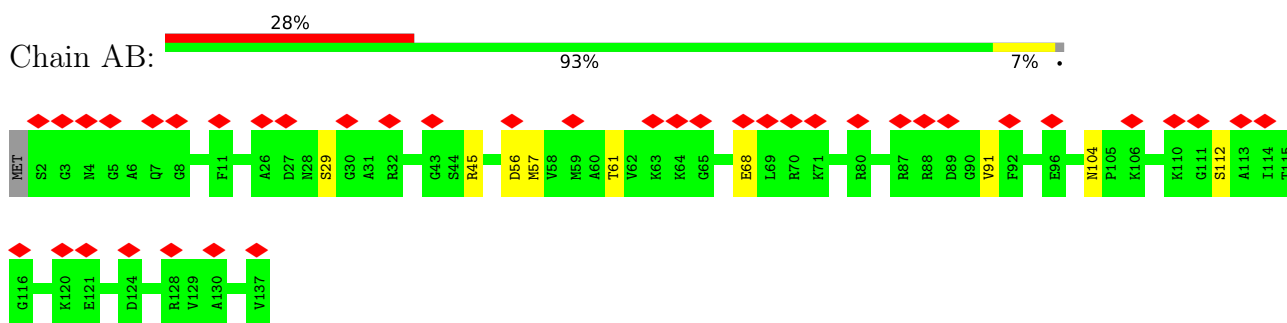
• Molecule 40: Antiviral protein SKI8



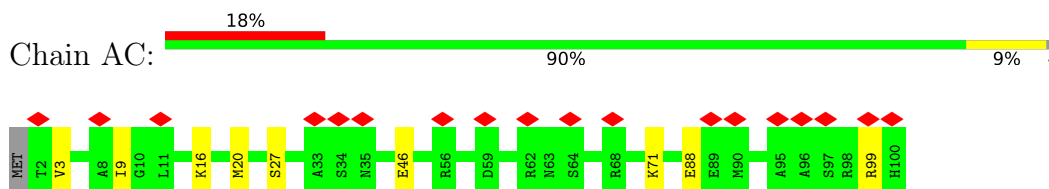
• Molecule 41: 60S ribosomal protein L8-A



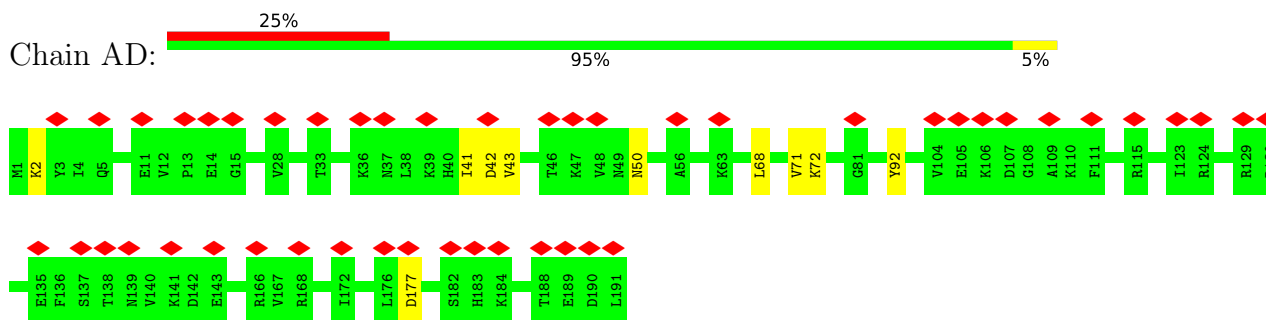
• Molecule 42: 60S ribosomal protein L23-A



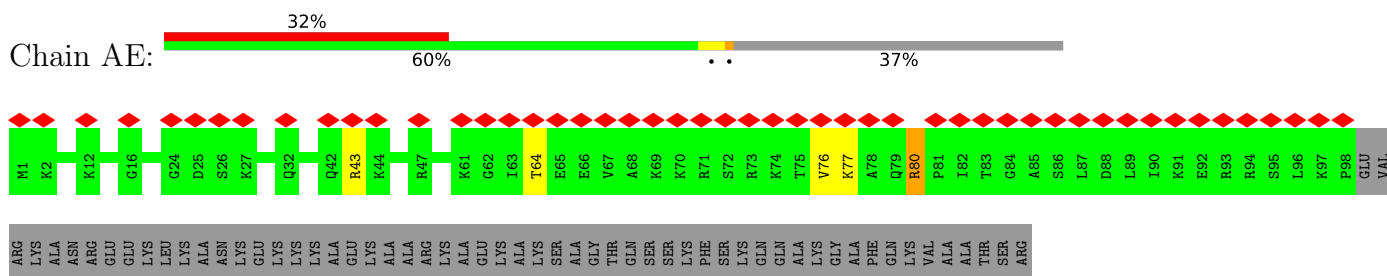
- Molecule 43: 60S ribosomal protein L36-A



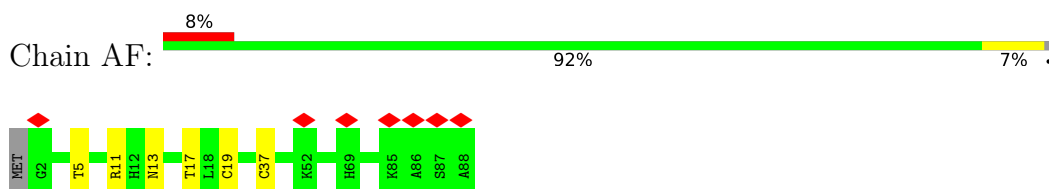
- Molecule 44: 60S ribosomal protein L9-A



- Molecule 45: 60S ribosomal protein L24-A

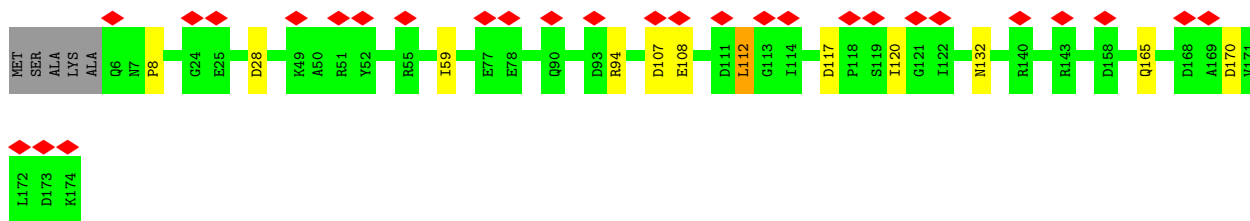


- Molecule 46: 60S ribosomal protein L37-A

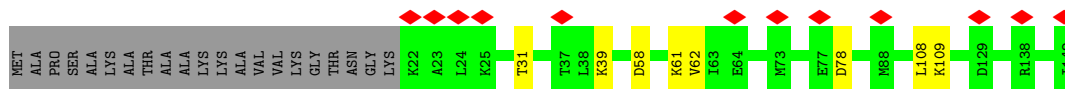
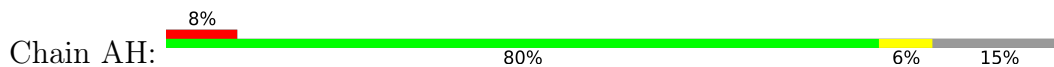


- Molecule 47: 60S ribosomal protein L11-A





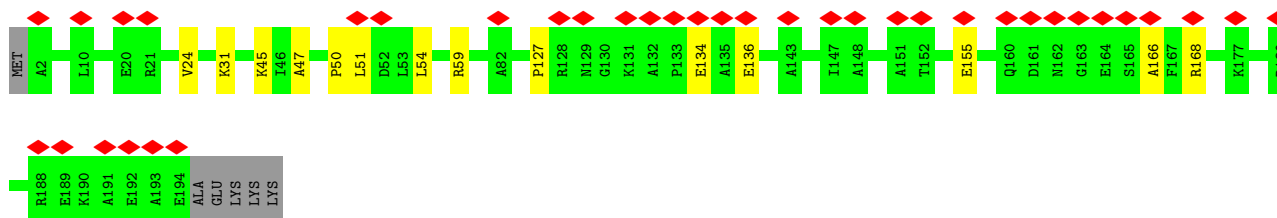
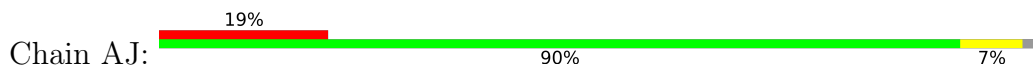
- Molecule 48: 60S ribosomal protein L25



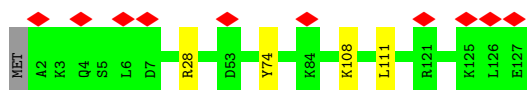
- Molecule 49: 60S ribosomal protein L38



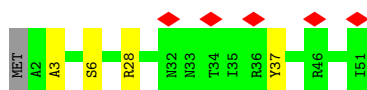
- Molecule 50: 60S ribosomal protein L13-A



- Molecule 51: 60S ribosomal protein L26-A



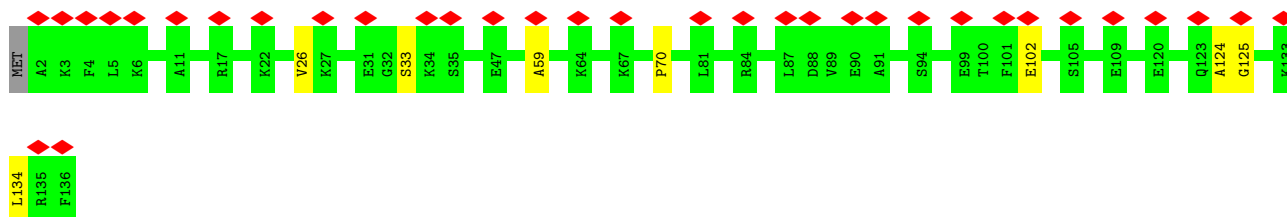
- Molecule 52: 60S ribosomal protein L39



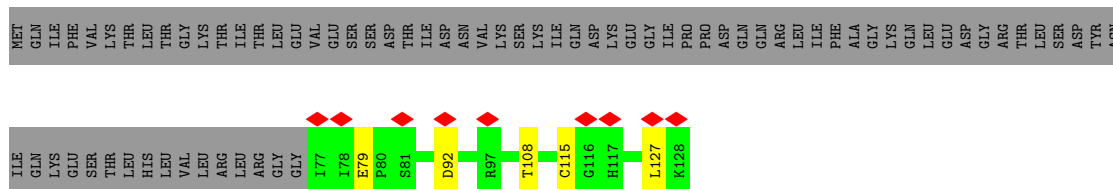
- Molecule 53: 60S ribosomal protein L14-A



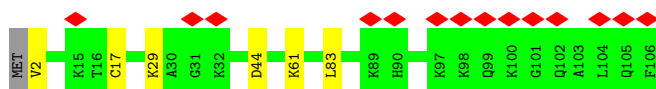
- Molecule 54: 60S ribosomal protein L27-A



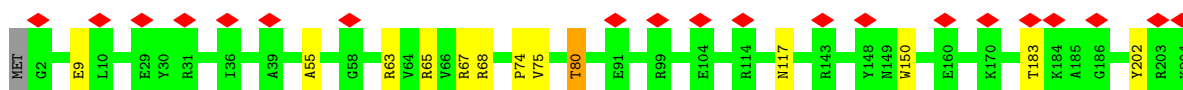
- Molecule 55: Ubiquitin-60S ribosomal protein L40



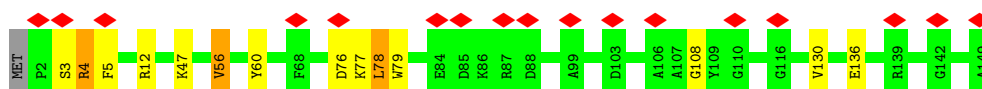
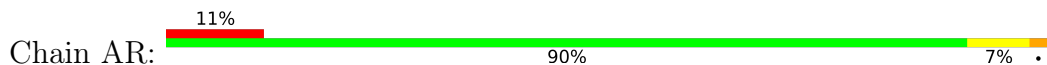
- Molecule 56: 60S ribosomal protein L42-A



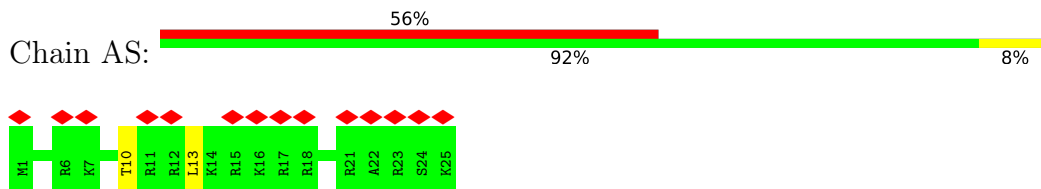
- Molecule 57: 60S ribosomal protein L15-A



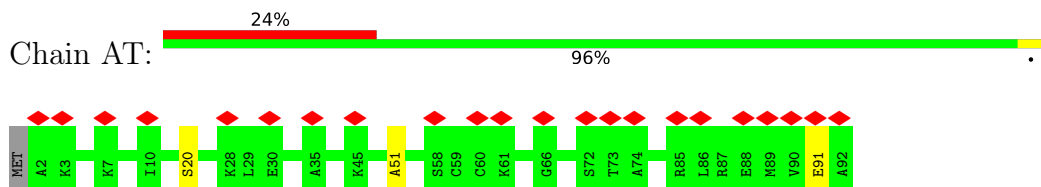
- Molecule 58: 60S ribosomal protein L28



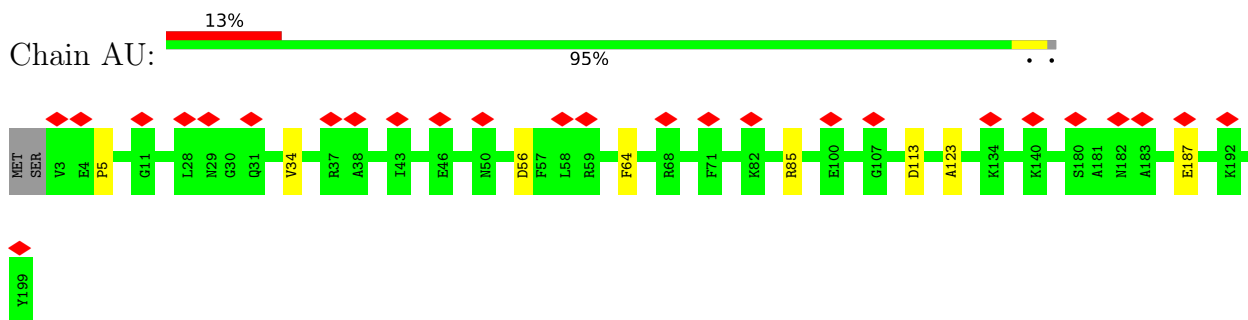
- Molecule 59: 60S ribosomal protein L41-A



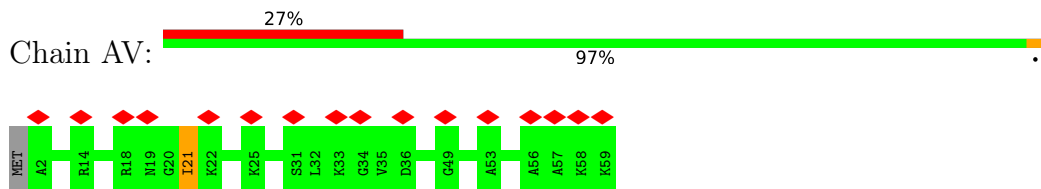
- Molecule 60: 60S ribosomal protein L43-A



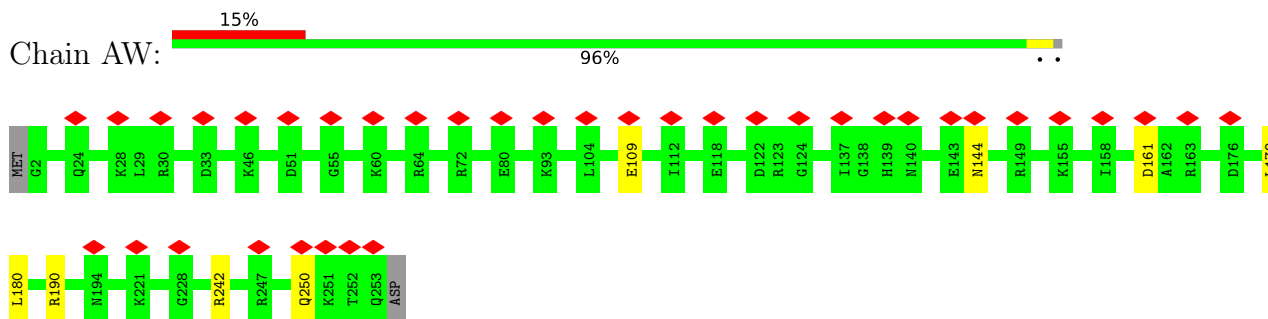
- Molecule 61: 60S ribosomal protein L16-A



- Molecule 62: 60S ribosomal protein L29



- Molecule 63: 60S ribosomal protein L2-A

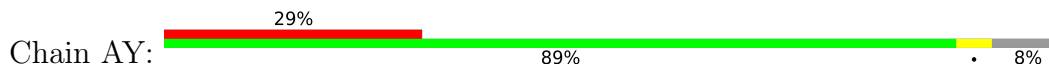


- Molecule 64: 60S ribosomal protein L17-A

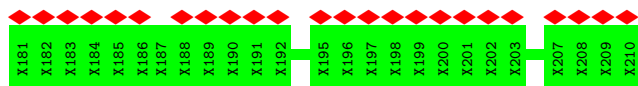
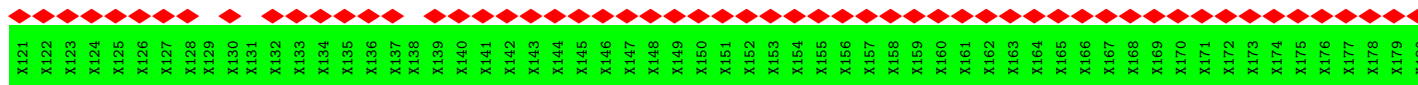
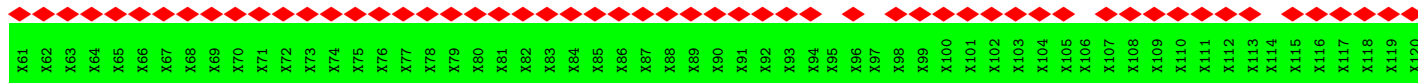
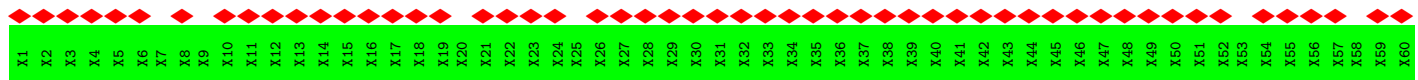
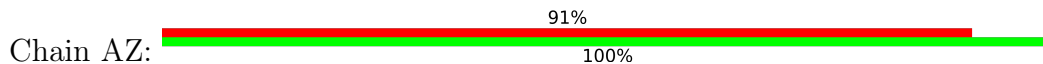




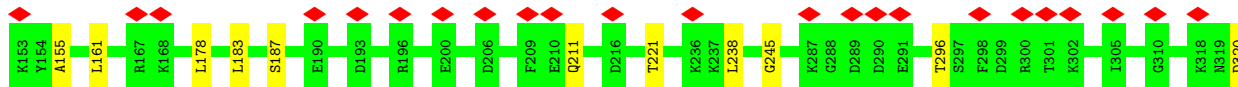
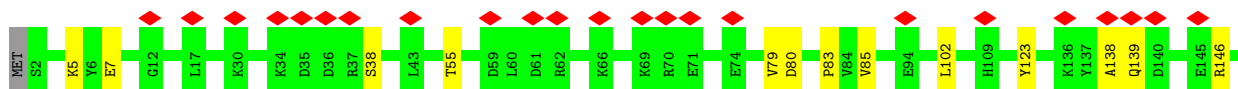
• Molecule 65: 60S ribosomal protein L30



• Molecule 66: uL1

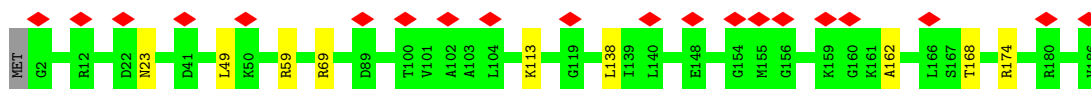


• Molecule 67: 60S ribosomal protein L3




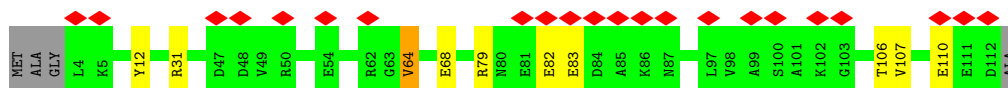
• Molecule 68: 60S ribosomal protein L18-A

Chain BB: 




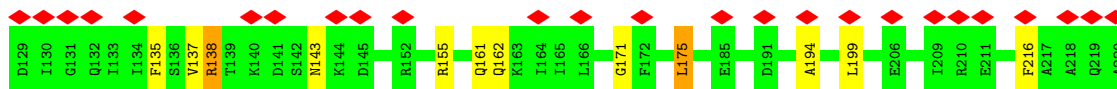
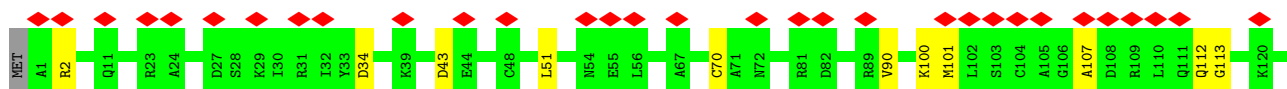
- Molecule 69: 60S ribosomal protein L31-A

Chain BC: 

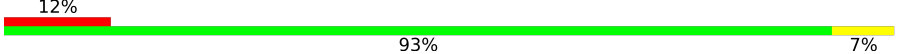


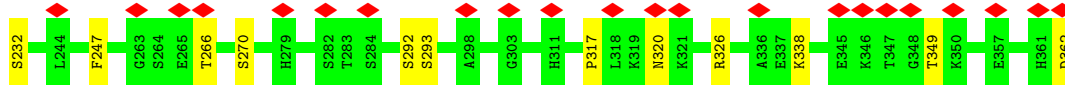
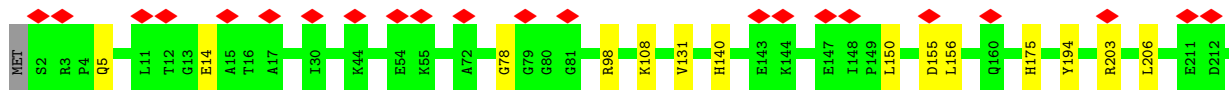
- Molecule 70: 60S ribosomal protein L10

Chain BD: 



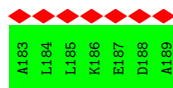
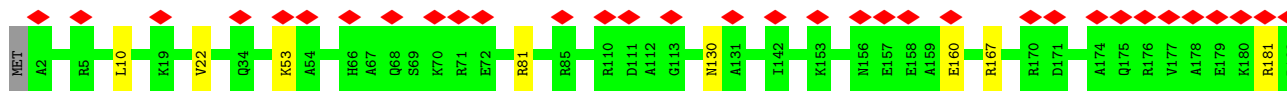
- Molecule 71: 60S ribosomal protein L4-A

Chain BE: 



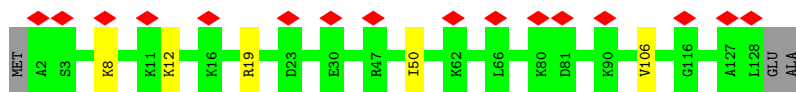
- Molecule 72: 60S ribosomal protein L19-A

Chain BF: 

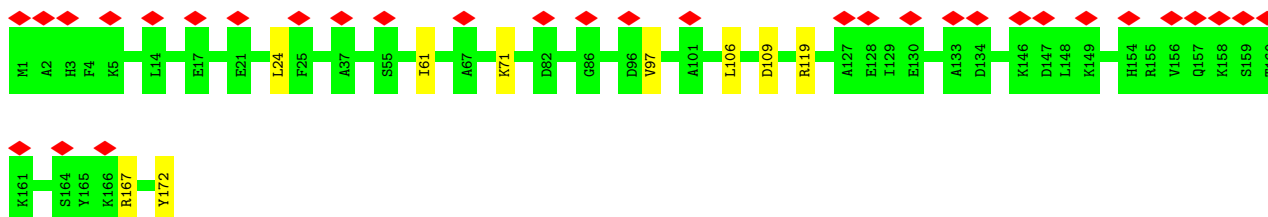


- Molecule 73: 60S ribosomal protein L32

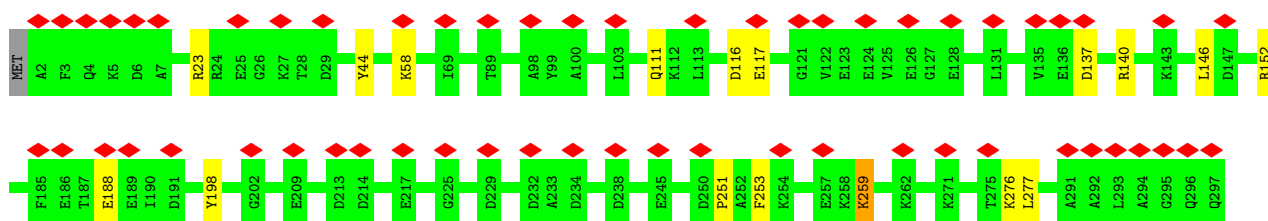
Chain BG: 



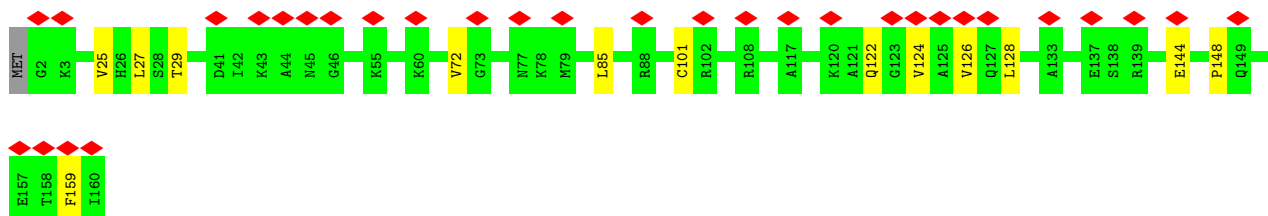
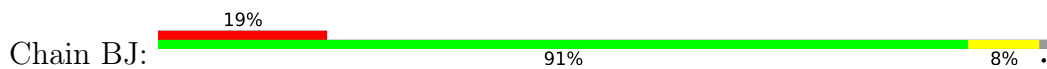
- Molecule 74: 60S ribosomal protein L20-A



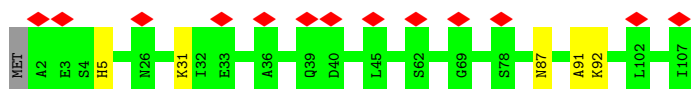
- Molecule 75: 60S ribosomal protein L5



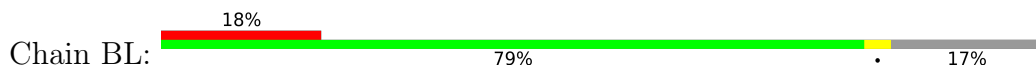
- Molecule 76: 60S ribosomal protein L21-A

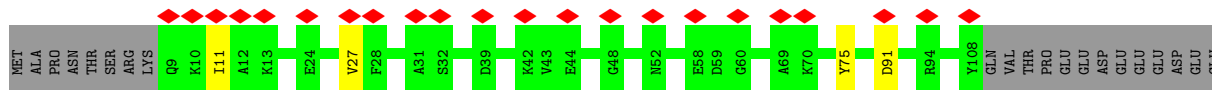


- Molecule 77: 60S ribosomal protein L33-A

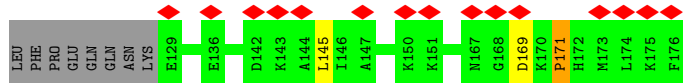
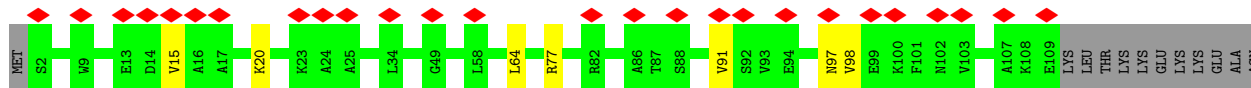
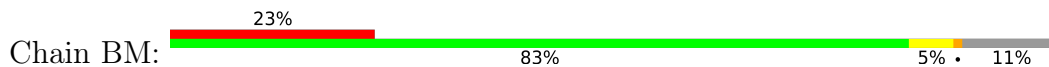


- Molecule 78: 60S ribosomal protein L22-A

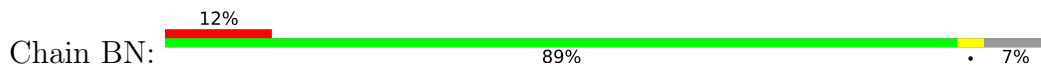




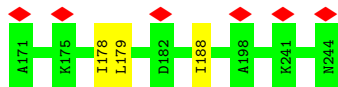
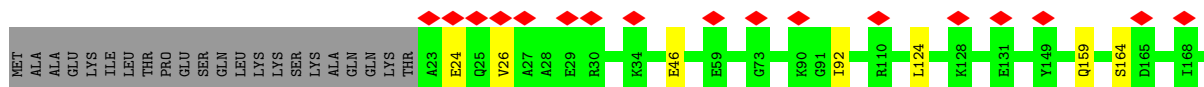
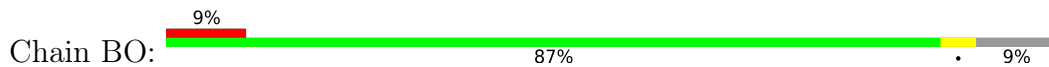
• Molecule 79: 60S ribosomal protein L6-A



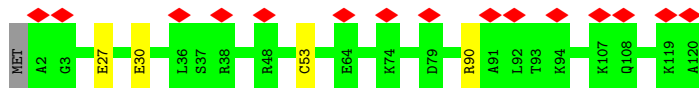
• Molecule 80: 60S ribosomal protein L34-A



• Molecule 81: 60S ribosomal protein L7-A

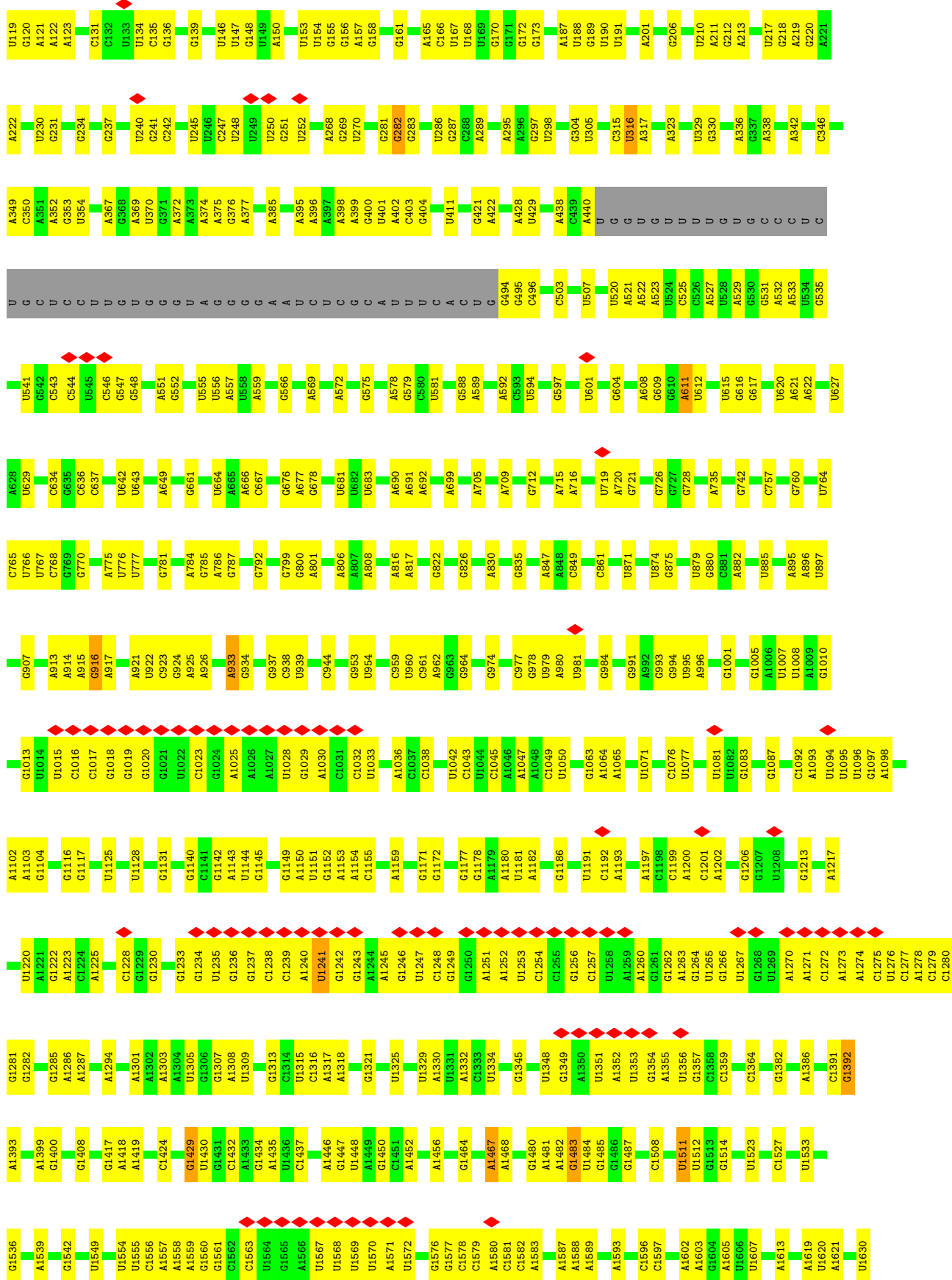


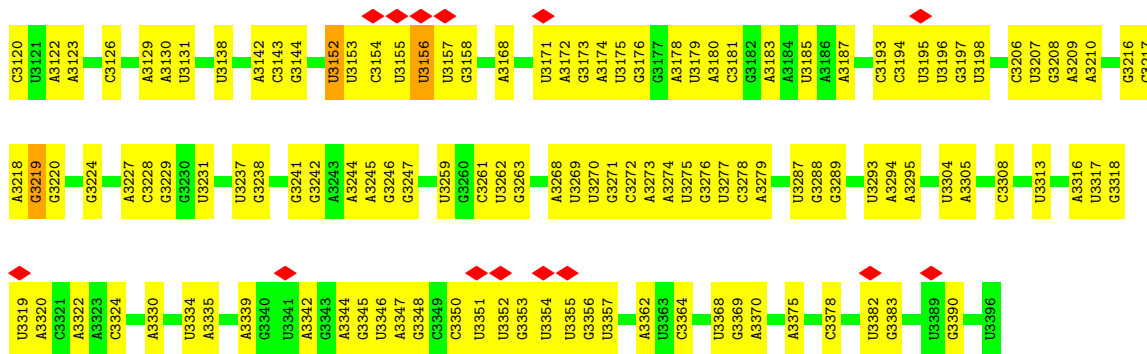
• Molecule 82: 60S ribosomal protein L35-A



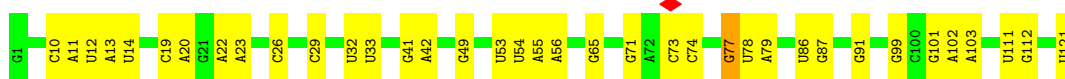
• Molecule 83: 25S ribosomal RNA







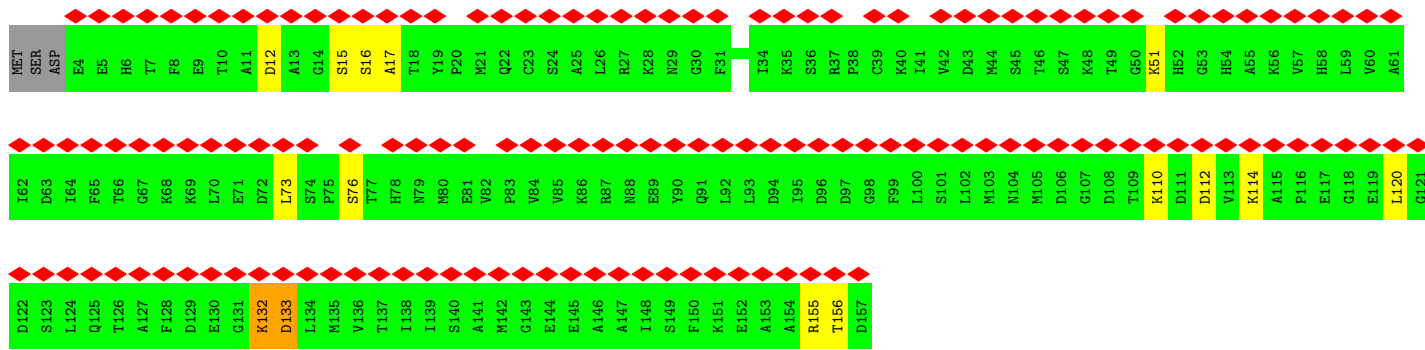
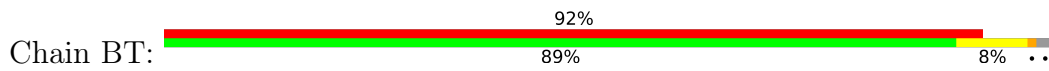
• Molecule 84: 5S ribosomal RNA



• Molecule 85: 5.8S ribosomal RNA



• Molecule 86: Eukaryotic translation initiation factor 5A-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.075	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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	2	0.33	2/42103 (0.0%)	0.73	20/65603 (0.0%)
2	A	0.37	0/1759	0.62	0/2368
3	B	0.39	0/1629	0.67	0/2202
4	C	0.39	0/833	0.59	0/1126
5	D	0.40	0/885	0.61	0/1202
6	E	0.40	0/998	0.64	0/1341
7	F	0.40	0/1125	0.69	1/1510 (0.1%)
8	G	0.49	2/754 (0.3%)	0.74	1/1005 (0.1%)
9	H	0.41	0/1211	0.75	0/1628
10	I	0.42	0/1130	0.68	0/1517
11	J	0.36	0/865	0.62	0/1169
12	K	0.40	0/571	0.65	0/768
13	L	0.37	0/499	0.69	0/670
14	M	0.38	0/452	0.63	0/600
15	N	0.39	0/404	0.61	0/542
16	O	0.35	0/2489	0.52	0/3389
17	P	0.39	0/1617	0.62	0/2215
18	Q	0.40	0/1735	0.62	0/2335
19	R	0.35	0/1702	0.57	0/2310
20	S	0.39	0/2109	0.61	0/2839
21	T	0.38	0/1823	0.62	0/2439
22	U	0.40	0/1506	0.57	0/2028
23	V	0.46	0/1514	0.78	1/2021 (0.0%)
24	W	0.40	0/1456	0.65	0/1949
25	X	0.42	2/1239 (0.2%)	0.56	0/1673
26	Y	0.39	0/1215	0.66	0/1638
27	Z	0.41	0/901	0.71	0/1217
28	a	0.38	0/693	0.64	0/935
29	b	0.35	0/1038	0.65	1/1395 (0.1%)
30	c	0.36	0/1139	0.61	0/1518
31	d	0.41	0/1074	0.70	2/1431 (0.1%)
32	e	0.61	0/782	0.80	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.37	0/620	0.57	0/838
34	g	0.39	0/481	0.60	0/640
35	l	0.47	1/764 (0.1%)	0.79	0/1179
36	m	0.26	0/1799	0.72	1/2801 (0.0%)
37	n	0.36	1/1835 (0.1%)	0.71	0/2858
38	h	0.40	2/8985 (0.0%)	0.56	1/12155 (0.0%)
39	i	0.38	0/10027	0.54	0/13707
40	j	0.37	0/3001	0.52	0/4083
40	k	0.37	0/2988	0.54	0/4060
41	AA	0.42	0/1836	0.63	0/2481
42	AB	0.39	0/1018	0.66	0/1369
43	AC	0.43	0/778	0.73	0/1034
44	AD	0.41	0/1539	0.66	0/2073
45	AE	0.42	0/712	0.66	1/958 (0.1%)
46	AF	0.45	0/696	0.74	0/923
47	AG	0.43	0/1374	0.71	0/1842
48	AH	0.38	0/979	0.64	0/1321
49	AI	0.40	0/618	0.61	0/826
50	AJ	0.45	0/1568	0.74	0/2106
51	AK	0.39	0/1004	0.67	0/1341
52	AL	0.44	0/443	0.74	0/588
53	AM	0.40	0/1068	0.70	0/1438
54	AN	0.41	0/1118	0.65	0/1497
55	AO	0.42	0/423	0.69	0/562
56	AP	0.41	0/860	0.66	0/1136
57	AQ	0.44	0/1757	0.77	1/2354 (0.0%)
58	AR	0.42	0/1204	0.73	1/1612 (0.1%)
59	AS	0.50	0/234	0.86	0/300
60	AT	0.39	0/701	0.72	0/934
61	AU	0.41	0/1585	0.66	0/2128
62	AV	0.39	0/473	0.66	0/629
63	AW	0.39	0/1948	0.75	0/2617
64	AX	0.42	0/1443	0.73	0/1944
65	AY	0.41	0/750	0.63	0/1008
67	BA	0.41	0/3146	0.69	0/4228
68	BB	0.40	0/1465	0.73	0/1965
69	BC	0.39	0/890	0.67	0/1196
70	BD	0.43	0/1807	0.71	0/2425
71	BE	0.41	0/2800	0.68	0/3790
72	BF	0.43	0/1538	0.71	0/2050
73	BG	0.39	0/1041	0.64	0/1394
74	BH	0.41	0/1481	0.67	0/1990
75	BI	0.42	0/2425	0.66	0/3271

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	BJ	0.40	0/1300	0.68	0/1743
77	BK	0.41	0/868	0.69	0/1168
78	BL	0.44	0/812	0.60	0/1099
79	BM	0.40	0/1260	0.65	0/1694
80	BN	0.41	0/890	0.71	0/1189
81	BO	0.42	0/1821	0.67	0/2451
82	BP	0.39	0/978	0.69	0/1301
83	BQ	0.34	4/75774 (0.0%)	0.75	37/118137 (0.0%)
84	BR	0.31	0/2883	0.73	1/4491 (0.0%)
85	BS	0.32	0/3745	0.73	1/5829 (0.0%)
86	BT	0.32	0/1142	0.61	0/1537
All	All	0.37	14/243945 (0.0%)	0.70	70/355920 (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
9	H	0	1
10	I	0	2
21	T	0	2
22	U	0	1
23	V	0	3
32	e	0	2
57	AQ	0	1
58	AR	0	2
63	AW	0	1
69	BC	0	1
70	BD	0	1
86	BT	0	1
All	All	0	18

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	52	U	O3'-P	23.25	1.89	1.61
83	BQ	683	U	N1-C2	10.32	1.47	1.38
37	n	1	G	OP3-P	-10.19	1.49	1.61
35	l	34	U	OP3-P	-10.13	1.49	1.61
83	BQ	683	U	C4-C5	8.78	1.51	1.43

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	52	U	P-O3'-C3'	-14.01	102.89	119.70
1	2	52	U	C5'-C4'-O4'	-13.02	93.47	109.10
83	BQ	2972	G	N9-C1'-C2'	-11.36	99.23	114.00
1	2	428	A	N9-C1'-C2'	-10.27	100.66	114.00
83	BQ	933	A	C2'-C3'-O3'	9.73	130.90	109.50

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	H	143	ARG	Peptide
10	I	88	VAL	Peptide
10	I	89	ARG	Peptide
21	T	196	ARG	Peptide
21	T	197	ASN	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	221/240 (92%)	194 (88%)	24 (11%)	3 (1%)	11	46
3	B	204/225 (91%)	172 (84%)	24 (12%)	8 (4%)	3	28
4	C	94/105 (90%)	72 (77%)	16 (17%)	6 (6%)	1	20
5	D	119/143 (83%)	92 (77%)	17 (14%)	10 (8%)	1	13
6	E	122/142 (86%)	101 (83%)	18 (15%)	3 (2%)	5	36
7	F	139/143 (97%)	119 (86%)	15 (11%)	5 (4%)	3	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	G	87/136 (64%)	73 (84%)	11 (13%)	3 (3%)	3	31
9	H	143/146 (98%)	123 (86%)	17 (12%)	3 (2%)	7	40
10	I	141/144 (98%)	112 (79%)	21 (15%)	8 (6%)	1	21
11	J	105/121 (87%)	94 (90%)	10 (10%)	1 (1%)	15	52
12	K	68/108 (63%)	54 (79%)	9 (13%)	5 (7%)	1	16
13	L	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
14	M	51/56 (91%)	41 (80%)	10 (20%)	0	100	100
15	N	49/152 (32%)	40 (82%)	6 (12%)	3 (6%)	1	20
16	O	316/319 (99%)	274 (87%)	37 (12%)	5 (2%)	9	44
17	P	204/252 (81%)	176 (86%)	20 (10%)	8 (4%)	3	28
18	Q	212/255 (83%)	170 (80%)	31 (15%)	11 (5%)	2	23
19	R	218/254 (86%)	184 (84%)	30 (14%)	4 (2%)	8	42
20	S	258/261 (99%)	213 (83%)	36 (14%)	9 (4%)	3	31
21	T	224/236 (95%)	188 (84%)	29 (13%)	7 (3%)	4	33
22	U	182/190 (96%)	142 (78%)	31 (17%)	9 (5%)	2	24
23	V	184/200 (92%)	128 (70%)	30 (16%)	26 (14%)	0	4
24	W	176/197 (89%)	149 (85%)	21 (12%)	6 (3%)	3	31
25	X	153/156 (98%)	129 (84%)	17 (11%)	7 (5%)	2	24
26	Y	148/151 (98%)	134 (90%)	11 (7%)	3 (2%)	7	41
27	Z	125/137 (91%)	103 (82%)	17 (14%)	5 (4%)	3	28
28	a	85/87 (98%)	67 (79%)	14 (16%)	4 (5%)	2	24
29	b	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	6	37
30	c	142/145 (98%)	120 (84%)	21 (15%)	1 (1%)	22	60
31	d	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	2	22
32	e	95/119 (80%)	70 (74%)	17 (18%)	8 (8%)	1	13
33	f	79/82 (96%)	61 (77%)	14 (18%)	4 (5%)	2	23
34	g	58/63 (92%)	48 (83%)	8 (14%)	2 (3%)	3	31
38	h	1107/1287 (86%)	965 (87%)	124 (11%)	18 (2%)	9	44
39	i	1355/1432 (95%)	1158 (86%)	172 (13%)	25 (2%)	8	42
40	j	388/397 (98%)	335 (86%)	46 (12%)	7 (2%)	8	42
40	k	382/397 (96%)	333 (87%)	40 (10%)	9 (2%)	6	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	AA	231/256 (90%)	194 (84%)	32 (14%)	5 (2%)	6	39
42	AB	134/137 (98%)	117 (87%)	14 (10%)	3 (2%)	6	39
43	AC	97/100 (97%)	80 (82%)	13 (13%)	4 (4%)	3	27
44	AD	189/191 (99%)	166 (88%)	19 (10%)	4 (2%)	7	40
45	AE	96/155 (62%)	73 (76%)	18 (19%)	5 (5%)	2	23
46	AF	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	13	50
47	AG	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	3	30
48	AH	119/142 (84%)	103 (87%)	14 (12%)	2 (2%)	9	43
49	AI	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	12	48
50	AJ	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	4	33
51	AK	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
52	AL	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	7	40
53	AM	134/138 (97%)	119 (89%)	12 (9%)	3 (2%)	6	39
54	AN	133/136 (98%)	118 (89%)	10 (8%)	5 (4%)	3	29
55	AO	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	3	28
56	AP	103/106 (97%)	86 (84%)	16 (16%)	1 (1%)	15	52
57	AQ	201/204 (98%)	175 (87%)	21 (10%)	5 (2%)	5	36
58	AR	146/149 (98%)	118 (81%)	21 (14%)	7 (5%)	2	24
59	AS	23/25 (92%)	23 (100%)	0	0	100	100
60	AT	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	14	51
61	AU	195/199 (98%)	177 (91%)	15 (8%)	3 (2%)	10	46
62	AV	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	8	42
63	AW	250/254 (98%)	218 (87%)	31 (12%)	1 (0%)	34	70
64	AX	181/184 (98%)	158 (87%)	19 (10%)	4 (2%)	6	39
65	AY	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	14	51
67	BA	384/387 (99%)	332 (86%)	41 (11%)	11 (3%)	4	34
68	BB	183/186 (98%)	163 (89%)	17 (9%)	3 (2%)	9	44
69	BC	107/113 (95%)	94 (88%)	11 (10%)	2 (2%)	8	42
70	BD	218/221 (99%)	185 (85%)	24 (11%)	9 (4%)	3	27
71	BE	359/362 (99%)	306 (85%)	38 (11%)	15 (4%)	3	26
72	BF	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	9	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	BG	125/130 (96%)	110 (88%)	13 (10%)	2 (2%)	9	44
74	BH	170/172 (99%)	151 (89%)	16 (9%)	3 (2%)	8	42
75	BI	294/297 (99%)	263 (90%)	22 (8%)	9 (3%)	4	33
76	BJ	157/160 (98%)	133 (85%)	18 (12%)	6 (4%)	3	29
77	BK	104/107 (97%)	93 (89%)	9 (9%)	2 (2%)	8	42
78	BL	98/121 (81%)	79 (81%)	16 (16%)	3 (3%)	4	33
79	BM	152/176 (86%)	137 (90%)	11 (7%)	4 (3%)	5	36
80	BN	110/121 (91%)	104 (94%)	3 (3%)	3 (3%)	5	35
81	BO	220/244 (90%)	199 (90%)	16 (7%)	5 (2%)	6	38
82	BP	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	17	54
86	BT	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	19
All	All	14299/15550 (92%)	12246 (86%)	1644 (12%)	409 (3%)	7	34

5 of 409 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	196	ARG
3	B	100	ASN
5	D	115	VAL
5	D	126	TRP
7	F	32	ASN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	182/195 (93%)	175 (96%)	7 (4%)	33	61
3	B	173/191 (91%)	162 (94%)	11 (6%)	17	48
4	C	88/98 (90%)	83 (94%)	5 (6%)	20	52
5	D	89/119 (75%)	85 (96%)	4 (4%)	27	57
6	E	101/118 (86%)	94 (93%)	7 (7%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	F	117/119 (98%)	113 (97%)	4 (3%)	37	64
8	G	80/124 (64%)	75 (94%)	5 (6%)	18	49
9	H	128/129 (99%)	117 (91%)	11 (9%)	10	40
10	I	115/116 (99%)	102 (89%)	13 (11%)	6	28
11	J	100/114 (88%)	94 (94%)	6 (6%)	19	50
12	K	61/89 (68%)	58 (95%)	3 (5%)	25	55
13	L	56/60 (93%)	54 (96%)	2 (4%)	35	63
14	M	47/49 (96%)	44 (94%)	3 (6%)	17	48
15	N	43/135 (32%)	42 (98%)	1 (2%)	50	72
16	O	259/262 (99%)	250 (96%)	9 (4%)	36	64
17	P	164/210 (78%)	157 (96%)	7 (4%)	29	58
18	Q	191/224 (85%)	182 (95%)	9 (5%)	26	56
19	R	180/205 (88%)	175 (97%)	5 (3%)	43	68
20	S	221/222 (100%)	217 (98%)	4 (2%)	59	77
21	T	188/201 (94%)	181 (96%)	7 (4%)	34	62
22	U	165/170 (97%)	160 (97%)	5 (3%)	41	66
23	V	150/161 (93%)	133 (89%)	17 (11%)	6	28
24	W	152/166 (92%)	150 (99%)	2 (1%)	69	82
25	X	129/137 (94%)	126 (98%)	3 (2%)	50	72
26	Y	127/128 (99%)	121 (95%)	6 (5%)	26	56
27	Z	81/105 (77%)	74 (91%)	7 (9%)	10	40
28	a	74/74 (100%)	72 (97%)	2 (3%)	44	69
29	b	110/111 (99%)	109 (99%)	1 (1%)	78	88
30	c	119/120 (99%)	115 (97%)	4 (3%)	37	64
31	d	111/113 (98%)	103 (93%)	8 (7%)	14	45
32	e	83/101 (82%)	77 (93%)	6 (7%)	14	45
33	f	70/71 (99%)	69 (99%)	1 (1%)	67	81
34	g	50/54 (93%)	50 (100%)	0	100	100
38	h	936/1139 (82%)	901 (96%)	35 (4%)	34	62
39	i	849/1279 (66%)	823 (97%)	26 (3%)	40	65
40	j	296/347 (85%)	288 (97%)	8 (3%)	44	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	k	295/347 (85%)	290 (98%)	5 (2%)	60	78
41	AA	187/208 (90%)	179 (96%)	8 (4%)	29	58
42	AB	104/105 (99%)	98 (94%)	6 (6%)	20	51
43	AC	81/82 (99%)	76 (94%)	5 (6%)	18	49
44	AD	171/171 (100%)	165 (96%)	6 (4%)	36	64
45	AE	57/129 (44%)	57 (100%)	0	100	100
46	AF	70/71 (99%)	65 (93%)	5 (7%)	14	45
47	AG	147/150 (98%)	140 (95%)	7 (5%)	25	56
48	AH	104/118 (88%)	98 (94%)	6 (6%)	20	51
49	AI	68/69 (99%)	67 (98%)	1 (2%)	65	81
50	AJ	154/159 (97%)	146 (95%)	8 (5%)	23	54
51	AK	109/110 (99%)	105 (96%)	4 (4%)	34	62
52	AL	45/46 (98%)	42 (93%)	3 (7%)	16	47
53	AM	107/109 (98%)	101 (94%)	6 (6%)	21	52
54	AN	115/116 (99%)	112 (97%)	3 (3%)	46	69
55	AO	47/116 (40%)	44 (94%)	3 (6%)	17	48
56	AP	90/91 (99%)	85 (94%)	5 (6%)	21	52
57	AQ	175/176 (99%)	168 (96%)	7 (4%)	31	59
58	AR	118/119 (99%)	111 (94%)	7 (6%)	19	51
59	AS	23/23 (100%)	21 (91%)	2 (9%)	10	38
60	AT	71/72 (99%)	69 (97%)	2 (3%)	43	68
61	AU	160/162 (99%)	155 (97%)	5 (3%)	40	65
62	AV	46/47 (98%)	45 (98%)	1 (2%)	52	72
63	AW	193/196 (98%)	187 (97%)	6 (3%)	40	65
64	AX	140/146 (96%)	133 (95%)	7 (5%)	24	55
65	AY	81/88 (92%)	78 (96%)	3 (4%)	34	62
67	BA	320/323 (99%)	304 (95%)	16 (5%)	24	55
68	BB	150/151 (99%)	144 (96%)	6 (4%)	31	59
69	BC	92/97 (95%)	84 (91%)	8 (9%)	10	38
70	BD	184/187 (98%)	169 (92%)	15 (8%)	11	40
71	BE	288/289 (100%)	277 (96%)	11 (4%)	33	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	BF	153/154 (99%)	148 (97%)	5 (3%)	38	65
73	BG	109/111 (98%)	106 (97%)	3 (3%)	43	68
74	BH	156/156 (100%)	150 (96%)	6 (4%)	33	61
75	BI	244/245 (100%)	235 (96%)	9 (4%)	34	62
76	BJ	136/137 (99%)	129 (95%)	7 (5%)	24	54
77	BK	90/91 (99%)	87 (97%)	3 (3%)	38	65
78	BL	87/107 (81%)	86 (99%)	1 (1%)	73	85
79	BM	134/153 (88%)	127 (95%)	7 (5%)	23	54
80	BN	95/103 (92%)	94 (99%)	1 (1%)	73	85
81	BO	186/205 (91%)	181 (97%)	5 (3%)	44	69
82	BP	104/105 (99%)	101 (97%)	3 (3%)	42	67
86	BT	118/132 (89%)	113 (96%)	5 (4%)	30	58
All	All	11689/13228 (88%)	11203 (96%)	486 (4%)	33	58

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	i	505	PHE
74	BH	119	ARG
46	AF	17	THR
73	BG	106	VAL
81	BO	24	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
56	AP	27	GLN
65	AY	71	GLN
58	AR	65	GLN
63	AW	209	HIS
71	BE	59	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1800 (98%)	729 (41%)	100 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	l	33/34 (97%)	20 (60%)	0
36	m	75/76 (98%)	34 (45%)	0
37	n	76/77 (98%)	30 (39%)	0
83	BQ	3162/3396 (93%)	1066 (33%)	177 (5%)
84	BR	120/121 (99%)	35 (29%)	7 (5%)
85	BS	157/158 (99%)	50 (31%)	10 (6%)
All	All	5387/5662 (95%)	1964 (36%)	294 (5%)

5 of 1964 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	17	C
1	2	25	C

5 of 294 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	BQ	2625	C
85	BS	33	A
83	BQ	2754	G
83	BQ	3172	A
1	2	1761	U

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

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
86	5CT	BT	51	86	13,14,15	0.34	0	9,15,17	1.20	2 (22%)

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
86	5CT	BT	51	86	-	5/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	BT	51	5CT	C1-NZ-CE	-2.30	108.27	113.42
86	BT	51	5CT	C4-C3-C2	-2.03	109.19	113.47

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	BT	51	5CT	O-C-CA-CB
86	BT	51	5CT	C2-C3-C4-N1
86	BT	51	5CT	CG-CD-CE-NZ
86	BT	51	5CT	C2-C1-NZ-CE
86	BT	51	5CT	CD-CE-NZ-C1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	52:U	O3'	53:G	P	1.89

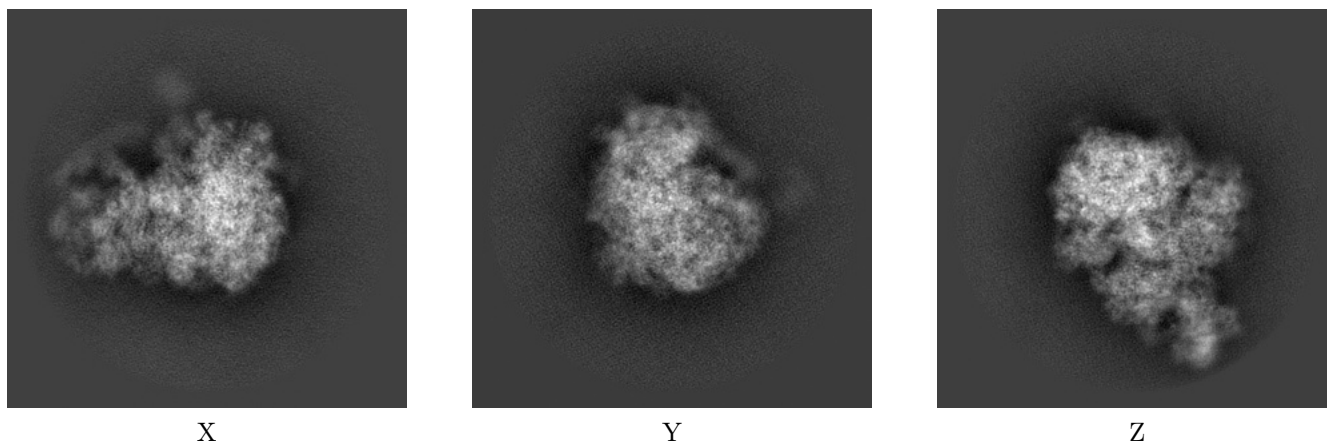
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3461. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

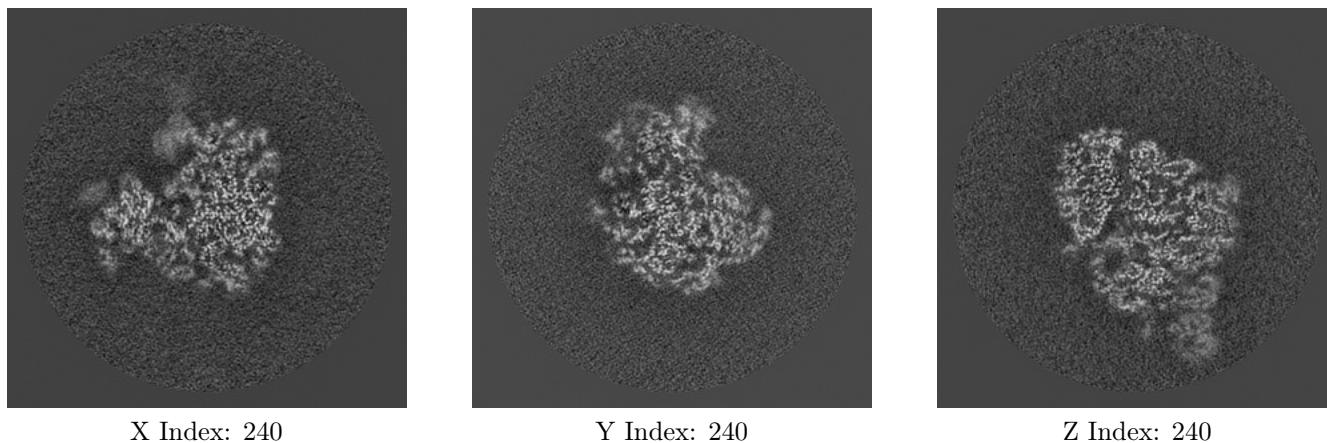
6.1.1 Primary map



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

6.2 Central slices [i](#)

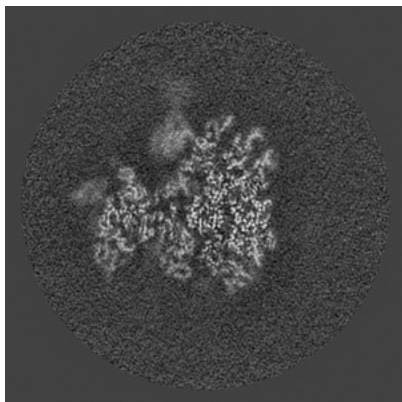
6.2.1 Primary map



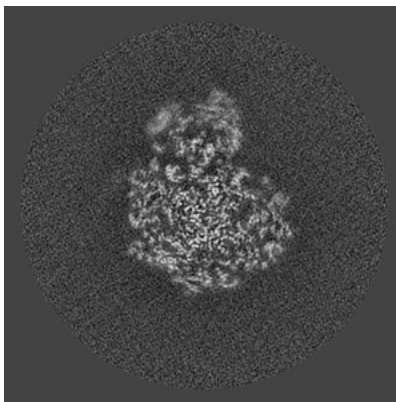
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

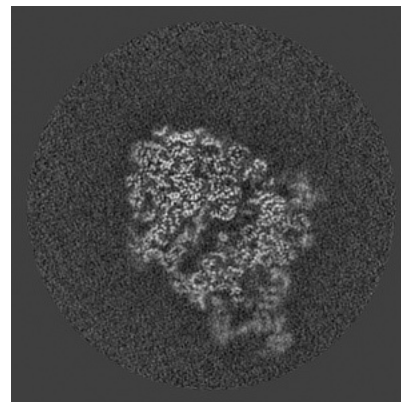
6.3.1 Primary map



X Index: 245



Y Index: 253



Z Index: 247

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

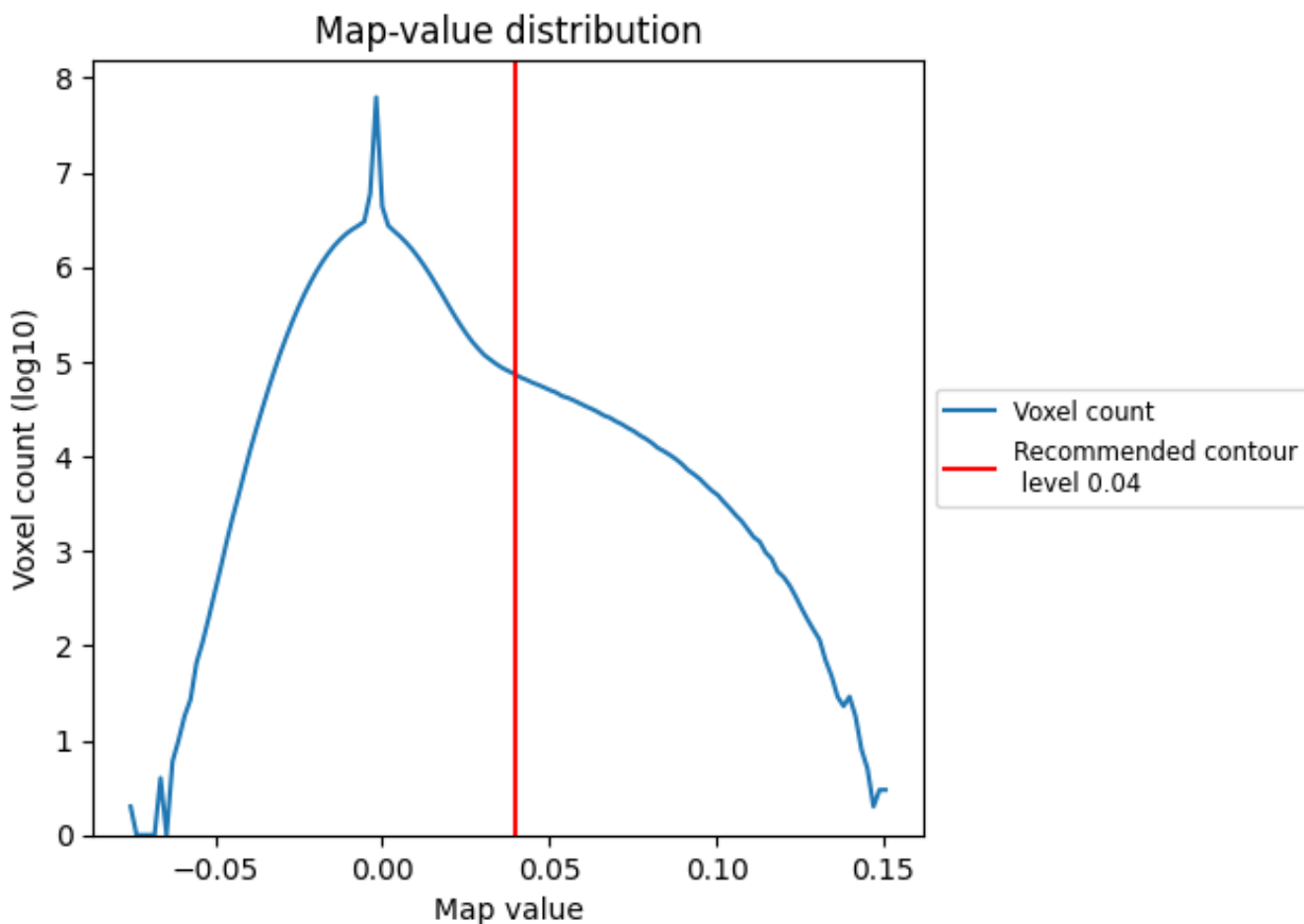
6.5 Mask visualisation

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

7 Map analysis [i](#)

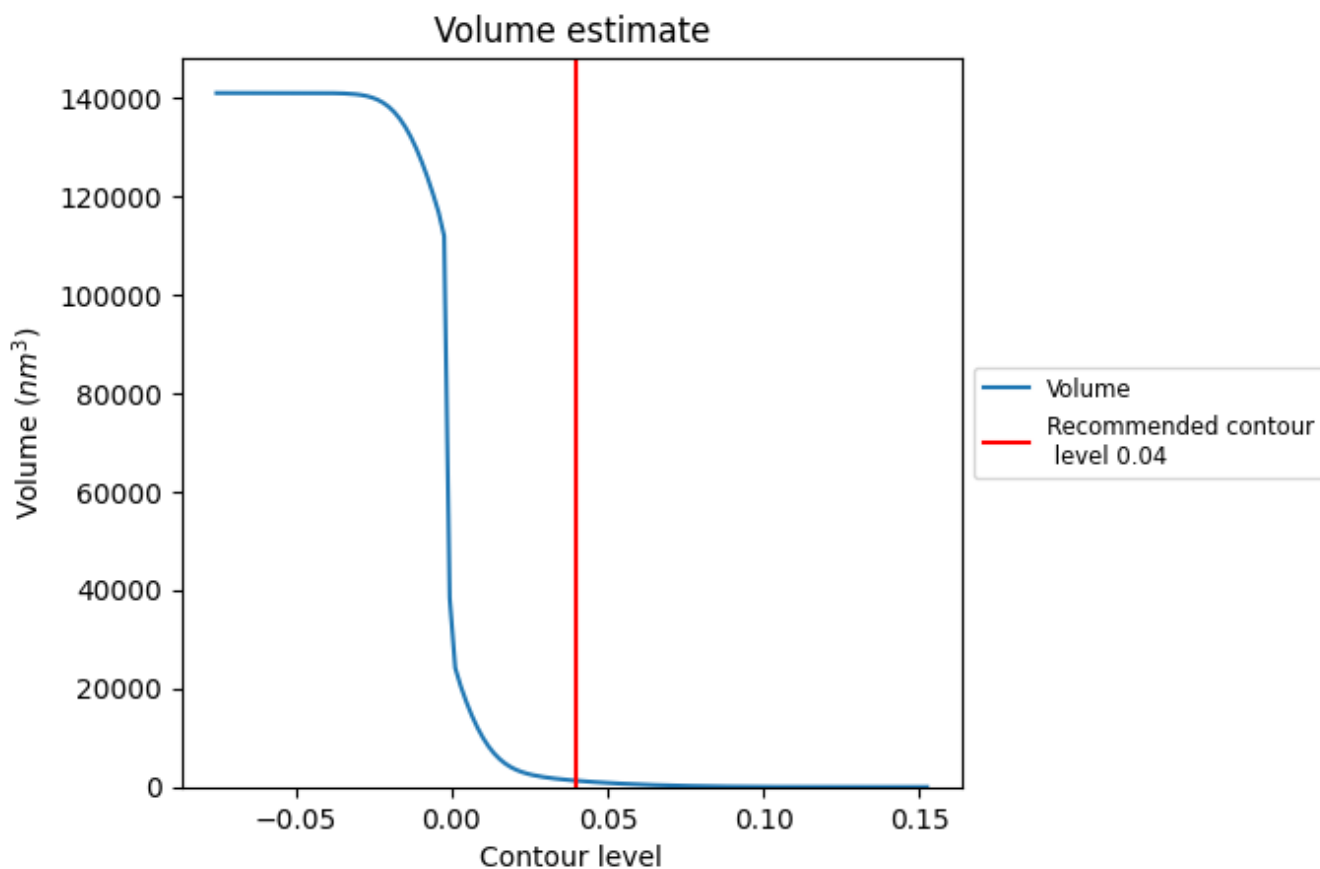
This section contains the results of statistical analysis of the map.

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.

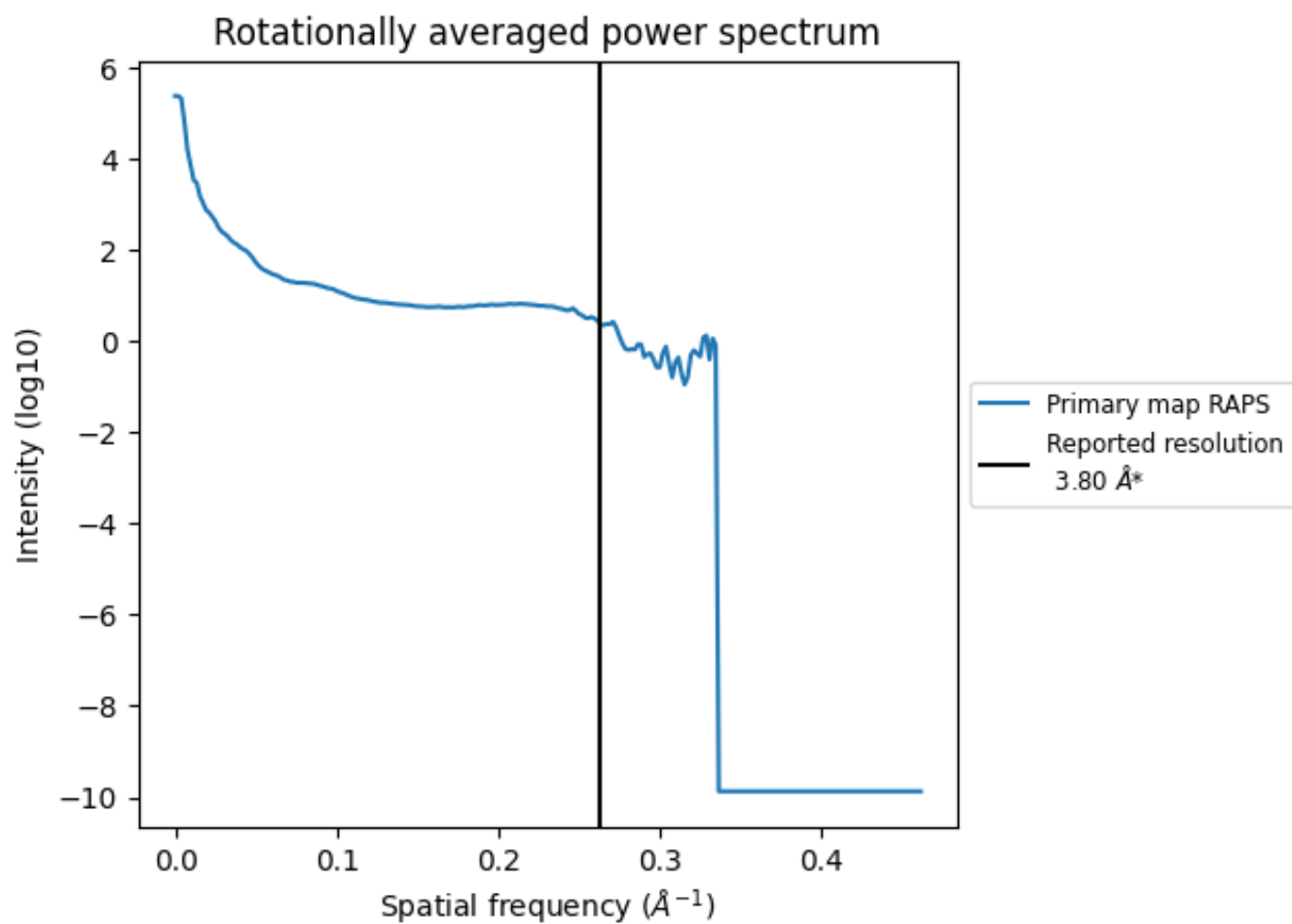
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1270 nm^3 ; this corresponds to an approximate mass of 1147 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

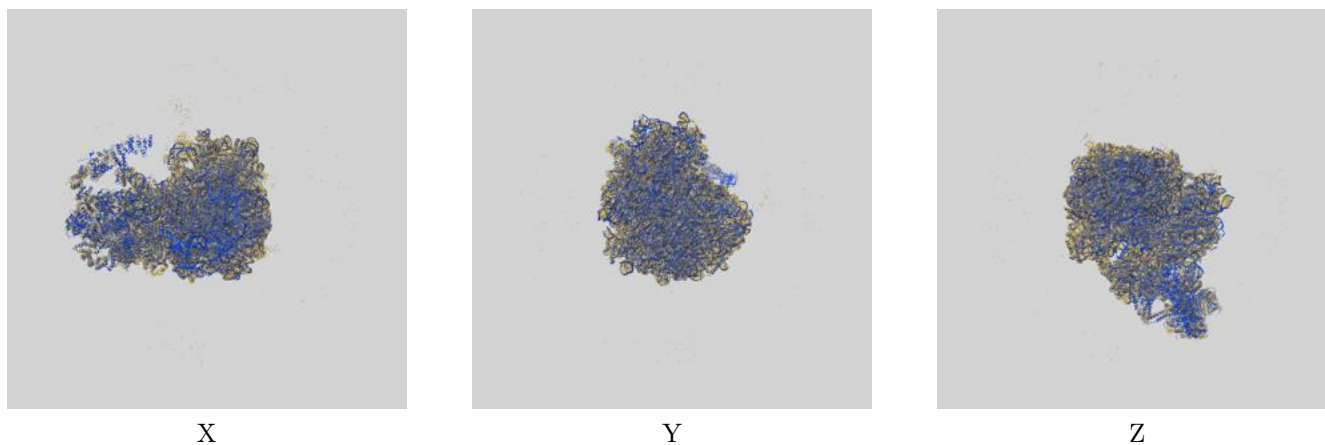
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

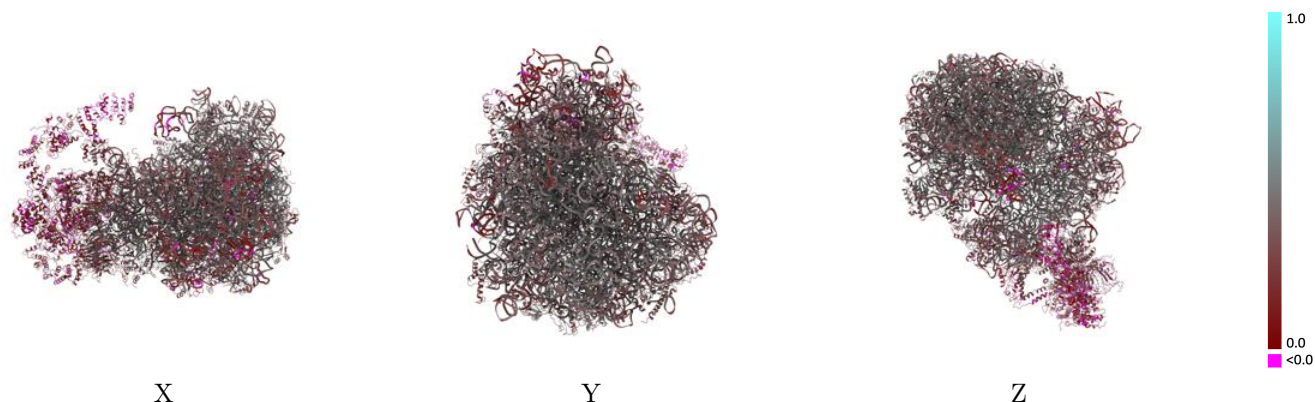
This section contains information regarding the fit between EMDB map EMD-3461 and PDB model 5MC6. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



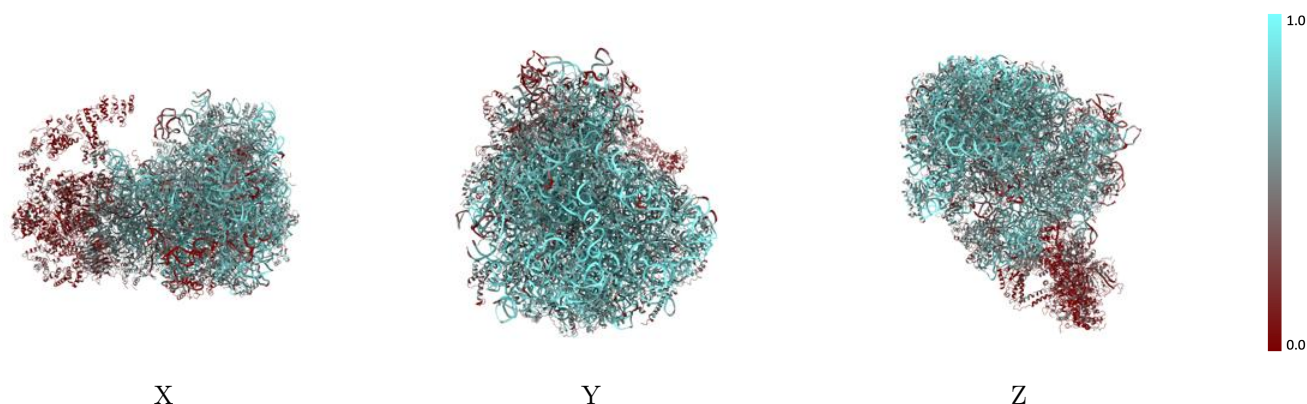
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



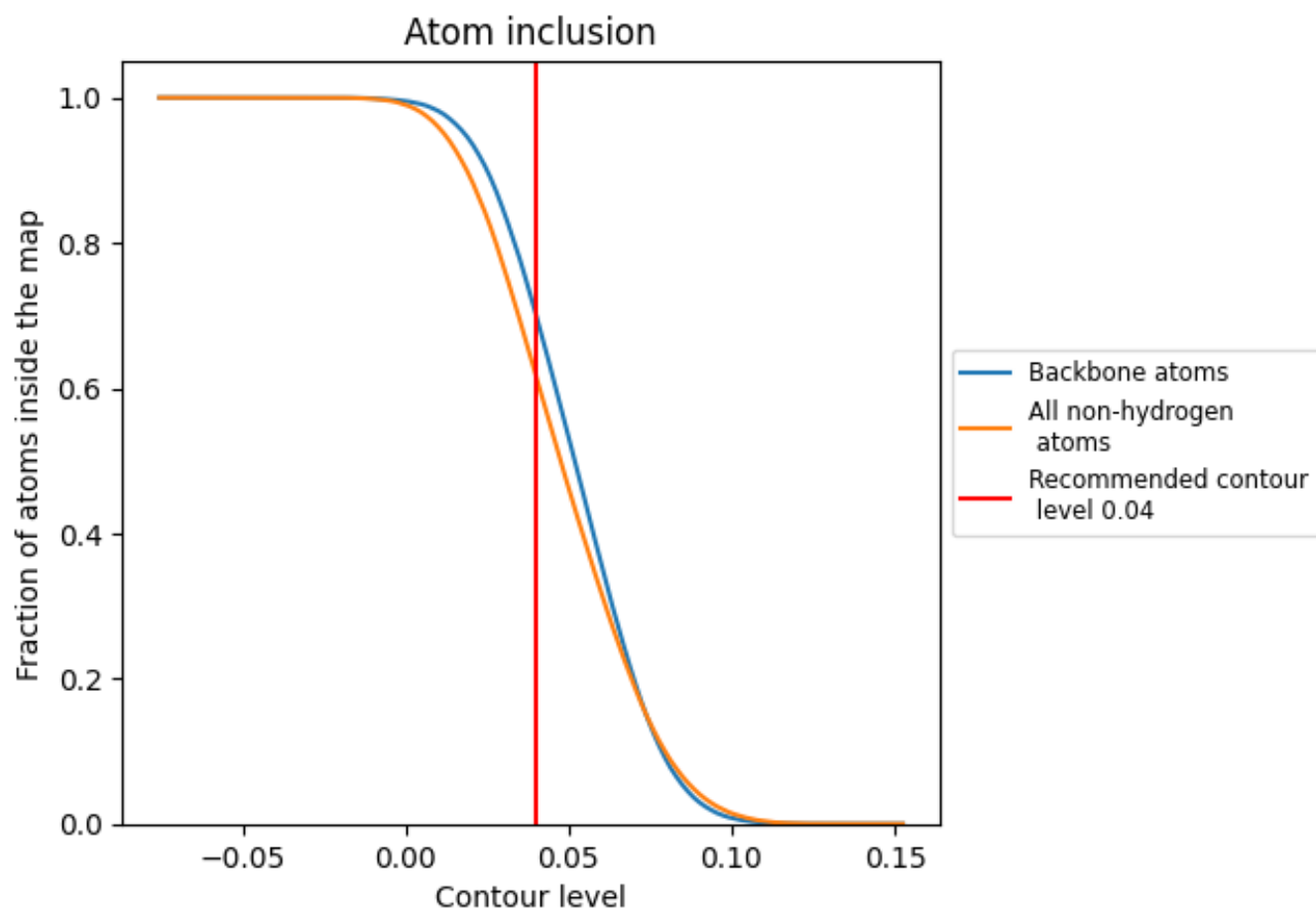
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6174	 0.3620
2	 0.7276	 0.3590
A	 0.4944	 0.3910
AA	 0.5147	 0.3680
AB	 0.5169	 0.4220
AC	 0.5584	 0.3700
AD	 0.5208	 0.3780
AE	 0.4085	 0.3450
AF	 0.6687	 0.4610
AG	 0.5802	 0.3740
AH	 0.6242	 0.4290
AI	 0.5159	 0.3720
AJ	 0.5992	 0.3970
AK	 0.6429	 0.4260
AL	 0.6241	 0.4640
AM	 0.5595	 0.3630
AN	 0.5397	 0.3760
AO	 0.5856	 0.4030
AP	 0.5882	 0.4350
AQ	 0.6359	 0.4330
AR	 0.6322	 0.4220
AS	 0.4009	 0.3980
AT	 0.5590	 0.4280
AU	 0.5951	 0.4140
AV	 0.5686	 0.3950
AW	 0.5982	 0.4500
AX	 0.6265	 0.4410
AY	 0.5164	 0.3840
AZ	 0.1600	 0.3360
B	 0.4322	 0.3190
BA	 0.6074	 0.4230
BB	 0.6194	 0.4260
BC	 0.5776	 0.4330
BD	 0.5236	 0.3950
BE	 0.6266	 0.4240

























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Chain	Atom inclusion	Q-score
BF	0.5682	0.3980
BG	0.6016	0.4350
BH	0.5735	0.4020
BI	0.5982	0.3630
BJ	0.5685	0.4280
BK	0.6127	0.4340
BL	0.5358	0.3630
BM	0.5598	0.3760
BN	0.5852	0.4230
BO	0.6062	0.3950
BP	0.6193	0.3980
BQ	0.8208	0.4040
BR	0.8841	0.4050
BS	0.8616	0.4220
BT	0.1121	0.2900
C	0.4711	0.3480
D	0.2722	0.2450
E	0.4299	0.2960
F	0.5134	0.3470
G	0.4917	0.3700
H	0.4705	0.3120
I	0.4422	0.2390
J	0.4857	0.3610
K	0.4516	0.2770
L	0.3312	0.3320
M	0.6288	0.4270
N	0.2972	0.1920
O	0.4575	0.3280
P	0.5107	0.3600
Q	0.4163	0.3170
R	0.5481	0.4150
S	0.4374	0.3460
T	0.4164	0.3090
U	0.3127	0.2740
V	0.4666	0.2950
W	0.5198	0.3250
X	0.4484	0.3800
Y	0.4978	0.3600
Z	0.4838	0.3360
a	0.5000	0.3860
b	0.5381	0.4090
c	0.4945	0.4090

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Chain	Atom inclusion	Q-score
d	 0.4222	 0.2950
e	 0.4357	 0.3140
f	 0.4359	 0.3540
g	 0.4420	 0.3550
h	 0.1761	 0.2120
i	 0.1487	 0.1490
j	 0.1567	 0.1890
k	 0.2925	 0.2970
l	 0.3367	 0.3130
m	 0.6034	 0.3260
n	 0.6442	 0.3490