



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 12:41 PM UTC

PDB ID : 5MC6 / pdb_00005mc6
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:

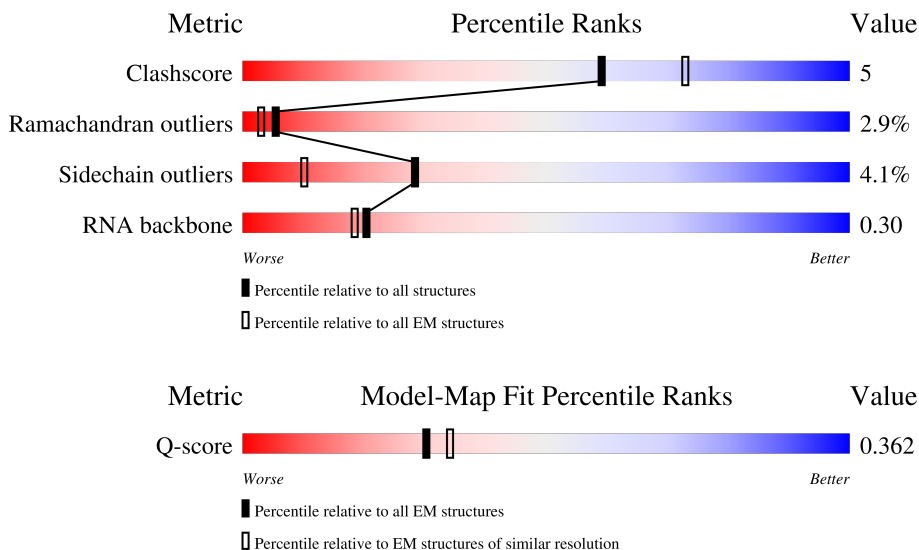
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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)	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	10198 (3.30 - 4.30)

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	

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Mol	Chain	Length	Quality of chain
4	C	105	27% 68% 23% 9%
5	D	143	64% 66% 17% 15%
6	E	142	41% 75% 13% 13%
7	F	143	22% 81% 13% ..
8	G	136	20% 54% 12% 33%
9	H	146	40% 75% 20% ..
10	I	144	42% 78% 17% ..
11	J	121	28% 73% 15% 12%
12	K	108	29% 51% 13% 35%
13	L	67	61% 85% 9% 6%
14	M	56	12% 86% 7% 5%
15	N	152	24% 28% 5% 66%
16	O	319	38% 90% 9%
17	P	252	21% 75% 6% 18%
18	Q	255	41% 71% 12% 16%
19	R	254	15% 76% 9% 13%
20	S	261	44% 87% 10% .
21	T	236	43% 81% 14% .
22	U	190	61% 81% 15% ..
23	V	200	37% 64% 20% 6% 6%
24	W	197	32% 81% 9% 10%
25	X	156	38% 88% 11% ..
26	Y	151	34% 88% 10% ..
27	Z	137	32% 81% 11% 7%
28	a	87	30% 89% 9% .

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Mol	Chain	Length	Quality of chain
29	b	130	23% 89% 10%
30	c	145	30% 88% 11%
31	d	135	42% 79% 14%
32	e	119	35% 62% 13% 5% 18%
33	f	82	40% 90% 9%
34	g	63	37% 89% 6% 5%
35	l	34	62% 29% 62% 9%
36	m	76	14% 45% 46% 9%
37	n	77	10% 49% 43% 6%
38	h	1287	76% 78% 8% 13%
39	i	1432	87% 85% 10% 5%
40	j	397	88% 87% 11%
40	k	397	70% 87% 10%
41	AA	256	24% 79% 11% 9%
42	AB	137	28% 85% 15%
43	AC	100	18% 82% 16%
44	AD	191	25% 87% 10%
45	AE	155	32% 56% 6% 37%
46	AF	88	8% 78% 17%
47	AG	174	16% 82% 14%
48	AH	142	8% 75% 10% 15%
49	AI	78	28% 96%
50	AJ	199	19% 86% 9%
51	AK	127	8% 91% 9%
52	AL	51	10% 84% 12%

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Mol	Chain	Length	Quality of chain
78	BL	121	
79	BM	176	
80	BN	121	
81	BO	244	
82	BP	120	
83	BQ	3396	
84	BR	121	
85	BS	158	
86	BT	157	

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

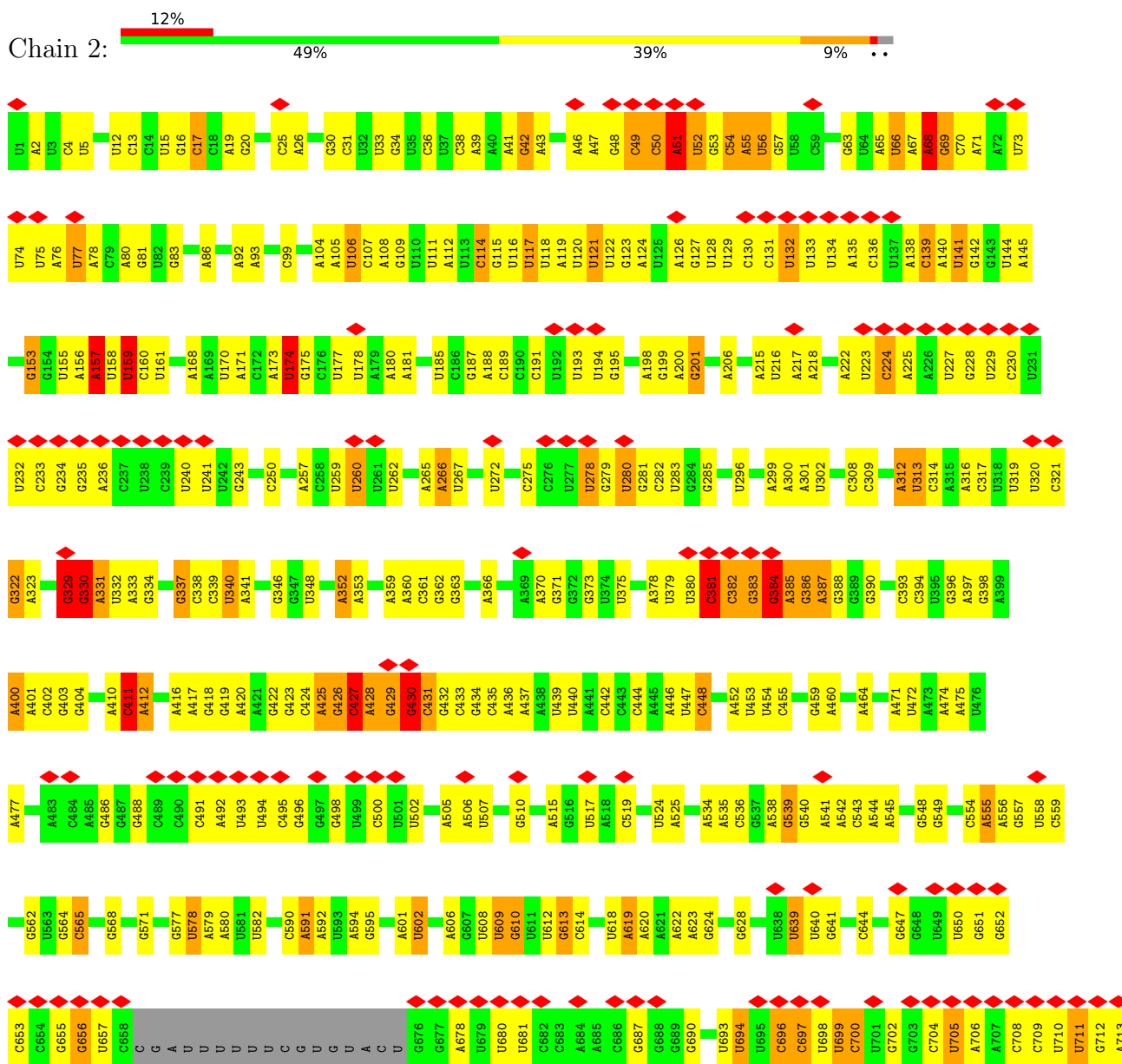
- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

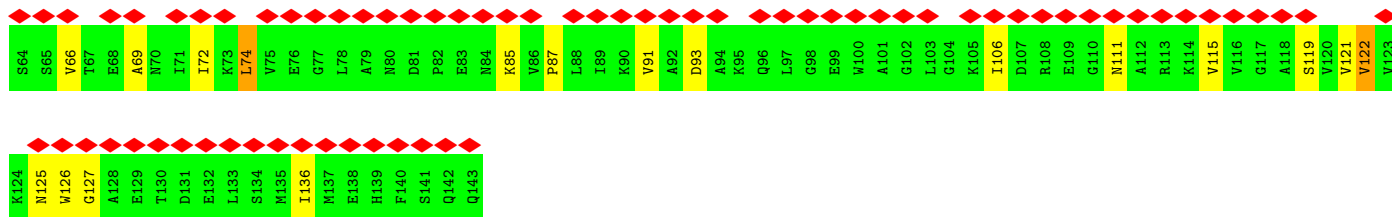
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	BT	154	1143	709	195	230	9	0	0

3 Residue-property plots

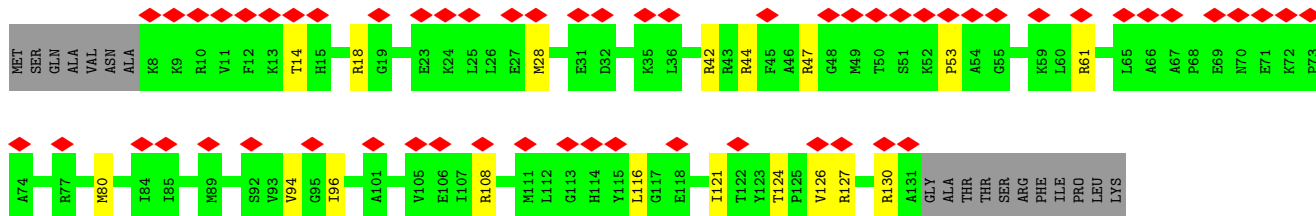
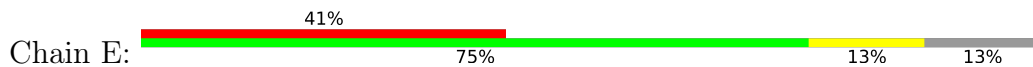
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

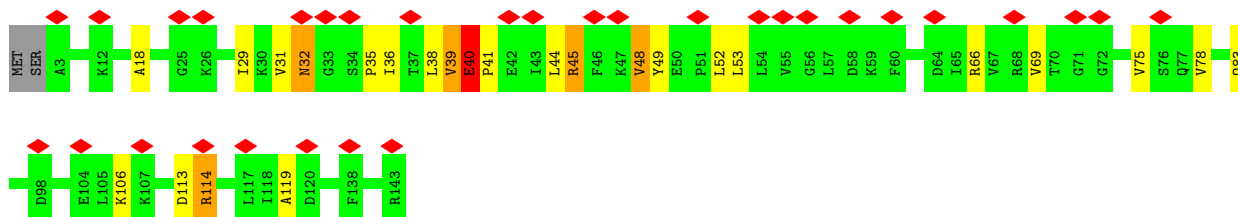
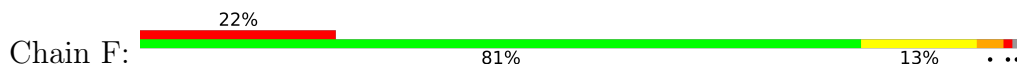




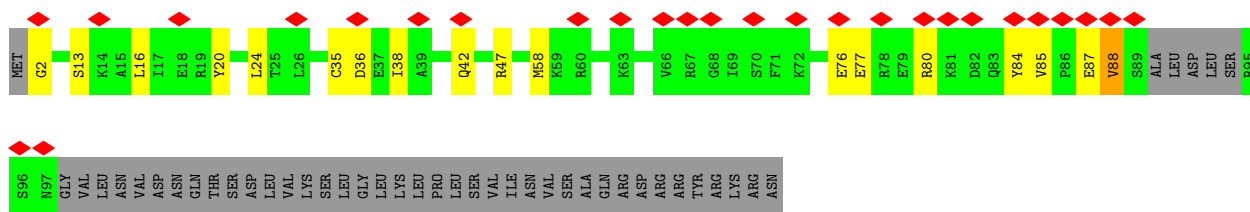
• Molecule 6: 40S ribosomal protein S15



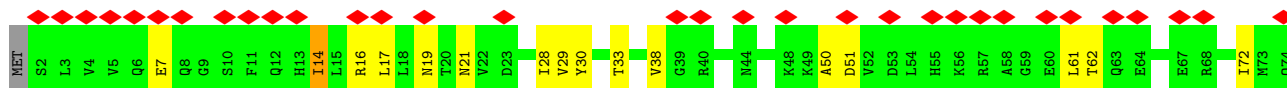
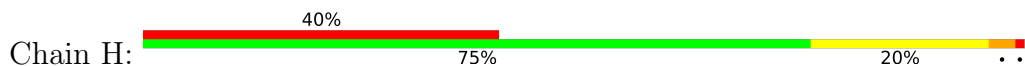
• Molecule 7: 40S ribosomal protein S16-A

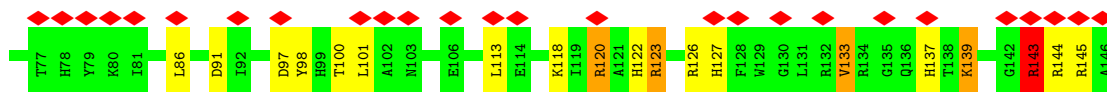


• Molecule 8: 40S ribosomal protein S17-B

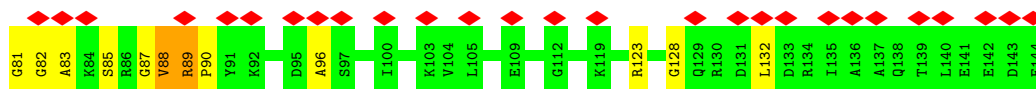
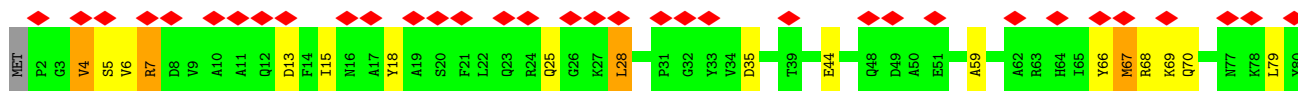
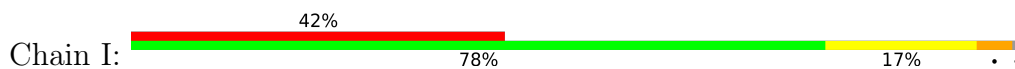


• Molecule 9: 40S ribosomal protein S18-A

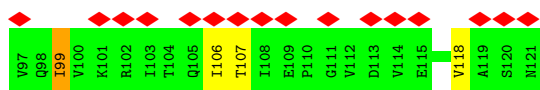
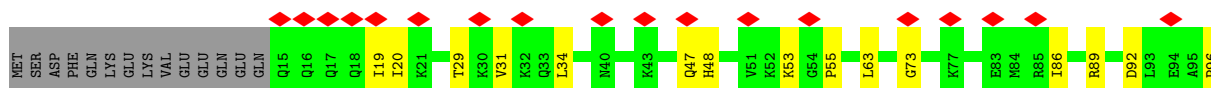
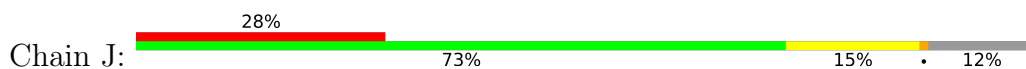




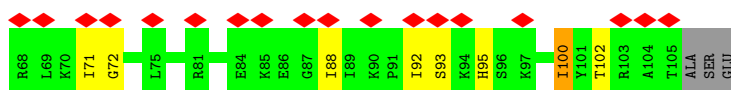
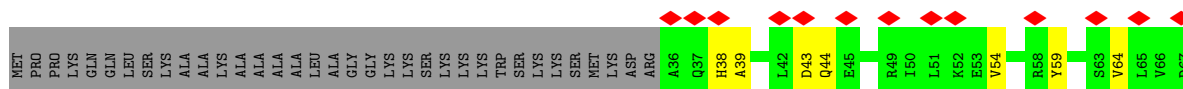
- Molecule 10: 40S ribosomal protein S19-A



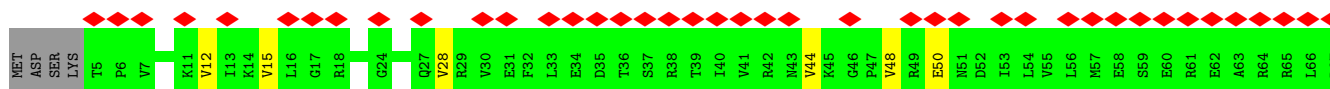
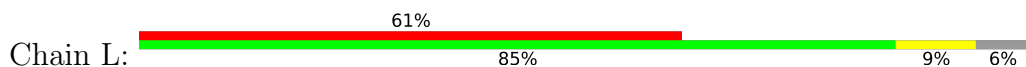
- Molecule 11: 40S ribosomal protein S20



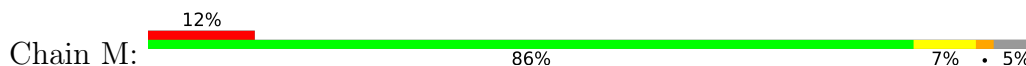
- Molecule 12: 40S ribosomal protein S25-A

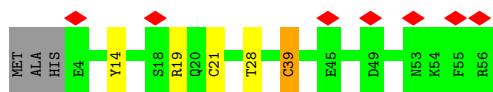


- Molecule 13: 40S ribosomal protein S28-B

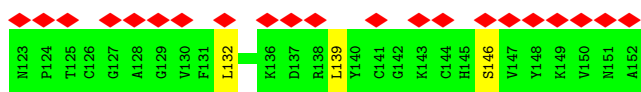
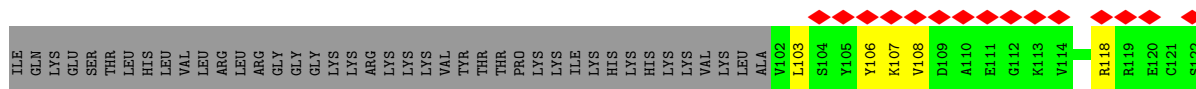
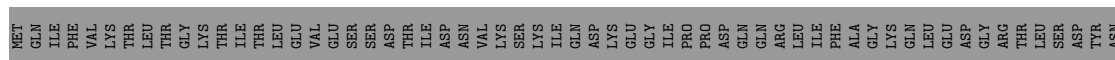


- Molecule 14: 40S ribosomal protein S29-A

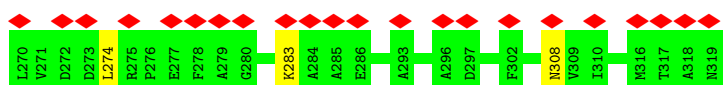
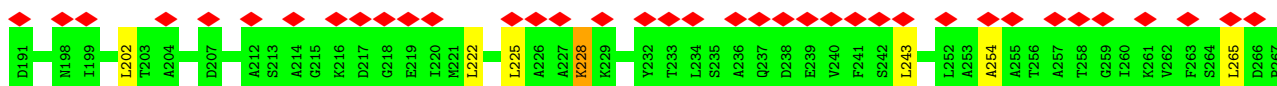
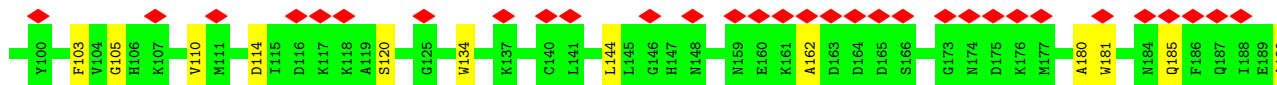
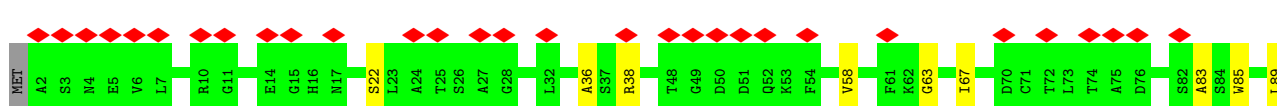
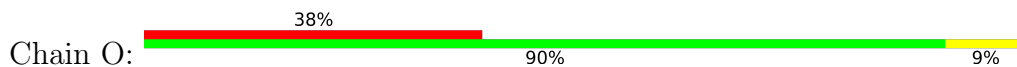




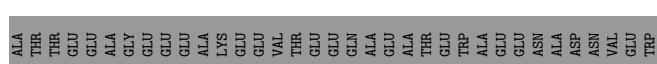
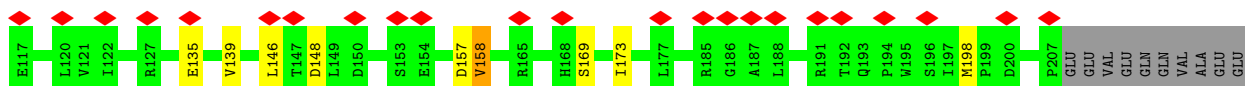
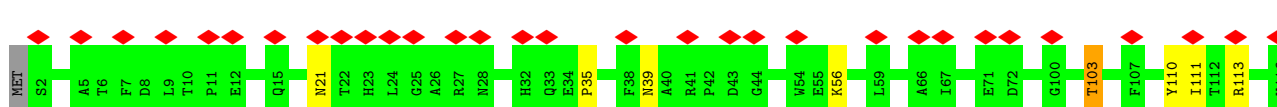
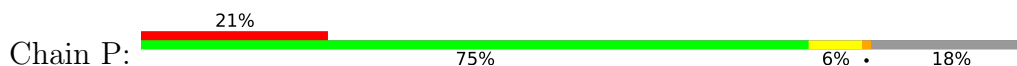
• Molecule 15: Ubiquitin-40S ribosomal protein S31



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

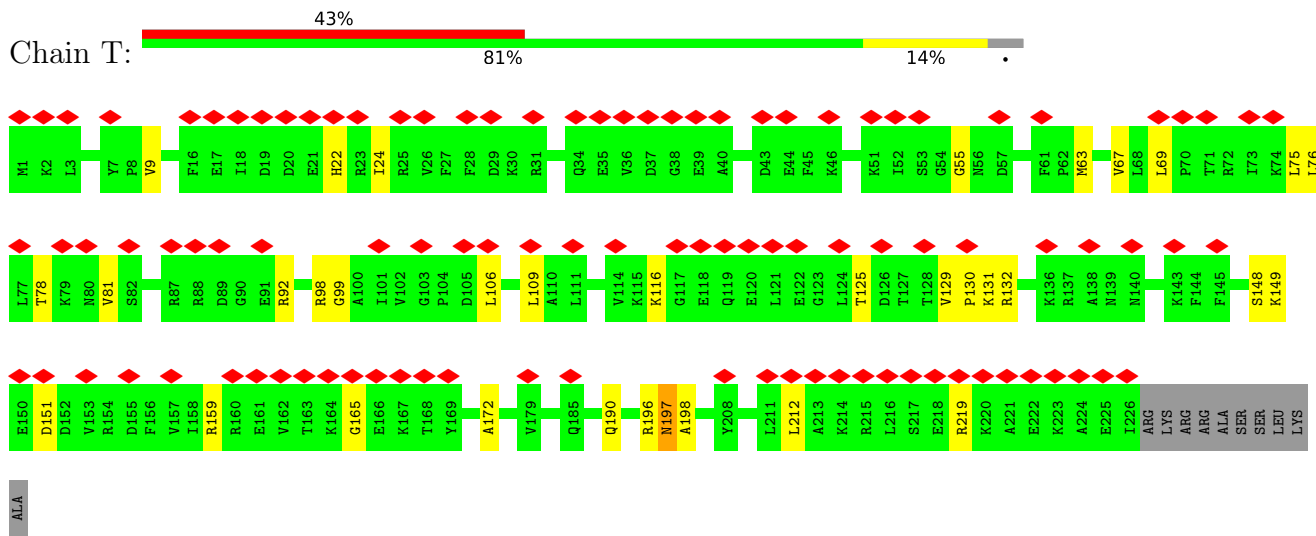


• Molecule 17: 40S ribosomal protein S0-A

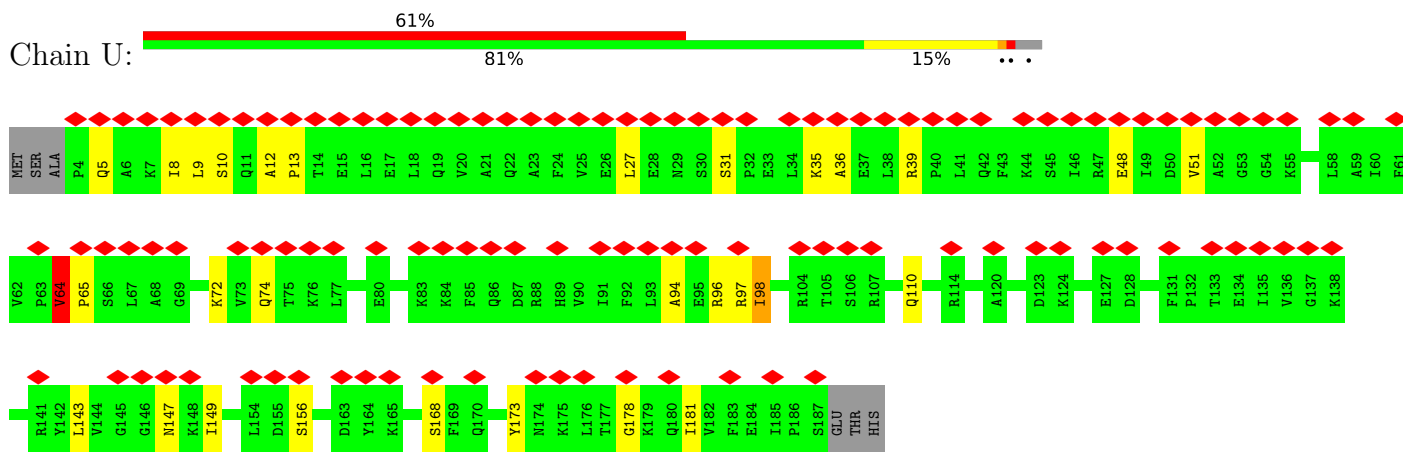


• Molecule 18: 40S ribosomal protein S1-A

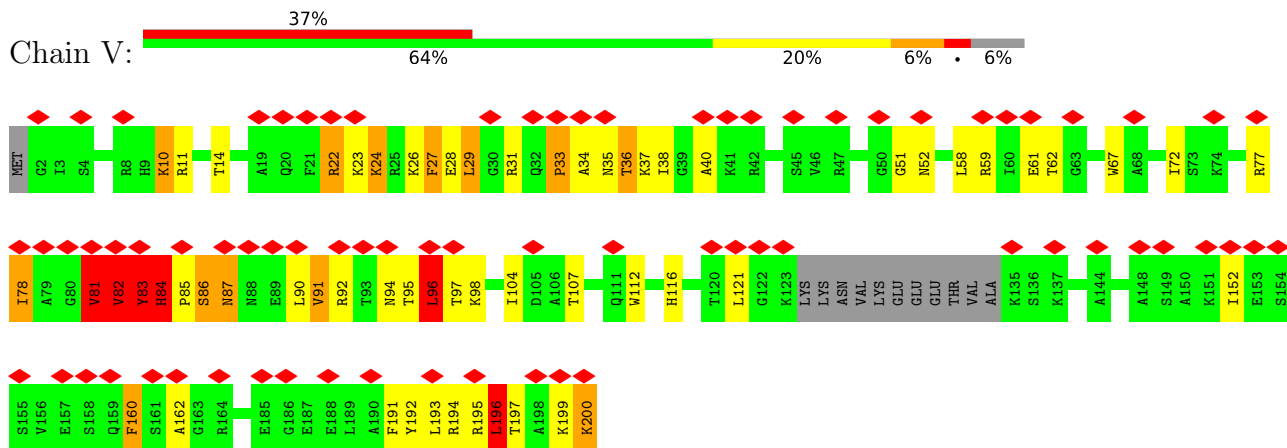
• Molecule 21: 40S ribosomal protein S6-A



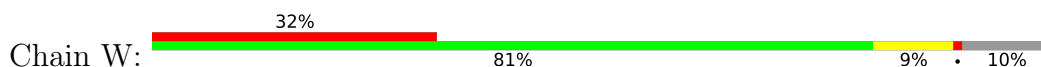
• Molecule 22: 40S ribosomal protein S7-A

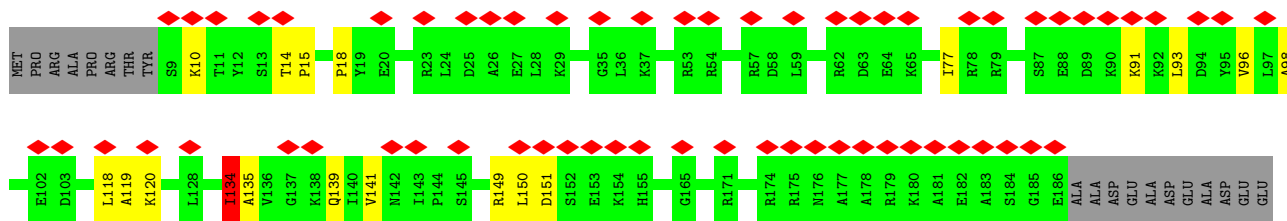


• Molecule 23: 40S ribosomal protein S8-A



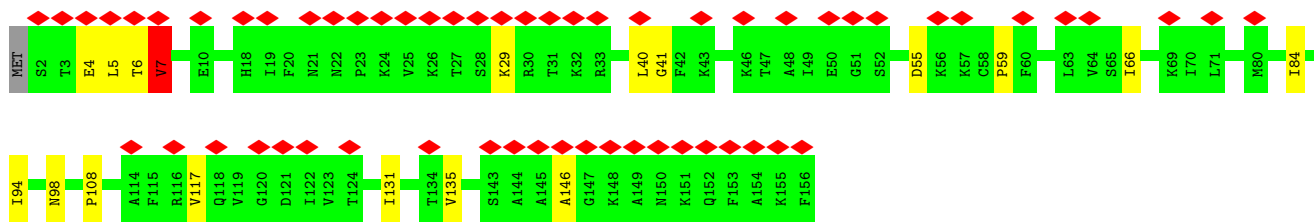
• Molecule 24: 40S ribosomal protein S9-A





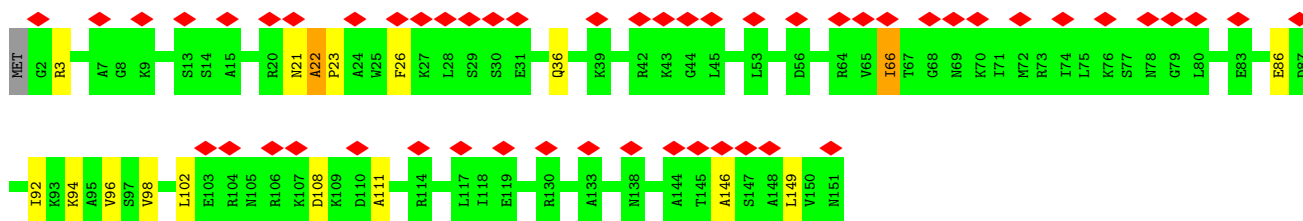
- Molecule 25: 40S ribosomal protein S11-A

Chain X:



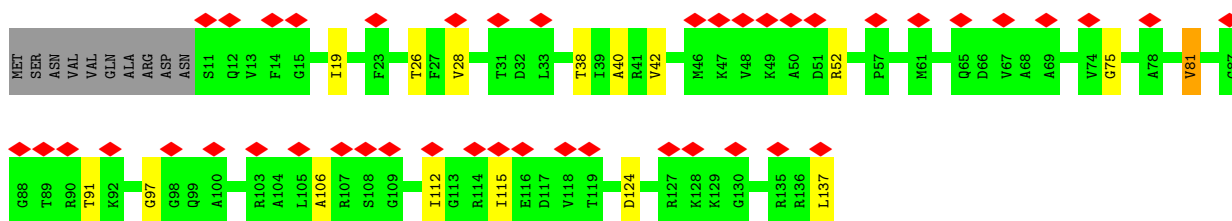
- Molecule 26: 40S ribosomal protein S13

Chain Y:



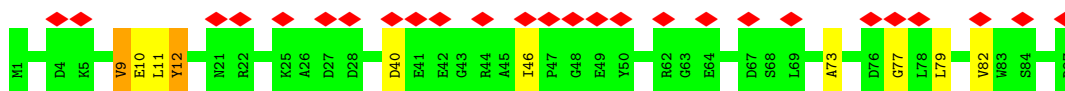
- Molecule 27: 40S ribosomal protein S14-A

Chain Z:

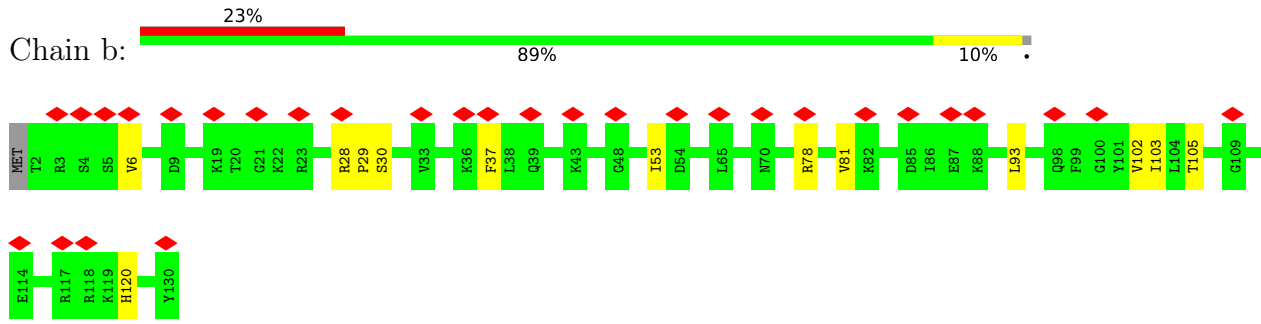


- Molecule 28: 40S ribosomal protein S21-A

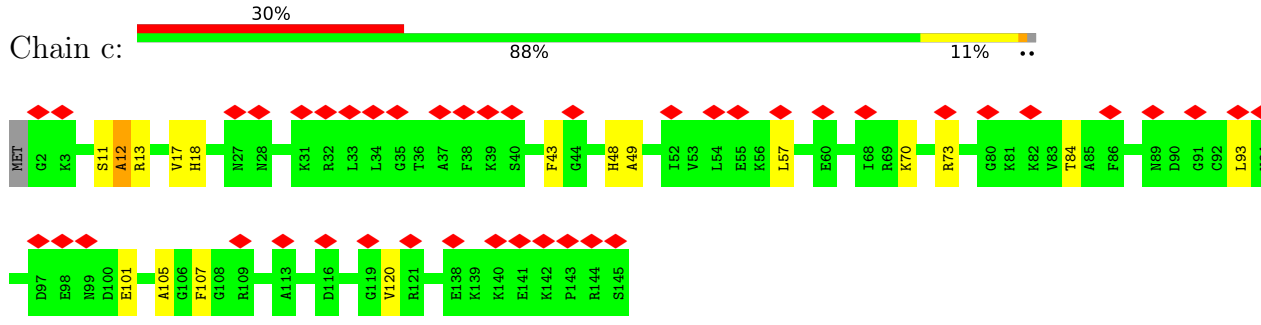
Chain a:



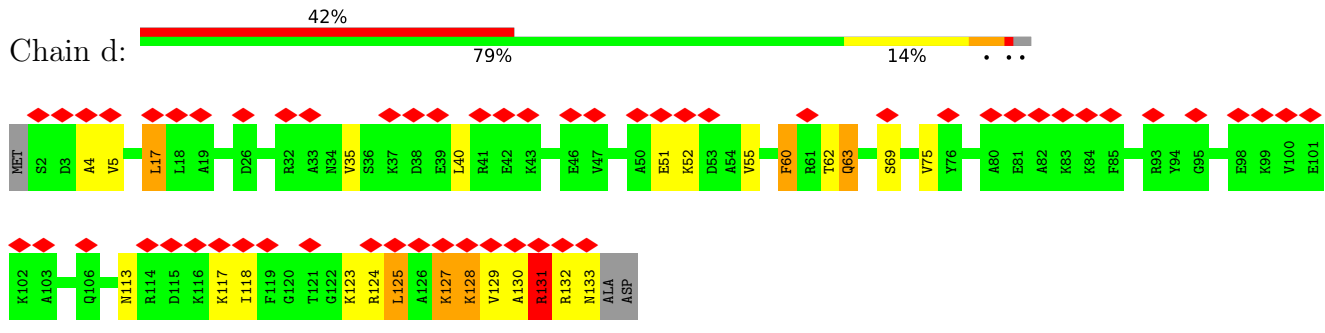
- Molecule 29: 40S ribosomal protein S22-A



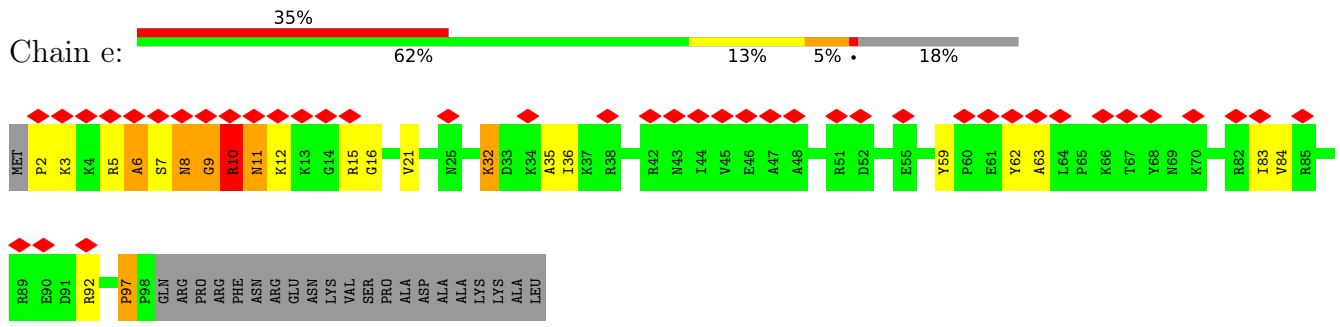
• Molecule 30: 40S ribosomal protein S23-A



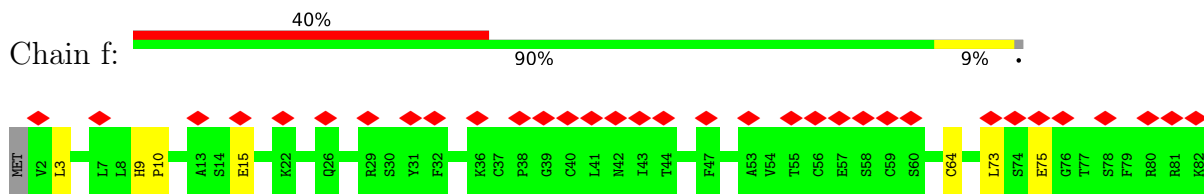
• Molecule 31: 40S ribosomal protein S24-A



• Molecule 32: 40S ribosomal protein S26-A



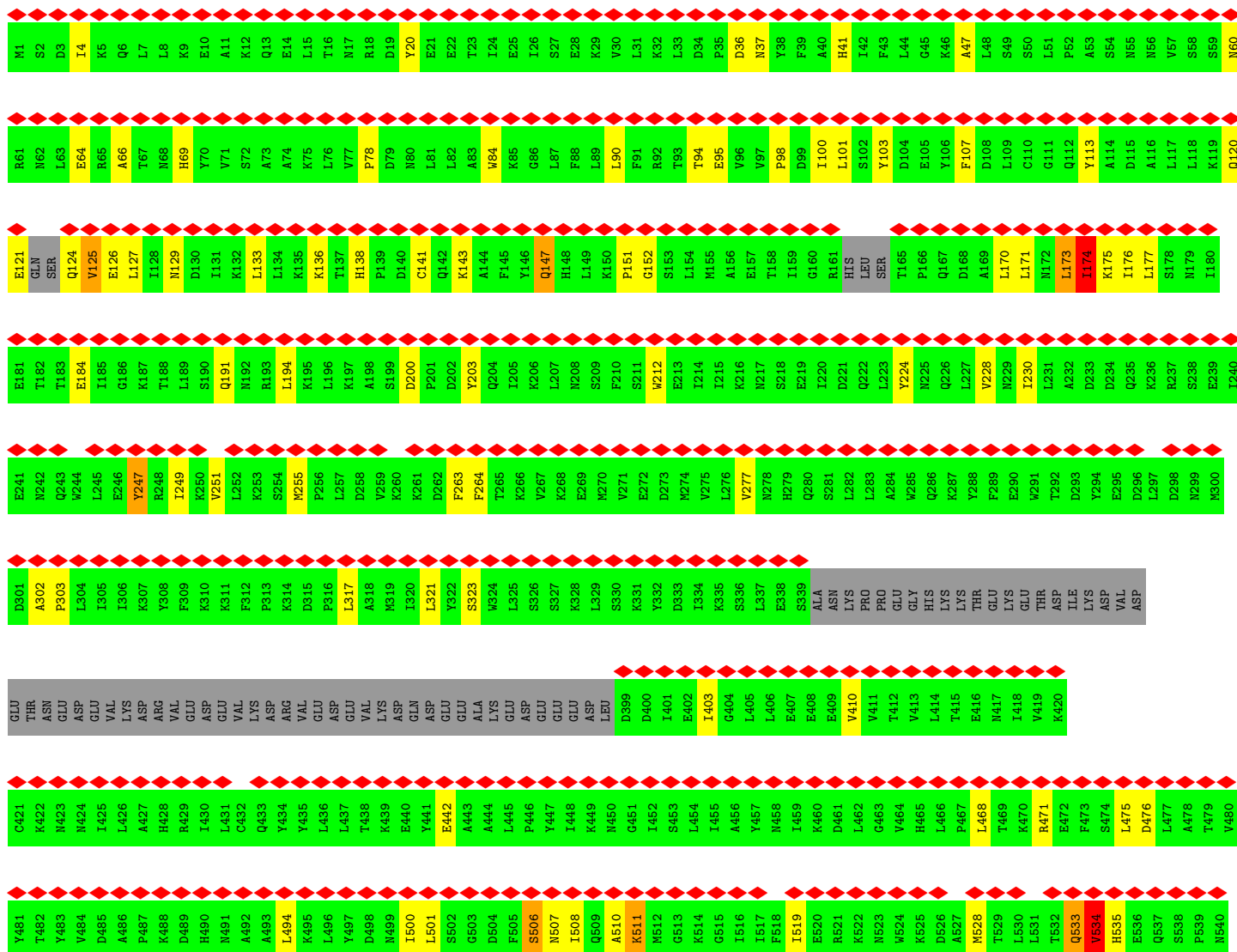
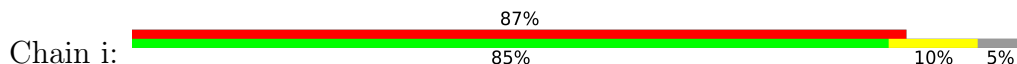
• Molecule 33: 40S ribosomal protein S27-A



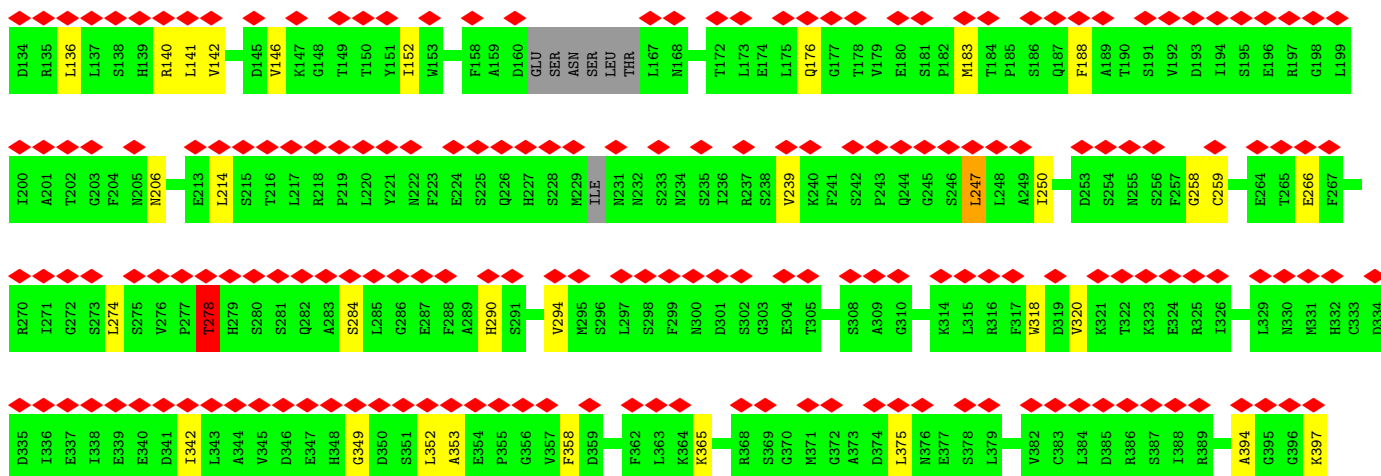
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E362	Y363	A364	I365	A366	M367	A368	H369	K370	N371	M372	T373	K374	T375	I376	T377	T378	S379	P380	I381	K382	A383	L384	S385	N386	Q387	K388	F389	R390	D391	F392	K393	E394	T395	F396	D397	D398	V399	G402	L403	I404	G406	D407	V408	Q409	V469	I410	M411	P412	D413	A414	M415	C416	I418	M419	T420	T421	E422					
I423	L424	R425	S426	M427	L428	Y429	G431	A432	D433	L434	I435	R436	D437	V438	E439	F440	V441	I442	F443	D444	E445	V446	H447	Y448	V449	M450	D451	Q452	D453	R454	G455	V456	V457	V458	E459	E460	V461	I462	I463	M464	L465	P466	Q467	H468	V469	F471	I472	L473	L474	A476	T477	V478	P479	M480	T481	Y482						
E483	F484	A485	M486	M487	I488	G489	R490	T491	K492	Q493	K494	M495	I496	Y497	V498	I499	S500	T501	P502	K503	R504	T505	V506	P507	L508	E509	I510	N511	I512	M513	A514	K515	G516	E517	L518	I519	P520	V521	I522	N523	Q524	N525	S526	E527	F528	L529	E530	A531	N532	F533	R534	K535	H536	K537	E538	I539	L540	N541	GLY			
GLU	SER	ALA	LVS	GLY	ALA	PRO	SER	LVS	THR	ASN	GLY	ARG	GLY	THR	ALA	ALA	ARG	GLY	GLY	GLY	ASN	THR	ASP	GLY	ARG	GLY	I510	ASN	SER	THR	ARG	GLY	ALA	ASN	ARG	GLY	GLY	SER	ARG	GLY	ALA	ALA	ILE	G997	S998	N999	K000	R001	K002													
F603	F604	T605	Q606	D607	K611	K612	T613	E616	Y620	L621	R622	K623	R624	E625	L626	L627	P628	M629	F632	V633	E641	Y642	A643	D644	M645	L646	E647	G648	I649	M650	F651	G652	K655	S668	H661	M662	F663	I664	E665	K666	S667	I668	T669	R670	L671	K672	E673	E674	D675	R676	D677											
L678	P679	Q680	K683	T684	R685	S686	L687	L688	E689	A693	V694	G697	G698	L699	L700	P701	I702	V703	K704	E705	L706	I707	E708	I709	F711	K712	S713	L714	G714	F715	I716	K717	V718	L719	F720	A721	T722	E723	T724	F725	A726	M727	G728	L729	L730	L731	P732	T733	R734	V735	I737	F738	S739	S740								
I741	R742	K743	H744	D745	G746	M747	G748	L749	R750	E751	L752	G755	E756	M760	A761	G762	R763	A764	G765	R766	R767	G768	L769	D770	S771	T772	G773	T774	V775	I776	V777	M778	A779	Y780	N781	S782	P783	L784	S785	I786	A787	T788	F789	K790	E791	V792	L793	M794	G795	V796	F797	T798	R799	L800	Q801	S802	Q803					
F804	R805	L806	T807	Y808	N809	H810	T811	L812	N813	L814	L815	R816	L817	E818	A819	L820	R821	V822	E824	R825	I826	K827	Y828	S829	F830	S831	E832	K835	E836	T837	L838	Q839	F840	E841	H842	E843	K844	Q845	I846	K847	V848	L849	R850	E851	E852	L853	R854	T855	I856	E857	Y858	K859	S860	C861	E862	I863	C864					
D865	N866	D867	I868	E869	K870	F871	L872	E873	L874	M875	L876	A877	Y878	K879	E880	A881	T882	W883	N884	L885	M886	Q887	E888	M889	W890	K891	S892	R893	S894	I895	L896	H897	I898	L899	K900	E901	G902	R903	L904	Y905	A906	F907	R908	D909	F910	N911	D912	C913	L914	K915	L916	G917	F918	Y919	F920	Q921	V922	S923	L924			
K925	D926	A927	V928	C929	V930	L931	M932	T933	F934	T935	K936	P937	Y938	Y939	K939	L940	P941	N942	G943	E944	P945	N946	H947	L948	I949	Y950	F951	E952	K953	A954	D955	G956	Y957	R958	R959	R960	F963	K964	F965	Q966	K967	T968	D969	F970	Y971	M972	E973	E974	Y975	P976	Y977	T978	A979	I980	E981	F982	I983	T984	K985			
R886	K987	F988	A989	A990	P991	L992	G993	K994	V995	I996	K997	K998	D999	V1000	A1001	A1002	A1003	N1004	E1005	F1006	I1070	N1007	A1008	E1009	I1074	N1010	N1011	N1012	I1013	L1014	D1015	G1016	K1017	Y1018	N1018	L1019	K1020	A1021	A1022	I1023	N1024	I1025	E1026	K1027	Q1028	G1029	L1030	N1031	R1032	H1033	V1034	L1035	L1036	D1037	D1038	R1039	T1040	N1041	I1042	V1043	I1044	D1045
I1046	F1047	K1048	L1049	K1050	S1051	I1052	K1053	C1054	P1055	M1056	H1060	P1063	K1064	F1065	K1066	A1067	H1068	V1069	I1070	K1071	K1072	K1073	I1074	N1075	E1076	L1077	Y1078	H1079	L1080	M1081	S1082	D1083	Q1084	M1085	L1086	S1087	L1088	L1089	P1090	D1091	Y1092	E1093	K1094	R1095	L1096	A1097	V1098	L1099	K1100	D1101	T1102	E1103	F1104	I1105	D1106	Q1107	M1108					



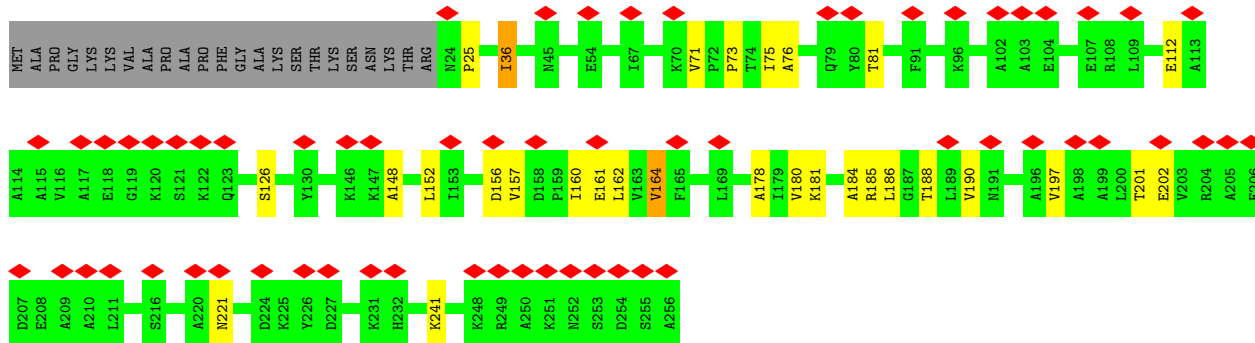
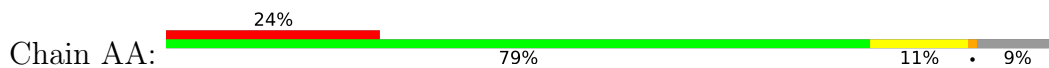
● Molecule 39: Superkiller protein 3



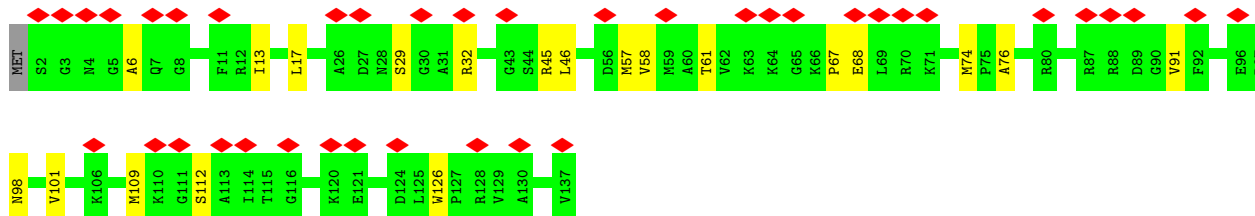
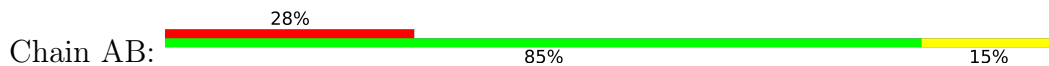
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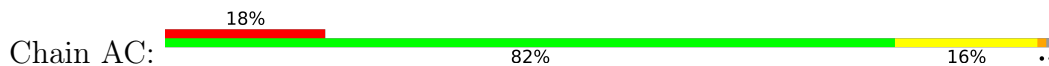
• Molecule 41: 60S ribosomal protein L8-A



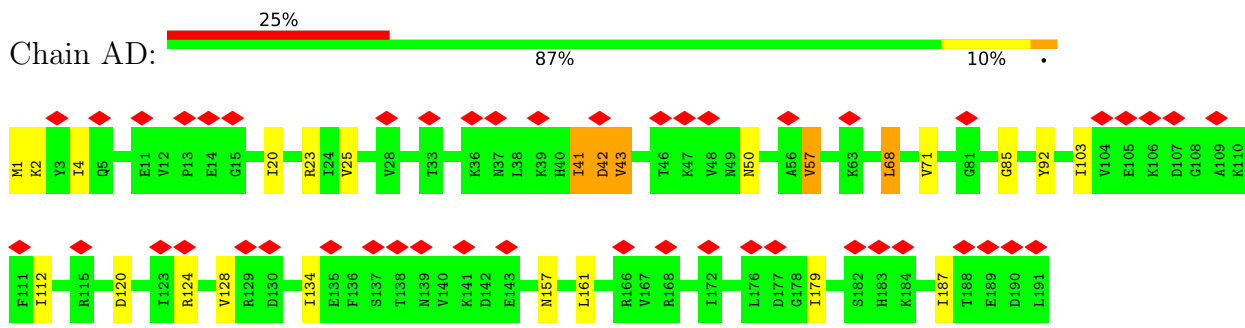
• Molecule 42: 60S ribosomal protein L23-A



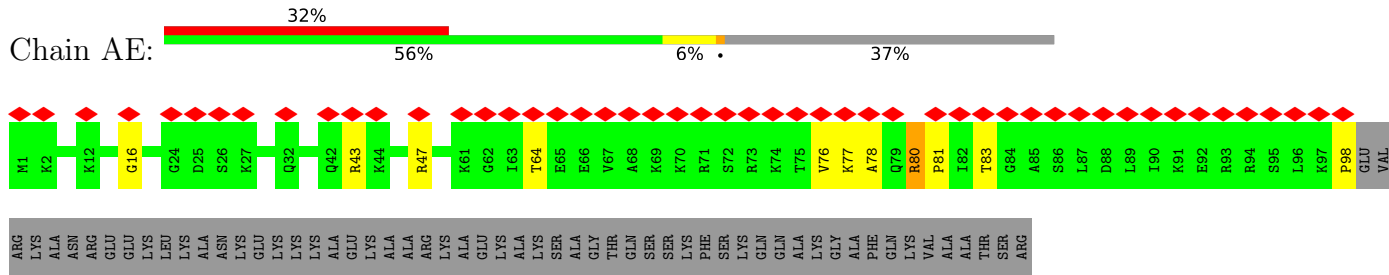
• Molecule 43: 60S ribosomal protein L36-A



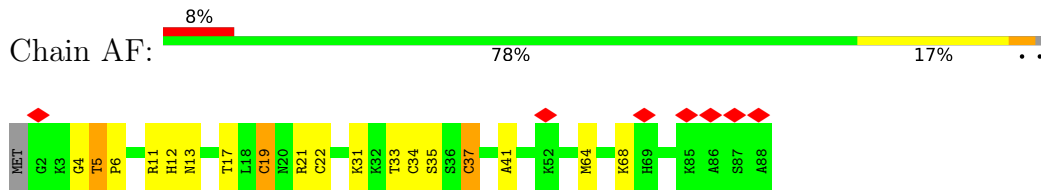
• Molecule 44: 60S ribosomal protein L9-A



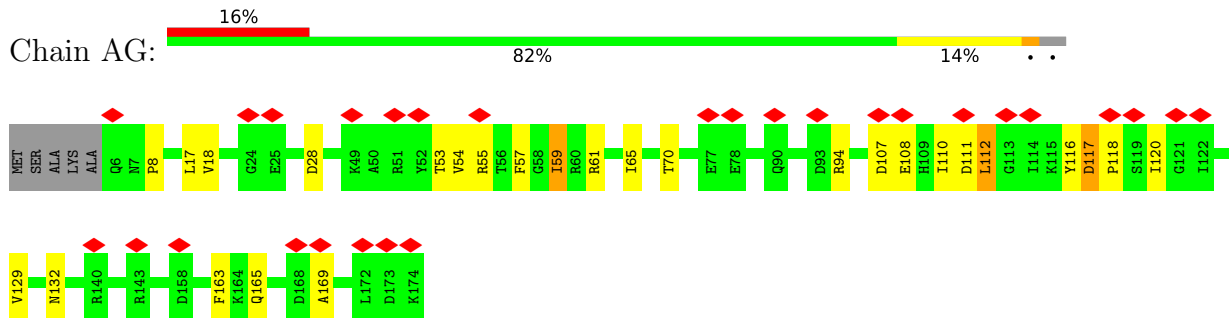
• Molecule 45: 60S ribosomal protein L24-A



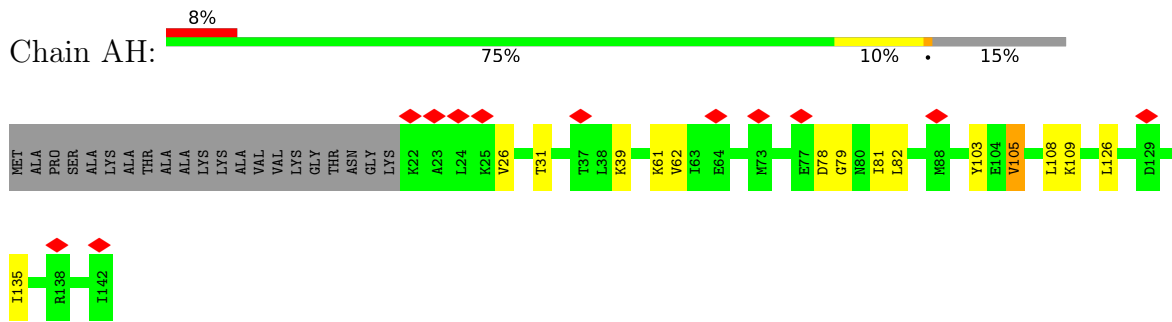
• Molecule 46: 60S ribosomal protein L37-A



• Molecule 47: 60S ribosomal protein L11-A



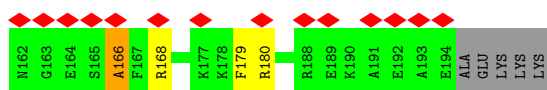
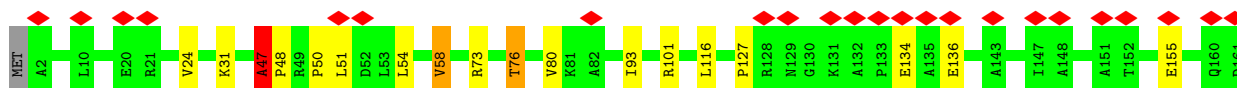
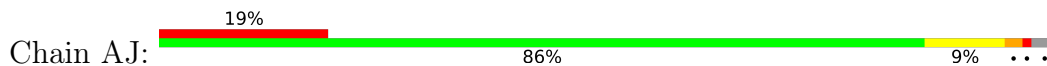
• Molecule 48: 60S ribosomal protein L25



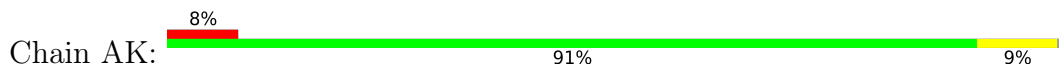
• Molecule 49: 60S ribosomal protein L38



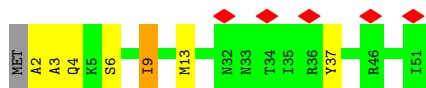
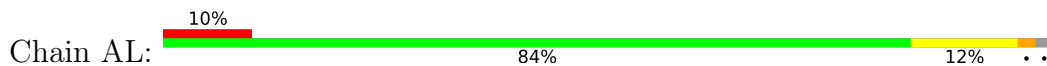
- Molecule 50: 60S ribosomal protein L13-A



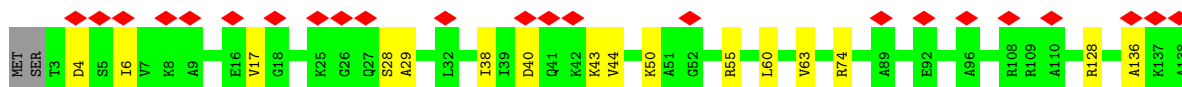
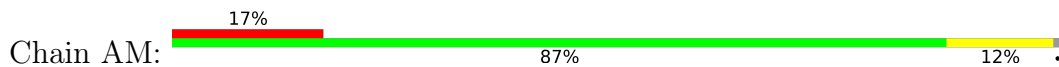
- Molecule 51: 60S ribosomal protein L26-A



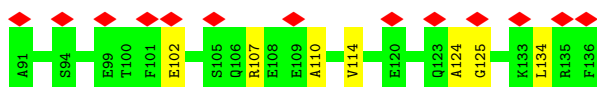
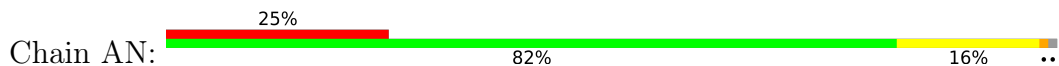
- Molecule 52: 60S ribosomal protein L39



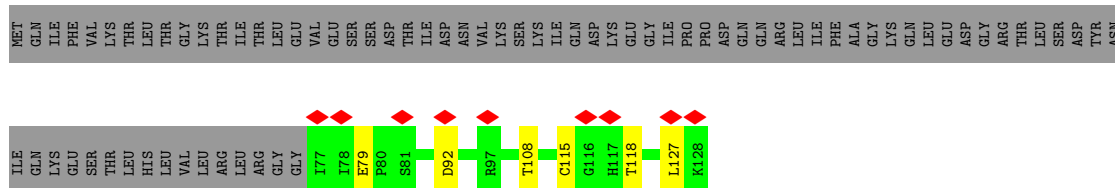
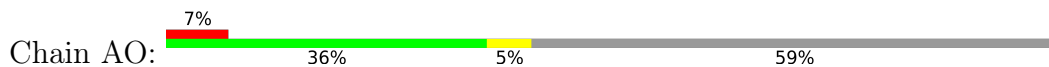
- Molecule 53: 60S ribosomal protein L14-A



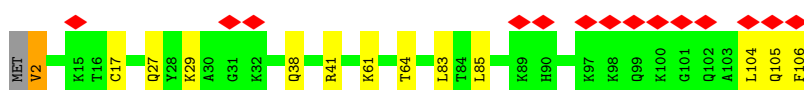
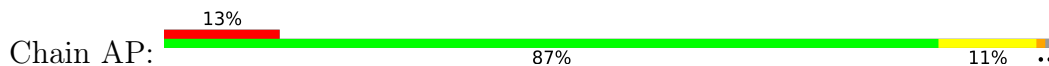
- Molecule 54: 60S ribosomal protein L27-A



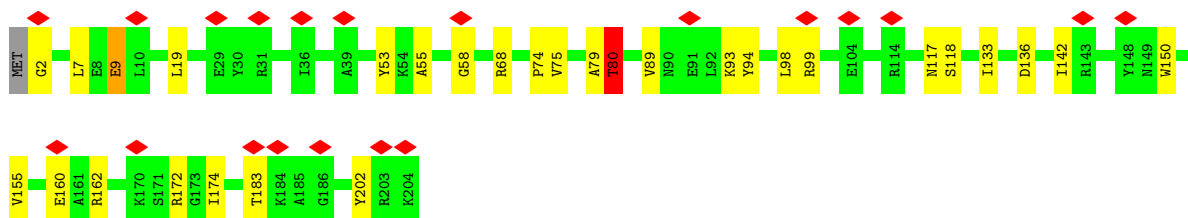
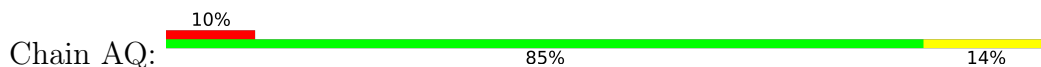
• Molecule 55: Ubiquitin-60S ribosomal protein L40



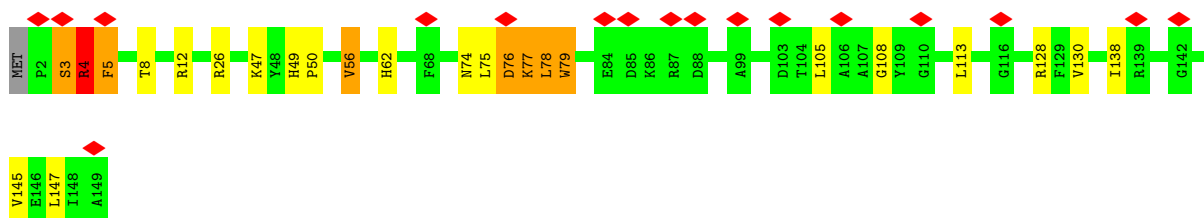
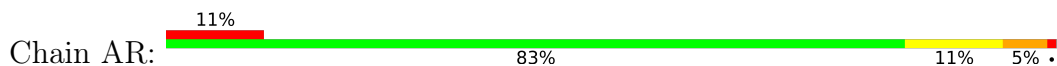
• Molecule 56: 60S ribosomal protein L42-A



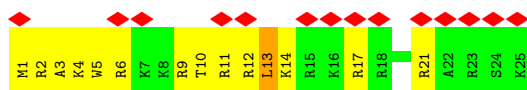
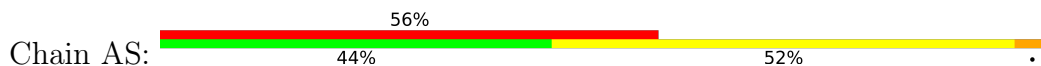
• Molecule 57: 60S ribosomal protein L15-A



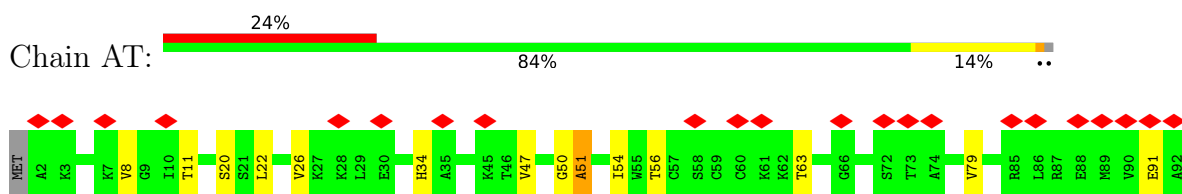
• Molecule 58: 60S ribosomal protein L28



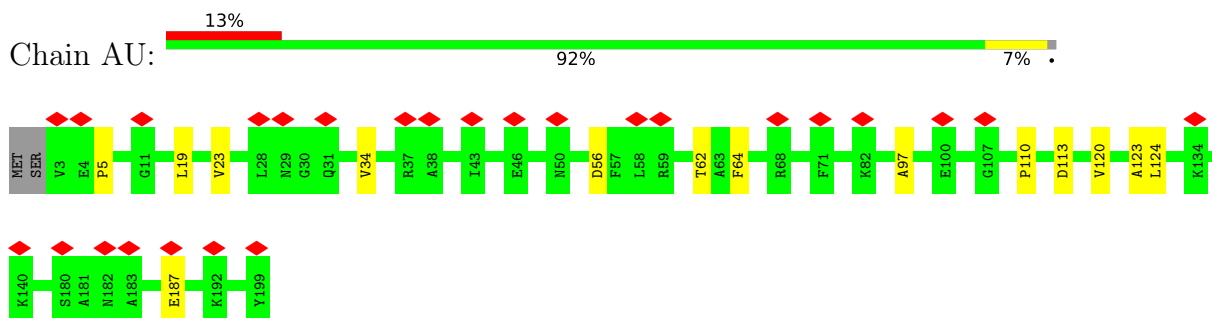
• Molecule 59: 60S ribosomal protein L41-A



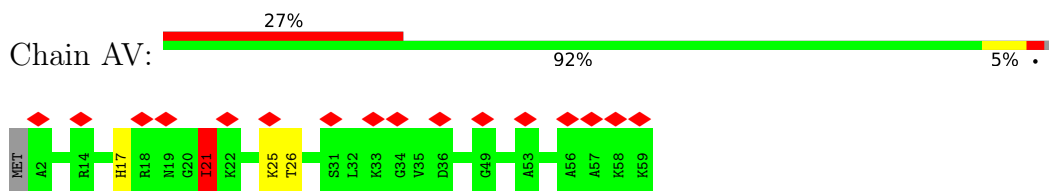
• Molecule 60: 60S ribosomal protein L43-A



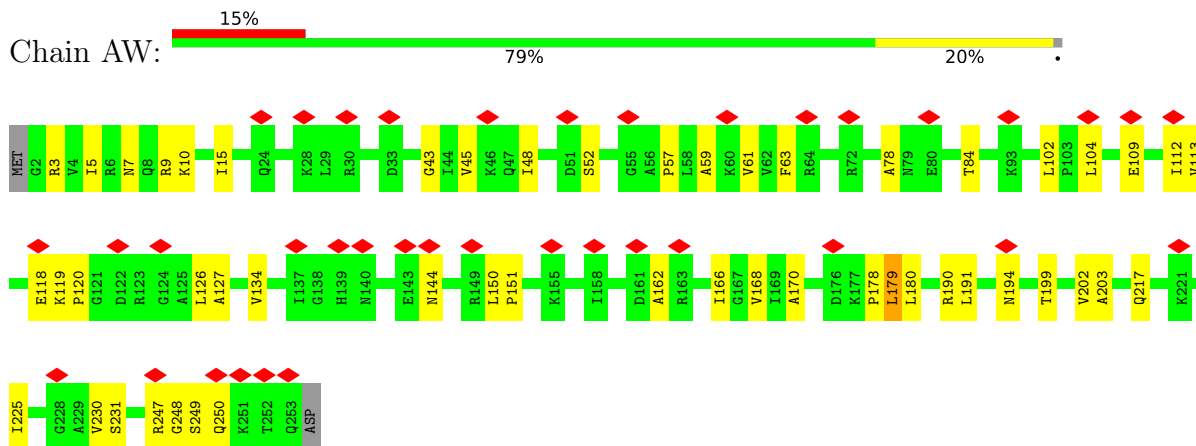
- Molecule 61: 60S ribosomal protein L16-A



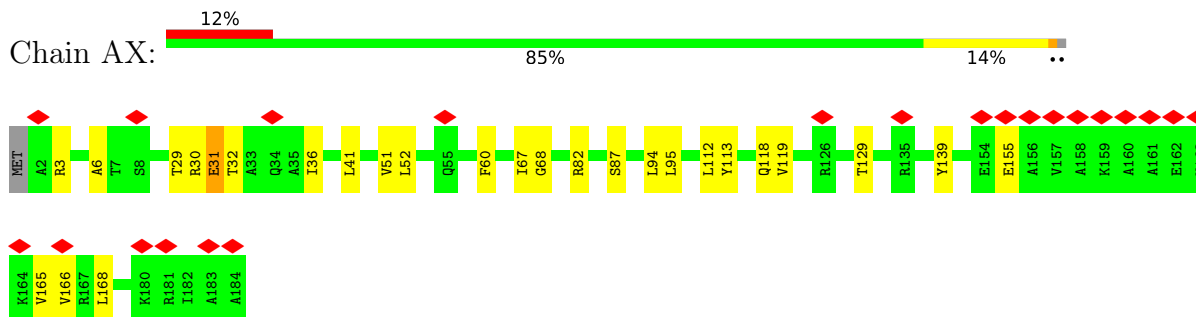
- Molecule 62: 60S ribosomal protein L29



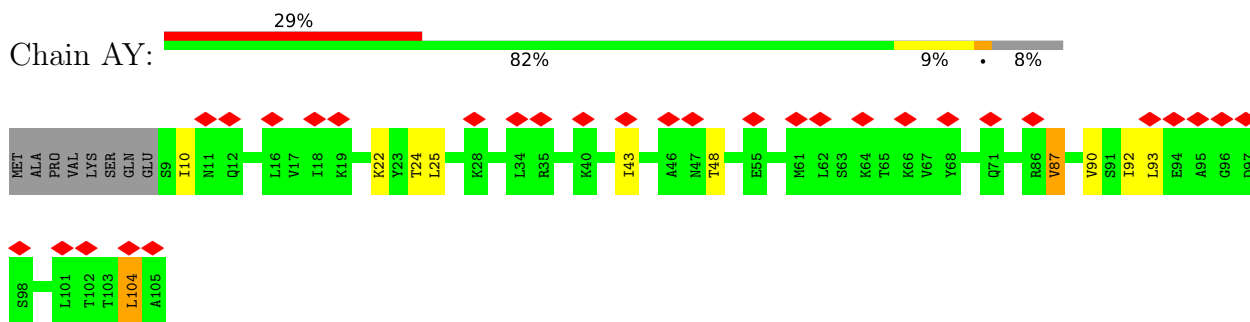
- Molecule 63: 60S ribosomal protein L2-A



- Molecule 64: 60S ribosomal protein L17-A



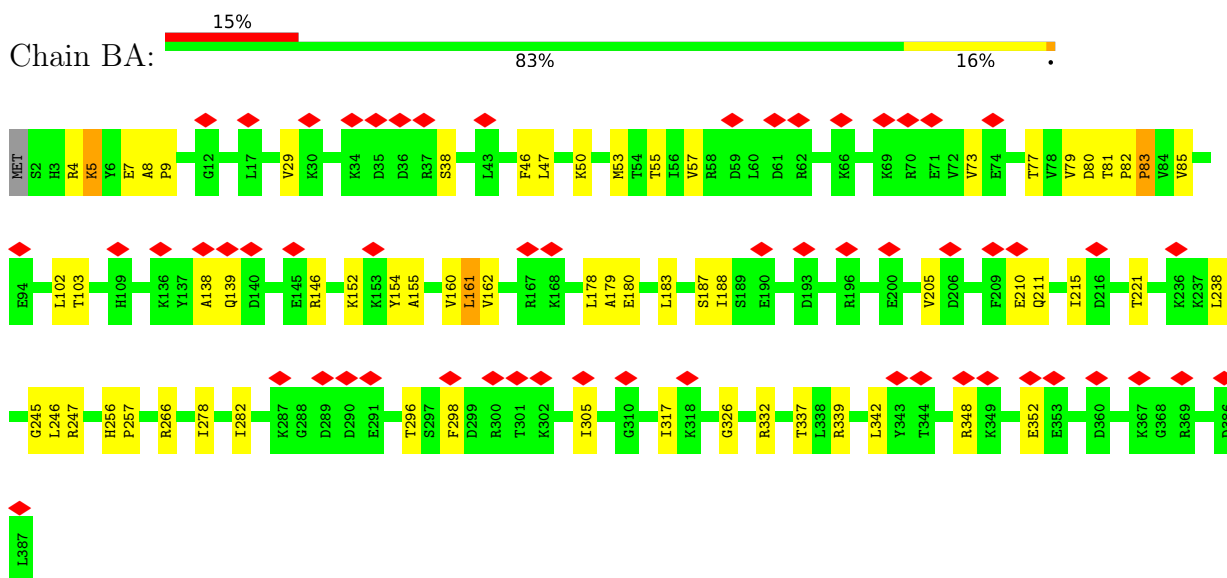
• Molecule 65: 60S ribosomal protein L30



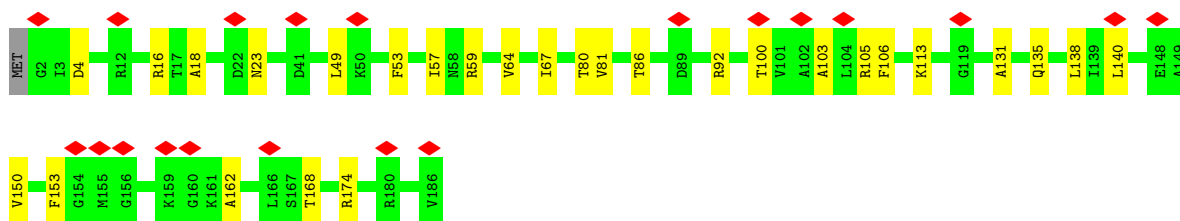
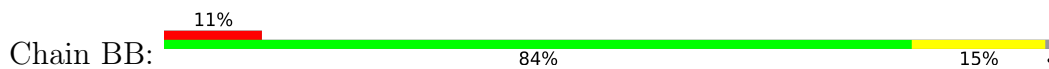
• Molecule 66: uL1



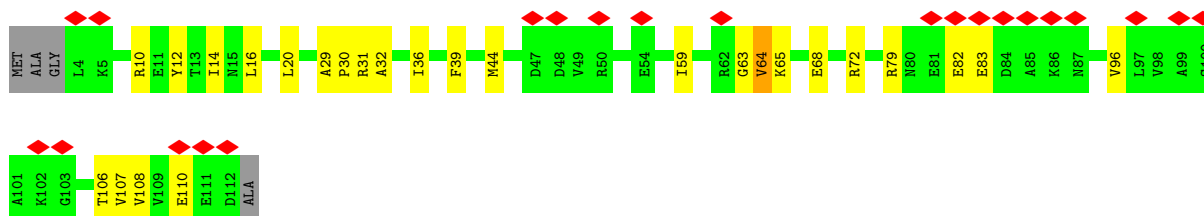
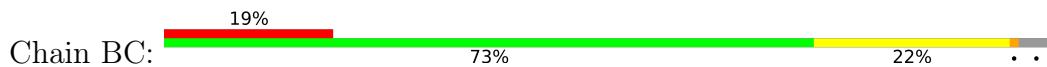
• Molecule 67: 60S ribosomal protein L3



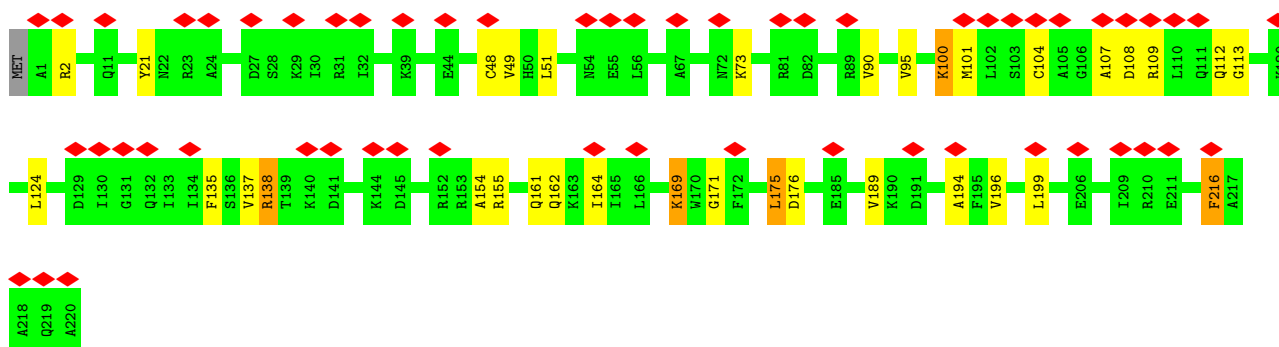
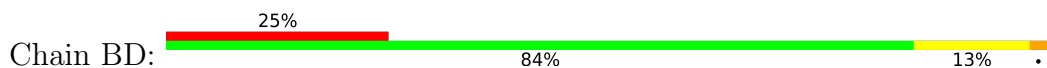
• Molecule 68: 60S ribosomal protein L18-A



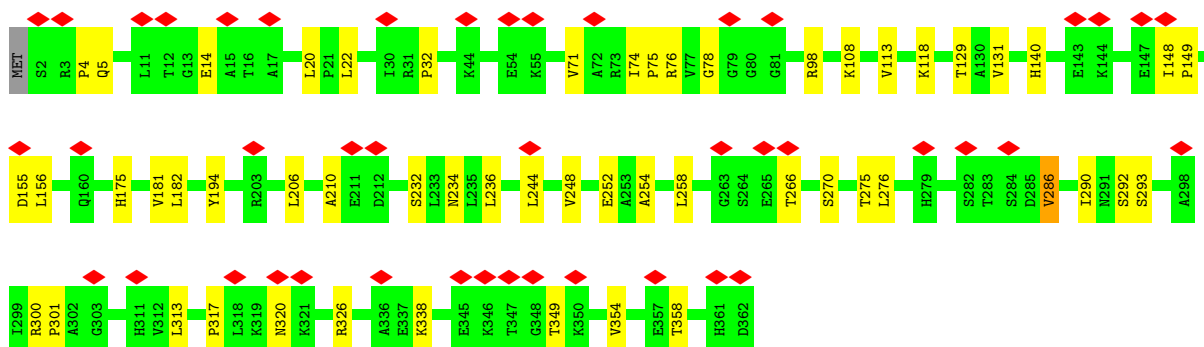
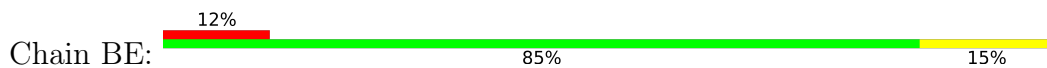
- Molecule 69: 60S ribosomal protein L31-A



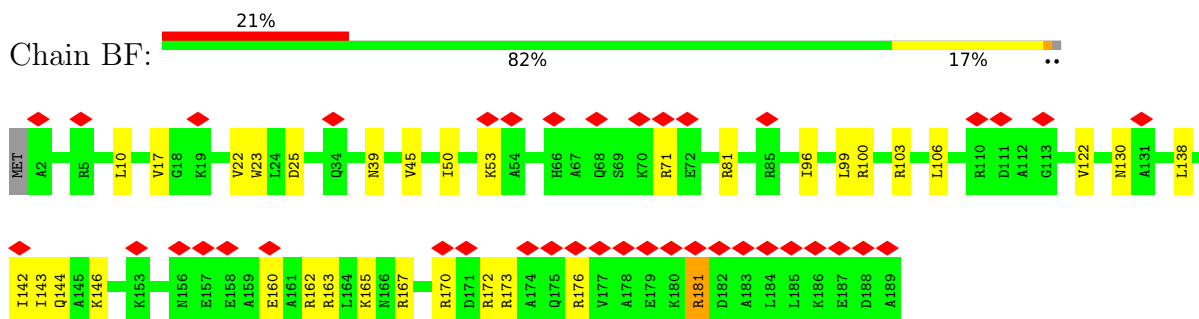
- Molecule 70: 60S ribosomal protein L10



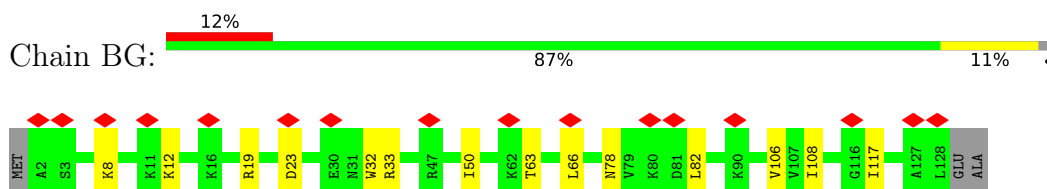
- Molecule 71: 60S ribosomal protein L4-A



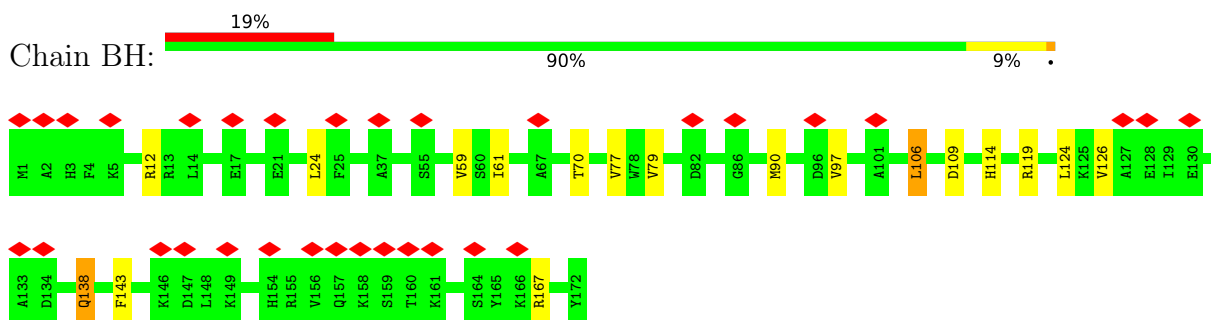
- Molecule 72: 60S ribosomal protein L19-A



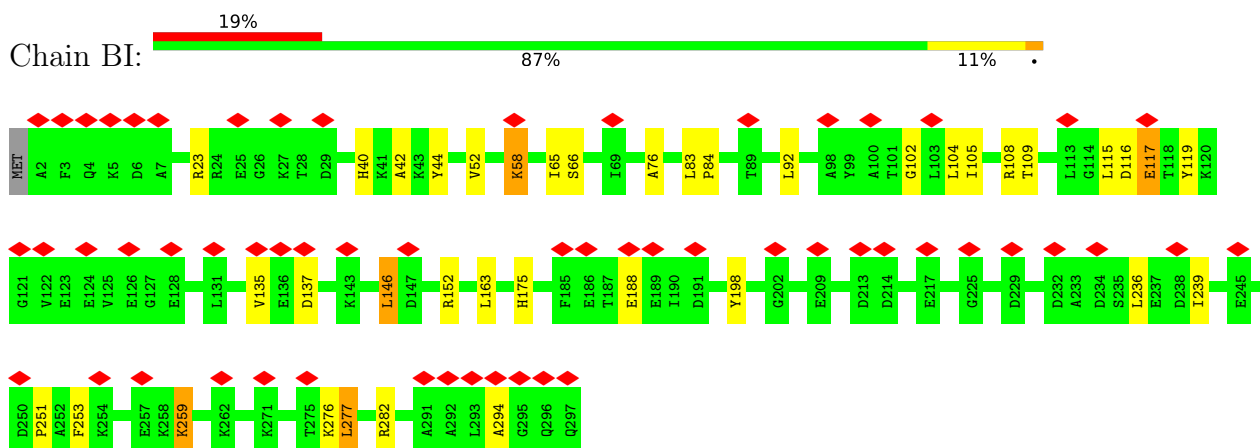
- Molecule 73: 60S ribosomal protein L32



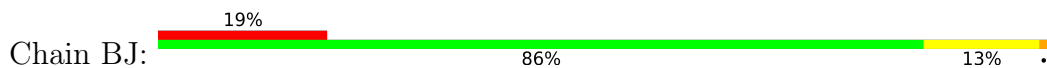
- Molecule 74: 60S ribosomal protein L20-A

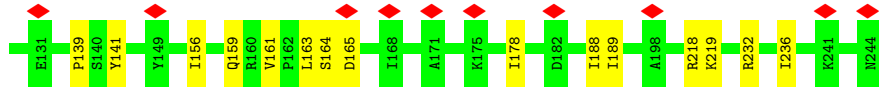


- Molecule 75: 60S ribosomal protein L5

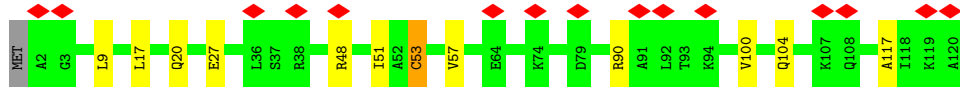
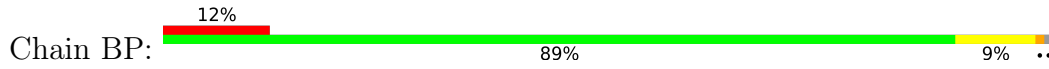


- Molecule 76: 60S ribosomal protein L21-A

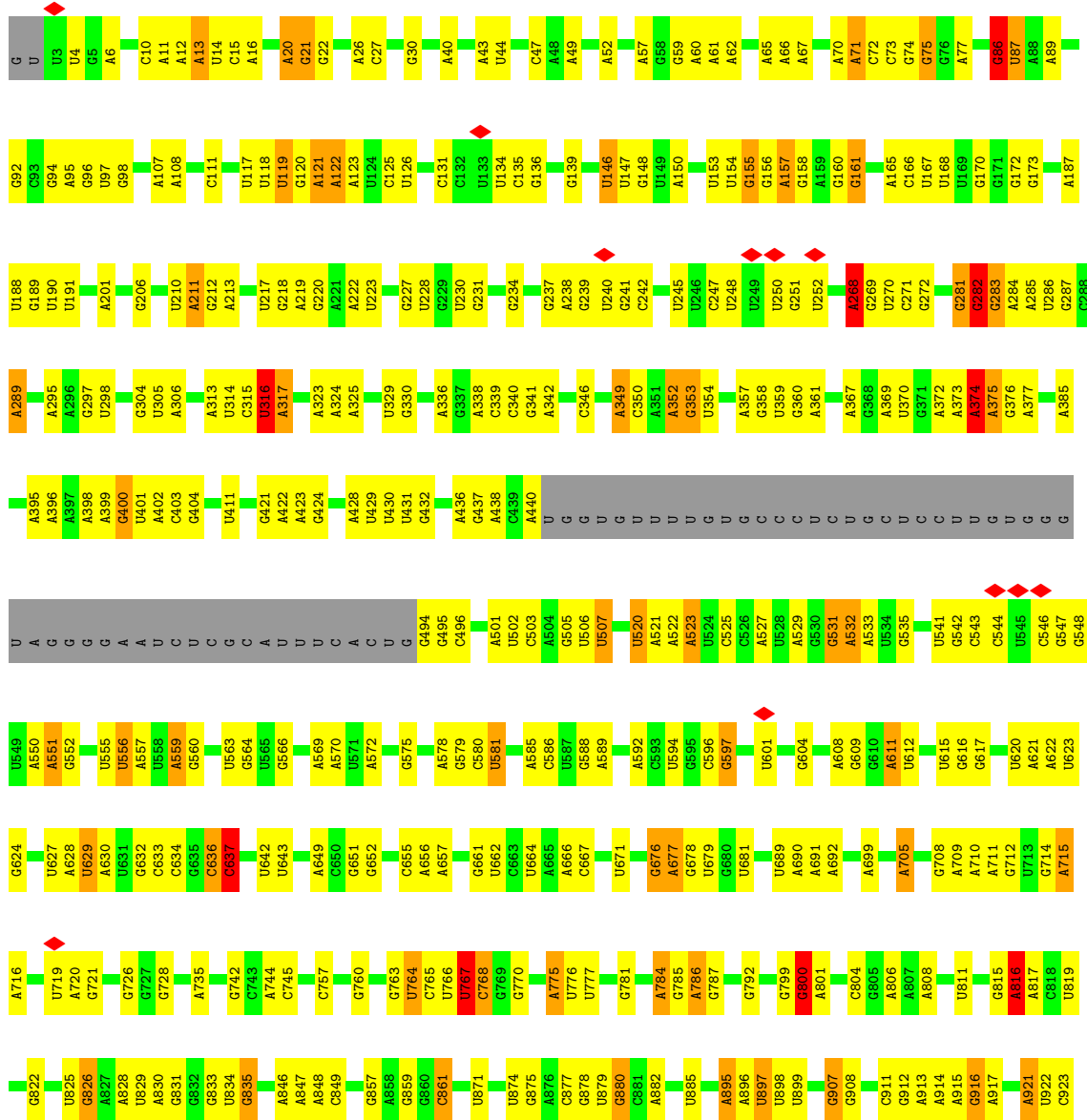




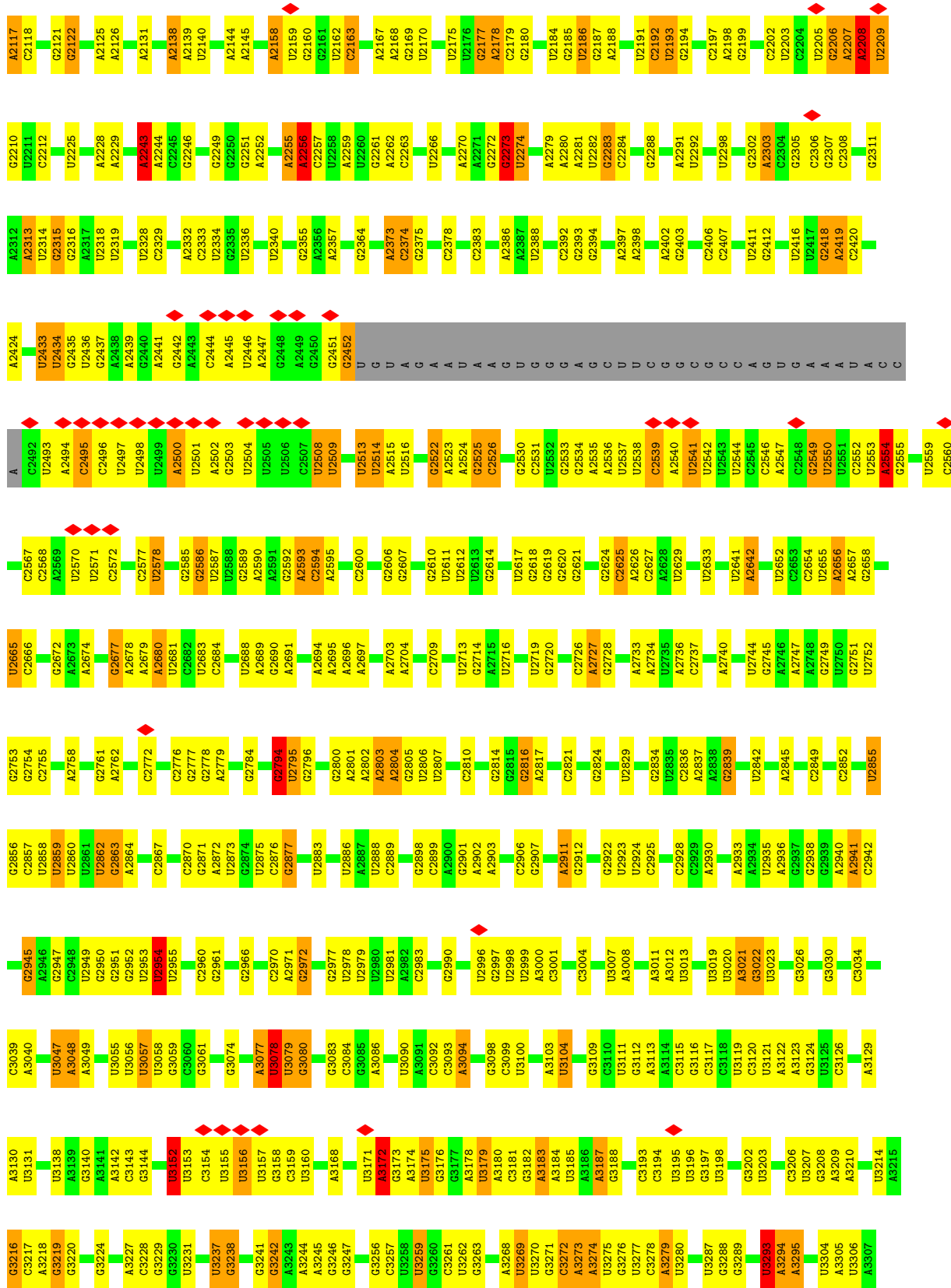
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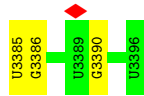
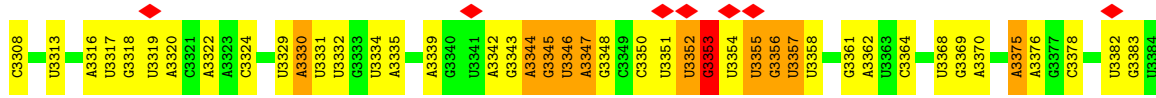


• Molecule 83: 25S ribosomal RNA

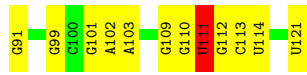
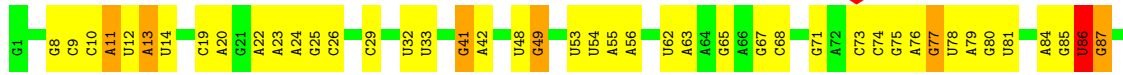


G	A2093	A2099	A2100	C2101	U2102	A2106	A2107	C2108	G2111	U2112	A2113	G2114	G2115	G2116	G																																									
C	U1820	U1821	C1822	U1834	A1835	U1839	U1840	A1841	A1842	G1845	C1846	A1847	G1848	C1849	A1850	G1851	C1854	U1855	C1856	C1857	A1858	A1864	A1865	A1866	A1867	U1871	U1877	G1878	A1879	U1880	A1881	A1884	U1885	A1886	A1887	U1888	A1893	U1894	A1895	A1896	A1897	G1898	G1899	A1900	A1901	G1905	G1906	G	U1912	G						
U	A1913	G1914	C1918	C1926	G1927	A1839	U1840	A1841	A1842	G1845	C1846	A1847	G1848	C1849	A1850	G1851	C1854	U1855	C1856	C1857	A1858	A1864	A1865	A1866	A1867	U1871	U1877	G1878	A1879	U1880	A1881	A1884	U1885	A1886	A1887	U1888	A1893	U1894	A1895	A1896	A1897	G1898	G1899	A1900	A1901	G1905	G1906	G	U1912	G						
C	U1724	C1725	G1728	U1729	G1730	A1731	G1735	U1740	A1741	G1747	G1748	U1749	G1750	G1751	A1752	A1760	C1761	U1762	U1763	U1764	U1765	G1766	G1769	G1770	G1775	G1780	C1781	U1782	U1783	U1784	U1785	G1786	A1787	C1788	C1792	C1793	G1794	A1797	A1798	G1808	A1809	A1813	A1814	U1815	A1816	G1817	U1818	U1819	G							
G	A1613	G1617	G1618	A1619	U1620	A1621	G1624	A1625	A1626	U1630	C1631	A1632	C1633	U1645	U1646	A1656	A1657	A1658	C1657	G1658	U1659	C1660	G1661	G1662	G1668	A1676	G1677	A1683	U1684	U1689	C1693	U1694	U1695	A1696	A1697	U1702	U1703	A1704	C1708	G1713	A1714	U1717	G1718	G1719	U1720	U1721	U1722	A1723	G							
C	U1526	C1527	U1532	C1533	U1536	A1537	G1538	A1539	G1542	U1549	U1554	C1555	C1556	A1557	A1558	A1559	G1560	G1561	C1562	C1563	U1564	G1565	A1566	U1568	U1569	U1570	A1571	U1572	G1576	G1577	C1578	A1580	C1581	A1582	A1583	A1587	A1588	A1589	A1593	C1596	C1597	A1602	A1603	G1604	A1605	U1606	U1607	G								
U	G1429	U1430	G1431	C1432	A1433	G1434	U1436	C1437	G1444	U1445	A1446	U1447	U1448	A1449	C1451	A1452	U1455	G1456	A1462	U1463	G1464	A1467	U1479	G1480	A1481	A1482	G1483	U1484	U1485	G1486	G1487	U1494	U1495	A1504	C1505	A1506	G1507	C1508	U1511	U1512	G1513	G1514	G1520	G1521	U1522	U1523	A1524	G								
C	U1315	C1316	A1317	G1319	C1320	G1321	U1325	A1326	C1327	C1328	U1329	A1330	U1331	C1333	U1334	A1337	C1338	G1345	U1348	G1349	A1350	U1351	A1352	G1354	A1355	U1356	G1357	C1358	C1359	C1364	G1380	A1381	G1382	A1386	C1391	G1392	A1393	A1399	G1400	A1407	G1408	G1417	A1418	A1419	C1424	G										
G	U1246	U1247	C1248	G1249	G1250	A1251	A1252	U1253	C1254	C1255	G1256	C1257	U1258	A1259	A1260	G1261	G1262	A1263	G1264	U1265	G1266	U1267	G1268	U1269	A1270	A1271	C1272	A1273	A1274	C1275	U1276	C1277	A1278	C1279	C1280	G1281	C1282	C1283	G1284	A1285	A1286	A1287	A1290	A1291	A1294	A1301	A1302	A1303	A1304	U1305	G1306	G1307	A1308	U1309	G1313	G
C	A1180	U1181	A1182	C1185	G1186	C1187	U1188	U1191	C1192	A1193	G1194	A1195	C1196	A1197	C1198	C1199	C1201	A1202	A1203	A1204	A1205	G1206	U1207	U1208	G1209	U1210	G1213	A1217	U1220	G1221	G1222	A1223	A1224	C1225	G1226	C1227	C1228	G1229	G1230	A1231	A1232	C1233	G1234	U1235	G1236	G1237	C1238	C1239	U1241	G1242	G1243	A1244	A1245	G		
U	G1087	C1092	U1093	U1094	U1095	U1096	G1097	A1098	A1102	A1103	G1104	U1105	G1106	U1110	U1111	G1113	G1116	G1117	U1125	G1126	C1127	U1128	A1129	A1130	G1131	G1134	G1140	G1141	G1142	A1143	A1144	G1145	G1149	A1150	U1151	G1152	A1153	A1154	C1155	A1159	C1160	A1169	U1170	G1171	G1172	G1177	G1178	A1179	U1081	U1082	G1083	A1084	A1085	A1086	G	
G	U1010	G1013	U1014	U1015	C1016	C1017	G1018	U1019	G1020	G1021	U1022	C1023	G1024	A1025	A1026	A1027	U1028	G1029	A1030	C1031	C1032	U1033	A1036	C1037	C1038	U1042	G1043	U1044	C1045	A1046	A1047	A1048	C1049	U1050	U1051	U1052	A1055	G1063	A1064	A1065	U1071	G1072	U1073	U1074	A1075	G1076	U1077	U1081	U1082	G1083	A1084	A1085	A1086	G		
C	G924	A925	A926	A933	G934	U935	A936	G937	C938	U939	U942	U943	C944	C945	U946	C949	G950	C953	U954	C959	U960	C961	A962	C964	G974	C977	G978	U979	A980	U981	G984	U988	A989	U990	G991	A992	G993	G994	U995	A996	G1001	A1002	A1003	U1004	G1005	A1006	U1007	U1008	A1009	G						

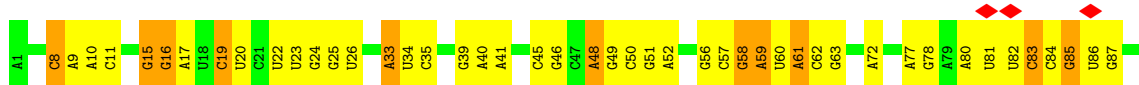




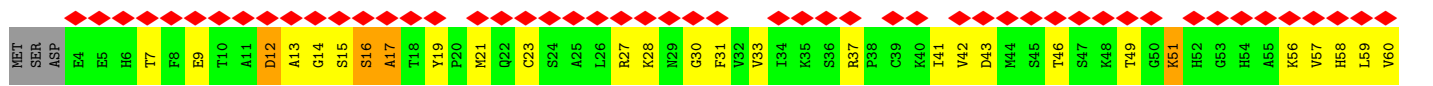
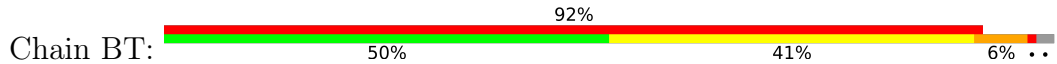
• Molecule 84: 5S ribosomal RNA



• 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	0.41	1/42103 (0.0%)	0.78	99/65603 (0.2%)
2	A	0.54	0/1759	0.83	0/2368
3	B	0.58	0/1629	0.91	0/2202
4	C	0.55	0/833	0.81	0/1126
5	D	0.63	0/885	0.89	0/1202
6	E	0.58	0/998	0.84	0/1341
7	F	0.59	0/1125	0.92	1/1510 (0.1%)
8	G	0.67	2/754 (0.3%)	0.96	0/1005
9	H	0.62	0/1211	0.95	2/1628 (0.1%)
10	I	0.63	0/1130	0.95	3/1517 (0.2%)
11	J	0.55	0/865	0.84	1/1169 (0.1%)
12	K	0.61	0/571	0.90	0/768
13	L	0.54	0/499	0.70	0/670
14	M	0.50	0/452	0.74	0/600
15	N	0.58	0/404	0.79	0/542
16	O	0.52	0/2489	0.66	0/3389
17	P	0.56	0/1617	0.86	0/2215
18	Q	0.62	0/1735	0.84	0/2335
19	R	0.51	0/1702	0.80	0/2310
20	S	0.60	1/2109 (0.0%)	0.80	1/2839 (0.0%)
21	T	0.57	0/1823	0.78	1/2439 (0.0%)
22	U	0.61	0/1506	0.81	2/2028 (0.1%)
23	V	0.69	0/1514	0.99	5/2021 (0.2%)
24	W	0.60	0/1456	0.87	0/1949
25	X	0.55	0/1239	0.72	0/1673
26	Y	0.58	0/1215	0.96	0/1638
27	Z	0.64	0/901	0.91	0/1217
28	a	0.57	0/693	0.80	0/935
29	b	0.49	0/1038	0.88	1/1395 (0.1%)
30	c	0.51	0/1139	0.77	0/1518
31	d	0.62	0/1074	0.91	3/1431 (0.2%)
32	e	1.01	5/782 (0.6%)	1.06	5/1047 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.55	0/620	0.74	0/838
34	g	0.63	1/481 (0.2%)	0.79	0/640
35	l	0.41	0/764	0.85	1/1179 (0.1%)
36	m	0.40	0/1799	0.80	4/2801 (0.1%)
37	n	0.39	0/1835	0.75	4/2858 (0.1%)
38	h	0.57	0/8985	0.84	3/12155 (0.0%)
39	i	0.55	1/10027 (0.0%)	0.87	6/13707 (0.0%)
40	j	0.54	0/3001	0.69	0/4083
40	k	0.52	0/2988	0.70	0/4060
41	AA	0.64	0/1836	0.90	1/2481 (0.0%)
42	AB	0.57	0/1018	0.89	1/1369 (0.1%)
43	AC	0.63	0/778	0.93	0/1034
44	AD	0.58	0/1539	0.85	0/2073
45	AE	0.61	0/712	1.26	2/958 (0.2%)
46	AF	0.63	0/696	0.88	1/923 (0.1%)
47	AG	0.61	0/1374	0.88	2/1842 (0.1%)
48	AH	0.52	0/979	0.83	0/1321
49	AI	0.61	0/618	0.77	0/826
50	AJ	0.63	0/1568	0.92	2/2106 (0.1%)
51	AK	0.59	0/1004	0.89	0/1341
52	AL	0.55	0/443	0.82	0/588
53	AM	0.60	0/1068	0.94	0/1438
54	AN	0.57	0/1118	0.88	0/1497
55	AO	0.62	0/423	0.90	0/562
56	AP	0.53	0/860	0.80	0/1136
57	AQ	0.58	0/1757	0.89	1/2354 (0.0%)
58	AR	0.57	0/1204	0.90	2/1612 (0.1%)
59	AS	0.67	0/234	1.01	0/300
60	AT	0.56	0/701	0.87	0/934
61	AU	0.58	0/1585	0.89	1/2128 (0.0%)
62	AV	0.52	0/473	0.88	0/629
63	AW	0.54	0/1948	0.85	1/2617 (0.0%)
64	AX	0.58	0/1443	0.89	0/1944
65	AY	0.57	0/750	0.88	0/1008
67	BA	0.56	0/3146	0.83	0/4228
68	BB	0.56	0/1465	0.90	0/1965
69	BC	0.53	0/890	0.79	0/1196
70	BD	0.59	0/1807	0.89	2/2425 (0.1%)
71	BE	0.59	0/2800	0.92	0/3790
72	BF	0.64	0/1538	0.94	3/2050 (0.1%)
73	BG	0.55	0/1041	0.80	0/1394
74	BH	0.54	0/1481	0.83	0/1990
75	BI	0.58	0/2425	0.86	0/3271

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	BJ	0.53	0/1300	0.83	0/1743
77	BK	0.56	0/868	0.80	0/1168
78	BL	0.62	0/812	0.82	0/1099
79	BM	0.57	0/1260	0.87	2/1694 (0.1%)
80	BN	0.57	0/890	0.89	2/1189 (0.2%)
81	BO	0.59	0/1821	0.92	0/2451
82	BP	0.55	0/978	0.91	0/1301
83	BQ	0.42	0/75774	0.83	160/118137 (0.1%)
84	BR	0.40	0/2883	0.79	5/4491 (0.1%)
85	BS	0.41	0/3745	0.80	4/5829 (0.1%)
86	BT	0.30	0/1142	0.75	0/1537
All	All	0.50	11/243945 (0.0%)	0.83	334/355920 (0.1%)

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 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	52	U	O3'-P	18.60	1.89	1.61
32	e	8	ASN	CA-C	8.98	1.61	1.53
8	G	36	ASP	CG-OD1	7.28	1.39	1.25
8	G	36	ASP	CG-OD2	6.06	1.36	1.25
39	i	147	GLN	C-O	-5.92	1.16	1.24

The worst 5 of 334 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	AE	80	ARG	CA-C-N	19.43	144.12	119.84
45	AE	80	ARG	C-N-CA	19.43	144.12	119.84
83	BQ	933	A	C2'-C3'-O3'	14.27	130.90	109.50
83	BQ	1808	G	C2'-C3'-O3'	13.57	129.86	109.50
83	BQ	1429	G	C2'-C3'-O3'	11.78	127.17	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](#)

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	2	37645	0	18938	405	0
2	A	1734	0	1817	17	0
3	B	1609	0	1675	18	0
4	C	813	0	800	9	0
5	D	877	0	883	8	0
6	E	977	0	1002	7	0
7	F	1105	0	1166	14	0
8	G	746	0	781	11	0
9	H	1192	0	1220	50	0
10	I	1112	0	1124	12	0
11	J	855	0	917	8	0
12	K	563	0	603	9	0
13	L	497	0	535	2	0
14	M	442	0	428	2	0
15	N	397	0	399	2	0
16	O	2436	0	2386	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	P	1577	0	1567	4	0
18	Q	1709	0	1784	10	0
19	R	1671	0	1768	13	0
20	S	2068	0	2154	15	0
21	T	1799	0	1879	43	0
22	U	1481	0	1572	16	0
23	V	1489	0	1525	35	0
24	W	1434	0	1511	8	0
25	X	1213	0	1257	7	0
26	Y	1192	0	1255	8	0
27	Z	891	0	883	4	0
28	a	684	0	672	3	0
29	b	1021	0	1060	4	0
30	c	1121	0	1196	10	0
31	d	1060	0	1123	33	0
32	e	769	0	818	5	0
33	f	610	0	633	1	0
34	g	473	0	518	1	0
35	l	692	0	347	5	0
36	m	1611	0	817	55	0
37	n	1644	0	831	65	0
38	h	8814	0	8710	45	0
39	i	9827	0	8617	109	0
40	j	2933	0	2695	21	0
40	k	2919	0	2682	17	0
41	AA	1804	0	1877	14	0
42	AB	1003	0	1048	12	0
43	AC	771	0	849	5	0
44	AD	1518	0	1587	14	0
45	AE	699	0	638	38	0
46	AF	681	0	684	8	0
47	AG	1353	0	1381	43	0
48	AH	964	0	1025	4	0
49	AI	612	0	682	1	0
50	AJ	1543	0	1608	8	0
51	AK	993	0	1081	5	0
52	AL	436	0	475	2	0
53	AM	1053	0	1149	4	0
54	AN	1092	0	1155	9	0
55	AO	417	0	459	1	0
56	AP	847	0	918	35	0
57	AQ	1720	0	1779	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AR	1173	0	1215	13	0
59	AS	233	0	282	57	0
60	AT	694	0	738	11	0
61	AU	1555	0	1659	3	0
62	AV	462	0	491	2	0
63	AW	1914	0	1980	53	0
64	AX	1420	0	1437	15	0
65	AY	742	0	797	4	0
66	AZ	1050	0	245	1	0
67	BA	3075	0	3142	35	0
68	BB	1441	0	1543	18	0
69	BC	876	0	912	10	0
70	BD	1770	0	1808	27	0
71	BE	2748	0	2859	18	0
72	BF	1521	0	1611	72	0
73	BG	1020	0	1090	5	0
74	BH	1445	0	1487	10	0
75	BI	2375	0	2325	15	0
76	BJ	1276	0	1323	7	0
77	BK	850	0	880	8	0
78	BL	796	0	812	2	0
79	BM	1239	0	1326	11	0
80	BN	880	0	945	5	0
81	BO	1784	0	1862	13	0
82	BP	969	0	1078	5	0
83	BQ	67695	0	34019	506	0
84	BR	2579	0	1304	16	0
85	BS	3352	0	1695	19	0
86	BT	1143	0	1103	99	0
All	All	229285	0	172911	1849	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 5.

The worst 5 of 1849 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)
83:BQ:2418:G:C2	86:BT:73:LEU:HD11	1.29	1.63
39:i:147:GLN:NE2	39:i:177:LEU:CD1	1.68	1.52
31:d:125:LEU:CB	31:d:128:LYS:HE2	1.41	1.49
1:2:1645:G:C5'	83:BQ:2255:A:N6	1.76	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:815:G:N3	72:BF:162:ARG:CZ	1.82	1.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	221/240 (92%)	194 (88%)	24 (11%)	3 (1%)	9	37
3	B	204/225 (91%)	172 (84%)	24 (12%)	8 (4%)	2	20
4	C	94/105 (90%)	72 (77%)	16 (17%)	6 (6%)	1	14
5	D	119/143 (83%)	92 (77%)	17 (14%)	10 (8%)	0	9
6	E	122/142 (86%)	101 (83%)	18 (15%)	3 (2%)	4	28
7	F	139/143 (97%)	119 (86%)	15 (11%)	5 (4%)	2	22
8	G	87/136 (64%)	73 (84%)	11 (13%)	3 (3%)	3	23
9	H	143/146 (98%)	123 (86%)	17 (12%)	3 (2%)	5	31
10	I	141/144 (98%)	112 (79%)	21 (15%)	8 (6%)	1	15
11	J	105/121 (87%)	94 (90%)	10 (10%)	1 (1%)	12	43
12	K	68/108 (63%)	54 (79%)	9 (13%)	5 (7%)	1	11
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	14
16	O	316/319 (99%)	274 (87%)	37 (12%)	5 (2%)	7	35
17	P	204/252 (81%)	176 (86%)	20 (10%)	8 (4%)	2	20
18	Q	212/255 (83%)	170 (80%)	31 (15%)	11 (5%)	1	17
19	R	218/254 (86%)	184 (84%)	30 (14%)	4 (2%)	6	33
20	S	258/261 (99%)	213 (83%)	36 (14%)	9 (4%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	T	224/236 (95%)	188 (84%)	29 (13%)	7 (3%)	3	25
22	U	182/190 (96%)	142 (78%)	31 (17%)	9 (5%)	1	17
23	V	184/200 (92%)	128 (70%)	30 (16%)	26 (14%)	0	3
24	W	176/197 (89%)	149 (85%)	21 (12%)	6 (3%)	3	23
25	X	153/156 (98%)	129 (84%)	17 (11%)	7 (5%)	2	18
26	Y	148/151 (98%)	134 (90%)	11 (7%)	3 (2%)	6	32
27	Z	125/137 (91%)	103 (82%)	17 (14%)	5 (4%)	2	20
28	a	85/87 (98%)	67 (79%)	14 (16%)	4 (5%)	2	18
29	b	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	4	29
30	c	142/145 (98%)	120 (84%)	21 (15%)	1 (1%)	18	51
31	d	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	1	16
32	e	95/119 (80%)	70 (74%)	17 (18%)	8 (8%)	0	9
33	f	79/82 (96%)	61 (77%)	14 (18%)	4 (5%)	1	17
34	g	58/63 (92%)	48 (83%)	8 (14%)	2 (3%)	3	23
38	h	1107/1287 (86%)	965 (87%)	124 (11%)	18 (2%)	7	35
39	i	1355/1432 (95%)	1158 (86%)	172 (13%)	25 (2%)	6	33
40	j	388/397 (98%)	335 (86%)	46 (12%)	7 (2%)	6	33
40	k	382/397 (96%)	333 (87%)	40 (10%)	9 (2%)	4	29
41	AA	231/256 (90%)	194 (84%)	32 (14%)	5 (2%)	5	30
42	AB	134/137 (98%)	117 (87%)	14 (10%)	3 (2%)	5	30
43	AC	97/100 (97%)	80 (82%)	13 (13%)	4 (4%)	2	20
44	AD	189/191 (99%)	166 (88%)	19 (10%)	4 (2%)	5	31
45	AE	96/155 (62%)	73 (76%)	18 (19%)	5 (5%)	1	17
46	AF	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	10	40
47	AG	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	2	22
48	AH	119/142 (84%)	103 (87%)	14 (12%)	2 (2%)	7	34
49	AI	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	9	38
50	AJ	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	3	25
51	AK	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
52	AL	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	5	31
53	AM	134/138 (97%)	119 (89%)	12 (9%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AN	133/136 (98%)	118 (89%)	10 (8%)	5 (4%)	2	21
55	AO	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	2	20
56	AP	103/106 (97%)	86 (84%)	16 (16%)	1 (1%)	12	43
57	AQ	201/204 (98%)	175 (87%)	21 (10%)	5 (2%)	4	28
58	AR	146/149 (98%)	118 (81%)	21 (14%)	7 (5%)	2	17
59	AS	23/25 (92%)	23 (100%)	0	0	100	100
60	AT	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	11	41
61	AU	195/199 (98%)	177 (91%)	15 (8%)	3 (2%)	8	36
62	AV	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	6	33
63	AW	250/254 (98%)	218 (87%)	31 (12%)	1 (0%)	30	62
64	AX	181/184 (98%)	158 (87%)	19 (10%)	4 (2%)	5	30
65	AY	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	11	41
67	BA	384/387 (99%)	332 (86%)	41 (11%)	11 (3%)	3	25
68	BB	183/186 (98%)	163 (89%)	17 (9%)	3 (2%)	7	35
69	BC	107/113 (95%)	94 (88%)	11 (10%)	2 (2%)	6	32
70	BD	218/221 (99%)	185 (85%)	24 (11%)	9 (4%)	2	20
71	BE	359/362 (99%)	306 (85%)	38 (11%)	15 (4%)	2	19
72	BF	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	7	35
73	BG	125/130 (96%)	110 (88%)	13 (10%)	2 (2%)	7	35
74	BH	170/172 (99%)	151 (89%)	16 (9%)	3 (2%)	6	33
75	BI	294/297 (99%)	263 (90%)	22 (8%)	9 (3%)	3	25
76	BJ	157/160 (98%)	133 (85%)	18 (12%)	6 (4%)	2	21
77	BK	104/107 (97%)	93 (89%)	9 (9%)	2 (2%)	6	32
78	BL	98/121 (81%)	79 (81%)	16 (16%)	3 (3%)	3	25
79	BM	152/176 (86%)	137 (90%)	11 (7%)	4 (3%)	4	27
80	BN	110/121 (91%)	104 (94%)	3 (3%)	3 (3%)	4	27
81	BO	220/244 (90%)	199 (90%)	16 (7%)	5 (2%)	5	30
82	BP	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	45
86	BT	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	13
All	All	14299/15550 (92%)	12246 (86%)	1644 (12%)	409 (3%)	5	25

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%)	176 (97%)	6 (3%)	33 56
3	B	173/191 (91%)	159 (92%)	14 (8%)	11 35
4	C	88/98 (90%)	82 (93%)	6 (7%)	14 40
5	D	89/119 (75%)	83 (93%)	6 (7%)	15 41
6	E	101/118 (86%)	92 (91%)	9 (9%)	9 32
7	F	117/119 (98%)	112 (96%)	5 (4%)	26 50
8	G	80/124 (64%)	77 (96%)	3 (4%)	29 53
9	H	128/129 (99%)	116 (91%)	12 (9%)	8 30
10	I	115/116 (99%)	104 (90%)	11 (10%)	8 29
11	J	100/114 (88%)	95 (95%)	5 (5%)	22 47
12	K	61/89 (68%)	58 (95%)	3 (5%)	22 47
13	L	56/60 (93%)	54 (96%)	2 (4%)	31 54
14	M	47/49 (96%)	44 (94%)	3 (6%)	16 42
15	N	43/135 (32%)	41 (95%)	2 (5%)	23 48
16	O	259/262 (99%)	252 (97%)	7 (3%)	39 59
17	P	164/210 (78%)	159 (97%)	5 (3%)	36 57
18	Q	191/224 (85%)	183 (96%)	8 (4%)	26 50
19	R	180/205 (88%)	174 (97%)	6 (3%)	33 56
20	S	221/222 (100%)	216 (98%)	5 (2%)	44 63
21	T	188/201 (94%)	179 (95%)	9 (5%)	23 47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	U	165/170 (97%)	159 (96%)	6 (4%)	31	54
23	V	150/161 (93%)	131 (87%)	19 (13%)	4	21
24	W	152/166 (92%)	149 (98%)	3 (2%)	48	65
25	X	129/137 (94%)	125 (97%)	4 (3%)	35	57
26	Y	127/128 (99%)	121 (95%)	6 (5%)	23	48
27	Z	81/105 (77%)	77 (95%)	4 (5%)	22	47
28	a	74/74 (100%)	72 (97%)	2 (3%)	39	59
29	b	110/111 (99%)	108 (98%)	2 (2%)	51	67
30	c	119/120 (99%)	115 (97%)	4 (3%)	32	55
31	d	111/113 (98%)	103 (93%)	8 (7%)	13	39
32	e	83/101 (82%)	75 (90%)	8 (10%)	8	29
33	f	70/71 (99%)	69 (99%)	1 (1%)	59	70
34	g	50/54 (93%)	50 (100%)	0	100	100
38	h	936/1139 (82%)	900 (96%)	36 (4%)	29	53
39	i	849/1279 (66%)	830 (98%)	19 (2%)	45	63
40	j	296/347 (85%)	291 (98%)	5 (2%)	53	67
40	k	295/347 (85%)	288 (98%)	7 (2%)	43	62
41	AA	187/208 (90%)	179 (96%)	8 (4%)	26	50
42	AB	104/105 (99%)	99 (95%)	5 (5%)	23	47
43	AC	81/82 (99%)	75 (93%)	6 (7%)	13	38
44	AD	171/171 (100%)	166 (97%)	5 (3%)	37	58
45	AE	57/129 (44%)	57 (100%)	0	100	100
46	AF	70/71 (99%)	65 (93%)	5 (7%)	13	39
47	AG	147/150 (98%)	141 (96%)	6 (4%)	27	51
48	AH	104/118 (88%)	97 (93%)	7 (7%)	15	41
49	AI	68/69 (99%)	68 (100%)	0	100	100
50	AJ	154/159 (97%)	143 (93%)	11 (7%)	13	39
51	AK	109/110 (99%)	106 (97%)	3 (3%)	38	58
52	AL	45/46 (98%)	42 (93%)	3 (7%)	15	41
53	AM	107/109 (98%)	101 (94%)	6 (6%)	19	45
54	AN	115/116 (99%)	111 (96%)	4 (4%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	AO	47/116 (40%)	45 (96%)	2 (4%)	26	50
56	AP	90/91 (99%)	85 (94%)	5 (6%)	19	45
57	AQ	175/176 (99%)	168 (96%)	7 (4%)	28	52
58	AR	118/119 (99%)	114 (97%)	4 (3%)	32	55
59	AS	23/23 (100%)	21 (91%)	2 (9%)	9	33
60	AT	71/72 (99%)	69 (97%)	2 (3%)	38	58
61	AU	160/162 (99%)	155 (97%)	5 (3%)	35	57
62	AV	46/47 (98%)	44 (96%)	2 (4%)	26	50
63	AW	193/196 (98%)	186 (96%)	7 (4%)	31	54
64	AX	140/146 (96%)	135 (96%)	5 (4%)	31	54
65	AY	81/88 (92%)	77 (95%)	4 (5%)	22	47
67	BA	320/323 (99%)	305 (95%)	15 (5%)	23	48
68	BB	150/151 (99%)	145 (97%)	5 (3%)	33	56
69	BC	92/97 (95%)	83 (90%)	9 (10%)	7	29
70	BD	184/187 (98%)	172 (94%)	12 (6%)	15	42
71	BE	288/289 (100%)	278 (96%)	10 (4%)	32	54
72	BF	153/154 (99%)	142 (93%)	11 (7%)	13	39
73	BG	109/111 (98%)	106 (97%)	3 (3%)	38	58
74	BH	156/156 (100%)	150 (96%)	6 (4%)	29	53
75	BI	244/245 (100%)	235 (96%)	9 (4%)	30	54
76	BJ	136/137 (99%)	130 (96%)	6 (4%)	25	49
77	BK	90/91 (99%)	86 (96%)	4 (4%)	25	49
78	BL	87/107 (81%)	87 (100%)	0	100	100
79	BM	134/153 (88%)	129 (96%)	5 (4%)	30	54
80	BN	95/103 (92%)	93 (98%)	2 (2%)	47	64
81	BO	186/205 (91%)	182 (98%)	4 (2%)	45	63
82	BP	104/105 (99%)	101 (97%)	3 (3%)	37	58
86	BT	118/132 (89%)	113 (96%)	5 (4%)	26	50
All	All	11689/13228 (88%)	11205 (96%)	484 (4%)	28	51

5 of 484 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	i	174	ILE
74	BH	109	ASP
46	AF	13	ASN
73	BG	19	ARG
81	BO	46	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 215 such sidechains are listed below:

Mol	Chain	Res	Type
40	k	300	ASN
53	AM	56	GLN
76	BJ	16	GLN
41	AA	192	GLN
47	AG	68	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1800 (98%)	729 (41%)	100 (5%)
35	l	33/34 (97%)	21 (63%)	0
36	m	75/76 (98%)	34 (45%)	0
37	n	76/77 (98%)	30 (39%)	0
83	BQ	3162/3396 (93%)	1076 (34%)	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%)	1975 (36%)	294 (5%)

5 of 1975 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

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Mol	Chain	Res	Type
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	0.32	0	8,15,17	1.21	2 (25%)

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	-	7/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
86	BT	51	5CT	C1-NZ-CE	-2.34	108.27	113.38
86	BT	51	5CT	C4-C3-C2	-2.03	109.19	113.47

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	BT	51	5CT	O-C-CA-CB
86	BT	51	5CT	C2-C1-NZ-CE

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	BT	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
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

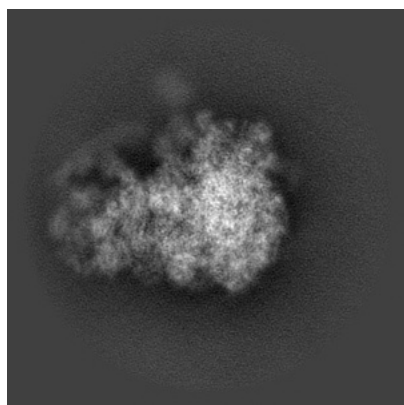
6 Map visualisation [i](#)

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.

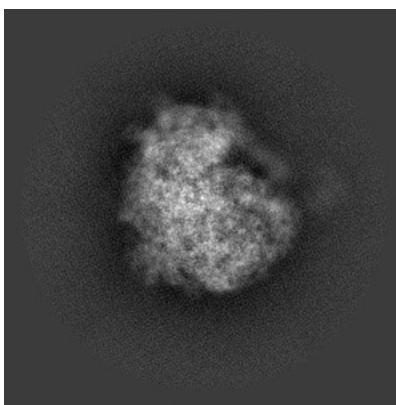
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

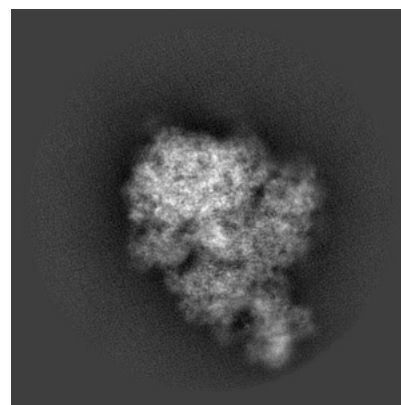
6.1.1 Primary map



X



Y

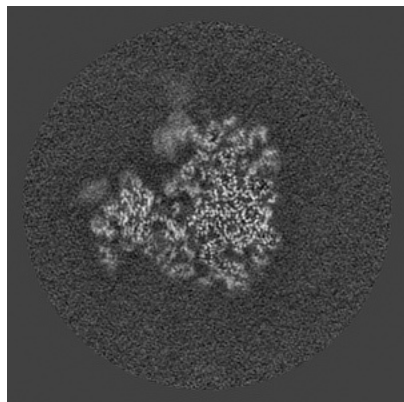


Z

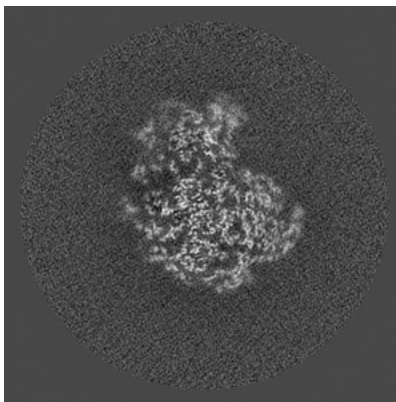
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

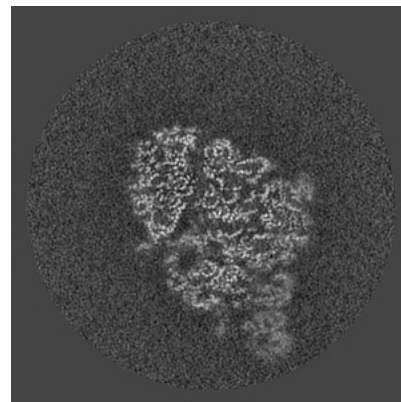
6.2.1 Primary map



X Index: 240



Y Index: 240

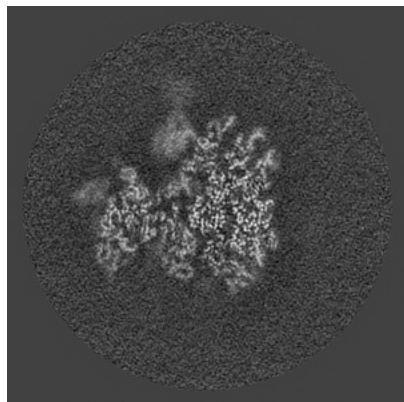


Z Index: 240

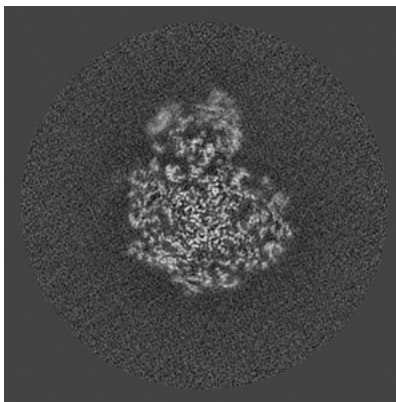
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

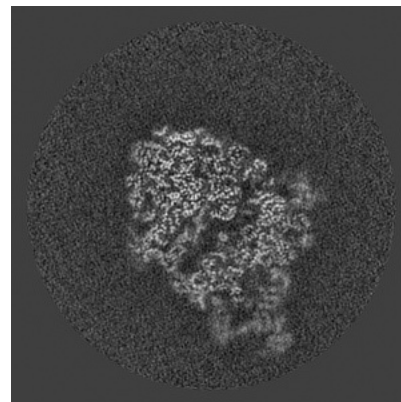
6.3.1 Primary map



X Index: 245



Y Index: 253

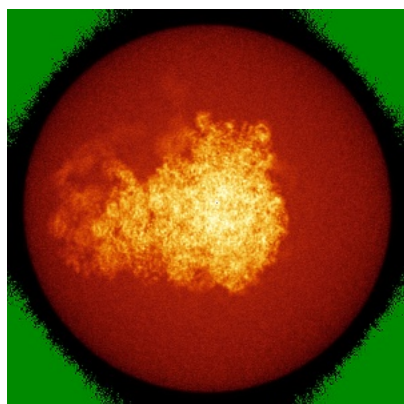


Z Index: 247

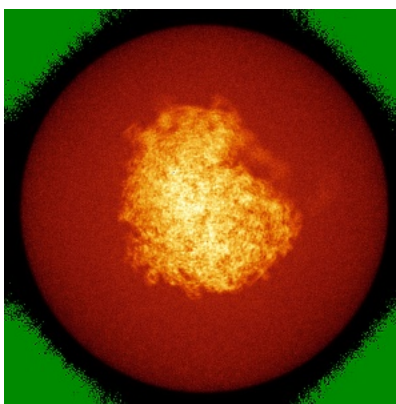
The images above show the largest variance slices of the map in three orthogonal directions.

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

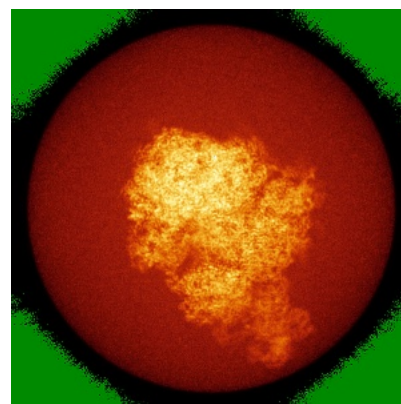
6.4.1 Primary map



X



Y

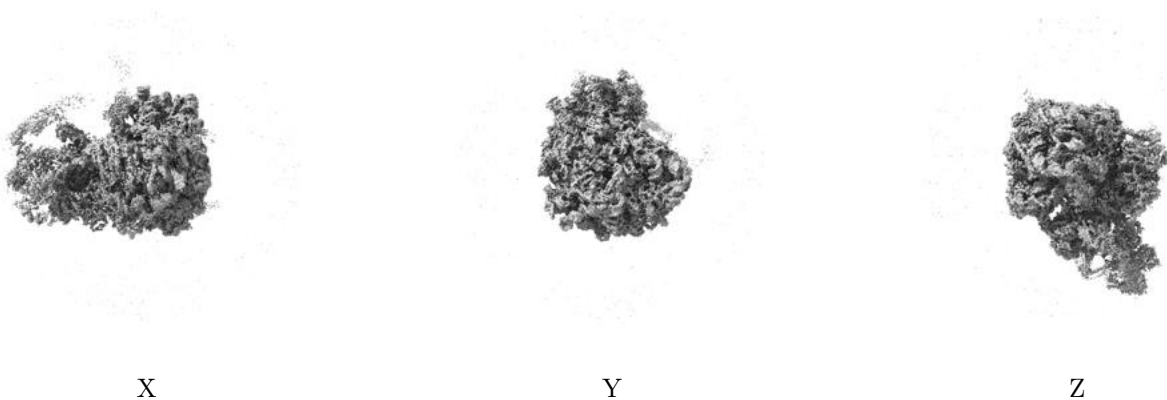


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

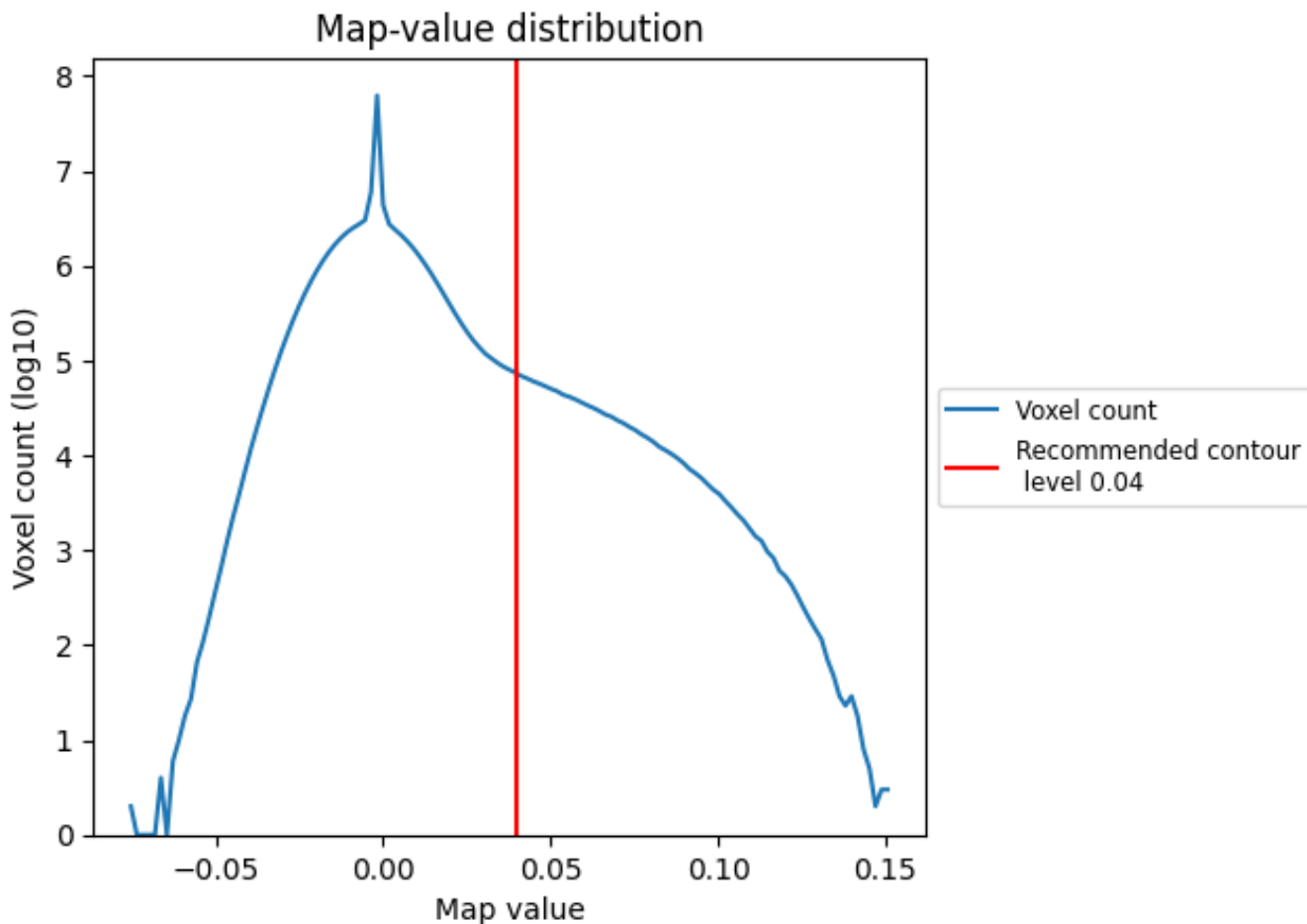
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

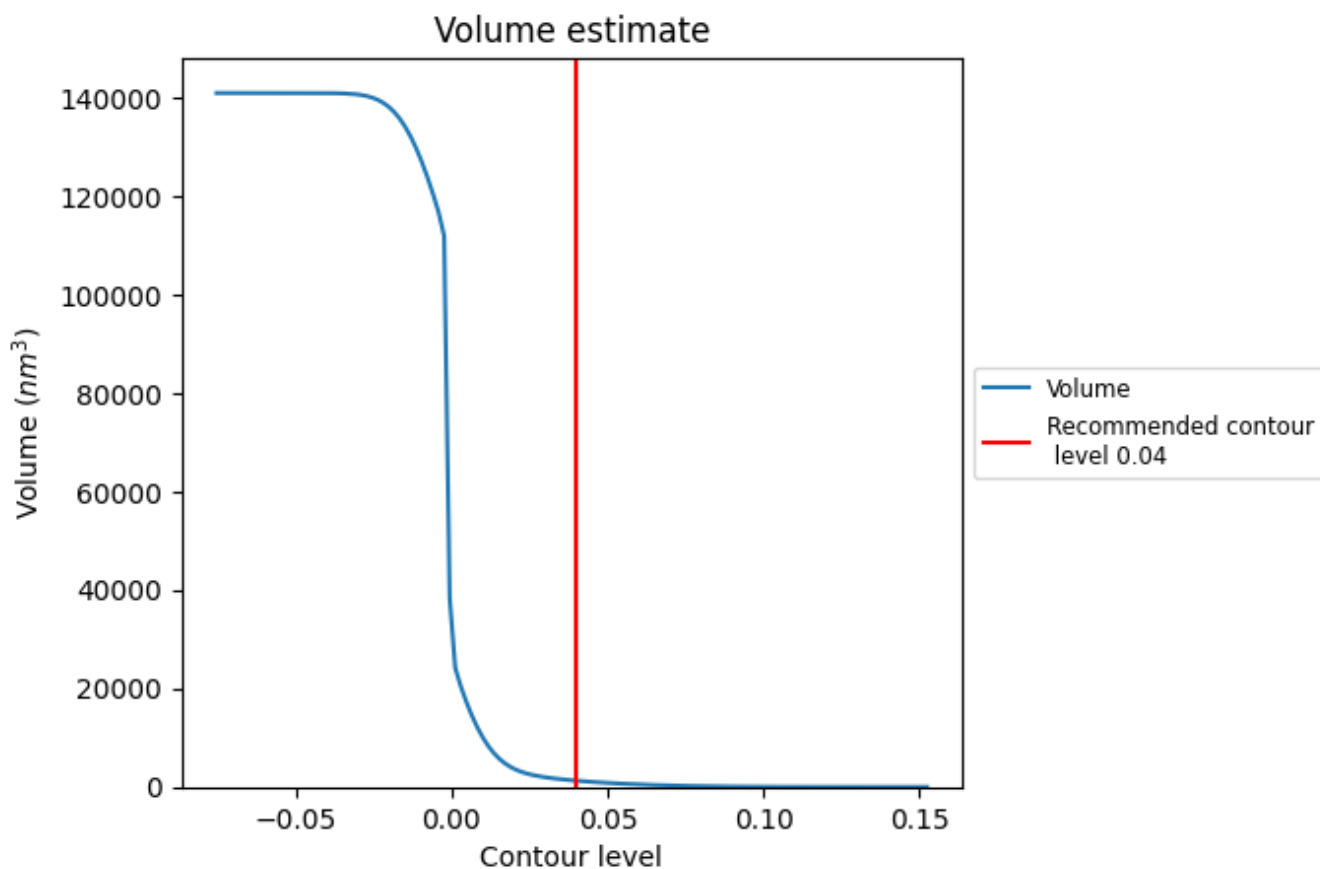
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

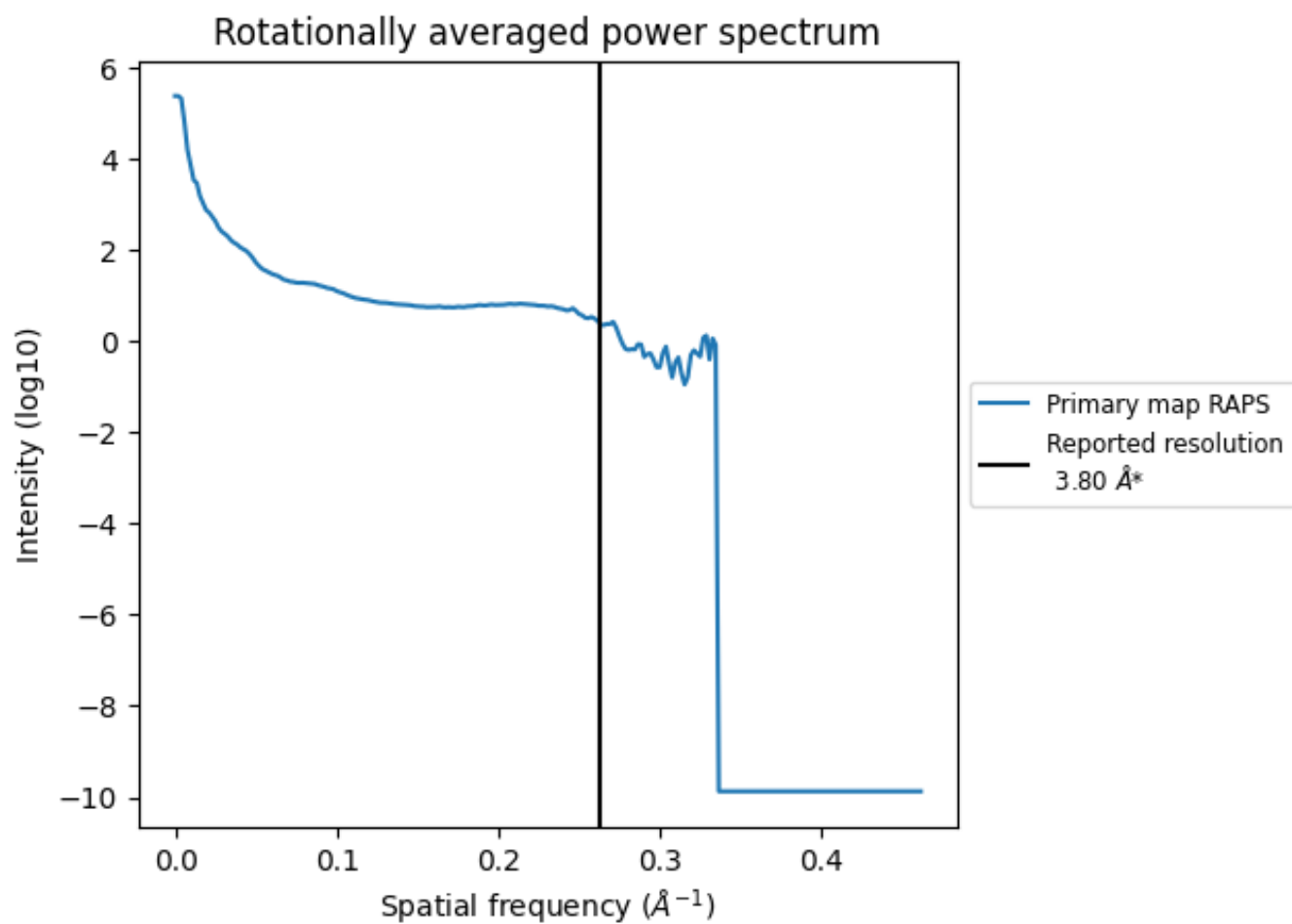
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1270 nm³; 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

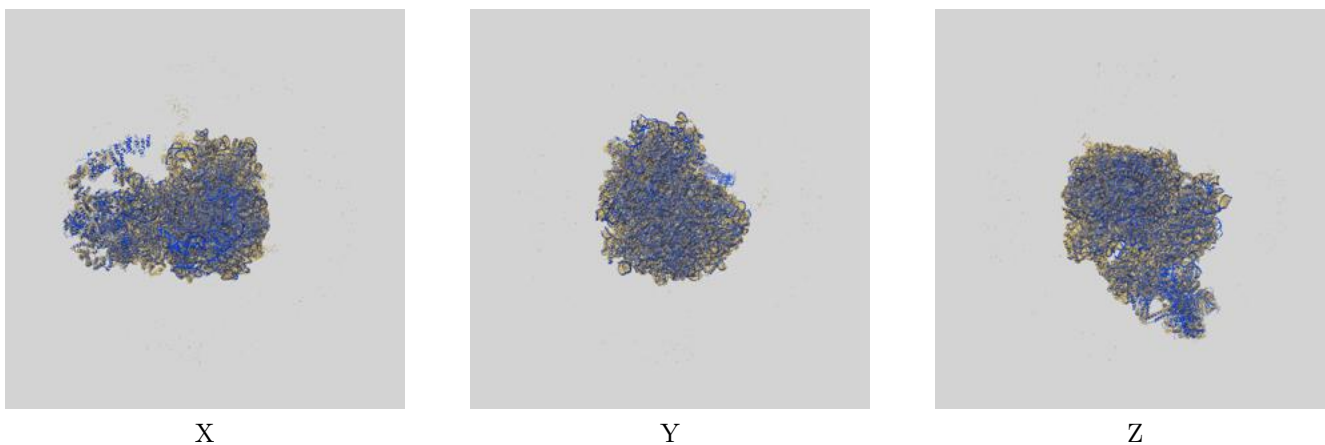
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

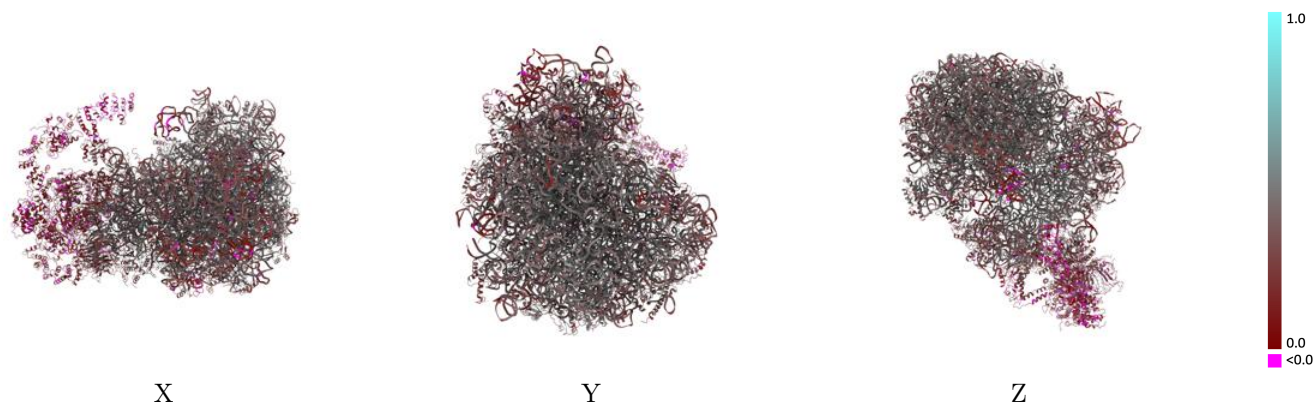
This section contains information regarding the fit between EMDB map EMD-3461 and PDB model 5MC6. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



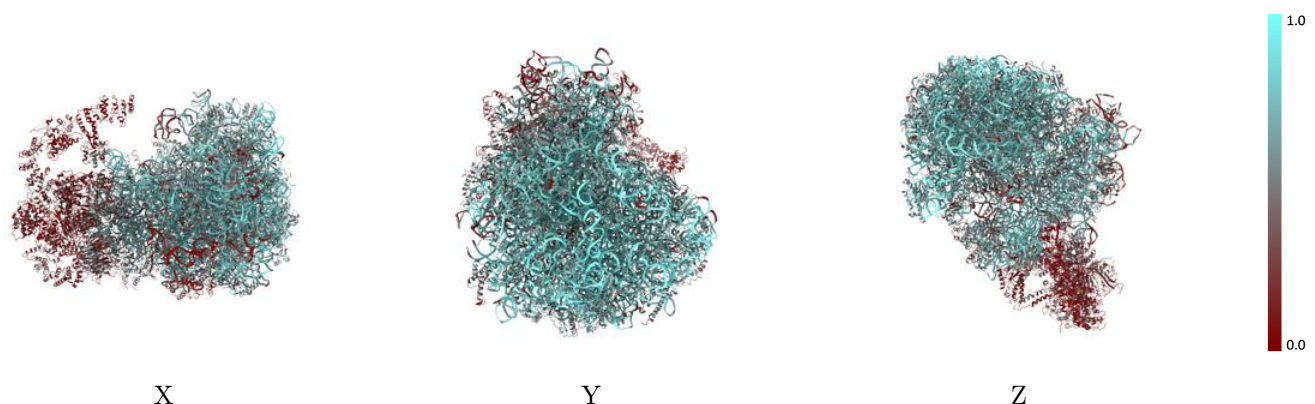
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



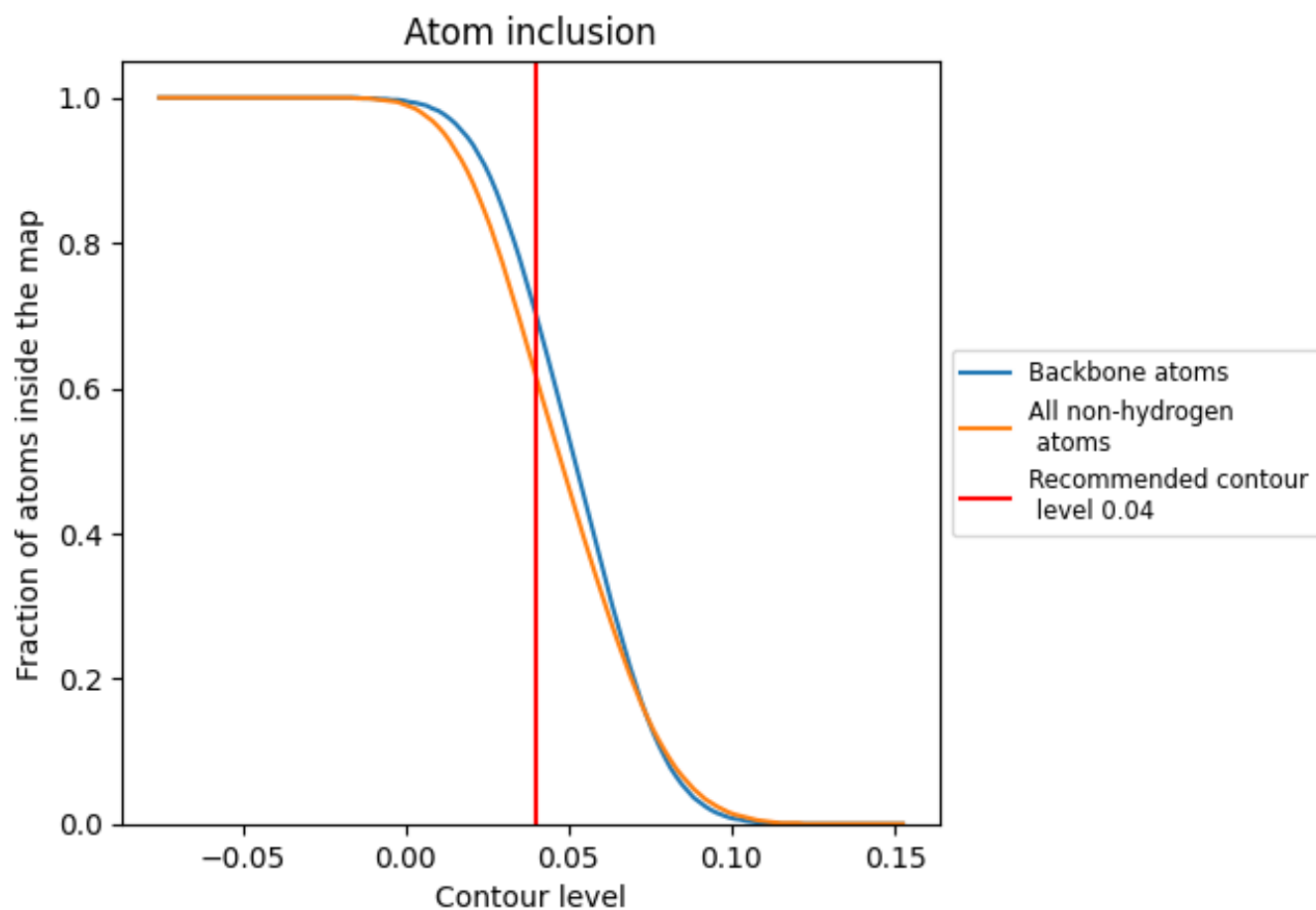
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.6170	 0.3620
2	 0.7280	 0.3590
A	 0.4940	 0.3910
AA	 0.5150	 0.3680
AB	 0.5170	 0.4220
AC	 0.5580	 0.3700
AD	 0.5210	 0.3780
AE	 0.4080	 0.3450
AF	 0.6690	 0.4610
AG	 0.5800	 0.3740
AH	 0.6240	 0.4290
AI	 0.5160	 0.3720
AJ	 0.5990	 0.3970
AK	 0.6430	 0.4260
AL	 0.6240	 0.4640
AM	 0.5590	 0.3630
AN	 0.5400	 0.3760
AO	 0.5860	 0.4030
AP	 0.5880	 0.4350
AQ	 0.6360	 0.4330
AR	 0.6320	 0.4220
AS	 0.4010	 0.3980
AT	 0.5590	 0.4280
AU	 0.5950	 0.4140
AV	 0.5690	 0.3950
AW	 0.5980	 0.4500
AX	 0.6260	 0.4410
AY	 0.5160	 0.3840
AZ	 0.1600	 0.3360
B	 0.4320	 0.3190
BA	 0.6070	 0.4230
BB	 0.6190	 0.4260
BC	 0.5780	 0.4330
BD	 0.5240	 0.3950
BE	 0.6270	 0.4240

























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Chain	Atom inclusion	Q-score
BF	0.5680	0.3980
BG	0.6020	0.4350
BH	0.5740	0.4020
BI	0.5980	0.3630
BJ	0.5690	0.4280
BK	0.6130	0.4340
BL	0.5360	0.3630
BM	0.5600	0.3760
BN	0.5850	0.4230
BO	0.6060	0.3950
BP	0.6190	0.3980
BQ	0.8210	0.4040
BR	0.8840	0.4050
BS	0.8620	0.4220
BT	0.1120	0.2900
C	0.4710	0.3480
D	0.2720	0.2450
E	0.4300	0.2960
F	0.5130	0.3470
G	0.4920	0.3700
H	0.4700	0.3120
I	0.4420	0.2390
J	0.4860	0.3610
K	0.4520	0.2770
L	0.3310	0.3320
M	0.6290	0.4270
N	0.2970	0.1920
O	0.4580	0.3280
P	0.5110	0.3600
Q	0.4160	0.3170
R	0.5480	0.4150
S	0.4370	0.3460
T	0.4160	0.3090
U	0.3130	0.2740
V	0.4670	0.2950
W	0.5200	0.3250
X	0.4480	0.3800
Y	0.4980	0.3600
Z	0.4840	0.3360
a	0.5000	0.3860
b	0.5380	0.4090
c	0.4940	0.4090

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Chain	Atom inclusion	Q-score
d	 0.4220	 0.2950
e	 0.4360	 0.3140
f	 0.4360	 0.3540
g	 0.4420	 0.3550
h	 0.1760	 0.2120
i	 0.1490	 0.1490
j	 0.1570	 0.1890
k	 0.2920	 0.2970
l	 0.3370	 0.3130
m	 0.6030	 0.3250
n	 0.6440	 0.3480