



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:01 AM UTC

PDB ID : 8T3C / pdb_00008t3c
EMDB ID : EMD-40999
Title : Hypomethylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2, GDP, and sordarin, Structure II
Authors : Zhao, Y.; Li, H.
Deposited on : 2023-06-07
Resolution : 3.86 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:

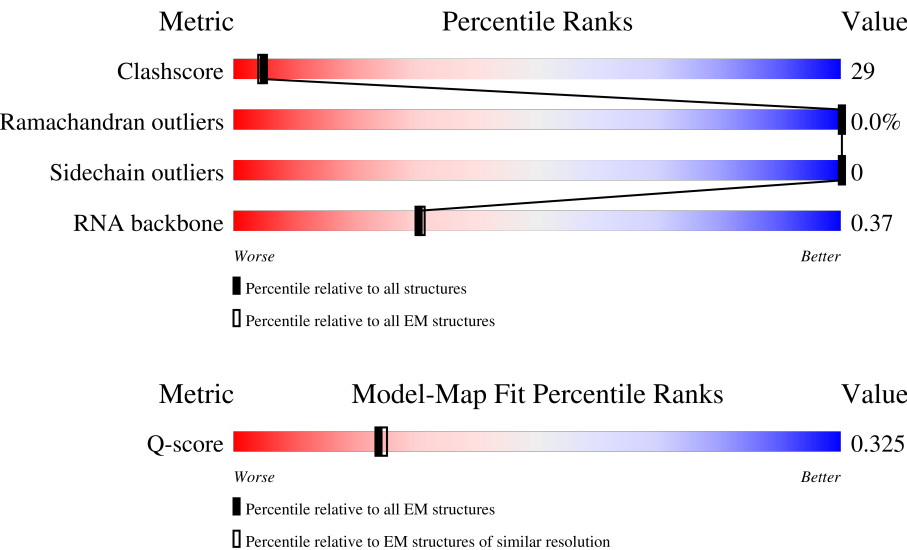
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.86 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	8889 (3.36 - 4.35)

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	BA	252	23% 42% 40% 18%
2	BB	255	48% 37% 47% 16%
3	BC	254	20% 38% 48% 15%

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Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	

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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	222	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

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Mol	Chain	Length	Quality of chain
54	AR	189	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	

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Mol	Chain	Length	Quality of chain
79	E	217	
80	DC	842	
81	EC	202	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
85	SO1	DC	903	X	-	-	-

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 212449 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	BA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BG	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	BH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

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

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 12 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 13 is a protein called RPS22A isoform 1.

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

- Molecule 14 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 16 is a protein called RPS26B isoform 1.

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

- Molecule 17 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Be	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 22 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 27 is a protein called RPS20 isoform 1.

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

- Molecule 28 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	71	Total	C	N	O	0	0
			574	366	108	100		

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

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

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	75	Total	C	N	O	S	0	0
			605	386	116	99	4		

- Molecule 33 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 34 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	1757	Total	C	N	O	P	1	0
			37463	16754	6635	12317	1757		

- Molecule 35 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

- Molecule 38 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3216	Total	C	N	O	P	0	0
			68786	30729	12387	22454	3216		

- Molecule 39 is a RNA chain called 5s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 40 is a RNA chain called 5.8 S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 41 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 42 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AE	167	Total	C	N	O	S	0	0
			1303	840	234	228	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	120	LYS	ASN	conflict	UNP Q02326

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AG	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 46 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	222	Total	C	N	O	S	0	0
			1804	1147	339	310	8		

- Molecule 47 is a protein called RPL11A isoform 1.

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

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	AP	175	Total	C	N	O		
			1388	862	277	249	0	0

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L20.

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

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AX	121	Total	C	N	O	S	0	0
			968	623	170	173	2		

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AY	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ac	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ad	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 67 is a protein called RPL32 isoform 1.

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

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	E	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DC	824	Total	C	N	O	S	0	0
			6419	4085	1096	1208	30		

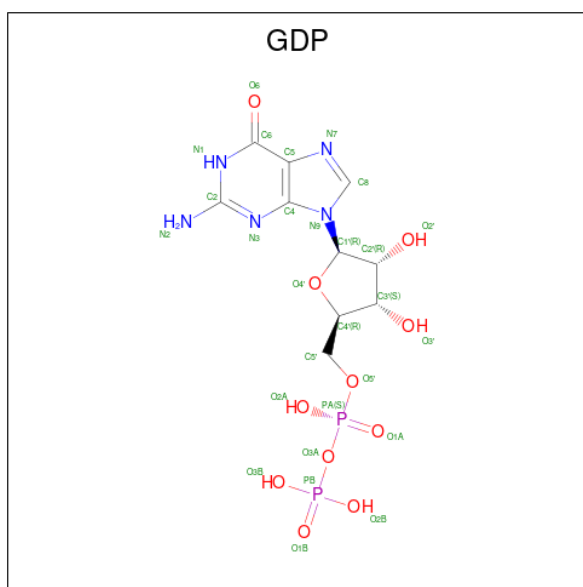
- Molecule 81 is a RNA chain called TSV IRES.

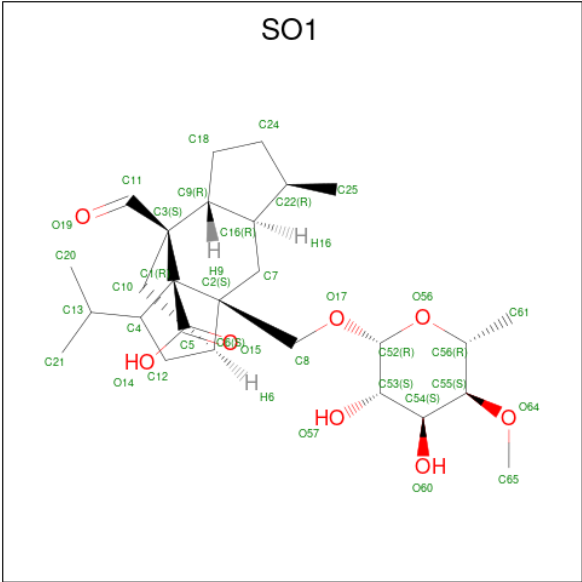
Mol	Chain	Residues	Atoms					AltConf	Trace
81	EC	200	Total	C	N	O	P	0	0
			4235	1891	751	1393	200		

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	Ao	1	Total	Zn	0
			1	1	

- Molecule 83 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



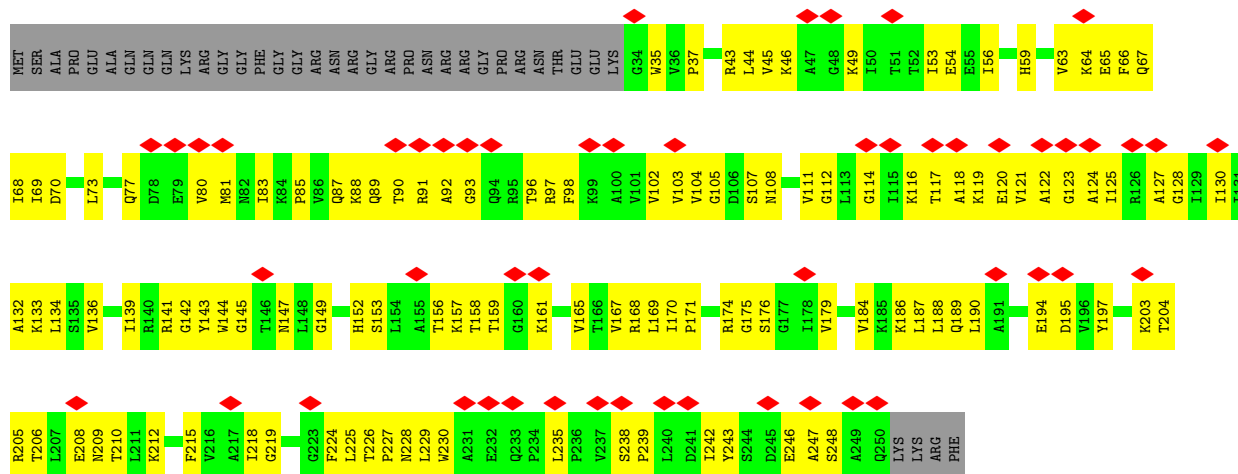


Mol	Chain	Residues	Atoms			AltConf
85	DC	1	Total	C	O	0
			35	27	8	

PHE
LYS
ASP
GLU
PRO
VAL
LEU
GLU
THR
VAL

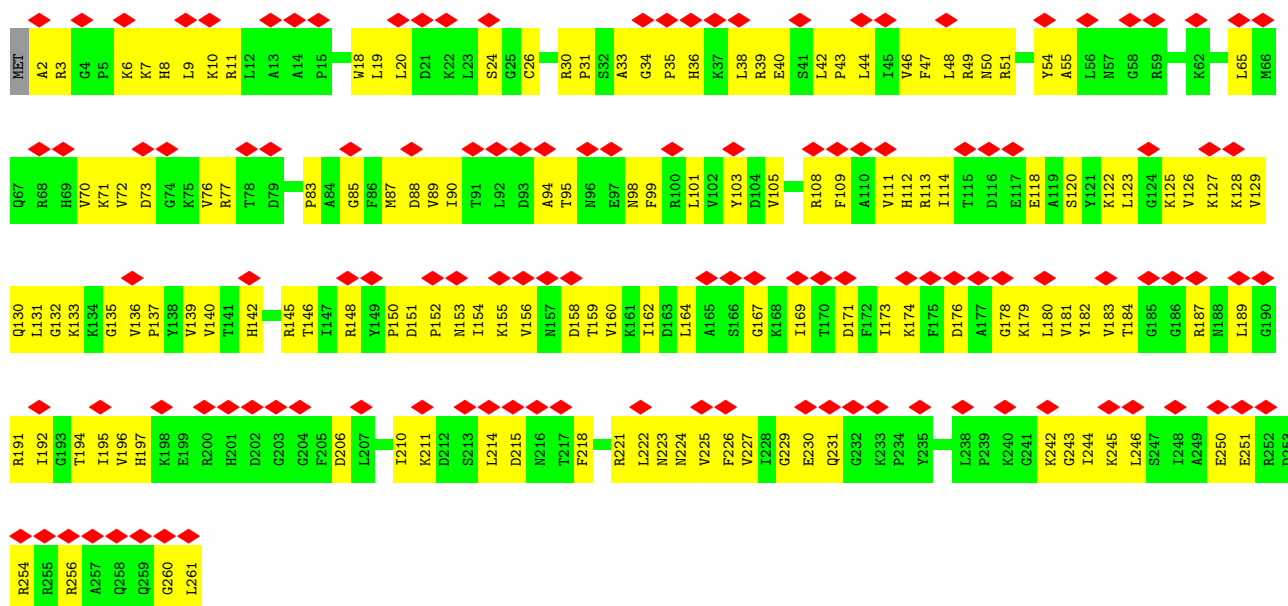
• Molecule 3: RPS2 isoform 1

Chain BC: 20% 38% 48% 15%



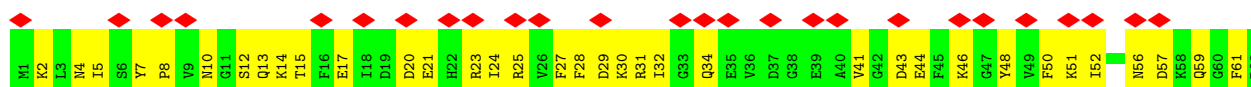
• Molecule 4: 40S ribosomal protein S4-A

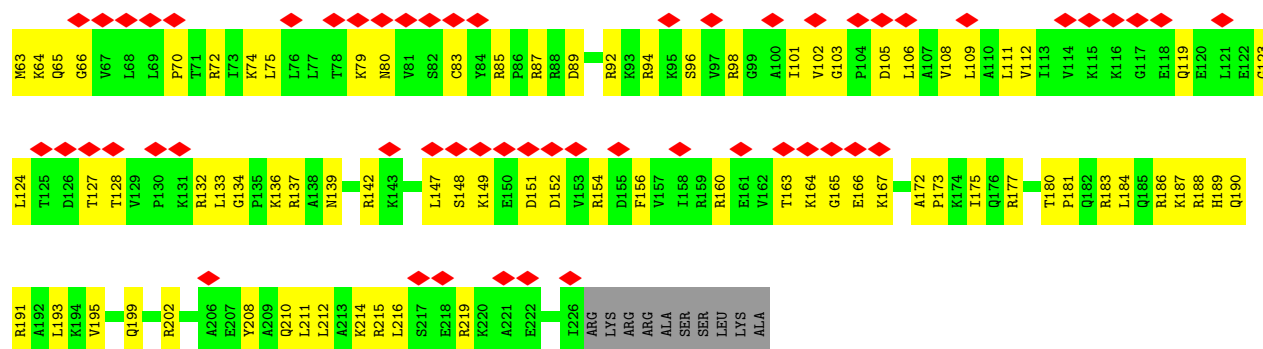
Chain BE: 47% 46% 54%



• Molecule 5: 40S ribosomal protein S6-A

Chain BG: 34% 48% 48%

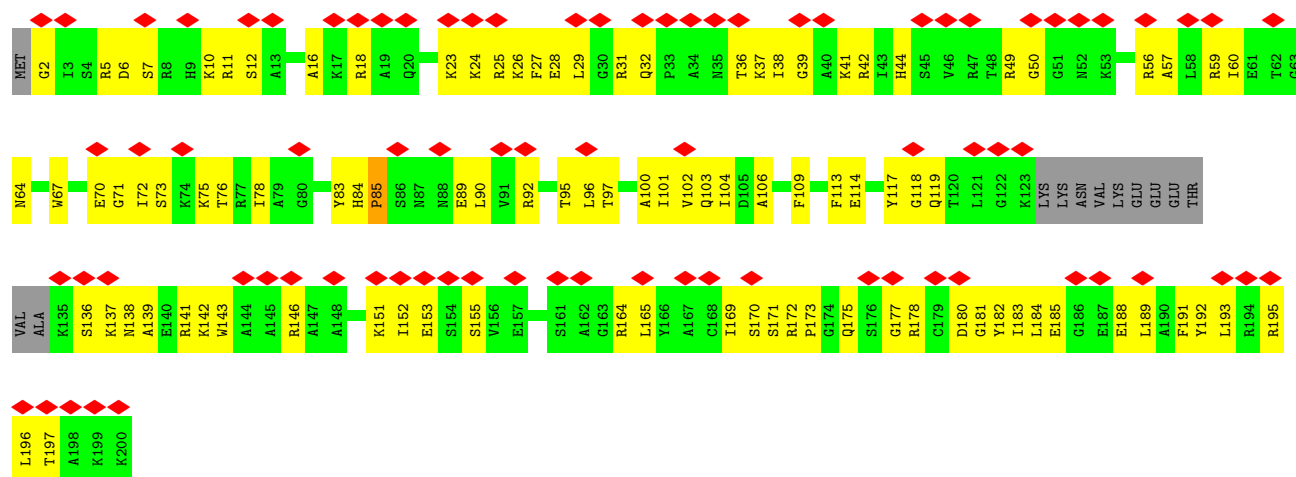




• Molecule 6: 40S ribosomal protein S7-A

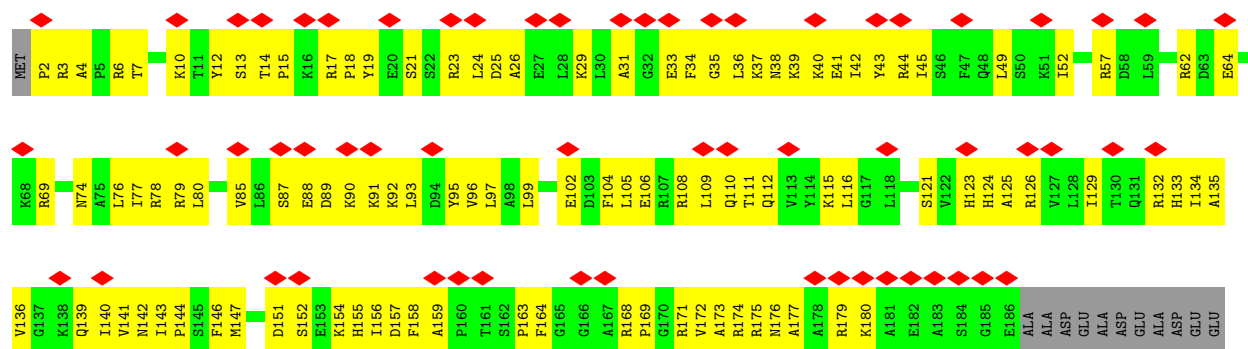


• Molecule 7: 40S ribosomal protein S8-A

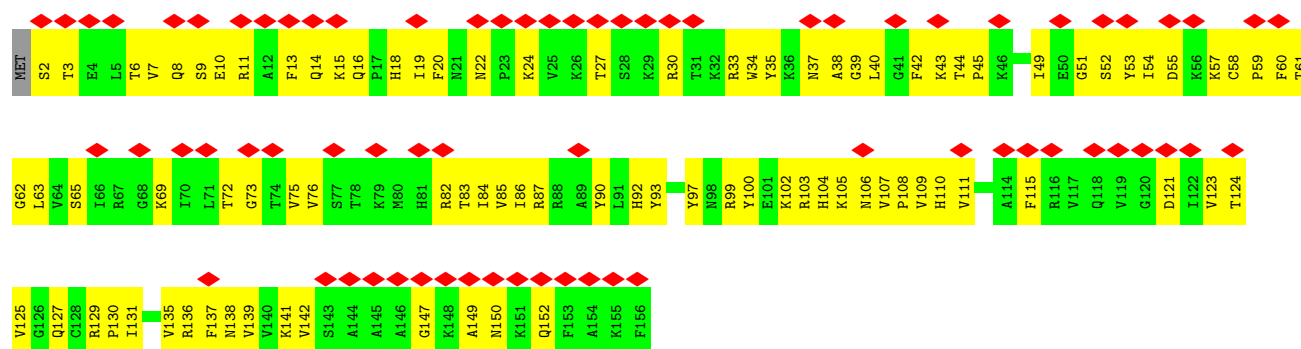


• Molecule 8: 40S ribosomal protein S9-A

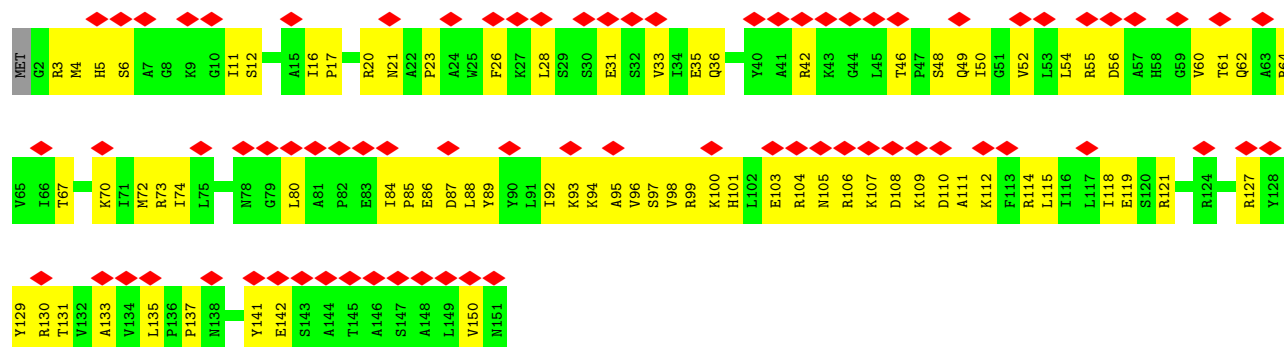




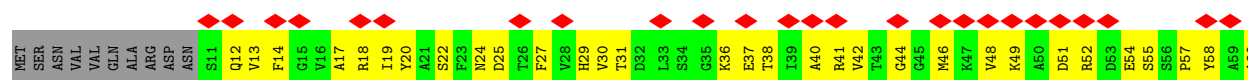
• Molecule 9: 40S ribosomal protein S11-A

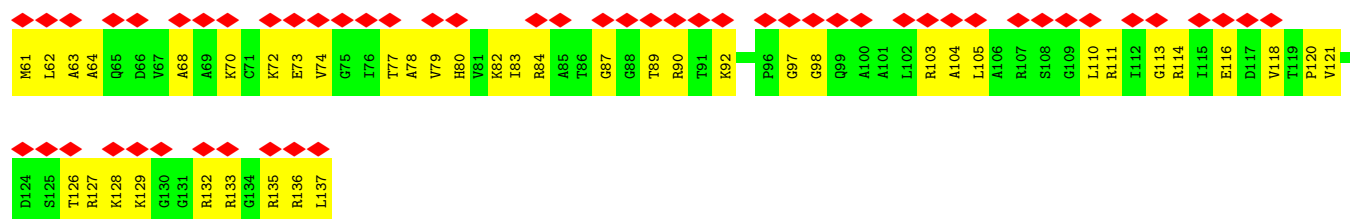


• Molecule 10: 40S ribosomal protein S13



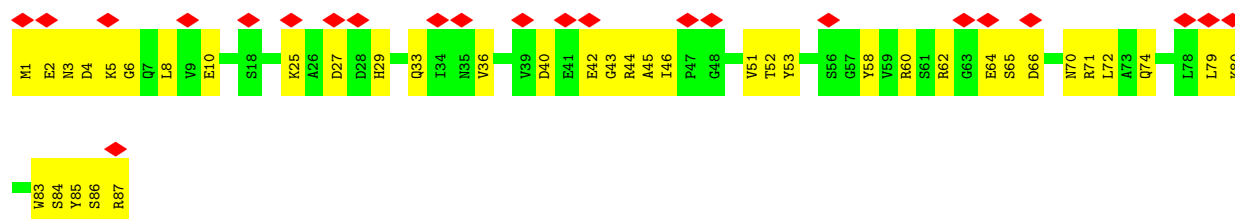
• Molecule 11: 40S ribosomal protein S14-A





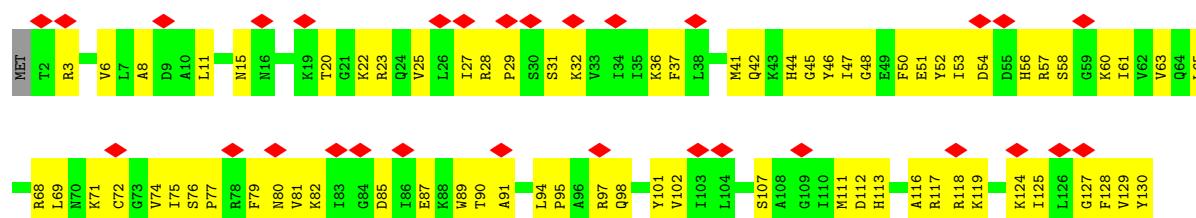
• Molecule 12: 40S ribosomal protein S21-A

Chain BV:



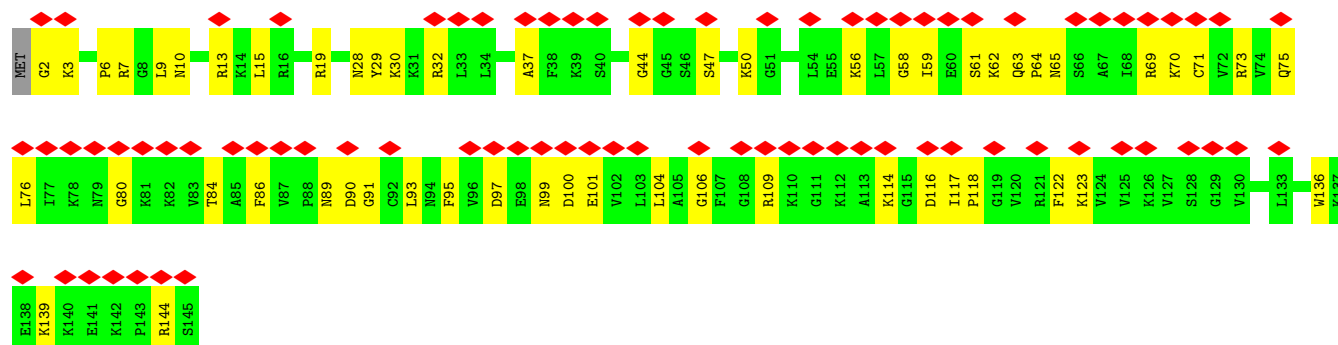
• Molecule 13: RPS22A isoform 1

Chain BW:



• Molecule 14: 40S ribosomal protein S23-A

Chain BX:

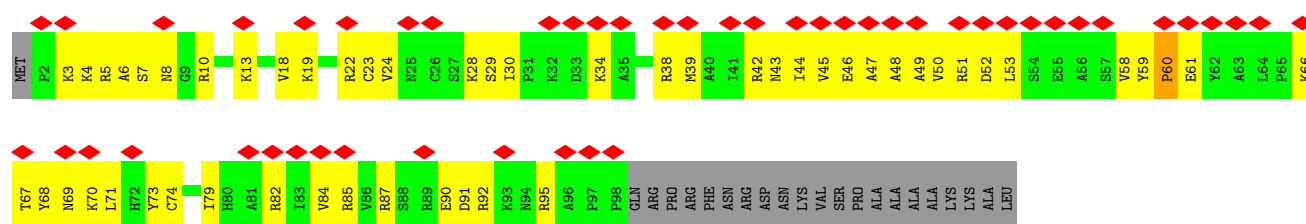
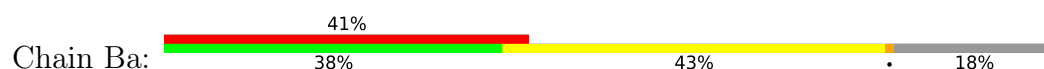


• Molecule 15: 40S ribosomal protein S24-A

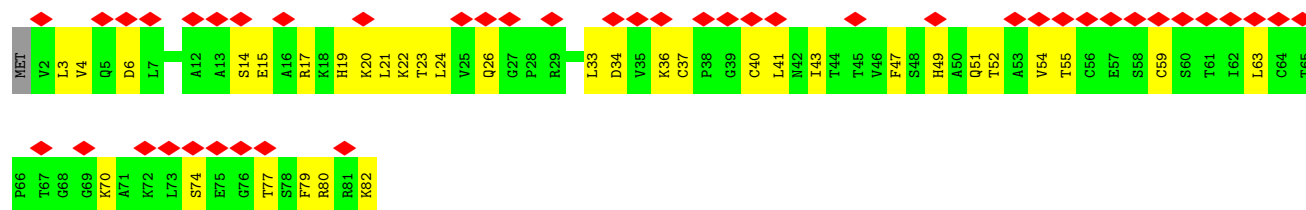
Chain BY:



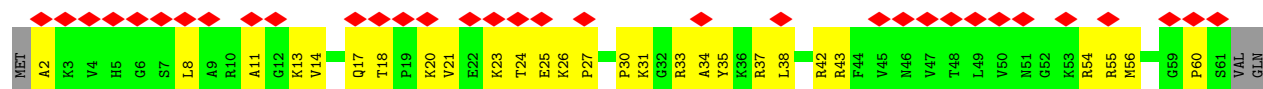
• Molecule 16: RPS26B isoform 1



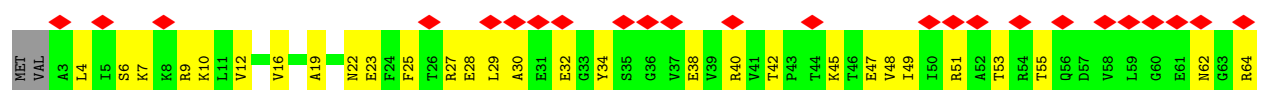
• Molecule 17: 40S ribosomal protein S27-A

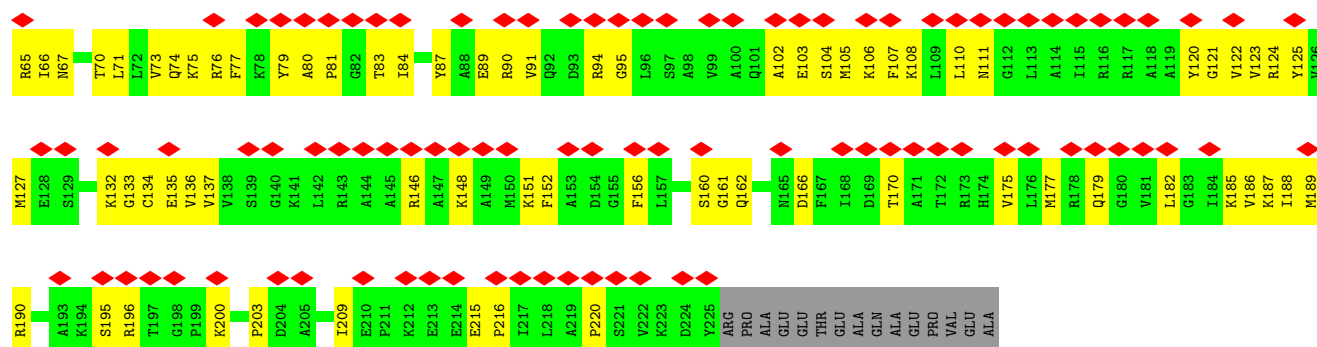


• Molecule 18: 40S ribosomal protein S30-A

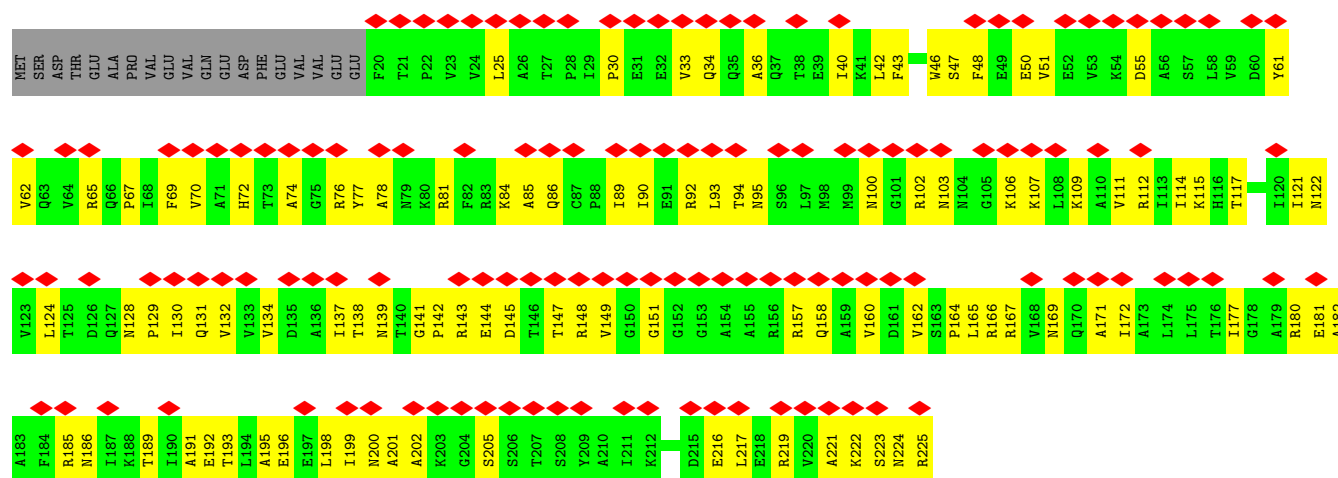


• Molecule 19: RPS3 isoform 1

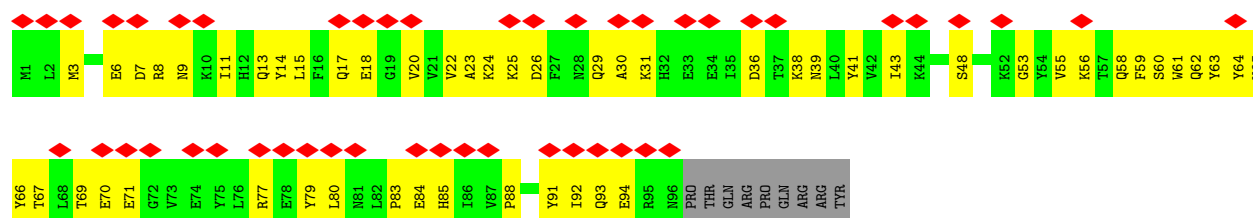
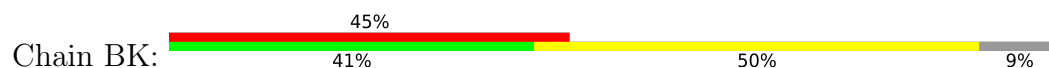




• Molecule 20: Rps5p

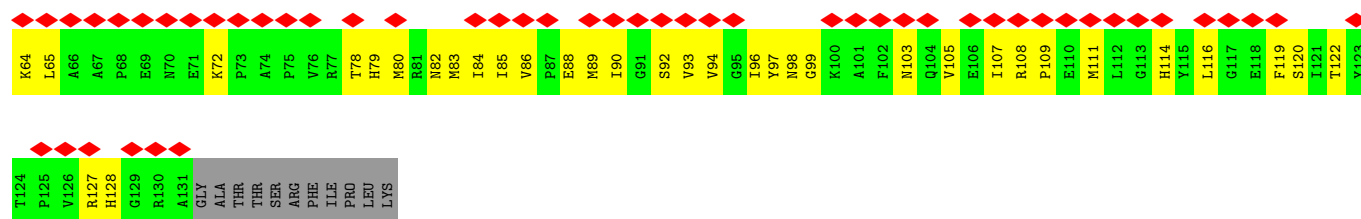


• Molecule 21: 40S ribosomal protein S10-A

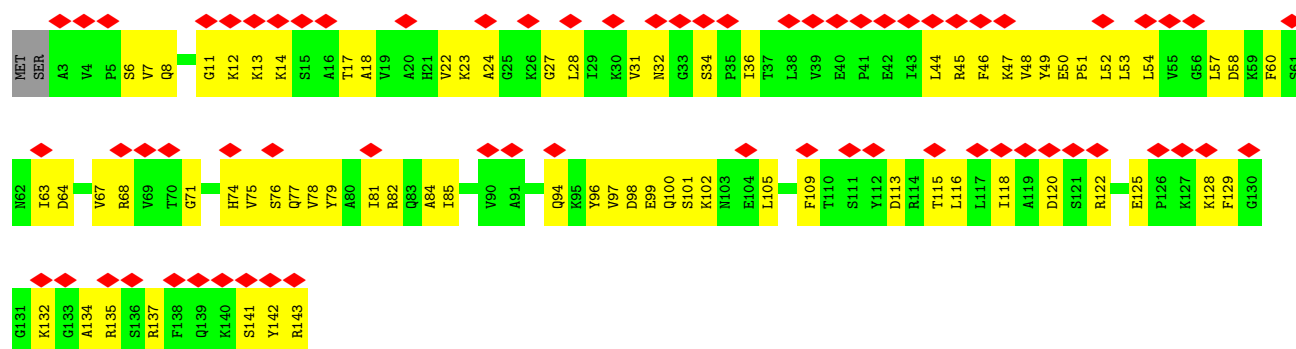


• Molecule 22: RPS15 isoform 1

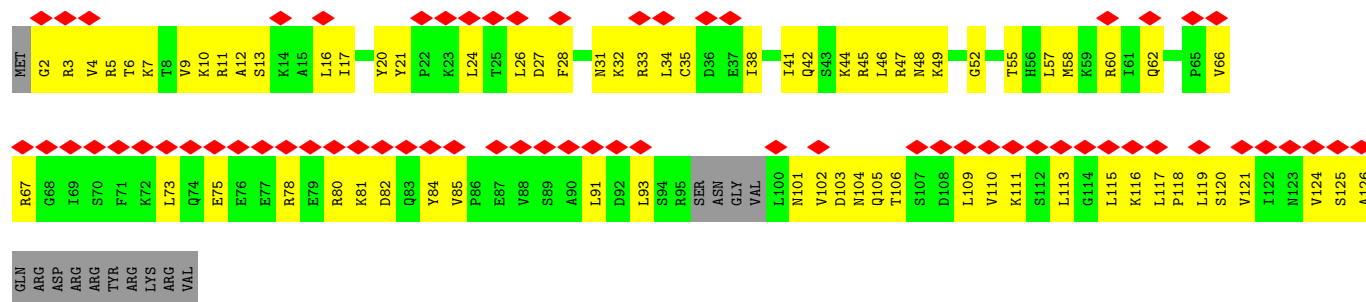
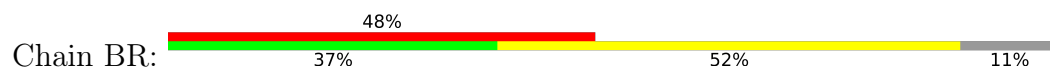




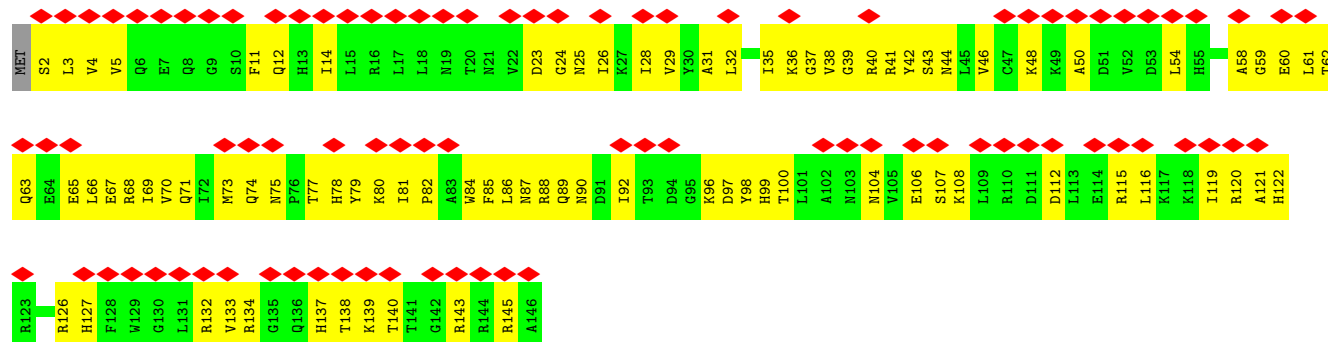
• Molecule 23: 40S ribosomal protein S16-A



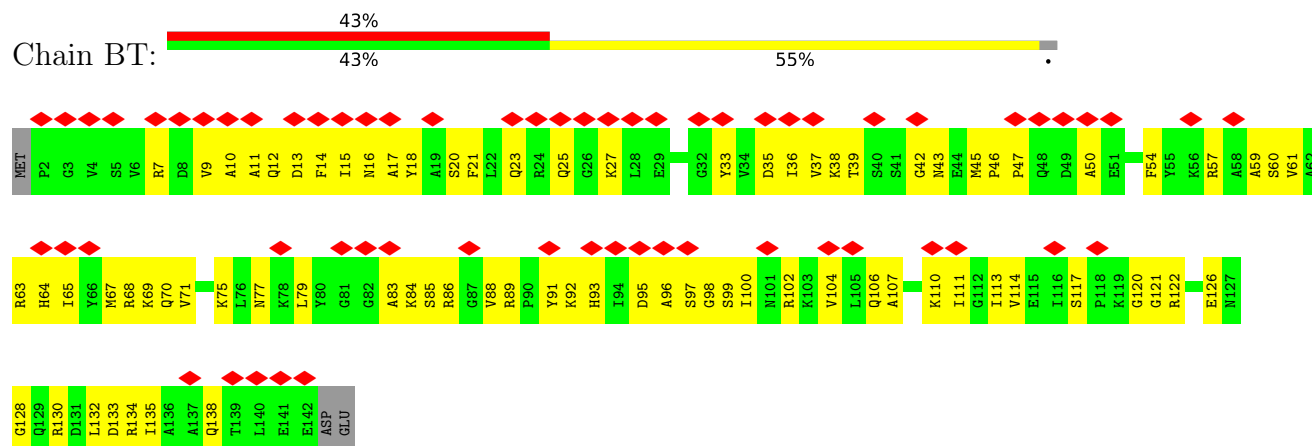
• Molecule 24: 40S ribosomal protein S17-A



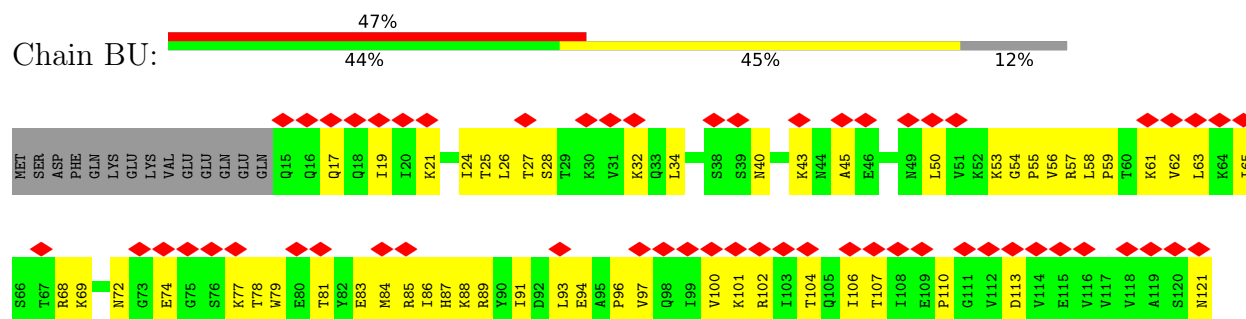
• Molecule 25: 40S ribosomal protein S18-A



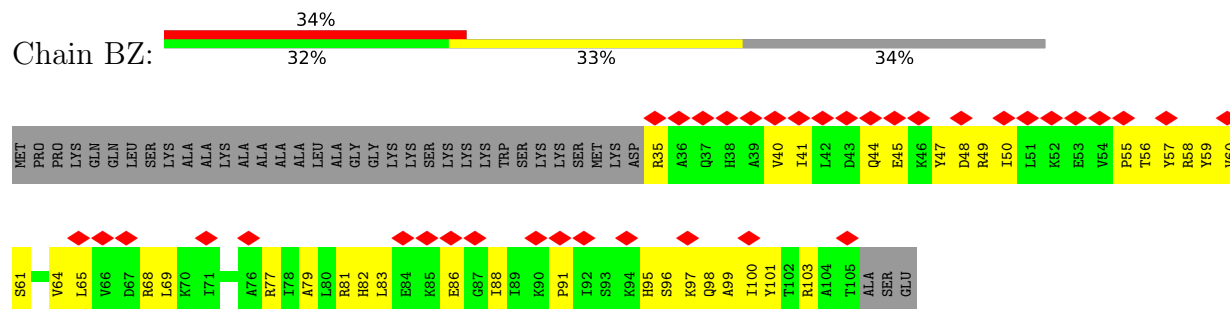
- Molecule 26: 40S ribosomal protein S19-A



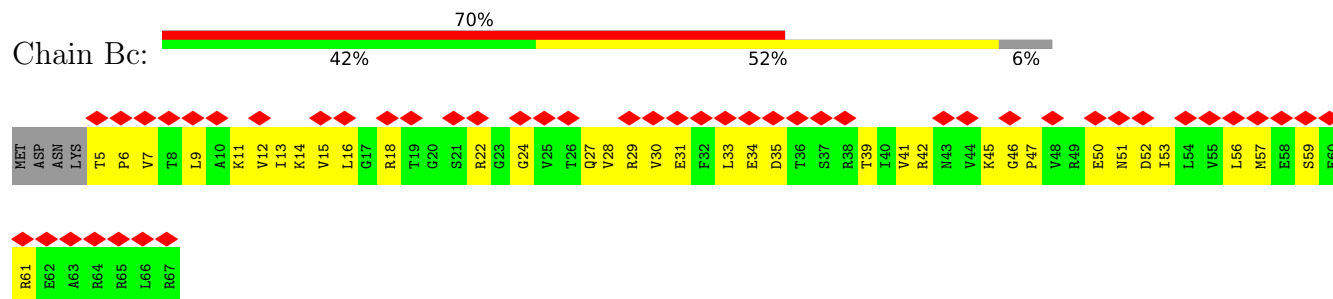
- Molecule 27: RPS20 isoform 1



- Molecule 28: RPS25A isoform 1



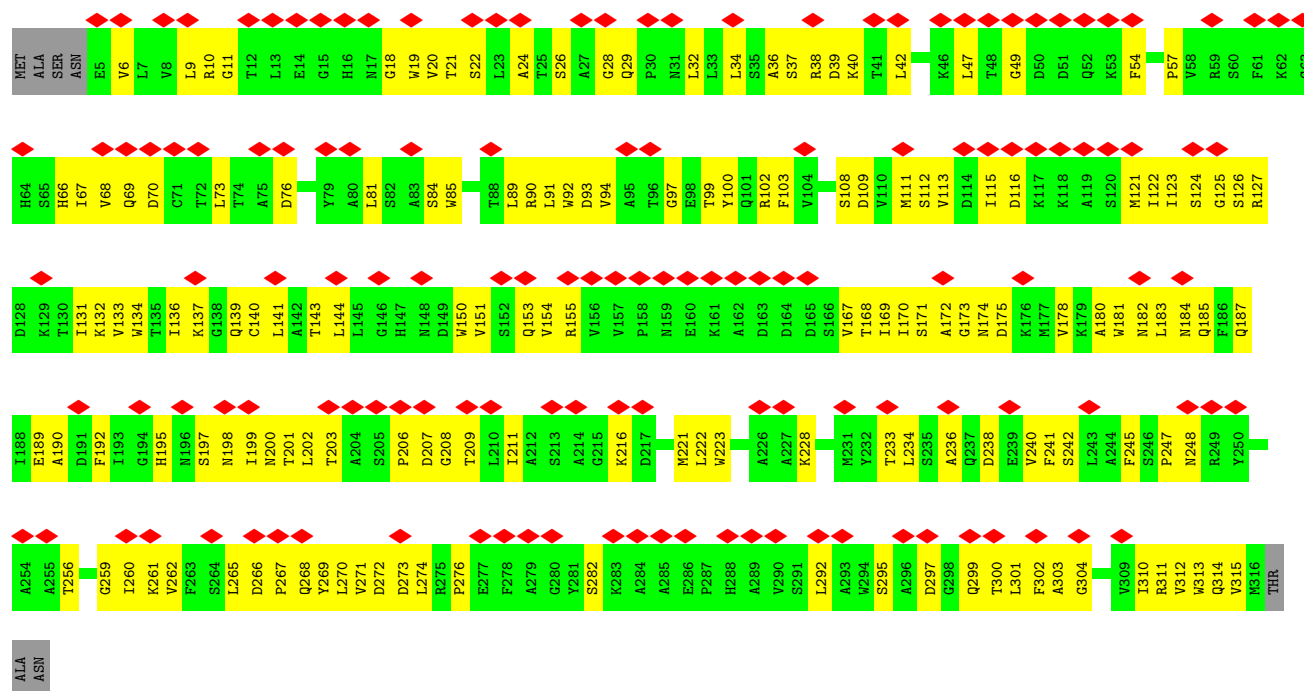
- Molecule 29: RPS28A isoform 1



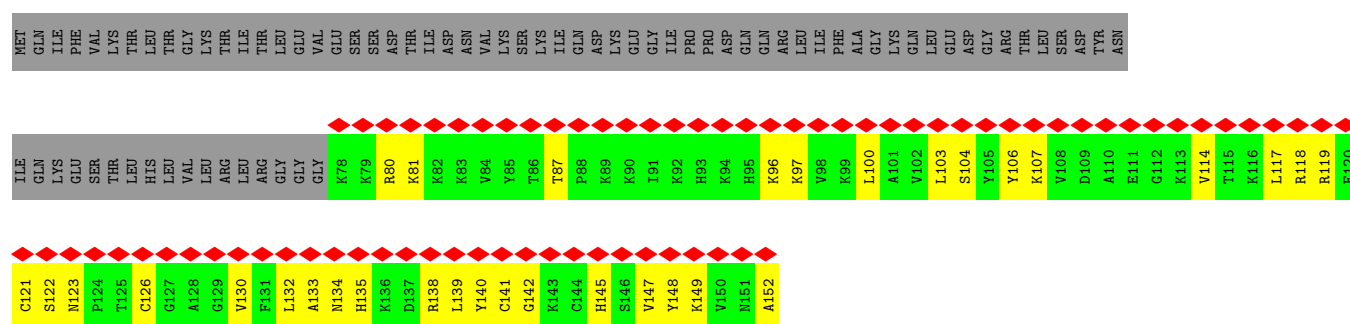
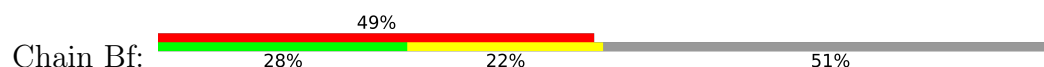
- Molecule 30: RPS29A isoform 1



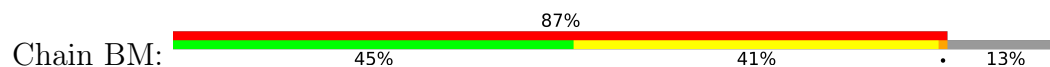
- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

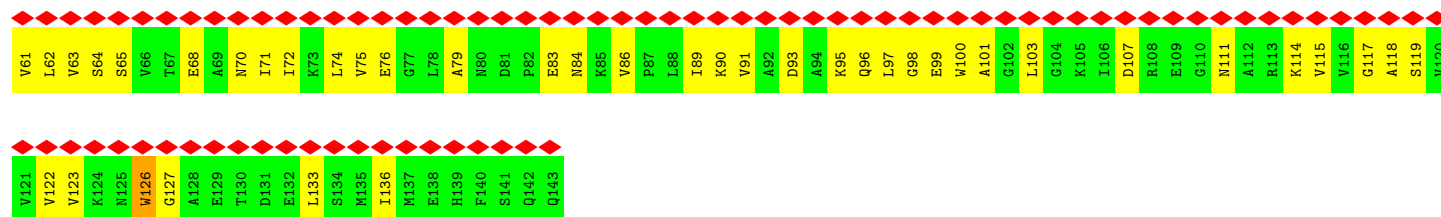


- Molecule 32: Ubiquitin-40S ribosomal protein S31

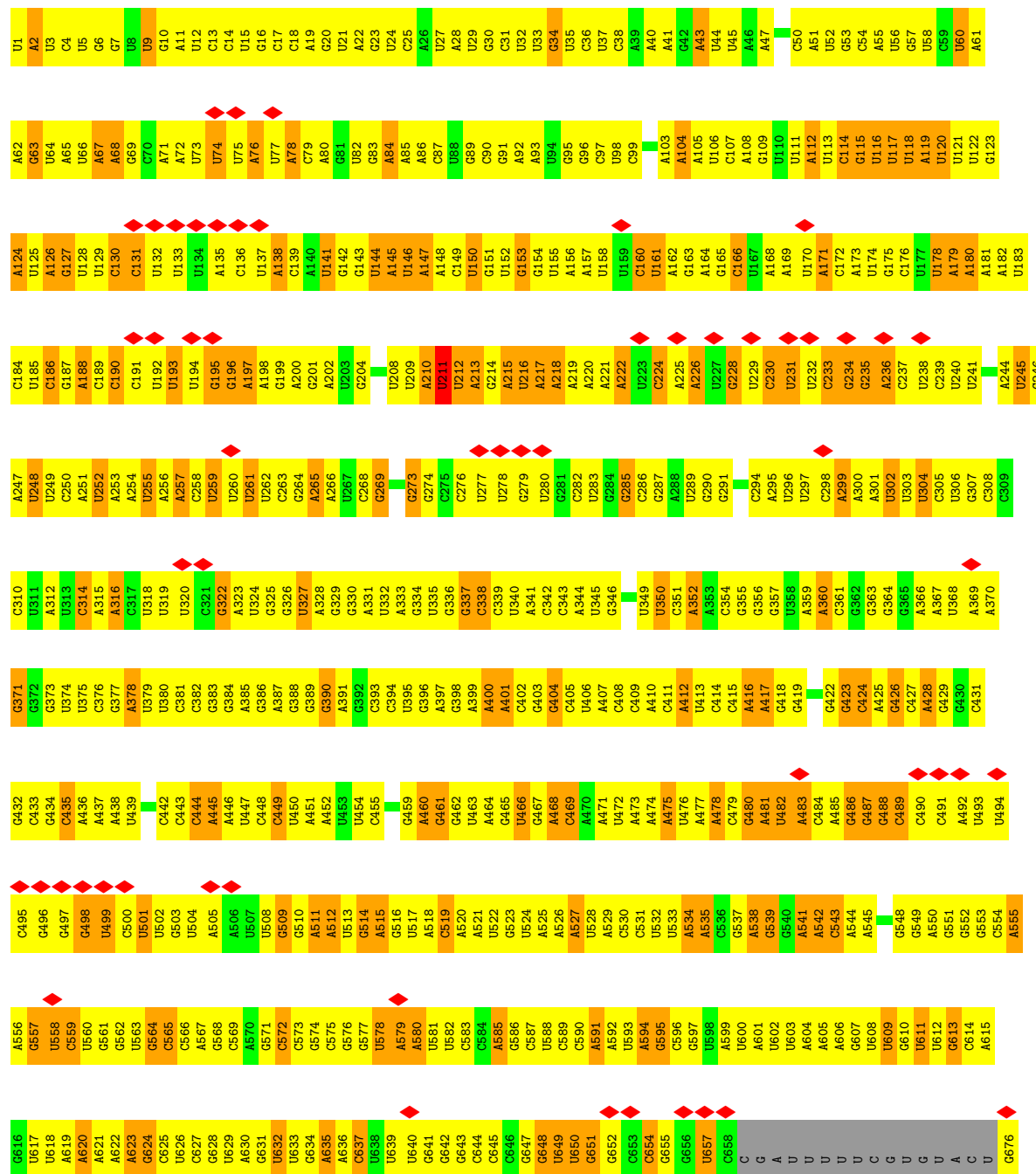
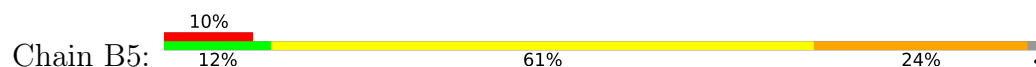


- Molecule 33: 40S ribosomal protein S12

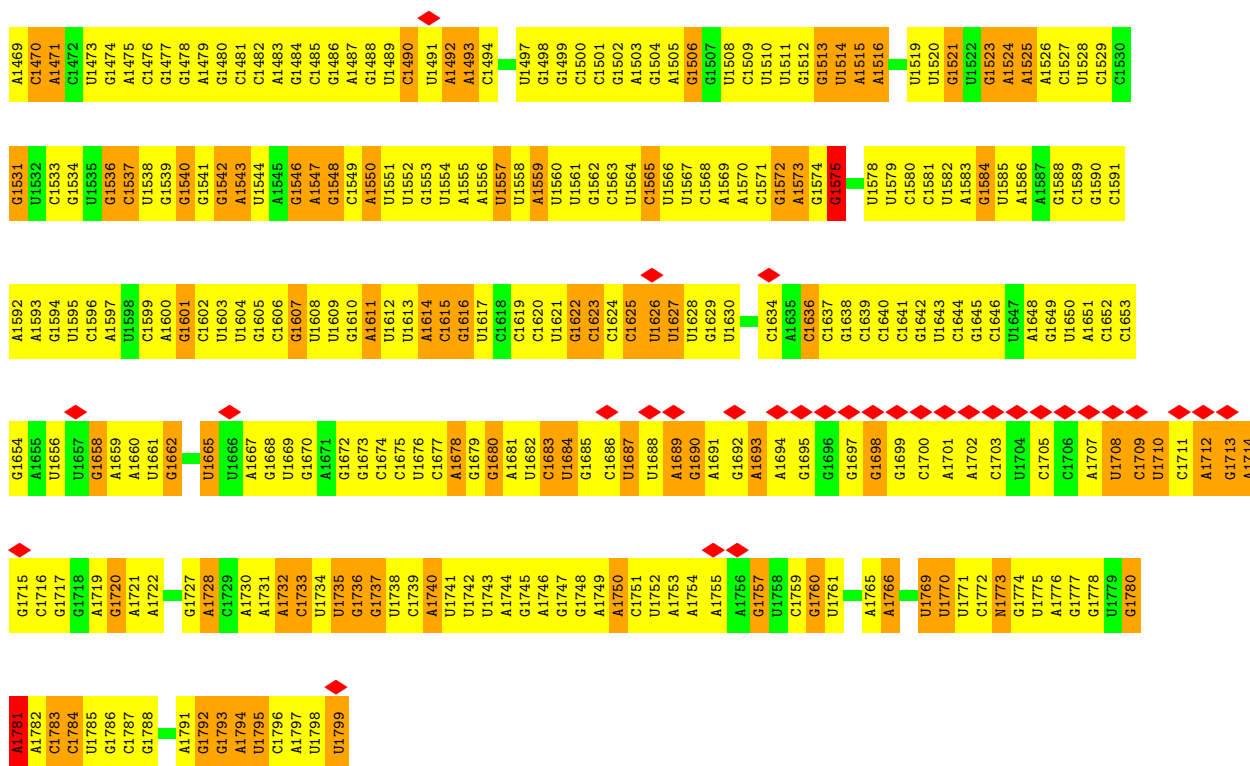




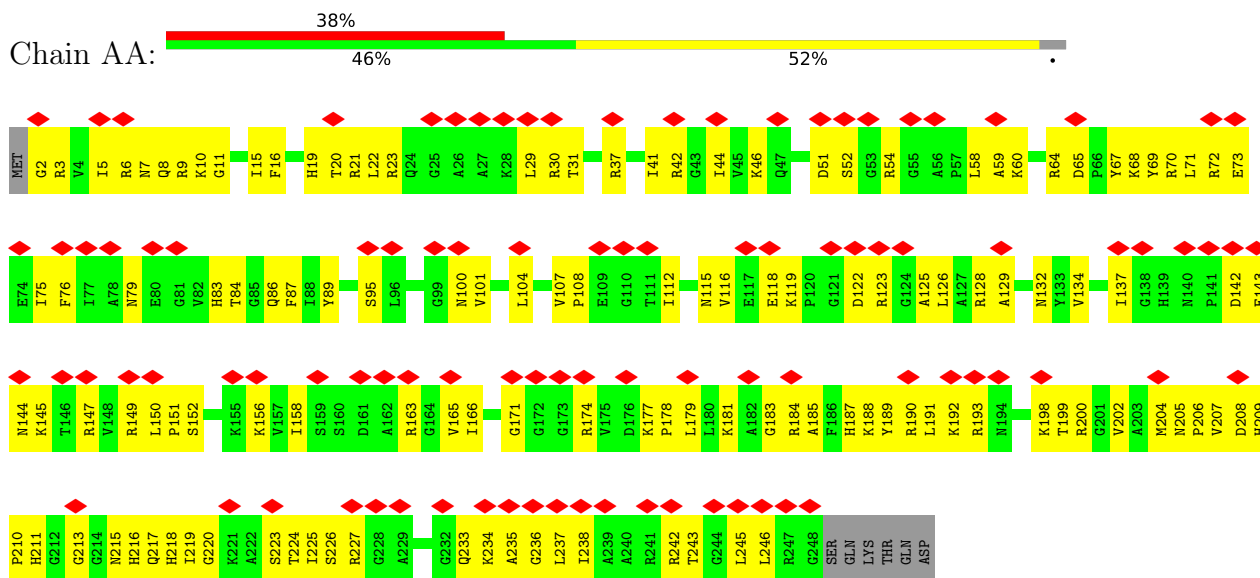
• Molecule 34: 18S rRNA



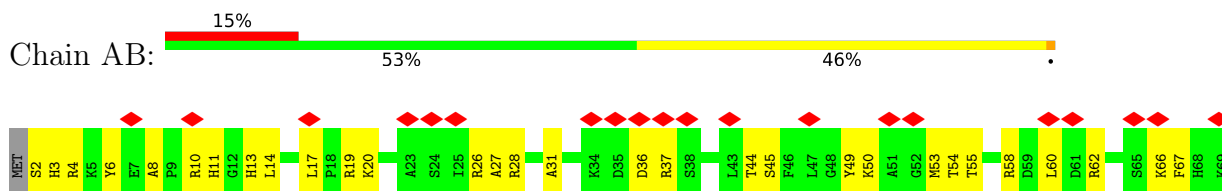
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G1409	G1349	A1287	G1165	G1042	G980	U860	A799	G738	A678
A1410	U1350	G1288	A1166	A1043	U981	U861	U900	G739	U679
G1411	G1351	A1227	G1167	U1044	U982	U862	G801	A740	U680
G1412	G1352	G1228	U1168	C1045	A983	A863	A923	C741	U681
U1413	U1353	G1229	G1169	G1046	G984	U864	A924	U742	C682
U1414	G1354	A1230	A1170	G1047	G985	A925	A926	U743	C683
U1415	C1355	U1231	G1171	G1048	G986	G866	U806	U744	A684
G1416	U1356	U1232	C1172	U1049	A988	G867	A907	U745	C685
G1417	A1357	U1233	C1173	G1050	U989	G868	U808	U746	A686
U1418	G1358	G1234	U1174	G1051	G990	A869	A809	C747	C687
G1419	C1359	A1234	U1175	U1052	C991	C870	G810	U748	G688
C1420	U1360	G1235	G1176	U1053	A992	G872	A811	U749	G689
U1423	U1361	A1236	G1177	U1054	A993	C873	G751	G690	G691
U1424	U1362	G1237	G1178	U1055	G994	U874	U813	C692	C692
A1425	U1363	A1238	U1179	U1056	A995	G875	A753	U752	U693
G1426	G1364	U1239	G1180	U1057	U996	G876	A754	A755	U694
A1427	C1365	U1240	U1181	U1058	G997	G877	G816	A756	U695
G1428	G1367	U1241	U1182	U1059	A998	G878	A757	A758	C696
U1430	U1368	G241	A1183	U1060	U999	G879	U759	U759	U697
U1431	U1369	A1242	A1184	A1061	C1000	C880	A760	A760	U699
U1432	U1370	G1243	U1185	A1062	A1001	A881	A761	A761	C700
G1433	U1371	A1244	G1186	G1063	G1002	U882	A762	A762	U701
A1434	A1372	C1246	U1187	U1064	A1003	C883	A763	A763	G702
G1435	C1373	U1247	U1188	C1066	U1004	G884	A764	A764	G703
A1436	C1374	U1248	G1189	C1067	A1005	G885	A765	A765	C704
U1437	A1375	C1248	A1190	U1068	C1006	U886	U766	U766	U
G1438	C1376	U1249	C1192	A1069	C1007	U887	U767	U767	A
C1439	U1377	U1250	A1193	C1070	C1008	U888	U768	U768	A
C1440	U1378	U1251	A1194	U1071	U1009	U889	U769	U769	C
U1441	C1379	C1252	C1195	C1072	C1010	C890	U770	U770	C
U1442	U1380	U1253	A1196	G1073	A951	U891	U771	U771	C
U1443	U1381	G1254	G1197	G1074	A952	U892	U772	U772	U
A1444	A1382	U1255	G1198	C1075	G953	U893	U773	U773	U
G1445	G1383	U1256	G1199	A1076	A954	U894	U774	U774	U
A1446	A1384	G1257	G1200	C1077	C956	U895	U775	U775	G
C1447	G1385	U1258	G1201	U1078	G957	U896	U776	U776	A
G1448	U1386	G1259	G1202	C1079	U958	C897	U777	U777	G
U1449	G1387	U1260	A1203	U1080	U959	A898	U778	U778	U
U1450	A1388	G1261	A1204	A1081	U960	G899	U779	U779	C
C1451	C1389	G1262	C1205	C1082	U961	A900	U780	U780	C
U1452	U1390	U1263	U1206	G1083	C962	G901	U781	U781	C
G1453	C1391	G1264	C1207	U1084	A963	G902	U782	U782	U
U1454	U1392	U1265	A1208	G1085	U964	U903	U783	U783	G
G1455	C1393	G1266	C1209	A1086	U965	G904	U784	U784	G
U1456	U1394	G1267	C1210	A1087	A966	A905	U785	U785	C
C1457	G1395	U1268	A1211	U1088	U967	A906	U786	U786	U
G1458	A1396	G1269	G1212	U1089	U968	A907	U787	U787	C
U1459	C1397	U1270	G1213	C1090	C969	U908	U788	U788	U
A1460	U1398	G1271	U1214	A1091	A970	C910	U789	U789	U
C1461	C1399	U1272	G1215	A1092	A971	U911	U790	U790	G
G1462	A1400	G1273	C1216	A1093	A972	U912	U791	U791	U
C1463	A1401	U1274	A1217	C1096	A973	G913	U792	U792	U
G1464	G1402	G1275	G1218	U1097	C975	G914	U793	U793	U
C1465	C1403	A1276	A1219	C1037	G976	A855	U794	U794	U
U1466	A1404	U1277	C1220	U1038	A977	A856	U795	U795	U
G1467	G1405	G1278	A1221	U1098	A978	U916	U796	U796	U
U1468	A1406	U1279	C1222	U1099	G1040	U917	U797	U797	U
		U1280	A1223	G1101		U918			
		G1281							
		U1282							
		U1285							

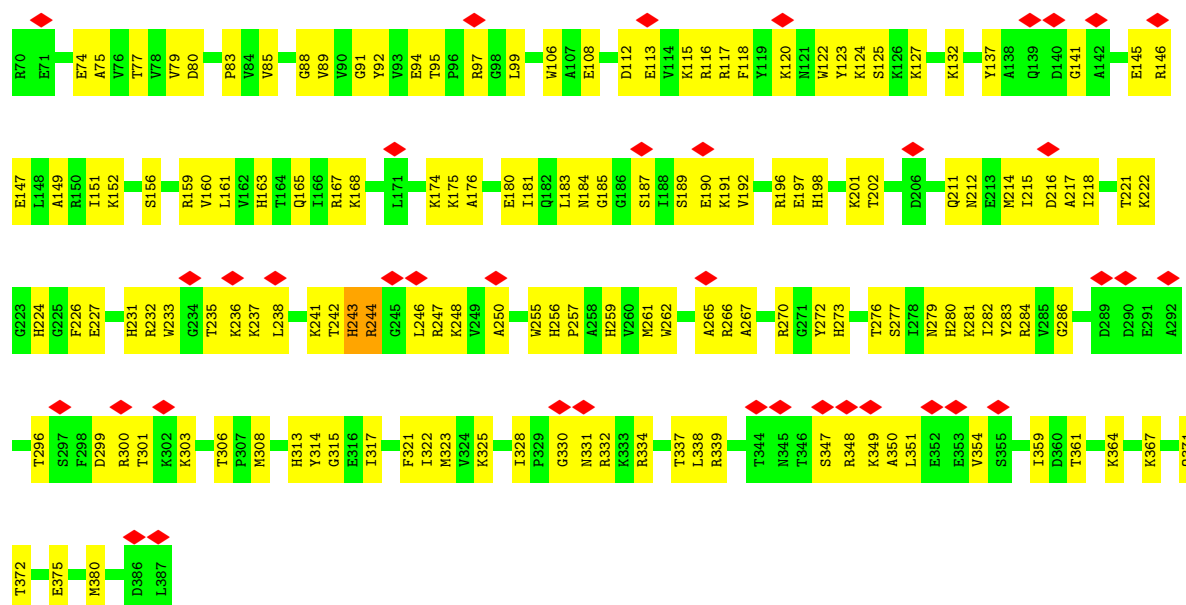


- Molecule 35: 60S ribosomal protein L2-A

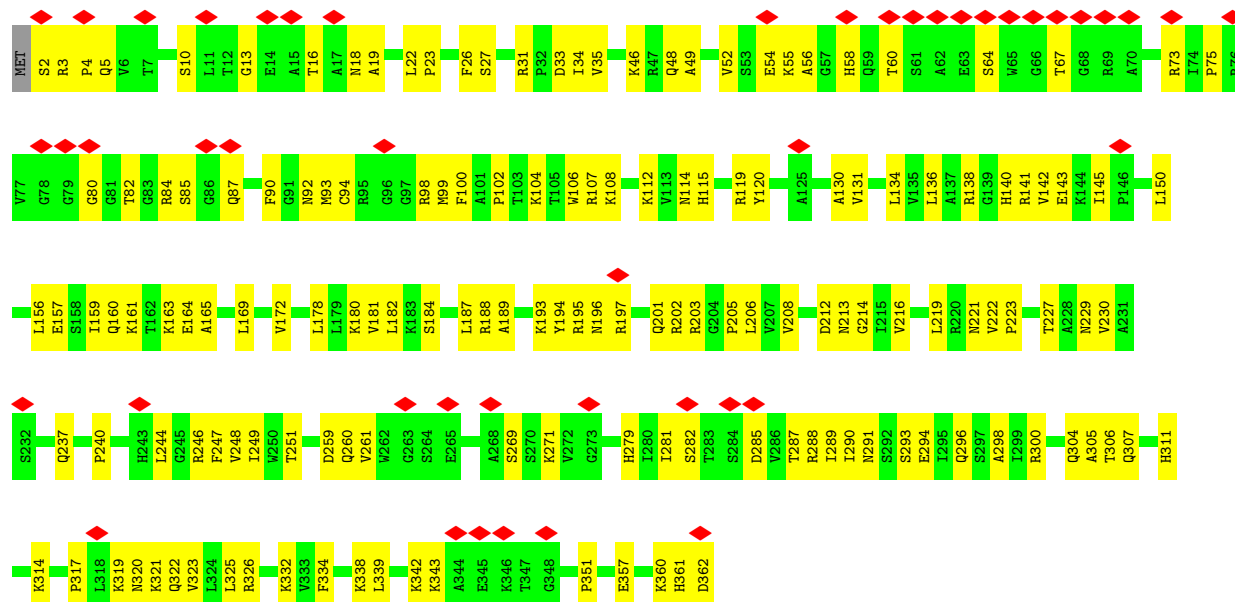


- Molecule 36: 60S ribosomal protein L3

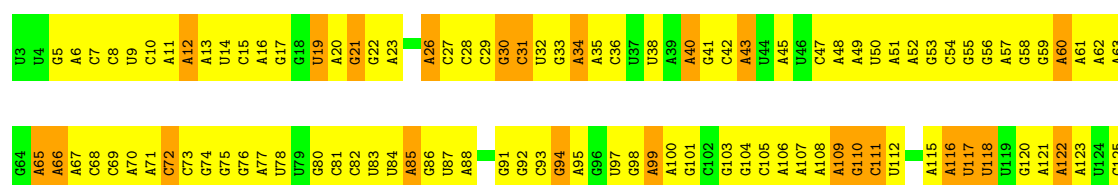
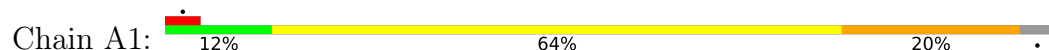


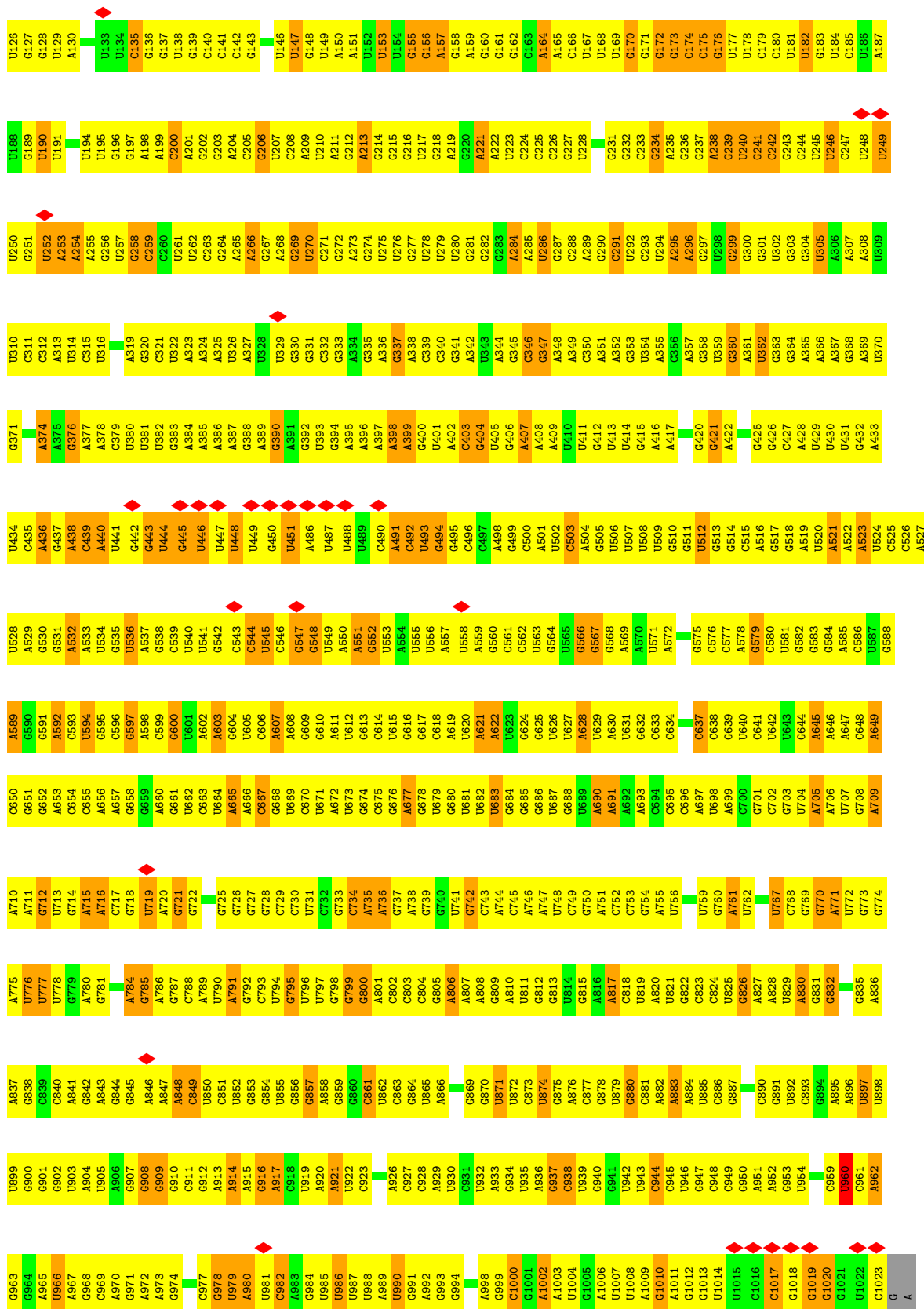


• Molecule 37: RPL4A isoform 1



• Molecule 38: 25S rRNA

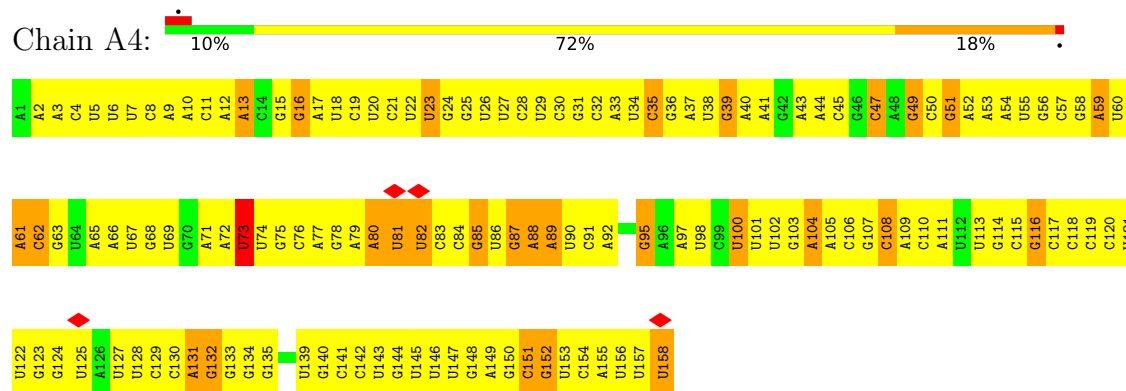




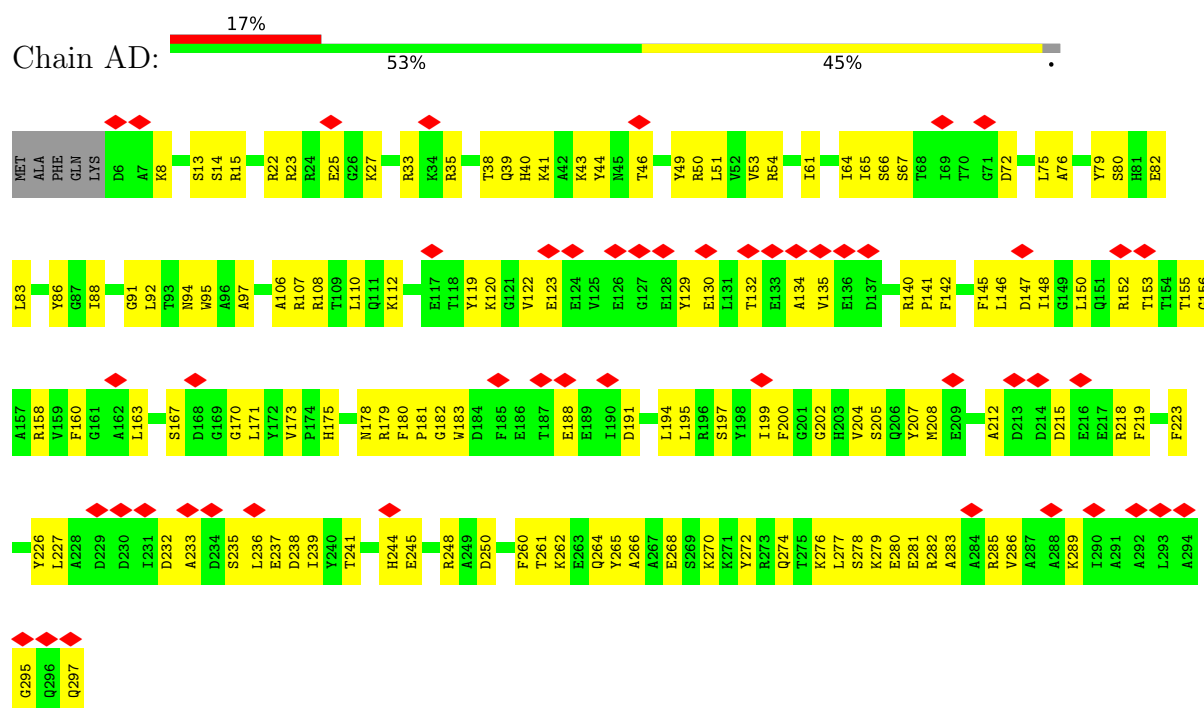
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U1821	C1761	A1699	C1633	U1512	C1451	C1391	U1331	A1270	G1147	G1087	A
A1822	U1762	G1700	G1634	G1513	A1452	C1392	A1332	A1271	G1148	G1088	U
U1823	U1763		G1635	G1514		A1393	C1333	C1272	G1149	G1089	G
U1824	U1764	U1703	A1636	A1515	A1455	A1394	U1334	C1273	U1151	A1091	A1030
C1825	U1765	U1705	A1637	C1516	A1456	C1395	C1335	A1274	G1152	C1092	C1031
C1826	C1766	G1706	A1638	G1517	U1457	C1396	U1336	C1275	G1153	C1093	C1032
C1827	G1767	C1707	C1639	U1518	U1458	C1397	A1337	C1276	A1153	U1093	U1033
A1828	U1768	A1707	G1640	G1519	C1459	U1398	C1338	U1277	A1154	U1094	U1034
G1829	U1769	C1708	A1641	G1520	A1460	A1399	C1339	A1278	C1155	U1095	G1035
G1830	C1770	C1709	A1642	G1521	A1461	G1400	G1340	C1279	C1156	U1096	A1036
U1831	G1771	C1710	A1643	U1522	A1462	A1401	U1341	C1280	G1157	G1097	C1037
C1832	C1772	C1711	A1644	U1523	A1463	C1402	C1342	G1281	A1158	A1098	C1038
G1833	U1773	A1582	G1645	A1524	G1464	C1403	A1343	G1282	A1159	A1099	U1039
U1834	C1773	C1583	A1646	G1525	A1465	G1404	G1344	C1283	G1161	U1100	A1040
A1835	C1774			U1526	A1466	U1405	G1345	C1284	U1162	G1101	U1041
C1836	G1775	G1586		C1527	A1467	A1406	U1346	C1285	U1163	U1042	U1042
U1837	G1776	A1587	G1650	G1528	A1468	A1407	U1347	G1286	A1164	C1043	C1043
G1838	U1777	A1588	U1651	C1529	C1469	G1408	U1348	A1287	G1165	U1044	U1044
A1839		A1589	G1652	U1530	U1470	G1409	G1349	C1288	A1166	A1105	C1045
U1940	C1778	G1718	C1653	C1531	U1471	U1410	G1350	C1289	U1167	G1106	A1046
A1841	G1779	G1719	A1654	U1532	U1472	C1411	A1350	G1290	C1107	C1107	A1047
A1842	C1780	G1720	G1655	U1533	G1473	G1412	U1351	G1291	U1108	U1108	A1048
C1843	C1781	U1721	A1656	U1534	A1474	G1413	A1352	C1292	U1109	C1049	C1049
C1844	U1782	U1722	A1657	A1535	A1475	G1414	U1353	C1293	A1170	U1050	U1050
U1845	U1783	A1723	C1658	G1536	G1476	U1415	G1354	G1294	U1111	U1111	U1051
C1846	U1724	U1724	U1659	A1537	A1477	C1416	U1355	A1295	G1172	U1112	U1052
A1847	C1725	C1725	C1660	G1538	U1478	G1417	U1356	C1296	G1173	C1113	A1053
C1848	G1726	G1726	A1661	U1539	U1479	A1418	G1357	C1297	G1174	U1114	A1054
G1849	G1727	G1727	G1662	A1540	U1480	A1419	C1358	C1298	G1175	G1115	A1055
C1849	U1728	G1728	C1663	G1541	A1481	C1420	C1359	U1299	G1176	G1116	U1056
A1850	U1729	U1729	A1664	U1542	A1482	G1421	U1360	G1300	C1177	G1117	A1057
G1851	C1791	U1730	C1665	G1543	U1483	C1422	U1361	A1301	G1178	C1118	U1058
U1852	C1792	A1803	A1666	U1544	U1484	C1423	G1362	A1302	A1179	C1119	G1059
C1853	G1793	G1603	A1667	A1545	G1485	C1424	A1363	U1305	U1180	U1181	U1060
U1854	G1794	U1606	U1668	A1546	G1486	U1425	G1364	G1306	U1182	A1061	A1061
C1855	G1795	A1805		G1547	G1487	C1426	G1365	G1307	U1122	A1062	A1062
G1856	U1796	U1607	G1673	C1548	G1488	U1427	A1366	A1244	G1063	U1123	G1063
C1857	U1797	U1608		U1549	U1489	G1428	G1367	A1245	A1064	U1124	A1064
A1858	A1797	G1809	G1677	C1550	A1490	U1430	U1368	A1309	U1125	U1125	A1065
G1860	U1798	G1610	G1678	G1551	A1491	G1431	G1370	G1310	G1126	G1126	G1066
C1861	A1800	A1611	A1679	U1552	G1492	C1432	G1371	C1311	U1127	U1127	U1067
U1862	U1801	A1612	G1680	U1553	G1493	A1433	C1372	C1312	U1128	U1128	C1068
A1863	C1802	A1613	U1681	U1554	U1494	G1434	A1373	G1313	A1129	C1069	C1069
C1864	C1803	C1614	U1682	U1555	U1495	U1435	G1374	C1314	A1130	A1130	U1070
A1865	A1804	C1615	A1683	C1556	C1496	U1436	G1375	U1315	U1191	G1131	U1071
C1866	C1805	U1616	U1684	A1557	C1497	U1437	C1376	C1316	C1192	C1132	G1072
A1867	A1806	G1617	C1685	U1558	A1498	C1437	C1377	C1317	G1194	G1133	U1073
G1868	G1807	G1618	U1686	A1559	C1499	U1438	U1378	A1318	C1196	G1134	U1074
C1869	U1687	A1619	U1687	U1560	G1500	U1439	U1379	C1254	A1195	A1135	A1075
U1870	U1688	U1620	U1688	U1501	U1501	G1440	G1380	G1255	C1196	A1136	C1076
A1871	A1809	A1621	G1689	C1502	C1502	G1441	G1381	G1256	C1197	A1137	U1077
G1872	G1751	U1622	U1689	C1562	A1503	U1442	G1382	C1257	C1198	U1138	U1078
U1873	A1752	G1623	C1690	U1563	A1504	G1443	G1383	U1258	G1139	G1139	A1079
C1874	G1812	G1624	U1691	U1564	U1505	U1444	G1384	C1259	C1199	U1138	U1079
A1875	A1813	A1625	G1692	G1565	A1506	U1445	U1384	A1260	A1200	G1140	A1080
G1876	U1814	U1626	A1693	A1566	G1507	U1446	C1385	C1261	C1201	C1141	C1141
U1877	U1815	U1627	U1694	U1567	C1508	G1447	G1386	G1262	A1202	G1142	U1081
C1878	A1816	C1628	A1695	U1568	U1508	U1448	A1387	A1263	A1143	A1143	G1082
A1879	G1817	U1629	A1696	U1569	A1509	U1449	G1388	G1264	A1203	A1144	G1083
	U1818	U1630	A1697	U1570	G1510	A1449	U1389	U1265	A1204	G1145	A1084
		C1631						G1266	A1205		A1085



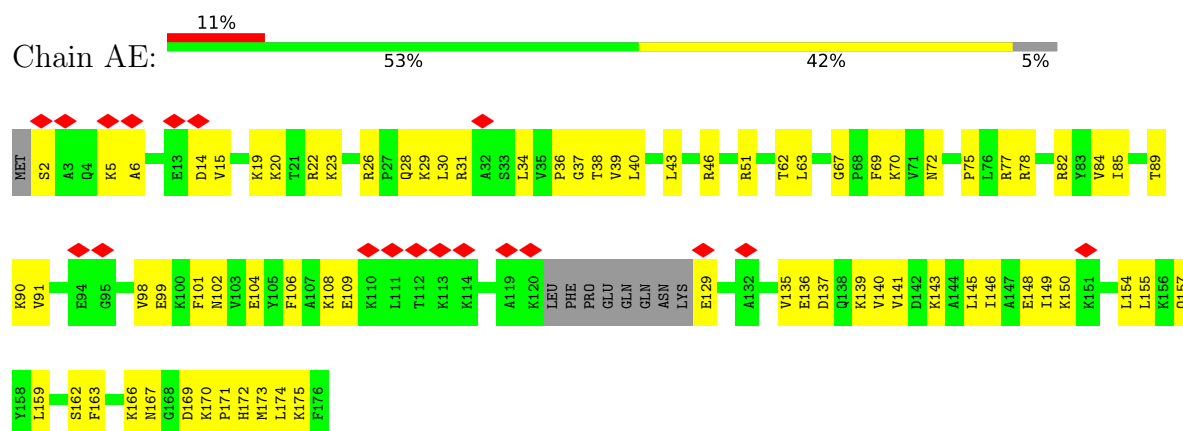
- Molecule 40: 5.8 S rRNA



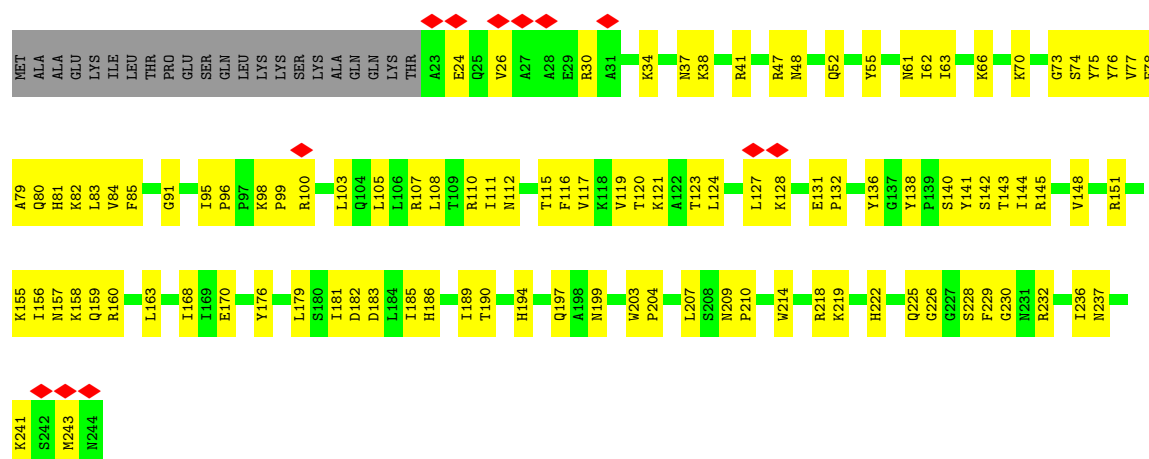
- Molecule 41: RPL5 isoform 1



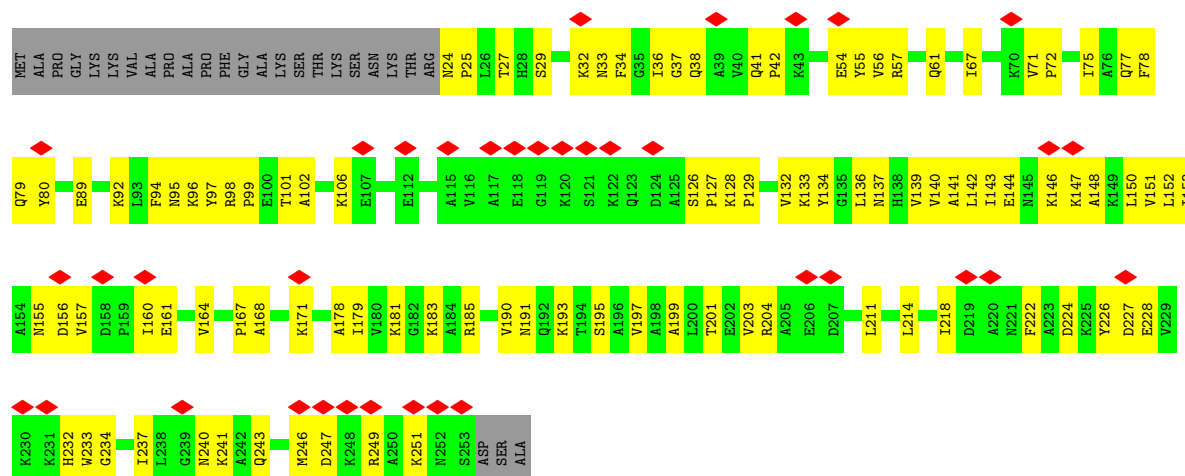
- Molecule 42: 60S ribosomal protein L6-A



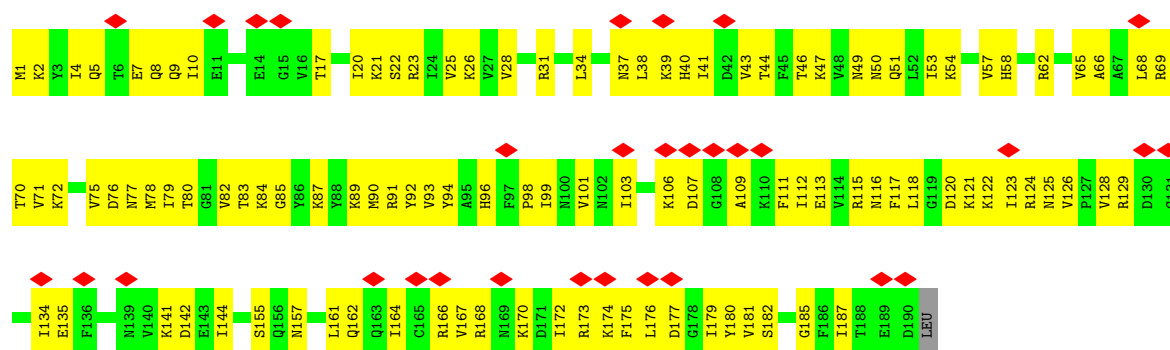
- Molecule 43: 60S ribosomal protein L7-A



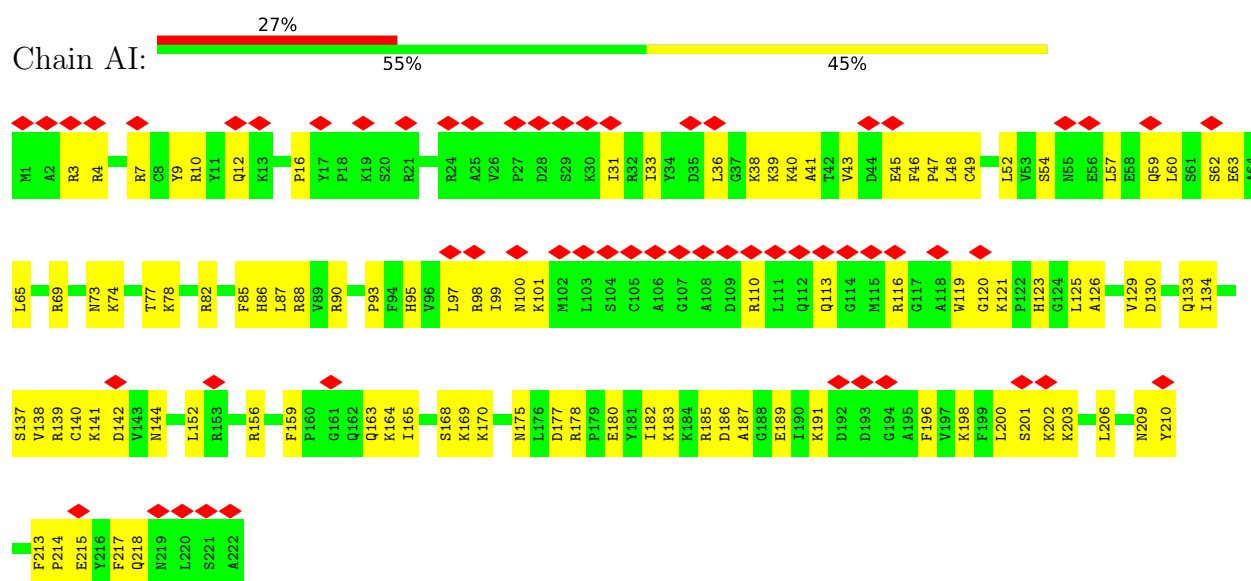
• Molecule 44: 60S ribosomal protein L8-A



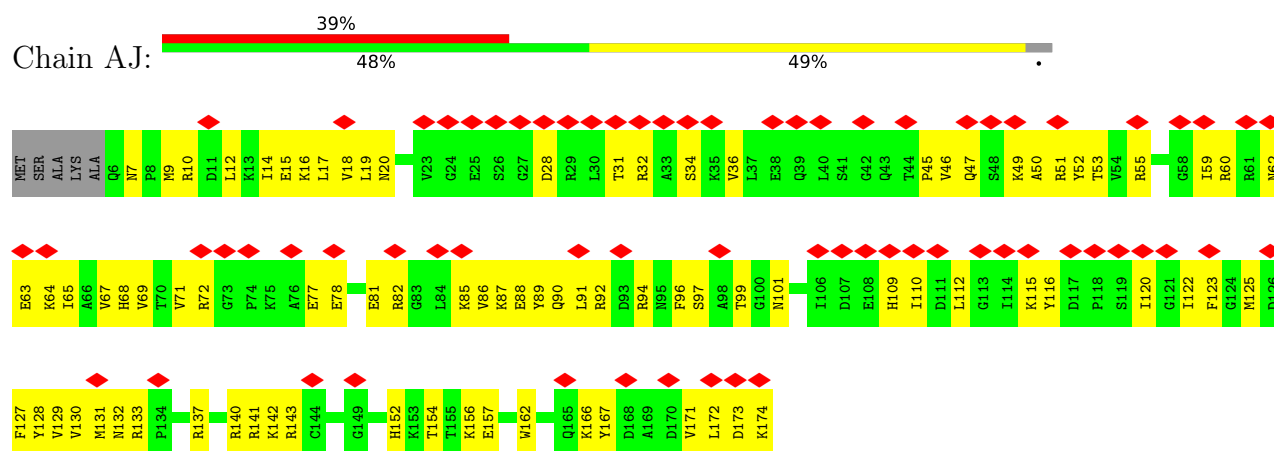
• Molecule 45: 60S ribosomal protein L9-A



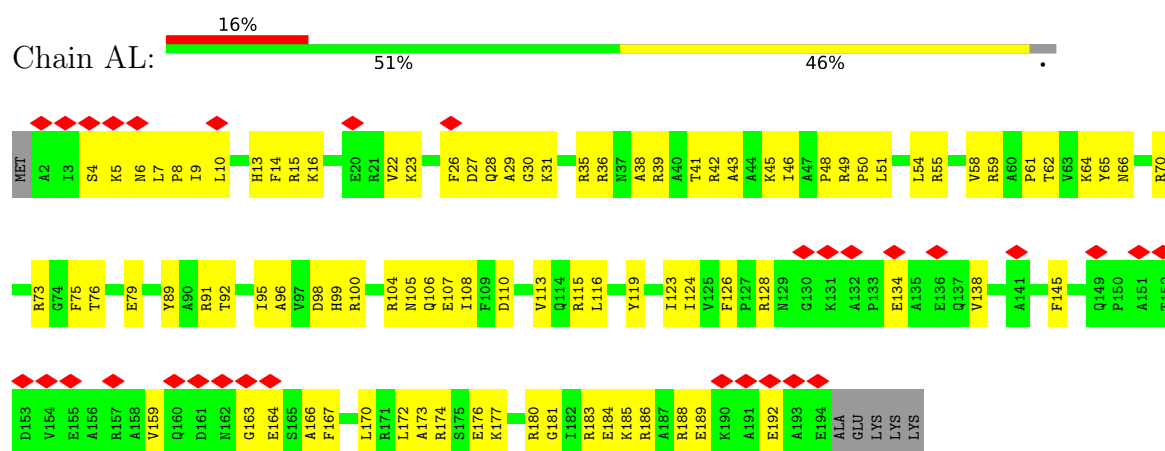
• Molecule 46: 60S ribosomal protein L10



• Molecule 47: RPL11A isoform 1



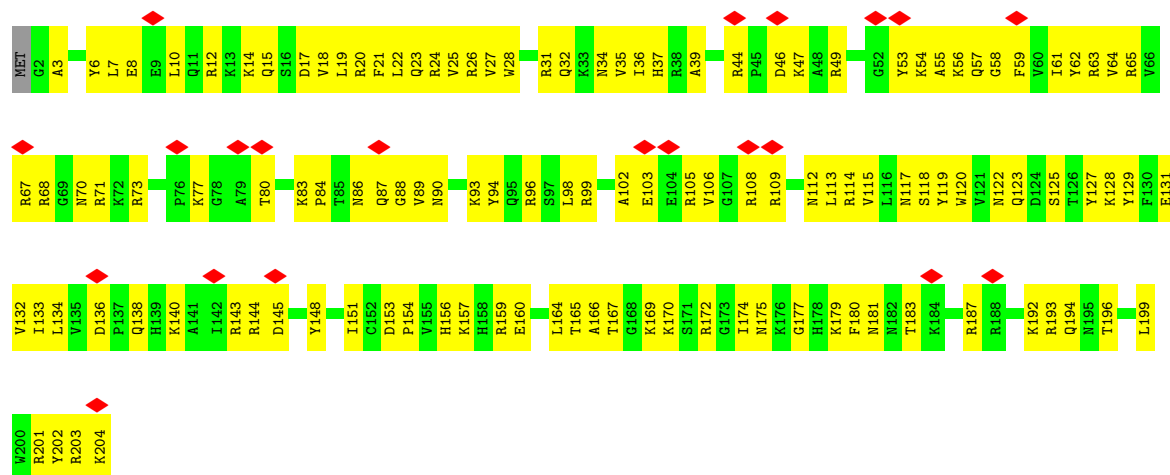
• Molecule 48: 60S ribosomal protein L13-A



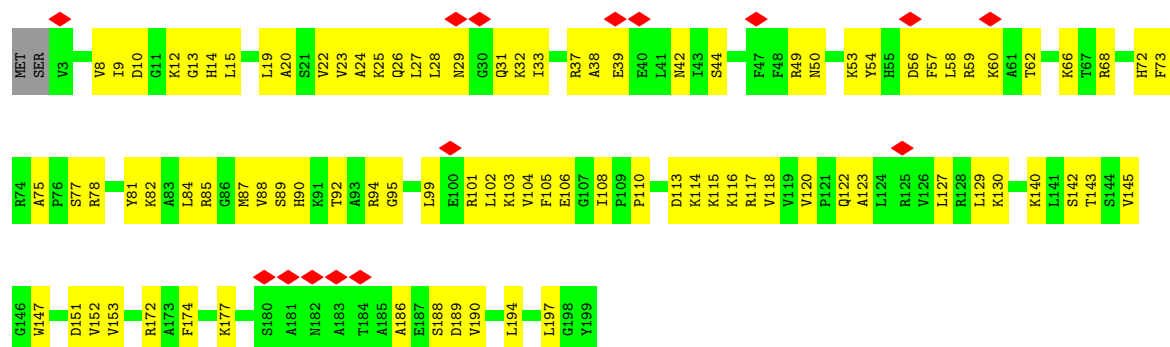
• Molecule 49: 60S ribosomal protein L14-A



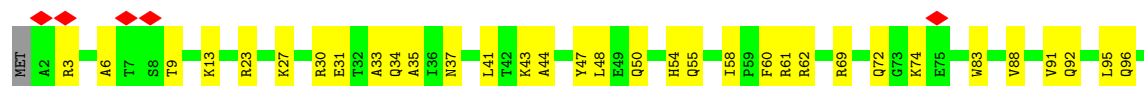
- Molecule 50: 60S ribosomal protein L15-A

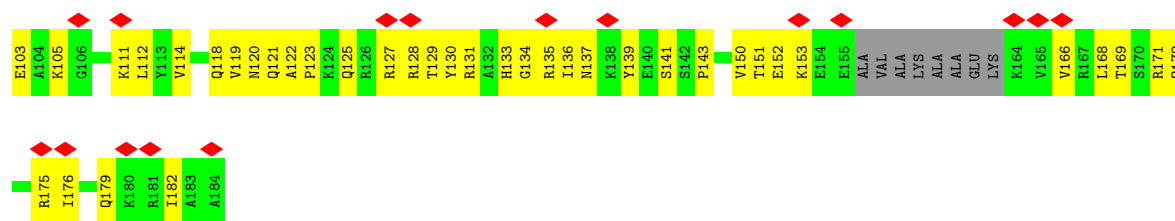


- Molecule 51: 60S ribosomal protein L16-A

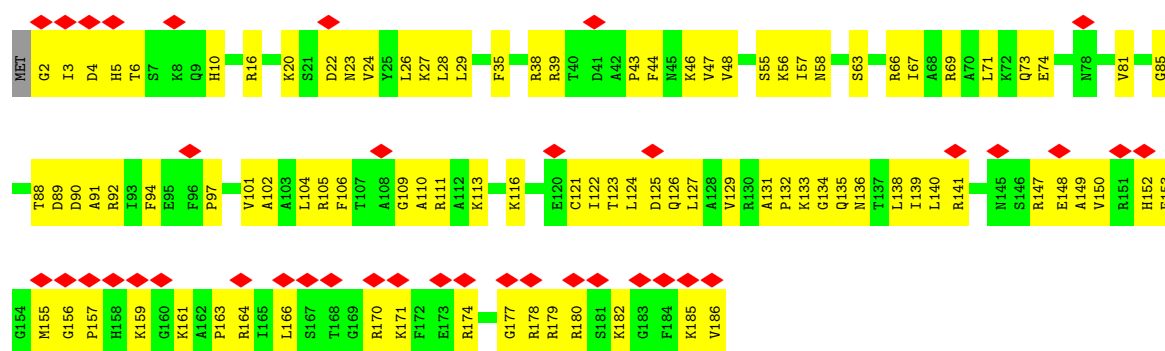


- Molecule 52: 60S ribosomal protein L17-A

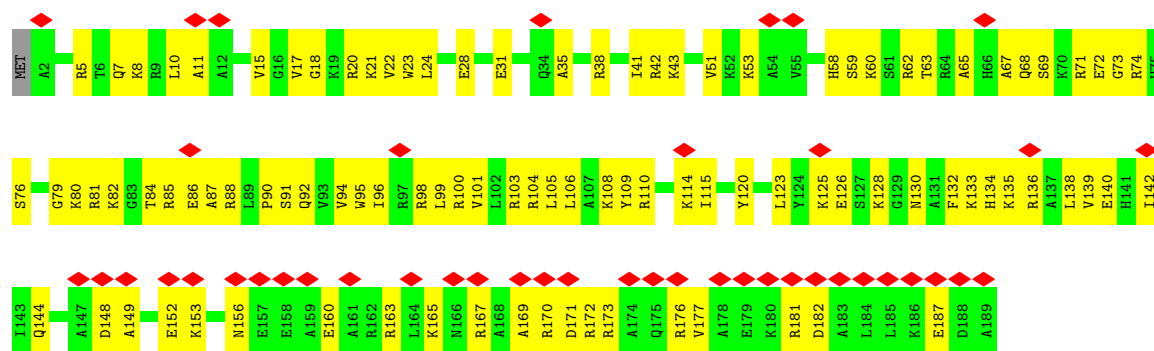




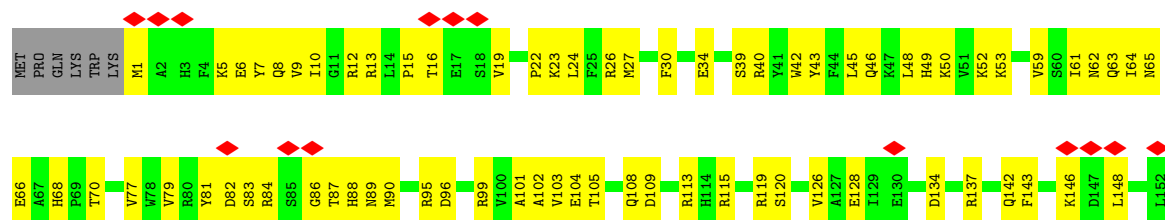
• Molecule 53: 60S ribosomal protein L18-A



• Molecule 54: 60S ribosomal protein L19-A

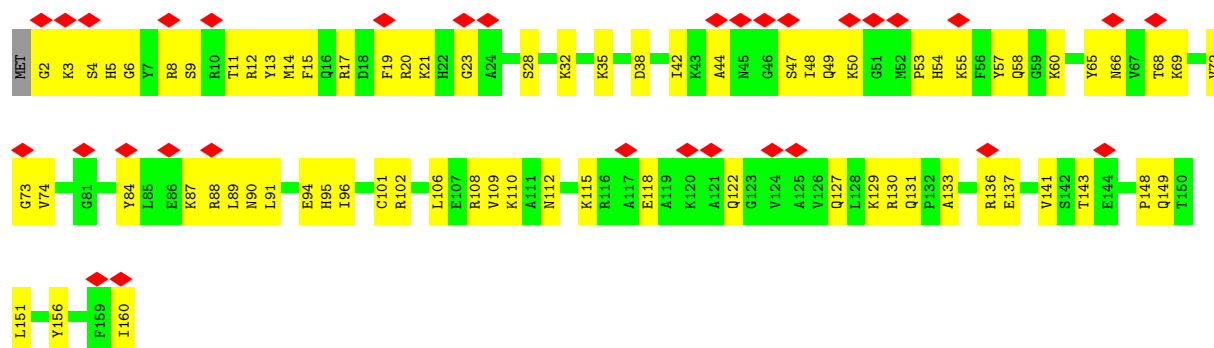


• Molecule 55: 60S ribosomal protein L20

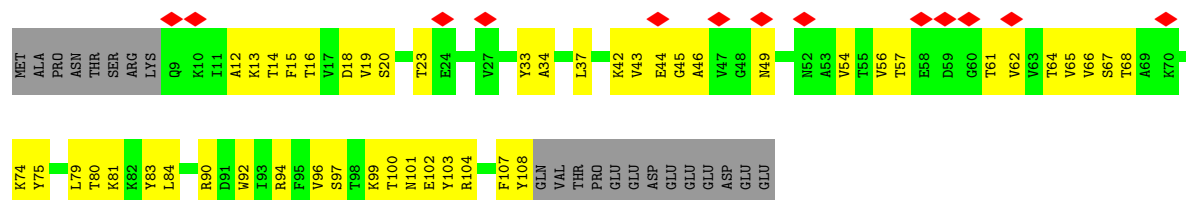
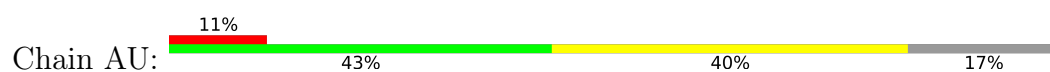




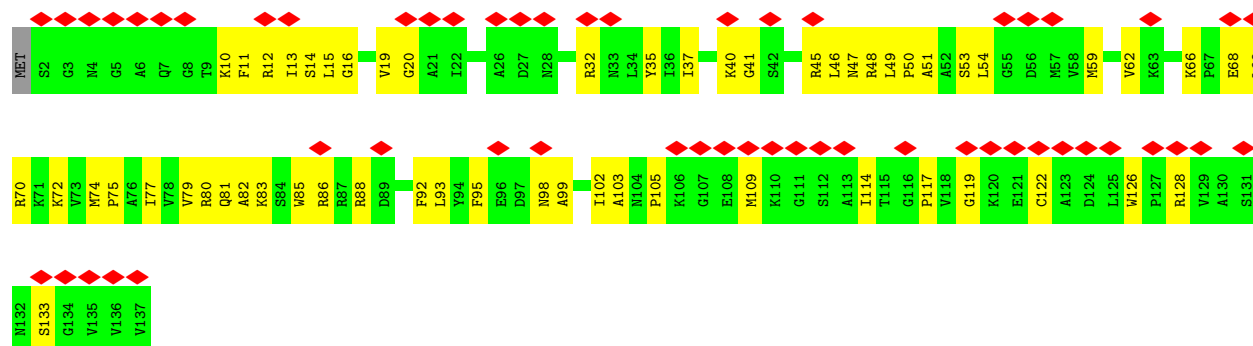
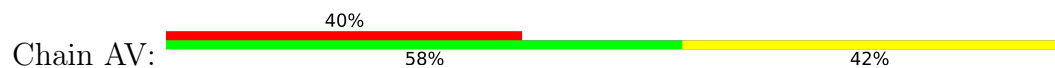
• Molecule 56: 60S ribosomal protein L21-A



• Molecule 57: 60S ribosomal protein L22-A

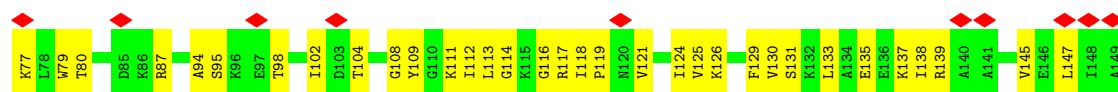


• Molecule 58: 60S ribosomal protein L23-A



• Molecule 59: RPL24A isoform 1

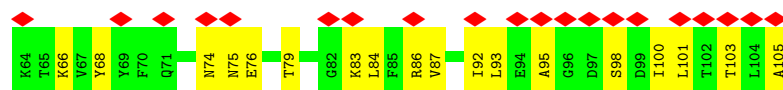
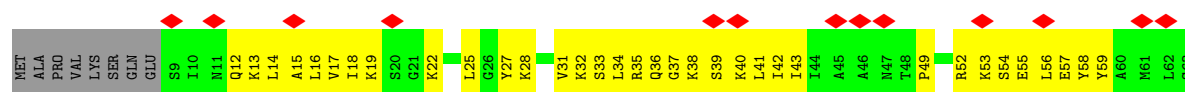




• Molecule 64: RPL29 isoform 1



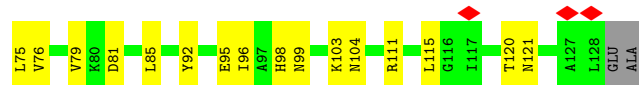
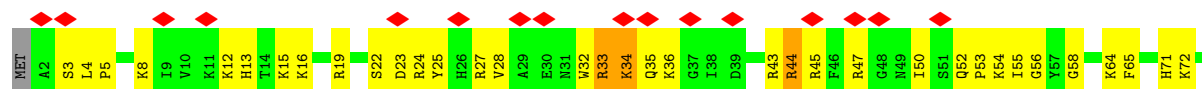
• Molecule 65: 60S ribosomal protein L30



• Molecule 66: 60S ribosomal protein L31-A

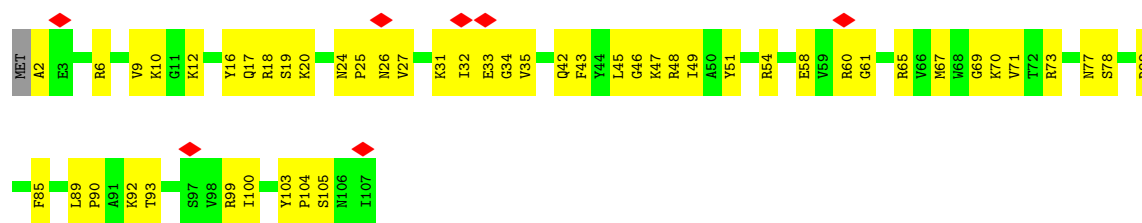


• Molecule 67: RPL32 isoform 1

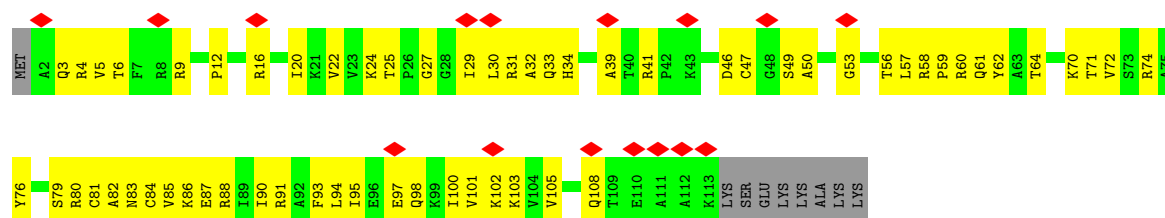


• Molecule 68: 60S ribosomal protein L33-A

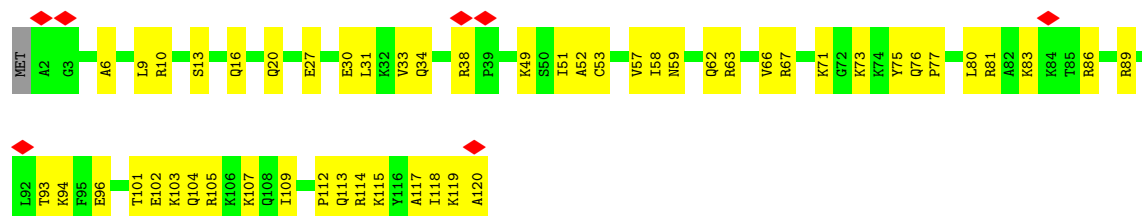




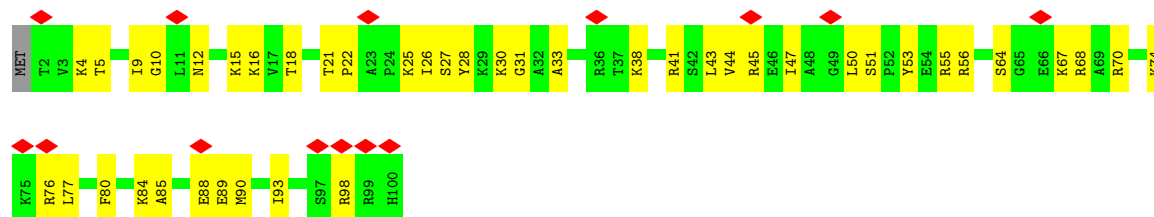
- Molecule 69: 60S ribosomal protein L34-A



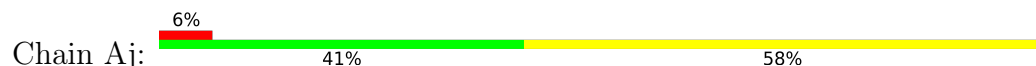
- Molecule 70: 60S ribosomal protein L35-A

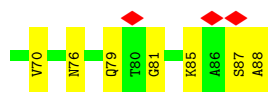


- Molecule 71: 60S ribosomal protein L36-A



- Molecule 72: 60S ribosomal protein L37-A





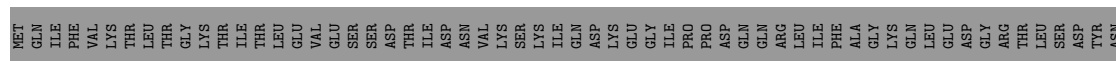
• Molecule 73: RPL38 isoform 1



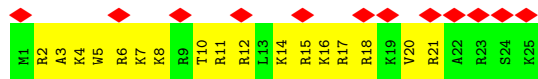
• Molecule 74: 60S ribosomal protein L39



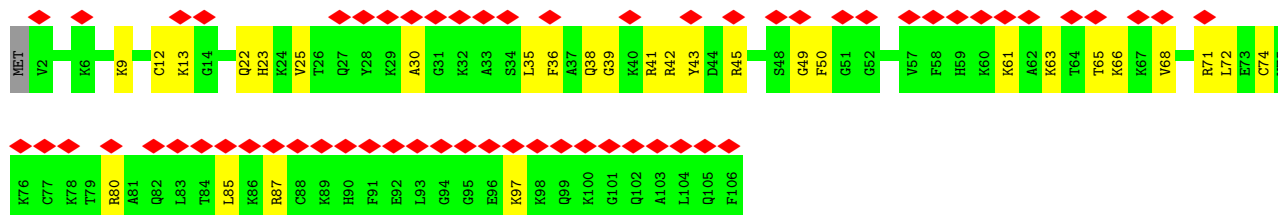
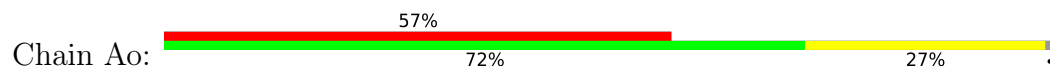
• Molecule 75: Ubiquitin-60S ribosomal protein L40



• Molecule 76: 60S ribosomal protein L41-A

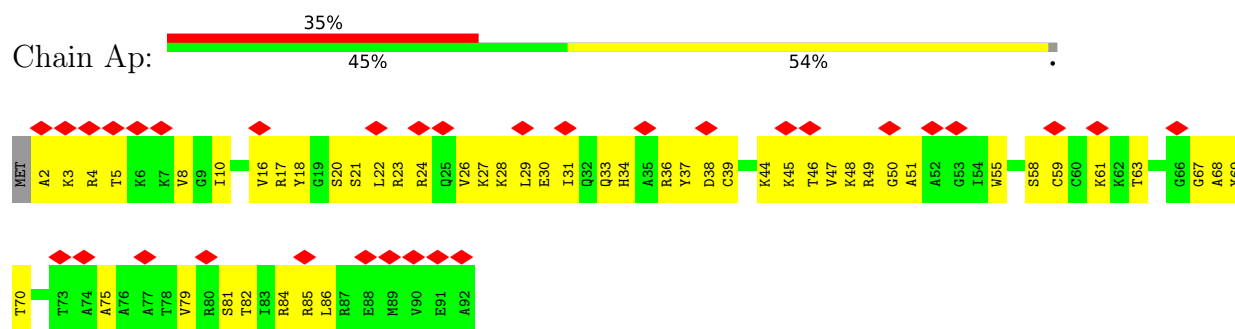


• Molecule 77: 60S ribosomal protein L42-A



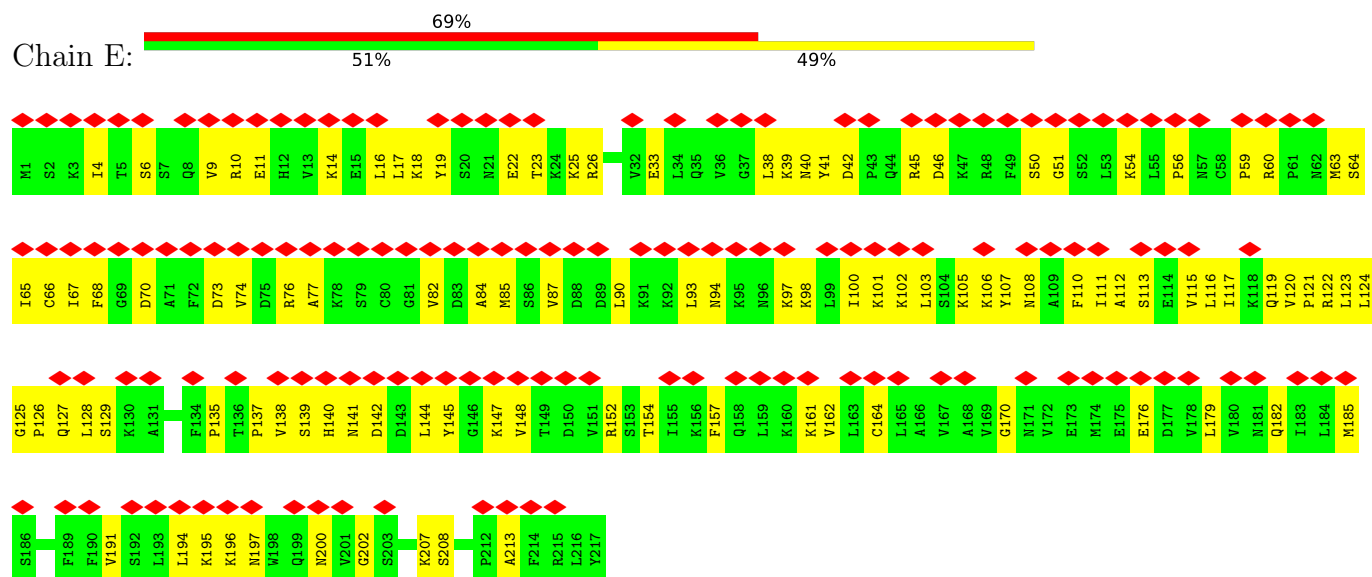
- Molecule 78: 60S ribosomal protein L43-A

Chain Ap:



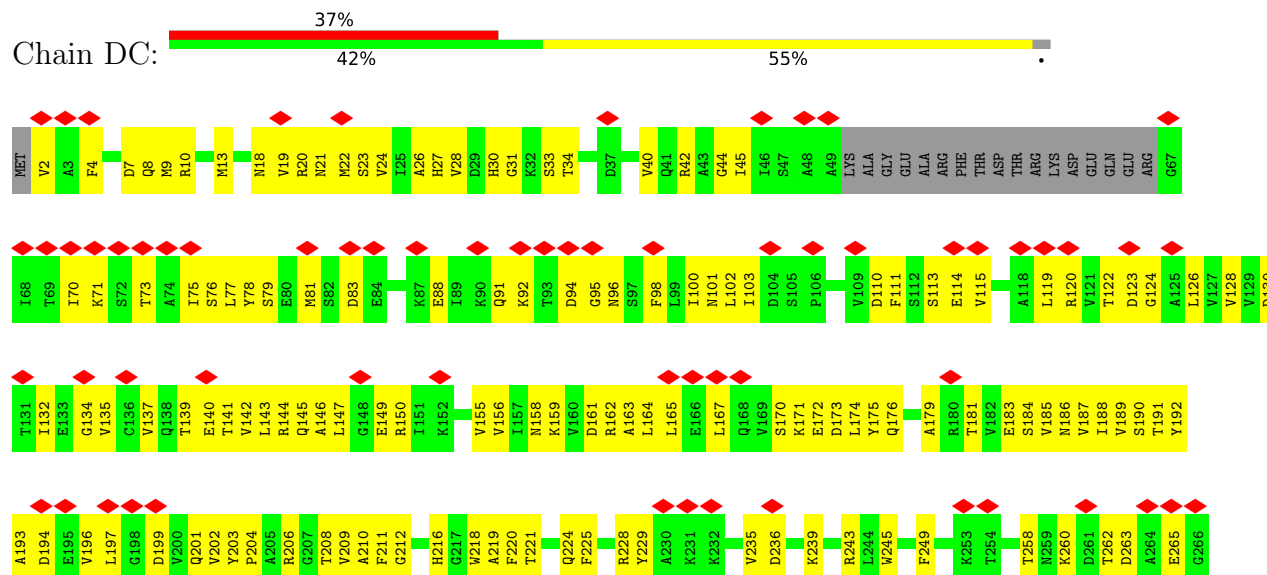
- Molecule 79: RPL1A isoform 1

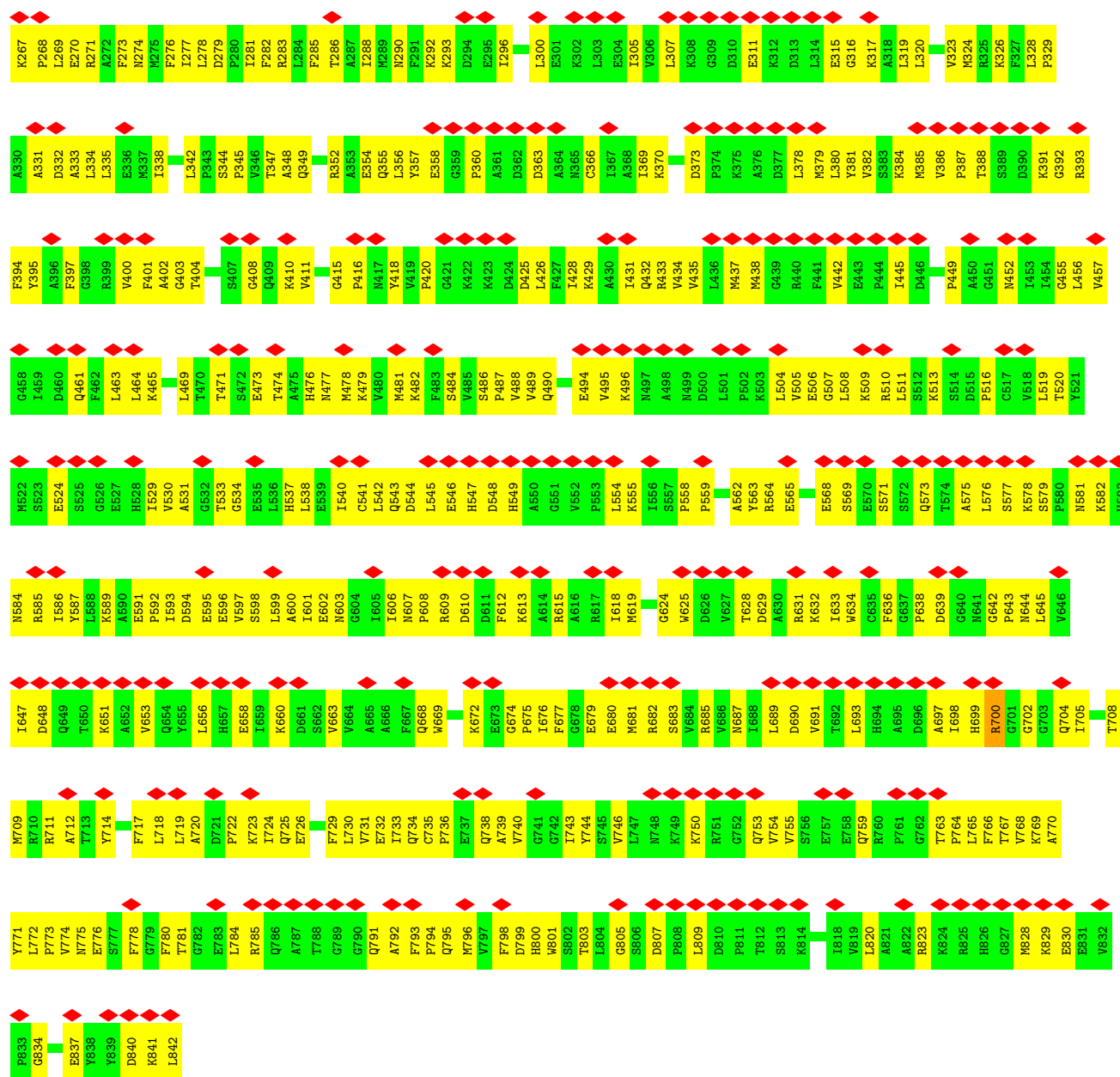
Chain E:



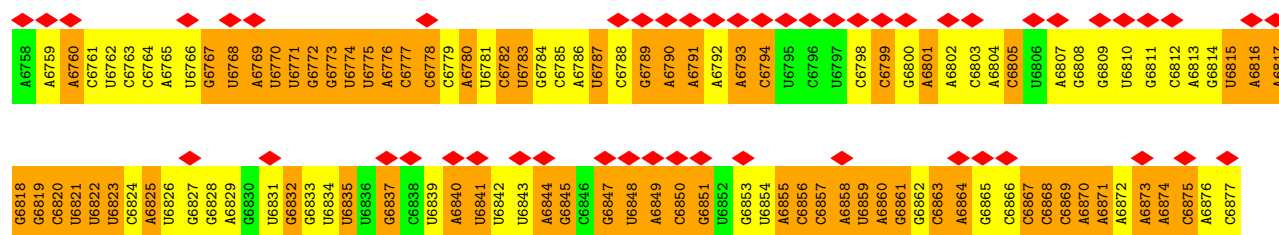
- Molecule 80: Elongation factor 2

Chain DC:





• Molecule 81: TSV IRES





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22050	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.296	Depositor
Minimum map value	-0.490	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PSU, ZN, GDP, G7M, 4AC, HIC, UR3, B8N, MA6, OMG, 5MC, OMU, DDE, SO1, 1MA

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	BA	0.19	0/1653	0.38	0/2261
2	BB	0.19	0/1735	0.46	0/2335
3	BC	0.20	0/1665	0.37	0/2263
4	BE	0.17	0/2109	0.37	0/2839
5	BG	0.15	0/1844	0.32	0/2464
6	BH	0.16	0/1506	0.39	0/2028
7	BI	0.20	0/1514	0.46	1/2021 (0.0%)
8	BJ	0.17	0/1519	0.38	0/2035
9	BL	0.20	0/1272	0.41	0/1712
10	BN	0.21	0/1215	0.45	0/1638
11	BO	0.21	0/952	0.47	0/1279
12	BV	0.22	0/693	0.44	0/935
13	BW	0.20	0/1038	0.37	0/1395
14	BX	0.19	0/1139	0.37	0/1518
15	BY	0.16	0/1087	0.37	0/1449
16	Ba	0.26	0/782	0.56	2/1047 (0.2%)
17	Bb	0.15	0/620	0.34	0/838
18	Be	0.23	0/483	0.58	1/643 (0.2%)
19	BD	0.16	0/1759	0.37	0/2368
20	BF	0.16	0/1629	0.36	0/2202
21	BK	0.16	0/837	0.42	0/1131
22	BP	0.18	0/1012	0.38	0/1356
23	BQ	0.15	0/1125	0.33	0/1510
24	BR	0.25	0/958	0.50	0/1286
25	BS	0.15	0/1211	0.36	0/1628
26	BT	0.14	0/1113	0.34	0/1494
27	BU	0.15	0/865	0.33	0/1169
28	BZ	0.12	0/582	0.31	0/782
29	Bc	0.14	0/499	0.36	0/670
30	Bd	0.17	0/452	0.37	0/600
31	Bg	0.14	0/2454	0.35	0/3340
32	Bf	0.14	0/616	0.36	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.12	0/943	0.47	2/1274 (0.2%)
34	B5	0.21	0/41450	0.32	0/64582
35	AA	0.27	0/1912	0.45	0/2569
36	AB	0.26	0/3139	0.41	0/4219
37	AC	0.24	0/2800	0.40	0/3790
38	A1	0.27	0/76161	0.34	0/118749
39	A3	0.23	0/2861	0.33	0/4457
40	A4	0.28	0/3724	0.34	0/5798
41	AD	0.17	0/2390	0.33	0/3225
42	AE	0.20	0/1324	0.34	0/1782
43	AF	0.25	0/1821	0.36	0/2451
44	AG	0.21	0/1830	0.38	0/2469
45	AH	0.23	0/1531	0.43	0/2062
46	AI	0.21	0/1843	0.33	0/2471
47	AJ	0.16	0/1374	0.38	0/1842
48	AL	0.22	0/1568	0.36	0/2106
49	AM	0.21	0/1068	0.33	0/1438
50	AN	0.29	0/1757	0.45	0/2354
51	AO	0.25	0/1585	0.41	0/2128
52	AP	0.24	0/1410	0.33	0/1893
53	AQ	0.24	0/1465	0.38	0/1965
54	AR	0.22	0/1538	0.42	0/2050
55	AS	0.26	0/1481	0.41	0/1990
56	AT	0.20	0/1300	0.37	0/1743
57	AU	0.19	0/812	0.38	0/1099
58	AV	0.27	0/1018	0.45	1/1369 (0.1%)
59	AW	0.23	0/533	0.39	0/707
60	AX	0.22	0/983	0.35	0/1325
61	AY	0.22	0/1004	0.38	0/1341
62	AZ	0.24	0/1118	0.39	0/1497
63	Aa	0.24	0/1204	0.34	0/1612
64	Ab	0.19	0/473	0.43	0/629
65	Ac	0.26	0/751	0.42	0/1008
66	Ad	0.24	0/904	0.39	0/1213
67	Ae	0.24	0/1041	0.52	1/1394 (0.1%)
68	Af	0.28	0/868	0.43	0/1168
69	Ag	0.23	0/890	0.44	0/1189
70	Ah	0.21	0/978	0.34	0/1301
71	Ai	0.21	0/778	0.35	0/1034
72	Aj	0.27	0/696	0.42	0/923
73	Ak	0.19	0/618	0.33	0/826
74	Al	0.27	0/443	0.55	0/588
75	Am	0.22	0/423	0.39	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	An	0.40	0/234	0.68	0/300
77	Ao	0.18	0/860	0.36	0/1136
78	Ap	0.25	0/701	0.44	0/934
79	E	0.16	0/1745	0.40	0/2342
80	DC	0.19	0/6521	0.44	2/8830 (0.0%)
81	EC	0.15	0/4733	0.34	0/7369
All	All	0.23	0/226542	0.36	10/332156 (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
1	BA	0	1
67	Ae	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BM	126	TRP	CA-C-N	8.46	136.92	121.70
33	BM	126	TRP	C-N-CA	8.46	136.92	121.70
16	Ba	60	PRO	CA-N-CD	-8.07	100.70	112.00
18	Be	60	PRO	CA-N-CD	-7.33	101.73	112.00
80	DC	774	VAL	CA-C-N	-7.30	112.71	121.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
67	Ae	33	ARG	Peptide
67	Ae	44	ARG	Peptide
1	BA	195	TRP	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	BA	1612	0	1623	89	0
2	BB	1709	0	1784	136	0
3	BC	1635	0	1723	111	0
4	BE	2068	0	2154	129	0
5	BG	1820	0	1918	110	0
6	BH	1481	0	1572	79	0
7	BI	1489	0	1525	117	0
8	BJ	1494	0	1573	109	0
9	BL	1244	0	1314	101	0
10	BN	1192	0	1255	79	0
11	BO	941	0	979	98	0
12	BV	684	0	672	35	0
13	BW	1021	0	1060	74	0
14	BX	1121	0	1196	62	0
15	BY	1073	0	1132	75	0
16	Ba	769	0	818	66	0
17	Bb	610	0	633	30	0
18	Be	475	0	525	37	0
19	BD	1734	0	1817	92	0
20	BF	1609	0	1675	101	0
21	BK	817	0	804	51	0
22	BP	991	0	1035	51	0
23	BQ	1105	0	1166	78	0
24	BR	948	0	991	65	0
25	BS	1192	0	1222	91	0
26	BT	1095	0	1114	78	0
27	BU	855	0	917	67	0
28	BZ	574	0	616	36	0
29	Bc	497	0	535	34	0
30	Bd	442	0	432	33	0
31	Bg	2401	0	2356	138	0
32	Bf	605	0	654	37	0
33	BM	935	0	975	57	0
34	B5	37463	0	18842	2149	0
35	AA	1878	0	1946	161	0
36	AB	3081	0	3160	192	0
37	AC	2748	0	2859	168	0
38	A1	68786	0	34575	3724	0
39	A3	2579	0	1304	154	0
40	A4	3353	0	1695	237	0
41	AD	2341	0	2290	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	AE	1303	0	1376	73	0
43	AF	1784	0	1862	87	0
44	AG	1798	0	1894	87	0
45	AH	1510	0	1576	105	0
46	AI	1804	0	1854	93	0
47	AJ	1353	0	1383	84	0
48	AL	1543	0	1608	107	0
49	AM	1053	0	1149	62	0
50	AN	1720	0	1779	163	0
51	AO	1555	0	1659	97	0
52	AP	1388	0	1423	80	0
53	AQ	1441	0	1543	86	0
54	AR	1521	0	1617	118	0
55	AS	1445	0	1487	80	0
56	AT	1276	0	1323	78	0
57	AU	796	0	812	39	0
58	AV	1003	0	1047	69	0
59	AW	521	0	551	30	0
60	AX	968	0	1036	43	0
61	AY	993	0	1081	56	0
62	AZ	1092	0	1155	72	0
63	Aa	1173	0	1215	72	0
64	Ab	462	0	490	22	0
65	Ac	743	0	797	61	0
66	Ad	890	0	938	53	0
67	Ae	1020	0	1090	67	0
68	Af	850	0	880	57	0
69	Ag	880	0	945	75	0
70	Ah	969	0	1078	58	0
71	Ai	771	0	849	44	0
72	Aj	681	0	687	71	0
73	Ak	612	0	682	40	0
74	Al	436	0	475	38	0
75	Am	417	0	459	27	0
76	An	233	0	281	29	0
77	Ao	847	0	914	38	0
78	Ap	694	0	738	58	0
79	E	1718	0	1811	102	0
80	DC	6419	0	6487	436	0
81	EC	4235	0	2135	191	0
82	Ao	1	0	0	0	0
83	DC	28	0	12	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	DC	1	0	0	0	0
85	DC	35	0	40	6	0
All	All	212449	0	158654	10677	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 29.

The worst 5 of 10677 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)
34:B5:883:C:N4	34:B5:945:U:H3	1.53	1.05
34:B5:1175:U:H3	34:B5:1464:G:H1	1.07	1.02
15:BY:20:ARG:HH12	15:BY:22:GLN:HB2	1.24	1.01
38:A1:2276:G:H1	38:A1:2310:U:H3	1.05	1.01
38:A1:160:G:H1	38:A1:261:U:H3	1.07	1.00

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	182 (89%)	22 (11%)	0	100	100
2	BB	212/255 (83%)	176 (83%)	36 (17%)	0	100	100
3	BC	215/254 (85%)	202 (94%)	13 (6%)	0	100	100
4	BE	258/261 (99%)	230 (89%)	28 (11%)	0	100	100
5	BG	224/236 (95%)	208 (93%)	16 (7%)	0	100	100
6	BH	182/190 (96%)	167 (92%)	15 (8%)	0	100	100
7	BI	184/200 (92%)	156 (85%)	28 (15%)	0	100	100
8	BJ	183/197 (93%)	173 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	BL	153/156 (98%)	137 (90%)	16 (10%)	0	100	100
10	BN	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
11	BO	125/137 (91%)	104 (83%)	21 (17%)	0	100	100
12	BV	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
13	BW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
14	BX	142/145 (98%)	129 (91%)	13 (9%)	0	100	100
15	BY	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
16	Ba	95/119 (80%)	83 (87%)	12 (13%)	0	100	100
17	Bb	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
18	Be	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
19	BD	221/240 (92%)	208 (94%)	13 (6%)	0	100	100
20	BF	204/225 (91%)	186 (91%)	18 (9%)	0	100	100
21	BK	94/105 (90%)	83 (88%)	11 (12%)	0	100	100
22	BP	122/142 (86%)	112 (92%)	10 (8%)	0	100	100
23	BQ	139/143 (97%)	131 (94%)	8 (6%)	0	100	100
24	BR	119/136 (88%)	107 (90%)	12 (10%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100
26	BT	139/144 (96%)	127 (91%)	12 (9%)	0	100	100
27	BU	105/121 (87%)	98 (93%)	7 (7%)	0	100	100
28	BZ	69/108 (64%)	63 (91%)	6 (9%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Bg	310/319 (97%)	273 (88%)	37 (12%)	0	100	100
32	Bf	73/152 (48%)	60 (82%)	13 (18%)	0	100	100
33	BM	122/143 (85%)	117 (96%)	5 (4%)	0	100	100
35	AA	245/254 (96%)	226 (92%)	19 (8%)	0	100	100
36	AB	383/387 (99%)	338 (88%)	44 (12%)	1 (0%)	36	69
37	AC	359/362 (99%)	323 (90%)	36 (10%)	0	100	100
41	AD	290/297 (98%)	268 (92%)	22 (8%)	0	100	100
42	AE	163/176 (93%)	143 (88%)	20 (12%)	0	100	100
43	AF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	AG	228/256 (89%)	208 (91%)	20 (9%)	0	100	100
45	AH	188/191 (98%)	166 (88%)	22 (12%)	0	100	100
46	AI	220/222 (99%)	204 (93%)	16 (7%)	0	100	100
47	AJ	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
48	AL	191/199 (96%)	181 (95%)	10 (5%)	0	100	100
49	AM	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
50	AN	201/204 (98%)	178 (89%)	23 (11%)	0	100	100
51	AO	195/199 (98%)	185 (95%)	10 (5%)	0	100	100
52	AP	171/184 (93%)	157 (92%)	14 (8%)	0	100	100
53	AQ	183/186 (98%)	170 (93%)	13 (7%)	0	100	100
54	AR	186/189 (98%)	167 (90%)	19 (10%)	0	100	100
55	AS	170/178 (96%)	154 (91%)	16 (9%)	0	100	100
56	AT	157/160 (98%)	141 (90%)	16 (10%)	0	100	100
57	AU	98/121 (81%)	86 (88%)	12 (12%)	0	100	100
58	AV	134/137 (98%)	127 (95%)	7 (5%)	0	100	100
59	AW	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
60	AX	119/142 (84%)	108 (91%)	11 (9%)	0	100	100
61	AY	124/127 (98%)	113 (91%)	11 (9%)	0	100	100
62	AZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
63	Aa	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
64	Ab	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
65	Ac	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
66	Ad	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
67	Ae	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
68	Af	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
69	Ag	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
70	Ah	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
71	Ai	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
72	Aj	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
73	Ak	75/78 (96%)	67 (89%)	8 (11%)	0	100	100
74	Al	48/51 (94%)	43 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Am	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
76	An	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
77	Ao	103/106 (97%)	95 (92%)	8 (8%)	0	100	100
78	Ap	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
79	E	215/217 (99%)	195 (91%)	20 (9%)	0	100	100
80	DC	819/842 (97%)	735 (90%)	81 (10%)	3 (0%)	30	64
All	All	11962/12946 (92%)	10881 (91%)	1077 (9%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	DC	700	ARG
80	DC	698	ILE
80	DC	773	PRO
36	AB	244	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	101/124 (82%)	101 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	62/89 (70%)	62 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	137/153 (90%)	137 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	AI	190/190 (100%)	190 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
80	DC	699/714 (98%)	699 (100%)	0	100	100
All	All	10195/10903 (94%)	10195 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
47	AJ	20	ASN
54	AR	118	HIS
80	DC	91	GLN
48	AL	19	GLN
51	AO	26[A]	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1754/1798 (97%)	565 (32%)	15 (0%)
38	A1	3212/3360 (95%)	875 (27%)	29 (0%)
39	A3	120/121 (99%)	27 (22%)	1 (0%)
40	A4	157/158 (99%)	39 (24%)	2 (1%)
81	EC	196/202 (97%)	113 (57%)	6 (3%)
All	All	5439/5639 (96%)	1619 (29%)	53 (0%)

5 of 1619 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	9	U
34	B5	25	C
34	B5	34	G
34	B5	43	A

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	1560	G
38	A1	2437	G
81	EC	6868	C
38	A1	1588	A
38	A1	2094	C

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

60 non-standard protein/DNA/RNA residues are 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
80	DDE	DC	699	-	18,20,21	1.08	1 (5%)	17,28,30	1.09	2 (11%)
38	PSU	A1	2191	38	18,21,22	1.50	5 (27%)	21,30,33	2.06	4 (19%)
36	HIC	AB	243	36	10,11,12	1.47	1 (10%)	9,14,16	1.34	2 (22%)
38	PSU	A1	990	38	18,21,22	1.38	2 (11%)	21,30,33	2.17	4 (19%)
38	PSU	A1	776	38	18,21,22	1.39	5 (27%)	21,30,33	2.08	3 (14%)
38	5MC	A1	2870	38	19,22,23	1.48	3 (15%)	26,32,35	1.15	3 (11%)
38	1MA	A1	645	38	21,25,26	1.36	5 (23%)	30,37,40	1.67	4 (13%)
38	PSU	A1	2260	38	18,21,22	1.36	3 (16%)	21,30,33	2.14	4 (19%)
38	PSU	A1	2923	38	18,21,22	1.34	2 (11%)	21,30,33	2.09	4 (19%)
34	G7M	B5	1575	34	23,26,27	2.52	7 (30%)	34,39,42	1.72	7 (20%)
38	UR3	A1	2634	38	19,22,23	0.90	0	26,32,35	1.72	3 (11%)
34	PSU	B5	759	34	18,21,22	1.36	2 (11%)	21,30,33	2.07	3 (14%)
38	PSU	A1	2340	38	18,21,22	1.36	3 (16%)	21,30,33	2.01	4 (19%)
34	PSU	B5	1290	34	18,21,22	1.40	3 (16%)	21,30,33	2.17	4 (19%)
34	PSU	B5	302	34	18,21,22	1.38	4 (22%)	21,30,33	2.03	4 (19%)
38	PSU	A1	960	38	18,21,22	1.39	2 (11%)	21,30,33	2.12	4 (19%)
38	OMG	A1	2922	38	23,26,27	1.19	4 (17%)	32,38,41	1.92	6 (18%)
38	PSU	A1	2349	38	18,21,22	1.40	2 (11%)	21,30,33	2.08	4 (19%)
38	PSU	A1	2258	38	18,21,22	1.35	2 (11%)	21,30,33	2.04	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	PSU	A1	2975	38	18,21,22	1.38	3 (16%)	21,30,33	2.10	4 (19%)
38	PSU	A1	2129	38	18,21,22	1.41	4 (22%)	21,30,33	2.11	3 (14%)
34	B8N	B5	1191	34	25,29,30	1.40	3 (12%)	28,42,45	1.62	4 (14%)
38	PSU	A1	2314	38	18,21,22	1.42	3 (16%)	21,30,33	2.13	4 (19%)
38	PSU	A1	1004	38	18,21,22	1.40	2 (11%)	21,30,33	2.08	3 (14%)
38	5MC	A1	2278	38	19,22,23	1.42	2 (10%)	26,32,35	1.50	5 (19%)
38	PSU	A1	2880	38	18,21,22	1.45	4 (22%)	21,30,33	2.11	4 (19%)
34	MA6	B5	1782	34	23,26,27	1.42	5 (21%)	33,38,41	2.08	10 (30%)
38	PSU	A1	2735	38	18,21,22	1.38	3 (16%)	21,30,33	2.06	3 (14%)
34	PSU	B5	999	34	18,21,22	1.35	2 (11%)	21,30,33	2.03	4 (19%)
34	4AC	B5	1280	34	21,24,25	1.14	1 (4%)	28,34,37	1.15	2 (7%)
38	PSU	A1	2865	38	18,21,22	1.44	3 (16%)	21,30,33	2.06	4 (19%)
34	PSU	B5	466	34	18,21,22	1.35	2 (11%)	21,30,33	2.05	5 (23%)
34	PSU	B5	1187	34	18,21,22	1.38	2 (11%)	21,30,33	2.05	4 (19%)
38	PSU	A1	1124	38	18,21,22	1.38	3 (16%)	21,30,33	2.00	4 (19%)
38	PSU	A1	2133	38	18,21,22	1.41	3 (16%)	21,30,33	2.22	4 (19%)
38	PSU	A1	2944	38	18,21,22	1.41	4 (22%)	21,30,33	2.06	4 (19%)
38	PSU	A1	1056	38	18,21,22	1.38	3 (16%)	21,30,33	2.14	4 (19%)
34	PSU	B5	1415	34	18,21,22	1.38	2 (11%)	21,30,33	1.99	3 (14%)
38	1MA	A1	2142	38	21,25,26	1.33	4 (19%)	30,37,40	1.74	6 (20%)
34	PSU	B5	1181	34	18,21,22	1.37	2 (11%)	21,30,33	2.11	3 (14%)
38	OMU	A1	2921	38	19,22,23	1.23	3 (15%)	25,31,34	1.85	5 (20%)
34	PSU	B5	120	34	18,21,22	1.42	3 (16%)	21,30,33	2.00	4 (19%)
38	PSU	A1	1042	38	18,21,22	1.41	4 (22%)	21,30,33	2.09	5 (23%)
38	PSU	A1	2351	38	18,21,22	1.42	4 (22%)	21,30,33	2.19	4 (19%)
38	PSU	A1	2826	38	18,21,22	1.39	4 (22%)	21,30,33	1.97	3 (14%)
34	PSU	B5	211	34	18,21,22	1.42	3 (16%)	21,30,33	2.04	3 (14%)
38	PSU	A1	966	38	18,21,22	1.39	4 (22%)	21,30,33	2.05	4 (19%)
34	PSU	B5	766	34	18,21,22	1.38	3 (16%)	21,30,33	2.01	4 (19%)
39	PSU	A3	50	39	18,21,22	1.40	2 (11%)	21,30,33	2.02	3 (14%)
40	PSU	A4	73	40	18,21,22	1.42	3 (16%)	21,30,33	2.20	5 (23%)
34	MA6	B5	1781	34	23,26,27	1.44	5 (21%)	33,38,41	2.06	11 (33%)
38	PSU	A1	2266	38	18,21,22	1.55	5 (27%)	21,30,33	1.94	3 (14%)
34	4AC	B5	1773	34	21,24,25	1.06	1 (4%)	28,34,37	1.06	3 (10%)
38	PSU	A1	1110	38	18,21,22	1.42	4 (22%)	21,30,33	2.43	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	PSU	A1	2264	38	18,21,22	1.46	4 (22%)	21,30,33	2.16	3 (14%)
34	PSU	B5	632	34	18,21,22	1.38	3 (16%)	21,30,33	2.07	3 (14%)
38	PSU	A1	1052	38	18,21,22	1.37	3 (16%)	21,30,33	2.05	4 (19%)
34	PSU	B5	106	34	18,21,22	1.38	2 (11%)	21,30,33	2.01	3 (14%)
38	PSU	A1	986	38	18,21,22	1.41	3 (16%)	21,30,33	2.06	3 (14%)
38	PSU	A1	2416	38	18,21,22	1.47	5 (27%)	21,30,33	2.19	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
80	DDE	DC	699	-	-	10/20/21/23	0/1/1/1
38	PSU	A1	2191	38	-	3/7/25/26	0/2/2/2
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	PSU	A1	990	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	776	38	-	3/7/25/26	0/2/2/2
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
38	1MA	A1	645	38	-	2/7/25/26	0/3/3/3
38	PSU	A1	2260	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2923	38	-	3/7/25/26	0/2/2/2
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	759	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2340	38	-	3/7/25/26	0/2/2/2
34	PSU	B5	1290	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	302	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	960	38	-	2/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	PSU	A1	2349	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2258	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2975	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2129	38	-	0/7/25/26	0/2/2/2
34	B8N	B5	1191	34	-	2/16/34/35	0/2/2/2
38	PSU	A1	2314	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1004	38	-	0/7/25/26	0/2/2/2
38	5MC	A1	2278	38	-	5/7/25/26	0/2/2/2
38	PSU	A1	2880	38	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	MA6	B5	1782	34	-	3/11/29/30	0/3/3/3
38	PSU	A1	2735	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	999	34	-	1/7/25/26	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	PSU	A1	2865	38	-	2/7/25/26	0/2/2/2
34	PSU	B5	466	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	1187	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1124	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2133	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2944	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1056	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1415	34	-	2/7/25/26	0/2/2/2
38	1MA	A1	2142	38	-	0/7/25/26	0/3/3/3
34	PSU	B5	1181	34	-	0/7/25/26	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	PSU	B5	120	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1042	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	2351	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2826	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	211	34	-	2/7/25/26	0/2/2/2
38	PSU	A1	966	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	766	34	-	0/7/25/26	0/2/2/2
39	PSU	A3	50	39	-	4/7/25/26	0/2/2/2
40	PSU	A4	73	40	-	3/7/25/26	0/2/2/2
34	MA6	B5	1781	34	-	6/11/29/30	0/3/3/3
38	PSU	A1	2266	38	-	4/7/25/26	0/2/2/2
34	4AC	B5	1773	34	-	0/11/29/30	0/2/2/2
38	PSU	A1	1110	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2264	38	-	5/7/25/26	0/2/2/2
34	PSU	B5	632	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1052	38	-	1/7/25/26	0/2/2/2
34	PSU	B5	106	34	-	1/7/25/26	0/2/2/2
38	PSU	A1	986	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2416	38	-	0/7/25/26	0/2/2/2

The worst 5 of 184 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O6-C6	7.52	1.37	1.23
34	B5	1575	G7M	C2-N2	5.61	1.47	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2870	5MC	C5-C4	5.22	1.48	1.44
34	B5	1575	G7M	C5-N7	-4.98	1.33	1.39
34	B5	1782	MA6	C5-C4	4.43	1.47	1.39

The worst 5 of 242 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2634	UR3	C4-N3-C2	-7.01	118.94	124.58
38	A1	2416	PSU	N1-C2-N3	6.89	122.44	115.17
38	A1	2264	PSU	N1-C2-N3	6.86	122.41	115.17
38	A1	2133	PSU	N1-C2-N3	6.83	122.37	115.17
38	A1	2351	PSU	N1-C2-N3	6.82	122.36	115.17

There are no chirality outliers.

5 of 75 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	A3	50	PSU	C2'-C1'-C5-C4
39	A3	50	PSU	C2'-C1'-C5-C6
80	DC	699	DDE	N-CA-CB-CG
80	DC	699	DDE	C-CA-CB-CG
80	DC	699	DDE	CBI-CBW-NCB-CAB

There are no ring outliers.

44 monomers are involved in 97 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2191	PSU	1	0
36	AB	243	HIC	2	0
38	A1	990	PSU	4	0
38	A1	776	PSU	2	0
38	A1	645	1MA	1	0
38	A1	2260	PSU	2	0
38	A1	2923	PSU	1	0
34	B5	1575	G7M	1	0
38	A1	2634	UR3	1	0
34	B5	759	PSU	3	0
38	A1	2340	PSU	3	0
34	B5	1290	PSU	2	0
34	B5	302	PSU	3	0
38	A1	960	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2349	PSU	1	0
38	A1	2258	PSU	3	0
38	A1	2975	PSU	3	0
38	A1	2129	PSU	2	0
38	A1	2314	PSU	2	0
38	A1	2880	PSU	4	0
38	A1	2735	PSU	1	0
34	B5	999	PSU	2	0
34	B5	1280	4AC	4	0
38	A1	2865	PSU	2	0
34	B5	466	PSU	2	0
34	B5	1187	PSU	3	0
38	A1	1056	PSU	2	0
34	B5	1181	PSU	2	0
34	B5	120	PSU	2	0
38	A1	1042	PSU	2	0
38	A1	2351	PSU	1	0
34	B5	211	PSU	3	0
38	A1	966	PSU	5	0
34	B5	766	PSU	1	0
39	A3	50	PSU	1	0
40	A4	73	PSU	2	0
34	B5	1781	MA6	2	0
34	B5	1773	4AC	3	0
38	A1	1110	PSU	2	0
38	A1	2264	PSU	1	0
34	B5	632	PSU	6	0
38	A1	1052	PSU	1	0
38	A1	986	PSU	1	0
38	A1	2416	PSU	4	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	GDP	DC	901	84	29,30,30	1.14	3 (10%)	45,47,47	1.86	8 (17%)
85	SO1	DC	903	-	34,39,39	0.69	1 (2%)	38,64,64	1.33	6 (15%)

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
83	GDP	DC	901	84	-	5/16/32/32	0/3/3/3
85	SO1	DC	903	-	1/1/15/16	5/21/104/104	0/7/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	DC	901	GDP	C5-C4	3.02	1.47	1.38
85	DC	903	SO1	O14-C5	-2.95	1.19	1.30
83	DC	901	GDP	C6-N1	-2.21	1.34	1.38
83	DC	901	GDP	C5-N7	-2.14	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	DC	901	GDP	C5-C4-N3	-6.32	118.34	128.39
83	DC	901	GDP	C2-N3-C4	5.19	121.24	112.30
85	DC	903	SO1	C12-C6-C2	-5.10	97.19	105.09
83	DC	901	GDP	N9-C4-N3	4.41	134.77	125.95
83	DC	901	GDP	C6-C5-N7	3.27	136.25	130.29

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	DC	903	SO1	C4

5 of 10 torsion outliers are listed below:

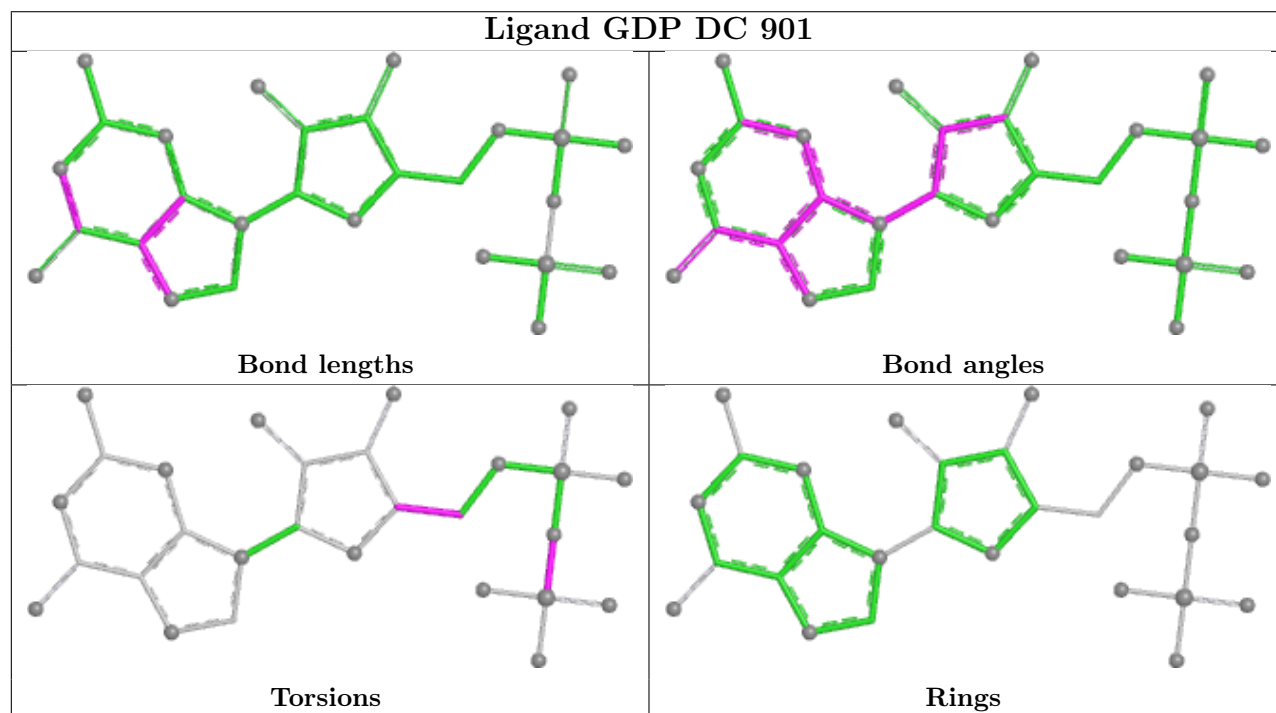
Mol	Chain	Res	Type	Atoms
85	DC	903	SO1	C2-C1-C5-O14
85	DC	903	SO1	C2-C1-C5-O15
85	DC	903	SO1	O56-C52-O17-C8
83	DC	901	GDP	O4'-C4'-C5'-O5'
83	DC	901	GDP	C3'-C4'-C5'-O5'

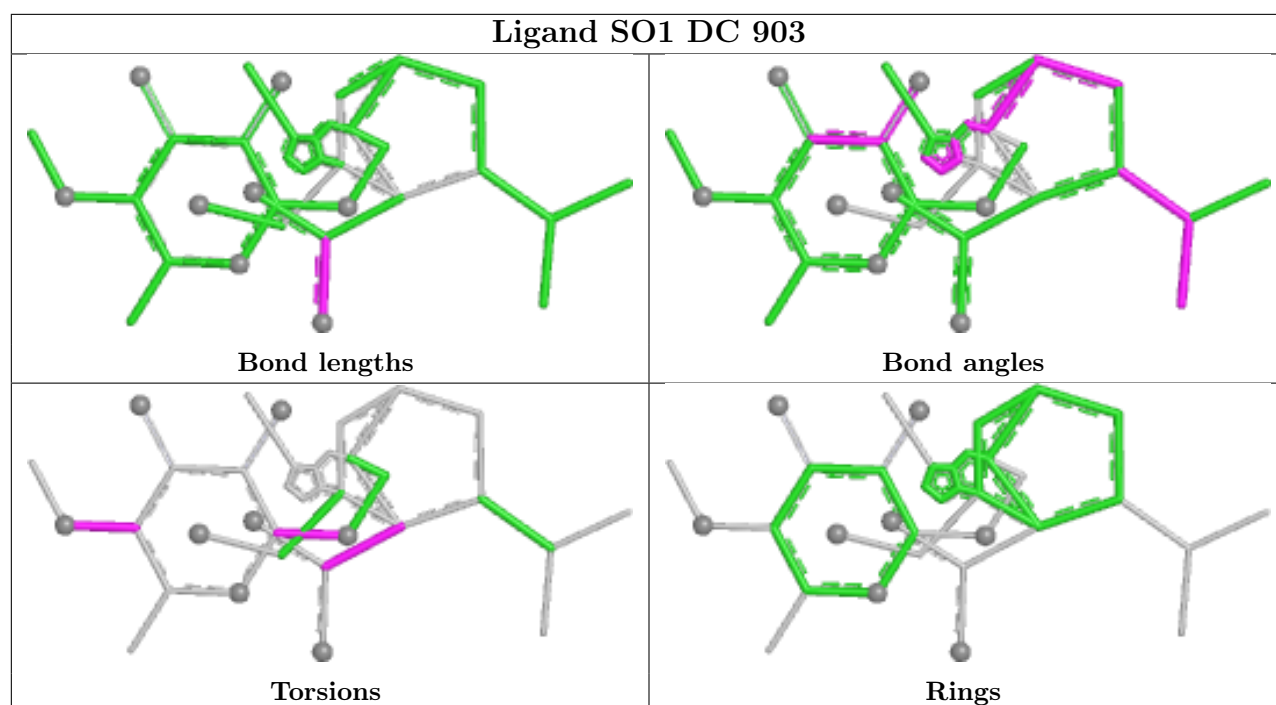
There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	DC	901	GDP	6	0
85	DC	903	SO1	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	451:U	O3'	486:A	P	15.26

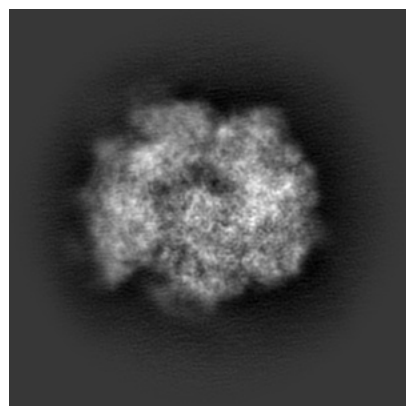
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40999. These allow visual inspection of the internal detail of the map and identification of artifacts.

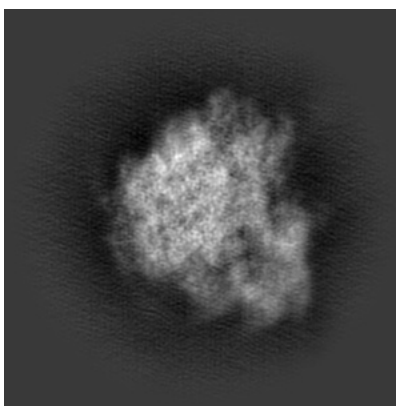
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

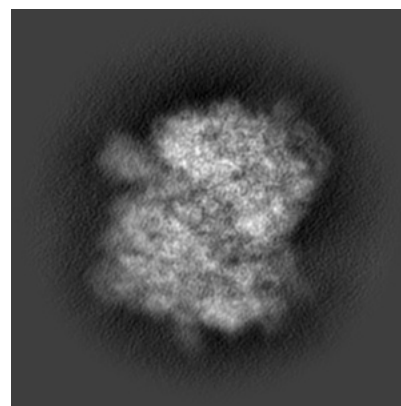
6.1.1 Primary map



X

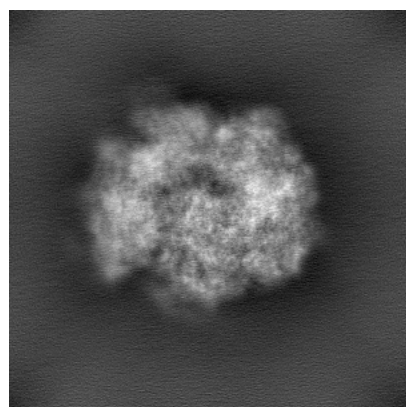


Y

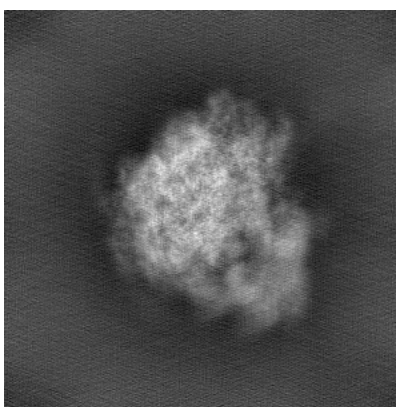


Z

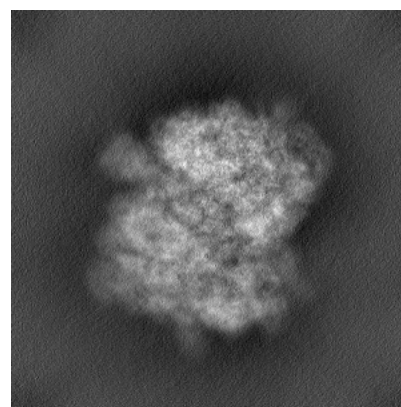
6.1.2 Raw map



X



Y

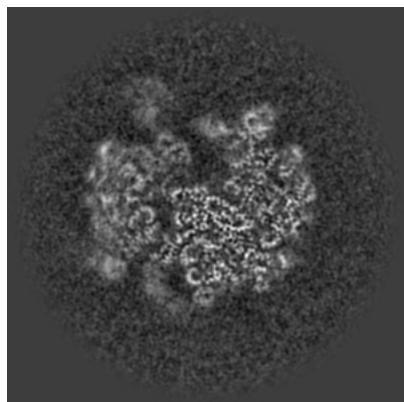


Z

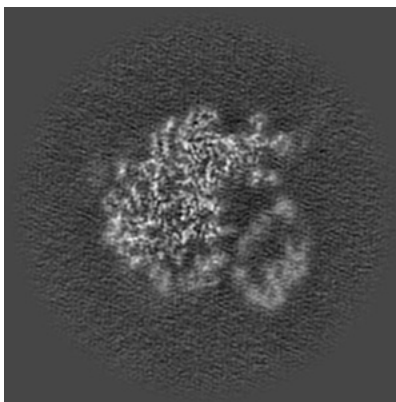
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

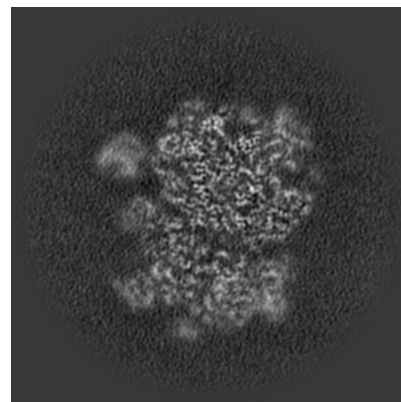
6.2.1 Primary map



X Index: 200

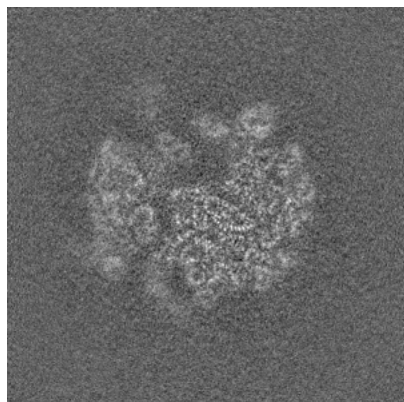


Y Index: 200

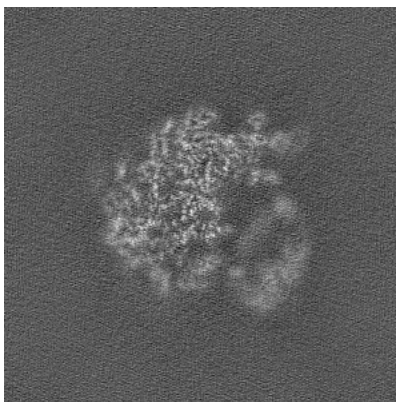


Z Index: 200

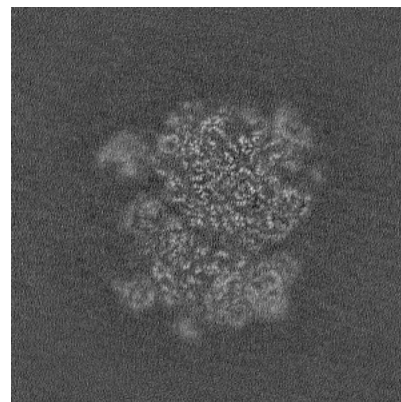
6.2.2 Raw map



X Index: 200



Y Index: 200

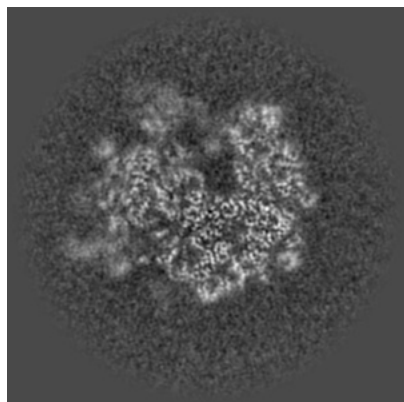


Z Index: 200

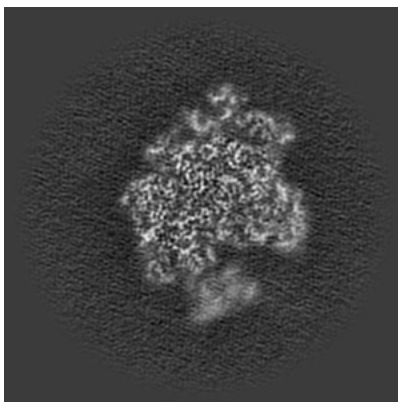
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

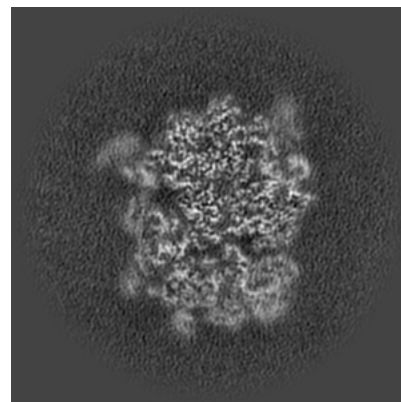
6.3.1 Primary map



X Index: 186

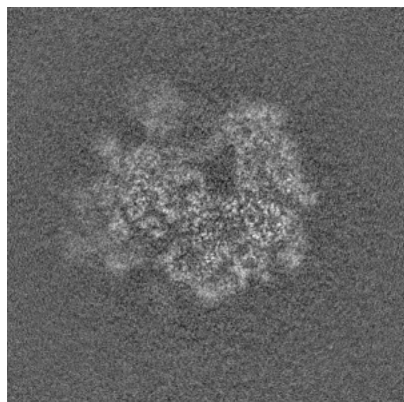


Y Index: 245

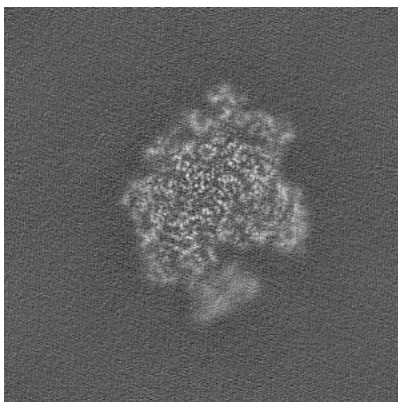


Z Index: 190

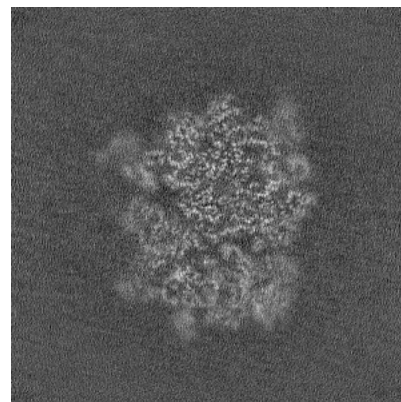
6.3.2 Raw map



X Index: 184



Y Index: 245

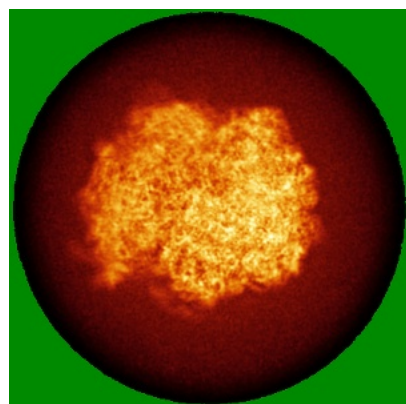


Z Index: 191

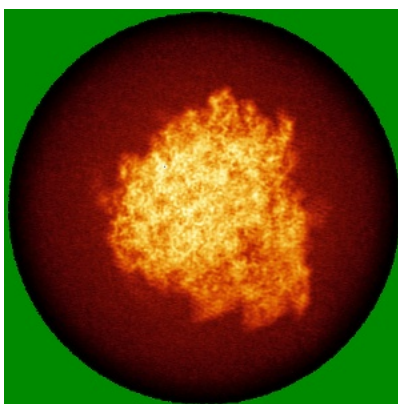
The images above show the largest variance slices of the map in three orthogonal directions.

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

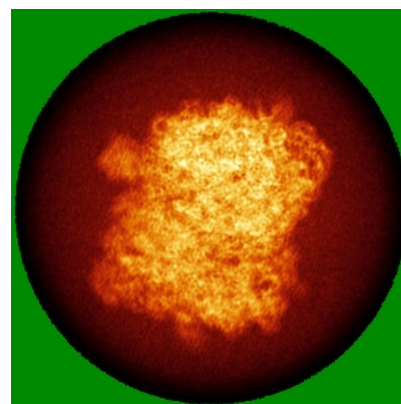
6.4.1 Primary map



X

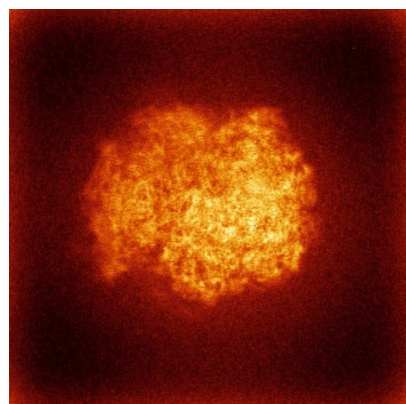


Y

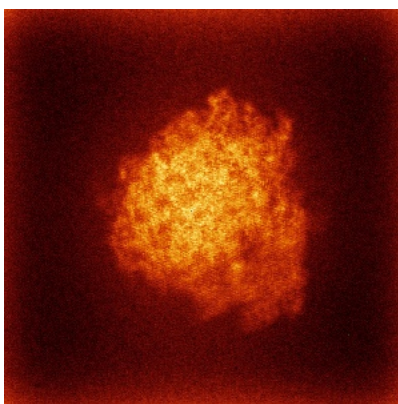


Z

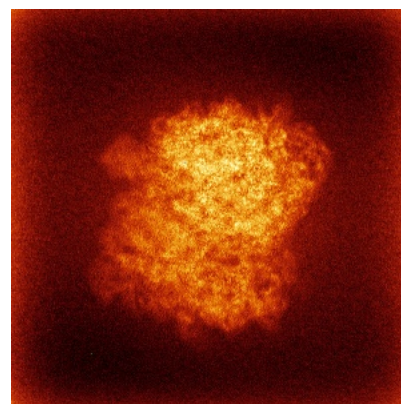
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



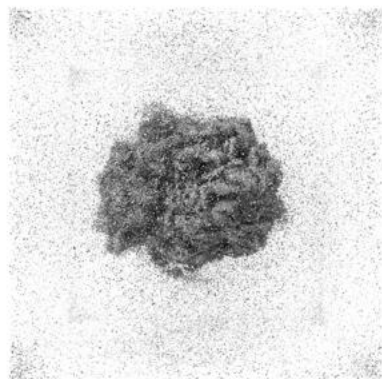
Y



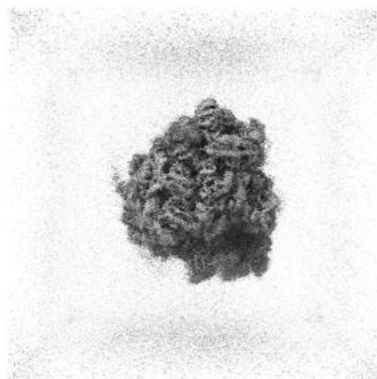
Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

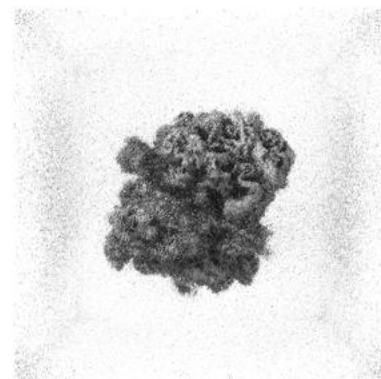
6.5.2 Raw map



X



Y



Z

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

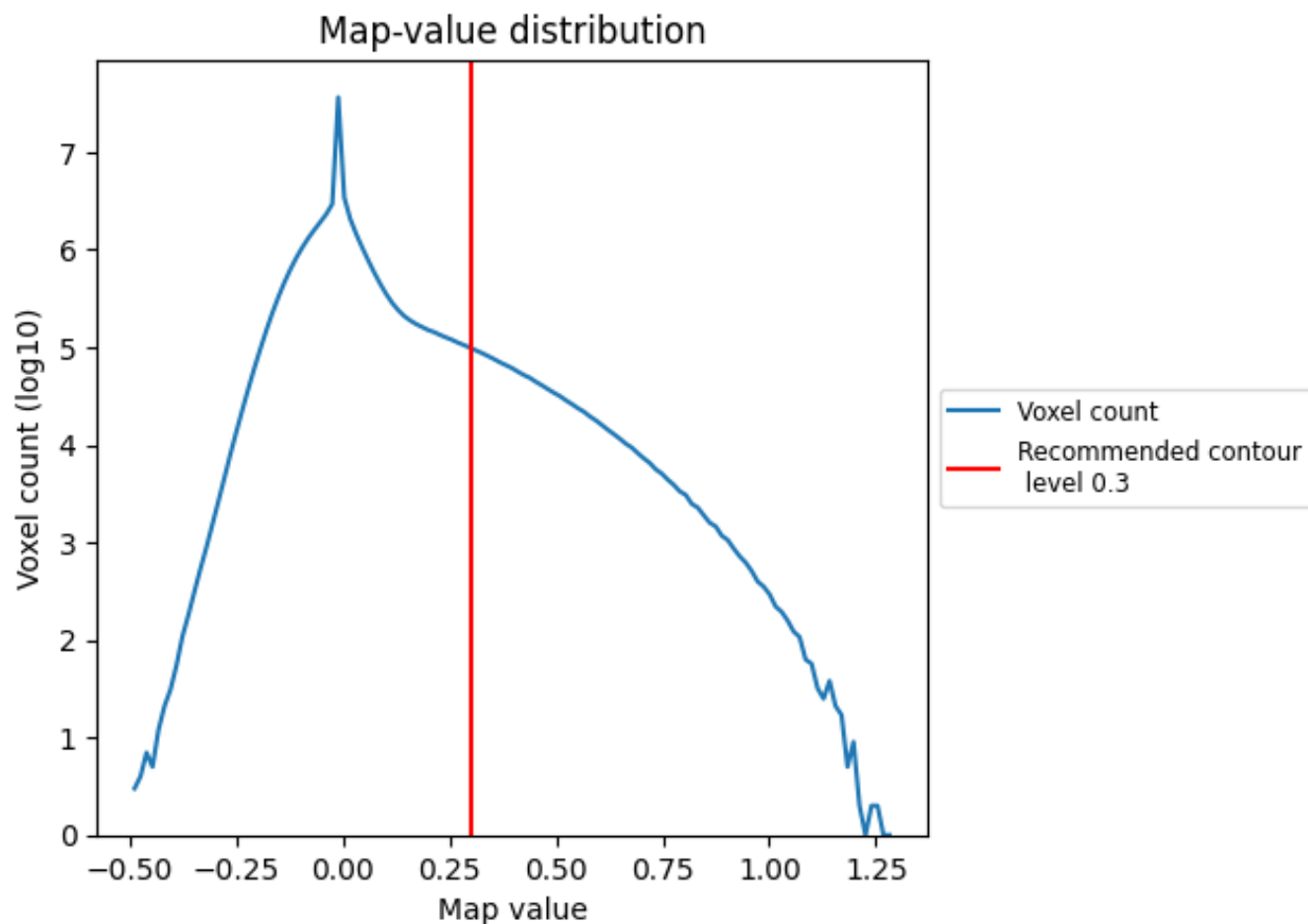
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

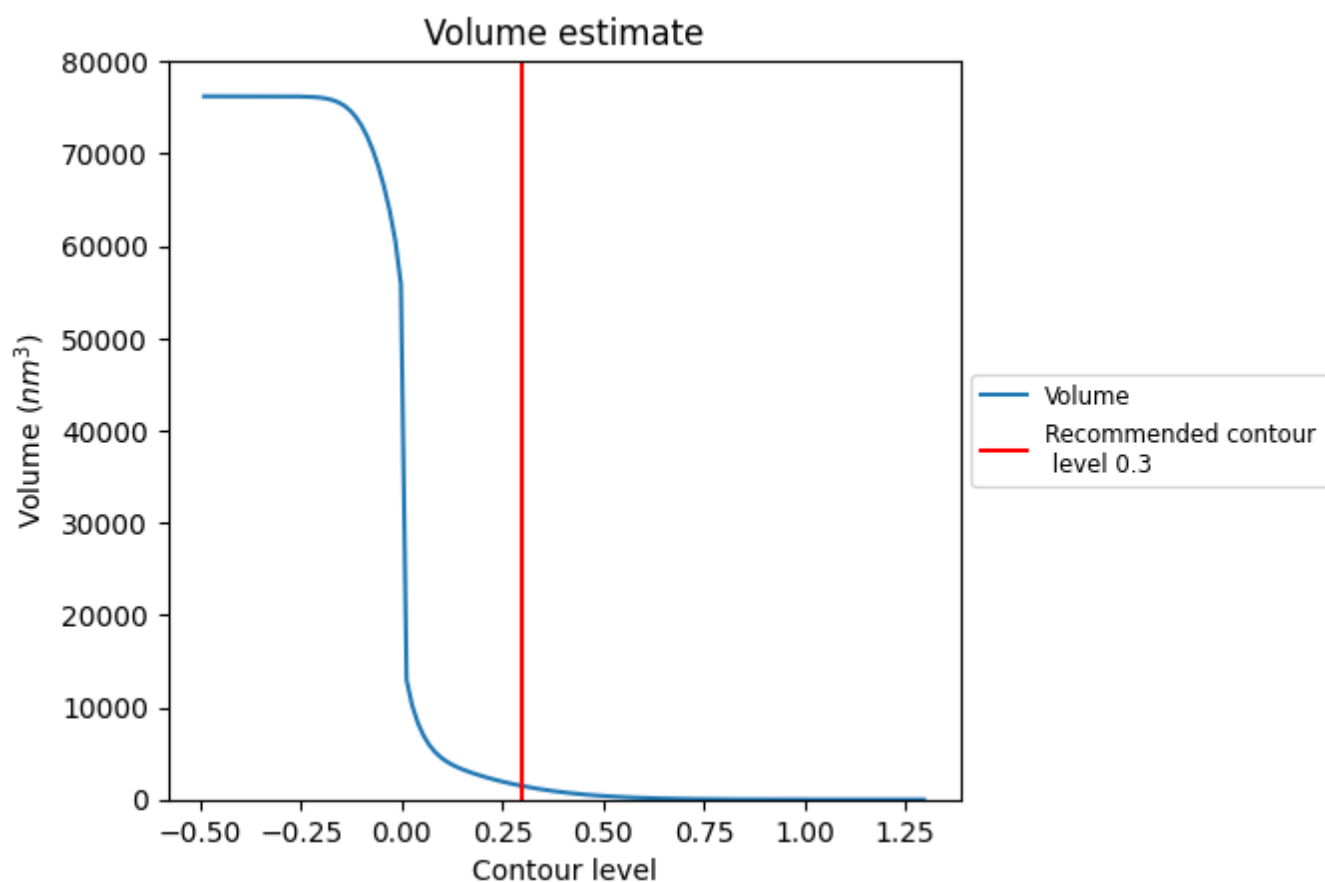
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

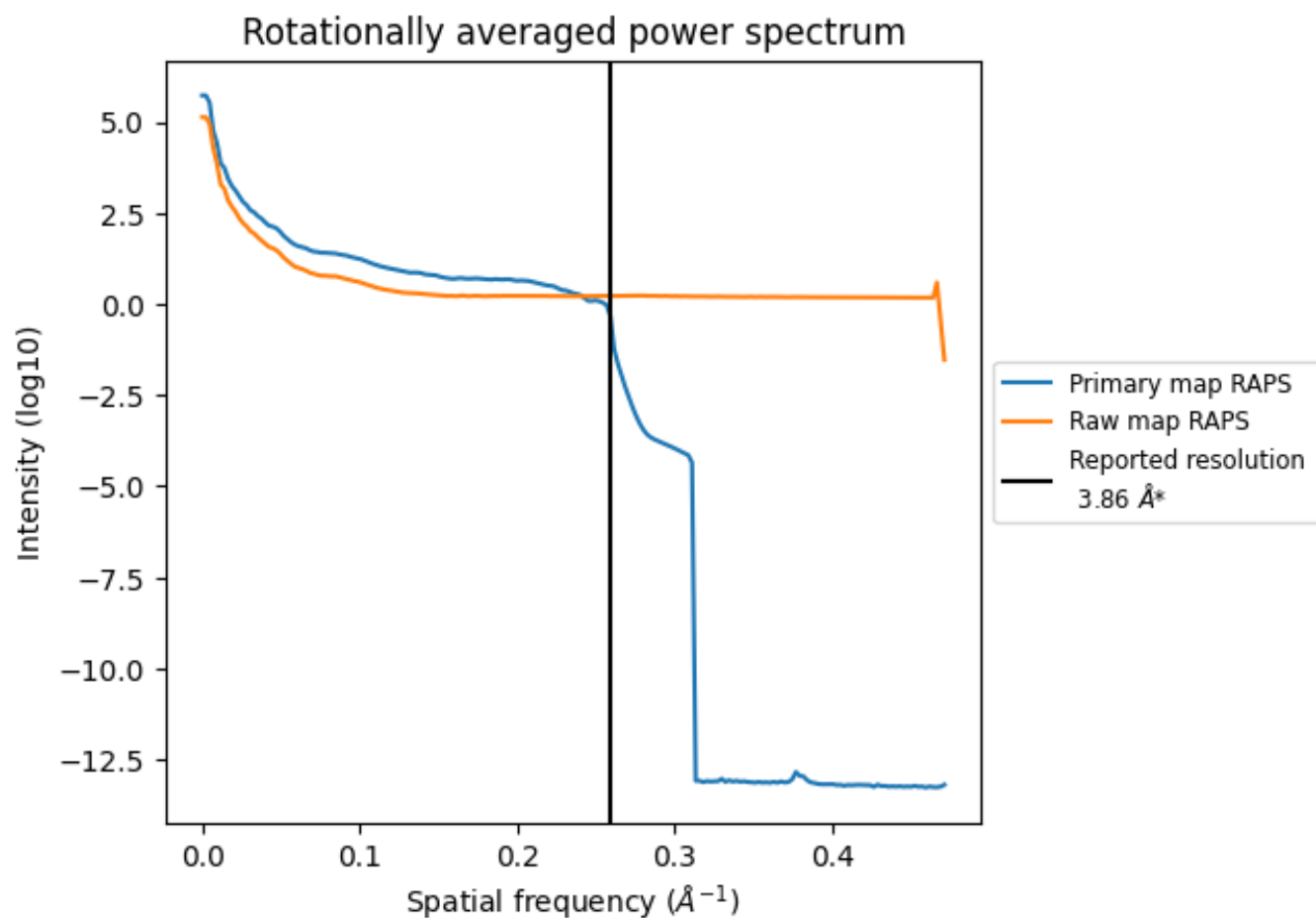
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1472 nm³; this corresponds to an approximate mass of 1329 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

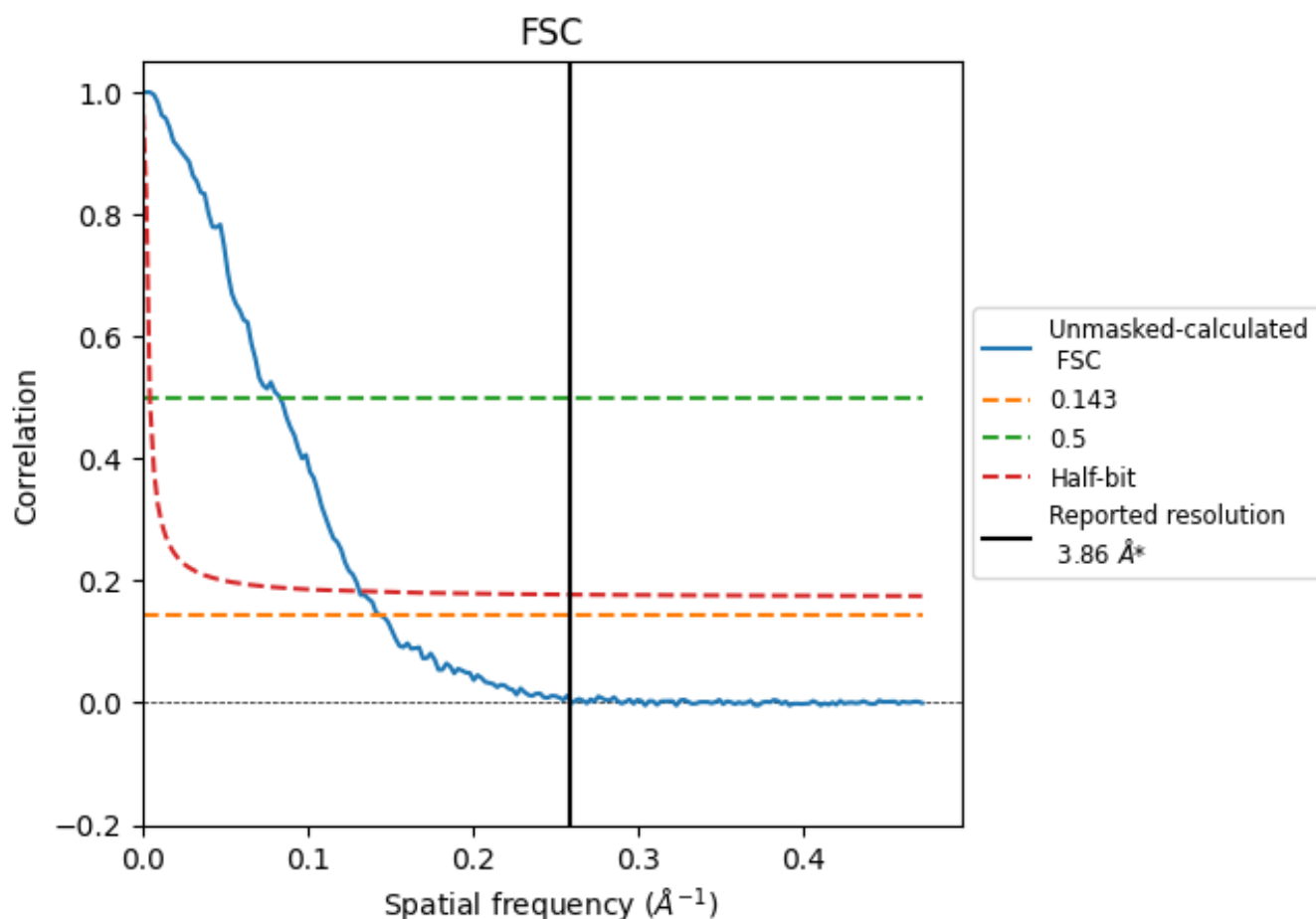


*Reported resolution corresponds to spatial frequency of 0.259 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.259 Å⁻¹

8.2 Resolution estimates [i](#)

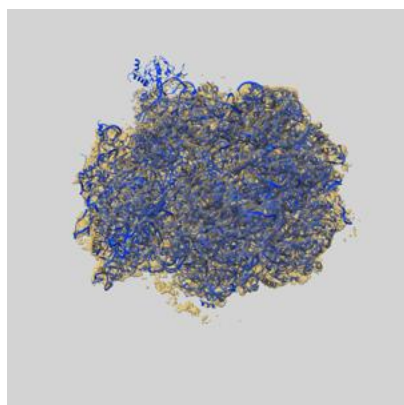
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.86	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.94	12.05	7.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.94 differs from the reported value 3.86 by more than 10 %

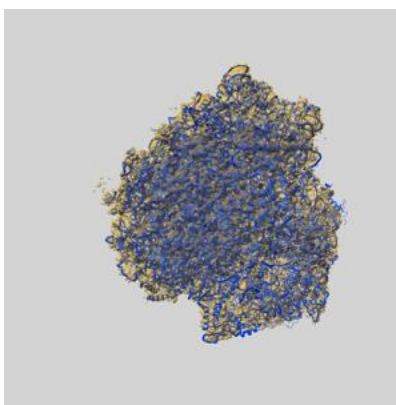
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40999 and PDB model 8T3C. Per-residue inclusion information can be found in section [3](#) on page [21](#).

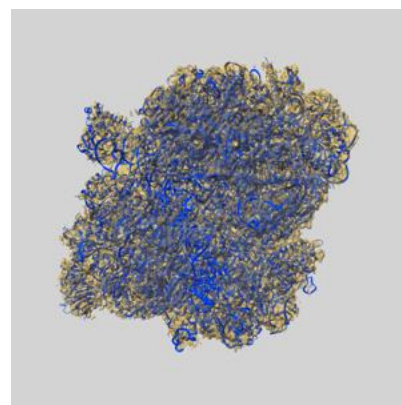
9.1 Map-model overlay [i](#)



X



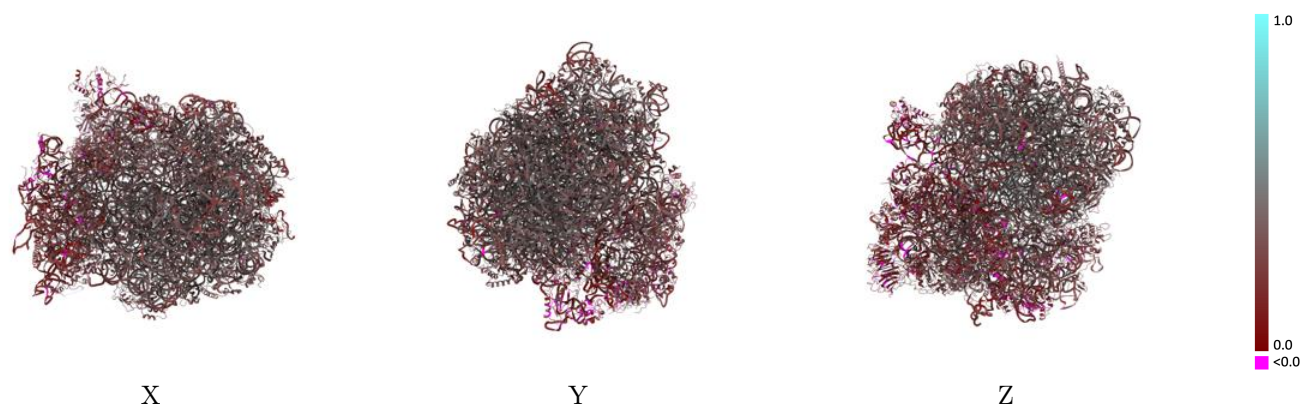
Y



Z

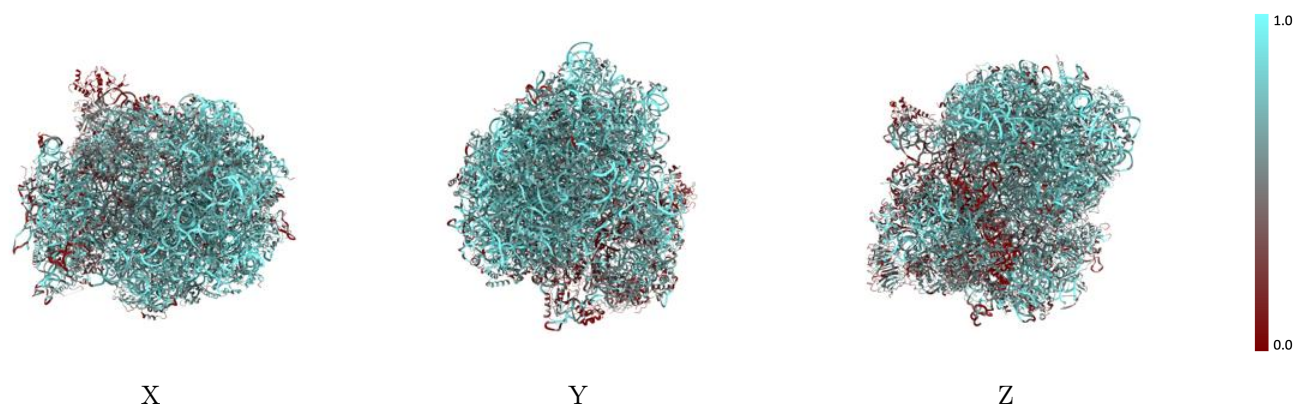
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



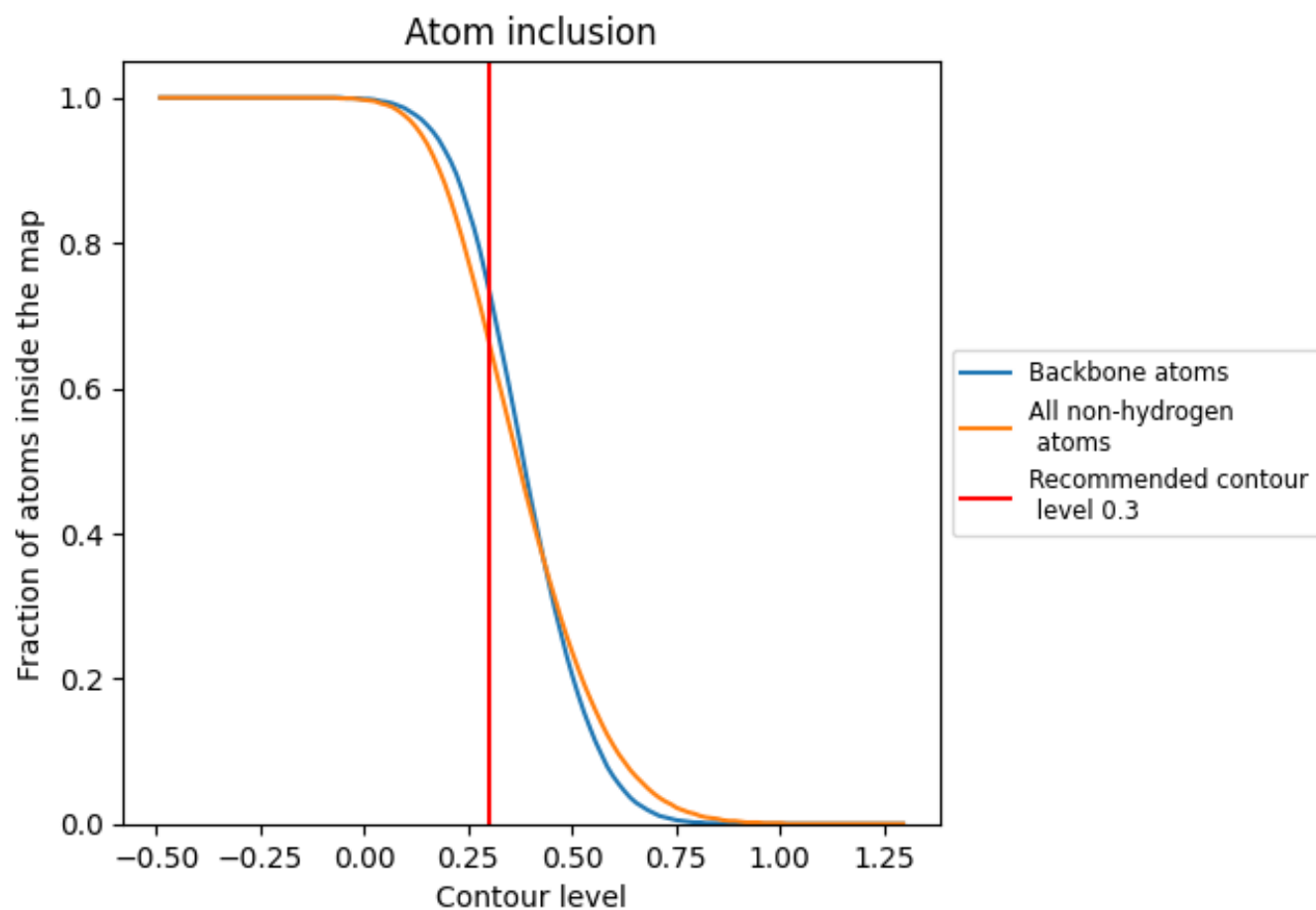
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 66% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6650	 0.3250
A1	 0.8290	 0.3610
A3	 0.9120	 0.3390
A4	 0.8720	 0.3810
AA	 0.4920	 0.4130
AB	 0.6320	 0.3830
AC	 0.6570	 0.3940
AD	 0.6360	 0.3140
AE	 0.6810	 0.3440
AF	 0.7170	 0.3920
AG	 0.6230	 0.3600
AH	 0.6010	 0.3560
AI	 0.5460	 0.3490
AJ	 0.4580	 0.2970
AL	 0.6780	 0.3810
AM	 0.6620	 0.3510
AN	 0.6320	 0.4000
AO	 0.6370	 0.3870
AP	 0.6650	 0.3920
AQ	 0.5790	 0.3920
AR	 0.5600	 0.3470
AS	 0.7060	 0.3910
AT	 0.5940	 0.3790
AU	 0.6390	 0.3370
AV	 0.4540	 0.3960
AW	 0.6020	 0.3770
AX	 0.6130	 0.3870
AY	 0.7070	 0.3760
AZ	 0.6480	 0.3580
Aa	 0.6330	 0.4020
Ab	 0.5330	 0.3680
Ac	 0.4910	 0.3710
Ad	 0.6520	 0.3830
Ae	 0.6340	 0.4080
Af	 0.6860	 0.4140



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Chain	Atom inclusion	Q-score
Ag	 0.5790	 0.3910
Ah	 0.6940	 0.3590
Ai	 0.6280	 0.3430
Aj	 0.6960	 0.4130
Ak	 0.3970	 0.3410
Al	 0.6050	 0.4030
Am	 0.5960	 0.4180
An	 0.4810	 0.3490
Ao	 0.3780	 0.3700
Ap	 0.4890	 0.3900
B5	 0.7380	 0.2840
BA	 0.5300	 0.3020
BB	 0.3510	 0.2720
BC	 0.5680	 0.3360
BD	 0.4040	 0.2640
BE	 0.4400	 0.2490
BF	 0.3010	 0.2590
BG	 0.5200	 0.2470
BH	 0.4260	 0.2950
BI	 0.4670	 0.2980
BJ	 0.5240	 0.2150
BK	 0.4170	 0.2280
BL	 0.4270	 0.3190
BM	 0.0100	 0.1990
BN	 0.4240	 0.3220
BO	 0.3290	 0.2990
BP	 0.2300	 0.2150
BQ	 0.3980	 0.2400
BR	 0.4000	 0.2780
BS	 0.3710	 0.2180
BT	 0.4480	 0.1910
BU	 0.3740	 0.2450
BV	 0.5440	 0.3130
BW	 0.5610	 0.3420
BX	 0.3910	 0.3460
BY	 0.4560	 0.1910
BZ	 0.4150	 0.2390
Ba	 0.3790	 0.3510
Bb	 0.3540	 0.3200
Bc	 0.2580	 0.2420
Bd	 0.6290	 0.2860
Be	 0.3770	 0.2710

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Chain	Atom inclusion	Q-score
Bf	 0.0170	 0.1870
Bg	 0.4520	 0.1890
DC	 0.4780	 0.2840
E	 0.2830	 0.1420
EC	 0.3220	 0.1580