



## wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 09:34 AM EST

PDB ID : 6OLZ  
EMDB ID : EMD-0598  
Title : Human ribosome nascent chain complex (PCSK9-RNC) stalled by a drug-like molecule with PP tRNA  
Authors : Li, W.; Cate, J.H.D.  
Deposited on : 2019-04-17  
Resolution : 3.90 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](mailto: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>.

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

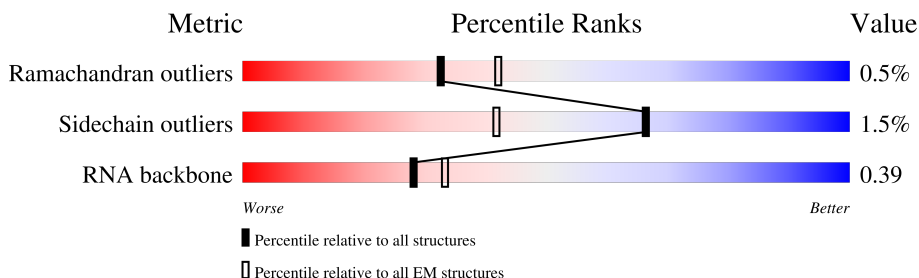
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	AA	248	
2	BA	215	
3	AB	394	
4	BB	212	
5	AC	363	
6	BC	222	
7	A3	157	
8	A4	119	

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Mol	Chain	Length	Quality of chain
9	AD	294	19% 97%
10	AE	247	21% 88% 9%
11	AF	234	9% 97%
12	AG	234	26% 99%
13	AH	191	19% 99%
14	AI	211	17% 95%
15	AJ	169	30% 99%
16	AL	205	19% 95%
17	AM	139	12% 99%
18	AN	203	5% 98%
19	AO	195	9% 97%
20	AP	153	5% 100%
21	AQ	187	13% 99%
22	AR	181	17% 98%
23	AS	175	8% 99%
24	AT	157	13% 99%
25	AU	99	34% 99%
26	AV	129	11% 99%
27	AW	121	55% 98%
28	AX	117	10% 100%
29	AY	127	7% 98%
30	AZ	134	15% 99%
31	Aa	147	10% 99%
32	Ab	118	27% 76% 5% 18%
33	Ac	103	20% 98%

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Mol	Chain	Length	Quality of chain
34	Ad	106	10% 100%
35	Ae	129	11% 98%
36	Af	109	10% 98%
37	Ag	114	14% 100%
38	Ah	122	11% 97%
39	Ai	97	18% 99%
40	Aj	84	5% 98%
41	Ak	69	29% 97%
42	Al	50	20% 94% 6%
43	Am	50	8% 96%
44	An	25	36% 100%
45	Ao	105	21% 98%
46	Ap	91	13% 98%
47	At	122	7% 97%
48	A2	3643	9% 66% 30%
49	B1	1708	17% 63% 33%
50	BD	220	77% 98%
51	BE	257	39% 97%
52	BF	190	70% 97%
53	BG	232	57% 99%
54	BH	183	61% 98%
55	BI	207	30% 99%
56	BJ	179	41% 98%
57	BK	98	88% 98%
58	BL	153	36% 99%

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Mol	Chain	Length	Quality of chain
59	BM	120	99% 98%
60	BN	149	37% 99%
61	BO	136	31% 99%
62	BP	120	67% 97%
63	BQ	139	68% 100%
64	BR	125	68% 98%
65	BS	139	65% 96%
66	BT	143	69% 97%
67	BU	97	70% 100%
68	BV	81	41% 98%
69	BW	129	26% 98%
70	BX	139	30% 99%
71	BY	125	46% 98%
72	BZ	86	72% 95% 5%
73	Ba	97	32% 99%
74	Bb	80	41% 99%
75	Bc	62	73% 97%
76	Bd	51	59% 98%
77	Be	55	47% 93% 7%
78	Bf	73	93% 99%
79	Bg	314	92% 99%
80	Bv	76	91% 58% 39%
81	Bx	16	88% 44% 56%
82	A	26	92% 81% 19%

## 2 Entry composition [i](#)

There are 85 unique types of molecules in this entry. The entry contains 214215 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 60S ribosomal protein L8.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	BA	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	BB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AC	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	BC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	A3	157	3337	1489	587	1104	157	0	0

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	A4	119	2541	1132	454	836	119	0	0

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AD	294	2392	1510	436	432	14	0	0

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AE	226	1838	1180	350	304	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AF	234	1950	1252	376	313	9	0	0

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AG	234	1880	1197	362	317	4	0	0

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AH	191	1526	960	285	275	6	0	0

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AI	208	1692	1074	327	278	13	0	0

- Molecule 15 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AJ	169	1353	855	252	240	6	0	0

- Molecule 16 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AL	205	1657	1036	344	273	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AM	139	1138	730	218	183	7	0	0

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

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

- Molecule 19 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AO	195	1606	1034	315	252	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AP	153	1242	776	241	216	9	0	0

- Molecule 21 is a protein called 60S ribosomal protein L18.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	AQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 22 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 23 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AS	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 24 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AT	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AU	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 27 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AW	121	Total	C	N	O	S	0	0
			989	617	202	167	3		

- Molecule 28 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	AX	117	958	612	180	165	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AY	127	1064	668	216	177	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AZ	134	1103	712	207	181	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Aa	147	1162	736	237	186	3	0	0

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	Ab	97	792	492	175	122	3	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Ac	103	801	508	141	145	7	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Ad	106	879	555	170	152	2	0	0

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Ae	129	1064	673	220	166	5	0	0

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Af	109	876	555	174	144	3	0	0

- Molecule 37 is a protein called 60S ribosomal protein L34.

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

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ah	122	1015	641	205	168	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Ai	97	794	497	168	124	5	0	0

- Molecule 40 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Aj	84	689	423	152	109	5	0	0

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Al	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 43 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Am	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 44 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	An	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 45 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ao	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 46 is a protein called 60S ribosomal protein L37a.

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

- Molecule 47 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	At	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A2	3643	Total	C	N	O	P	0	0
			78102	34781	14290	25388	3643		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	B1	1708	36456	16274	6546	11928	1708	0	0

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BD	220	1709	1090	308	304	7	0	0

- Molecule 51 is a protein called 40S ribosomal protein S4, Y isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	BE	257	2031	1298	381	344	8	0	0

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	BF	190	1502	939	285	271	7	0	0

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	BG	232	1884	1176	379	322	7	0	0

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	BH	183	1479	941	272	265	1	0	0

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	BI	207	1696	1064	334	293	5	0	0

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	BJ	179	1495	953	299	241	2	0	0

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	BK	98	827	539	148	134	6	0	0

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	BL	153	1258	804	235	213	6	0	0

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	BM	120	931	584	164	174	9	0	0

- Molecule 60 is a protein called 40S ribosomal protein S13.

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

- Molecule 61 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	BO	136	1016	621	199	190	6	0	0

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	BP	120	999	636	188	168	7	0	0

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	BQ	139	1109	704	210	192	3	0	0

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	BR	125	1011	634	187	186	4	0	0

- Molecule 65 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	BS	139	1154	725	233	195	1	0	0

- Molecule 66 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	BT	143	1112	697	214	198	3	0	0

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	BU	97	769	483	144	138	4	0	0

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	BV	81	617	380	114	118	5	0	0

- Molecule 69 is a protein called 40S ribosomal protein S15a.

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

- Molecule 70 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BZ	86	Total	C	N	O	S	0	0
			688	442	129	116	1		

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ba	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 75 is a protein called 40S ribosomal protein S28.

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

- Molecule 76 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bd	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 77 is a protein called 40S ribosomal protein S30.



Mol	Chain	Residues	Atoms					AltConf	Trace
77	Be	55	Total	C	N	O	S	0	0
			437	272	96	68	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bf	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 79 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bx	16	Total	C	N	O	P	0	0
			320	144	32	128	16		

- Molecule 82 is a protein called Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	A	26	Total	C	N	O	0	0
			128	76	26	26		

- Molecule 83 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	AA	1	Total	Mg	0
			1	1	
83	AB	2	Total	Mg	0
			2	2	
83	BC	1	Total	Mg	0
			1	1	

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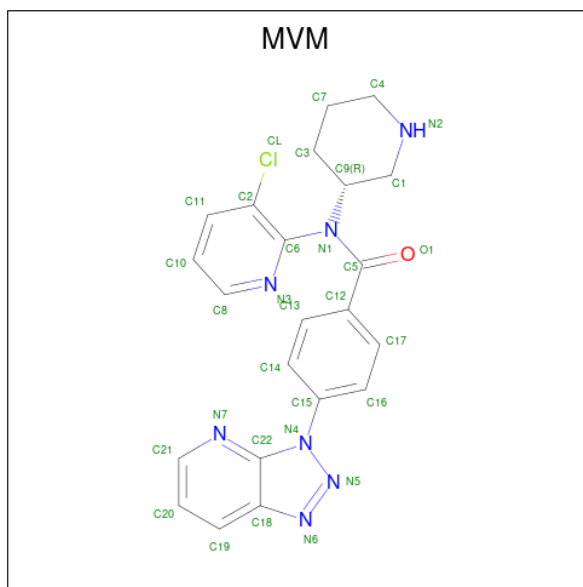
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
83	A3	8	8	8	0
83	A4	9	9	9	0
83	AN	1	1	1	0
83	AP	2	2	2	0
83	Aa	2	2	2	0
83	Ae	1	1	1	0
83	Aj	1	1	1	0
83	Al	1	1	1	0
83	An	1	1	1	0
83	A2	220	220	220	0
83	B1	73	73	73	0
83	BI	1	1	1	0
83	Bv	2	2	2	0

- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
84	Aj	1	1	1	0
84	Ao	1	1	1	0
84	Ap	1	1	1	0
84	Ba	1	1	1	0
84	Bd	1	1	1	0

- Molecule 85 is N-(3-chloropyridin-2-yl)-N-[(3R)-piperidin-3-yl]-4-(3H-[1,2,3]triazolo[4,5-b]pyridin-3-yl)benzamide (three-letter code: MVM) (formula: C<sub>22</sub>H<sub>20</sub>ClN<sub>7</sub>O).

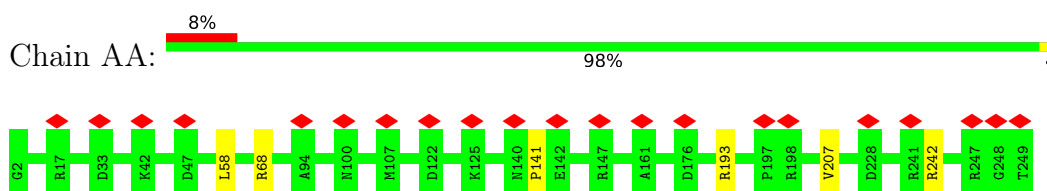


Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
85	A	1	31	22	1	7	1	0

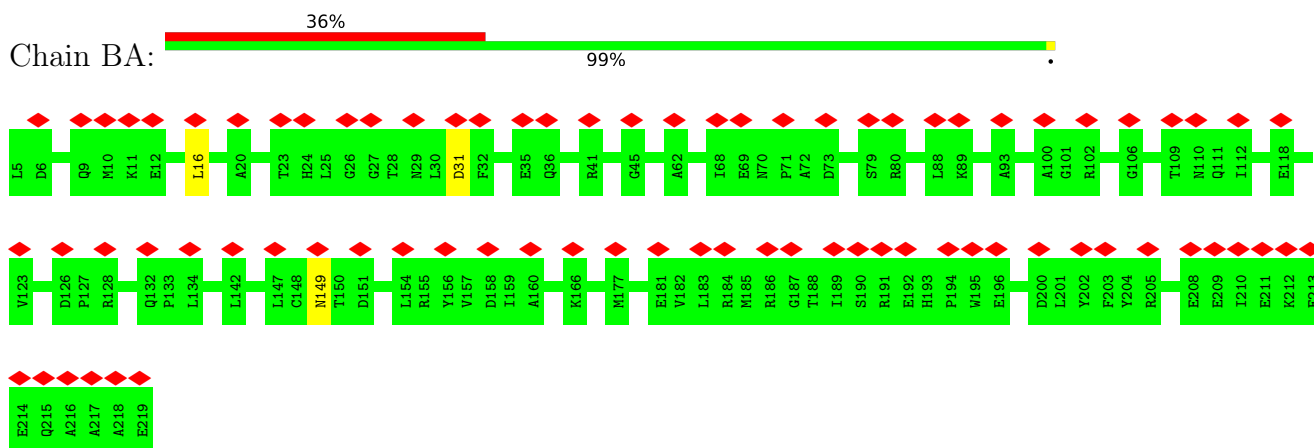
### 3 Residue-property plots [i](#)

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.

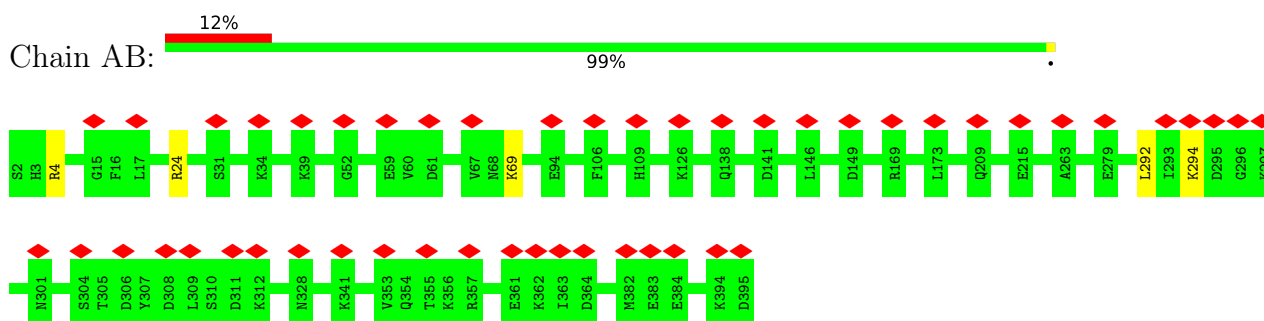
- Molecule 1: 60S ribosomal protein L8



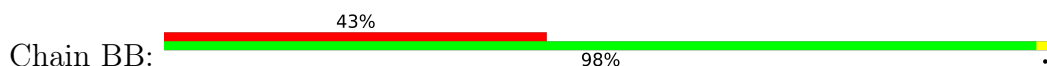
- Molecule 2: 40S ribosomal protein SA

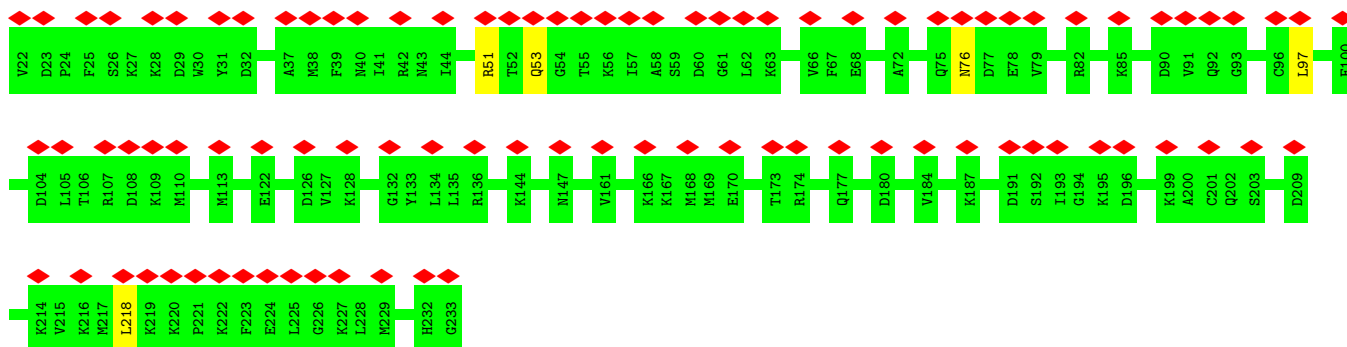


- Molecule 3: 60S ribosomal protein L3



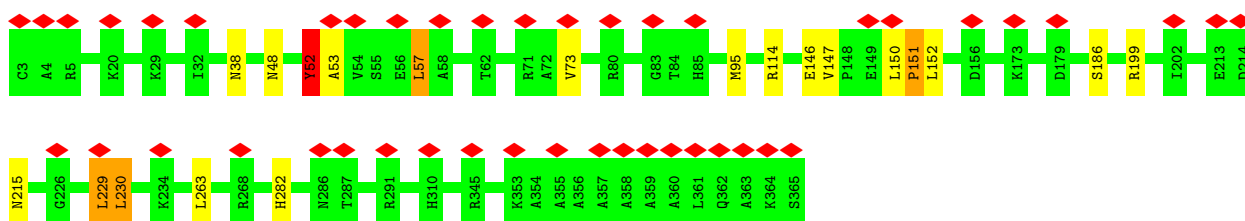
- Molecule 4: 40S ribosomal protein S3a





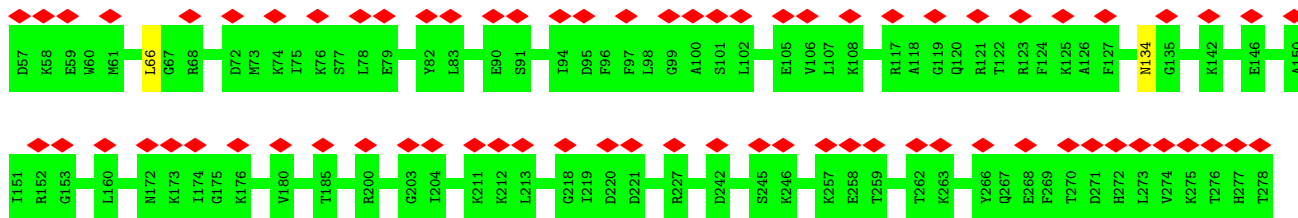
- Molecule 5: 60S ribosomal protein L4

Chain AC: 12% 94%



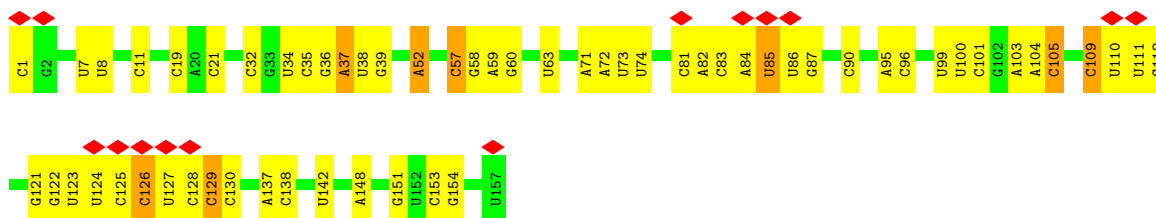
- Molecule 6: 40S ribosomal protein S2

Chain BC: 32% 99%



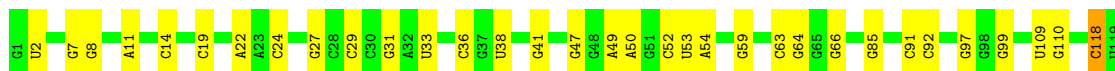
- Molecule 7: 5.8S ribosomal RNA

Chain A3: 9% 62% 33% 5%

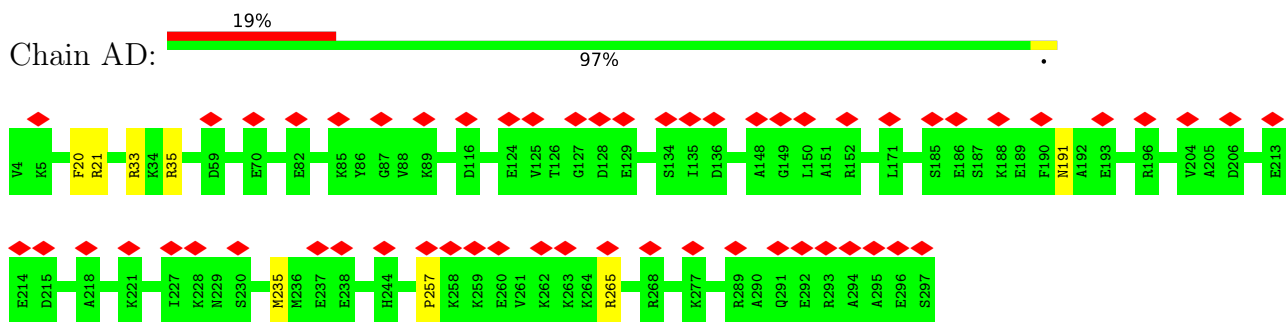


- Molecule 8: 5S ribosomal RNA

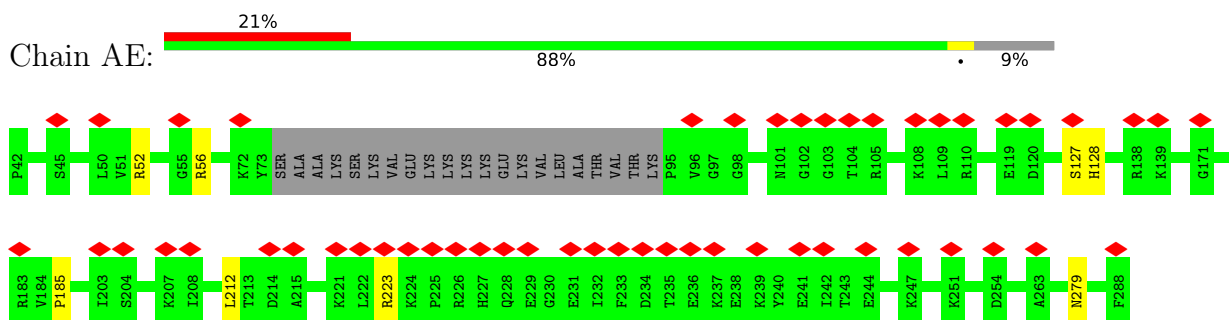
Chain A4: 72% 27%



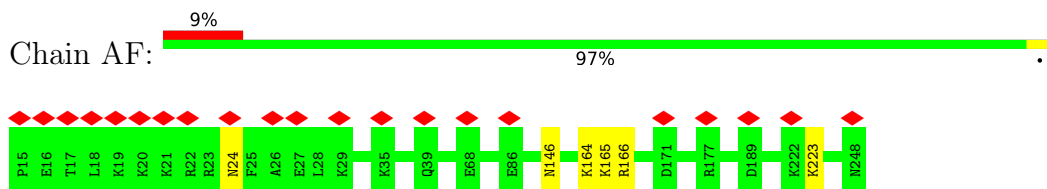
- Molecule 9: 60S ribosomal protein L5



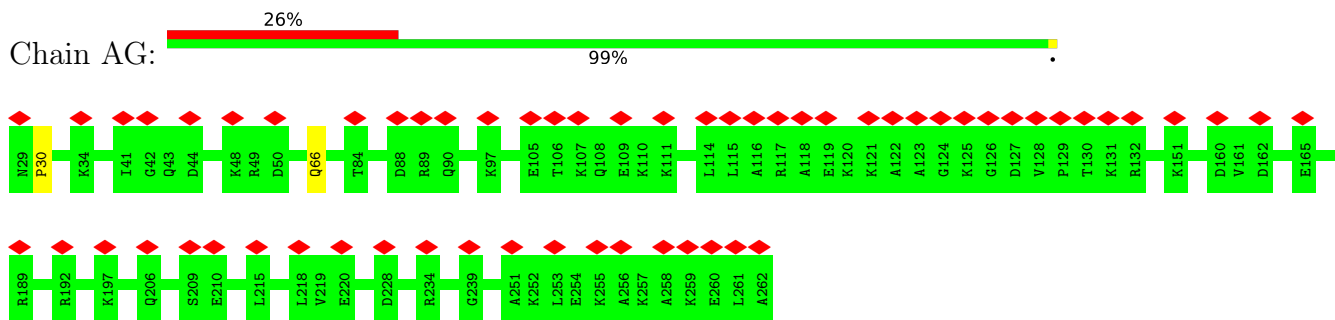
- Molecule 10: 60S ribosomal protein L6



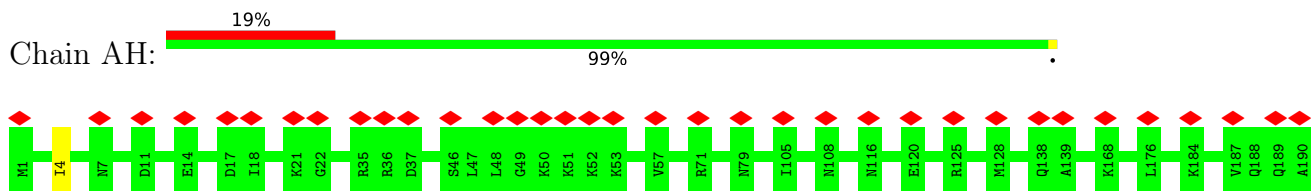
- Molecule 11: 60S ribosomal protein L7



- Molecule 12: 60S ribosomal protein L7a

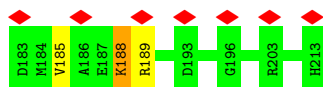
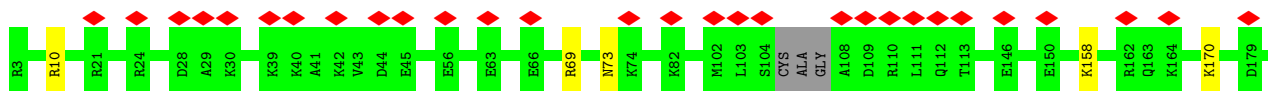


- Molecule 13: 60S ribosomal protein L9

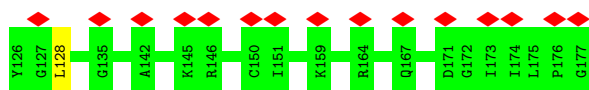
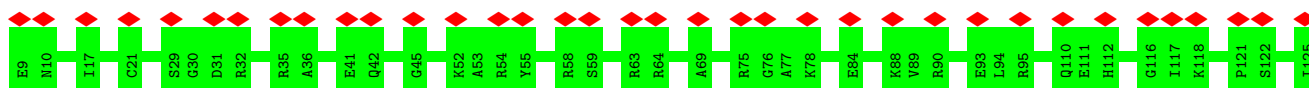




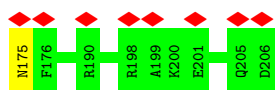
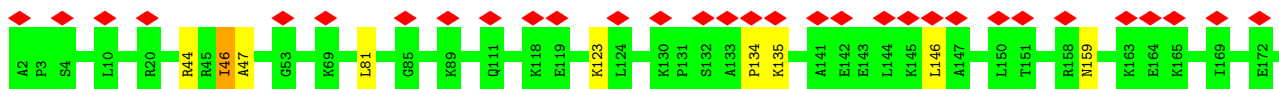
- Molecule 14: 60S ribosomal protein L10



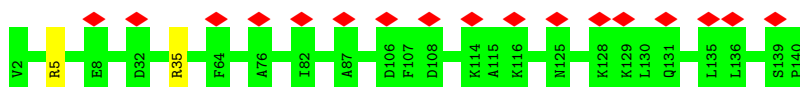
- Molecule 15: 60S ribosomal protein L11



- Molecule 16: 60S ribosomal protein L13

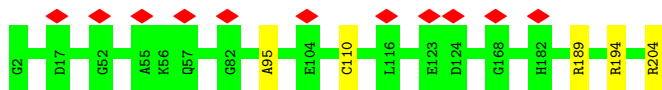


- Molecule 17: 60S ribosomal protein L14

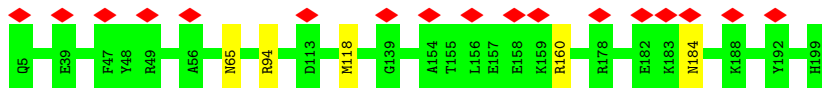


- Molecule 18: 60S ribosomal protein L15

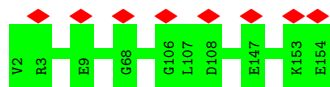




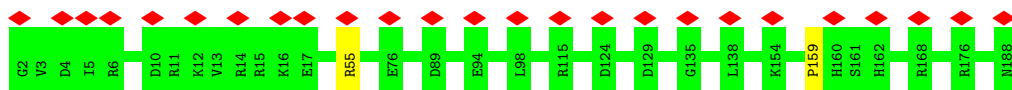
- Molecule 19: 60S ribosomal protein L13a



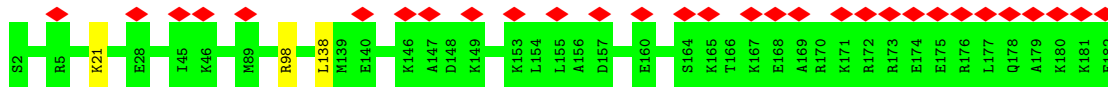
- Molecule 20: 60S ribosomal protein L17



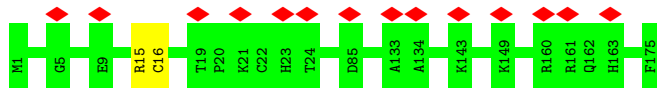
- Molecule 21: 60S ribosomal protein L18



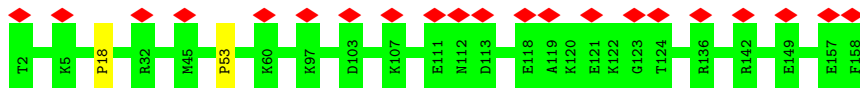
- Molecule 22: 60S ribosomal protein L19



- Molecule 23: 60S ribosomal protein L18a

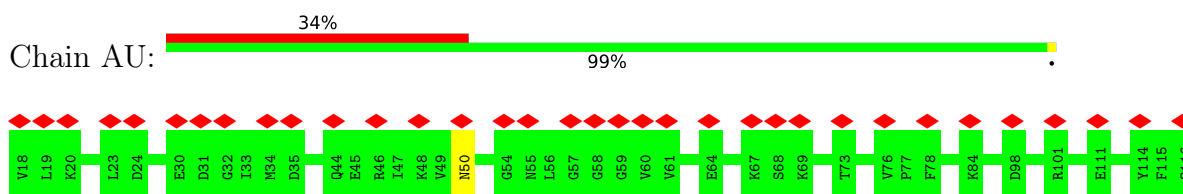


- Molecule 24: 60S ribosomal protein L21

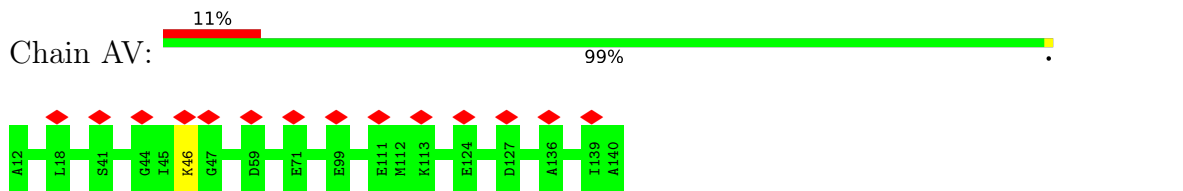


- Molecule 25: 60S ribosomal protein L22

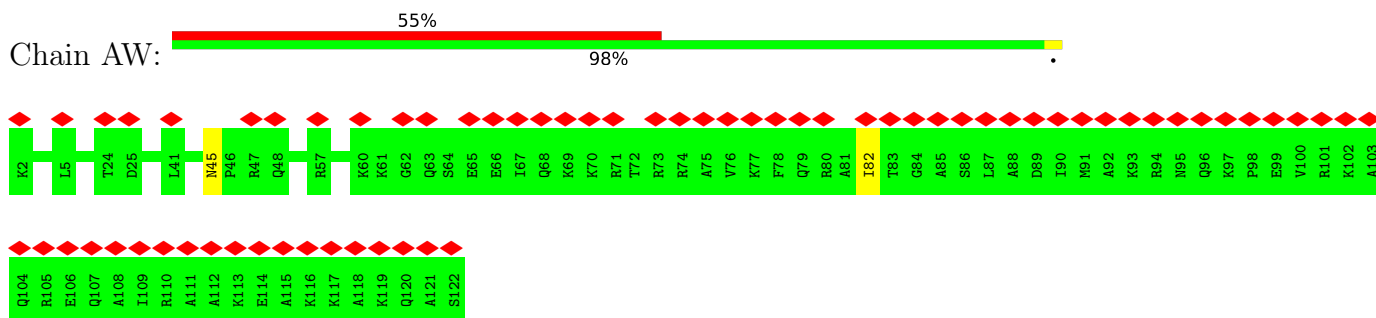




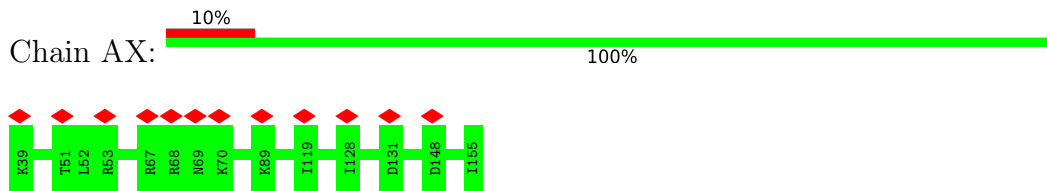
- Molecule 26: 60S ribosomal protein L23



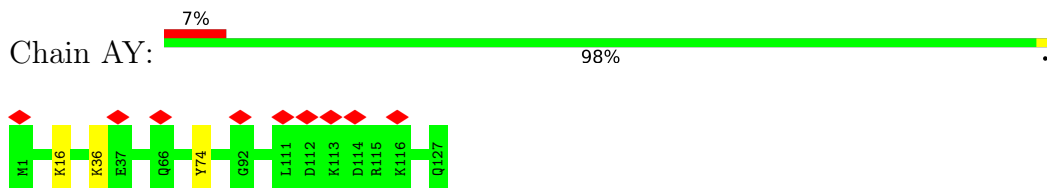
- Molecule 27: 60S ribosomal protein L24



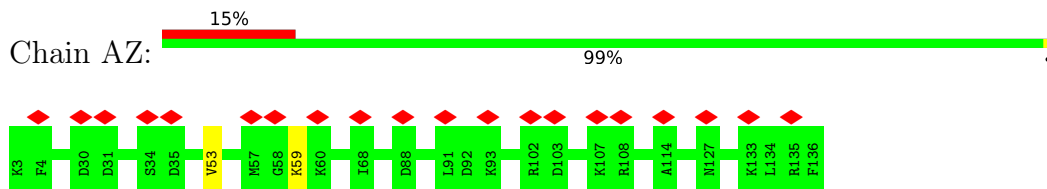
- Molecule 28: 60S ribosomal protein L23a



- Molecule 29: 60S ribosomal protein L26

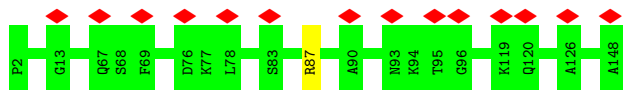


- Molecule 30: 60S ribosomal protein L27

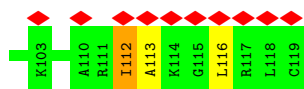
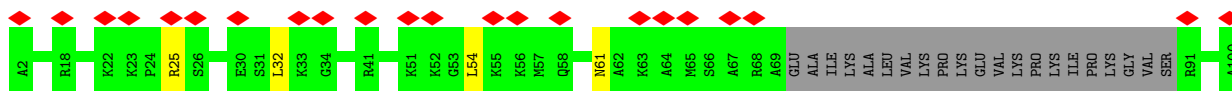
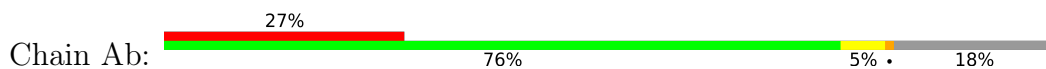


- Molecule 31: 60S ribosomal protein L27a

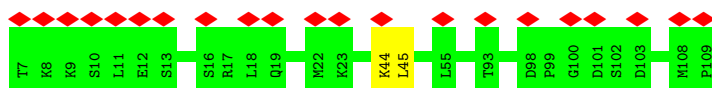




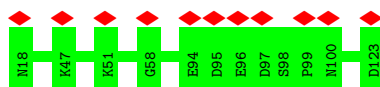
- Molecule 32: 60S ribosomal protein L29



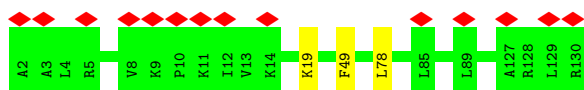
- Molecule 33: 60S ribosomal protein L30



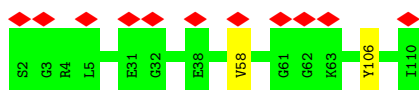
- Molecule 34: 60S ribosomal protein L31



- Molecule 35: 60S ribosomal protein L32

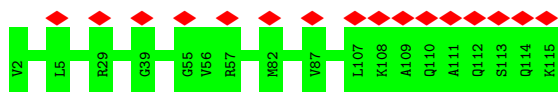


- Molecule 36: 60S ribosomal protein L35a

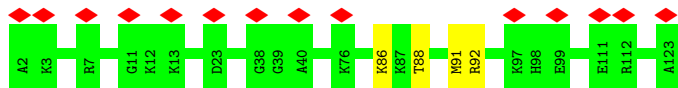


- Molecule 37: 60S ribosomal protein L34

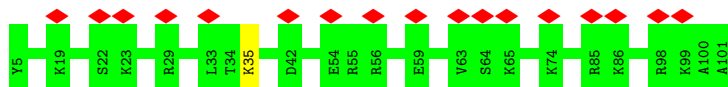




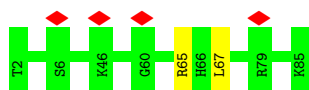
- Molecule 38: 60S ribosomal protein L35



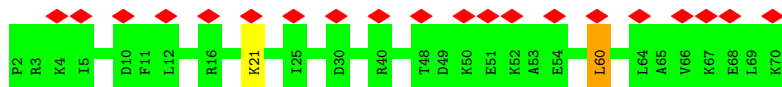
- Molecule 39: 60S ribosomal protein L36



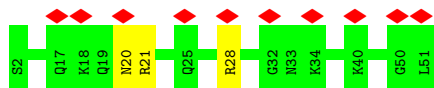
- Molecule 40: 60S ribosomal protein L37



- Molecule 41: 60S ribosomal protein L38



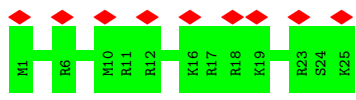
- Molecule 42: 60S ribosomal protein L39



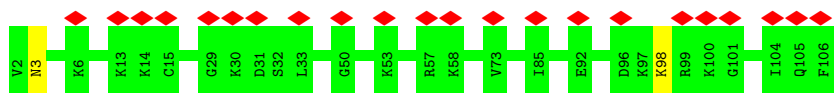
- Molecule 43: 60S ribosomal protein L40



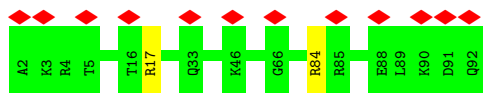
- Molecule 44: 60S ribosomal protein L41



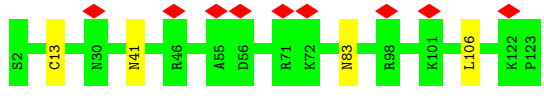
• Molecule 45: 60S ribosomal protein L36a



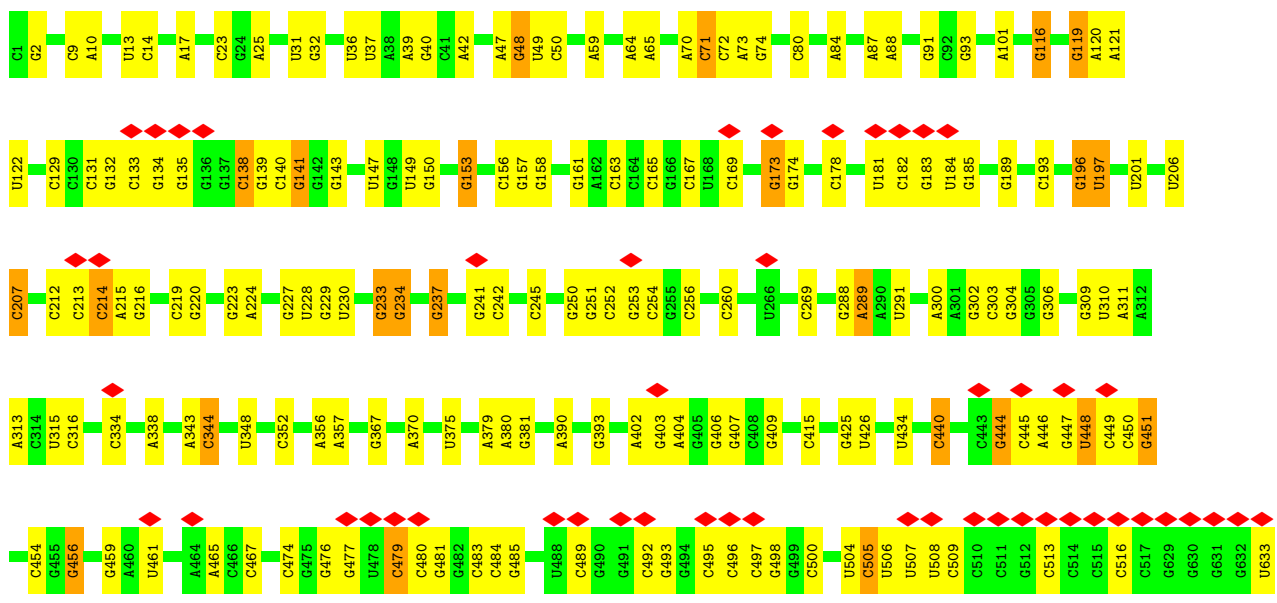
• Molecule 46: 60S ribosomal protein L37a

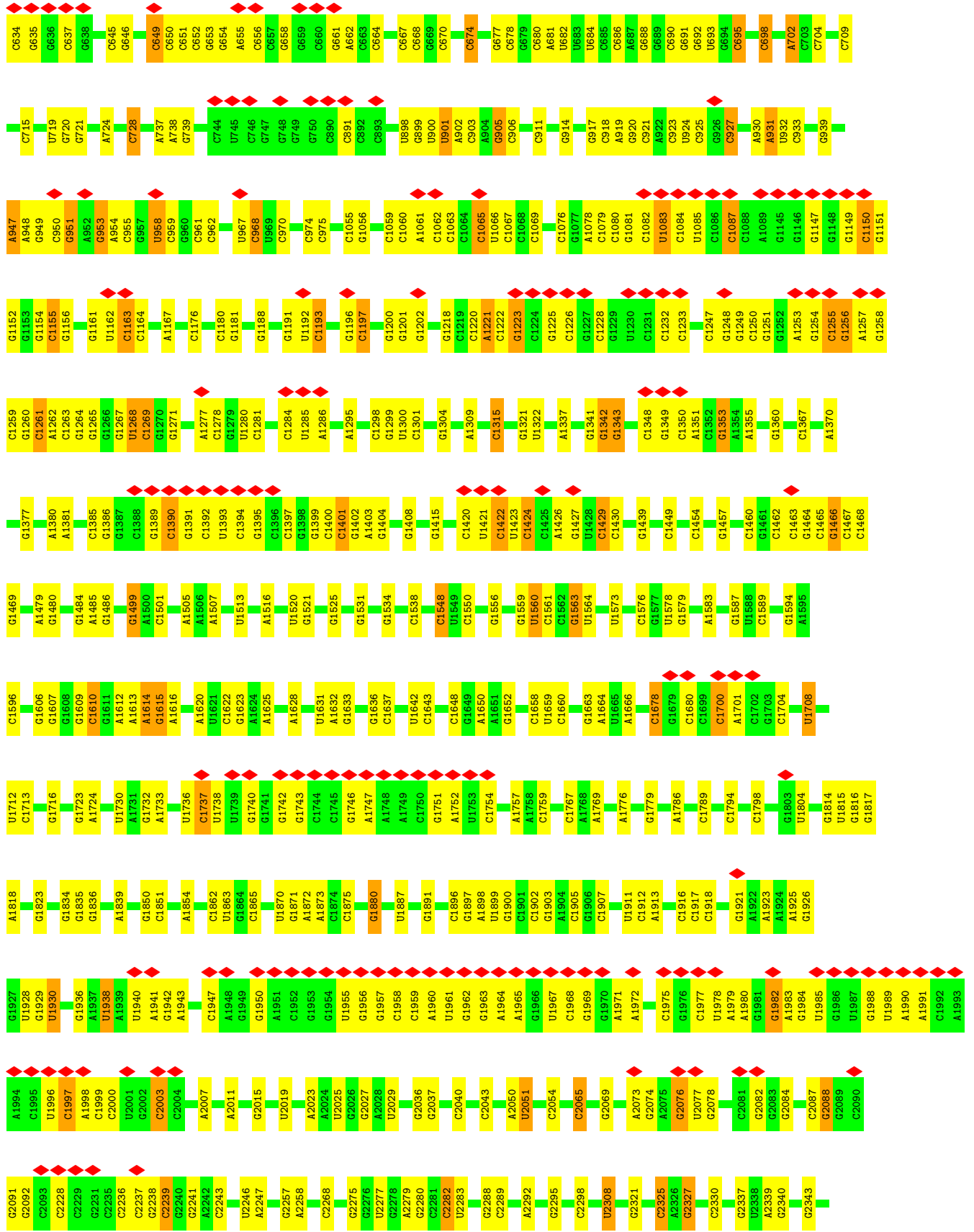


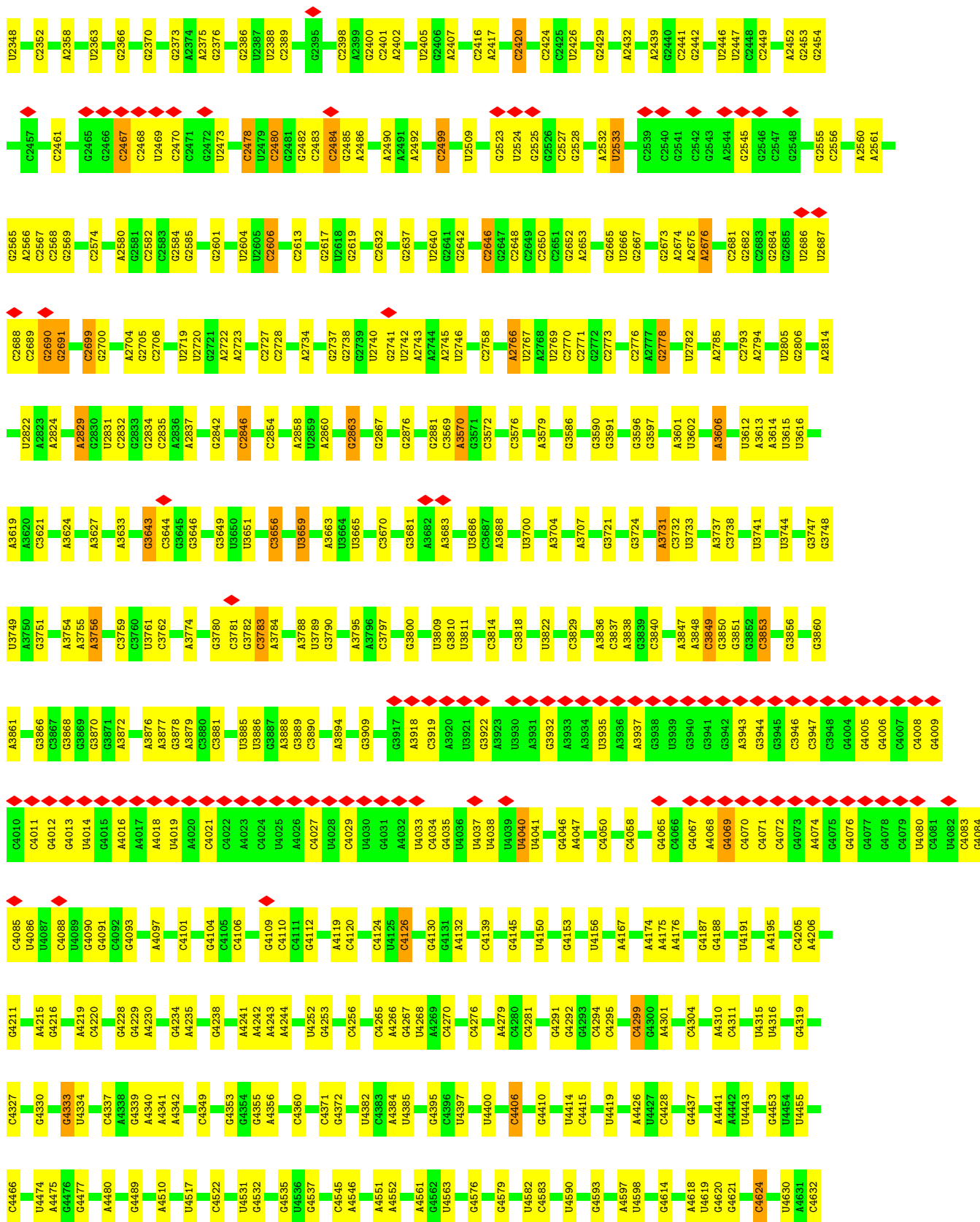
• Molecule 47: 60S ribosomal protein L28

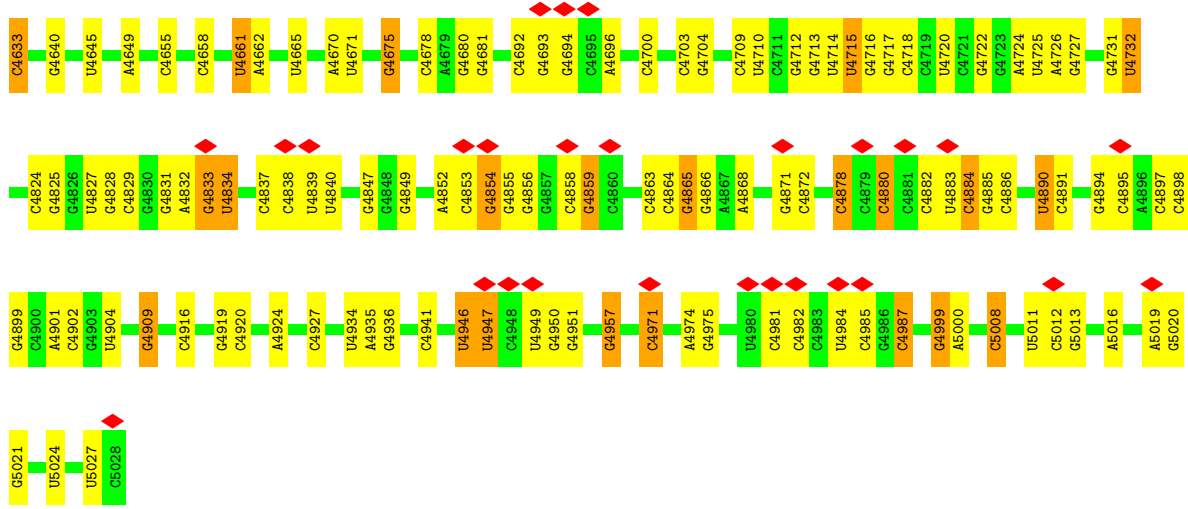


• Molecule 48: 28S ribosomal RNA

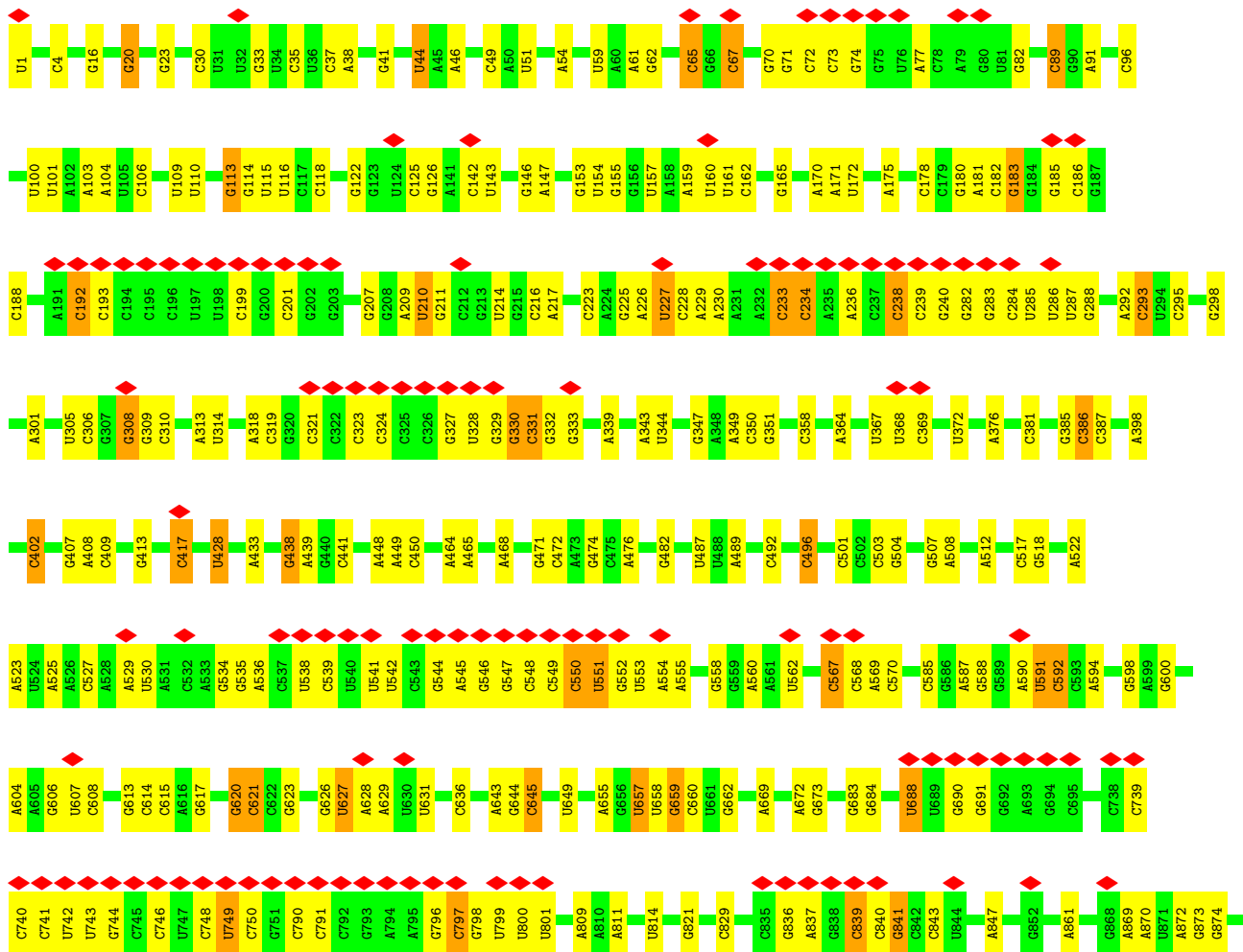


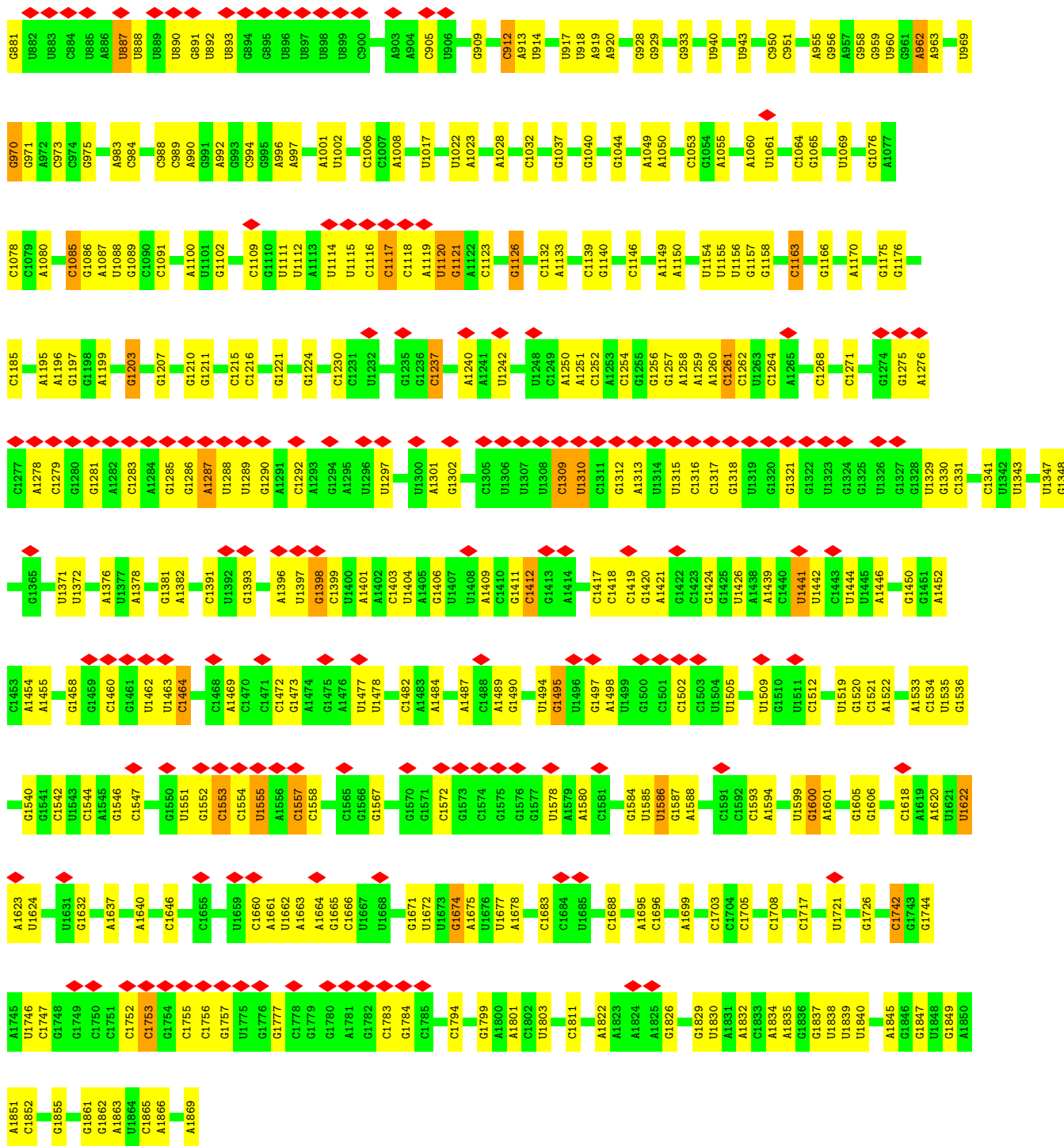




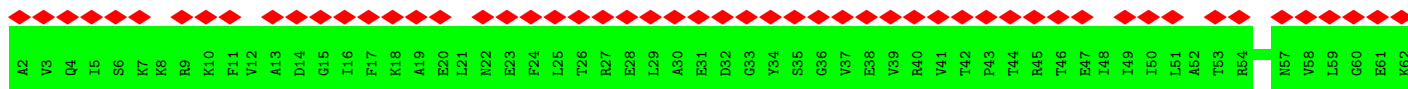
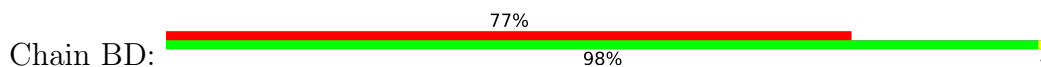


• Molecule 49: 18S ribosomal RNA

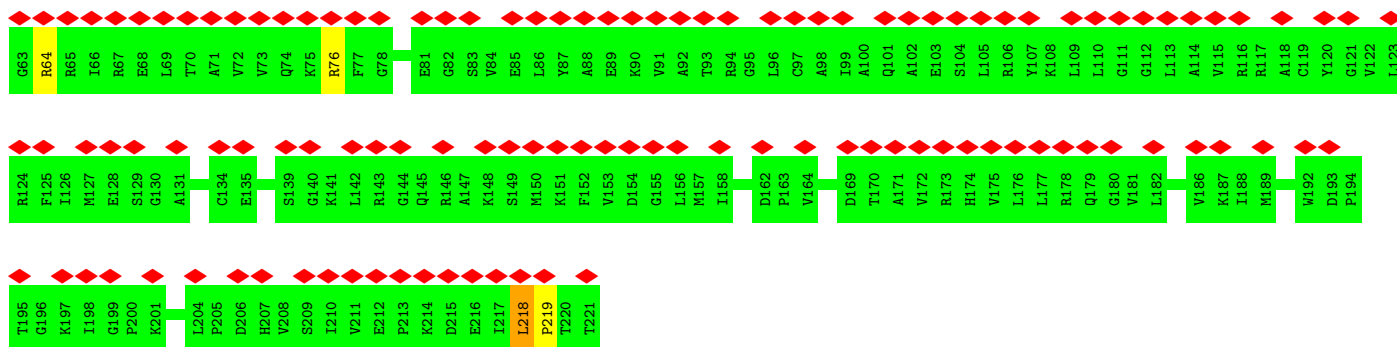




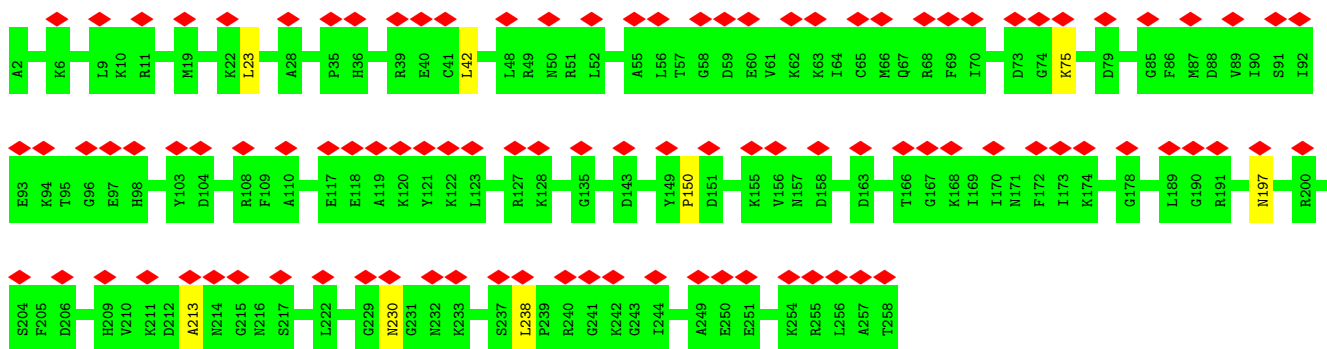
• Molecule 50: 40S ribosomal protein S3



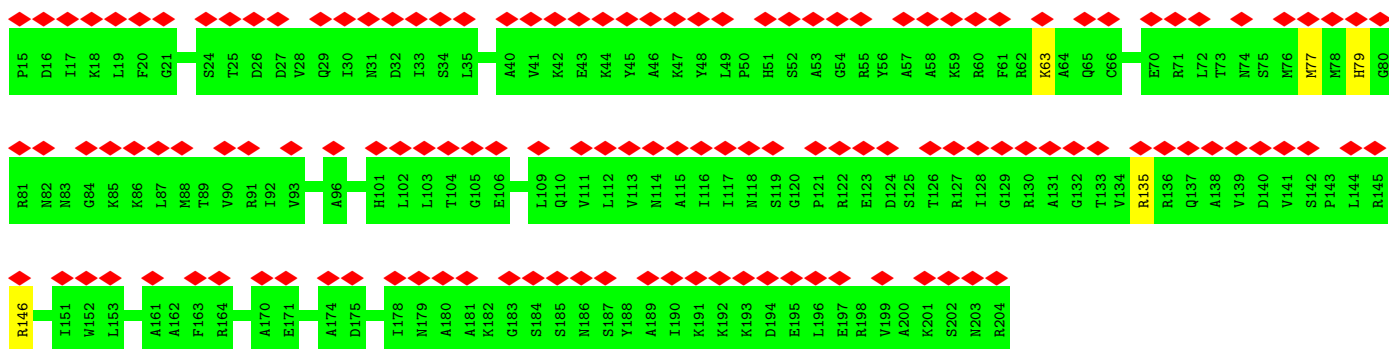




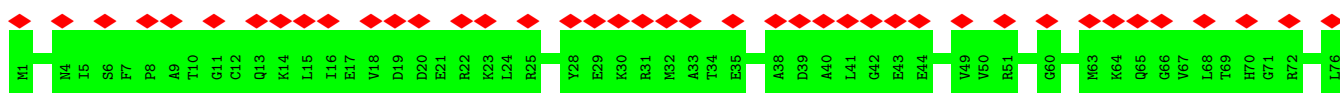
• Molecule 51: 40S ribosomal protein S4, Y isoform 1

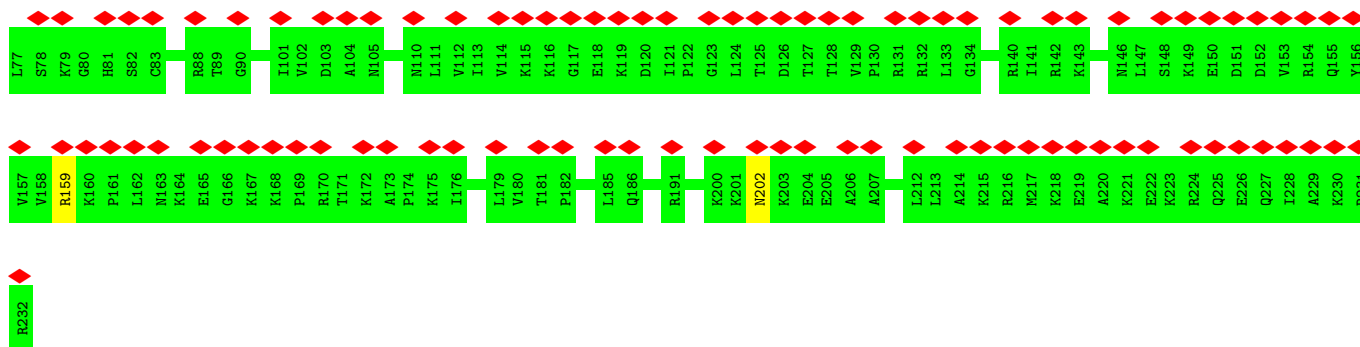


• Molecule 52: 40S ribosomal protein S5

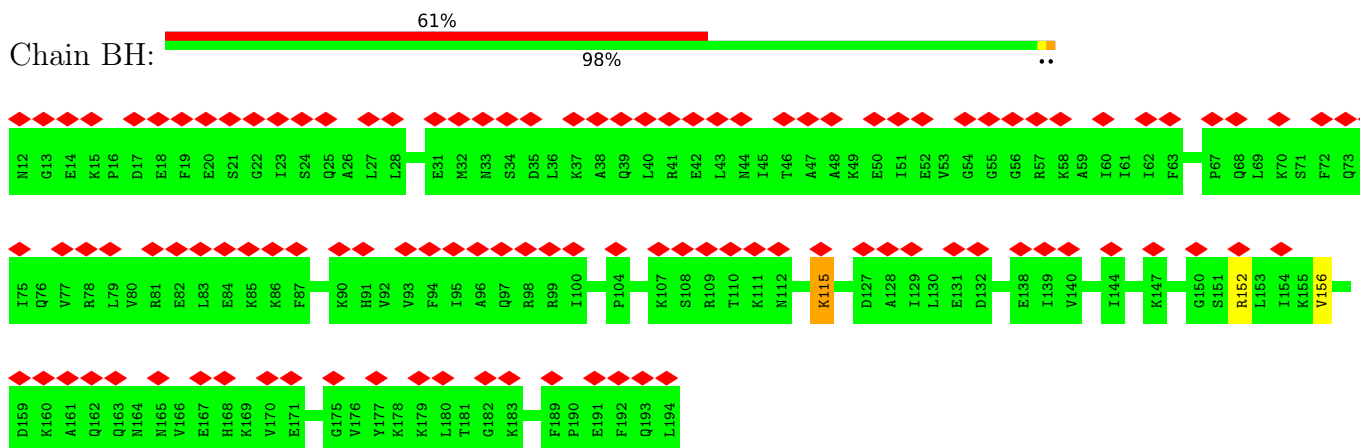


• Molecule 53: 40S ribosomal protein S6

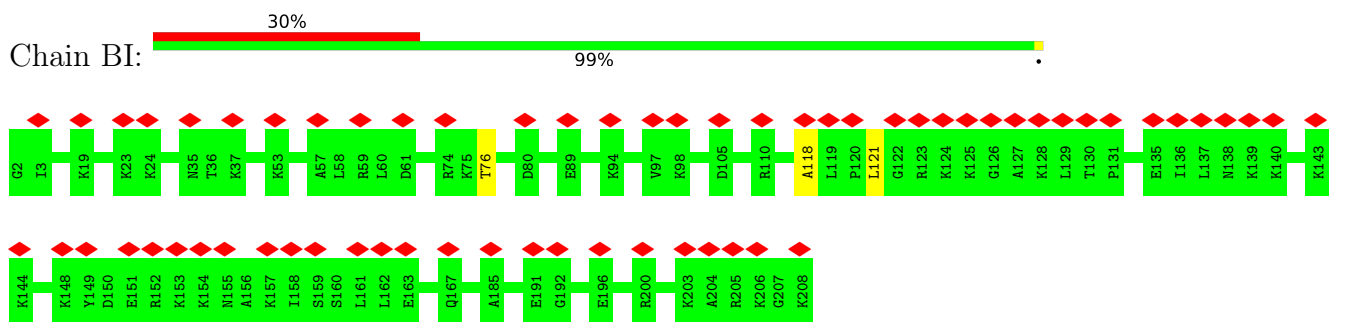




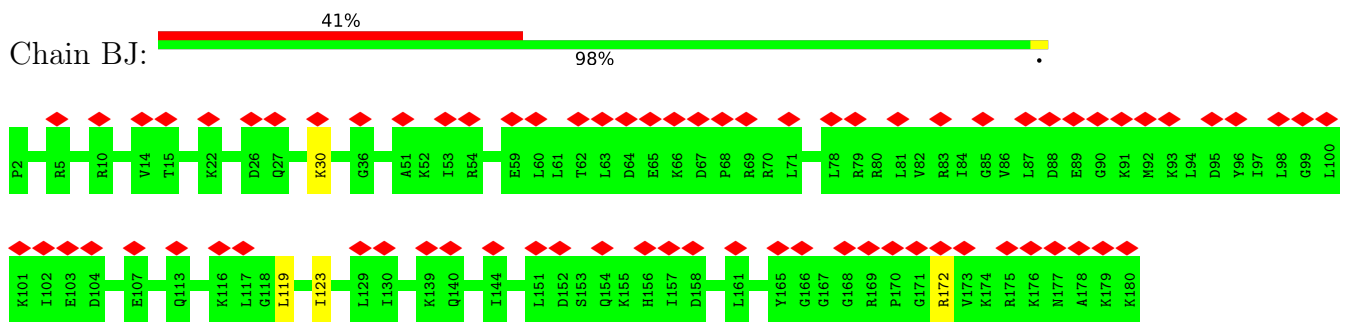
• Molecule 54: 40S ribosomal protein S7



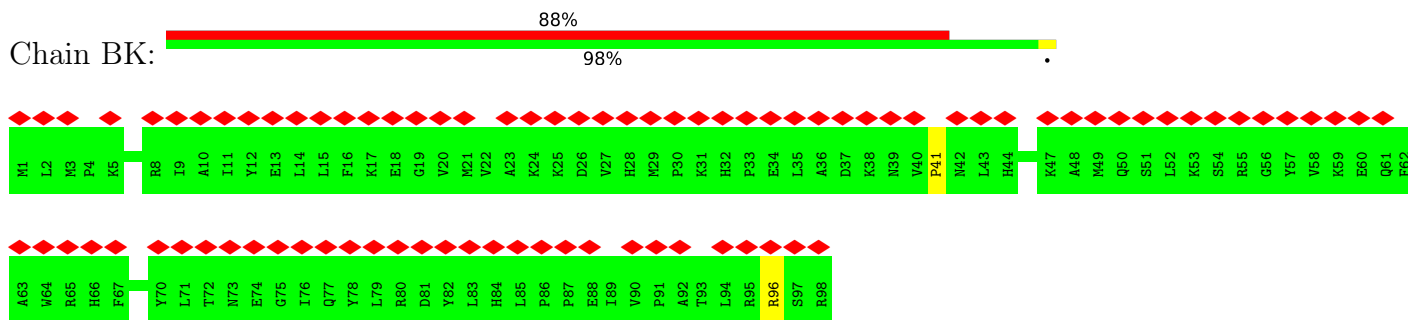
• Molecule 55: 40S ribosomal protein S8



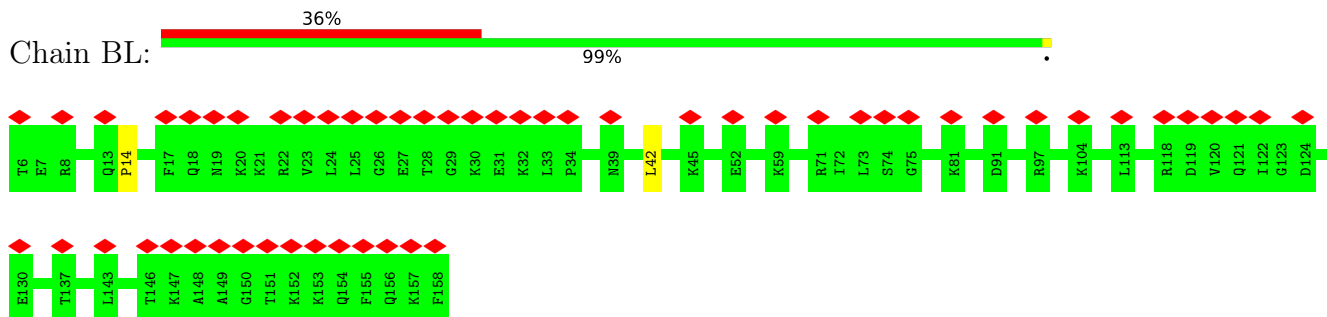
• Molecule 56: 40S ribosomal protein S9



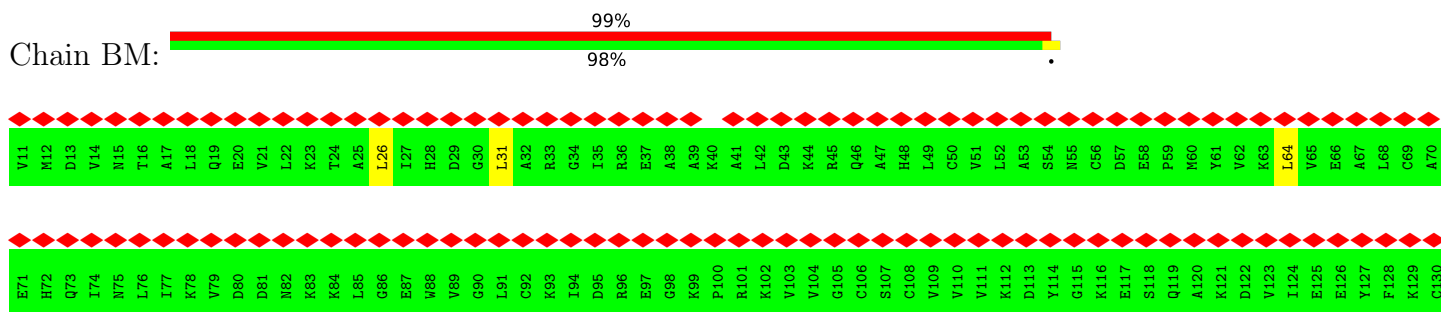
• Molecule 57: 40S ribosomal protein S10



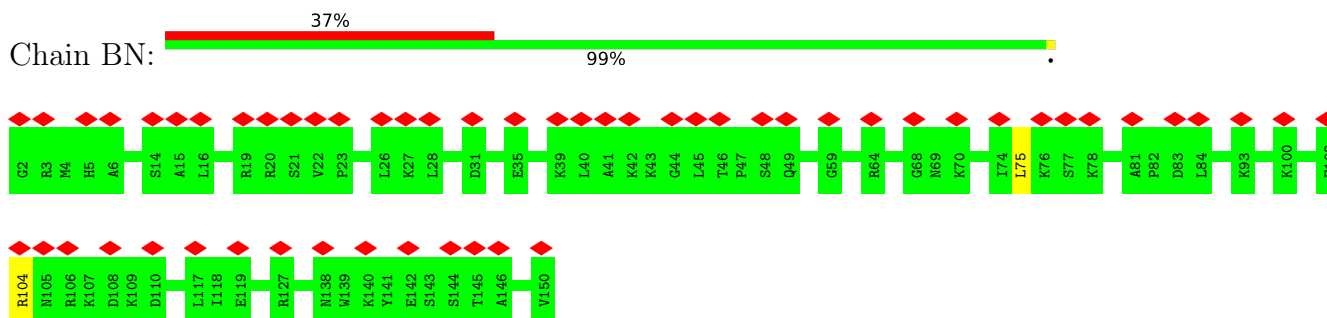
• Molecule 58: 40S ribosomal protein S11



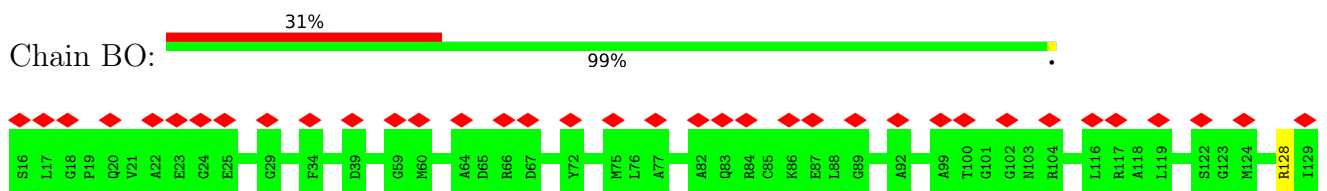
• Molecule 59: 40S ribosomal protein S12

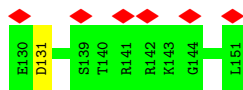


• Molecule 60: 40S ribosomal protein S13



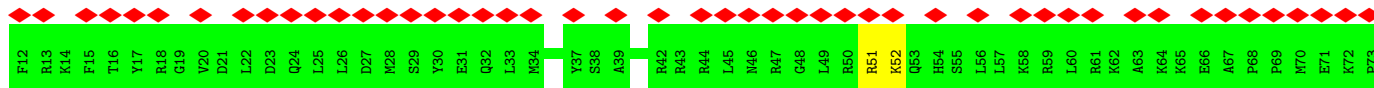
• Molecule 61: 40S ribosomal protein S14





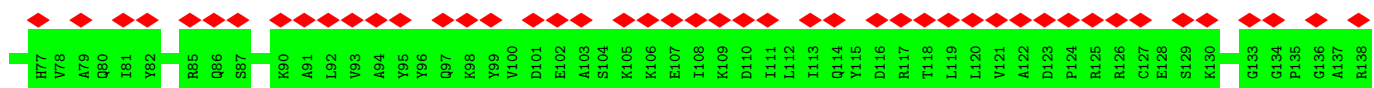
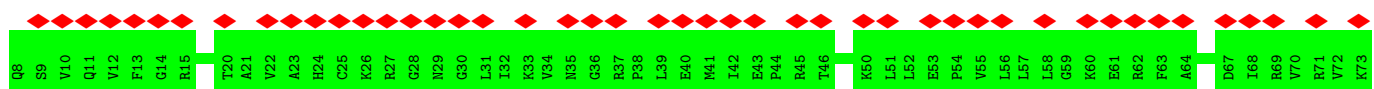
- Molecule 62: 40S ribosomal protein S15

Chain BP: 67%  
97%



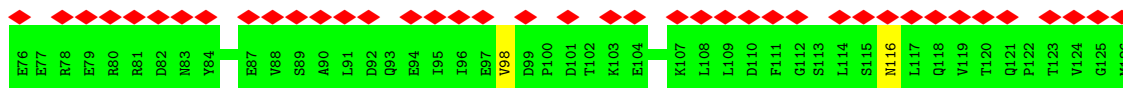
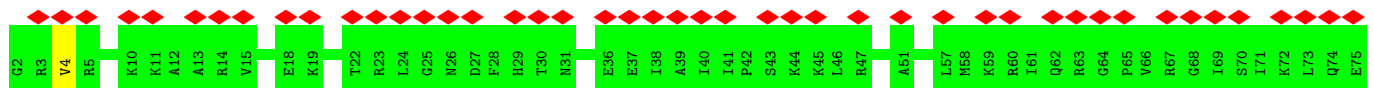
- Molecule 63: 40S ribosomal protein S16

Chain BQ: 68%  
100%



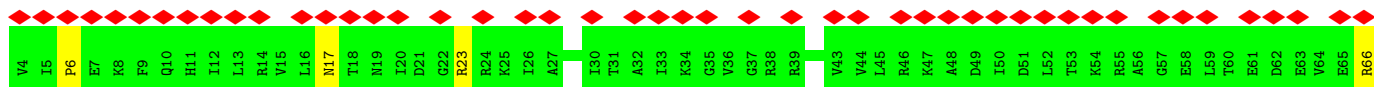
- Molecule 64: 40S ribosomal protein S17

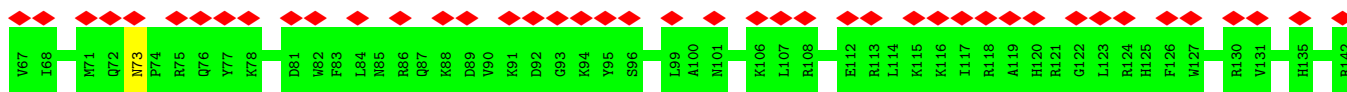
Chain BR: 68%  
98%



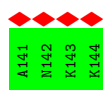
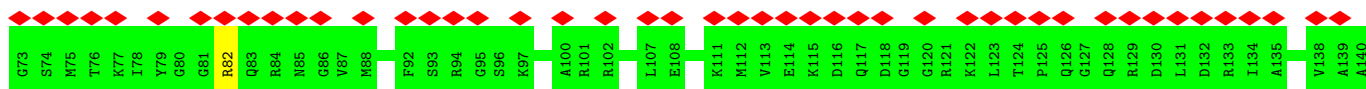
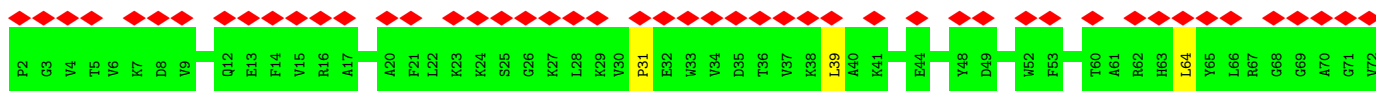
- Molecule 65: 40S ribosomal protein S18

Chain BS: 65%  
96%

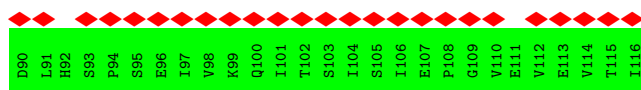
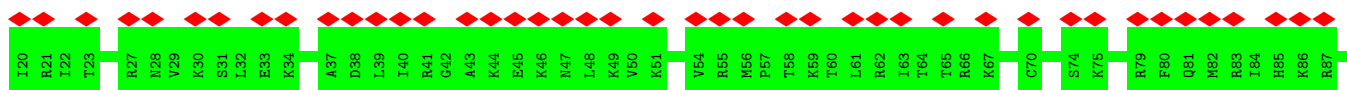




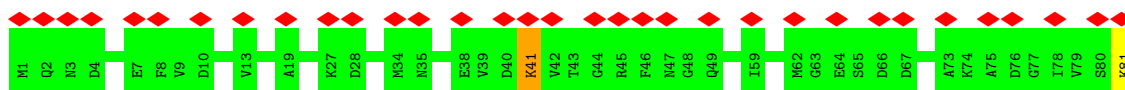
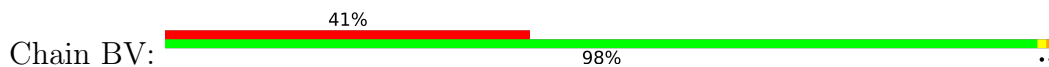
• Molecule 66: 40S ribosomal protein S19



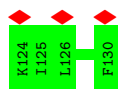
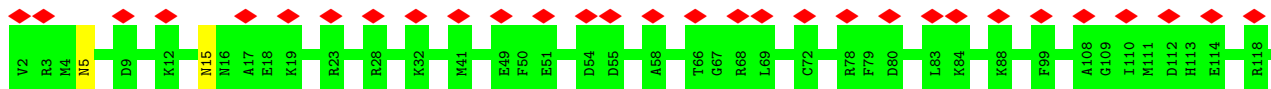
• Molecule 67: 40S ribosomal protein S20



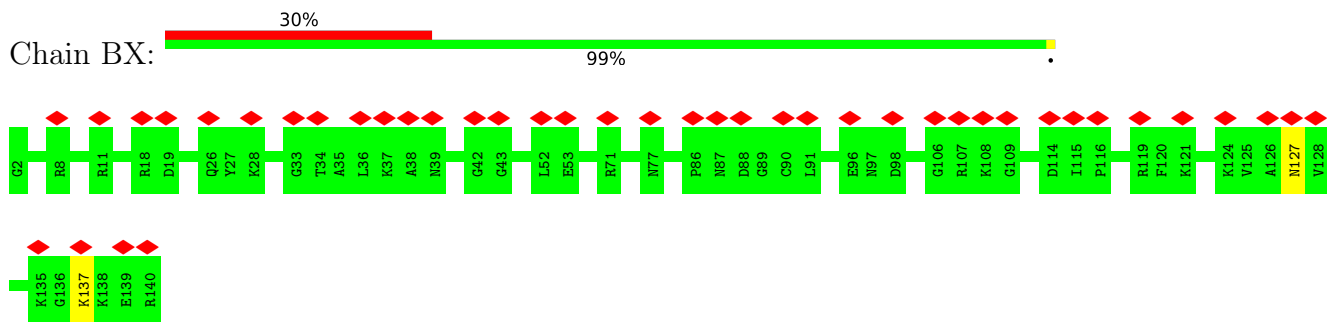
• Molecule 68: 40S ribosomal protein S21



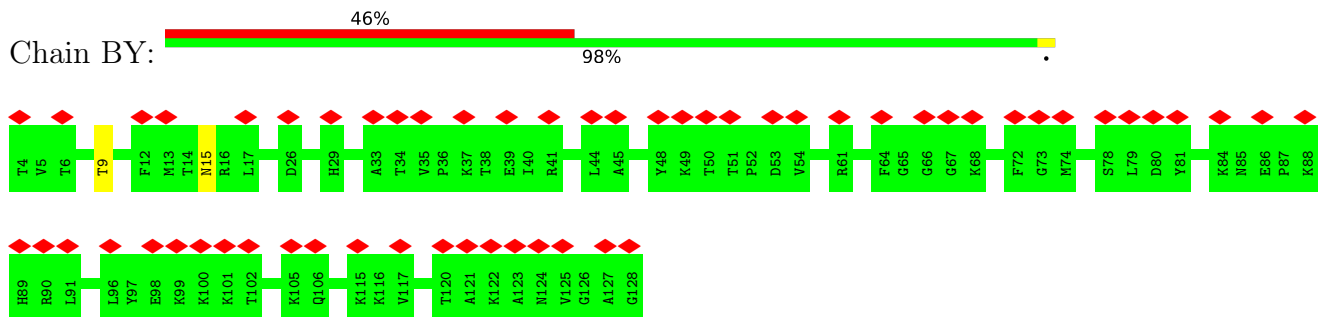
• Molecule 69: 40S ribosomal protein S15a



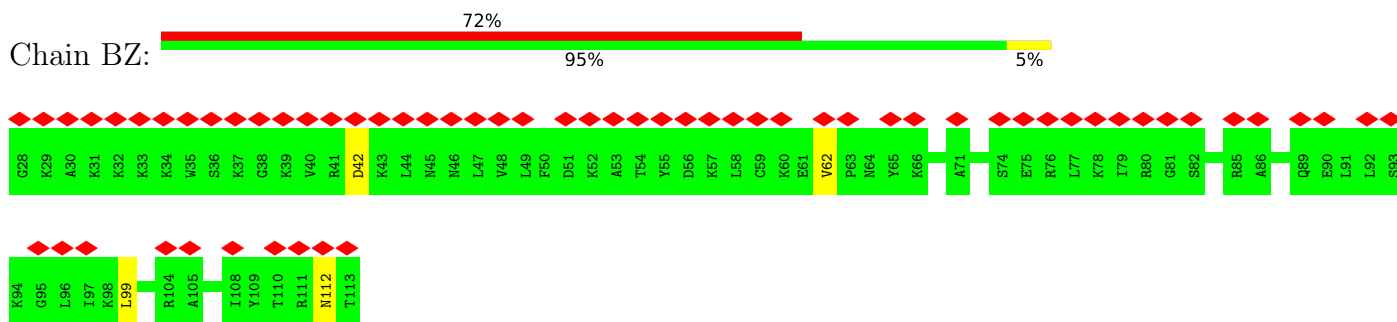
• Molecule 70: 40S ribosomal protein S23



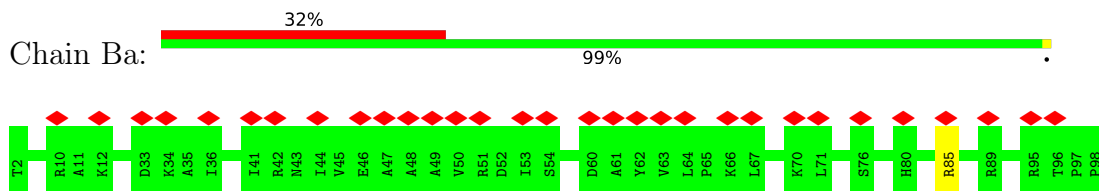
• Molecule 71: 40S ribosomal protein S24



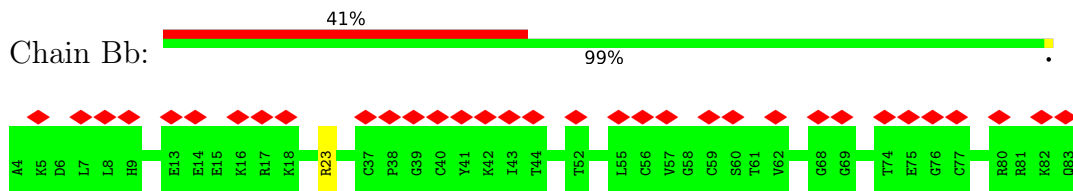
• Molecule 72: 40S ribosomal protein S25



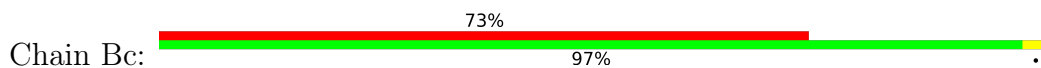
• Molecule 73: 40S ribosomal protein S26

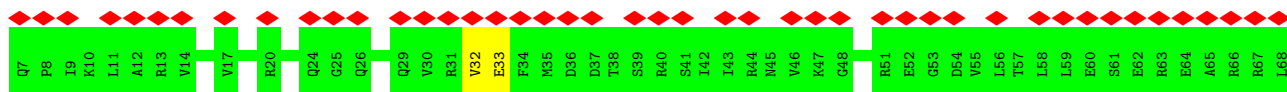


• Molecule 74: 40S ribosomal protein S27

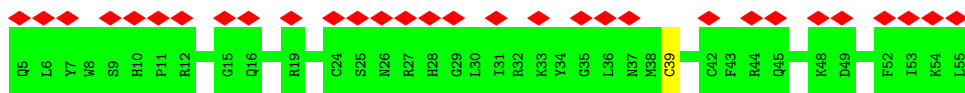


• Molecule 75: 40S ribosomal protein S28

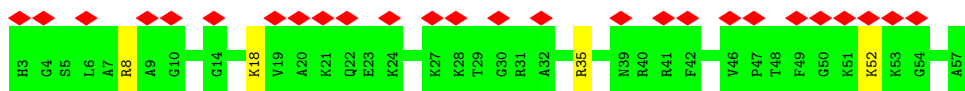




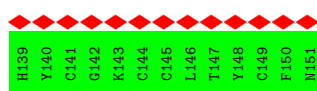
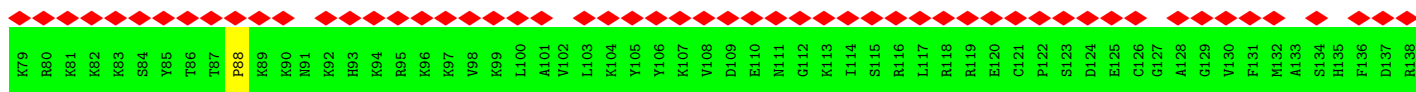
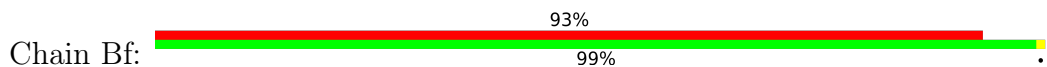
• Molecule 76: 40S ribosomal protein S29



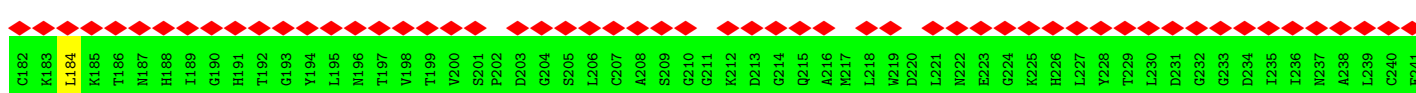
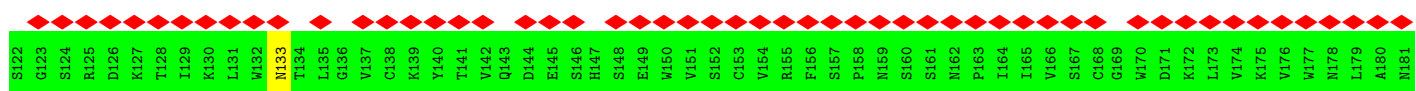
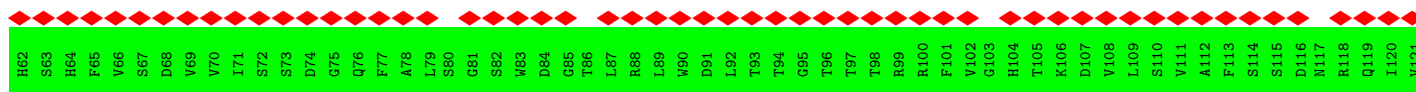
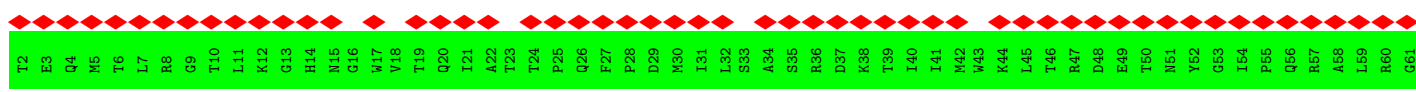
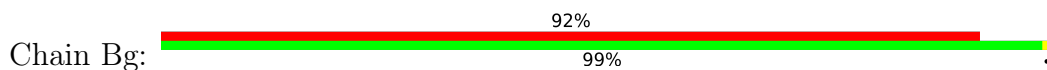
• Molecule 77: 40S ribosomal protein S30

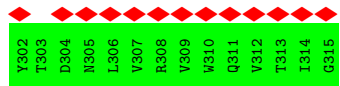
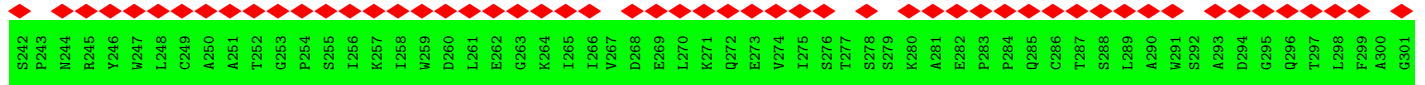


• Molecule 78: Ubiquitin-40S ribosomal protein S27a

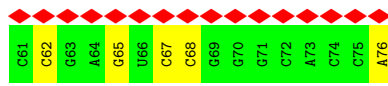
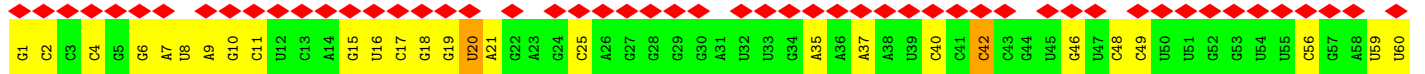
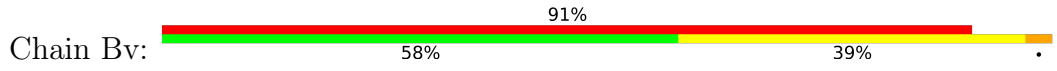


• Molecule 79: Receptor of activated protein C kinase 1

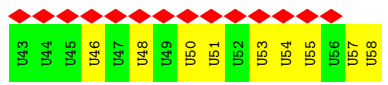
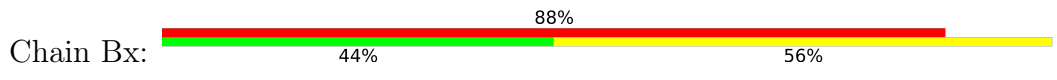




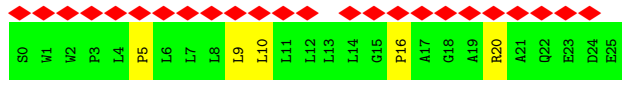
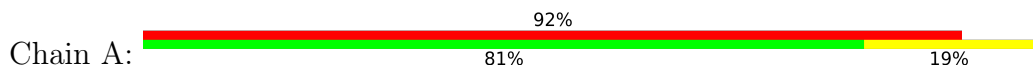
• Molecule 80: tRNA



• Molecule 81: mRNA



• Molecule 82: Proprotein convertase subtilisin/kexin type 9





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7214	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.104	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.022	Depositor
Map size ( $\text{\AA}$ )	488.0, 488.0, 488.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.22, 1.22, 1.22	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: ZN, MG, MVM

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	AA	0.55	0/1936	0.67	0/2596
2	BA	0.44	0/1741	0.71	1/2366 (0.0%)
3	AB	0.54	0/3246	0.71	1/4345 (0.0%)
4	BB	0.41	0/1749	0.71	1/2340 (0.0%)
5	AC	0.58	1/2942 (0.0%)	0.82	7/3951 (0.2%)
6	BC	0.46	0/1761	0.66	0/2379
7	A3	0.98	1/3726 (0.0%)	1.29	46/5804 (0.8%)
8	A4	0.91	0/2839	1.14	7/4425 (0.2%)
9	AD	0.46	0/2437	0.66	0/3262
10	AE	0.45	0/1876	0.75	1/2514 (0.0%)
11	AF	0.57	0/1986	0.72	2/2644 (0.1%)
12	AG	0.45	0/1913	0.68	0/2576
13	AH	0.46	0/1545	0.71	1/2077 (0.0%)
14	AI	0.50	0/1730	0.68	0/2311
15	AJ	0.44	0/1376	0.69	1/1841 (0.1%)
16	AL	0.53	0/1688	0.76	2/2260 (0.1%)
17	AM	0.47	0/1161	0.65	0/1554
18	AN	0.61	1/1746 (0.1%)	0.70	0/2338
19	AO	0.51	0/1638	0.70	0/2191
20	AP	0.50	0/1268	0.61	0/1701
21	AQ	0.58	0/1537	0.79	0/2052
22	AR	0.43	0/1533	0.68	1/2025 (0.0%)
23	AS	0.53	1/1488 (0.1%)	0.68	0/1997
24	AT	0.55	0/1312	0.69	0/1753
25	AU	0.43	0/822	0.65	0/1103
26	AV	0.48	0/983	0.68	0/1319
27	AW	0.46	0/1004	0.68	1/1332 (0.1%)
28	AX	0.45	0/975	0.67	0/1312
29	AY	0.48	0/1081	0.67	0/1439
30	AZ	0.52	0/1126	0.71	0/1502
31	Aa	0.55	0/1191	0.68	0/1591
32	Ab	2.58	2/804 (0.2%)	0.78	2/1060 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Ac	0.48	0/812	0.64	0/1089
34	Ad	0.51	0/894	0.68	0/1204
35	Ae	0.55	0/1082	0.70	2/1443 (0.1%)
36	Af	0.56	0/895	0.73	0/1198
37	Ag	0.51	0/916	0.76	0/1220
38	Ah	0.55	1/1023 (0.1%)	0.73	0/1351
39	Ai	0.45	0/805	0.69	0/1065
40	Aj	0.55	0/703	0.76	1/929 (0.1%)
41	Ak	0.44	0/575	0.70	1/761 (0.1%)
42	Al	0.45	0/454	0.68	0/599
43	Am	0.45	0/417	0.67	0/553
44	An	0.49	0/241	0.85	0/305
45	Ao	0.51	0/877	0.69	0/1156
46	Ap	0.54	0/718	0.71	0/953
47	At	0.51	0/995	0.77	2/1334 (0.1%)
48	A2	1.27	17/87365 (0.0%)	1.27	737/136272 (0.5%)
49	B1	0.76	1/40767 (0.0%)	1.24	314/63536 (0.5%)
50	BD	0.40	0/1736	0.68	1/2338 (0.0%)
51	BE	0.41	0/2072	0.71	3/2793 (0.1%)
52	BF	0.39	0/1524	0.70	1/2048 (0.0%)
53	BG	0.38	0/1907	0.71	0/2538
54	BH	0.39	0/1501	0.70	1/2009 (0.0%)
55	BI	0.44	0/1725	0.70	0/2298
56	BJ	0.41	0/1520	0.70	1/2030 (0.0%)
57	BK	0.40	0/851	0.71	0/1147
58	BL	0.46	0/1281	0.74	1/1710 (0.1%)
59	BM	0.37	0/941	0.71	2/1264 (0.2%)
60	BN	0.40	0/1226	0.69	1/1649 (0.1%)
61	BO	0.45	1/1029 (0.1%)	0.70	0/1380
62	BP	0.41	0/1019	0.80	0/1361
63	BQ	0.37	0/1126	0.70	0/1506
64	BR	0.36	0/1023	0.68	0/1373
65	BS	0.39	0/1172	0.69	0/1570
66	BT	0.40	0/1131	0.70	1/1515 (0.1%)
67	BU	0.35	0/778	0.68	0/1045
68	BV	0.38	0/623	0.68	0/833
69	BW	0.44	0/1051	0.71	0/1406
70	BX	0.46	0/1097	0.69	0/1464
71	BY	0.37	0/1032	0.65	0/1371
72	BZ	0.36	0/696	0.77	1/929 (0.1%)
73	Ba	0.44	0/786	0.66	0/1053
74	Bb	0.46	0/637	0.72	0/854
75	Bc	0.32	0/490	0.70	0/656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Bd	0.43	0/437	0.79	1/580 (0.2%)
77	Be	0.38	0/443	0.71	0/583
78	Bf	0.35	0/613	0.66	0/811
79	Bg	0.35	0/2497	0.68	1/3399 (0.0%)
80	Bv	0.56	1/1813 (0.1%)	1.16	7/2823 (0.2%)
81	Bx	0.40	0/351	1.05	0/540
82	A	0.19	0/127	0.56	0/175
All	All	0.92	27/229954 (0.0%)	1.09	1153/337979 (0.3%)

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
22	AR	0	1
52	BF	0	1
All	All	0	2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	A2	1254	G	N3-C4	132.95	2.28	1.35
48	A2	1254	G	C2-N3	109.51	2.20	1.32
48	A2	1254	G	C6-N1	99.11	2.08	1.39
48	A2	1254	G	N1-C2	89.30	2.09	1.37
48	A2	1254	G	C5-C4	82.35	1.96	1.38

The worst 5 of 1153 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	A2	1254	G	C2-N3-C4	39.26	131.53	111.90
48	A2	1254	G	C4-C5-N7	-37.76	95.70	110.80
48	A2	1254	G	N3-C4-C5	-34.88	111.16	128.60
48	A2	1254	G	N3-C4-N9	33.78	146.27	126.00
48	A2	1254	G	N1-C2-N3	-29.77	106.04	123.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	AR	21	LYS	Peptide
52	BF	79	HIS	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	246/248 (99%)	216 (88%)	29 (12%)	1 (0%)	34	71
2	BA	213/215 (99%)	193 (91%)	20 (9%)	0	100	100
3	AB	392/394 (100%)	352 (90%)	39 (10%)	1 (0%)	41	75
4	BB	210/212 (99%)	175 (83%)	34 (16%)	1 (0%)	29	67
5	AC	361/363 (99%)	323 (90%)	32 (9%)	6 (2%)	9	43
6	BC	220/222 (99%)	196 (89%)	24 (11%)	0	100	100
9	AD	292/294 (99%)	261 (89%)	30 (10%)	1 (0%)	41	75
10	AE	222/247 (90%)	184 (83%)	35 (16%)	3 (1%)	11	46
11	AF	232/234 (99%)	201 (87%)	30 (13%)	1 (0%)	34	71
12	AG	232/234 (99%)	208 (90%)	23 (10%)	1 (0%)	34	71
13	AH	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
14	AI	204/211 (97%)	181 (89%)	21 (10%)	2 (1%)	15	52
15	AJ	167/169 (99%)	146 (87%)	21 (13%)	0	100	100
16	AL	203/205 (99%)	174 (86%)	26 (13%)	3 (2%)	10	45
17	AM	137/139 (99%)	119 (87%)	18 (13%)	0	100	100
18	AN	201/203 (99%)	172 (86%)	28 (14%)	1 (0%)	29	67
19	AO	193/195 (99%)	183 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
21	AQ	185/187 (99%)	165 (89%)	19 (10%)	1 (0%)	29	67
22	AR	179/181 (99%)	170 (95%)	9 (5%)	0	100	100
23	AS	173/175 (99%)	153 (88%)	20 (12%)	0	100	100
24	AT	155/157 (99%)	131 (84%)	22 (14%)	2 (1%)	12	48
25	AU	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
26	AV	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
27	AW	119/121 (98%)	103 (87%)	16 (13%)	0	100	100
28	AX	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
29	AY	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
30	AZ	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
31	Aa	145/147 (99%)	124 (86%)	21 (14%)	0	100	100
32	Ab	93/118 (79%)	81 (87%)	9 (10%)	3 (3%)	4	32
33	Ac	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
34	Ad	104/106 (98%)	91 (88%)	13 (12%)	0	100	100
35	Ae	127/129 (98%)	107 (84%)	20 (16%)	0	100	100
36	Af	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
37	Ag	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
38	Ah	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
39	Ai	95/97 (98%)	81 (85%)	13 (14%)	1 (1%)	14	51
40	Aj	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
41	Ak	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
42	Al	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
43	Am	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
44	An	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
45	Ao	103/105 (98%)	92 (89%)	11 (11%)	0	100	100
46	Ap	89/91 (98%)	78 (88%)	11 (12%)	0	100	100
47	At	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
50	BD	218/220 (99%)	193 (88%)	23 (11%)	2 (1%)	17	54
51	BE	255/257 (99%)	231 (91%)	23 (9%)	1 (0%)	34	71
52	BF	188/190 (99%)	163 (87%)	25 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	BG	230/232 (99%)	197 (86%)	33 (14%)	0	100	100
54	BH	181/183 (99%)	158 (87%)	22 (12%)	1 (1%)	25	63
55	BI	205/207 (99%)	170 (83%)	34 (17%)	1 (0%)	29	67
56	BJ	177/179 (99%)	157 (89%)	19 (11%)	1 (1%)	25	63
57	BK	96/98 (98%)	77 (80%)	18 (19%)	1 (1%)	15	52
58	BL	151/153 (99%)	131 (87%)	19 (13%)	1 (1%)	22	60
59	BM	118/120 (98%)	110 (93%)	8 (7%)	0	100	100
60	BN	147/149 (99%)	129 (88%)	18 (12%)	0	100	100
61	BO	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
62	BP	118/120 (98%)	100 (85%)	16 (14%)	2 (2%)	9	43
63	BQ	137/139 (99%)	121 (88%)	16 (12%)	0	100	100
64	BR	123/125 (98%)	107 (87%)	15 (12%)	1 (1%)	19	57
65	BS	137/139 (99%)	117 (85%)	19 (14%)	1 (1%)	22	60
66	BT	141/143 (99%)	126 (89%)	14 (10%)	1 (1%)	22	60
67	BU	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
68	BV	79/81 (98%)	72 (91%)	6 (8%)	1 (1%)	12	48
69	BW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
70	BX	137/139 (99%)	124 (90%)	13 (10%)	0	100	100
71	BY	123/125 (98%)	113 (92%)	10 (8%)	0	100	100
72	BZ	84/86 (98%)	71 (84%)	12 (14%)	1 (1%)	13	49
73	Ba	95/97 (98%)	84 (88%)	10 (10%)	1 (1%)	14	51
74	Bb	78/80 (98%)	68 (87%)	10 (13%)	0	100	100
75	Bc	60/62 (97%)	52 (87%)	6 (10%)	2 (3%)	4	31
76	Bd	49/51 (96%)	38 (78%)	11 (22%)	0	100	100
77	Be	53/55 (96%)	45 (85%)	8 (15%)	0	100	100
78	Bf	71/73 (97%)	61 (86%)	9 (13%)	1 (1%)	11	46
79	Bg	312/314 (99%)	273 (88%)	39 (12%)	0	100	100
82	A	24/26 (92%)	16 (67%)	3 (12%)	5 (21%)	0	2
All	All	11199/11402 (98%)	9901 (88%)	1246 (11%)	52 (0%)	32	67

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AB	4	ARG
5	AC	53	ALA
5	AC	151	PRO
14	AI	189	ARG
16	AL	46	ILE

### 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	
1	AA	190/190 (100%)	185 (97%)	5 (3%)	46	68
2	BA	180/180 (100%)	178 (99%)	2 (1%)	73	84
3	AB	343/343 (100%)	340 (99%)	3 (1%)	78	87
4	BB	193/193 (100%)	190 (98%)	3 (2%)	62	79
5	AC	302/302 (100%)	289 (96%)	13 (4%)	29	57
6	BC	188/188 (100%)	186 (99%)	2 (1%)	73	84
9	AD	248/248 (100%)	241 (97%)	7 (3%)	43	66
10	AE	202/220 (92%)	198 (98%)	4 (2%)	55	74
11	AF	203/203 (100%)	200 (98%)	3 (2%)	65	80
12	AG	199/199 (100%)	198 (100%)	1 (0%)	88	93
13	AH	170/170 (100%)	170 (100%)	0	100	100
14	AI	178/179 (99%)	171 (96%)	7 (4%)	32	59
15	AJ	142/142 (100%)	142 (100%)	0	100	100
16	AL	171/171 (100%)	165 (96%)	6 (4%)	36	62
17	AM	118/118 (100%)	116 (98%)	2 (2%)	60	78
18	AN	171/171 (100%)	168 (98%)	3 (2%)	59	77
19	AO	168/168 (100%)	163 (97%)	5 (3%)	41	64
20	AP	134/134 (100%)	134 (100%)	0	100	100
21	AQ	164/164 (100%)	163 (99%)	1 (1%)	86	91
22	AR	160/160 (100%)	159 (99%)	1 (1%)	86	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	AS	156/156 (100%)	155 (99%)	1 (1%)	86	91
24	AT	138/138 (100%)	138 (100%)	0	100	100
25	AU	89/89 (100%)	88 (99%)	1 (1%)	73	84
26	AV	100/100 (100%)	99 (99%)	1 (1%)	76	86
27	AW	100/100 (100%)	99 (99%)	1 (1%)	76	86
28	AX	105/105 (100%)	105 (100%)	0	100	100
29	AY	119/119 (100%)	116 (98%)	3 (2%)	47	69
30	AZ	117/117 (100%)	115 (98%)	2 (2%)	60	78
31	Aa	120/120 (100%)	119 (99%)	1 (1%)	81	89
32	Ab	79/98 (81%)	75 (95%)	4 (5%)	24	53
33	Ac	88/88 (100%)	86 (98%)	2 (2%)	50	71
34	Ad	97/97 (100%)	97 (100%)	0	100	100
35	Ae	115/115 (100%)	114 (99%)	1 (1%)	78	87
36	Af	88/88 (100%)	86 (98%)	2 (2%)	50	71
37	Ag	98/98 (100%)	98 (100%)	0	100	100
38	Ah	109/109 (100%)	106 (97%)	3 (3%)	43	66
39	Ai	83/83 (100%)	83 (100%)	0	100	100
40	Aj	71/71 (100%)	70 (99%)	1 (1%)	67	81
41	Ak	64/64 (100%)	62 (97%)	2 (3%)	40	64
42	Al	47/47 (100%)	44 (94%)	3 (6%)	17	47
43	Am	46/46 (100%)	44 (96%)	2 (4%)	29	57
44	An	24/24 (100%)	24 (100%)	0	100	100
45	Ao	93/93 (100%)	91 (98%)	2 (2%)	52	71
46	Ap	74/74 (100%)	72 (97%)	2 (3%)	44	67
47	At	106/106 (100%)	104 (98%)	2 (2%)	57	75
50	BD	183/183 (100%)	181 (99%)	2 (1%)	73	84
51	BE	220/220 (100%)	216 (98%)	4 (2%)	59	77
52	BF	160/160 (100%)	157 (98%)	3 (2%)	57	75
53	BG	202/202 (100%)	200 (99%)	2 (1%)	76	86
54	BH	164/164 (100%)	162 (99%)	2 (1%)	71	83
55	BI	179/179 (100%)	177 (99%)	2 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	BJ	160/160 (100%)	158 (99%)	2 (1%)	69	82
57	BK	89/89 (100%)	88 (99%)	1 (1%)	73	84
58	BL	138/138 (100%)	138 (100%)	0	100	100
59	BM	102/102 (100%)	101 (99%)	1 (1%)	76	86
60	BN	130/130 (100%)	129 (99%)	1 (1%)	81	89
61	BO	106/106 (100%)	105 (99%)	1 (1%)	78	87
62	BP	109/109 (100%)	107 (98%)	2 (2%)	59	77
63	BQ	115/115 (100%)	115 (100%)	0	100	100
64	BR	113/113 (100%)	111 (98%)	2 (2%)	59	77
65	BS	121/121 (100%)	117 (97%)	4 (3%)	38	63
66	BT	113/113 (100%)	111 (98%)	2 (2%)	59	77
67	BU	90/90 (100%)	90 (100%)	0	100	100
68	BV	65/65 (100%)	63 (97%)	2 (3%)	40	64
69	BW	112/112 (100%)	110 (98%)	2 (2%)	59	77
70	BX	111/111 (100%)	109 (98%)	2 (2%)	59	77
71	BY	107/107 (100%)	105 (98%)	2 (2%)	57	75
72	BZ	75/75 (100%)	73 (97%)	2 (3%)	44	67
73	Ba	84/84 (100%)	84 (100%)	0	100	100
74	Bb	72/72 (100%)	71 (99%)	1 (1%)	67	81
75	Bc	55/55 (100%)	55 (100%)	0	100	100
76	Bd	45/45 (100%)	45 (100%)	0	100	100
77	Be	44/44 (100%)	40 (91%)	4 (9%)	9	35
78	Bf	66/66 (100%)	66 (100%)	0	100	100
79	Bg	272/272 (100%)	271 (100%)	1 (0%)	91	94
All	All	9752/9790 (100%)	9601 (98%)	151 (2%)	66	80

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	BH	152	ARG
72	BZ	62	VAL
56	BJ	30	LYS
65	BS	23	ARG
79	Bg	133	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 127 such sidechains are listed below:

Mol	Chain	Res	Type
21	AQ	44	ASN
69	BW	5	ASN
32	Ab	60	ASN
65	BS	19	ASN
72	BZ	89	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	A2	3626/3643 (99%)	1021 (28%)	12 (0%)
49	B1	1701/1708 (99%)	533 (31%)	6 (0%)
7	A3	156/157 (99%)	49 (31%)	1 (0%)
8	A4	118/119 (99%)	29 (24%)	0
80	Bv	75/76 (98%)	28 (37%)	0
81	Bx	15/16 (93%)	9 (60%)	0
All	All	5691/5719 (99%)	1669 (29%)	19 (0%)

5 of 1669 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A3	8	U
7	A3	32	C
7	A3	34	U
7	A3	35	C
7	A3	36	G

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	B1	216	C
49	B1	869	A
49	B1	1398	G
49	B1	797	C
48	A2	3755	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 332 ligands modelled in this entry, 331 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
85	MVM	A	101	-	33,35,35	1.75	6 (18%)	36,49,49	2.50	14 (38%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	MVM	A	101	-	-	3/20/28/28	0/5/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	A	101	MVM	C5-N1	5.88	1.45	1.37
85	A	101	MVM	N5-N4	-4.53	1.30	1.37
85	A	101	MVM	C6-N1	2.72	1.45	1.39
85	A	101	MVM	O1-C5	-2.28	1.18	1.22
85	A	101	MVM	C2-CL	2.07	1.78	1.73

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	A	101	MVM	C15-N4-C22	-8.27	121.07	129.98
85	A	101	MVM	C15-N4-N5	4.81	127.66	119.95
85	A	101	MVM	N3-C6-N1	4.32	120.91	116.33
85	A	101	MVM	C21-N7-C22	3.93	121.65	116.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	A	101	MVM	C7-C3-C9	3.66	118.09	110.82

There are no chirality outliers.

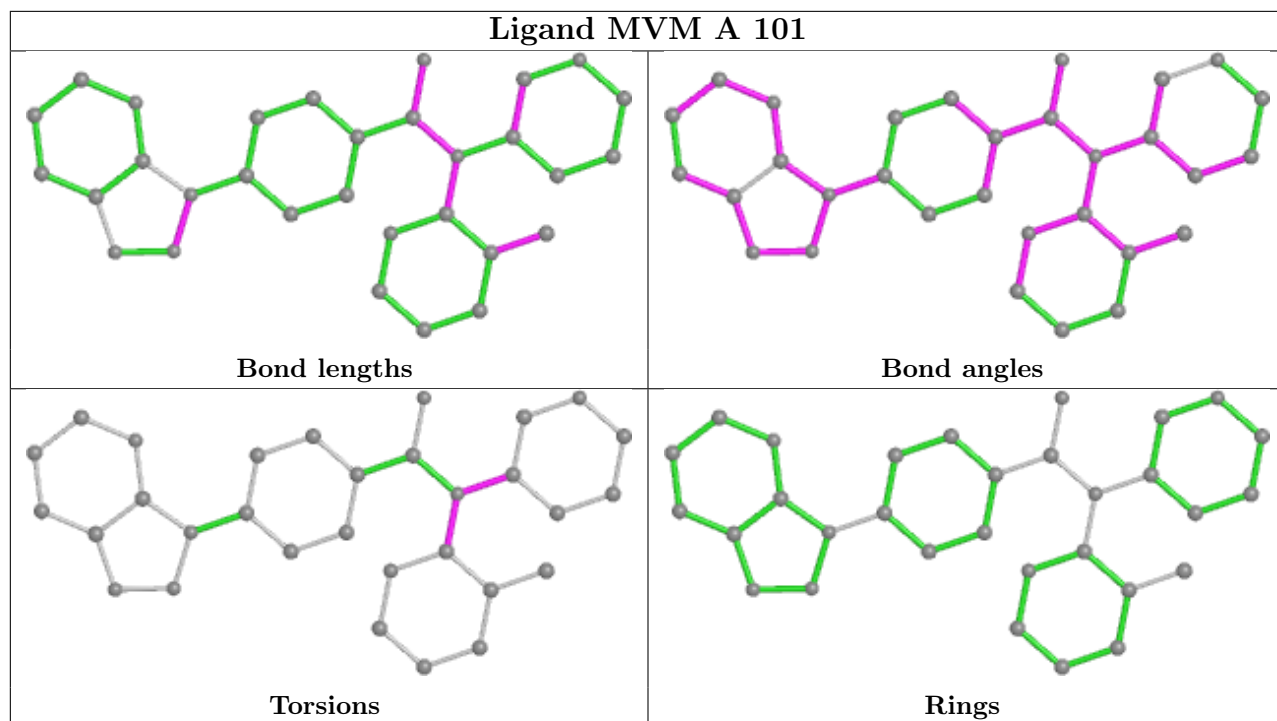
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	A	101	MVM	C3-C9-N1-C5
85	A	101	MVM	C3-C9-N1-C6
85	A	101	MVM	N3-C6-N1-C5

There are no ring outliers.

No monomer is involved in short contacts.

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
48	A2	16
49	B1	6

The worst 5 of 22 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	3923:A	O3'	3930:U	P	31.28
1	B1	126:G	O3'	141:A	P	22.59
1	A2	2231:G	O3'	2235:C	P	21.97
1	A2	3948:C	O3'	4004:G	P	18.85
1	B1	1426:U	O3'	1438:A	P	18.66

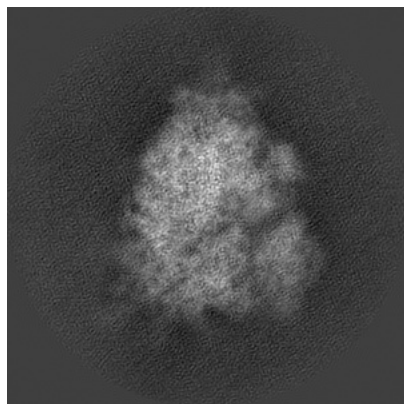
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0598. These allow visual inspection of the internal detail of the map and identification of artifacts.

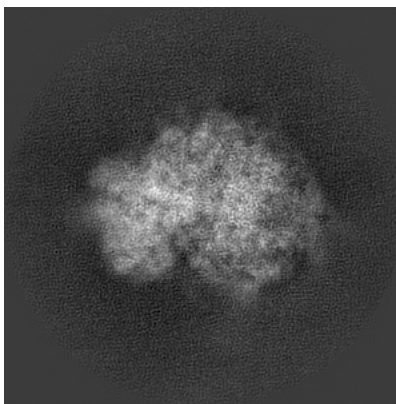
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

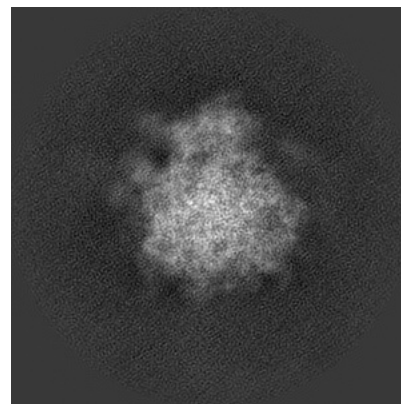
#### 6.1.1 Primary map



X

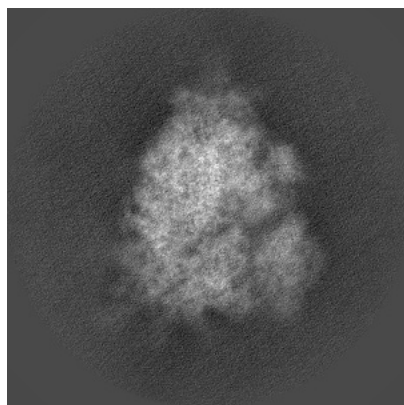


Y

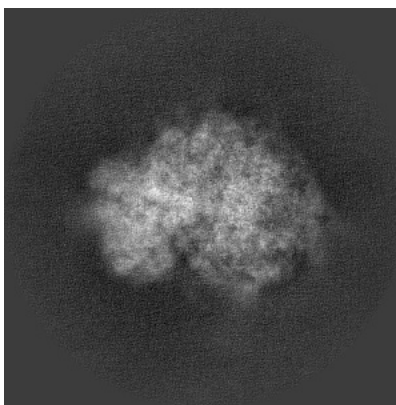


Z

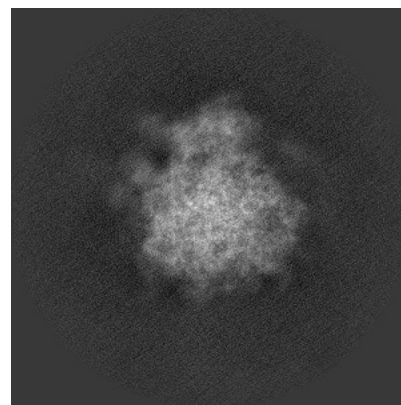
#### 6.1.2 Raw map



X



Y



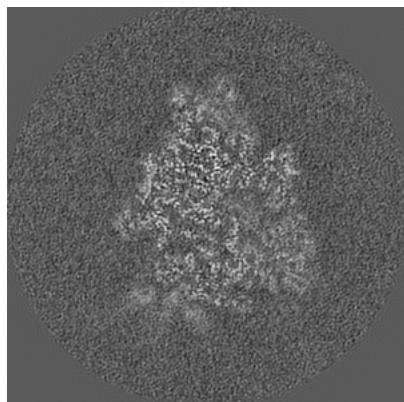
Z

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

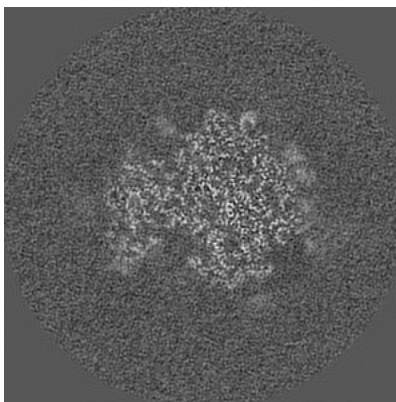


## 6.2 Central slices [i](#)

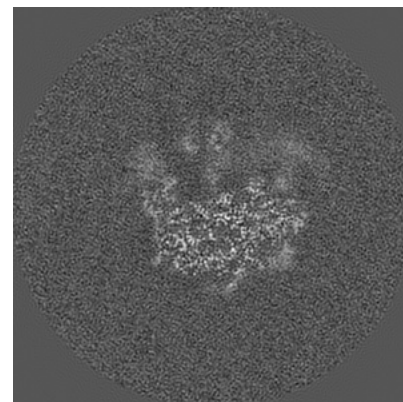
### 6.2.1 Primary map



X Index: 200

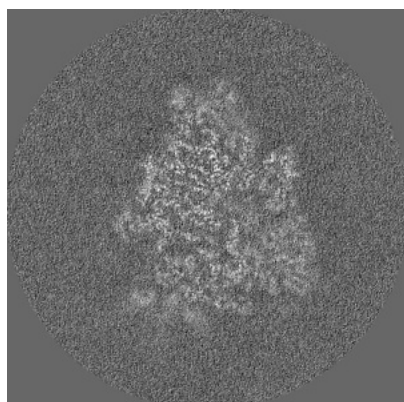


Y Index: 200

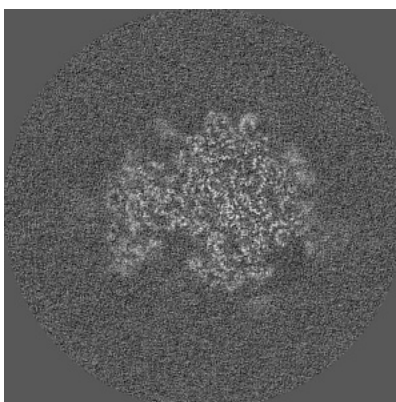


Z Index: 200

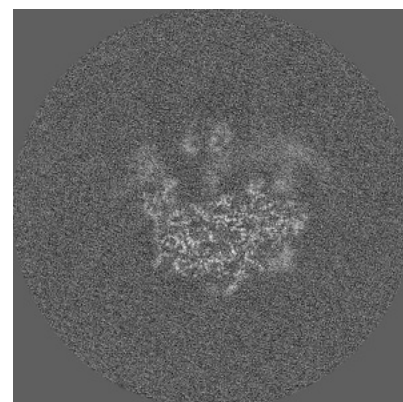
### 6.2.2 Raw map



X Index: 200



Y Index: 200



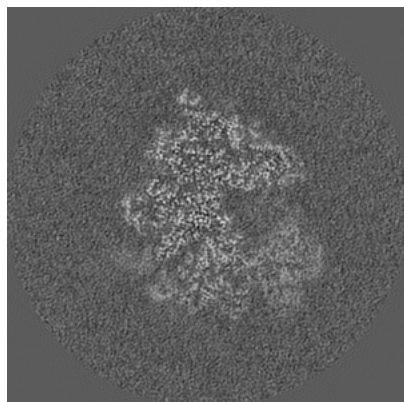
Z Index: 200

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

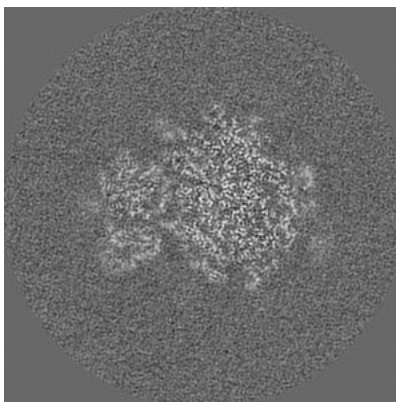


## 6.3 Largest variance slices [i](#)

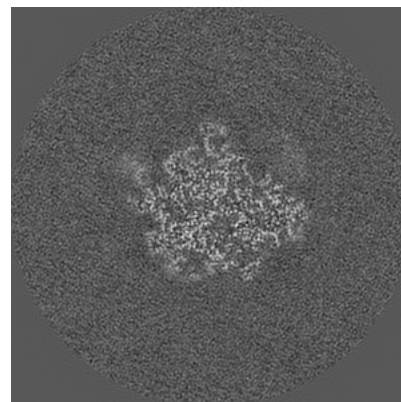
### 6.3.1 Primary map



X Index: 217

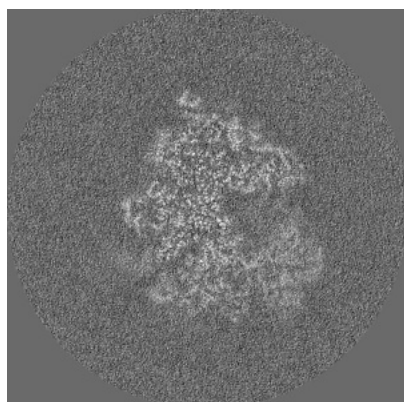


Y Index: 194

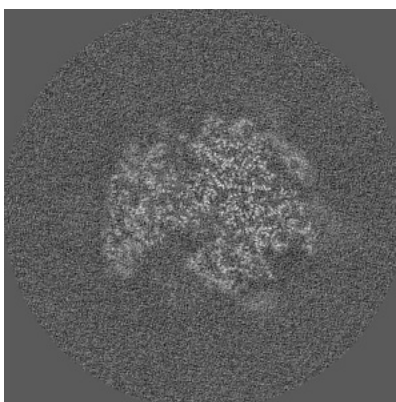


Z Index: 220

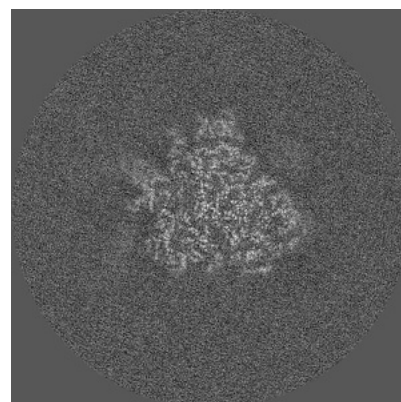
### 6.3.2 Raw map



X Index: 217



Y Index: 205

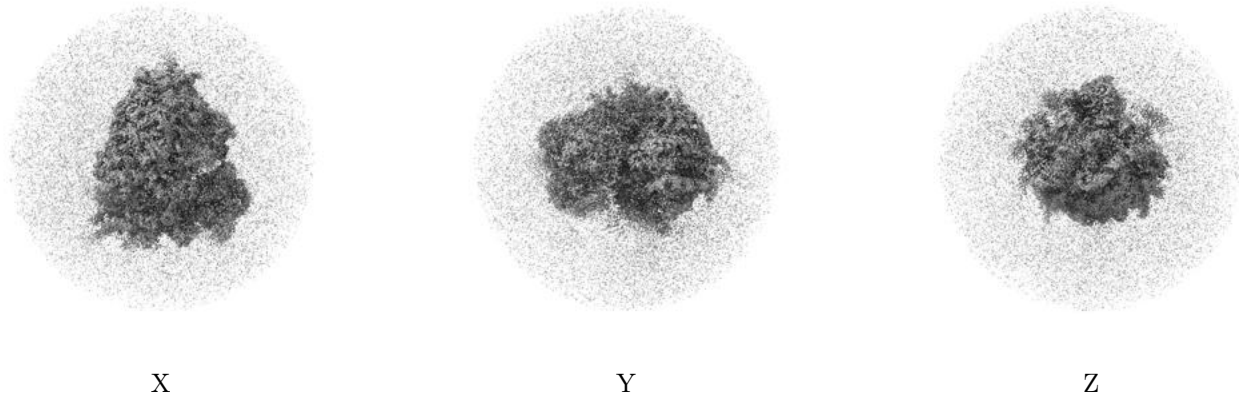


Z Index: 228

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

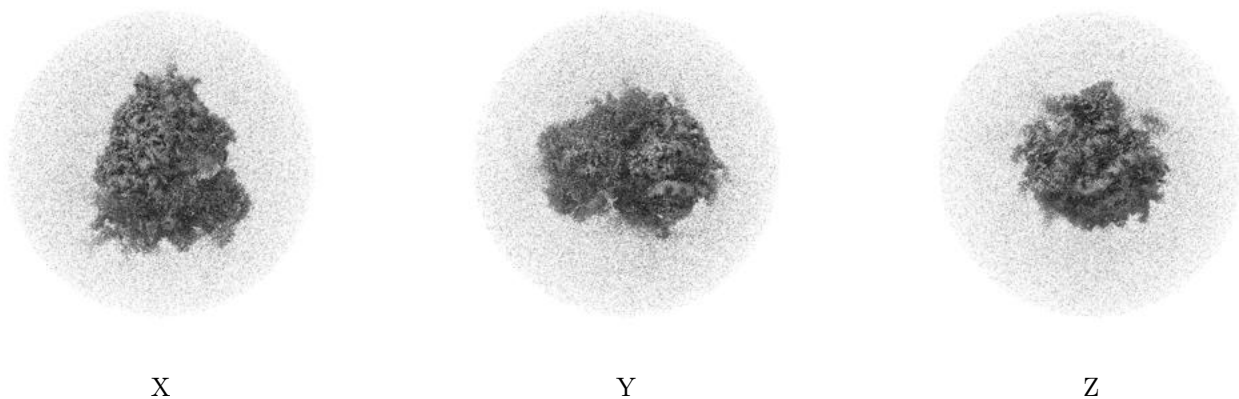
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



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

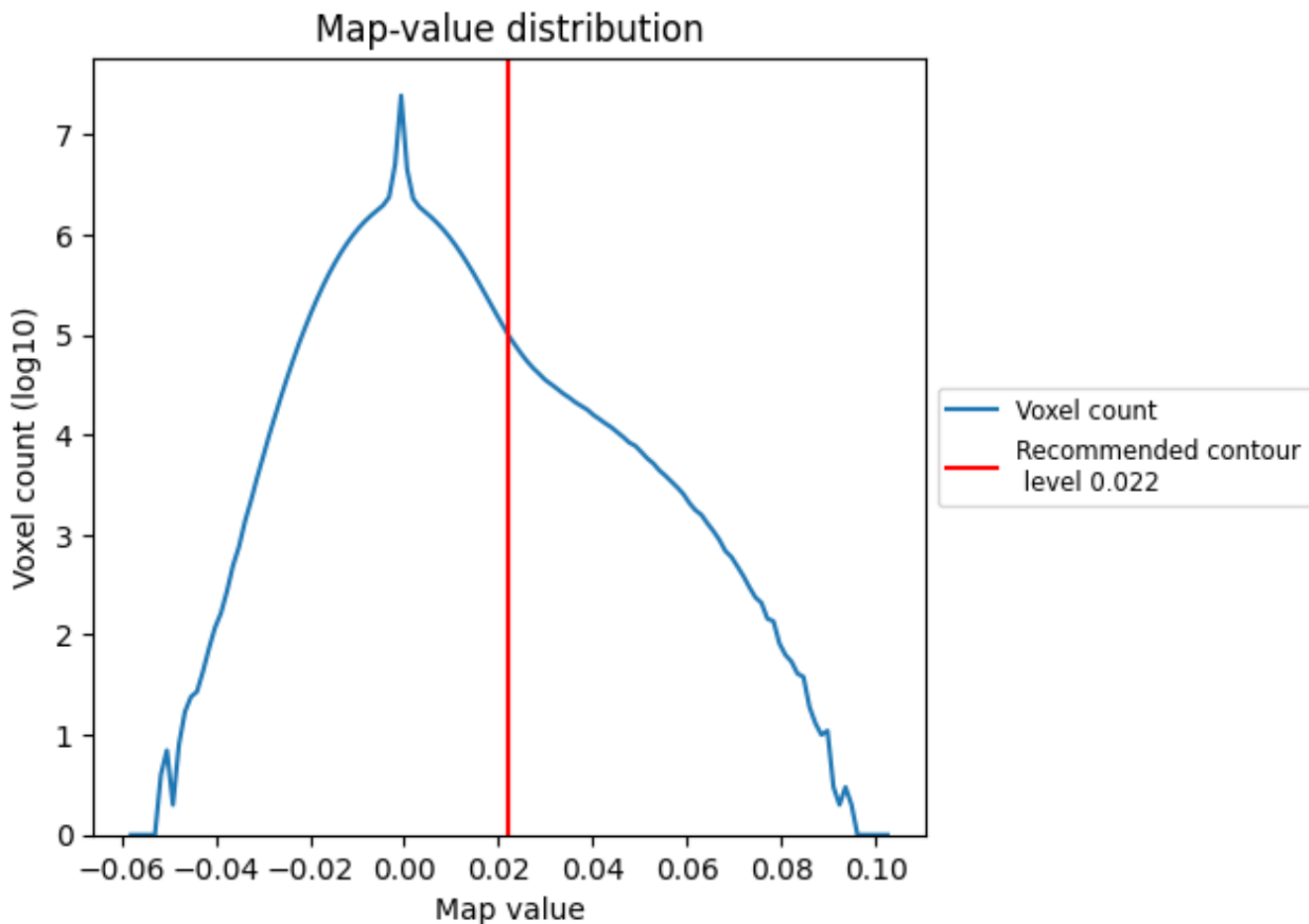
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

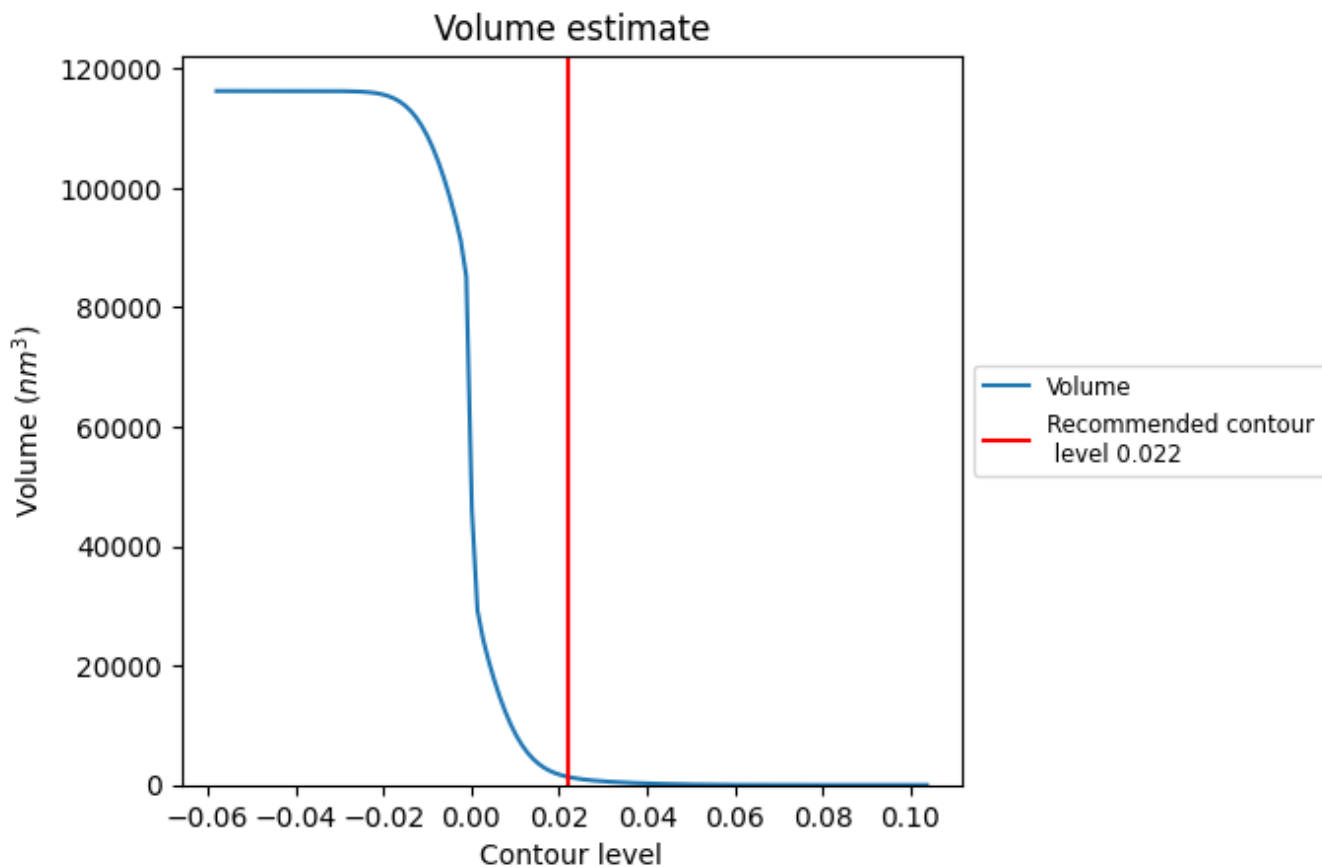
This section contains the results of statistical analysis of the map.

### 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.

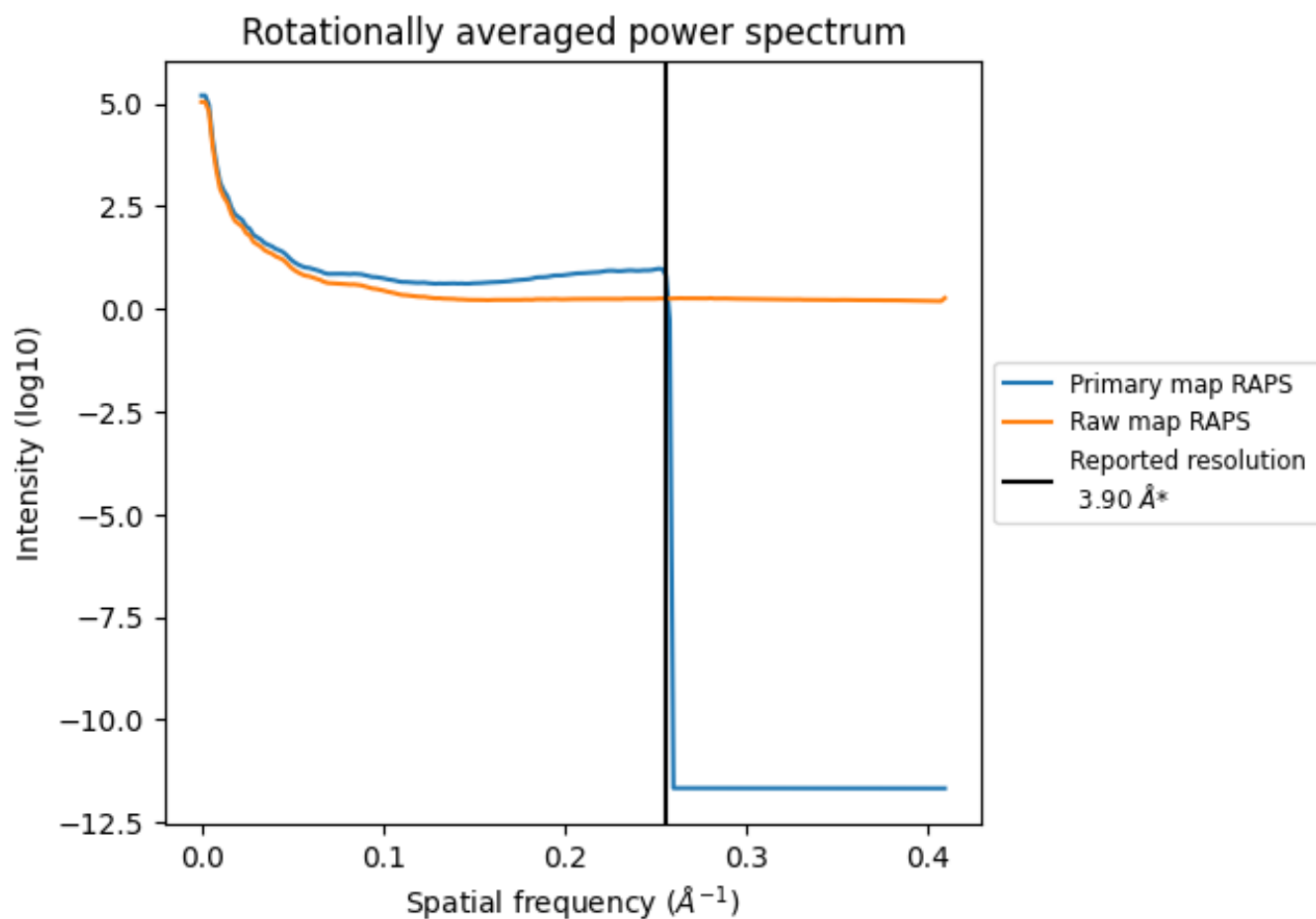
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1361 nm<sup>3</sup>; this corresponds to an approximate mass of 1230 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](#)

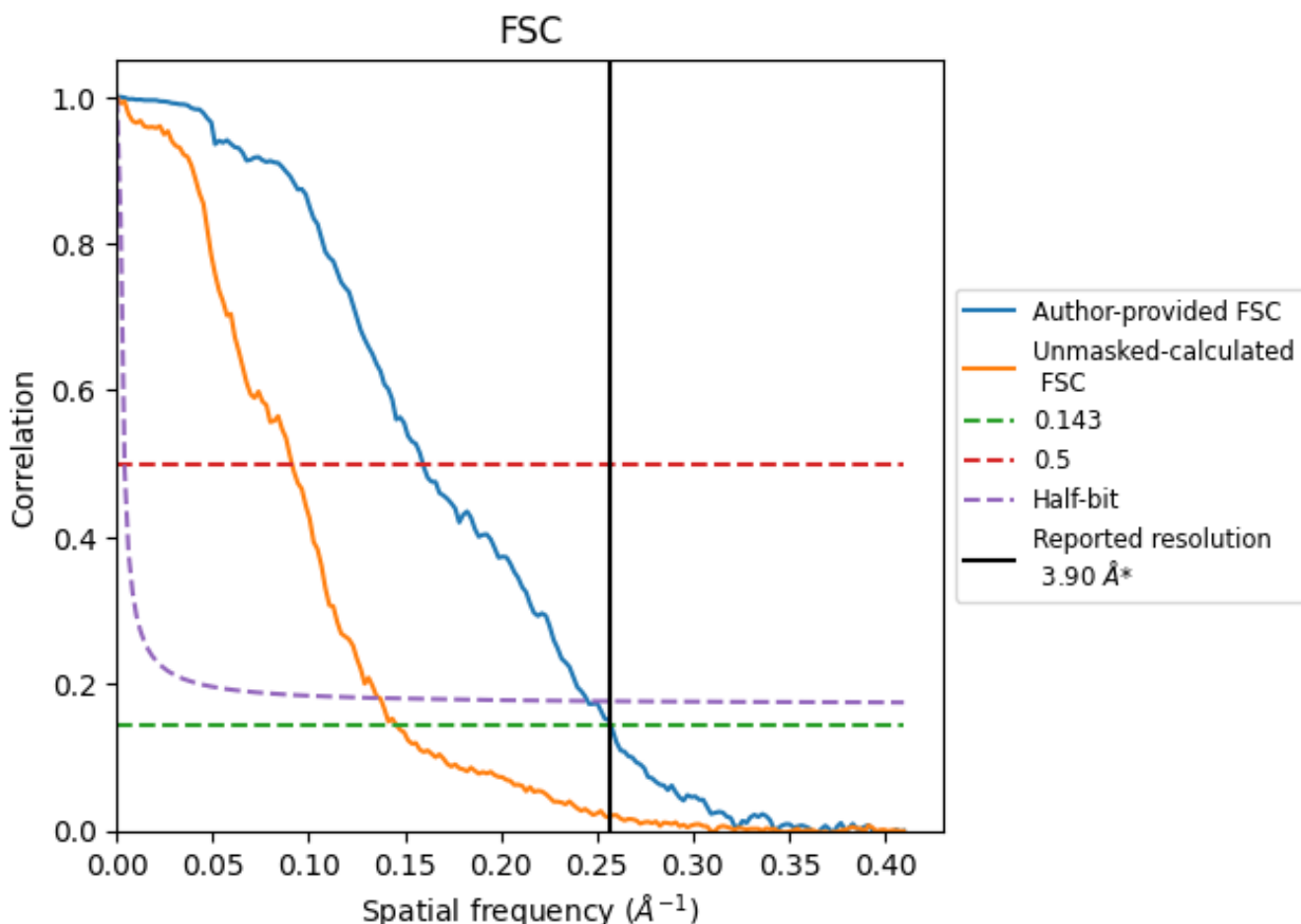


\*Reported resolution corresponds to spatial frequency of 0.256 Å<sup>-1</sup>

## 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 0.256 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

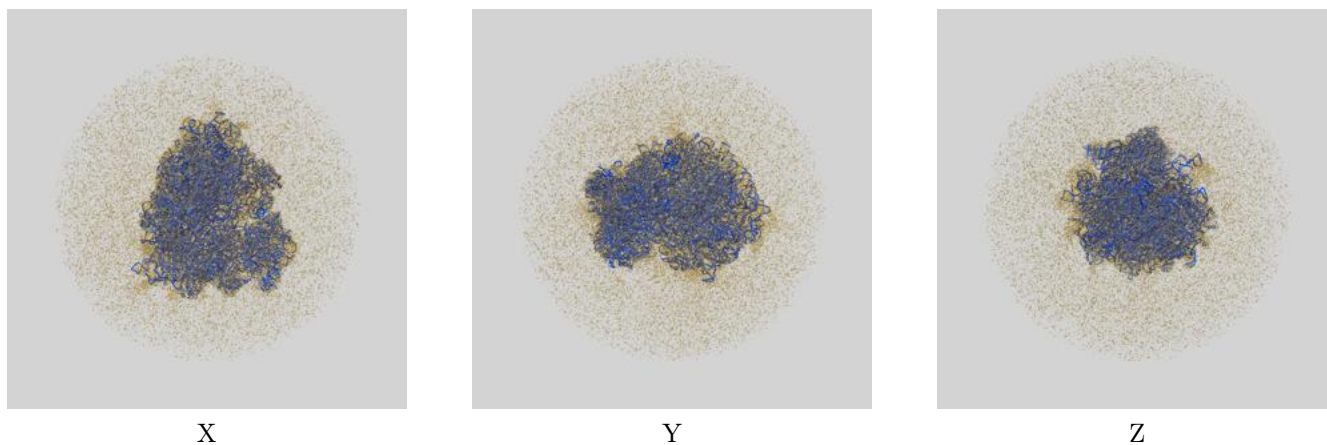
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.89	6.27	4.08
Unmasked-calculated*	6.86	10.96	7.30

\*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 6.86 differs from the reported value 3.9 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0598 and PDB model 6OLZ. Per-residue inclusion information can be found in section 3 on page 20.

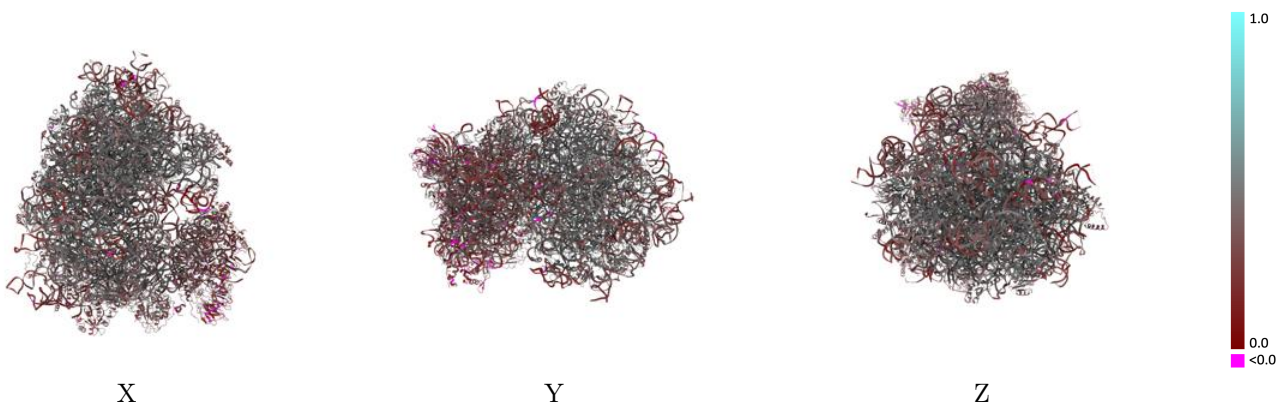
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.022 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.

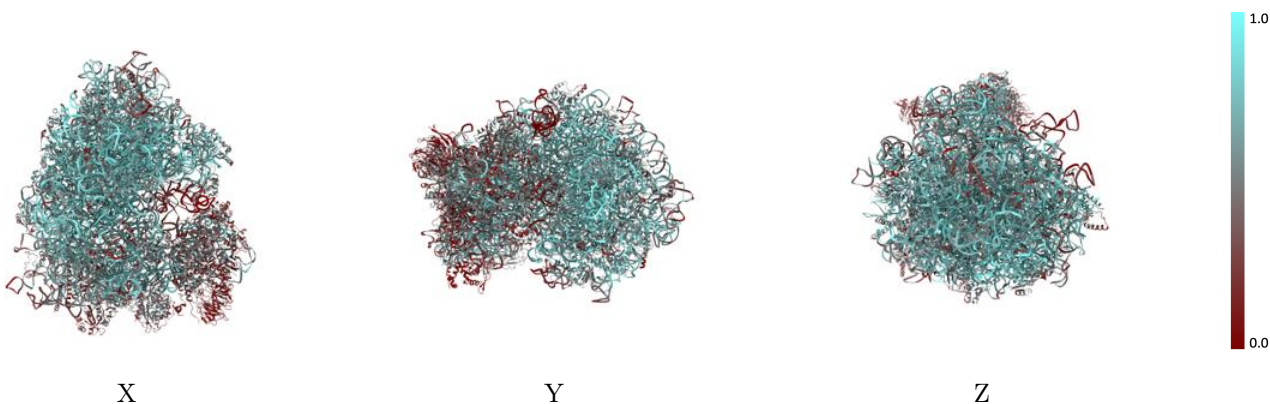


## 9.2 Q-score mapped to coordinate model [i](#)



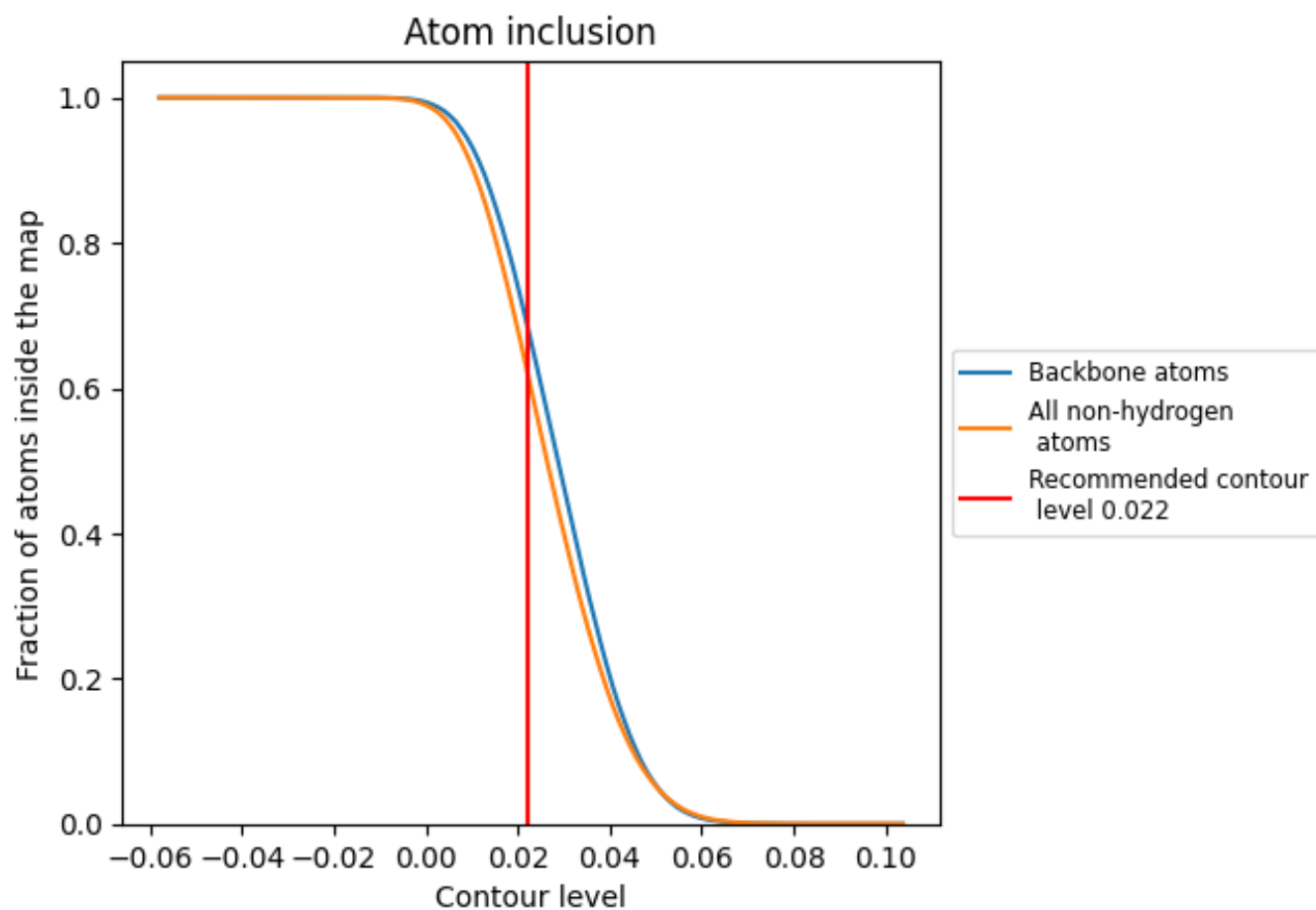
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 69% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6244	 0.3940
A	 0.2516	 0.3170
A2	 0.7482	 0.4090
A3	 0.7584	 0.4190
A4	 0.8396	 0.4390
AA	 0.6536	 0.4800
AB	 0.6307	 0.4530
AC	 0.6539	 0.4610
AD	 0.5624	 0.3920
AE	 0.5303	 0.3990
AF	 0.6219	 0.4410
AG	 0.5416	 0.4000
AH	 0.5625	 0.4300
AI	 0.5915	 0.4410
AJ	 0.5137	 0.3780
AL	 0.5931	 0.4140
AM	 0.6251	 0.4380
AN	 0.6915	 0.4760
AO	 0.6334	 0.4560
AP	 0.6656	 0.4730
AQ	 0.6436	 0.4640
AR	 0.5938	 0.4170
AS	 0.6478	 0.4620
AT	 0.6093	 0.4610
AU	 0.5114	 0.3850
AV	 0.6177	 0.4720
AW	 0.3679	 0.3430
AX	 0.6284	 0.4480
AY	 0.6485	 0.4620
AZ	 0.6006	 0.4220
Aa	 0.6749	 0.4650
Ab	 0.5334	 0.3850
Ac	 0.5536	 0.4100
Ad	 0.6215	 0.4460
Ae	 0.6573	 0.4720















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Chain	Atom inclusion	Q-score
Af	 0.6401	 0.4720
Ag	 0.6110	 0.4530
Ah	 0.6106	 0.4220
Ai	 0.6024	 0.4130
Aj	 0.7158	 0.4890
Ak	 0.5081	 0.3880
Al	 0.5849	 0.4380
Am	 0.6373	 0.4520
An	 0.5273	 0.4190
Ao	 0.6229	 0.4480
Ap	 0.6096	 0.4430
At	 0.6578	 0.4510
B1	 0.6445	 0.3640
BA	 0.4474	 0.3730
BB	 0.4622	 0.3870
BC	 0.4956	 0.3990
BD	 0.2437	 0.2790
BE	 0.4566	 0.3800
BF	 0.3025	 0.3080
BG	 0.3636	 0.3210
BH	 0.3393	 0.3290
BI	 0.5159	 0.4110
BJ	 0.4446	 0.3500
BK	 0.2025	 0.2460
BL	 0.4873	 0.4030
BM	 0.0436	 0.1750
BN	 0.4889	 0.3940
BO	 0.4965	 0.4110
BP	 0.2916	 0.2920
BQ	 0.3178	 0.2950
BR	 0.2879	 0.2990
BS	 0.3141	 0.2870
BT	 0.2930	 0.2630
BU	 0.2853	 0.2960
BV	 0.4328	 0.3670
BW	 0.5257	 0.4170
BX	 0.5185	 0.4040
BY	 0.4193	 0.3250
BZ	 0.2396	 0.2770
Ba	 0.5188	 0.4030
Bb	 0.4796	 0.4030
Bc	 0.2532	 0.3040

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Chain	Atom inclusion	Q-score
Bd	 0.3439	 0.3100
Be	 0.4242	 0.3860
Bf	 0.1096	 0.2150
Bg	 0.1365	 0.2190
Bv	 0.2000	 0.2750
Bx	 0.1250	 0.2270