



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:29 PM UTC

PDB ID : 6IP6 / pdb_00006ip6
EMDB ID : EMD-9702
Title : Cryo-EM structure of the CMV-stalled human 80S ribosome with HCV IRES
(Structure iii)
Authors : Yokoyama, T.; Shigematsu, H.; Shirouzu, M.; Imataka, H.; Ito, T.
Deposited on : 2018-11-02
Resolution : 4.50 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:

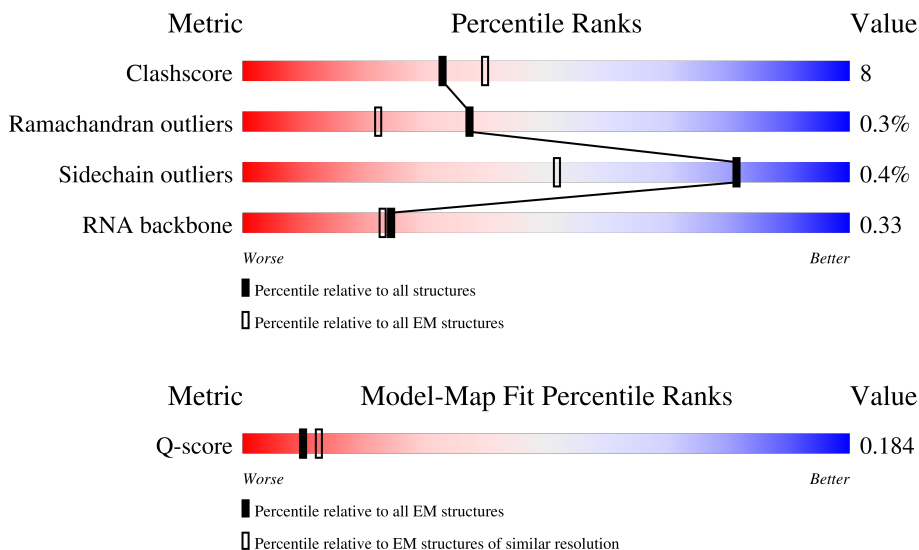
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

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	1A	5070	
2	1B	121	
3	1C	157	

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Mol	Chain	Length	Quality of chain
4	1D	257	56% 79% 18%
5	1E	403	19% 82% 17%
6	1F	427	41% 74% 12% 14%
7	1G	297	49% 81% 17%
8	1H	288	19% 60% 20% 18%
9	2A	248	28% 63% 27% 9%
10	2B	266	64% 75% 16% 9%
11	2C	192	11% 76% 21%
12	2D	214	25% 74% 26%
13	2E	178	42% 70% 29%
14	2F	211	63% 83% 17%
15	2G	215	9% 55% 9% 35%
16	2H	204	61% 78% 22%
17	2I	203	7% 82% 17%
18	2J	184	23% 70% 13% 17%
19	2K	188	55% 84% 16%
20	2L	196	46% 73% 22% 5%
21	2M	176	13% 78% 22%
22	2N	160	39% 76% 22%
23	2O	128	50% 64% 15% 21%
24	2P	140	14% 72% 20% 6%
25	2Q	157	48% 67% 11% 21%
26	2R	156	49% 67% 10% 24%
27	2S	145	48% 73% 19% 8%
28	2T	136	58% 80% 18%

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Mol	Chain	Length	Quality of chain
29	2U	148	53% 82% 18%
30	2V	159	31% 60% 8% 31%
31	2W	115	46% 77% 8% 15%
32	2X	125	30% 76% 10% 14%
33	2Y	135	29% 78% 16% 5%
34	2Z	110	11% 72% 27%
35	2a	117	55% 75% 21%
36	2b	123	59% 89% 11%
37	2c	105	69% 84% 13%
38	2d	97	40% 53% 35% 11%
39	2e	70	53% 73% 24%
40	2f	51	51% 80% 18%
41	2g	128	31% 9% 59%
42	2h	25	12% 92%
43	2i	106	43% 85% 14%
44	2j	92	48% 76% 23%
45	2k	137	42% 75% 16% 9%
46	2m	1869	9% 36% 42% 15% 7%
47	2n	295	31% 59% 16% 25%
48	2o	264	56% 66% 15% 19%
49	2p	243	52% 81% 12% 7%
50	2q	263	49% 75% 25%
51	2r	204	52% 72% 19% 8%
52	2s	194	61% 74% 23%
53	2t	208	54% 79% 20%

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Mol	Chain	Length	Quality of chain
54	2u	165	41% 49% 10% 41%
55	2v	158	56% 78% 18%
56	2w	145	39% 42% 24% 33%
57	2x	146	57% 73% 25%
58	2y	135	53% 76% 21%
59	2z	152	61% 77% 19%
60	20	145	56% 74% 25%
61	21	119	55% 62% 25% 13%
62	3A	83	39% 83% 17%
63	3B	143	24% 78% 20%
64	3C	115	39% 71% 22% 7%
65	3D	69	67% 62% 29% 7%
66	3E	56	32% 59% 36% 5%
67	3F	317	64% 70% 28%
68	3G	293	18% 59% 16% 24%
69	3H	249	54% 71% 24% 5%
70	3I	194	34% 72% 22% 5%
71	3J	132	92% 75% 17% 8%
72	3K	151	50% 91% 7%
73	3L	151	63% 68% 24% 7%
74	3M	130	31% 81% 18%
75	3N	133	39% 78% 20%
76	3O	125	42% 40% 19% 40%
77	3P	84	67% 69% 26%
78	3Q	59	36% 88% 10%

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Mol	Chain	Length	Quality of chain
79	3R	156	
80	zV	6	
81	zX	17	
82	zY	75	
83	zZ	290	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 219084 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1A	3667	78599	35000	14383	25550	3666	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1B	120	2558	1141	456	842	119	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	1C	156	3314	1480	585	1094	155	0	0

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	1D	248	1898	1189	389	314	6	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	1E	402	3238	2060	608	556	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	1F	368	2927	1840	583	489	15	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	1G	293	2382	1507	434	427	14	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	1H	237	1913	1228	363	318	4	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	2A	225	1870	1202	358	301	9	0	0

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	2B	241	1927	1228	371	324	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	2C	190	1518	956	284	272	6	0	0

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	2D	213	1711	1082	329	285	15	0	0

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	2E	176	1410	888	263	253	6	0	0

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2F	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2G	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2H	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2L	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	2M	175	1453	925	283	235	10	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	2N	159	1298	823	252	217	6	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	2O	101	825	529	144	150	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	2P	131	979	618	184	172	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	2Q	124	1015	634	207	170	4	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	2R	119	976	625	184	166	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	2S	134	1115	700	226	186	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	2V	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	2W	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

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

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2Z	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2a	113	Total	C	N	O	S	0	0
			895	560	183	146	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2d	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2e	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	2h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	2i	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2m	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2n	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2o	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	2p	227	1765	1125	317	315	8	0	0

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	2q	262	2076	1324	386	358	8	0	0

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	2r	187	1479	924	282	266	7	0	0

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	2s	189	1521	969	280	271	1	0	0

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	2t	206	1686	1058	332	291	5	0	0

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	2u	98	827	539	148	134	6	0	0

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	2v	153	1247	793	234	214	6	0	0

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	2w	97	804	505	155	138	6	0	0

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	2x	146	1158	736	218	200	4	0	0

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	2y	132	1072	673	199	195	5	0	0

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	2z	150	1235	776	250	208	1	0	0

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	20	143	1112	697	214	198	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	21	104	821	514	155	148	4	0	0

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	3A	83	636	393	117	121	5	0	0

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	3B	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	3C	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	3D	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
66	3E	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	3F	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	3G	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	3H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	3I	185	1525	969	306	248	2	0	0

- Molecule 71 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	3J	122	952	596	169	179	8	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3J	52	GLN	LEU	conflict	UNP P25398
3J	69	LEU	CYS	conflict	UNP P25398
3J	99	ASN	LYS	conflict	UNP P25398

- Molecule 72 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	3K	150	1208	773	229	205	1	0	0

- Molecule 73 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	3L	140	1049	642	204	197	6	0	0

- Molecule 74 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	3M	129	1034	659	193	176	6	0	0

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	3N	131	1065	673	209	178	5	0	0

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	3O	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	3P	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	3Q	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	3R	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zv	6	Total	C	N	O	P	0	0
			123	55	19	43	6		

- Molecule 81 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zx	17	Total	C	N	O	S	0	0
			129	86	20	22	1		

- Molecule 82 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		

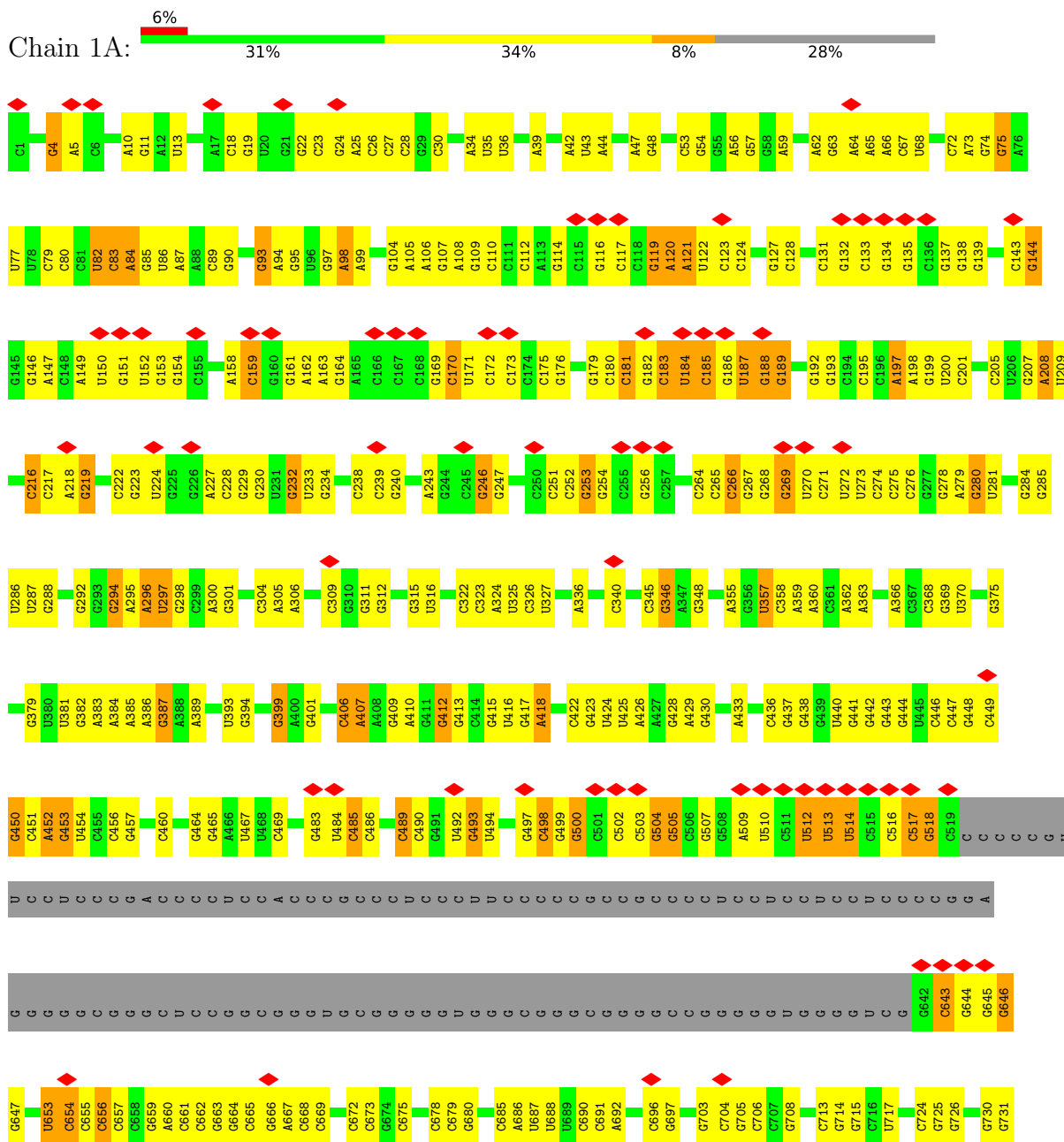
- Molecule 83 is a RNA chain called HCV-IRES RNA.

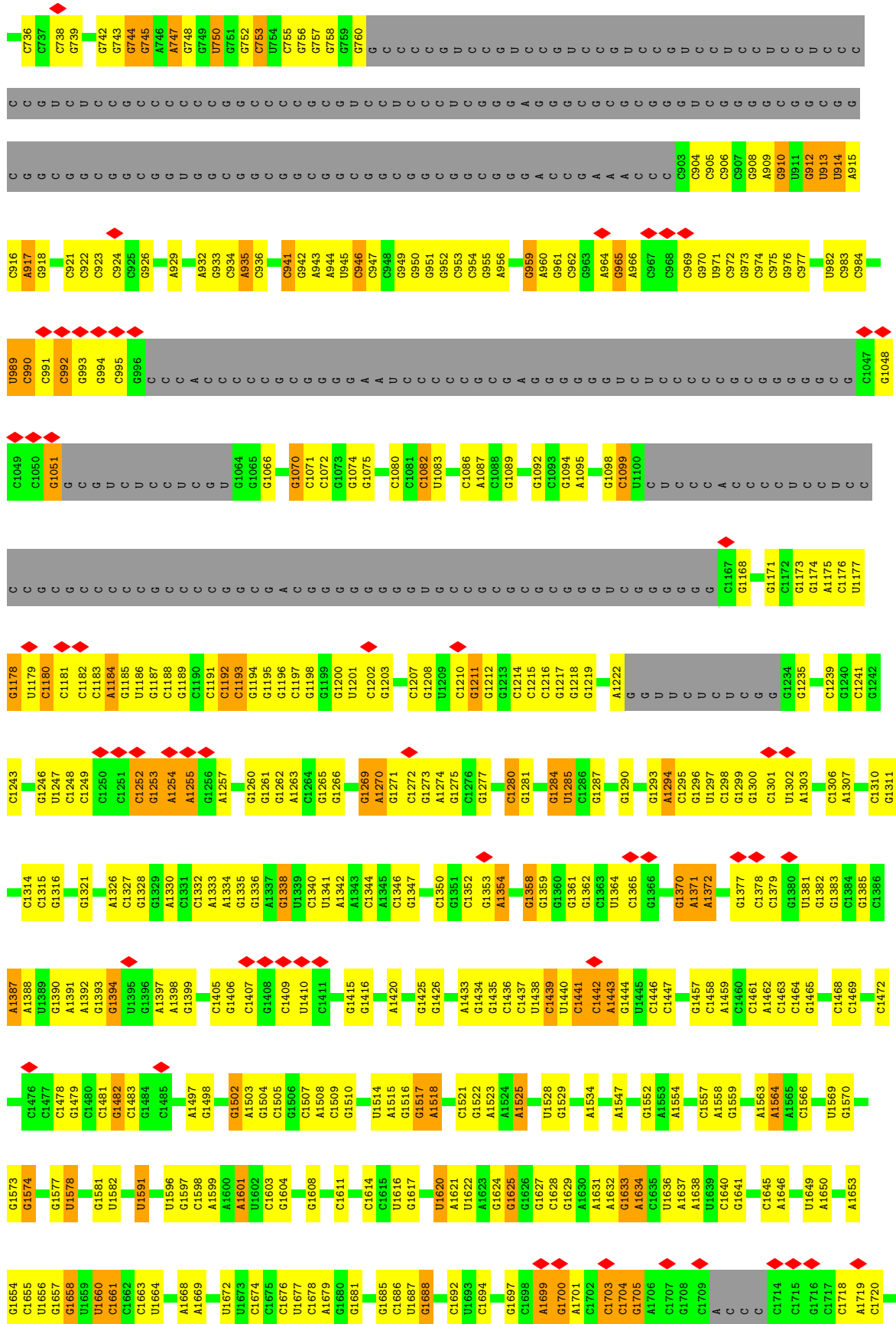
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	<i>zz</i>	163	3492	1553	627	1149	163	0	0

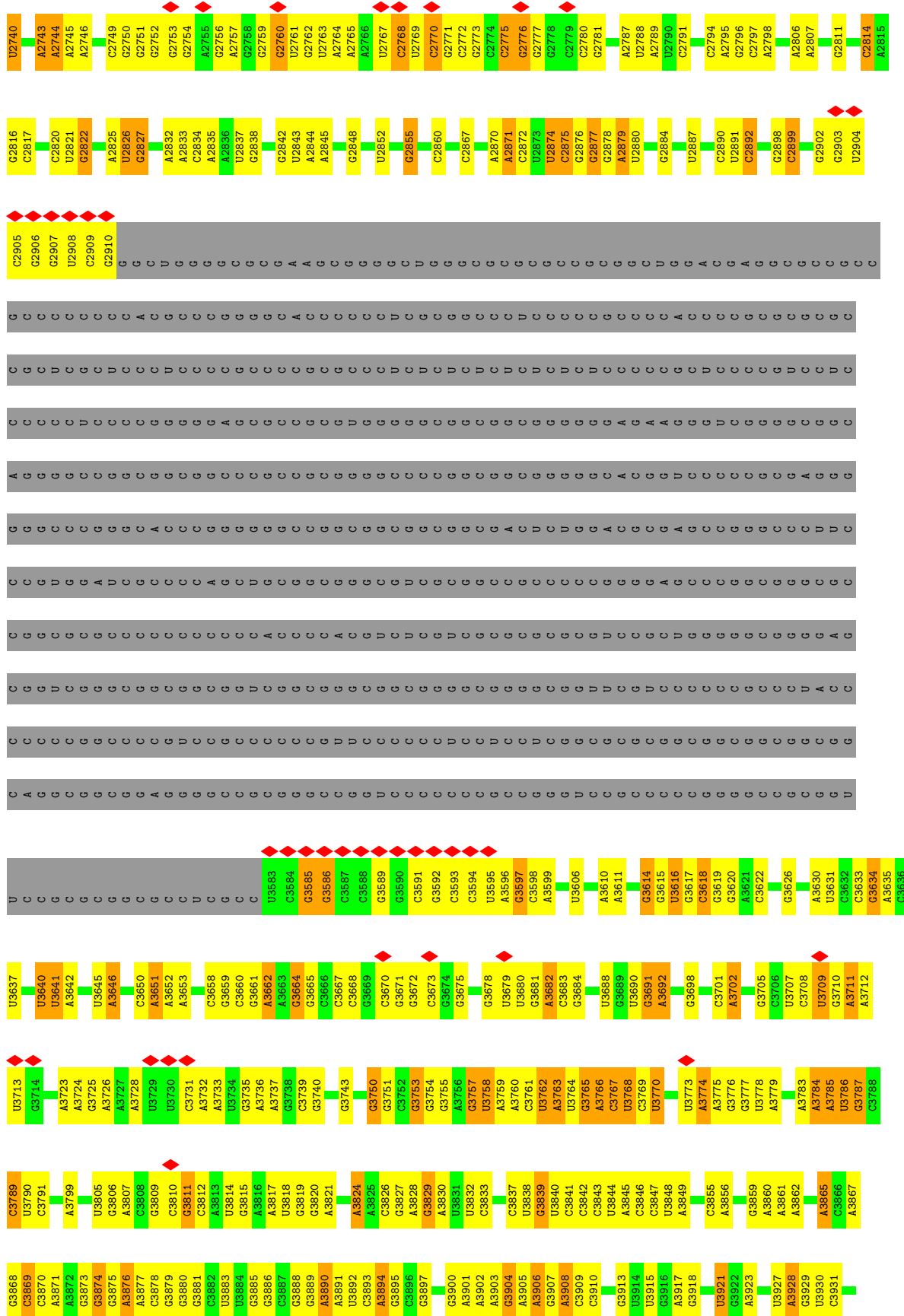
3 Residue-property plots

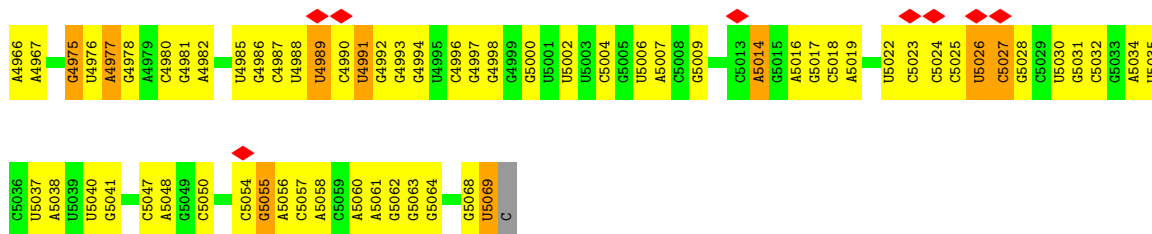
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 28S ribosomal RNA

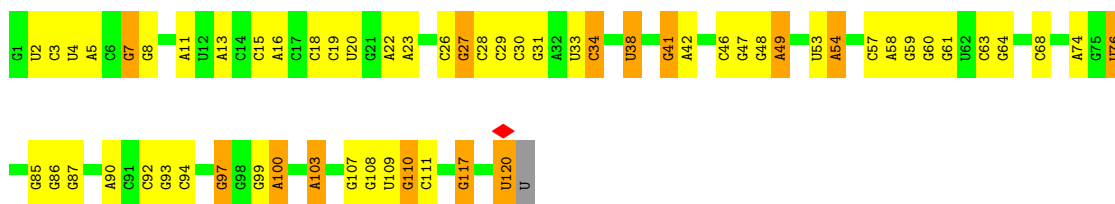




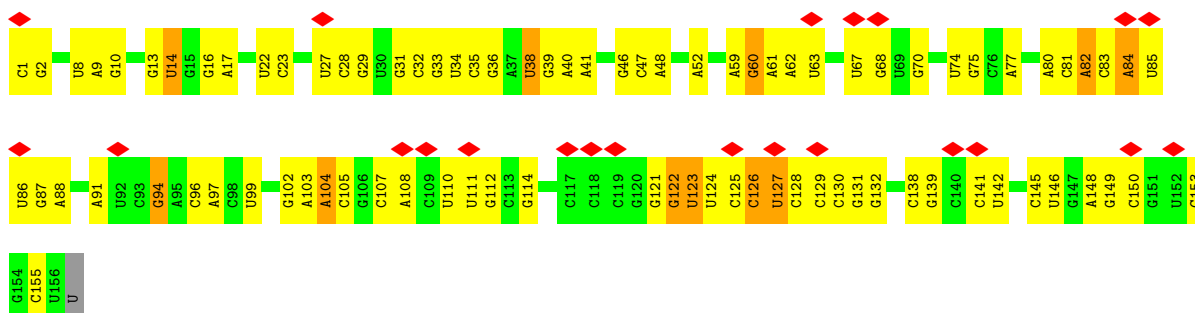




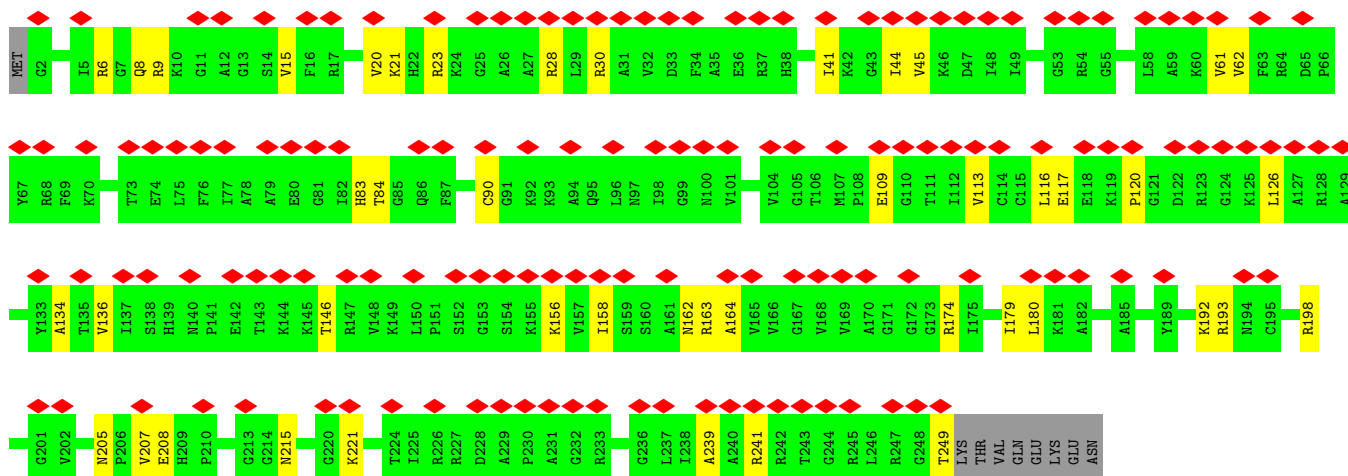
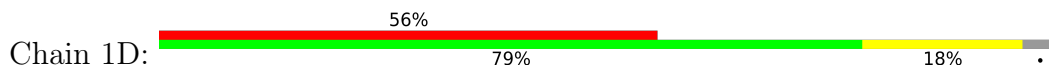
• Molecule 2: 5S ribosomal RNA



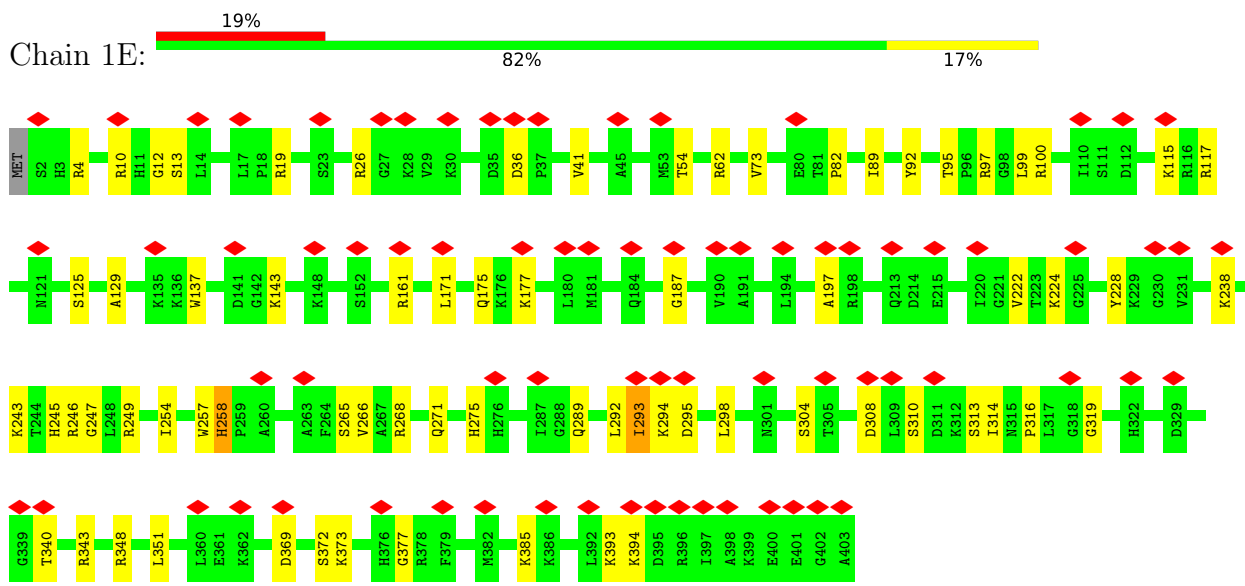
• Molecule 3: 5.8S ribosomal RNA



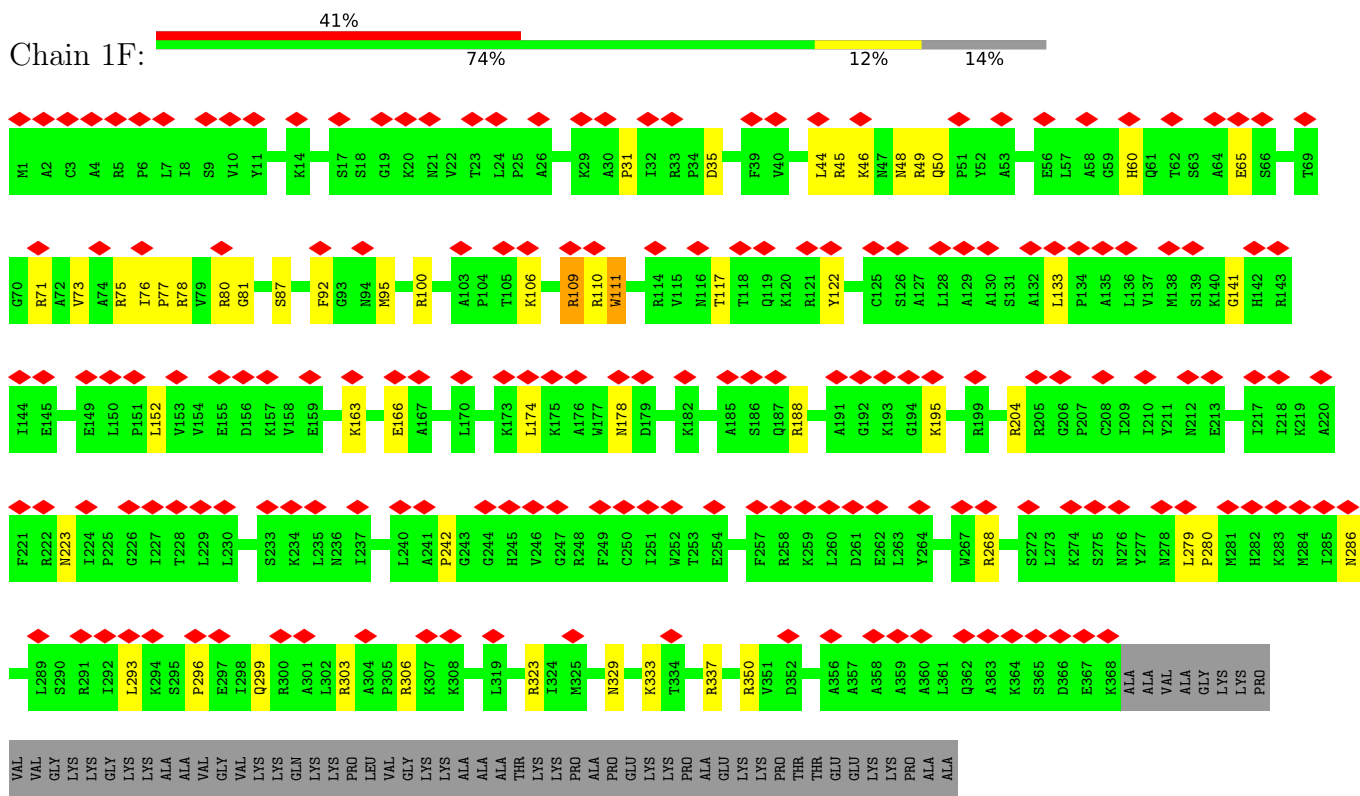
• Molecule 4: 60S ribosomal protein L8



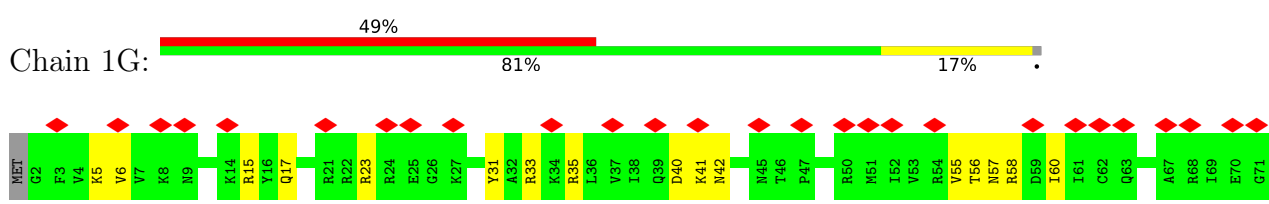
• Molecule 5: 60S ribosomal protein L3

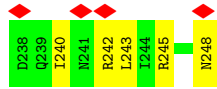


• Molecule 6: 60S ribosomal protein L4

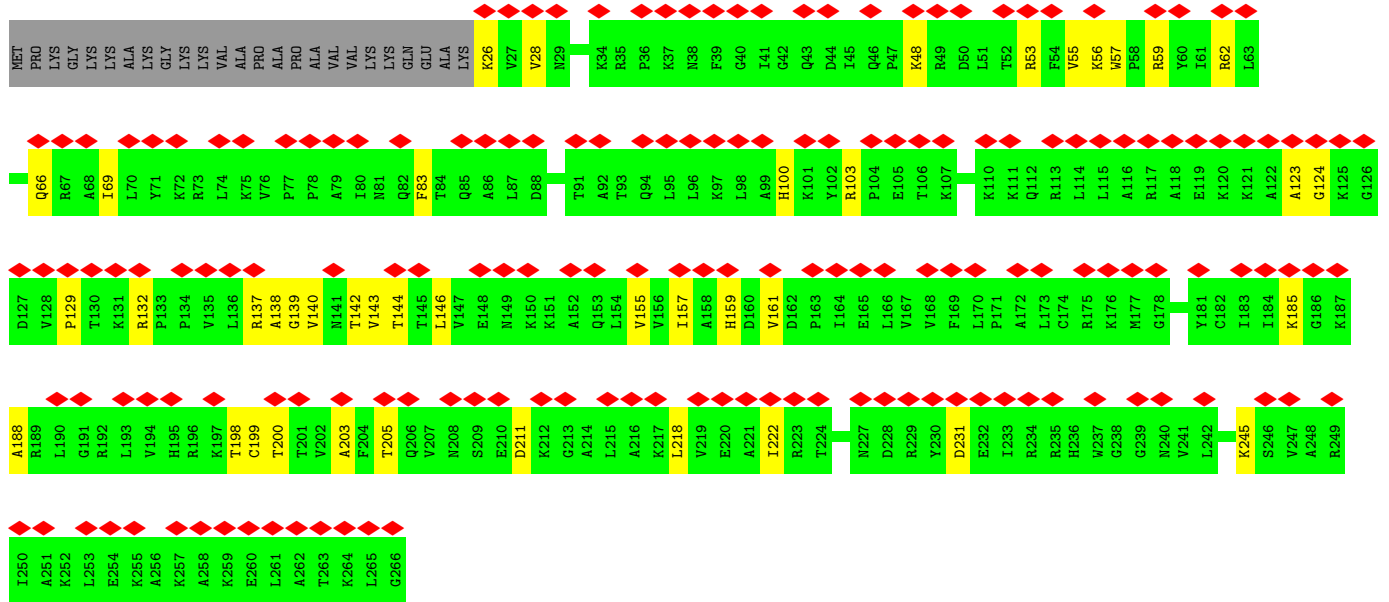
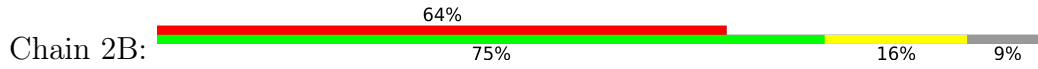


• Molecule 7: 60S ribosomal protein L5

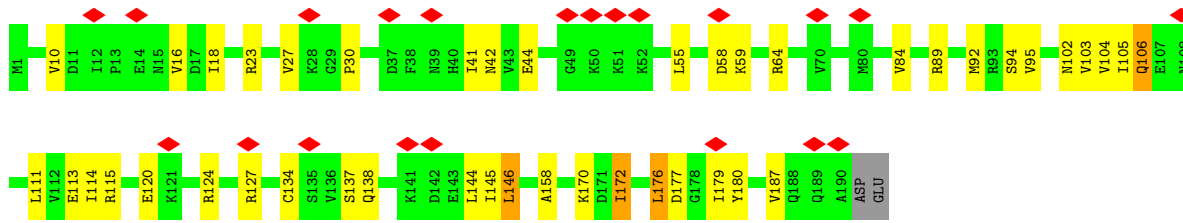
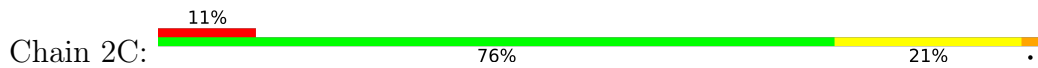




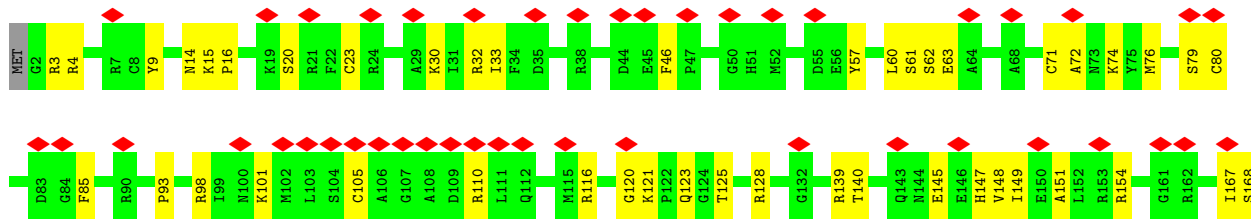
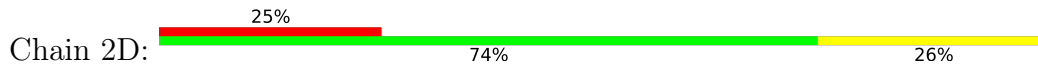
• Molecule 10: 60S ribosomal protein L7a



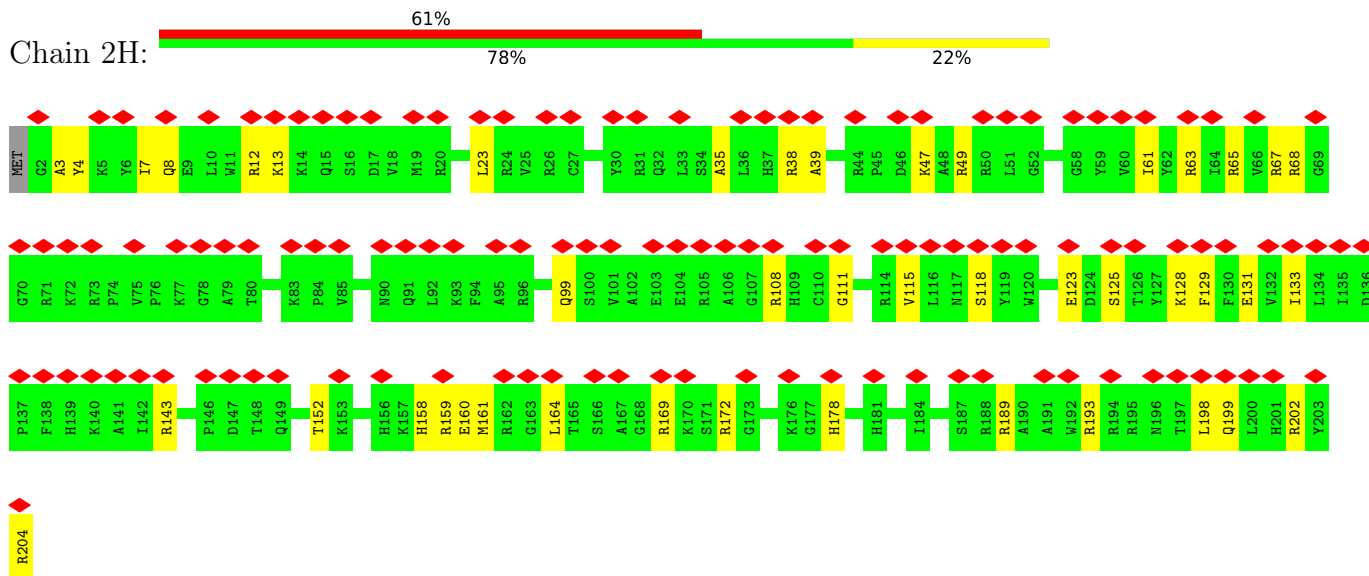
• Molecule 11: 60S ribosomal protein L9



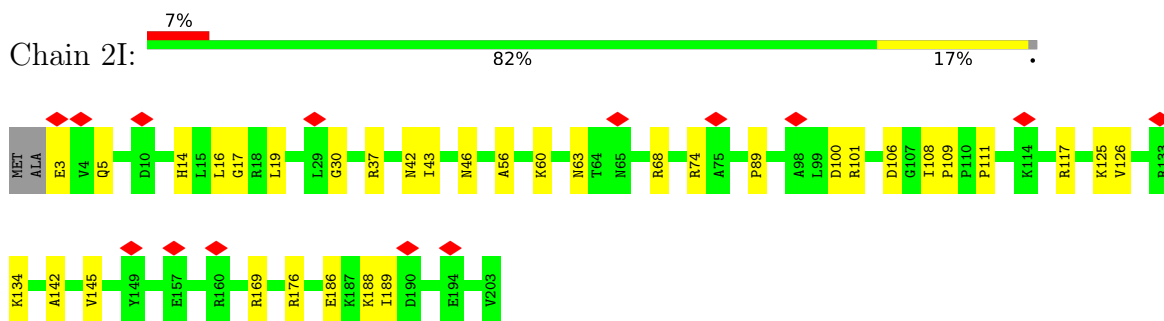
• Molecule 12: 60S ribosomal protein L10-like



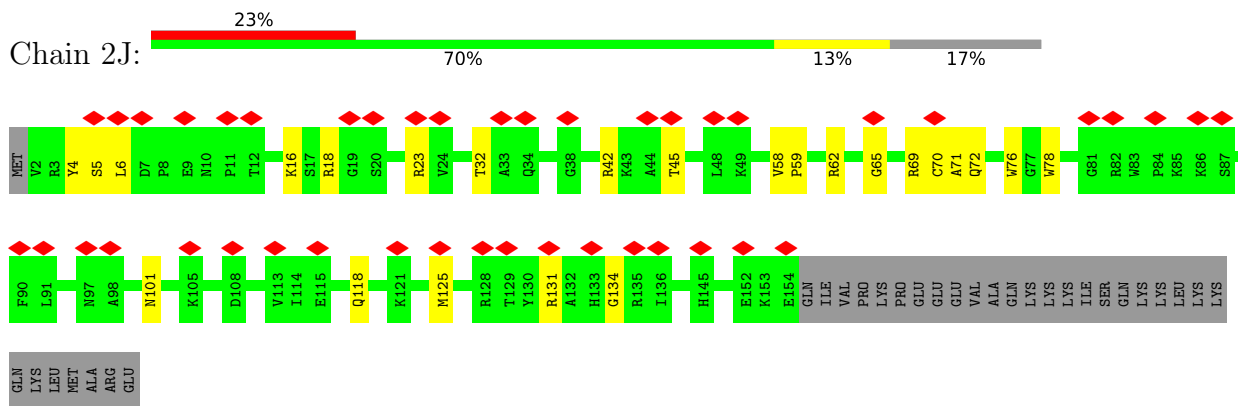
• Molecule 16: 60S ribosomal protein L15



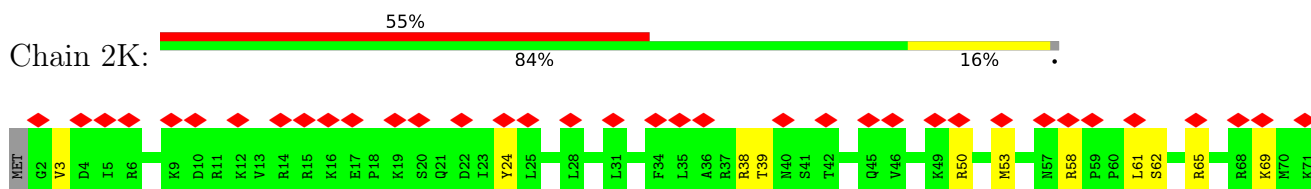
• Molecule 17: 60S ribosomal protein L13a

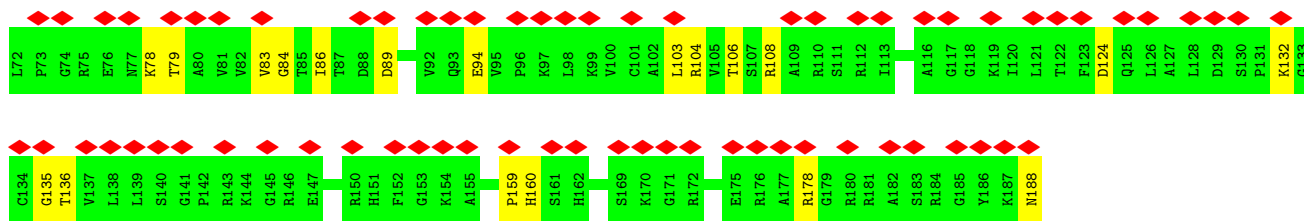


• Molecule 18: 60S ribosomal protein L17

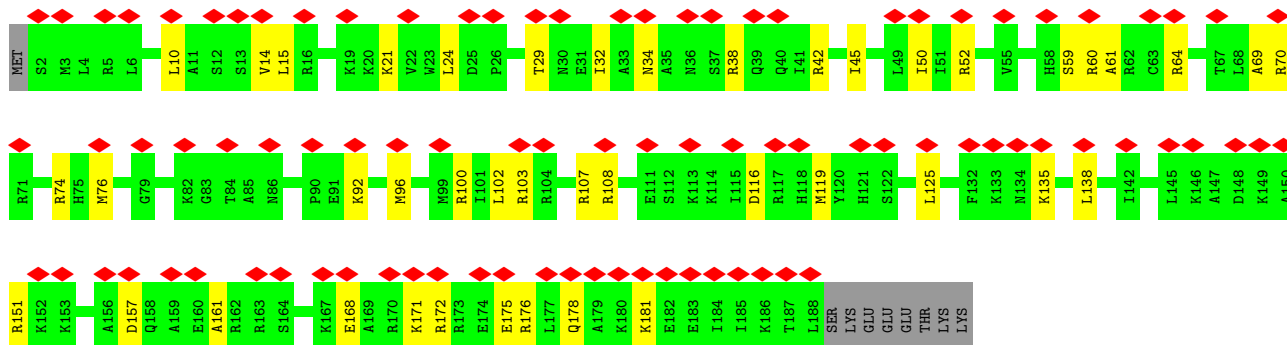
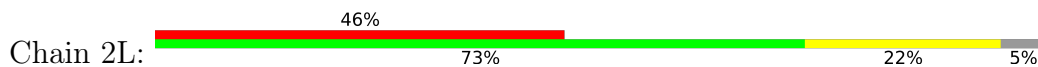


• Molecule 19: 60S ribosomal protein L18

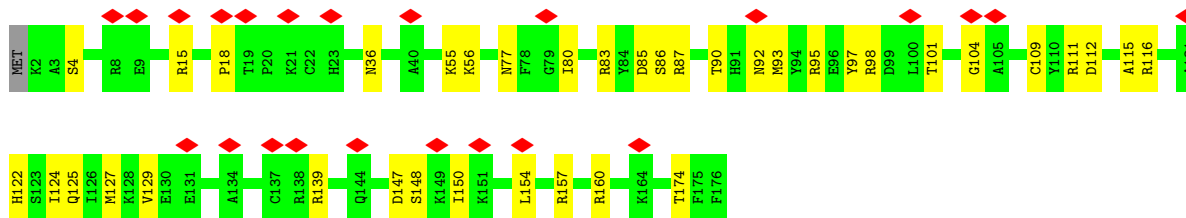
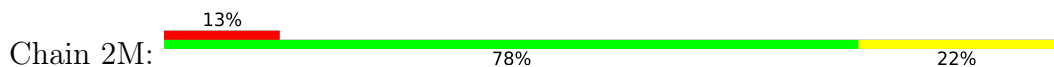




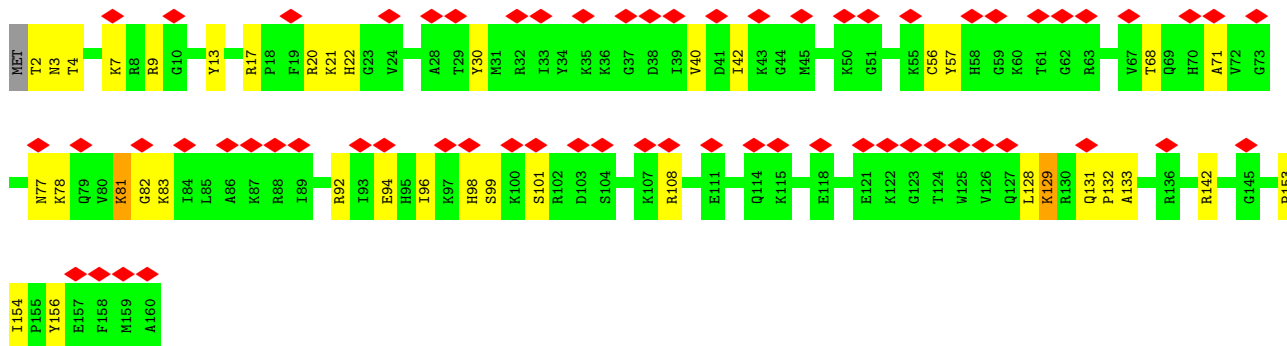
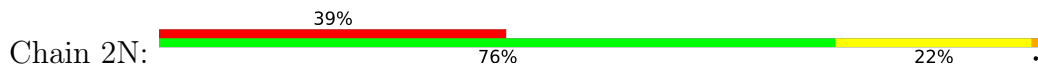
• Molecule 20: 60S ribosomal protein L19



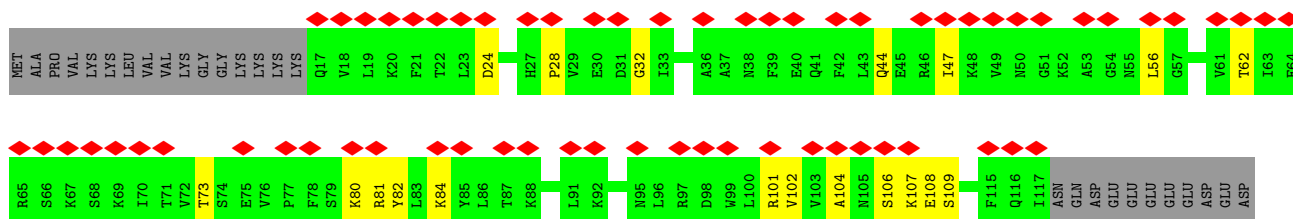
• Molecule 21: 60S ribosomal protein L18a



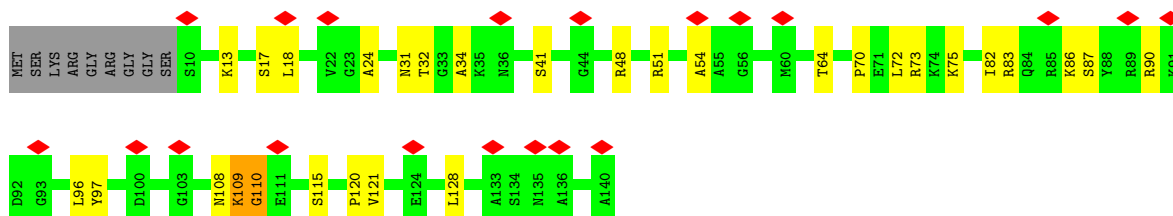
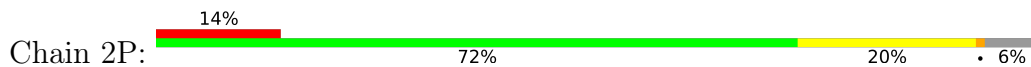
• Molecule 22: 60S ribosomal protein L21



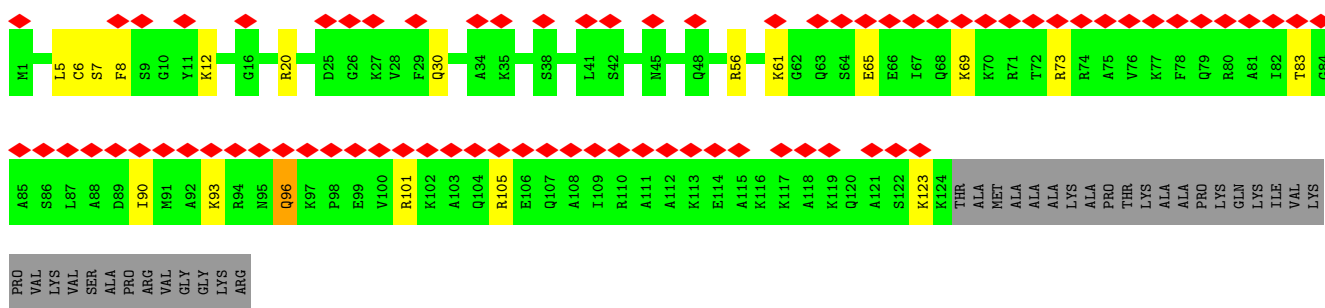
• Molecule 23: 60S ribosomal protein L22



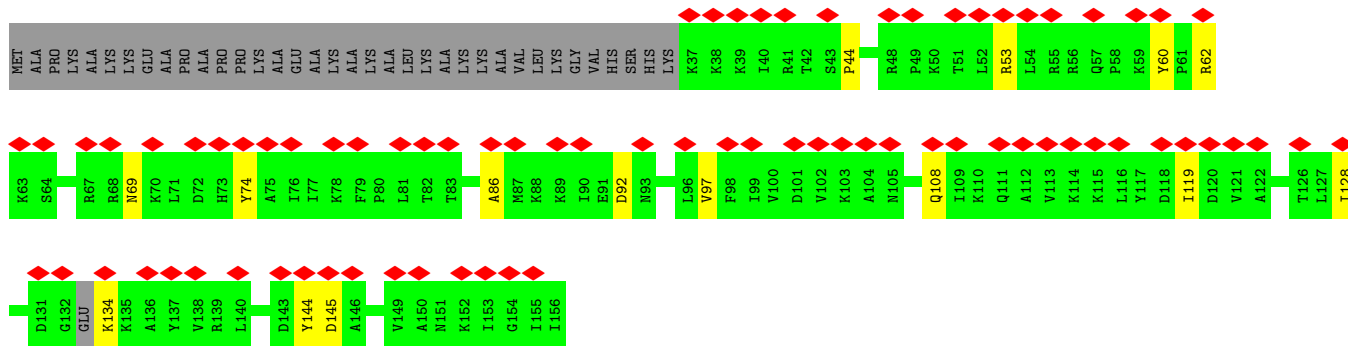
- Molecule 24: 60S ribosomal protein L23



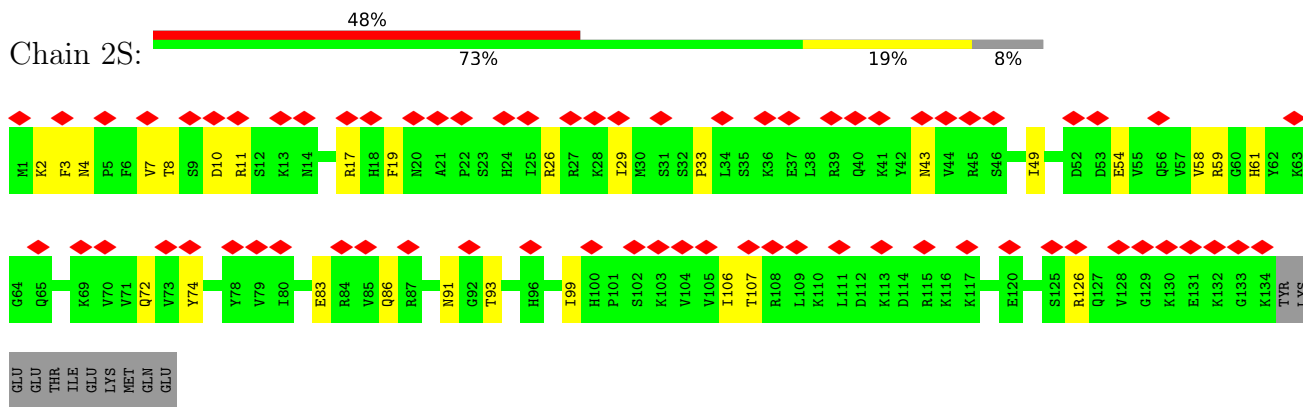
- Molecule 25: 60S ribosomal protein L24



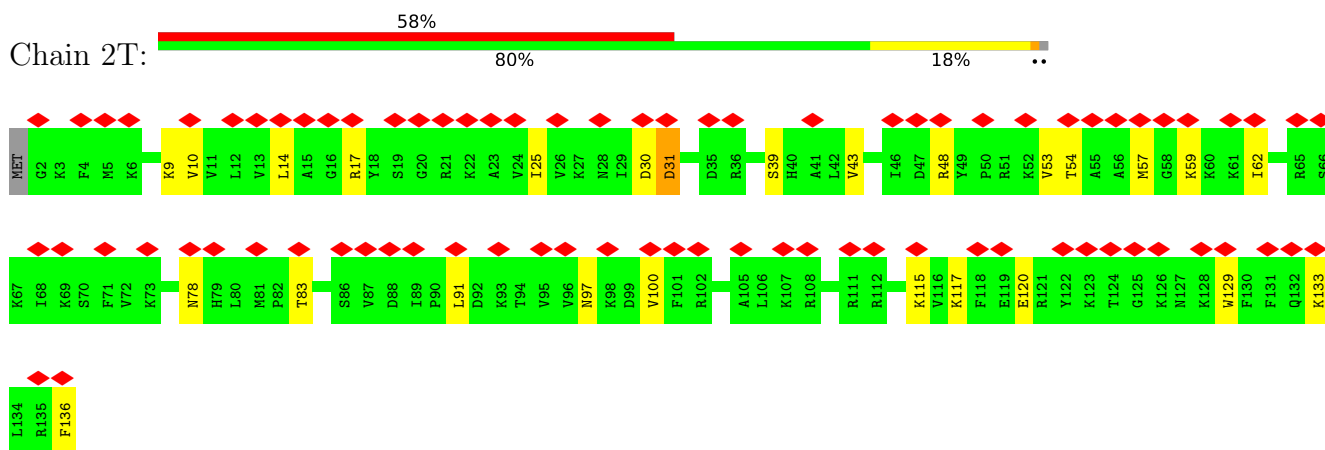
- Molecule 26: 60S ribosomal protein L23a



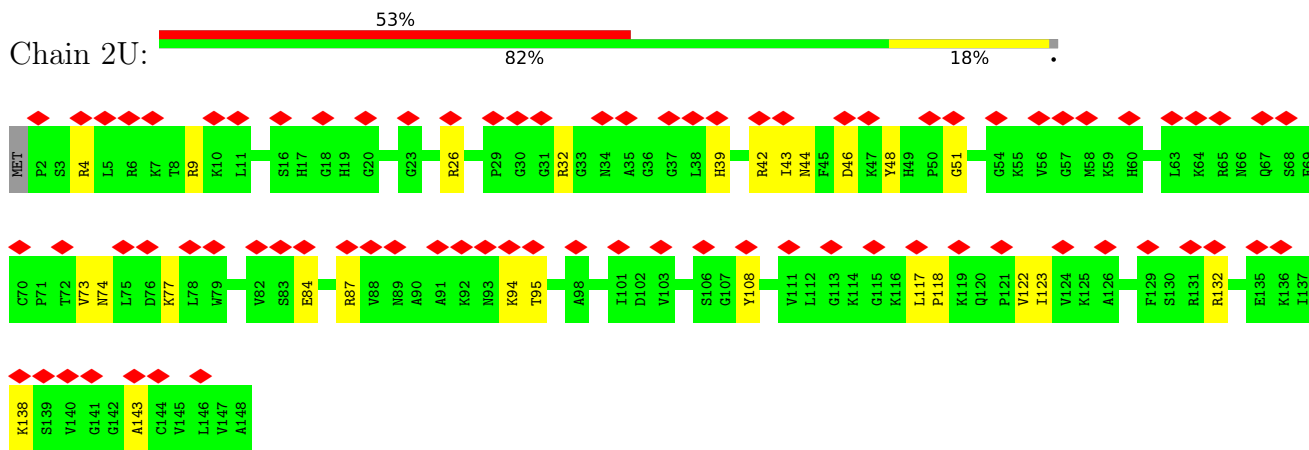
- Molecule 27: 60S ribosomal protein L26



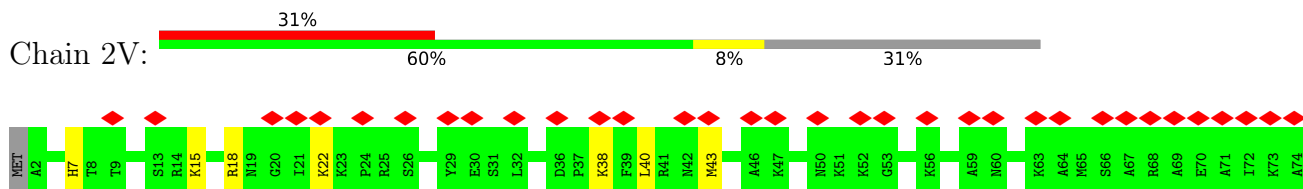
• Molecule 28: 60S ribosomal protein L27

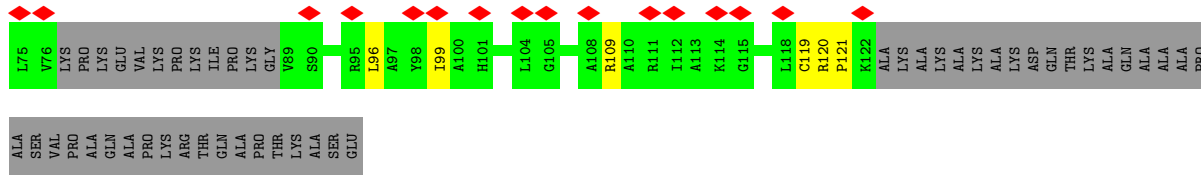


• Molecule 29: 60S ribosomal protein L27a

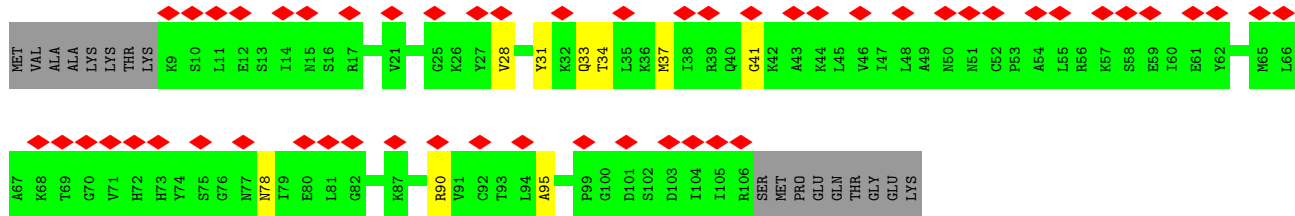
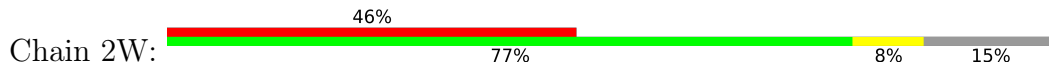


• Molecule 30: 60S ribosomal protein L29

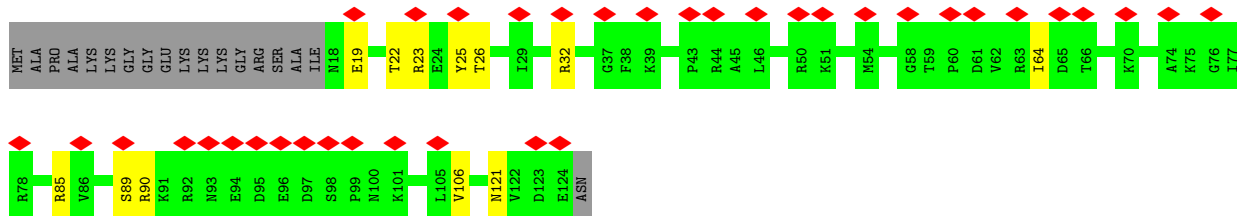
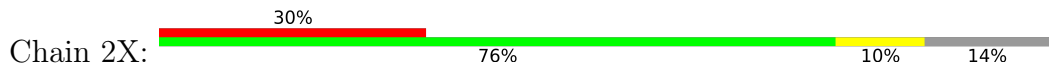




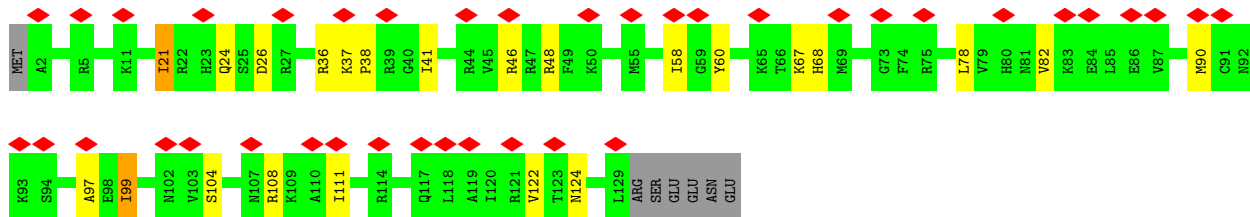
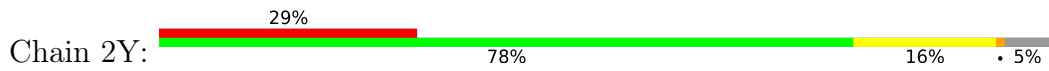
• Molecule 31: 60S ribosomal protein L30



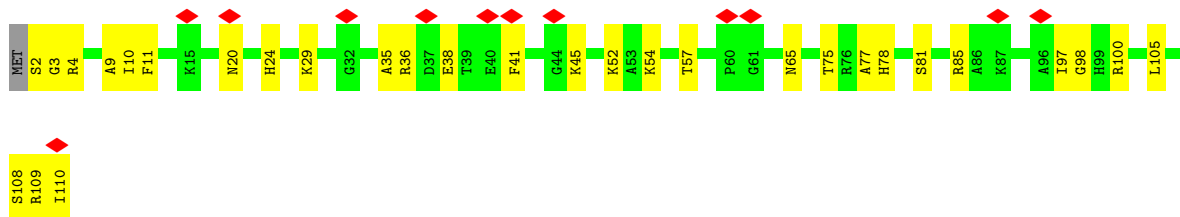
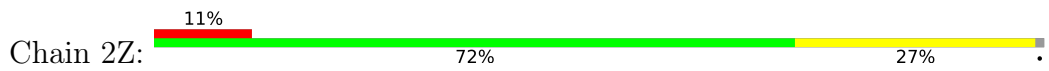
• Molecule 32: 60S ribosomal protein L31

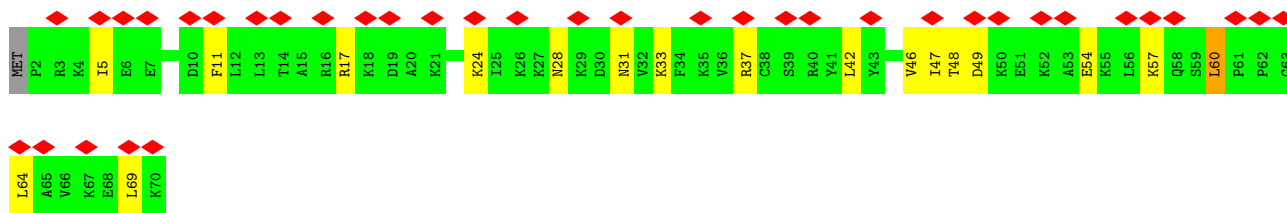


• Molecule 33: 60S ribosomal protein L32

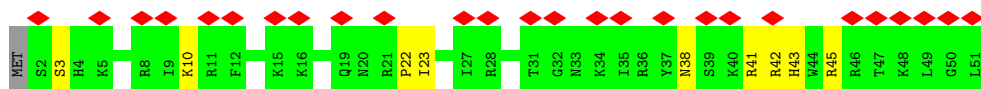
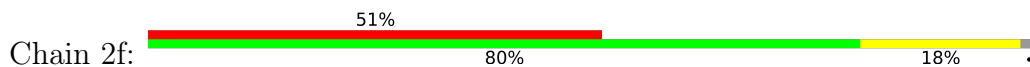


• Molecule 34: 60S ribosomal protein L35a

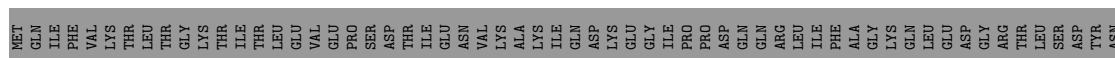




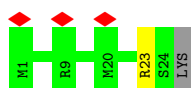
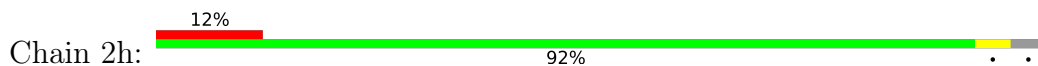
• Molecule 40: 60S ribosomal protein L39



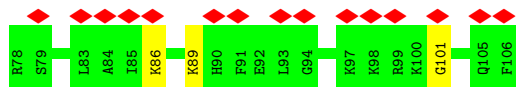
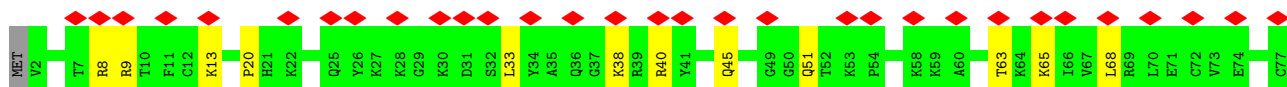
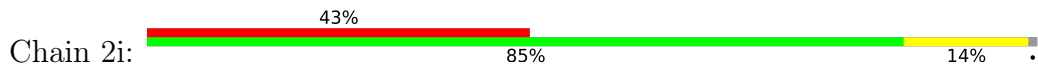
• Molecule 41: Ubiquitin-60S ribosomal protein L40



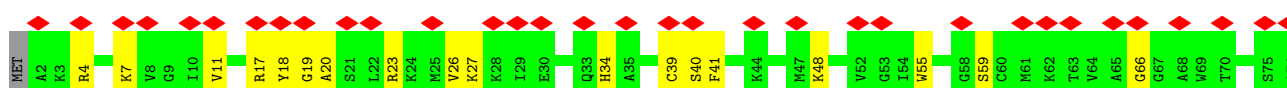
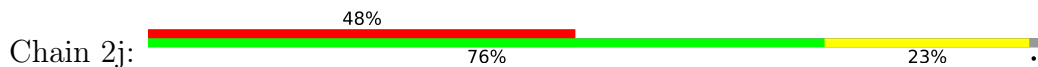
• Molecule 42: 60S ribosomal protein L41

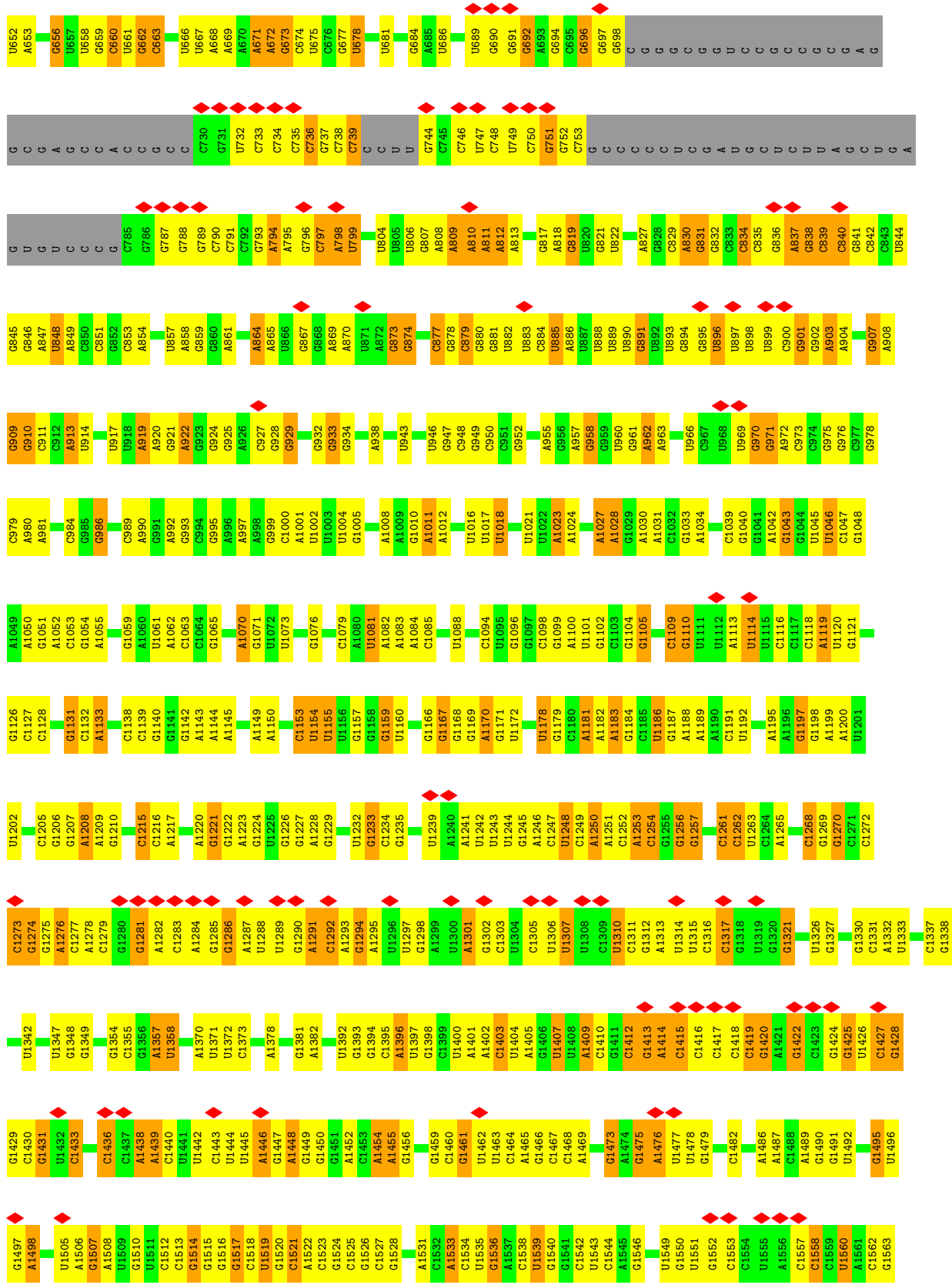


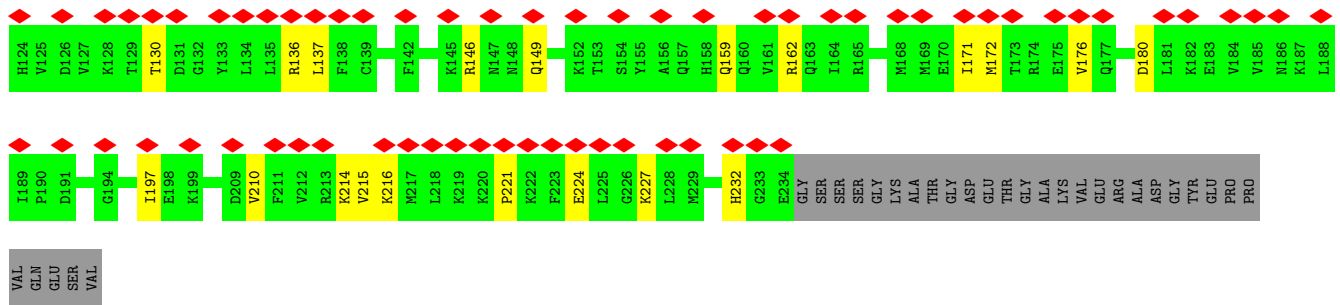
• Molecule 43: 60S ribosomal protein L36a



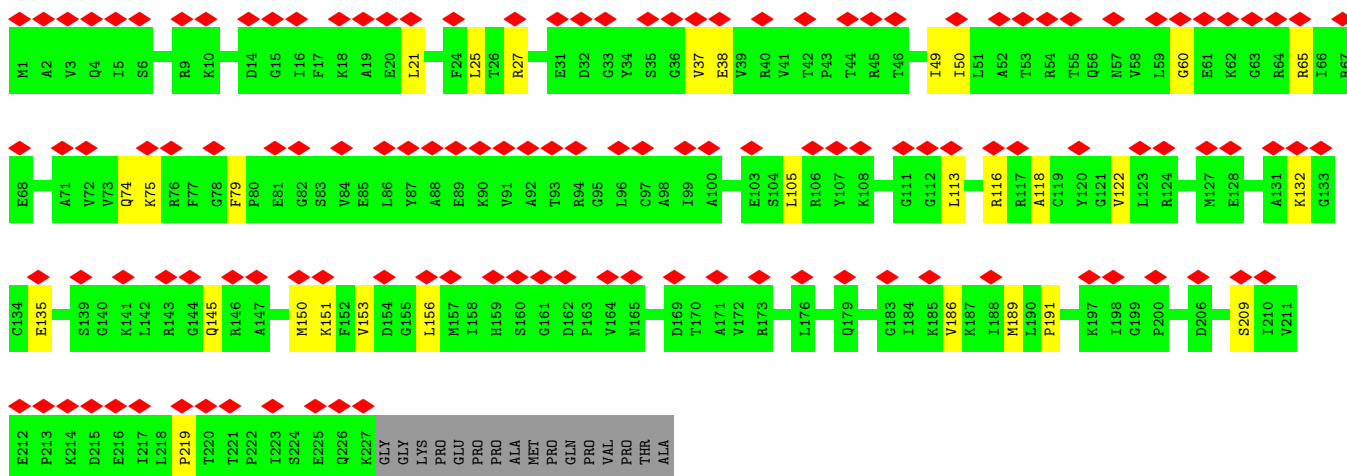
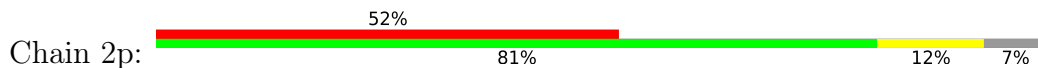
• Molecule 44: 60S ribosomal protein L37a



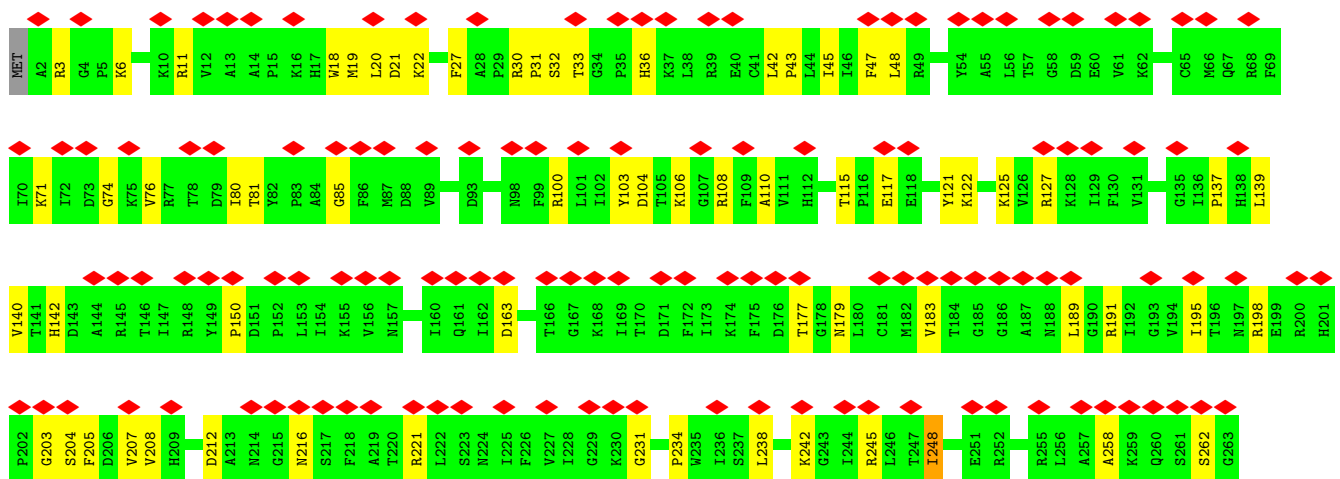
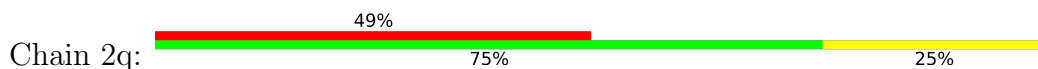




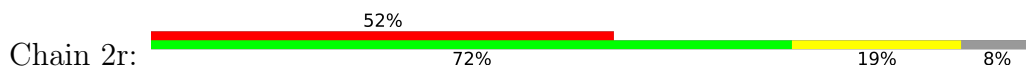
• Molecule 49: 40S ribosomal protein S3

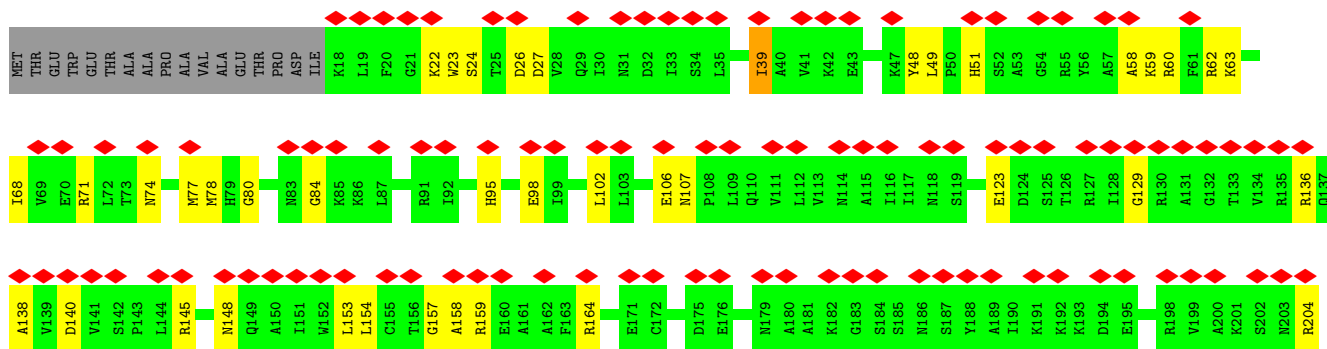


• Molecule 50: 40S ribosomal protein S4, X isoform

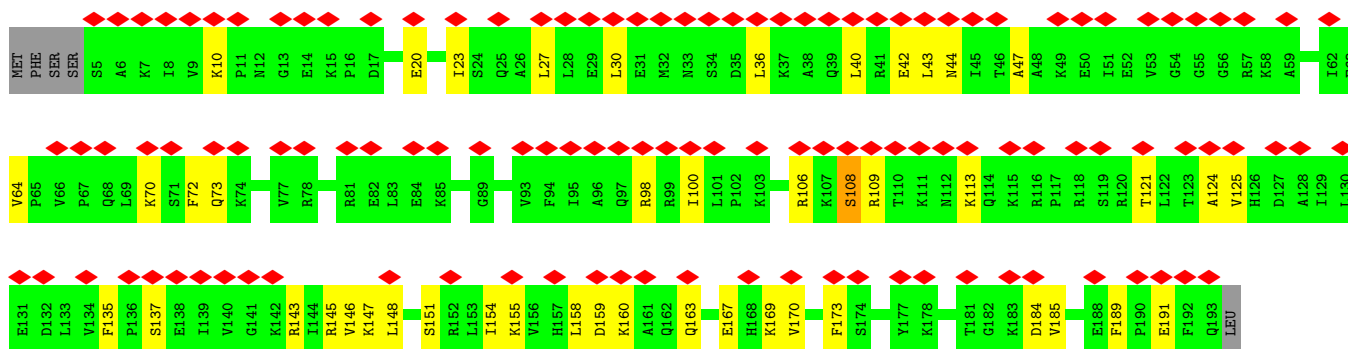
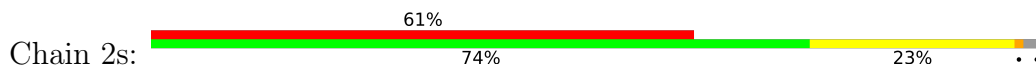


• Molecule 51: 40S ribosomal protein S5

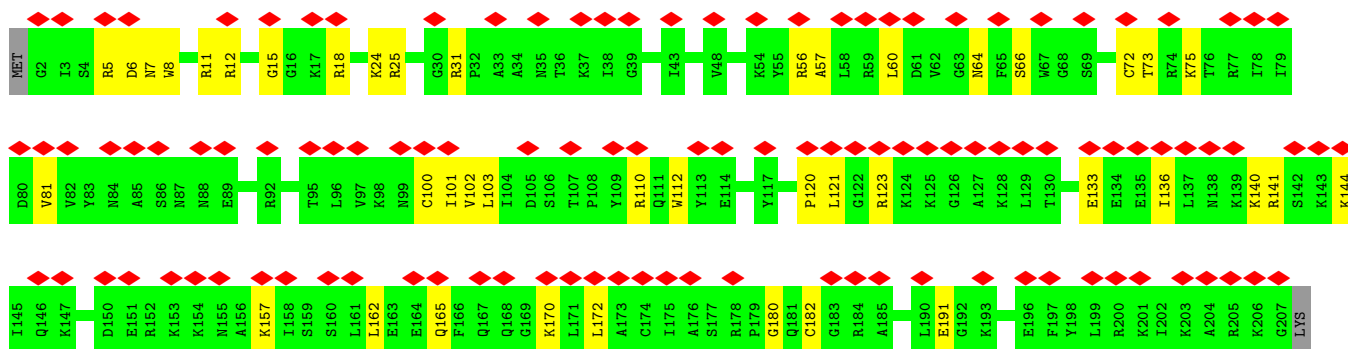
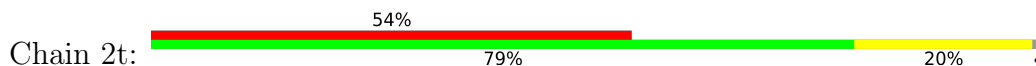




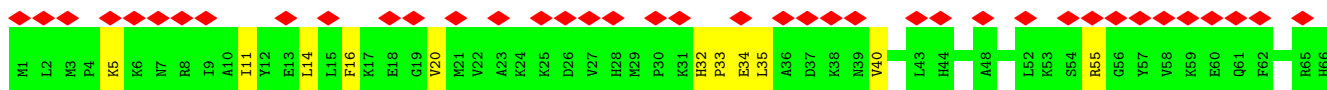
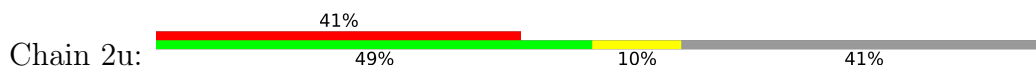
- Molecule 52: 40S ribosomal protein S7

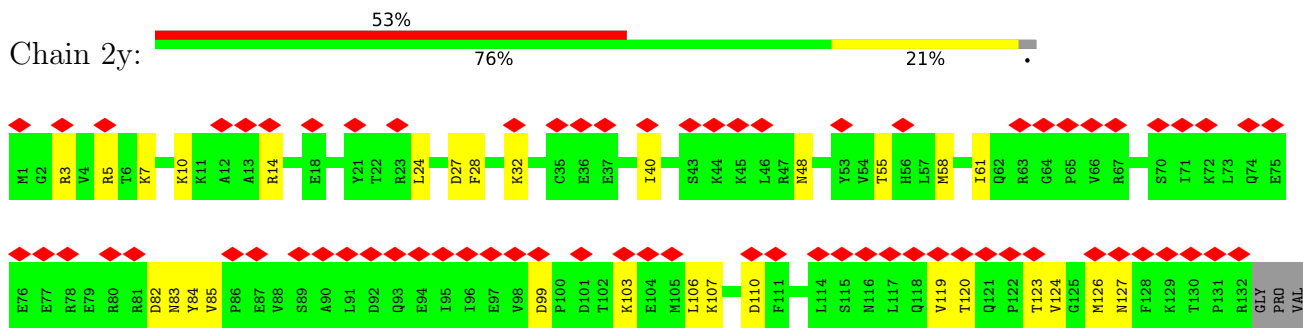


- Molecule 53: 40S ribosomal protein S8

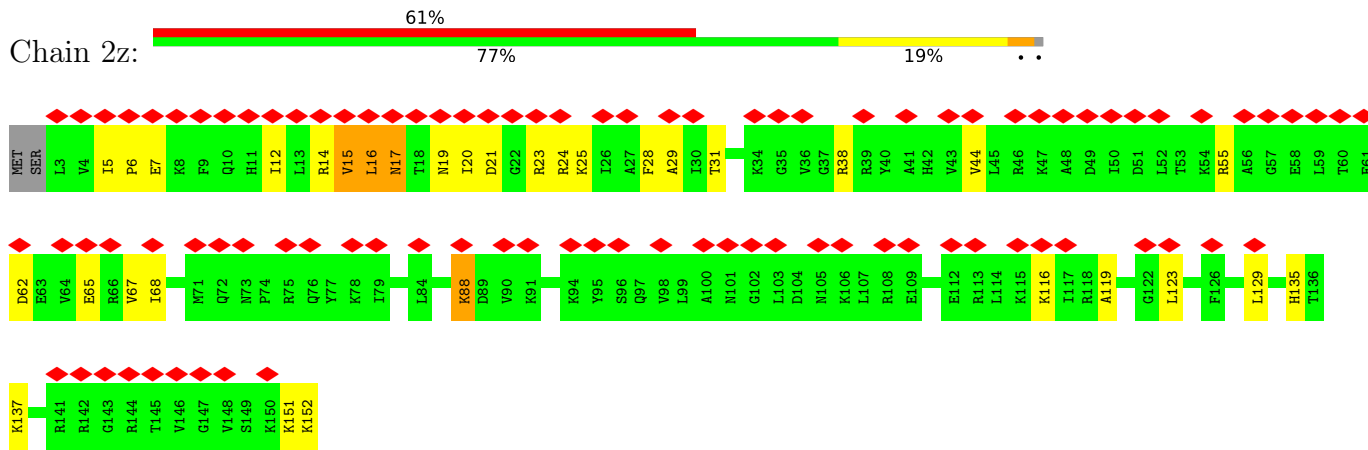


- Molecule 54: 40S ribosomal protein S10

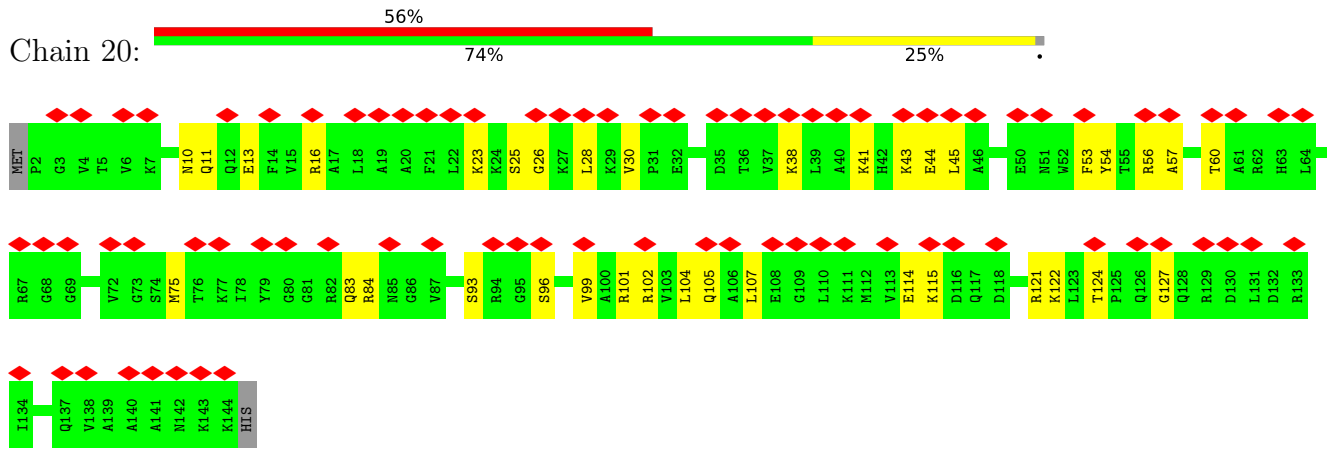




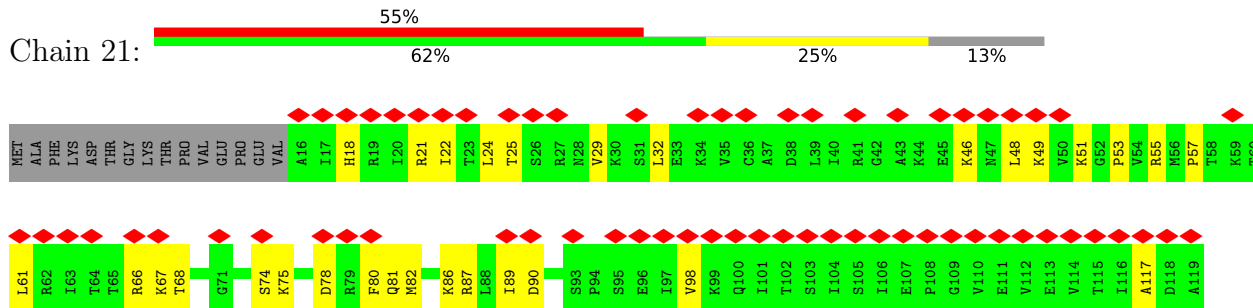
• Molecule 59: 40S ribosomal protein S18



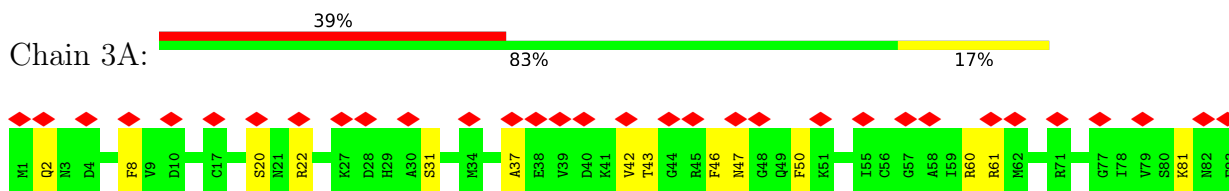
• Molecule 60: 40S ribosomal protein S19



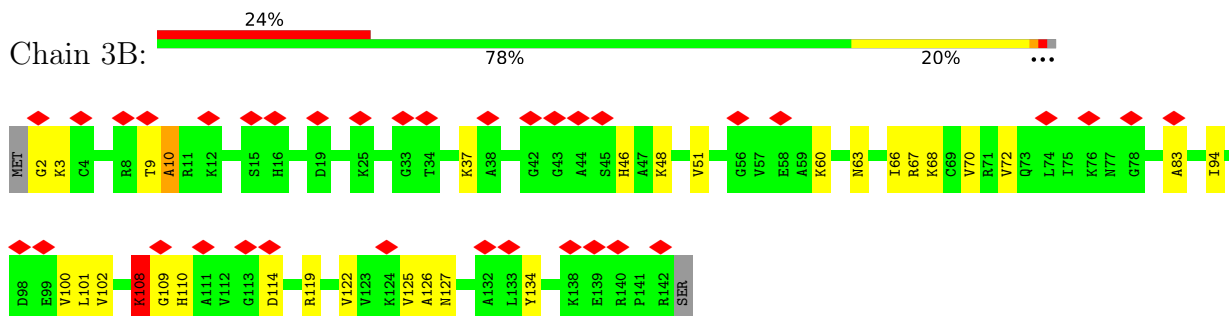
• Molecule 61: 40S ribosomal protein S20



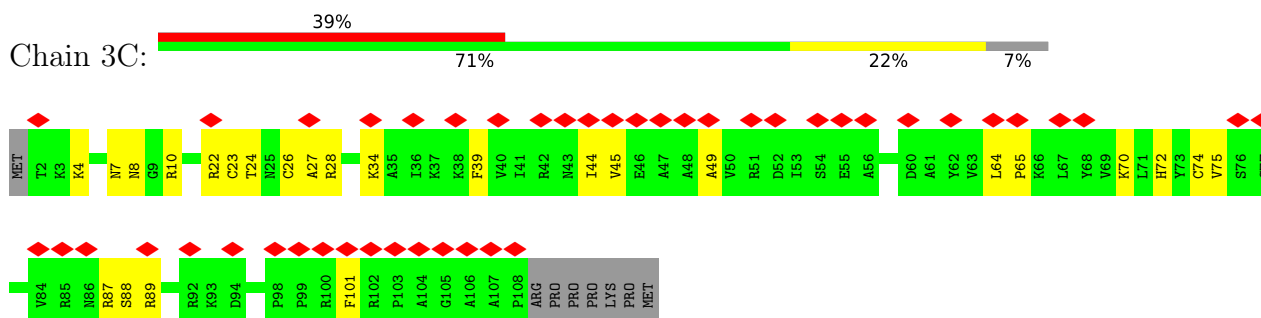
- Molecule 62: 40S ribosomal protein S21



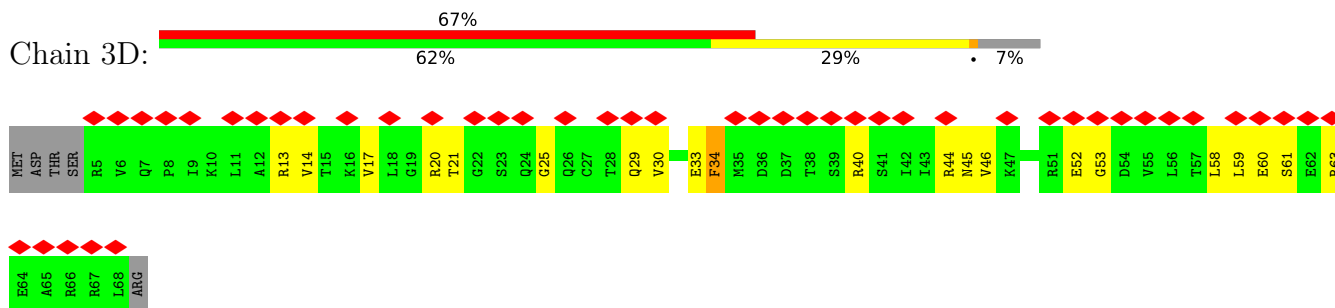
- Molecule 63: 40S ribosomal protein S23



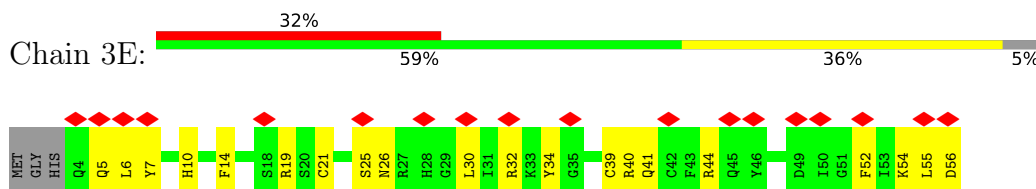
- Molecule 64: 40S ribosomal protein S26



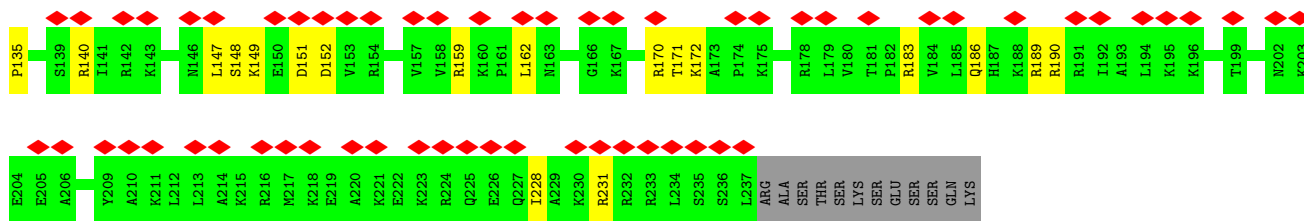
- Molecule 65: 40S ribosomal protein S28



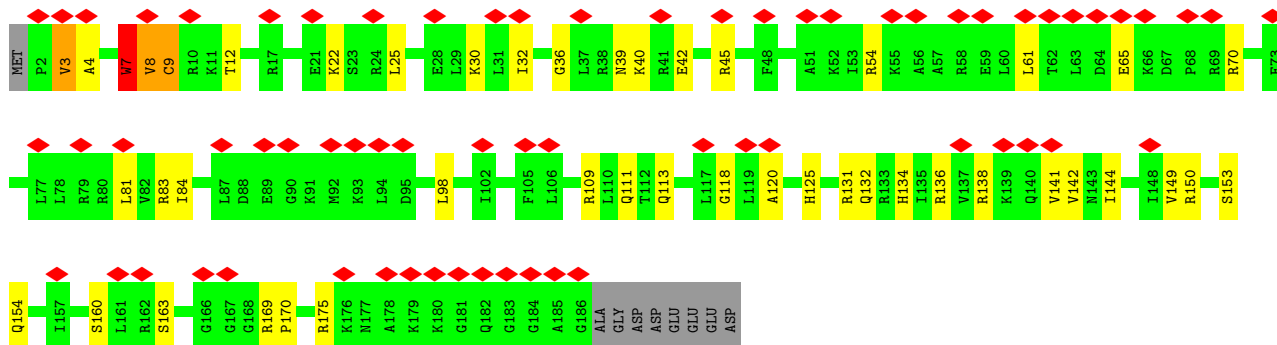
- Molecule 66: 40S ribosomal protein S29



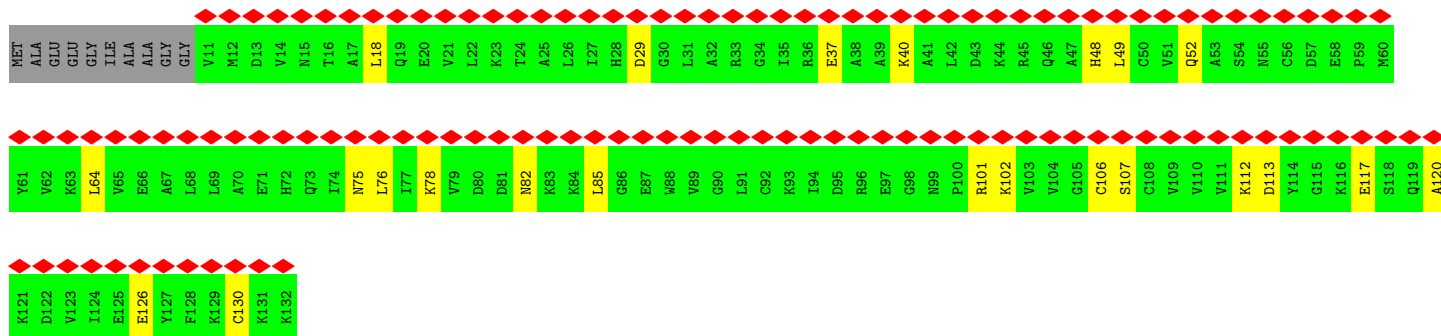
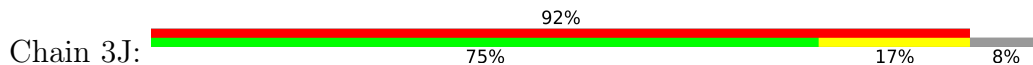
- Molecule 67: Receptor of activated protein C kinase 1



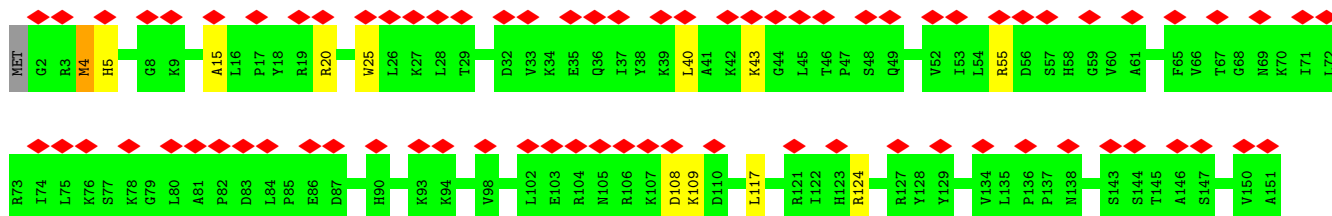
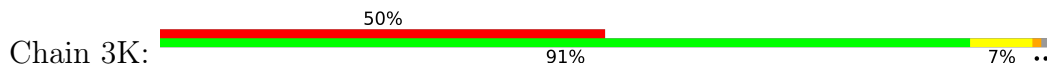
• Molecule 70: 40S ribosomal protein S9



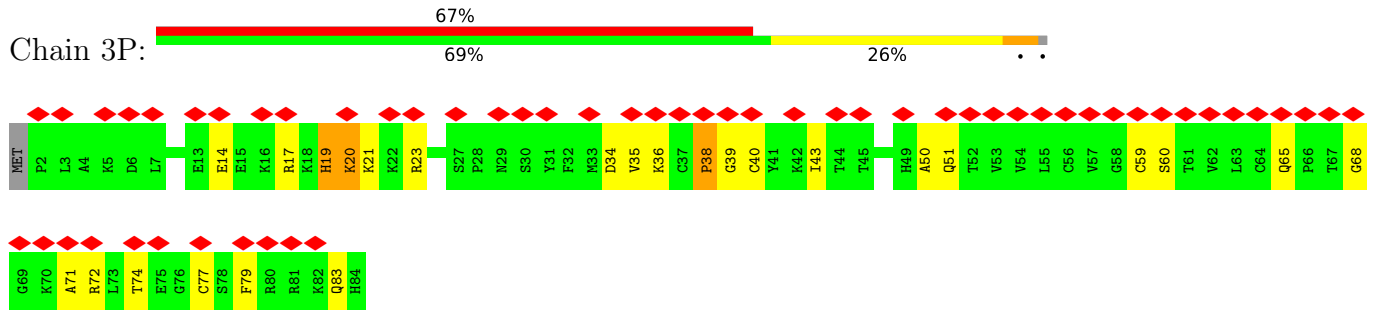
• Molecule 71: 40S ribosomal protein S12



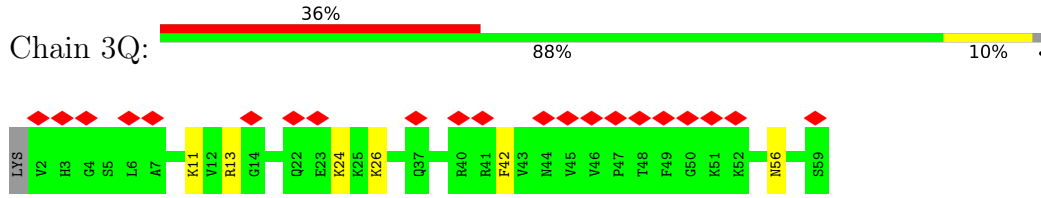
• Molecule 72: 40S ribosomal protein S13



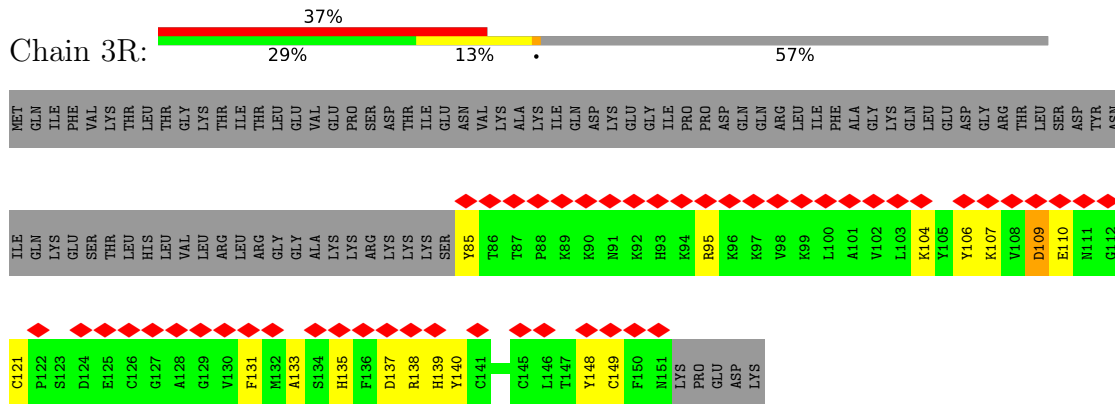
• Molecule 73: 40S ribosomal protein S14



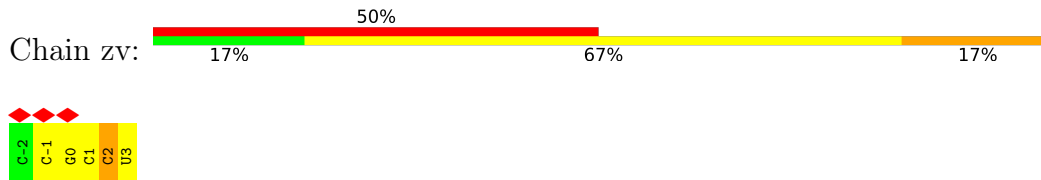
• Molecule 78: 40S ribosomal protein S30



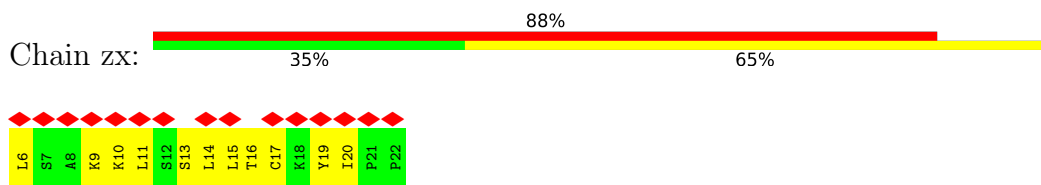
• Molecule 79: Ubiquitin-40S ribosomal protein S27a



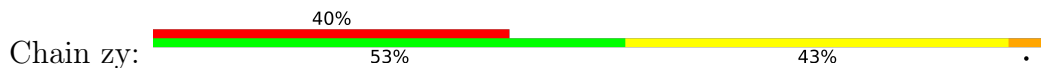
• Molecule 80: mRNA

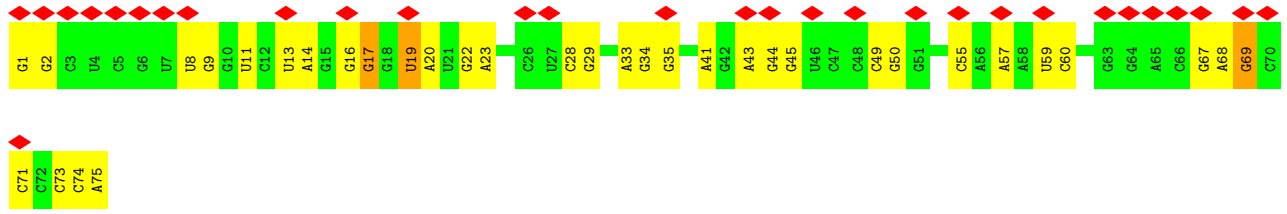


• Molecule 81: nascent peptide

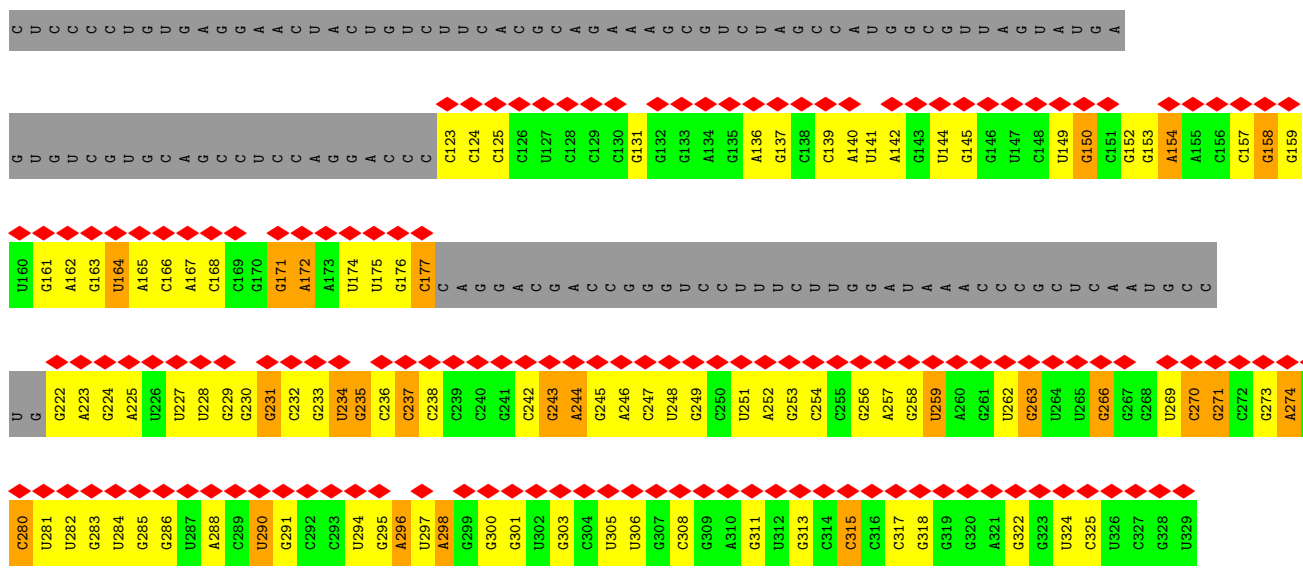


• Molecule 82: P-site tRNA





● Molecule 83: HCV-IRES RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21303	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	33557	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.219	Depositor
Minimum map value	-0.109	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	625.8, 625.8, 625.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.49, 1.49, 1.49	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1A	0.48	0/87922	0.54	6/137154 (0.0%)
2	1B	0.49	0/2858	0.51	0/4455
3	1C	0.46	0/3701	0.50	0/5766
4	1D	0.45	0/1936	0.72	0/2596
5	1E	0.44	0/3306	0.69	2/4424 (0.0%)
6	1F	0.43	0/2981	0.70	2/4002 (0.0%)
7	1G	0.37	0/2428	0.66	0/3252
8	1H	0.40	0/1951	0.81	0/2618
9	2A	0.49	0/1905	0.75	3/2539 (0.1%)
10	2B	0.36	0/1960	0.67	2/2637 (0.1%)
11	2C	0.39	0/1537	0.69	0/2066
12	2D	0.44	0/1751	0.73	1/2340 (0.0%)
13	2E	0.36	0/1433	0.65	0/1915
14	2F	0.40	0/1732	0.72	0/2315
15	2G	0.40	0/1161	0.63	0/1554
16	2H	0.47	0/1746	0.72	0/2338
17	2I	0.45	0/1682	0.66	0/2250
18	2J	0.51	0/1268	0.75	0/1701
19	2K	0.48	0/1537	0.69	0/2052
20	2L	0.39	0/1582	0.67	0/2091
21	2M	0.50	0/1493	0.67	0/2003
22	2N	0.40	0/1326	0.70	0/1770
23	2O	0.33	0/839	0.63	0/1126
24	2P	0.43	0/993	0.68	1/1332 (0.1%)
25	2Q	0.37	0/1030	0.68	0/1364
26	2R	0.40	0/992	0.62	0/1330
27	2S	0.36	0/1132	0.63	0/1504
28	2T	0.36	0/1130	0.64	0/1507
29	2U	0.47	0/1191	0.67	0/1591
30	2V	0.39	0/889	0.67	0/1175
31	2W	0.39	0/774	0.55	0/1038
32	2X	0.39	0/903	0.63	0/1216
33	2Y	0.46	0/1071	0.67	0/1429
34	2Z	0.47	0/895	0.72	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	2a	0.40	0/904	0.67	0/1203
36	2b	0.36	0/1023	0.64	0/1351
37	2c	0.34	0/843	0.67	0/1115
38	2d	0.48	0/720	0.76	0/952
39	2e	0.37	0/575	0.68	0/761
40	2f	0.47	0/454	0.71	0/599
41	2g	0.42	0/435	0.70	0/575
42	2h	0.41	0/231	0.72	0/294
43	2i	0.42	0/876	0.66	2/1156 (0.2%)
44	2j	0.48	0/718	0.70	0/953
45	2k	0.44	0/1017	0.71	0/1364
46	2m	0.39	0/41243	0.52	2/64257 (0.0%)
47	2n	0.34	0/1778	0.65	0/2416
48	2o	0.29	0/1765	0.60	3/2362 (0.1%)
49	2p	0.32	0/1793	0.65	0/2414
50	2q	0.32	0/2118	0.66	0/2849
51	2r	0.29	0/1500	0.68	0/2015
52	2s	0.32	0/1544	0.66	0/2068
53	2t	0.35	0/1715	0.64	0/2287
54	2u	0.31	0/851	0.69	0/1147
55	2v	0.37	0/1268	0.64	0/1696
56	2w	0.33	0/815	0.78	2/1087 (0.2%)
57	2x	0.33	0/1177	0.68	0/1575
58	2y	0.30	0/1086	0.67	0/1457
59	2z	0.37	0/1253	0.80	0/1676
60	20	0.28	0/1131	0.59	0/1515
61	21	0.34	0/831	0.71	0/1115
62	3A	0.32	0/643	0.66	0/860
63	3B	0.37	0/1116	0.73	0/1490
64	3C	0.37	0/863	0.76	2/1159 (0.2%)
65	3D	0.31	0/508	0.83	0/680
66	3E	0.37	0/455	0.67	0/603
67	3F	0.31	0/2493	0.70	0/3394
68	3G	0.35	0/1762	0.66	0/2381
69	3H	0.31	0/1946	0.71	0/2590
70	3I	0.35	0/1550	0.77	5/2069 (0.2%)
71	3J	0.27	0/962	0.69	0/1290
72	3K	0.38	0/1232	0.70	0/1656
73	3L	0.33	0/1062	0.70	2/1425 (0.1%)
74	3M	0.40	0/1051	0.71	0/1406
75	3N	0.33	0/1083	0.58	0/1438
76	3O	0.30	0/604	0.75	2/810 (0.2%)
77	3P	0.34	0/665	0.71	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	3Q	0.31	0/465	0.64	0/612
79	3R	0.26	0/560	0.68	0/745
80	zv	0.28	0/135	0.49	0/207
81	zx	0.31	0/131	0.71	0/176
82	zy	0.28	0/1786	0.44	0/2784
83	zz	0.25	0/3902	0.51	0/6084
All	All	0.42	0/235673	0.59	37/346657 (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
4	1D	0	1
5	1E	0	2
7	1G	0	1
8	1H	0	4
11	2C	0	1
12	2D	0	1
14	2F	0	3
15	2G	0	2
16	2H	0	1
18	2J	0	2
19	2K	0	1
22	2N	0	2
24	2P	0	2
25	2Q	0	1
28	2T	0	1
38	2d	0	1
48	2o	0	1
51	2r	0	1
52	2s	0	2
57	2x	0	4
59	2z	0	3
62	3A	0	1
63	3B	0	3
67	3F	0	1
68	3G	0	1
69	3H	0	1
70	3I	0	5
71	3J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
76	3O	0	1
77	3P	0	2
79	3R	0	1
81	zx	0	1
All	All	0	55

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	3C	101	PHE	CA-C-N	7.56	128.22	119.83
64	3C	101	PHE	C-N-CA	7.56	128.22	119.83
48	2o	176	VAL	N-CA-C	-6.28	107.37	113.53
43	2i	101	GLY	CA-C-N	5.73	132.02	121.70
43	2i	101	GLY	C-N-CA	5.73	132.02	121.70

There are no chirality outliers.

5 of 55 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	1D	239	ALA	Peptide
5	1E	258	HIS	Peptide
5	1E	293	ILE	Peptide
7	1G	124	GLU	Peptide
8	1H	109	LEU	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	1A	78599	0	39720	1091	0
2	1B	2558	0	1296	48	0
3	1C	3314	0	1683	48	0
4	1D	1898	0	1993	35	0
5	1E	3238	0	3376	52	0
6	1F	2927	0	3104	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	1G	2382	0	2410	40	0
8	1H	1913	0	2067	49	0
9	2A	1870	0	1996	53	0
10	2B	1927	0	2074	30	0
11	2C	1518	0	1601	25	0
12	2D	1711	0	1749	36	0
13	2E	1410	0	1441	32	0
14	2F	1701	0	1818	24	0
15	2G	1138	0	1204	15	0
16	2H	1701	0	1749	38	0
17	2I	1650	0	1794	29	0
18	2J	1242	0	1269	16	0
19	2K	1513	0	1628	21	0
20	2L	1566	0	1729	35	0
21	2M	1453	0	1490	28	0
22	2N	1298	0	1366	28	0
23	2O	825	0	850	13	0
24	2P	979	0	1039	17	0
25	2Q	1015	0	1079	12	0
26	2R	976	0	1059	11	0
27	2S	1115	0	1205	20	0
28	2T	1107	0	1182	19	0
29	2U	1162	0	1213	21	0
30	2V	876	0	948	11	0
31	2W	764	0	804	7	0
32	2X	888	0	930	8	0
33	2Y	1053	0	1147	21	0
34	2Z	876	0	912	23	0
35	2a	895	0	988	19	0
36	2b	1015	0	1148	13	0
37	2c	832	0	917	12	0
38	2d	705	0	741	31	0
39	2e	569	0	637	13	0
40	2f	444	0	483	6	0
41	2g	429	0	469	10	0
42	2h	230	0	276	1	0
43	2i	862	0	933	10	0
44	2j	708	0	760	16	0
45	2k	1002	0	1068	14	0
46	2m	36900	0	18599	593	0
47	2n	1741	0	1746	29	0
48	2o	1738	0	1809	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	2p	1765	0	1865	19	0
50	2q	2076	0	2177	44	0
51	2r	1479	0	1534	28	0
52	2s	1521	0	1616	29	0
53	2t	1686	0	1772	32	0
54	2u	827	0	854	13	0
55	2v	1247	0	1323	22	0
56	2w	804	0	841	24	0
57	2x	1158	0	1232	30	0
58	2y	1072	0	1130	20	0
59	2z	1235	0	1309	28	0
60	20	1112	0	1146	24	0
61	21	821	0	883	22	0
62	3A	636	0	637	8	0
63	3B	1098	0	1167	18	0
64	3C	847	0	899	20	0
65	3D	506	0	536	16	0
66	3E	445	0	442	19	0
67	3F	2436	0	2393	60	0
68	3G	1725	0	1813	33	0
69	3H	1923	0	2089	54	0
70	3I	1525	0	1640	29	0
71	3J	952	0	983	16	0
72	3K	1208	0	1294	11	0
73	3L	1049	0	1073	37	0
74	3M	1034	0	1080	19	0
75	3N	1065	0	1142	17	0
76	3O	598	0	656	18	0
77	3P	651	0	672	17	0
78	3Q	459	0	503	7	0
79	3R	548	0	555	16	0
80	zv	123	0	66	2	0
81	zx	129	0	148	8	0
82	zy	1599	0	809	19	0
83	zz	3492	0	1761	49	0
All	All	219084	0	161539	2979	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 8.

The worst 5 of 2979 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)
46:2m:902:G:O6	46:2m:904:A:C6	1.71	1.44
2:1B:30:C:C2	2:1B:48:G:N2	2.20	1.10
46:2m:902:G:O6	46:2m:904:A:N6	1.87	1.07
1:1A:120:A:H62	1:1A:151:G:N2	1.56	1.03
46:2m:677:G:N2	46:2m:1028:A:H62	1.57	1.01

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	
4	1D	246/257 (96%)	219 (89%)	27 (11%)	0	100	100
5	1E	400/403 (99%)	355 (89%)	43 (11%)	2 (0%)	24	63
6	1F	366/427 (86%)	324 (88%)	41 (11%)	1 (0%)	36	71
7	1G	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
8	1H	233/288 (81%)	201 (86%)	30 (13%)	2 (1%)	14	49
9	2A	223/248 (90%)	204 (92%)	19 (8%)	0	100	100
10	2B	239/266 (90%)	209 (87%)	30 (13%)	0	100	100
11	2C	188/192 (98%)	166 (88%)	21 (11%)	1 (0%)	24	63
12	2D	211/214 (99%)	184 (87%)	27 (13%)	0	100	100
13	2E	174/178 (98%)	156 (90%)	18 (10%)	0	100	100
14	2F	208/211 (99%)	180 (86%)	27 (13%)	1 (0%)	24	63
15	2G	137/215 (64%)	125 (91%)	12 (9%)	0	100	100
16	2H	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
17	2I	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
18	2J	151/184 (82%)	134 (89%)	17 (11%)	0	100	100
19	2K	185/188 (98%)	172 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	2L	185/196 (94%)	177 (96%)	8 (4%)	0	100	100
21	2M	173/176 (98%)	149 (86%)	24 (14%)	0	100	100
22	2N	157/160 (98%)	138 (88%)	17 (11%)	2 (1%)	9	41
23	2O	99/128 (77%)	90 (91%)	9 (9%)	0	100	100
24	2P	129/140 (92%)	118 (92%)	9 (7%)	2 (2%)	7	37
25	2Q	122/157 (78%)	111 (91%)	11 (9%)	0	100	100
26	2R	115/156 (74%)	103 (90%)	12 (10%)	0	100	100
27	2S	132/145 (91%)	120 (91%)	12 (9%)	0	100	100
28	2T	133/136 (98%)	119 (90%)	13 (10%)	1 (1%)	16	53
29	2U	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
30	2V	105/159 (66%)	92 (88%)	13 (12%)	0	100	100
31	2W	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
32	2X	105/125 (84%)	96 (91%)	9 (9%)	0	100	100
33	2Y	126/135 (93%)	116 (92%)	10 (8%)	0	100	100
34	2Z	107/110 (97%)	97 (91%)	10 (9%)	0	100	100
35	2a	109/117 (93%)	104 (95%)	5 (5%)	0	100	100
36	2b	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
37	2c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	2d	84/97 (87%)	68 (81%)	16 (19%)	0	100	100
39	2e	67/70 (96%)	58 (87%)	9 (13%)	0	100	100
40	2f	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	2g	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	2h	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
43	2i	103/106 (97%)	92 (89%)	11 (11%)	0	100	100
44	2j	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
45	2k	123/137 (90%)	112 (91%)	11 (9%)	0	100	100
47	2n	219/295 (74%)	198 (90%)	20 (9%)	1 (0%)	24	63
48	2o	212/264 (80%)	193 (91%)	19 (9%)	0	100	100
49	2p	225/243 (93%)	192 (85%)	33 (15%)	0	100	100
50	2q	260/263 (99%)	232 (89%)	28 (11%)	0	100	100
51	2r	185/204 (91%)	162 (88%)	21 (11%)	2 (1%)	11	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	2s	187/194 (96%)	167 (89%)	20 (11%)	0	100	100
53	2t	204/208 (98%)	181 (89%)	23 (11%)	0	100	100
54	2u	96/165 (58%)	88 (92%)	8 (8%)	0	100	100
55	2v	151/158 (96%)	129 (85%)	22 (15%)	0	100	100
56	2w	95/145 (66%)	76 (80%)	19 (20%)	0	100	100
57	2x	144/146 (99%)	124 (86%)	19 (13%)	1 (1%)	18	55
58	2y	130/135 (96%)	113 (87%)	17 (13%)	0	100	100
59	2z	148/152 (97%)	123 (83%)	24 (16%)	1 (1%)	18	55
60	20	141/145 (97%)	128 (91%)	13 (9%)	0	100	100
61	21	102/119 (86%)	92 (90%)	10 (10%)	0	100	100
62	3A	81/83 (98%)	71 (88%)	9 (11%)	1 (1%)	10	43
63	3B	139/143 (97%)	121 (87%)	14 (10%)	4 (3%)	3	23
64	3C	105/115 (91%)	96 (91%)	9 (9%)	0	100	100
65	3D	62/69 (90%)	48 (77%)	14 (23%)	0	100	100
66	3E	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
67	3F	311/317 (98%)	265 (85%)	45 (14%)	1 (0%)	36	71
68	3G	220/293 (75%)	205 (93%)	14 (6%)	1 (0%)	24	63
69	3H	235/249 (94%)	206 (88%)	29 (12%)	0	100	100
70	3I	183/194 (94%)	158 (86%)	22 (12%)	3 (2%)	7	37
71	3J	120/132 (91%)	101 (84%)	19 (16%)	0	100	100
72	3K	148/151 (98%)	137 (93%)	10 (7%)	1 (1%)	18	55
73	3L	138/151 (91%)	120 (87%)	17 (12%)	1 (1%)	18	55
74	3M	127/130 (98%)	113 (89%)	14 (11%)	0	100	100
75	3N	129/133 (97%)	121 (94%)	8 (6%)	0	100	100
76	3O	73/125 (58%)	62 (85%)	11 (15%)	0	100	100
77	3P	81/84 (96%)	65 (80%)	14 (17%)	2 (2%)	4	26
78	3Q	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
79	3R	65/156 (42%)	53 (82%)	12 (18%)	0	100	100
81	zx	15/17 (88%)	10 (67%)	5 (33%)	0	100	100
All	All	11334/12705 (89%)	10113 (89%)	1190 (10%)	31 (0%)	37	71

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	1H	111	LYS
24	2P	110	GLY
59	2z	17	ASN
70	3I	8	VAL
77	3P	20	LYS

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	
4	1D	190/199 (96%)	190 (100%)	0	100	100
5	1E	348/349 (100%)	347 (100%)	1 (0%)	86	84
6	1F	306/348 (88%)	306 (100%)	0	100	100
7	1G	246/250 (98%)	246 (100%)	0	100	100
8	1H	210/252 (83%)	208 (99%)	2 (1%)	68	76
9	2A	194/215 (90%)	191 (98%)	3 (2%)	57	70
10	2B	203/223 (91%)	203 (100%)	0	100	100
11	2C	169/171 (99%)	164 (97%)	5 (3%)	36	57
12	2D	180/181 (99%)	178 (99%)	2 (1%)	65	74
13	2E	148/149 (99%)	147 (99%)	1 (1%)	76	79
14	2F	176/177 (99%)	176 (100%)	0	100	100
15	2G	118/161 (73%)	116 (98%)	2 (2%)	53	67
16	2H	171/172 (99%)	171 (100%)	0	100	100
17	2I	173/174 (99%)	173 (100%)	0	100	100
18	2J	134/163 (82%)	133 (99%)	1 (1%)	76	79
19	2K	164/165 (99%)	164 (100%)	0	100	100
20	2L	166/175 (95%)	166 (100%)	0	100	100
21	2M	156/157 (99%)	155 (99%)	1 (1%)	78	80
22	2N	139/140 (99%)	139 (100%)	0	100	100
23	2O	91/115 (79%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	2P	101/107 (94%)	101 (100%)	0	100	100
25	2Q	103/126 (82%)	103 (100%)	0	100	100
26	2R	107/133 (80%)	107 (100%)	0	100	100
27	2S	124/135 (92%)	123 (99%)	1 (1%)	73	77
28	2T	117/118 (99%)	117 (100%)	0	100	100
29	2U	120/121 (99%)	120 (100%)	0	100	100
30	2V	88/126 (70%)	88 (100%)	0	100	100
31	2W	83/97 (86%)	83 (100%)	0	100	100
32	2X	98/110 (89%)	97 (99%)	1 (1%)	68	76
33	2Y	114/121 (94%)	112 (98%)	2 (2%)	51	67
34	2Z	88/89 (99%)	88 (100%)	0	100	100
35	2a	97/100 (97%)	97 (100%)	0	100	100
36	2b	109/110 (99%)	109 (100%)	0	100	100
37	2c	86/89 (97%)	86 (100%)	0	100	100
38	2d	73/80 (91%)	73 (100%)	0	100	100
39	2e	64/65 (98%)	63 (98%)	1 (2%)	55	69
40	2f	47/48 (98%)	47 (100%)	0	100	100
41	2g	48/116 (41%)	48 (100%)	0	100	100
42	2h	23/24 (96%)	23 (100%)	0	100	100
43	2i	93/94 (99%)	92 (99%)	1 (1%)	65	74
44	2j	74/75 (99%)	74 (100%)	0	100	100
45	2k	109/121 (90%)	106 (97%)	3 (3%)	38	59
47	2n	183/243 (75%)	181 (99%)	2 (1%)	65	74
48	2o	195/231 (84%)	194 (100%)	1 (0%)	81	81
49	2p	190/202 (94%)	189 (100%)	1 (0%)	81	81
50	2q	224/225 (100%)	223 (100%)	1 (0%)	84	82
51	2r	157/170 (92%)	157 (100%)	0	100	100
52	2s	169/174 (97%)	169 (100%)	0	100	100
53	2t	178/180 (99%)	178 (100%)	0	100	100
54	2u	89/136 (65%)	89 (100%)	0	100	100
55	2v	137/142 (96%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	2w	87/130 (67%)	87 (100%)	0	100	100
57	2x	121/121 (100%)	121 (100%)	0	100	100
58	2y	120/122 (98%)	120 (100%)	0	100	100
59	2z	130/132 (98%)	128 (98%)	2 (2%)	57	70
60	20	113/115 (98%)	113 (100%)	0	100	100
61	21	94/107 (88%)	94 (100%)	0	100	100
62	3A	67/67 (100%)	67 (100%)	0	100	100
63	3B	113/115 (98%)	113 (100%)	0	100	100
64	3C	90/98 (92%)	90 (100%)	0	100	100
65	3D	57/62 (92%)	56 (98%)	1 (2%)	51	67
66	3E	47/49 (96%)	47 (100%)	0	100	100
67	3F	272/275 (99%)	269 (99%)	3 (1%)	65	74
68	3G	188/225 (84%)	188 (100%)	0	100	100
69	3H	207/218 (95%)	207 (100%)	0	100	100
70	3I	161/168 (96%)	160 (99%)	1 (1%)	78	80
71	3J	104/108 (96%)	104 (100%)	0	100	100
72	3K	130/131 (99%)	130 (100%)	0	100	100
73	3L	110/119 (92%)	110 (100%)	0	100	100
74	3M	112/113 (99%)	112 (100%)	0	100	100
75	3N	113/115 (98%)	113 (100%)	0	100	100
76	3O	66/103 (64%)	65 (98%)	1 (2%)	57	70
77	3P	75/76 (99%)	75 (100%)	0	100	100
78	3Q	47/48 (98%)	47 (100%)	0	100	100
79	3R	60/140 (43%)	60 (100%)	0	100	100
81	zx	16/16 (100%)	16 (100%)	0	100	100
All	All	9870/10817 (91%)	9830 (100%)	40 (0%)	81	82

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	2n	112	ILE
67	3F	11	LEU
48	2o	171	ILE

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Mol	Chain	Res	Type
59	2z	12	ILE
67	3F	109	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
70	3I	143	ASN
71	3J	99	ASN
76	3O	89	GLN
21	2M	163	HIS
21	2M	156	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	3655/5070 (72%)	1231 (33%)	30 (0%)
2	1B	119/121 (98%)	29 (24%)	1 (0%)
3	1C	155/157 (98%)	44 (28%)	2 (1%)
46	2m	1714/1869 (91%)	658 (38%)	0
80	zv	5/6 (83%)	4 (80%)	0
82	zy	74/75 (98%)	16 (21%)	0
83	zz	161/290 (55%)	76 (47%)	0
All	All	5883/7588 (77%)	2058 (34%)	33 (0%)

5 of 2058 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	4	G
1	1A	13	U
1	1A	18	C
1	1A	22	G
1	1A	23	C

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	4913	G
1	1A	4949	G
3	1C	87	G
1	1A	2408	U

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Mol	Chain	Res	Type
1	1A	2389	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

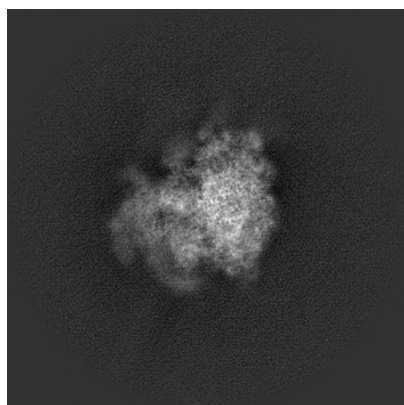
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9702. These allow visual inspection of the internal detail of the map and identification of artifacts.

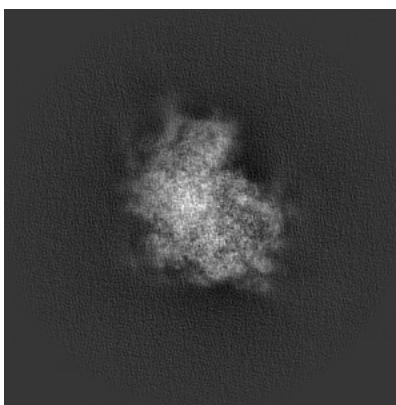
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

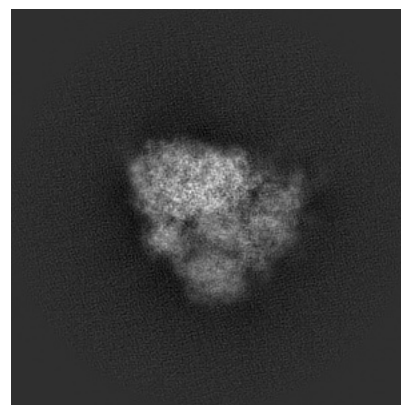
6.1.1 Primary map



X



Y

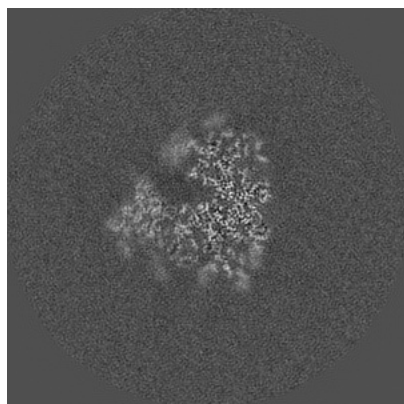


Z

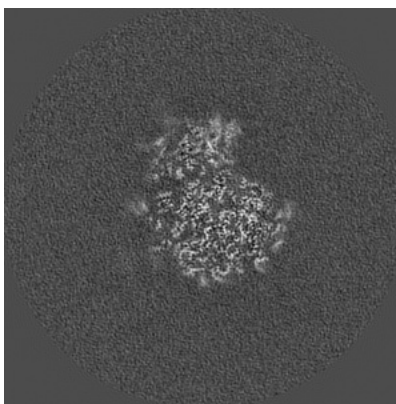
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

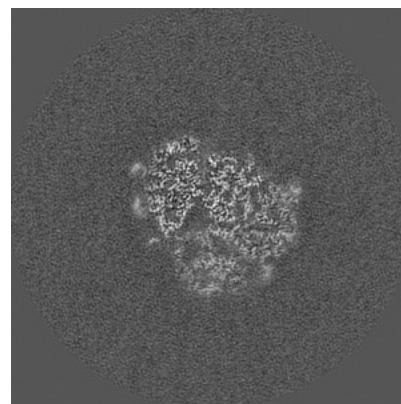
6.2.1 Primary map



X Index: 210



Y Index: 210

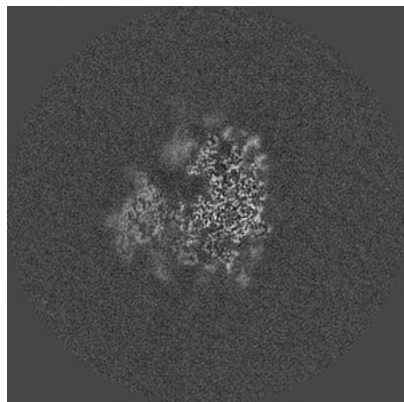


Z Index: 210

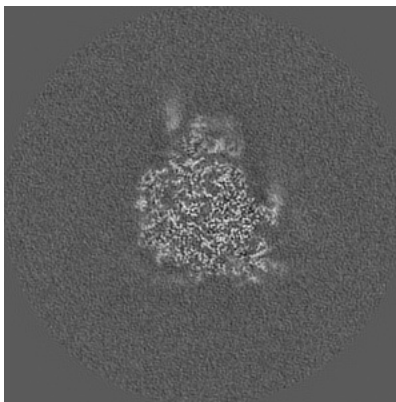
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

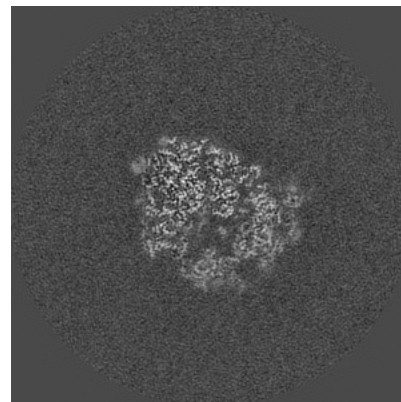
6.3.1 Primary map



X Index: 214



Y Index: 232

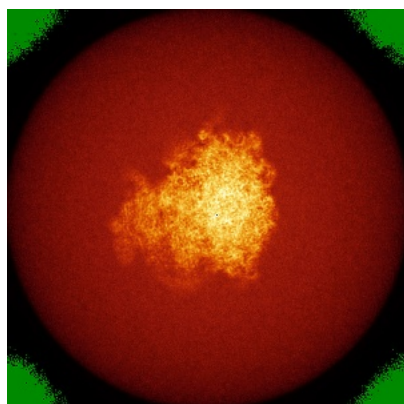


Z Index: 217

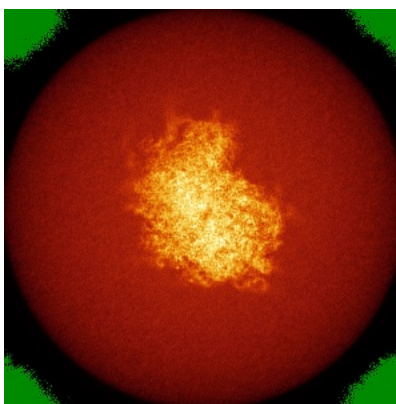
The images above show the largest variance slices of the map in three orthogonal directions.

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

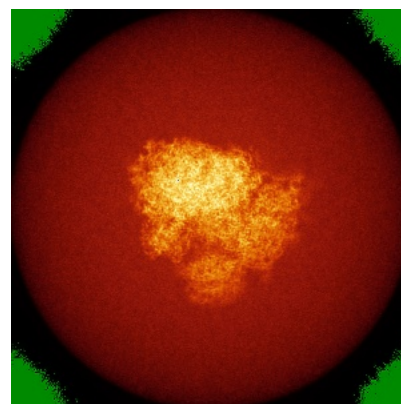
6.4.1 Primary map



X



Y

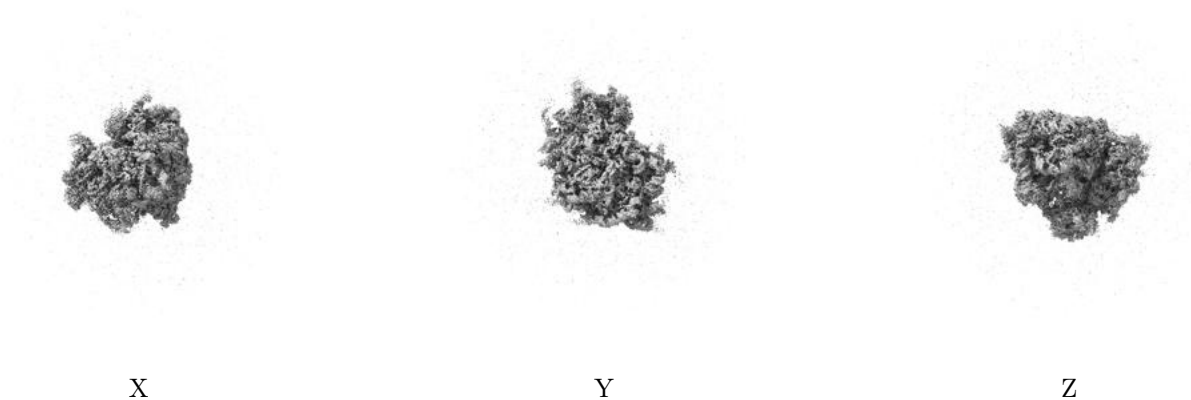


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

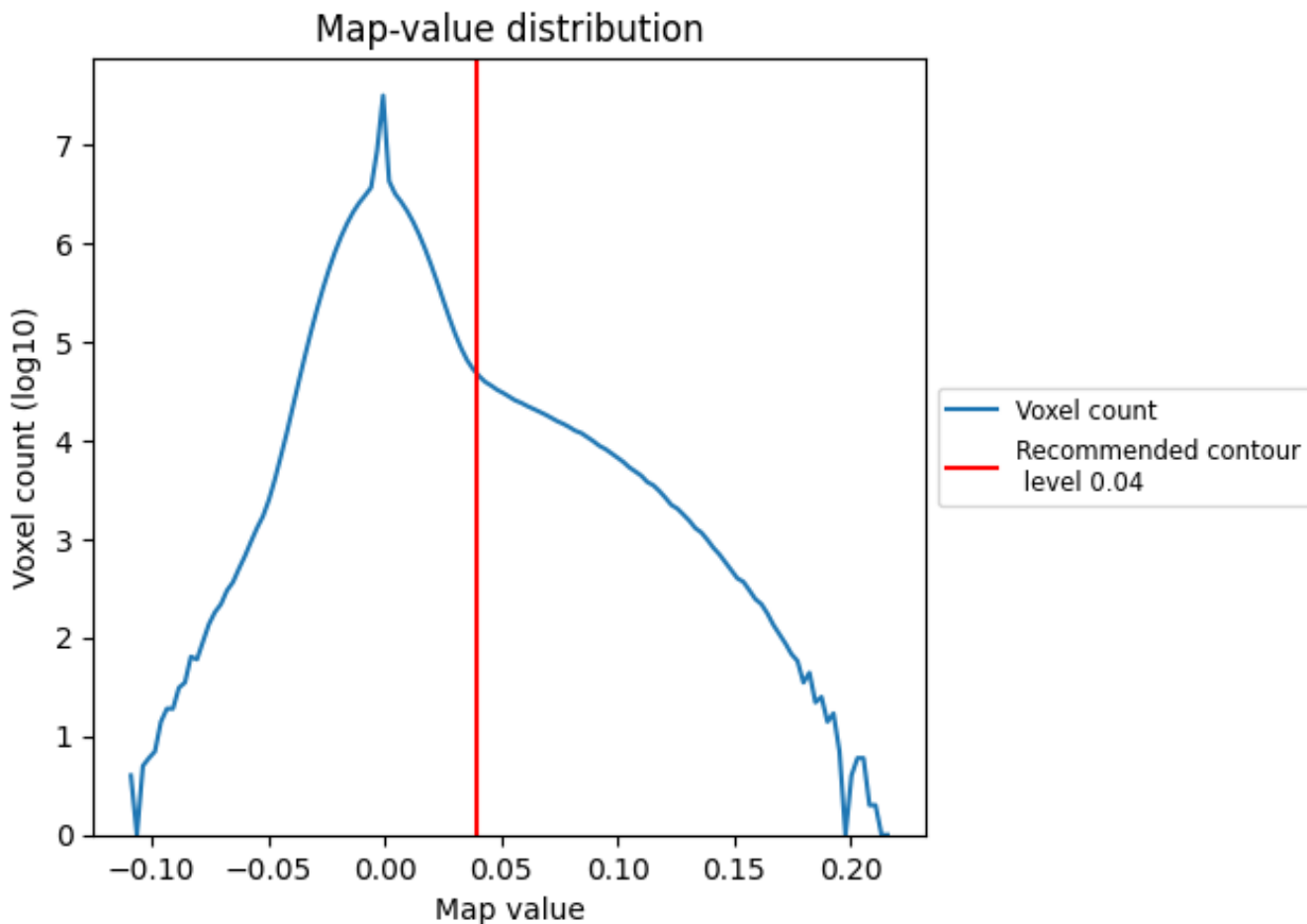
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

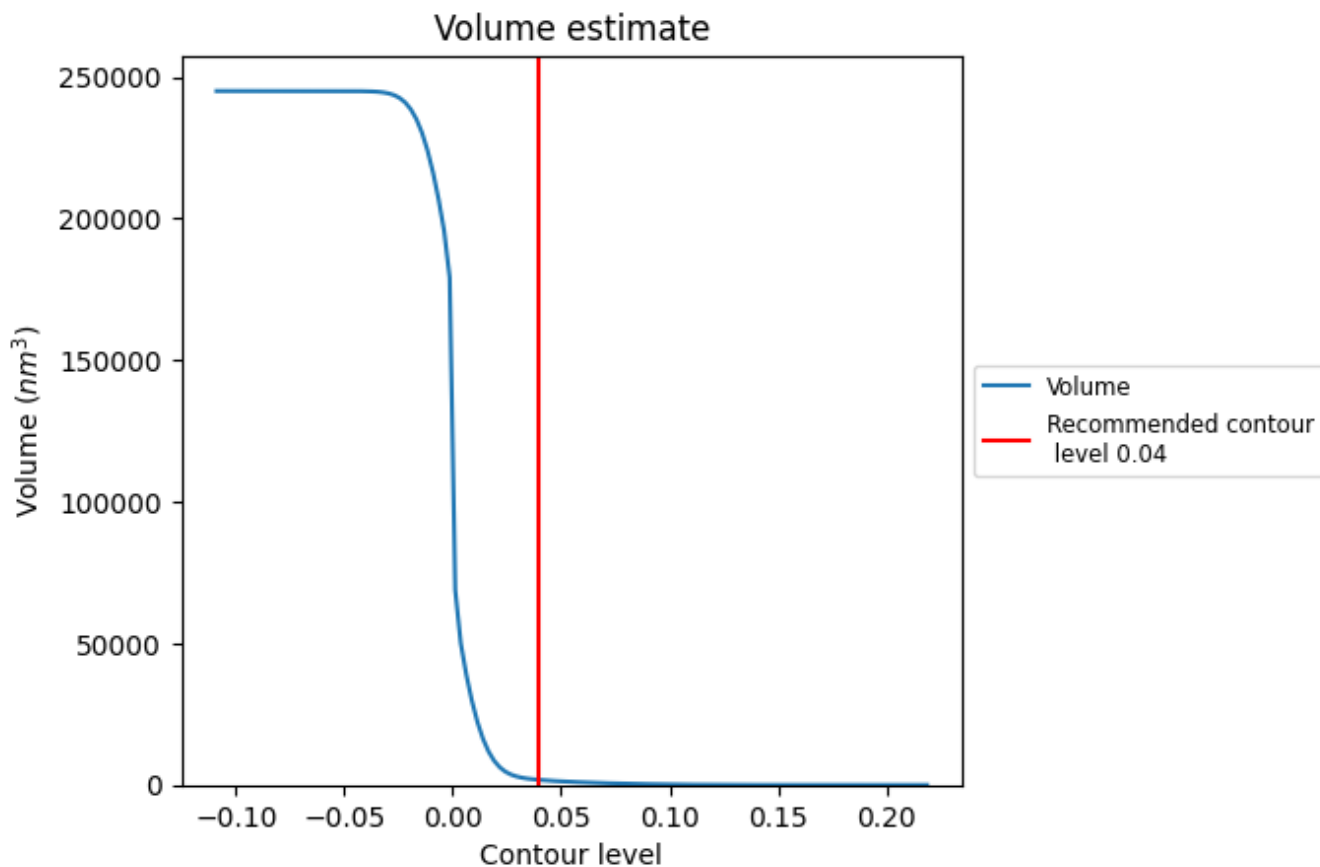
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

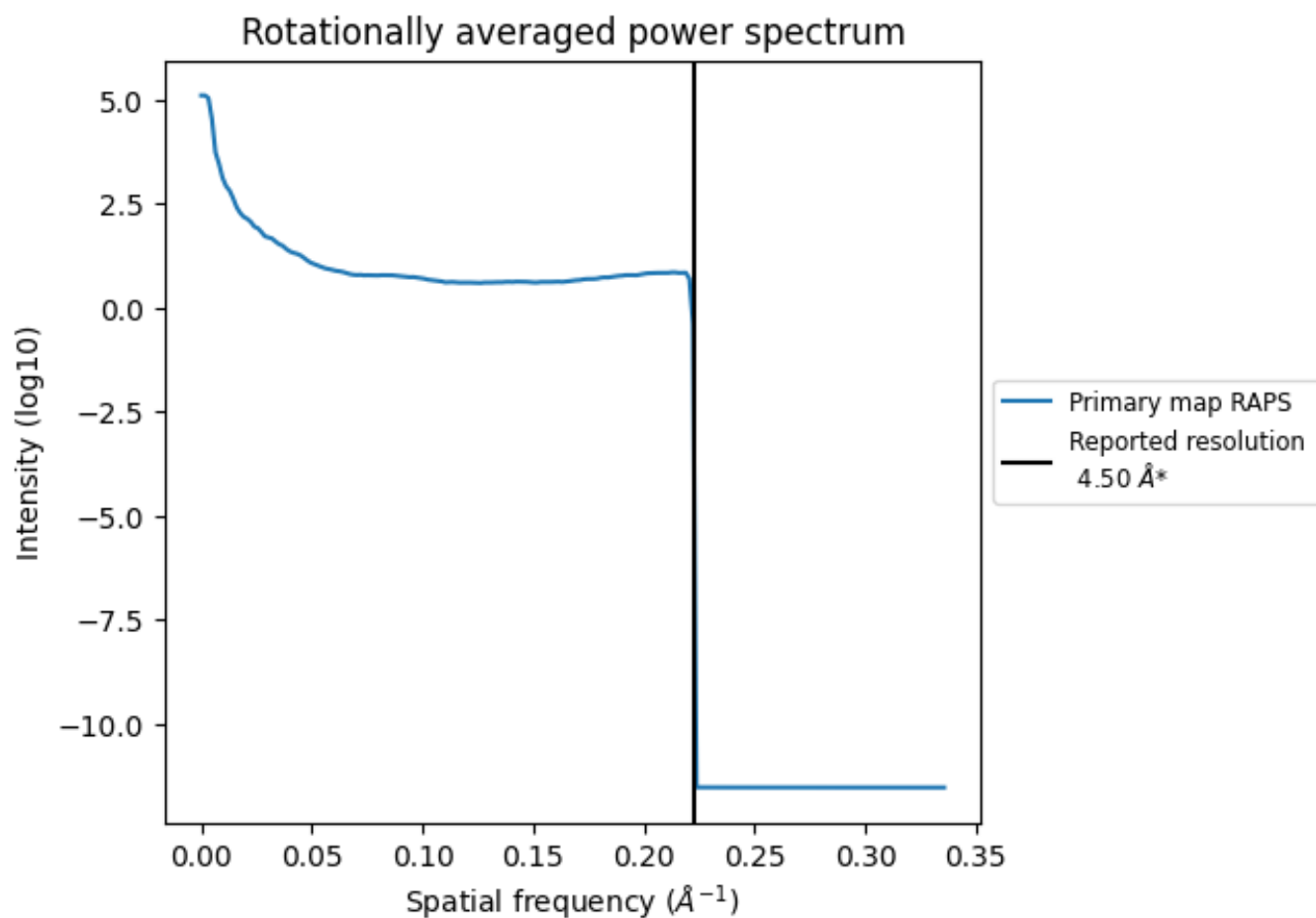
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1785 nm^3 ; this corresponds to an approximate mass of 1612 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](#)

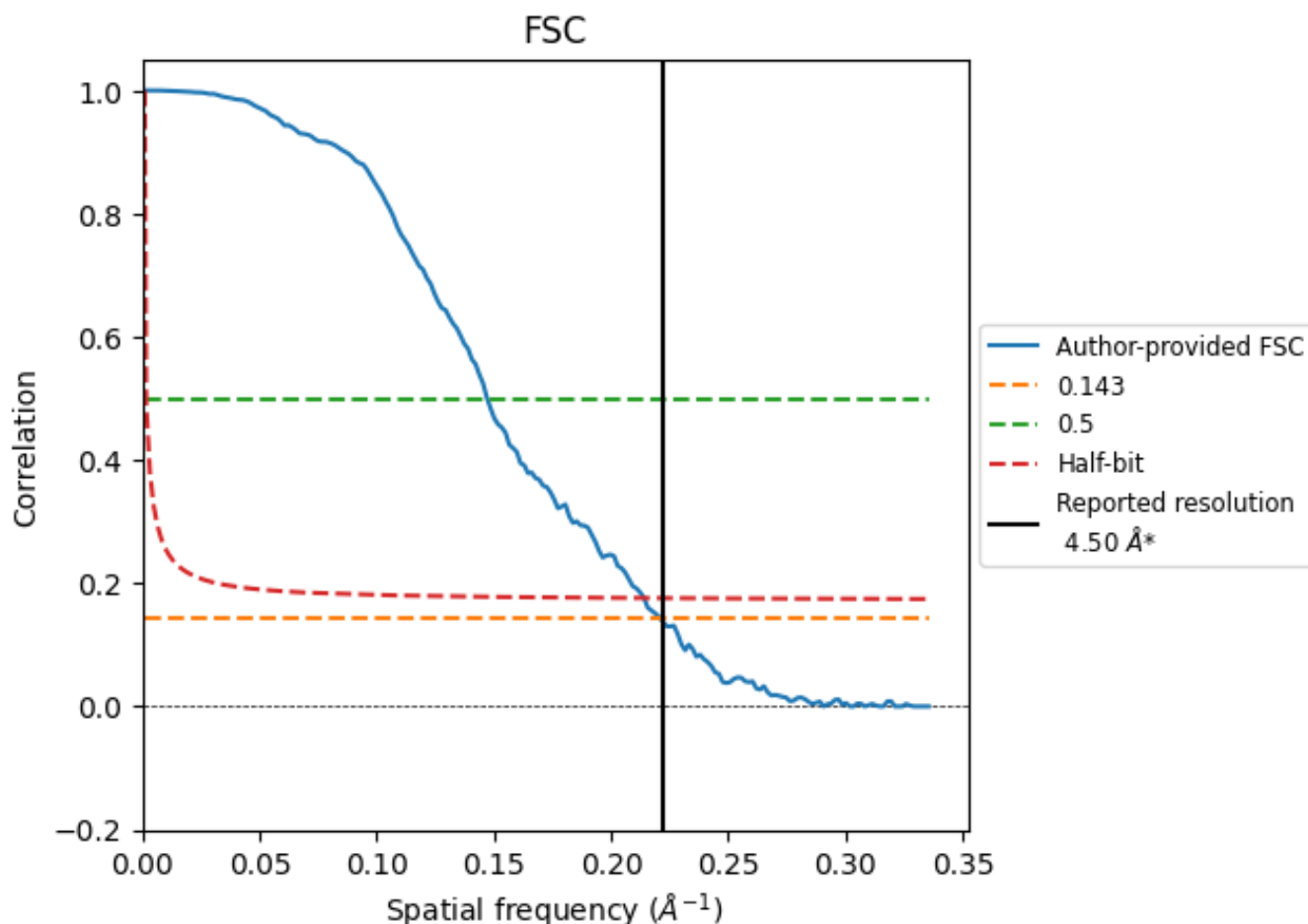


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

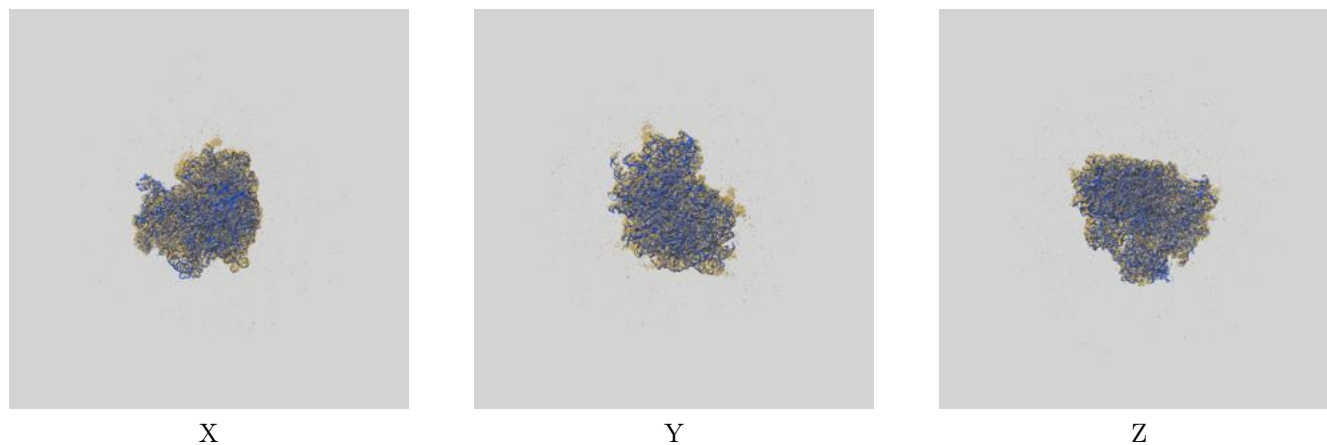
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.52	6.79	4.67
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

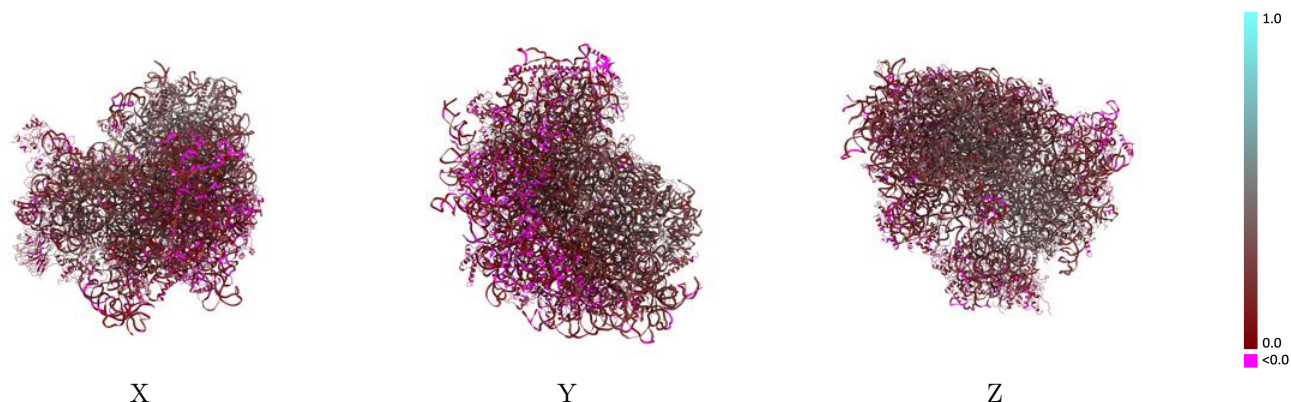
This section contains information regarding the fit between EMDB map EMD-9702 and PDB model 6IP6. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



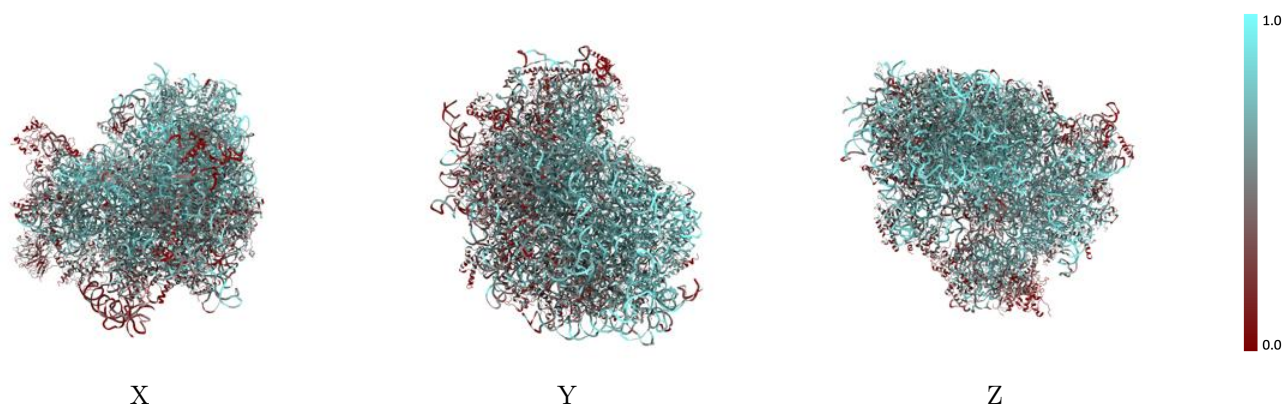
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



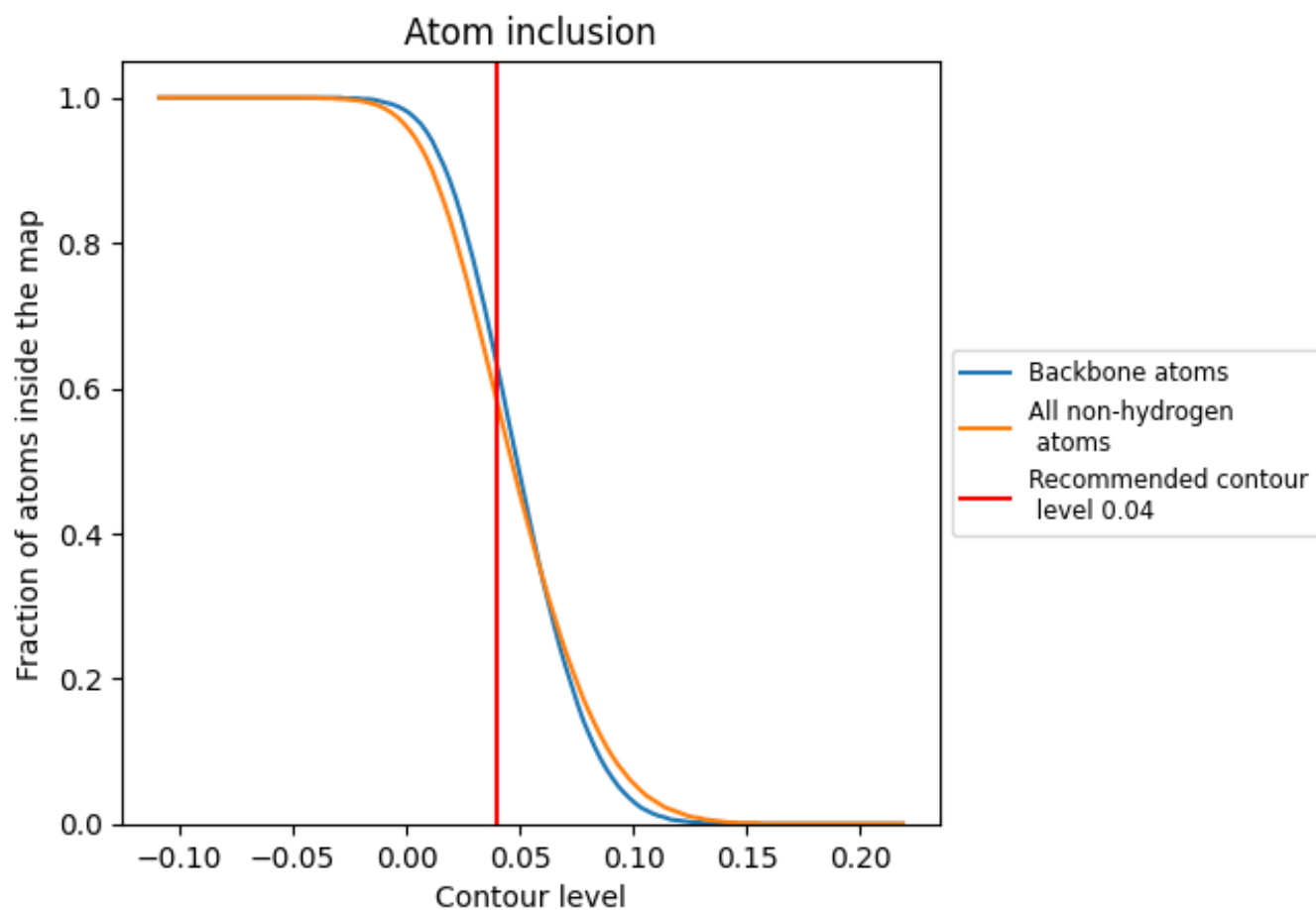
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

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

Chain	Atom inclusion	Q-score
All	 0.5800	 0.1840
1A	 0.7000	 0.1930
1B	 0.7750	 0.1950
1C	 0.5970	 0.1010
1D	 0.3890	 0.1250
1E	 0.5890	 0.2710
1F	 0.4210	 0.1150
1G	 0.4360	 0.0990
1H	 0.5540	 0.2490
20	 0.3900	 0.1300
21	 0.3410	 0.1770
2A	 0.5270	 0.2150
2B	 0.2790	 0.0400
2C	 0.6360	 0.3140
2D	 0.5470	 0.2510
2E	 0.4530	 0.1350
2F	 0.3380	 0.0640
2G	 0.6370	 0.2930
2H	 0.3560	 0.0340
2I	 0.6500	 0.3390
2J	 0.5430	 0.2030
2K	 0.4010	 0.0820
2L	 0.4240	 0.1260
2M	 0.6320	 0.2810
2N	 0.4770	 0.1740
2O	 0.3230	 0.0410
2P	 0.6050	 0.3170
2Q	 0.3330	 0.1290
2R	 0.3590	 0.0450
2S	 0.4200	 0.0490
2T	 0.3470	 0.0430
2U	 0.4000	 0.1030
2V	 0.4580	 0.1520
2W	 0.3860	 0.1020
2X	 0.5100	 0.1840

















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Chain	Atom inclusion	Q-score
2Y	0.5210	0.2160
2Z	0.6540	0.3100
2a	0.3700	0.0850
2b	0.3640	0.0470
2c	0.3200	0.0670
2d	0.4390	0.0830
2e	0.3860	0.0670
2f	0.4300	0.1430
2g	0.6670	0.3370
2h	0.6360	0.3140
2i	0.4320	0.1190
2j	0.4560	0.1810
2k	0.4700	0.1200
2m	0.7190	0.2230
2n	0.4680	0.2320
2o	0.2940	0.1350
2p	0.3810	0.2260
2q	0.3970	0.1390
2r	0.3590	0.1260
2s	0.3410	0.1560
2t	0.3730	0.1070
2u	0.3070	0.1730
2v	0.3630	0.1640
2w	0.3440	0.1370
2x	0.3880	0.1280
2y	0.3620	0.1940
2z	0.3640	0.1360
3A	0.4890	0.2670
3B	0.5520	0.3260
3C	0.4560	0.2300
3D	0.2390	0.1690
3E	0.5320	0.2130
3F	0.3100	0.1440
3G	0.5520	0.2910
3H	0.3740	0.1370
3I	0.5030	0.2390
3J	0.0360	0.0850
3K	0.4140	0.1720
3L	0.3250	0.1360
3M	0.5260	0.2500
3N	0.4700	0.1700
3O	0.2620	0.0920

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Chain	Atom inclusion	Q-score
3P	 0.3350	 0.1900
3Q	 0.4620	 0.2540
3R	 0.1410	 0.0760
zV	 0.4310	 0.2670
zX	 0.1250	 0.1160
zY	 0.4390	 0.2210
zZ	 0.1650	 0.0770