



wwPDB EM Validation Summary Report ⓘ

Sep 15, 2026 – 03:10 pm BST

PDB ID : 4V8Z / pdb_00004v8z
EMDB ID : EMD-2422
Title : Cryo-EM reconstruction of the 80S-eIF5B-Met-itRNAMet Eukaryotic Translation Initiation Complex
Authors : Fernandez, I.S.; Bai, X.C.; Hussain, T.; Kelley, A.C.; Lorsch, J.R.; Ramakrishnan, V.; Scheres, S.H.W.
Deposited on : 2013-07-20
Resolution : 6.60 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:

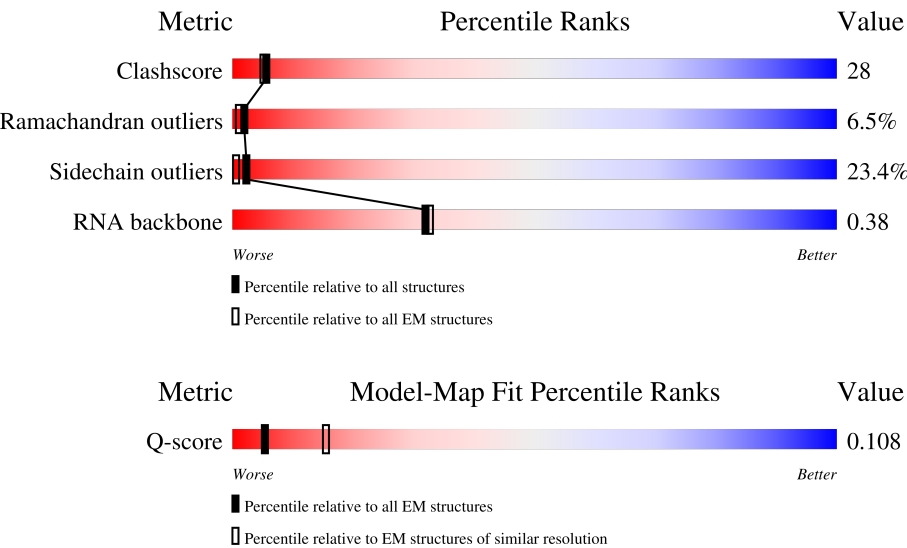
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 6.60 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	531 (6.10 - 7.10)

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	A0	119	51% 28%34%15%5%18%
2	A1	82	48% 52%30%15%..
3	A2	67	82% 27%43%24%6%

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Mol	Chain	Length	Quality of chain
4	A3	56	
5	A4	63	
6	A5	152	
7	A6	319	
8	A7	273	
9	AA	252	
10	AB	255	
11	AC	254	
12	AD	240	
13	AE	261	
14	AF	225	
15	AG	236	
16	AH	190	
17	AI	200	
18	AJ	197	
19	AK	105	
20	AL	156	
21	AM	143	
22	AN	151	
23	AO	137	
24	AP	142	
25	AQ	143	
26	AR	136	
27	AS	146	
28	AT	144	

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Mol	Chain	Length	Quality of chain
29	AU	121	
30	AV	87	
31	AW	130	
32	AX	145	
33	AY	135	
34	AZ	108	
35	BA	253	
36	BB	386	
37	BC	361	
38	BD	296	
39	BE	175	
40	BF	243	
41	BG	255	
42	BH	191	
43	BI	220	
44	BJ	173	
45	BK	174	
46	BL	198	
47	BM	137	
48	BN	203	
49	BO	218	
50	BP	183	
51	BQ	185	
52	BR	188	
53	BS	172	

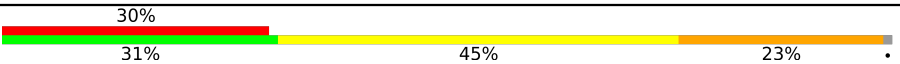
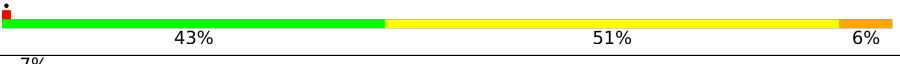
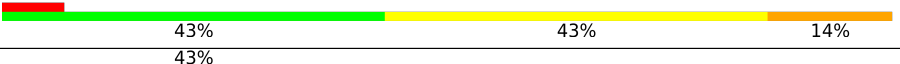
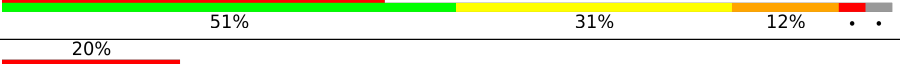
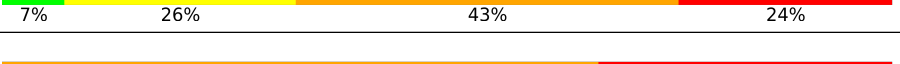
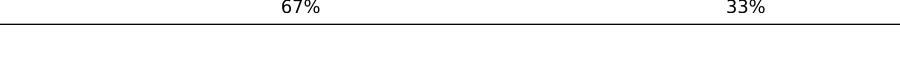
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Mol	Chain	Length	Quality of chain
54	BT	159	
55	BU	120	
56	BV	136	
57	BW	155	
58	BX	141	
59	BY	126	
60	BZ	135	
61	Ba	148	
62	Bb	58	
63	Bc	104	
64	Bd	112	
65	Be	129	
66	Bf	106	
67	Bg	120	
68	Bh	119	
69	Bi	99	
70	Bj	87	
71	Bk	77	
72	Bl	50	
73	Bm	128	
74	Bn	25	
75	Bo	105	
76	Bq	312	
77	Br	47	
78	Bs	46	

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Mol	Chain	Length	Quality of chain
79	B2	1800	
80	B5	3396	
81	B7	121	
82	B8	158	
83	CV	586	
84	CW	76	
85	CX	3	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
88	OHX	A3	102	-	-	X	-
88	OHX	AC	301	-	-	X	-
88	OHX	B2	1907	-	-	X	-
88	OHX	B2	1915	-	-	X	-
88	OHX	B2	1918	-	-	X	-
88	OHX	B2	1921	-	-	X	-
88	OHX	B2	1922	-	-	X	-
88	OHX	B2	1939	-	-	X	-
88	OHX	B2	1953	-	-	X	-
88	OHX	B2	1960	-	-	X	-
88	OHX	B2	1962	-	-	X	-
88	OHX	B2	1963	-	-	X	-
88	OHX	B2	1967	-	-	X	-
88	OHX	B2	1968	-	-	X	-
88	OHX	B2	1973	-	-	X	-
88	OHX	B2	1976	-	-	X	-
88	OHX	B2	1981	-	-	X	-
88	OHX	B2	1987	-	-	X	-
88	OHX	B2	2011	-	-	X	-
88	OHX	B2	2014	-	-	X	-
88	OHX	B2	2025	-	-	X	-
88	OHX	B2	2044	-	-	X	-
88	OHX	B2	2048	-	-	X	-
88	OHX	B2	2062	-	-	X	-
88	OHX	B2	2066	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
88	OHX	B2	2069	-	-	X	-
88	OHX	B2	2071	-	-	X	-
88	OHX	B2	2077	-	-	X	-
88	OHX	B2	2081	-	-	X	-
88	OHX	B7	203	-	-	X	-
88	OHX	B7	219	-	-	X	-
88	OHX	BR	201	-	-	X	-
88	OHX	CV	601	-	-	X	-
89	GCP	CV	602	-	-	X	-

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 219371 atoms, of which 8407 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S RIBOSOMAL PROTEIN S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A1	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A3	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A4	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 6 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A5	71	Total	C	N	O	S	0	0
			516	328	93	91	4		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5	82	UNK	LYS	SEE REMARK 999	UNP P05759
A5	83	UNK	LYS	SEE REMARK 999	UNP P05759
A5	84	UNK	VAL	SEE REMARK 999	UNP P05759
A5	85	UNK	TYR	SEE REMARK 999	UNP P05759
A5	86	UNK	THR	SEE REMARK 999	UNP P05759
A5	87	UNK	THR	SEE REMARK 999	UNP P05759
A5	88	UNK	PRO	SEE REMARK 999	UNP P05759
A5	89	UNK	LYS	SEE REMARK 999	UNP P05759
A5	90	UNK	LYS	SEE REMARK 999	UNP P05759
A5	91	UNK	ILE	SEE REMARK 999	UNP P05759
A5	92	UNK	LYS	SEE REMARK 999	UNP P05759
A5	93	UNK	HIS	SEE REMARK 999	UNP P05759
A5	94	UNK	LYS	SEE REMARK 999	UNP P05759
A5	95	UNK	HIS	SEE REMARK 999	UNP P05759
A5	96	UNK	LYS	SEE REMARK 999	UNP P05759
A5	97	UNK	LYS	SEE REMARK 999	UNP P05759
A5	98	UNK	VAL	SEE REMARK 999	UNP P05759
A5	99	UNK	LYS	SEE REMARK 999	UNP P05759
A5	100	UNK	LEU	SEE REMARK 999	UNP P05759
A5	101	UNK	ALA	SEE REMARK 999	UNP P05759

- Molecule 7 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 8 is a protein called SUPPRESSOR PROTEIN STM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	A7	159	Total	C	N	O	0	0
			1105	653	221	231		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A7	9	UNK	GLY	SEE REMARK 999	UNP P39015
A7	10	UNK	ASN	SEE REMARK 999	UNP P39015
A7	11	UNK	ASP	SEE REMARK 999	UNP P39015
A7	12	UNK	VAL	SEE REMARK 999	UNP P39015

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Chain	Residue	Modelled	Actual	Comment	Reference
A7	13	UNK	GLU	SEE REMARK 999	UNP P39015
A7	14	UNK	ASP	SEE REMARK 999	UNP P39015
A7	15	UNK	ALA	SEE REMARK 999	UNP P39015
A7	16	UNK	ASP	SEE REMARK 999	UNP P39015
A7	17	UNK	VAL	SEE REMARK 999	UNP P39015
A7	18	UNK	VAL	SEE REMARK 999	UNP P39015
A7	19	UNK	VAL	SEE REMARK 999	UNP P39015
A7	20	UNK	LEU	SEE REMARK 999	UNP P39015
A7	151	UNK	LEU	SEE REMARK 999	UNP P39015
A7	152	UNK	GLN	SEE REMARK 999	UNP P39015
A7	153	UNK	ASP	SEE REMARK 999	UNP P39015
A7	154	UNK	TYR	SEE REMARK 999	UNP P39015
A7	155	UNK	LEU	SEE REMARK 999	UNP P39015
A7	156	UNK	ASN	SEE REMARK 999	UNP P39015
A7	157	UNK	GLN	SEE REMARK 999	UNP P39015
A7	158	UNK	GLN	SEE REMARK 999	UNP P39015
A7	159	UNK	ALA	SEE REMARK 999	UNP P39015
A7	160	UNK	ASN	SEE REMARK 999	UNP P39015
A7	161	UNK	ASN	SEE REMARK 999	UNP P39015
A7	162	UNK	GLN	SEE REMARK 999	UNP P39015
A7	163	UNK	PHE	SEE REMARK 999	UNP P39015
A7	164	UNK	ASN	SEE REMARK 999	UNP P39015
A7	165	UNK	LYS	SEE REMARK 999	UNP P39015
A7	166	UNK	VAL	SEE REMARK 999	UNP P39015
A7	167	UNK	PRO	SEE REMARK 999	UNP P39015
A7	168	UNK	GLU	SEE REMARK 999	UNP P39015
A7	169	UNK	ALA	SEE REMARK 999	UNP P39015
A7	170	UNK	LYS	SEE REMARK 999	UNP P39015
A7	171	UNK	LYS	SEE REMARK 999	UNP P39015
A7	172	UNK	VAL	SEE REMARK 999	UNP P39015
A7	173	UNK	GLU	SEE REMARK 999	UNP P39015
A7	174	UNK	LEU	SEE REMARK 999	UNP P39015
A7	175	UNK	ASP	SEE REMARK 999	UNP P39015

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S0-A.

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

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S1-A.

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

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S2.

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

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S3.

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

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S4-A.

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

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S5.

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

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S6-A.

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

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	184	Total	C	N	O		0	0
			1481	951	265	265			

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S8-A.

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

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S9-A.

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

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AK	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S11-A.

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

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AM	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S13.

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

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S14-A.

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

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S15.

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

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AR	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S18-A.

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

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S19-A.

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

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S20.

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

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S21-A.

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

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S22-A.

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

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S23-A.

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

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN S25-A.

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

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L2-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L3.

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

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L4-A.

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

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L9-A.

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

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BI	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L11-A.

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

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	153	Total	C	H	N	O	0	3
			1509	450	756	153	150		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	89	ALA	GLY	conflict	UNP P38754

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L15-A.

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

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BO	197	Total	C	N	O	S	197	0
			3119	2008	581	528	2		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BO	3	VAL	SER	microheterogeneity	UNP P26784
BO	4	GLU	GLN	microheterogeneity	UNP P26784
BO	11	GLY	ALA	microheterogeneity	UNP P26784
BO	13	GLY	ASP	microheterogeneity	UNP P26784
BO	16	VAL	LEU	microheterogeneity	UNP P26784
BO	22	VAL	THR	microheterogeneity	UNP P26784
BO	23	VAL	ILE	microheterogeneity	UNP P26784

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Chain	Residue	Modelled	Actual	Comment	Reference
BO	27	LEU	VAL	microheterogeneity	UNP P26784
BO	40	GLU	ALA	microheterogeneity	UNP P26784
BO	80	PHE	LEU	microheterogeneity	UNP P26784
BO	84	LEU	ILE	microheterogeneity	UNP P26784
BO	104	VAL	ILE	microheterogeneity	UNP P26784
BO	158	ALA	ASP	microheterogeneity	UNP P26784
BO	163	SER	ARG	microheterogeneity	UNP P26784
BO	179	ALA	SER	microheterogeneity	UNP P26784
BO	182	ASN	SER	microheterogeneity	UNP P26784
BO	184	THR	ALA	microheterogeneity	UNP P26784
BO	186	ALA	SER	microheterogeneity	UNP P26784
BO	196	ALA	SER	microheterogeneity	UNP P26784
BO	197	LEU	PHE	microheterogeneity	UNP P26784

- Molecule 50 is a protein called 60S RIBOSOMAL PROTEIN L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BP	155	Total	C	N	O	0	0
			1227	764	238	225		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L18-A.

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

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L19-B.

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

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L20-B.

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

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L21-A.

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

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BU	98	Total	C	N	O		0	0
			778	505	127	146			

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L23-A.

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

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BW	135	Total	C	N	O	S	0	0
			1038	651	206	180	1		

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L26-A.

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

- Molecule 60 is a protein called 60S RIBOSOMAL PROTEIN L27-A.

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

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L28.

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

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L29.

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

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bd	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 65 is a protein called 60S RIBOSOMAL PROTEIN L32.

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

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L33-A.

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

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L34-A.

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

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L35-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bi	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L37-A.

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

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bk	77	Total	C	N	O		0	0
			608	388	114	106			

- Molecule 72 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

- Molecule 73 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

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

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L41-B.

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

- Molecule 75 is a protein called 60S RIBOSOMAL PROTEIN L42-A.

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

- Molecule 76 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace	
76	Bq	145	Total	C	H	N	O	S	0	2
			2185	683	1110	194	195	3		

- Molecule 77 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Br	47	Total	C	H	N	O	0	0
			473	141	237	47	48		

- Molecule 78 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bs	46	Total	C	H	N	O	0	0
			463	138	232	46	47		

- Molecule 79 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	B2	1781	Total	C	N	O	P	1	0
			37835	16910	6661	12482	1782		

- Molecule 80 is a RNA chain called 25S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	B5	3147	Total	C	H	N	O	P	0	0
			67972	30066	664	12132	21965	3145		

- Molecule 81 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 82 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	B8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 83 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 5B, PROBABLE TRANSLATION INITIATION FACTOR IF-2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
83	CV	570	Total	C	H	N	O	S	0	2
			9036	2819	4585	766	847	19		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CV	340	ASP	-	linker	UNP P39730
CV	341	LEU	-	linker	UNP P39730
CV	342	THR	-	linker	UNP P39730
CV	343	GLY	-	linker	UNP P39730
CV	344	LEU	-	linker	UNP P39730
CV	345	LEU	-	linker	UNP P39730
CV	346	ASP	-	linker	UNP P39730
CV	347	SER	-	linker	UNP P39730
CV	348	VAL	-	linker	UNP P39730
CV	349	ASP	-	linker	UNP P39730
CV	350	THR	-	linker	UNP P39730

- Molecule 84 is a RNA chain called EUKARYOTIC RIBOSOMAL PI TRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	CW	76	Total	C	H	N	O	P	0	0
			2403	721	789	285	533	75		

- Molecule 85 is a RNA chain called 5'-R(*AP*UP*GP)-3'.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	CX	3	Total	C	H	N	O	P	0	0
			96	29	34	12	19	2		

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	A0	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	A1	1	Total 1	Zn 1	0
86	A3	1	Total 1	Zn 1	0
86	A5	1	Total 1	Zn 1	0
86	Bj	1	Total 1	Zn 1	0
86	Bm	1	Total 1	Zn 1	0

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

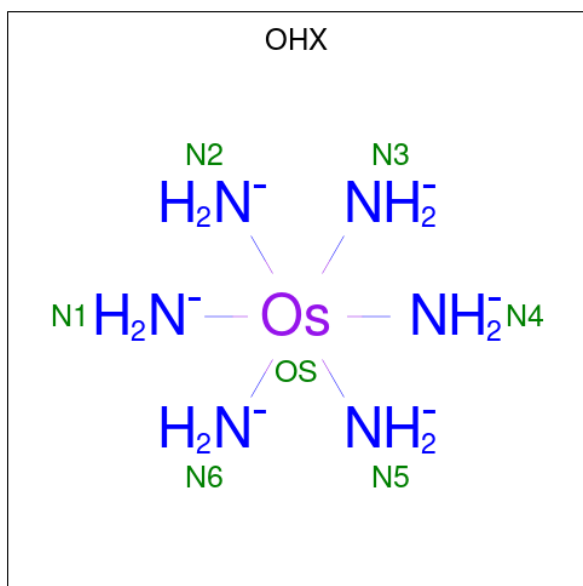
Mol	Chain	Residues	Atoms		AltConf
87	A0	2	Total 2	Mg 2	0
87	A3	3	Total 3	Mg 3	0
87	A5	1	Total 1	Mg 1	0
87	AB	1	Total 1	Mg 1	0
87	AC	2	Total 2	Mg 2	0
87	AE	1	Total 1	Mg 1	0
87	AG	1	Total 1	Mg 1	0
87	AI	1	Total 1	Mg 1	0
87	AJ	1	Total 1	Mg 1	0
87	AL	2	Total 2	Mg 2	0
87	AN	1	Total 1	Mg 1	0
87	AP	1	Total 1	Mg 1	0
87	AS	1	Total 1	Mg 1	0
87	AU	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
87	BD	4	Total 4	Mg 4	0
87	BF	1	Total 1	Mg 1	0
87	BS	3	Total 3	Mg 3	0
87	B2	168	Total 168	Mg 168	0
87	B5	3	Total 3	Mg 3	0
87	B7	27	Total 27	Mg 27	0
87	CW	1	Total 1	Mg 1	0

- Molecule 88 is osmium (III) hexammine (CCD ID: OHX) (formula: $\text{H}_{12}\text{N}_6\text{Os}$).



Mol	Chain	Residues	Atoms			AltConf
88	A3	1	Total 7	N 6	Os 1	0
88	A6	1	Total 7	N 6	Os 1	0
88	AC	1	Total 7	N 6	Os 1	0
88	AI	1	Total 7	N 6	Os 1	0

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Mol	Chain	Residues	Atoms			AltConf
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	
88	B2	1	Total	N	Os	0
			7	6	1	

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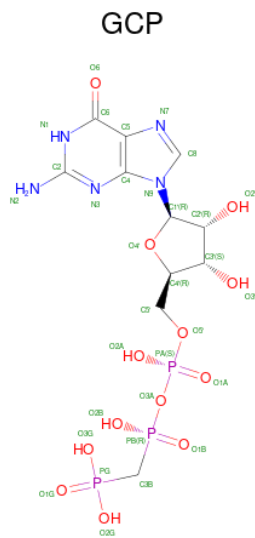
Mol	Chain	Residues	Atoms			AltConf
			Total	N	Os	
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B2	1	7	6	1	0
88	B5	1	7	6	1	0

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Mol	Chain	Residues	Atoms			AltConf
88	B5	1	Total	N	Os	0
			7	6	1	
88	B5	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	B7	1	Total	N	Os	0
			7	6	1	
88	CV	1	Total	N	Os	0
			7	6	1	
88	CX	1	Total	N	Os	0
			7	6	1	

- Molecule 89 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

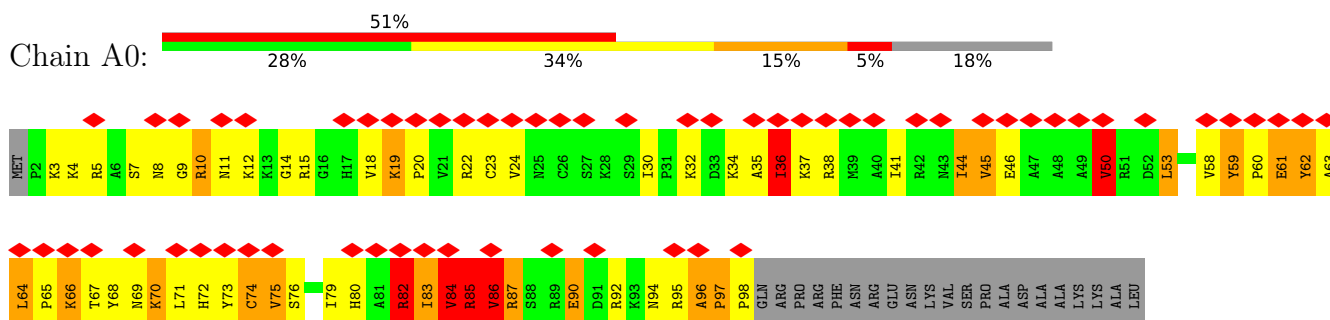


Mol	Chain	Residues	Atoms					AltConf
89	CV	1	Total 32	C 11	N 5	O 13	P 3	0

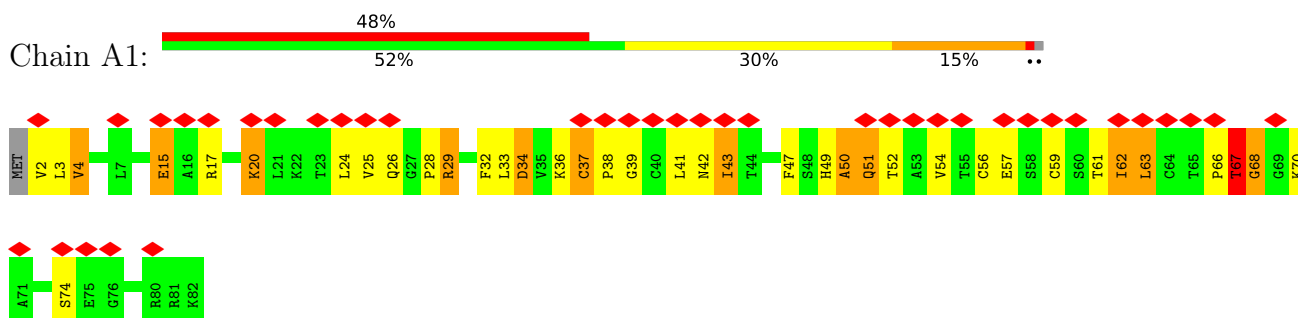
3 Residue-property plots

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.

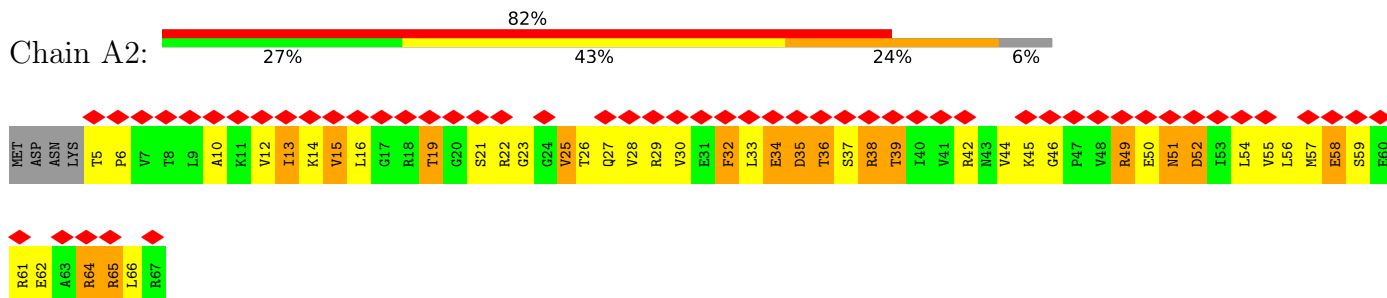
• Molecule 1: 40S RIBOSOMAL PROTEIN S26-A



• Molecule 2: 40S RIBOSOMAL PROTEIN S27-A

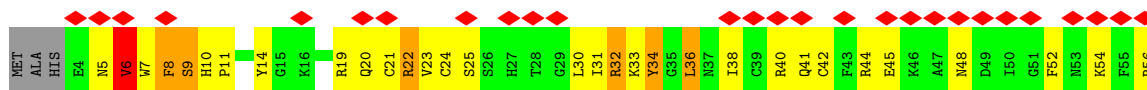


• Molecule 3: 40S RIBOSOMAL PROTEIN S28-A

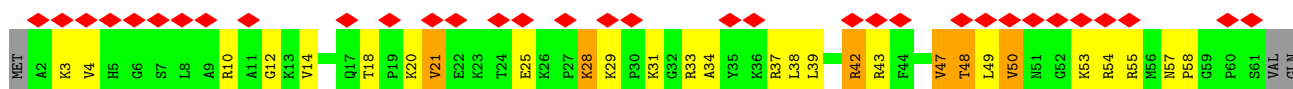


• Molecule 4: 40S RIBOSOMAL PROTEIN S29-A

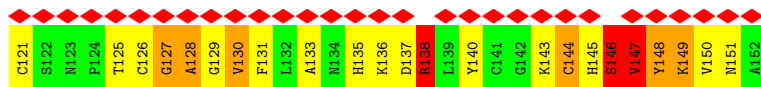
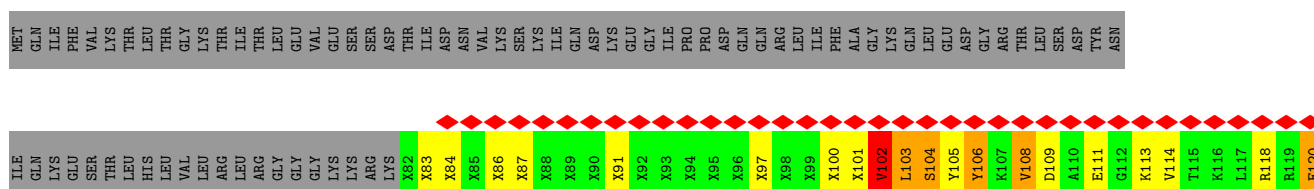
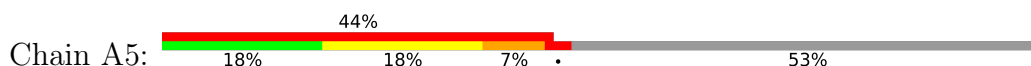




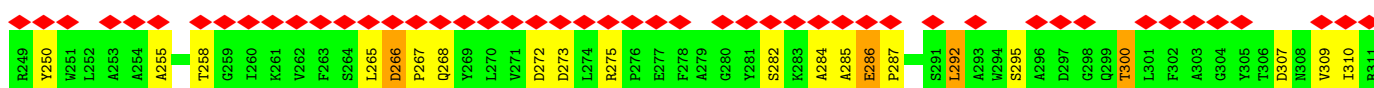
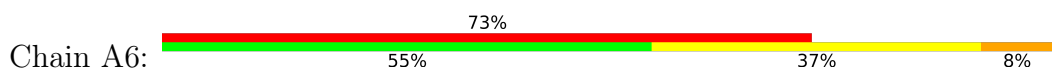
• Molecule 5: 40S RIBOSOMAL PROTEIN S30-A



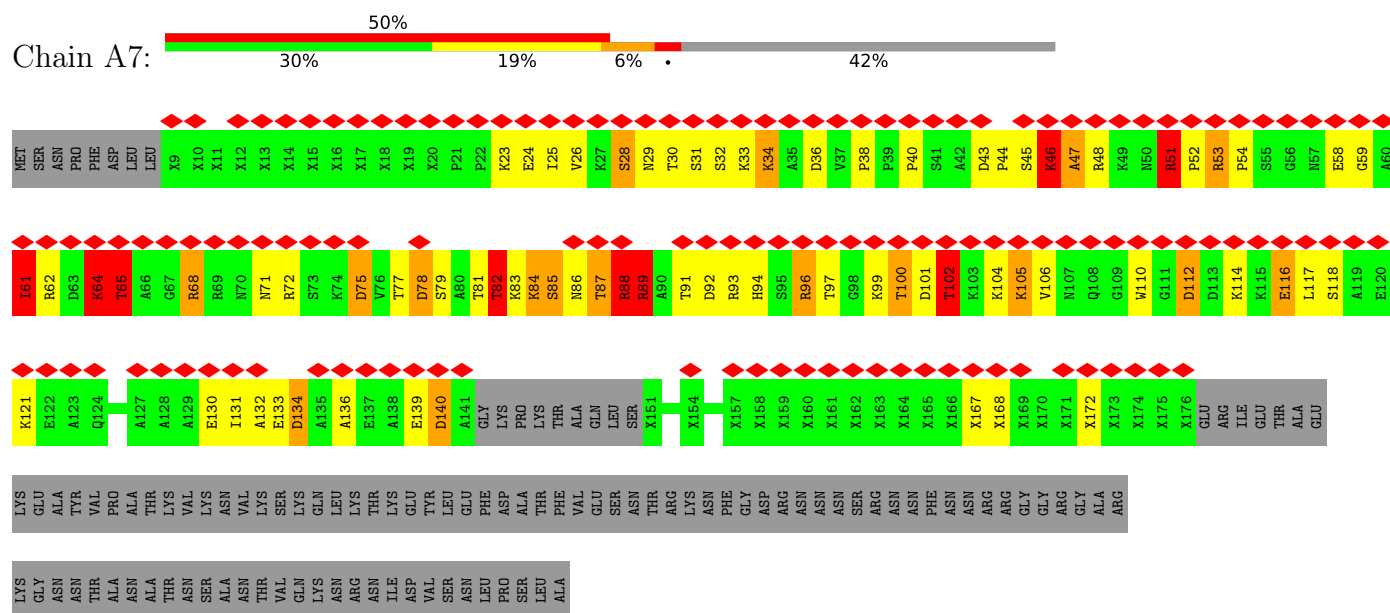
• Molecule 6: UBIQUITIN-40S RIBOSOMAL PROTEIN S31



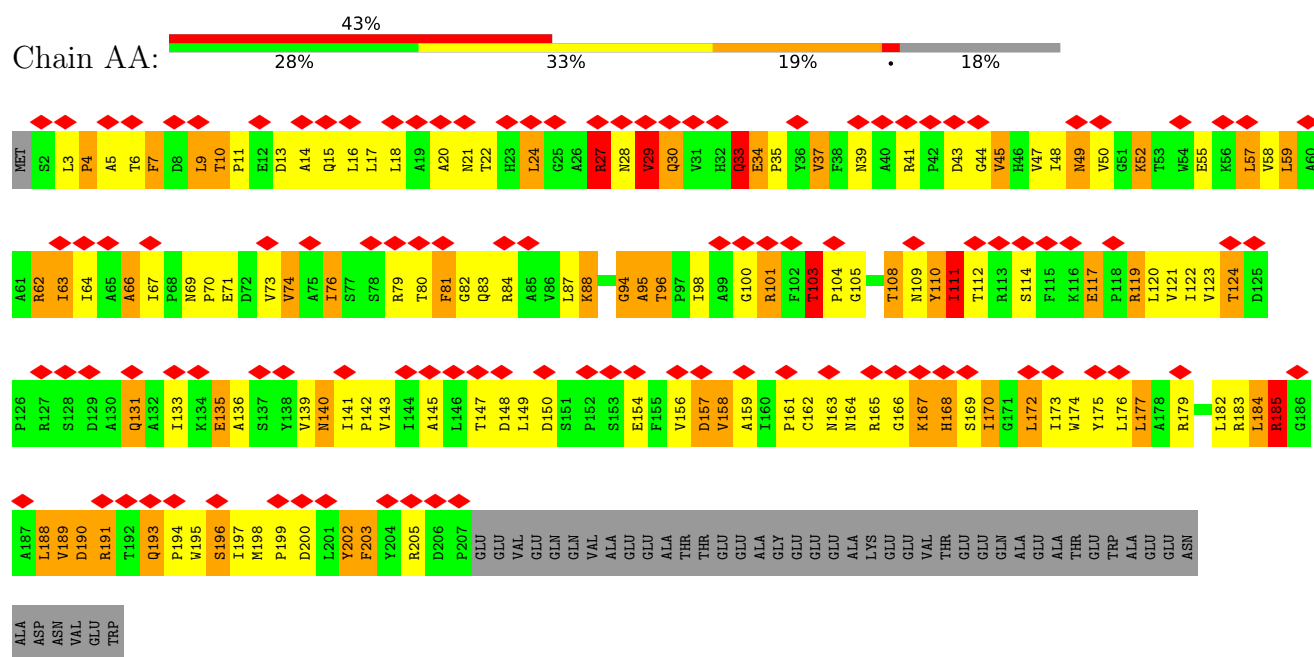
• Molecule 7: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-LIKE PROTEIN



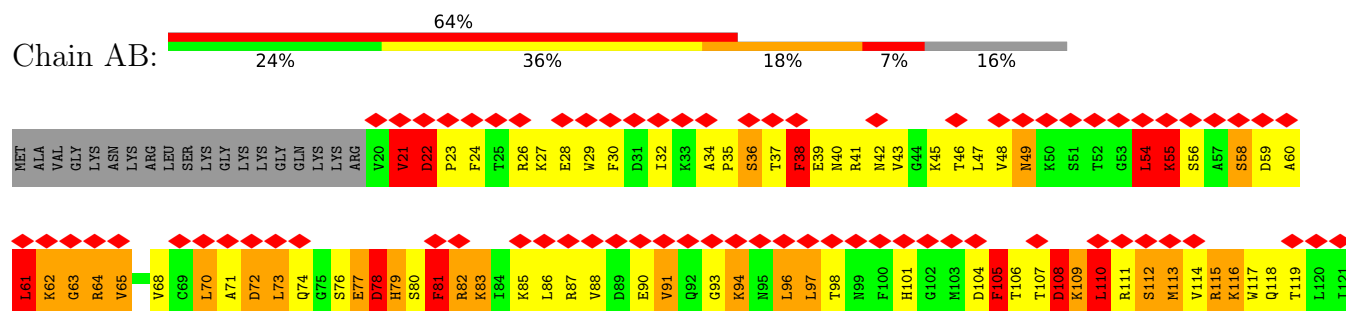
• Molecule 8: SUPPRESSOR PROTEIN STM1

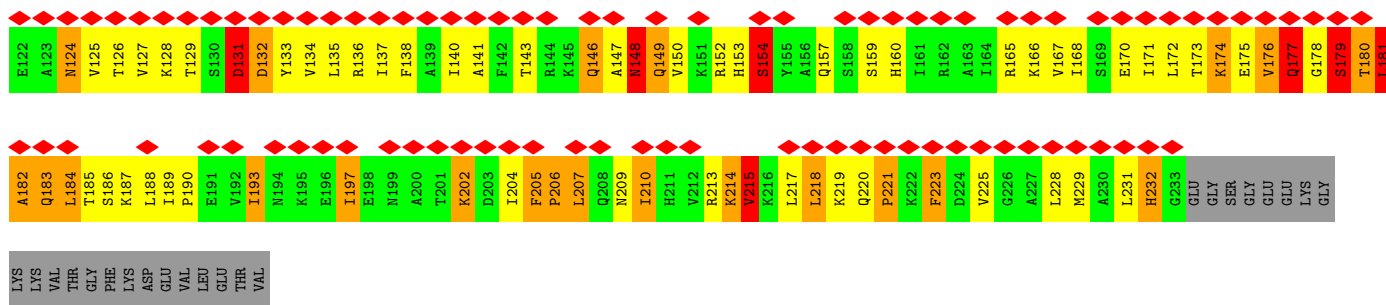


• Molecule 9: 40S RIBOSOMAL PROTEIN S0-A

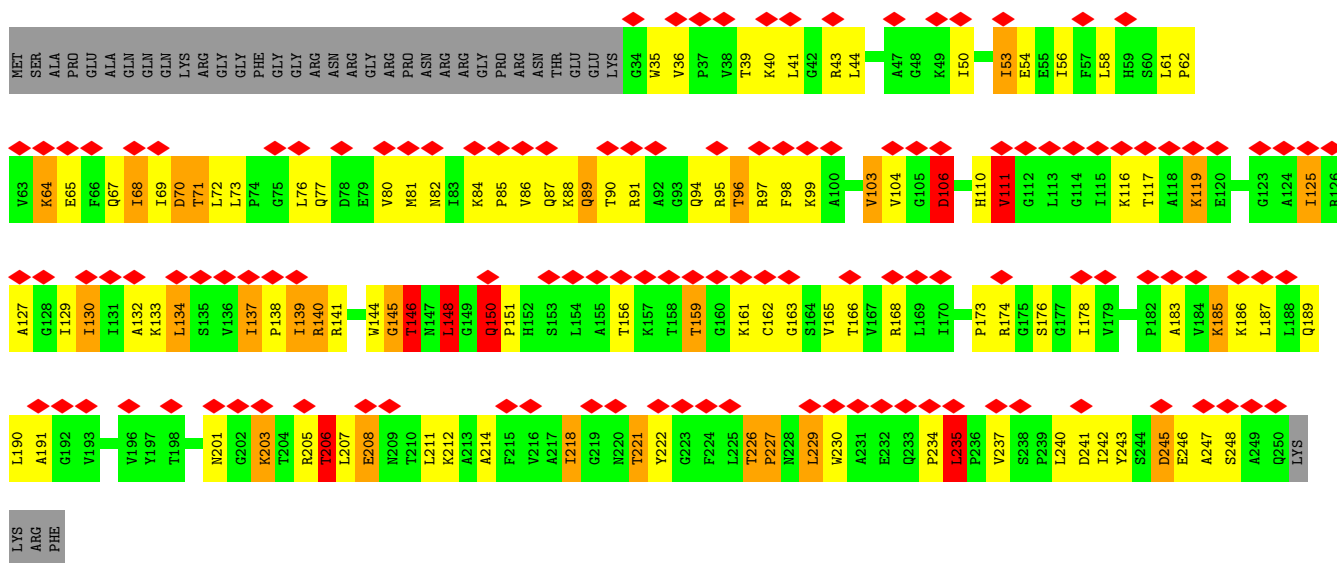


• Molecule 10: 40S RIBOSOMAL PROTEIN S1-A

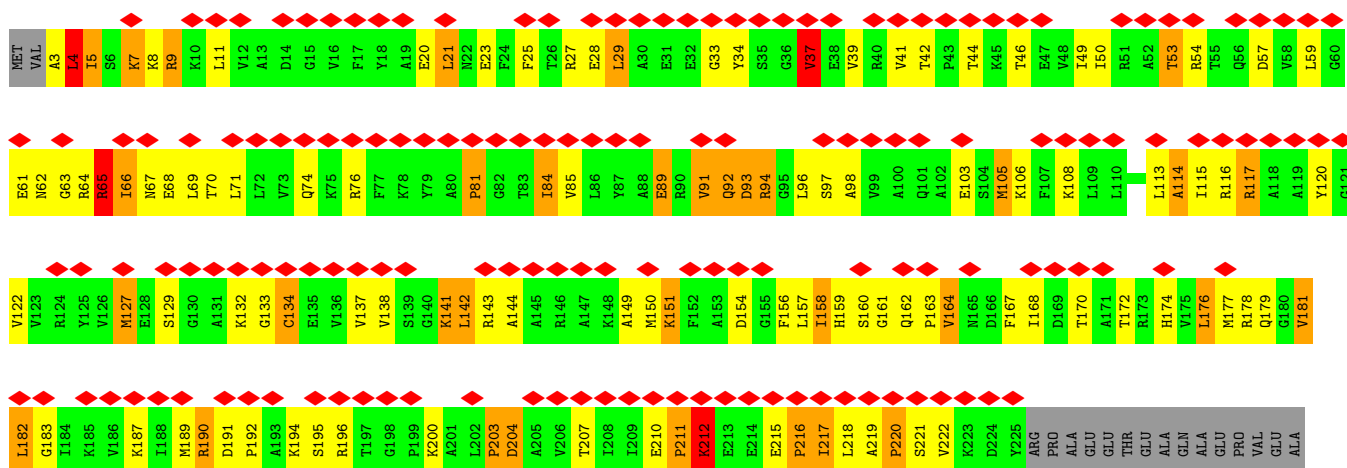




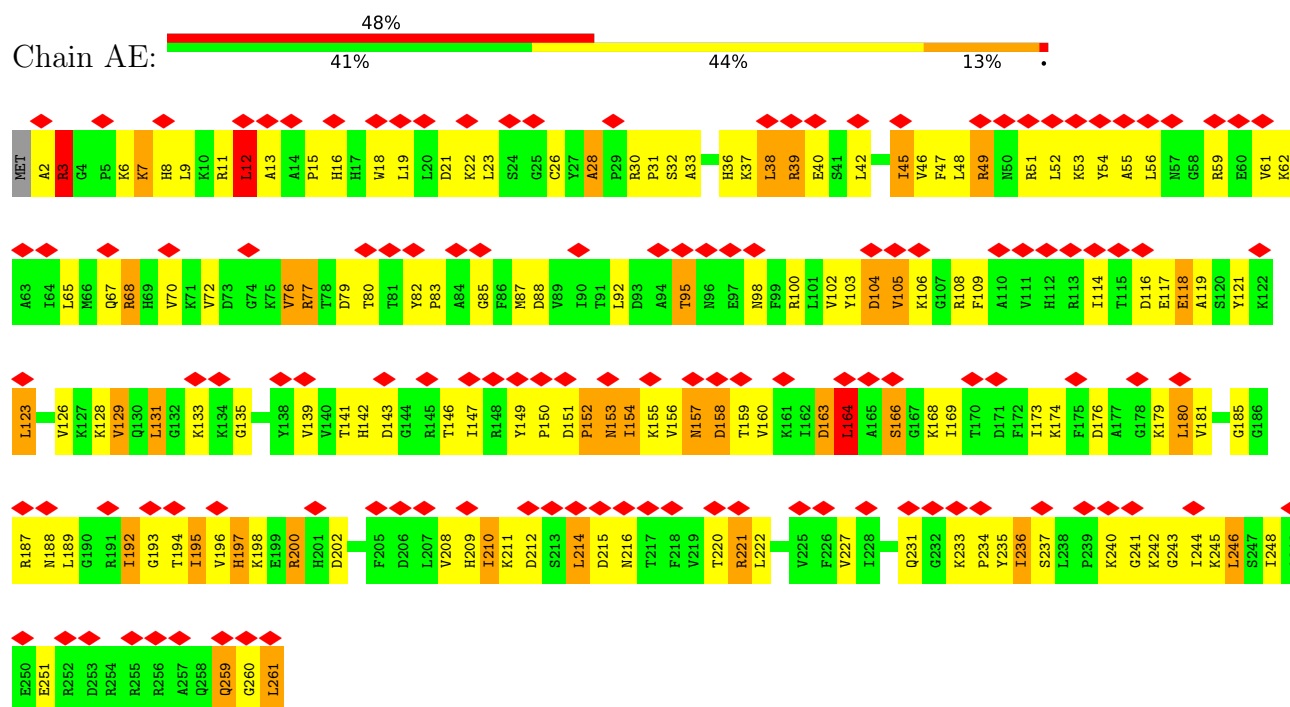
• Molecule 11: 40S RIBOSOMAL PROTEIN S2



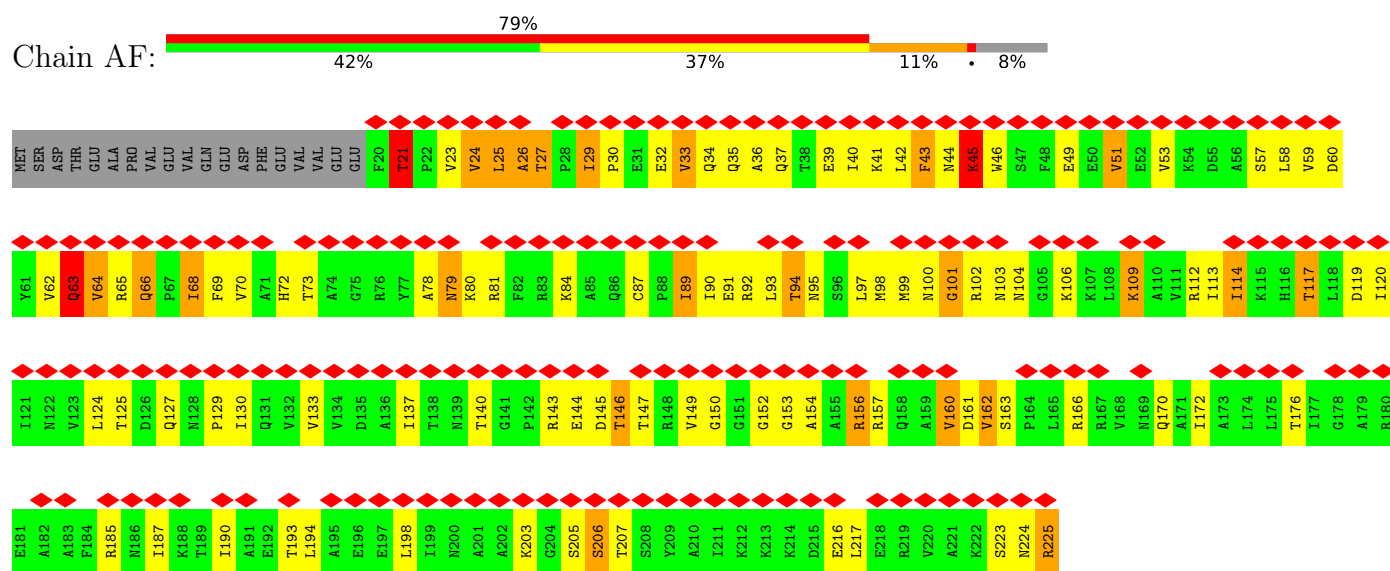
• Molecule 12: 40S RIBOSOMAL PROTEIN S3



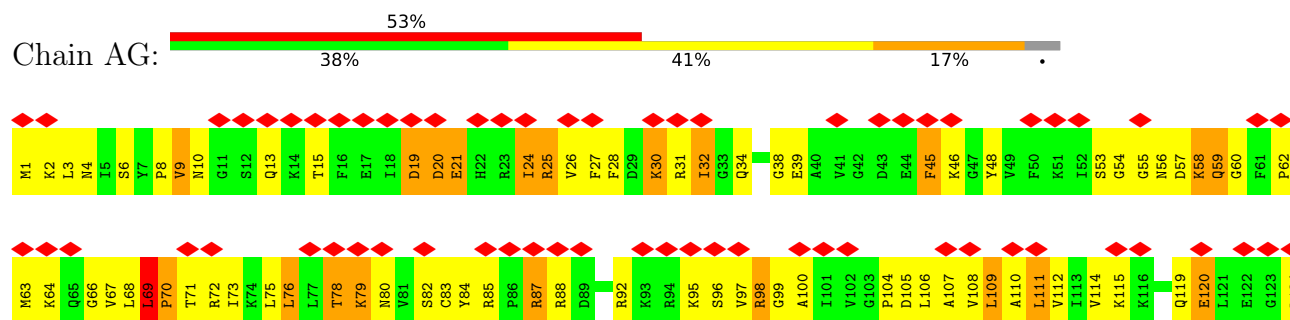
• Molecule 13: 40S RIBOSOMAL PROTEIN S4-A

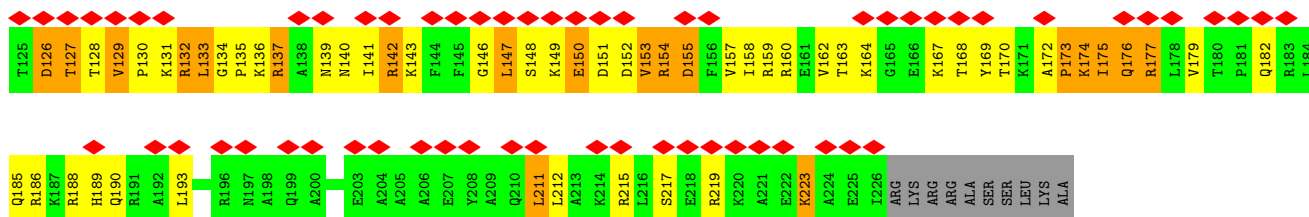


• Molecule 14: 40S RIBOSOMAL PROTEIN S5

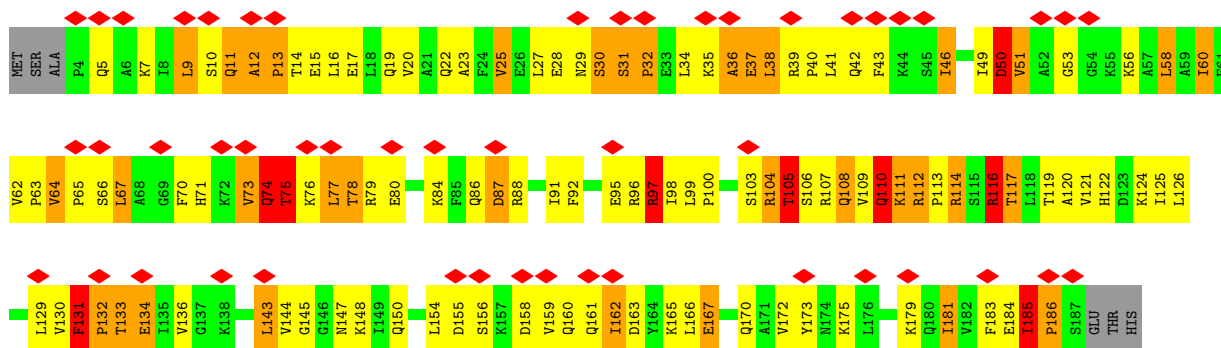


• Molecule 15: 40S RIBOSOMAL PROTEIN S6-A

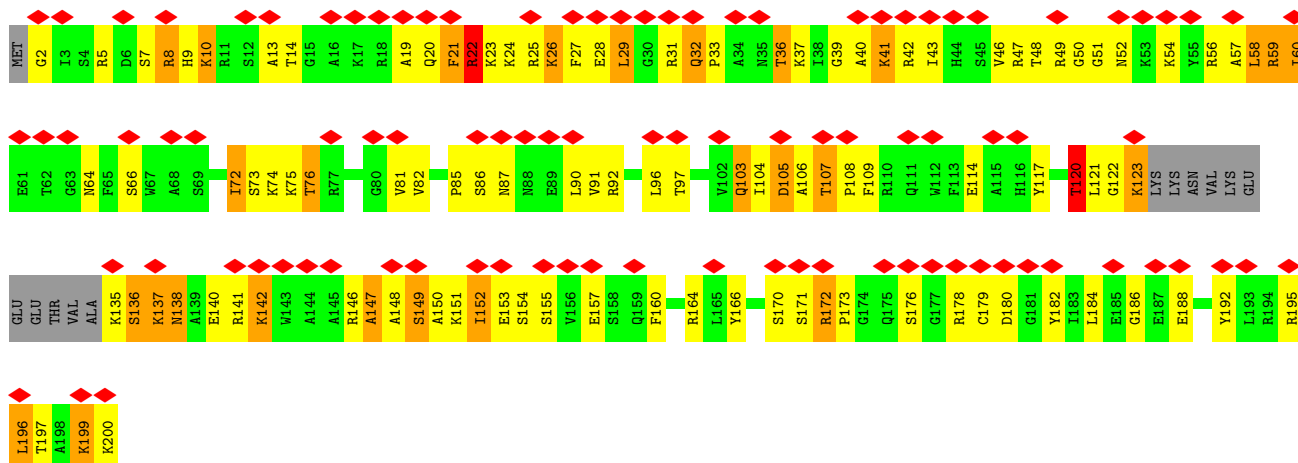




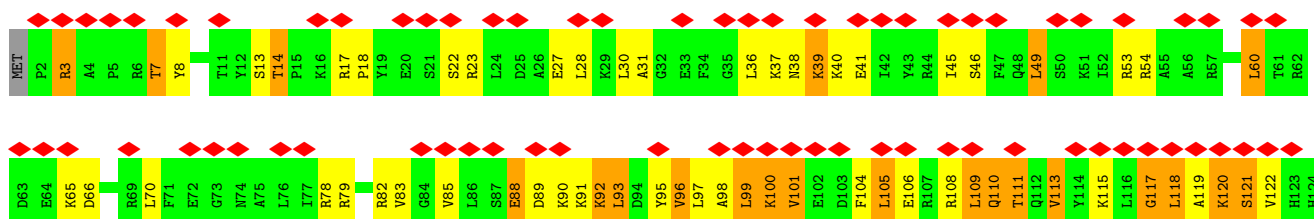
• Molecule 16: 40S RIBOSOMAL PROTEIN S7-A

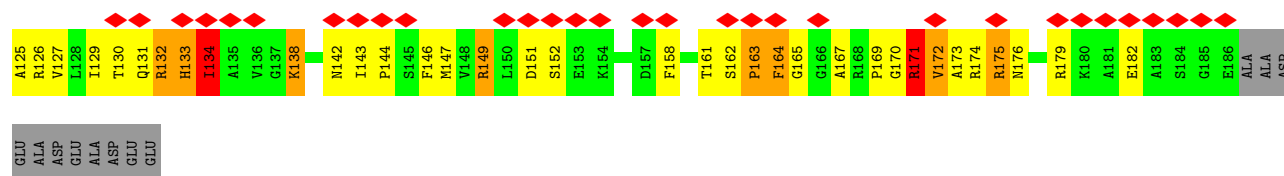


• Molecule 17: 40S RIBOSOMAL PROTEIN S8-A

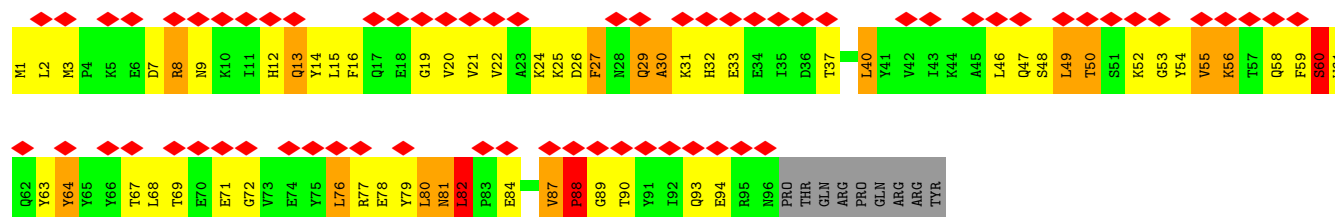


• Molecule 18: 40S RIBOSOMAL PROTEIN S9-A

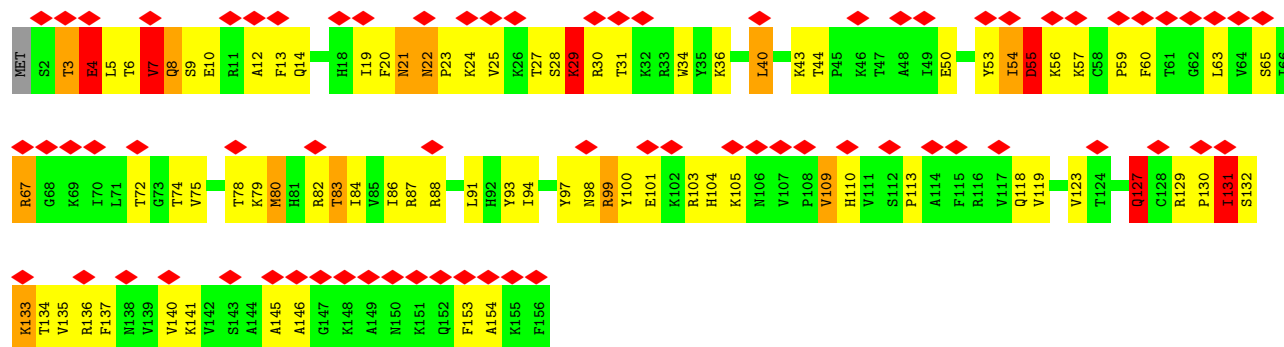




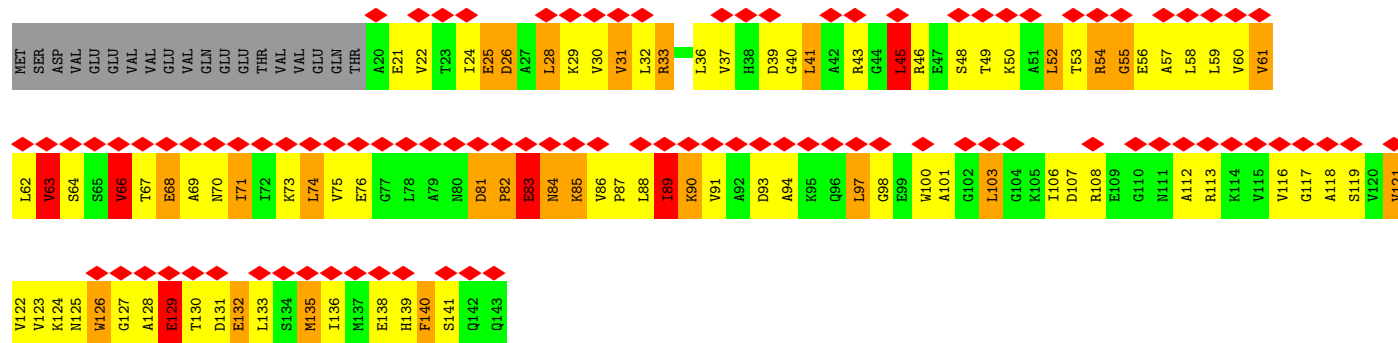
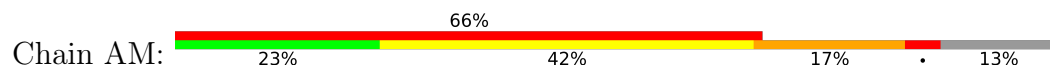
• Molecule 19: 40S RIBOSOMAL PROTEIN S10-A



• Molecule 20: 40S RIBOSOMAL PROTEIN S11-A

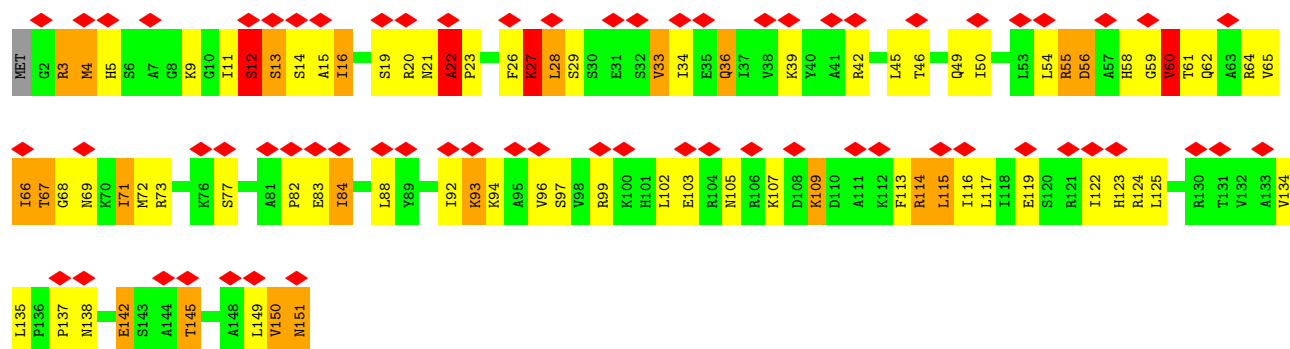


• Molecule 21: 40S RIBOSOMAL PROTEIN S12

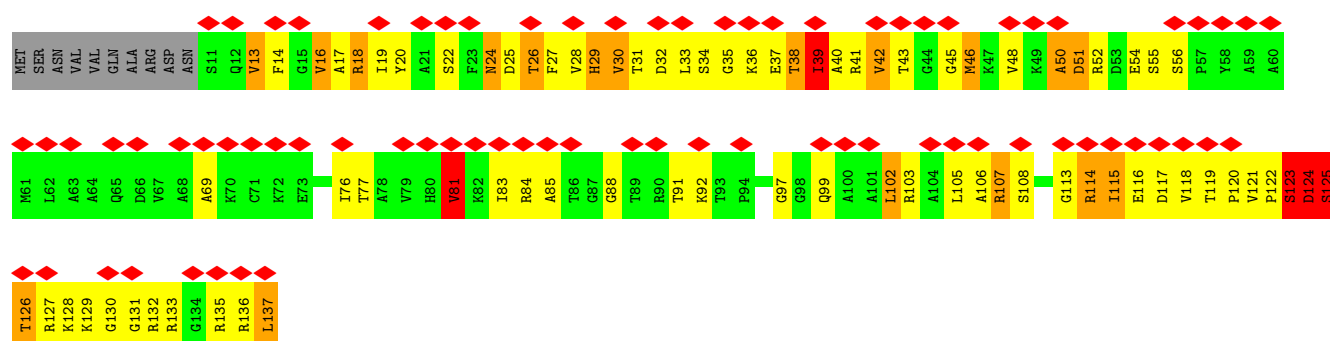


• Molecule 22: 40S RIBOSOMAL PROTEIN S13

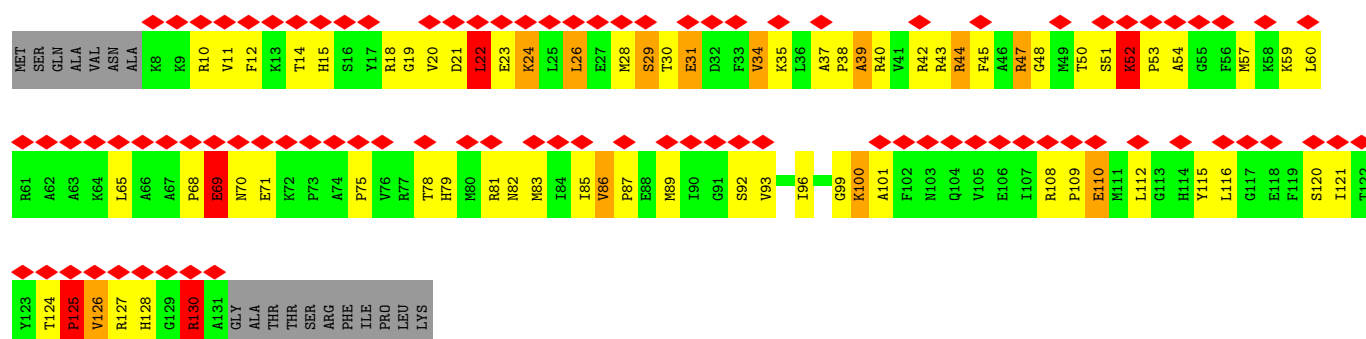




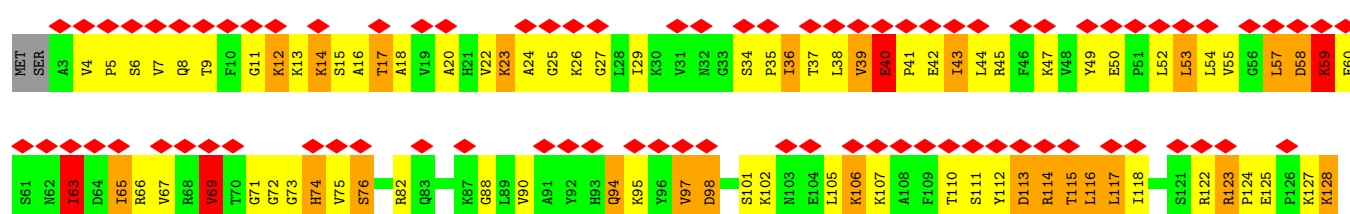
• Molecule 23: 40S RIBOSOMAL PROTEIN S14-A



• Molecule 24: 40S RIBOSOMAL PROTEIN S15

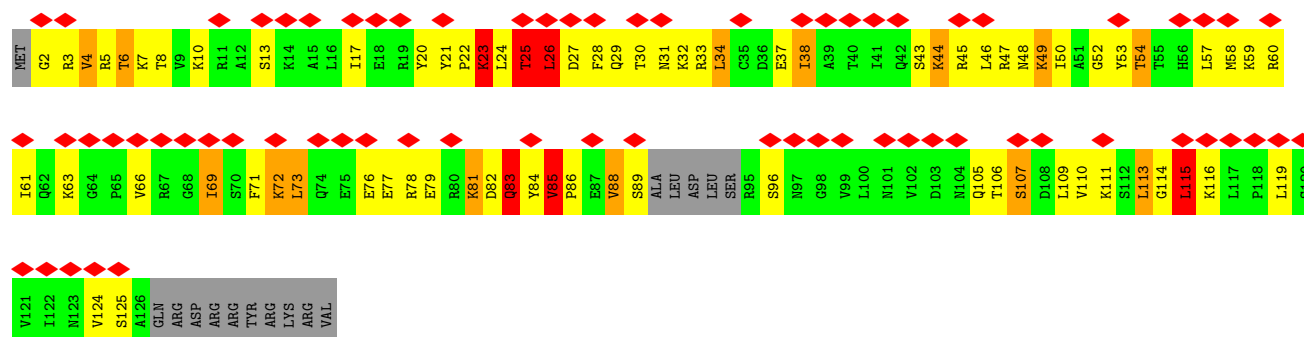


• Molecule 25: 40S RIBOSOMAL PROTEIN S16-A

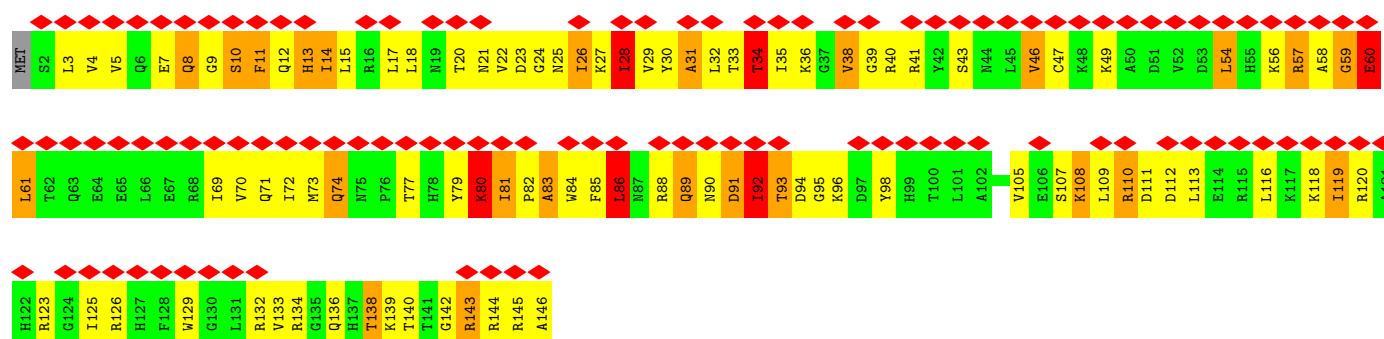
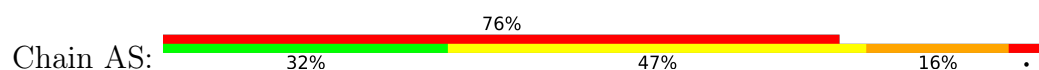




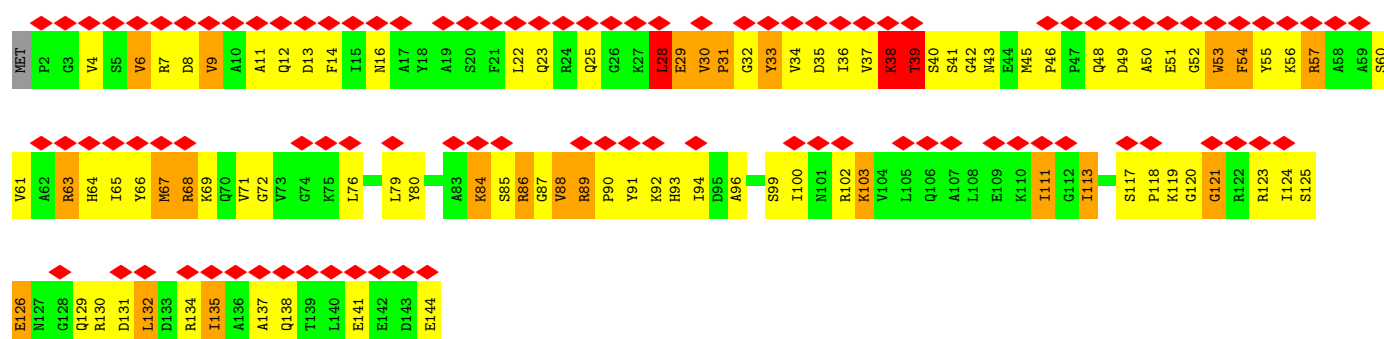
• Molecule 26: 40S RIBOSOMAL PROTEIN S17-A



• Molecule 27: 40S RIBOSOMAL PROTEIN S18-A

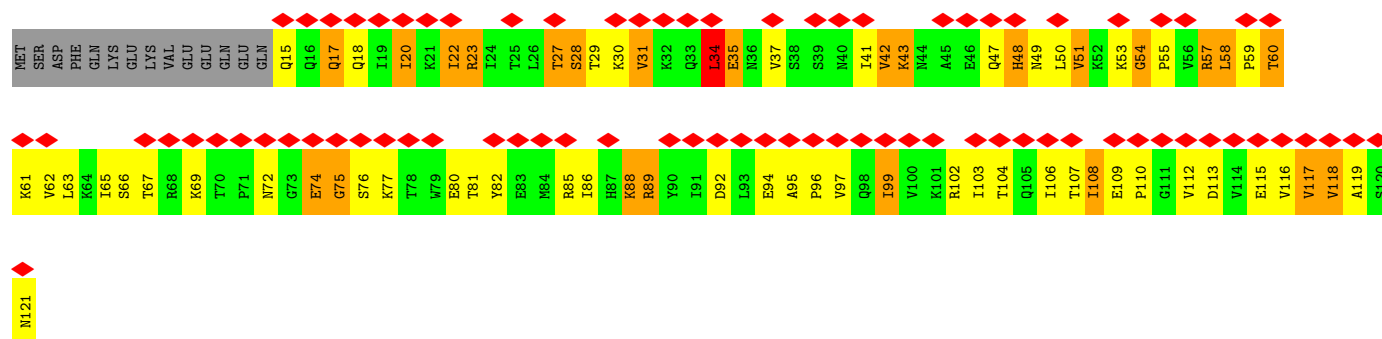


• Molecule 28: 40S RIBOSOMAL PROTEIN S19-A

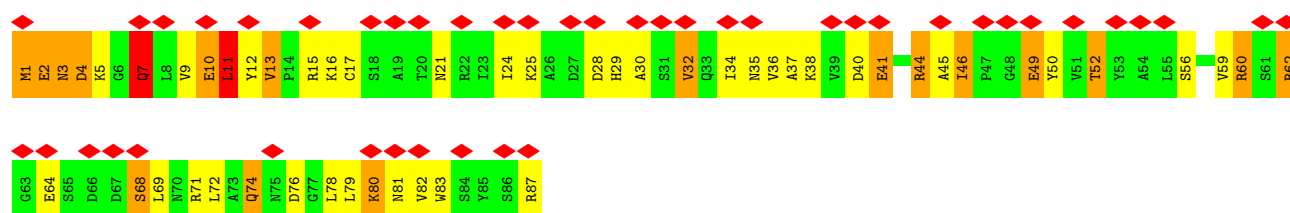


• Molecule 29: 40S RIBOSOMAL PROTEIN S20

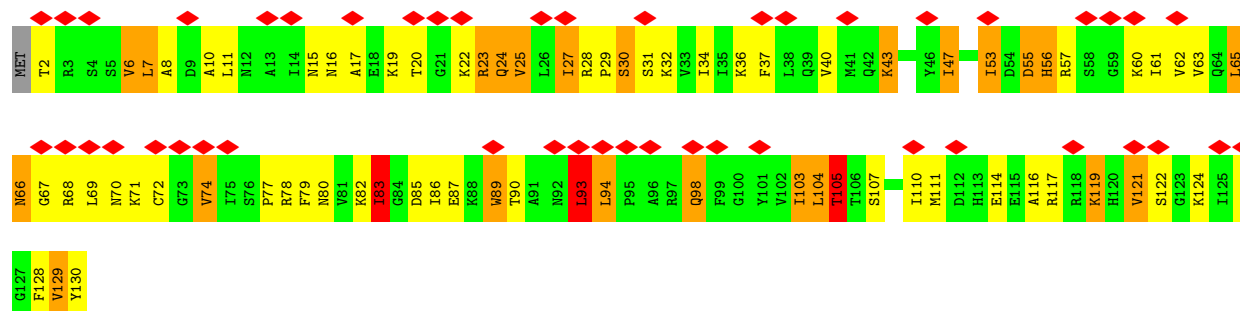




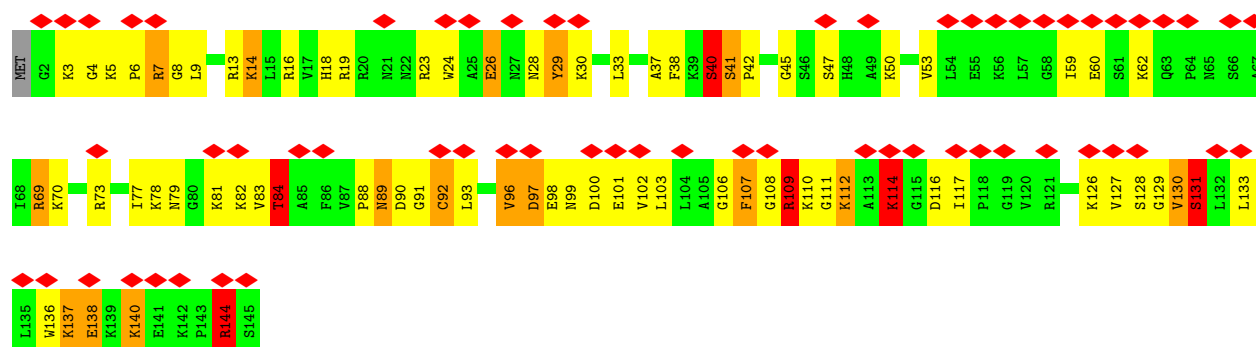
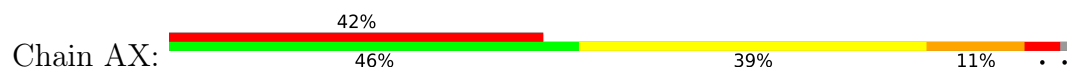
• Molecule 30: 40S RIBOSOMAL PROTEIN S21-A



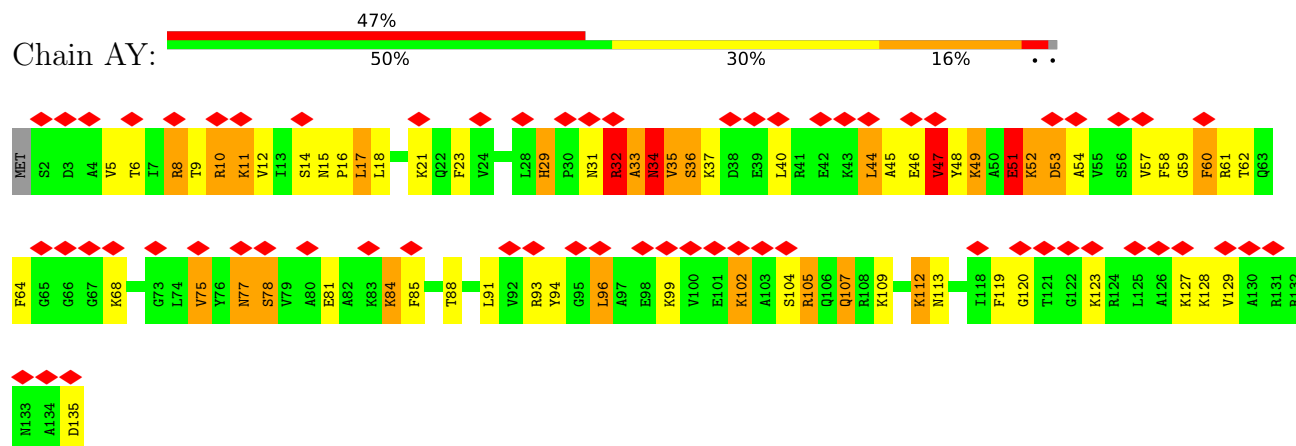
• Molecule 31: 40S RIBOSOMAL PROTEIN S22-A



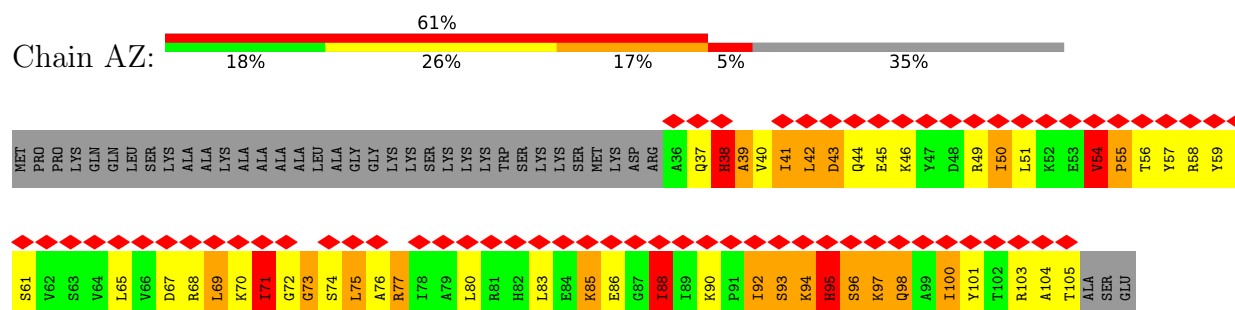
• Molecule 32: 40S RIBOSOMAL PROTEIN S23-A



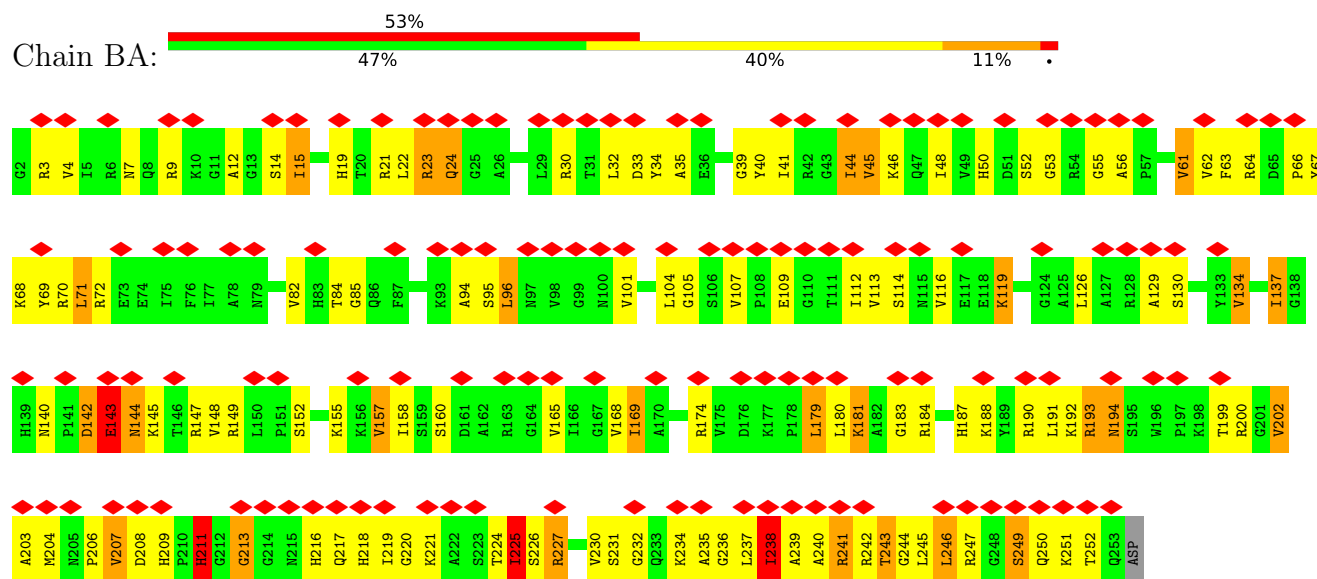
- Molecule 33: 40S RIBOSOMAL PROTEIN S24-A



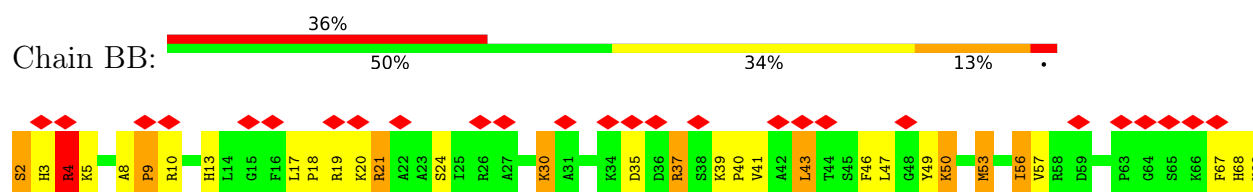
- Molecule 34: 40S RIBOSOMAL PROTEIN S25-A

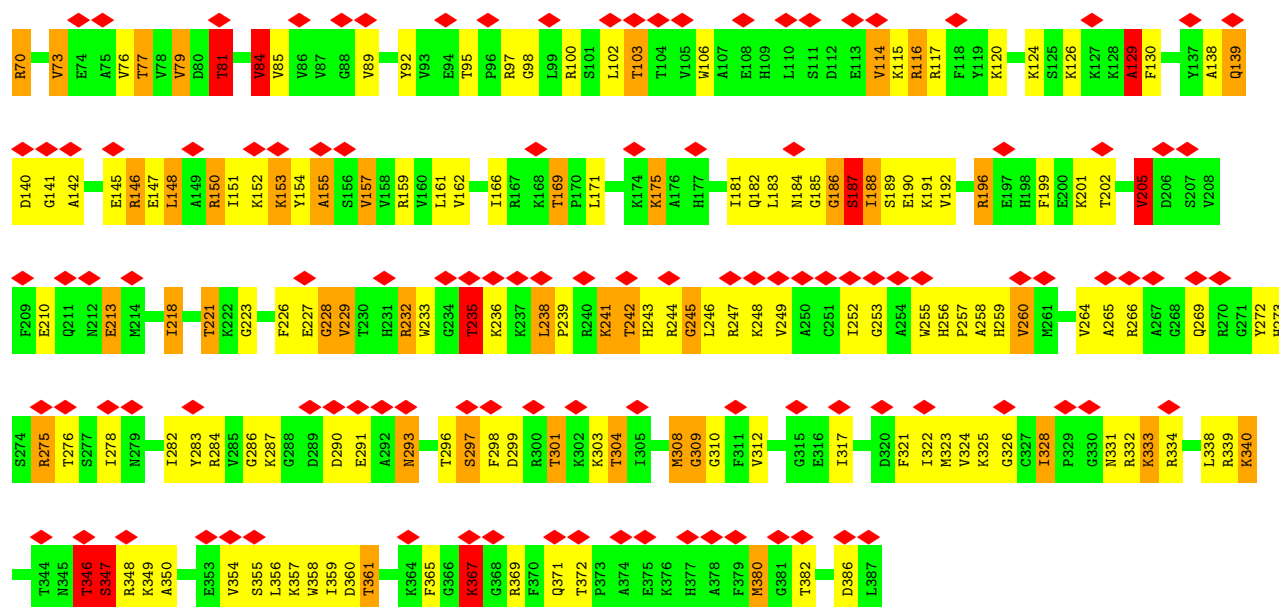


- Molecule 35: 60S RIBOSOMAL PROTEIN L2-B

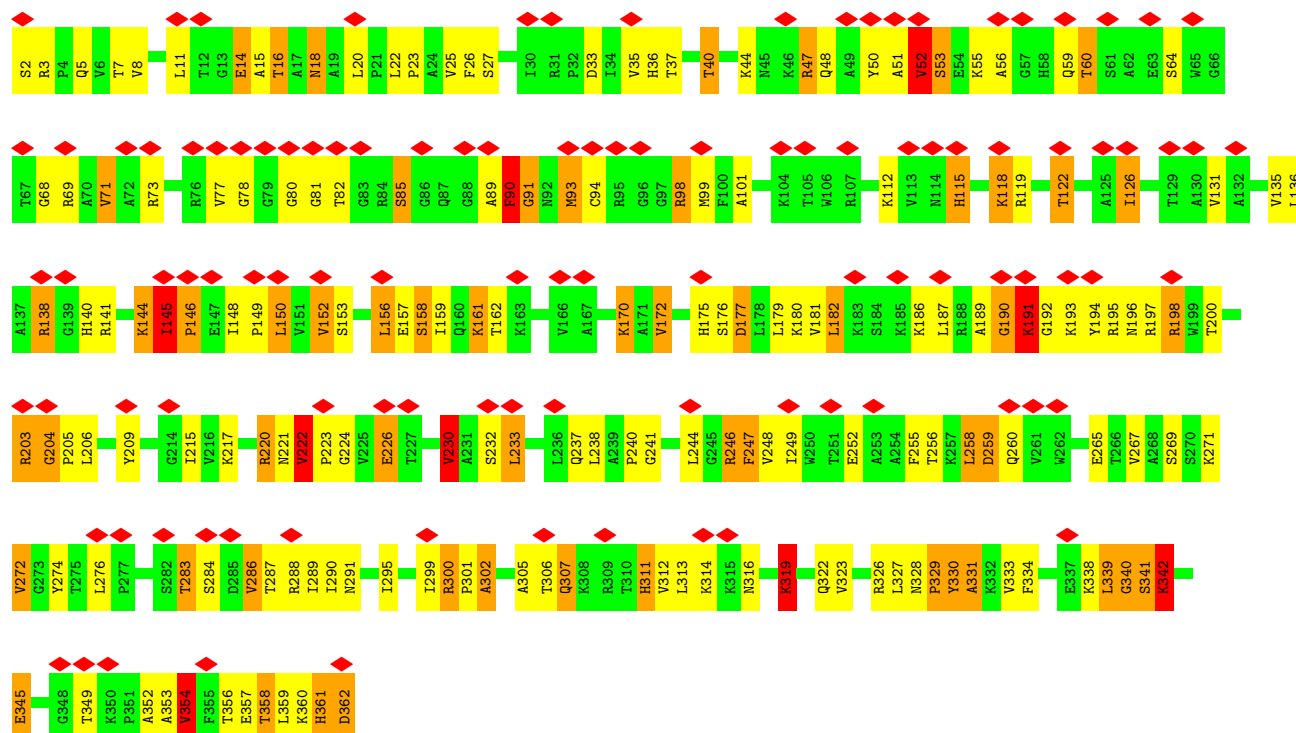


- Molecule 36: 60S RIBOSOMAL PROTEIN L3

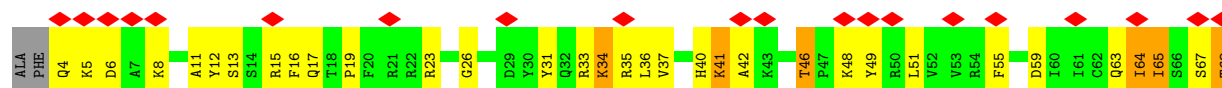


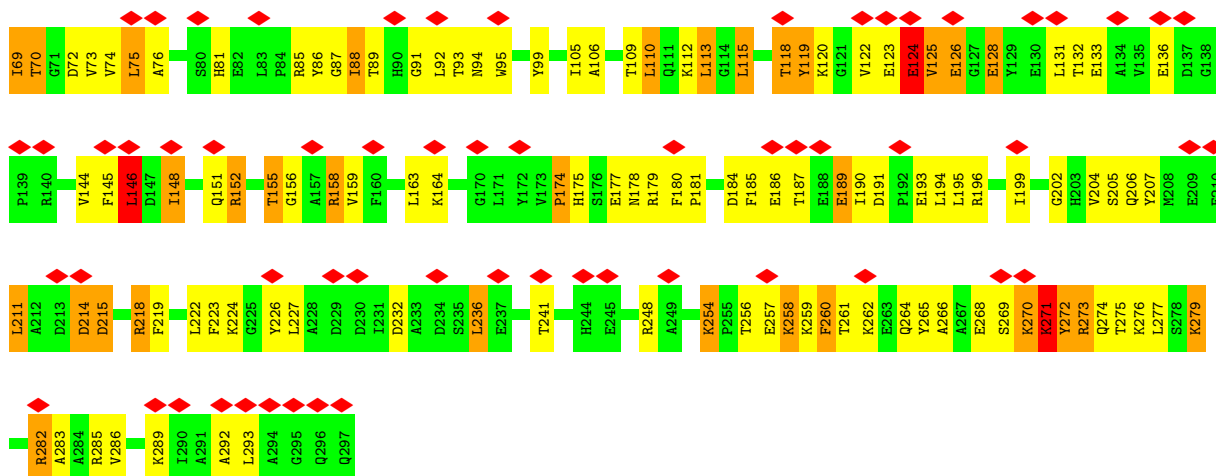


• Molecule 37: 60S RIBOSOMAL PROTEIN L4-A

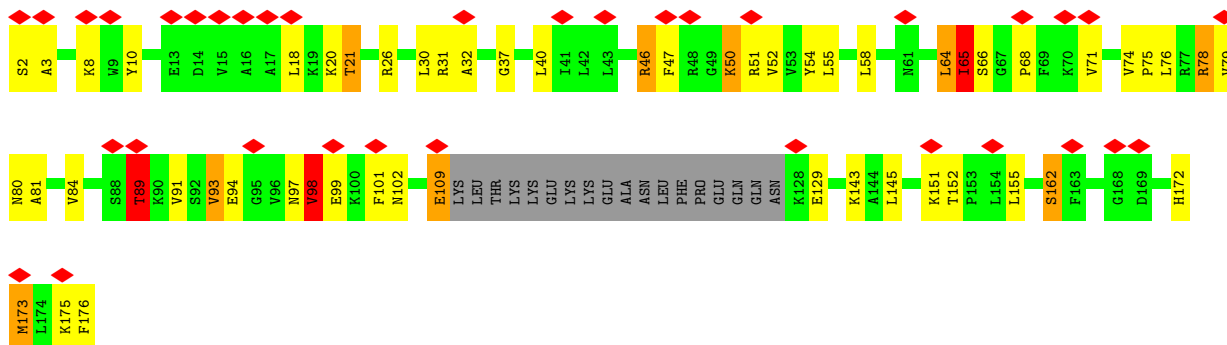


• Molecule 38: 60S RIBOSOMAL PROTEIN L5

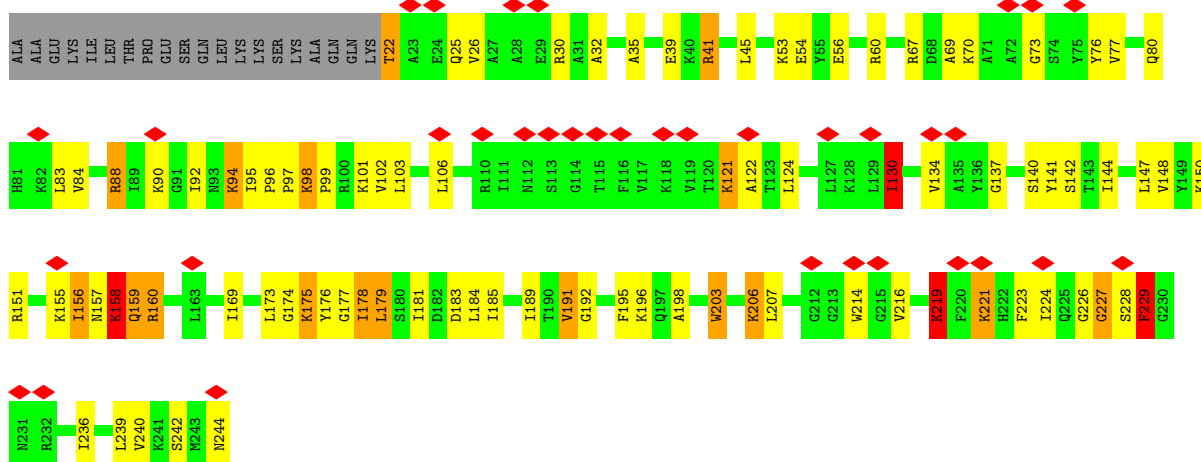




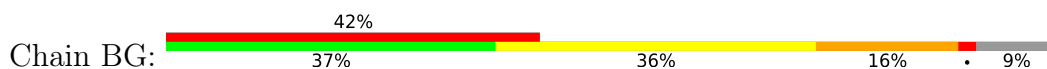
• Molecule 39: 60S RIBOSOMAL PROTEIN L6-A

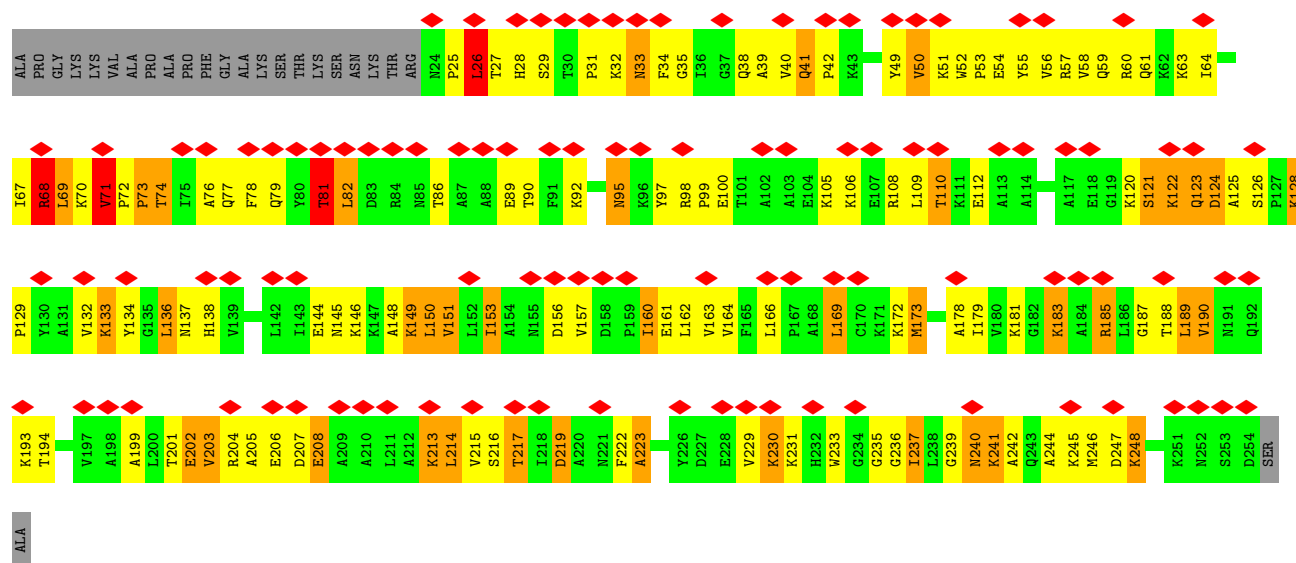


• Molecule 40: 60S RIBOSOMAL PROTEIN L7-A

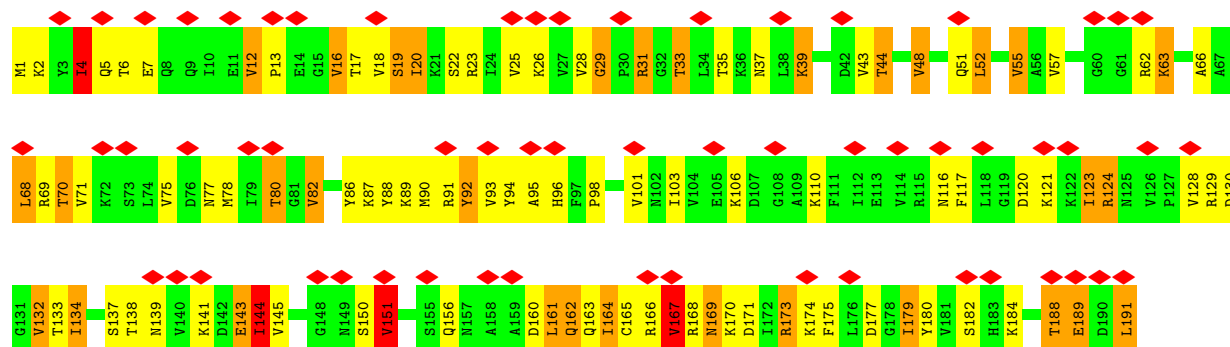


• Molecule 41: 60S RIBOSOMAL PROTEIN L8-A

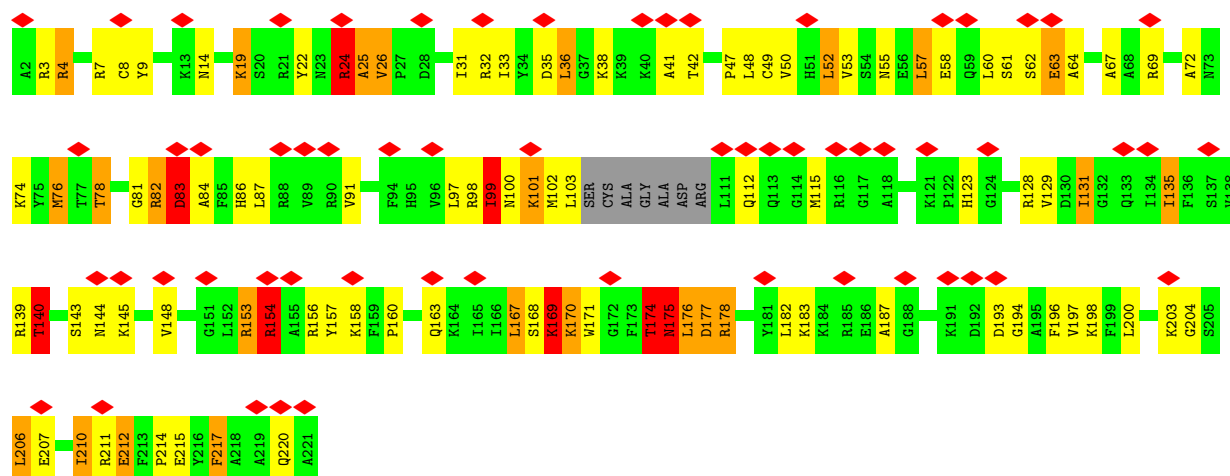




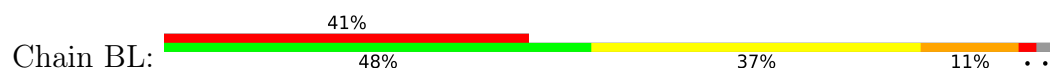
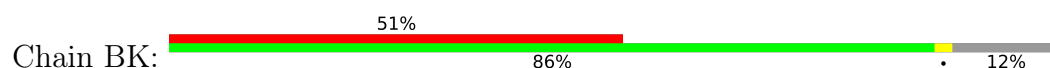
• Molecule 42: 60S RIBOSOMAL PROTEIN L9-A

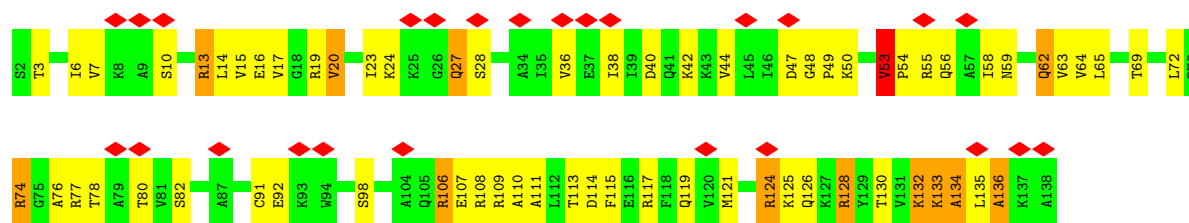


• Molecule 43: 60S RIBOSOMAL PROTEIN L10



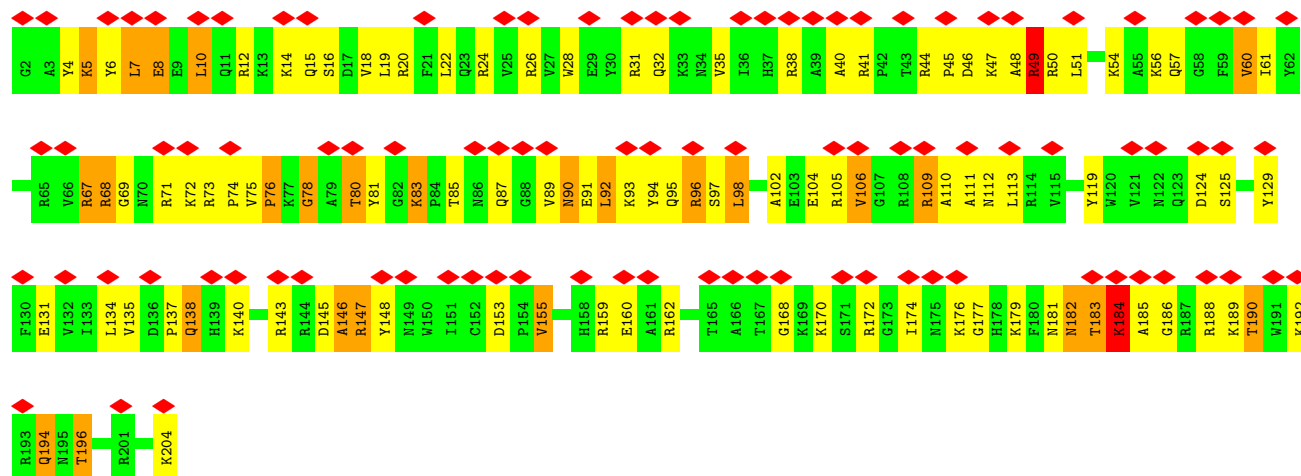
Chain BJ:





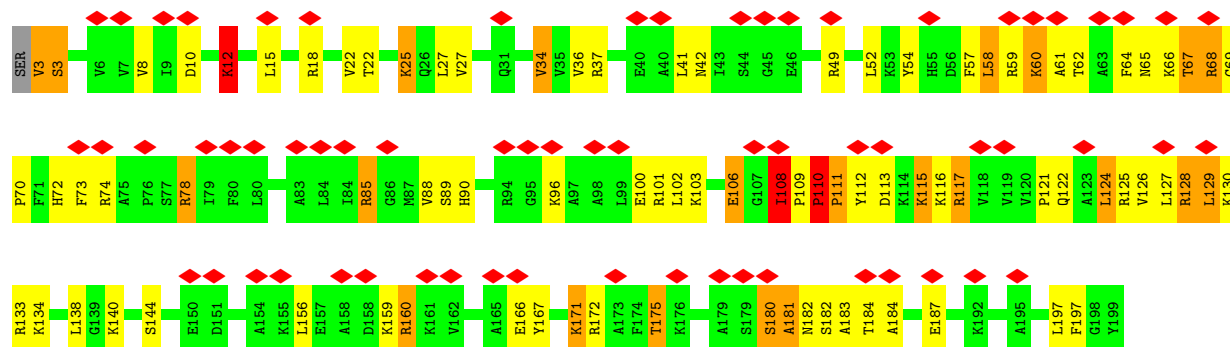
• Molecule 48: 60S RIBOSOMAL PROTEIN L15-A

Chain BN: .



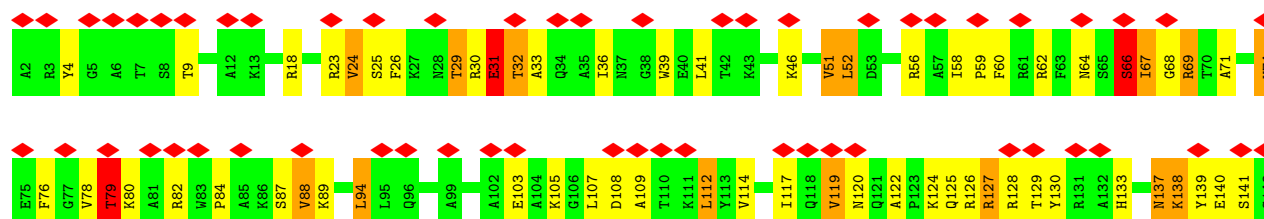
• Molecule 49: 60S RIBOSOMAL PROTEIN L16-A

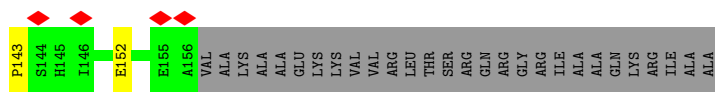
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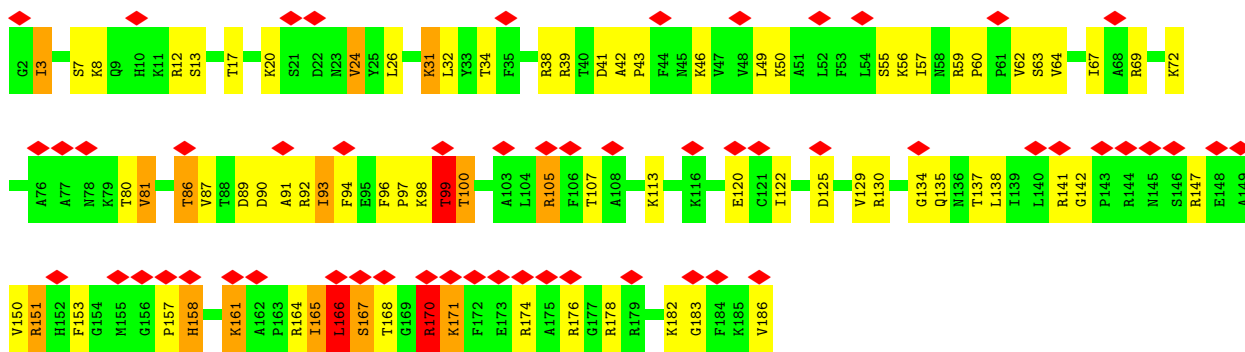
• Molecule 50: 60S RIBOSOMAL PROTEIN L17-A

Chain BP: .

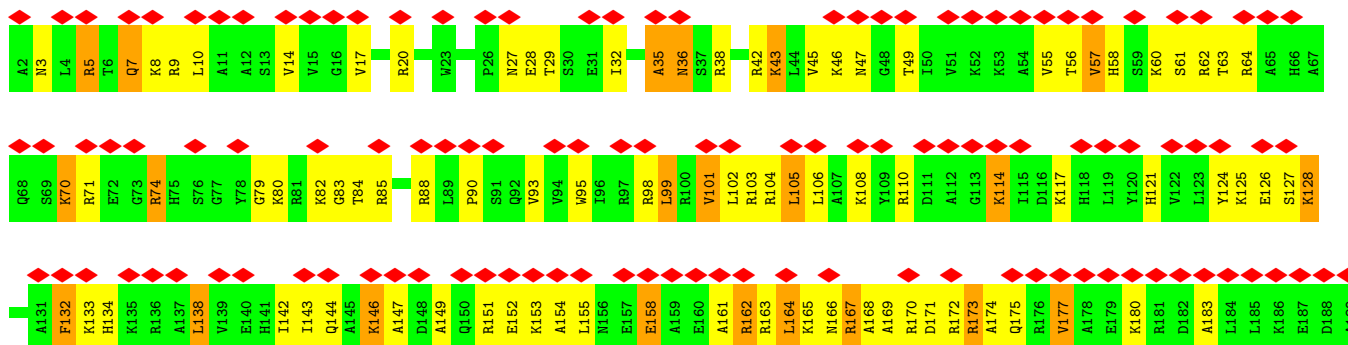




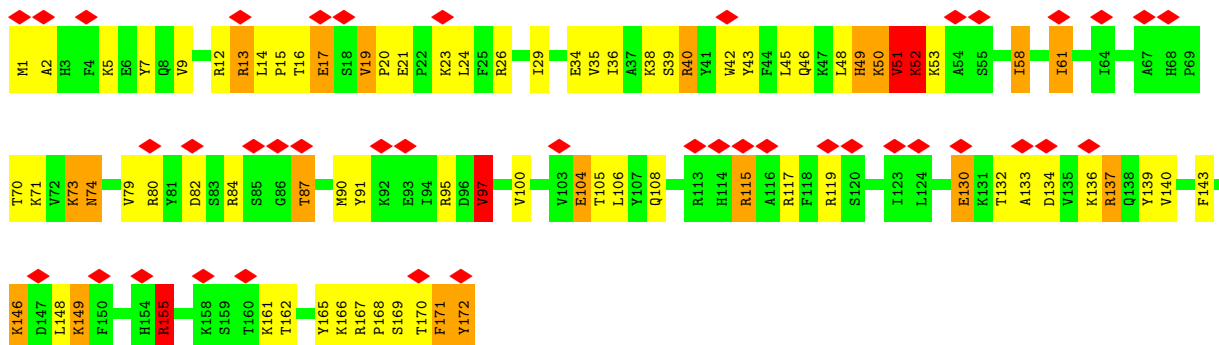
• Molecule 51: 60S RIBOSOMAL PROTEIN L18-A



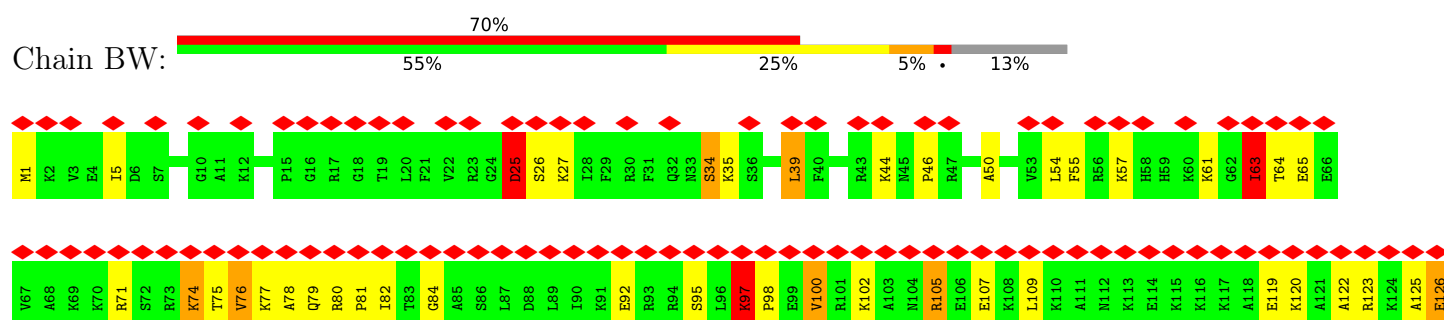
• Molecule 52: 60S RIBOSOMAL PROTEIN L19-B

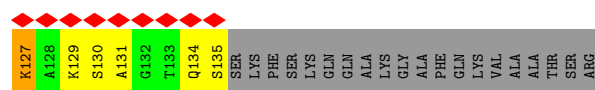


• Molecule 53: 60S RIBOSOMAL PROTEIN L20-B

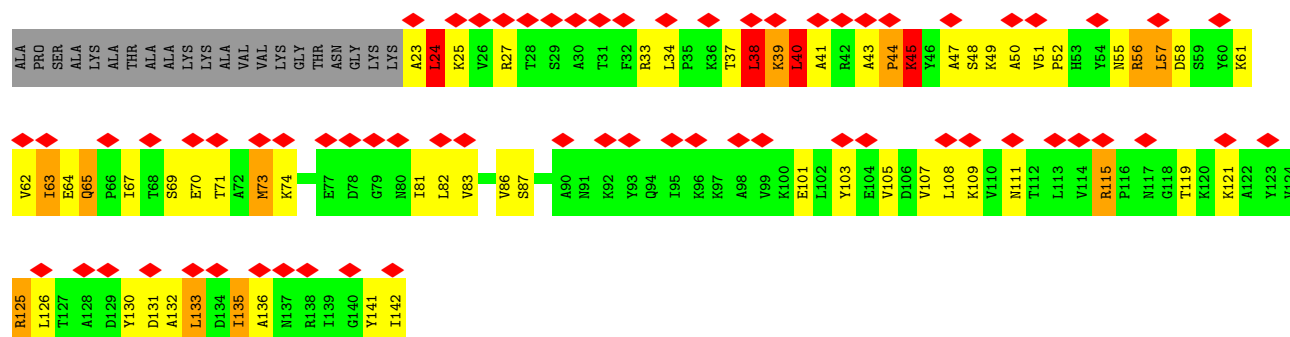


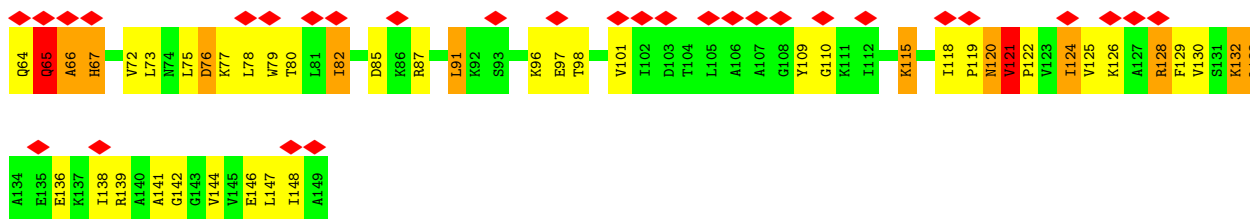
• Molecule 54: 60S RIBOSOMAL PROTEIN L21-A



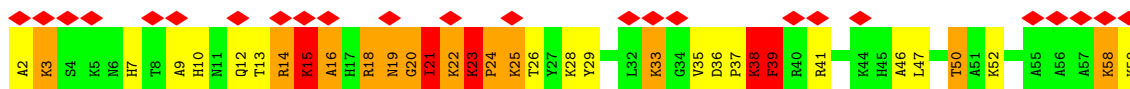


• Molecule 58: 60S RIBOSOMAL PROTEIN L25

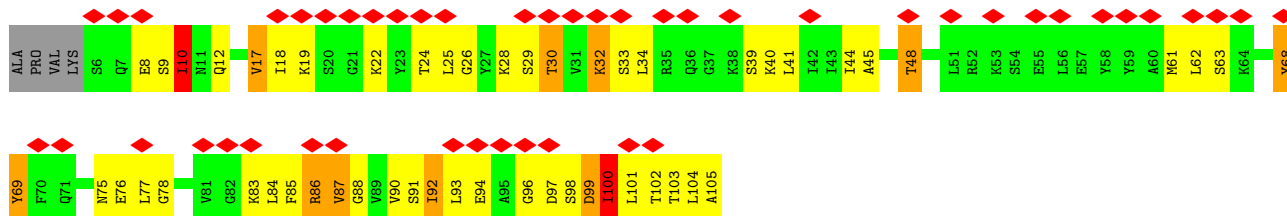




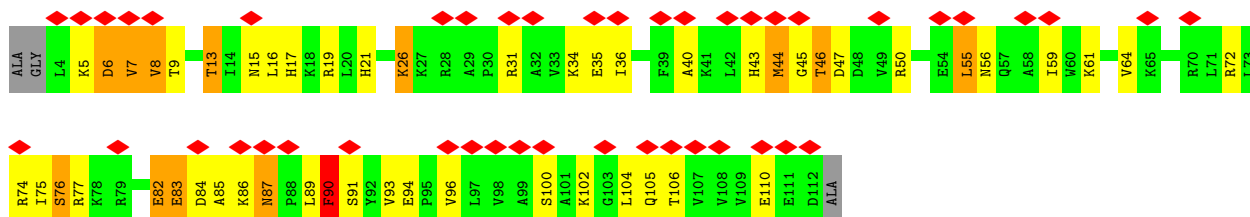
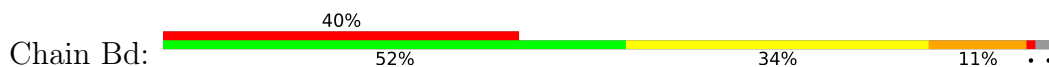
• Molecule 62: 60S RIBOSOMAL PROTEIN L29



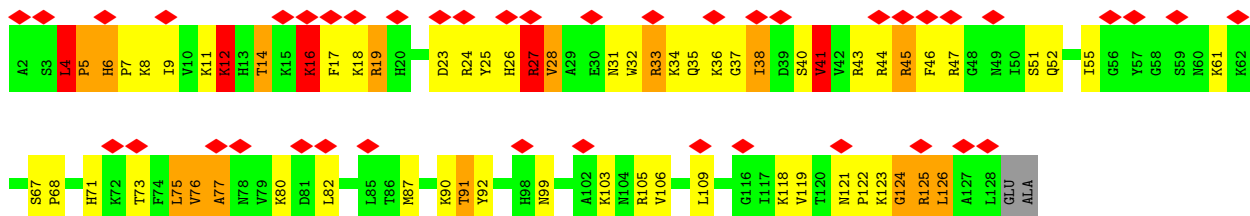
• Molecule 63: 60S RIBOSOMAL PROTEIN L30



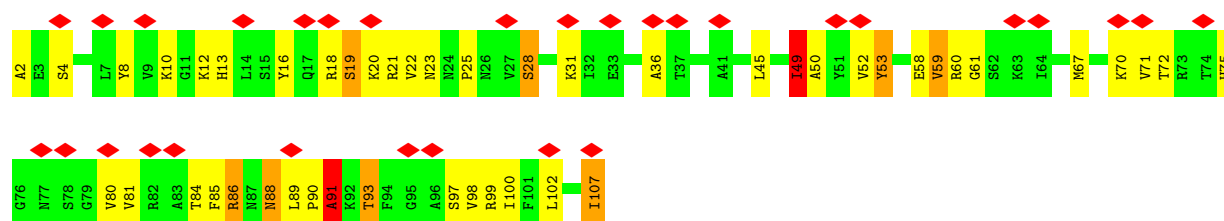
• Molecule 64: 60S RIBOSOMAL PROTEIN L31-A



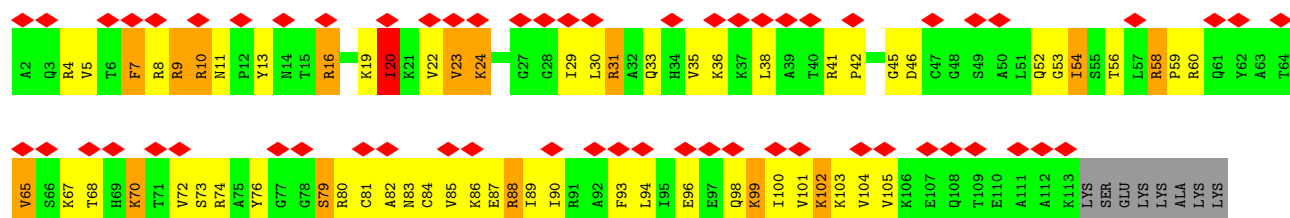
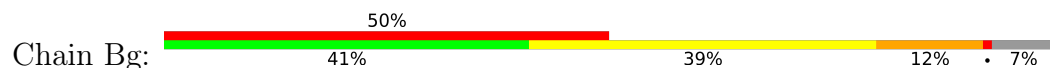
• Molecule 65: 60S RIBOSOMAL PROTEIN L32



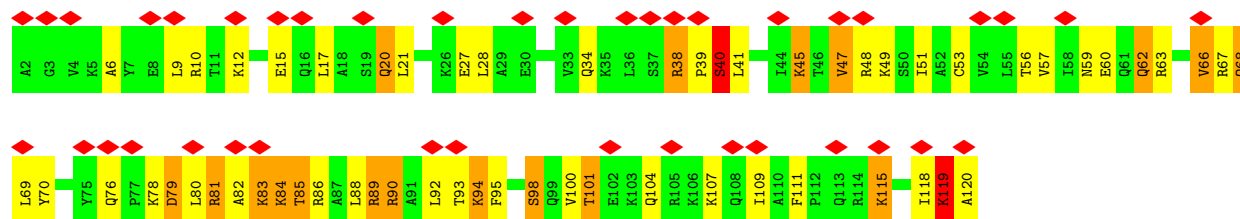
• Molecule 66: 60S RIBOSOMAL PROTEIN L33-A



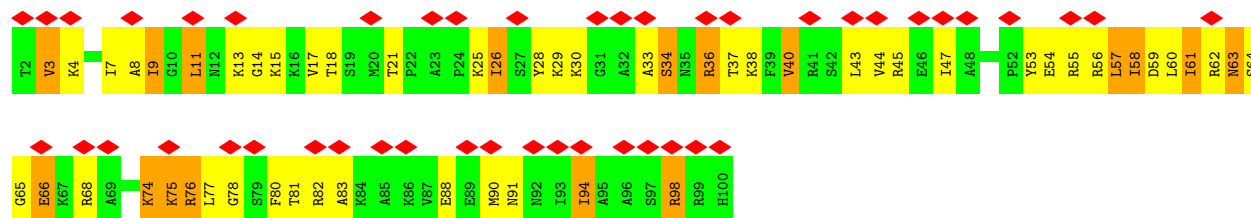
• Molecule 67: 60S RIBOSOMAL PROTEIN L34-A



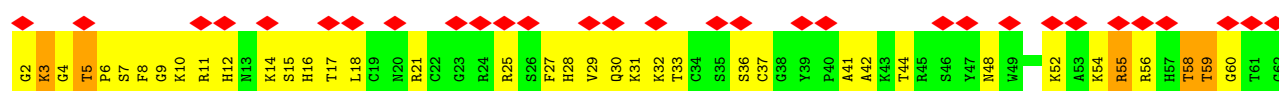
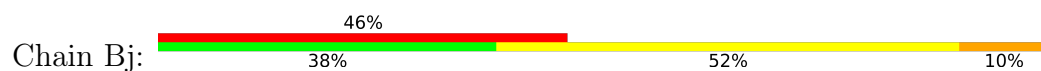
• Molecule 68: 60S RIBOSOMAL PROTEIN L35-B

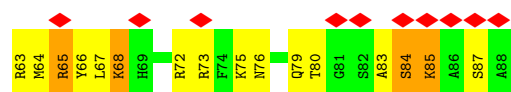


• Molecule 69: 60S RIBOSOMAL PROTEIN L36-A

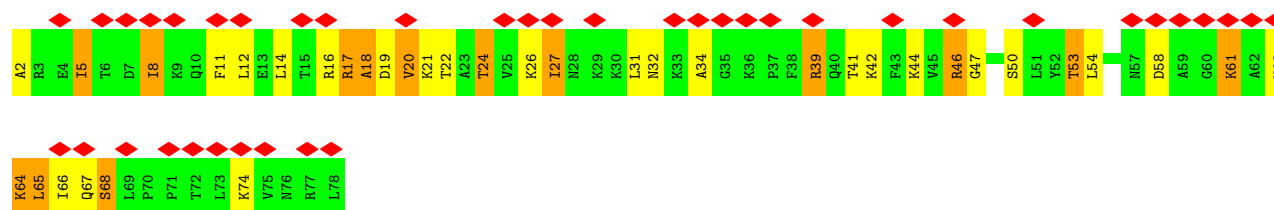


• Molecule 70: 60S RIBOSOMAL PROTEIN L37-A





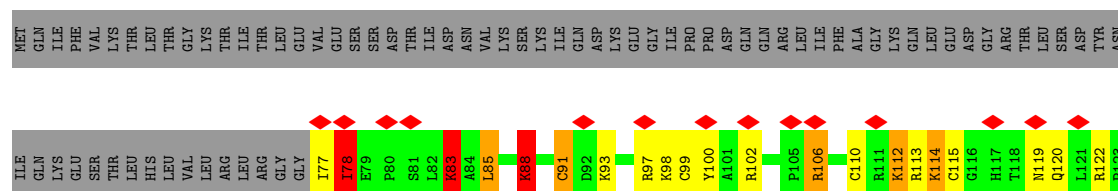
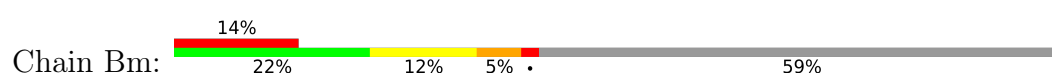
• Molecule 71: 60S RIBOSOMAL PROTEIN L38



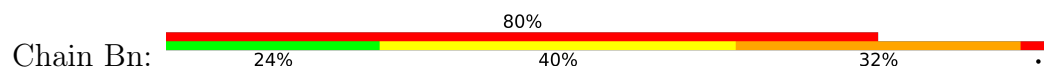
• Molecule 72: 60S RIBOSOMAL PROTEIN L39



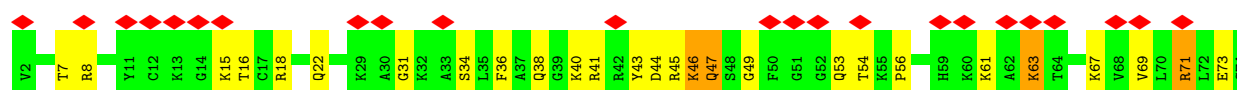
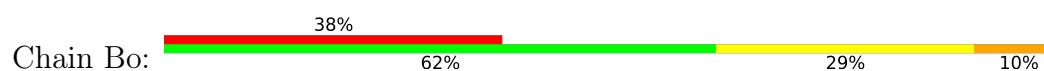
• Molecule 73: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

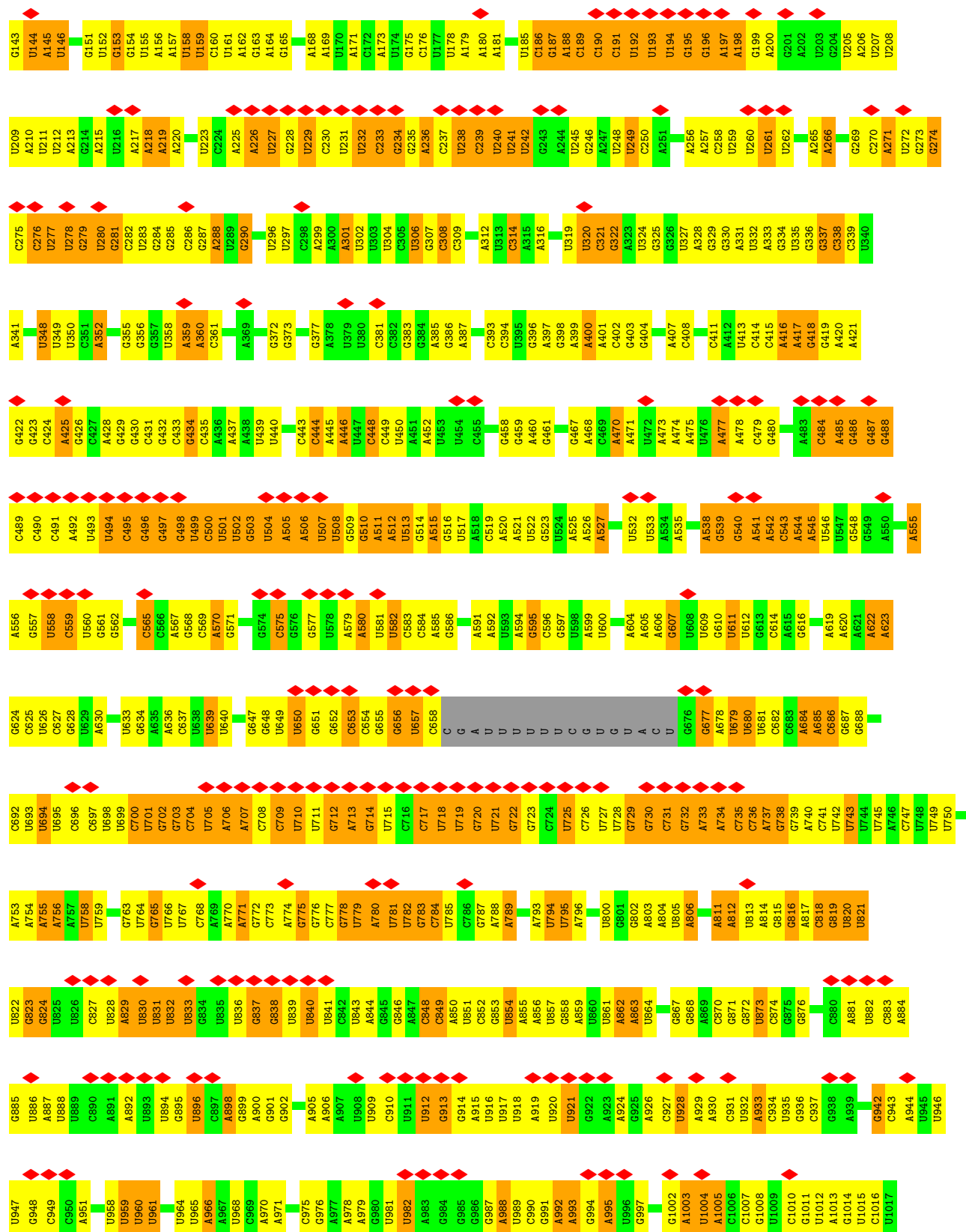


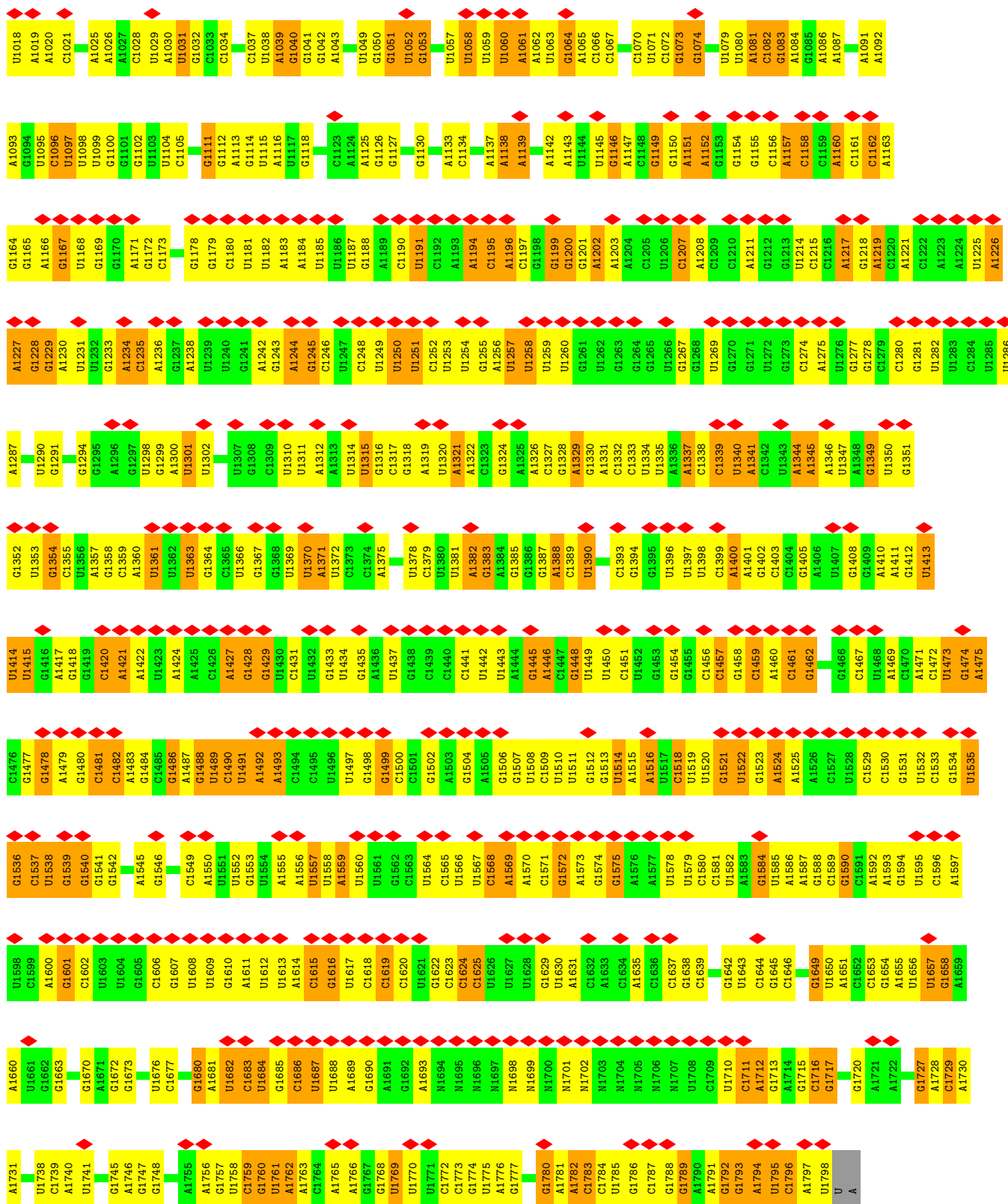
• Molecule 74: 60S RIBOSOMAL PROTEIN L41-B

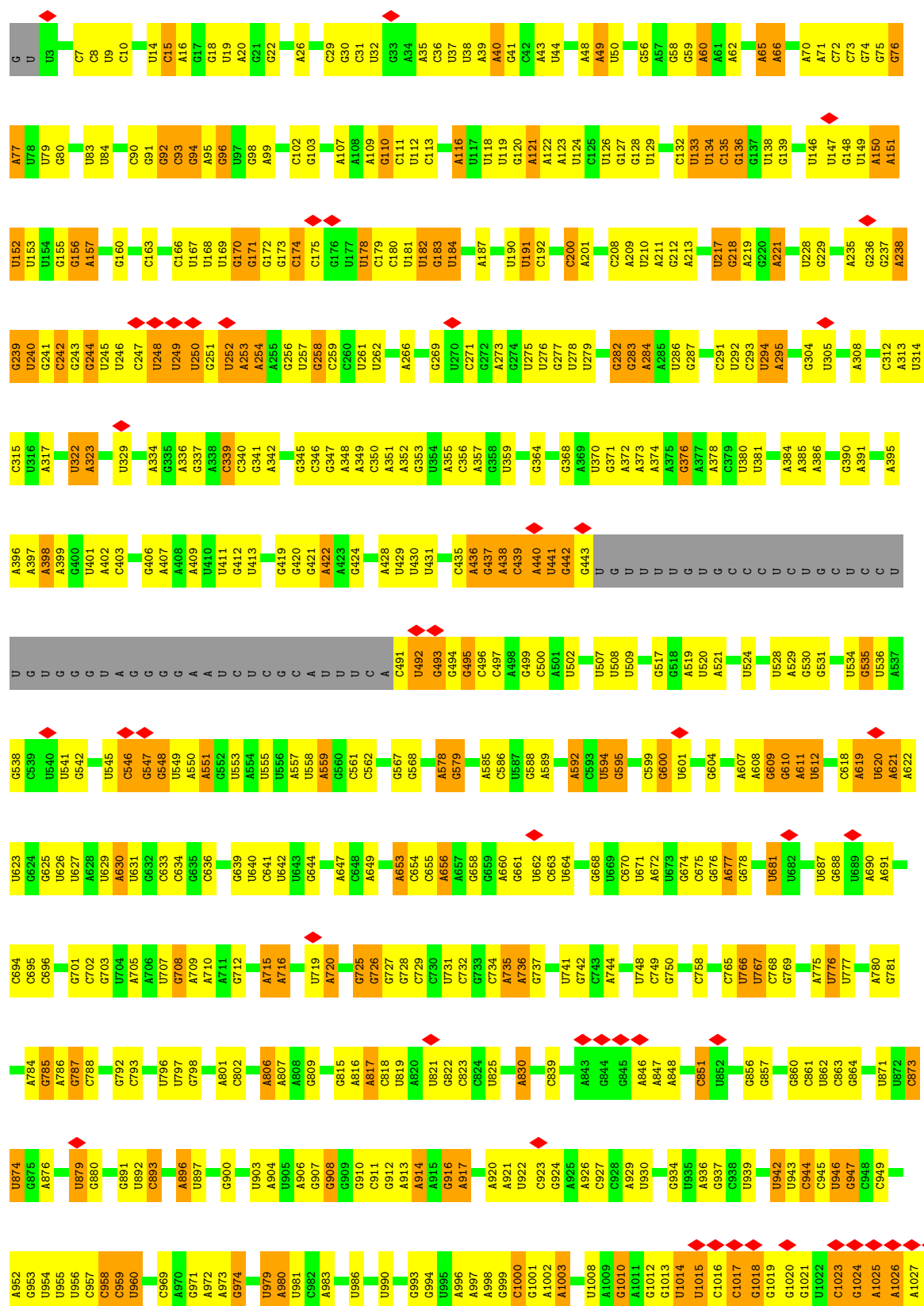


• Molecule 75: 60S RIBOSOMAL PROTEIN L42-A



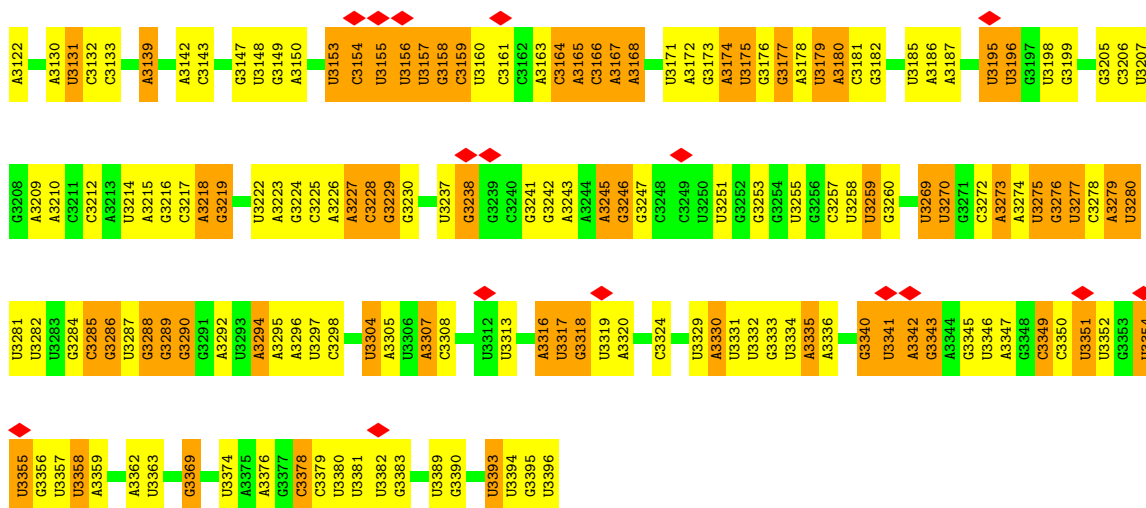




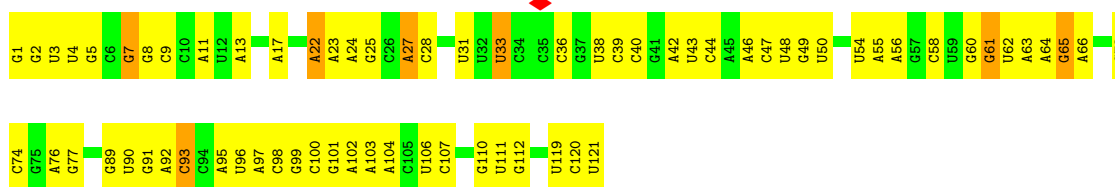




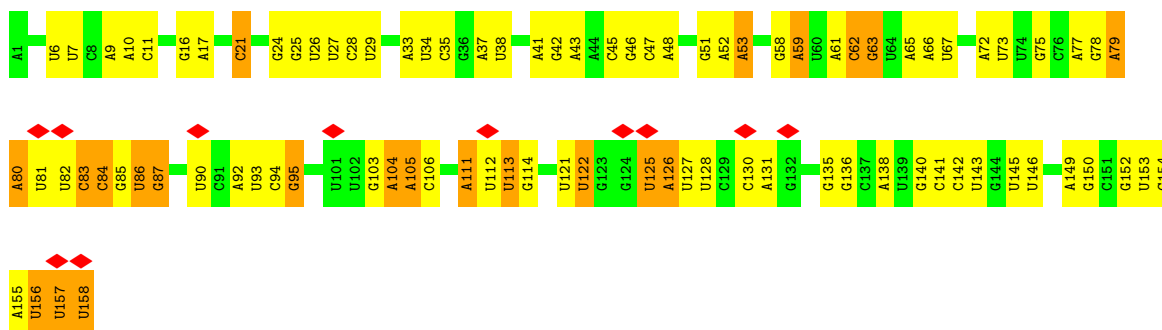
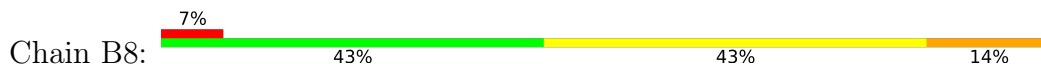
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G3044	A2946	U2853	U2763	U2681	G2606	U2532	U	G2400	A2223	U2154	U
G3045	C2947	U2854	C2764	C2682	G2607	G2533	U	A2401	A2224	G2155	C
U2948	U2948	U2865	U2768	U2687	G2610	G2534	G	A2402	U2225	U2156	G
A3048	U2950	G2866	U2769	U2688	G2614	A2535	C	G2403	U2226	G2157	U
A3049	G2951	U2867	G2770	U2689	G2615	U2536	C	C2405	U2227	A2158	G
U3050	U2952	U2868	U2771	G2690	C2616	U2537	C	C2406	G2234	G2161	C
U3051	U2953	C2870	C2772	G2691	G2617	U2538	C	C2407	G2235	U2162	U
G3052	U2954	G2871	C2773	A2692	G2618	C2539	A	U2408	G2236	C2163	A
G3053	G2957	A2872	C2774	C2693	G2621	A2540	G	U2411	A2244	A2164	C
U3056	C2960	U2873	U2775	A2694	G2622	U2541	U	G2418	G2249	A2166	A
U3057	G2961	U2874	C2776	A2695	G2623	U2542	A	U2421	G2250	A2167	U
U3058	C2962	U2875	G2777	U2696	G2624	U2543	A	G2425	C2253	A2168	C
G3059	U2967	G2878	C2778	G2698	G2625	U2544	U	U2426	U2254	G2169	A
C3060	A2967	U2879	A2779	G2699	A2626	C2546	C	U2427	A2255	U2170	U
G3061	C2970	C2881	A2780	G2700	C2627	A2547	C	G2428	C2257	G2171	U
U3068	A2971	U2882	G2792	U2701	G2630	C2548	A	G2429	U2258	G2174	C
G3069	G2972	U2883	G2793	A2702	U2631	G2549	C	U2433	A2259	U2175	U
A3070	U2978	A2887	G2794	A2703	G2632	U2550	U	U2434	U2260	A2178	C
U3078	U2979	U2888	G2795	A2704	A2637	U2551	C	U2435	U2261	C2179	C
G3080	C2983	C2889	C2796	G2705	U2638	C2552	C	U2436	G2262	G2180	U
C3084	U2985	G2894	U2797	G2706	G2639	U2553	U	U2437	A2182	C2181	C
G3085	C2986	A2895	G2798	C2707	A2640	G2554	U	A2438	A2183	U2184	C
A3086	A2987	A2896	G2799	G2708	U2641	G2555	U	A2439	G2185	U2186	C
G3088	C2988	G2897	G2800	G2709	A2642	A2556	A	G2440	C2265	G2187	C
U3089	U2989	G2898	A2801	G2710	U2643	A2557	U	A2441	U2266	U2191	C
C3089	G2990	C2899	U2722	U2722	A2647	U2558	C	G2442	C2267	C2192	C
U3090	U2992	U2901	U2723	U2724	G2648	C2560	U	A2443	U2268	U2193	C
A3091	U2994	U2904	U2725	U2725	U2652	A2562	A	C2444	U2269	G2194	C
C3092	G2997	U2907	C2726	C2726	A2656	U2565	C	A	A2270	C2195	C
G3093	U2996	A2907	A2727	A2727	A2657	U2566	C	U	G2273	G2196	C
A3094	C2997	U2908	U2728	U2728	G2658	C2567	A	G	U2274	A2199	C
U3095	A2999	A2910	U2729	U2729	G2659	C2568	A	A	A2275	U2200	C
U3107	A3000	A2911	A2733	A2733	G2660	U2569	G	G	G2276	G2201	C
G3112	C3001	G2912	A2734	A2734	G2661	A2569	C	U	C2277	A2204	C
U3121	A3006	G2913	U2735	U2735	G2662	U2570	G	U	A2278	U2205	C
		G2914	A2736	A2736	G2663	U2571	C	U	C2279	G2206	C
		U2921	G2737	C2737	G2664	G2572	C	U	U2282	C2283	C
						G2573	C	U	C2284	C2285	C
						G2574	C	U			
						C2583	C	U			
						G2585	C	U			



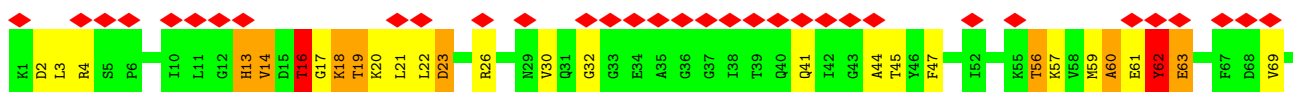
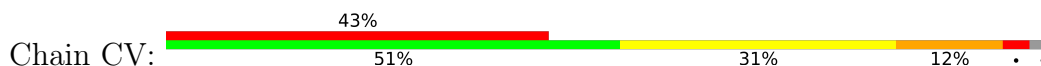
• Molecule 81: 5S RIBOSOMAL RNA

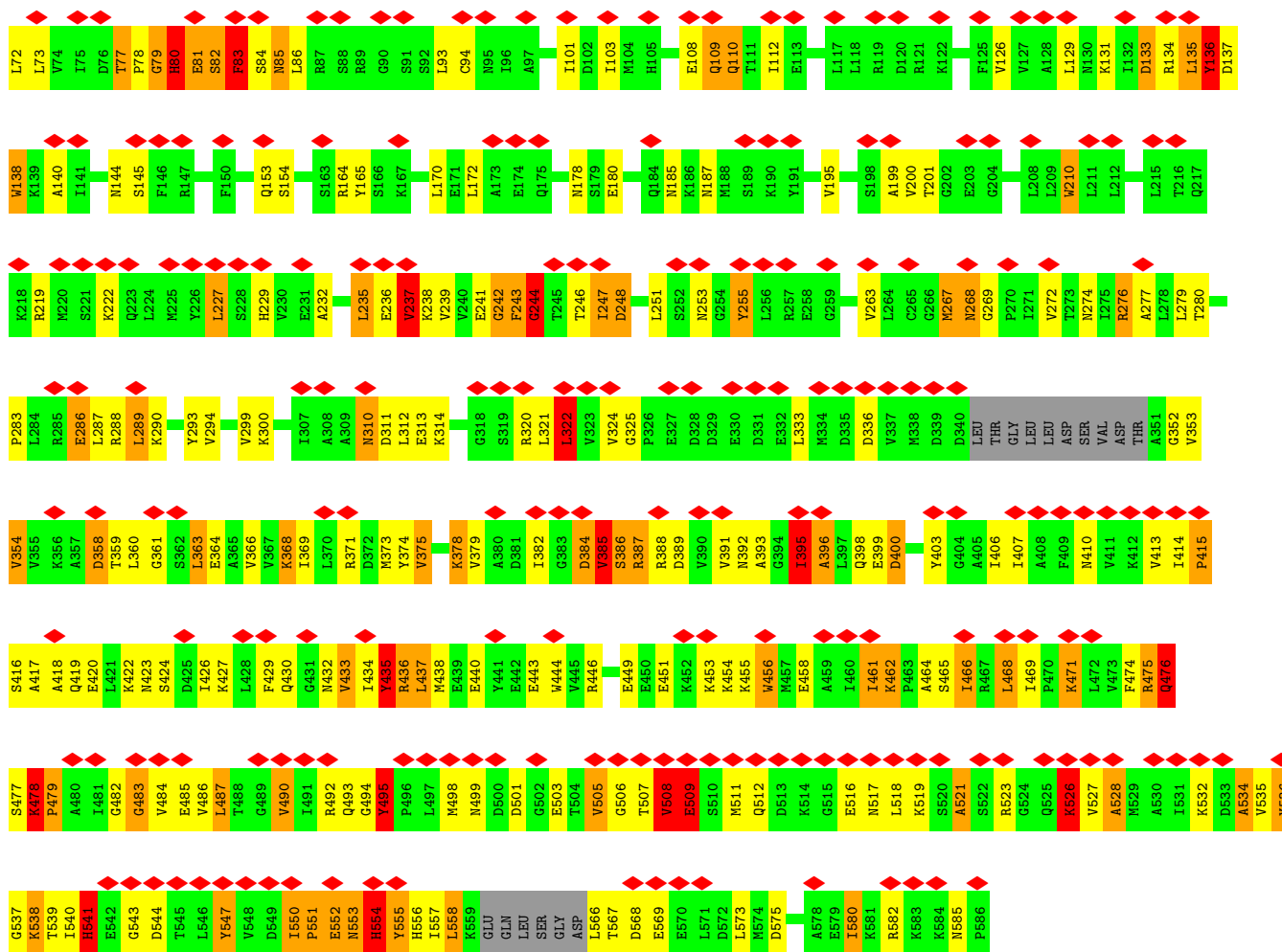


• Molecule 82: 5.8S RIBOSOMAL RNA

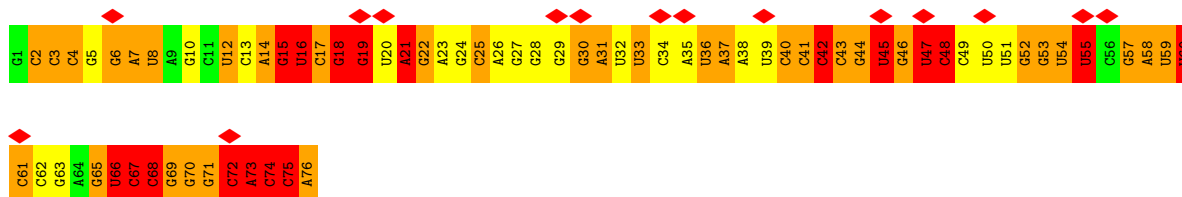


• Molecule 83: EUKARYOTIC TRANSLATION INITIATION FACTOR 5B, PROBABLE TRANSLATION INITIATION FACTOR IF-2

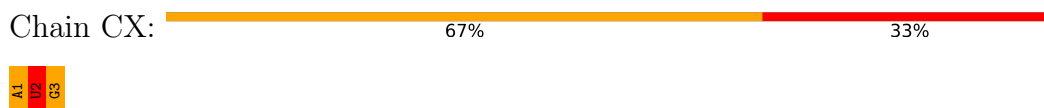




• Molecule 84: EUKARYOTIC RIBOSOMAL PI TRNA



• Molecule 85: 5'-R(*AP*UP*GP)-3'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5143	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	3900	Depositor
Magnification	79096	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	0.643	Depositor
Minimum map value	-0.362	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	424.8, 424.8, 424.8	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.77, 1.77, 1.77	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OHX, ZN, MG, GCP

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	A0	0.76	0/782	1.15	4/1047 (0.4%)
2	A1	0.69	0/620	1.23	7/838 (0.8%)
3	A2	0.54	0/499	1.08	0/670
4	A3	0.85	1/452 (0.2%)	1.24	2/600 (0.3%)
5	A4	0.61	0/483	1.13	2/643 (0.3%)
6	A5	0.72	0/404	1.37	5/542 (0.9%)
7	A6	0.63	0/2490	1.03	7/3389 (0.2%)
8	A7	1.09	3/925 (0.3%)	1.29	8/1240 (0.6%)
9	AA	0.71	1/1617 (0.1%)	1.22	18/2215 (0.8%)
10	AB	0.62	0/1735	1.13	11/2335 (0.5%)
11	AC	0.81	3/1665 (0.2%)	1.19	6/2263 (0.3%)
12	AD	0.76	0/1759	1.15	11/2368 (0.5%)
13	AE	0.74	0/2109	1.20	17/2839 (0.6%)
14	AF	0.65	0/1629	1.10	7/2202 (0.3%)
15	AG	0.70	0/1823	1.12	7/2439 (0.3%)
16	AH	0.68	0/1506	1.15	12/2028 (0.6%)
17	AI	0.84	0/1514	1.17	7/2021 (0.3%)
18	AJ	0.73	0/1519	1.18	7/2035 (0.3%)
19	AK	0.71	0/789	1.20	7/1067 (0.7%)
20	AL	0.85	0/1239	1.17	6/1673 (0.4%)
21	AM	0.70	0/898	1.13	4/1220 (0.3%)
22	AN	0.79	0/1215	1.17	7/1638 (0.4%)
23	AO	0.69	0/901	1.24	7/1217 (0.6%)
24	AP	0.75	0/998	1.20	8/1341 (0.6%)
25	AQ	0.70	0/1125	1.18	8/1510 (0.5%)
26	AR	0.73	0/935	1.25	7/1254 (0.6%)
27	AS	0.74	0/1211	1.14	5/1628 (0.3%)
28	AT	0.72	1/1130 (0.1%)	1.09	5/1517 (0.3%)
29	AU	0.71	0/865	1.18	8/1169 (0.7%)
30	AV	0.68	1/693 (0.1%)	1.07	3/935 (0.3%)
31	AW	0.83	0/1038	1.23	8/1395 (0.6%)
32	AX	0.91	1/1139 (0.1%)	1.26	6/1518 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AY	0.70	1/1087 (0.1%)	1.08	2/1449 (0.1%)
34	AZ	0.65	0/571	1.22	4/768 (0.5%)
35	BA	1.11	4/1946 (0.2%)	1.43	18/2614 (0.7%)
36	BB	1.23	5/3146 (0.2%)	1.44	26/4228 (0.6%)
37	BC	1.12	6/2800 (0.2%)	1.43	34/3790 (0.9%)
38	BD	1.02	1/2408 (0.0%)	1.27	21/3248 (0.6%)
39	BE	1.07	0/1269	1.37	11/1705 (0.6%)
40	BF	1.17	2/1828 (0.1%)	1.43	26/2461 (1.1%)
41	BG	0.78	0/1795	1.18	14/2429 (0.6%)
42	BH	1.18	0/1539	1.45	13/2073 (0.6%)
43	BI	1.11	0/1758	1.38	12/2358 (0.5%)
44	BJ	0.99	1/1374 (0.1%)	1.36	17/1842 (0.9%)
46	BL	1.06	3/1573 (0.2%)	1.40	19/2113 (0.9%)
47	BM	1.19	0/1074	1.36	9/1446 (0.6%)
48	BN	0.99	2/1757 (0.1%)	1.30	14/2354 (0.6%)
49	BO	0.64	0/3159	0.95	14/4205 (0.3%)
50	BP	1.34	4/1250 (0.3%)	1.41	6/1683 (0.4%)
51	BQ	1.08	1/1465 (0.1%)	1.42	10/1965 (0.5%)
52	BR	0.95	0/1538	1.21	5/2050 (0.2%)
53	BS	1.20	3/1481 (0.2%)	1.43	17/1990 (0.9%)
54	BT	1.16	2/1300 (0.2%)	1.35	6/1743 (0.3%)
55	BU	0.67	0/794	1.20	8/1076 (0.7%)
56	BV	1.25	2/1018 (0.2%)	1.42	6/1369 (0.4%)
57	BW	0.99	0/1052	1.22	7/1398 (0.5%)
58	BX	0.88	0/974	1.24	7/1314 (0.5%)
59	BY	0.94	0/1004	1.31	6/1341 (0.4%)
60	BZ	0.65	0/1118	1.18	9/1497 (0.6%)
61	Ba	1.20	7/1204 (0.6%)	1.59	28/1612 (1.7%)
62	Bb	1.20	2/473 (0.4%)	1.61	10/629 (1.6%)
63	Bc	0.72	0/775	1.11	3/1040 (0.3%)
64	Bd	1.11	1/897 (0.1%)	1.32	8/1205 (0.7%)
65	Be	1.23	3/1041 (0.3%)	1.58	9/1394 (0.6%)
66	Bf	1.34	6/868 (0.7%)	1.40	6/1168 (0.5%)
67	Bg	0.87	0/890	1.26	3/1189 (0.3%)
68	Bh	0.81	0/974	1.15	2/1297 (0.2%)
69	Bi	0.84	0/777	1.17	2/1033 (0.2%)
70	Bj	1.03	0/696	1.35	4/923 (0.4%)
71	Bk	0.66	0/614	1.07	1/822 (0.1%)
72	Bl	1.03	0/443	1.28	0/588
73	Bm	1.29	0/423	1.42	5/562 (0.9%)
74	Bn	1.05	0/234	1.25	2/300 (0.7%)
75	Bo	0.95	0/860	1.24	0/1136
76	Bq	1.53	6/1090 (0.6%)	1.82	30/1474 (2.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
79	B2	0.53	1/42128 (0.0%)	0.58	0/65642
80	B5	0.84	29/75336 (0.0%)	0.72	69/117449 (0.1%)
81	B7	0.78	0/2883	0.63	0/4491
82	B8	0.66	0/3746	0.61	0/5832
83	CV	2.36	35/4514 (0.8%)	2.08	206/6090 (3.4%)
84	CW	1.35	8/1801 (0.4%)	2.19	71/2803 (2.5%)
85	CX	1.30	0/69	1.99	3/106 (2.8%)
All	All	0.89	146/222521 (0.1%)	1.00	1030/326090 (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
2	A1	0	1
6	A5	0	2
8	A7	0	1
10	AB	0	1
16	AH	0	1
20	AL	0	1
23	AO	0	1
26	AR	0	2
34	AZ	0	3
35	BA	0	2
37	BC	0	1
38	BD	0	1
39	BE	0	1
40	BF	0	2
49	BO	0	2
53	BS	0	1
56	BV	0	1
59	BY	0	1
60	BZ	0	1
61	Ba	0	3
62	Bb	0	1
76	Bq	0	7
77	Br	0	1
80	B5	0	35
83	CV	0	20
84	CW	0	32
85	CX	0	2
All	All	0	127

The worst 5 of 146 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	CV	63	GLU	N-CA	99.89	2.84	1.46
83	CV	210	TRP	CD2-CE3	32.65	1.92	1.40
83	CV	210	TRP	CE2-CZ2	25.81	1.94	1.39
83	CV	210	TRP	CZ2-CH2	23.93	1.82	1.37
83	CV	210	TRP	CD2-CE2	23.30	1.80	1.41

The worst 5 of 1030 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	CW	36	U	P-O3'-C3'	-48.26	47.81	120.20
80	B5	1256	G	P-O3'-C3'	25.89	159.04	120.20
84	CW	36	U	O3'-P-O5'	21.56	136.34	104.00
84	CW	36	U	OP1-P-O3'	-17.49	55.52	108.00
80	B5	1238	C	P-O3'-C3'	17.46	146.38	120.20

There are no chirality outliers.

5 of 127 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A1	42	ASN	Peptide
6	A5	105	TYR	Peptide
6	A5	138	ARG	Peptide
8	A7	134	ASP	Sidechain
10	AB	131	ASP	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	A0	769	0	814	122	0
2	A1	610	0	630	53	0
3	A2	497	0	535	32	0
4	A3	442	0	428	57	0
5	A4	475	0	525	21	0
6	A5	516	0	517	41	0
7	A6	2437	0	2386	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A7	1105	0	933	457	0
9	AA	1577	0	1567	101	0
10	AB	1709	0	1784	200	0
11	AC	1635	0	1723	82	0
12	AD	1734	0	1817	123	0
13	AE	2068	0	2154	95	0
14	AF	1609	0	1675	118	0
15	AG	1799	0	1874	442	0
16	AH	1481	0	1572	84	0
17	AI	1489	0	1523	193	0
18	AJ	1494	0	1573	98	0
19	AK	772	0	727	48	0
20	AL	1213	0	1257	104	0
21	AM	890	0	887	53	0
22	AN	1192	0	1252	66	0
23	AO	891	0	880	300	0
24	AP	977	0	1002	78	0
25	AQ	1105	0	1164	147	0
26	AR	926	0	930	135	0
27	AS	1192	0	1220	118	0
28	AT	1112	0	1123	111	0
29	AU	855	0	917	118	0
30	AV	684	0	672	47	0
31	AW	1021	0	1060	70	0
32	AX	1121	0	1195	90	0
33	AY	1073	0	1132	115	0
34	AZ	563	0	602	54	0
35	BA	1912	0	1973	284	0
36	BB	3075	0	3142	153	0
37	BC	2748	0	2859	137	0
38	BD	2359	0	2311	272	0
39	BE	1248	0	1339	41	0
40	BF	1791	0	1869	60	0
41	BG	1763	0	1819	152	0
42	BH	1518	0	1587	85	0
43	BI	1722	0	1754	115	0
44	BJ	1353	0	1380	119	0
45	BK	753	756	195	3	0
46	BL	1548	0	1613	99	0
47	BM	1059	0	1154	45	0
48	BN	1720	0	1779	139	0
49	BO	3119	0	3302	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	BP	1227	0	1236	43	0
51	BQ	1441	0	1543	78	0
52	BR	1521	0	1605	196	0
53	BS	1445	0	1487	67	0
54	BT	1276	0	1323	141	0
55	BU	778	0	791	24	0
56	BV	1003	0	1048	52	0
57	BW	1038	0	1071	45	0
58	BX	959	0	1023	41	0
59	BY	993	0	1081	46	0
60	BZ	1092	0	1154	119	0
61	Ba	1173	0	1215	108	0
62	Bb	462	0	491	39	0
63	Bc	767	0	816	78	0
64	Bd	883	0	918	32	0
65	Be	1020	0	1090	62	0
66	Bf	850	0	880	36	0
67	Bg	880	0	944	106	0
68	Bh	965	0	1067	56	0
69	Bi	770	0	846	61	0
70	Bj	681	0	683	71	0
71	Bk	608	0	671	23	0
72	Bl	436	0	475	46	0
73	Bm	417	0	455	26	0
74	Bn	233	0	271	71	0
75	Bo	847	0	918	80	0
76	Bq	1075	1110	1021	30	0
77	Br	236	237	65	0	0
78	Bs	231	232	67	0	0
79	B2	37835	0	19045	3195	0
80	B5	67308	664	33785	2782	0
81	B7	2579	0	1303	192	0
82	B8	3353	0	1695	158	0
83	CV	4451	4585	4534	561	0
84	CW	1614	789	802	496	0
85	CX	62	34	34	34	0
86	A0	1	0	0	0	0
86	A1	1	0	0	0	0
86	A3	1	0	0	0	0
86	A5	1	0	0	0	0
86	Bj	1	0	0	0	0
86	Bm	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	A0	2	0	0	0	0
87	A3	3	0	0	0	0
87	A5	1	0	0	0	0
87	AB	1	0	0	0	0
87	AC	2	0	0	0	0
87	AE	1	0	0	0	0
87	AG	1	0	0	0	0
87	AI	1	0	0	0	0
87	AJ	1	0	0	0	0
87	AL	2	0	0	0	0
87	AN	1	0	0	0	0
87	AP	1	0	0	0	0
87	AS	1	0	0	0	0
87	AU	1	0	0	0	0
87	B2	168	0	0	0	0
87	B5	3	0	0	0	0
87	B7	27	0	0	0	0
87	BD	4	0	0	0	0
87	BF	1	0	0	0	0
87	BS	3	0	0	0	0
87	CW	1	0	0	0	0
88	A3	7	0	0	4	0
88	A6	7	0	0	2	0
88	AC	7	0	0	5	0
88	AI	14	0	0	2	0
88	AL	7	0	0	3	0
88	AN	7	0	0	2	0
88	AP	7	0	0	3	0
88	B2	1274	0	0	223	0
88	B5	21	0	0	4	0
88	B7	91	0	0	8	0
88	BR	7	0	0	9	0
88	Bn	7	0	0	0	0
88	CV	7	0	0	10	0
88	CX	7	0	0	2	0
89	CV	32	0	7	62	0
All	All	210964	8407	155586	10038	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 28.

The worst 5 of 10038 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)
80:B5:2621:G:C8	84:CW:75:C:C5	1.76	1.69
8:A7:85:SER:HB2	84:CW:30:G:C8	1.24	1.66
15:AG:175:ILE:HG12	79:B2:78:A:C4	1.29	1.65
83:CV:210:TRP:CH2	83:CV:210:TRP:CZ3	1.78	1.63
83:CV:210:TRP:CZ3	83:CV:210:TRP:CE3	1.83	1.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A0	95/119 (80%)	57 (60%)	21 (22%)	17 (18%)	0	2
2	A1	79/82 (96%)	62 (78%)	13 (16%)	4 (5%)	1	15
3	A2	61/67 (91%)	47 (77%)	9 (15%)	5 (8%)	0	9
4	A3	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	2	18
5	A4	58/63 (92%)	49 (84%)	7 (12%)	2 (3%)	3	21
6	A5	50/152 (33%)	30 (60%)	9 (18%)	11 (22%)	0	1
7	A6	316/319 (99%)	273 (86%)	30 (10%)	13 (4%)	2	18
8	A7	120/273 (44%)	92 (77%)	17 (14%)	11 (9%)	0	8
9	AA	204/252 (81%)	143 (70%)	35 (17%)	26 (13%)	0	4
10	AB	212/255 (83%)	132 (62%)	42 (20%)	38 (18%)	0	2
11	AC	215/254 (85%)	187 (87%)	16 (7%)	12 (6%)	1	14
12	AD	221/240 (92%)	180 (81%)	27 (12%)	14 (6%)	1	12
13	AE	258/261 (99%)	201 (78%)	36 (14%)	21 (8%)	1	9
14	AF	204/225 (91%)	155 (76%)	30 (15%)	19 (9%)	0	8
15	AG	224/236 (95%)	190 (85%)	23 (10%)	11 (5%)	1	16
16	AH	182/190 (96%)	128 (70%)	27 (15%)	27 (15%)	0	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AI	184/200 (92%)	155 (84%)	14 (8%)	15 (8%)	0	9
18	AJ	183/197 (93%)	153 (84%)	18 (10%)	12 (7%)	1	12
19	AK	94/105 (90%)	66 (70%)	18 (19%)	10 (11%)	0	6
20	AL	153/156 (98%)	125 (82%)	19 (12%)	9 (6%)	1	13
21	AM	122/143 (85%)	66 (54%)	23 (19%)	33 (27%)	0	0
22	AN	148/151 (98%)	125 (84%)	15 (10%)	8 (5%)	1	14
23	AO	125/137 (91%)	94 (75%)	16 (13%)	15 (12%)	0	4
24	AP	122/142 (86%)	92 (75%)	15 (12%)	15 (12%)	0	4
25	AQ	139/143 (97%)	114 (82%)	14 (10%)	11 (8%)	1	9
26	AR	116/136 (85%)	87 (75%)	17 (15%)	12 (10%)	0	6
27	AS	143/146 (98%)	110 (77%)	19 (13%)	14 (10%)	0	7
28	AT	141/144 (98%)	111 (79%)	18 (13%)	12 (8%)	0	9
29	AU	105/121 (87%)	87 (83%)	13 (12%)	5 (5%)	2	16
30	AV	85/87 (98%)	64 (75%)	11 (13%)	10 (12%)	0	4
31	AW	127/130 (98%)	114 (90%)	10 (8%)	3 (2%)	4	27
32	AX	142/145 (98%)	111 (78%)	13 (9%)	18 (13%)	0	4
33	AY	132/135 (98%)	106 (80%)	13 (10%)	13 (10%)	0	7
34	AZ	68/108 (63%)	46 (68%)	11 (16%)	11 (16%)	0	2
35	BA	250/253 (99%)	213 (85%)	30 (12%)	7 (3%)	4	24
36	BB	384/386 (100%)	341 (89%)	34 (9%)	9 (2%)	5	28
37	BC	359/361 (99%)	306 (85%)	32 (9%)	21 (6%)	1	13
38	BD	292/296 (99%)	267 (91%)	19 (6%)	6 (2%)	5	30
39	BE	153/175 (87%)	134 (88%)	15 (10%)	4 (3%)	4	25
40	BF	221/243 (91%)	201 (91%)	16 (7%)	4 (2%)	6	34
41	BG	229/255 (90%)	180 (79%)	28 (12%)	21 (9%)	0	8
42	BH	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	5	30
43	BI	209/220 (95%)	175 (84%)	22 (10%)	12 (6%)	1	14
44	BJ	167/173 (96%)	135 (81%)	19 (11%)	13 (8%)	1	10
46	BL	192/198 (97%)	161 (84%)	20 (10%)	11 (6%)	1	14
47	BM	135/137 (98%)	124 (92%)	10 (7%)	1 (1%)	18	56
48	BN	201/203 (99%)	182 (90%)	13 (6%)	6 (3%)	3	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	BO	352/218 (162%)	324 (92%)	18 (5%)	10 (3%)	4	24
50	BP	153/183 (84%)	142 (93%)	9 (6%)	2 (1%)	9	42
51	BQ	183/185 (99%)	168 (92%)	9 (5%)	6 (3%)	3	21
52	BR	186/188 (99%)	167 (90%)	16 (9%)	3 (2%)	7	38
53	BS	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	21	59
54	BT	157/159 (99%)	146 (93%)	9 (6%)	2 (1%)	9	42
55	BU	96/120 (80%)	80 (83%)	13 (14%)	3 (3%)	3	22
56	BV	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	8	40
57	BW	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	1	13
58	BX	118/141 (84%)	104 (88%)	6 (5%)	8 (7%)	1	11
59	BY	124/126 (98%)	107 (86%)	12 (10%)	5 (4%)	2	18
60	BZ	133/135 (98%)	107 (80%)	13 (10%)	13 (10%)	0	7
61	Ba	146/148 (99%)	123 (84%)	18 (12%)	5 (3%)	3	21
62	Bb	56/58 (97%)	44 (79%)	7 (12%)	5 (9%)	0	8
63	Bc	98/104 (94%)	87 (89%)	8 (8%)	3 (3%)	3	22
64	Bd	107/112 (96%)	88 (82%)	13 (12%)	6 (6%)	1	14
65	Be	125/129 (97%)	110 (88%)	9 (7%)	6 (5%)	2	16
66	Bf	104/106 (98%)	96 (92%)	5 (5%)	3 (3%)	3	23
67	Bg	110/120 (92%)	93 (84%)	13 (12%)	4 (4%)	2	20
68	Bh	117/119 (98%)	99 (85%)	14 (12%)	4 (3%)	3	21
69	Bi	97/99 (98%)	77 (79%)	13 (13%)	7 (7%)	1	11
70	Bj	85/87 (98%)	75 (88%)	8 (9%)	2 (2%)	4	27
71	Bk	75/77 (97%)	61 (81%)	10 (13%)	4 (5%)	1	14
72	Bl	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	30
73	Bm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
74	Bn	23/25 (92%)	22 (96%)	0	1 (4%)	2	17
75	Bo	103/105 (98%)	90 (87%)	11 (11%)	2 (2%)	6	32
76	Bq	141/312 (45%)	105 (74%)	14 (10%)	22 (16%)	0	2
83	CV	564/586 (96%)	457 (81%)	63 (11%)	44 (8%)	1	10
All	All	11848/12944 (92%)	9840 (83%)	1247 (10%)	761 (6%)	2	12

5 of 761 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A0	19	LYS
1	A0	45	VAL
1	A0	46	GLU
1	A0	62	TYR
1	A0	65	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A0	83/101 (82%)	61 (74%)	22 (26%)	0	3
2	A1	70/71 (99%)	60 (86%)	10 (14%)	3	13
3	A2	56/60 (93%)	36 (64%)	20 (36%)	0	1
4	A3	47/49 (96%)	40 (85%)	7 (15%)	3	13
5	A4	51/54 (94%)	41 (80%)	10 (20%)	1	7
6	A5	43/116 (37%)	31 (72%)	12 (28%)	0	3
7	A6	259/262 (99%)	215 (83%)	44 (17%)	2	10
8	A7	97/195 (50%)	71 (73%)	26 (27%)	0	3
9	AA	164/210 (78%)	114 (70%)	50 (30%)	0	2
10	AB	191/224 (85%)	137 (72%)	54 (28%)	0	3
11	AC	176/205 (86%)	124 (70%)	52 (30%)	0	2
12	AD	182/195 (93%)	133 (73%)	49 (27%)	0	3
13	AE	221/222 (100%)	160 (72%)	61 (28%)	0	3
14	AF	173/191 (91%)	139 (80%)	34 (20%)	1	7
15	AG	188/201 (94%)	145 (77%)	43 (23%)	1	6
16	AH	165/170 (97%)	116 (70%)	49 (30%)	0	2
17	AI	150/161 (93%)	114 (76%)	36 (24%)	1	4
18	AJ	158/166 (95%)	121 (77%)	37 (23%)	1	5
19	AK	77/98 (79%)	57 (74%)	20 (26%)	0	3
20	AL	129/137 (94%)	102 (79%)	27 (21%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AM	88/119 (74%)	53 (60%)	35 (40%)	0	1
22	AN	127/128 (99%)	86 (68%)	41 (32%)	0	2
23	AO	81/105 (77%)	57 (70%)	24 (30%)	0	2
24	AP	101/118 (86%)	81 (80%)	20 (20%)	1	7
25	AQ	117/119 (98%)	82 (70%)	35 (30%)	0	2
26	AR	94/124 (76%)	72 (77%)	22 (23%)	1	5
27	AS	128/129 (99%)	87 (68%)	41 (32%)	0	2
28	AT	115/116 (99%)	84 (73%)	31 (27%)	0	3
29	AU	100/114 (88%)	69 (69%)	31 (31%)	0	2
30	AV	74/74 (100%)	54 (73%)	20 (27%)	0	3
31	AW	110/111 (99%)	82 (74%)	28 (26%)	0	3
32	AX	119/120 (99%)	93 (78%)	26 (22%)	1	6
33	AY	112/113 (99%)	81 (72%)	31 (28%)	0	3
34	AZ	61/89 (68%)	42 (69%)	19 (31%)	0	2
35	BA	192/195 (98%)	149 (78%)	43 (22%)	1	6
36	BB	320/322 (99%)	241 (75%)	79 (25%)	1	4
37	BC	288/288 (100%)	213 (74%)	75 (26%)	0	3
38	BD	243/244 (100%)	185 (76%)	58 (24%)	1	4
39	BE	135/152 (89%)	113 (84%)	22 (16%)	2	10
40	BF	187/204 (92%)	158 (84%)	29 (16%)	2	12
41	BG	177/207 (86%)	136 (77%)	41 (23%)	1	5
42	BH	171/171 (100%)	128 (75%)	43 (25%)	0	4
43	BI	179/186 (96%)	134 (75%)	45 (25%)	0	4
44	BJ	147/149 (99%)	113 (77%)	34 (23%)	1	5
46	BL	154/158 (98%)	126 (82%)	28 (18%)	2	9
47	BM	108/108 (100%)	80 (74%)	28 (26%)	0	3
48	BN	175/175 (100%)	139 (79%)	36 (21%)	1	7
49	BO	323/178 (182%)	254 (79%)	69 (21%)	1	6
50	BP	125/145 (86%)	98 (78%)	27 (22%)	1	6
51	BQ	150/150 (100%)	121 (81%)	29 (19%)	1	7
52	BR	153/153 (100%)	113 (74%)	40 (26%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	BS	156/156 (100%)	119 (76%)	37 (24%)	1	4
54	BT	136/136 (100%)	107 (79%)	29 (21%)	1	6
55	BU	85/106 (80%)	60 (71%)	25 (29%)	0	2
56	BV	104/104 (100%)	93 (89%)	11 (11%)	6	21
57	BW	100/129 (78%)	83 (83%)	17 (17%)	2	10
58	BX	104/117 (89%)	77 (74%)	27 (26%)	0	3
59	BY	109/109 (100%)	81 (74%)	28 (26%)	0	3
60	BZ	115/115 (100%)	87 (76%)	28 (24%)	1	4
61	Ba	118/118 (100%)	90 (76%)	28 (24%)	1	4
62	Bb	46/46 (100%)	32 (70%)	14 (30%)	0	2
63	Bc	84/87 (97%)	65 (77%)	19 (23%)	1	6
64	Bd	94/96 (98%)	72 (77%)	22 (23%)	1	5
65	Be	109/110 (99%)	85 (78%)	24 (22%)	1	6
66	Bf	90/90 (100%)	80 (89%)	10 (11%)	6	20
67	Bg	95/102 (93%)	70 (74%)	25 (26%)	0	3
68	Bh	103/104 (99%)	75 (73%)	28 (27%)	0	3
69	Bi	80/81 (99%)	51 (64%)	29 (36%)	0	1
70	Bj	70/70 (100%)	55 (79%)	15 (21%)	1	6
71	Bk	67/68 (98%)	50 (75%)	17 (25%)	0	3
72	Bl	45/45 (100%)	30 (67%)	15 (33%)	0	2
73	Bm	47/116 (40%)	35 (74%)	12 (26%)	0	3
74	Bn	23/23 (100%)	13 (56%)	10 (44%)	0	0
75	Bo	90/90 (100%)	72 (80%)	18 (20%)	1	7
76	Bq	101/254 (40%)	91 (90%)	10 (10%)	7	24
83	CV	490/506 (97%)	448 (91%)	42 (9%)	10	29
All	All	9995/10830 (92%)	7662 (77%)	2333 (23%)	2	5

5 of 2333 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	BT	139	ARG
83	CV	16	THR
57	BW	105	ARG

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Mol	Chain	Res	Type
54	BT	131	GLN
65	Be	14	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 166 such sidechains are listed below:

Mol	Chain	Res	Type
54	BT	26	HIS
72	Bl	4	GLN
56	BV	33	ASN
61	Ba	65	GLN
76	Bq	56	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
79	B2	1763/1800 (97%)	548 (31%)	86 (4%)
80	B5	3140/3396 (92%)	756 (24%)	131 (4%)
81	B7	120/121 (99%)	18 (15%)	0
82	B8	157/158 (99%)	33 (21%)	3 (1%)
84	CW	74/76 (97%)	23 (31%)	5 (6%)
85	CX	2/3 (66%)	0	0
All	All	5256/5554 (94%)	1378 (26%)	225 (4%)

5 of 1378 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
79	B2	2	A
79	B2	4	C
79	B2	8	U
79	B2	16	G
79	B2	20	G

5 of 225 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	B5	908	G
84	CW	20	U
80	B5	1434	G
82	B8	156	U
80	B5	2996	U

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](#)

Of 443 ligands modelled in this entry, 232 are monoatomic - leaving 211 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	$\# Z > 2$
88	OHX	B2	1972	-	0,6,6	-	-	-		
88	OHX	B2	2036	-	0,6,6	-	-	-		
88	OHX	B2	2043	-	0,6,6	-	-	-		
88	OHX	B2	1973	-	0,6,6	-	-	-		
88	OHX	B2	1993	-	0,6,6	-	-	-		
88	OHX	B2	1949	-	0,6,6	-	-	-		
88	OHX	B2	1923	-	0,6,6	-	-	-		
88	OHX	B2	1913	87	0,6,6	-	-	-		
88	OHX	B2	2035	-	0,6,6	-	-	-		
88	OHX	B2	2078	-	0,6,6	-	-	-		
88	OHX	B2	1951	-	0,6,6	-	-	-		
88	OHX	B2	1922	87	0,6,6	-	-	-		
88	OHX	B7	212	87	0,6,6	-	-	-		
88	OHX	B7	220	87	0,6,6	-	-	-		
88	OHX	B2	2080	-	0,6,6	-	-	-		
88	OHX	B2	2028	-	0,6,6	-	-	-		
88	OHX	B2	1952	87	0,6,6	-	-	-		
88	OHX	B2	1986	-	0,6,6	-	-	-		
88	OHX	B2	2005	87	0,6,6	-	-	-		
88	OHX	B2	1977	-	0,6,6	-	-	-		
88	OHX	B7	204	87	0,6,6	-	-	-		
88	OHX	B2	1989	-	0,6,6	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	OHX	B2	1960	-	0,6,6	-	-	-		
88	OHX	B2	1907	-	0,6,6	-	-	-		
88	OHX	B2	2055	-	0,6,6	-	-	-		
88	OHX	B2	2008	-	0,6,6	-	-	-		
88	OHX	B2	2044	-	0,6,6	-	-	-		
88	OHX	B2	2049	87	0,6,6	-	-	-		
88	OHX	B2	2060	-	0,6,6	-	-	-		
88	OHX	B7	221	-	0,6,6	-	-	-		
88	OHX	B2	1917	-	0,6,6	-	-	-		
88	OHX	B2	1954	-	0,6,6	-	-	-		
88	OHX	B2	2019	87	0,6,6	-	-	-		
88	OHX	B2	2022	-	0,6,6	-	-	-		
88	OHX	B2	1930	-	0,6,6	-	-	-		
88	OHX	B2	2081	-	0,6,6	-	-	-		
88	OHX	B2	1978	-	0,6,6	-	-	-		
88	OHX	B2	2020	-	0,6,6	-	-	-		
88	OHX	B2	2010	-	0,6,6	-	-	-		
88	OHX	B2	2032	-	0,6,6	-	-	-		
88	OHX	B2	1997	-	0,6,6	-	-	-		
88	OHX	B2	1938	-	0,6,6	-	-	-		
88	OHX	B2	2053	-	0,6,6	-	-	-		
88	OHX	B2	2046	-	0,6,6	-	-	-		
88	OHX	B2	1935	87	0,6,6	-	-	-		
88	OHX	B2	1915	-	0,6,6	-	-	-		
88	OHX	B7	206	-	0,6,6	-	-	-		
88	OHX	B2	1958	-	0,6,6	-	-	-		
88	OHX	B2	1963	-	0,6,6	-	-	-		
88	OHX	B2	2014	-	0,6,6	-	-	-		
88	OHX	CV	601	83	0,6,6	-	-	-		
88	OHX	B2	2037	-	0,6,6	-	-	-		
88	OHX	B2	1925	-	0,6,6	-	-	-		
88	OHX	B2	2027	-	0,6,6	-	-	-		
88	OHX	B2	2050	-	0,6,6	-	-	-		
88	OHX	B2	2065	-	0,6,6	-	-	-		
88	OHX	B2	1928	87	0,6,6	-	-	-		
88	OHX	B2	1955	-	0,6,6	-	-	-		
88	OHX	B2	1999	-	0,6,6	-	-	-		
88	OHX	B2	2018	-	0,6,6	-	-	-		
88	OHX	B2	2040	-	0,6,6	-	-	-		
88	OHX	B2	1903	-	0,6,6	-	-	-		
88	OHX	B2	2064	-	0,6,6	-	-	-		
88	OHX	B2	1944	-	0,6,6	-	-	-		
88	OHX	B2	1975	-	0,6,6	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	OHX	B2	2062	88,87	0,6,6	-	-	-		
88	OHX	B2	2011	-	0,6,6	-	-	-		
88	OHX	B2	2000	-	0,6,6	-	-	-		
88	OHX	B2	1964	87	0,6,6	-	-	-		
88	OHX	B2	2030	-	0,6,6	-	-	-		
88	OHX	B7	203	87	0,6,6	-	-	-		
88	OHX	B2	1904	-	0,6,6	-	-	-		
88	OHX	B7	202	-	0,6,6	-	-	-		
88	OHX	B2	1959	-	0,6,6	-	-	-		
88	OHX	B2	2025	-	0,6,6	-	-	-		
88	OHX	B2	1939	-	0,6,6	-	-	-		
88	OHX	B2	1908	-	0,6,6	-	-	-		
88	OHX	B2	1956	-	0,6,6	-	-	-		
88	OHX	B2	1936	-	0,6,6	-	-	-		
88	OHX	B2	2074	-	0,6,6	-	-	-		
88	OHX	B2	2076	-	0,6,6	-	-	-		
88	OHX	B2	1995	-	0,6,6	-	-	-		
88	OHX	B2	2012	-	0,6,6	-	-	-		
88	OHX	B5	3401	-	0,6,6	-	-	-		
88	OHX	B2	1931	-	0,6,6	-	-	-		
88	OHX	B2	1940	-	0,6,6	-	-	-		
88	OHX	B2	1965	-	0,6,6	-	-	-		
88	OHX	B7	201	-	0,6,6	-	-	-		
88	OHX	B2	2066	-	0,6,6	-	-	-		
88	OHX	B2	1919	-	0,6,6	-	-	-		
88	OHX	B2	1911	87	0,6,6	-	-	-		
88	OHX	B2	2063	-	0,6,6	-	-	-		
88	OHX	B2	2033	-	0,6,6	-	-	-		
88	OHX	B2	1920	-	0,6,6	-	-	-		
88	OHX	B2	1996	-	0,6,6	-	-	-		
88	OHX	B2	1976	-	0,6,6	-	-	-		
88	OHX	B2	1946	87	0,6,6	-	-	-		
88	OHX	B2	2023	-	0,6,6	-	-	-		
88	OHX	B2	2071	-	0,6,6	-	-	-		
88	OHX	B2	2067	-	0,6,6	-	-	-		
88	OHX	B2	1983	-	0,6,6	-	-	-		
88	OHX	B2	2082	-	0,6,6	-	-	-		
88	OHX	B2	1933	-	0,6,6	-	-	-		
88	OHX	B2	2039	-	0,6,6	-	-	-		
88	OHX	B5	3403	-	0,6,6	-	-	-		
88	OHX	B2	1947	87	0,6,6	-	-	-		
88	OHX	B2	1943	87	0,6,6	-	-	-		
88	OHX	B2	2024	-	0,6,6	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	OHX	B2	2007	87	0,6,6	-	-	-		
88	OHX	B2	1934	-	0,6,6	-	-	-		
88	OHX	B2	1905	-	0,6,6	-	-	-		
88	OHX	B2	1994	-	0,6,6	-	-	-		
88	OHX	B2	1968	-	0,6,6	-	-	-		
88	OHX	B2	1990	87	0,6,6	-	-	-		
88	OHX	B2	2058	-	0,6,6	-	-	-		
88	OHX	AC	301	-	0,6,6	-	-	-		
88	OHX	AI	301	-	0,6,6	-	-	-		
88	OHX	B2	2017	-	0,6,6	-	-	-		
88	OHX	B2	2048	87	0,6,6	-	-	-		
88	OHX	AL	201	-	0,6,6	-	-	-		
88	OHX	B2	1924	87	0,6,6	-	-	-		
88	OHX	B2	2001	-	0,6,6	-	-	-		
88	OHX	B2	1921	87	0,6,6	-	-	-		
88	OHX	B2	2068	-	0,6,6	-	-	-		
88	OHX	B2	2073	-	0,6,6	-	-	-		
88	OHX	B2	1998	-	0,6,6	-	-	-		
88	OHX	AP	201	-	0,6,6	-	-	-		
88	OHX	B2	1992	-	0,6,6	-	-	-		
88	OHX	B2	1982	87	0,6,6	-	-	-		
88	OHX	B2	2004	-	0,6,6	-	-	-		
88	OHX	B7	205	-	0,6,6	-	-	-		
88	OHX	B2	1932	-	0,6,6	-	-	-		
88	OHX	A6	401	-	0,6,6	-	-	-		
88	OHX	B2	2003	-	0,6,6	-	-	-		
88	OHX	B2	1926	87	0,6,6	-	-	-		
88	OHX	A3	102	-	0,6,6	-	-	-		
88	OHX	B2	1948	-	0,6,6	-	-	-		
88	OHX	B2	1916	-	0,6,6	-	-	-		
88	OHX	B2	1914	-	0,6,6	-	-	-		
88	OHX	B2	1971	-	0,6,6	-	-	-		
88	OHX	B2	1979	-	0,6,6	-	-	-		
88	OHX	B2	1984	-	0,6,6	-	-	-		
88	OHX	B2	1902	-	0,6,6	-	-	-		
88	OHX	B2	2045	-	0,6,6	-	-	-		
88	OHX	B2	2059	-	0,6,6	-	-	-		
88	OHX	B2	2029	88	0,6,6	-	-	-		
88	OHX	B2	1969	-	0,6,6	-	-	-		
88	OHX	Bn	101	-	0,6,6	-	-	-		
88	OHX	B2	1970	-	0,6,6	-	-	-		
88	OHX	B2	2051	87	0,6,6	-	-	-		
88	OHX	B2	2077	-	0,6,6	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	OHX	B2	1945	-	0,6,6	-	-	-		
88	OHX	B2	2070	-	0,6,6	-	-	-		
88	OHX	B2	2009	-	0,6,6	-	-	-		
88	OHX	B2	1953	-	0,6,6	-	-	-		
88	OHX	B2	2002	-	0,6,6	-	-	-		
88	OHX	B2	2042	-	0,6,6	-	-	-		
88	OHX	B2	2013	-	0,6,6	-	-	-		
88	OHX	B2	2054	-	0,6,6	-	-	-		
88	OHX	B2	2034	-	0,6,6	-	-	-		
88	OHX	B2	1966	-	0,6,6	-	-	-		
88	OHX	B2	2069	79	0,6,6	-	-	-		
88	OHX	B2	1974	-	0,6,6	-	-	-		
88	OHX	B2	2016	-	0,6,6	-	-	-		
88	OHX	B2	1909	88	0,6,6	-	-	-		
88	OHX	B5	3402	-	0,6,6	-	-	-		
88	OHX	B7	219	87	0,6,6	-	-	-		
88	OHX	B2	1942	-	0,6,6	-	-	-		
89	GCP	CV	602	-	31,34,34	1.28	3 (9%)	47,54,54	1.57	4 (8%)
88	OHX	B2	2079	-	0,6,6	-	-	-		
88	OHX	B2	1912	-	0,6,6	-	-	-		
88	OHX	B2	1927	-	0,6,6	-	-	-		
88	OHX	B2	2006	-	0,6,6	-	-	-		
88	OHX	B7	214	87	0,6,6	-	-	-		
88	OHX	B2	1941	87	0,6,6	-	-	-		
88	OHX	B2	2075	-	0,6,6	-	-	-		
88	OHX	B2	1981	-	0,6,6	-	-	-		
88	OHX	B2	2038	87	0,6,6	-	-	-		
88	OHX	B7	210	-	0,6,6	-	-	-		
88	OHX	B2	1910	-	0,6,6	-	-	-		
88	OHX	B2	1967	-	0,6,6	-	-	-		
88	OHX	B2	2047	-	0,6,6	-	-	-		
88	OHX	B2	2052	-	0,6,6	-	-	-		
88	OHX	B2	1906	87	0,6,6	-	-	-		
88	OHX	AN	201	-	0,6,6	-	-	-		
88	OHX	B2	1950	-	0,6,6	-	-	-		
88	OHX	B2	2057	-	0,6,6	-	-	-		
88	OHX	B2	1957	87	0,6,6	-	-	-		
88	OHX	B2	1918	88	0,6,6	-	-	-		
88	OHX	B2	2015	87	0,6,6	-	-	-		
88	OHX	B2	2026	87	0,6,6	-	-	-		
88	OHX	B2	2041	-	0,6,6	-	-	-		
88	OHX	B2	1985	-	0,6,6	-	-	-		
88	OHX	AI	302	-	0,6,6	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	OHX	B2	1937	-	0,6,6	-	-	-		
88	OHX	B2	2061	-	0,6,6	-	-	-		
88	OHX	B2	1901	-	0,6,6	-	-	-		
88	OHX	CX	101	-	0,6,6	-	-	-		
88	OHX	B2	1962	-	0,6,6	-	-	-		
88	OHX	B2	2072	-	0,6,6	-	-	-		
88	OHX	B2	2021	-	0,6,6	-	-	-		
88	OHX	BR	201	52	0,6,6	-	-	-		
88	OHX	B2	1987	-	0,6,6	-	-	-		
88	OHX	B2	1961	-	0,6,6	-	-	-		
88	OHX	B2	1980	-	0,6,6	-	-	-		
88	OHX	B2	2031	87	0,6,6	-	-	-		
88	OHX	B2	1991	-	0,6,6	-	-	-		
88	OHX	B2	1929	-	0,6,6	-	-	-		
88	OHX	B7	215	-	0,6,6	-	-	-		
88	OHX	B2	2056	-	0,6,6	-	-	-		
88	OHX	B2	1988	-	0,6,6	-	-	-		

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
89	GCP	CV	602	-	-	1/19/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	CV	602	GCP	C2'-C1'	-2.99	1.43	1.53
89	CV	602	GCP	C4-N3	2.44	1.40	1.34
89	CV	602	GCP	PB-O3A	-2.31	1.55	1.58

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	CV	602	GCP	O3G-PG-C3B	-7.36	88.55	106.40
89	CV	602	GCP	O1B-PB-C3B	2.89	116.72	109.07
89	CV	602	GCP	O2G-PG-O1G	2.71	119.54	112.39
89	CV	602	GCP	C1'-N9-C8	2.21	133.00	126.70

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	CV	602	GCP	PB-C3B-PG-O1G

There are no ring outliers.

126 monomers are involved in 332 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	1972	OHX	1	0
88	B2	2036	OHX	1	0
88	B2	2043	OHX	1	0
88	B2	1973	OHX	7	0
88	B2	1949	OHX	2	0
88	B2	1923	OHX	1	0
88	B2	2078	OHX	1	0
88	B2	1951	OHX	2	0
88	B2	1922	OHX	7	0
88	B7	220	OHX	1	0
88	B2	2028	OHX	1	0
88	B2	1952	OHX	2	0
88	B2	1986	OHX	1	0
88	B2	1977	OHX	1	0
88	B2	1989	OHX	1	0
88	B2	1960	OHX	4	0
88	B2	1907	OHX	6	0
88	B2	2044	OHX	5	0
88	B2	1917	OHX	2	0
88	B2	1954	OHX	1	0
88	B2	2022	OHX	1	0
88	B2	2081	OHX	11	0
88	B2	1978	OHX	1	0
88	B2	2020	OHX	3	0
88	B2	2010	OHX	1	0
88	B2	2032	OHX	1	0
88	B2	2046	OHX	1	0
88	B2	1915	OHX	6	0
88	B2	1963	OHX	6	0
88	B2	2014	OHX	7	0
88	CV	601	OHX	10	0
88	B2	2037	OHX	1	0
88	B2	1925	OHX	1	0
88	B2	1928	OHX	1	0
88	B2	1999	OHX	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	2040	OHX	1	0
88	B2	1944	OHX	1	0
88	B2	2062	OHX	6	0
88	B2	2011	OHX	11	0
88	B2	1964	OHX	2	0
88	B7	203	OHX	6	0
88	B7	202	OHX	1	0
88	B2	1959	OHX	1	0
88	B2	2025	OHX	7	0
88	B2	1939	OHX	5	0
88	B2	1956	OHX	1	0
88	B2	1936	OHX	1	0
88	B2	2074	OHX	1	0
88	B2	2076	OHX	1	0
88	B2	1995	OHX	1	0
88	B2	2012	OHX	1	0
88	B5	3401	OHX	1	0
88	B2	2066	OHX	6	0
88	B2	1919	OHX	1	0
88	B2	2063	OHX	2	0
88	B2	2033	OHX	2	0
88	B2	1976	OHX	7	0
88	B2	2023	OHX	2	0
88	B2	2071	OHX	6	0
88	B2	2067	OHX	2	0
88	B2	2082	OHX	1	0
88	B2	1947	OHX	1	0
88	B2	2024	OHX	2	0
88	B2	2007	OHX	2	0
88	B2	1968	OHX	7	0
88	B2	1990	OHX	3	0
88	B2	2058	OHX	1	0
88	AC	301	OHX	5	0
88	B2	2048	OHX	7	0
88	AL	201	OHX	3	0
88	B2	1924	OHX	1	0
88	B2	1921	OHX	6	0
88	B2	2068	OHX	1	0
88	B2	2073	OHX	1	0
88	AP	201	OHX	3	0
88	B2	1982	OHX	1	0
88	A6	401	OHX	2	0

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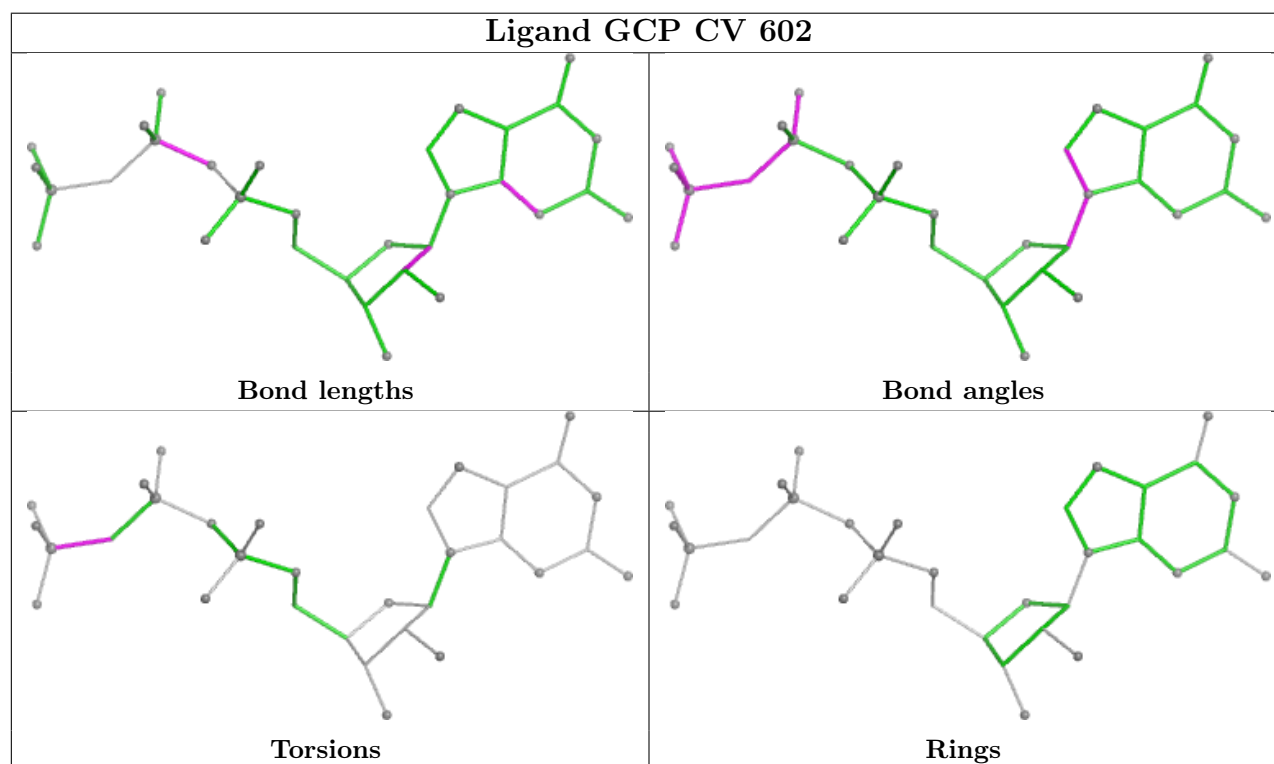
Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	A3	102	OHX	4	0
88	B2	1948	OHX	1	0
88	B2	1916	OHX	1	0
88	B2	1914	OHX	3	0
88	B2	1971	OHX	2	0
88	B2	2045	OHX	1	0
88	B2	2059	OHX	1	0
88	B2	2029	OHX	1	0
88	B2	1969	OHX	1	0
88	B2	2051	OHX	1	0
88	B2	2077	OHX	5	0
88	B2	1945	OHX	1	0
88	B2	2009	OHX	2	0
88	B2	1953	OHX	6	0
88	B2	2002	OHX	1	0
88	B2	2013	OHX	1	0
88	B2	2069	OHX	17	0
88	B2	1974	OHX	3	0
88	B2	1909	OHX	2	0
88	B5	3402	OHX	3	0
88	B7	219	OHX	6	0
89	CV	602	GCP	62	0
88	B2	1927	OHX	1	0
88	B2	2006	OHX	1	0
88	B2	1941	OHX	1	0
88	B2	2075	OHX	2	0
88	B2	1981	OHX	5	0
88	B2	2038	OHX	1	0
88	B2	1910	OHX	2	0
88	B2	1967	OHX	5	0
88	B2	2047	OHX	3	0
88	B2	1906	OHX	3	0
88	AN	201	OHX	2	0
88	B2	2057	OHX	1	0
88	B2	1918	OHX	8	0
88	B2	2041	OHX	1	0
88	B2	1985	OHX	3	0
88	AI	302	OHX	2	0
88	B2	1937	OHX	1	0
88	B2	2061	OHX	1	0
88	B2	1901	OHX	1	0
88	CX	101	OHX	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	1962	OHX	4	0
88	BR	201	OHX	9	0
88	B2	1987	OHX	8	0
88	B2	1961	OHX	1	0
88	B2	1929	OHX	1	0
88	B2	2056	OHX	1	0
88	B2	1988	OHX	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
80	B5	1
84	CW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B5	1285:G	O3'	1286:A	P	6.77
1	CW	33:U	O3'	34:C	P	4.25

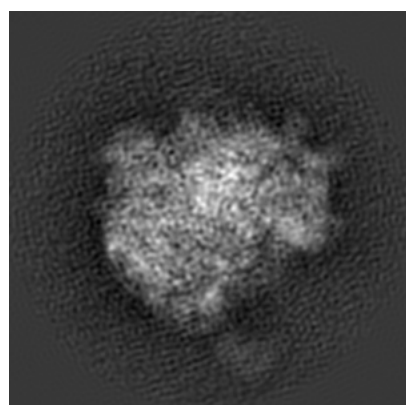
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2422. These allow visual inspection of the internal detail of the map and identification of artifacts.

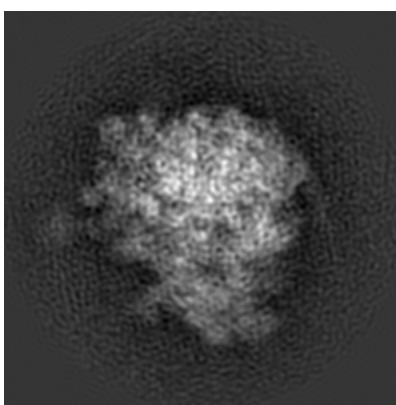
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

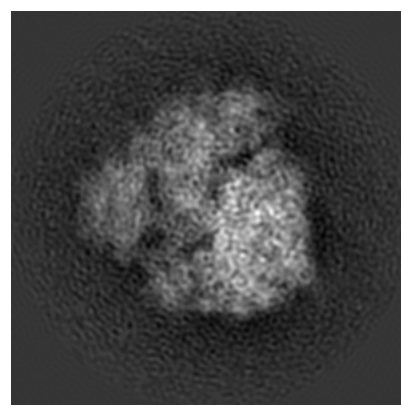
6.1.1 Primary map



X



Y

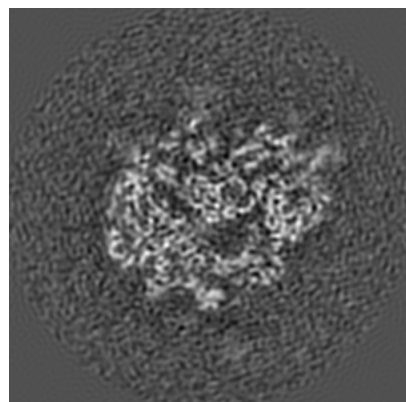


Z

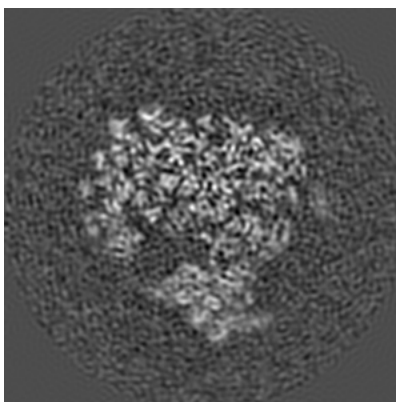
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

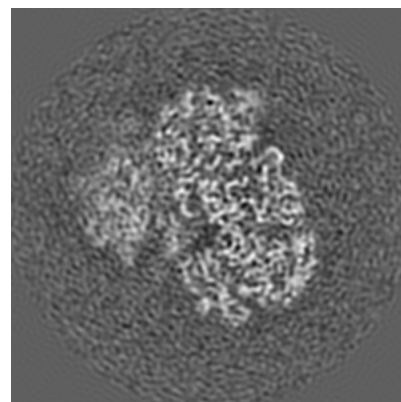
6.2.1 Primary map



X Index: 120



Y Index: 120

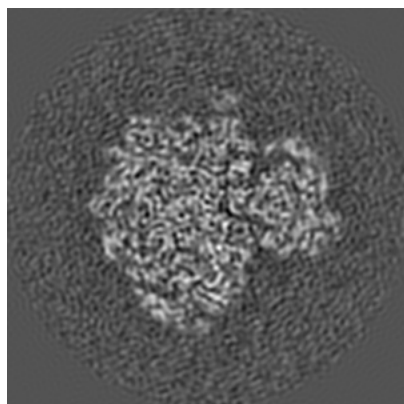


Z Index: 120

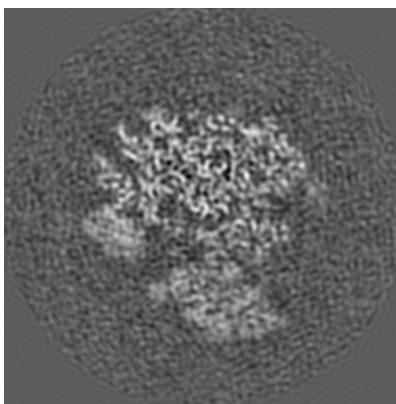
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

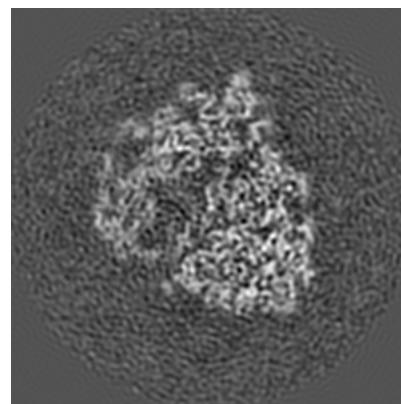
6.3.1 Primary map



X Index: 133



Y Index: 124

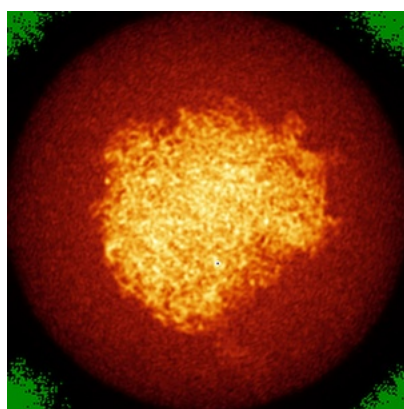


Z Index: 113

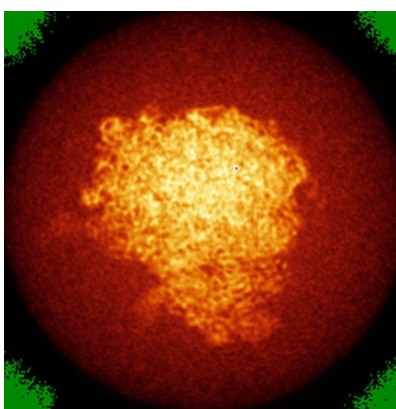
The images above show the largest variance slices of the map in three orthogonal directions.

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

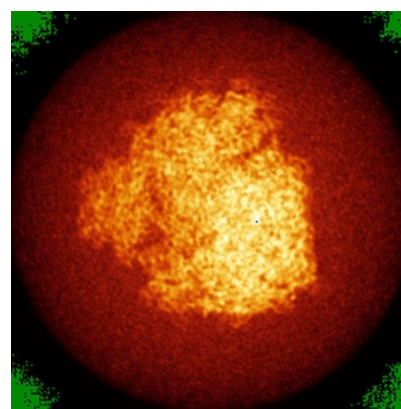
6.4.1 Primary map



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 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

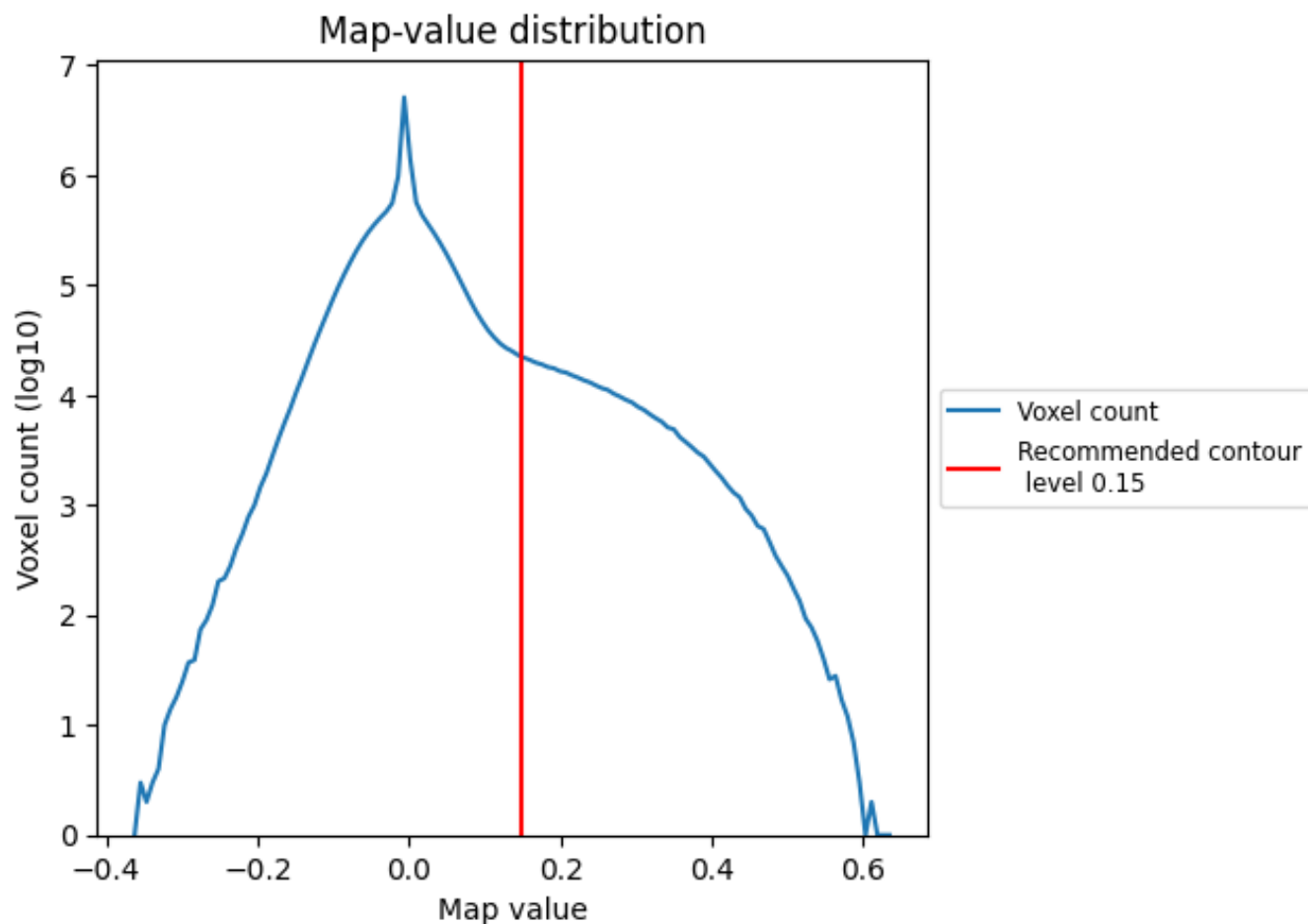
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

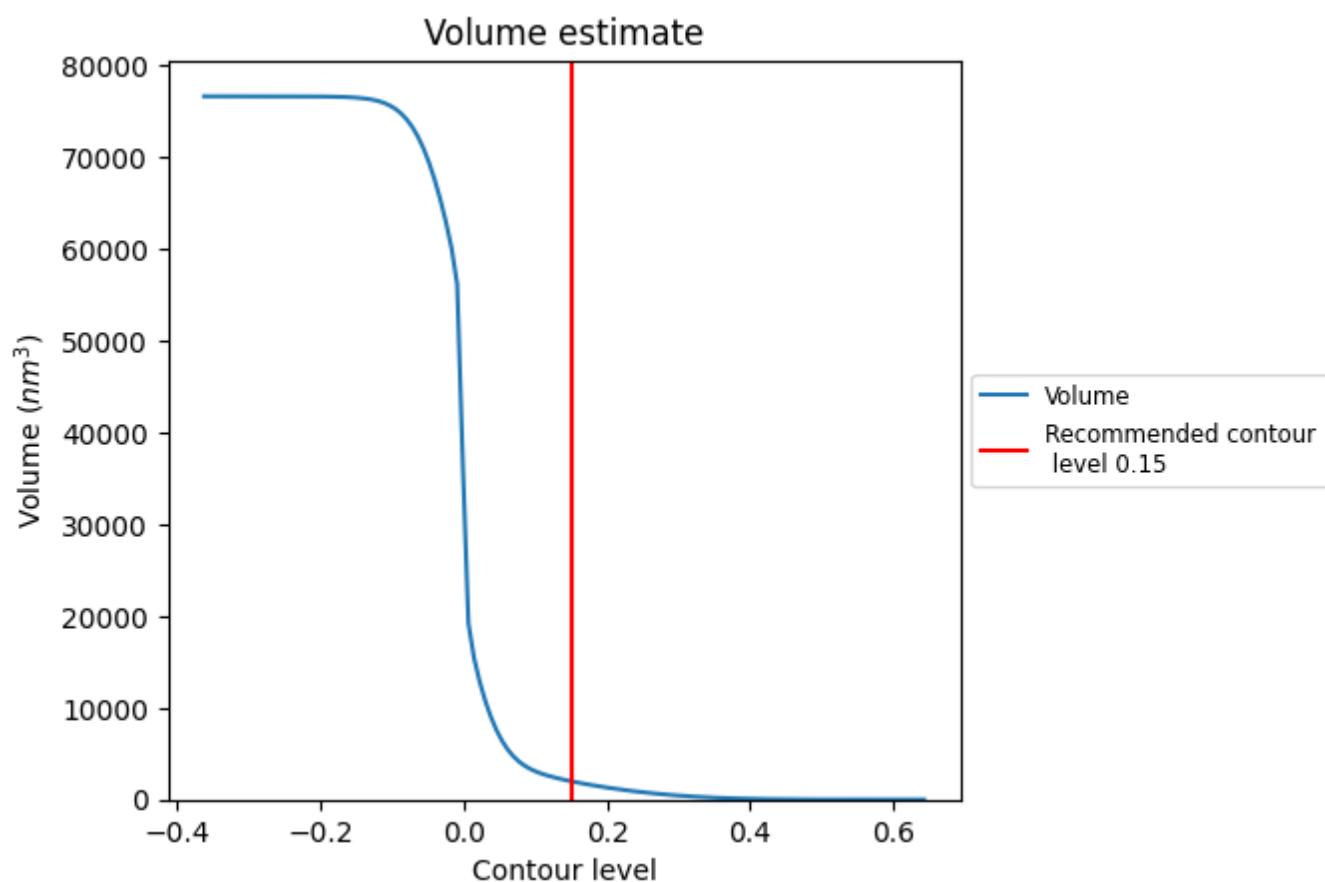
This section contains the results of statistical analysis of the map.

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.

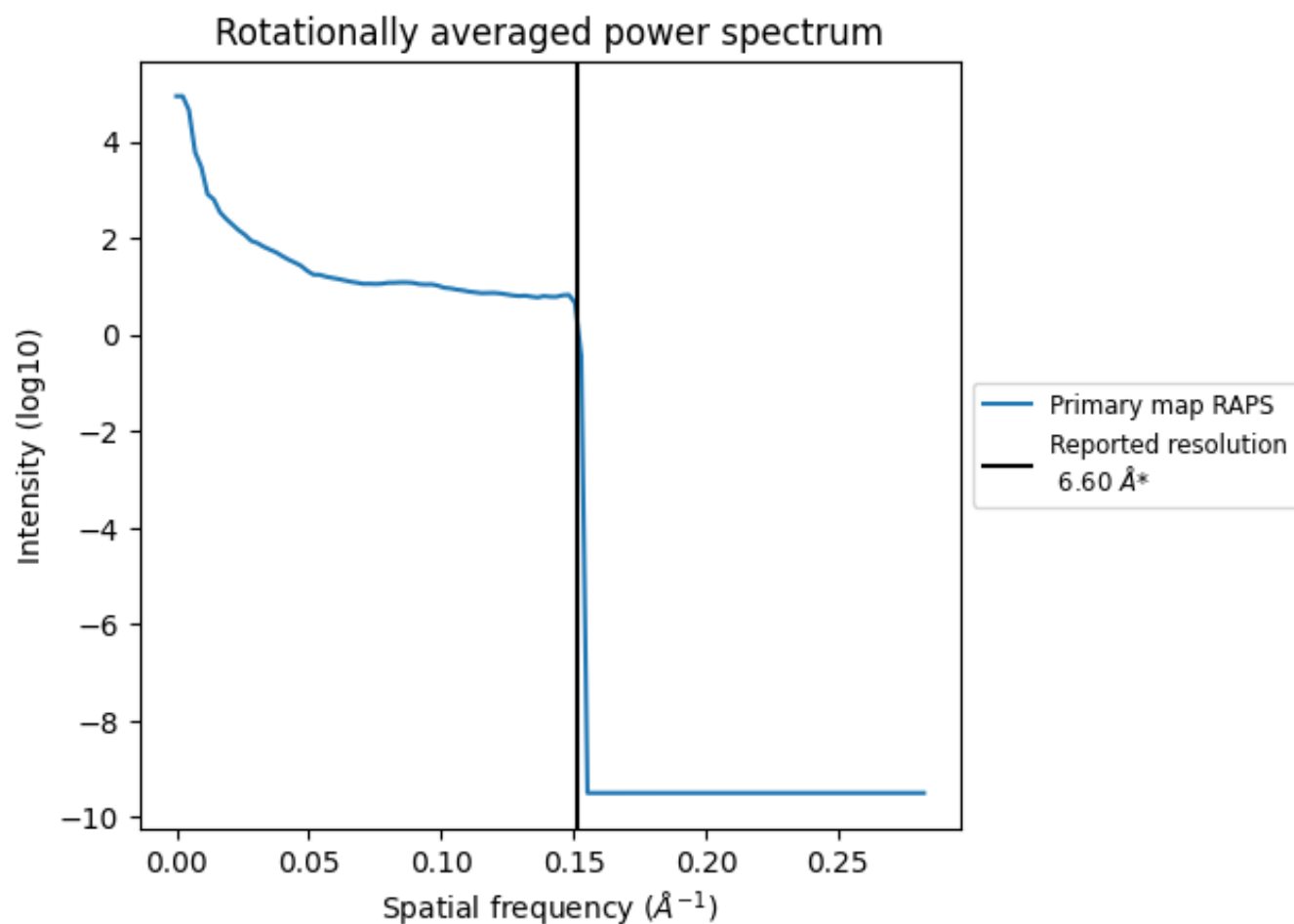
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1997 nm³; this corresponds to an approximate mass of 1804 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.152 $\text{\AA}^{-1}$

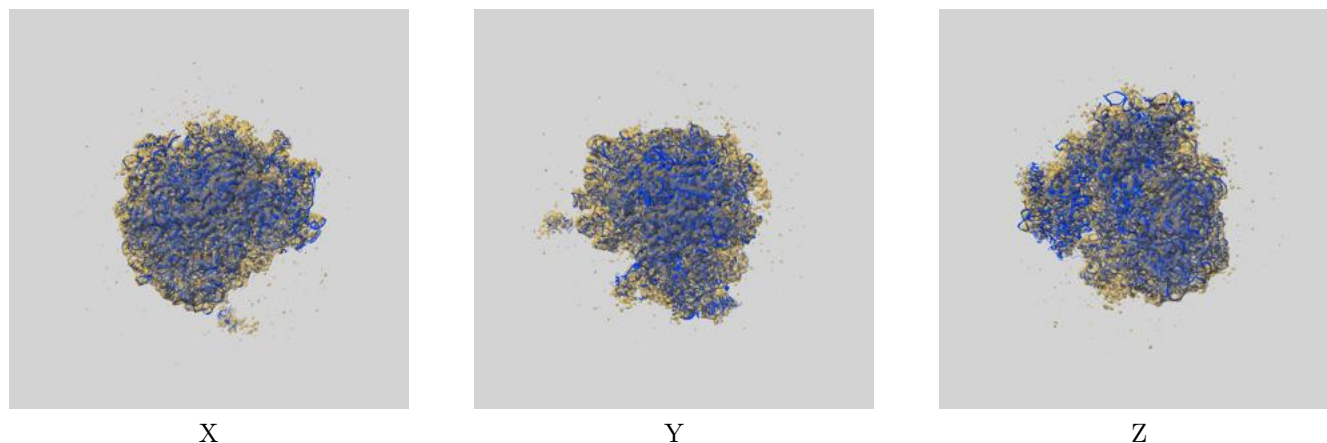
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

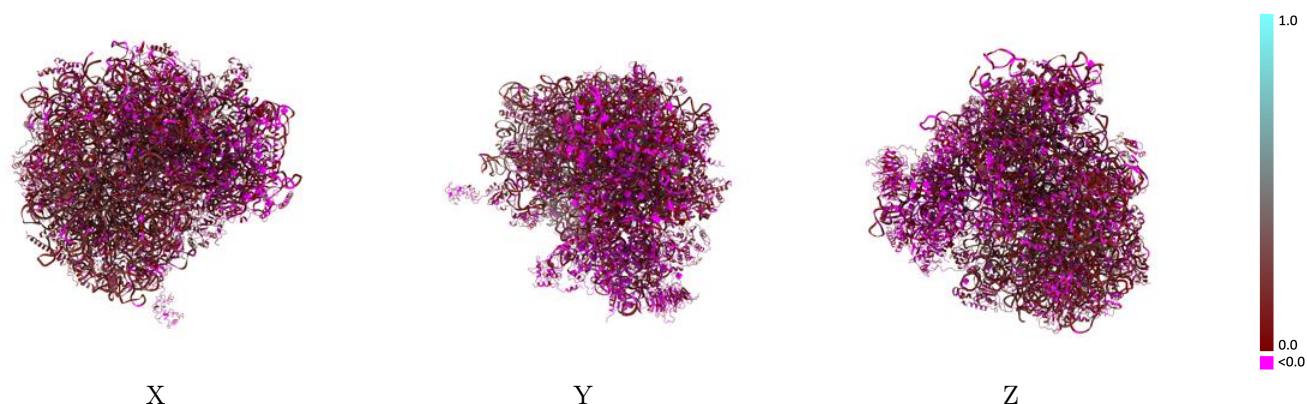
This section contains information regarding the fit between EMDB map EMD-2422 and PDB model 4V8Z. Per-residue inclusion information can be found in section [3](#) on page [36](#).

9.1 Map-model overlay [i](#)



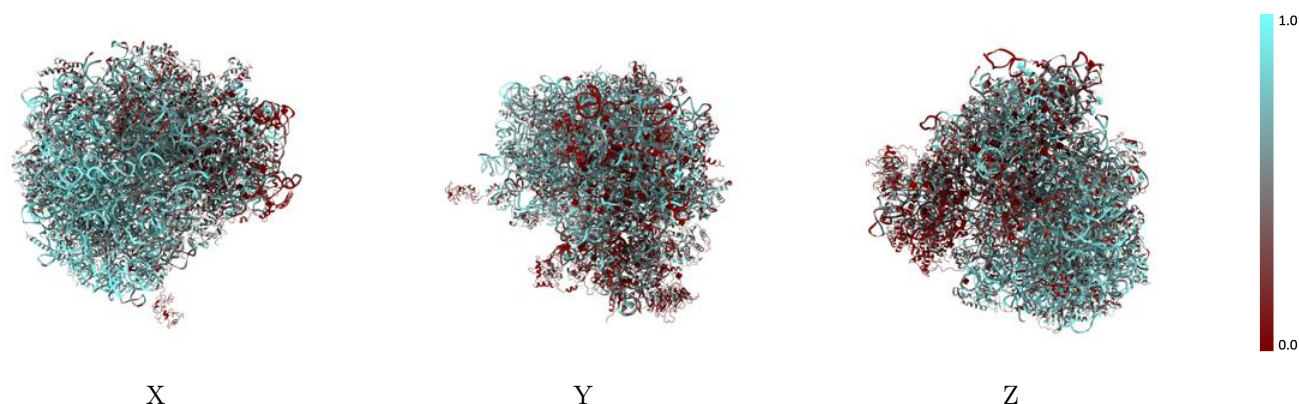
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



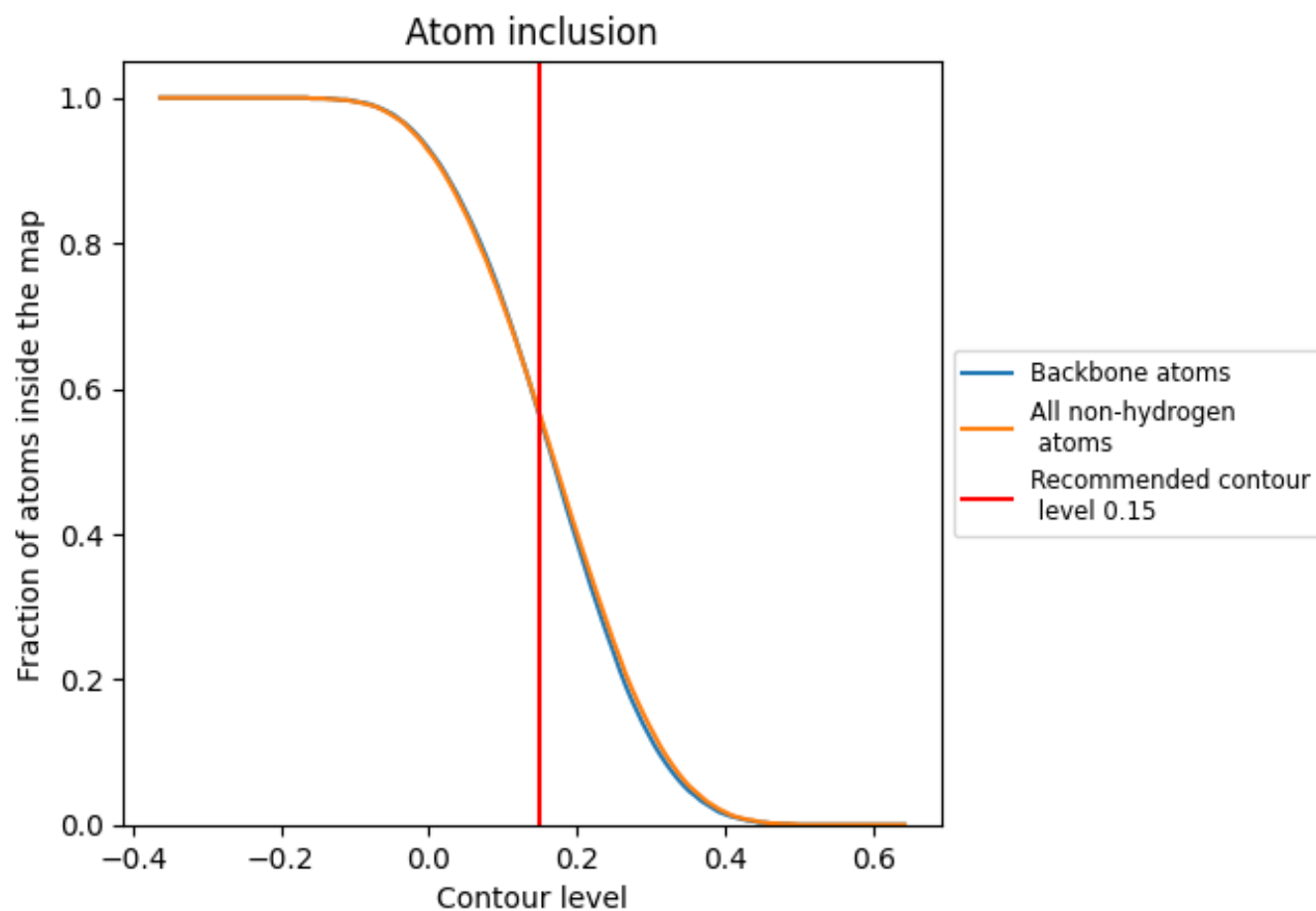
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5650	 0.1080
A0	 0.3320	 -0.0020
A1	 0.4120	 0.0760
A2	 0.1150	 -0.0000
A3	 0.3690	 0.0080
A4	 0.3790	 0.0510
A5	 0.0510	 -0.0100
A6	 0.2510	 0.0200
A7	 0.1380	 0.0190
AA	 0.4130	 0.0530
AB	 0.2240	 0.0100
AC	 0.3920	 0.0420
AD	 0.2870	 -0.0120
AE	 0.4220	 0.0540
AF	 0.1330	 -0.0030
AG	 0.3770	 0.0160
AH	 0.5540	 0.1420
AI	 0.4250	 0.0370
AJ	 0.4320	 0.0580
AK	 0.2860	 -0.0190
AL	 0.4350	 0.0800
AM	 0.2030	 0.0190
AN	 0.4650	 0.1190
AO	 0.3700	 -0.0040
AP	 0.2320	 0.0100
AQ	 0.3110	 0.0080
AR	 0.3940	 0.0950
AS	 0.2200	 0.0110
AT	 0.3010	 0.0260
AU	 0.2410	 0.0090
AV	 0.4280	 0.0470
AW	 0.4880	 0.1130
AX	 0.4390	 0.1160
AY	 0.4470	 0.0390
AZ	 0.0530	 0.0150



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Chain	Atom inclusion	Q-score
B2	 0.5480	 0.0840
B5	 0.7490	 0.1610
B7	 0.8480	 0.1770
B8	 0.7510	 0.1470
BA	 0.3860	 0.0620
BB	 0.4890	 0.1010
BC	 0.5560	 0.1160
BD	 0.5700	 0.1270
BE	 0.5990	 0.1360
BF	 0.5950	 0.1490
BG	 0.4710	 0.0510
BH	 0.5440	 0.1110
BI	 0.5400	 0.1340
BJ	 0.5390	 0.1260
BK	 0.4410	 0.0840
BL	 0.4930	 0.0910
BM	 0.6360	 0.1480
BN	 0.4470	 0.0670
BO	 0.5480	 0.1400
BP	 0.5210	 0.0980
BQ	 0.5330	 0.1170
BR	 0.3290	 0.0290
BS	 0.5670	 0.1260
BT	 0.5300	 0.1380
BU	 0.4250	 0.0610
BV	 0.4430	 0.1270
BW	 0.2180	 0.0370
BX	 0.3940	 0.0650
BY	 0.5560	 0.0940
BZ	 0.4560	 0.0410
Ba	 0.4820	 0.1010
Bb	 0.4930	 0.1510
Bc	 0.4110	 0.0580
Bd	 0.4880	 0.0570
Be	 0.5370	 0.1380
Bf	 0.5500	 0.1240
Bg	 0.4010	 0.0400
Bh	 0.4970	 0.1060
Bi	 0.4660	 0.0640
Bj	 0.4790	 0.0670
Bk	 0.4290	 0.0610
Bl	 0.4170	 0.0610

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Chain	Atom inclusion	Q-score
Bm	 0.4850	 0.1270
Bn	 0.1780	 0.0130
Bo	 0.4660	 0.1040
Bq	 0.4810	 0.1050
Br	 0.1360	 0.0410
Bs	 0.1170	 0.0360
CV	 0.4620	 0.1390
CW	 0.5950	 0.2240
CX	 0.5800	 0.1470