



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 09:00 PM UTC

PDB ID : 4V6W / pdb_00004v6w
EMDB ID : EMD-5591
Title : Structure of the D. melanogaster 80S ribosome
Authors : Anger, A.M.; Armache, J.-P.; Berninghausen, O.; Habeck, M.; Subklewe, M.;
Wilson, D.N.; Beckmann, R.
Deposited on : 2013-02-27
Resolution : 6.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

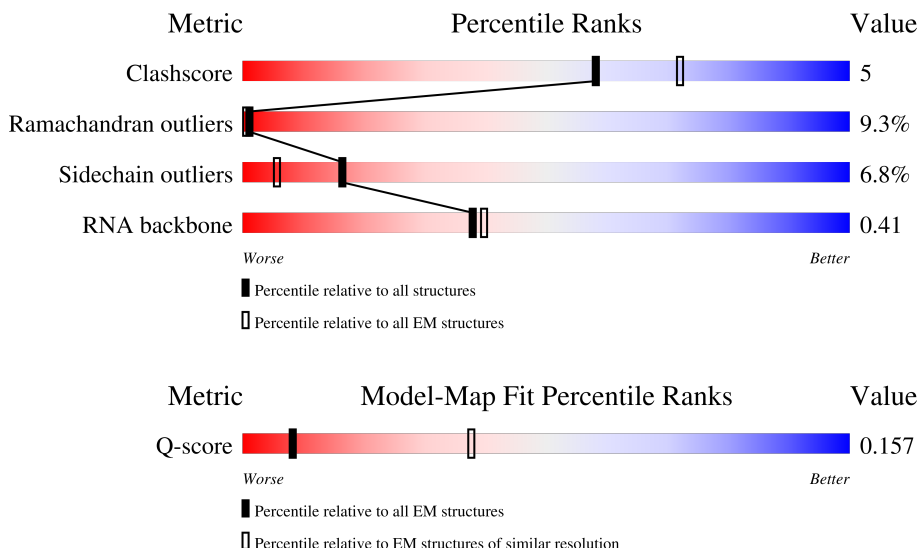
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 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.



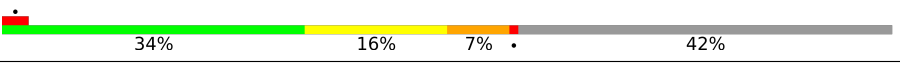
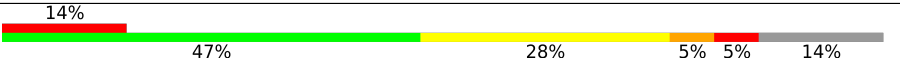
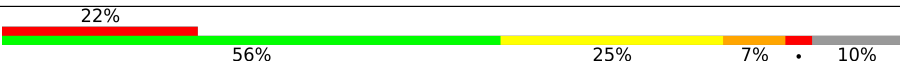
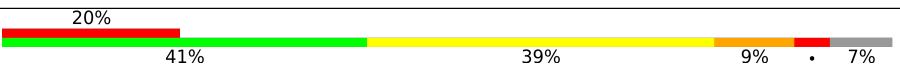
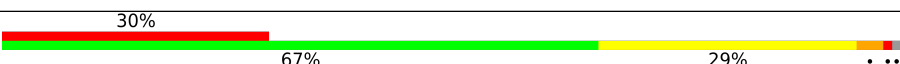
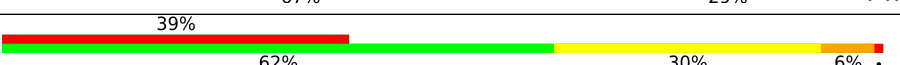
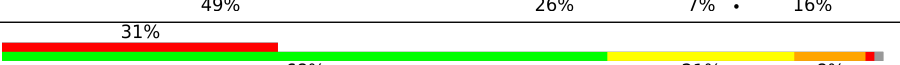
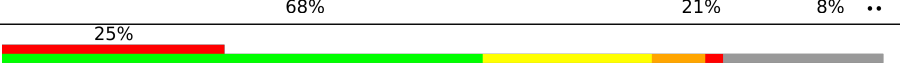
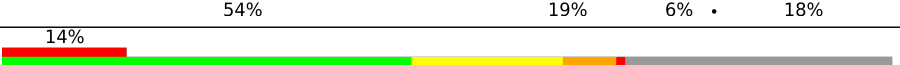
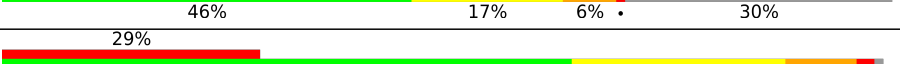
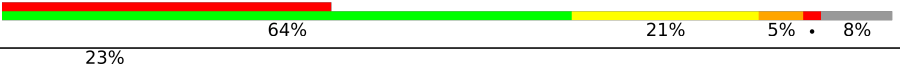
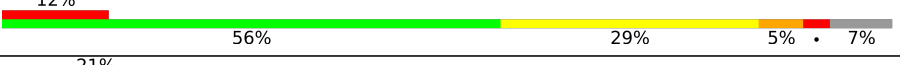
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	525 (5.50 - 6.50)

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	Az	844	43% 53% 31% 11% • •
2	Ag	318	29% 75% 22% • •
3	AU	120	24% 59% 18% 5% • 15%

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Mol	Chain	Length	Quality of chain
4	AK	163	
5	AO	151	
6	AX	143	
7	AM	139	
8	AS	152	
9	Ad	56	
10	AN	151	
11	AL	155	
12	AR	131	
13	AP	148	
14	AT	156	
15	AB	268	
16	AA	313	
17	AV	83	
18	AY	131	
19	AZ	117	
20	Aa	114	
21	Ab	84	
22	Ac	65	
23	AD	246	
24	Ae	132	
25	Af	80	
26	AJ	195	
27	AE	261	
28	AC	267	

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Mol	Chain	Length	Quality of chain
29	AG	248	
30	AF	228	
31	AH	194	
32	AW	130	
33	AI	208	
34	AQ	148	
35	Ah	121	
36	B2	1995	
37	BC	75	
38	Cz	218	
39	Cq	223	
40	CK	165	
41	CO	205	
42	CL	218	
43	CV	140	
44	CM	166	
45	Ca	149	
46	CN	204	
47	CI	218	
48	CD	299	
49	CQ	188	
50	CR	203	
51	CA	256	
52	CS	177	
53	CT	159	

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Mol	Chain	Length	Quality of chain
54	CP	186	
55	CU	299	
56	CX	277	
57	CY	149	
58	CW	155	
59	CZ	135	
60	Cr	144	
61	Ch	123	
62	Cb	76	
63	CB	416	
64	CF	252	
65	Cc	111	
66	Cd	124	
67	Ce	134	
68	Cf	157	
69	Cg	162	
70	Ci	115	
71	Cj	93	
72	Ck	70	
73	Cl	51	
74	CC	401	
75	Cm	52	
76	Cn	25	
77	Cp	92	
78	Co	104	

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Mol	Chain	Length	Quality of chain
79	CJ	184	
80	CH	190	
81	CE	243	
82	CG	271	
83	A5	3970	
84	A9	30	
85	A7	120	
86	A8	123	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 230721 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Az	837	Total	C	N	O	S	0	0
			6574	4170	1123	1235	46		

- Molecule 2 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 3 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 4 is a protein called 40S ribosomal protein S10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AK	95	Total	C	N	O	S	0	0
			797	522	136	137	2		

- Molecule 5 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AO	134	Total	C	N	O	S	0	0
			1003	616	196	187	4		

- Molecule 6 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 7 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 8 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS	137	Total	C	N	O	S	0	0
			1128	707	220	198	3		

- Molecule 9 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 13 is a protein called 40S ribosomal protein S15, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 14 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AT	154	Total	C	N	O	S	0	0
			1203	762	230	207	4		

- Molecule 15 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

- Molecule 16 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927
AV	80	SER	THR	conflict	UNP O76927

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 19 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AZ	74	Total	C	N	O		0	0
			608	390	112	106			

- Molecule 20 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 21 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 22 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 24 is a protein called 40S ribosomal protein S30, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ae	58	Total	C	N	O		0	0
			469	289	105	75			

- Molecule 25 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 27 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 29 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 30 is a protein called 40S ribosomal protein S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	190	Total	C	N	O	S	0	0
			1497	934	285	269	9		

- Molecule 31 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 32 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 33 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 34 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 35 is a protein called Vig2, isoform B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ah	58	Total	C	N	O	S	0	0
			486	298	93	94	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	212	LYS	GLU	conflict	UNP Q9VBX3
Ah	213	GLU	ASP	conflict	UNP Q9VBX3
Ah	215	PRO	SER	conflict	UNP Q9VBX3
Ah	217	GLU	GLN	conflict	UNP Q9VBX3
Ah	226	ILE	LEU	conflict	UNP Q9VBX3
Ah	227	GLN	ARG	conflict	UNP Q9VBX3
Ah	228	ASN	ASP	conflict	UNP Q9VBX3

- Molecule 36 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B2	1957	Total	C	N	O	P	0	0
			39523	17589	6780	13198	1956		

- Molecule 37 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	75	Total	C	N	O	P	0	0
			1605	717	296	518	74		

- Molecule 38 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cz	72A	SER	-	expression tag	UNP Q9VTP4

- Molecule 39 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cq	223	Total	C	N	O	S	0	0
			1710	1089	297	314	10		

- Molecule 40 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CK	158	Total	C	N	O	S	0	0
			1180	739	213	222	6		

- Molecule 41 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 42 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 43 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 45 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 49 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 50 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 51 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

- Molecule 52 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 53 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 54 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 55 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CU	116	Total	C	N	O	S	0	0
			961	607	167	185	2		

- Molecule 56 is a protein called 60S ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 57 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CW	130	Total	C	N	O	S	0	0
			1047	662	207	172	6		

- Molecule 59 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cr	134	Total	C	N	O	S	0	0
			1051	670	205	176			

- Molecule 61 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 63 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 64 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CF	229	Total	C	N	O	S	0	0
			1921	1234	372	312	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	111	Total	C	N	O	S	0	0
			924	573	180	169	2		

- Molecule 67 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 68 is a protein called 60S ribosomal protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 69 is a protein called 60S ribosomal protein L34a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cg	113	Total	C	N	O	S	0	0
			926	575	193	152	6		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cj	92	Total	C	N	O	S	0	0
			737	450	160	122	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 74 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 78 is a protein called 60S ribosomal protein L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 79 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 80 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 81 is a protein called 60S ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 82 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 83 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A5	3806	Total	C	N	O	P	0	0
			77967	34770	13566	25827	3804		

- Molecule 84 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 85 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

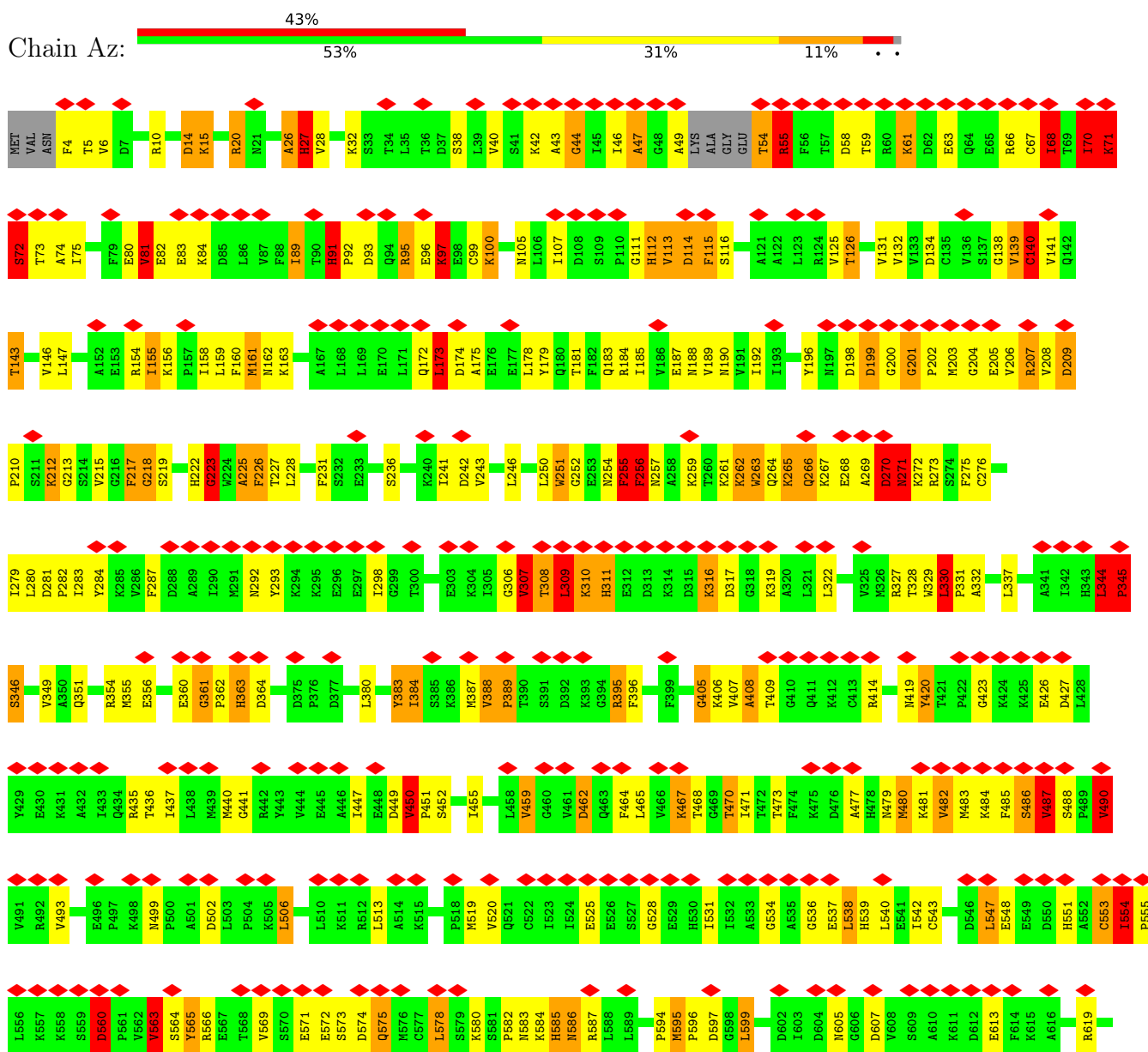
- Molecule 86 is a RNA chain called 5.8S ribosomal RNA.

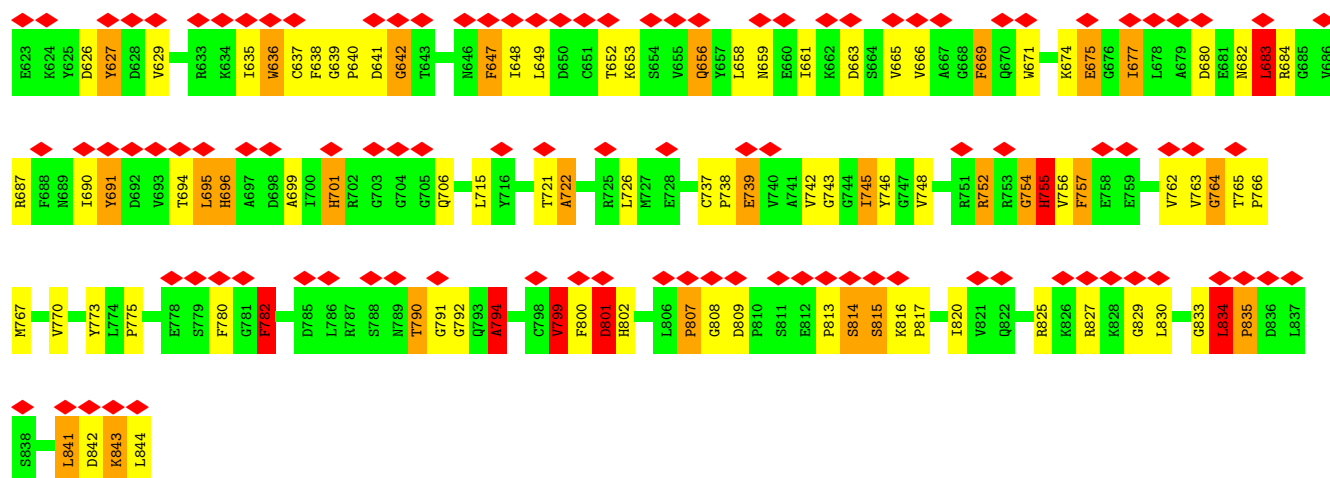
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
86	A8	123	2621	1173	474	852	122	0	0

3 Residue-property plots

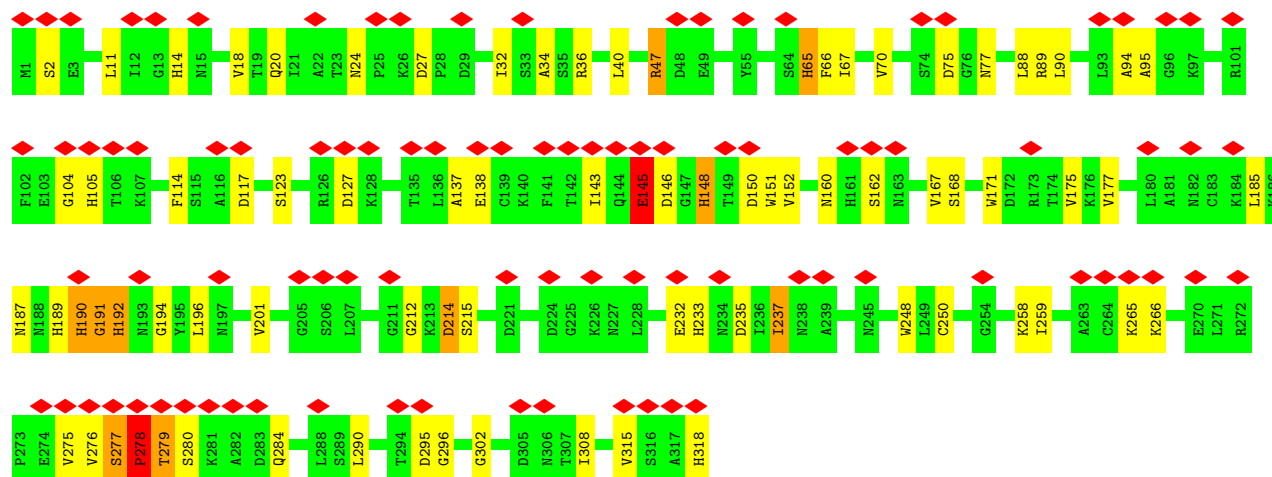
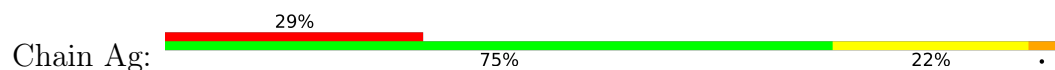
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Elongation factor 2

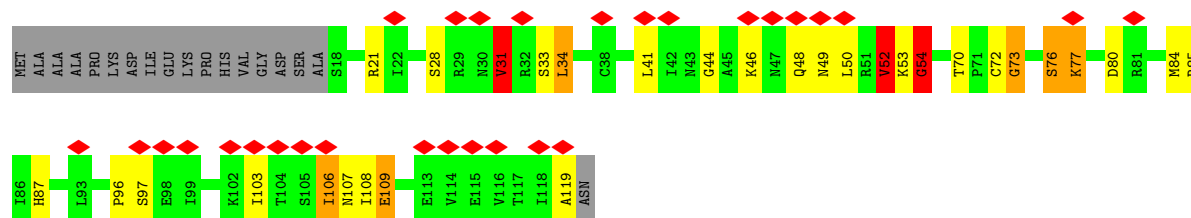




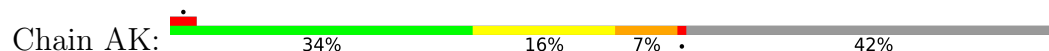
• Molecule 2: Guanine nucleotide-binding protein subunit beta-like protein

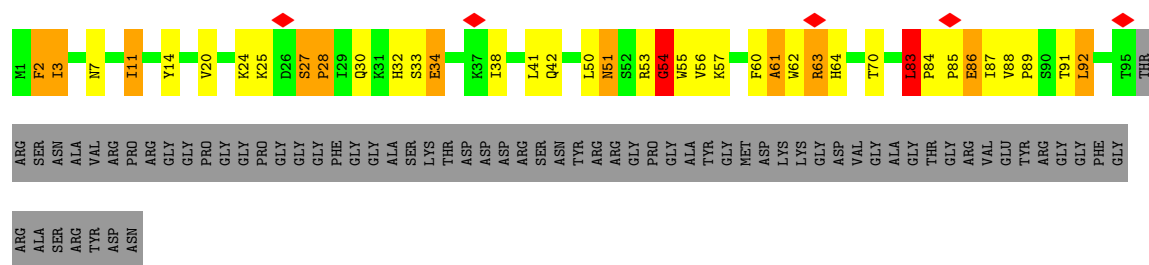


• Molecule 3: 40S ribosomal protein S20

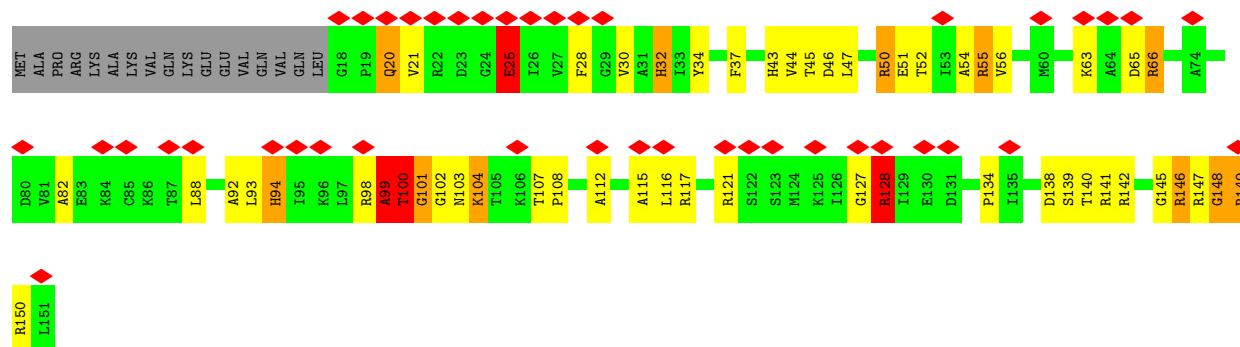


• Molecule 4: 40S ribosomal protein S10a

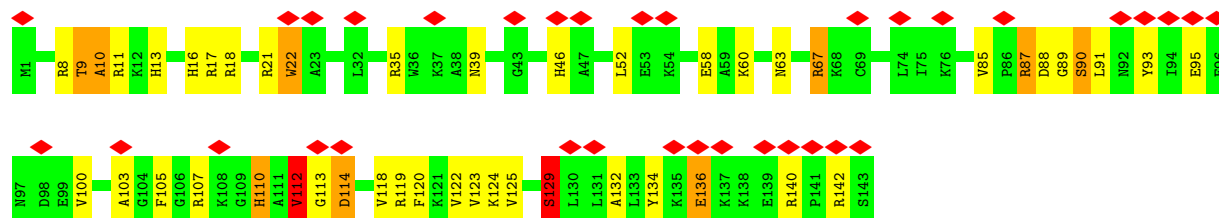




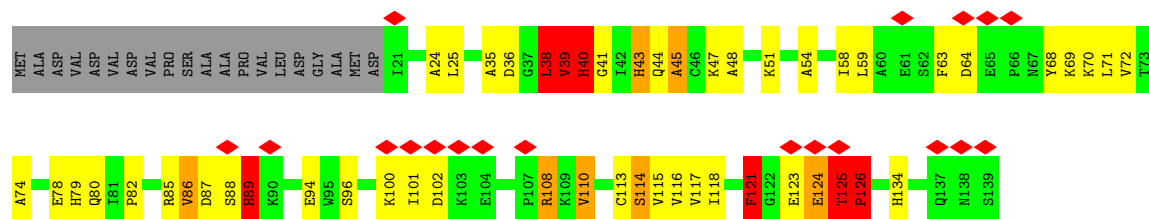
• Molecule 5: 40S ribosomal protein S14



• Molecule 6: 40S ribosomal protein S23

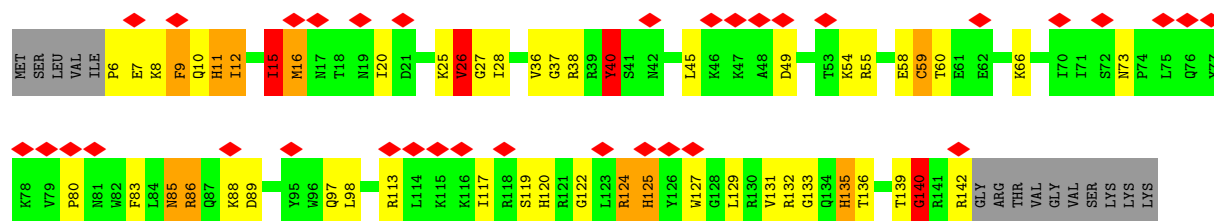


• Molecule 7: 40S ribosomal protein S12

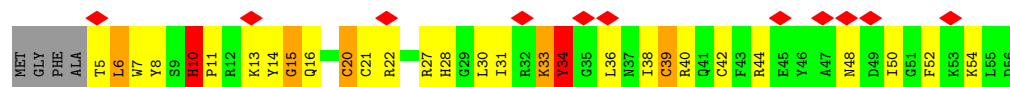
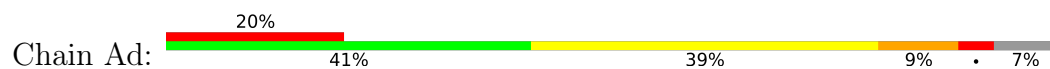


• Molecule 8: 40S ribosomal protein S18

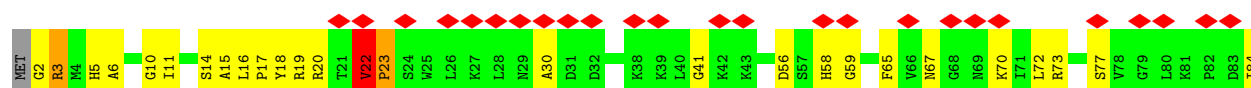




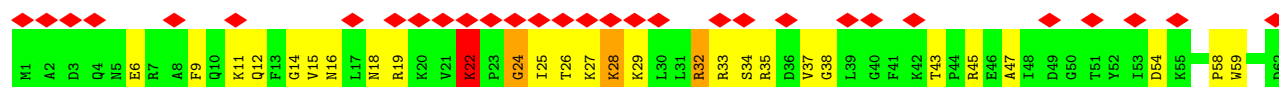
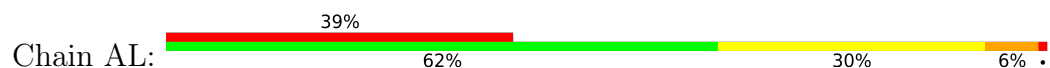
• Molecule 9: 40S ribosomal protein S29



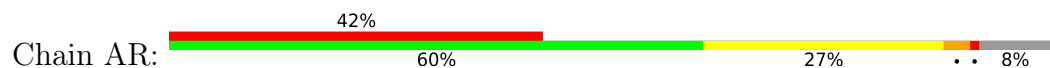
• Molecule 10: 40S ribosomal protein S13



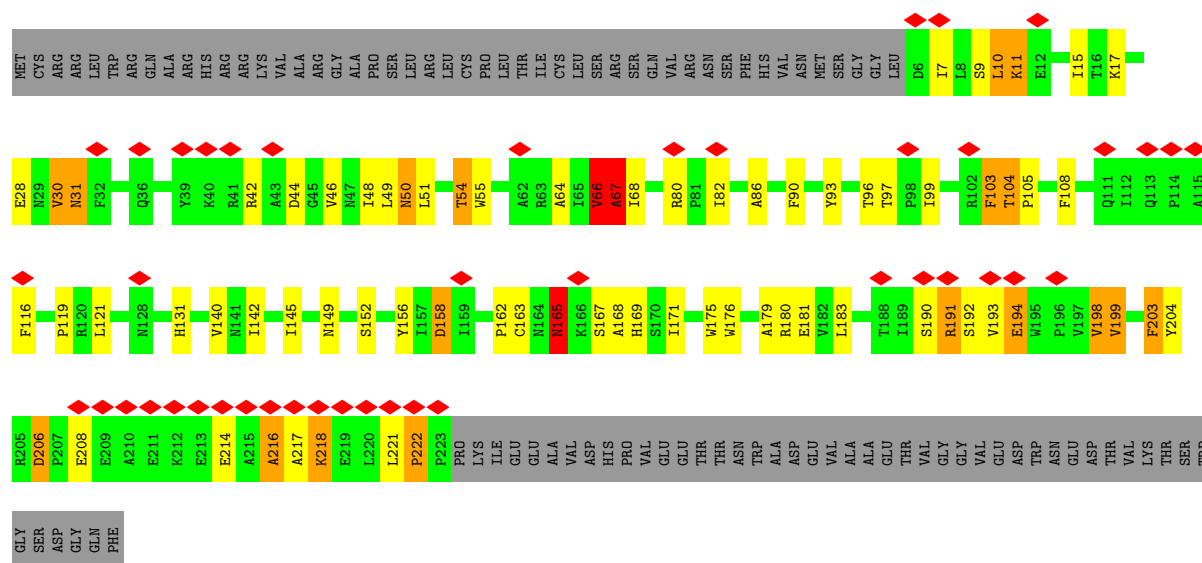
• Molecule 11: 40S ribosomal protein S11



• Molecule 12: 40S ribosomal protein S17

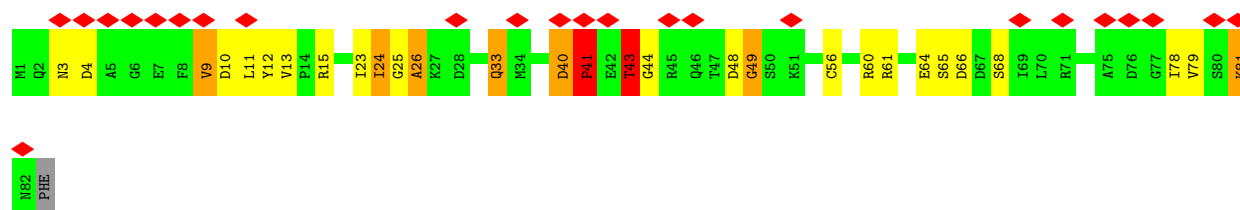






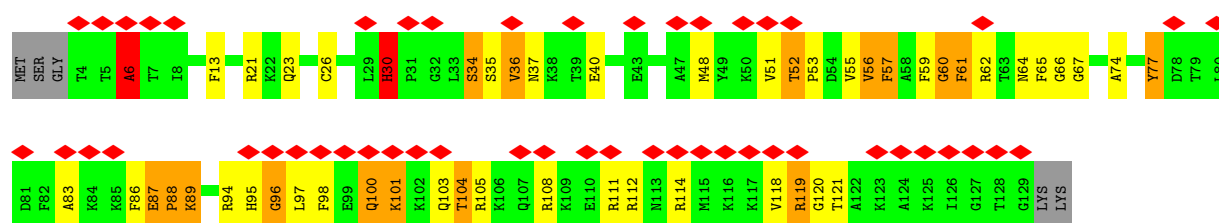
• Molecule 17: 40S ribosomal protein S21

Chain AV: 29% 64% 24% 8% ..



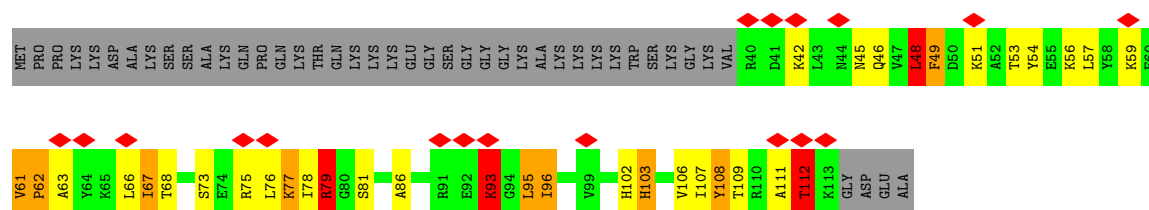
• Molecule 18: 40S ribosomal protein S24

Chain AY: 38% 57% 25% 12% ..

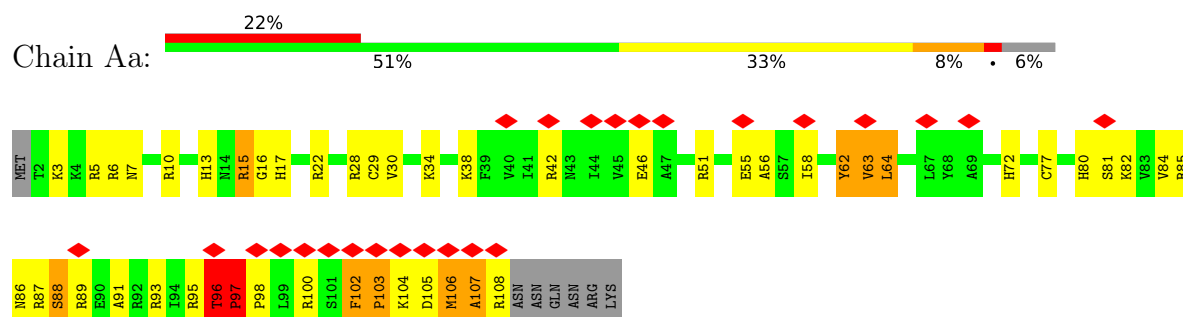


• Molecule 19: 40S ribosomal protein S25

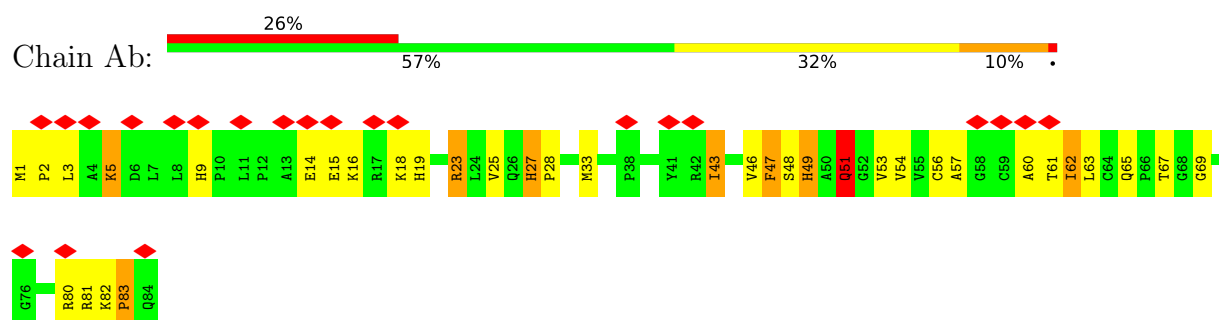
Chain AZ: 15% 32% 20% 8% . 37%



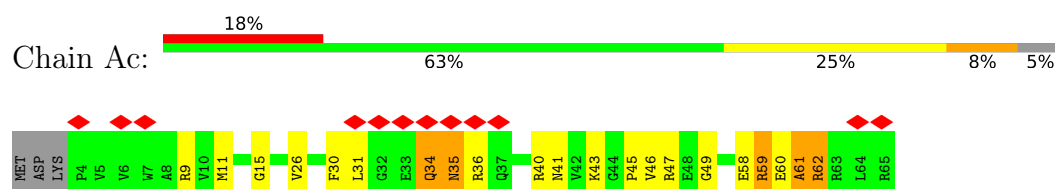
• Molecule 20: 40S ribosomal protein S26



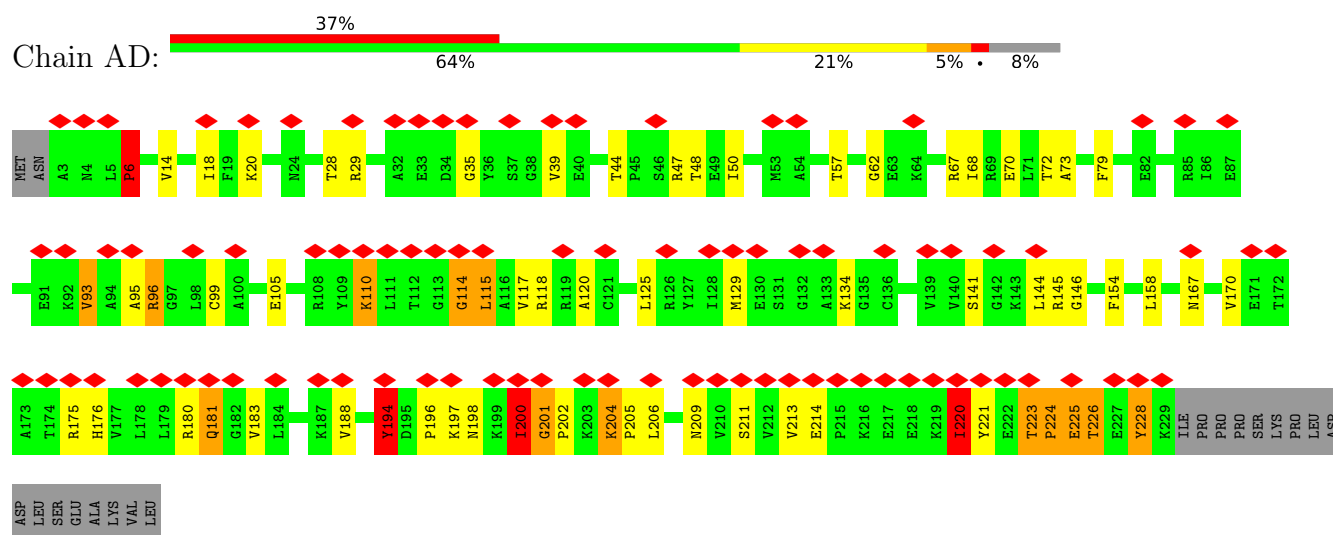
• Molecule 21: 40S ribosomal protein S27



• Molecule 22: 40S ribosomal protein S28

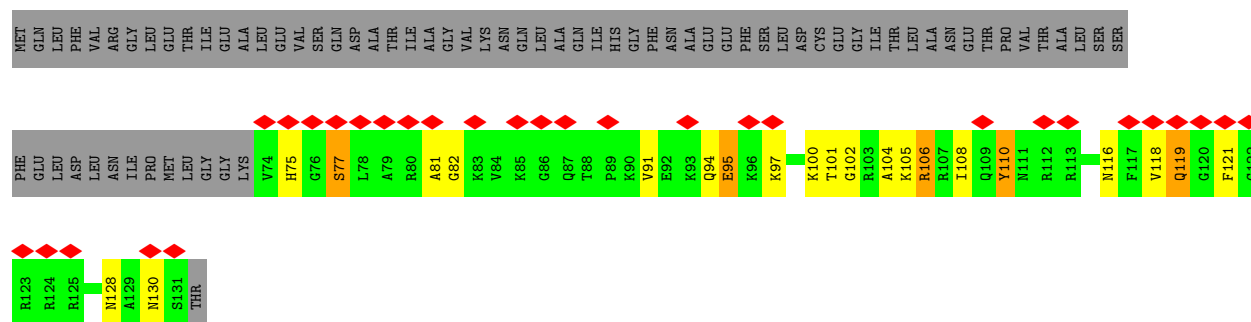


• Molecule 23: 40S ribosomal protein S3



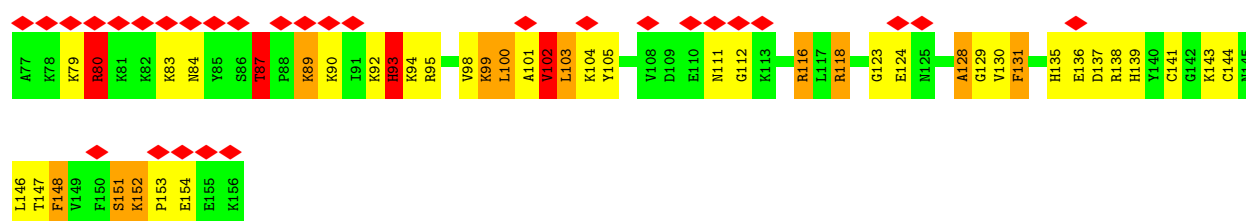
• Molecule 24: 40S ribosomal protein S30, isoform A





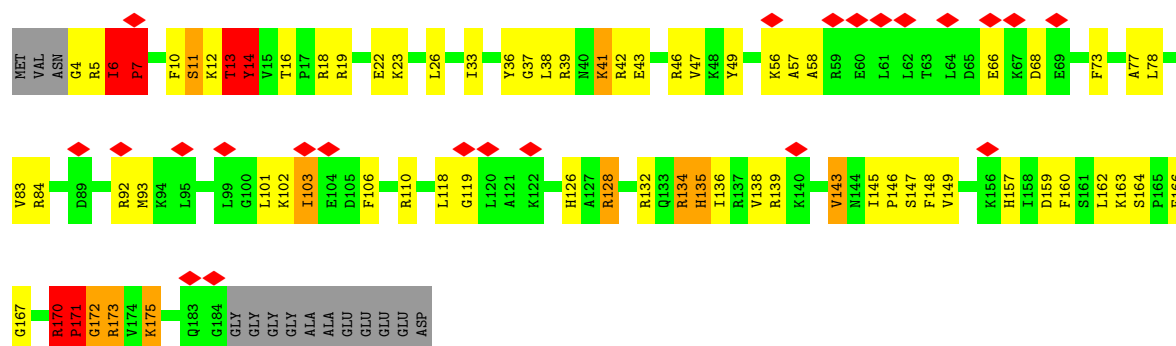
• Molecule 25: 40S ribosomal protein S27a

Chain Af: 36% 45% 36% 14% 5%



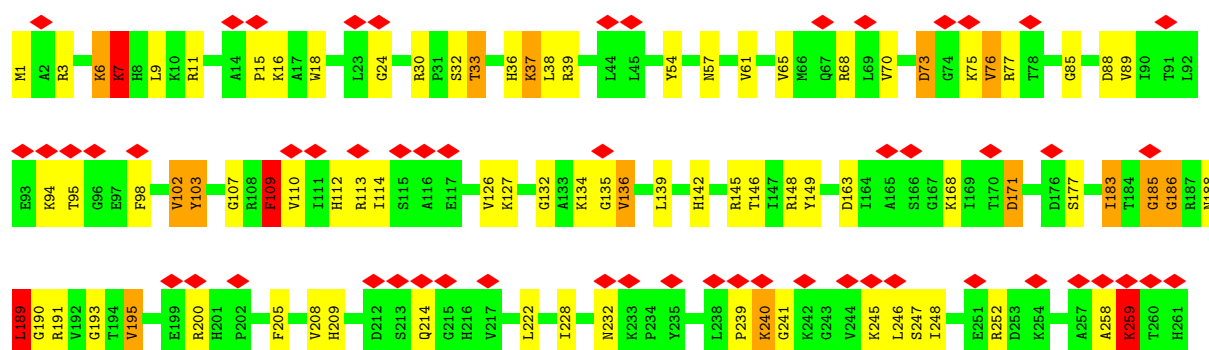
• Molecule 26: 40S ribosomal protein S9

Chain AJ: 12% 56% 29% 5% 7%

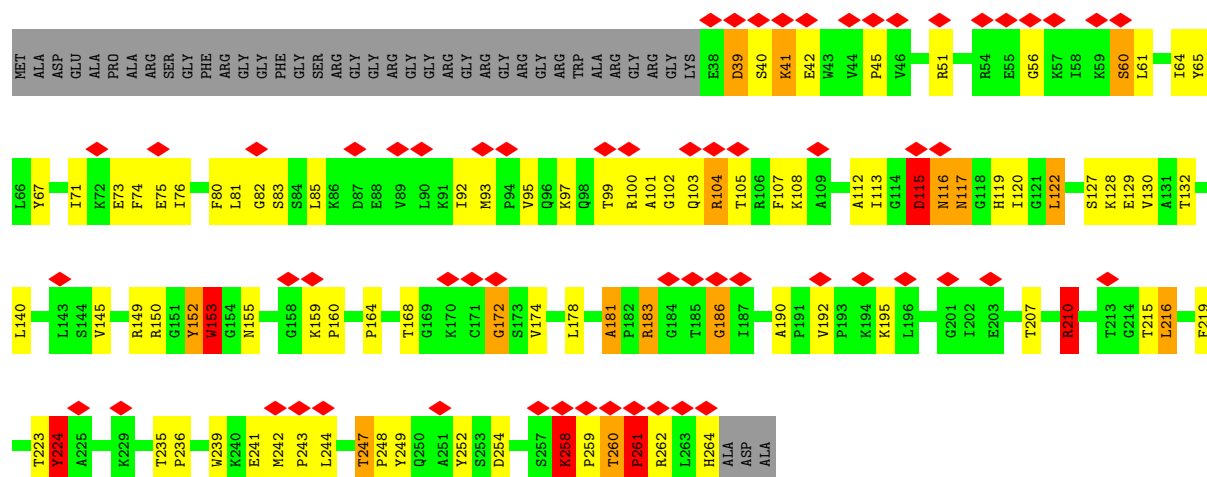


• Molecule 27: 40S ribosomal protein S4

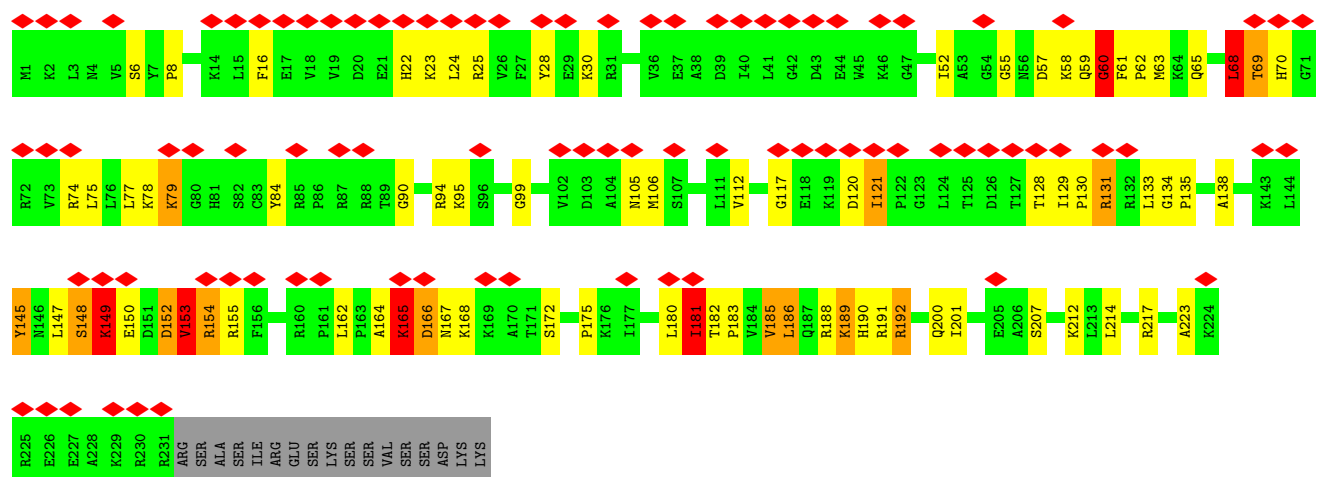
Chain AE: 21% 68% 25% 5%



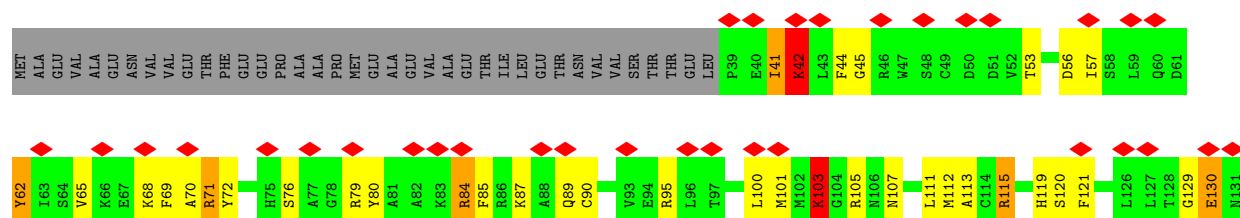
Chain AC:

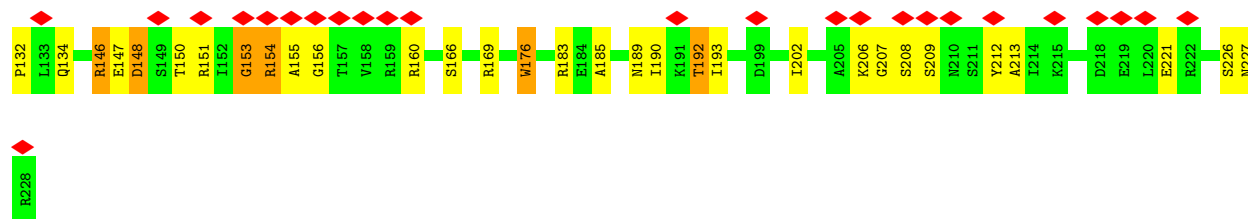


Chain AG:

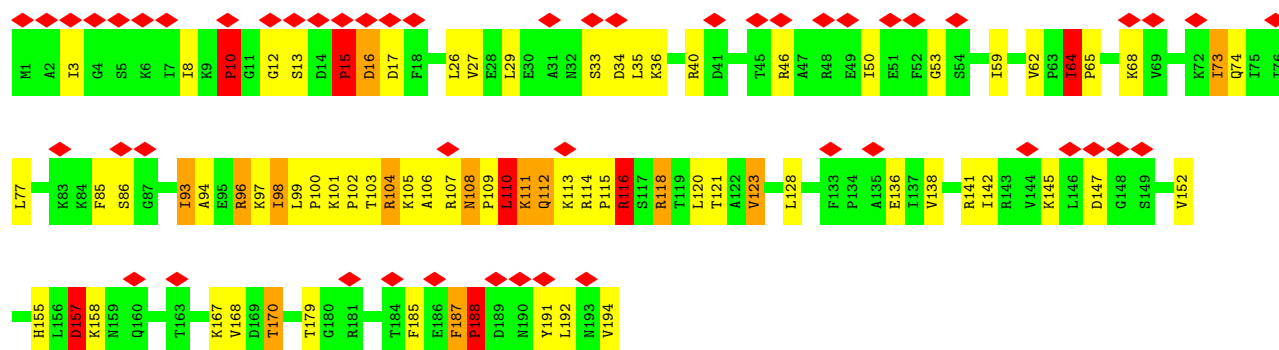


Chain AF:

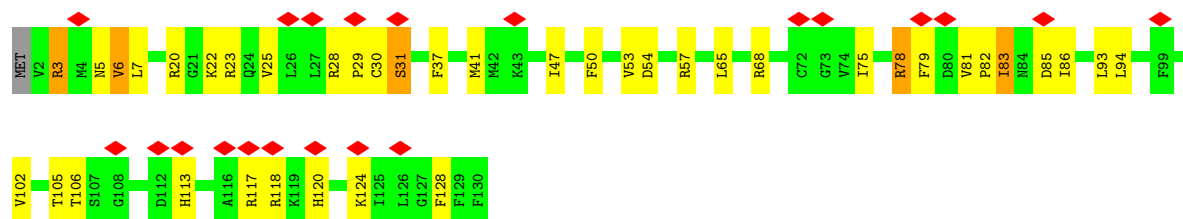
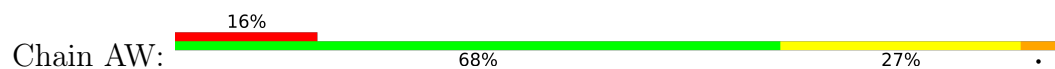




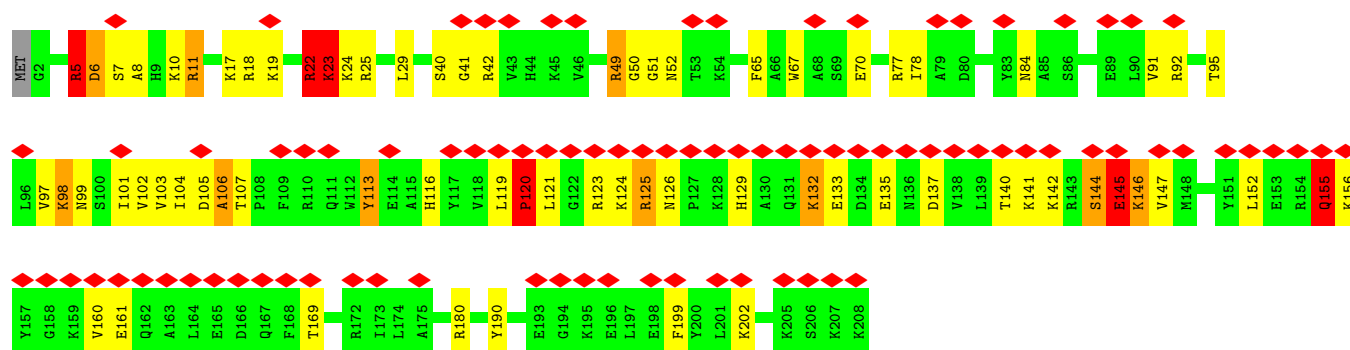
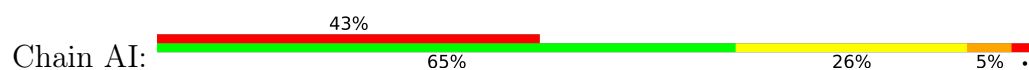
• Molecule 31: 40S ribosomal protein S7



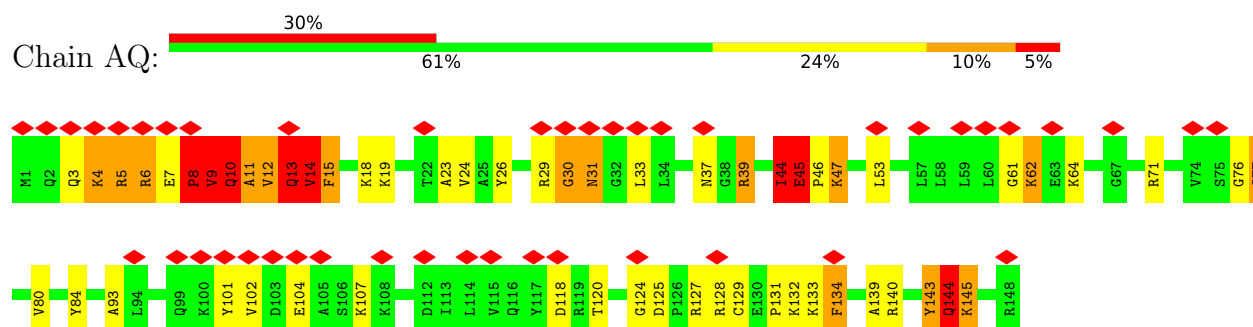
• Molecule 32: 40S ribosomal protein S15Aa



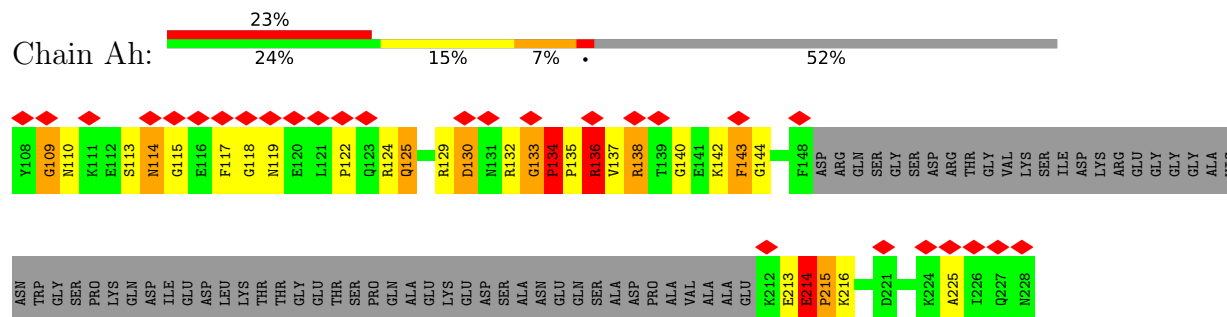
• Molecule 33: 40S ribosomal protein S8



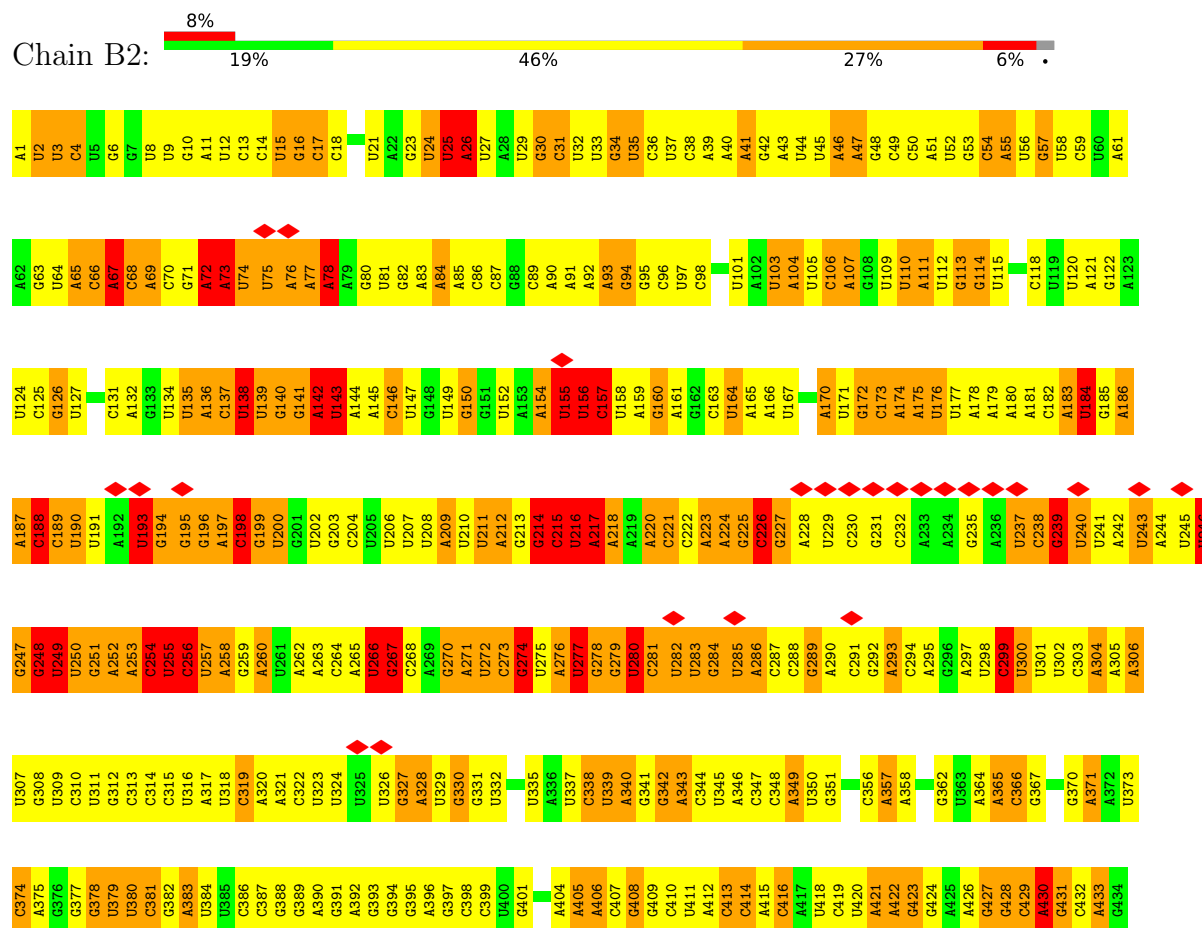
• Molecule 34: 40S ribosomal protein S16



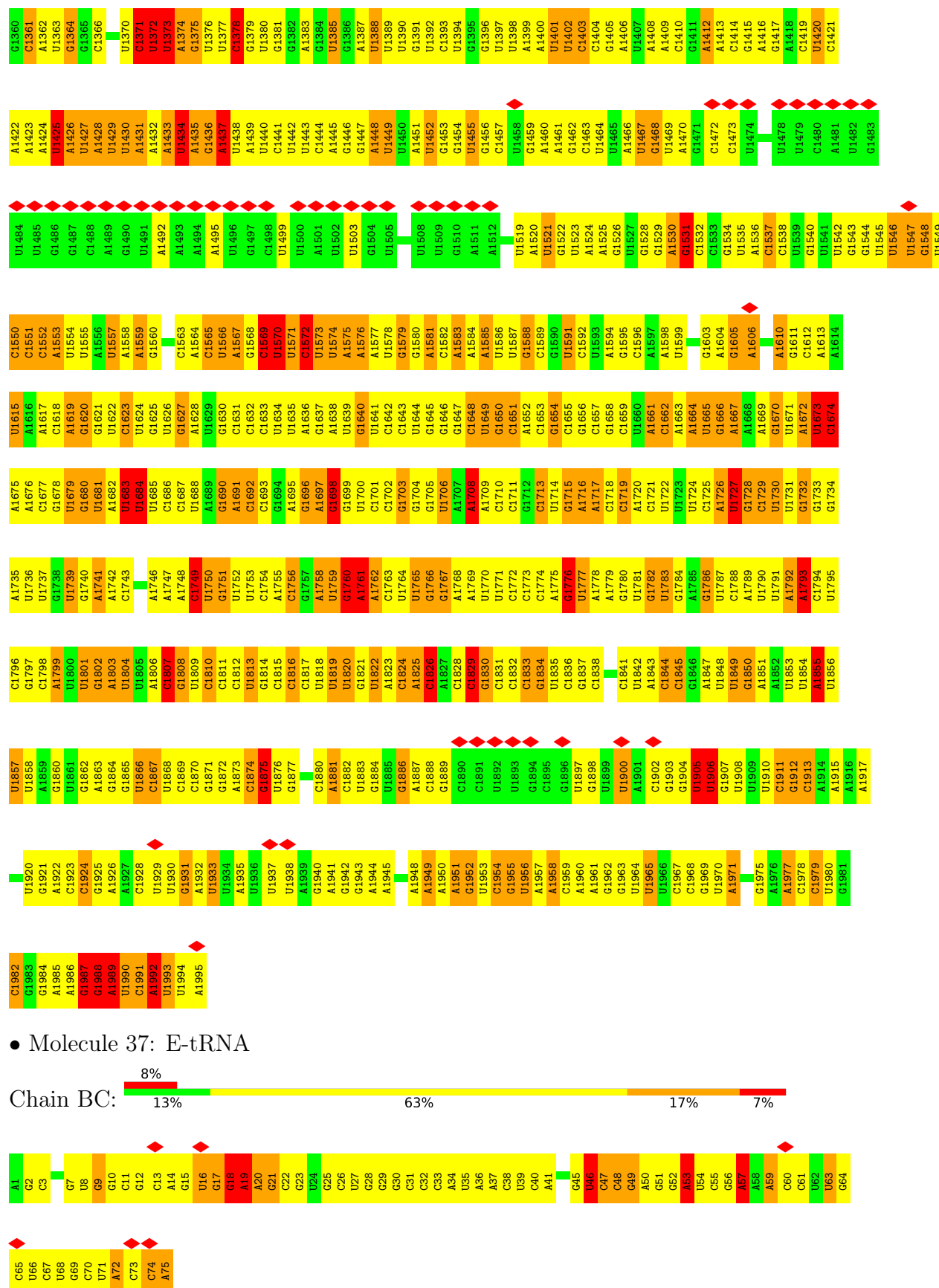
• Molecule 35: Vig2, isoform B



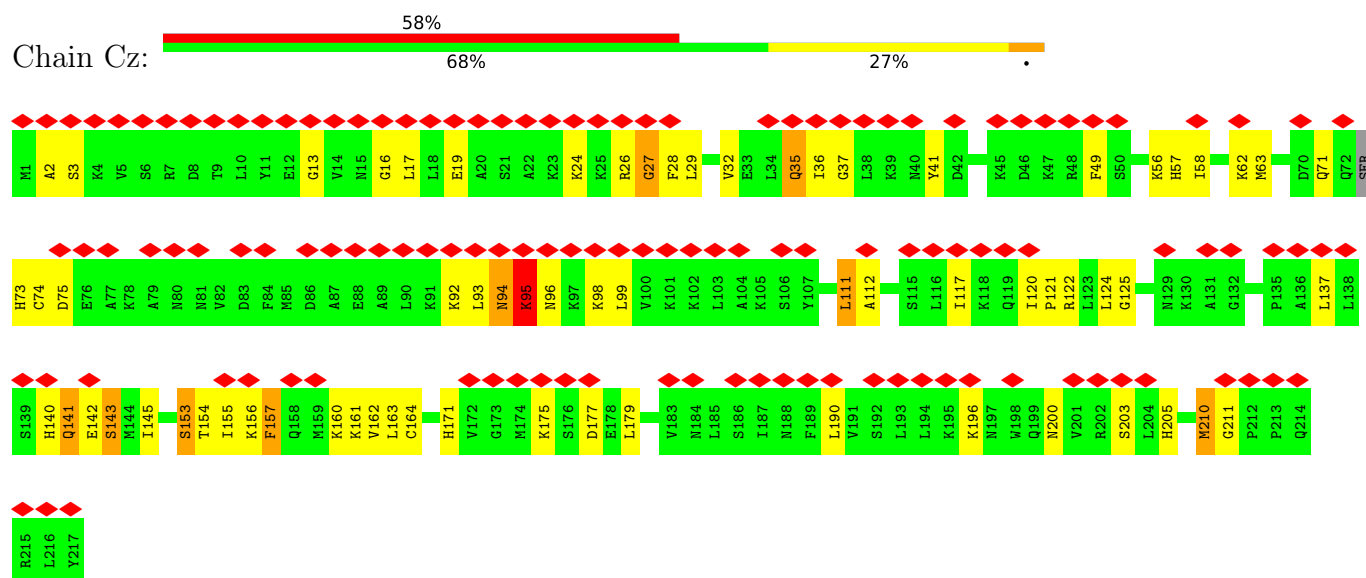
• Molecule 36: 18S ribosomal RNA



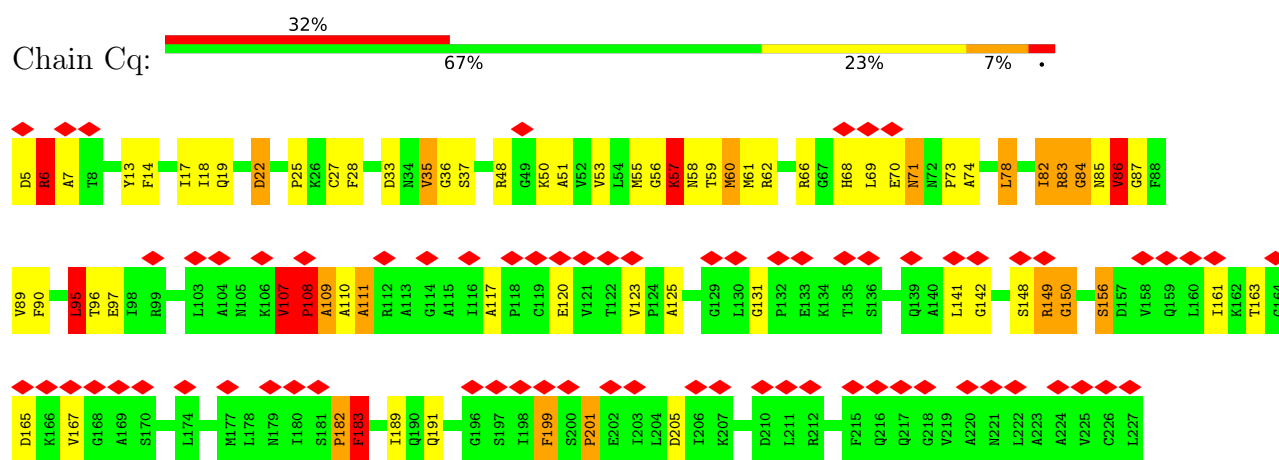




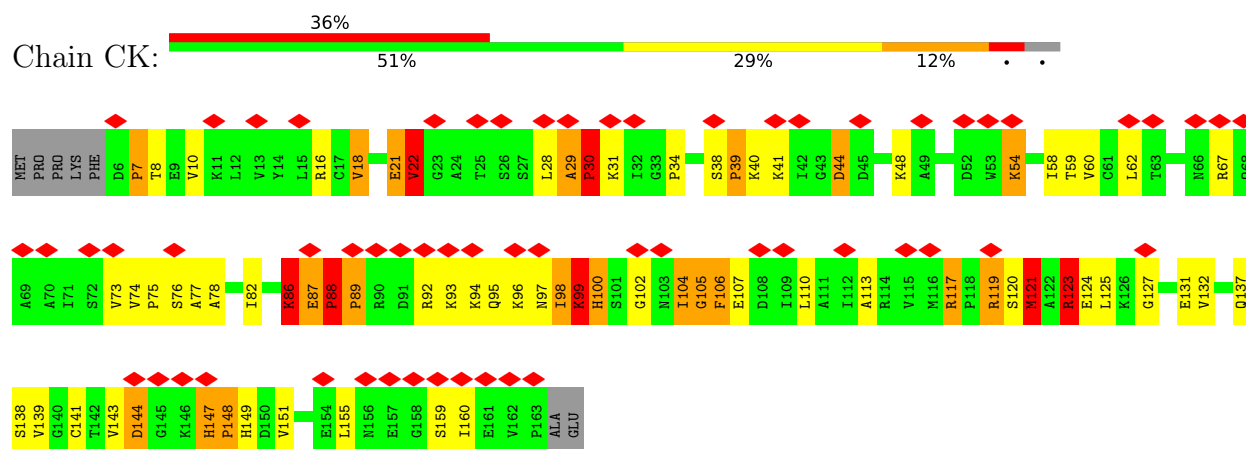
- Molecule 38: 60S ribosomal protein L10a-2



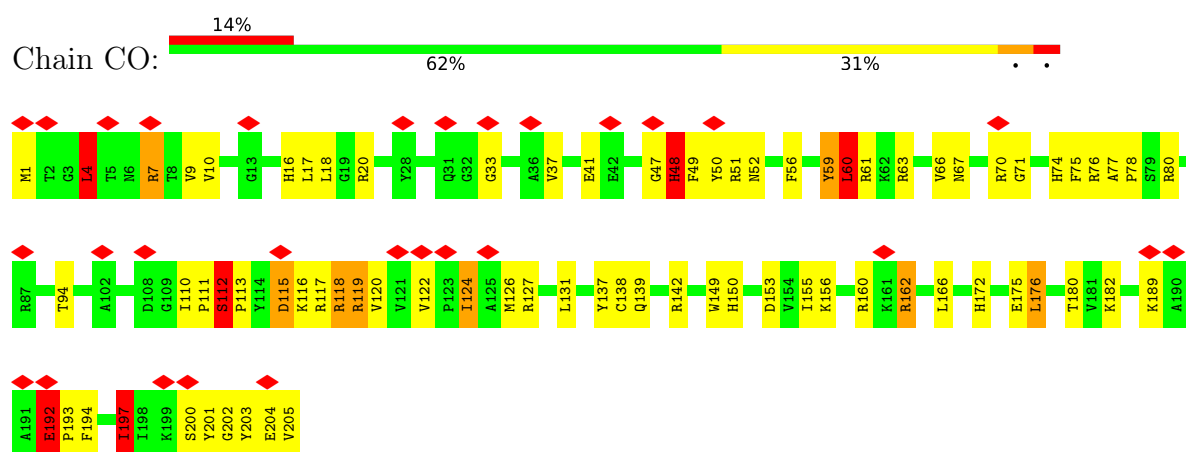
- Molecule 39: 60S acidic ribosomal protein P0



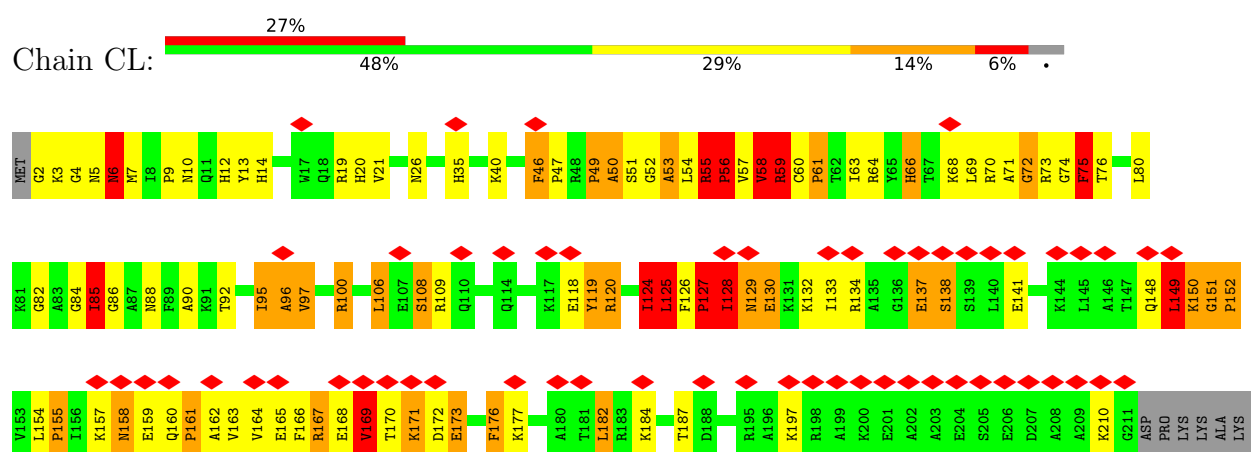
- Molecule 40: 60S ribosomal protein L12



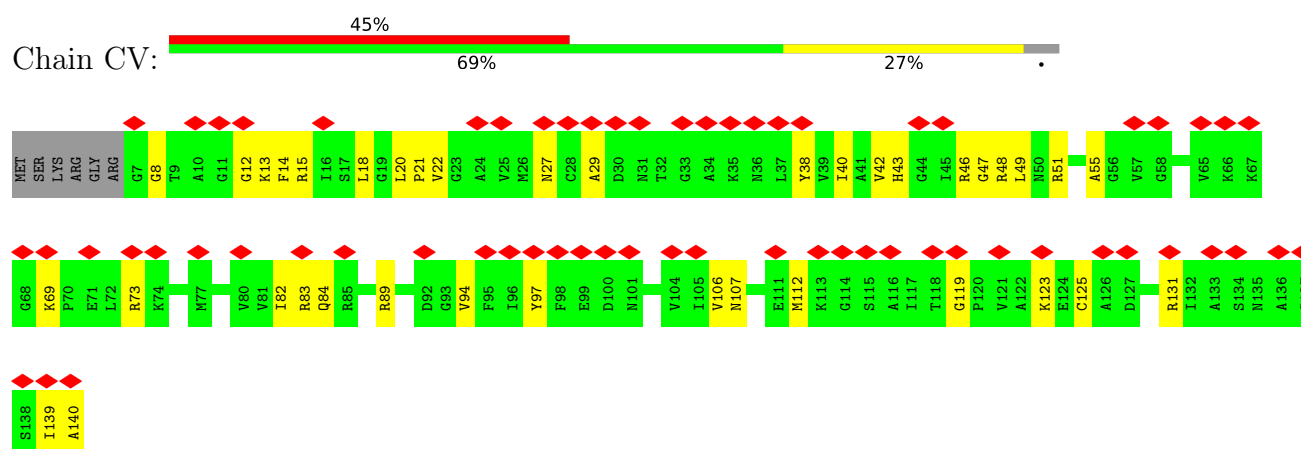
- Molecule 41: 60S ribosomal protein L13a



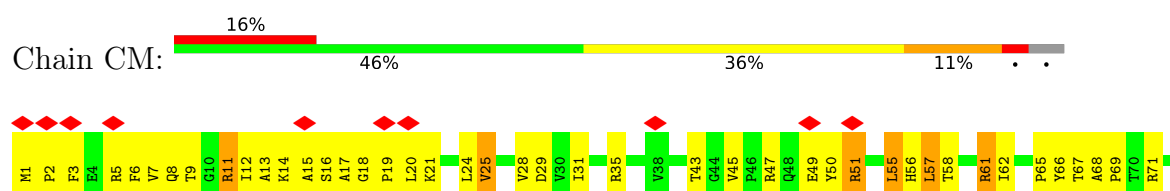
• Molecule 42: 60S ribosomal protein L13

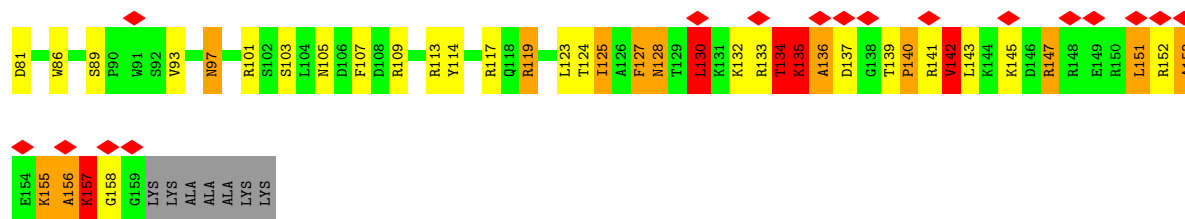


• Molecule 43: 60S ribosomal protein L23

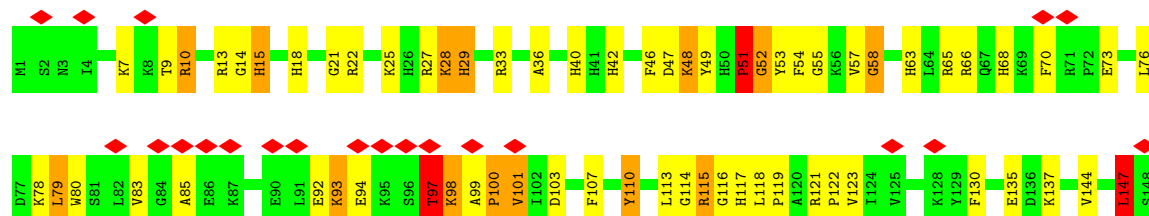


• Molecule 44: 60S ribosomal protein L14

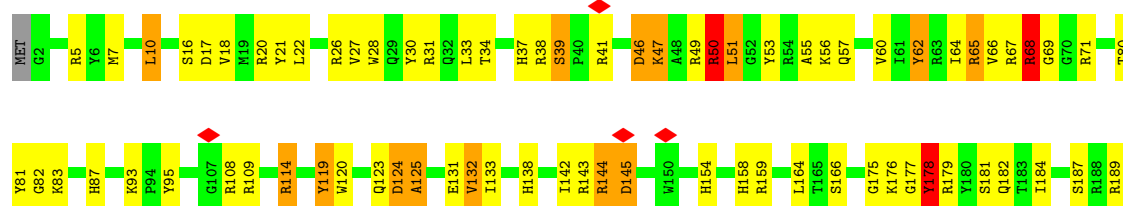




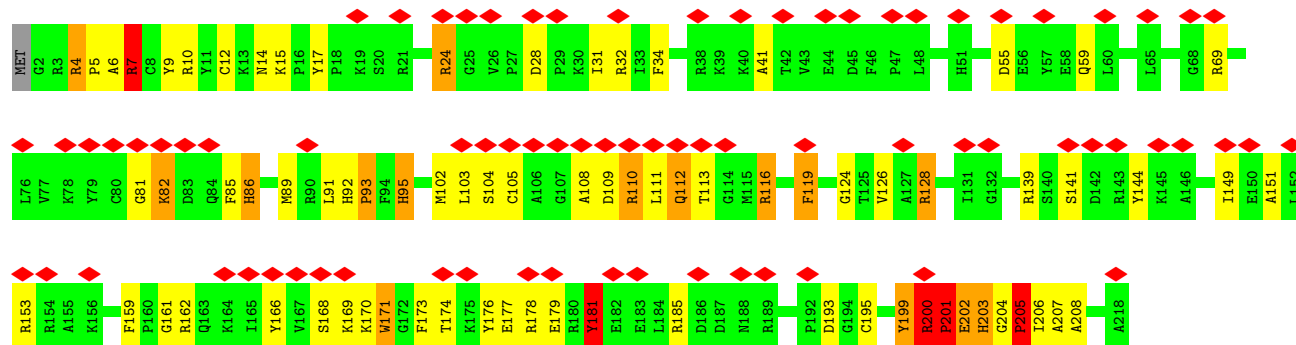
• Molecule 45: 60S ribosomal protein L27a



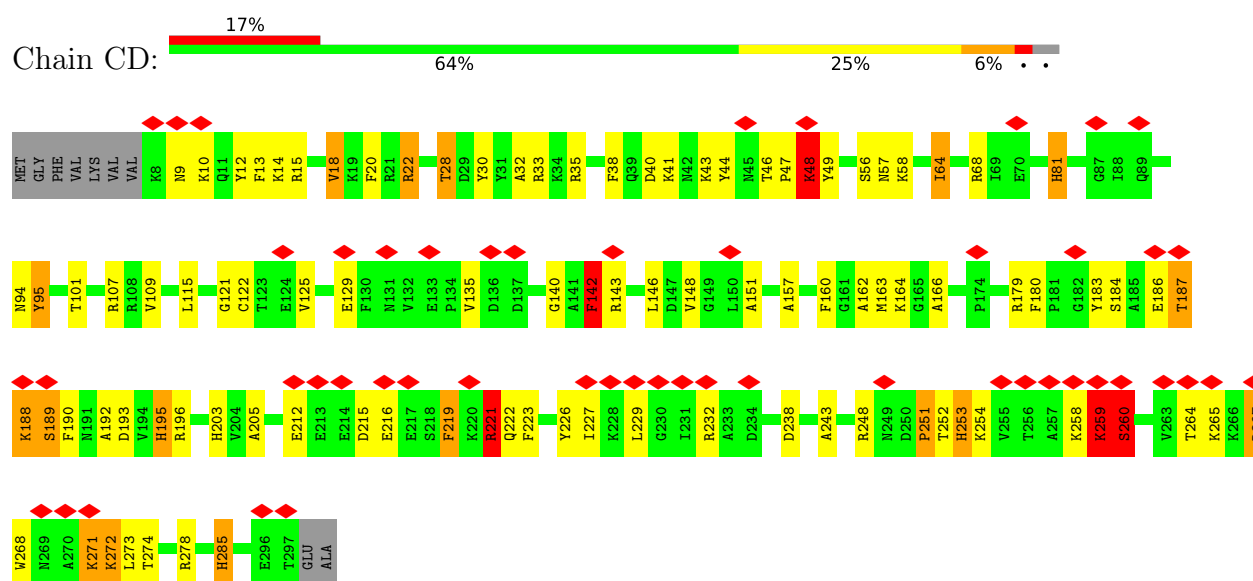
• Molecule 46: 60S ribosomal protein L15



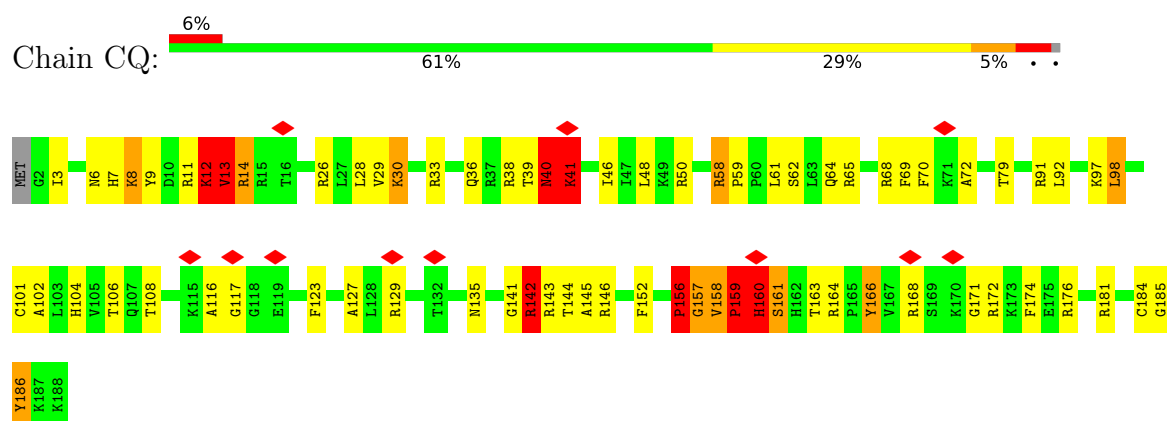
• Molecule 47: 60S ribosomal protein L10



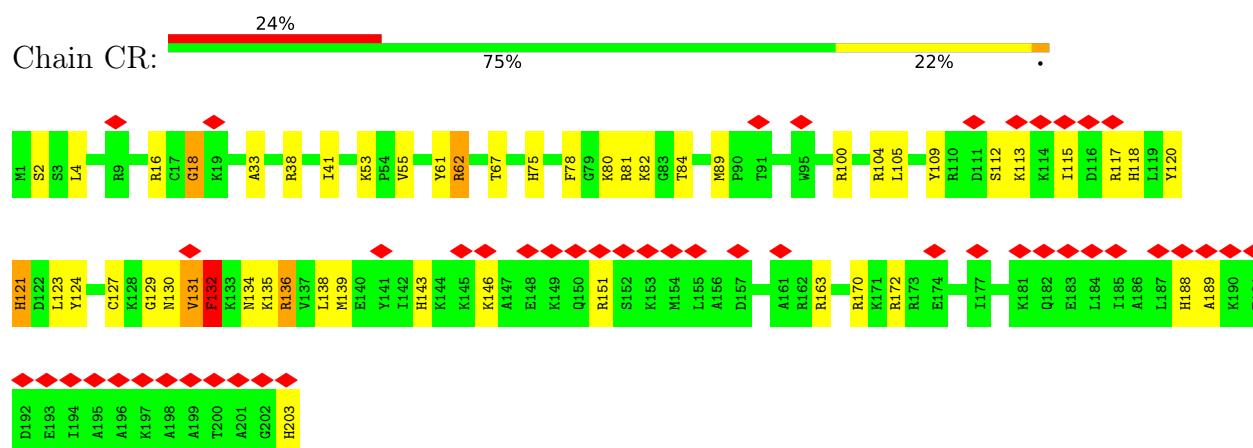
• Molecule 48: 60S ribosomal protein L5



• Molecule 49: 60S ribosomal protein L18

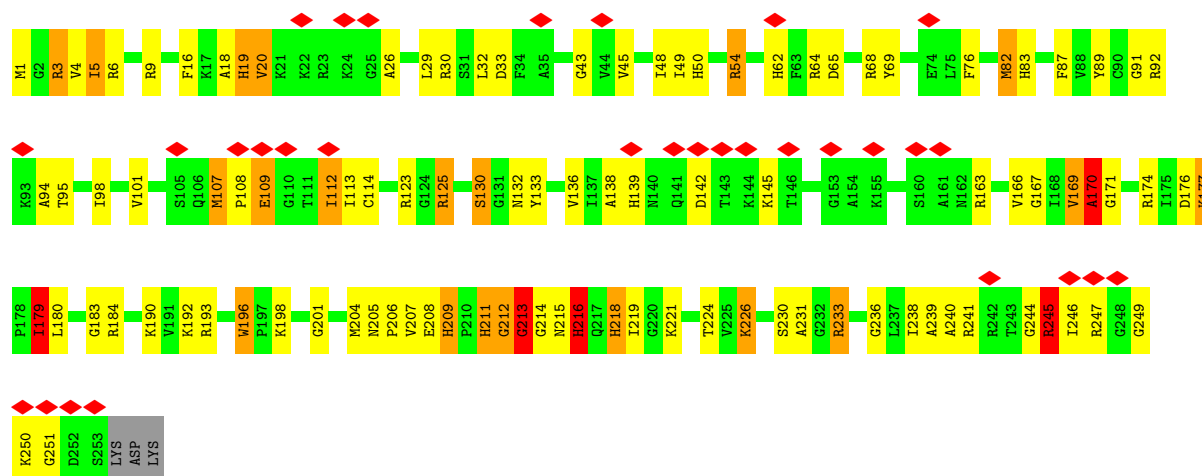


• Molecule 50: 60S ribosomal protein L19

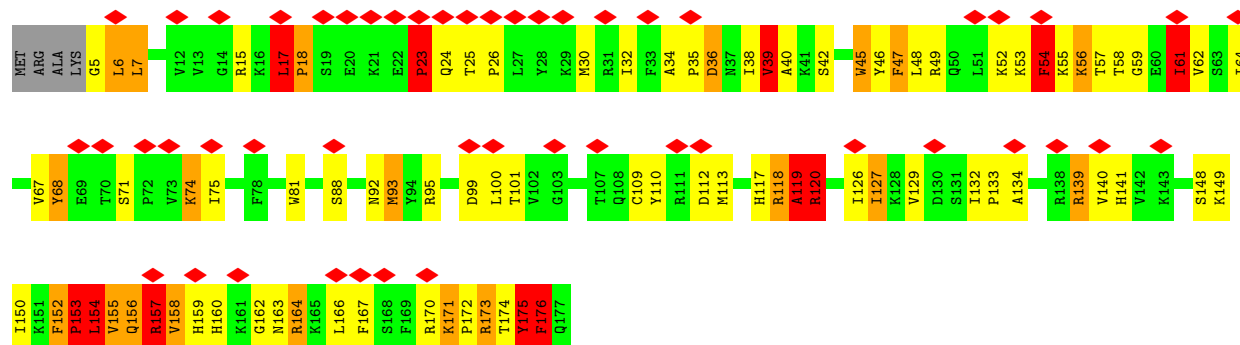


• Molecule 51: 60S ribosomal protein L8

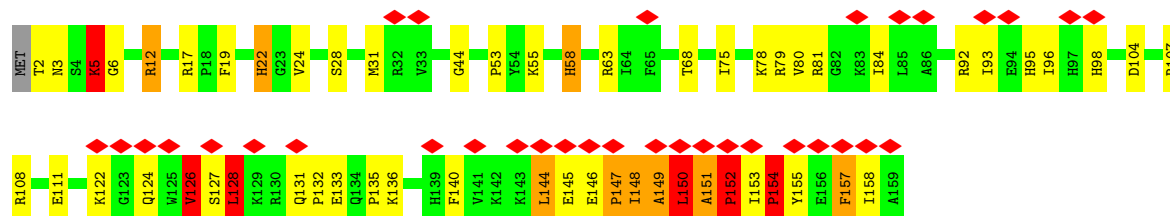




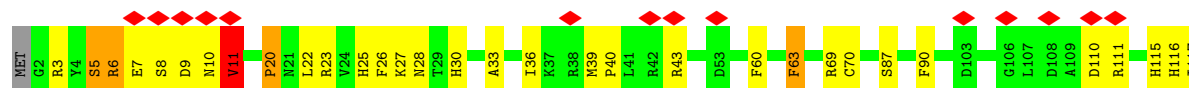
• Molecule 52: 60S ribosomal protein L18a

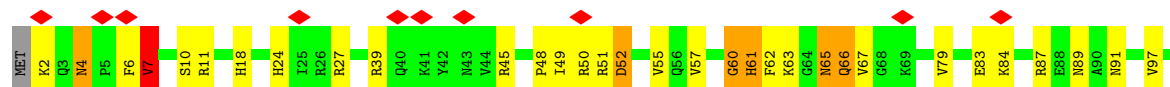


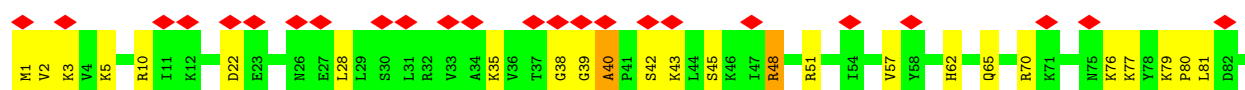
• Molecule 53: 60S ribosomal protein L21

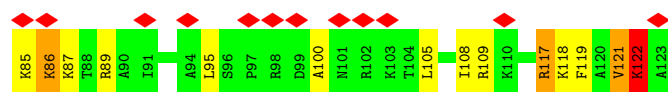


• Molecule 54: 60S ribosomal protein L17

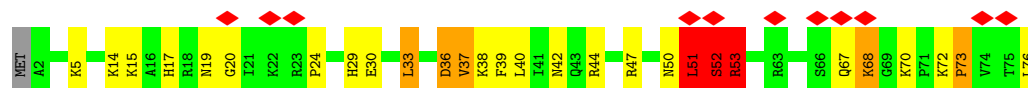




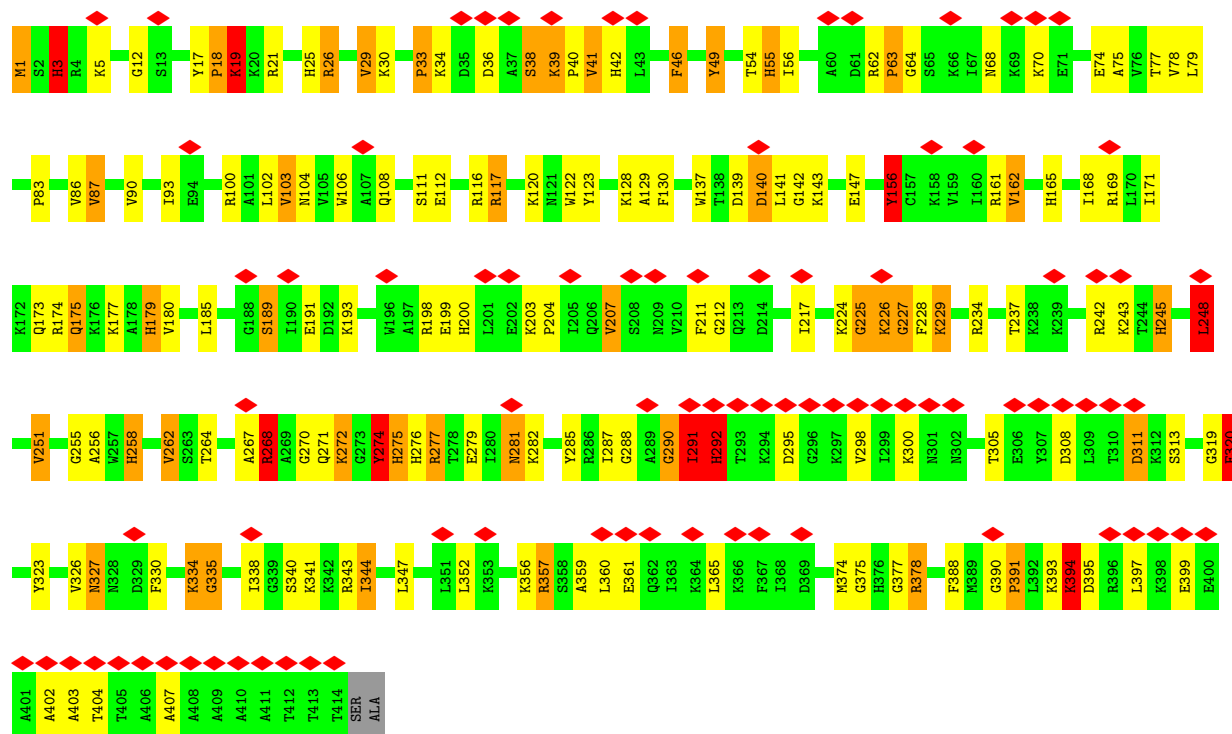




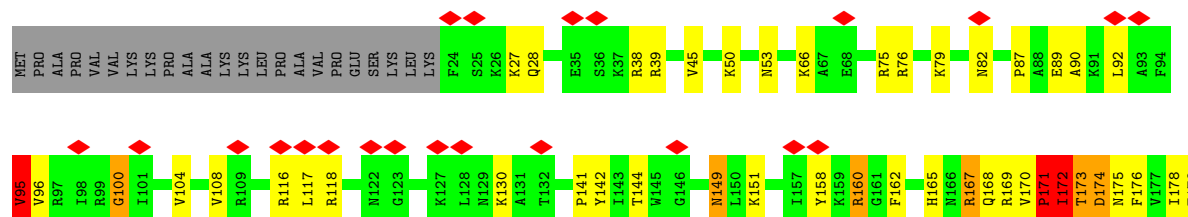
- Molecule 62: 60S ribosomal protein L29

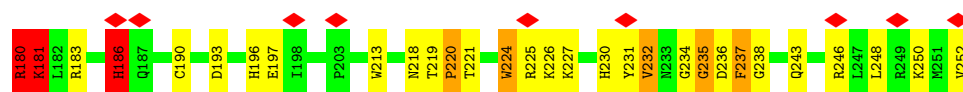


- Molecule 63: 60S ribosomal protein L3

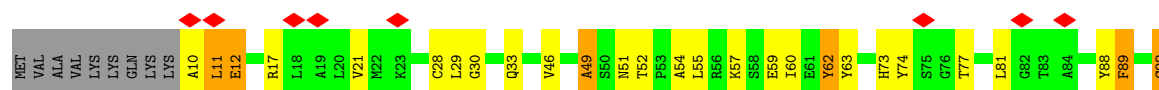


- Molecule 64: 60S ribosomal protein L7

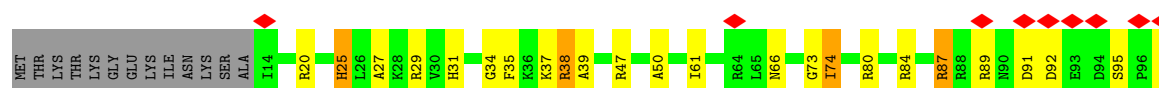




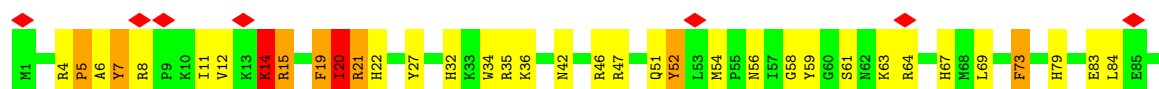
- Molecule 65: 60S ribosomal protein L30



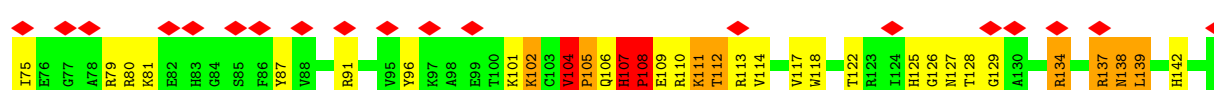
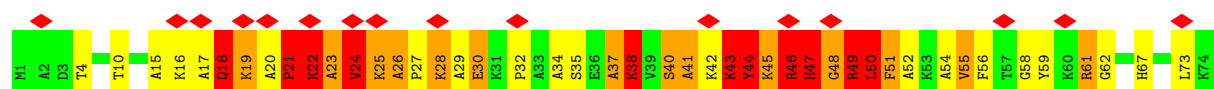
- Molecule 66: 60S ribosomal protein L31



- Molecule 67: 60S ribosomal protein L32

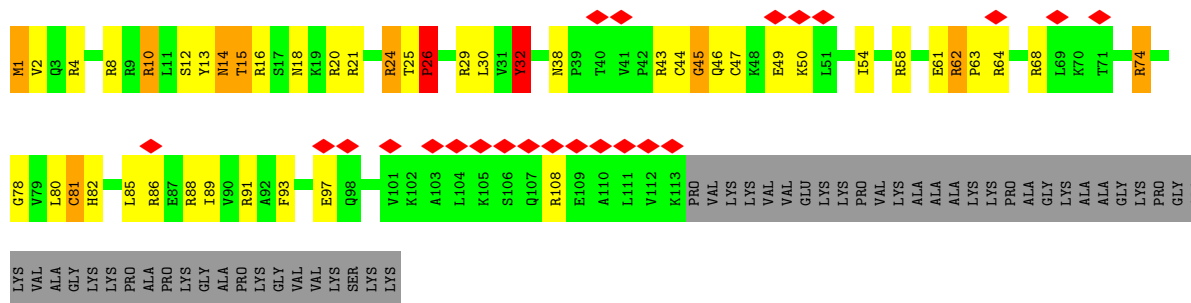


- Molecule 68: 60S ribosomal protein L35A

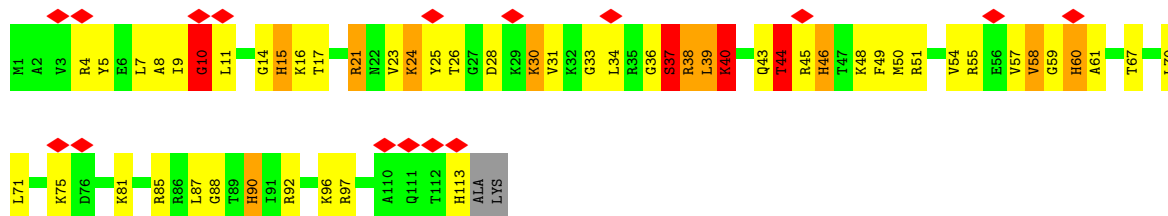




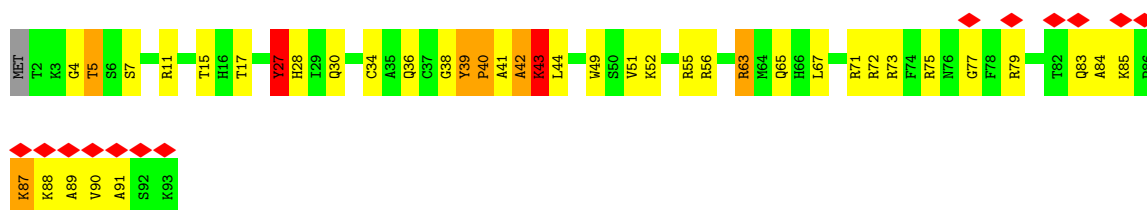
- Molecule 69: 60S ribosomal protein L34a



- Molecule 70: 60S ribosomal protein L36



- Molecule 71: 60S ribosomal protein L37-A

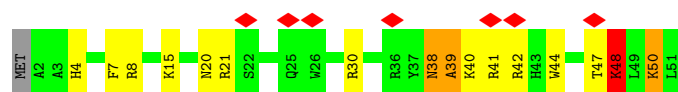


- Molecule 72: 60S ribosomal protein L38

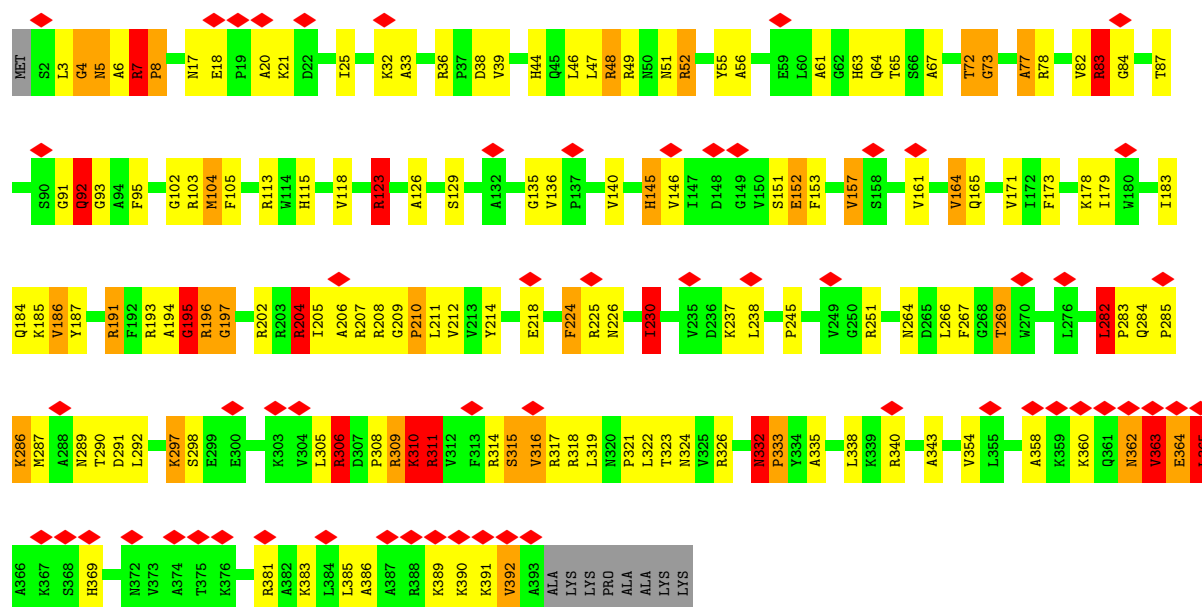


- Molecule 73: 60S ribosomal protein L39

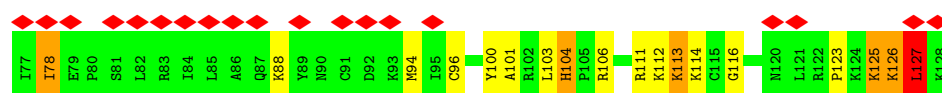
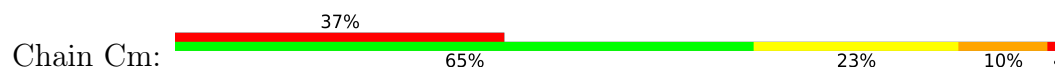




- Molecule 74: 60S ribosomal protein L4



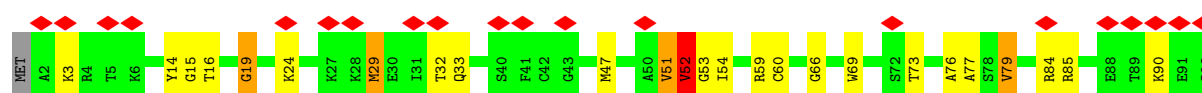
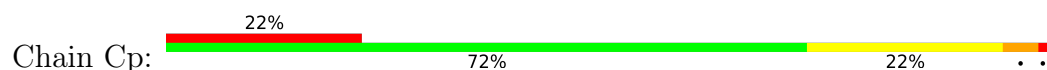
- Molecule 75: 60S ribosomal protein L40



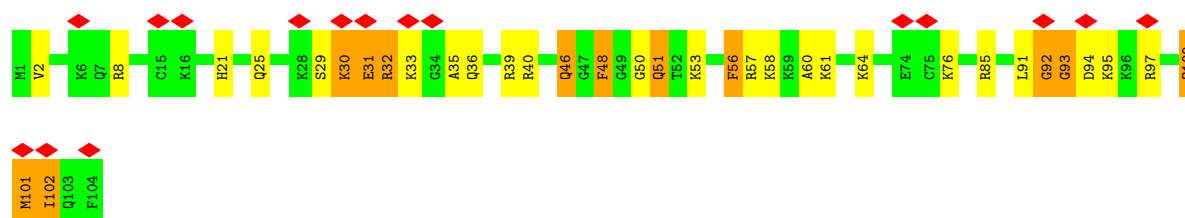
- Molecule 76: 60S ribosomal protein L41



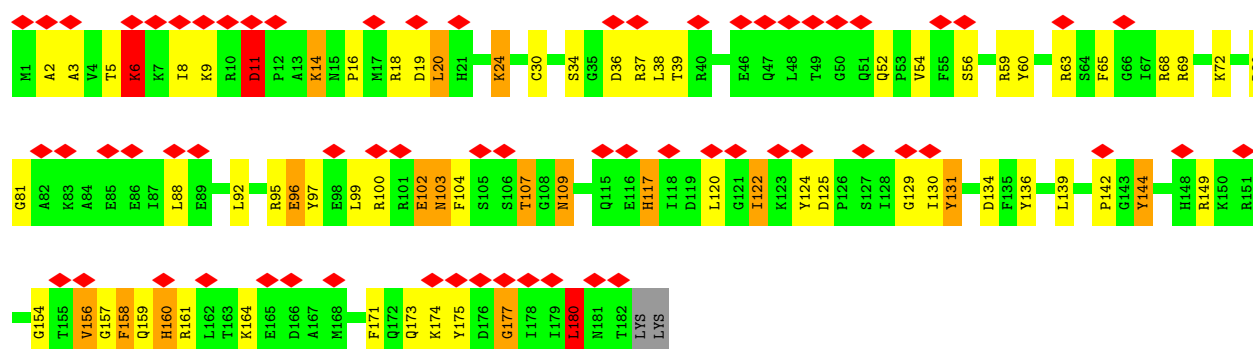
- Molecule 77: 60S ribosomal protein L37a



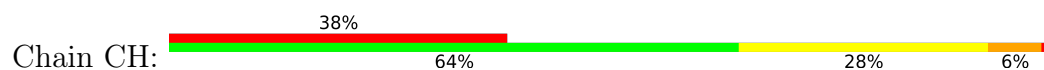
- Molecule 78: 60S ribosomal protein L36A



• Molecule 79: 60S ribosomal protein L11

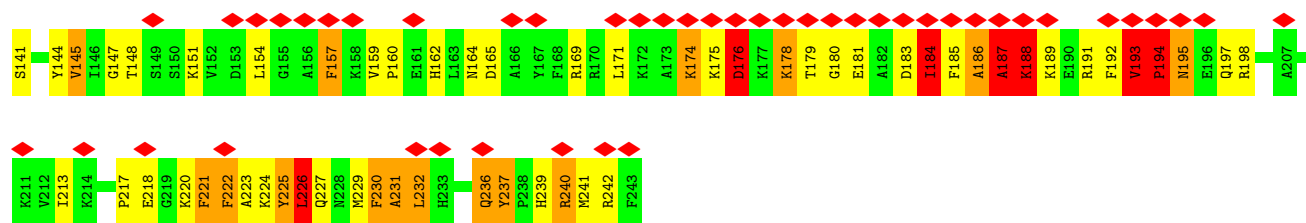


• Molecule 80: 60S ribosomal protein L9

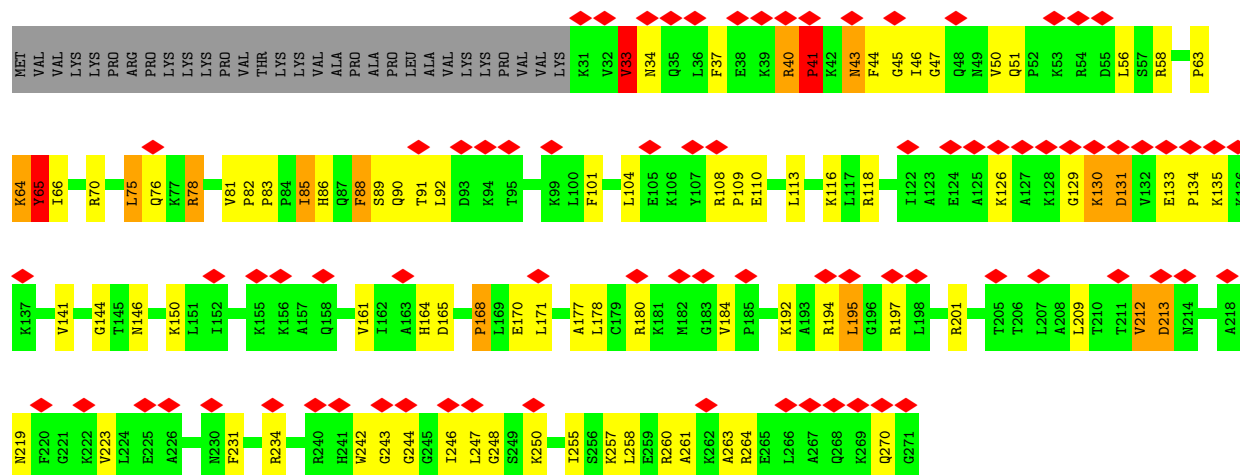


• Molecule 81: 60S ribosomal protein L6, isoform A

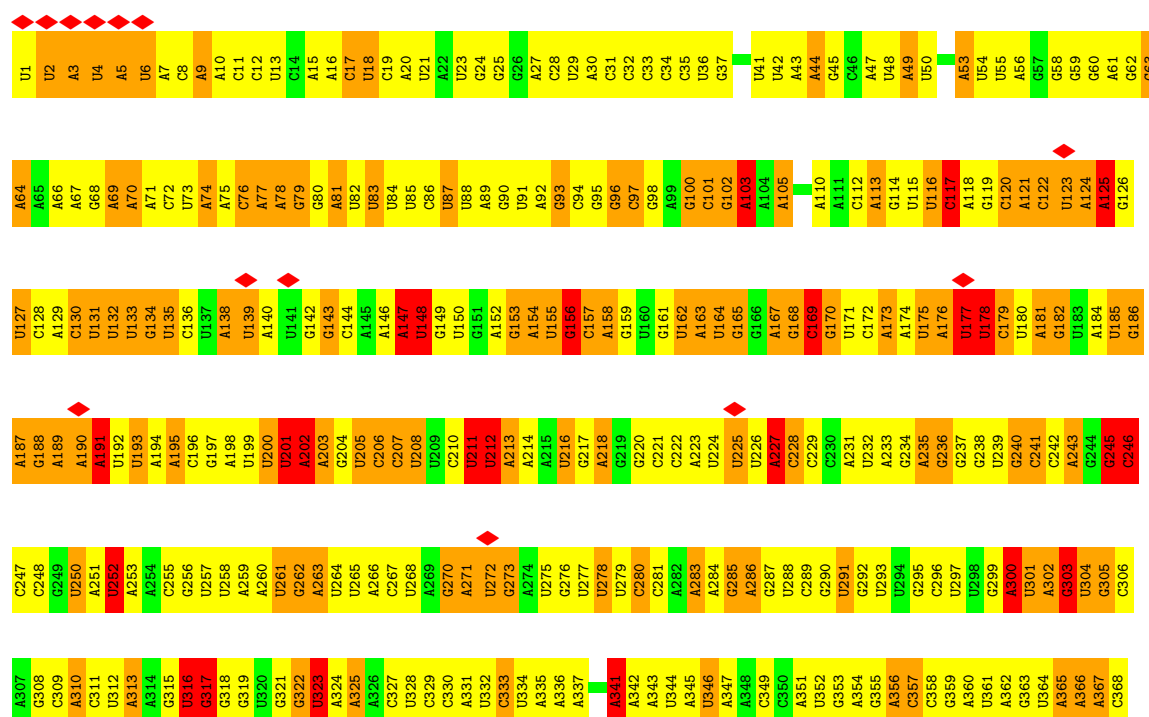
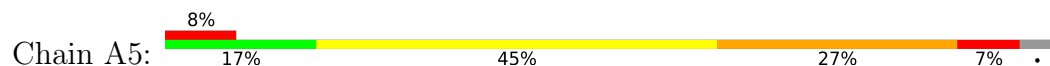




• Molecule 82: 60S ribosomal protein L7a



• Molecule 83: 28S ribosomal RNA

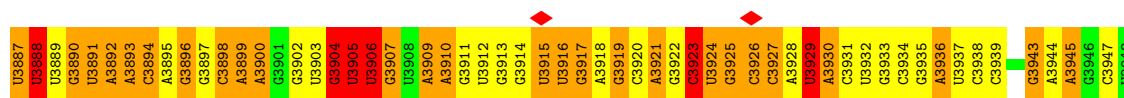




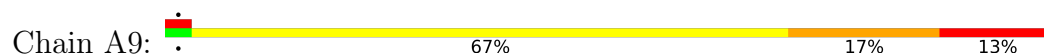
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G2102	G2041	A1979	U1918	A	A1797	G1735			A1487	A1426	A1304
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C2105	G2043	U1859	U1859	U1859	U1799	U1737	G1615	A1552	A1489	C1553	G1367
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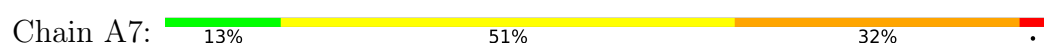
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C3885	U3825	A3765	G3702	U3642	G3582	U3520	C3461	C3398	A3336	A3272	G3145	U3145	U3072
U3886	A3826	U3766	C3703	G3642	A3582	A3521			G3337		A3211	G3146	U3073
												C3148	G3074
												U3149	A3074
													U3075
													U3076
													U3077
													G3078
													A3079
													A3080
													A3081
													A3082
													U3083



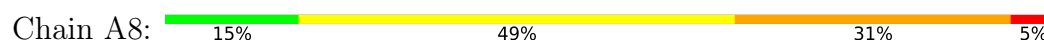
• Molecule 84: 2S ribosomal RNA



• Molecule 85: 5S ribosomal RNA



• Molecule 86: 5.8S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134500	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	each subvolume	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	90000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	1.943	Depositor
Minimum map value	-0.877	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.168	Depositor
Recommended contour level	0.49	Depositor
Map size ($\text{\AA}$)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2375, 1.2375, 1.2375	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Az	1.61	28/6704 (0.4%)	2.30	405/9051 (4.5%)
2	Ag	1.60	9/2574 (0.3%)	1.86	61/3506 (1.7%)
3	AU	1.73	5/825 (0.6%)	2.01	33/1111 (3.0%)
4	AK	1.57	1/819 (0.1%)	2.05	32/1110 (2.9%)
5	AO	1.67	10/1016 (1.0%)	2.15	44/1364 (3.2%)
6	AX	1.70	5/1152 (0.4%)	2.05	42/1540 (2.7%)
7	AM	1.60	6/937 (0.6%)	2.26	37/1260 (2.9%)
8	AS	1.66	7/1146 (0.6%)	2.14	39/1535 (2.5%)
9	Ad	1.71	4/443 (0.9%)	2.13	22/589 (3.7%)
10	AN	1.64	7/1225 (0.6%)	2.14	42/1641 (2.6%)
11	AL	1.73	13/1296 (1.0%)	1.96	31/1725 (1.8%)
12	AR	1.69	5/993 (0.5%)	2.05	34/1333 (2.6%)
13	AP	1.59	5/1036 (0.5%)	2.07	48/1383 (3.5%)
14	AT	1.70	9/1228 (0.7%)	2.19	44/1653 (2.7%)
15	AB	1.61	8/1825 (0.4%)	2.03	70/2448 (2.9%)
16	AA	1.61	8/1777 (0.5%)	2.16	80/2422 (3.3%)
17	AV	1.71	4/622 (0.6%)	2.02	22/835 (2.6%)
18	AY	2.04	12/1032 (1.2%)	2.05	45/1373 (3.3%)
19	AZ	1.66	3/616 (0.5%)	2.23	33/826 (4.0%)
20	Aa	1.74	8/883 (0.9%)	2.20	42/1184 (3.5%)
21	Ab	1.73	6/668 (0.9%)	2.11	30/898 (3.3%)
22	Ac	1.88	6/502 (1.2%)	1.96	14/670 (2.1%)
23	AD	1.65	10/1808 (0.6%)	2.02	54/2427 (2.2%)
24	Ae	1.68	3/475 (0.6%)	2.06	20/625 (3.2%)
25	Af	1.70	7/672 (1.0%)	2.22	32/887 (3.6%)
26	AJ	1.70	10/1526 (0.7%)	2.20	64/2037 (3.1%)
27	AE	1.65	18/2096 (0.9%)	1.99	58/2819 (2.1%)
28	AC	1.62	6/1785 (0.3%)	2.11	81/2415 (3.4%)
29	AG	1.71	19/1891 (1.0%)	2.11	77/2519 (3.1%)
30	AF	1.66	10/1518 (0.7%)	2.14	52/2037 (2.6%)
31	AH	1.64	4/1593 (0.3%)	2.15	75/2145 (3.5%)
32	AW	1.67	7/1046 (0.7%)	1.98	18/1402 (1.3%)
33	AI	1.64	8/1689 (0.5%)	2.07	58/2250 (2.6%)
34	AQ	1.67	6/1202 (0.5%)	2.35	61/1608 (3.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ah	1.62	3/495 (0.6%)	2.17	19/658 (2.9%)
36	B2	1.85	1372/44058 (3.1%)	1.82	1875/68404 (2.7%)
37	BC	1.81	52/1796 (2.9%)	1.68	62/2800 (2.2%)
38	Cz	1.57	7/1727 (0.4%)	2.00	48/2308 (2.1%)
39	Cq	1.59	6/1736 (0.3%)	2.07	61/2342 (2.6%)
40	CK	1.64	5/1196 (0.4%)	2.17	60/1614 (3.7%)
41	CO	1.70	15/1700 (0.9%)	2.04	66/2277 (2.9%)
42	CL	1.74	16/1726 (0.9%)	2.43	128/2308 (5.5%)
43	CV	1.65	5/1014 (0.5%)	2.03	36/1362 (2.6%)
44	CM	1.72	10/1326 (0.8%)	2.13	59/1780 (3.3%)
45	Ca	1.66	5/1235 (0.4%)	2.27	58/1640 (3.5%)
46	CN	1.82	24/1750 (1.4%)	2.10	68/2335 (2.9%)
47	CI	1.65	11/1827 (0.6%)	1.96	64/2447 (2.6%)
48	CD	1.67	11/2379 (0.5%)	2.01	75/3196 (2.3%)
49	CQ	1.70	13/1544 (0.8%)	2.10	71/2069 (3.4%)
50	CR	1.65	7/1703 (0.4%)	2.08	52/2255 (2.3%)
51	CA	1.77	23/1970 (1.2%)	2.13	75/2635 (2.8%)
52	CS	1.66	7/1491 (0.5%)	2.19	79/1998 (4.0%)
53	CT	1.66	8/1326 (0.6%)	2.09	48/1773 (2.7%)
54	CP	1.70	14/1529 (0.9%)	1.99	41/2042 (2.0%)
55	CU	1.56	2/974 (0.2%)	1.87	24/1302 (1.8%)
56	CX	1.69	9/1001 (0.9%)	2.10	34/1348 (2.5%)
57	CY	1.75	6/1094 (0.5%)	2.05	33/1456 (2.3%)
58	CW	1.69	9/1063 (0.8%)	2.17	56/1410 (4.0%)
59	CZ	1.65	6/1141 (0.5%)	2.04	37/1517 (2.4%)
60	Cr	1.69	8/1069 (0.7%)	2.31	63/1432 (4.4%)
61	Ch	1.64	5/1024 (0.5%)	2.04	29/1353 (2.1%)
62	Cb	1.67	1/628 (0.2%)	2.20	30/832 (3.6%)
63	CB	1.67	22/3356 (0.7%)	2.13	145/4494 (3.2%)
64	CF	1.70	14/1958 (0.7%)	2.11	72/2622 (2.7%)
65	Cc	1.56	4/779 (0.5%)	1.99	23/1048 (2.2%)
66	Cd	1.70	4/939 (0.4%)	2.03	28/1262 (2.2%)
67	Ce	1.70	10/1132 (0.9%)	2.14	50/1508 (3.3%)
68	Cf	1.81	11/1270 (0.9%)	2.29	80/1696 (4.7%)
69	Cg	1.86	14/938 (1.5%)	2.16	40/1252 (3.2%)
70	Ci	1.67	6/944 (0.6%)	2.22	45/1250 (3.6%)
71	Cj	1.80	8/750 (1.1%)	2.06	30/993 (3.0%)
72	Ck	1.69	2/583 (0.3%)	2.32	19/774 (2.5%)
73	Cl	1.76	4/445 (0.9%)	2.04	10/589 (1.7%)
74	CC	1.70	18/3163 (0.6%)	2.14	119/4253 (2.8%)
75	Cm	1.60	1/435 (0.2%)	2.05	15/575 (2.6%)
76	Cn	1.91	4/237 (1.7%)	1.91	2/300 (0.7%)
77	Cp	1.66	2/719 (0.3%)	2.00	19/954 (2.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Co	1.69	5/887 (0.6%)	2.11	40/1162 (3.4%)
79	CJ	1.69	10/1494 (0.7%)	2.05	47/2001 (2.3%)
80	CH	1.60	9/1519 (0.6%)	1.99	47/2042 (2.3%)
81	CE	1.66	13/1883 (0.7%)	2.36	125/2514 (5.0%)
82	CG	1.63	12/1968 (0.6%)	2.14	94/2637 (3.6%)
83	A5	1.86	2670/87035 (3.1%)	1.86	3981/135254 (2.9%)
84	A9	1.81	27/714 (3.8%)	1.99	33/1112 (3.0%)
85	A7	1.87	95/2854 (3.3%)	1.89	129/4447 (2.9%)
86	A8	1.82	88/2932 (3.0%)	1.86	126/4568 (2.8%)
All	All	1.78	4990/247076 (2.0%)	1.96	10570/360828 (2.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Az	105	86
2	Ag	0	4
3	AU	0	3
4	AK	0	8
5	AO	2	1
6	AX	0	3
7	AM	1	7
8	AS	0	6
9	Ad	0	4
10	AN	0	6
11	AL	0	9
12	AR	0	5
13	AP	1	4
14	AT	2	11
15	AB	0	4
16	AA	0	6
17	AV	0	2
18	AY	0	11
19	AZ	1	2
20	Aa	1	6
21	Ab	0	4
22	Ac	0	3
23	AD	1	10
24	Ae	0	2
25	Af	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	AJ	0	7
27	AE	0	13
28	AC	0	14
29	AG	0	11
30	AF	0	7
31	AH	2	8
32	AW	0	2
33	AI	0	12
34	AQ	0	12
35	Ah	0	6
36	B2	1	0
38	Cz	1	2
39	Cq	1	16
40	CK	0	13
41	CO	0	9
42	CL	29	21
43	CV	0	4
44	CM	2	15
45	Ca	1	12
46	CN	1	13
47	CI	0	11
48	CD	1	8
49	CQ	0	7
50	CR	0	5
51	CA	0	8
52	CS	28	22
53	CT	1	12
54	CP	1	4
55	CU	0	4
56	CX	1	4
57	CY	0	4
58	CW	0	10
59	CZ	0	6
60	Cr	0	14
61	Ch	0	3
62	Cb	0	4
63	CB	1	24
64	CF	1	7
65	Cc	0	5
66	Cd	1	3
67	Ce	0	8
68	Cf	7	22

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	Cg	0	7
70	Ci	0	5
71	Cj	0	3
72	Ck	0	2
73	Cl	0	4
74	CC	1	21
75	Cm	0	2
76	Cn	0	2
77	Cp	0	2
78	Co	0	5
79	CJ	1	10
80	CH	1	11
81	CE	3	26
82	CG	1	7
83	A5	7	0
All	All	208	716

The worst 5 of 4990 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	A5	1668	U	C2'-C1'	-22.84	1.19	1.53
36	B2	1320	G	C2'-C1'	-22.10	1.20	1.53
83	A5	973	G	C2'-C1'	-20.15	1.23	1.53
83	A5	2767	U	C2'-C1'	-18.93	1.25	1.53
83	A5	3474	G	C2'-C1'	-18.53	1.25	1.53

The worst 5 of 10570 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	A5	668	A	C4'-C3'-O3'	25.46	151.19	113.00
83	A5	3842	A	P-O5'-C5'	24.91	158.27	120.90
36	B2	1472	C	P-O3'-C3'	24.24	156.56	120.20
83	A5	668	A	P-O3'-C3'	23.93	156.09	120.20
36	B2	199	G	C4'-C3'-O3'	-23.63	77.55	113.00

5 of 208 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Az	4	PHE	CA
1	Az	15	LYS	CA
1	Az	49	ALA	CA
1	Az	55	ARG	CA

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Mol	Chain	Res	Type	Atom
1	Az	68	ILE	CA

5 of 716 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Az	14	ASP	Peptide
1	Az	20	ARG	Sidechain
1	Az	27	HIS	Peptide
1	Az	47	ALA	Peptide
1	Az	49	ALA	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	Az	6574	0	6616	45	0
2	Ag	2511	0	2438	12	0
3	AU	815	0	871	1	0
4	AK	797	0	817	7	0
5	AO	1003	0	1035	9	0
6	AX	1131	0	1190	5	0
7	AM	924	0	960	17	0
8	AS	1128	0	1177	13	0
9	Ad	433	0	424	4	0
10	AN	1202	0	1291	4	0
11	AL	1274	0	1351	10	0
12	AR	981	0	1038	1	0
13	AP	1016	0	1086	6	0
14	AT	1203	0	1250	7	0
15	AB	1798	0	1867	11	0
16	AA	1737	0	1750	7	0
17	AV	617	0	613	2	0
18	AY	1016	0	1073	17	0
19	AZ	608	0	658	5	0
20	Aa	867	0	920	7	0
21	Ab	653	0	680	7	0
22	Ac	498	0	525	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AD	1782	0	1862	5	0
24	Ae	469	0	503	1	0
25	Af	659	0	695	7	0
26	AJ	1503	0	1620	34	0
27	AE	2054	0	2165	11	0
28	AC	1746	0	1827	12	0
29	AG	1866	0	2028	17	0
30	AF	1497	0	1556	7	0
31	AH	1566	0	1664	9	0
32	AW	1028	0	1071	9	0
33	AI	1665	0	1746	4	0
34	AQ	1183	0	1255	11	0
35	Ah	486	0	458	6	0
36	B2	39523	0	19572	381	0
37	BC	1605	0	814	15	0
38	Cz	1702	0	1814	17	0
39	Cq	1710	0	1777	10	0
40	CK	1180	0	1246	8	0
41	CO	1668	0	1783	13	0
42	CL	1695	0	1790	24	0
43	CV	998	0	1046	2	0
44	CM	1302	0	1388	22	0
45	Ca	1204	0	1260	9	0
46	CN	1710	0	1778	13	0
47	CI	1785	0	1805	17	0
48	CD	2334	0	2354	27	0
49	CQ	1518	0	1626	10	0
50	CR	1683	0	1827	5	0
51	CA	1935	0	2037	24	0
52	CS	1454	0	1503	24	0
53	CT	1297	0	1364	8	0
54	CP	1505	0	1556	6	0
55	CU	961	0	975	3	0
56	CX	984	0	1058	4	0
57	CY	1078	0	1159	8	0
58	CW	1047	0	1140	4	0
59	CZ	1115	0	1199	9	0
60	Cr	1051	0	1148	7	0
61	Ch	1015	0	1163	5	0
62	Cb	619	0	650	5	0
63	CB	3287	0	3432	55	0
64	CF	1921	0	2039	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	Cc	770	0	802	7	0
66	Cd	924	0	942	4	0
67	Ce	1110	0	1181	9	0
68	Cf	1244	0	1316	36	0
69	Cg	926	0	1013	4	0
70	Ci	934	0	1029	19	0
71	Cj	737	0	770	4	0
72	Ck	576	0	634	1	0
73	Cl	437	0	483	6	0
74	CC	3109	0	3298	25	0
75	Cm	429	0	472	3	0
76	Cn	236	0	286	1	0
77	Cp	710	0	756	3	0
78	Co	874	0	956	0	0
79	CJ	1468	0	1507	10	0
80	CH	1499	0	1569	12	0
81	CE	1845	0	1981	28	0
82	CG	1936	0	2103	5	0
83	A5	77967	0	38740	862	0
84	A9	639	0	321	5	0
85	A7	2554	0	1296	37	0
86	A8	2621	0	1328	53	0
All	All	230721	0	173166	1848	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1848 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)
18:AY:77:TYR:CE1	18:AY:77:TYR:CZ	1.77	1.73
18:AY:77:TYR:CG	18:AY:77:TYR:CD1	1.74	1.64
18:AY:77:TYR:CZ	18:AY:77:TYR:CE2	1.76	1.63
83:A5:3843:U:C1'	83:A5:3843:U:C2'	1.74	1.47
42:CL:59:ARG:HG2	83:A5:77:A:N3	1.17	1.44

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	Az	835/844 (99%)	647 (78%)	96 (12%)	92 (11%)	0	5
2	Ag	316/318 (99%)	274 (87%)	25 (8%)	17 (5%)	1	14
3	AU	100/120 (83%)	84 (84%)	6 (6%)	10 (10%)	0	7
4	AK	93/163 (57%)	75 (81%)	7 (8%)	11 (12%)	0	4
5	AO	132/151 (87%)	104 (79%)	13 (10%)	15 (11%)	0	5
6	AX	141/143 (99%)	118 (84%)	15 (11%)	8 (6%)	1	14
7	AM	117/139 (84%)	85 (73%)	16 (14%)	16 (14%)	0	4
8	AS	135/152 (89%)	107 (79%)	16 (12%)	12 (9%)	0	8
9	Ad	50/56 (89%)	30 (60%)	10 (20%)	10 (20%)	0	2
10	AN	148/151 (98%)	136 (92%)	7 (5%)	5 (3%)	3	21
11	AL	153/155 (99%)	128 (84%)	16 (10%)	9 (6%)	1	13
12	AR	118/131 (90%)	99 (84%)	12 (10%)	7 (6%)	1	13
13	AP	122/148 (82%)	95 (78%)	13 (11%)	14 (12%)	0	5
14	AT	152/156 (97%)	125 (82%)	17 (11%)	10 (7%)	1	12
15	AB	218/268 (81%)	179 (82%)	23 (11%)	16 (7%)	1	10
16	AA	216/313 (69%)	174 (81%)	22 (10%)	20 (9%)	0	8
17	AV	80/83 (96%)	64 (80%)	6 (8%)	10 (12%)	0	4
18	AY	124/131 (95%)	96 (77%)	10 (8%)	18 (14%)	0	3
19	AZ	72/117 (62%)	49 (68%)	11 (15%)	12 (17%)	0	2
20	Aa	105/114 (92%)	75 (71%)	14 (13%)	16 (15%)	0	3
21	Ab	82/84 (98%)	64 (78%)	12 (15%)	6 (7%)	1	10
22	Ac	60/65 (92%)	53 (88%)	1 (2%)	6 (10%)	0	7
23	AD	225/246 (92%)	183 (81%)	29 (13%)	13 (6%)	1	13
24	Ae	56/132 (42%)	37 (66%)	10 (18%)	9 (16%)	0	2
25	Af	78/80 (98%)	46 (59%)	15 (19%)	17 (22%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AJ	179/195 (92%)	148 (83%)	17 (10%)	14 (8%)	1	9
27	AE	259/261 (99%)	204 (79%)	37 (14%)	18 (7%)	1	11
28	AC	225/267 (84%)	186 (83%)	17 (8%)	22 (10%)	0	7
29	AG	229/248 (92%)	196 (86%)	20 (9%)	13 (6%)	1	14
30	AF	188/228 (82%)	152 (81%)	20 (11%)	16 (8%)	0	9
31	AH	192/194 (99%)	147 (77%)	28 (15%)	17 (9%)	0	8
32	AW	127/130 (98%)	114 (90%)	10 (8%)	3 (2%)	4	27
33	AI	205/208 (99%)	164 (80%)	12 (6%)	29 (14%)	0	3
34	AQ	146/148 (99%)	114 (78%)	14 (10%)	18 (12%)	0	4
35	Ah	54/121 (45%)	31 (57%)	6 (11%)	17 (32%)	0	0
38	Cz	215/218 (99%)	186 (86%)	17 (8%)	12 (6%)	1	14
39	Cq	221/223 (99%)	183 (83%)	21 (10%)	17 (8%)	1	9
40	CK	156/165 (94%)	95 (61%)	29 (19%)	32 (20%)	0	2
41	CO	203/205 (99%)	183 (90%)	12 (6%)	8 (4%)	2	18
42	CL	208/218 (95%)	141 (68%)	28 (14%)	39 (19%)	0	2
43	CV	132/140 (94%)	116 (88%)	13 (10%)	3 (2%)	5	28
44	CM	157/166 (95%)	123 (78%)	20 (13%)	14 (9%)	0	8
45	Ca	147/149 (99%)	116 (79%)	17 (12%)	14 (10%)	0	8
46	CN	201/204 (98%)	175 (87%)	20 (10%)	6 (3%)	3	22
47	CI	215/218 (99%)	176 (82%)	19 (9%)	20 (9%)	0	8
48	CD	288/299 (96%)	242 (84%)	20 (7%)	26 (9%)	0	8
49	CQ	185/188 (98%)	153 (83%)	18 (10%)	14 (8%)	1	10
50	CR	201/203 (99%)	187 (93%)	7 (4%)	7 (4%)	3	20
51	CA	251/256 (98%)	205 (82%)	27 (11%)	19 (8%)	1	10
52	CS	171/177 (97%)	131 (77%)	18 (10%)	22 (13%)	0	4
53	CT	156/159 (98%)	122 (78%)	17 (11%)	17 (11%)	0	6
54	CP	183/186 (98%)	154 (84%)	16 (9%)	13 (7%)	1	10
55	CU	114/299 (38%)	88 (77%)	18 (16%)	8 (7%)	1	11
56	CX	118/277 (43%)	96 (81%)	15 (13%)	7 (6%)	1	13
57	CY	129/149 (87%)	113 (88%)	9 (7%)	7 (5%)	1	14
58	CW	128/155 (83%)	102 (80%)	12 (9%)	14 (11%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	CZ	132/135 (98%)	111 (84%)	15 (11%)	6 (4%)	2	16
60	Cr	132/144 (92%)	88 (67%)	22 (17%)	22 (17%)	0	2
61	Ch	121/123 (98%)	99 (82%)	10 (8%)	12 (10%)	0	7
62	Cb	73/76 (96%)	53 (73%)	11 (15%)	9 (12%)	0	4
63	CB	412/416 (99%)	325 (79%)	56 (14%)	31 (8%)	1	10
64	CF	227/252 (90%)	195 (86%)	17 (8%)	15 (7%)	1	12
65	Cc	98/111 (88%)	91 (93%)	3 (3%)	4 (4%)	2	17
66	Cd	109/124 (88%)	91 (84%)	14 (13%)	4 (4%)	2	19
67	Ce	130/134 (97%)	101 (78%)	16 (12%)	13 (10%)	0	7
68	Cf	155/157 (99%)	115 (74%)	14 (9%)	26 (17%)	0	2
69	Cg	111/162 (68%)	92 (83%)	12 (11%)	7 (6%)	1	12
70	Ci	111/115 (96%)	82 (74%)	16 (14%)	13 (12%)	0	4
71	Cj	90/93 (97%)	75 (83%)	9 (10%)	6 (7%)	1	11
72	Ck	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	17
73	Cl	48/51 (94%)	40 (83%)	4 (8%)	4 (8%)	0	9
74	CC	390/401 (97%)	309 (79%)	36 (9%)	45 (12%)	0	5
75	Cm	50/52 (96%)	38 (76%)	6 (12%)	6 (12%)	0	4
76	Cn	23/25 (92%)	22 (96%)	0	1 (4%)	2	17
77	Cp	89/92 (97%)	77 (86%)	8 (9%)	4 (4%)	2	16
78	Co	102/104 (98%)	79 (78%)	10 (10%)	13 (13%)	0	4
79	CJ	180/184 (98%)	139 (77%)	17 (9%)	24 (13%)	0	4
80	CH	188/190 (99%)	160 (85%)	16 (8%)	12 (6%)	1	12
81	CE	226/243 (93%)	149 (66%)	34 (15%)	43 (19%)	0	2
82	CG	239/271 (88%)	197 (82%)	22 (9%)	20 (8%)	0	9
All	All	13015/14439 (90%)	10459 (80%)	1348 (10%)	1208 (9%)	1	8

5 of 1208 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Az	5	THR
1	Az	15	LYS
1	Az	44	GLY
1	Az	54	THR
1	Az	82	GLU

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	Az	721/726 (99%)	670 (93%)	51 (7%)	13	35
2	Ag	280/280 (100%)	271 (97%)	9 (3%)	34	56
3	AU	95/108 (88%)	91 (96%)	4 (4%)	26	48
4	AK	88/132 (67%)	79 (90%)	9 (10%)	7	23
5	AO	103/118 (87%)	92 (89%)	11 (11%)	6	21
6	AX	116/116 (100%)	110 (95%)	6 (5%)	21	42
7	AM	104/119 (87%)	97 (93%)	7 (7%)	15	36
8	AS	123/136 (90%)	118 (96%)	5 (4%)	27	48
9	Ad	45/47 (96%)	45 (100%)	0	100	100
10	AN	130/131 (99%)	122 (94%)	8 (6%)	16	38
11	AL	138/138 (100%)	127 (92%)	11 (8%)	11	31
12	AR	108/118 (92%)	97 (90%)	11 (10%)	7	23
13	AP	111/130 (85%)	106 (96%)	5 (4%)	24	46
14	AT	125/127 (98%)	116 (93%)	9 (7%)	13	35
15	AB	199/233 (85%)	181 (91%)	18 (9%)	9	28
16	AA	190/271 (70%)	180 (95%)	10 (5%)	20	41
17	AV	67/68 (98%)	60 (90%)	7 (10%)	7	22
18	AY	105/110 (96%)	103 (98%)	2 (2%)	50	67
19	AZ	67/100 (67%)	57 (85%)	10 (15%)	3	12
20	Aa	94/101 (93%)	92 (98%)	2 (2%)	47	65
21	Ab	72/72 (100%)	69 (96%)	3 (4%)	26	48
22	Ac	54/57 (95%)	50 (93%)	4 (7%)	13	33
23	AD	192/210 (91%)	176 (92%)	16 (8%)	10	30
24	Ae	47/108 (44%)	46 (98%)	1 (2%)	47	65
25	Af	70/70 (100%)	61 (87%)	9 (13%)	4	15
26	AJ	161/169 (95%)	154 (96%)	7 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	AE	220/220 (100%)	206 (94%)	14 (6%)	16	37
28	AC	188/209 (90%)	177 (94%)	11 (6%)	18	39
29	AG	200/216 (93%)	190 (95%)	10 (5%)	22	43
30	AF	161/193 (83%)	152 (94%)	9 (6%)	19	40
31	AH	175/175 (100%)	152 (87%)	23 (13%)	4	15
32	AW	113/114 (99%)	106 (94%)	7 (6%)	16	38
33	AI	175/176 (99%)	166 (95%)	9 (5%)	21	42
34	AQ	122/122 (100%)	112 (92%)	10 (8%)	10	31
35	Ah	51/100 (51%)	49 (96%)	2 (4%)	28	49
38	Cz	190/191 (100%)	172 (90%)	18 (10%)	8	25
39	Cq	186/186 (100%)	172 (92%)	14 (8%)	12	33
40	CK	131/137 (96%)	125 (95%)	6 (5%)	24	45
41	CO	175/175 (100%)	157 (90%)	18 (10%)	7	23
42	CL	173/180 (96%)	160 (92%)	13 (8%)	12	33
43	CV	101/106 (95%)	99 (98%)	2 (2%)	48	66
44	CM	138/142 (97%)	124 (90%)	14 (10%)	7	23
45	Ca	122/122 (100%)	114 (93%)	8 (7%)	15	37
46	CN	174/175 (99%)	167 (96%)	7 (4%)	28	49
47	CI	187/188 (100%)	180 (96%)	7 (4%)	30	51
48	CD	241/248 (97%)	235 (98%)	6 (2%)	42	62
49	CQ	164/165 (99%)	150 (92%)	14 (8%)	10	29
50	CR	176/176 (100%)	170 (97%)	6 (3%)	32	54
51	CA	195/198 (98%)	175 (90%)	20 (10%)	7	23
52	CS	156/159 (98%)	141 (90%)	15 (10%)	8	25
53	CT	137/138 (99%)	130 (95%)	7 (5%)	21	42
54	CP	160/161 (99%)	156 (98%)	4 (2%)	42	62
55	CU	108/203 (53%)	102 (94%)	6 (6%)	19	40
56	CX	106/205 (52%)	101 (95%)	5 (5%)	23	44
57	CY	116/130 (89%)	111 (96%)	5 (4%)	26	47
58	CW	107/124 (86%)	102 (95%)	5 (5%)	23	44
59	CZ	121/122 (99%)	106 (88%)	15 (12%)	4	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	Cr	112/120 (93%)	101 (90%)	11 (10%)	7	24
61	Ch	112/112 (100%)	109 (97%)	3 (3%)	39	60
62	Cb	67/68 (98%)	62 (92%)	5 (8%)	12	33
63	CB	349/350 (100%)	330 (95%)	19 (5%)	20	41
64	CF	203/222 (91%)	190 (94%)	13 (6%)	16	37
65	Cc	84/93 (90%)	79 (94%)	5 (6%)	17	39
66	Cd	103/114 (90%)	97 (94%)	6 (6%)	18	40
67	Ce	120/122 (98%)	110 (92%)	10 (8%)	10	30
68	Cf	123/123 (100%)	110 (89%)	13 (11%)	6	21
69	Cg	104/137 (76%)	95 (91%)	9 (9%)	9	29
70	Ci	100/101 (99%)	90 (90%)	10 (10%)	7	24
71	Cj	77/78 (99%)	67 (87%)	10 (13%)	4	15
72	Ck	65/65 (100%)	57 (88%)	8 (12%)	4	17
73	Cl	45/46 (98%)	44 (98%)	1 (2%)	45	64
74	CC	323/329 (98%)	294 (91%)	29 (9%)	9	28
75	Cm	48/48 (100%)	46 (96%)	2 (4%)	26	48
76	Cn	23/23 (100%)	22 (96%)	1 (4%)	26	47
77	Cp	74/75 (99%)	68 (92%)	6 (8%)	11	31
78	Co	94/94 (100%)	90 (96%)	4 (4%)	26	47
79	CJ	155/157 (99%)	143 (92%)	12 (8%)	12	32
80	CH	169/169 (100%)	155 (92%)	14 (8%)	10	30
81	CE	197/208 (95%)	179 (91%)	18 (9%)	9	27
82	CG	210/237 (89%)	197 (94%)	13 (6%)	16	38
All	All	11331/12242 (93%)	10564 (93%)	767 (7%)	16	36

5 of 767 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	CA	45	VAL
63	CB	168	ILE
51	CA	193	ARG
50	CR	163	ARG
57	CY	7	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 296 such sidechains are listed below:

Mol	Chain	Res	Type
63	CB	55	HIS
80	CH	114	ASN
63	CB	271	GLN
68	Cf	47	HIS
27	AE	201	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	B2	1791/1995 (89%)	506 (28%)	117 (6%)
37	BC	74/75 (98%)	13 (17%)	3 (4%)
83	A5	3562/3970 (89%)	954 (26%)	263 (7%)
84	A9	29/30 (96%)	7 (24%)	2 (6%)
85	A7	119/120 (99%)	23 (19%)	5 (4%)
86	A8	122/123 (99%)	18 (14%)	4 (3%)
All	All	5697/6313 (90%)	1521 (26%)	394 (6%)

5 of 1521 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	B2	2	U
36	B2	3	U
36	B2	4	C
36	B2	8	U
36	B2	16	G

5 of 394 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	A5	1407	C
83	A5	2200	A
83	A5	1522	G
83	A5	1793	C
83	A5	2750	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

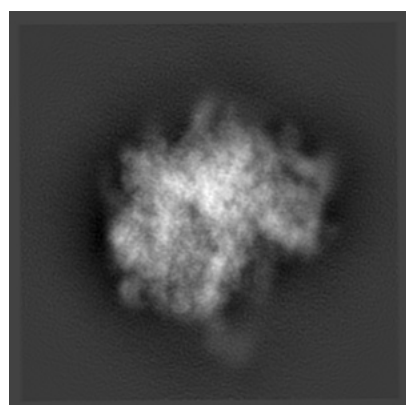
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5591. These allow visual inspection of the internal detail of the map and identification of artifacts.

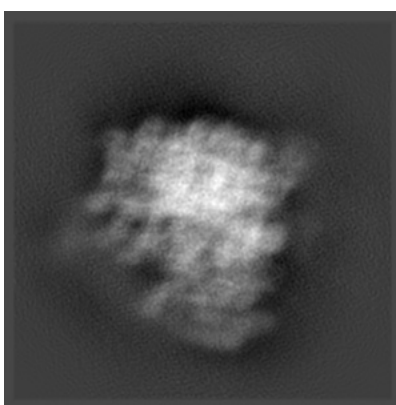
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

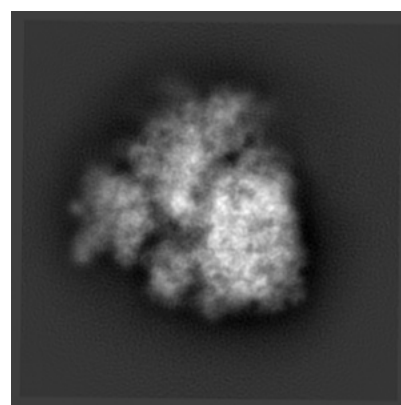
6.1.1 Primary map



X



Y

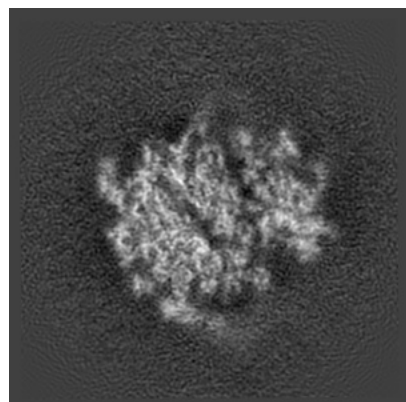


Z

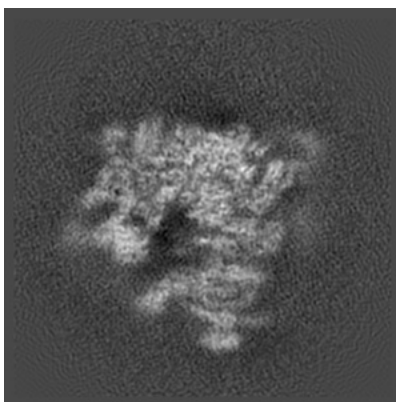
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

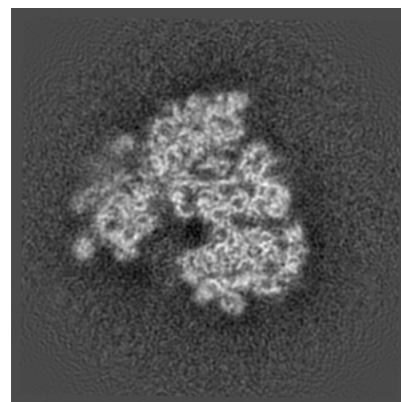
6.2.1 Primary map



X Index: 184



Y Index: 184

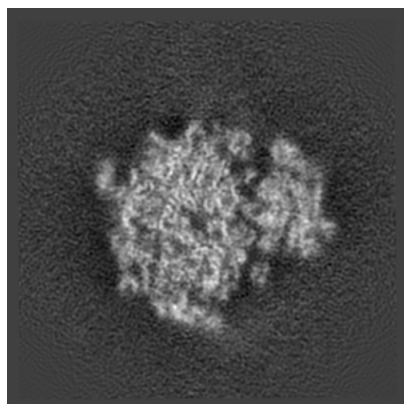


Z Index: 184

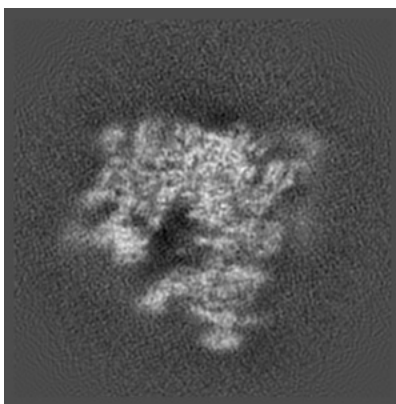
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

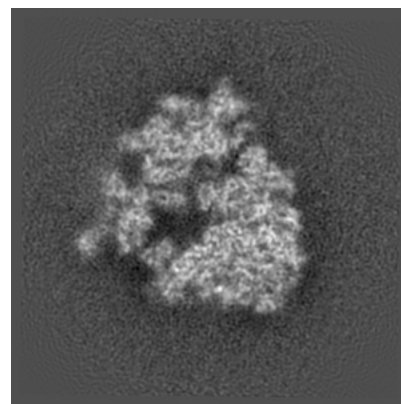
6.3.1 Primary map



X Index: 190



Y Index: 183

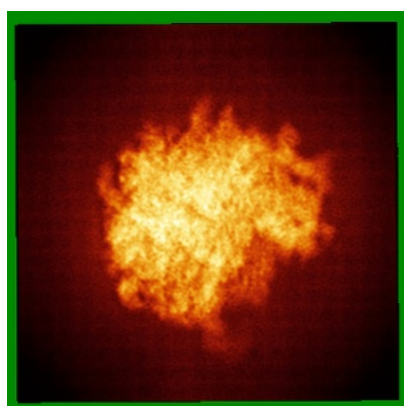


Z Index: 172

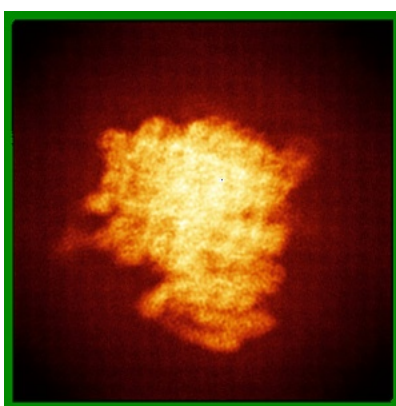
The images above show the largest variance slices of the map in three orthogonal directions.

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

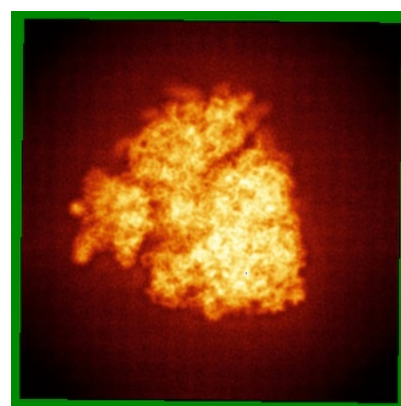
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.49. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

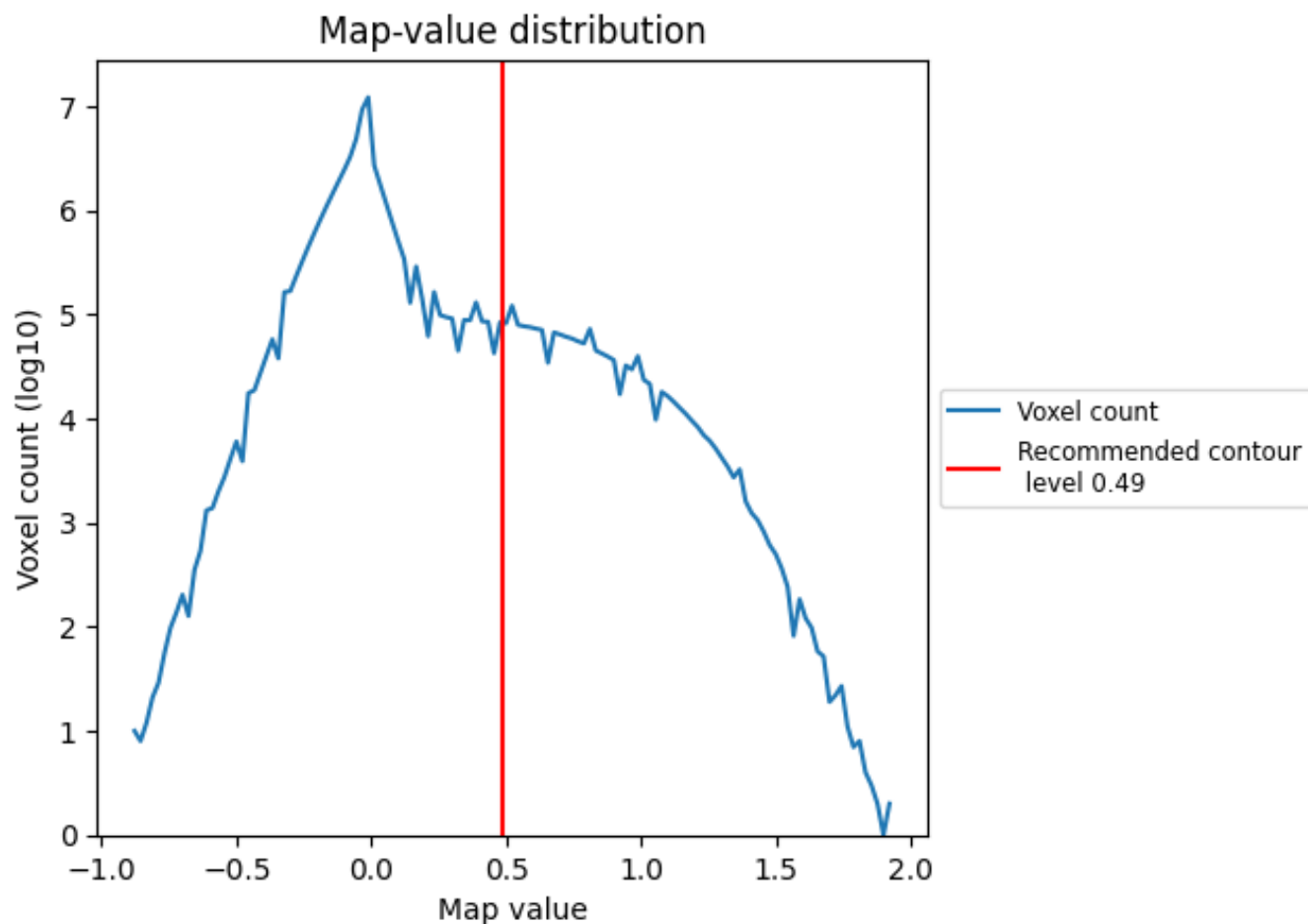
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

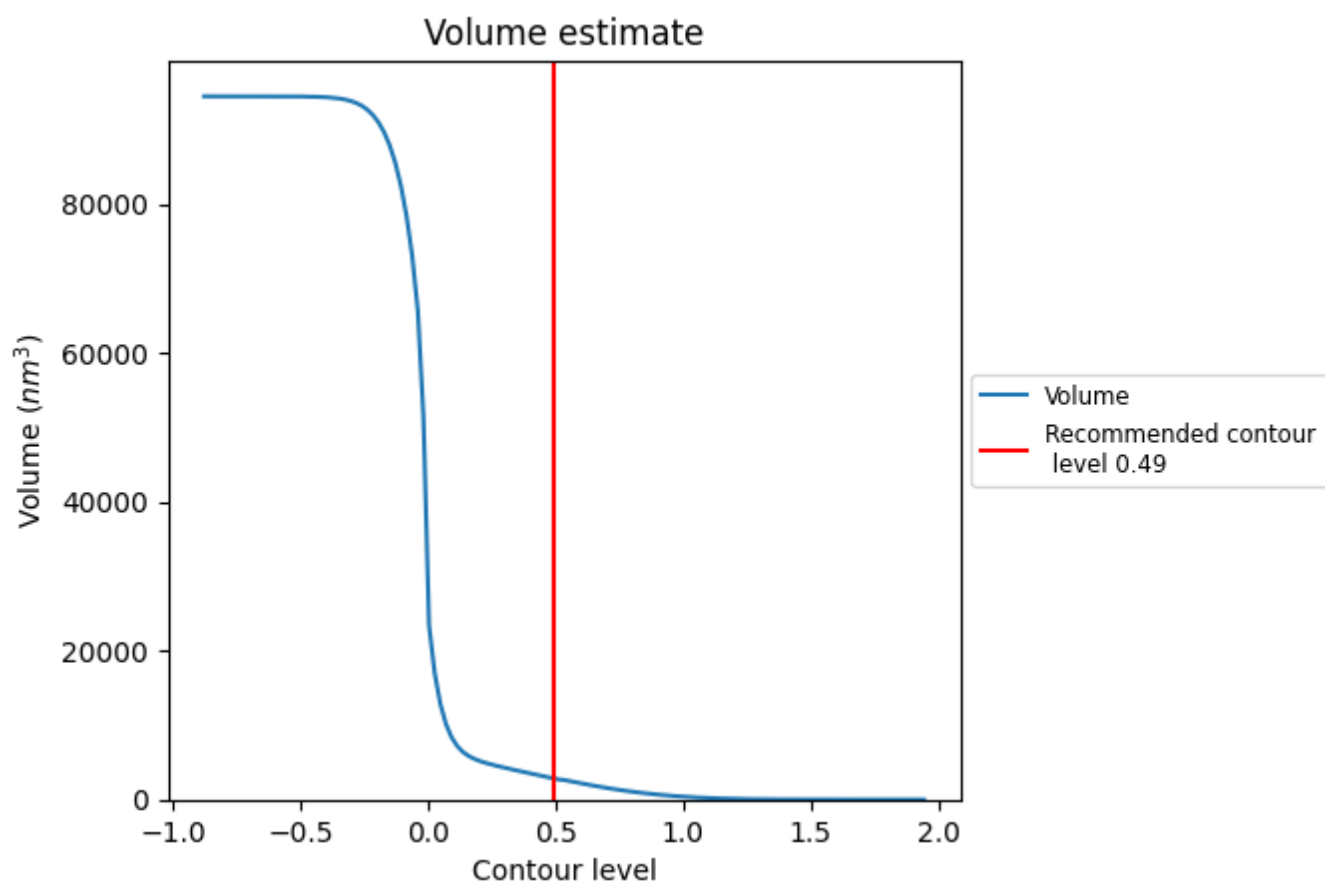
This section contains the results of statistical analysis of the map.

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.

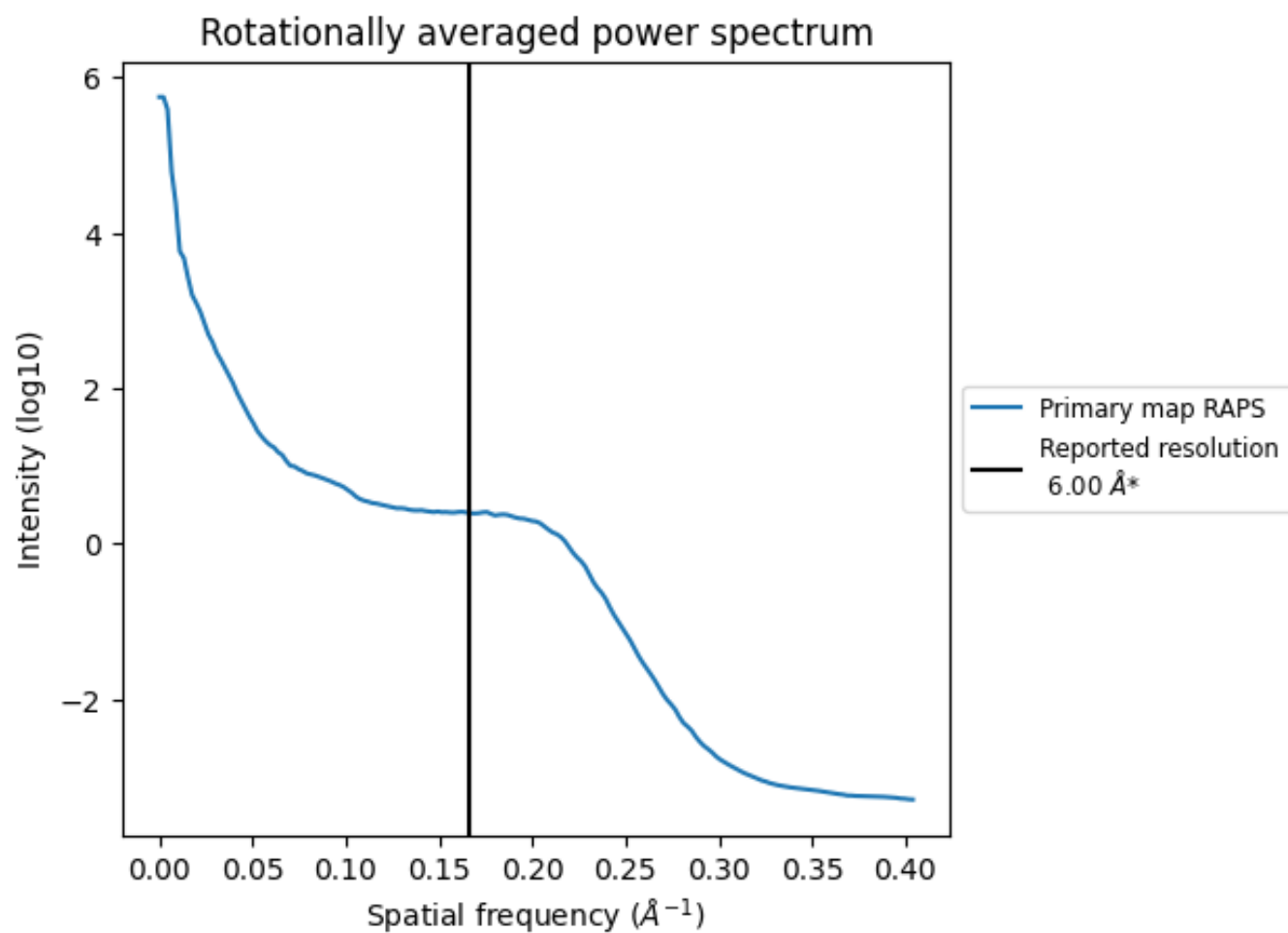
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2852 nm³; this corresponds to an approximate mass of 2576 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 0.167 Å⁻¹

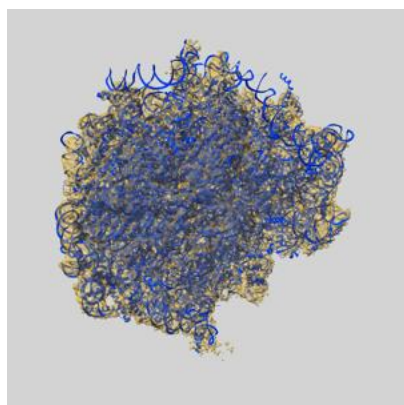
8 Fourier-Shell correlation ⓘ

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

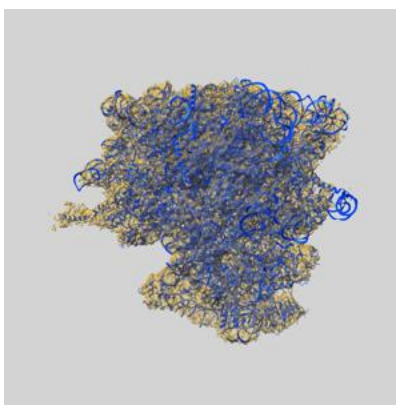
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5591 and PDB model 4V6W. Per-residue inclusion information can be found in section [3](#) on page [21](#).

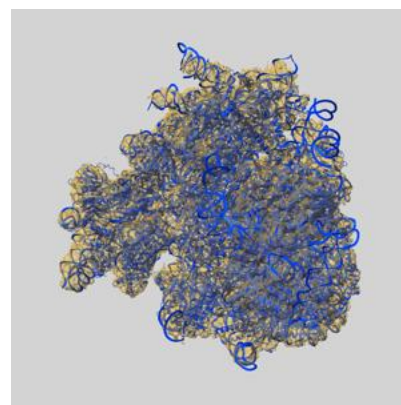
9.1 Map-model overlay [i](#)



X



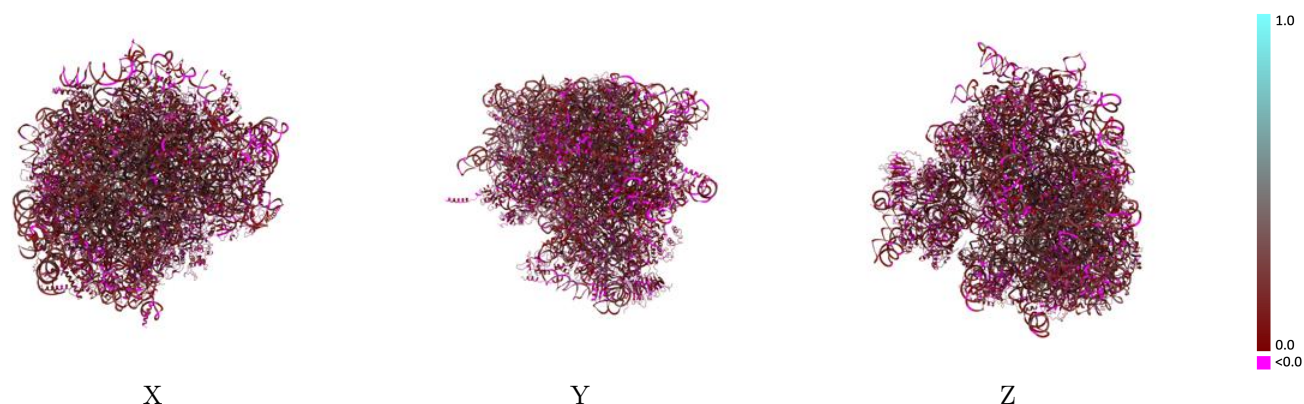
Y



Z

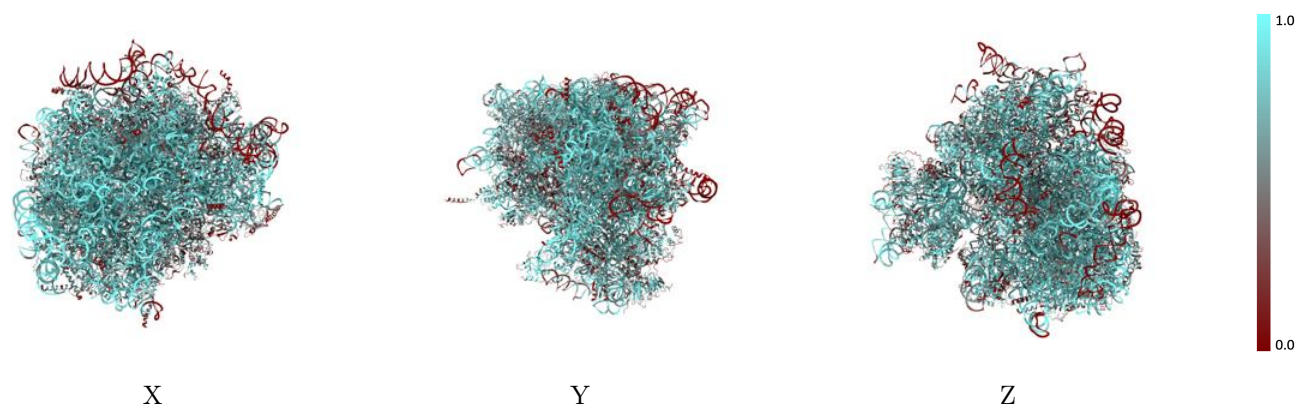
The images above show the 3D surface view of the map at the recommended contour level 0.49 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



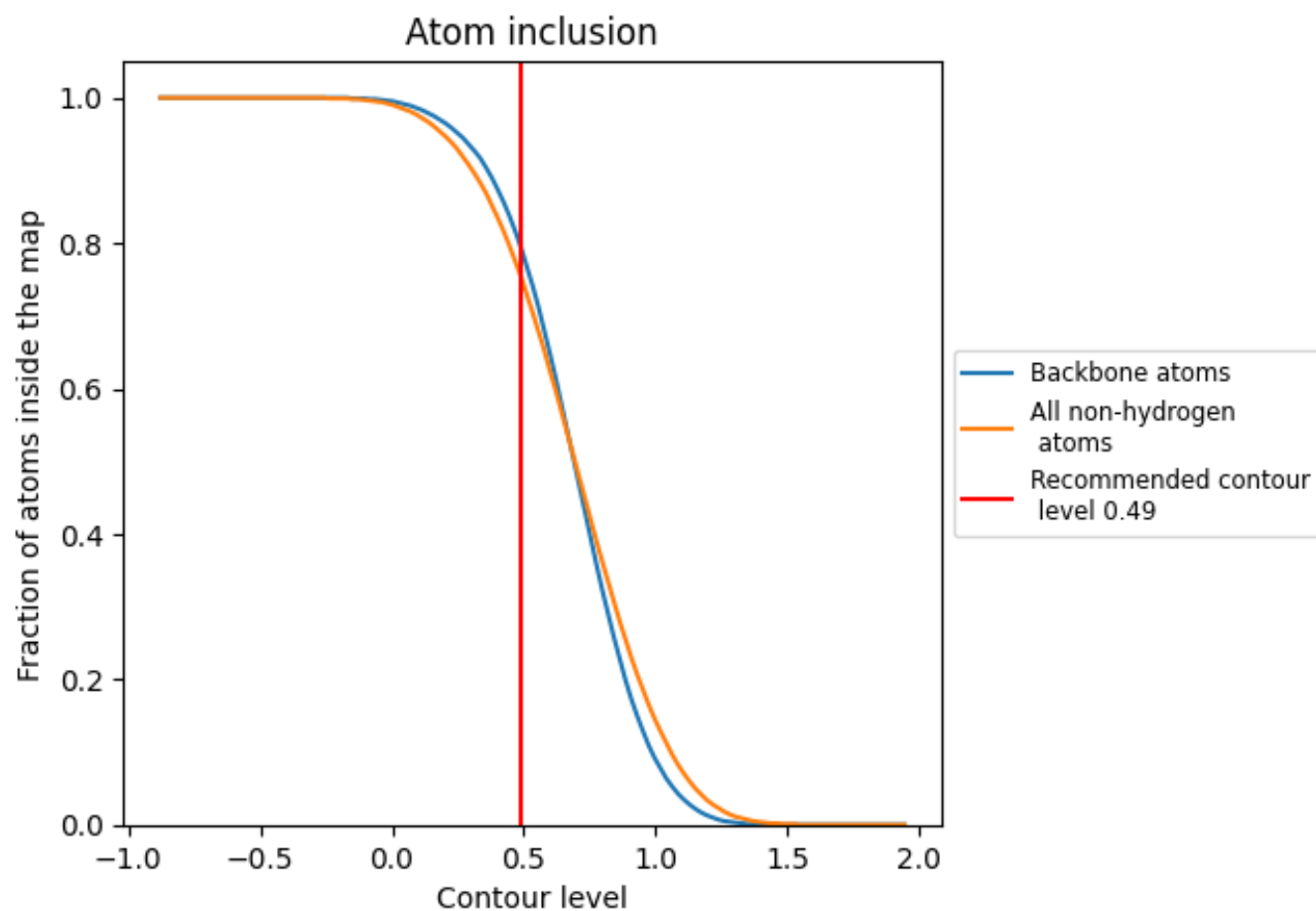
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.49).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.49) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.1570
A5	 0.8870	 0.2040
A7	 0.9450	 0.2030
A8	 0.9250	 0.2330
A9	 0.8220	 0.2100
AA	 0.6570	 0.1060
AB	 0.5770	 0.0940
AC	 0.5680	 0.1340
AD	 0.4870	 0.1230
AE	 0.6540	 0.1060
AF	 0.5940	 0.0880
AG	 0.5120	 0.0690
AH	 0.6120	 0.1000
AI	 0.4730	 0.0910
AJ	 0.7220	 0.1220
AK	 0.8140	 0.1170
AL	 0.5220	 0.0890
AM	 0.7370	 0.0940
AN	 0.5950	 0.1050
AO	 0.5890	 0.0500
AP	 0.4210	 0.0960
AQ	 0.5710	 0.0960
AR	 0.4410	 0.1060
AS	 0.5940	 0.1060
AT	 0.5530	 0.0950
AU	 0.6190	 0.1120
AV	 0.5740	 0.1020
AW	 0.6500	 0.1020
AX	 0.6130	 0.1020
AY	 0.5320	 0.0900
AZ	 0.6270	 0.1060
Aa	 0.6380	 0.1240
Ab	 0.6450	 0.1240
Ac	 0.6660	 0.0940
Ad	 0.7100	 0.0920



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Chain	Atom inclusion	Q-score
Ae	 0.4380	 0.1370
Af	 0.5770	 0.0610
Ag	 0.5920	 0.1010
Ah	 0.4280	 0.0890
Az	 0.4650	 0.1100
B2	 0.8710	 0.1770
BC	 0.7150	 0.1770
CA	 0.7250	 0.1370
CB	 0.6330	 0.1340
CC	 0.6910	 0.1210
CD	 0.6850	 0.1110
CE	 0.6220	 0.1160
CF	 0.6430	 0.1340
CG	 0.5220	 0.1280
CH	 0.4970	 0.1400
CI	 0.5550	 0.1330
CJ	 0.5230	 0.1410
CK	 0.5290	 0.1020
CL	 0.6260	 0.1150
CM	 0.6610	 0.1170
CN	 0.8290	 0.1090
CO	 0.6450	 0.1390
CP	 0.6660	 0.1160
CQ	 0.7570	 0.1090
CR	 0.6420	 0.1390
CS	 0.5930	 0.1190
CT	 0.6330	 0.1250
CU	 0.4220	 0.1090
CV	 0.4170	 0.1400
CW	 0.3250	 0.1040
CX	 0.4050	 0.1310
CY	 0.6930	 0.1370
CZ	 0.5870	 0.1250
Ca	 0.7410	 0.1160
Cb	 0.7360	 0.1450
Cc	 0.6720	 0.1420
Cd	 0.7280	 0.1300
Ce	 0.7180	 0.1490
Cf	 0.5730	 0.0630
Cg	 0.6800	 0.1540
Ch	 0.5370	 0.1190
Ci	 0.7090	 0.1360

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Chain	Atom inclusion	Q-score
Cj	 0.7400	 0.1370
Ck	 0.5590	 0.0880
Cl	 0.7210	 0.1180
Cm	 0.5200	 0.1570
Cn	 0.6740	 0.1080
Co	 0.6710	 0.0950
Cp	 0.6270	 0.1340
Cq	 0.6170	 0.0900
Cr	 0.6140	 0.1170
Cz	 0.3550	 0.0350