



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:38 PM UTC

PDB ID : 7MDZ / pdb_00007mdz
EMDB ID : EMD-23785
Title : 80S rabbit ribosome stalled with benzamide-CHX
Authors : Koga, Y.; Hoang, E.M.; Park, Y.; Keszei, A.F.A.; Murray, J.; Shao, S.; Liao, B.B.
Deposited on : 2021-04-06
Resolution : 3.20 Å(reported)
Based on initial model : 6SGC

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

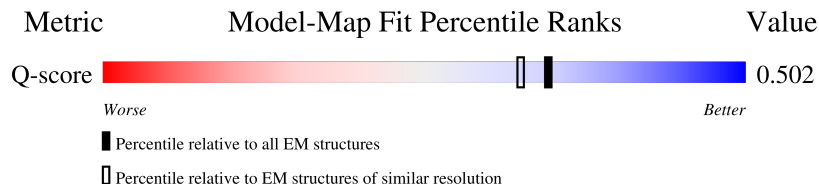
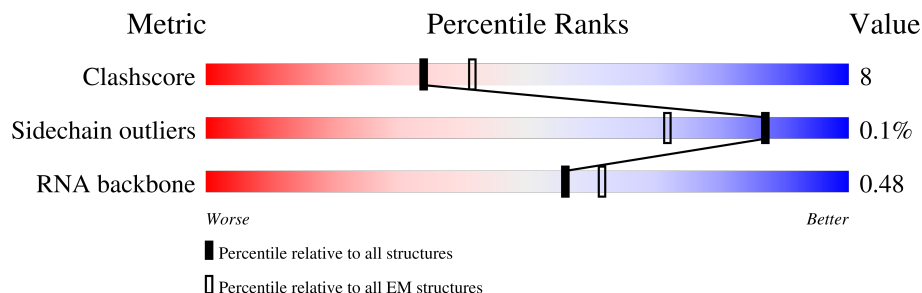
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	257	
2	B	403	
3	C	425	
4	D	297	

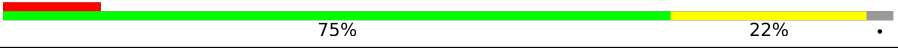
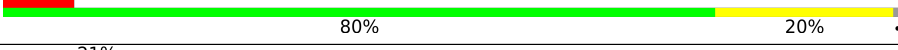
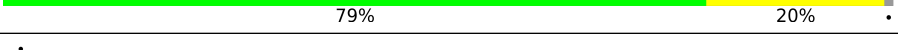
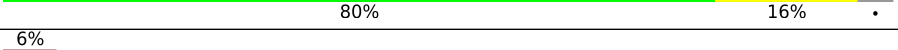
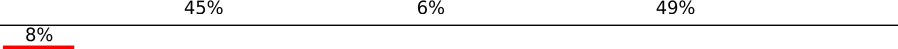
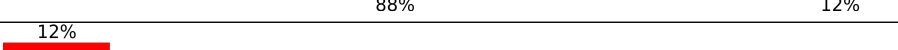
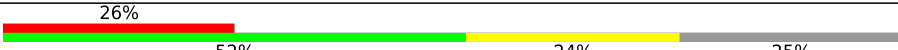
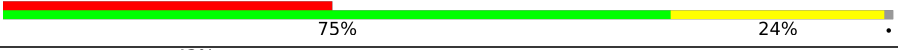
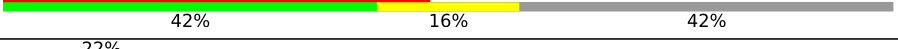
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Mol	Chain	Length	Quality of chain
5	E	291	
6	F	247	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	
29	d	125	

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Mol	Chain	Length	Quality of chain
30	e	135	
31	f	110	
32	g	116	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	AA	295	
44	BB	264	
45	CC	293	
46	DD	243	
47	EE	263	
48	FF	204	
49	GG	249	
50	HH	194	
51	II	208	
52	JJ	194	
53	KK	165	
54	LL	158	

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Mol	Chain	Length	Quality of chain
55	MM	132	
56	NN	151	
57	OO	168	
58	PP	145	
59	QQ	146	
60	RR	135	
61	SS	152	
62	TT	145	
63	UU	119	
64	VV	83	
65	WW	130	
66	XX	143	
67	YY	130	
68	ZZ	125	
69	aa	115	
70	bb	84	
71	cc	69	
72	dd	56	
73	ee	133	
74	ff	156	
75	gg	317	
76	5	3603	
77	7	120	
78	8	156	
79	2	76	

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Mol	Chain	Length	Quality of chain
80	9	1869	19% 50% 32% 9% 9%
81	6	10	70% 50% 20% 30%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 211192 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 Ribosomal protein L8.

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

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	113	Total	C	N	O	S	0	0
			897	560	185	146	6		

- Molecule 33 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	49	Total	C	N	O	S	0	0
			438	280	95	62	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AA	217	Total	C	N	O	S	0	0
			1712	1087	300	317	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 44 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 45 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 46 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 47 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 48 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 49 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 50 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	HH	184	Total	C	N	O	S	0	0
			1480	948	269	262	1		

- Molecule 51 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 52 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 53 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 54 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 55 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 56 is a protein called uS15.

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

- Molecule 57 is a protein called uS11.

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

- Molecule 58 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 59 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 60 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 61 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 62 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 63 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 64 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 65 is a protein called uS8.

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

- Molecule 66 is a protein called uS12.

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

- Molecule 67 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 68 is a protein called eS25.

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

- Molecule 69 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8
aa	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 70 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 71 is a protein called eS28.

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

- Molecule 72 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 73 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 74 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 75 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 76 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	5	3541	Total	C	N	O	P	0	0
			75929	33814	13902	24672	3541		

- Molecule 77 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 78 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 79 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	2	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 80 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	9	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	6	10	Total	C	N	O	P	0	0
			210	94	33	73	10		

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	A	1	Total	Mg	0
			1	1	
82	B	1	Total	Mg	0
			1	1	
82	P	1	Total	Mg	0
			1	1	
82	V	1	Total	Mg	0
			1	1	
82	g	1	Total	Mg	0
			1	1	
82	LL	1	Total	Mg	0
			1	1	
82	5	189	Total	Mg	0
			189	189	
82	7	6	Total	Mg	0
			6	6	
82	8	5	Total	Mg	0
			5	5	

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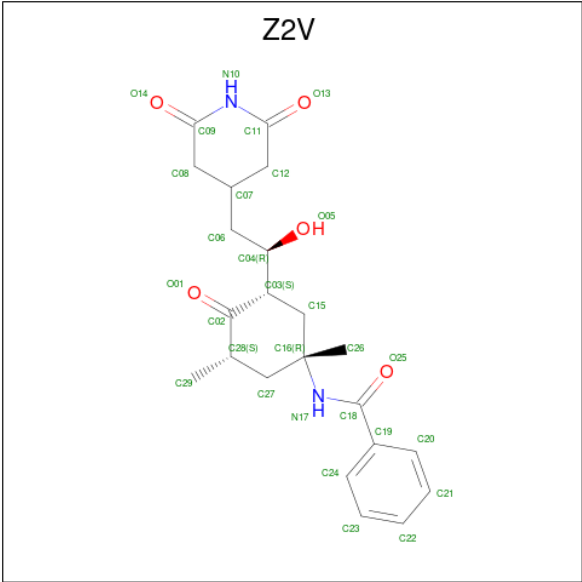
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Mol	Chain	Residues	Atoms		AltConf
82	2	2	Total 2	Mg 2	0
82	9	69	Total 69	Mg 69	0

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	g	1	Total 1	Zn 1	0
83	j	1	Total 1	Zn 1	0
83	m	1	Total 1	Zn 1	0
83	o	1	Total 1	Zn 1	0
83	p	1	Total 1	Zn 1	0
83	aa	1	Total 1	Zn 1	0
83	dd	1	Total 1	Zn 1	0
83	ff	1	Total 1	Zn 1	0

- Molecule 84 is N-[(1R,3S,4R,5S)-3-{(1R)-2-[(2R,4r,6S)-2,6-dihydroxypiperidin-4-yl]-1-hydroxyethyl}-4-hydroxy-1,5-dimethylcyclohexyl]benzamide (CCD ID: Z2V) (formula: C₂₂H₂₈N₂O₅) (labeled as "Ligand of Interest" by depositor).

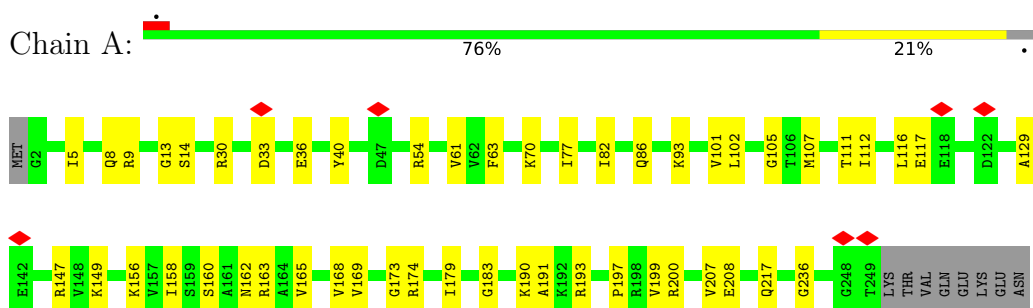


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
84	5	1	29	22	2	5	0

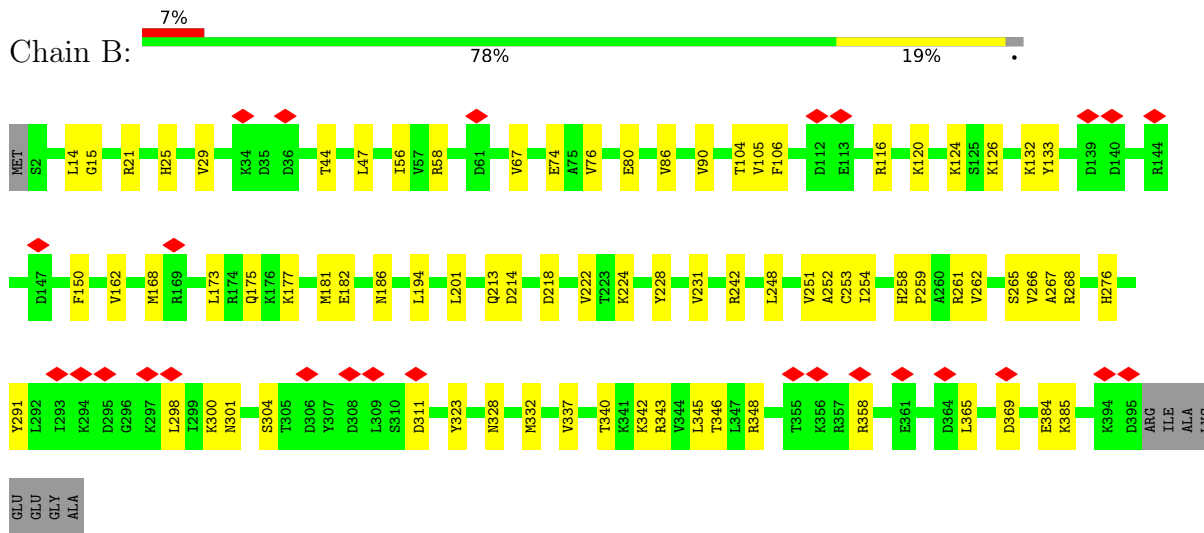
3 Residue-property plots

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.

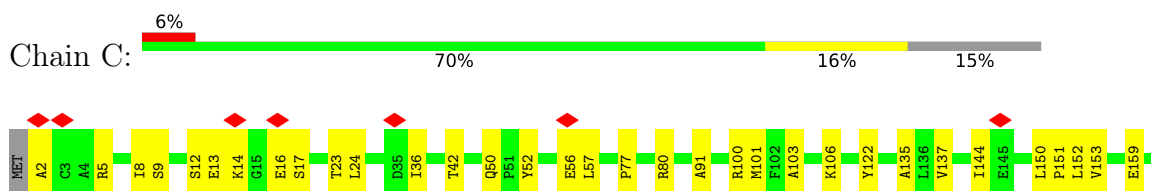
• Molecule 1: Ribosomal protein L8

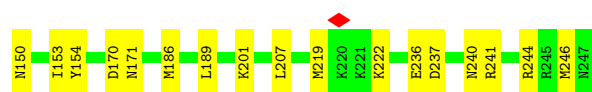


• Molecule 2: uL3

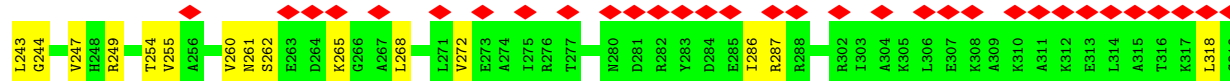
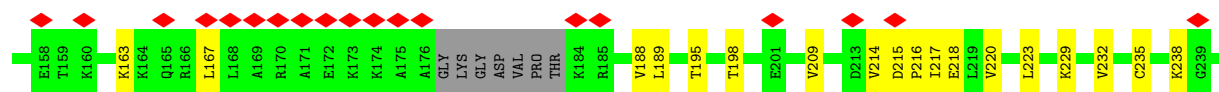
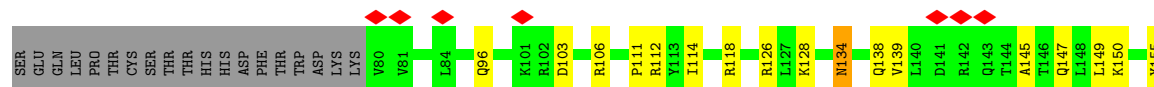
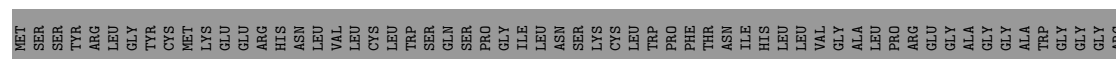


• Molecule 3: 60S ribosomal protein L4

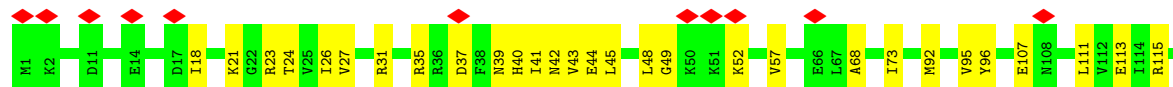




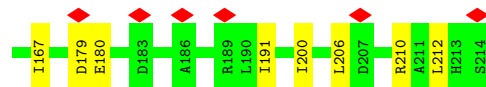
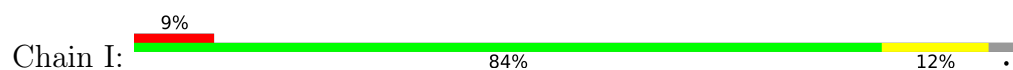
• Molecule 7: 60S ribosomal protein L7a



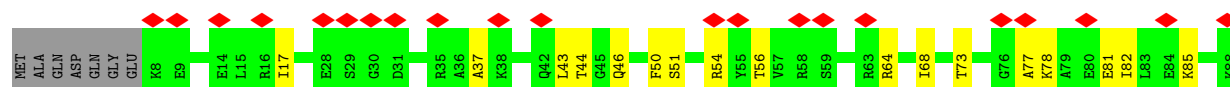
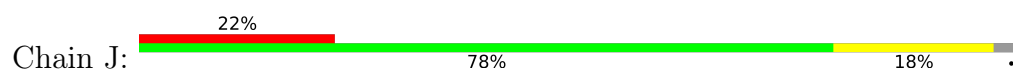
• Molecule 8: 60S ribosomal protein L9

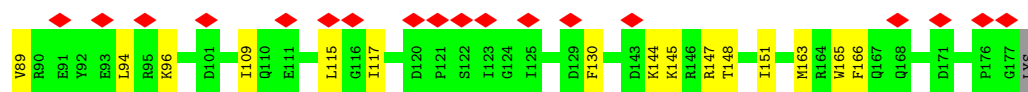


• Molecule 9: 60S ribosomal protein L10

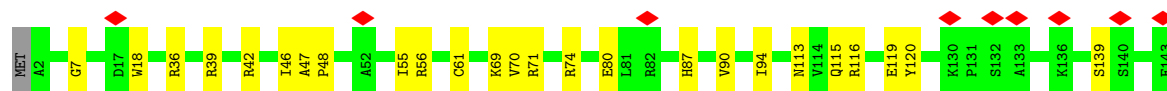
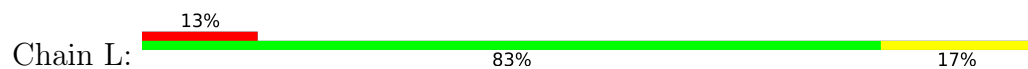


• Molecule 10: 60S ribosomal protein L11

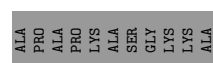
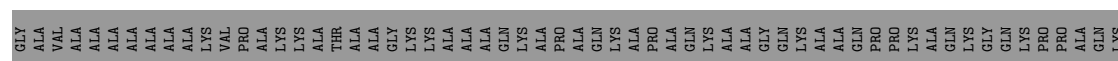




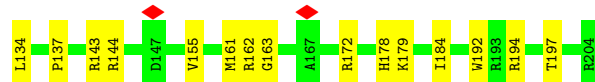
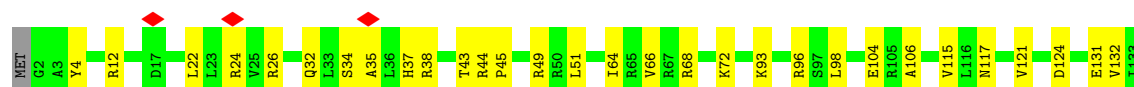
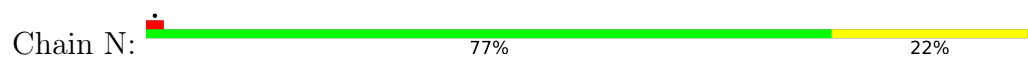
- Molecule 11: 60S ribosomal protein L13



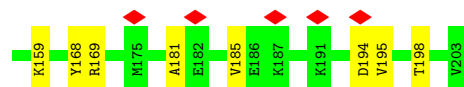
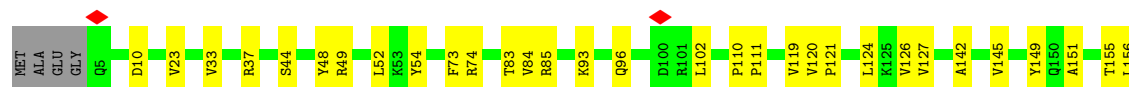
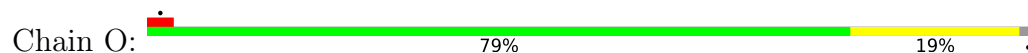
- Molecule 12: 60S ribosomal protein L14



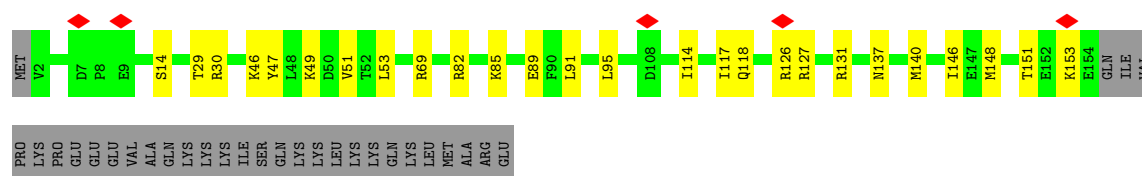
- Molecule 13: Ribosomal protein L15



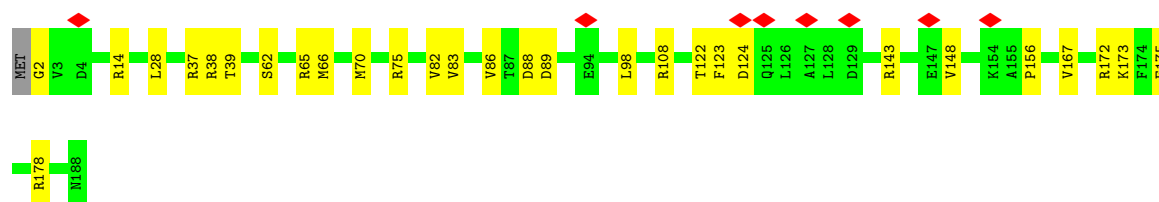
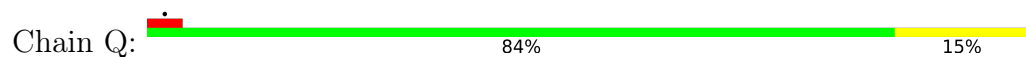
- Molecule 14: uL13



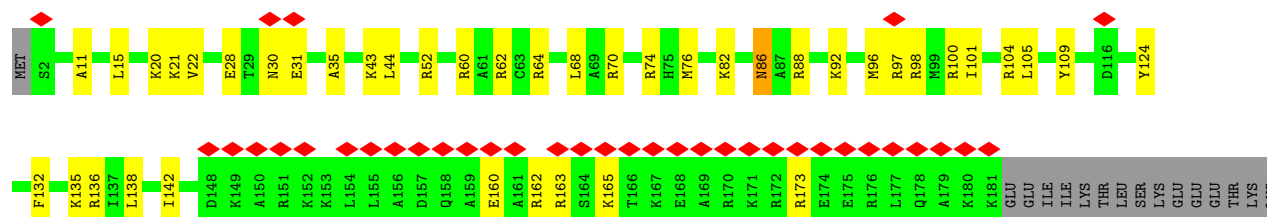
- Molecule 15: uL22



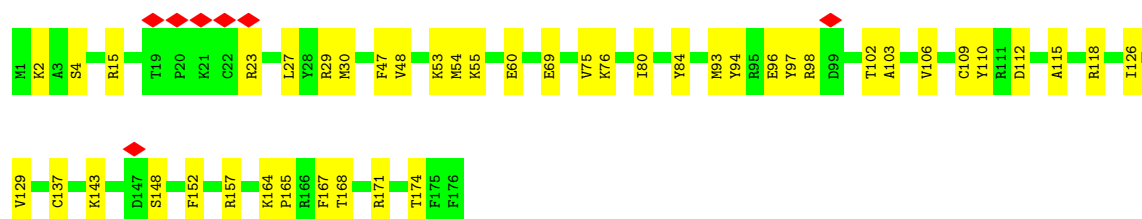
- Molecule 16: Ribosomal protein L18



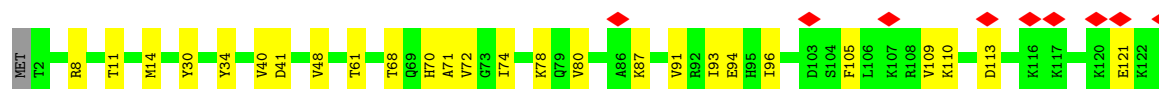
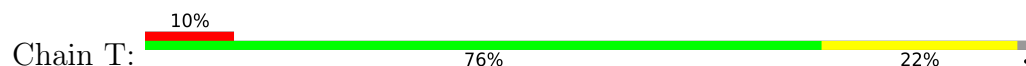
- Molecule 17: Ribosomal protein L19



- Molecule 18: 60S ribosomal protein L18a

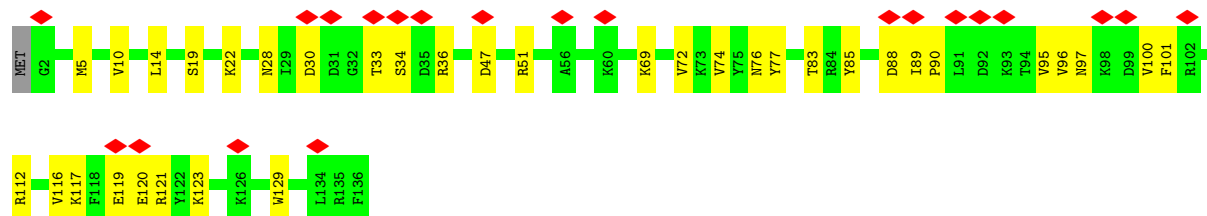
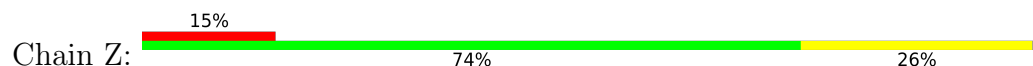


- Molecule 19: eL21

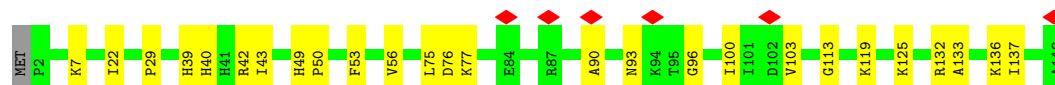
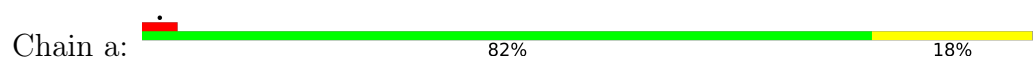




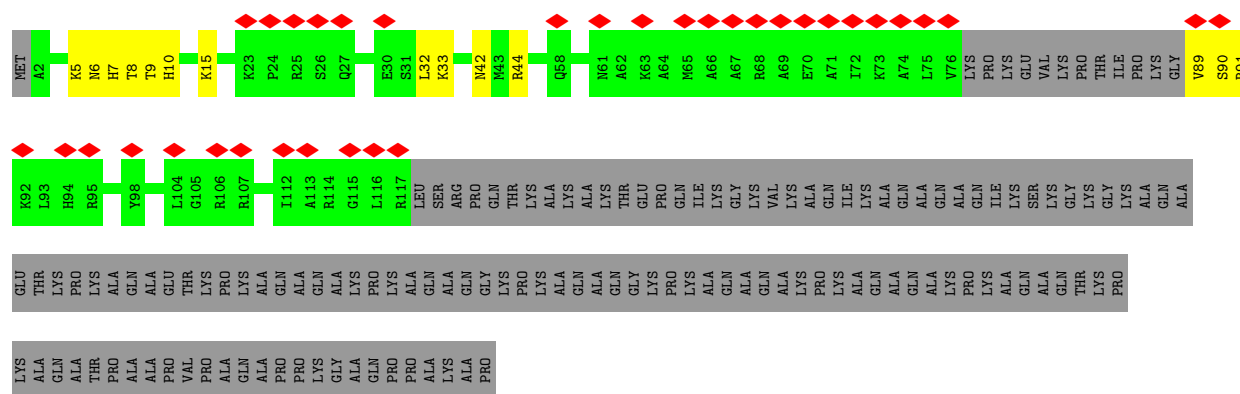
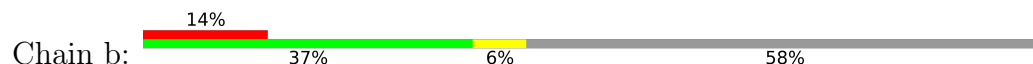
- Molecule 25: 60S ribosomal protein L27



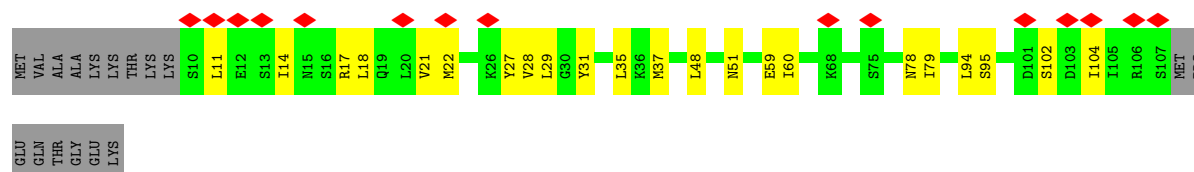
- Molecule 26: 60S ribosomal protein L27a



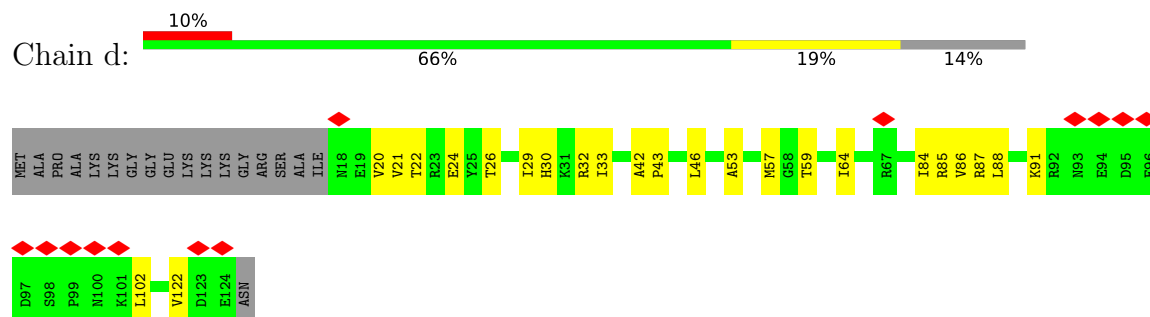
- Molecule 27: 60S ribosomal protein L29



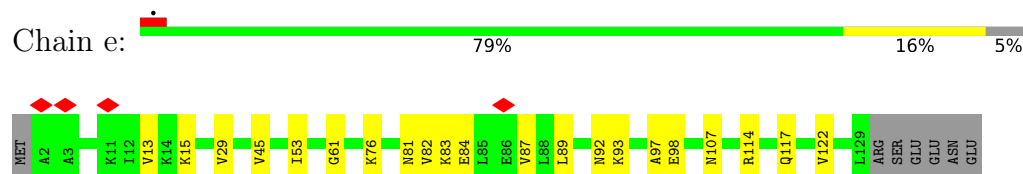
- Molecule 28: eL30



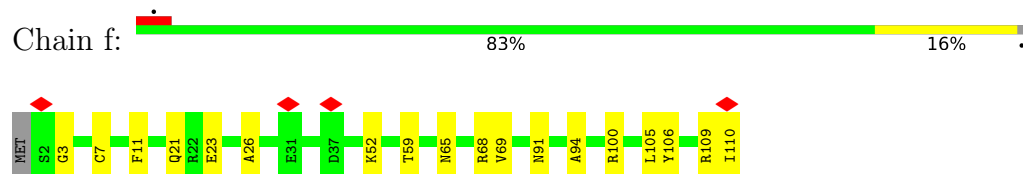
- Molecule 29: eL31



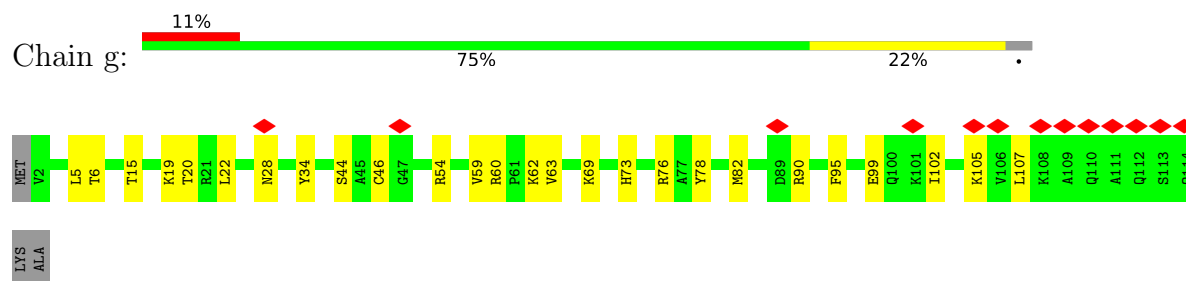
- Molecule 30: eL32



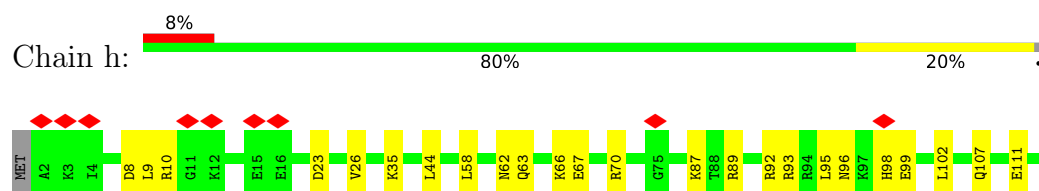
- Molecule 31: eL33



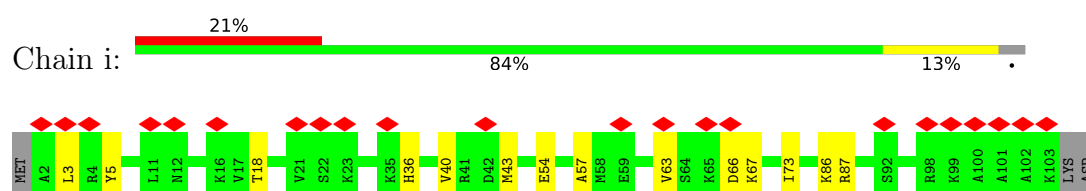
- Molecule 32: 60S ribosomal protein L34



- Molecule 33: eL35



- Molecule 34: 60S ribosomal protein L36



- Molecule 35: Ribosomal protein L37

Chain j:  72% 16% 11%



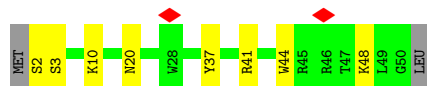
- Molecule 36: 60S ribosomal protein L38

Chain k:  37% 79% 20%

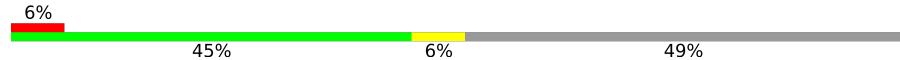


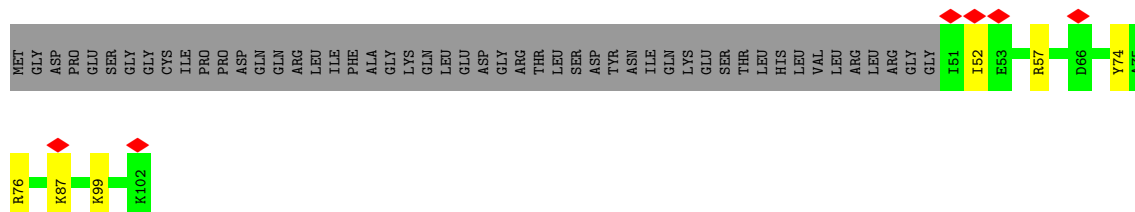
- Molecule 37: eL39

Chain l:  80% 16%



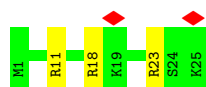
- Molecule 38: eL40

Chain m:  6% 45% 6% 49%



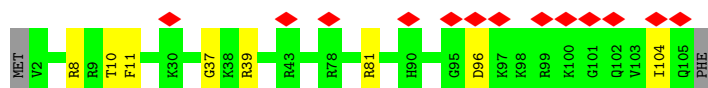
- Molecule 39: 60s ribosomal protein l41

Chain n:  8% 88% 12%

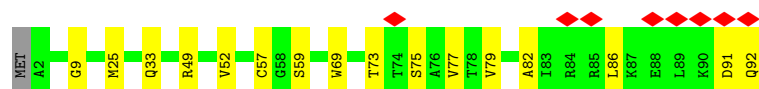
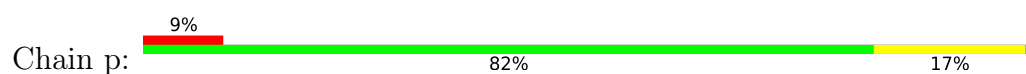


- Molecule 40: eL42

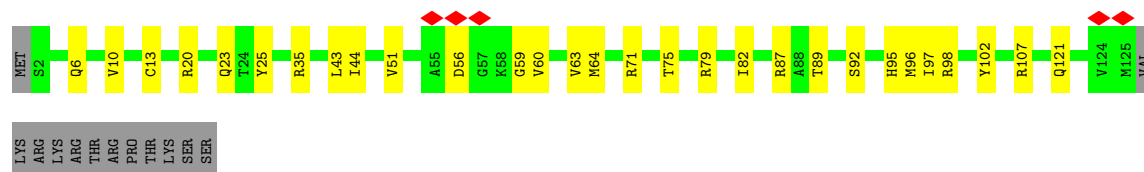
Chain o:  12% 91% 8%



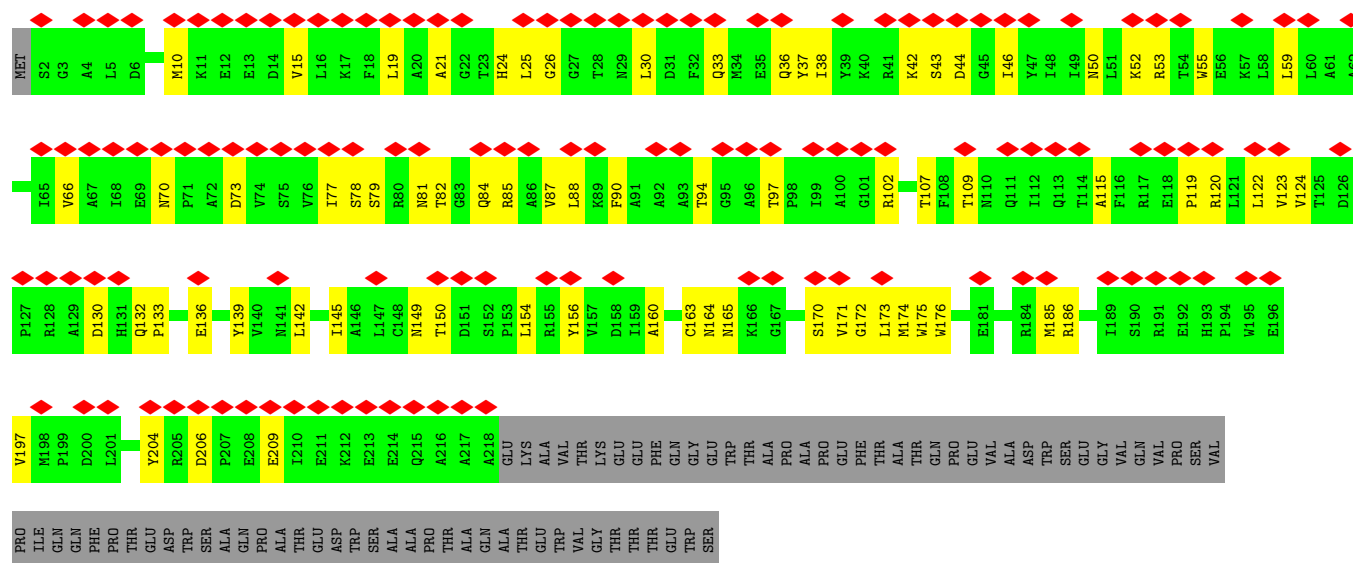
- Molecule 41: eL43



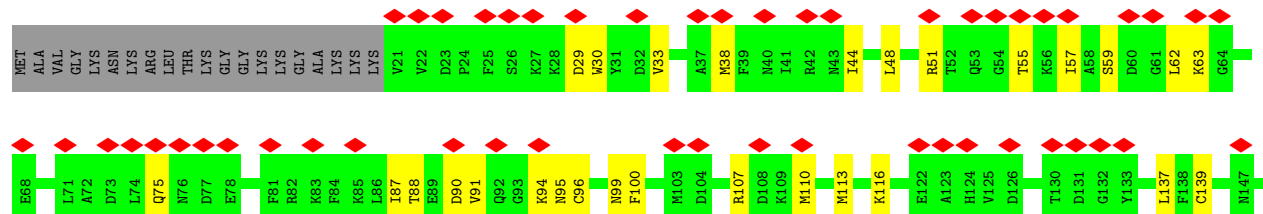
• Molecule 42: eL28

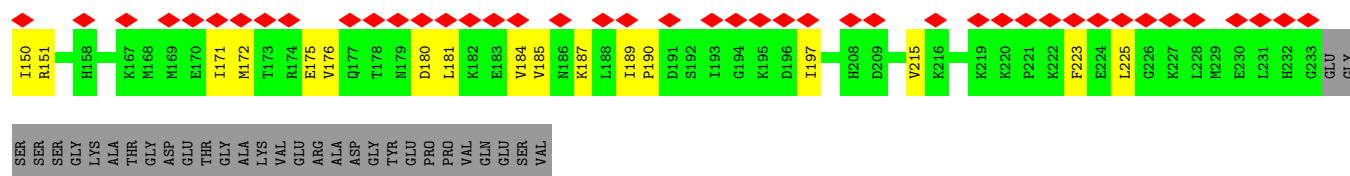


• Molecule 43: 40S ribosomal protein SA

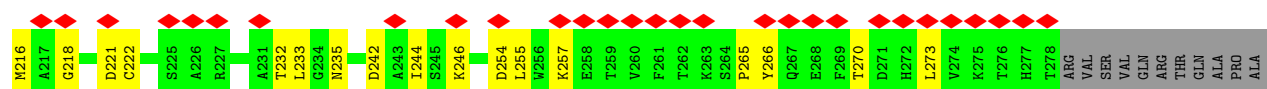
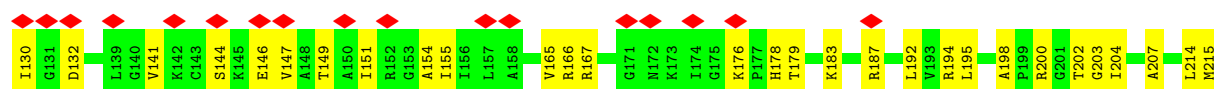
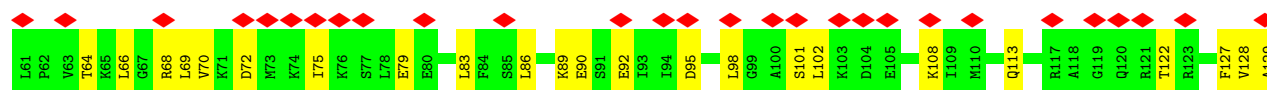
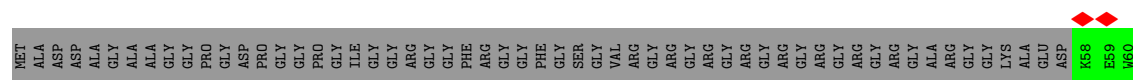


• Molecule 44: eS1

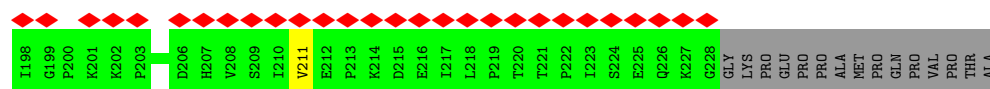
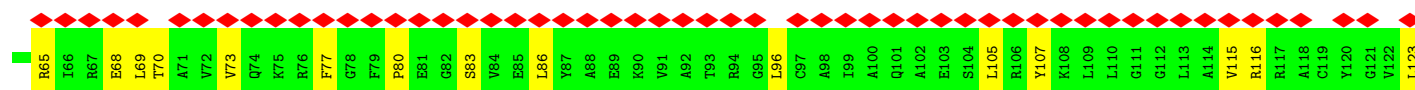
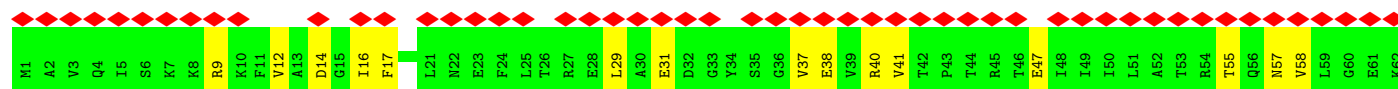
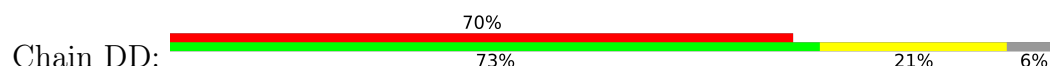




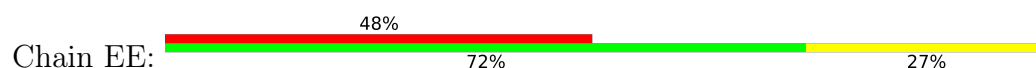
• Molecule 45: uS5

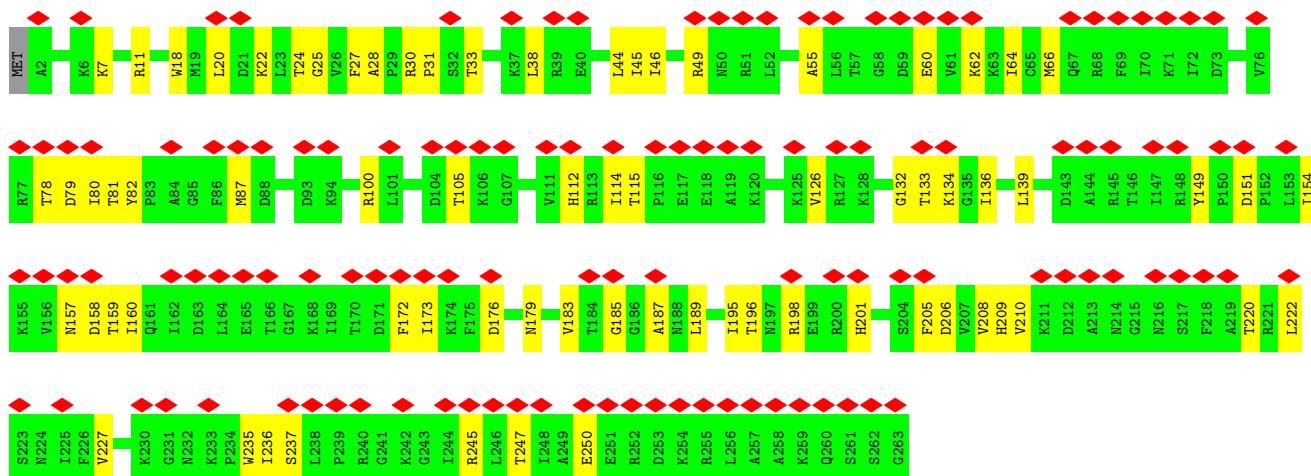


• Molecule 46: Ribosomal protein S3

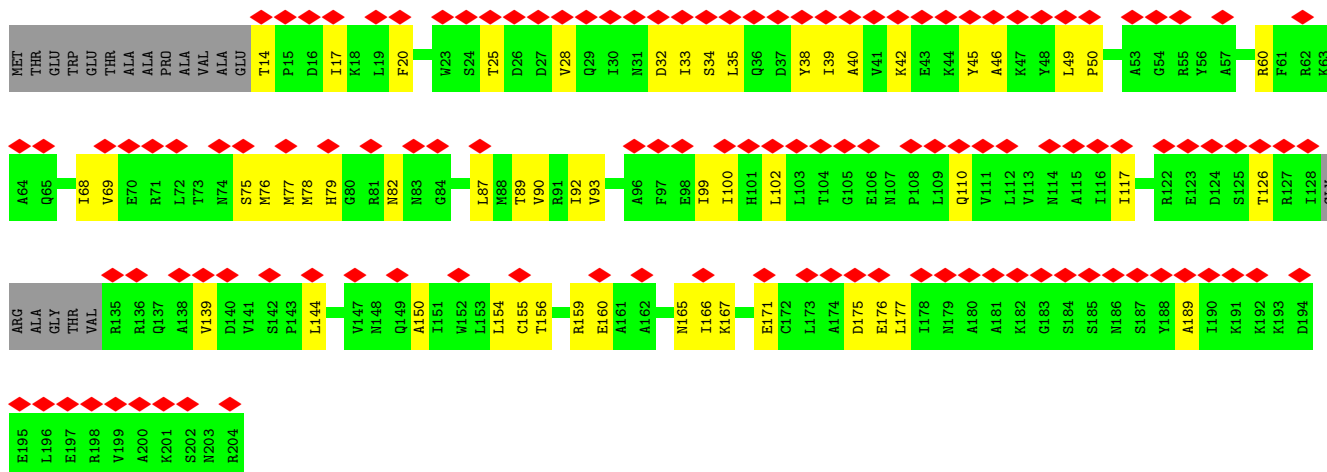


• Molecule 47: 40S ribosomal protein S4

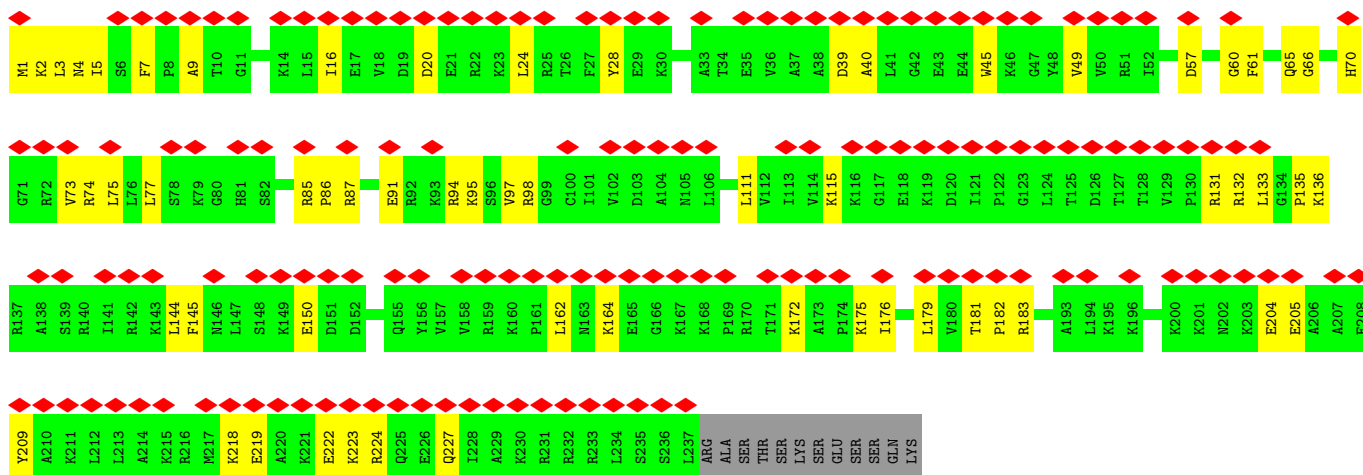
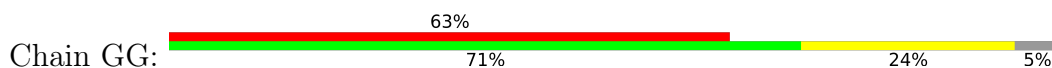




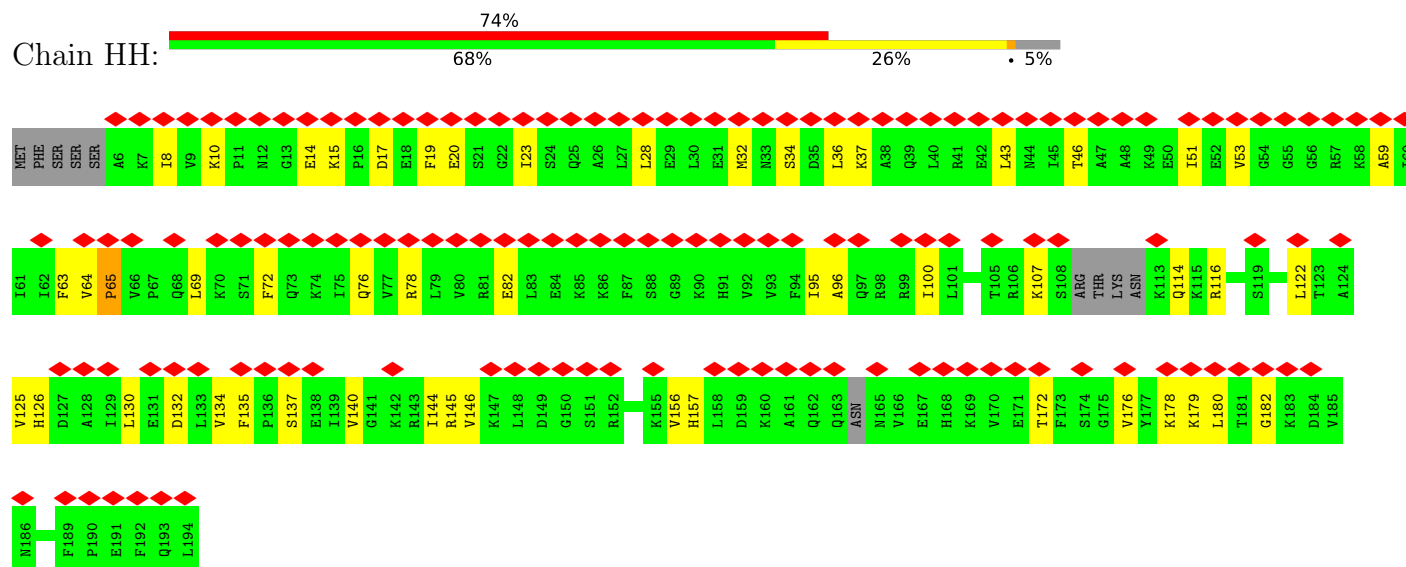
• Molecule 48: uS7



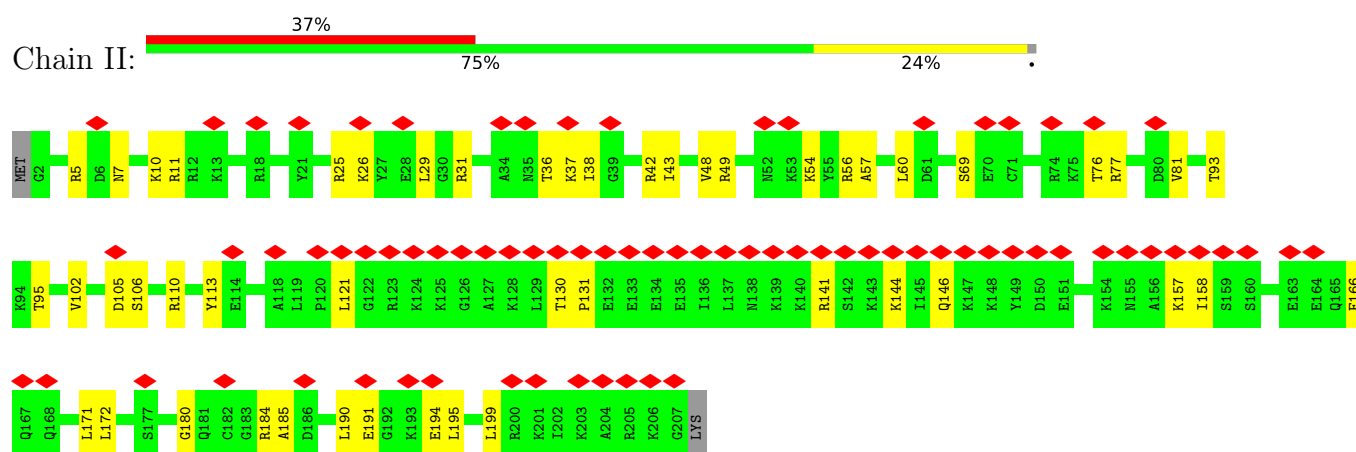
• Molecule 49: eS6



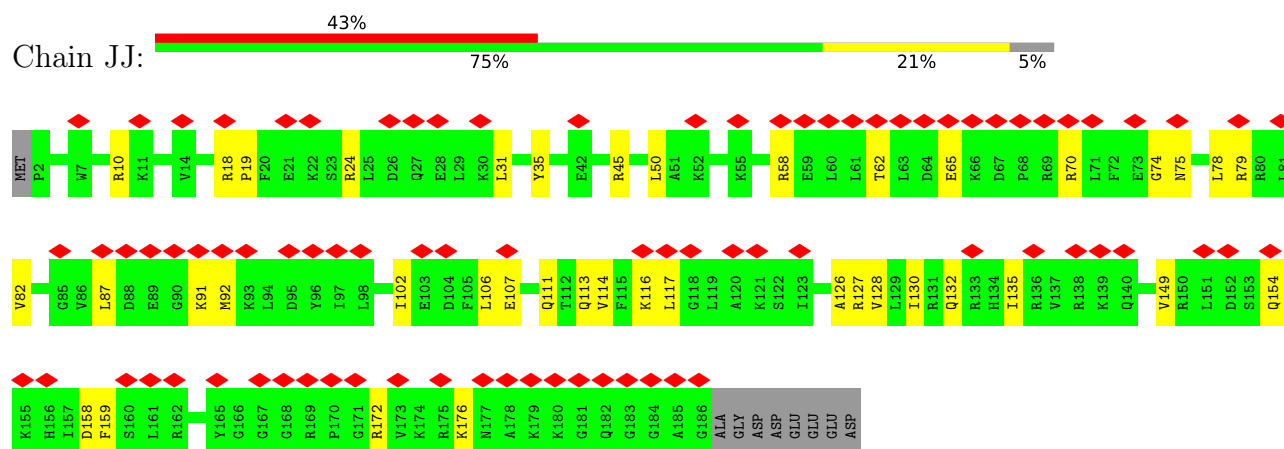
- Molecule 50: eS7



- Molecule 51: eS8

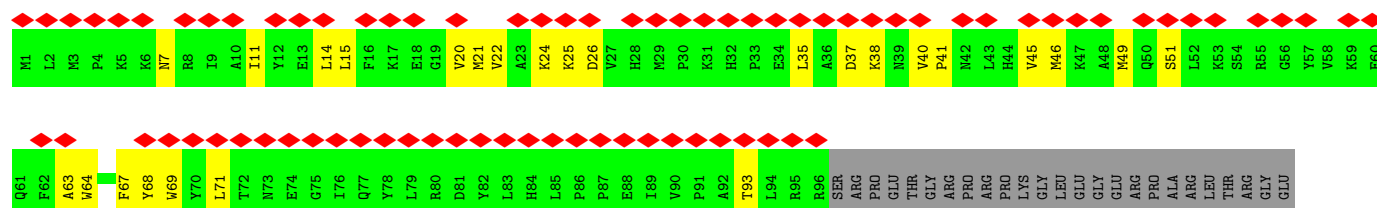


- Molecule 52: uS4

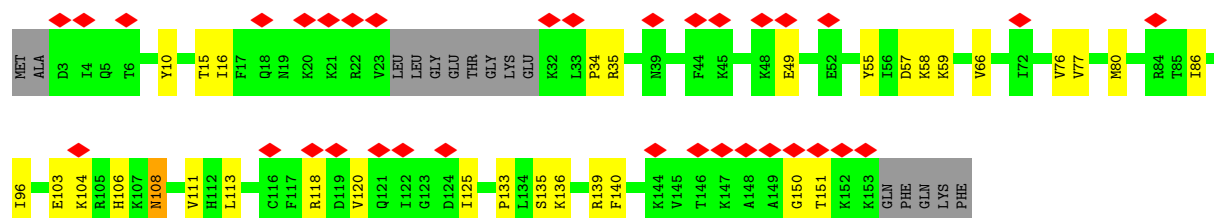


- Molecule 53: S10_ plectin domain-containing protein

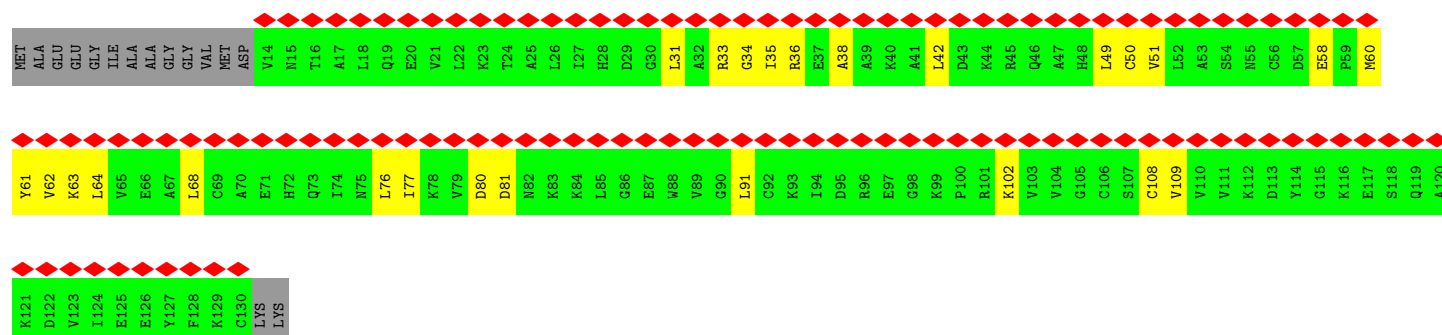
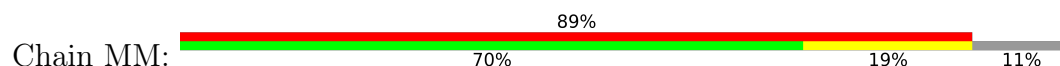




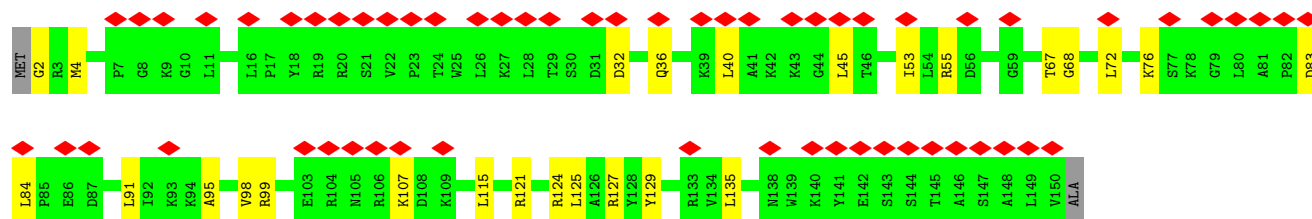
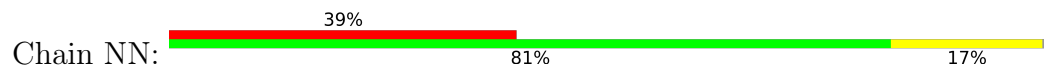
• Molecule 54: uS17



• Molecule 55: eS12

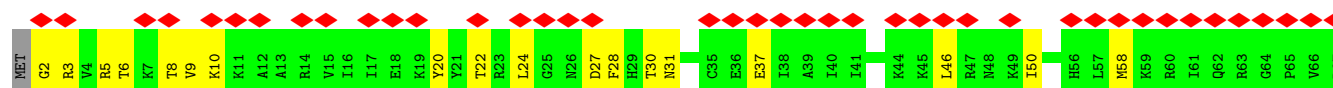


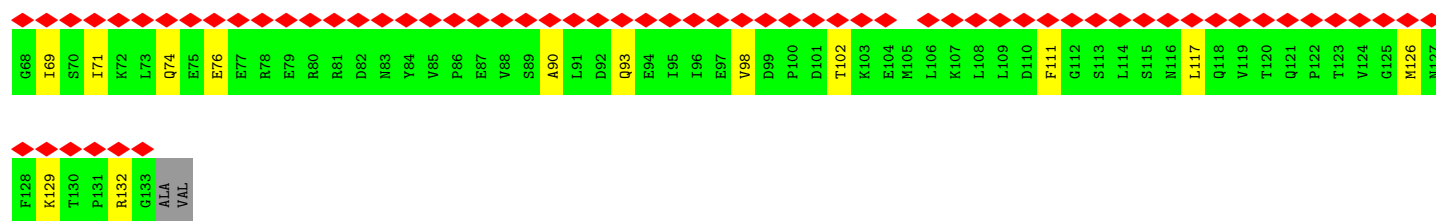
• Molecule 56: uS15



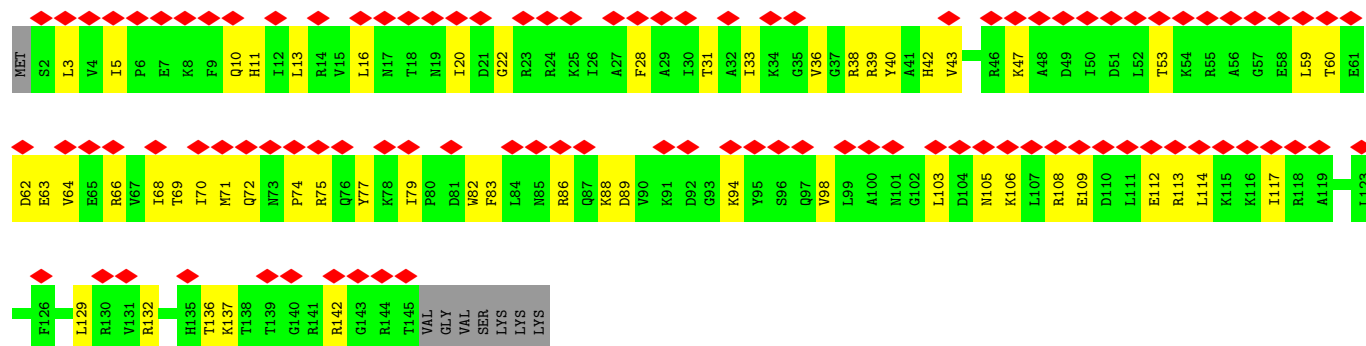
• Molecule 57: uS11



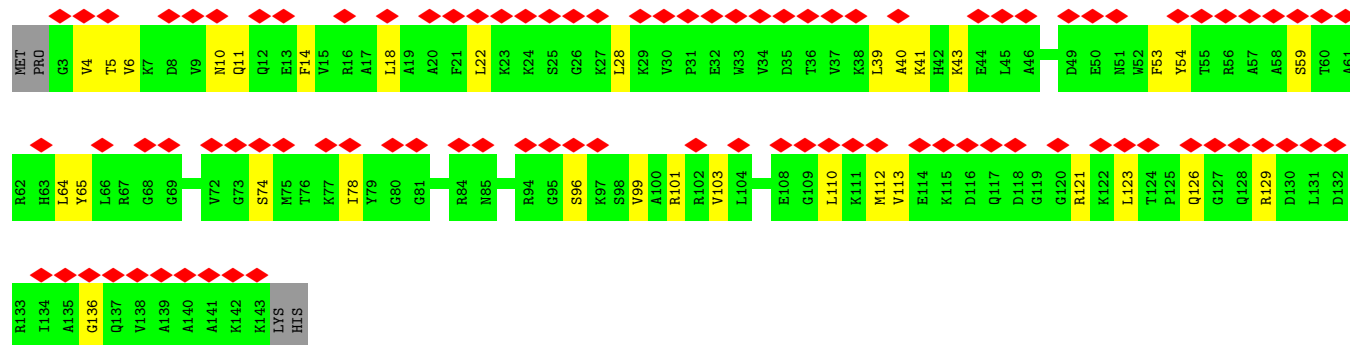
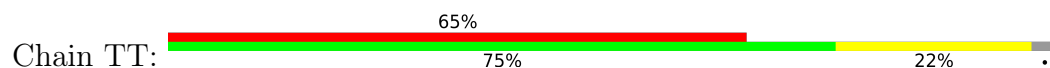




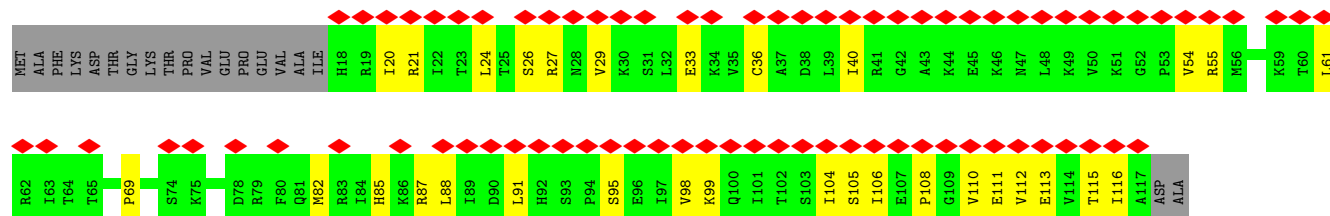
• Molecule 61: uS13



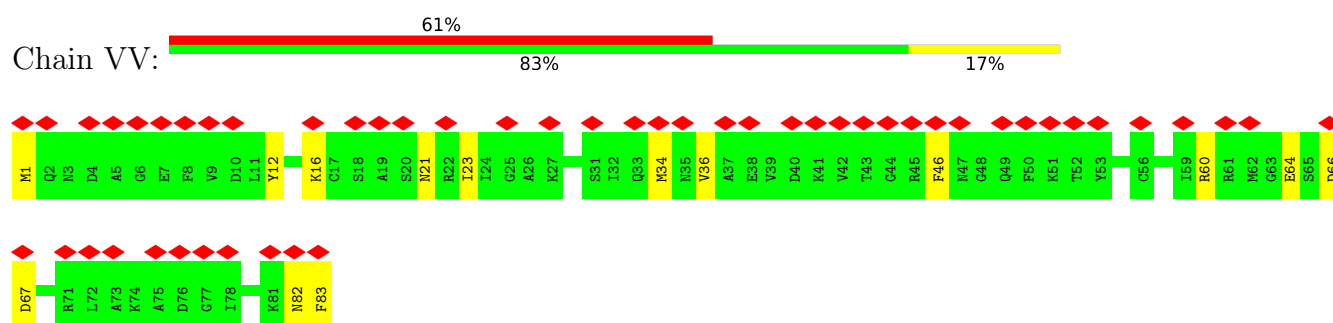
• Molecule 62: eS19



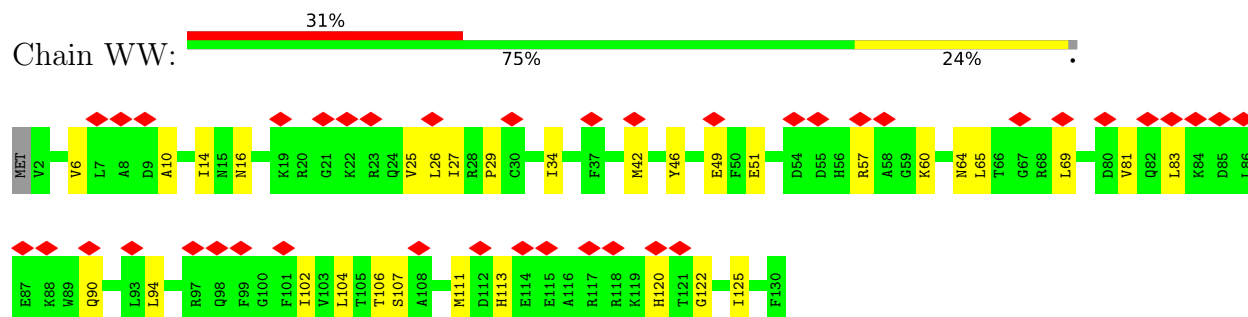
• Molecule 63: uS10



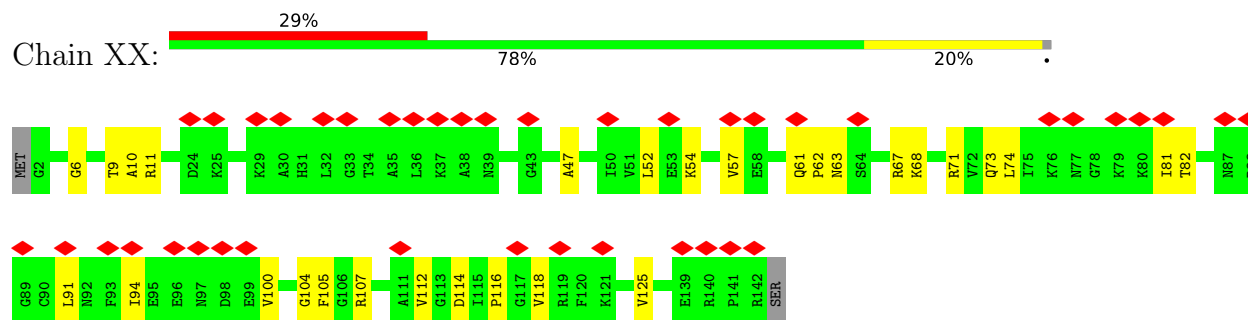
• Molecule 64: 40S ribosomal protein S21



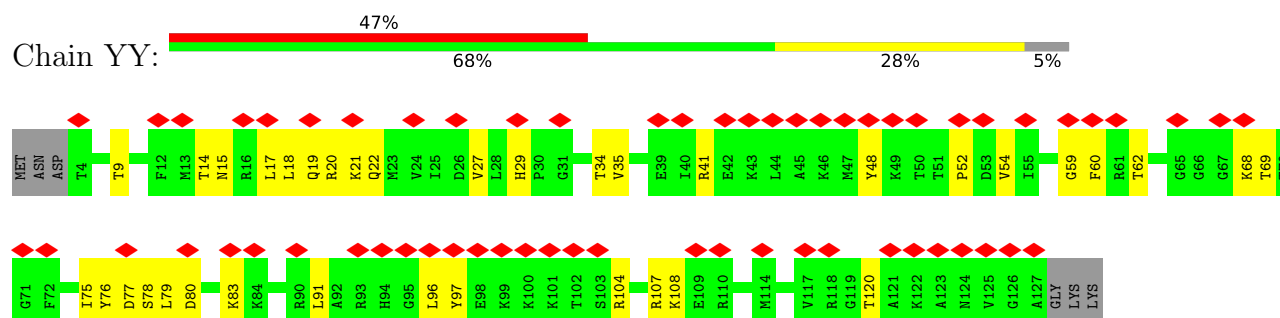
• Molecule 65: uS8



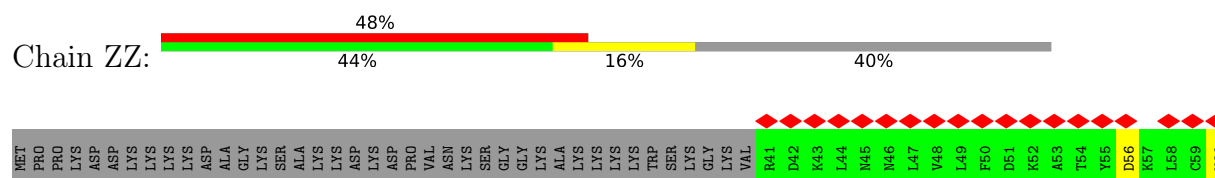
• Molecule 66: uS12

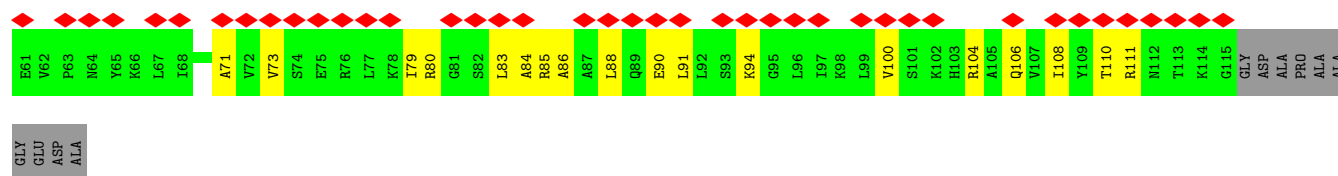


• Molecule 67: 40S ribosomal protein S24

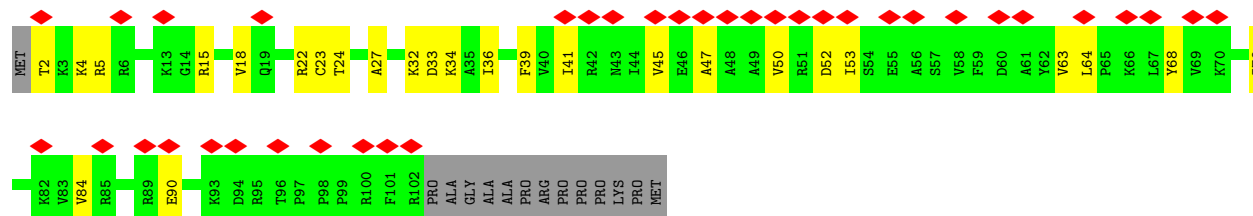


• Molecule 68: eS25

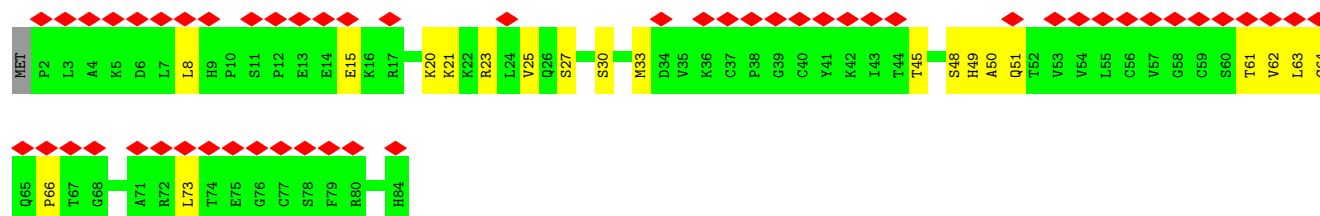
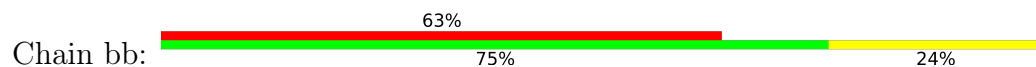




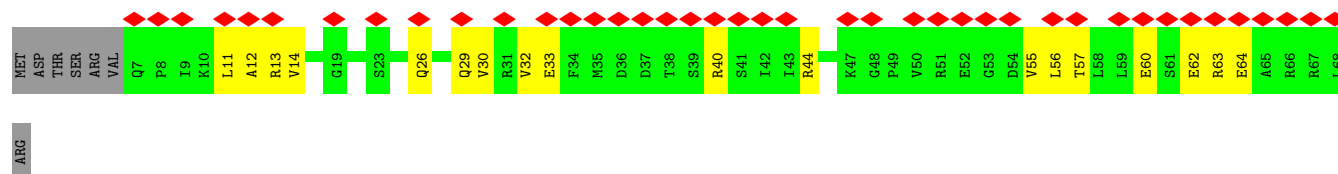
- Molecule 69: 40S ribosomal protein S26



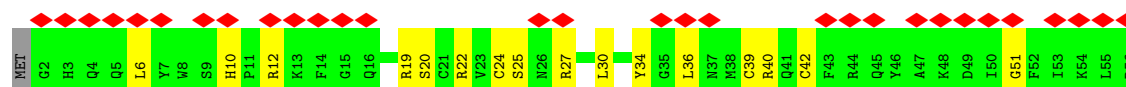
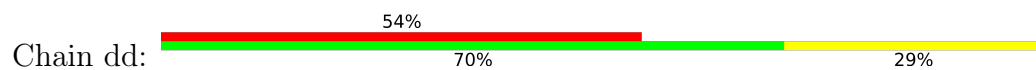
- Molecule 70: eS27



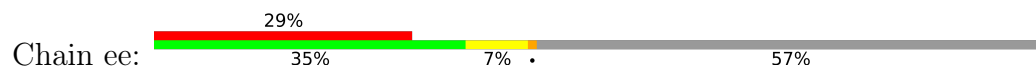
- Molecule 71: eS28

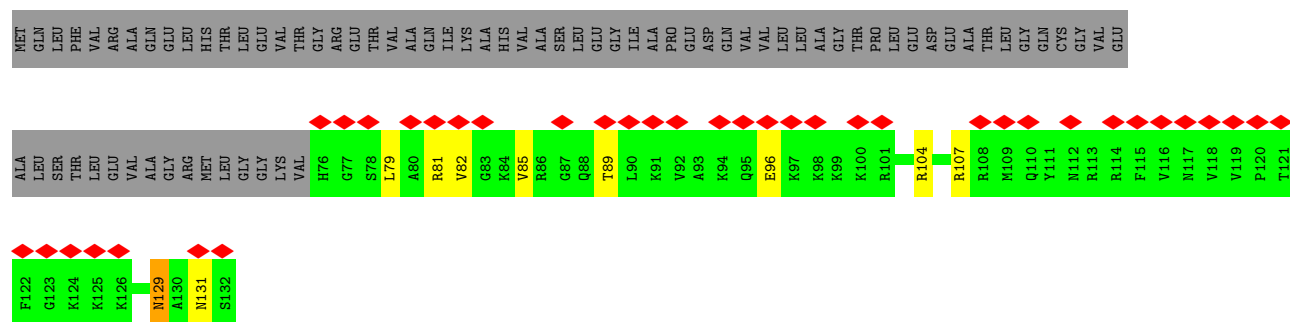


- Molecule 72: eS29

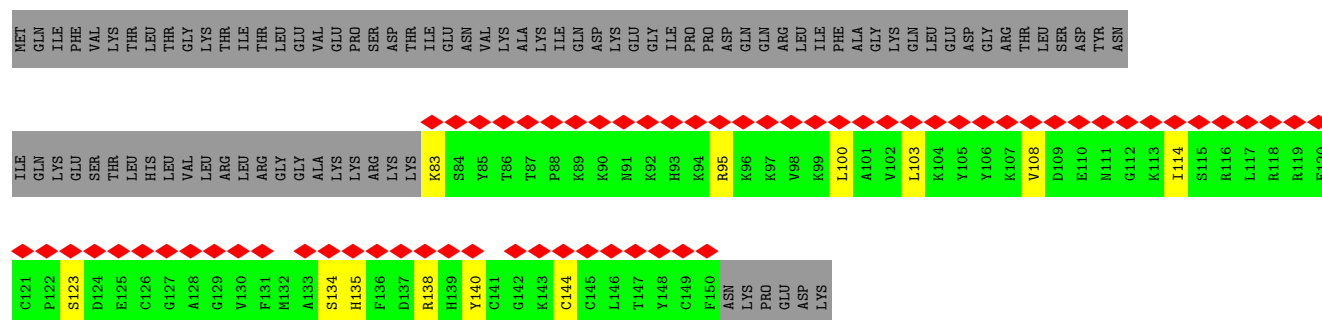
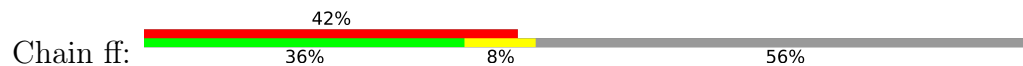


- Molecule 73: eS30

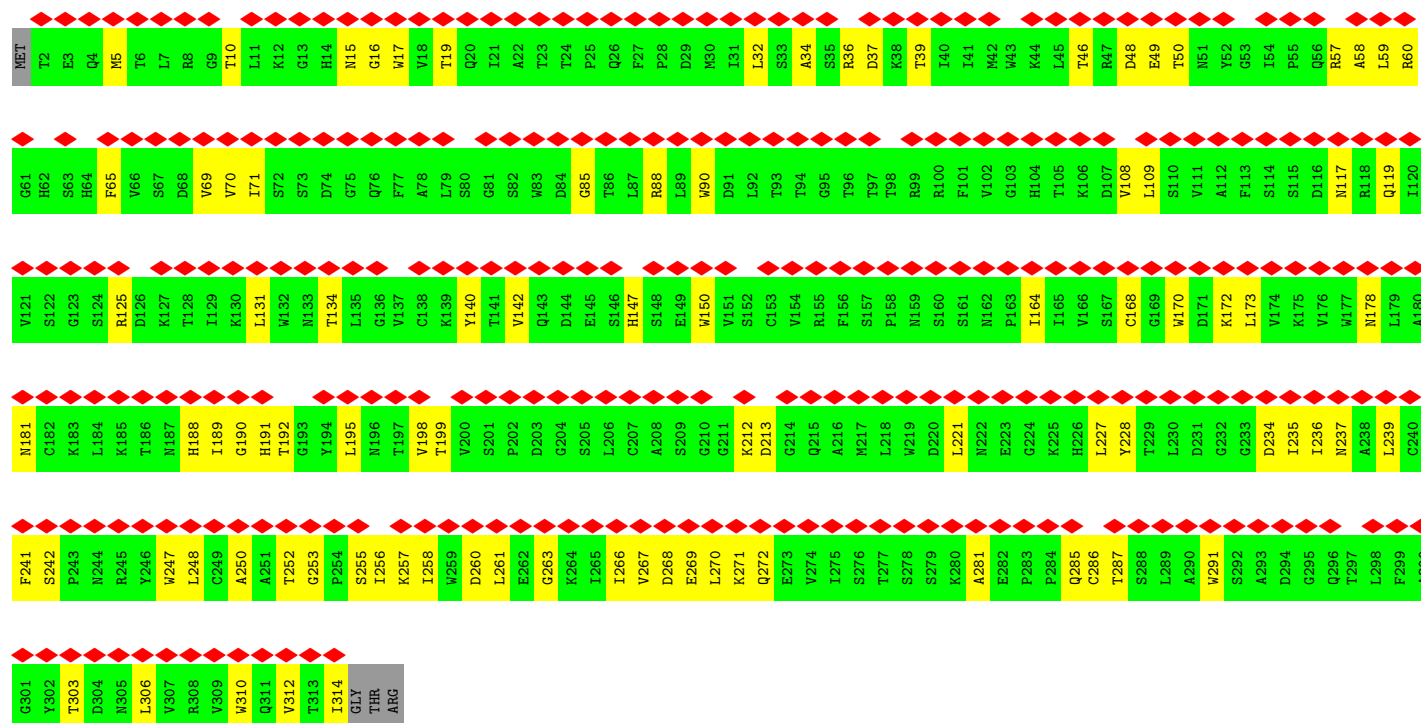
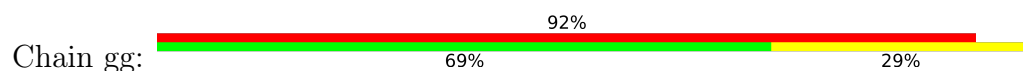




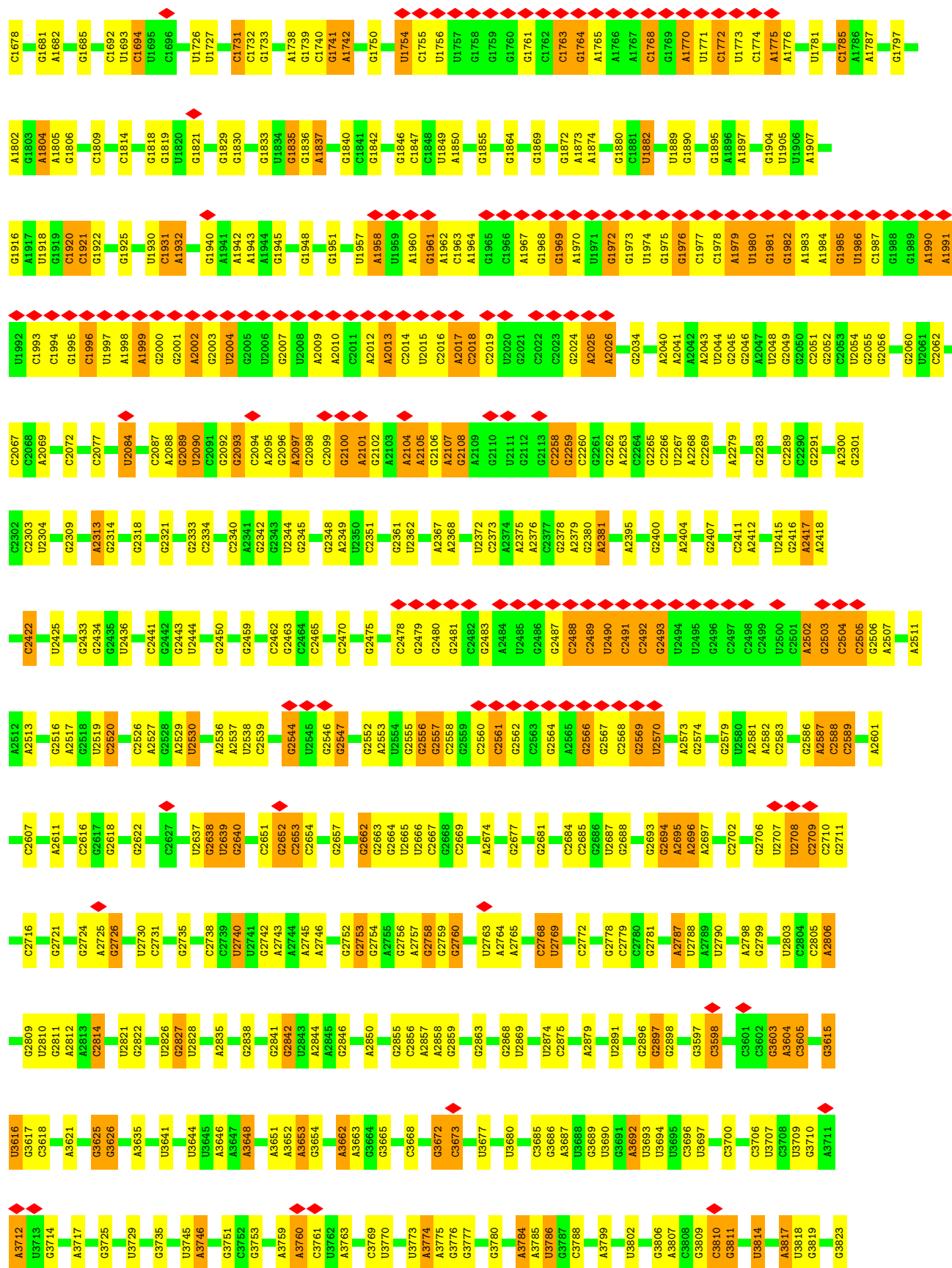
• Molecule 74: eS31

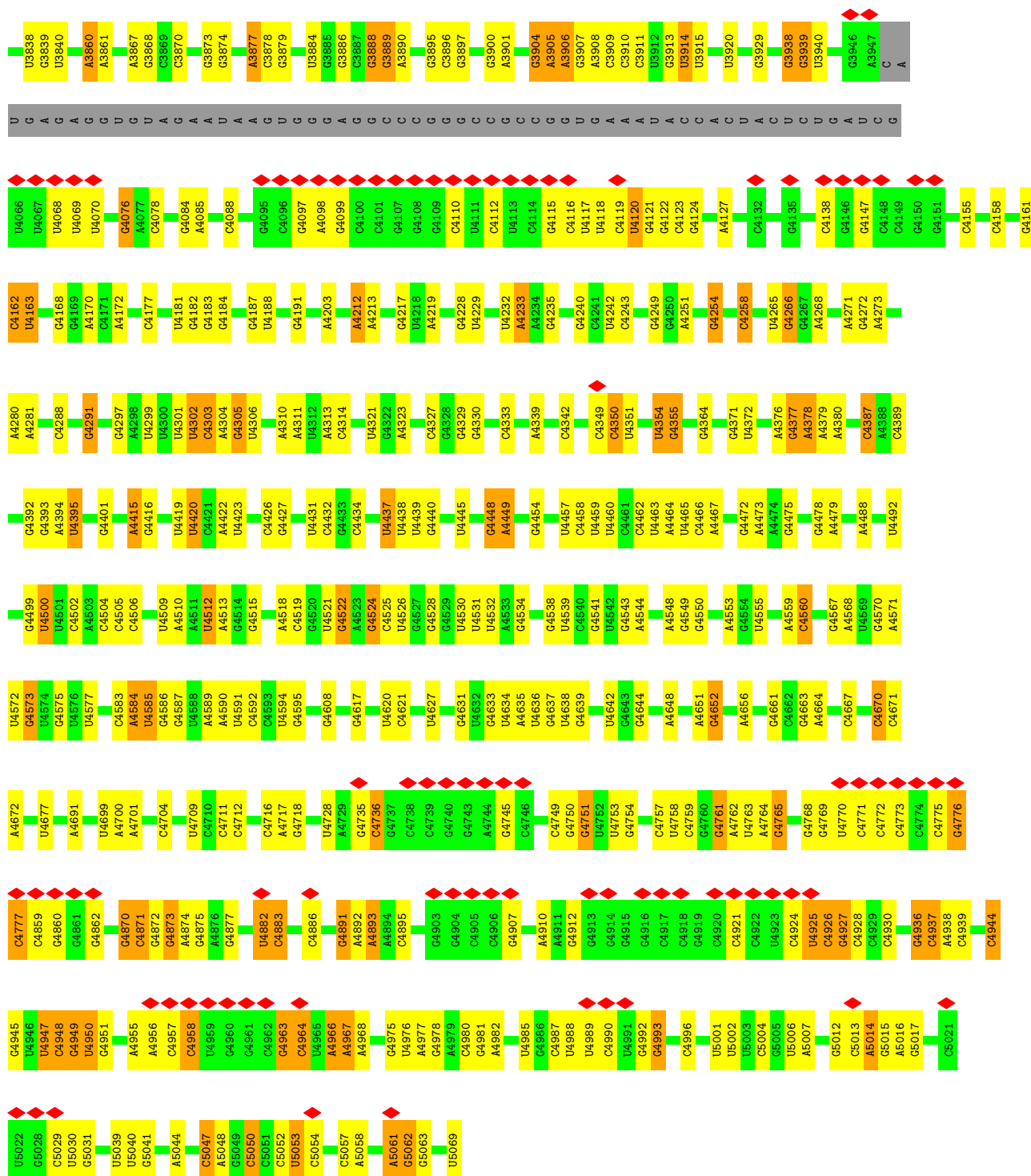


• Molecule 75: RACK1



• Molecule 76: 28S rRNA





• Molecule 77: 5S rRNA

Chain 7: 69% 29% ..

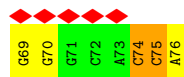


• Molecule 78: 5.8S rRNA

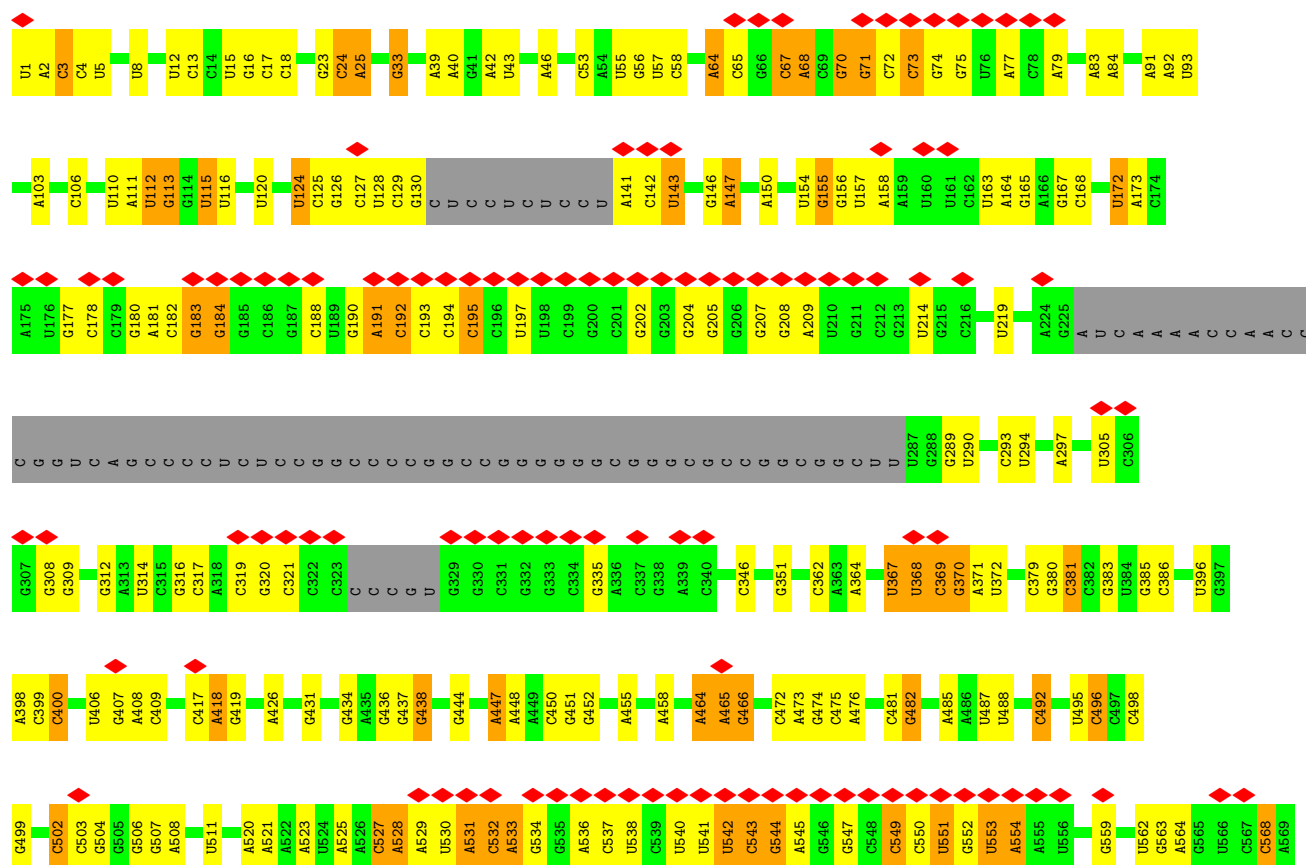
Chain 8:

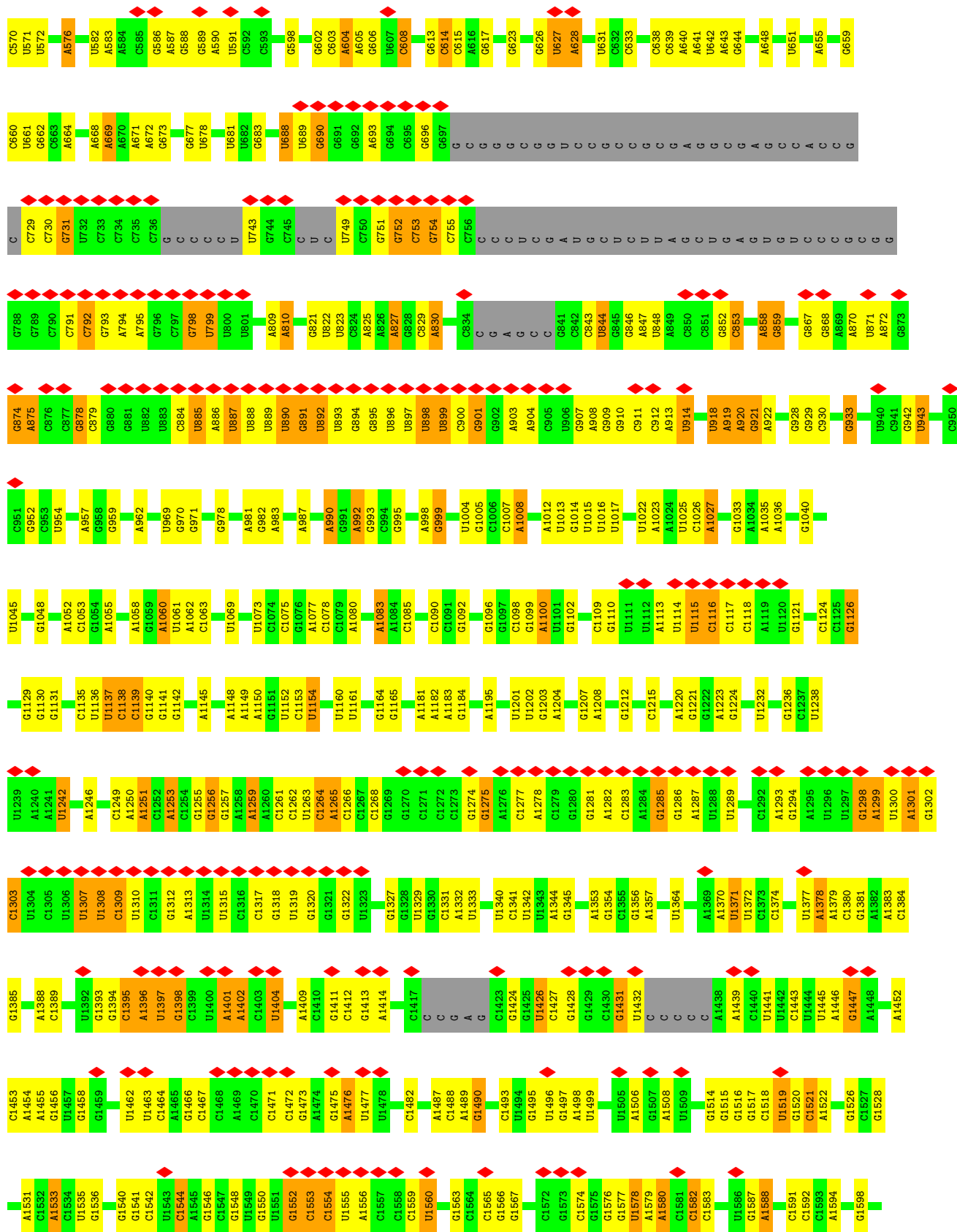


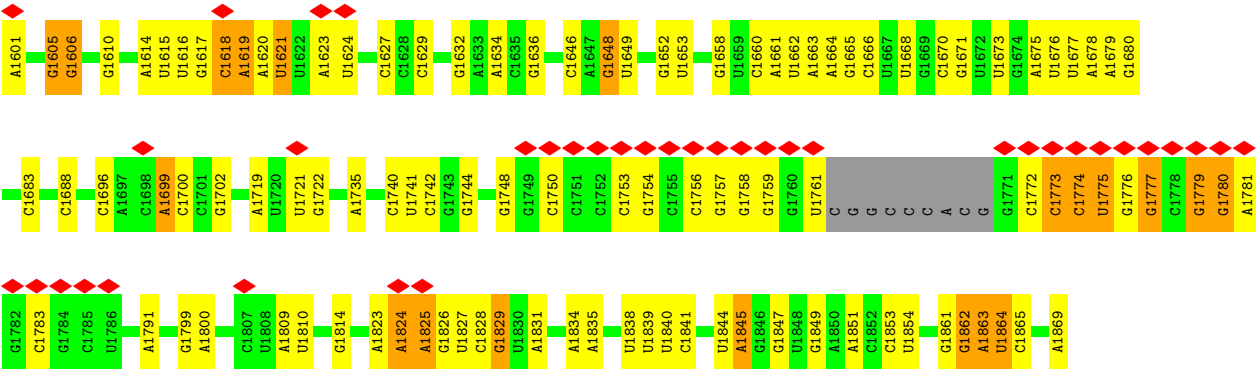
Chain 2:



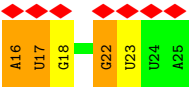
Chain 9:







• Molecule 81: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34783	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.231	Depositor
Minimum map value	-0.135	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	442.80002, 442.80002, 442.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: Z2V, MG, ZN

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	A	0.22	0/1936	0.39	0/2596
2	B	0.22	0/3240	0.34	0/4339
3	C	0.21	0/2937	0.33	0/3946
4	D	0.17	0/2437	0.31	0/3264
5	E	0.17	0/1762	0.33	0/2362
6	F	0.22	0/1911	0.33	0/2549
7	G	0.18	0/1910	0.34	0/2569
8	H	0.18	0/1535	0.32	0/2063
9	I	0.19	0/1702	0.32	0/2272
10	J	0.17	0/1385	0.35	0/1852
11	L	0.19	0/1733	0.32	0/2316
12	M	0.19	0/1158	0.31	0/1547
13	N	0.22	0/1746	0.33	0/2338
14	O	0.20	0/1662	0.30	0/2222
15	P	0.22	0/1268	0.36	0/1700
16	Q	0.22	0/1539	0.32	0/2054
17	R	0.18	0/1524	0.31	0/2013
18	S	0.21	0/1501	0.32	0/2012
19	T	0.21	0/1312	0.31	0/1753
20	U	0.15	0/823	0.31	0/1104
21	V	0.19	0/1048	0.32	0/1402
22	W	0.20	0/541	0.31	0/720
23	X	0.18	0/984	0.29	0/1323
24	Y	0.19	0/1132	0.30	0/1504
25	Z	0.18	0/1130	0.37	0/1507
26	a	0.23	0/1191	0.32	0/1590
27	b	0.17	0/861	0.30	0/1138
28	c	0.19	0/771	0.38	0/1034
29	d	0.19	0/903	0.31	0/1216
30	e	0.22	0/1071	0.31	0/1429
31	f	0.23	0/895	0.38	0/1198
32	g	0.18	0/907	0.34	0/1209

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.17	0/1021	0.32	0/1348
34	i	0.16	0/841	0.29	0/1112
35	j	0.21	0/720	0.34	0/952
36	k	0.17	0/575	0.33	0/761
37	l	0.19	0/450	0.29	0/597
38	m	0.18	0/435	0.35	0/575
39	n	0.21	0/240	0.30	0/305
40	o	0.18	0/864	0.29	0/1140
41	p	0.19	0/718	0.30	0/953
42	r	0.20	0/1010	0.33	0/1354
43	AA	0.15	0/1749	0.33	0/2377
44	BB	0.16	0/1756	0.33	0/2350
45	CC	0.18	0/1753	0.37	0/2369
46	DD	0.15	0/1796	0.35	0/2417
47	EE	0.14	0/2118	0.33	0/2849
48	FF	0.14	0/1492	0.36	0/2005
49	GG	0.15	0/1946	0.33	0/2590
50	HH	0.17	0/1501	0.42	1/2008 (0.0%)
51	II	0.16	0/1715	0.34	0/2287
52	JJ	0.14	0/1550	0.31	0/2069
53	KK	0.16	0/834	0.34	0/1125
54	LL	0.16	0/1195	0.29	0/1597
55	MM	0.12	0/918	0.32	0/1233
56	NN	0.15	0/1226	0.33	0/1649
57	OO	0.17	0/1029	0.33	0/1380
58	PP	0.14	0/1079	0.32	0/1441
59	QQ	0.15	0/1146	0.34	0/1534
60	RR	0.13	0/1082	0.30	0/1452
61	SS	0.15	0/1208	0.34	0/1618
62	TT	0.13	0/1115	0.31	0/1493
63	UU	0.17	0/805	0.41	0/1081
64	VV	0.13	0/643	0.29	0/860
65	WW	0.17	0/1051	0.36	0/1406
66	XX	0.15	0/1116	0.31	0/1490
67	YY	0.14	0/1028	0.33	0/1366
68	ZZ	0.13	0/604	0.33	0/810
69	aa	0.17	0/828	0.33	0/1109
70	bb	0.13	0/665	0.29	0/891
71	cc	0.13	0/490	0.35	0/656
72	dd	0.16	0/470	0.30	0/623
73	ee	0.14	0/462	0.37	0/607
74	ff	0.12	0/567	0.32	0/753
75	gg	0.15	0/2493	0.36	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	5	0.22	0/84931	0.29	0/132457
77	7	0.20	0/2836	0.25	0/4421
78	8	0.21	0/3581	0.26	0/5577
79	2	0.13	0/1813	0.29	0/2823
80	9	0.15	0/40509	0.28	0/63128
81	6	0.14	0/233	0.34	0/360
All	All	0.19	0/226662	0.30	1/332893 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	HH	65	PRO	CA-N-CD	-8.88	99.57	112.00

There are no chirality outliers.

There are no planarity outliers.

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	A	1898	0	1993	47	0
2	B	3172	0	3310	61	0
3	C	2883	0	3053	60	0
4	D	2391	0	2424	45	0
5	E	1729	0	1887	46	0
6	F	1875	0	1995	27	0
7	G	1879	0	2027	38	0
8	H	1516	0	1597	44	0
9	I	1664	0	1712	18	0
10	J	1362	0	1399	22	0
11	L	1702	0	1820	26	0
12	M	1137	0	1211	19	0
13	N	1701	0	1749	42	0
14	O	1630	0	1778	28	0
15	P	1242	0	1274	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	Q	1515	0	1634	31	0
17	R	1508	0	1664	41	0
18	S	1462	0	1508	36	0
19	T	1284	0	1352	36	0
20	U	809	0	833	16	0
21	V	1034	0	1097	24	0
22	W	528	0	541	6	0
23	X	967	0	1040	18	0
24	Y	1115	0	1205	24	0
25	Z	1107	0	1182	27	0
26	a	1162	0	1209	24	0
27	b	848	0	920	14	0
28	c	761	0	794	19	0
29	d	888	0	930	18	0
30	e	1053	0	1147	15	0
31	f	876	0	912	17	0
32	g	897	0	985	22	0
33	h	1013	0	1147	17	0
34	i	830	0	916	10	0
35	j	705	0	737	17	0
36	k	569	0	637	14	0
37	l	438	0	469	7	0
38	m	429	0	465	6	0
39	n	239	0	289	3	0
40	o	851	0	920	8	0
41	p	708	0	756	12	0
42	r	994	0	1051	24	0
43	AA	1712	0	1713	58	0
44	BB	1729	0	1803	40	0
45	CC	1716	0	1806	54	0
46	DD	1768	0	1866	39	0
47	EE	2076	0	2177	55	0
48	FF	1471	0	1522	45	0
49	GG	1923	0	2089	50	0
50	HH	1480	0	1575	44	0
51	II	1686	0	1772	42	0
52	JJ	1525	0	1640	30	0
53	KK	810	0	836	27	0
54	LL	1175	0	1249	31	0
55	MM	908	0	939	25	0
56	NN	1202	0	1289	22	0
57	OO	1016	0	1039	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	PP	1058	0	1104	29	0
59	QQ	1128	0	1195	30	0
60	RR	1068	0	1121	25	0
61	SS	1190	0	1249	52	0
62	TT	1097	0	1132	29	0
63	UU	795	0	862	26	0
64	VV	636	0	637	13	0
65	WW	1034	0	1080	27	0
66	XX	1098	0	1167	25	0
67	YY	1011	0	1083	32	0
68	ZZ	598	0	656	15	0
69	aa	814	0	864	24	0
70	bb	651	0	672	18	0
71	cc	488	0	514	13	0
72	dd	459	0	448	17	0
73	ee	457	0	502	15	0
74	ff	555	0	564	16	0
75	gg	2436	0	2393	65	0
76	5	75929	0	38360	845	0
77	7	2538	0	1286	23	0
78	8	3208	0	1629	38	0
79	2	1623	0	821	32	0
80	9	36229	0	18298	504	0
81	6	210	0	106	4	0
82	2	2	0	0	0	0
82	5	189	0	0	0	0
82	7	6	0	0	0	0
82	8	5	0	0	0	0
82	9	69	0	0	0	0
82	A	1	0	0	0	0
82	B	1	0	0	0	0
82	LL	1	0	0	0	0
82	P	1	0	0	0	0
82	V	1	0	0	0	0
82	g	1	0	0	0	0
83	aa	1	0	0	0	0
83	dd	1	0	0	0	0
83	ff	1	0	0	0	0
83	g	1	0	0	0	0
83	j	1	0	0	0	0
83	m	1	0	0	0	0
83	o	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	p	1	0	0	0	0
84	5	29	0	0	0	0
All	All	211192	0	156627	2958	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2958 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)
5:E:41:LYS:N	76:5:981:C:HO2'	1.30	1.26
76:5:2411:C:HO2'	76:5:2526:C:HO2'	1.03	1.03
80:9:751:G:O2'	80:9:752:G:O4'	1.78	1.01
76:5:485:C:O2'	76:5:486:C:O5'	1.78	1.00
53:KK:45:VAL:HG12	53:KK:49:MET:HE1	1.37	1.00

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/199 (96%)	190 (100%)	0	100	100
2	B	342/348 (98%)	342 (100%)	0	100	100
3	C	302/347 (87%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	190/251 (76%)	190 (100%)	0	100	100
6	F	196/215 (91%)	196 (100%)	0	100	100
7	G	200/272 (74%)	199 (100%)	1 (0%)	81	85
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	175/181 (97%)	175 (100%)	0	100	100
10	J	143/149 (96%)	143 (100%)	0	100	100
11	L	175/176 (99%)	175 (100%)	0	100	100
12	M	117/161 (73%)	117 (100%)	0	100	100
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	171/173 (99%)	171 (100%)	0	100	100
15	P	134/163 (82%)	134 (100%)	0	100	100
16	Q	164/165 (99%)	164 (100%)	0	100	100
17	R	159/175 (91%)	158 (99%)	1 (1%)	78	84
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	138/140 (99%)	138 (100%)	0	100	100
20	U	89/114 (78%)	89 (100%)	0	100	100
21	V	106/107 (99%)	106 (100%)	0	100	100
22	W	55/126 (44%)	55 (100%)	0	100	100
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	124 (100%)	0	100	100
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	119 (100%)	0	100	100
27	b	84/184 (46%)	84 (100%)	0	100	100
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	98 (100%)	0	100	100
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	97/99 (98%)	97 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	46/48 (96%)	46 (100%)	0	100	100
38	m	48/90 (53%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	108 (100%)	0	100	100
43	AA	181/245 (74%)	181 (100%)	0	100	100
44	BB	194/231 (84%)	194 (100%)	0	100	100
45	CC	187/225 (83%)	187 (100%)	0	100	100
46	DD	190/202 (94%)	190 (100%)	0	100	100
47	EE	224/225 (100%)	224 (100%)	0	100	100
48	FF	158/170 (93%)	158 (100%)	0	100	100
49	GG	207/218 (95%)	207 (100%)	0	100	100
50	HH	164/174 (94%)	164 (100%)	0	100	100
51	II	178/180 (99%)	178 (100%)	0	100	100
52	JJ	161/168 (96%)	161 (100%)	0	100	100
53	KK	87/136 (64%)	87 (100%)	0	100	100
54	LL	130/142 (92%)	129 (99%)	1 (1%)	73	82
55	MM	99/108 (92%)	99 (100%)	0	100	100
56	NN	130/131 (99%)	130 (100%)	0	100	100
57	OO	106/130 (82%)	106 (100%)	0	100	100
58	PP	115/130 (88%)	115 (100%)	0	100	100
59	QQ	117/121 (97%)	117 (100%)	0	100	100
60	RR	119/121 (98%)	119 (100%)	0	100	100
61	SS	125/132 (95%)	125 (100%)	0	100	100
62	TT	111/115 (96%)	111 (100%)	0	100	100
63	UU	92/107 (86%)	92 (100%)	0	100	100
64	VV	67/67 (100%)	67 (100%)	0	100	100
65	WW	112/113 (99%)	112 (100%)	0	100	100
66	XX	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	YY	107/112 (96%)	107 (100%)	0	100	100
68	ZZ	66/103 (64%)	66 (100%)	0	100	100
69	aa	88/98 (90%)	88 (100%)	0	100	100
70	bb	75/76 (99%)	75 (100%)	0	100	100
71	cc	55/62 (89%)	54 (98%)	1 (2%)	51	74
72	dd	48/49 (98%)	48 (100%)	0	100	100
73	ee	47/106 (44%)	46 (98%)	1 (2%)	47	71
74	ff	61/140 (44%)	61 (100%)	0	100	100
75	gg	272/275 (99%)	272 (100%)	0	100	100
All	All	9731/10943 (89%)	9726 (100%)	5 (0%)	87	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	134	ASN
17	R	86	ASN
54	LL	108	ASN
71	cc	29	GLN
73	ee	129	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
19	T	144	ASN
70	bb	65	GLN
29	d	116	ASN
66	XX	23	HIS
53	KK	61	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	5	3518/3603 (97%)	675 (19%)	53 (1%)
77	7	118/120 (98%)	9 (7%)	0
78	8	149/156 (95%)	27 (18%)	1 (0%)
79	2	75/76 (98%)	21 (28%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
80	9	1685/1869 (90%)	344 (20%)	20 (1%)
81	6	10/10 (100%)	4 (40%)	1 (10%)
All	All	5555/5834 (95%)	1080 (19%)	76 (1%)

5 of 1080 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	5	13	U
76	5	39	A
76	5	42	A
76	5	56	A
76	5	58	G

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	9	369	C
80	9	1264	C
80	9	527	C
80	9	858	A
81	6	16	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 285 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	Z2V	5	5288	-	29,31,31	4.33	17 (58%)	36,45,45	3.92	11 (30%)

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
84	Z2V	5	5288	-	-	6/17/47/47	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	5	5288	Z2V	O01-C02	11.73	1.39	1.21
84	5	5288	Z2V	C11-N10	9.14	1.52	1.37
84	5	5288	Z2V	C18-N17	8.07	1.49	1.34
84	5	5288	Z2V	O13-C11	7.43	1.38	1.23
84	5	5288	Z2V	O14-C09	7.27	1.37	1.23

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	5	5288	Z2V	C11-N10-C09	-10.43	113.30	125.87
84	5	5288	Z2V	O01-C02-C03	-9.57	109.27	123.22
84	5	5288	Z2V	O01-C02-C28	-8.10	110.26	122.11
84	5	5288	Z2V	O13-C11-N10	-8.05	107.89	120.30
84	5	5288	Z2V	O13-C11-C12	-7.75	107.83	122.62

There are no chirality outliers.

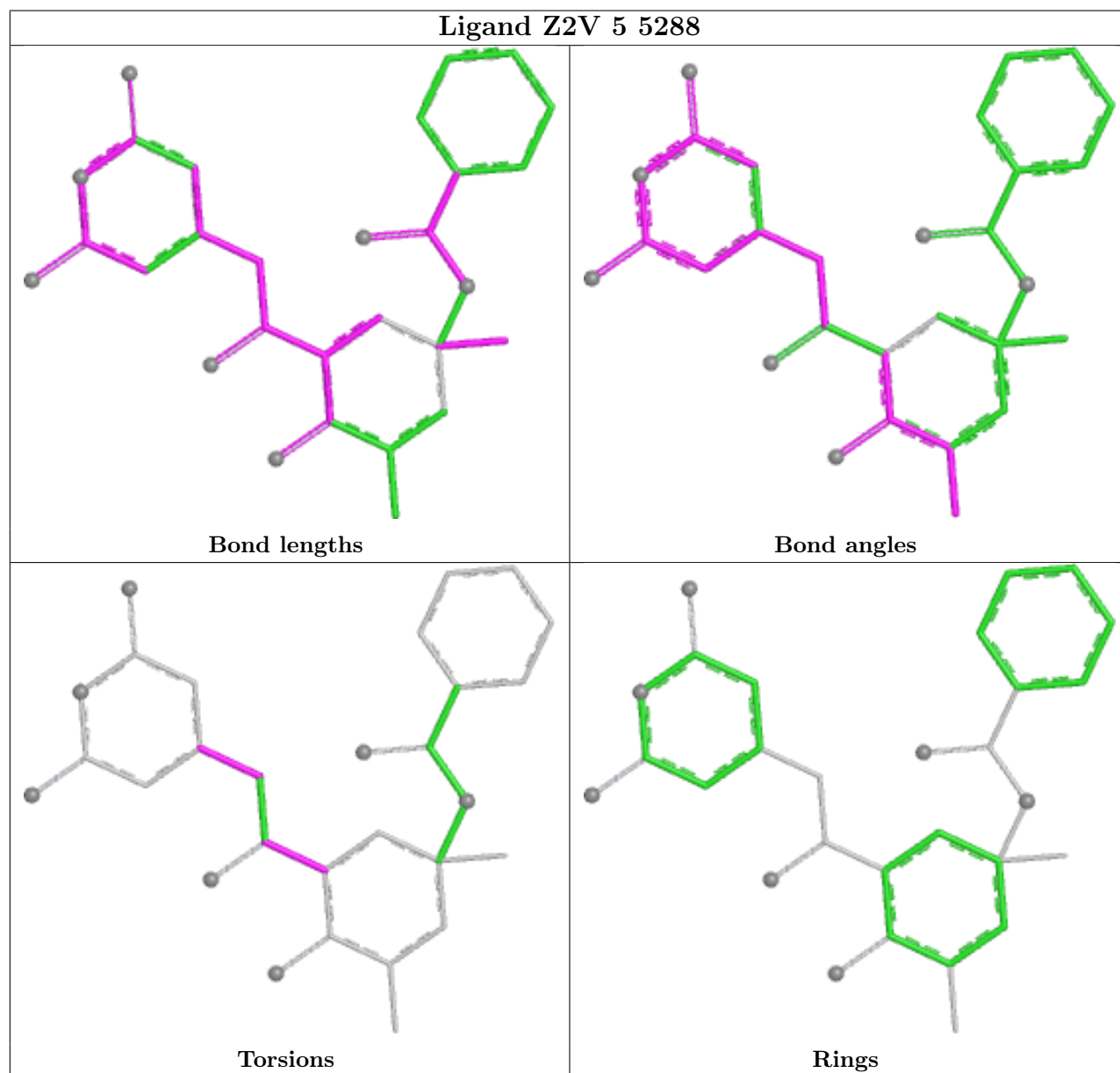
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	5	5288	Z2V	C02-C03-C04-O05
84	5	5288	Z2V	C15-C03-C04-C06
84	5	5288	Z2V	C15-C03-C04-O05
84	5	5288	Z2V	C04-C06-C07-C12
84	5	5288	Z2V	C04-C06-C07-C08

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
76	5	23

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.47
1	5	1252:C	O3'	1271:G	P	36.98
1	5	1219:G	O3'	1233:G	P	19.63
1	5	4138:C	O3'	4146:G	P	17.77
1	5	990:C	O3'	1064:G	P	17.68

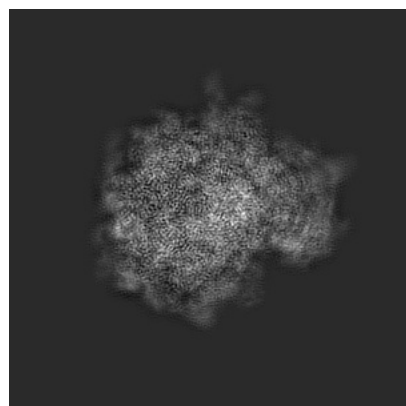
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23785. These allow visual inspection of the internal detail of the map and identification of artifacts.

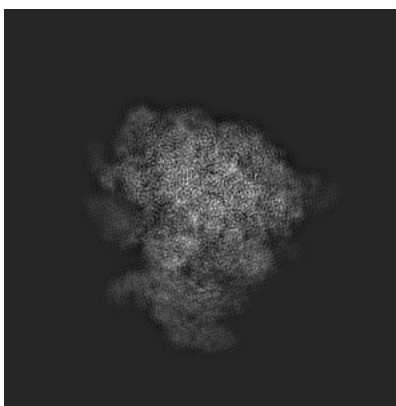
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

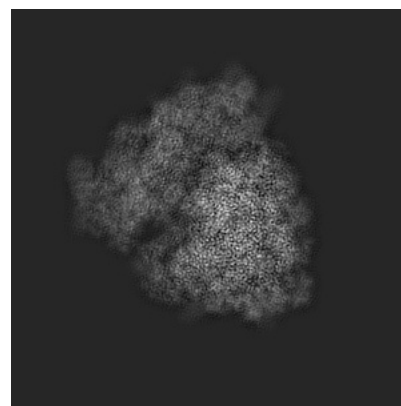
6.1.1 Primary map



X

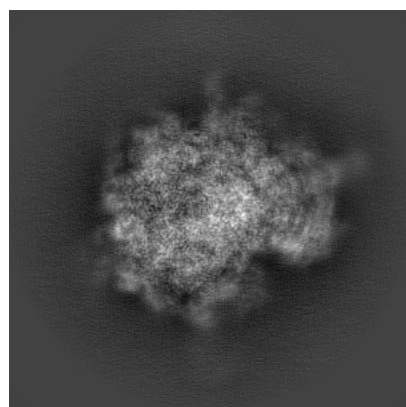


Y

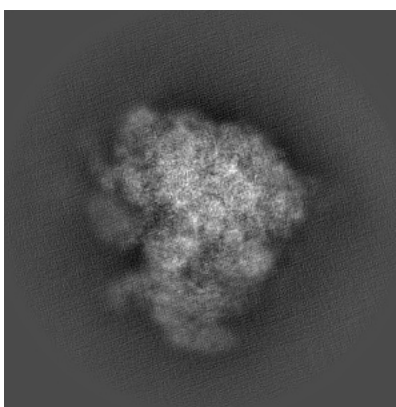


Z

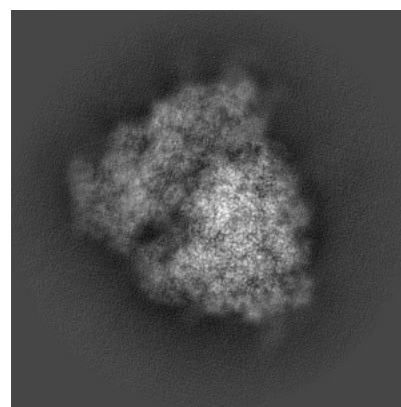
6.1.2 Raw map



X



Y

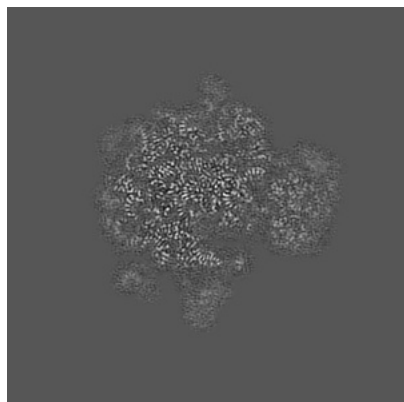


Z

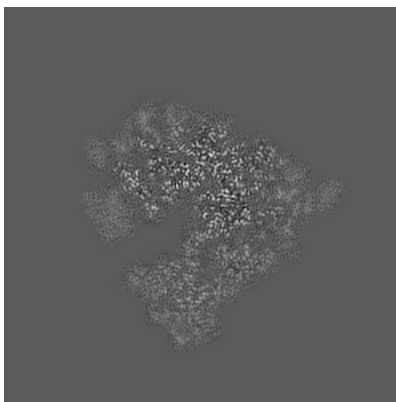
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

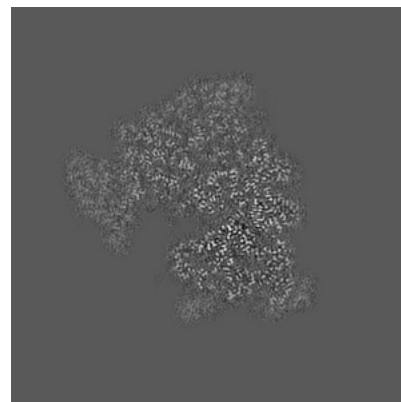
6.2.1 Primary map



X Index: 180

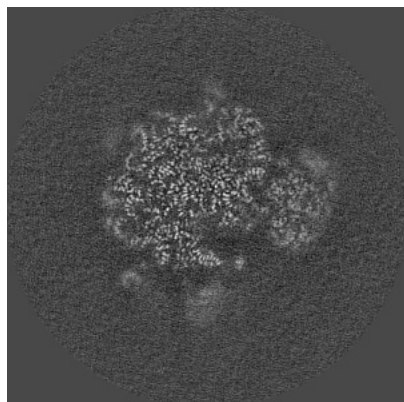


Y Index: 180

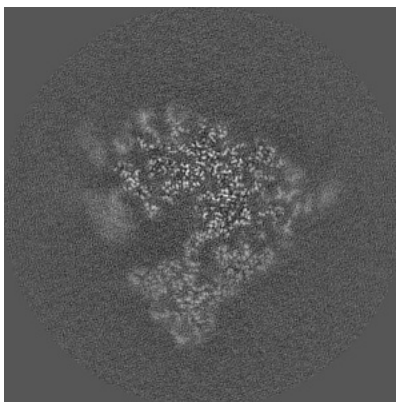


Z Index: 180

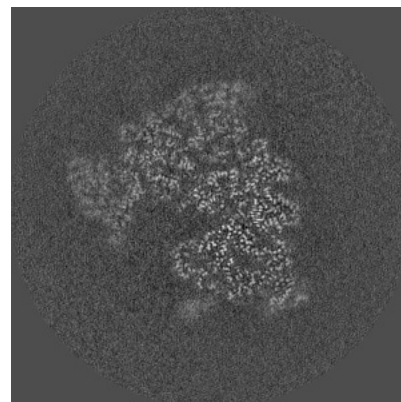
6.2.2 Raw map



X Index: 180



Y Index: 180

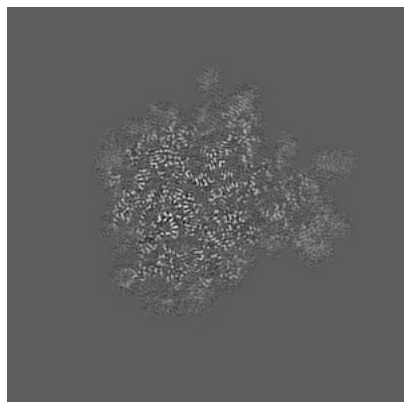


Z Index: 180

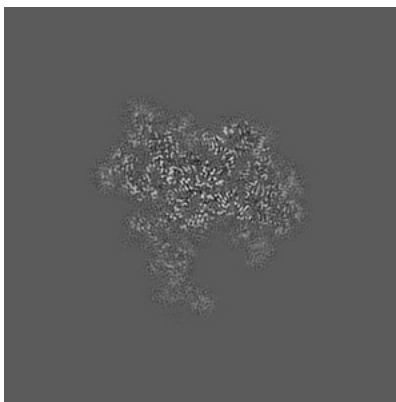
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

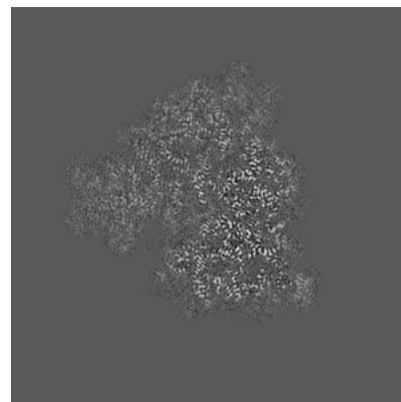
6.3.1 Primary map



X Index: 196

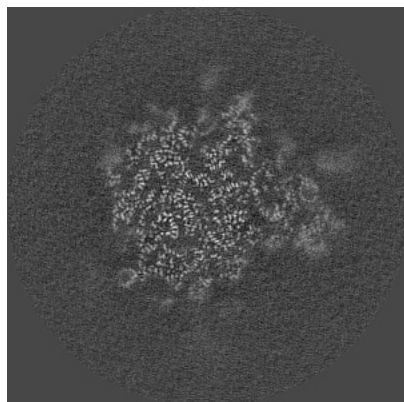


Y Index: 148

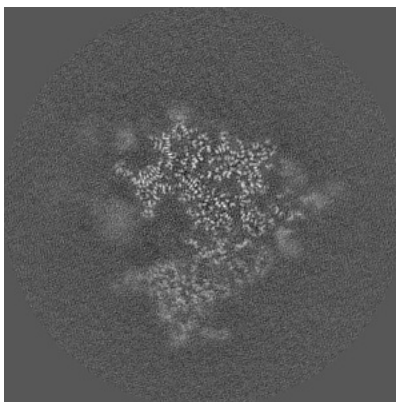


Z Index: 171

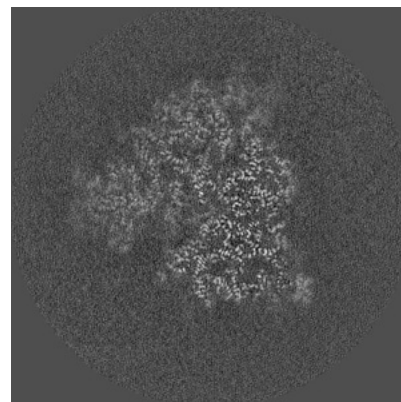
6.3.2 Raw map



X Index: 196



Y Index: 188

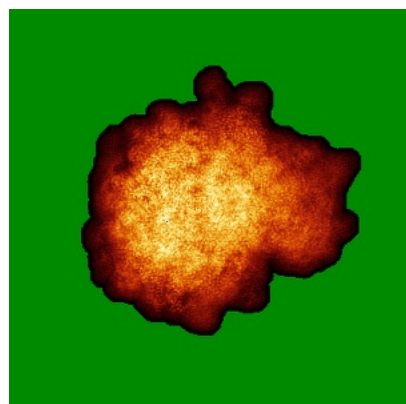


Z Index: 171

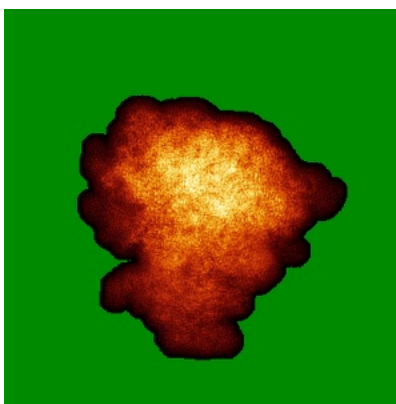
The images above show the largest variance slices of the map in three orthogonal directions.

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

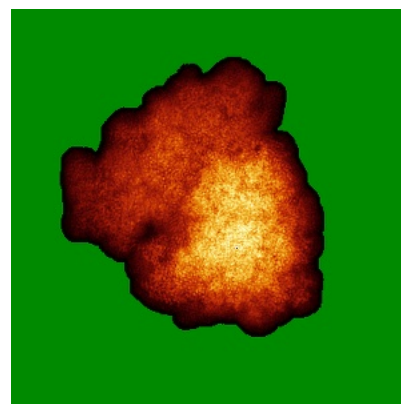
6.4.1 Primary map



X

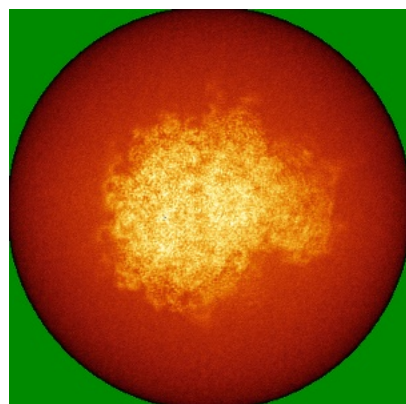


Y

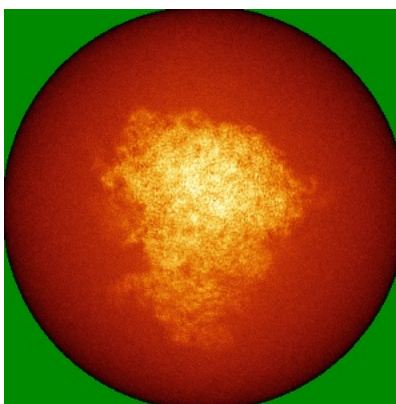


Z

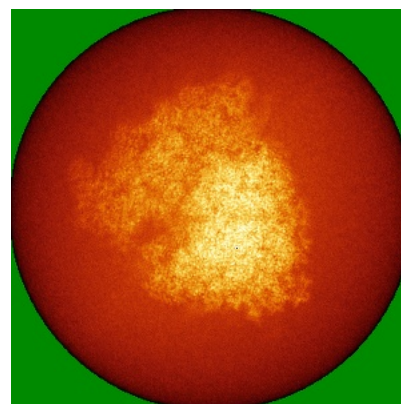
6.4.2 Raw map



X



Y

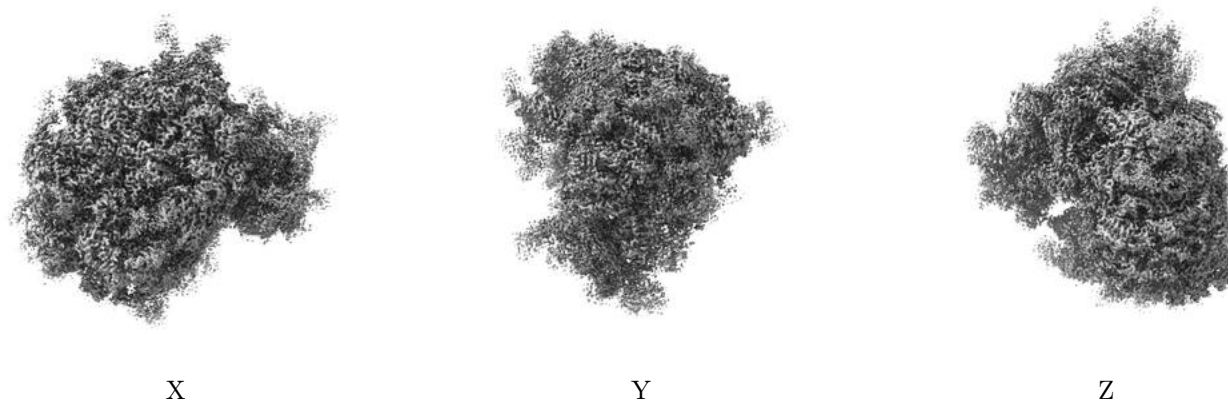


Z

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

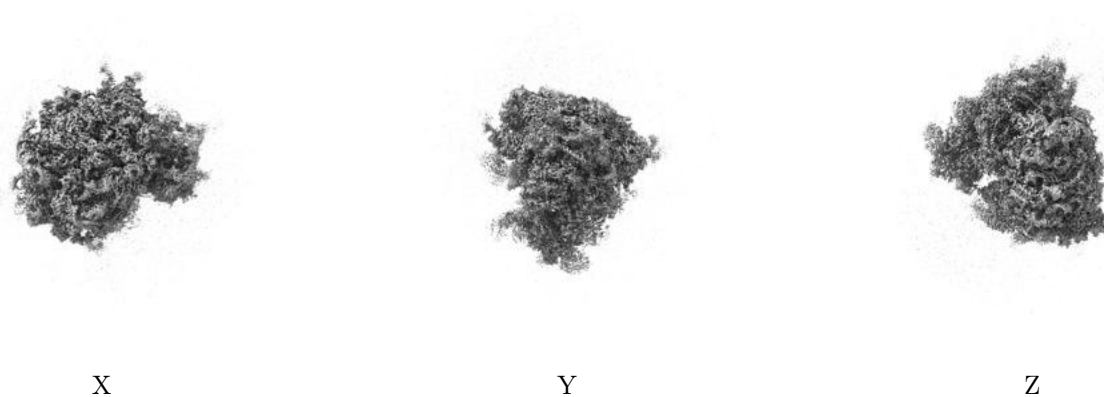
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

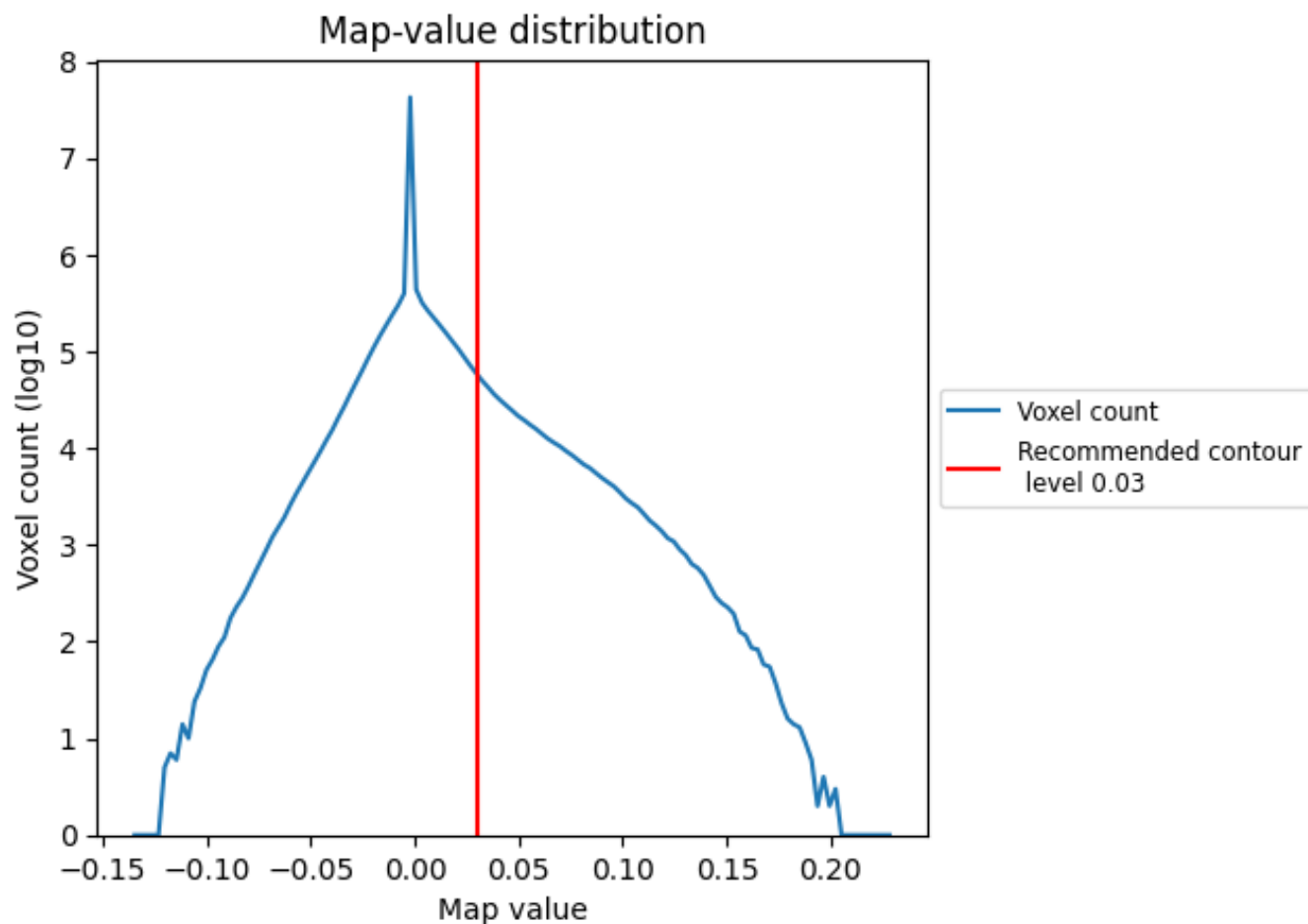
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

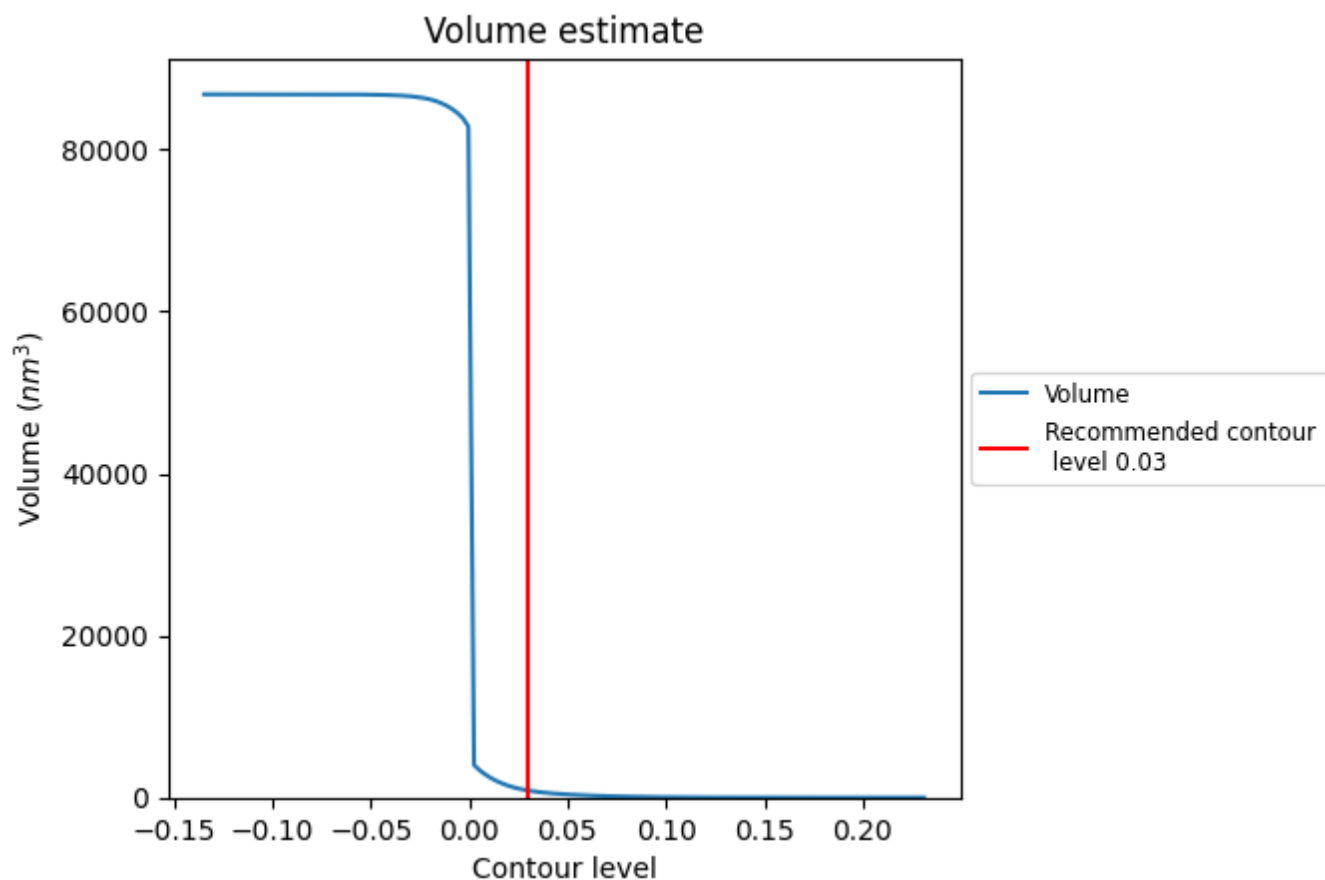
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

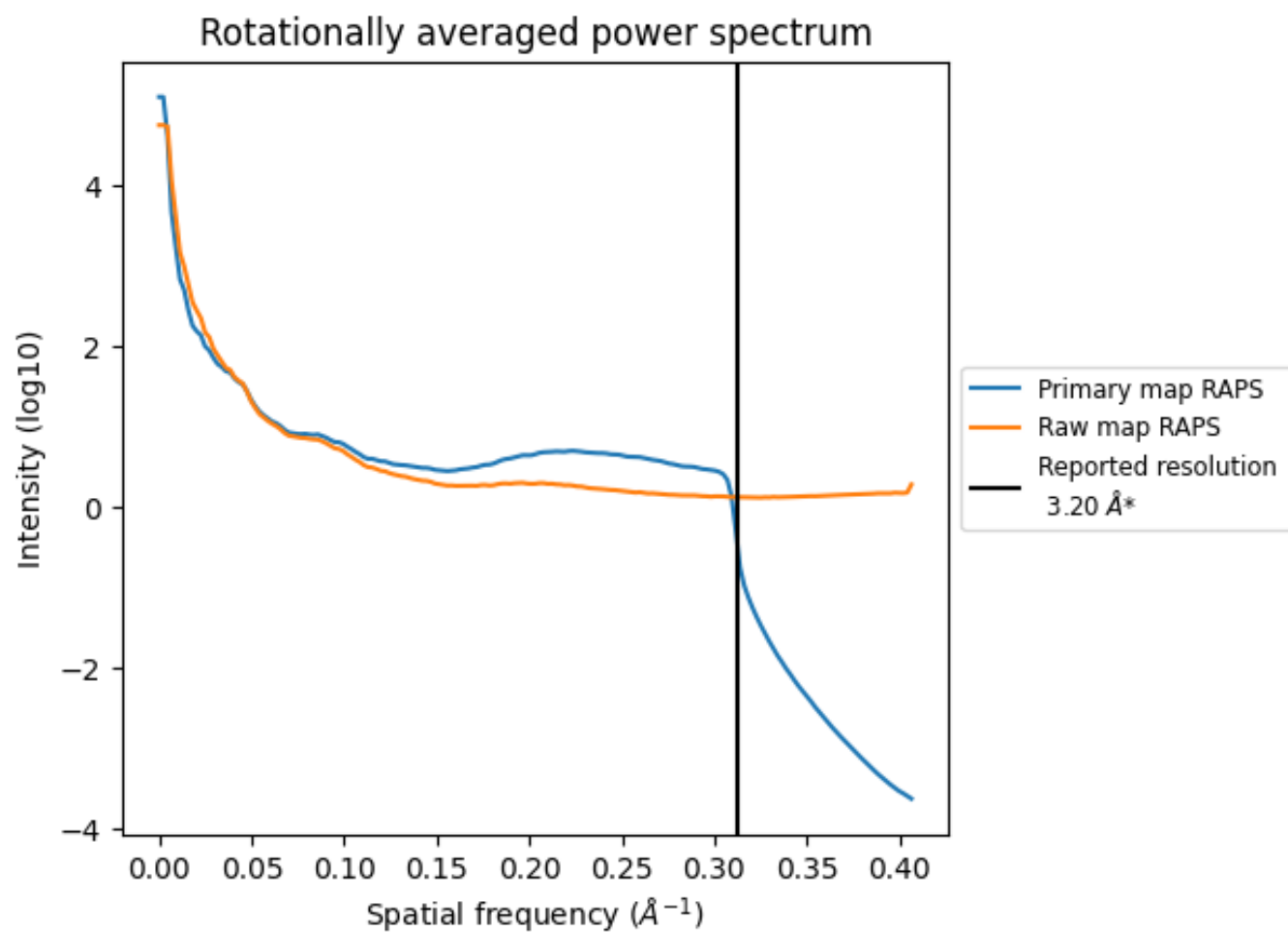
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 875 nm³; this corresponds to an approximate mass of 790 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 ⓘ

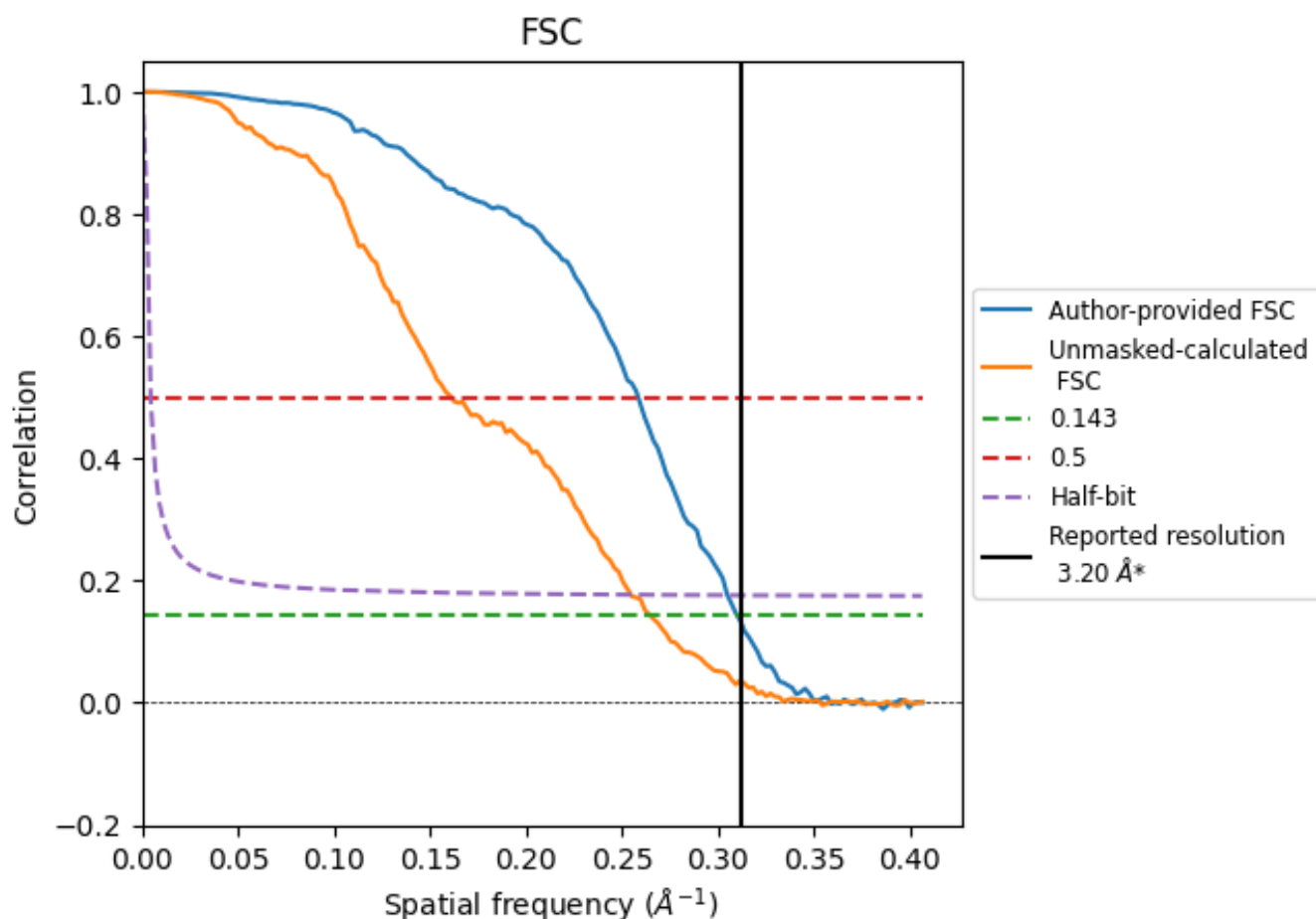


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

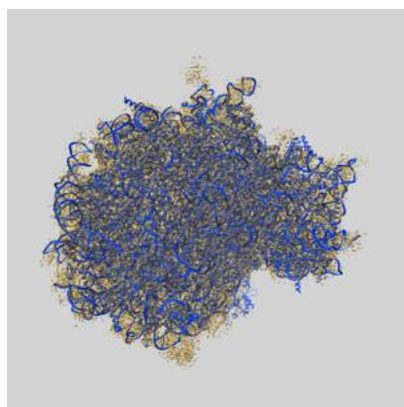
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.87	3.28
Unmasked-calculated*	3.78	6.21	3.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 3.2 by more than 10 %

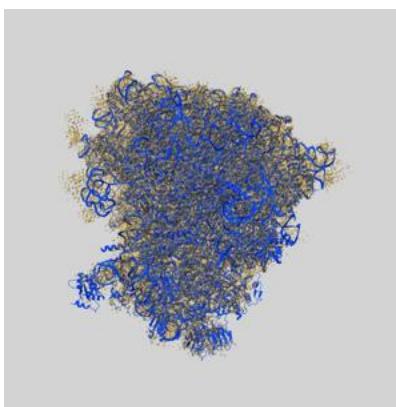
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23785 and PDB model 7MDZ. Per-residue inclusion information can be found in [section 3](#) on [page 25](#).

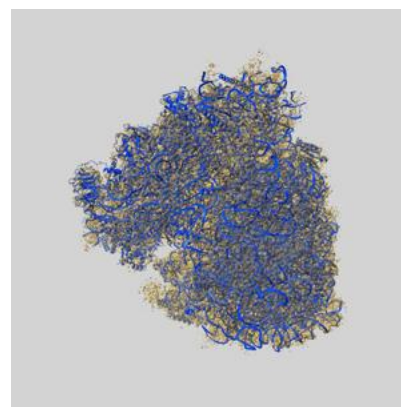
9.1 Map-model overlay [i](#)



X



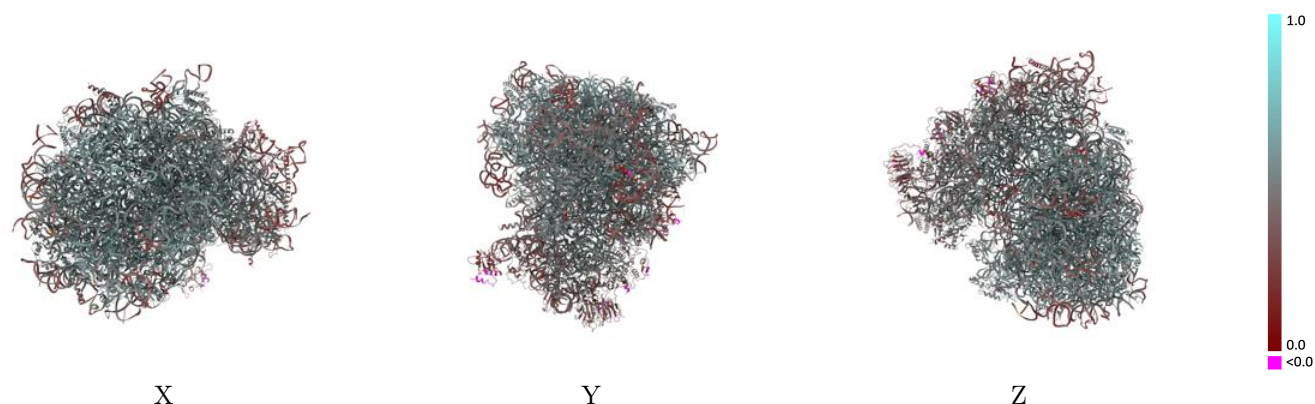
Y



Z

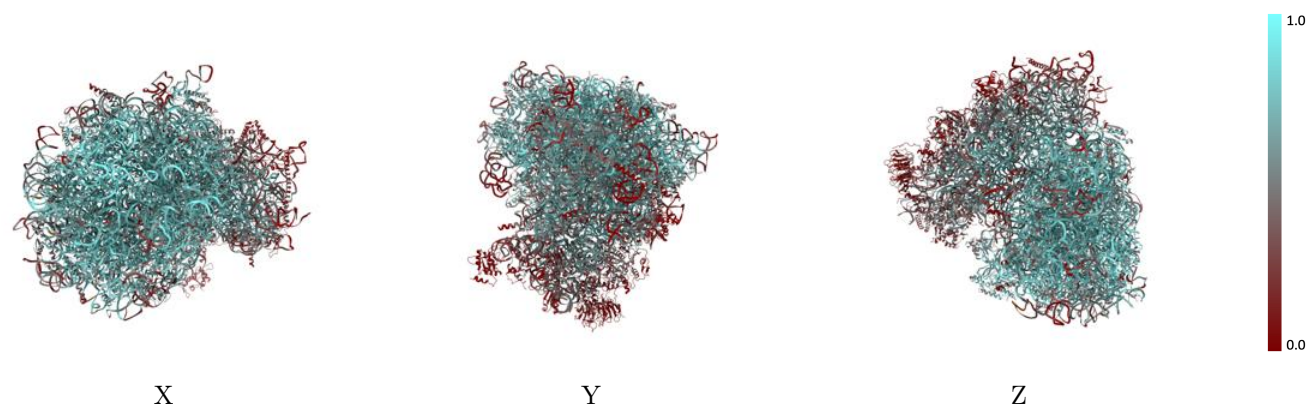
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



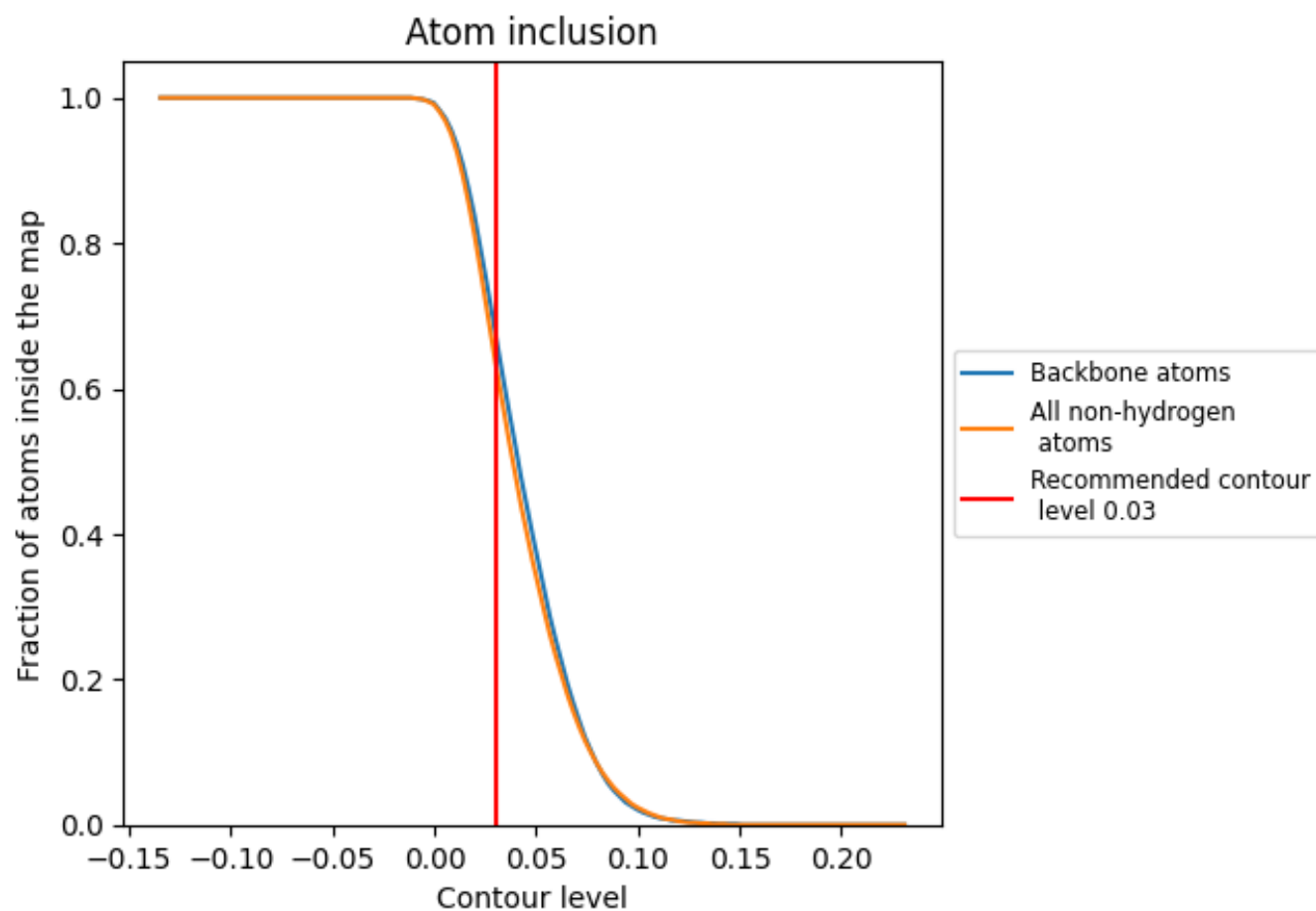
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 64% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6360	 0.5020
2	 0.3510	 0.4190
5	 0.7550	 0.5140
6	 0.2570	 0.4080
7	 0.8530	 0.5500
8	 0.7950	 0.5310
9	 0.5900	 0.4640
A	 0.7410	 0.5700
AA	 0.3350	 0.4510
B	 0.7410	 0.5710
BB	 0.4400	 0.4850
C	 0.7420	 0.5640
CC	 0.4770	 0.4910
D	 0.6810	 0.5290
DD	 0.2540	 0.4250
E	 0.6540	 0.5400
EE	 0.4360	 0.4950
F	 0.7420	 0.5690
FF	 0.3430	 0.4560
G	 0.5560	 0.4930
GG	 0.3210	 0.4230
H	 0.6580	 0.5420
HH	 0.2250	 0.3810
I	 0.7000	 0.5540
II	 0.4850	 0.4850
J	 0.5750	 0.5150
JJ	 0.4530	 0.4990
KK	 0.2350	 0.4120
L	 0.6690	 0.5400
LL	 0.5300	 0.5230
M	 0.7170	 0.5540
MM	 0.0290	 0.2030
N	 0.7920	 0.5820
NN	 0.4640	 0.4940
O	 0.7500	 0.5630



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Chain	Atom inclusion	Q-score
OO	 0.5060	 0.4960
P	 0.7700	 0.5780
PP	 0.2500	 0.4130
Q	 0.7500	 0.5740
QQ	 0.3390	 0.4390
R	 0.6360	 0.5260
RR	 0.2170	 0.3880
S	 0.7440	 0.5690
SS	 0.3170	 0.4360
T	 0.6950	 0.5510
TT	 0.3280	 0.4360
U	 0.5400	 0.5050
UU	 0.2380	 0.4090
V	 0.6790	 0.5530
VV	 0.3420	 0.4520
W	 0.7150	 0.5710
WW	 0.4810	 0.4990
X	 0.6550	 0.5430
XX	 0.5440	 0.5180
Y	 0.7100	 0.5590
YY	 0.4040	 0.4660
Z	 0.6340	 0.5300
ZZ	 0.2490	 0.4270
a	 0.7930	 0.5790
aa	 0.4900	 0.5110
b	 0.5530	 0.5090
bb	 0.3260	 0.4580
c	 0.6010	 0.5100
cc	 0.2960	 0.4400
d	 0.6910	 0.5570
dd	 0.3940	 0.4790
e	 0.7630	 0.5760
ee	 0.3160	 0.4430
f	 0.7970	 0.5840
ff	 0.0630	 0.2800
g	 0.6730	 0.5390
gg	 0.1430	 0.3550
h	 0.6660	 0.5440
i	 0.6120	 0.5210
j	 0.8130	 0.5770
k	 0.5130	 0.5040
l	 0.7420	 0.5740

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Chain	Atom inclusion	Q-score
m	 0.7070	 0.5570
n	 0.6560	 0.5550
o	 0.6950	 0.5780
p	 0.6680	 0.5530
r	 0.7620	 0.5590