wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 10:05 pm GMT

PDB ID	:	5LZS
EMDB ID	:	EMD-4130
Title	:	Structure of the mammalian ribosomal elongation complex with aminoacyl-tRNA, eEF1A, and didemnin B
Authors	:	Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on	:	2016-10-02
Resolution	:	3.31 Å(reported)

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

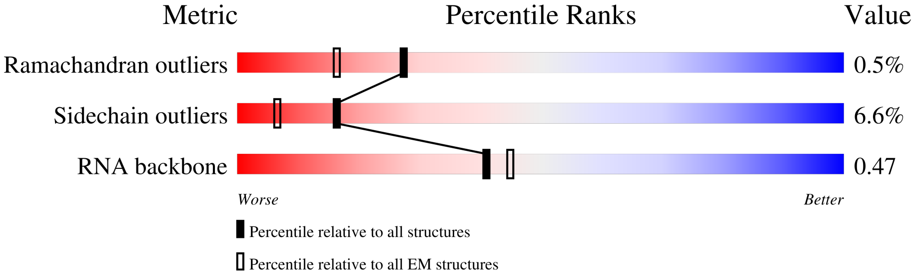
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance ⓘ

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

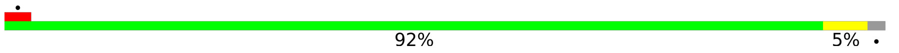
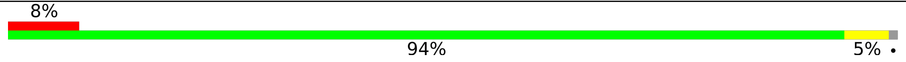
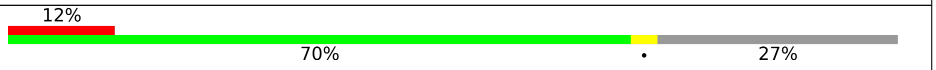
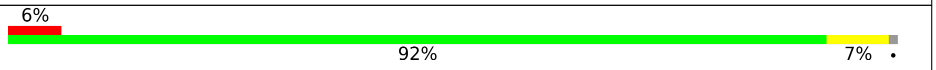
The reported resolution of this entry is 3.31 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 <=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	
5	E	291	
6	F	247	
7	G	319	
8	H	192	

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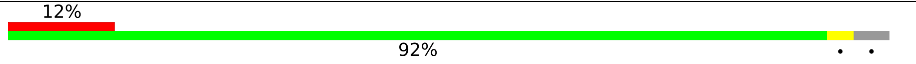
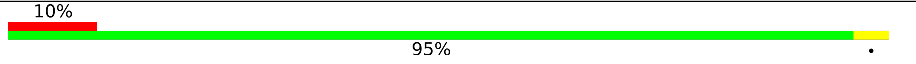
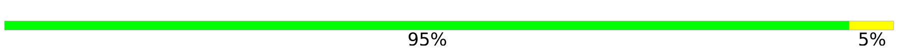
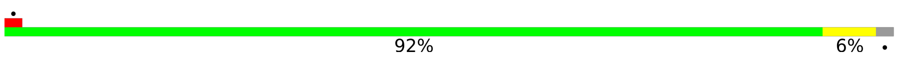
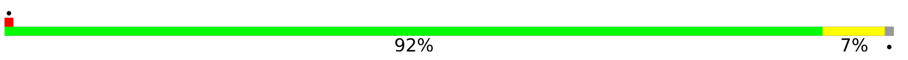
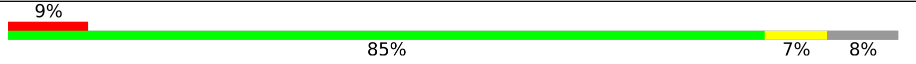
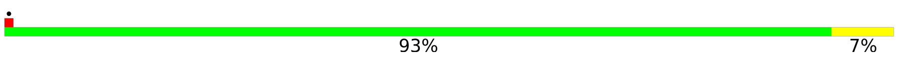
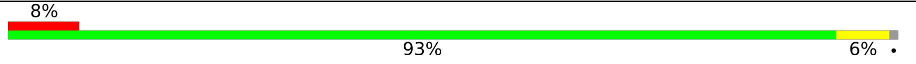
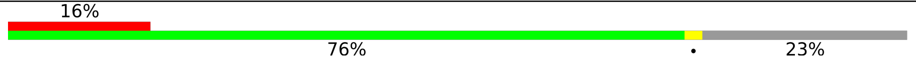
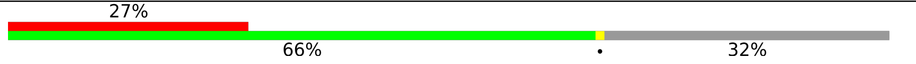
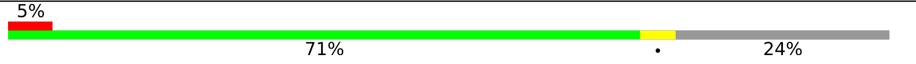
Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
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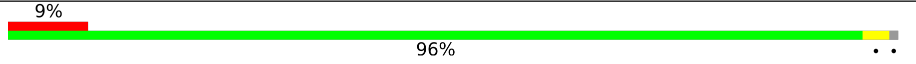
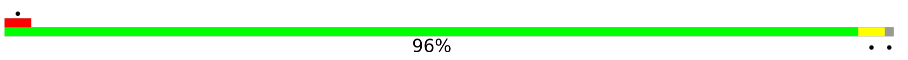
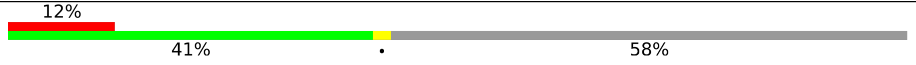
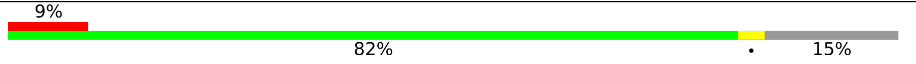
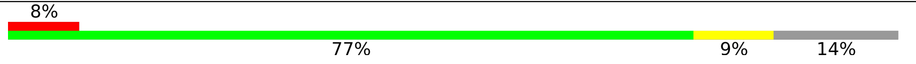
25	Z	136	
26	a	148	
27	b	245	
28	c	115	
29	d	125	
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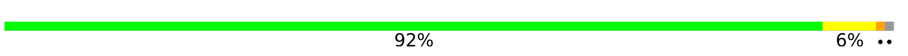
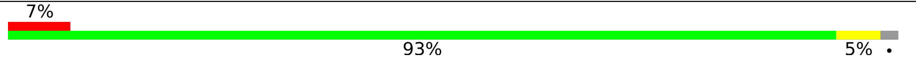
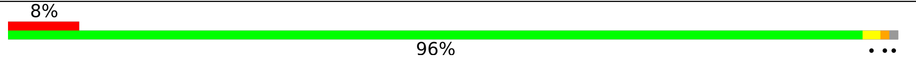
31	f	110	
32	g	116	
33	h	123	

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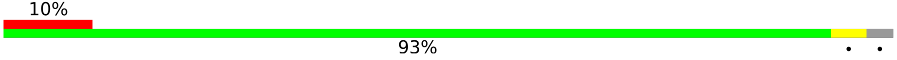
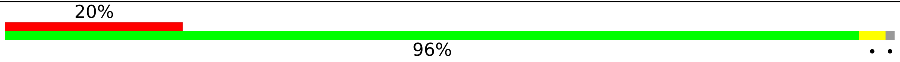
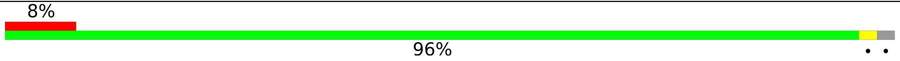
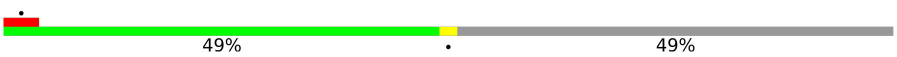
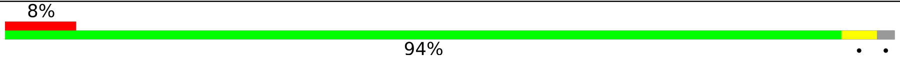
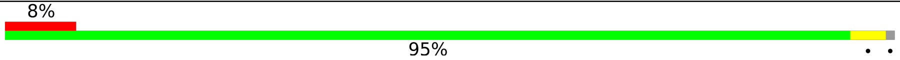
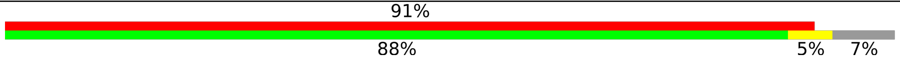
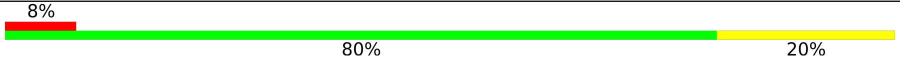
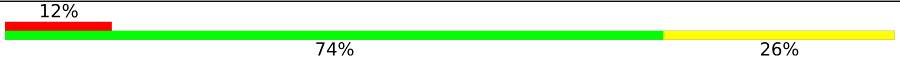
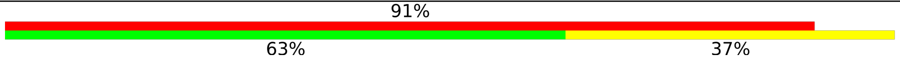
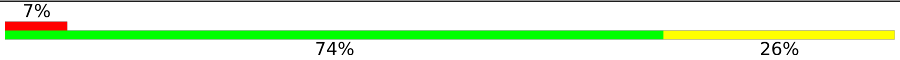
Mol	Chain	Length	Quality of chain
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	2	76	
45	ii	76	
46	3	75	
47	5	3543	
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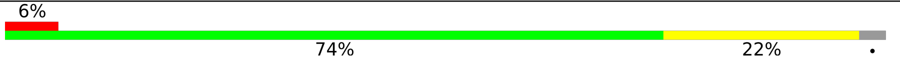
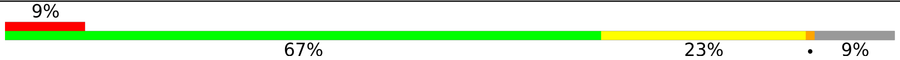
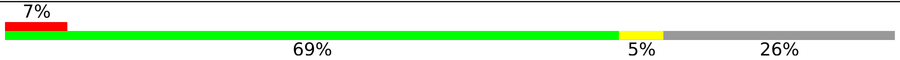
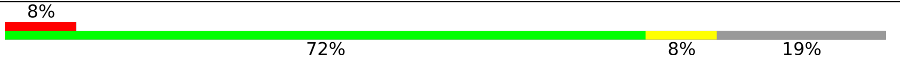
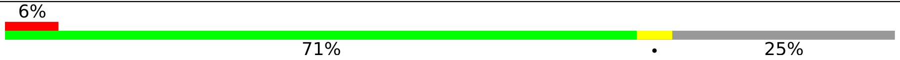
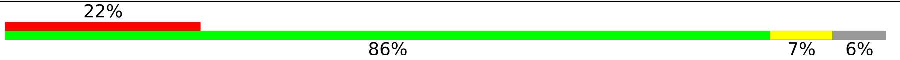
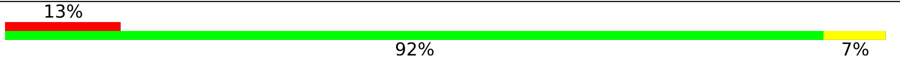
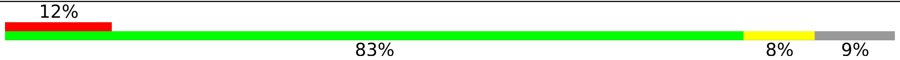
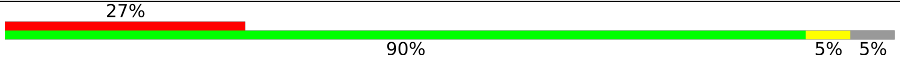
49	8	156	
50	9	1869	
51	AA	295	
52	BB	264	
53	CC	293	
54	DD	243	
55	EE	263	
56	FF	204	
57	GG	249	

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Mol	Chain	Length	Quality of chain
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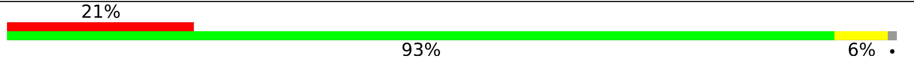
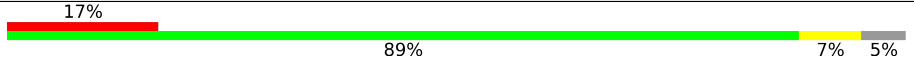
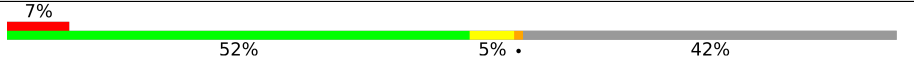
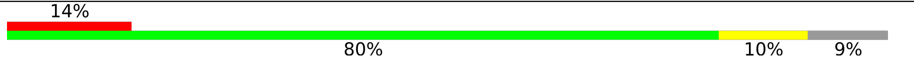
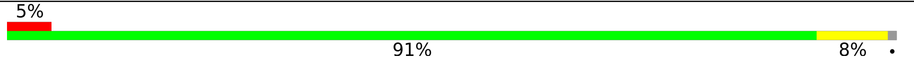
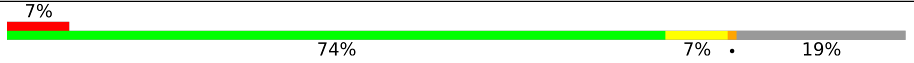
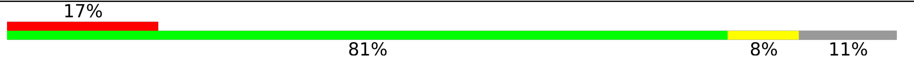
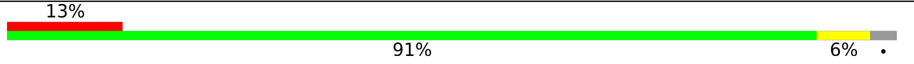
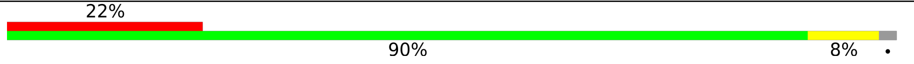
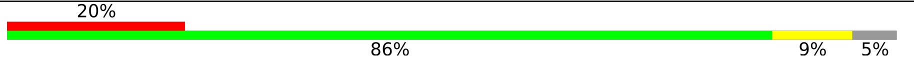
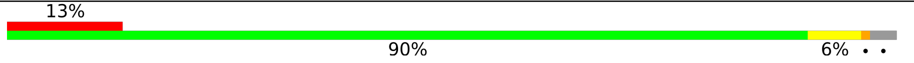
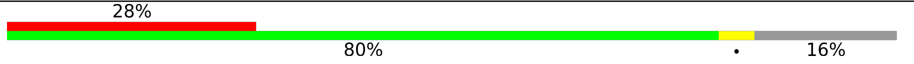
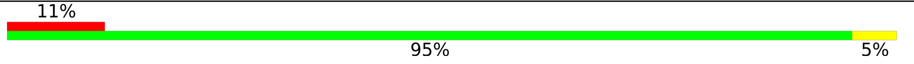
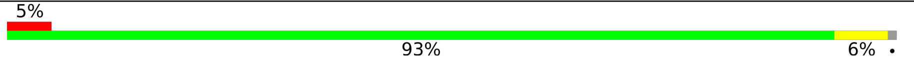
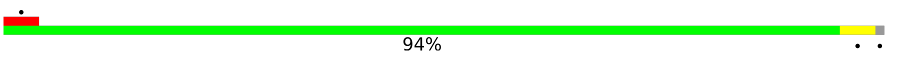
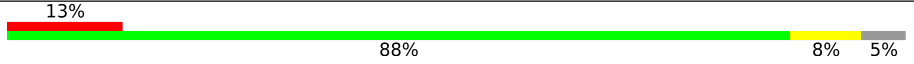
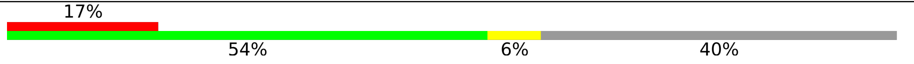
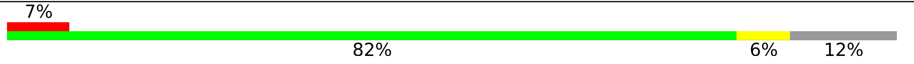
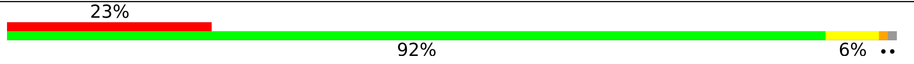
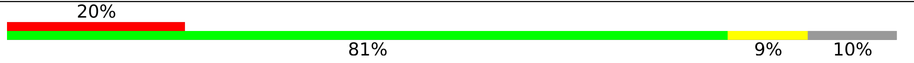
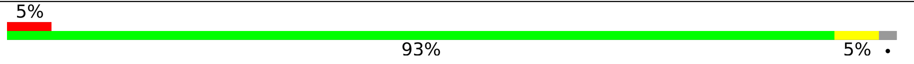
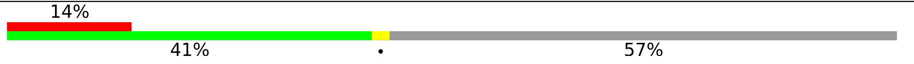
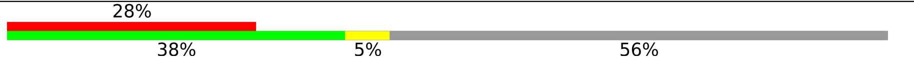
59	II	208	
60	JJ	194	
61	KK	165	
62	LL	158	
63	MM	132	
64	NN	151	
65	OO	168	
66	PP	145	
67	QQ	146	
68	RR	135	
69	SS	152	
70	TT	145	
71	UU	119	
72	VV	83	
73	WW	130	
74	XX	143	
75	YY	130	
76	ZZ	125	
77	aa	115	
78	bb	84	
79	cc	69	
80	dd	56	
81	ee	133	
82	ff	156	

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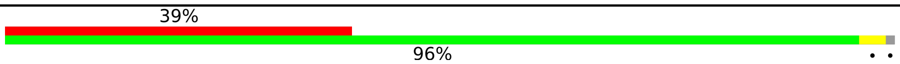
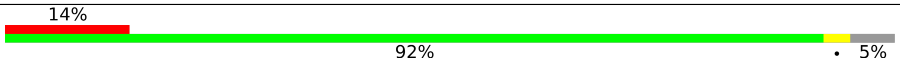
Mol	**Chain**	**Length**	**Quality of chain**
83	gg	317	
84	hh	10	
85	jj	462	

2 Entry composition ⓘ

There are 89 unique types of molecules in this entry. The entry contains 220934 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 uL2.

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

- Molecule 2 is a protein called uL3.

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

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 uL4.

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

- Molecule 4 is a protein called 60S ribosomal protein L5.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

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

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

- Molecule 6 is a protein called uL30.

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

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 eL8.

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

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 uL6.

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

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 10 is a protein called uL5.

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 eL13.

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

- Molecule 12 is a protein called eL14.

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 eL18.

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

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called uL14.

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

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	106	860	538	174	144	4	0	0

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

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

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

- Molecule 26 is a protein called uL15.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

- Molecule 33 is a protein called uL29.

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

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

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	l	50	447	286	96	64	1	0	0

- Molecule 38 is a protein called eL40.

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

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

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	s	196	1507	959	263	276	9	0	0

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	t	153	1160	722	218	217	3	0	0

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	2	76	1616	723	291	527	75	0	0
45	ii	76	1616	723	291	527	75	0	0

- Molecule 46 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
46	3	75	1593	712	281	526	74	0	0

- Molecule 47 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	5	3543	75972	33833	13910	24686	3543	0	0

- Molecule 48 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	7	119	2538	1132	454	834	118	0	0

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	8	151	3208	1432	564	1062	150	0	0

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	9	1697	36229	16171	6507	11855	1696	0	0

- Molecule 51 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	AA	217	1710	1086	300	316	8	0	0

- Molecule 52 is a protein called 40S ribosomal protein S3a.

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

- Molecule 53 is a protein called uS5.

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

- Molecule 54 is a protein called uS4.

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

- Molecule 55 is a protein called 40S ribosomal protein S4.

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

- Molecule 56 is a protein called Uncharacterized protein.

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

- Molecule 57 is a protein called 40S ribosomal protein S6.

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

- Molecule 58 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	HH	185	1488	952	271	264	1	0	0

- Molecule 59 is a protein called 40S ribosomal protein S8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 60 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 61 is a protein called eS10.

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

- Molecule 62 is a protein called uS17.

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

- Molecule 63 is a protein called 40S ribosomal protein S12.

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

- Molecule 64 is a protein called uS15.

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

- Molecule 65 is a protein called uS11.

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

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called uS9.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 71 is a protein called uS10.

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

- Molecule 72 is a protein called eS21.

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

- Molecule 73 is a protein called uS8.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called eS25.

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

- Molecule 77 is a protein called eS26.

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

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called eS28.

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

- Molecule 80 is a protein called uS14.

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

- Molecule 81 is a protein called eS30.

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

- Molecule 82 is a protein called eS31.

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

- Molecule 83 is a protein called RACK1.

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

- Molecule 84 is a RNA chain called mRNA.

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

- Molecule 85 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
85	jj	441	3383	2148	581	636	1	17	0	0

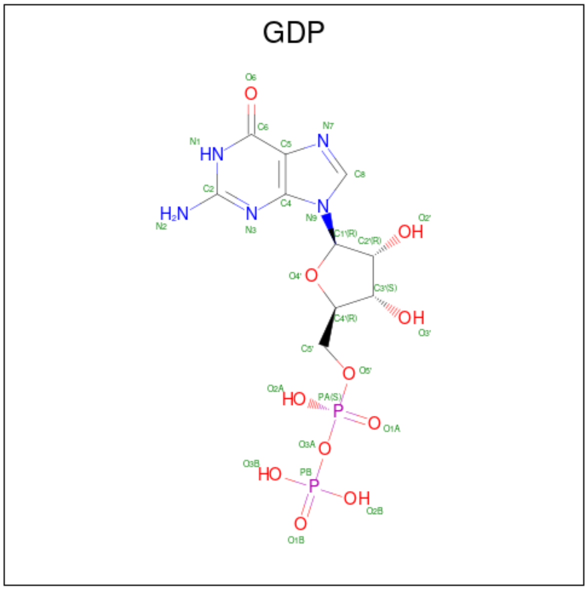
- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
86	B	1	1	1	0
86	I	1	1	1	0
86	P	1	1	1	0
86	Q	1	1	1	0
86	V	1	1	1	0
86	a	2	2	2	0
86	g	1	1	1	0
86	j	1	1	1	0
86	5	185	185	185	0
86	7	6	6	6	0
86	8	5	5	5	0
86	9	69	69	69	0
86	aa	1	1	1	0
86	jj	1	1	1	0

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

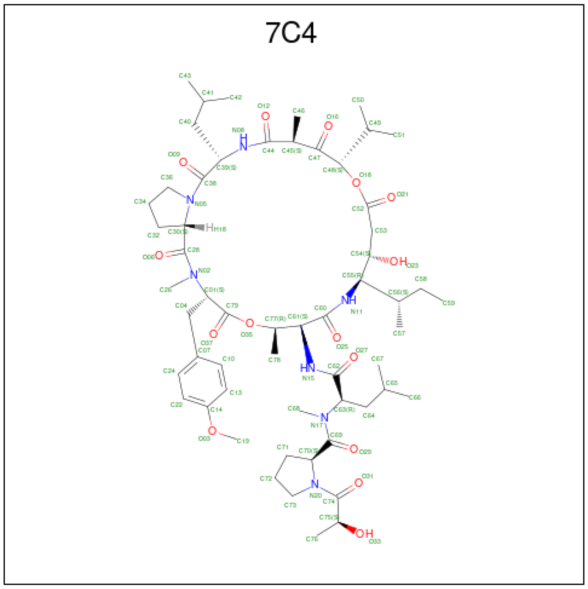
- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
88	jj	1	28	10	5	11	2	0

- Molecule 89 is (2 {S})- {N}-[(2 {R})-1-[[(3 {S},6 {S},8 {S},12 {S},13 {R},16 {S},17 {R},20 {S},23 {S})-13-[(2 {S})-butan-2-yl]-20-[(4-methoxyphenyl)methyl]-6,17,21-trimethyl-3-(2-methylpropyl)-12-oxidanyl-2,5,7,10,15,19,22-heptakis(oxidanylidene)-8-propan-2-yl-9,18-dioxa-1,4,14,21-tetrazabicyclo[21.3.0]hexacosan-16-yl]amino]-4-methyl-1-oxidanylidene-pentan

-2-yl]- {N}-methyl-1-[(2 {S})-2-oxidanylpropanoyl]pyrrolidine-2-carboxamide (three-letter code: 7C4) (formula: $C_{57}H_{89}N_{7}O_{15}$).



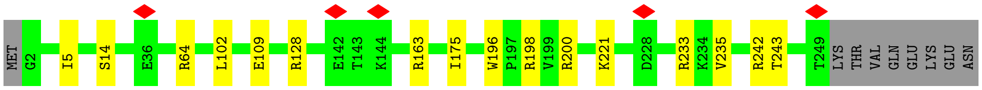
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
89	jj	1	79	57	7	15	0

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.

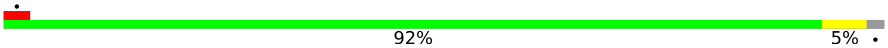
- Molecule 1: uL2

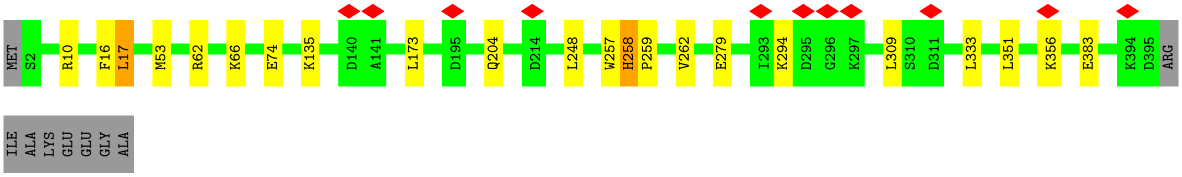
Chain A:



- Molecule 2: uL3

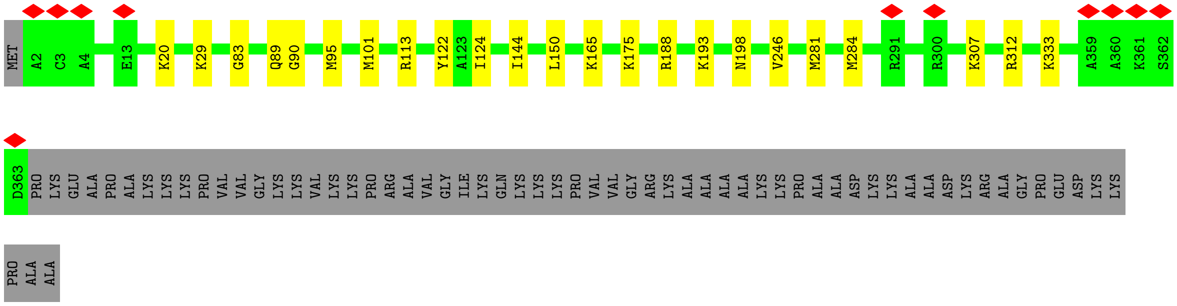
Chain B:





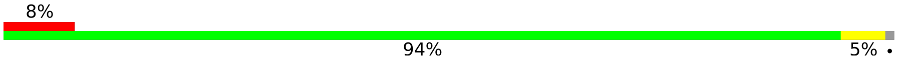
- Molecule 3: uL4

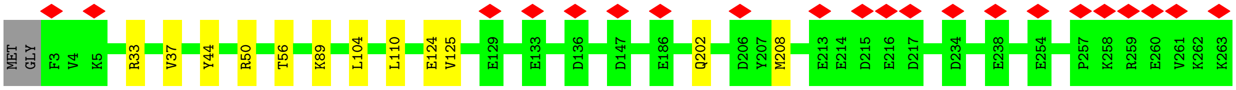
Chain C:

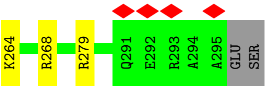


- Molecule 4: 60S ribosomal protein L5

Chain D:

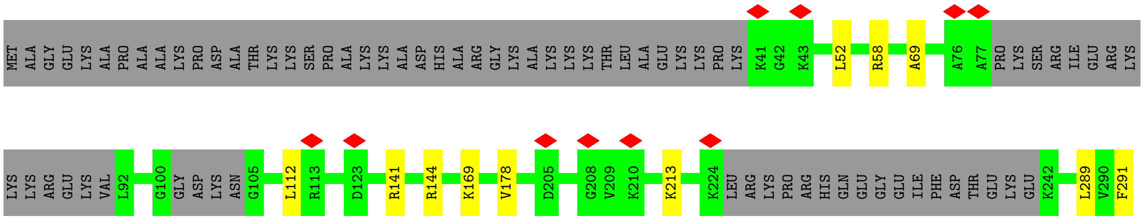






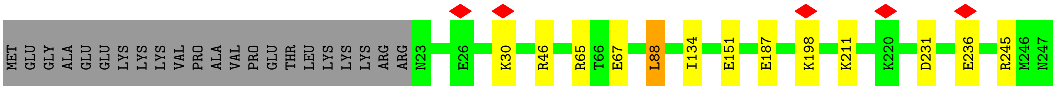
- Molecule 5: 60S ribosomal protein L6

Chain E:



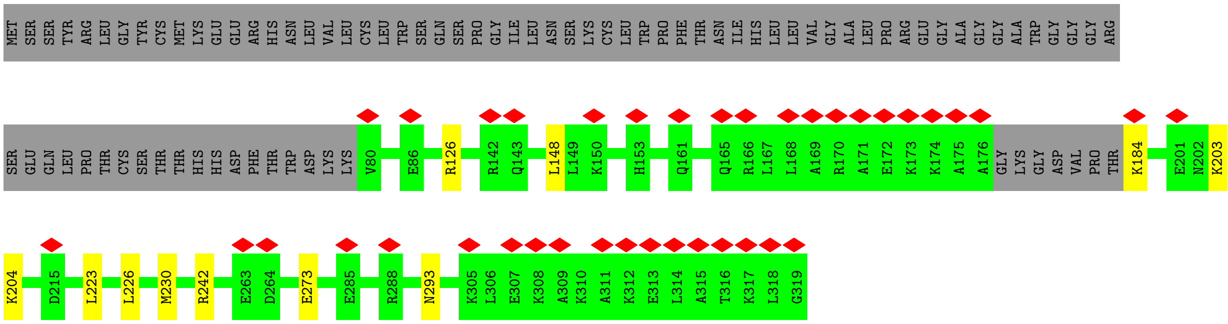
- Molecule 6: uL30

Chain F:



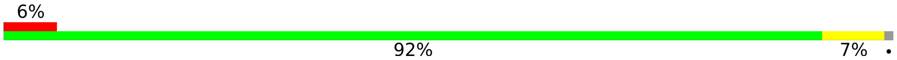
- Molecule 7: eL8

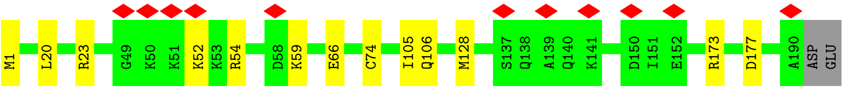
Chain G:



- Molecule 8: uL6

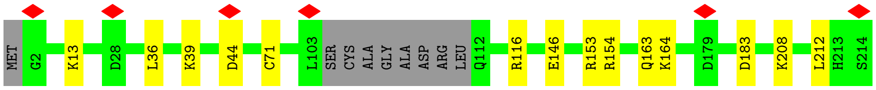
Chain H:





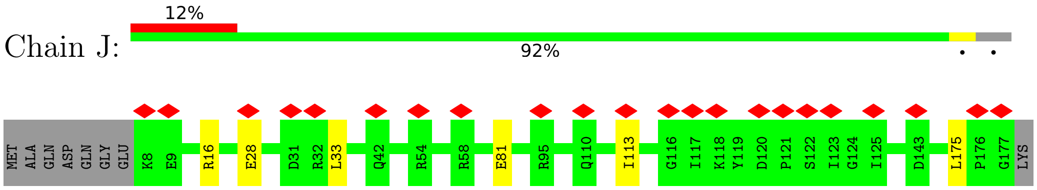
- Molecule 9: Ribosomal protein L10 (Predicted)

Chain I:



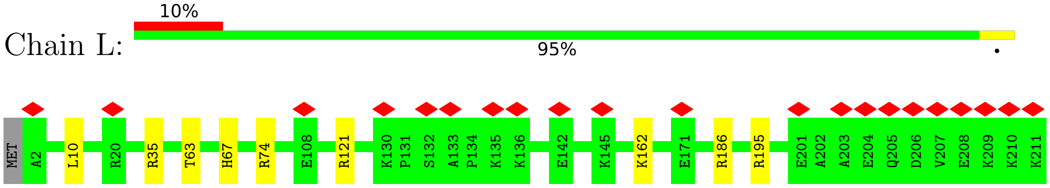
- Molecule 10: uL5

Chain J:



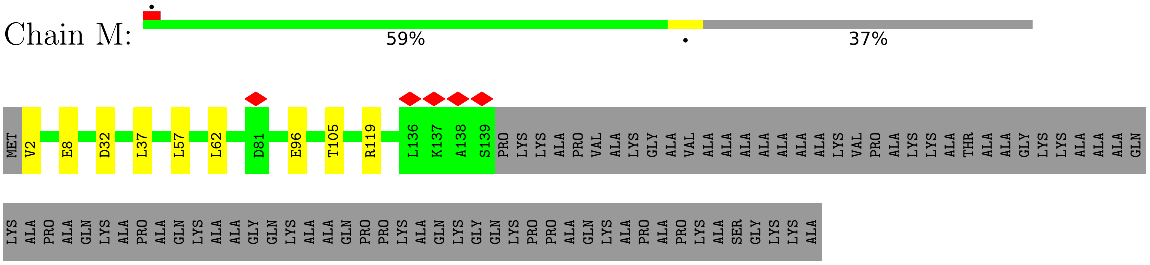
- Molecule 11: eL13

Chain L:



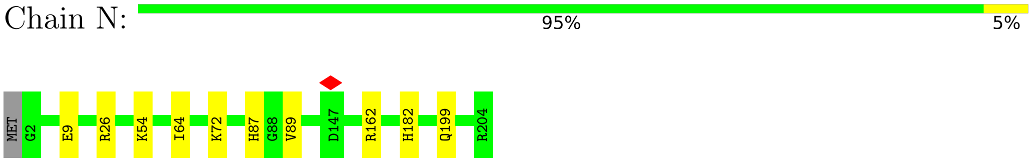
- Molecule 12: eL14

Chain M:



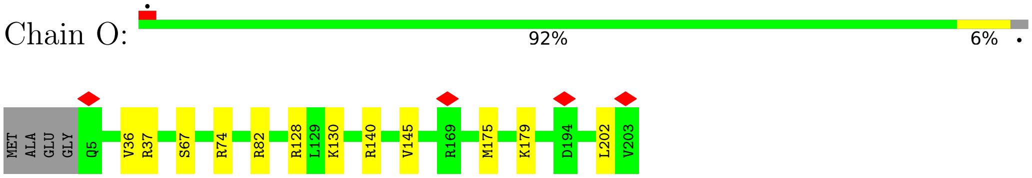
- Molecule 13: Ribosomal protein L15

Chain N:



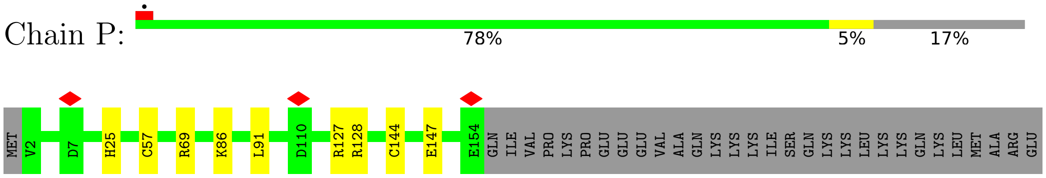
- Molecule 14: uL13

Chain O:



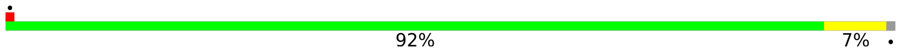
- Molecule 15: uL22

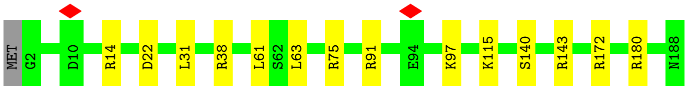
Chain P:



- Molecule 16: eL18

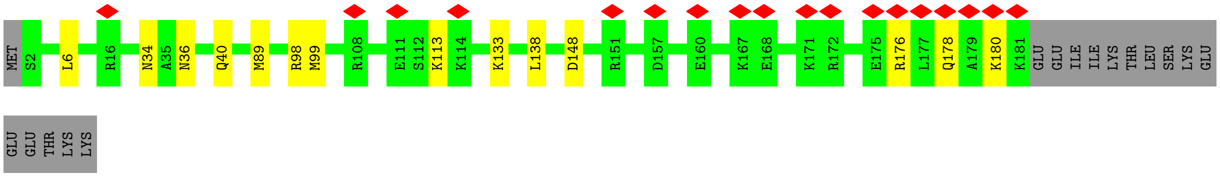
Chain Q:





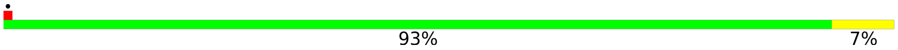
- Molecule 17: eL19

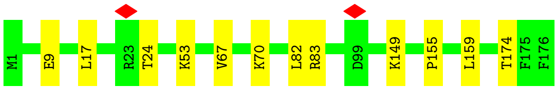
Chain R:



- Molecule 18: eL20

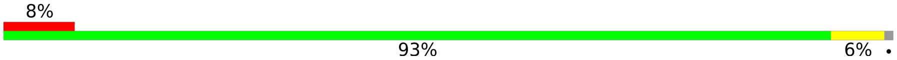
Chain S:

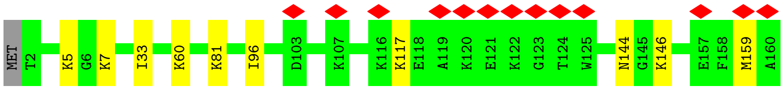




- Molecule 19: eL21

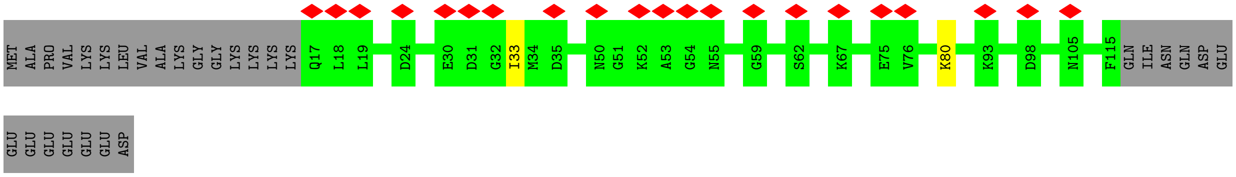
Chain T:





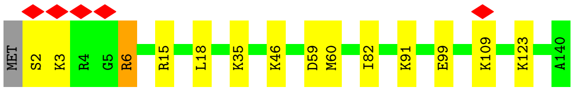
- Molecule 20: eL22

Chain U:



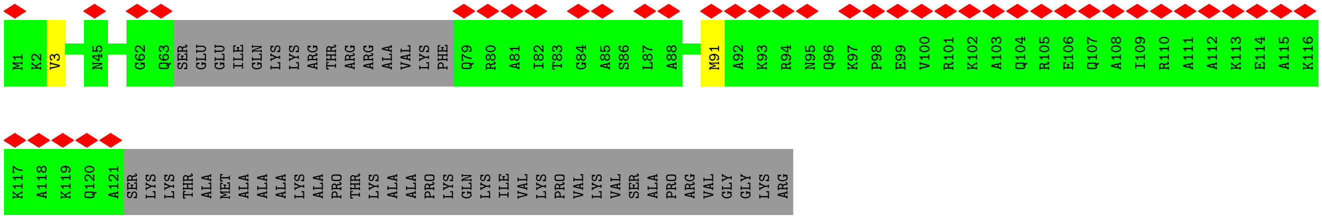
- Molecule 21: uL14

Chain V:



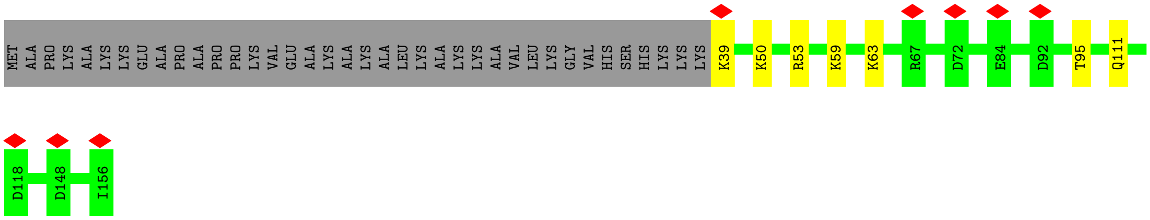
- Molecule 22: uL24

Chain W:



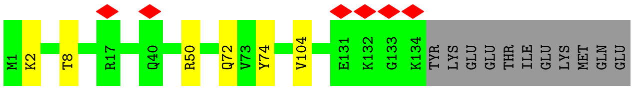
- Molecule 23: uL23

Chain X:



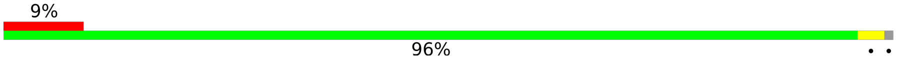
- Molecule 24: uL24

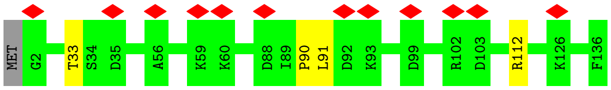
Chain Y:



- Molecule 25: 60S ribosomal protein L27

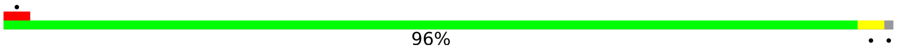
Chain Z:

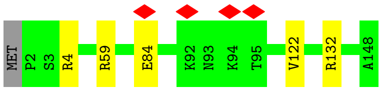




- Molecule 26: uL15

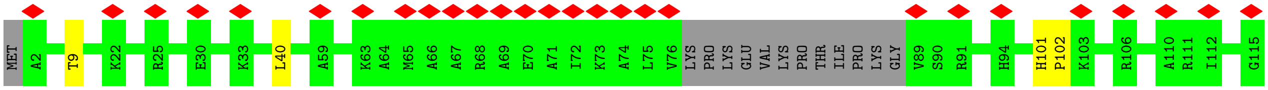
Chain a:

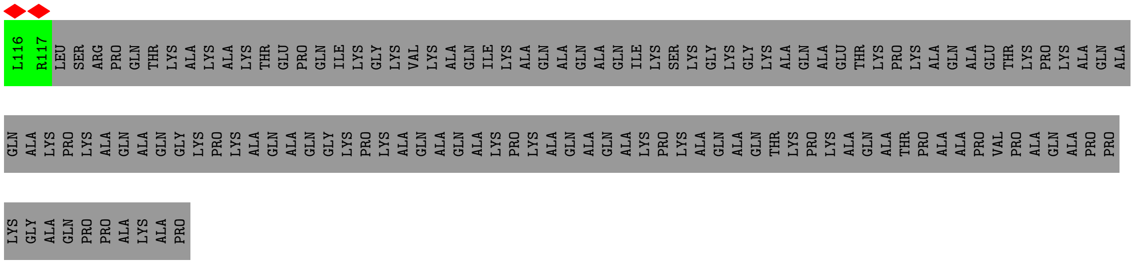




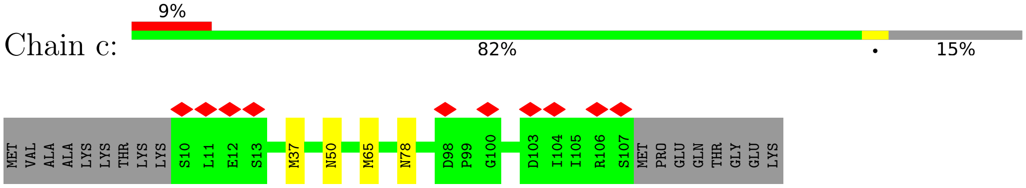
- Molecule 27: eL29

Chain b:

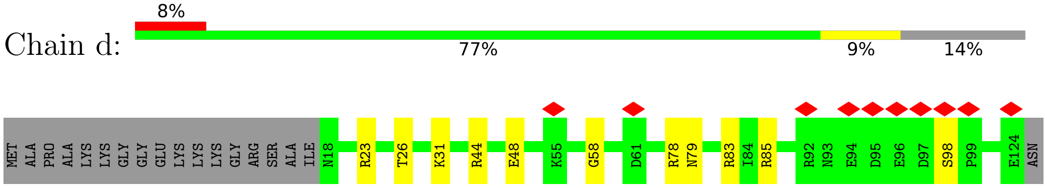




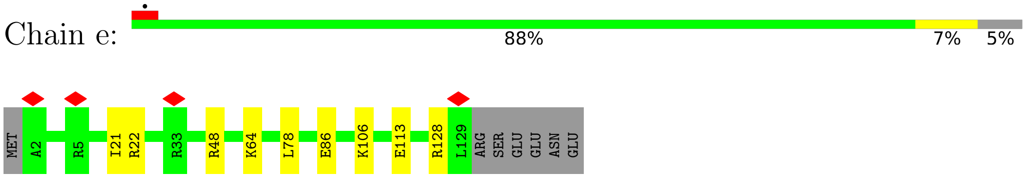
- Molecule 28: eL30



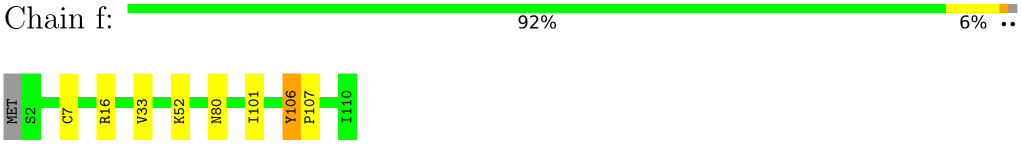
- Molecule 29: eL31



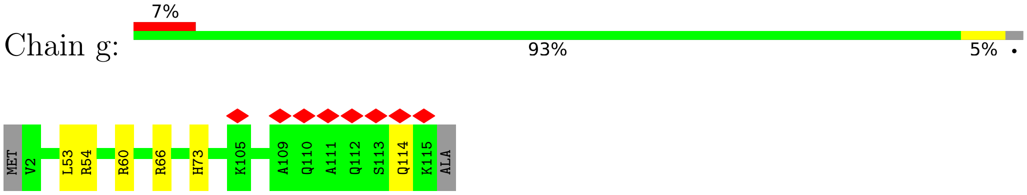
- Molecule 30: eL32



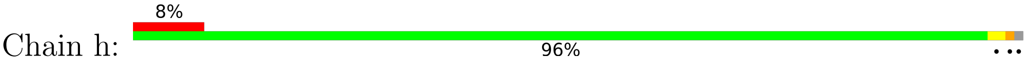
- Molecule 31: eL33

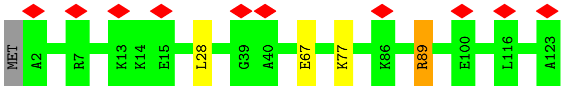


- Molecule 32: eL34



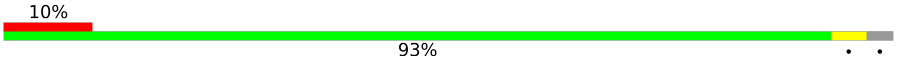
- Molecule 33: uL29

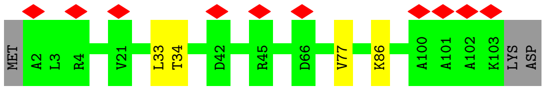




- Molecule 34: 60S ribosomal protein L36

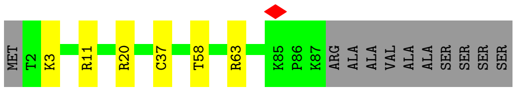
Chain i:





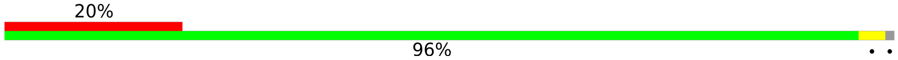
- Molecule 35: Ribosomal protein L37

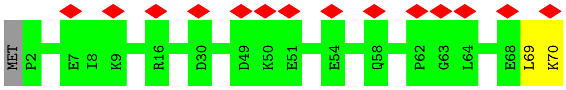
Chain j:



- Molecule 36: eL38

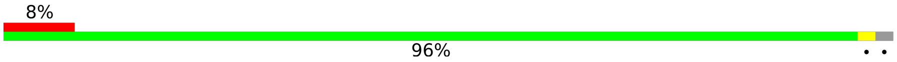
Chain k:

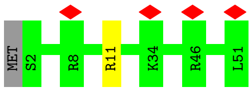




- Molecule 37: eL39

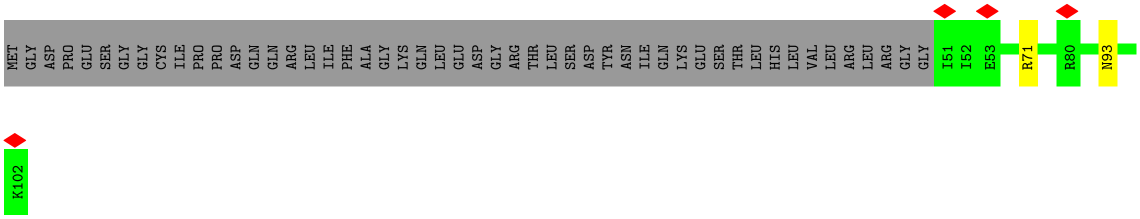
Chain l:





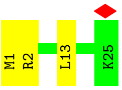
- Molecule 38: eL40

Chain m:



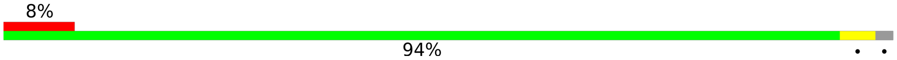
- Molecule 39: 60s ribosomal protein l41

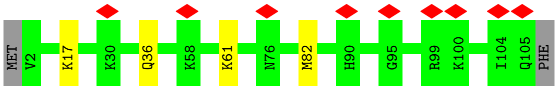
Chain n:



- Molecule 40: eL42

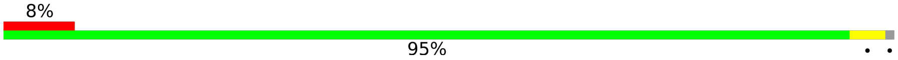
Chain o:

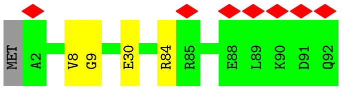




- Molecule 41: eL43

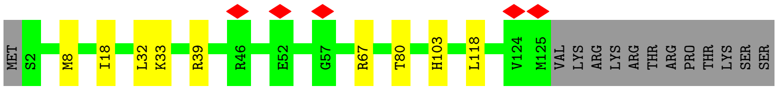
Chain p:





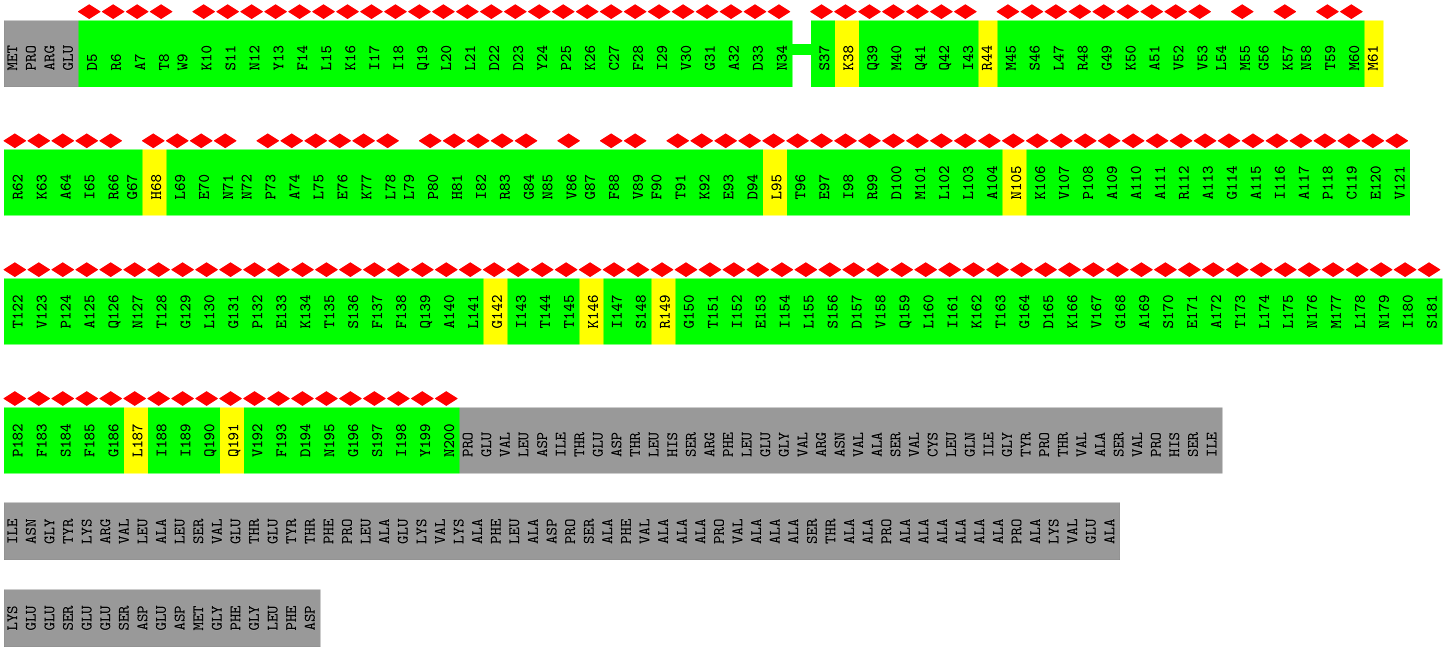
- Molecule 42: eL28

Chain r:



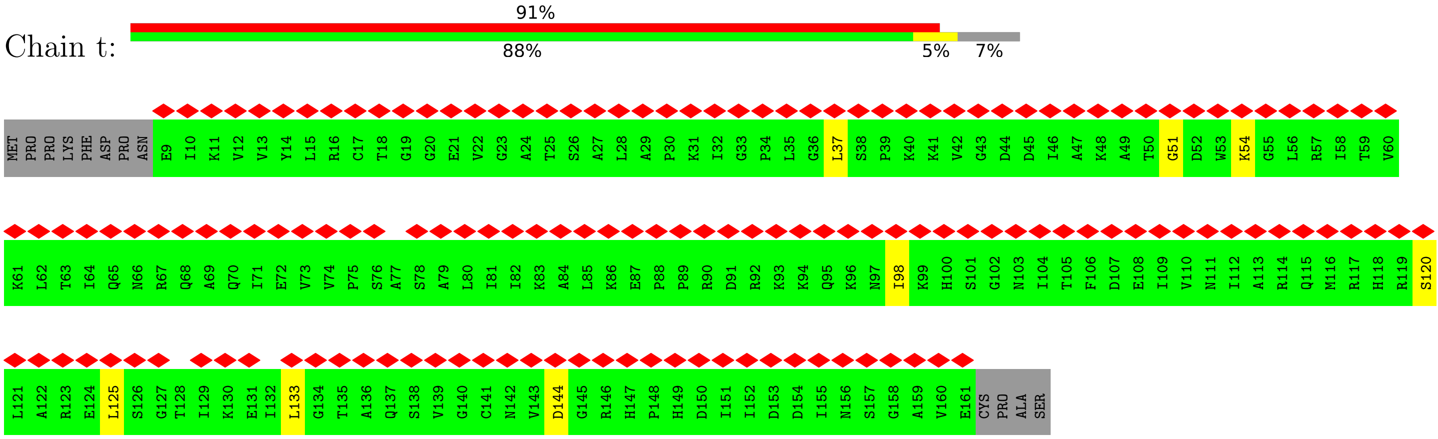
- Molecule 43: uL10

Chain s:



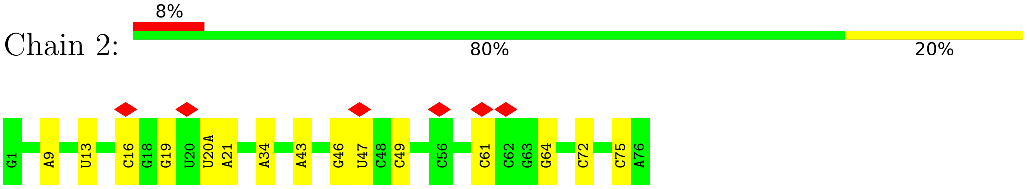
- Molecule 44: uL11

Chain t:



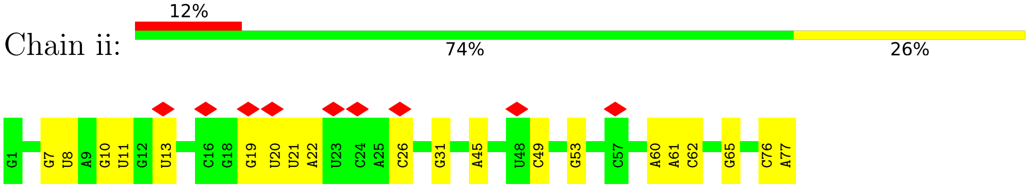
- Molecule 45: tRNA

Chain 2:



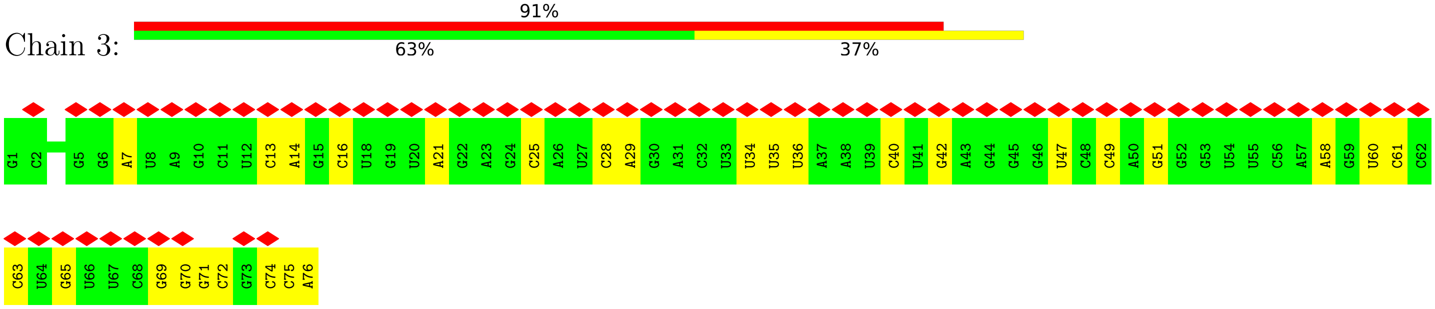
- Molecule 45: tRNA

Chain ii:



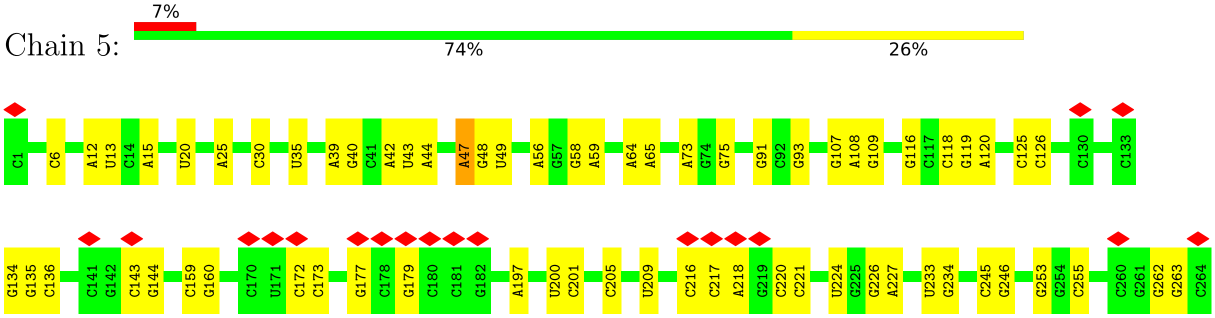
- Molecule 46: E-site tRNA

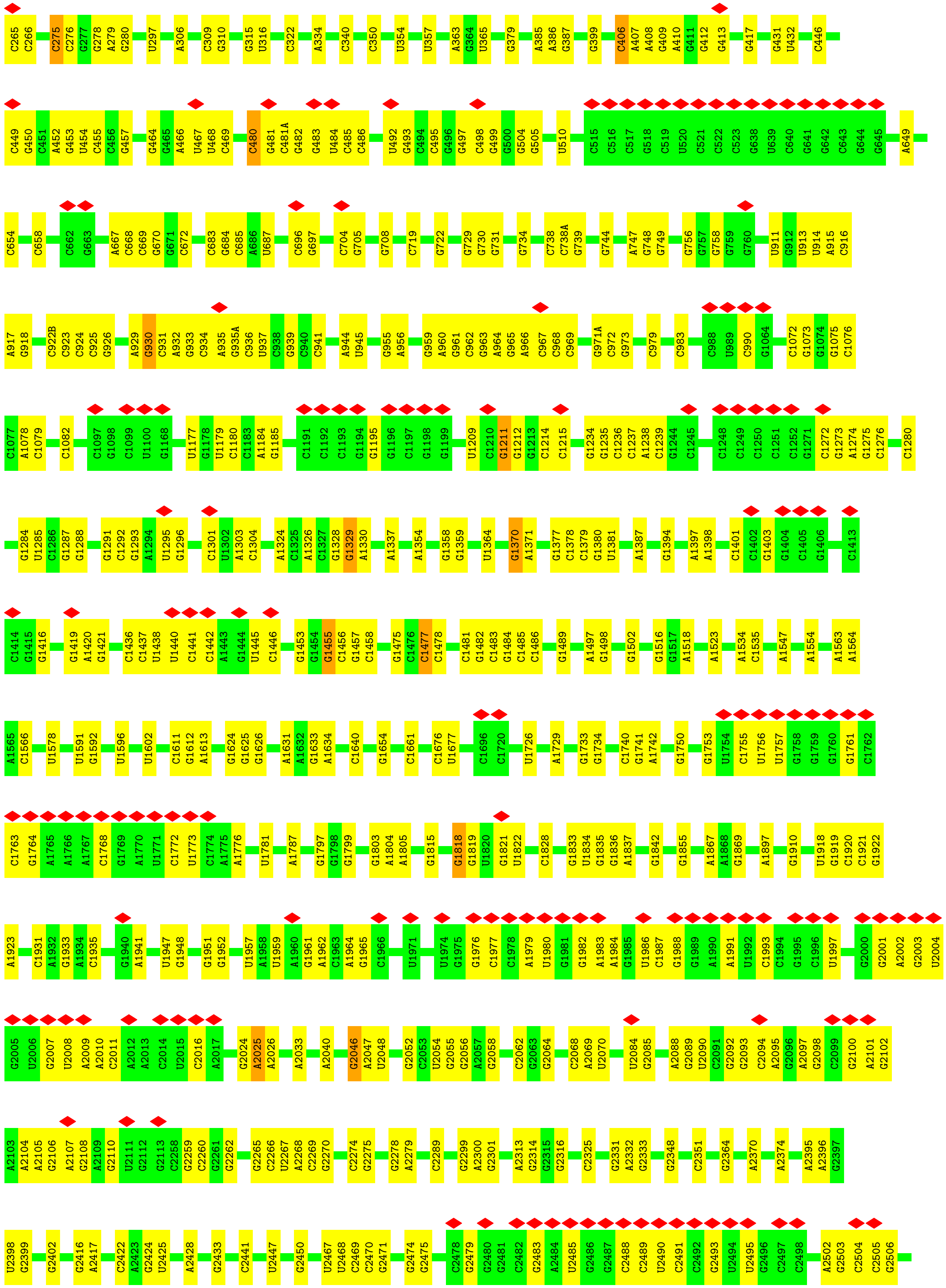
Chain 3:



- Molecule 47: 28S ribosomal RNA

Chain 5:




C265 C266 C275 C276 G277 G278 A279 G280 U297 A306 C309 G310 G315 U316 C322 A334 C340 C350 U354 U357 A363 G364 U365 G379 A385 A386 G387 G399 C406 A407 A408 G409 A410 G411 G412 G413 G417 G431 U432 C446
C449 G450 C451 A452 G453 U454 C455 C456 G457 G464 G465 A466 U467 U468 C469 C480 G481 C481A G482 G483 U484 C485 C486 U492 G493 C494 C495 G496 G497 C498 G499 G500 G504 G505 U510 C515 C516 C517 G518 C519 U520 C521 C522 C523 G638 U639 C640 G641 G642 C643 G644 G645 A649
C654 C658 C662 G663 A667 C668 C669 G670 G671 C672 C683 G684 C685 A686 U687 C696 G697 C704 G705 G708 C719 G722 G729 C730 G731 G734 C738 C738A G739 G744 A747 G748 G749 G756 G757 G758 G759 G760 U911 G912 U913 U914 A915 C916
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C1077 A1078 C1079 C1082 C1097 G1098 C1099 U1100 G1168 U1177 G1178 U1179 C1180 C1183 A1184 G1185 C1191 C1192 C1193 G1194 C1195 G1196 C1197 G1198 C1199 U1209 C1210 G1211 G1212 G1213 C1214 C1215 G1234 G1235 C1236 C1237 A1238 C1239 G1244 C1245 C1248 C1249 C1250 C1251 C1252 G1271 C1272 G1273 A1274 G1275 C1276 C1280
G1284 U1285 C1286 G1287 G1288 G1291 C1292 G1293 A1294 U1295 G1296 C1301 U1302 A1303 C1304 A1324 C1325 A1326 C1327 C1328 G1329 A1330 A1337 A1354 G1358 G1359 U1364 G1370 A1371 G1377 C1378 C1379 G1380 U1381 A1387 G1394 A1397 A1398 C1401 C1402 G1403 G1404 C1405 G1406 C1413
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A2103 A2104 A2105 G2106 A2107 G2108 A2109 G2110 U2111 G2112 G2113 C2258 G2259 C2260 G2261 G2262 G2265 C2266 U2267 A2268 G2269 G2270 C2274 G2275 G2278 A2279 C2289 G2299 A2300 G2301 A2313 G2314 G2315 G2316 C2325 G2331 A2332 G2333 G2348 C2351 G2364 A2370 A2374 A2395 A2396 G2397
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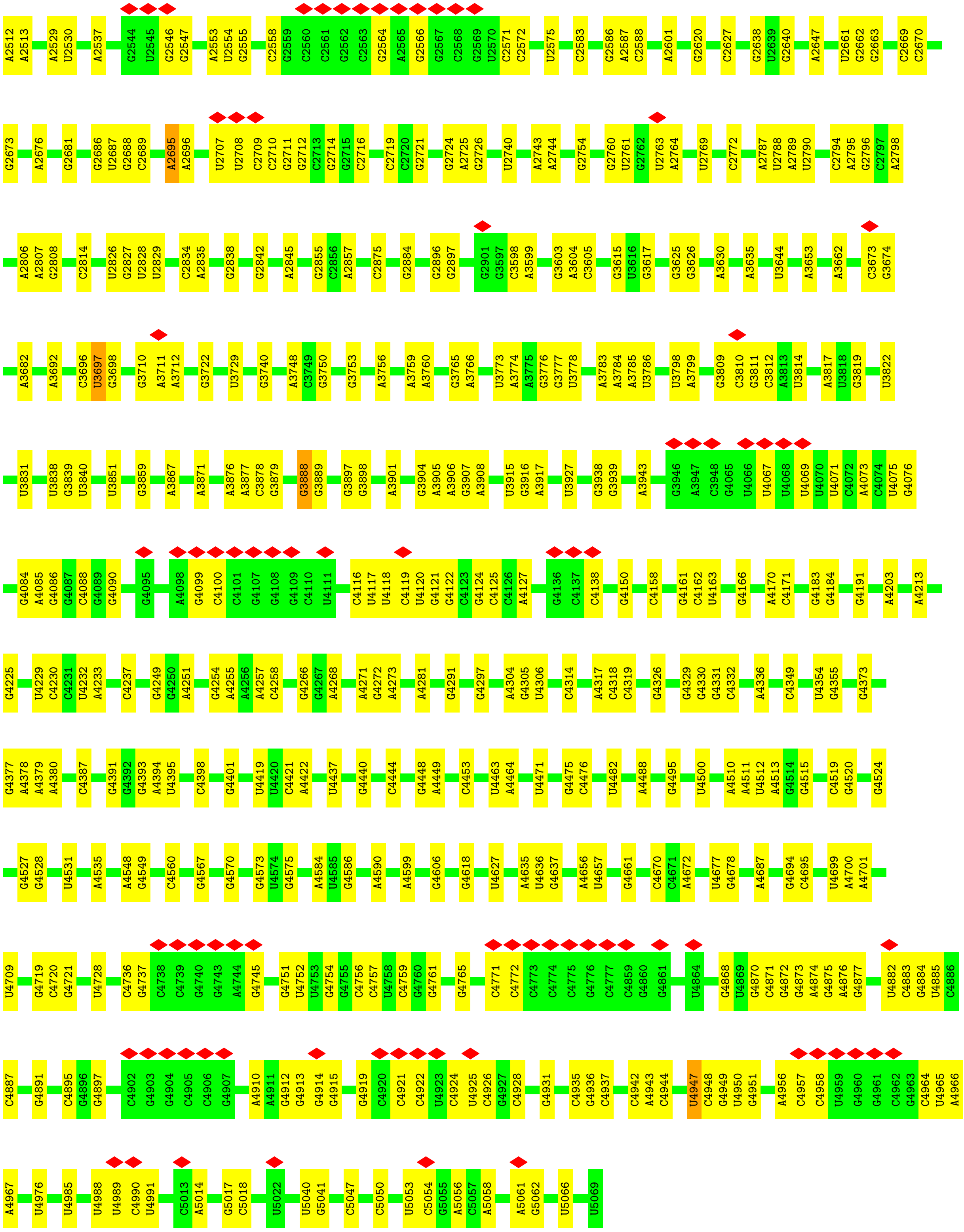
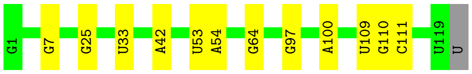
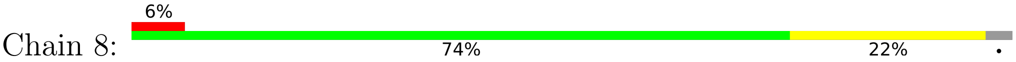


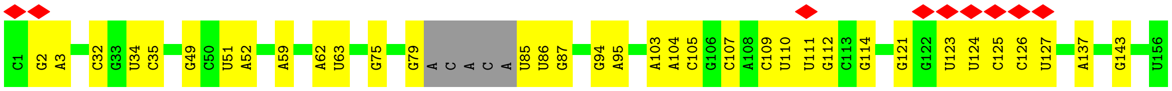
- Molecule 48: 5S ribosomal RNA

Chain 7:

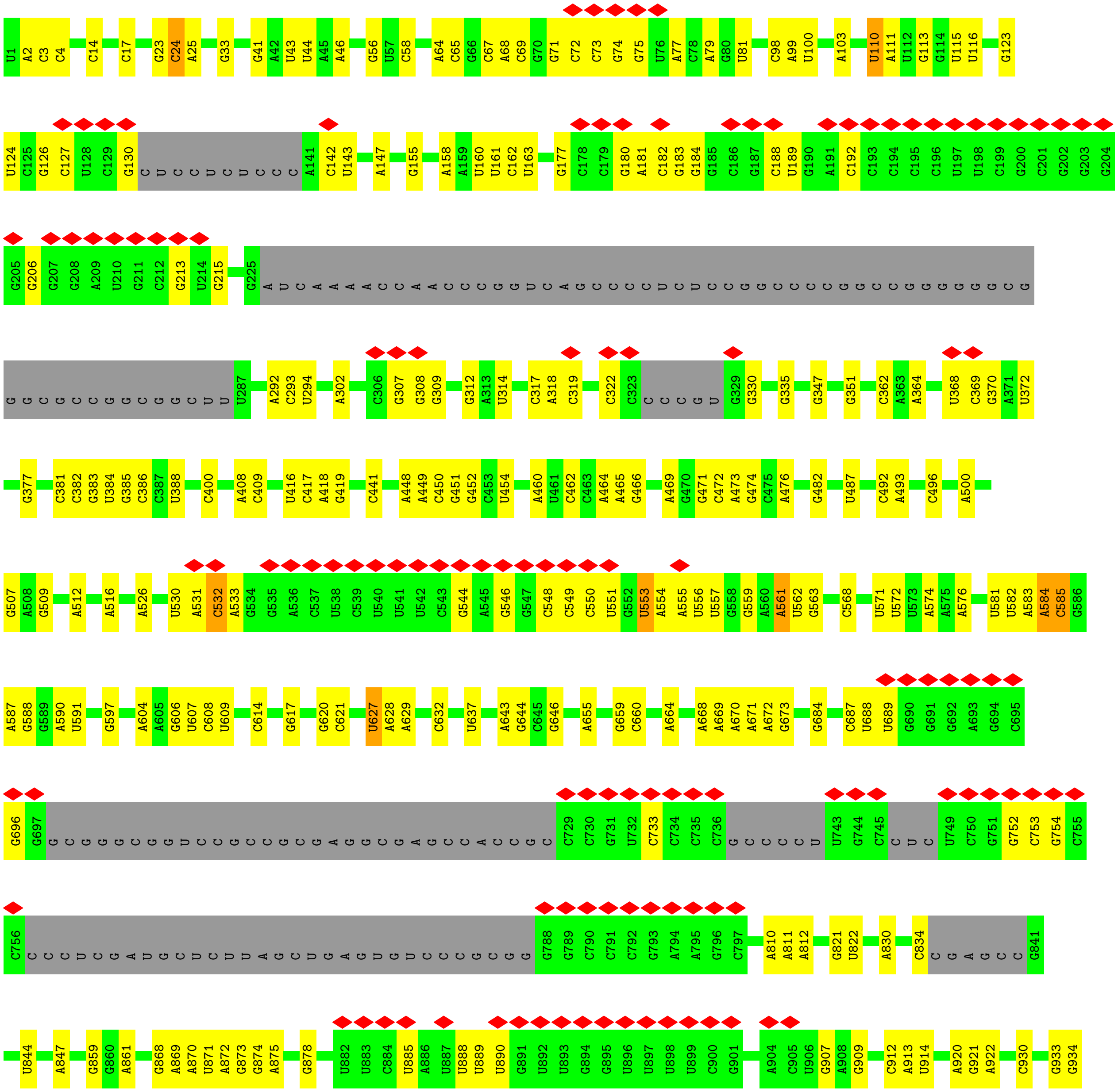


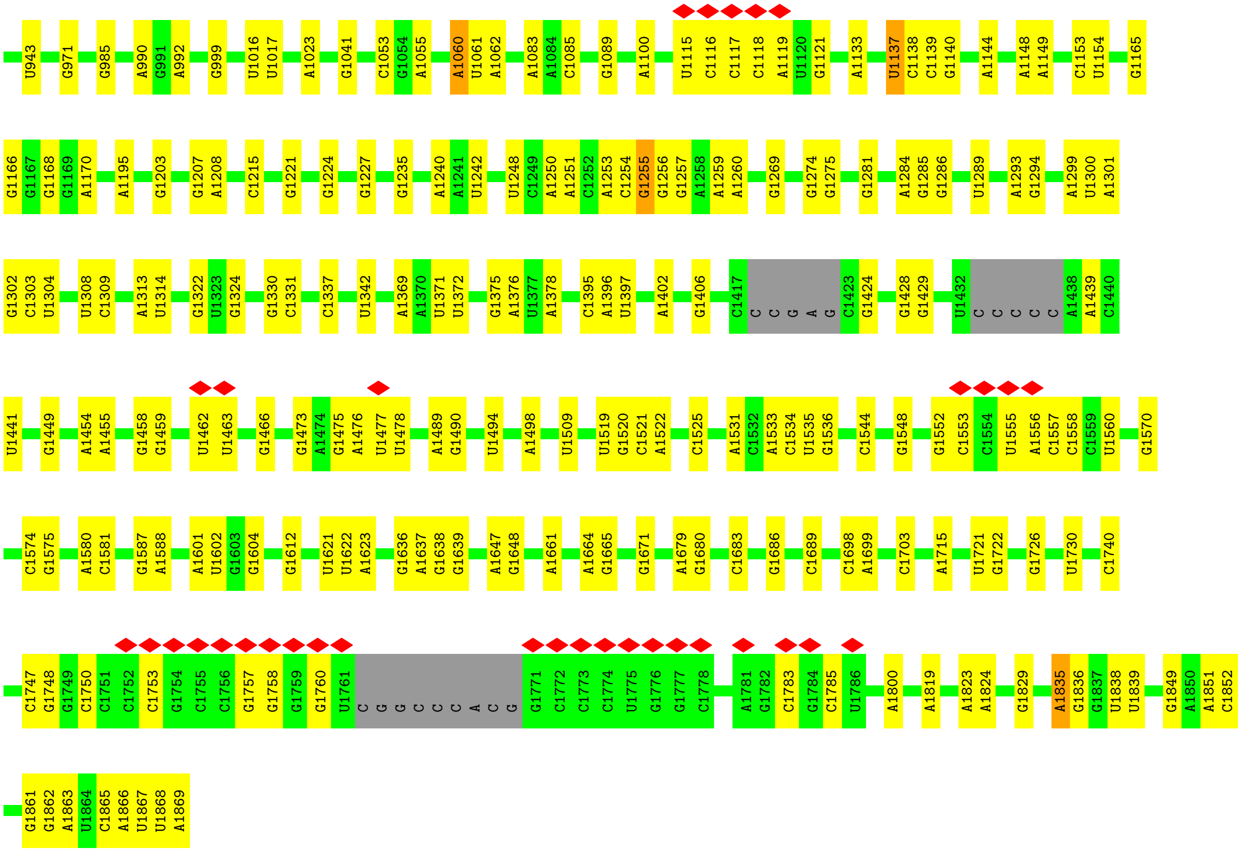
- Molecule 49: 5.8S ribosomal RNA





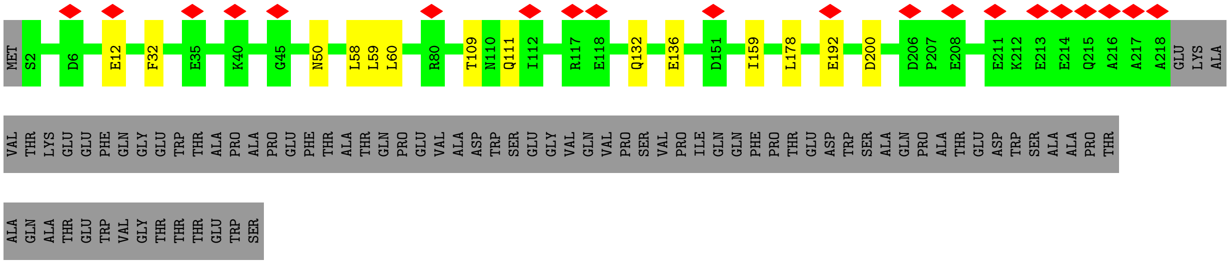
- Molecule 50: 18S ribosomal RNA





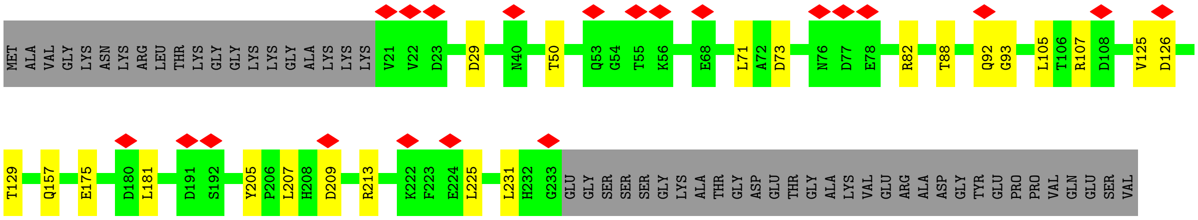
- Molecule 51: uS2

Chain AA:

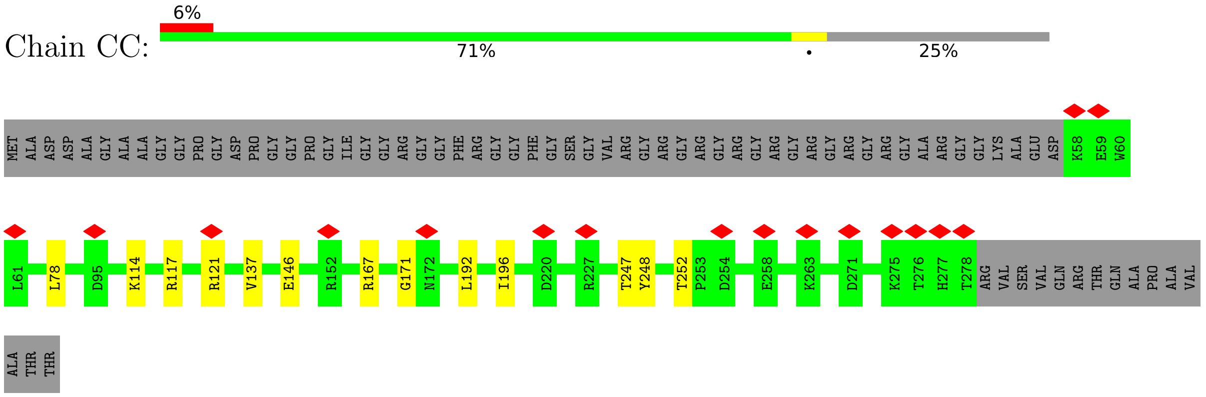


- Molecule 52: 40S ribosomal protein S3a

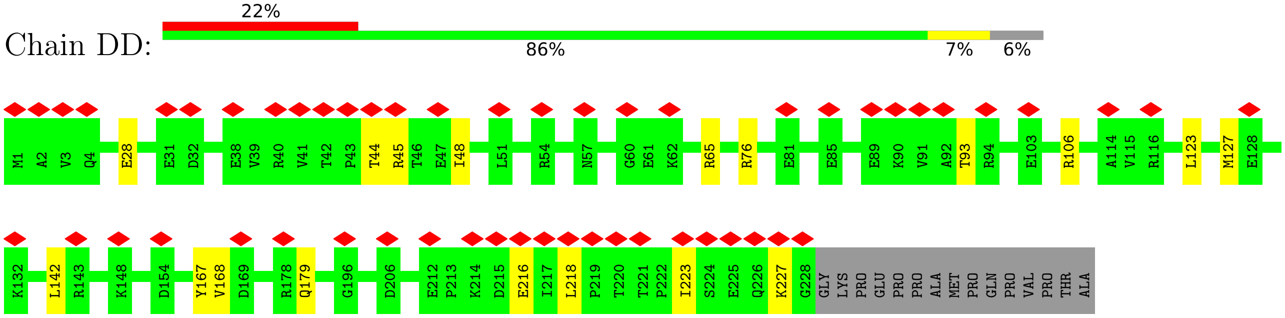
Chain BB:



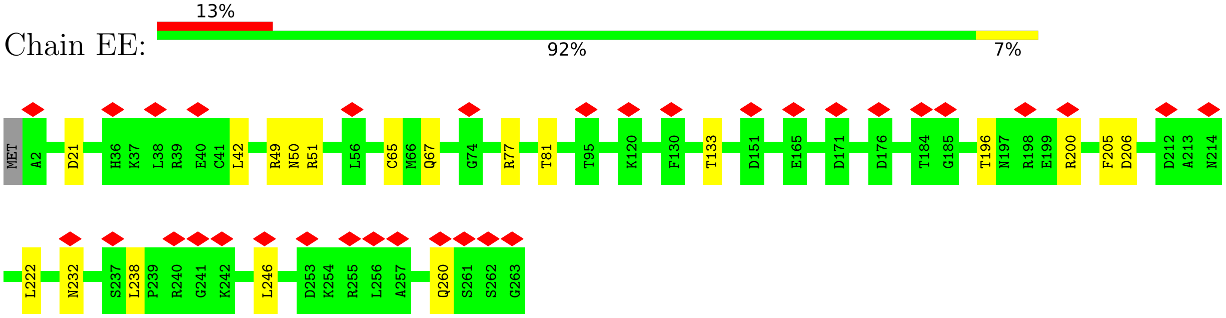
- Molecule 53: uS5



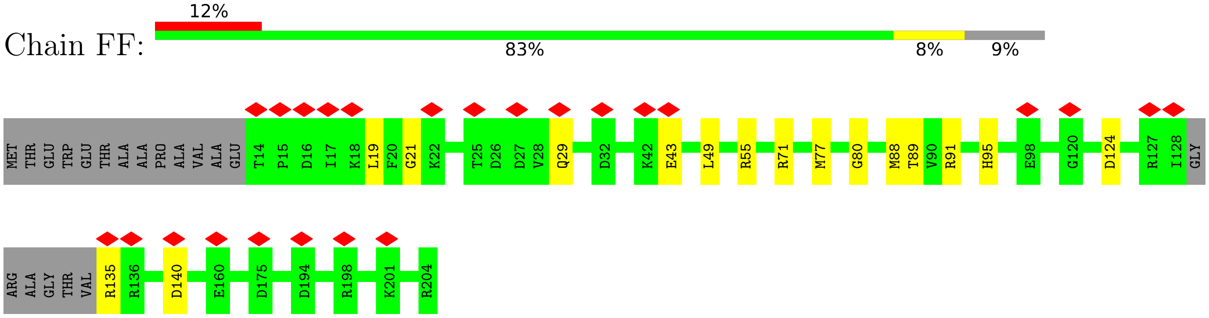
- Molecule 54: uS4



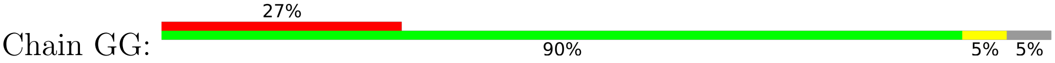
- Molecule 55: 40S ribosomal protein S4

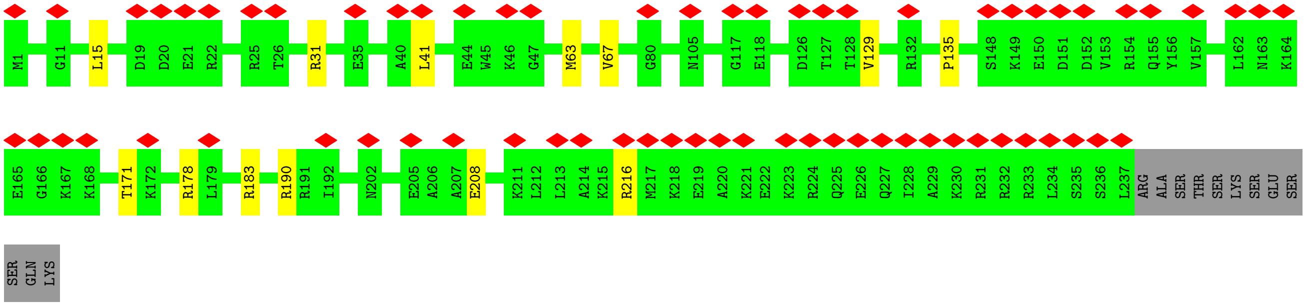


- Molecule 56: Uncharacterized protein



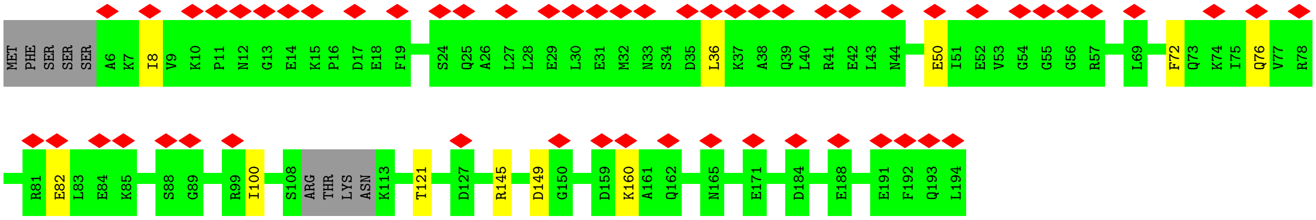
- Molecule 57: 40S ribosomal protein S6



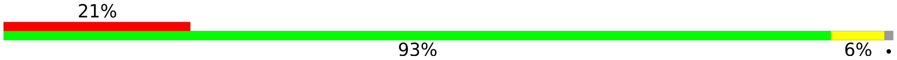


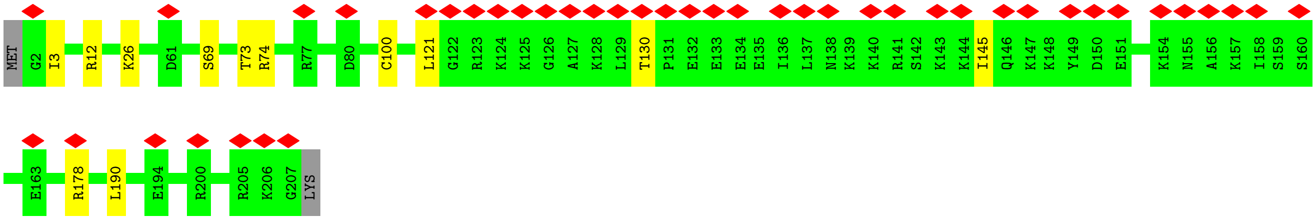
- Molecule 58: uS7

Chain HH:

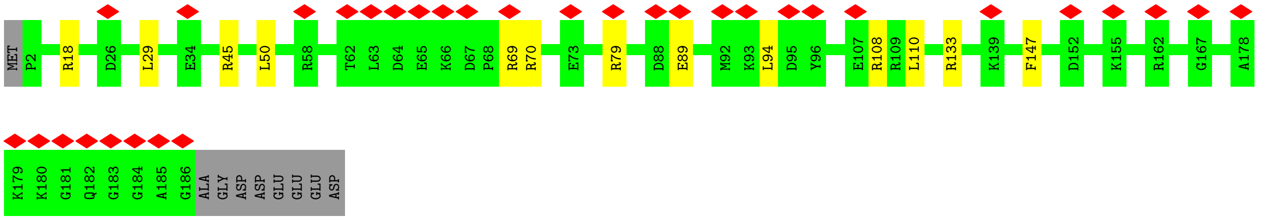
- Molecule 59: 40S ribosomal protein S8

Chain II:


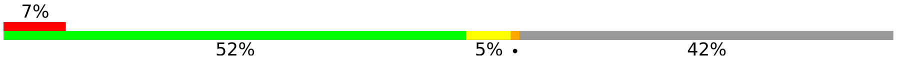


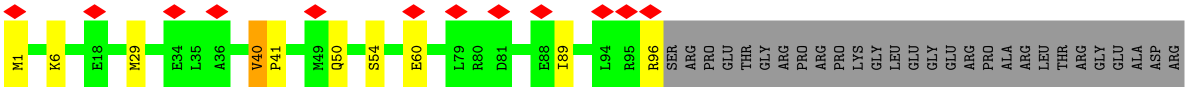
- Molecule 60: Ribosomal protein S9 (Predicted)

Chain JJ:

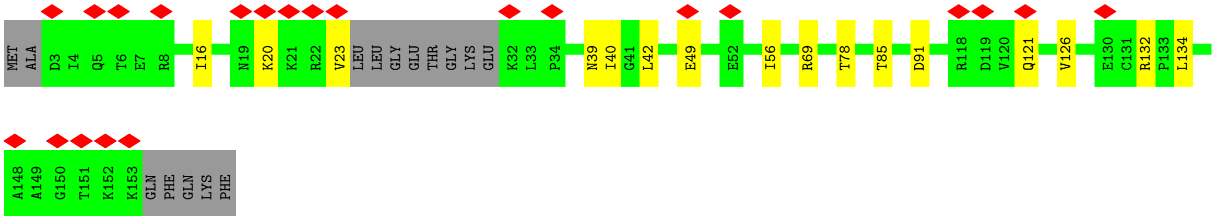
- Molecule 61: eS10

Chain KK:




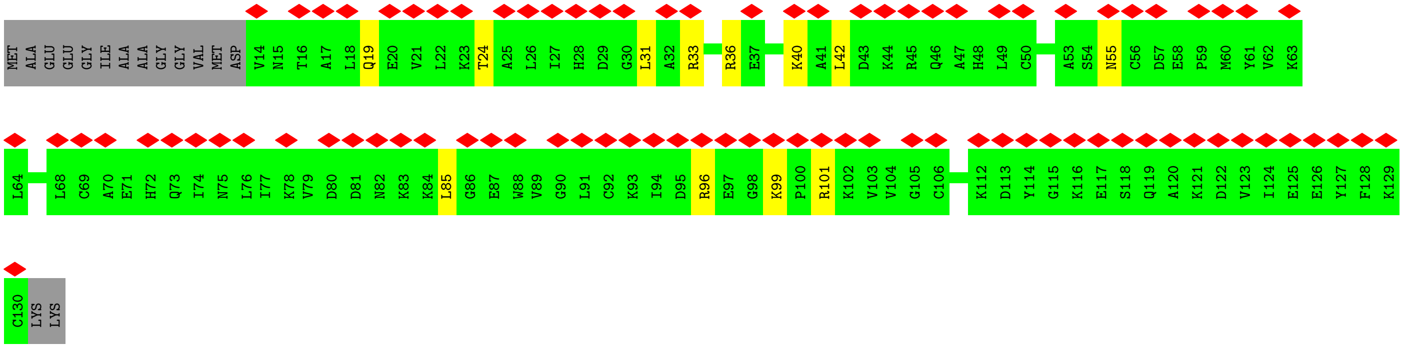
- Molecule 62: uS17

Chain LL:



- Molecule 63: 40S ribosomal protein S12

Chain MM:

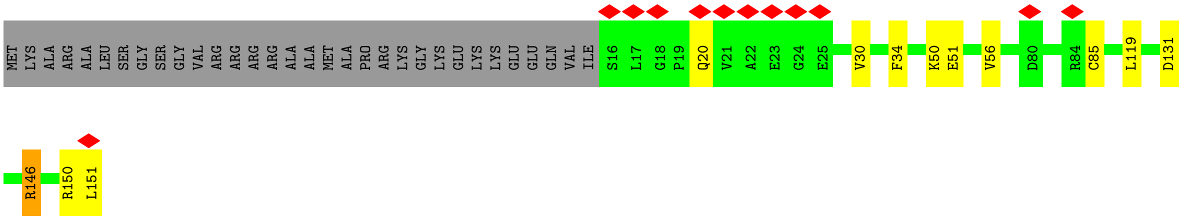


- Molecule 64: uS15

Chain NN:

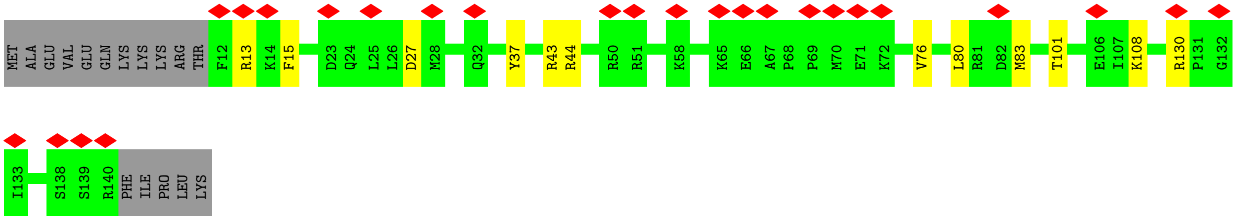
- Molecule 65: uS11

Chain OO:



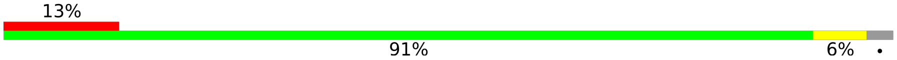
- Molecule 66: uS19

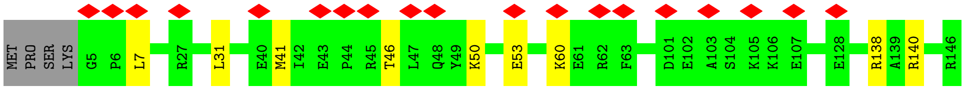
Chain PP:



- Molecule 67: uS9

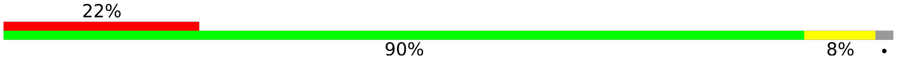
Chain QQ:

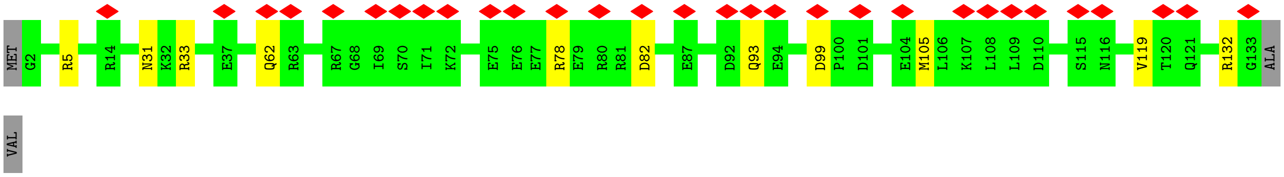




- Molecule 68: eS17

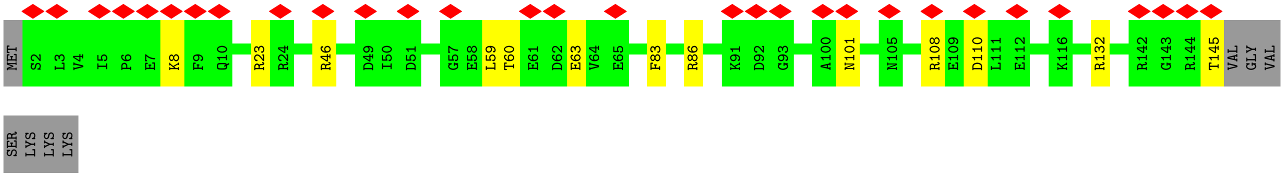
Chain RR:





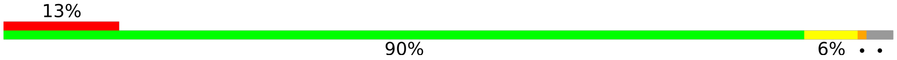
- Molecule 69: uS13

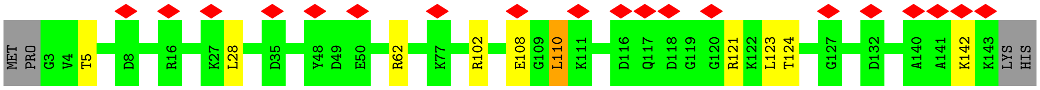
Chain SS:



- Molecule 70: eS19

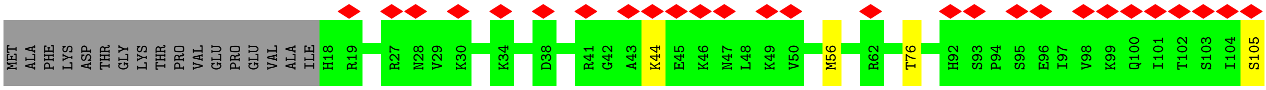
Chain TT:

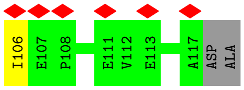




- Molecule 71: uS10

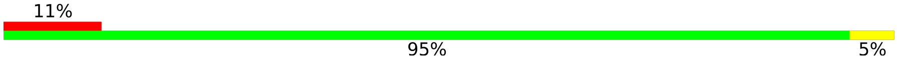
Chain UU:

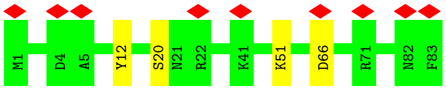




- Molecule 72: eS21

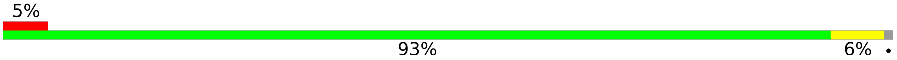
Chain VV:

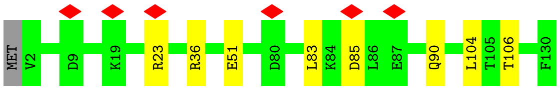




- Molecule 73: uS8

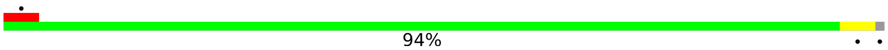
Chain WW:

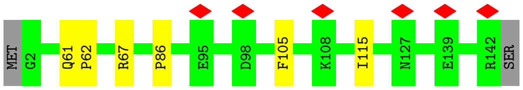




- Molecule 74: uS12

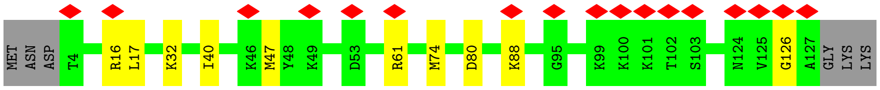
Chain XX:





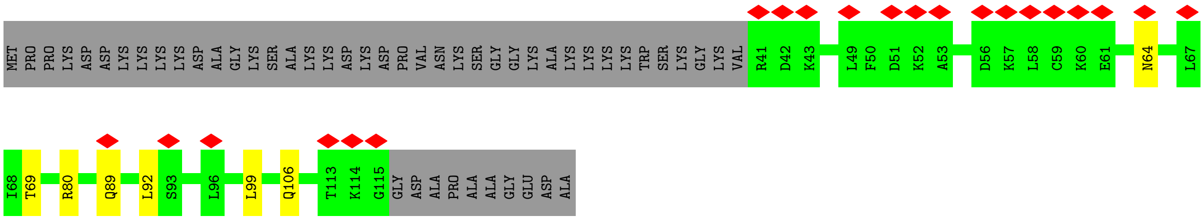
- Molecule 75: eS24

Chain YY:



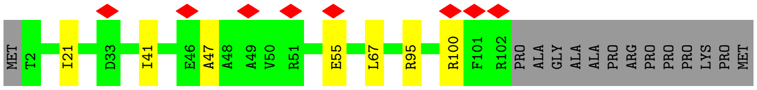
- Molecule 76: eS25

Chain ZZ:



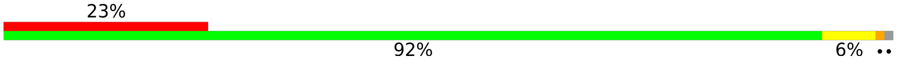
- Molecule 77: eS26

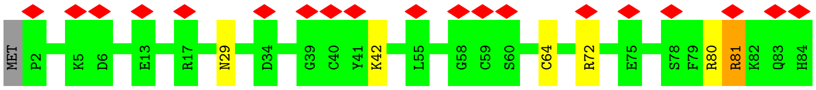
Chain aa:



- Molecule 78: 40S ribosomal protein S27

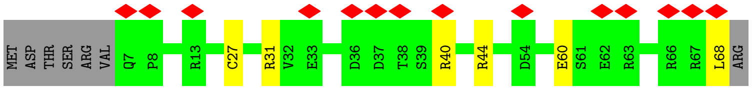
Chain bb:





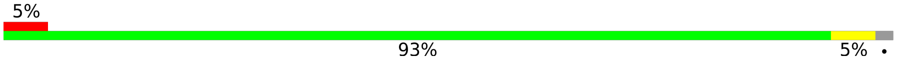
- Molecule 79: eS28

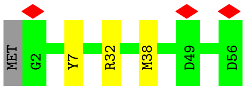
Chain cc:



- Molecule 80: uS14

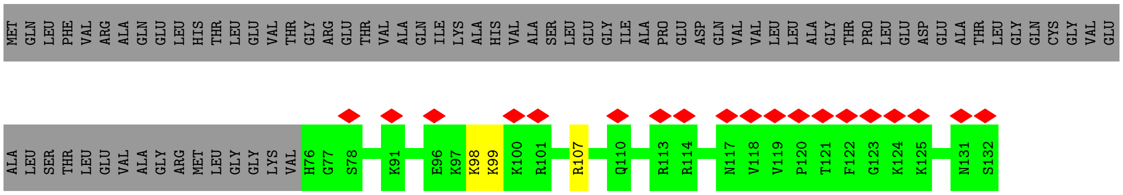
Chain dd:





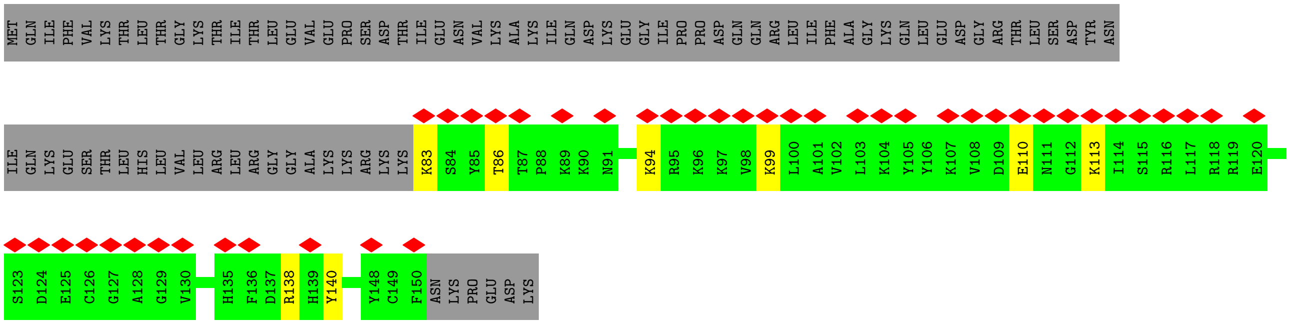
- Molecule 81: eS30

Chain ee:



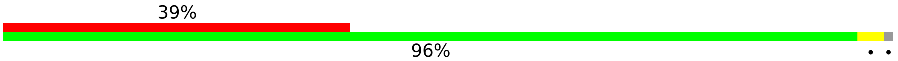
- Molecule 82: eS31

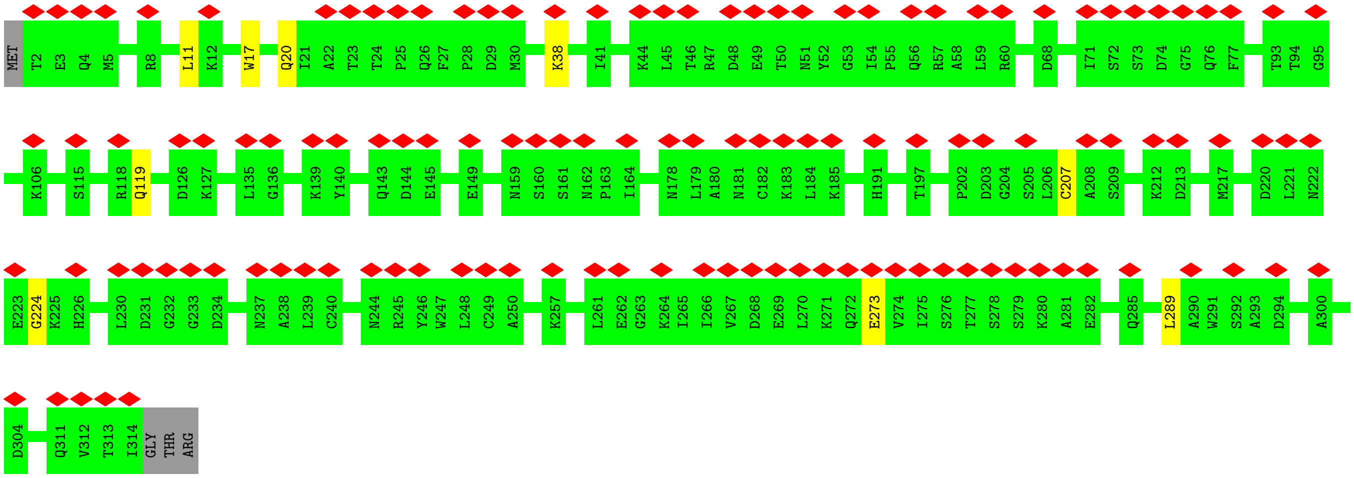
Chain ff:



- Molecule 83: RACK1

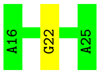
Chain gg:





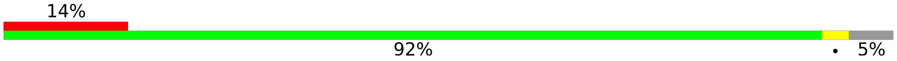
- Molecule 84: mRNA

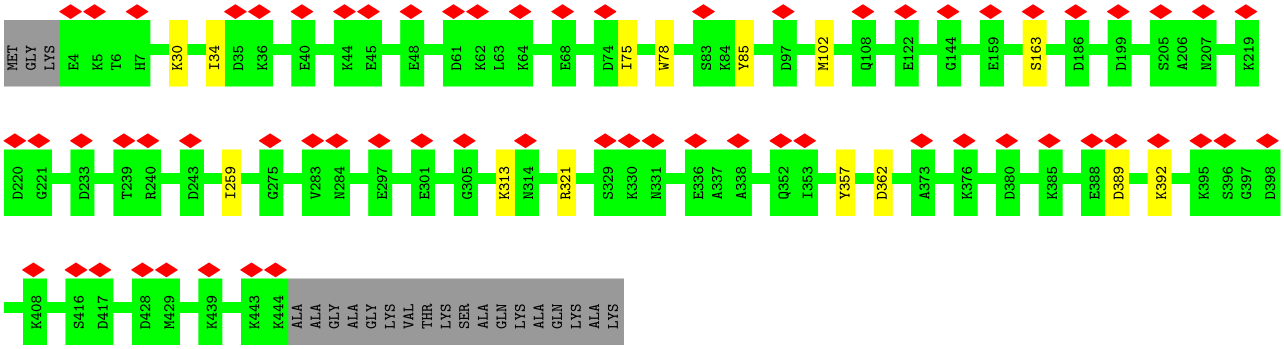
Chain hh:



- Molecule 85: Elongation factor 1-alpha 1

Chain jj:





4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	40347	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^{-}/\text{Å}^2)$	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	134615	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.600	Depositor
Minimum map value	-0.346	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	499.19998, 499.19998, 499.19998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, ZN, MG, 7C4, SEP

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	0.38	0/1936	0.71	0/2596
2	B	0.38	0/3240	0.68	0/4339
3	C	0.42	0/2937	0.73	0/3946
4	D	0.39	0/2437	0.63	0/3264
5	E	0.35	0/1762	0.65	0/2362
6	F	0.44	0/1911	0.74	1/2549 (0.0%)
7	G	0.42	0/1910	0.72	0/2569
8	H	0.34	0/1535	0.63	0/2063
9	I	0.36	0/1702	0.61	0/2272
10	J	0.33	0/1385	0.60	0/1852
11	L	0.43	0/1733	0.77	0/2316
12	M	0.43	0/1158	0.74	0/1547
13	N	0.43	0/1746	0.75	0/2338
14	O	0.47	0/1662	0.79	0/2222
15	P	0.41	0/1268	0.67	0/1700
16	Q	0.39	0/1539	0.77	0/2054
17	R	0.49	0/1524	0.82	0/2013
18	S	0.38	0/1501	0.69	0/2012
19	T	0.35	0/1326	0.62	0/1770
20	U	0.36	0/823	0.56	0/1104
21	V	0.38	0/1048	0.67	0/1402
22	W	0.36	0/873	0.61	0/1158
23	X	0.36	0/984	0.63	0/1323
24	Y	0.36	0/1132	0.65	0/1504
25	Z	0.38	0/1130	0.65	0/1507
26	a	0.39	0/1191	0.67	0/1590
27	b	0.40	0/861	0.67	0/1138
28	c	0.35	0/771	0.58	0/1034
29	d	0.38	0/903	0.68	0/1216
30	e	0.38	0/1071	0.68	0/1429
31	f	0.41	0/895	0.73	0/1198
32	g	0.35	0/916	0.72	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	h	0.51	0/1021	0.78	0/1348
34	i	0.50	0/841	0.77	0/1112
35	j	0.42	0/720	0.76	0/952
36	k	0.41	0/575	0.65	0/761
37	l	0.46	0/459	0.72	0/608
38	m	0.40	0/435	0.66	0/575
39	n	0.59	0/240	0.94	0/305
40	o	0.38	0/864	0.65	0/1140
41	p	0.44	0/718	0.72	0/953
42	r	0.44	0/1010	0.76	0/1354
43	s	0.44	0/1530	0.64	0/2064
44	t	0.47	0/1174	0.68	0/1582
45	2	0.23	0/1803	0.67	0/2801
45	ii	0.21	0/1805	0.71	0/2809
46	3	0.21	0/1777	0.65	0/2763
47	5	0.33	1/84973 (0.0%)	0.70	19/132508 (0.0%)
48	7	0.26	0/2836	0.65	0/4421
49	8	0.31	0/3581	0.68	0/5577
50	9	0.26	0/40502	0.70	15/63100 (0.0%)
51	AA	0.33	0/1747	0.58	0/2374
52	BB	0.33	0/1756	0.60	0/2350
53	CC	0.34	0/1753	0.62	0/2369
54	DD	0.36	0/1796	0.64	0/2417
55	EE	0.34	0/2118	0.63	0/2849
56	FF	0.34	0/1492	0.61	0/2005
57	GG	0.34	0/1946	0.66	0/2590
58	HH	0.34	0/1510	0.59	0/2022
59	II	0.34	0/1715	0.64	0/2287
60	JJ	0.36	0/1550	0.68	0/2069
61	KK	0.34	0/834	0.65	1/1125 (0.1%)
62	LL	0.35	0/1195	0.62	0/1597
63	MM	0.35	0/918	0.58	0/1233
64	NN	0.33	0/1226	0.63	0/1649
65	OO	0.35	0/1029	0.74	2/1380 (0.1%)
66	PP	0.35	0/1079	0.63	0/1441
67	QQ	0.33	0/1146	0.60	0/1534
68	RR	0.34	0/1082	0.58	0/1452
69	SS	0.35	0/1208	0.66	0/1618
70	TT	0.37	0/1115	0.62	1/1493 (0.1%)
71	UU	0.34	0/805	0.64	0/1081
72	VV	0.34	0/643	0.65	0/860
73	WW	0.37	0/1051	0.71	0/1406
74	XX	0.35	0/1116	0.67	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
75	YY	0.36	0/1028	0.63	0/1366
76	ZZ	0.34	0/604	0.60	0/810
77	aa	0.37	0/828	0.70	0/1109
78	bb	0.37	0/665	0.62	0/891
79	cc	0.35	0/490	0.68	0/656
80	dd	0.39	0/470	0.70	0/623
81	ee	0.35	0/462	0.68	0/607
82	ff	0.36	0/567	0.56	0/753
83	gg	0.33	0/2493	0.55	0/3394
84	hh	0.25	0/233	0.69	0/360
85	jj	0.35	0/3442	0.51	0/4656
All	All	0.34	1/236786 (0.0%)	0.68	39/347256 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3
21	V	0	1
31	f	0	1
74	XX	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	5	2025	A	O3'-P	-30.56	1.24	1.61

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	5	2025	A	OP1-P-O3'	-39.69	17.89	105.20
47	5	2025	A	P-O3'-C3'	-17.17	99.09	119.70
61	KK	40	VAL	C-N-CD	-10.98	96.44	120.60
50	9	581	U	N1-C1'-C2'	-10.17	100.77	114.00
50	9	582	U	N1-C1'-C2'	-9.01	102.09	112.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	16	PHE	Peptide
2	B	257	TRP	Peptide
2	B	258	HIS	Peptide
21	V	6	ARG	Sidechain
31	f	106	TYR	Peptide

5.2 Too-close contacts ⓘ

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

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	A	246/257 (96%)	225 (92%)	19 (8%)	2 (1%)	16	47
2	B	392/403 (97%)	364 (93%)	25 (6%)	3 (1%)	16	47
3	C	360/425 (85%)	337 (94%)	21 (6%)	2 (1%)	22	53
4	D	291/297 (98%)	275 (94%)	14 (5%)	2 (1%)	19	50
5	E	208/291 (72%)	189 (91%)	18 (9%)	1 (0%)	25	57
6	F	223/247 (90%)	211 (95%)	11 (5%)	1 (0%)	30	61
7	G	229/319 (72%)	217 (95%)	12 (5%)	0	100	100
8	H	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
9	I	201/214 (94%)	185 (92%)	16 (8%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
13	N	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
14	O	197/203 (97%)	189 (96%)	8 (4%)	0	100	100
15	P	151/184 (82%)	145 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	185/188 (98%)	175 (95%)	9 (5%)	1 (0%)	25	57
17	R	178/196 (91%)	172 (97%)	6 (3%)	0	100	100
18	S	174/176 (99%)	160 (92%)	12 (7%)	2 (1%)	12	41
19	T	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	22	53
20	U	97/128 (76%)	86 (89%)	11 (11%)	0	100	100
21	V	137/140 (98%)	125 (91%)	12 (9%)	0	100	100
22	W	102/157 (65%)	98 (96%)	3 (3%)	1 (1%)	13	42
23	X	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
24	Y	132/145 (91%)	125 (95%)	7 (5%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	8	34
26	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
27	b	100/245 (41%)	93 (93%)	6 (6%)	1 (1%)	13	42
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	94 (90%)	10 (10%)	1 (1%)	13	42
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	101 (94%)	4 (4%)	2 (2%)	6	30
32	g	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h	120/123 (98%)	118 (98%)	1 (1%)	1 (1%)	16	47
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
36	k	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	m	50/102 (49%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
41	p	89/92 (97%)	80 (90%)	8 (9%)	1 (1%)	12	41
42	r	122/137 (89%)	110 (90%)	11 (9%)	1 (1%)	16	47
43	s	194/318 (61%)	171 (88%)	22 (11%)	1 (0%)	25	57
44	t	151/165 (92%)	134 (89%)	13 (9%)	4 (3%)	4	24
51	AA	215/295 (73%)	204 (95%)	10 (5%)	1 (0%)	25	57
52	BB	211/264 (80%)	199 (94%)	11 (5%)	1 (0%)	25	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	CC	219/293 (75%)	205 (94%)	13 (6%)	1 (0%)	25	57
54	DD	226/243 (93%)	214 (95%)	9 (4%)	3 (1%)	10	37
55	EE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
56	FF	181/204 (89%)	166 (92%)	11 (6%)	4 (2%)	5	28
57	GG	235/249 (94%)	224 (95%)	10 (4%)	1 (0%)	30	61
58	HH	181/194 (93%)	171 (94%)	10 (6%)	0	100	100
59	II	204/208 (98%)	192 (94%)	11 (5%)	1 (0%)	25	57
60	JJ	183/194 (94%)	177 (97%)	5 (3%)	1 (0%)	25	57
61	KK	94/165 (57%)	88 (94%)	5 (5%)	1 (1%)	12	41
62	LL	139/158 (88%)	129 (93%)	10 (7%)	0	100	100
63	MM	115/132 (87%)	103 (90%)	12 (10%)	0	100	100
64	NN	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
65	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	8	34
66	PP	127/145 (88%)	117 (92%)	9 (7%)	1 (1%)	16	47
67	QQ	140/146 (96%)	130 (93%)	10 (7%)	0	100	100
68	RR	130/135 (96%)	118 (91%)	11 (8%)	1 (1%)	16	47
69	SS	142/152 (93%)	134 (94%)	8 (6%)	0	100	100
70	TT	139/145 (96%)	132 (95%)	7 (5%)	0	100	100
71	UU	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
72	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	WW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
74	XX	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	9	35
75	YY	122/130 (94%)	116 (95%)	5 (4%)	1 (1%)	16	47
76	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
77	aa	99/115 (86%)	90 (91%)	8 (8%)	1 (1%)	13	42
78	bb	81/84 (96%)	75 (93%)	5 (6%)	1 (1%)	11	39
79	cc	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
80	dd	53/56 (95%)	49 (92%)	3 (6%)	1 (2%)	6	30
81	ee	55/133 (41%)	52 (94%)	3 (6%)	0	100	100
82	ff	66/156 (42%)	61 (92%)	5 (8%)	0	100	100
83	gg	311/317 (98%)	282 (91%)	28 (9%)	1 (0%)	37	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
85	jj	438/462 (95%)	419 (96%)	18 (4%)	1 (0%)	44	72
All	All	11976/13836 (87%)	11207 (94%)	713 (6%)	56 (0%)	27	57

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
44	t	120	SER
44	t	125	LEU
74	XX	62	PRO
74	XX	86	PRO
3	C	83	GLY

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	A	190/199 (96%)	176 (93%)	14 (7%)	11	35
2	B	342/348 (98%)	324 (95%)	18 (5%)	19	47
3	C	302/347 (87%)	281 (93%)	21 (7%)	12	38
4	D	247/250 (99%)	234 (95%)	13 (5%)	19	47
5	E	190/251 (76%)	180 (95%)	10 (5%)	19	47
6	F	196/215 (91%)	184 (94%)	12 (6%)	15	42
7	G	200/272 (74%)	189 (94%)	11 (6%)	18	46
8	H	169/171 (99%)	156 (92%)	13 (8%)	10	34
9	I	175/181 (97%)	161 (92%)	14 (8%)	10	33
10	J	143/149 (96%)	137 (96%)	6 (4%)	25	54
11	L	175/176 (99%)	166 (95%)	9 (5%)	20	48
12	M	117/161 (73%)	108 (92%)	9 (8%)	10	34
13	N	171/172 (99%)	161 (94%)	10 (6%)	17	44
14	O	171/173 (99%)	159 (93%)	12 (7%)	12	38
15	P	134/163 (82%)	125 (93%)	9 (7%)	13	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	164/165 (99%)	151 (92%)	13 (8%)	10	33
17	R	159/175 (91%)	145 (91%)	14 (9%)	8	29
18	S	157/157 (100%)	147 (94%)	10 (6%)	14	41
19	T	139/140 (99%)	130 (94%)	9 (6%)	14	40
20	U	89/114 (78%)	87 (98%)	2 (2%)	47	70
21	V	106/107 (99%)	92 (87%)	14 (13%)	3	14
22	W	86/126 (68%)	85 (99%)	1 (1%)	67	81
23	X	106/134 (79%)	99 (93%)	7 (7%)	14	40
24	Y	124/135 (92%)	118 (95%)	6 (5%)	21	50
25	Z	117/118 (99%)	115 (98%)	2 (2%)	56	75
26	a	119/120 (99%)	114 (96%)	5 (4%)	25	54
27	b	84/184 (46%)	81 (96%)	3 (4%)	30	57
28	c	84/98 (86%)	80 (95%)	4 (5%)	21	50
29	d	98/110 (89%)	88 (90%)	10 (10%)	6	23
30	e	114/121 (94%)	105 (92%)	9 (8%)	10	33
31	f	88/89 (99%)	82 (93%)	6 (7%)	13	39
32	g	98/99 (99%)	92 (94%)	6 (6%)	15	42
33	h	109/110 (99%)	105 (96%)	4 (4%)	29	56
34	i	86/89 (97%)	82 (95%)	4 (5%)	22	51
35	j	73/80 (91%)	67 (92%)	6 (8%)	9	32
36	k	64/65 (98%)	62 (97%)	2 (3%)	35	62
37	l	47/48 (98%)	46 (98%)	1 (2%)	48	70
38	m	48/90 (53%)	46 (96%)	2 (4%)	25	54
39	n	24/24 (100%)	21 (88%)	3 (12%)	3	16
40	o	92/94 (98%)	88 (96%)	4 (4%)	25	53
41	p	74/75 (99%)	71 (96%)	3 (4%)	26	54
42	r	108/121 (89%)	100 (93%)	8 (7%)	11	35
43	s	164/258 (64%)	154 (94%)	10 (6%)	15	42
44	t	126/137 (92%)	122 (97%)	4 (3%)	34	61
51	AA	180/245 (74%)	167 (93%)	13 (7%)	12	37
52	BB	194/231 (84%)	173 (89%)	21 (11%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	CC	187/225 (83%)	175 (94%)	12 (6%)	14	41
54	DD	190/202 (94%)	175 (92%)	15 (8%)	10	33
55	EE	224/225 (100%)	205 (92%)	19 (8%)	8	31
56	FF	158/170 (93%)	146 (92%)	12 (8%)	11	35
57	GG	207/218 (95%)	195 (94%)	12 (6%)	17	44
58	HH	165/174 (95%)	154 (93%)	11 (7%)	13	40
59	II	178/180 (99%)	167 (94%)	11 (6%)	15	42
60	JJ	161/168 (96%)	149 (92%)	12 (8%)	11	35
61	KK	87/136 (64%)	78 (90%)	9 (10%)	6	22
62	LL	130/142 (92%)	114 (88%)	16 (12%)	4	16
63	MM	99/108 (92%)	87 (88%)	12 (12%)	4	17
64	NN	130/131 (99%)	118 (91%)	12 (9%)	7	27
65	OO	106/130 (82%)	96 (91%)	10 (9%)	7	26
66	PP	115/130 (88%)	104 (90%)	11 (10%)	7	25
67	QQ	117/121 (97%)	108 (92%)	9 (8%)	10	34
68	RR	119/121 (98%)	109 (92%)	10 (8%)	9	31
69	SS	125/132 (95%)	112 (90%)	13 (10%)	5	22
70	TT	111/115 (96%)	101 (91%)	10 (9%)	8	28
71	UU	92/107 (86%)	87 (95%)	5 (5%)	18	46
72	VV	67/67 (100%)	63 (94%)	4 (6%)	16	43
73	WW	112/113 (99%)	104 (93%)	8 (7%)	12	37
74	XX	113/115 (98%)	110 (97%)	3 (3%)	40	66
75	YY	107/112 (96%)	98 (92%)	9 (8%)	9	31
76	ZZ	66/103 (64%)	59 (89%)	7 (11%)	5	21
77	aa	88/98 (90%)	82 (93%)	6 (7%)	13	39
78	bb	75/76 (99%)	69 (92%)	6 (8%)	10	33
79	cc	55/62 (89%)	49 (89%)	6 (11%)	5	21
80	dd	48/49 (98%)	46 (96%)	2 (4%)	25	54
81	ee	47/106 (44%)	44 (94%)	3 (6%)	14	41
82	ff	61/140 (44%)	53 (87%)	8 (13%)	3	15
83	gg	272/275 (99%)	264 (97%)	8 (3%)	37	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
85	jj	365/378 (97%)	353 (97%)	12 (3%)	33	60
All	All	10420/11716 (89%)	9730 (93%)	690 (7%)	16	40

5 of 690 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	HH	100	ILE
68	RR	62	GLN
59	II	145	ILE
58	HH	82	GLU
63	MM	36	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
19	T	144	ASN
83	gg	14	HIS
85	jj	343	GLN
85	jj	367	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	73/76 (96%)	14 (19%)	1 (1%)
45	ii	74/76 (97%)	20 (27%)	0
46	3	72/75 (96%)	28 (38%)	2 (2%)
47	5	3514/3543 (99%)	869 (24%)	171 (4%)
48	7	118/120 (98%)	12 (10%)	1 (0%)
49	8	150/156 (96%)	34 (22%)	7 (4%)
50	9	1678/1869 (89%)	420 (25%)	65 (3%)
84	hh	9/10 (90%)	1 (11%)	0
All	All	5688/5925 (96%)	1398 (24%)	247 (4%)

5 of 1398 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	9	A
45	2	13	U
45	2	16	C

Continued on next page...

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Mol	Chain	Res	Type
45	2	19	G
45	2	21	A

5 of 247 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	5	2467	U
50	9	1137	U
47	5	4075	U
50	9	912	C
50	9	1534	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
85	SEP	jj	163	85	8,9,10	0.63	0	8,12,14	1.46	2 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	SEP	jj	163	85	-	5/5/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	jj	163	SEP	OG-CB-CA	2.47	110.55	108.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
85	jj	163	SEP	P-OG-CB	2.08	124.01	118.30

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	jj	163	SEP	N-CA-CB-OG
85	jj	163	SEP	CA-CB-OG-P
85	jj	163	SEP	CB-OG-P-O2P
85	jj	163	SEP	CB-OG-P-O3P
85	jj	163	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 286 ligands modelled in this entry, 284 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
88	GDP	jj	501	86	24,30,30	0.91	0	30,47,47	1.34	4 (13%)
89	7C4	jj	503	-	81,82,82	0.97	4 (4%)	111,117,117	1.22	12 (10%)

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
88	GDP	jj	501	86	-	0/12/32/32	0/3/3/3
89	7C4	jj	503	-	-	8/120/140/140	0/3/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	jj	503	7C4	C72-C71	-4.60	1.32	1.51
89	jj	503	7C4	C54-C55	-2.37	1.50	1.53
89	jj	503	7C4	C53-C54	2.08	1.56	1.53
89	jj	503	7C4	C45-C47	2.07	1.55	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
89	jj	503	7C4	O35-C79-C01	3.44	118.35	110.78
89	jj	503	7C4	C70-C69-N17	3.28	124.95	119.10
88	jj	501	GDP	C3'-C2'-C1'	3.10	105.64	100.98
89	jj	503	7C4	C36-N05-C30	-3.03	107.19	112.00
88	jj	501	GDP	PA-O3A-PB	-3.01	122.49	132.83

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	jj	503	7C4	C47-C48-O18-C52
89	jj	503	7C4	C62-C63-C64-C65
89	jj	503	7C4	C13-C14-O03-C19
89	jj	503	7C4	C22-C14-O03-C19
89	jj	503	7C4	N17-C63-C64-C65

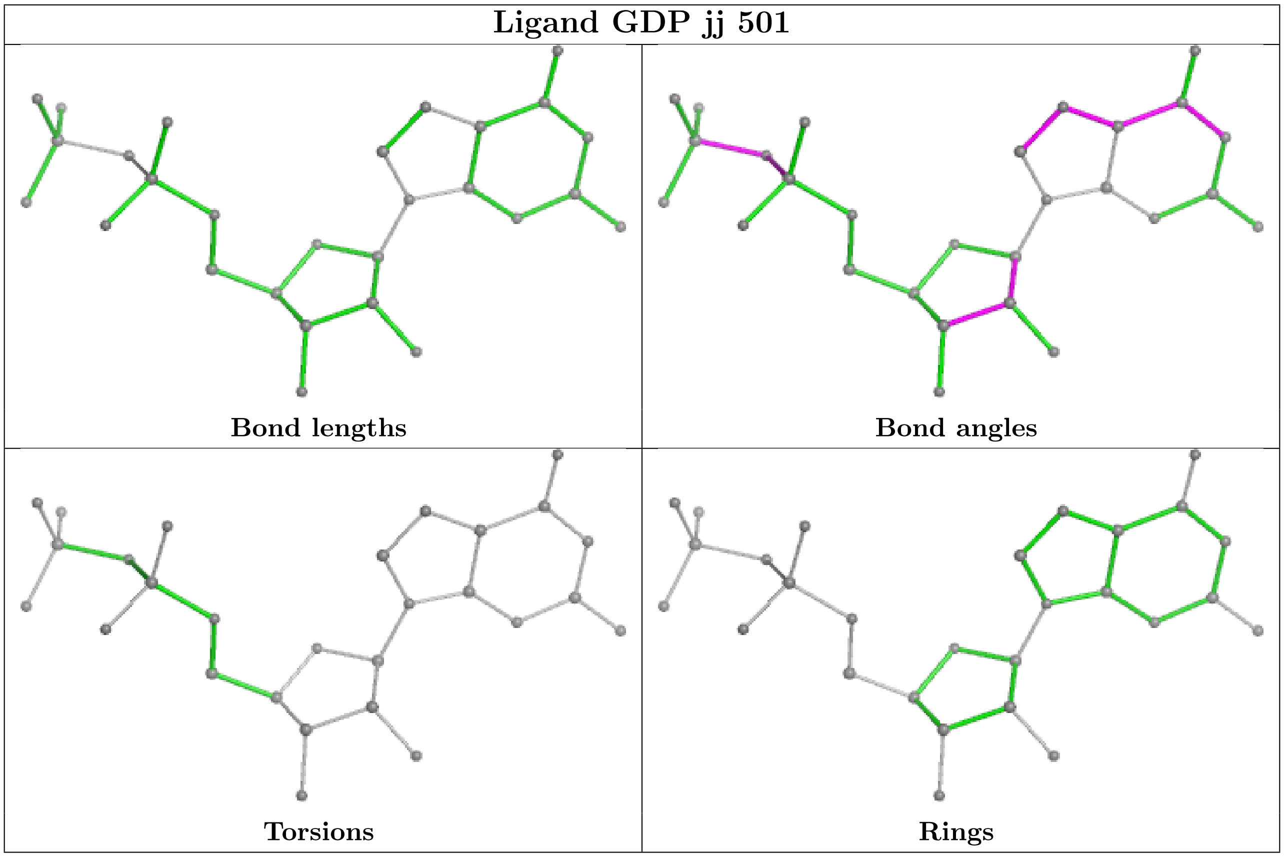
There are no ring outliers.

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 then 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.

Ligand GDP jj 501



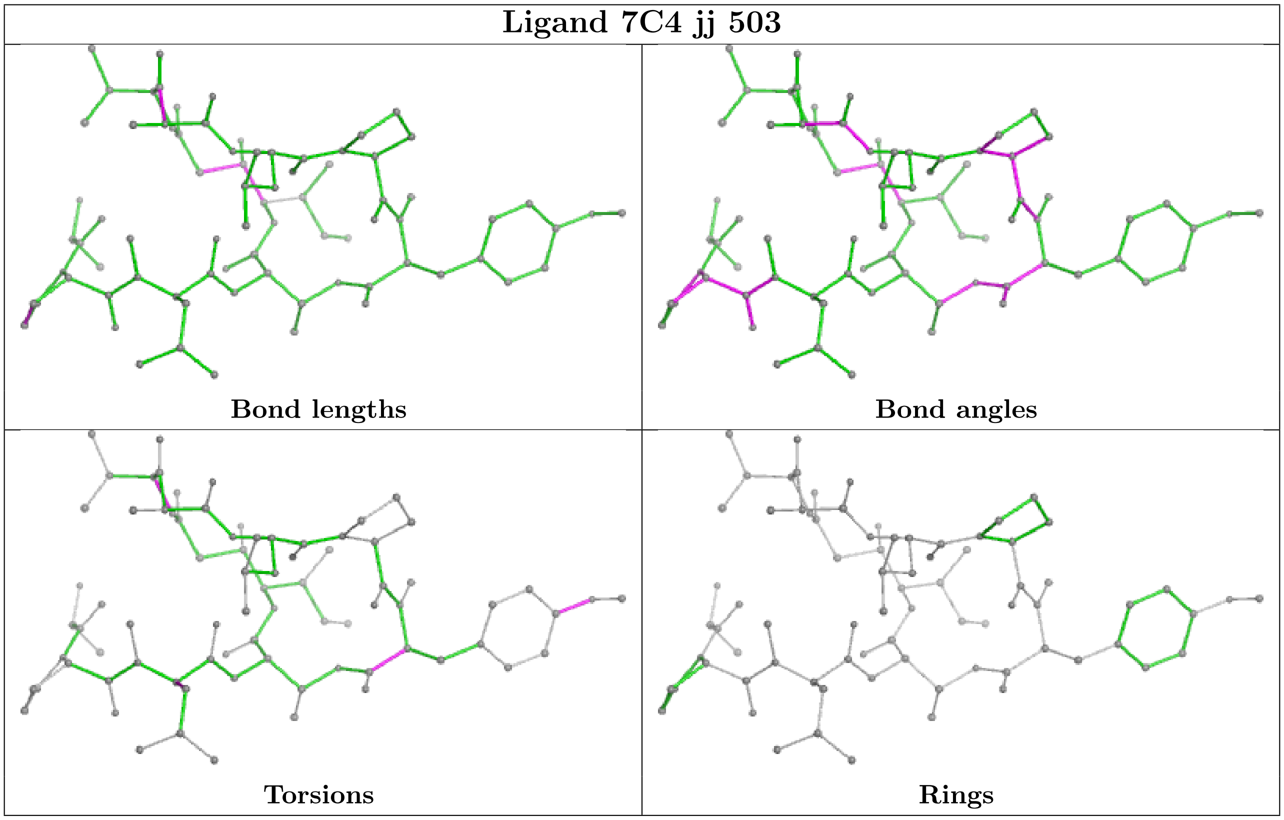
Bond lengths

Bond angles

Torsions

Rings

Ligand 7C4 jj 503



Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	5	31
50	9	7
45	2	3
46	3	2
45	ii	1

The worst 5 of 44 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	41.26
1	5	1252:C	O3’	1271:G	P	36.28
1	5	1219:G	O3’	1233:G	P	22.71
1	5	3948:C	O3’	4065:G	P	19.70
1	5	1406(C):G	O3’	1411:C	P	18.70

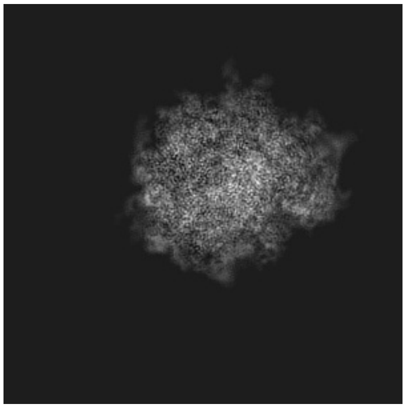
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4130. These allow visual inspection of the internal detail of the map and identification of artifacts.

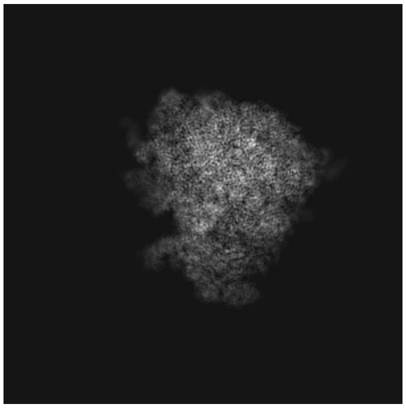
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

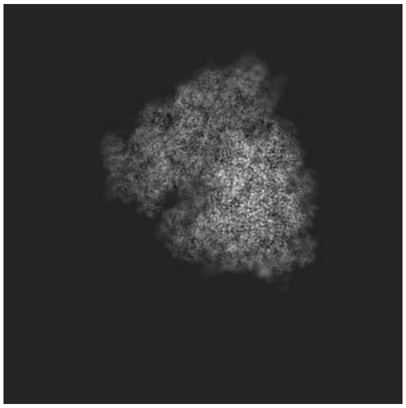
6.1.1 Primary map



X

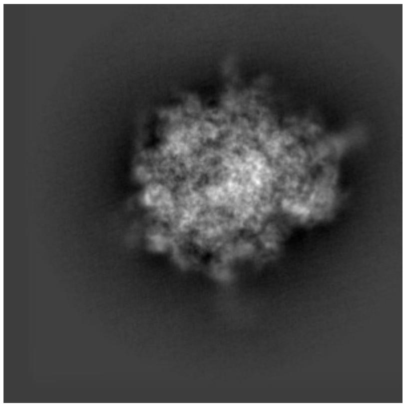


Y

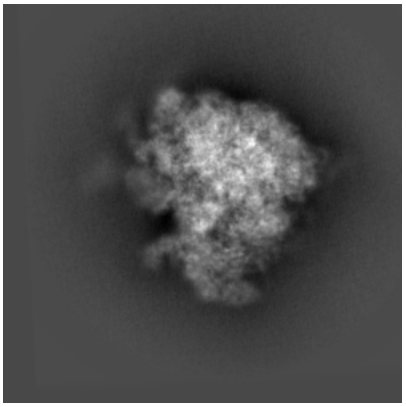


Z

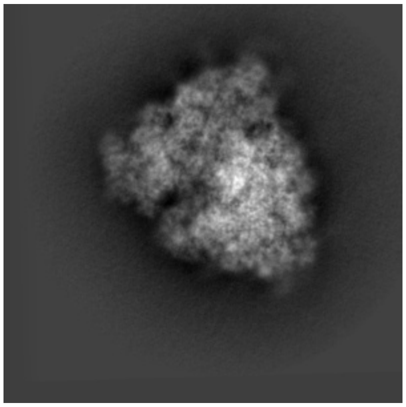
6.1.2 Raw map



X



Y

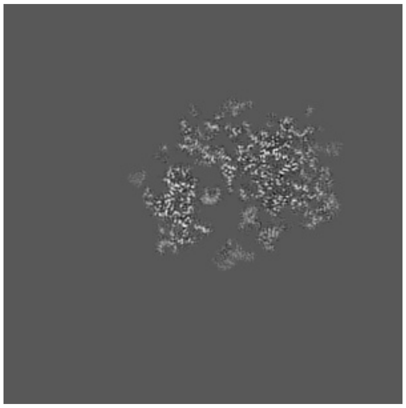


Z

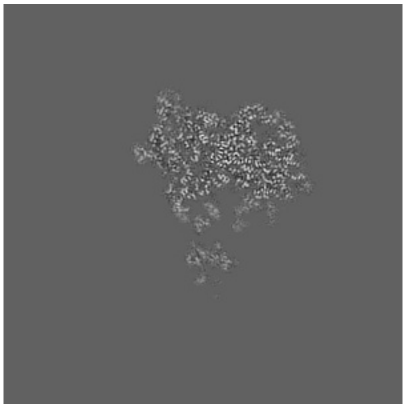
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

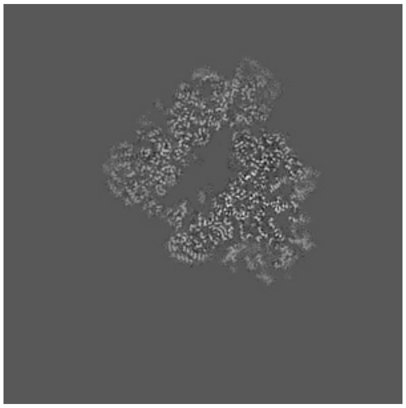
6.2.1 Primary map



X Index: 240

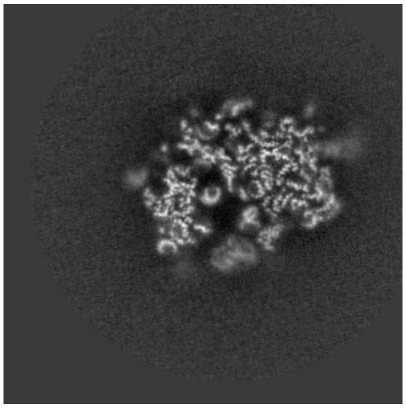


Y Index: 240

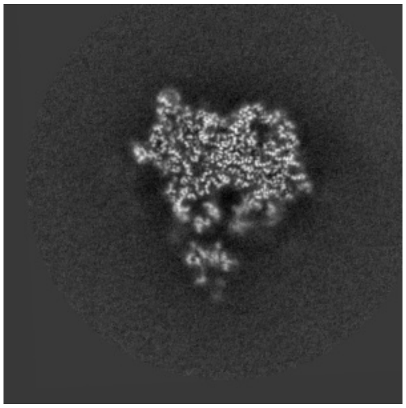


Z Index: 240

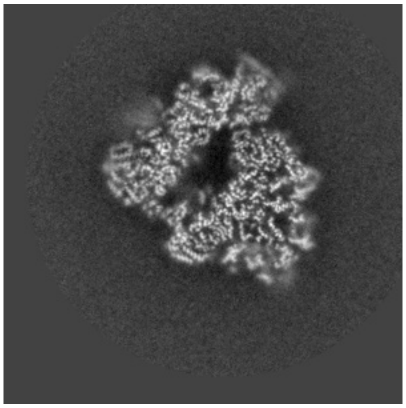
6.2.2 Raw map



X Index: 240



Y Index: 240

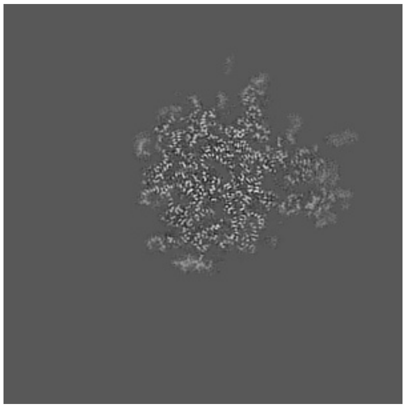


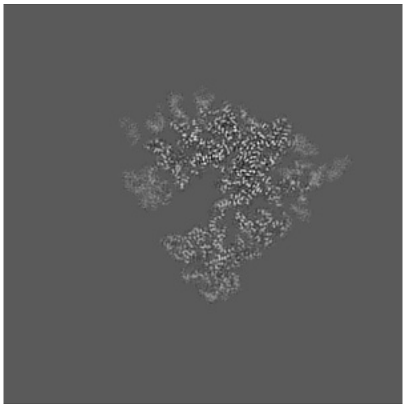
Z Index: 240

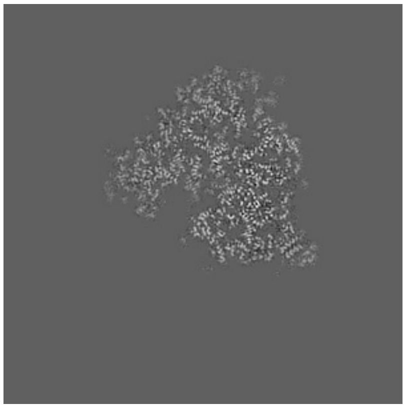
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

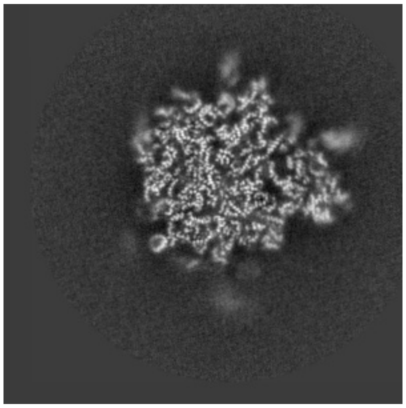
6.3.1 Primary map

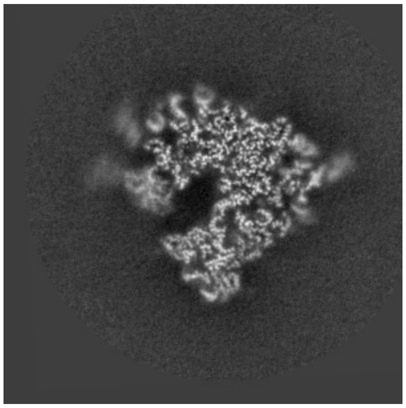

X Index: 294

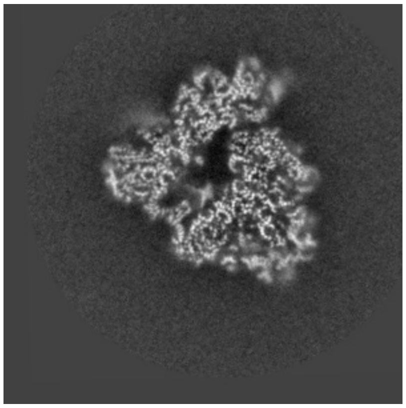

Y Index: 272


Z Index: 261

6.3.2 Raw map


X Index: 287

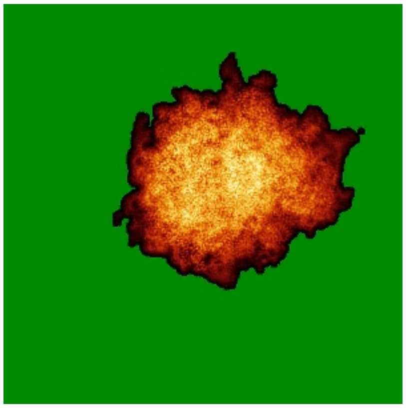

Y Index: 272

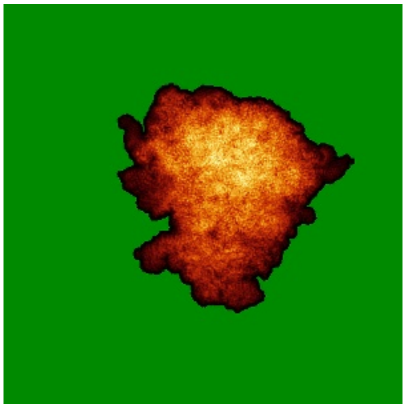

Z Index: 244

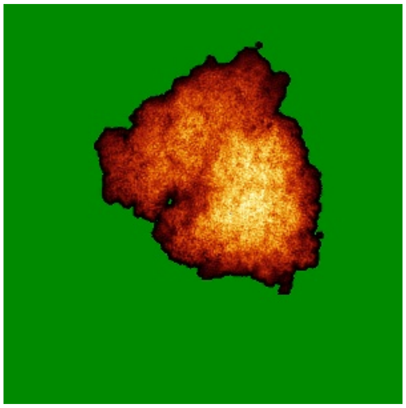
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

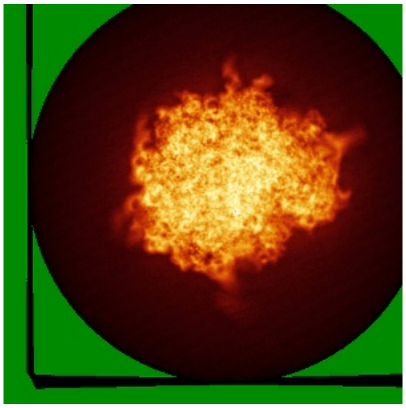
6.4.1 Primary map

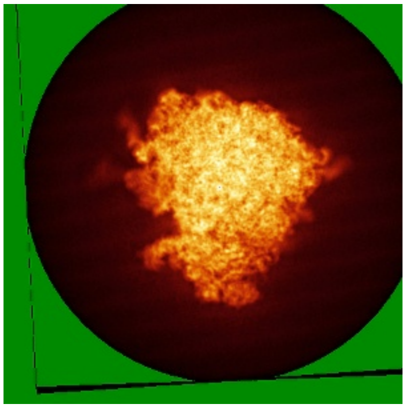

X

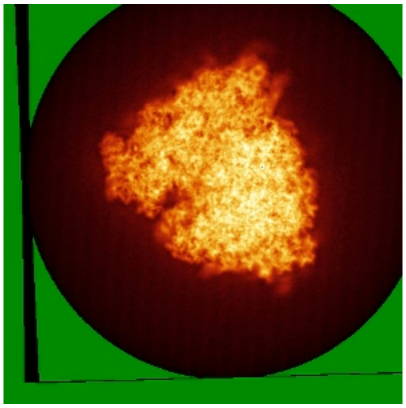

Y


Z

6.4.2 Raw map


X

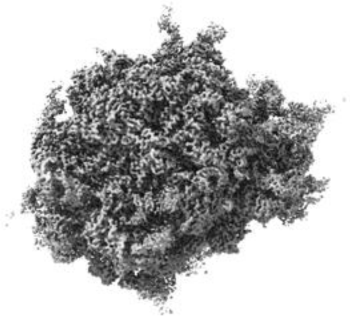

Y


Z

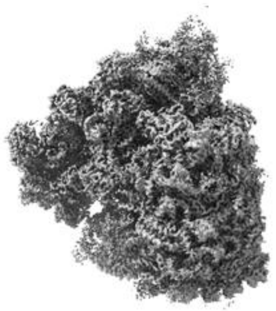
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

6.5.1 Primary map


X


Y


Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. 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


X


Y


Z

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.

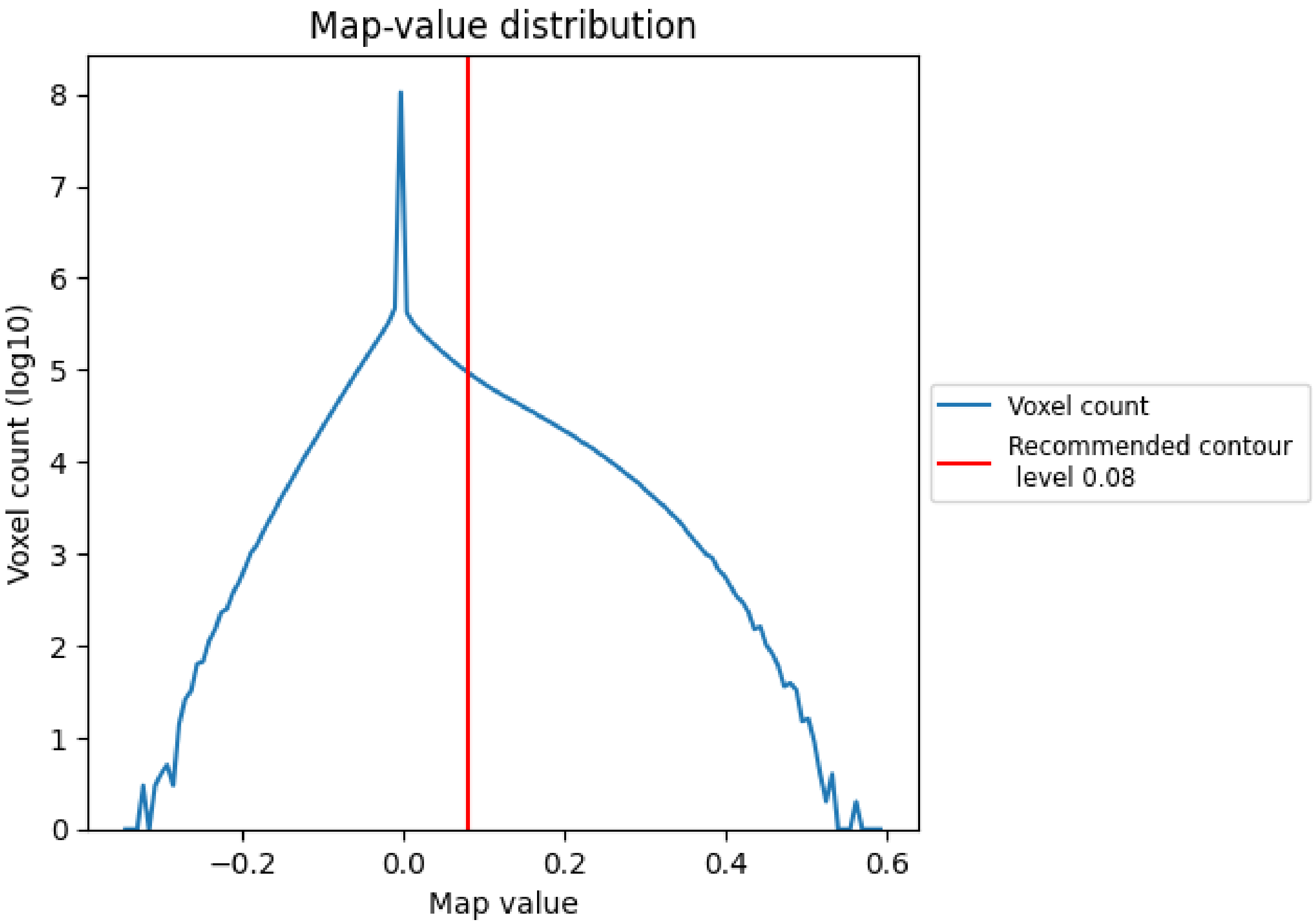
6.6 Mask visualisation

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

7 Map analysis ⓘ

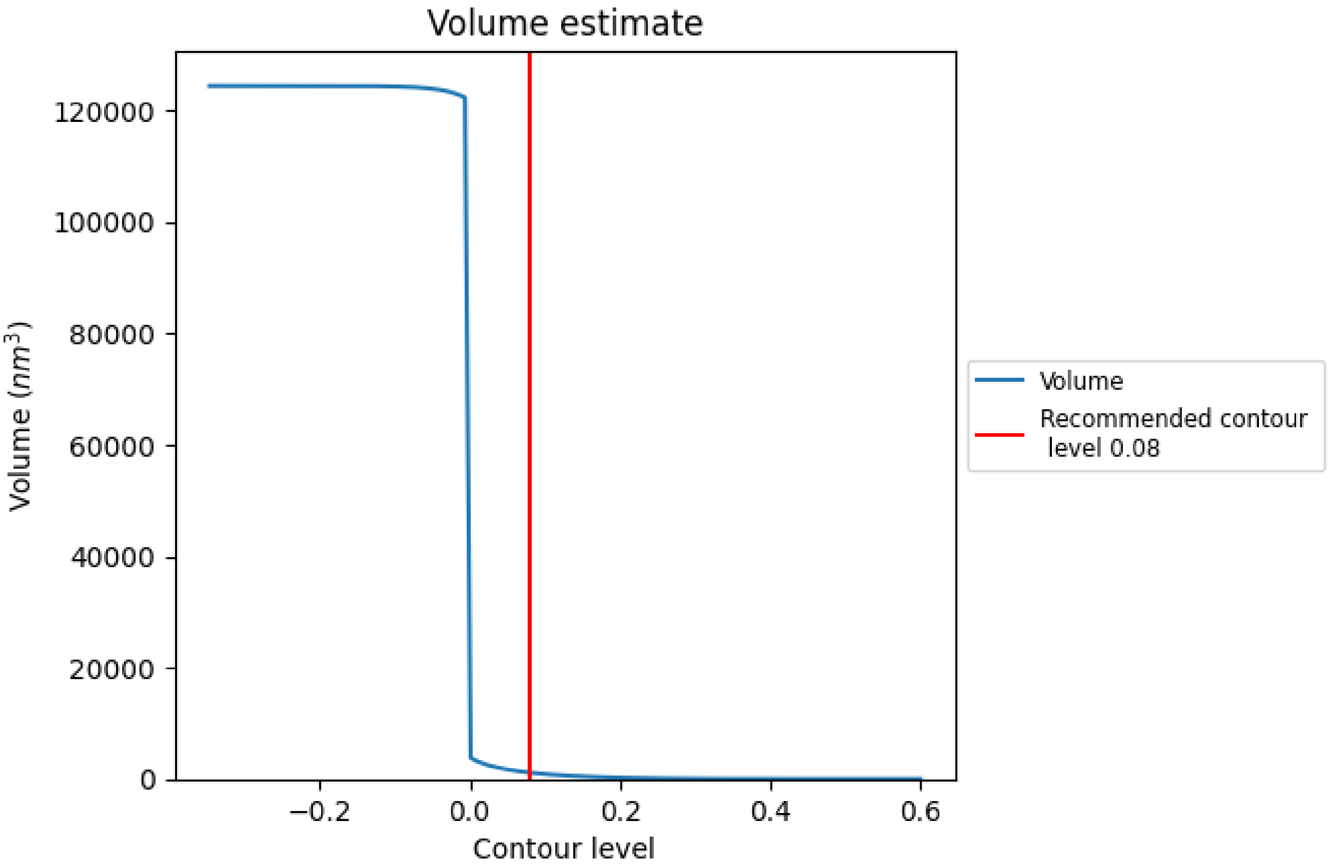
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

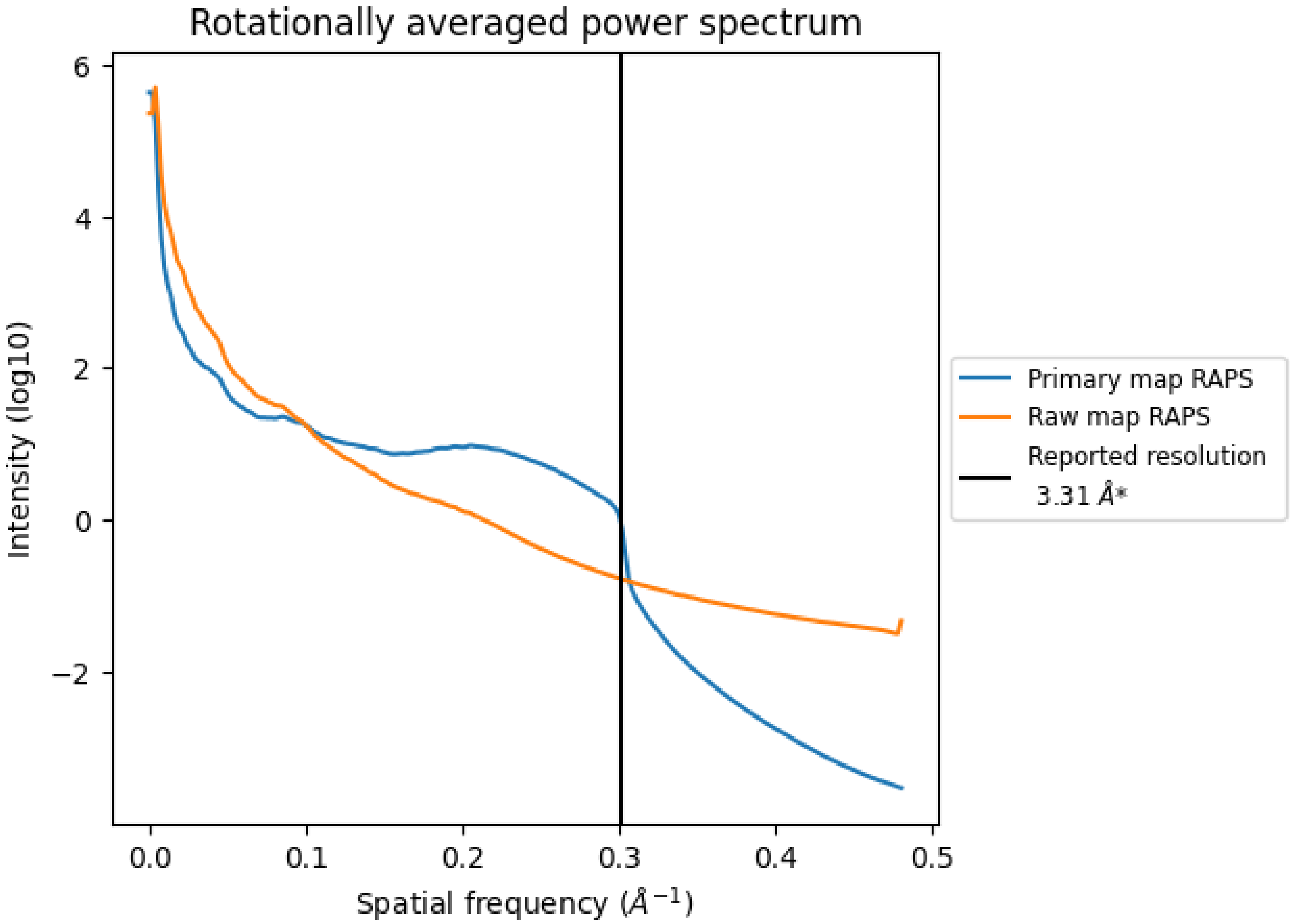
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1143 nm^3; this corresponds to an approximate mass of 1033 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 ⓘ

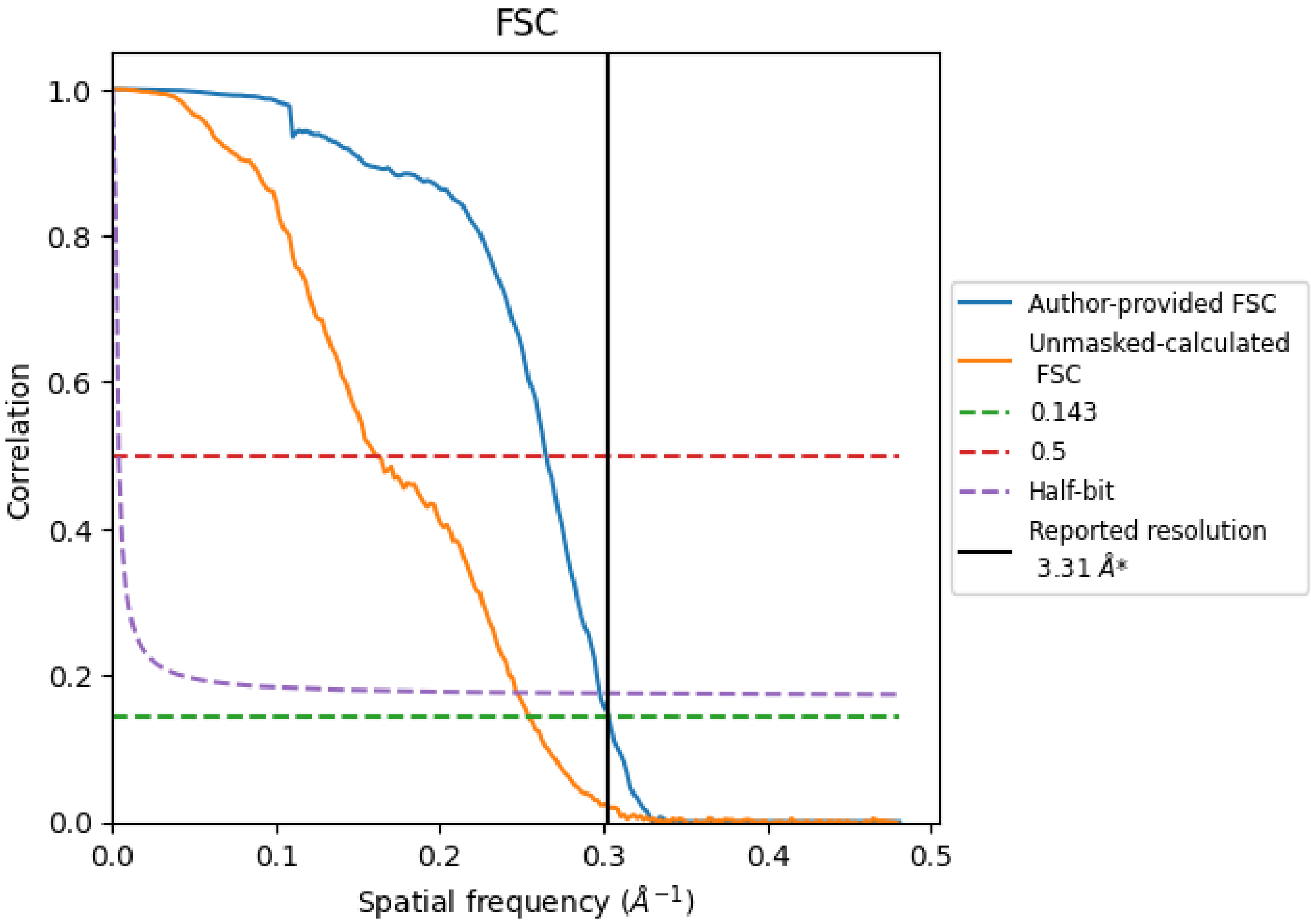


*Reported resolution corresponds to spatial frequency of 0.302 Å^{-1}

8 Fourier-Shell correlation ⓘ

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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.302 $Å^{-1}$

8.2 Resolution estimates ⓘ

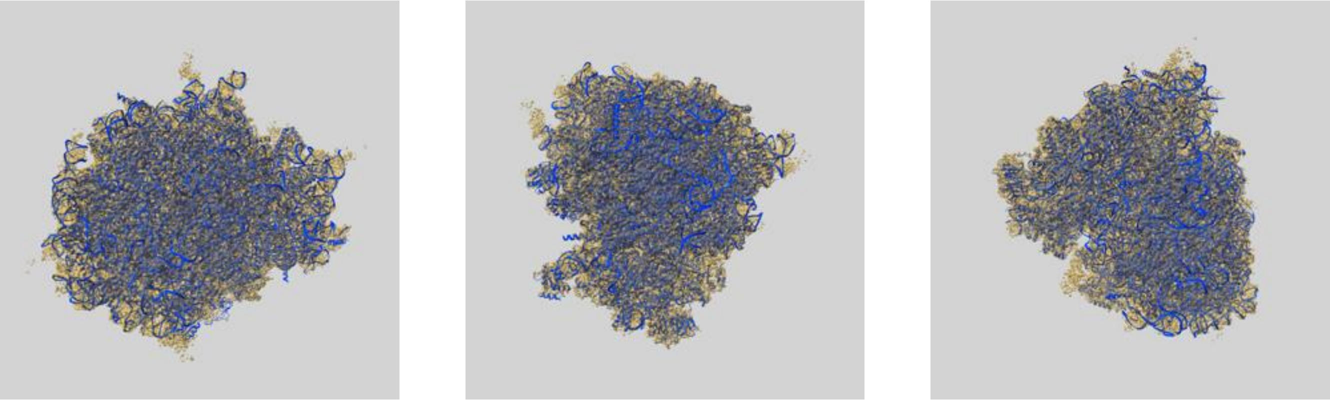
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	3.31	-	-
Author-provided FSC curve	3.30	3.78	3.36
Unmasked-calculated*	3.93	6.20	4.05

*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 3.93 differs from the reported value 3.31 by more than 10 %

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-4130 and PDB model 5LZS. Per-residue inclusion information can be found in section 3 on page 23.

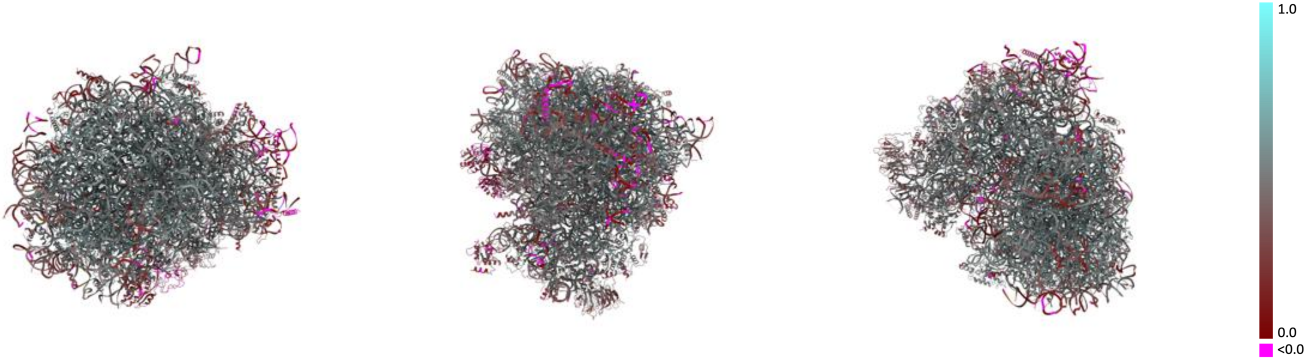
9.1 Map-model overlay ⓘ



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.08 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.

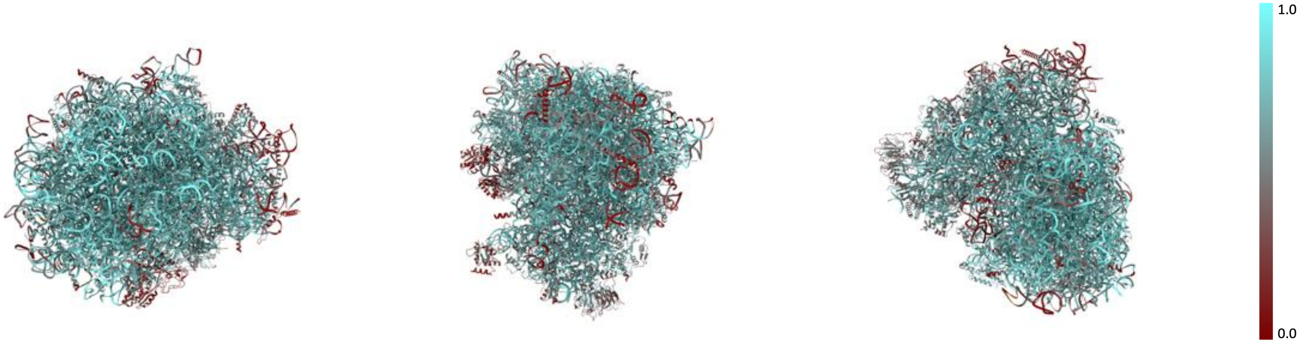
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

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.

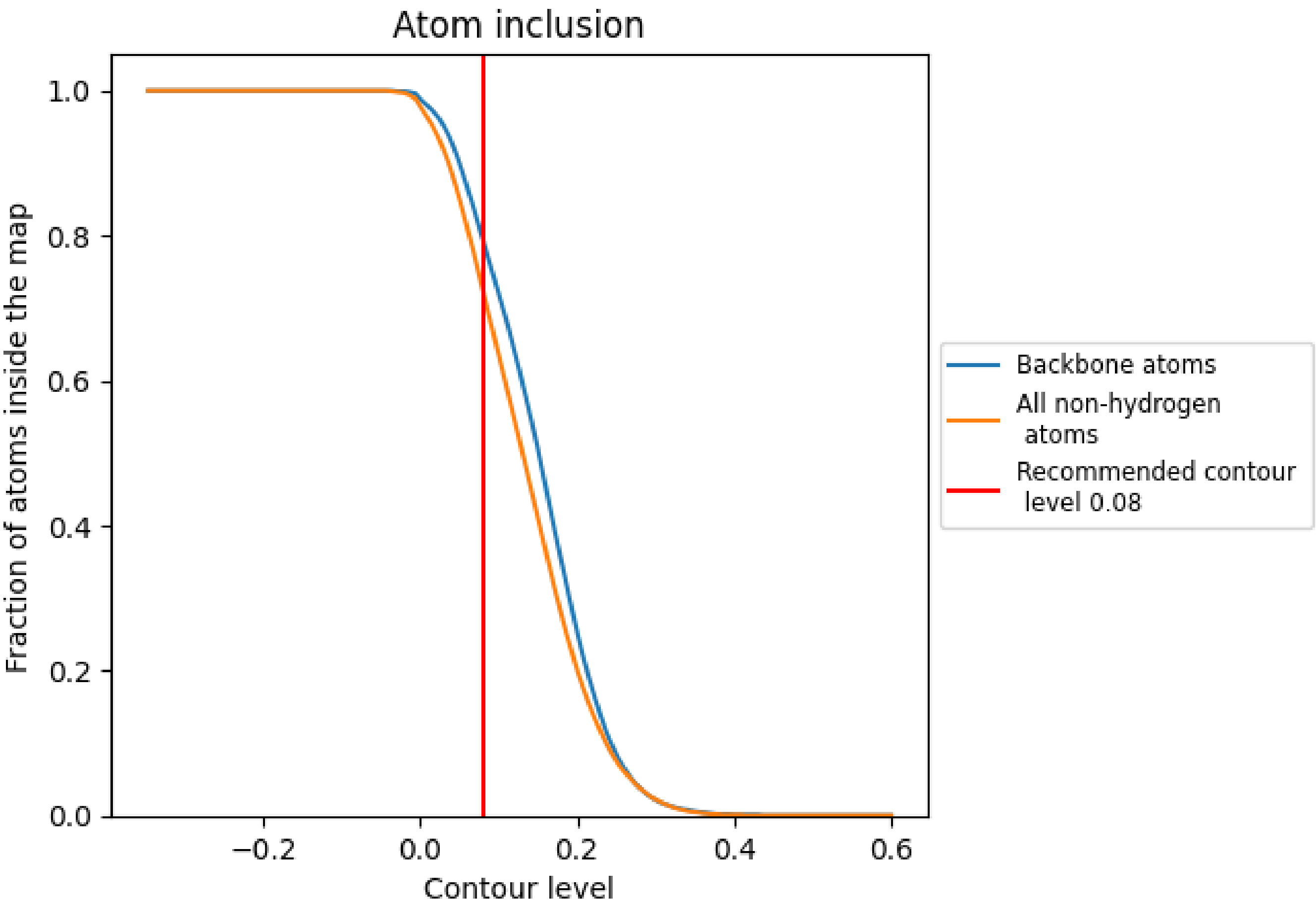
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

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 (0.08).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 72% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	■ 0.7250	■ 0.4620
2	■ 0.6650	■ 0.4170
3	■ 0.1690	■ 0.1890
5	■ 0.8060	■ 0.4770
7	■ 0.9050	■ 0.5270
8	■ 0.8400	■ 0.4910
9	■ 0.7780	■ 0.4560
A	■ 0.7570	■ 0.5370
AA	■ 0.6610	■ 0.4730
B	■ 0.7540	■ 0.5190
BB	■ 0.6360	■ 0.4670
C	■ 0.7520	■ 0.5160
CC	■ 0.6530	■ 0.4790
D	■ 0.7080	■ 0.4770
DD	■ 0.5390	■ 0.4150
E	■ 0.7100	■ 0.4840
EE	■ 0.6040	■ 0.4370
F	■ 0.7510	■ 0.5180
FF	■ 0.6050	■ 0.4390
G	■ 0.6280	■ 0.4380
GG	■ 0.5250	■ 0.3680
H	■ 0.7000	■ 0.4960
HH	■ 0.5240	■ 0.3910
I	■ 0.7310	■ 0.5040
II	■ 0.5800	■ 0.4110
J	■ 0.6230	■ 0.4380
JJ	■ 0.6060	■ 0.4230
KK	■ 0.6080	■ 0.4340
L	■ 0.7030	■ 0.4780
LL	■ 0.6280	■ 0.4650
M	■ 0.7230	■ 0.5010
MM	■ 0.2690	■ 0.1980
N	■ 0.7970	■ 0.5450
NN	■ 0.6860	■ 0.4910
O	■ 0.7550	■ 0.5130

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Chain	Atom inclusion	Q-score
OO	0.6430	0.4810
P	0.7610	0.5240
PP	0.5780	0.4070
Q	0.7480	0.5230
QQ	0.6260	0.4460
R	0.6730	0.4610
RR	0.5670	0.4160
S	0.7760	0.5310
SS	0.5620	0.3940
T	0.7110	0.5010
TT	0.6030	0.4250
U	0.6260	0.4140
UU	0.5180	0.3980
V	0.7030	0.5220
VV	0.6090	0.4710
W	0.4840	0.3220
WW	0.6980	0.5020
X	0.7030	0.4890
XX	0.6770	0.5040
Y	0.7200	0.4950
YY	0.5880	0.4210
Z	0.7180	0.4870
ZZ	0.5090	0.3720
a	0.7750	0.5320
aa	0.6510	0.4840
b	0.5940	0.4180
bb	0.5820	0.4360
c	0.6800	0.4860
cc	0.5490	0.4180
d	0.6930	0.4860
dd	0.7380	0.5010
e	0.7630	0.5350
ee	0.5070	0.3870
f	0.8080	0.5430
ff	0.3200	0.2000
g	0.7070	0.5040
gg	0.4700	0.3590
h	0.6860	0.4900
hh	0.7670	0.4640
i	0.6590	0.4560
ii	0.6790	0.4100
j	0.8040	0.5440

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Chain	Atom inclusion	Q-score
jj	■ 0.6000	■ 0.4490
k	■ 0.5890	■ 0.4140
l	■ 0.7310	■ 0.4960
m	■ 0.7430	■ 0.4970
n	■ 0.6830	■ 0.4480
o	■ 0.7010	■ 0.5140
p	■ 0.6810	■ 0.4840
r	■ 0.7450	■ 0.5140
s	■ 0.1380	■ 0.1250
t	■ 0.0590	■ 0.0750