wwPDB EM Validation Summary Report

Sep 8, 2026 – 06:12 pm BST

PDB ID	:	5LZV / pdb_00005lzv
EMDB ID	:	EMD-4133
Title	:	Structure of the mammalian ribosomal termination complex with accommodated eRF1(AAQ) and ABCE1.
Authors	:	Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on	:	2016-10-02
Resolution	:	3.35 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

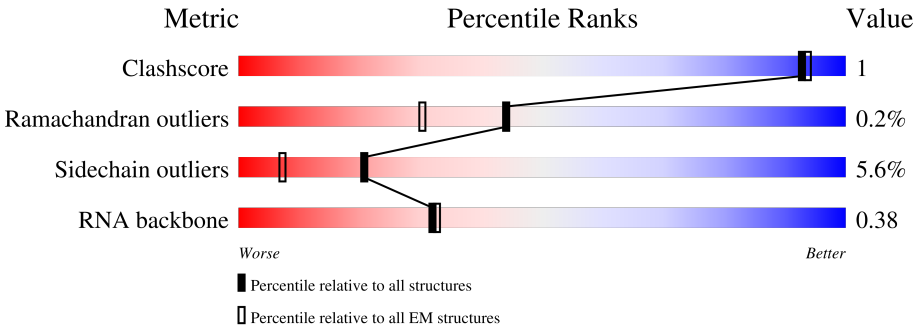
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal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

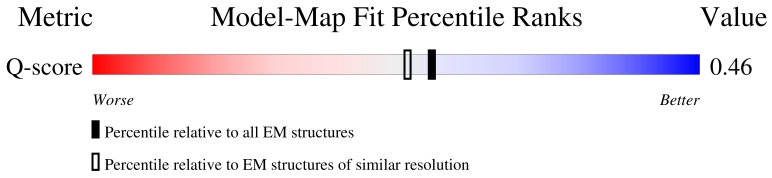
1 Overall quality at a glance

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

The reported resolution of this entry is 3.35 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14390 (2.85 - 3.85)

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	90% 6%
2	B	403	92% 5%
3	C	425	81% 15%

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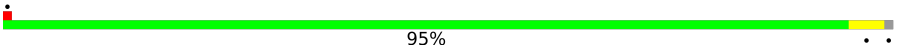
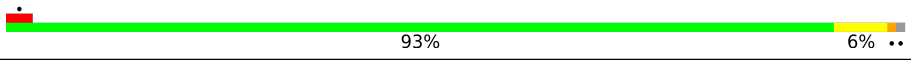
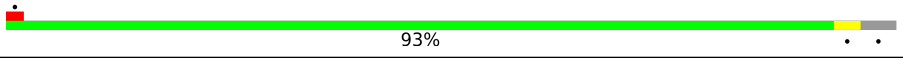
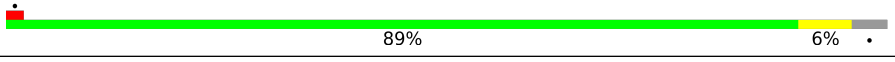
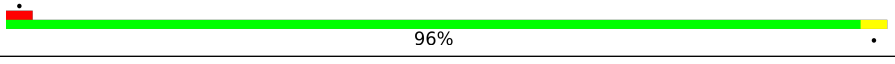
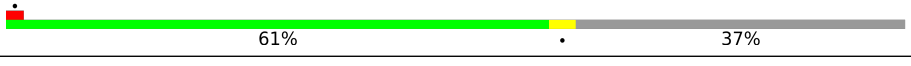
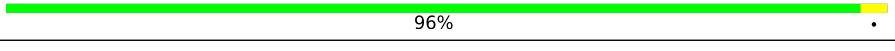
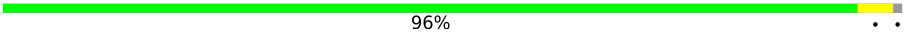
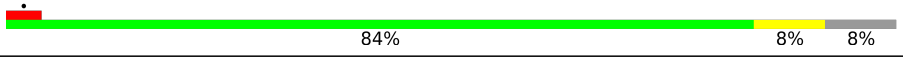
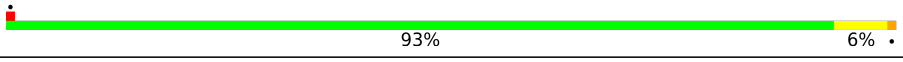
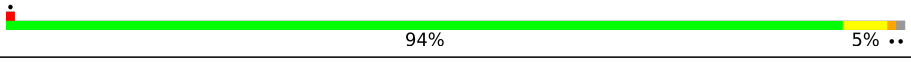
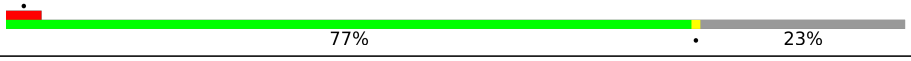
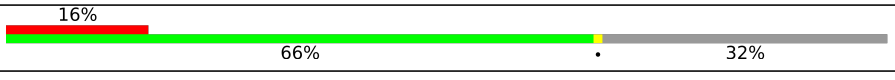
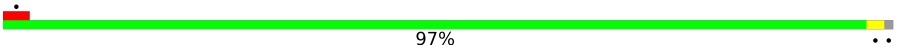
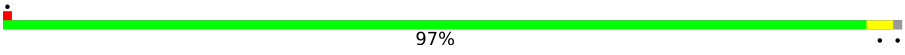
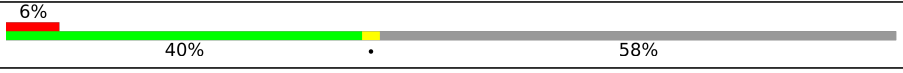
Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	

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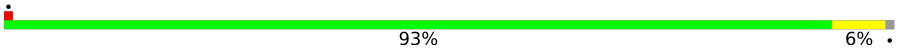
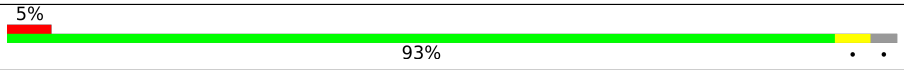
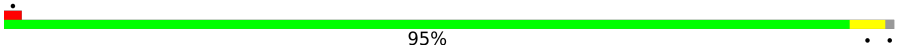
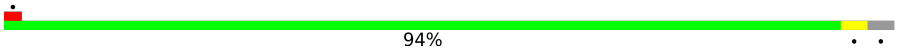
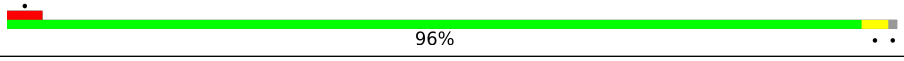
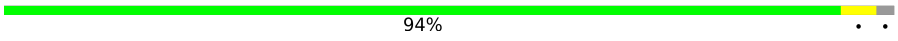
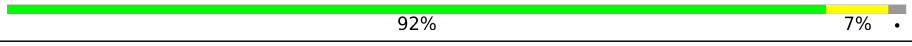
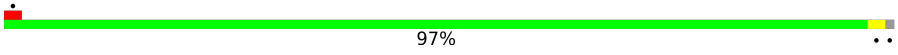
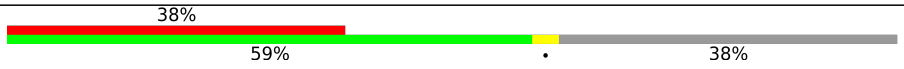
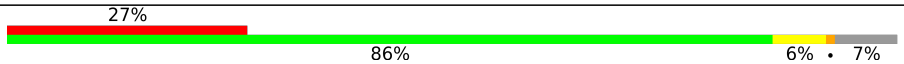
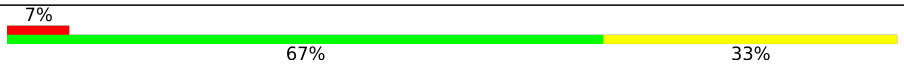
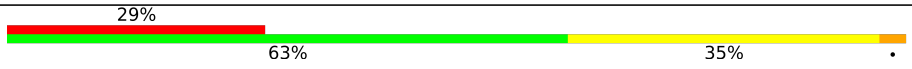
Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	1	15	
46	2	76	
47	3	75	
48	5	3543	
49	7	120	
50	8	156	
51	9	1869	
52	AA	295	
53	BB	264	

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Mol	Chain	Length	Quality of chain
54	CC	293	66% 9% 25%
55	DD	243	6% 84% 9% 6%
56	EE	263	86% 13%
57	FF	204	79% 10% 9%
58	GG	249	11% 87% 6% 5%
59	HH	194	10% 85% 10% 5%
60	II	208	7% 88% 10%
61	JJ	194	85% 10% 5%
62	KK	165	47% 9% 42%
63	LL	158	78% 12% 9%
64	MM	132	42% 66% 17% 6% 11%
65	NN	151	89% 9%
66	OO	168	69% 12% 19%
67	PP	145	71% 10% 17%
68	QQ	146	85% 12%
69	RR	135	90% 7%
70	SS	152	83% 11% 5%
71	TT	145	88% 8%
72	UU	119	7% 76% 8% 16%
73	VV	83	94%
74	WW	130	87% 12%
75	XX	143	87% 10%
76	YY	130	83% 12% 5%
77	ZZ	125	5% 54% 6% 40%
78	aa	115	77% 11% 12%

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Mol	Chain	Length	Quality of chain
79	bb	84	8% 92% 6%
80	cc	69	7% 81% 9% 10%
81	dd	56	96%
82	ee	133	5% 38% 59%
83	ff	156	16% 33% 9% 56%
84	gg	317	6% 91% 7%
85	hh	15	13% 47% 53%
86	ii	459	19% 81% 10% 9%
87	jj	599	14% 89% 7%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
89	ZN	ff	200	-	-	X	-

2 Entry composition (i)

There are 90 unique types of molecules in this entry. The entry contains 223874 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
1	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a protein called uL4.

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

- Molecule 4 is a protein called uL18.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 5 is a protein called eL6.

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

- Molecule 6 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 7 is a protein called eL8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 8 is a protein called uL6.

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

- Molecule 9 is a protein called uL16.

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

- Molecule 10 is a protein called 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 eL15.

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
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

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

- Molecule 26 is a protein called uL15.

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

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
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	117	LYS	-	insertion	UNP G1U945

- Molecule 33 is a protein called uL29.

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

- Molecule 34 is a protein called eL36.

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

- Molecule 35 is a protein called eL37.

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

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called uL10.

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

- Molecule 44 is a protein called uL11.

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

- Molecule 45 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 47 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 51 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 52 is a protein called uS2.

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

- Molecule 53 is a protein called eS1.

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

- Molecule 54 is a protein called uS5.

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

- Molecule 55 is a protein called uS3.

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

- Molecule 56 is a protein called eS4.

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

- Molecule 57 is a protein called uS7.

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

- Molecule 58 is a protein called eS6.

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

- Molecule 59 is a protein called eS7.

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

- Molecule 60 is a protein called eS8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 61 is a protein called uS4.

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

- Molecule 62 is a protein called eS10.

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

- Molecule 63 is a protein called uS17.

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

- Molecule 64 is a protein called eS12.

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

- Molecule 65 is a protein called uS15.

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

- Molecule 66 is a protein called uS11.

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

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

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

- Molecule 70 is a protein called uS13.

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

- Molecule 71 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called eS21.

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

- Molecule 74 is a protein called uS8.

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

- Molecule 75 is a protein called uS12.

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

- Molecule 76 is a protein called eS24.

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

- Molecule 77 is a protein called eS25.

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

- Molecule 78 is a protein called eS26.

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

- Molecule 79 is a protein called eS27.

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

- Molecule 80 is a protein called eS28.

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

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 83 is a protein called eS31.

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

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a RNA chain called mRNA (UGA stop codon).

Mol	Chain	Residues	Atoms					AltConf	Trace
85	hh	15	Total	C	N	O	P	0	0
			317	142	54	106	15		

- Molecule 86 is a protein called eRF1(AAQ).

Mol	Chain	Residues	Atoms					AltConf	Trace
86	ii	419	Total	C	N	O	S	0	0
			3309	2106	562	629	12		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	-21	MET	-	initiating methionine	UNP P62495
ii	-20	ARG	-	expression tag	UNP P62495
ii	-19	GLY	-	expression tag	UNP P62495
ii	-18	SER	-	expression tag	UNP P62495
ii	-17	HIS	-	expression tag	UNP P62495
ii	-16	HIS	-	expression tag	UNP P62495
ii	-15	HIS	-	expression tag	UNP P62495
ii	-14	HIS	-	expression tag	UNP P62495
ii	-13	HIS	-	expression tag	UNP P62495
ii	-12	HIS	-	expression tag	UNP P62495
ii	-11	GLY	-	expression tag	UNP P62495
ii	-10	MET	-	expression tag	UNP P62495
ii	-9	ALA	-	expression tag	UNP P62495
ii	-8	SER	-	expression tag	UNP P62495
ii	-7	GLU	-	expression tag	UNP P62495
ii	-6	ASN	-	expression tag	UNP P62495
ii	-5	LEU	-	expression tag	UNP P62495
ii	-4	TYR	-	expression tag	UNP P62495
ii	-3	PHE	-	expression tag	UNP P62495

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Chain	Residue	Modelled	Actual	Comment	Reference
ii	-2	GLN	-	expression tag	UNP P62495
ii	-1	GLY	-	expression tag	UNP P62495
ii	0	SER	-	expression tag	UNP P62495
ii	183	ALA	GLY	conflict	UNP P62495
ii	184	ALA	GLY	conflict	UNP P62495

- Molecule 87 is a protein called ABCE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	jj	577	Total	C	N	O	S	0	0
			4555	2914	780	830	31		

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	B	1	Total	Mg	0
			1	1	
88	I	1	Total	Mg	0
			1	1	
88	L	1	Total	Mg	0
			1	1	
88	P	1	Total	Mg	0
			1	1	
88	Q	1	Total	Mg	0
			1	1	
88	V	1	Total	Mg	0
			1	1	
88	a	2	Total	Mg	0
			2	2	
88	e	1	Total	Mg	0
			1	1	
88	g	1	Total	Mg	0
			1	1	
88	j	1	Total	Mg	0
			1	1	
88	5	197	Total	Mg	0
			197	197	
88	7	7	Total	Mg	0
			7	7	
88	8	5	Total	Mg	0
			5	5	
88	9	79	Total	Mg	0
			79	79	

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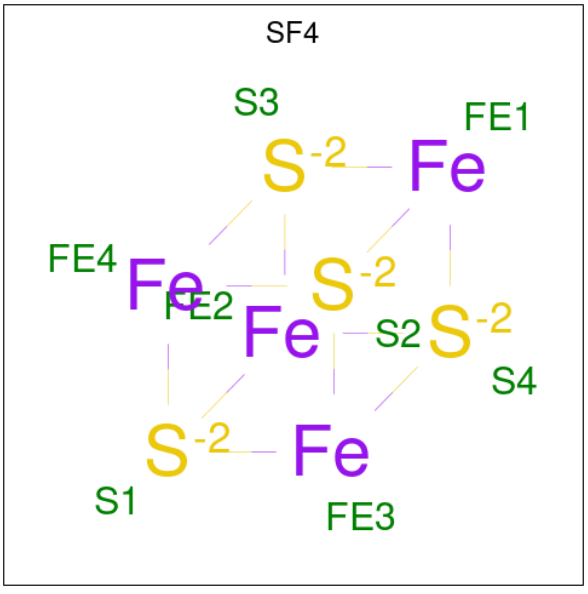
Mol	Chain	Residues	Atoms	AltConf
88	hh	1	Total Mg 1 1	0

- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 90 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



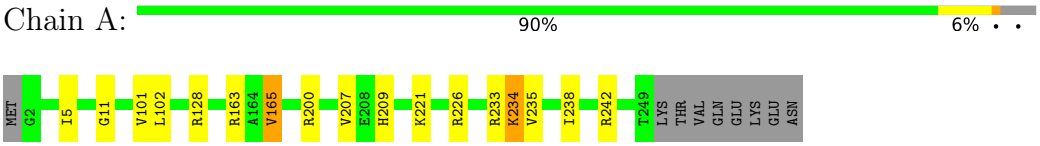
Mol	Chain	Residues	Atoms			AltConf
90	jj	1	Total 8	Fe 4	S 4	0
90	jj	1	Total 8	Fe 4	S 4	0

3 Residue-property plots (i)

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.

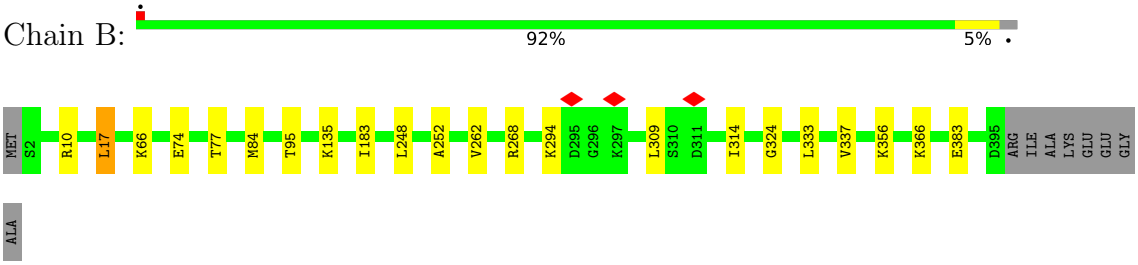
- Molecule 1: uL2

Chain A:



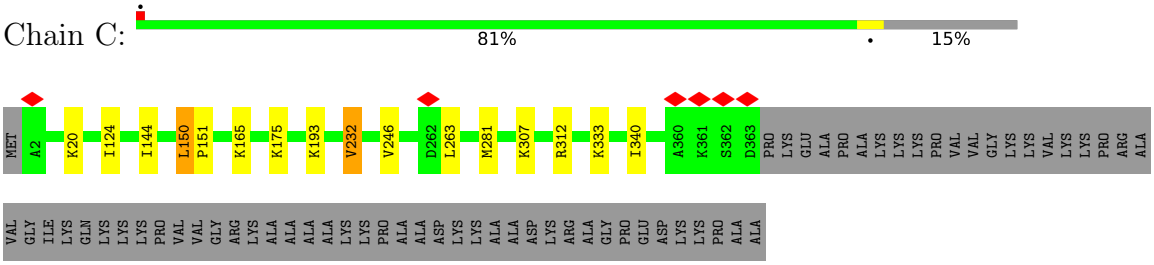
- Molecule 2: uL3

Chain B:



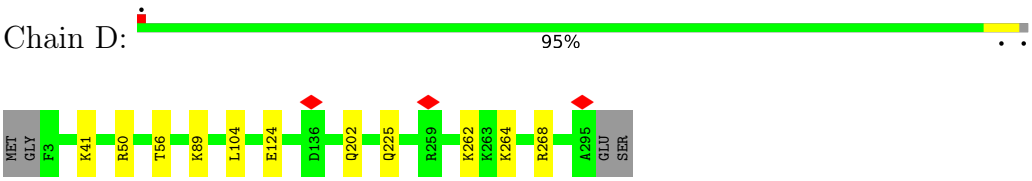
- Molecule 3: uL4

Chain C:



- Molecule 4: uL18

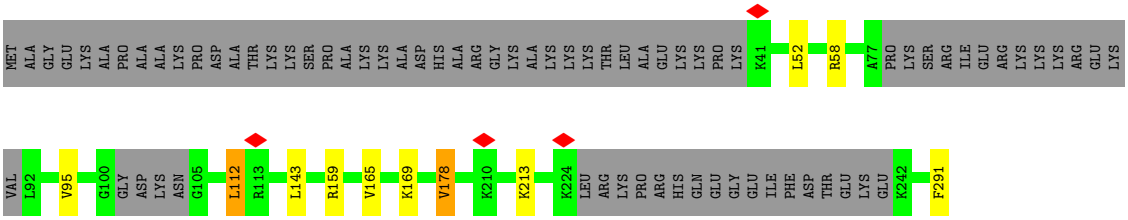
Chain D:



- Molecule 5: eL6

Chain E:

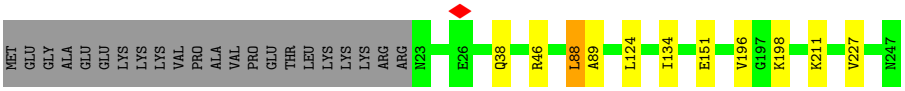




• Molecule 6: uL30

Chain F:

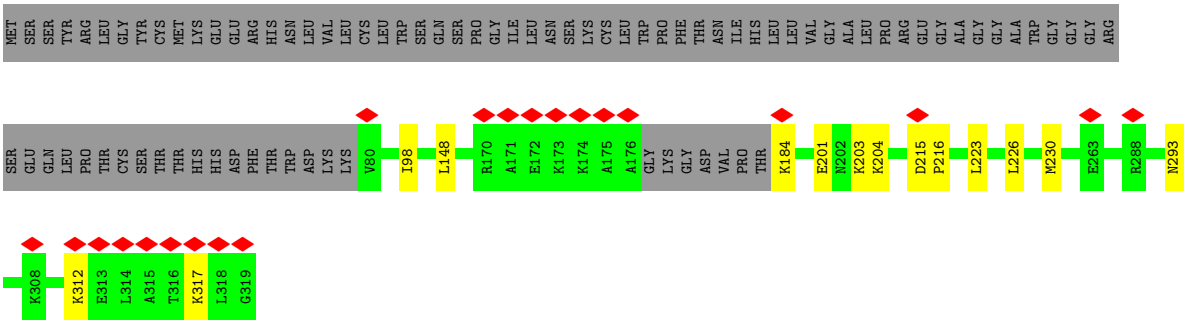




• Molecule 7: eL8

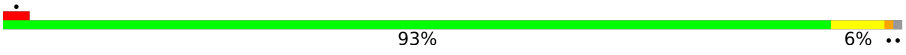
Chain G:

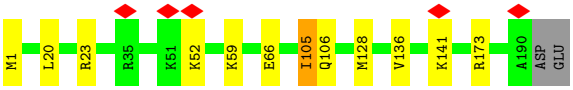




• Molecule 8: uL6

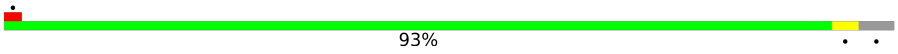
Chain H:

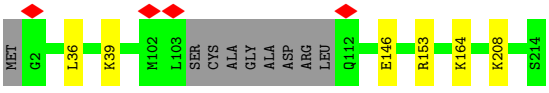




• Molecule 9: uL16

Chain I:

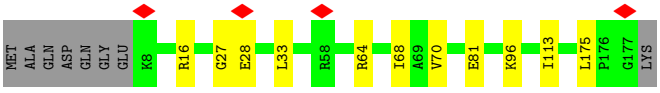




• Molecule 10: uL5

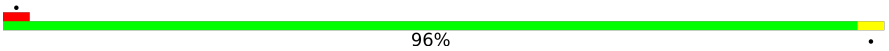
Chain J:

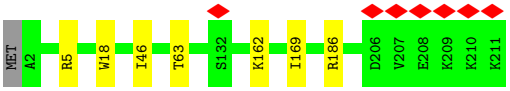




• Molecule 11: eL13

Chain L:

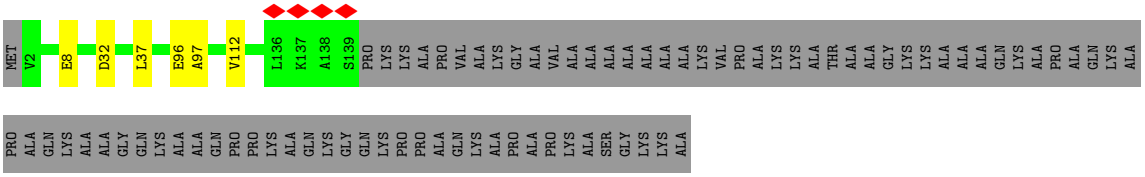




• Molecule 12: eL14

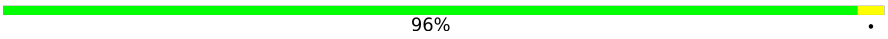
Chain M:





• Molecule 13: eL15

Chain N:

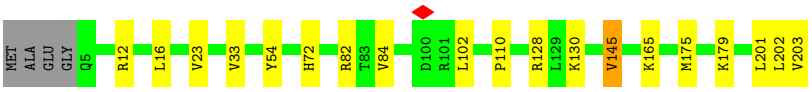




• Molecule 14: uL13

Chain O:

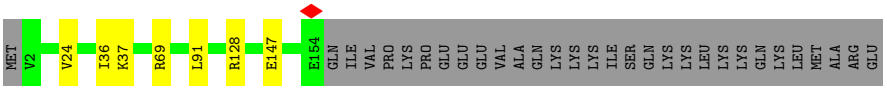




• Molecule 15: uL22

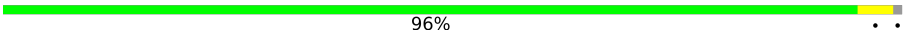
Chain P:





• Molecule 16: eL18

Chain Q:

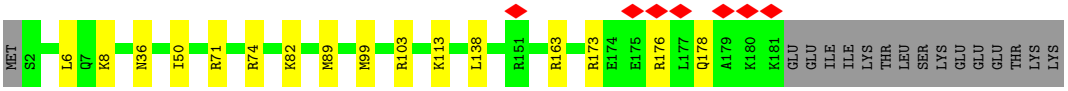




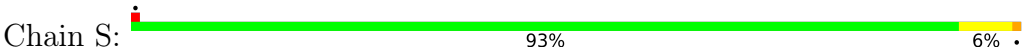
• Molecule 17: eL19

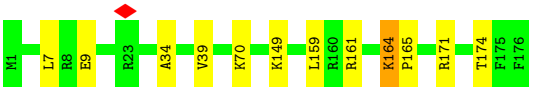
Chain R:



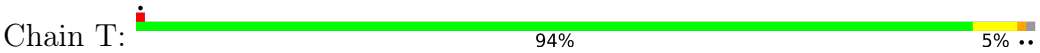


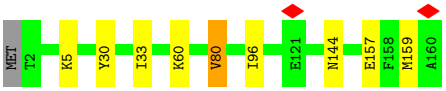
• Molecule 18: eL20





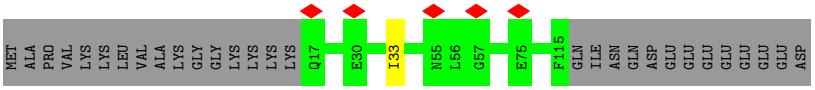
• Molecule 19: eL21



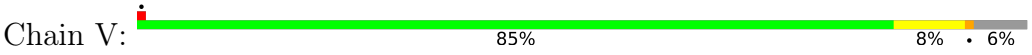


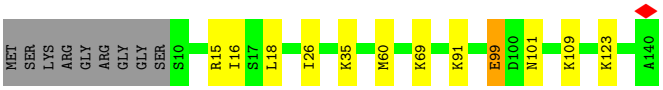
• Molecule 20: eL22





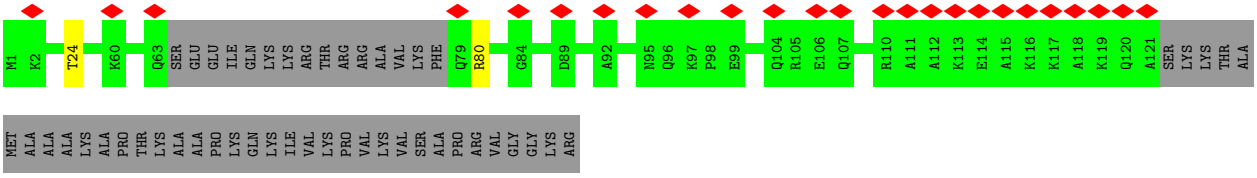
• Molecule 21: uL14





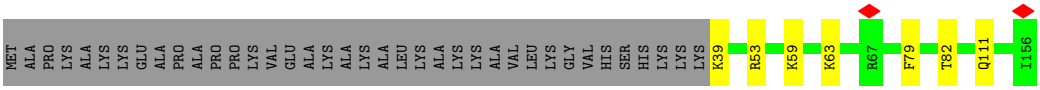
• Molecule 22: eL24





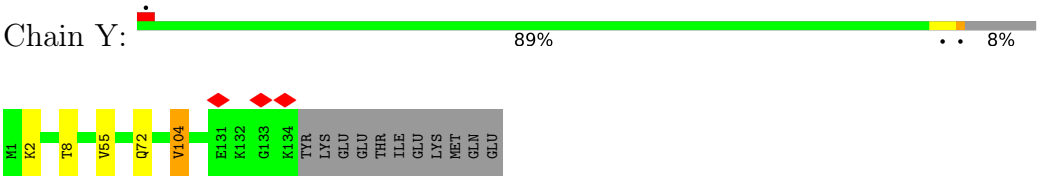
• Molecule 23: uL23





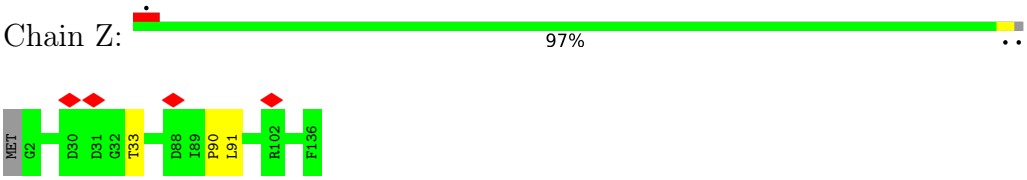
• Molecule 24: uL24

Chain Y:



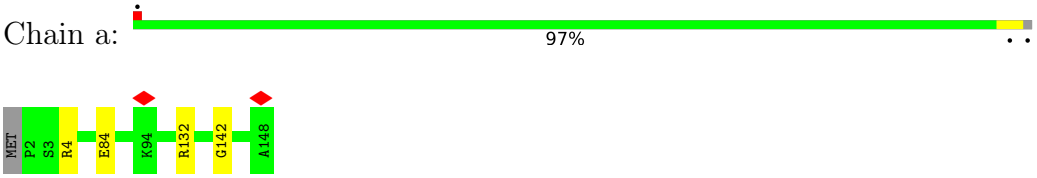
• Molecule 25: eL27

Chain Z:



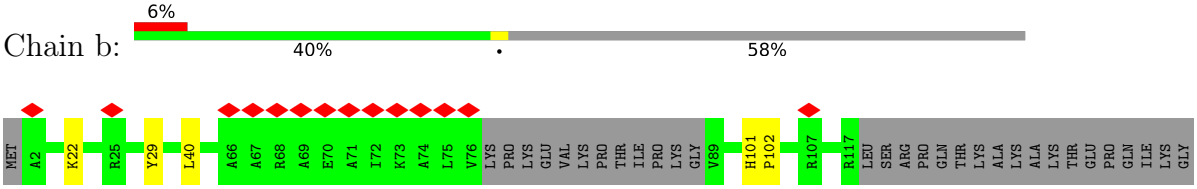
• Molecule 26: uL15

Chain a:



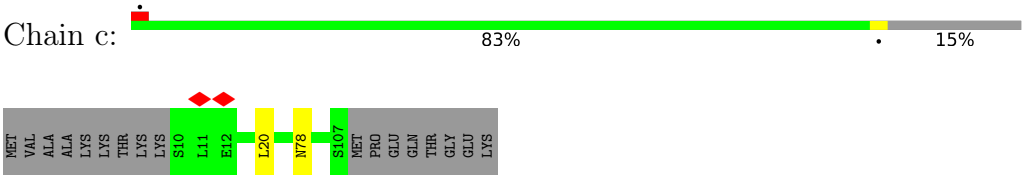
• Molecule 27: eL29

Chain b:



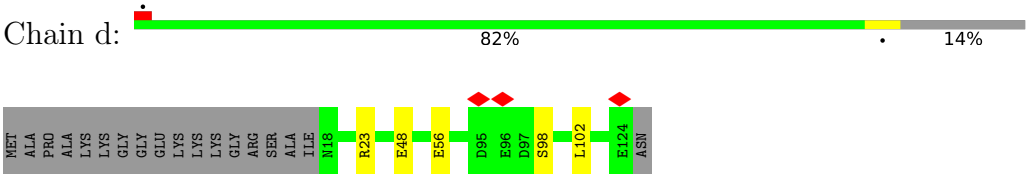
• Molecule 28: eL30

Chain c:



• Molecule 29: eL31

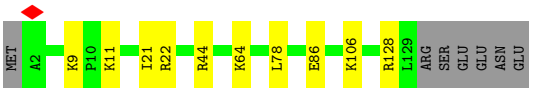
Chain d:



• Molecule 30: eL32

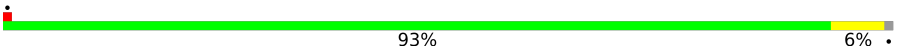
Chain e:





• Molecule 31: eL33

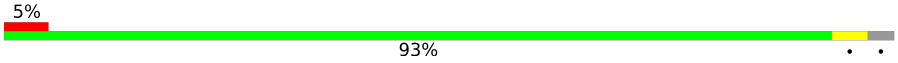
Chain f:

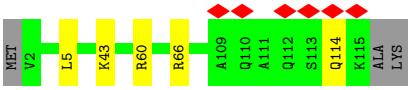




• Molecule 32: eL34

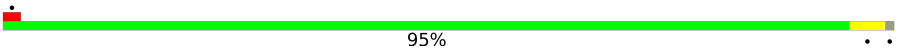
Chain g:

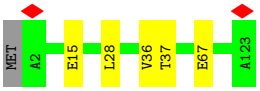




• Molecule 33: uL29

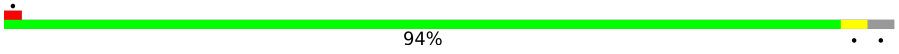
Chain h:

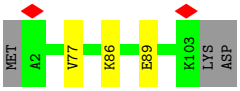




• Molecule 34: eL36

Chain i:

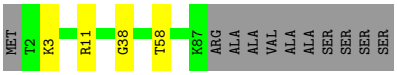




• Molecule 35: eL37

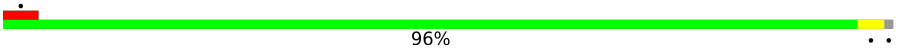
Chain j:

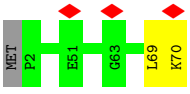




• Molecule 36: eL38

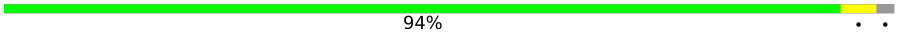
Chain k:

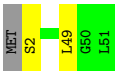




• Molecule 37: eL39

Chain l:

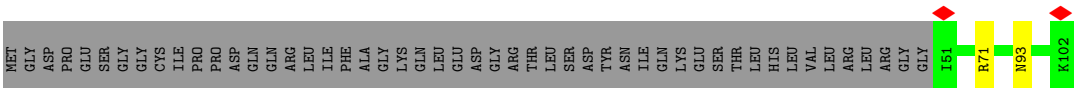




• Molecule 38: eL40

Chain m:





• Molecule 39: eL41

Chain n:





• Molecule 40: eL42

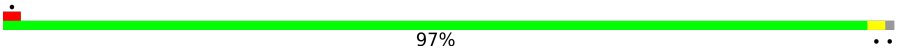
Chain o:

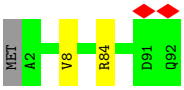




• Molecule 41: eL43

Chain p:

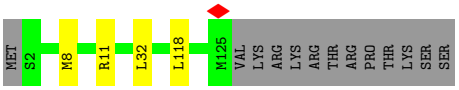




• Molecule 42: eL28

Chain r:

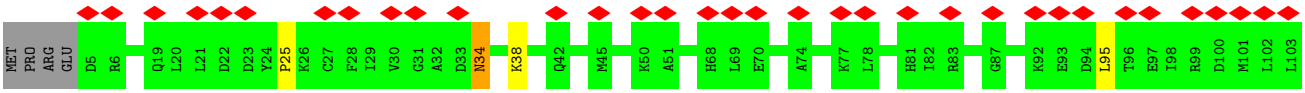


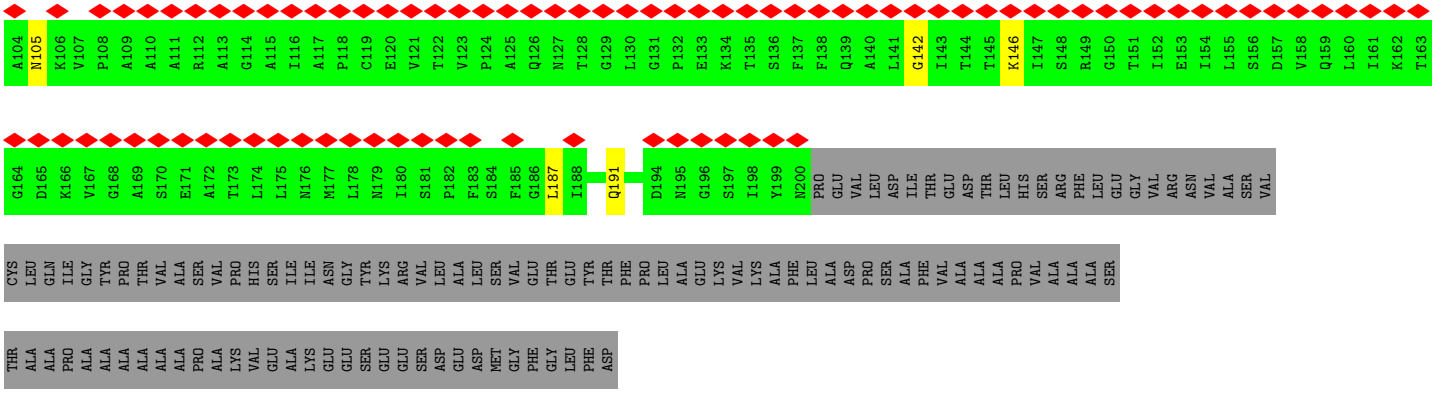


• Molecule 43: uL10

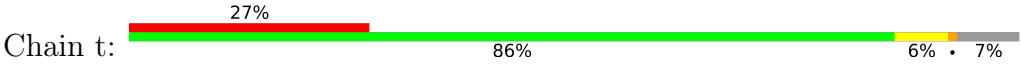
Chain s:

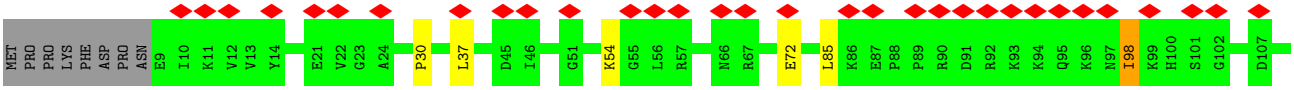


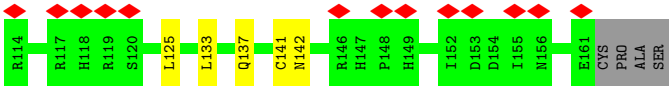




• Molecule 44: uL11

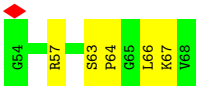






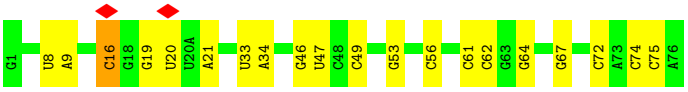
• Molecule 45: Nascent chain





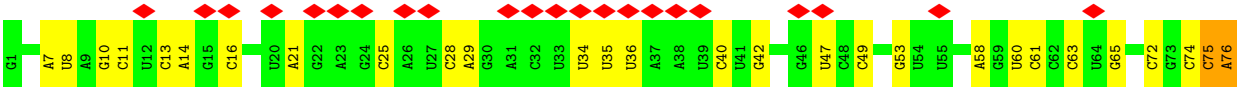
• Molecule 46: P-site tRNA





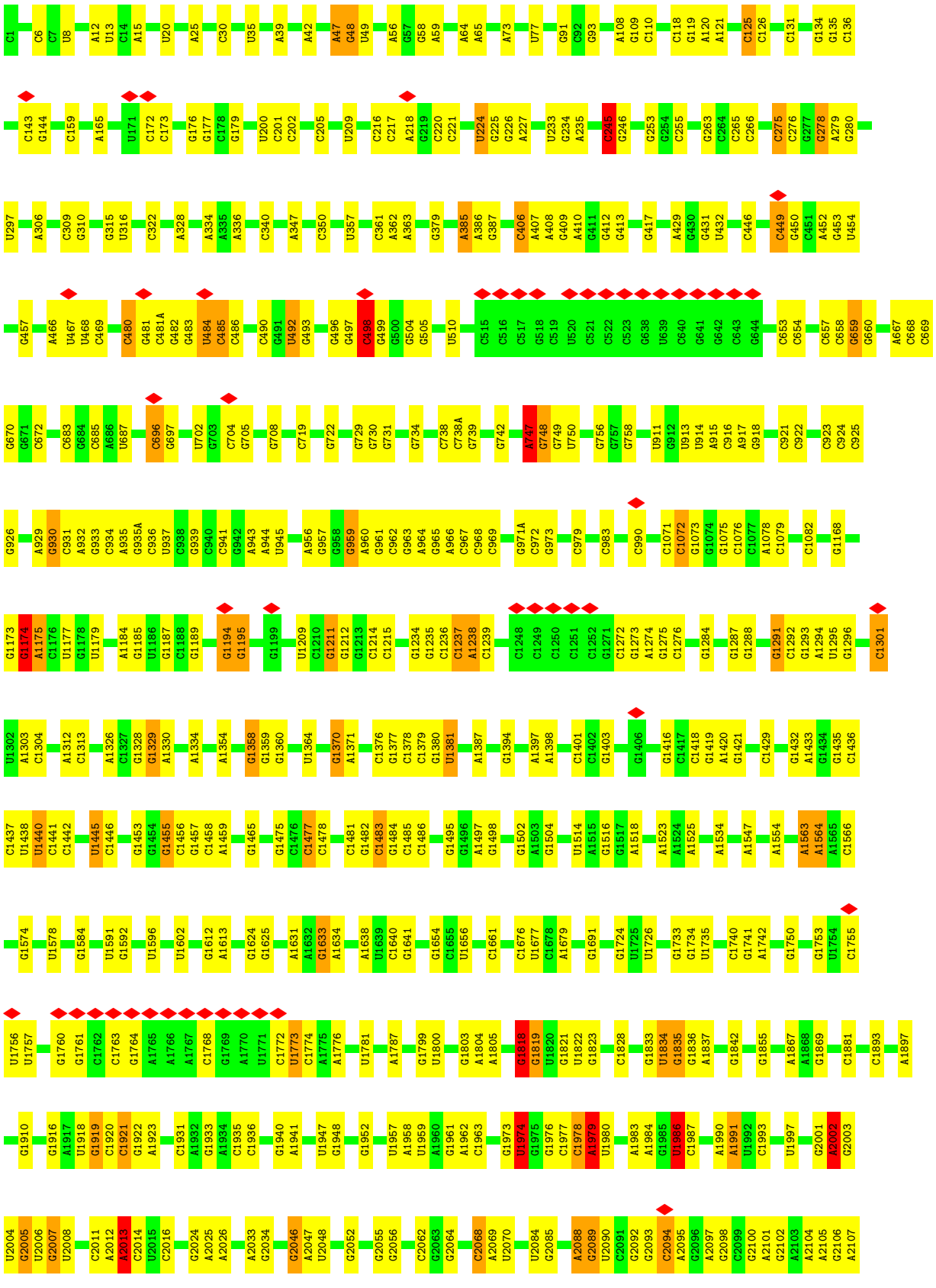
• Molecule 47: E-site tRNA

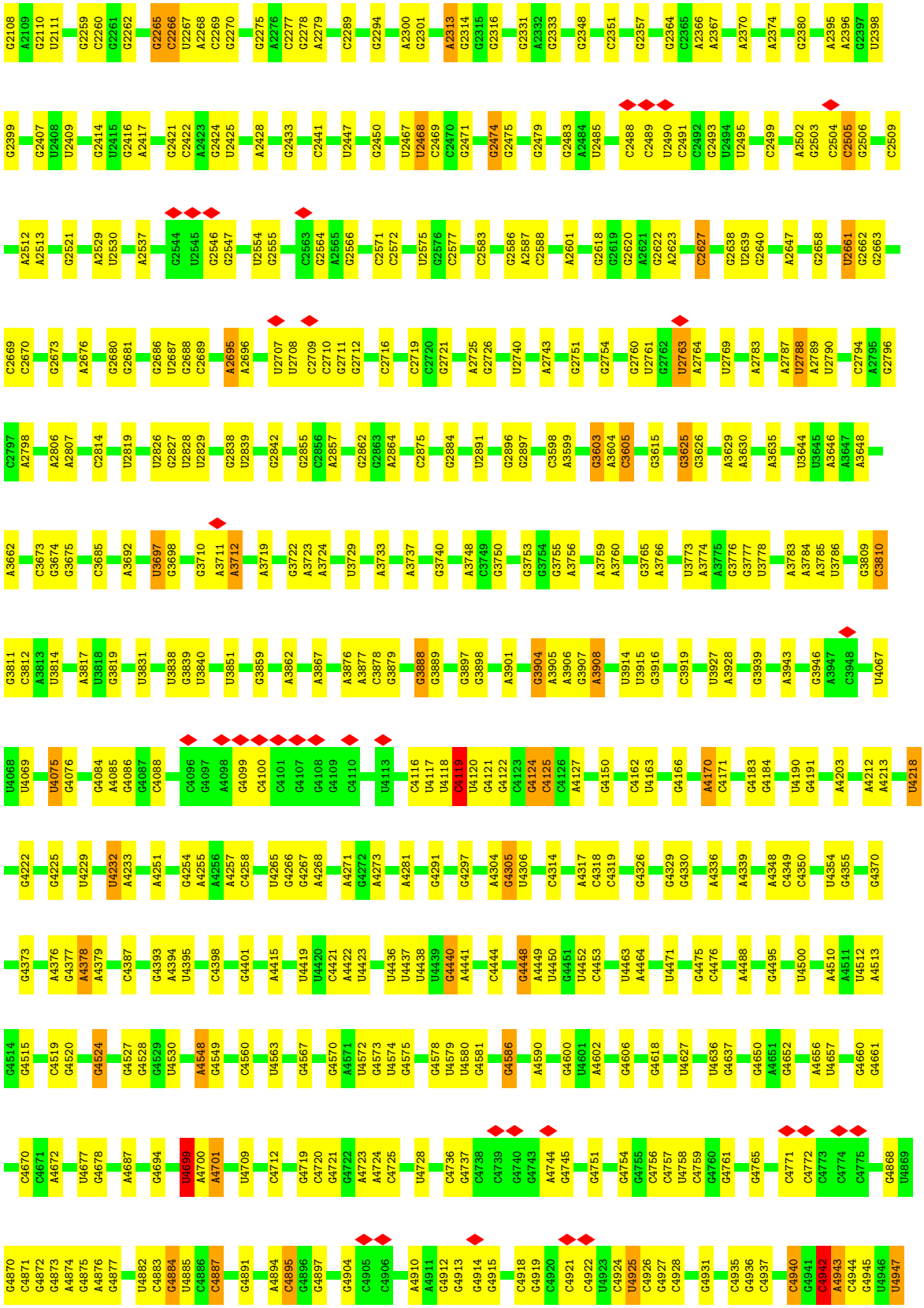


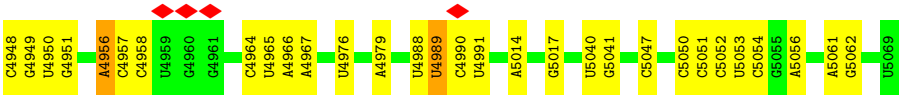


• Molecule 48: 28S ribosomal RNA




C1 C6 C7 U8 A12 U13 C14 A15 U20 A25 C30 U35 A39 A42 A47 G48 U49 A56 G57 G58 A59 A64 A65 A73 U77 G91 C92 G93 A108 G109 C110 C118 G119 A120 A121 C125 C126 C131 G134 G135 C136
C143 G144 C159 A165 U171 C172 C173 G176 G177 C178 G179 U200 C201 C202 C205 U209 C216 C217 A218 G219 C220 C221 U224 G225 G226 A227 U233 G234 A235 C245 G246 G253 G254 C255 G263 C264 C265 C266 C275 C276 G277 G278 A279 G280
U297 A306 C309 G310 G315 U316 C322 A328 A334 A335 A336 C340 A347 C350 U357 C361 A362 A363 G379 A385 A386 G387 C406 A407 A408 G409 A410 G411 G412 G413 G417 A429 G430 G431 U432 C446 C449 G450 C451 A452 G453 U454
G457 A466 U467 U468 C469 C480 G481 C481A G482 G483 U484 C485 C486 C490 G491 U492 G493 G496 G497 C498 G499 G500 G504 G505 U510 C515 C516 C517 G518 C519 U520 C521 C522 C523 G638 U639 C640 G641 G642 C643 G644 C653 C654 C657 C658 G659 G660 A667 C668 C669
G670 G671 C672 C683 G684 C685 A686 U687 C696 G697 U702 G703 C704 G705 G708 C719 G722 G729 G730 G731 G734 C738 C738A G739 G742 A747 G748 G749 U750 G756 G757 G758 U911 G912 U913 U914 A915 C916 A917 G918 C921 C922 C923 C924 C925
G926 A929 G930 C931 A932 G933 C934 A935 G935A C936 U937 C938 G939 C940 C941 G942 A943 A944 U945 A956 G957 G958 G959 A960 G961 C962 G963 A964 G965 A966 C967 C968 C969 G971A C972 G973 C979 C983 C990 C1071 C1072 G1073 G1074 G1075 C1076 C1077 A1078 C1079 C1082 G1168
G1173 G1174 A1175 C1176 U1177 G1178 U1179 A1184 G1185 U1186 G1187 C1188 G1189 G1194 G1195 G1199 U1209 C1210 G1211 G1212 G1213 C1214 C1215 G1234 G1235 C1236 C1237 A1238 C1239 C1248 C1249 C1250 C1251 C1252 G1271 C1272 G1273 A1274 G1275 C1276 G1284 G1287 G1288 G1291 C1292 G1293 A1294 U1295 G1296 C1301
U1302 A1303 C1304 A1312 C1313 A1326 C1327 G1328 G1329 A1330 A1334 A1354 G1358 G1359 G1360 U1364 G1370 A1371 C1376 G1377 C1378 C1379 G1380 U1381 A1387 G1394 A1397 A1398 C1401 C1402 G1403 G1406 G1416 C1417 C1418 G1419 A1420 G1421 C1429 G1432 A1433 G1434 G1435 C1436
C1437 U1438 U1440 C1441 C1442 U1445 C1446 G1453 G1454 G1455 C1456 G1457 C1458 A1459 G1465 G1475 C1476 C1477 C1478 C1481 G1482 C1483 G1484 C1485 C1486 G1495 G1496 A1497 G1498 G1502 A1503 G1504 U1514 A1515 G1516 G1517 A1518 A1523 A1524 A1525 A1534 A1547 A1554 A1563 A1564 A1565 C1566
G1574 U1578 G1584 U1591 G1592 U1596 U1602 G1612 A1613 G1624 G1625 A1631 A1632 G1633 A1634 A1638 U1639 C1640 G1641 G1654 C1655 U1656 C1661 C1676 U1677 C1678 A1679 G1691 G1724 U1725 U1726 G1733 G1734 U1735 C1740 G1741 A1742 G1750 G1753 U1754 C1755
U1756 U1757 G1760 G1761 C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771 C1772 U1773 C1774 A1775 A1776 U1781 A1787 G1799 U1800 G1803 A1804 A1805 G1818 G1819 U1820 G1821 U1822 G1823 C1828 G1833 U1834 G1835 G1836 A1837 G1842 G1855 A1867 A1868 G1869 C1881 C1893 A1897
G1910 G1916 A1917 U1918 G1919 C1920 C1921 G1922 A1923 C1931 A1932 G1933 A1934 C1935 C1936 G1940 A1941 U1947 G1948 G1952 U1957 A1958 U1959 A1960 G1961 A1962 C1963 G1973 U1974 G1975 G1976 C1977 C1978 A1979 U1980 A1983 A1984 G1985 U1986 C1987 A1990 A1991 U1992 C1993 U1997 G2001 A2002 G2003
U2004 G2005 U2006 G2007 U2008 C2011 A2012 A2013 C2014 U2015 C2016 G2024 A2025 A2026 A2033 G2034 G2046 A2047 U2048 G2052 G2055 G2056 C2062 G2063 G2064 C2068 A2069 U2070 U2084 G2085 A2088 G2089 U2090 C2091 G2092 G2093 C2094 A2095 G2096 A2097 G2098 C2099 G2100 A2101 G2102 A2103 A2104 A2105 G2106 A2107

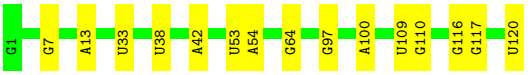




• Molecule 49: 5S ribosomal RNA

Chain 7:

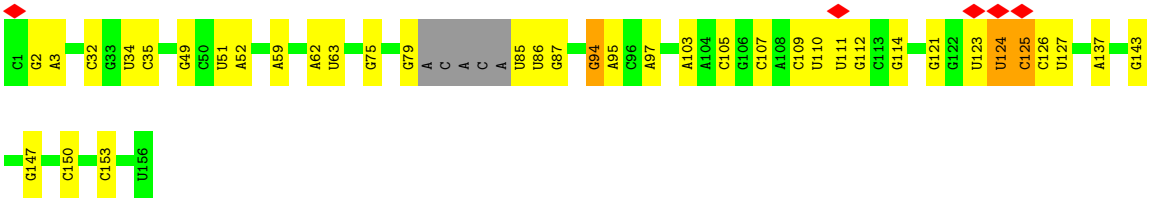




• Molecule 50: 5.8S ribosomal RNA

Chain 8:

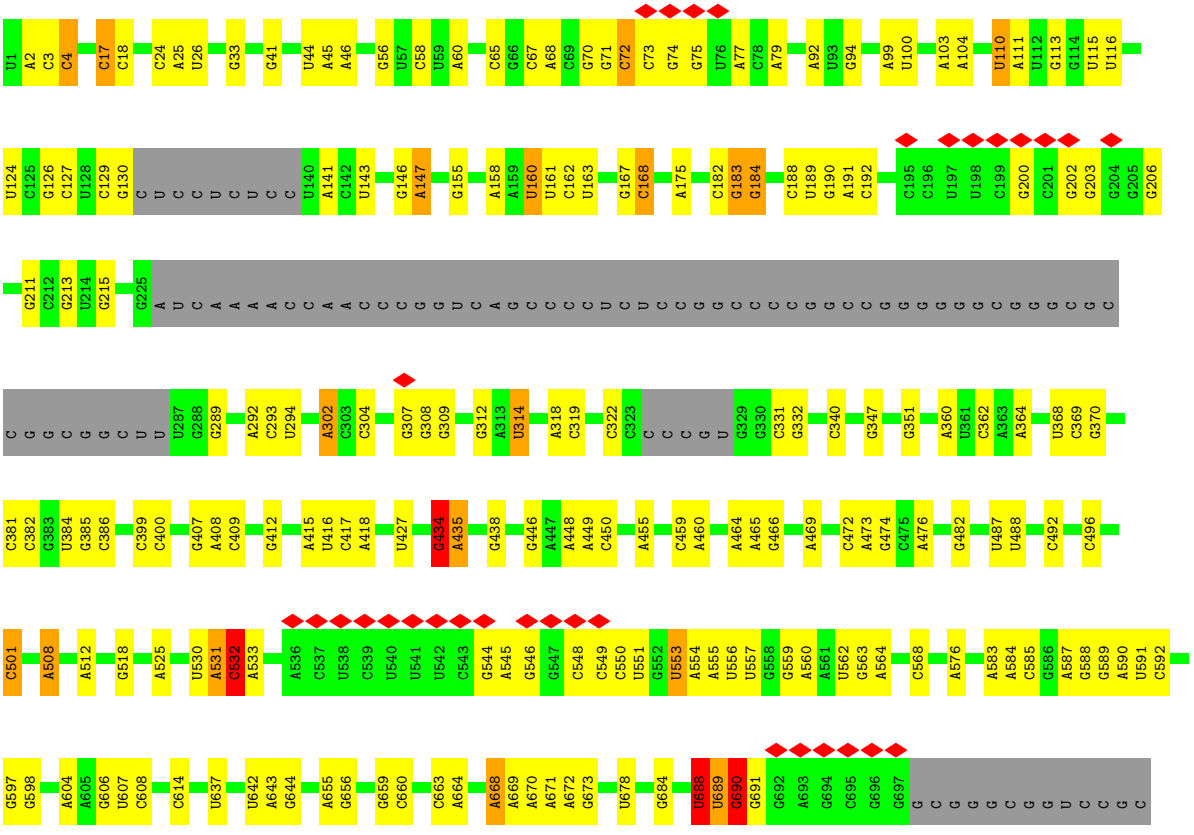


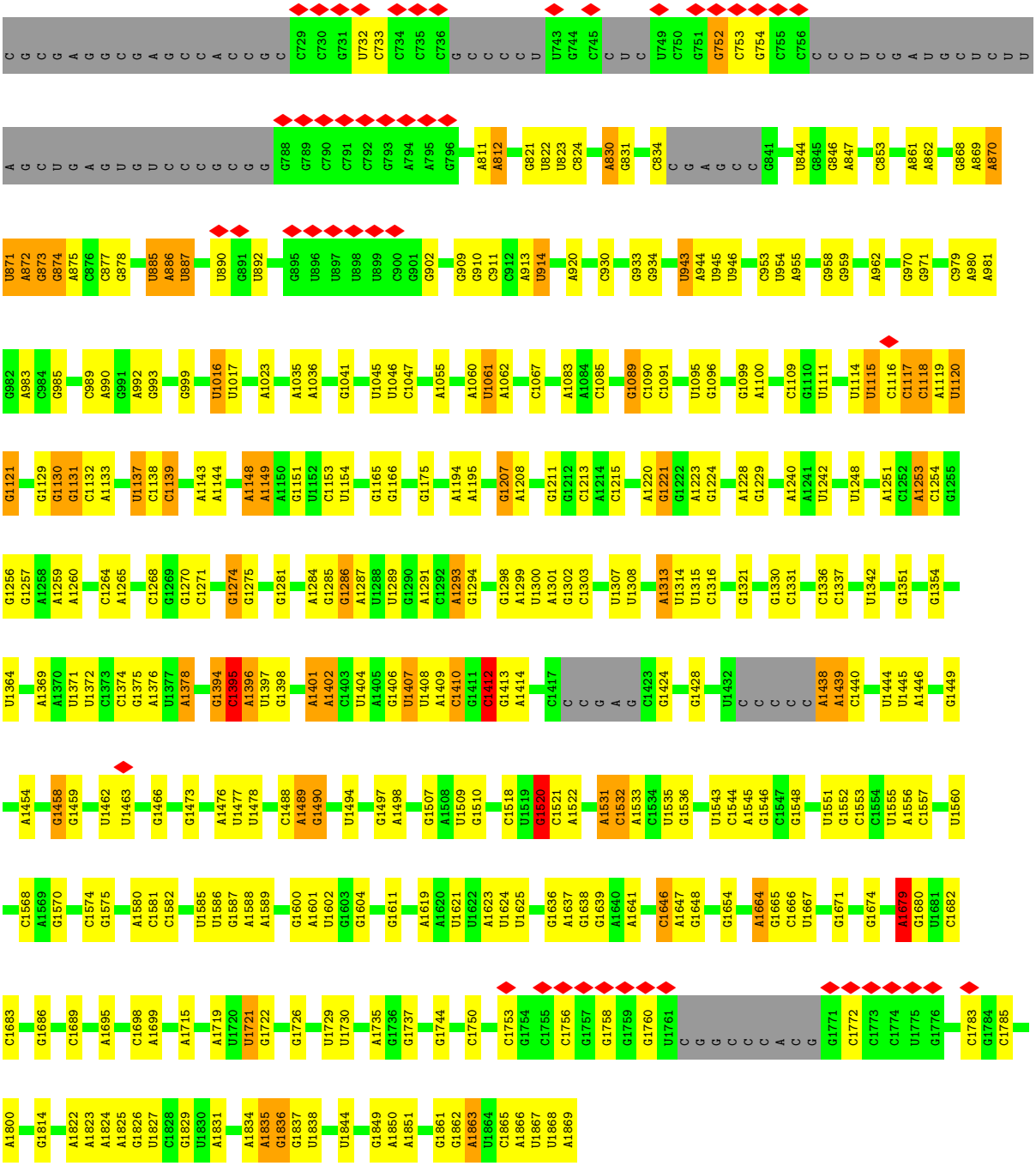


• Molecule 51: 18S ribosomal RNA

Chain 9:



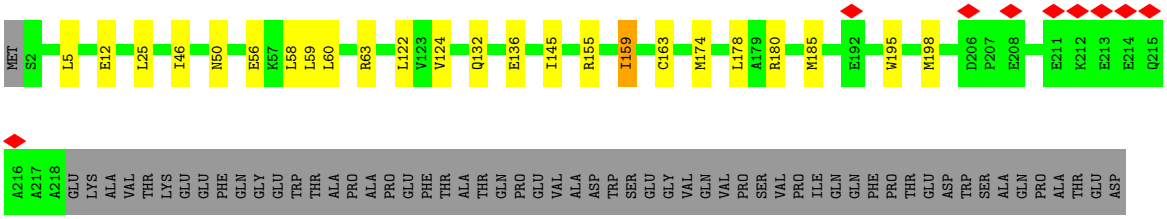




• Molecule 52: uS2

Chain AA:



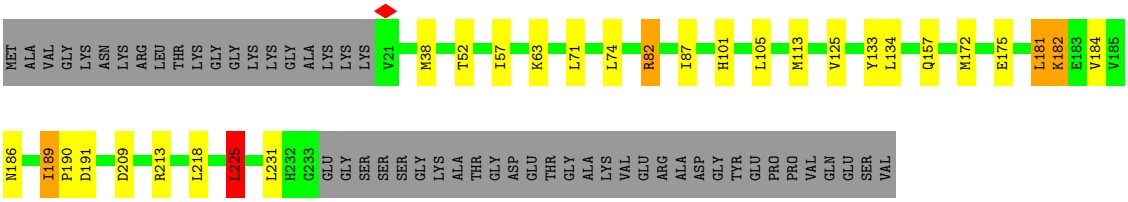




• Molecule 53: eS1

Chain BB:

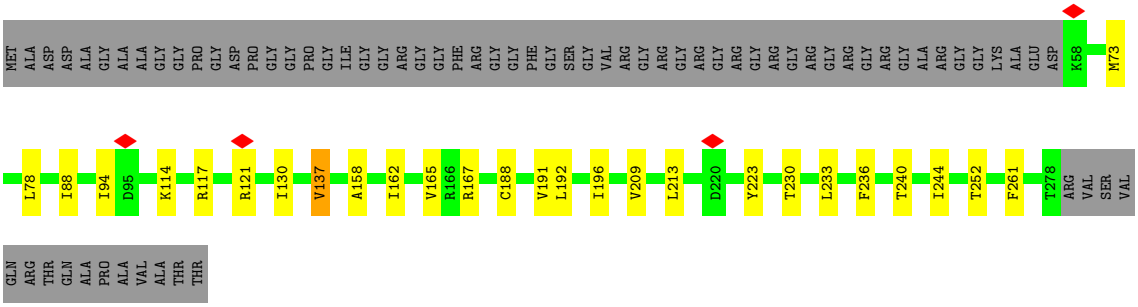




• Molecule 54: uS5

Chain CC:

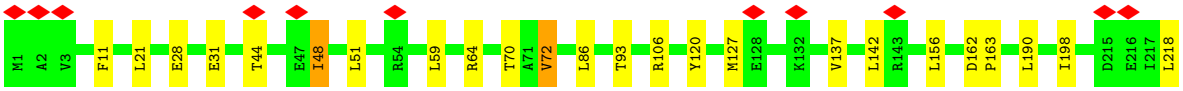


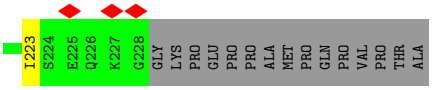


• Molecule 55: uS3

Chain DD:



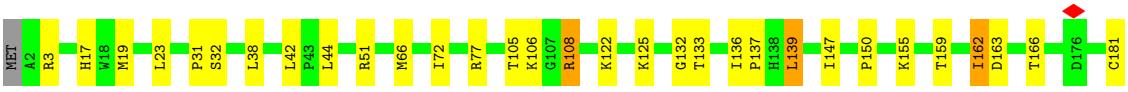


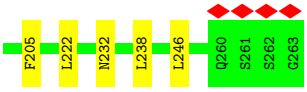


• Molecule 56: eS4

Chain EE:

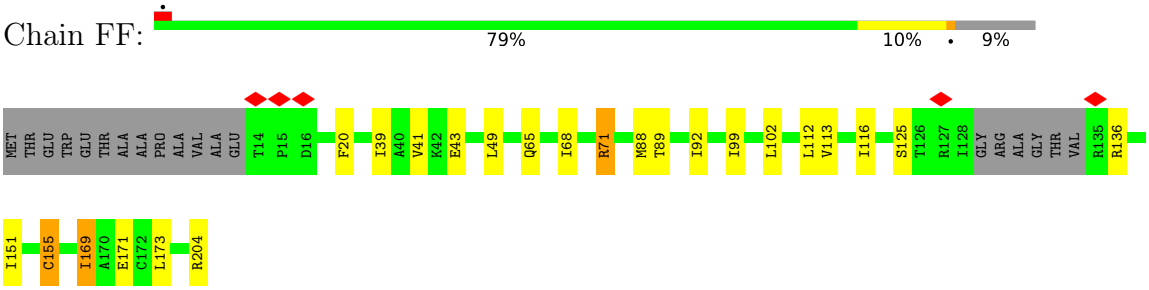






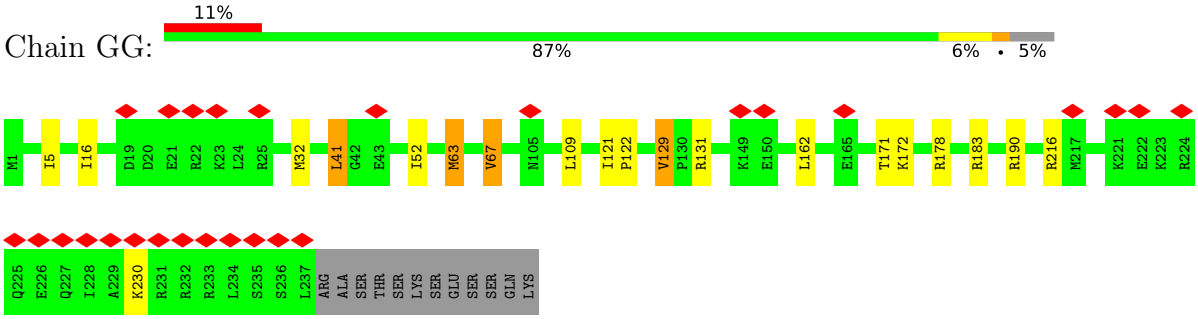
• Molecule 57: uS7

Chain FF:



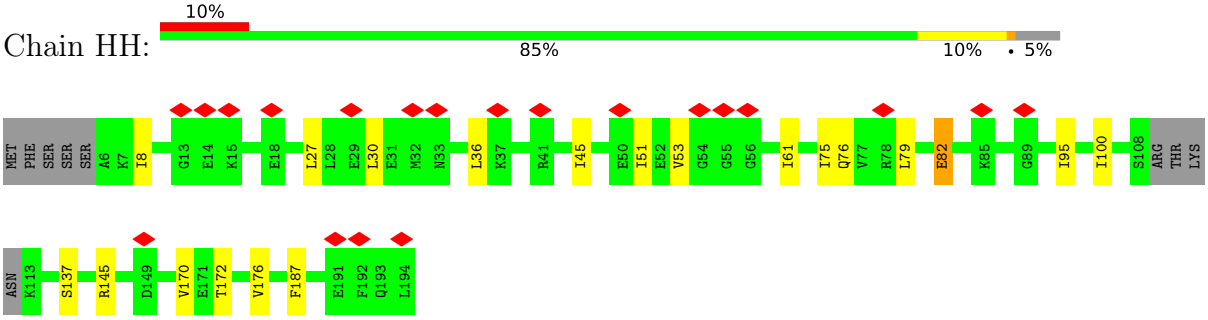
• Molecule 58: eS6

Chain GG:



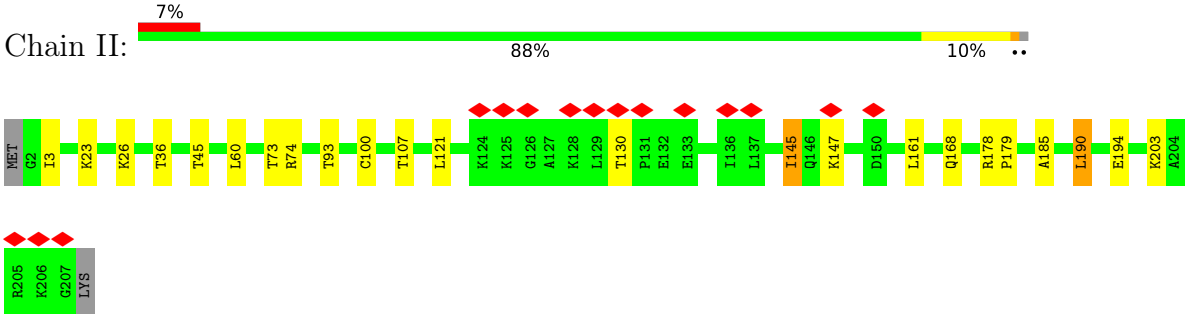
• Molecule 59: eS7

Chain HH:



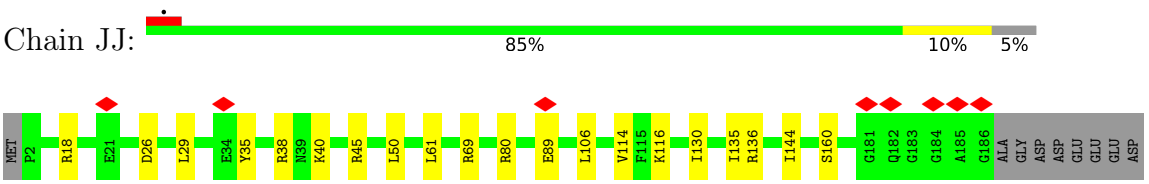
• Molecule 60: eS8

Chain II:



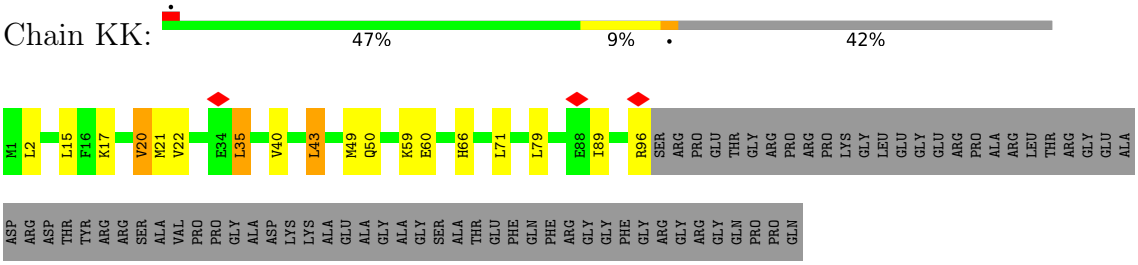
• Molecule 61: uS4

Chain JJ:



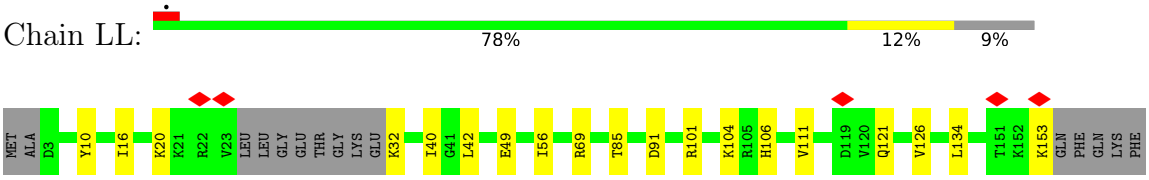
• Molecule 62: eS10

Chain KK:



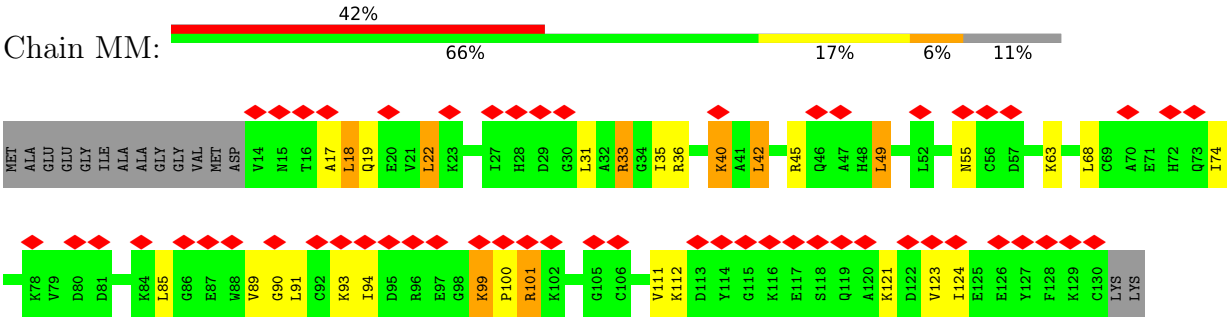
• Molecule 63: uS17

Chain LL:



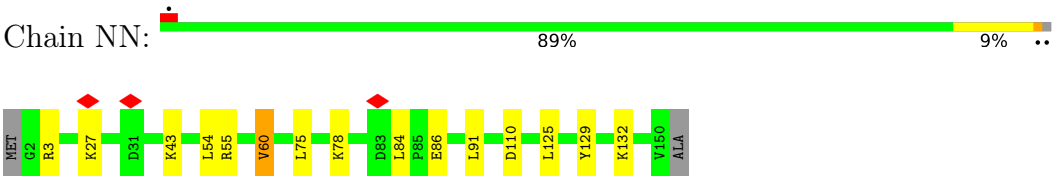
• Molecule 64: eS12

Chain MM:



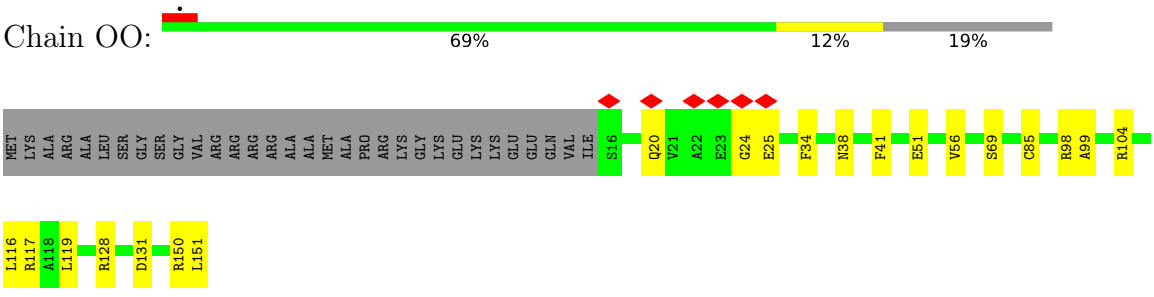
• Molecule 65: uS15

Chain NN:



• Molecule 66: uS11

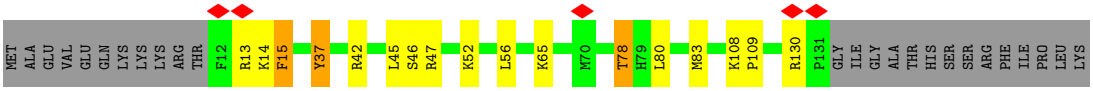
Chain OO:



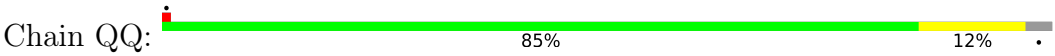
• Molecule 67: uS19

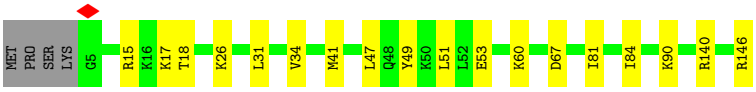
Chain PP:



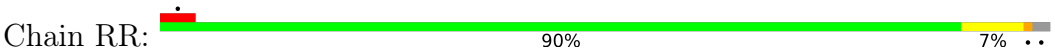


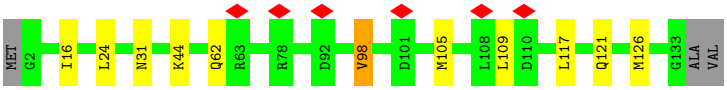
• Molecule 68: uS9



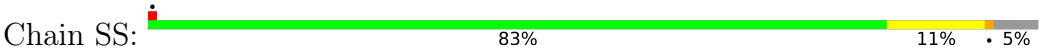


• Molecule 69: eS17



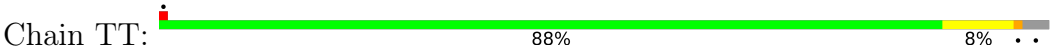


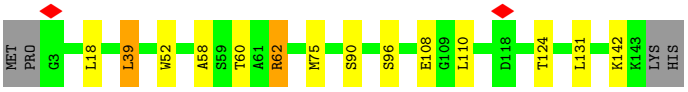
• Molecule 70: uS13



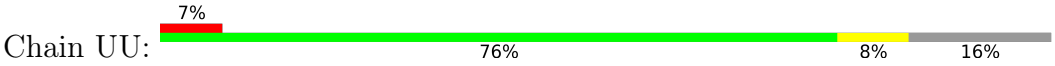


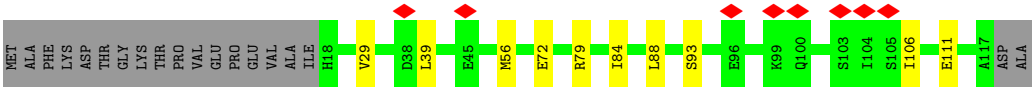
• Molecule 71: eS19





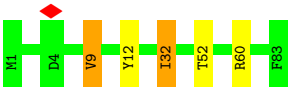
• Molecule 72: uS10





• Molecule 73: eS21





• Molecule 74: uS8

Chain WW:

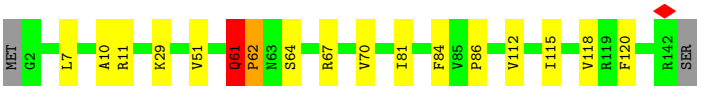




• Molecule 75: uS12

Chain XX:

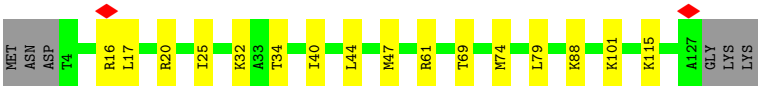




• Molecule 76: eS24

Chain YY:

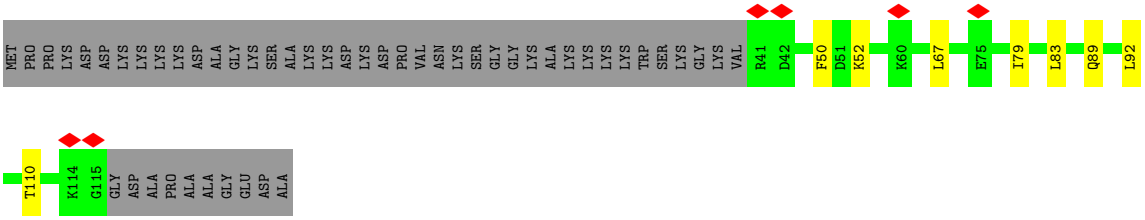




• Molecule 77: eS25

Chain ZZ:

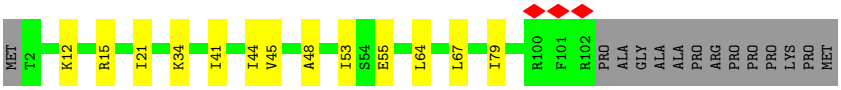




• Molecule 78: eS26

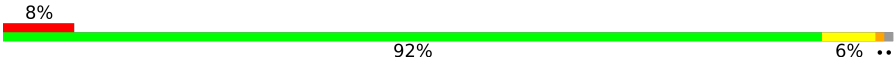
Chain aa:

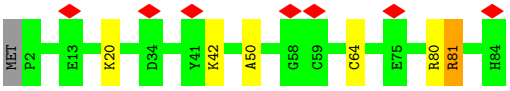




• Molecule 79: eS27

Chain bb:

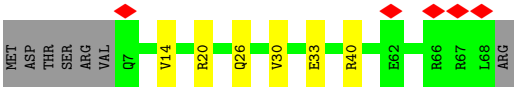




• Molecule 80: eS28

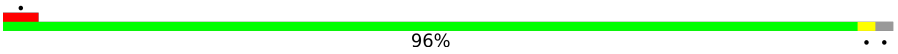
Chain cc:

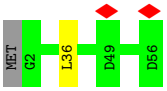




• Molecule 81: uS14

Chain dd:



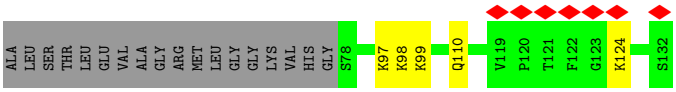


• Molecule 82: eS30

Chain ee:





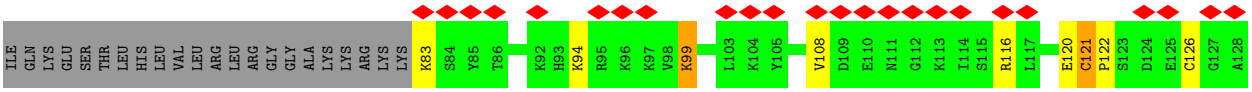


• Molecule 83: eS31

Chain ff:



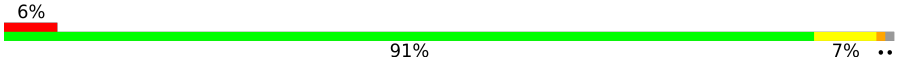


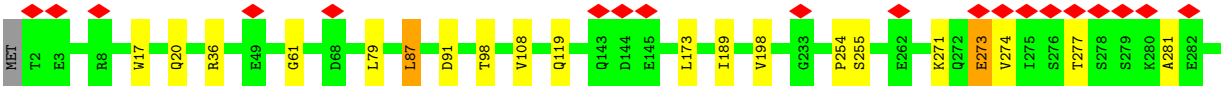


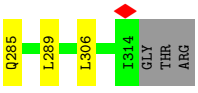


• Molecule 84: RACK1

Chain gg:



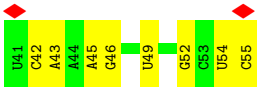




• Molecule 85: mRNA (UGA stop codon)

Chain hh:

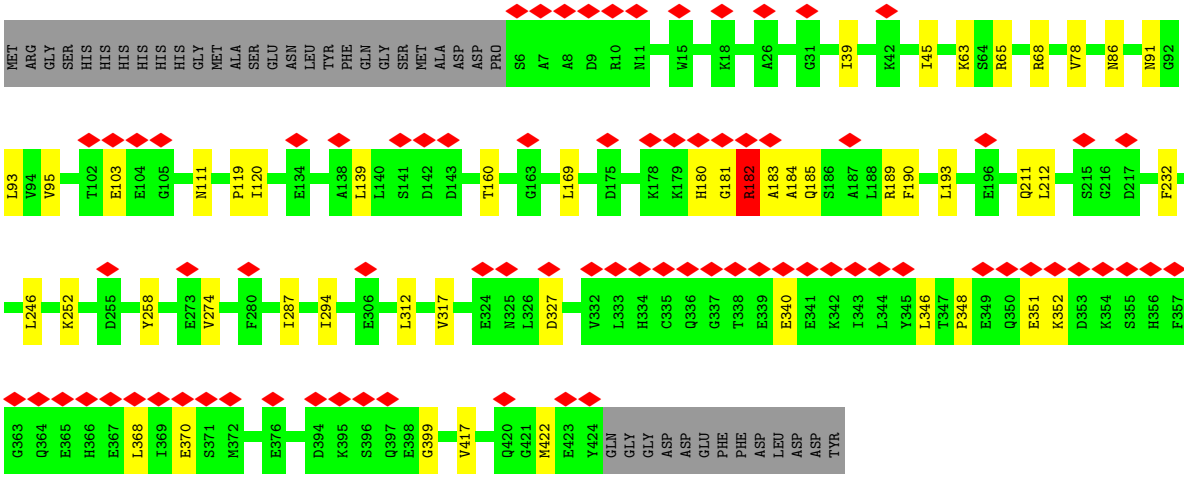




• Molecule 86: eRF1(AAQ)

Chain ii:

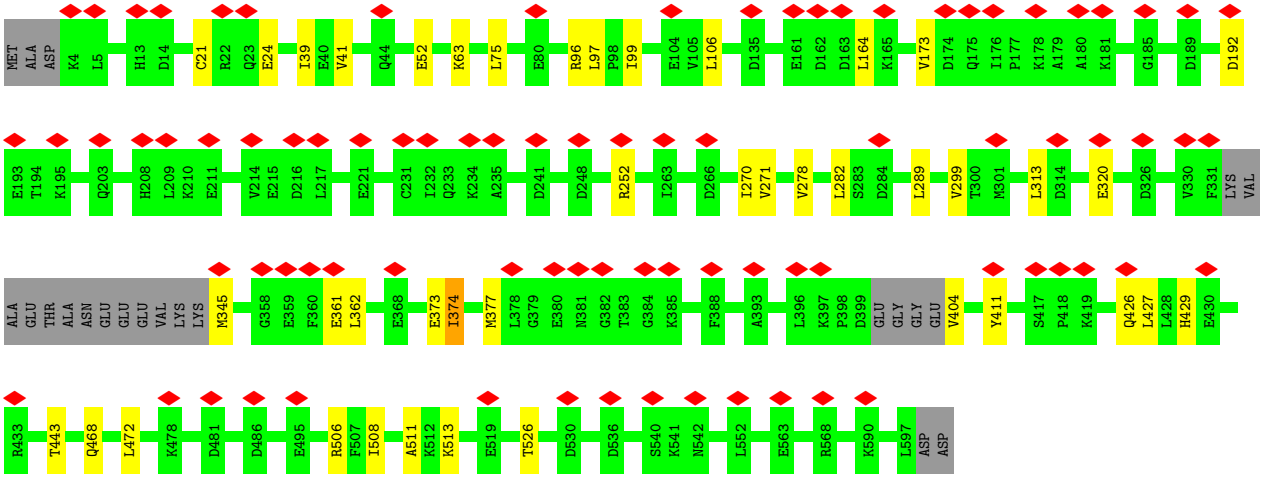




• Molecule 87: ABCE1

Chain jj:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80571	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 ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.749	Depositor
Minimum map value	-0.443	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, SF4

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	0.52	0/1936	0.74	0/2596
2	B	0.50	0/3240	0.70	0/4339
3	C	0.52	0/2937	0.76	0/3946
4	D	0.49	0/2437	0.77	0/3264
5	E	0.53	0/1762	0.73	0/2362
6	F	0.50	0/1911	0.77	0/2549
7	G	0.54	0/1910	0.81	0/2569
8	H	0.51	0/1535	0.72	0/2063
9	I	0.50	0/1702	0.74	0/2272
10	J	0.52	0/1385	0.76	0/1852
11	L	0.53	0/1733	0.81	0/2316
12	M	0.52	0/1158	0.81	0/1547
13	N	0.50	0/1746	0.78	0/2338
14	O	0.53	0/1662	0.82	1/2222 (0.0%)
15	P	0.49	0/1268	0.75	1/1700 (0.1%)
16	Q	0.52	0/1539	0.76	0/2054
17	R	0.52	0/1524	0.82	0/2013
18	S	0.50	0/1501	0.73	1/2012 (0.0%)
19	T	0.51	0/1326	0.72	0/1770
20	U	0.52	0/823	0.70	0/1104
21	V	0.51	0/993	0.73	0/1332
22	W	0.50	0/873	0.79	0/1158
23	X	0.50	0/984	0.73	0/1323
24	Y	0.50	0/1132	0.74	0/1504
25	Z	0.51	0/1130	0.72	0/1507
26	a	0.47	0/1191	0.77	0/1590
27	b	0.49	0/861	0.84	0/1138
28	c	0.49	0/771	0.79	0/1034
29	d	0.52	0/903	0.72	0/1216
30	e	0.51	0/1071	0.75	0/1429
31	f	0.52	0/895	0.68	0/1198
32	g	0.52	0/916	0.78	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	h	0.51	0/1021	0.84	0/1348
34	i	0.50	0/841	0.79	0/1112
35	j	0.51	0/720	0.84	0/952
36	k	0.50	0/575	0.72	0/761
37	l	0.51	0/459	0.75	0/608
38	m	0.51	0/435	0.75	0/575
39	n	0.45	0/240	0.86	0/305
40	o	0.50	0/864	0.72	0/1140
41	p	0.50	0/718	0.79	0/953
42	r	0.53	0/1010	0.81	0/1354
43	s	0.55	0/1530	0.76	0/2064
44	t	0.58	0/1174	0.85	0/1582
45	1	0.53	0/129	1.01	2/173 (1.2%)
46	2	0.37	0/1805	0.69	0/2809
47	3	0.37	0/1777	0.70	0/2763
48	5	0.37	1/84974 (0.0%)	0.68	68/132512 (0.1%)
49	7	0.37	0/2858	0.63	0/4455
50	8	0.37	0/3581	0.66	2/5577 (0.0%)
51	9	0.37	1/40524 (0.0%)	0.72	31/63134 (0.0%)
52	AA	0.52	0/1747	0.83	0/2374
53	BB	0.51	1/1756 (0.1%)	0.87	0/2350
54	CC	0.51	0/1753	0.88	0/2369
55	DD	0.54	0/1796	0.86	0/2417
56	EE	0.54	0/2118	0.82	2/2849 (0.1%)
57	FF	0.52	0/1492	0.97	0/2005
58	GG	0.52	0/1946	0.85	1/2590 (0.0%)
59	HH	0.54	0/1510	0.85	0/2022
60	II	0.50	0/1715	0.82	0/2287
61	JJ	0.50	0/1550	0.93	0/2069
62	KK	0.52	0/834	0.88	0/1125
63	LL	0.48	0/1195	0.72	0/1597
64	MM	0.55	0/918	0.98	1/1233 (0.1%)
65	NN	0.51	0/1226	0.93	0/1649
66	OO	0.52	0/1029	0.91	1/1380 (0.1%)
67	PP	0.52	0/1017	0.92	0/1358
68	QQ	0.52	0/1146	0.82	0/1534
69	RR	0.51	0/1082	0.89	0/1452
70	SS	0.53	0/1208	0.90	0/1618
71	TT	0.53	0/1115	0.95	0/1493
72	UU	0.50	0/805	0.87	2/1081 (0.2%)
73	VV	0.53	0/643	0.87	1/860 (0.1%)
74	WW	0.50	0/1051	0.83	0/1406
75	XX	0.48	0/1116	0.83	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	YY	0.51	0/1028	0.84	0/1366
77	ZZ	0.53	0/604	0.91	0/810
78	aa	0.53	0/828	0.86	0/1109
79	bb	0.50	0/665	0.74	1/891 (0.1%)
80	cc	0.51	0/490	0.78	0/656
81	dd	0.52	0/470	0.76	0/623
82	ee	0.50	0/447	0.86	0/587
83	ff	0.49	0/567	0.75	0/753
84	gg	0.50	0/2493	0.72	2/3394 (0.1%)
85	hh	0.37	0/353	0.75	0/547
86	ii	0.52	0/3363	0.88	2/4523 (0.0%)
87	jj	0.51	0/4640	0.84	0/6264
All	All	0.44	3/239706 (0.0%)	0.74	119/350845 (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
48	5	0	4
56	EE	0	1
75	XX	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	1974	U	C2-N3	7.09	1.51	1.37
51	9	1412	C	O3'-P	-6.32	1.51	1.61
53	BB	189	ILE	CA-CB	5.02	1.57	1.54

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
51	9	1835	A	C2'-C3'-O3'	11.25	126.38	109.50
51	9	1394	G	C2'-C3'-O3'	8.77	126.85	113.70
48	5	385	A	C4'-C3'-O3'	8.60	122.30	109.40
48	5	2474	G	C2'-C3'-O3'	8.39	122.08	109.50
48	5	2046	G	C2'-C3'-O3'	8.37	122.06	109.50

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	5	1974	U	Sidechain
48	5	1986	U	Sidechain
48	5	2002	A	Sidechain
48	5	2013	A	Sidechain
56	EE	155	LYS	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	0	1993	5	0
2	B	3172	0	3310	4	0
3	C	2883	0	3053	2	0
4	D	2391	0	2424	1	0
5	E	1729	0	1887	3	0
6	F	1875	0	1995	3	0
7	G	1879	0	2027	3	0
8	H	1516	0	1597	1	0
9	I	1664	0	1712	0	0
10	J	1362	0	1399	3	0
11	L	1702	0	1820	2	0
12	M	1137	0	1211	3	0
13	N	1701	0	1749	2	0
14	O	1630	0	1778	8	0
15	P	1242	0	1274	0	0
16	Q	1515	0	1634	1	0
17	R	1508	0	1664	6	0
18	S	1462	0	1508	5	0
19	T	1298	0	1366	2	0
20	U	809	0	833	0	0
21	V	979	0	1039	2	0
22	W	860	0	903	2	0
23	X	967	0	1040	2	0
24	Y	1115	0	1205	1	0
25	Z	1107	0	1182	0	0
26	a	1162	0	1209	1	0
27	b	848	0	920	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	c	761	0	794	1	0
29	d	888	0	930	0	0
30	e	1053	0	1147	1	0
31	f	876	0	912	2	0
32	g	906	0	999	0	0
33	h	1013	0	1147	2	0
34	i	830	0	916	0	0
35	j	705	0	737	0	0
36	k	569	0	637	0	0
37	l	447	0	480	1	0
38	m	429	0	466	0	0
39	n	239	0	289	3	0
40	o	851	0	920	4	0
41	p	708	0	756	0	0
42	r	994	0	1051	0	0
43	s	1507	0	1564	1	0
44	t	1160	0	1218	4	0
45	1	125	0	117	2	0
46	2	1616	0	824	6	0
47	3	1593	0	811	6	0
48	5	75972	0	38391	148	0
49	7	2558	0	1296	0	0
50	8	3208	0	1629	1	0
51	9	36249	0	18316	163	0
52	AA	1710	0	1708	5	0
53	BB	1729	0	1803	12	0
54	CC	1716	0	1806	10	0
55	DD	1768	0	1866	8	0
56	EE	2076	0	2177	16	0
57	FF	1471	0	1522	12	0
58	GG	1923	0	2089	8	0
59	HH	1488	0	1582	5	0
60	II	1686	0	1772	9	0
61	JJ	1525	0	1640	7	0
62	KK	810	0	836	6	0
63	LL	1175	0	1249	5	0
64	MM	908	0	939	23	0
65	NN	1202	0	1289	4	0
66	OO	1016	0	1039	5	0
67	PP	997	0	1045	6	0
68	QQ	1128	0	1195	8	0
69	RR	1068	0	1121	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	SS	1190	0	1249	4	0
71	TT	1097	0	1132	5	0
72	UU	795	0	862	2	0
73	VV	636	0	637	3	0
74	WW	1034	0	1080	6	0
75	XX	1098	0	1167	7	0
76	YY	1011	0	1083	2	0
77	ZZ	598	0	656	5	0
78	aa	814	0	864	7	0
79	bb	651	0	672	1	0
80	cc	488	0	514	5	0
81	dd	459	0	451	0	0
82	ee	443	0	492	0	0
83	ff	555	0	566	18	0
84	gg	2436	0	2393	9	0
85	hh	317	0	161	1	0
86	ii	3309	0	3350	31	0
87	jj	4555	0	4691	14	0
88	5	197	0	0	0	0
88	7	7	0	0	0	0
88	8	5	0	0	0	0
88	9	79	0	0	0	0
88	B	1	0	0	0	0
88	I	1	0	0	0	0
88	L	1	0	0	0	0
88	P	1	0	0	0	0
88	Q	1	0	0	0	0
88	V	1	0	0	0	0
88	a	2	0	0	0	0
88	e	1	0	0	0	0
88	g	1	0	0	0	0
88	hh	1	0	0	0	0
88	j	1	0	0	0	0
89	aa	1	0	0	0	0
89	dd	1	0	0	0	0
89	ff	1	0	0	2	0
89	g	1	0	0	0	0
89	j	1	0	0	0	0
89	m	1	0	0	0	0
89	o	1	0	0	0	0
89	p	1	0	0	0	0
90	jj	16	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	223874	0	168777	550	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 550 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:3914:U:O4	48:5:4378:A:N1	1.58	1.34
48:5:1986:U:C2	48:5:2006:U:O4	1.82	1.32
51:9:1137:U:O4	51:9:1148:A:N1	1.70	1.24
48:5:1986:U:O2	48:5:2006:U:C4	1.91	1.23
48:5:1986:U:O2	48:5:2006:U:O4	1.57	1.20

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	246/257 (96%)	224 (91%)	21 (8%)	1 (0%)	30 58
2	B	392/403 (97%)	365 (93%)	26 (7%)	1 (0%)	36 63
3	C	360/425 (85%)	339 (94%)	21 (6%)	0	100 100
4	D	291/297 (98%)	277 (95%)	14 (5%)	0	100 100
5	E	208/291 (72%)	193 (93%)	15 (7%)	0	100 100
6	F	223/247 (90%)	213 (96%)	9 (4%)	1 (0%)	30 58
7	G	229/319 (72%)	220 (96%)	9 (4%)	0	100 100
8	H	188/192 (98%)	177 (94%)	11 (6%)	0	100 100
9	I	201/214 (94%)	184 (92%)	17 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	168/178 (94%)	160 (95%)	8 (5%)	0	100	100
11	L	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
12	M	136/218 (62%)	128 (94%)	8 (6%)	0	100	100
13	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
14	O	197/203 (97%)	184 (93%)	13 (7%)	0	100	100
15	P	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
16	Q	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
17	R	178/196 (91%)	173 (97%)	5 (3%)	0	100	100
18	S	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
19	T	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
20	U	97/128 (76%)	86 (89%)	11 (11%)	0	100	100
21	V	129/140 (92%)	115 (89%)	14 (11%)	0	100	100
22	W	102/157 (65%)	97 (95%)	5 (5%)	0	100	100
23	X	116/156 (74%)	107 (92%)	9 (8%)	0	100	100
24	Y	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
25	Z	133/136 (98%)	127 (96%)	4 (3%)	2 (2%)	8	29
26	a	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
27	b	100/245 (41%)	93 (93%)	5 (5%)	2 (2%)	6	24
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	95 (90%)	10 (10%)	0	100	100
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	101 (94%)	4 (4%)	2 (2%)	6	25
32	g	112/117 (96%)	106 (95%)	6 (5%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j	84/97 (87%)	78 (93%)	5 (6%)	1 (1%)	10	33
36	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	44 (92%)	4 (8%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	r	122/137 (89%)	114 (93%)	7 (6%)	1 (1%)	16	44
43	s	194/318 (61%)	176 (91%)	16 (8%)	2 (1%)	12	38
44	t	151/165 (92%)	136 (90%)	13 (9%)	2 (1%)	9	32
45	1	13/15 (87%)	8 (62%)	4 (31%)	1 (8%)	1	5
52	AA	215/295 (73%)	201 (94%)	13 (6%)	1 (0%)	24	52
53	BB	211/264 (80%)	201 (95%)	9 (4%)	1 (0%)	24	52
54	CC	219/293 (75%)	209 (95%)	10 (5%)	0	100	100
55	DD	226/243 (93%)	214 (95%)	9 (4%)	3 (1%)	9	32
56	EE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
57	FF	181/204 (89%)	171 (94%)	10 (6%)	0	100	100
58	GG	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
59	HH	181/194 (93%)	171 (94%)	10 (6%)	0	100	100
60	II	204/208 (98%)	195 (96%)	8 (4%)	1 (0%)	24	52
61	JJ	183/194 (94%)	176 (96%)	7 (4%)	0	100	100
62	KK	94/165 (57%)	88 (94%)	6 (6%)	0	100	100
63	LL	139/158 (88%)	127 (91%)	12 (9%)	0	100	100
64	MM	115/132 (87%)	104 (90%)	11 (10%)	0	100	100
65	NN	147/151 (97%)	140 (95%)	7 (5%)	0	100	100
66	OO	134/168 (80%)	122 (91%)	11 (8%)	1 (1%)	18	46
67	PP	118/145 (81%)	108 (92%)	10 (8%)	0	100	100
68	QQ	140/146 (96%)	131 (94%)	9 (6%)	0	100	100
69	RR	130/135 (96%)	120 (92%)	10 (8%)	0	100	100
70	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
71	TT	139/145 (96%)	132 (95%)	7 (5%)	0	100	100
72	UU	98/119 (82%)	91 (93%)	7 (7%)	0	100	100
73	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
74	WW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
75	XX	139/143 (97%)	130 (94%)	6 (4%)	3 (2%)	5	23
76	YY	122/130 (94%)	113 (93%)	9 (7%)	0	100	100
77	ZZ	73/125 (58%)	68 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	aa	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
79	bb	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	10	33
80	cc	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
81	dd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
82	ee	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
83	ff	66/156 (42%)	61 (92%)	5 (8%)	0	100	100
84	gg	311/317 (98%)	290 (93%)	20 (6%)	1 (0%)	36	63
86	ii	417/459 (91%)	404 (97%)	12 (3%)	1 (0%)	43	70
87	jj	571/599 (95%)	538 (94%)	32 (6%)	1 (0%)	43	70
All	All	12520/14448 (87%)	11763 (94%)	727 (6%)	30 (0%)	44	70

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
75	XX	62	PRO
86	ii	182	ARG
43	s	142	GLY
44	t	125	LEU
52	AA	159	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/199 (96%)	178 (94%)	12 (6%)	16	43
2	B	342/348 (98%)	326 (95%)	16 (5%)	23	50
3	C	302/347 (87%)	288 (95%)	14 (5%)	24	50
4	D	247/250 (99%)	237 (96%)	10 (4%)	28	53
5	E	190/251 (76%)	182 (96%)	8 (4%)	26	52
6	F	196/215 (91%)	189 (96%)	7 (4%)	31	56
7	G	200/272 (74%)	190 (95%)	10 (5%)	22	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	169/171 (99%)	158 (94%)	11 (6%)	15	42
9	I	175/181 (97%)	169 (97%)	6 (3%)	32	58
10	J	143/149 (96%)	137 (96%)	6 (4%)	26	52
11	L	175/176 (99%)	170 (97%)	5 (3%)	37	60
12	M	117/161 (73%)	113 (97%)	4 (3%)	32	58
13	N	171/172 (99%)	164 (96%)	7 (4%)	27	53
14	O	171/173 (99%)	162 (95%)	9 (5%)	20	48
15	P	134/163 (82%)	128 (96%)	6 (4%)	24	51
16	Q	164/165 (99%)	159 (97%)	5 (3%)	36	60
17	R	159/175 (91%)	148 (93%)	11 (7%)	14	40
18	S	157/157 (100%)	150 (96%)	7 (4%)	24	51
19	T	139/140 (99%)	131 (94%)	8 (6%)	18	45
20	U	89/114 (78%)	88 (99%)	1 (1%)	65	73
21	V	101/107 (94%)	91 (90%)	10 (10%)	7	27
22	W	86/126 (68%)	86 (100%)	0	100	100
23	X	106/134 (79%)	101 (95%)	5 (5%)	23	50
24	Y	124/135 (92%)	120 (97%)	4 (3%)	34	58
25	Z	117/118 (99%)	116 (99%)	1 (1%)	70	75
26	a	119/120 (99%)	116 (98%)	3 (2%)	42	61
27	b	84/184 (46%)	81 (96%)	3 (4%)	31	56
28	c	84/98 (86%)	83 (99%)	1 (1%)	63	72
29	d	98/110 (89%)	93 (95%)	5 (5%)	21	48
30	e	114/121 (94%)	105 (92%)	9 (8%)	11	37
31	f	88/89 (99%)	84 (96%)	4 (4%)	24	51
32	g	98/100 (98%)	93 (95%)	5 (5%)	21	48
33	h	109/110 (99%)	106 (97%)	3 (3%)	38	60
34	i	86/89 (97%)	83 (96%)	3 (4%)	32	57
35	j	73/80 (91%)	70 (96%)	3 (4%)	27	53
36	k	64/65 (98%)	62 (97%)	2 (3%)	35	59
37	l	47/48 (98%)	46 (98%)	1 (2%)	47	64
38	m	48/90 (53%)	46 (96%)	2 (4%)	26	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	n	24/24 (100%)	22 (92%)	2 (8%)	10	35
40	o	92/94 (98%)	89 (97%)	3 (3%)	33	58
41	p	74/75 (99%)	72 (97%)	2 (3%)	39	60
42	r	108/121 (89%)	105 (97%)	3 (3%)	38	60
43	s	164/258 (64%)	157 (96%)	7 (4%)	26	52
44	t	126/137 (92%)	121 (96%)	5 (4%)	28	53
45	1	13/13 (100%)	12 (92%)	1 (8%)	12	37
52	AA	180/245 (74%)	164 (91%)	16 (9%)	9	31
53	BB	194/231 (84%)	175 (90%)	19 (10%)	7	27
54	CC	187/225 (83%)	173 (92%)	14 (8%)	12	38
55	DD	190/202 (94%)	174 (92%)	16 (8%)	10	34
56	EE	224/225 (100%)	209 (93%)	15 (7%)	15	41
57	FF	158/170 (93%)	148 (94%)	10 (6%)	16	43
58	GG	207/218 (95%)	197 (95%)	10 (5%)	23	49
59	HH	165/174 (95%)	154 (93%)	11 (7%)	15	41
60	II	178/180 (99%)	163 (92%)	15 (8%)	10	34
61	JJ	161/168 (96%)	150 (93%)	11 (7%)	14	41
62	KK	87/136 (64%)	74 (85%)	13 (15%)	3	12
63	LL	130/142 (92%)	115 (88%)	15 (12%)	5	20
64	MM	99/108 (92%)	83 (84%)	16 (16%)	2	10
65	NN	130/131 (99%)	120 (92%)	10 (8%)	12	37
66	OO	106/130 (82%)	94 (89%)	12 (11%)	5	20
67	PP	109/130 (84%)	98 (90%)	11 (10%)	7	26
68	QQ	117/121 (97%)	108 (92%)	9 (8%)	12	37
69	RR	119/121 (98%)	112 (94%)	7 (6%)	18	44
70	SS	125/132 (95%)	112 (90%)	13 (10%)	7	24
71	TT	111/115 (96%)	103 (93%)	8 (7%)	13	39
72	UU	92/107 (86%)	85 (92%)	7 (8%)	12	38
73	VV	67/67 (100%)	64 (96%)	3 (4%)	24	51
74	WW	112/113 (99%)	106 (95%)	6 (5%)	20	47
75	XX	113/115 (98%)	107 (95%)	6 (5%)	20	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
76	YY	107/112 (96%)	95 (89%)	12 (11%)	6 21
77	ZZ	66/103 (64%)	63 (96%)	3 (4%)	24 51
78	aa	88/98 (90%)	81 (92%)	7 (8%)	11 36
79	bb	75/76 (99%)	71 (95%)	4 (5%)	20 48
80	cc	55/62 (89%)	52 (94%)	3 (6%)	19 47
81	dd	48/49 (98%)	47 (98%)	1 (2%)	47 64
82	ee	46/106 (43%)	41 (89%)	5 (11%)	6 22
83	ff	61/140 (44%)	55 (90%)	6 (10%)	7 27
84	gg	272/275 (99%)	262 (96%)	10 (4%)	30 55
86	ii	361/394 (92%)	344 (95%)	17 (5%)	23 50
87	jj	509/526 (97%)	488 (96%)	21 (4%)	27 53
All	All	10926/12272 (89%)	10314 (94%)	612 (6%)	21 46

5 of 612 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
67	PP	130	ARG
84	gg	306	LEU
69	RR	98	VAL
67	PP	108	LYS
75	XX	67	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
73	VV	47	ASN
79	bb	51	GLN
86	ii	266	GLN
29	d	34	HIS
28	c	50	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	15 (20%)	0
47	3	72/75 (96%)	25 (34%)	2 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	5	3518/3543 (99%)	908 (25%)	167 (4%)
49	7	119/120 (99%)	15 (12%)	1 (0%)
50	8	150/156 (96%)	36 (24%)	7 (4%)
51	9	1682/1869 (89%)	423 (25%)	63 (3%)
85	hh	14/15 (93%)	7 (50%)	0
All	All	5629/5854 (96%)	1429 (25%)	240 (4%)

5 of 1429 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	8	U
46	2	9	A
46	2	16	C
46	2	19	G
46	2	20	U

5 of 240 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	2502	A
51	9	1286	G
48	5	4170	A
51	9	1264	C
51	9	1824	A

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 310 ligands modelled in this entry, 308 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	$\#\|Z\| > 2$
90	SF4	jj	601	87	0,12,12	-	-	-		
90	SF4	jj	600	87	0,12,12	-	-	-		

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
90	SF4	jj	601	87	-	-	0/6/5/5
90	SF4	jj	600	87	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	jj	601	SF4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
48	5	29
51	9	7
47	3	2
46	2	1

The worst 5 of 39 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	41.35
1	5	1252:C	O3'	1271:G	P	35.93
1	5	1219:G	O3'	1233:G	P	23.06
1	5	3948:C	O3'	4065:G	P	19.73
1	5	1406(C):G	O3'	1411:C	P	18.70

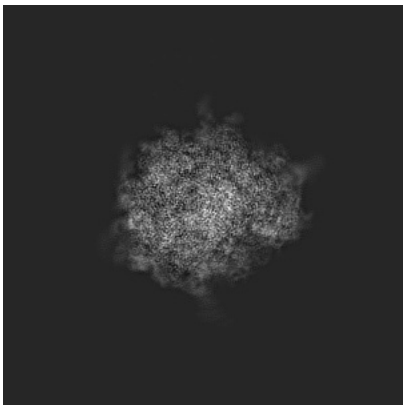
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4133. These allow visual inspection of the internal detail of the map and identification of artifacts.

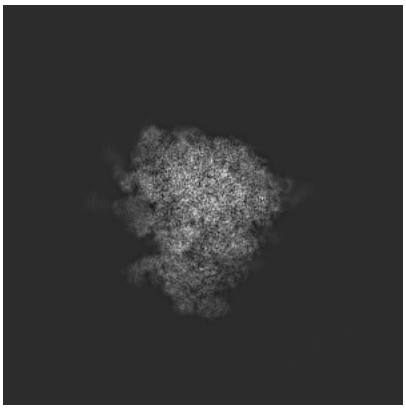
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

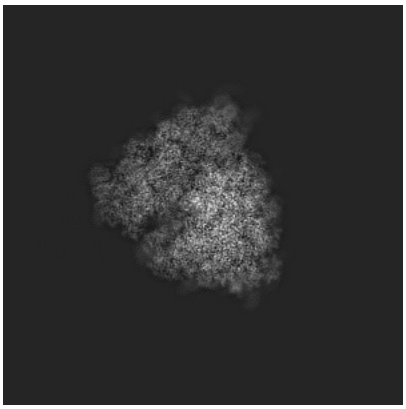
6.1.1 Primary map



X

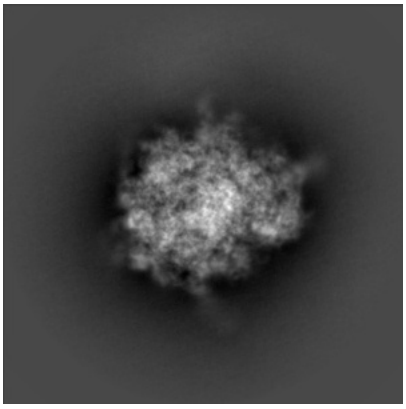


Y

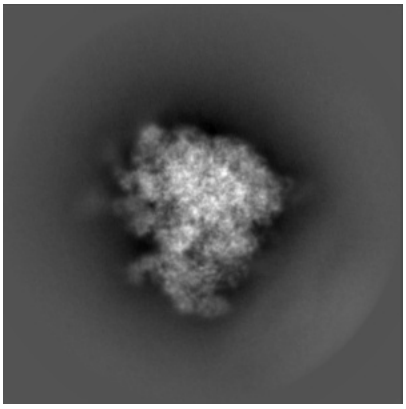


Z

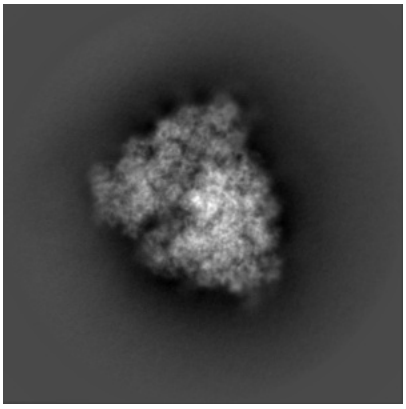
6.1.2 Raw map



X



Y



Z

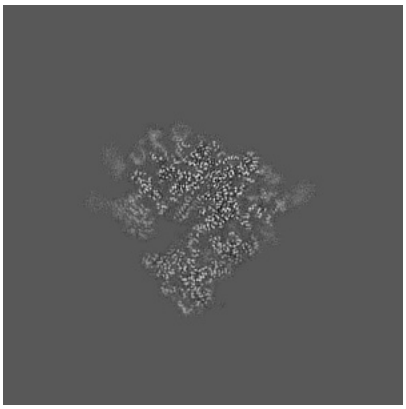
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

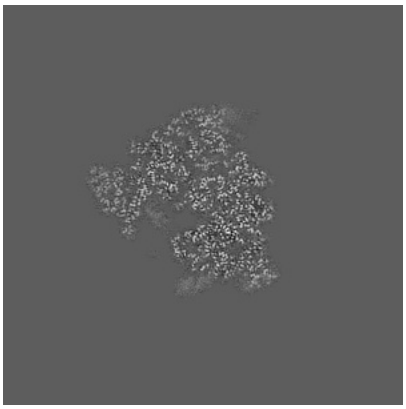
6.2.1 Primary map



X Index: 210

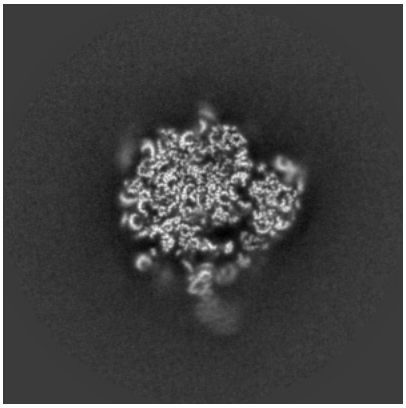


Y Index: 210

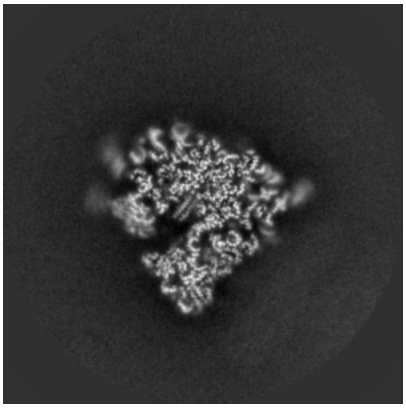


Z Index: 210

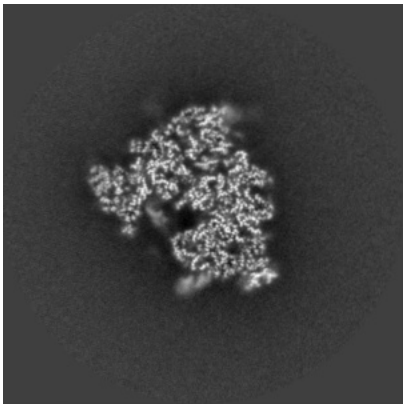
6.2.2 Raw map



X Index: 210



Y Index: 210

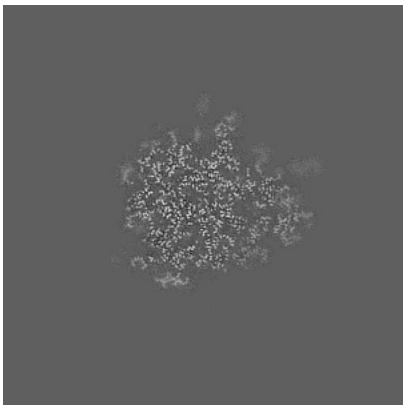


Z Index: 210

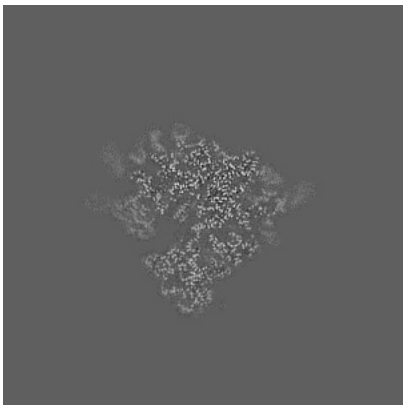
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 228

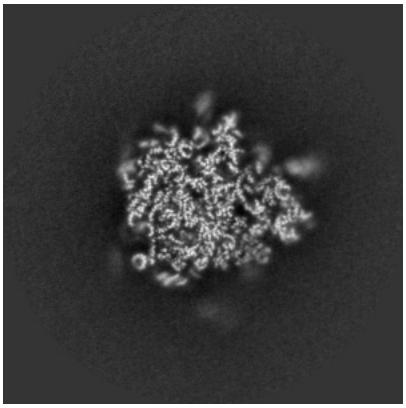


Y Index: 211

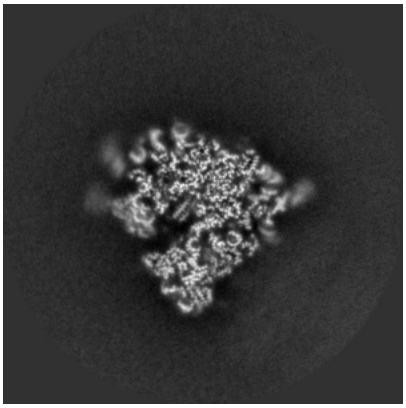


Z Index: 220

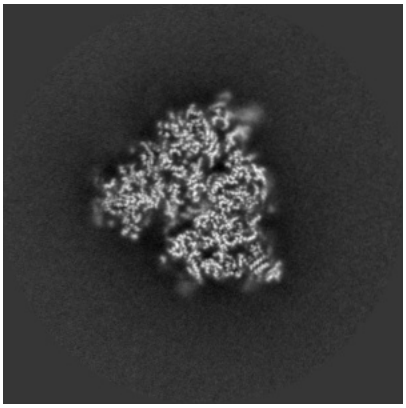
6.3.2 Raw map



X Index: 225



Y Index: 211

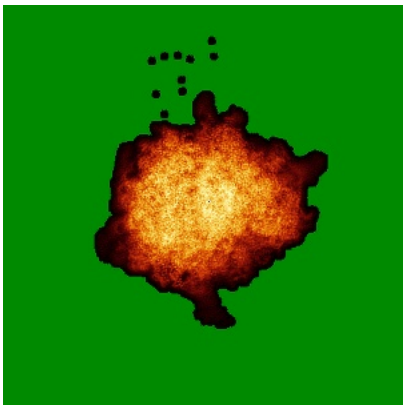


Z Index: 202

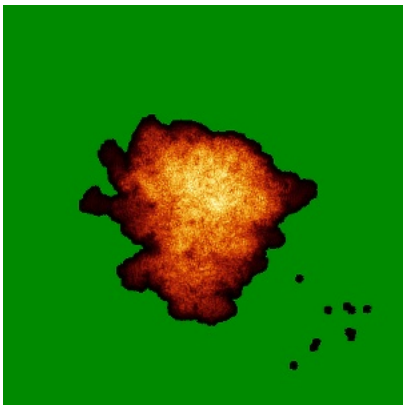
The images above show the largest variance slices of the map in three orthogonal directions.

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

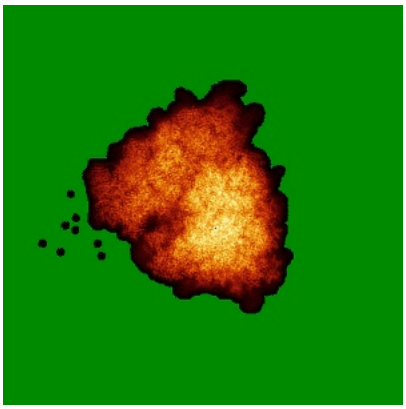
6.4.1 Primary map



X

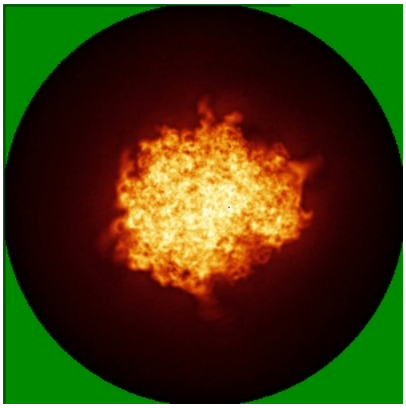


Y

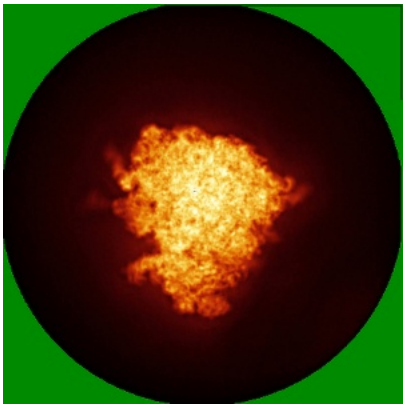


Z

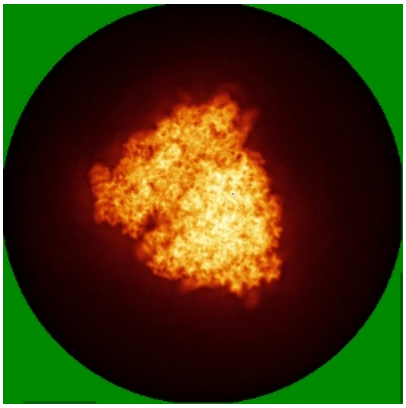
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

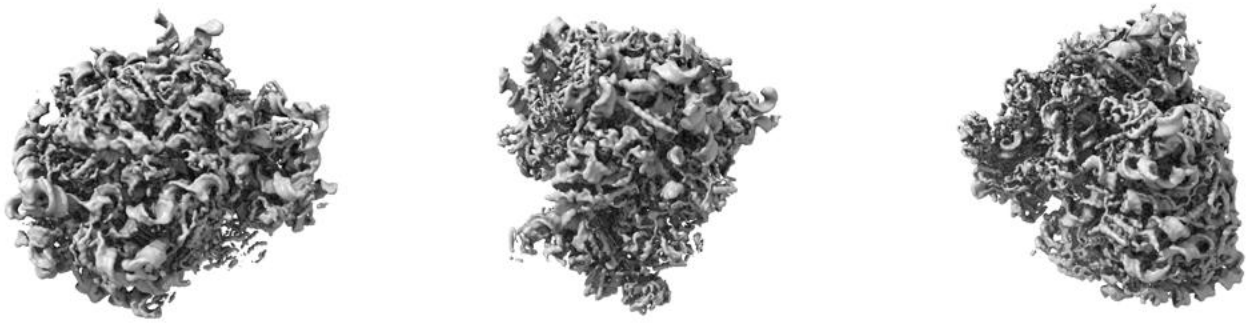
6.5.1 Primary map



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.

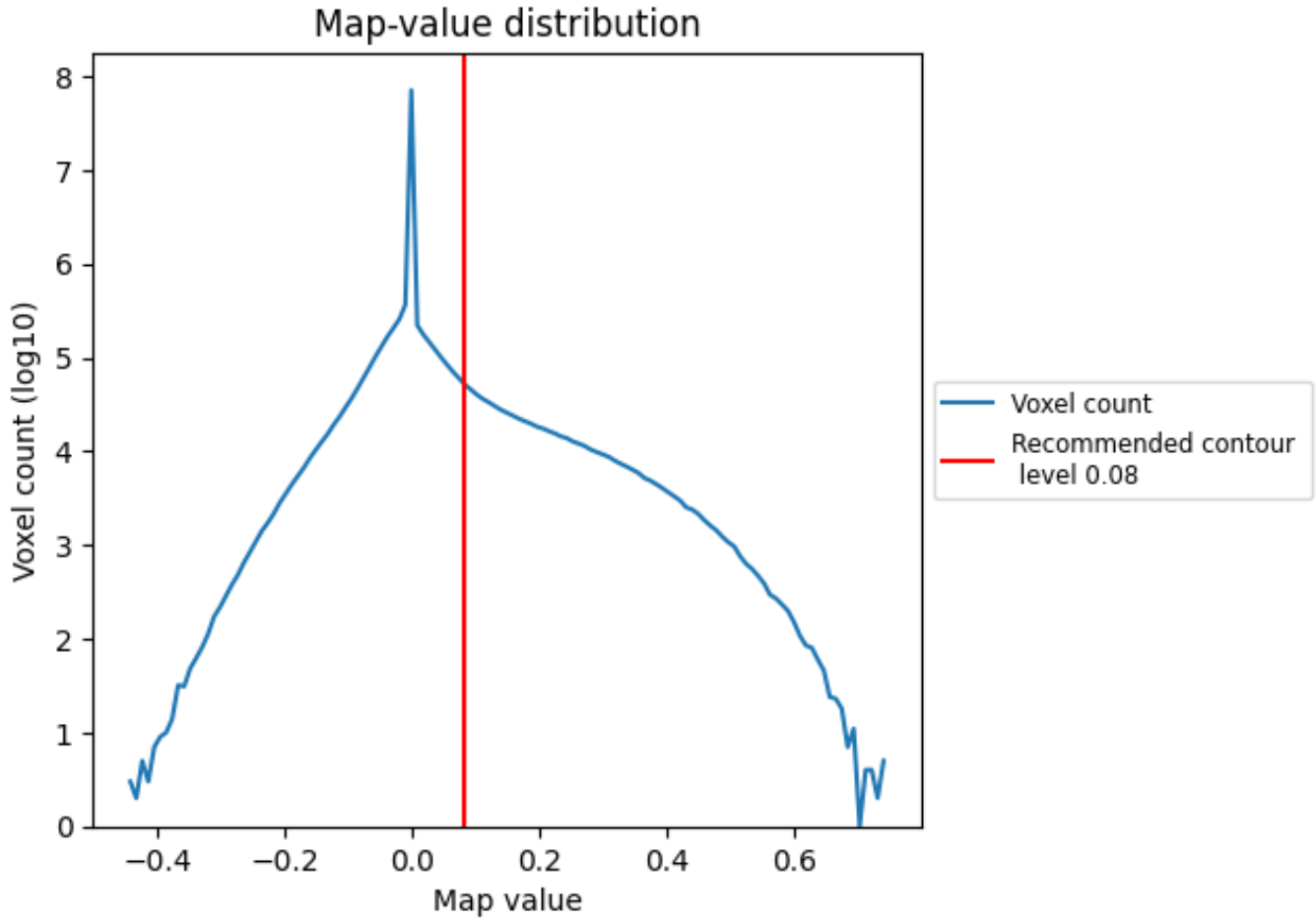
6.6 Mask visualisation (i)

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

7 Map analysis

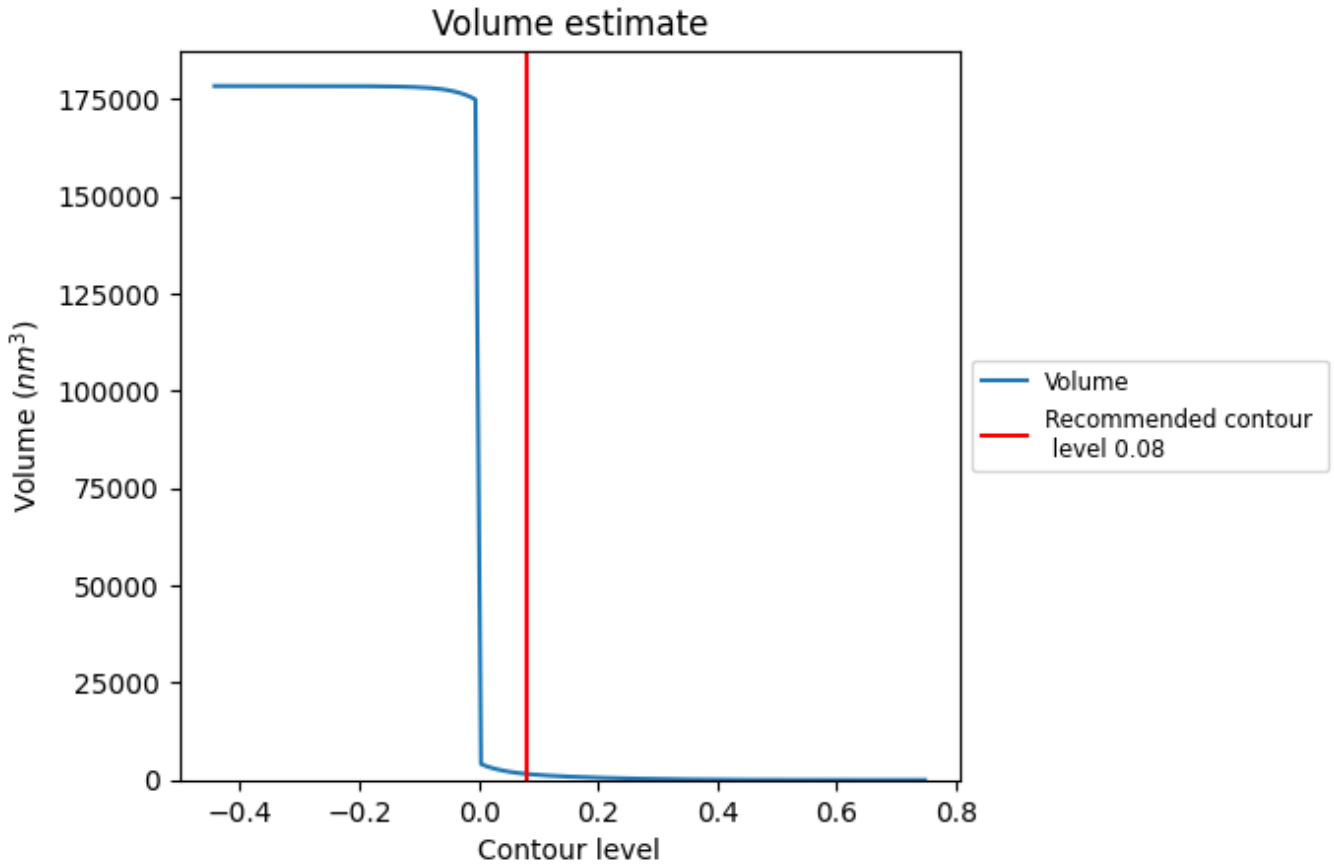
This section contains the results of statistical analysis of the map.

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.

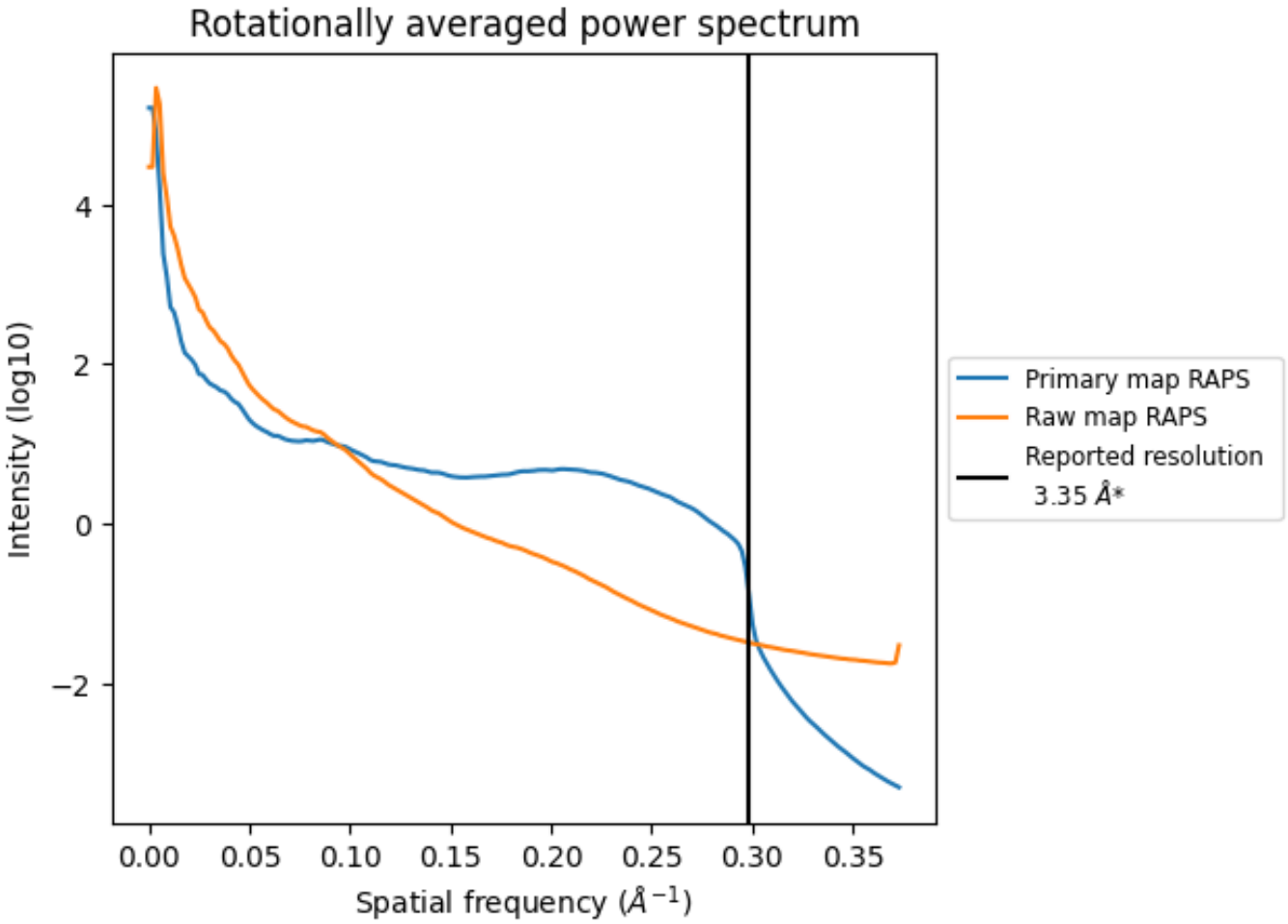
7.2 Volume estimate



The volume at the recommended contour level is 1553 nm^3; this corresponds to an approximate mass of 1402 kDa.

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

7.3 Rotationally averaged power spectrum (i)

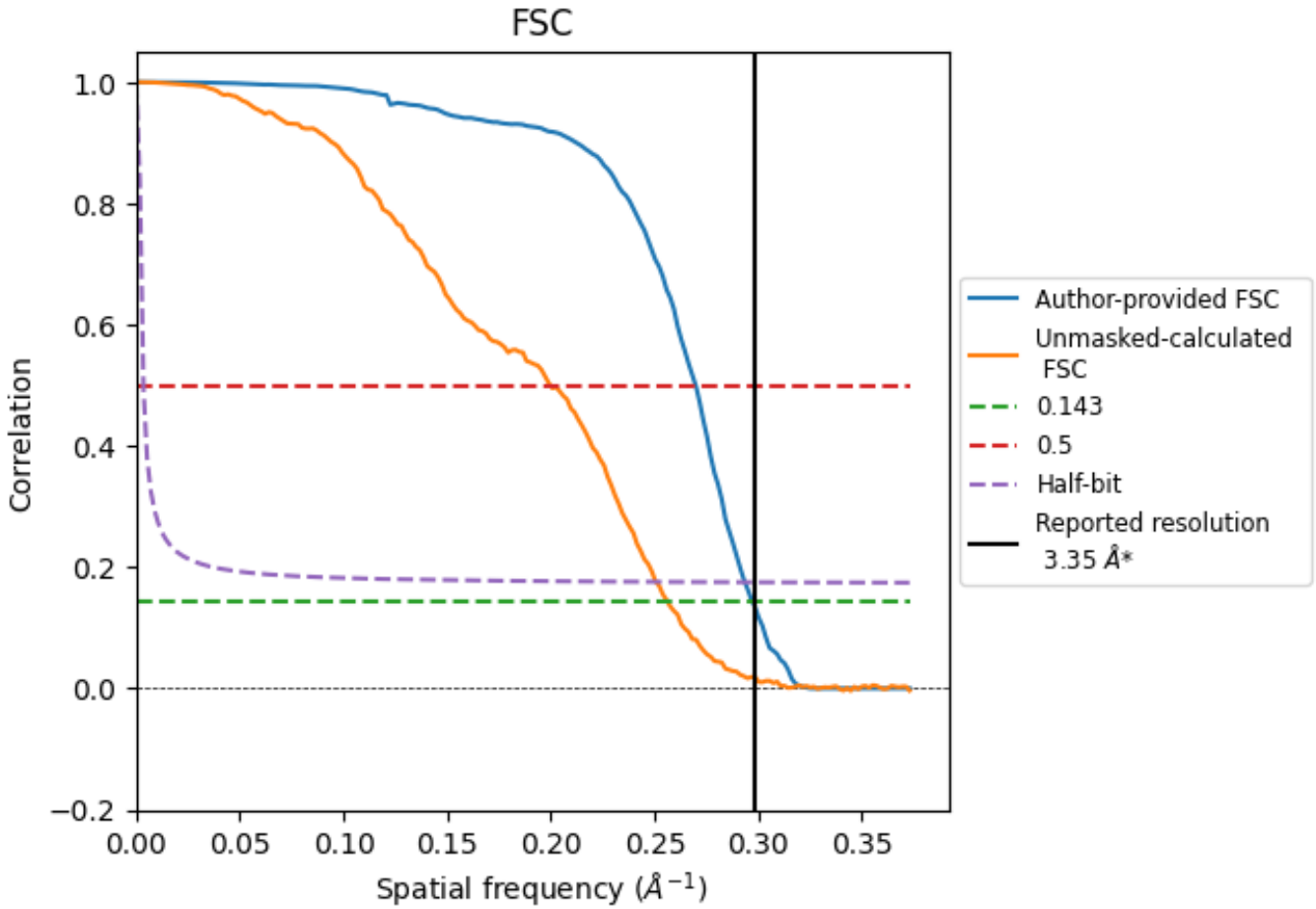


*Reported resolution corresponds to spatial frequency of 0.299 Å^{-1}

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 0.299 Å^{-1}

8.2 Resolution estimates (i)

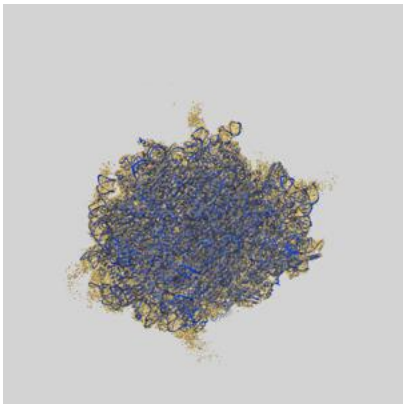
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	3.36	3.71	3.41
Unmasked-calculated*	3.90	5.01	3.99

*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 3.90 differs from the reported value 3.35 by more than 10 %

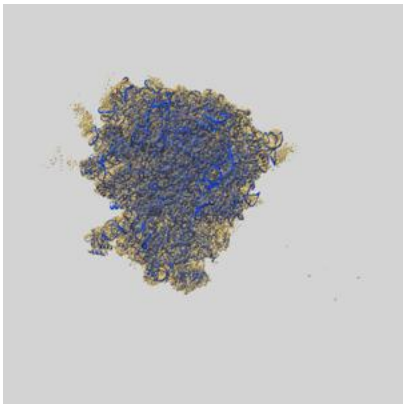
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4133 and PDB model 5LZV. Per-residue inclusion information can be found in section 3 on page 24.

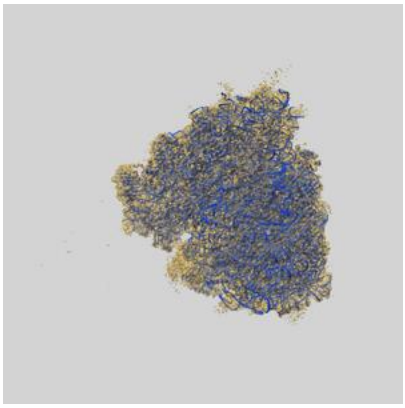
9.1 Map-model overlay



X



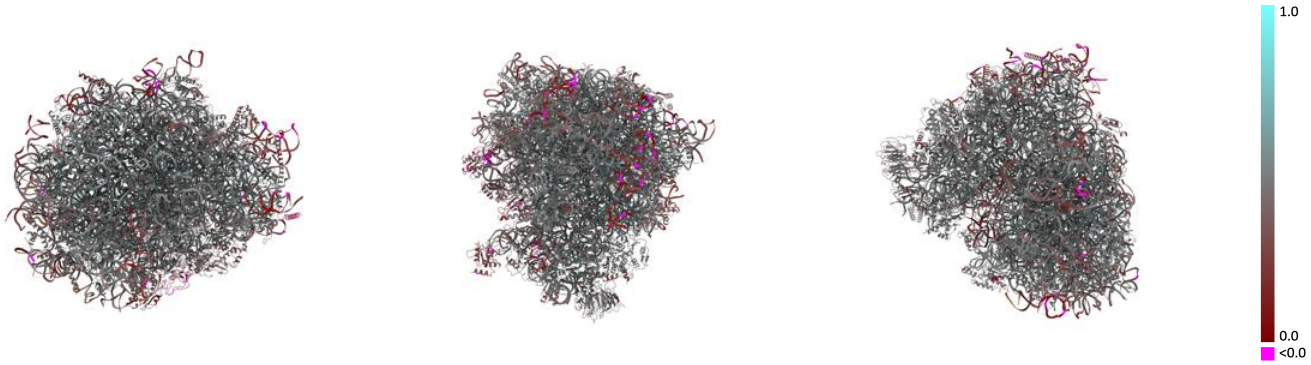
Y



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.

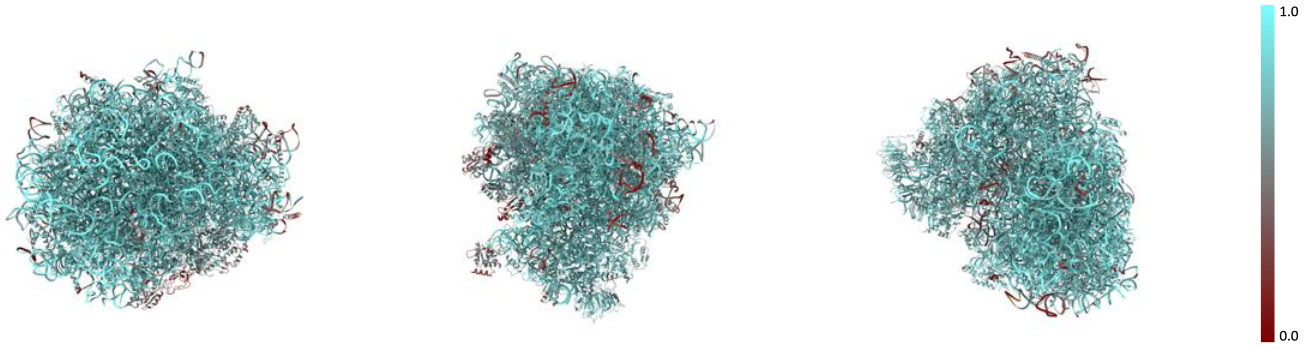
9.2 Q-score mapped to coordinate model



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.

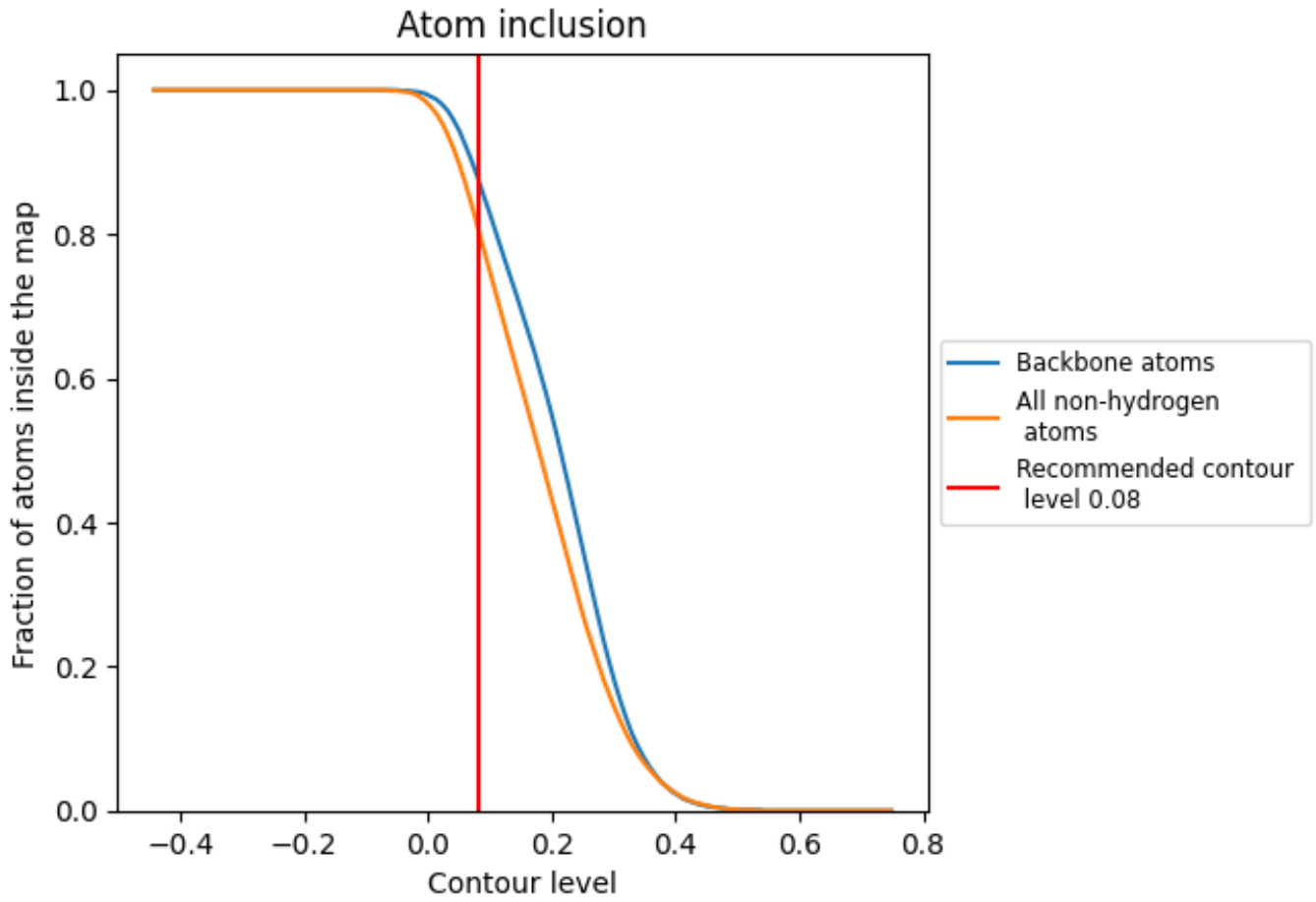
9.3 Atom inclusion mapped to coordinate model



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 (i)



At the recommended contour level, 88% of all backbone atoms, 81% 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	0.8100	0.4600
1	0.6940	0.4640
2	0.8290	0.4240
3	0.5220	0.2700
5	0.8750	0.4640
7	0.9270	0.4980
8	0.8880	0.4720
9	0.8650	0.4580
A	0.8170	0.5010
AA	0.7620	0.4790
B	0.7970	0.4860
BB	0.7620	0.4890
C	0.8120	0.4930
CC	0.7630	0.4860
D	0.8020	0.4710
DD	0.6950	0.4450
E	0.7860	0.4620
EE	0.7690	0.4830
F	0.7970	0.4930
FF	0.7330	0.4670
G	0.7260	0.4380
GG	0.7000	0.4270
H	0.7680	0.4710
HH	0.6720	0.4300
I	0.7660	0.4840
II	0.7570	0.4760
J	0.7450	0.4520
JJ	0.7580	0.4740
KK	0.7370	0.4460
L	0.7710	0.4640
LL	0.7890	0.4970
M	0.7890	0.4700
MM	0.4080	0.2890
N	0.8440	0.5100
NN	0.7740	0.4850



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Chain	Atom inclusion	Q-score
O	0.7960	0.4850
OO	0.7740	0.4920
P	0.8060	0.4980
PP	0.7400	0.4480
Q	0.8230	0.4930
QQ	0.7670	0.4780
R	0.7500	0.4510
RR	0.7060	0.4490
S	0.8160	0.4950
SS	0.7670	0.4670
T	0.7930	0.4810
TT	0.7680	0.4640
U	0.7380	0.4160
UU	0.6850	0.4390
V	0.7650	0.4880
VV	0.7480	0.4810
W	0.6340	0.3930
WW	0.7930	0.5020
X	0.7520	0.4580
XX	0.7910	0.5090
Y	0.7980	0.4760
YY	0.7650	0.4710
Z	0.7950	0.4630
ZZ	0.7190	0.4550
a	0.8480	0.5100
aa	0.7940	0.5010
b	0.6850	0.4250
bb	0.7200	0.4640
c	0.7470	0.4670
cc	0.7150	0.4700
d	0.7780	0.4710
dd	0.8100	0.5020
e	0.8100	0.5100
ee	0.6880	0.4560
f	0.8350	0.5020
ff	0.5100	0.3280
g	0.7800	0.4740
gg	0.6960	0.4420
h	0.7710	0.4740
hh	0.7450	0.4250
i	0.7450	0.4590
ii	0.5650	0.4080

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Chain	Atom inclusion	Q-score
j	0.8440	0.5030
jj	0.5990	0.4250
k	0.7110	0.4330
l	0.8310	0.4970
m	0.8100	0.4950
n	0.7750	0.4860
o	0.7930	0.4880
p	0.7530	0.4790
r	0.8350	0.5010
s	0.3340	0.2230
t	0.4890	0.3140