



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:19 PM UTC

PDB ID : 5LZY / pdb_00005lzy
EMDB ID : EMD-4136
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l assembled on a polyadenylated mRNA.
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.99 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

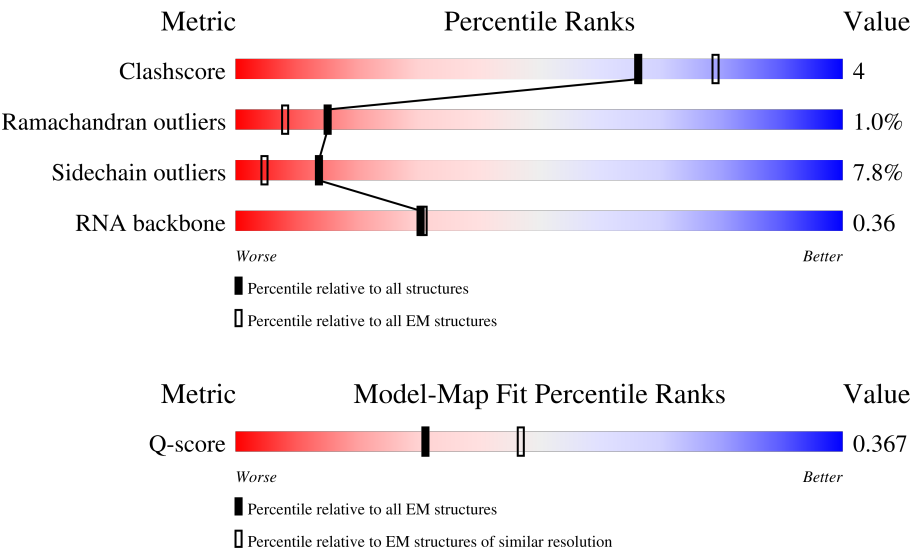
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.99 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.



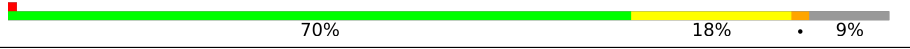
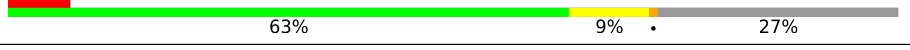
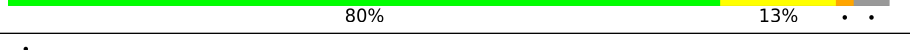
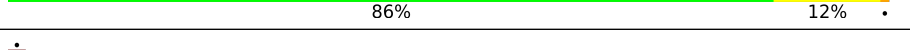
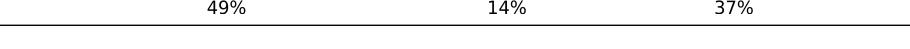
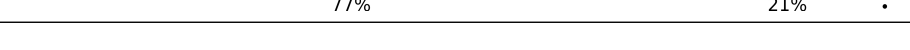
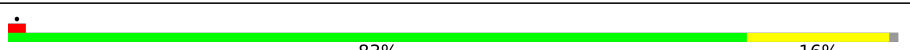
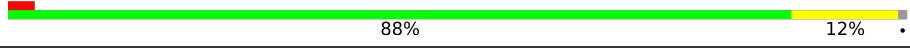
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7463 (3.49 - 4.49)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	425	

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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	2	75	
45	3	75	
46	5	3543	
47	7	120	
48	8	156	
49	9	1869	
50	AA	295	
51	BB	264	
52	CC	293	

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Mol	Chain	Length	Quality of chain
53	DD	243	
54	EE	263	
55	FF	204	
56	GG	249	
57	HH	194	
58	II	208	
59	JJ	194	
60	KK	165	
61	LL	158	
62	MM	132	
63	NN	151	
64	OO	168	
65	PP	145	
66	QQ	146	
67	RR	135	
68	SS	152	
69	TT	145	
70	UU	119	
71	VV	83	
72	WW	130	
73	XX	143	
74	YY	130	
75	ZZ	125	
76	aa	115	
77	bb	84	

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Mol	Chain	Length	Quality of chain
78	cc	69	
79	dd	56	
80	ee	133	
81	ff	156	
82	gg	317	
83	hh	8	
84	ii	403	
85	jj	710	

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
87	ZN	m	200	-	-	X	-
87	ZN	p	100	-	-	X	-

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221912 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	-	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 60S ribosomal protein L5.

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	-	initiating methionine	UNP G1SYJ6

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

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

- Molecule 6 is a protein called 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 Ribosomal protein L10 (Predicted).

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 Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
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 eL14.

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 eL23.

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

- Molecule 24 is a protein called uL24.

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

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

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

- Molecule 26 is a protein called 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		

- 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 60S ribosomal protein L36.

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

- Molecule 35 is a protein called 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
45	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 46 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 50 is a protein called uS2.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called uS5.

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

- Molecule 53 is a protein called uS3.

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

- Molecule 54 is a protein called eS4.

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

- Molecule 55 is a protein called uS7.

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

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called eS7.

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

- Molecule 58 is a protein called eS8.

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

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 60 is a protein called eS10.

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

- Molecule 61 is a protein called uS17.

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

- Molecule 62 is a protein called 40S ribosomal protein S12.

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

- Molecule 63 is a protein called uS15.

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

- Molecule 64 is a protein called uS11.

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

- Molecule 65 is a protein called uS19.

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

- Molecule 66 is a protein called uS9.

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

- Molecule 67 is a protein called eS17.

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

- Molecule 68 is a protein called uS13.

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

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	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 70 is a protein called uS10.

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

- Molecule 71 is a protein called eS21.

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

- Molecule 72 is a protein called uS8.

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

- Molecule 73 is a protein called uS12.

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

- Molecule 74 is a protein called eS24.

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

- Molecule 75 is a protein called eS25.

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

- Molecule 76 is a protein called eS26.

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

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called eS28.

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

- Molecule 79 is a protein called uS14.

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

- Molecule 80 is a protein called eS30.

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

- Molecule 81 is a protein called eS31.

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

- Molecule 82 is a protein called RACK1.

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

- Molecule 83 is a RNA chain called mRNA (polyadenylated).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	hh	8	Total	C	N	O	P	0	0
			176	80	40	48	8		

- Molecule 84 is a protein called Protein pelota homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ii	372	Total	C	N	O	S	0	0
			2947	1844	528	559	16		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	221	MET	LEU	variant	UNP Q9BRX2
ii	386	GLY	-	expression tag	UNP Q9BRX2
ii	387	SER	-	expression tag	UNP Q9BRX2
ii	388	GLU	-	expression tag	UNP Q9BRX2
ii	389	ASN	-	expression tag	UNP Q9BRX2
ii	390	LEU	-	expression tag	UNP Q9BRX2
ii	391	TYR	-	expression tag	UNP Q9BRX2
ii	392	PHE	-	expression tag	UNP Q9BRX2
ii	393	GLN	-	expression tag	UNP Q9BRX2
ii	394	GLY	-	expression tag	UNP Q9BRX2
ii	395	ALA	-	expression tag	UNP Q9BRX2
ii	396	HIS	-	expression tag	UNP Q9BRX2
ii	397	HIS	-	expression tag	UNP Q9BRX2
ii	398	HIS	-	expression tag	UNP Q9BRX2
ii	399	HIS	-	expression tag	UNP Q9BRX2
ii	400	HIS	-	expression tag	UNP Q9BRX2
ii	401	HIS	-	expression tag	UNP Q9BRX2
ii	402	SER	-	expression tag	UNP Q9BRX2
ii	403	THR	-	expression tag	UNP Q9BRX2

- Molecule 85 is a protein called HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	jj	425	Total	C	N	O	S	0	0
			3292	2100	565	609	18		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-25	MET	-	initiating methionine	UNP Q9Y450
jj	-24	ASP	-	expression tag	UNP Q9Y450
jj	-23	TYR	-	expression tag	UNP Q9Y450
jj	-22	LYS	-	expression tag	UNP Q9Y450
jj	-21	ASP	-	expression tag	UNP Q9Y450
jj	-20	HIS	-	expression tag	UNP Q9Y450
jj	-19	ASP	-	expression tag	UNP Q9Y450
jj	-18	GLY	-	expression tag	UNP Q9Y450
jj	-17	ASP	-	expression tag	UNP Q9Y450
jj	-16	TYR	-	expression tag	UNP Q9Y450
jj	-15	LYS	-	expression tag	UNP Q9Y450
jj	-14	ASP	-	expression tag	UNP Q9Y450
jj	-13	HIS	-	expression tag	UNP Q9Y450
jj	-12	ASP	-	expression tag	UNP Q9Y450

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Chain	Residue	Modelled	Actual	Comment	Reference
jj	-11	ILE	-	expression tag	UNP Q9Y450
jj	-10	ASP	-	expression tag	UNP Q9Y450
jj	-9	TYR	-	expression tag	UNP Q9Y450
jj	-8	LYS	-	expression tag	UNP Q9Y450
jj	-7	ASP	-	expression tag	UNP Q9Y450
jj	-6	ASP	-	expression tag	UNP Q9Y450
jj	-5	ASP	-	expression tag	UNP Q9Y450
jj	-4	ASP	-	expression tag	UNP Q9Y450
jj	-3	LYS	-	expression tag	UNP Q9Y450
jj	-2	ALA	-	expression tag	UNP Q9Y450
jj	-1	GLY	-	expression tag	UNP Q9Y450
jj	0	SER	-	expression tag	UNP Q9Y450

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	B	1	Total	Mg	0
			1	1	
86	I	1	Total	Mg	0
			1	1	
86	L	1	Total	Mg	0
			1	1	
86	P	1	Total	Mg	0
			1	1	
86	Q	1	Total	Mg	0
			1	1	
86	V	1	Total	Mg	0
			1	1	
86	a	1	Total	Mg	0
			1	1	
86	e	1	Total	Mg	0
			1	1	
86	j	1	Total	Mg	0
			1	1	
86	5	160	Total	Mg	0
			160	160	
86	7	5	Total	Mg	0
			5	5	
86	8	3	Total	Mg	0
			3	3	
86	9	58	Total	Mg	0
			58	58	

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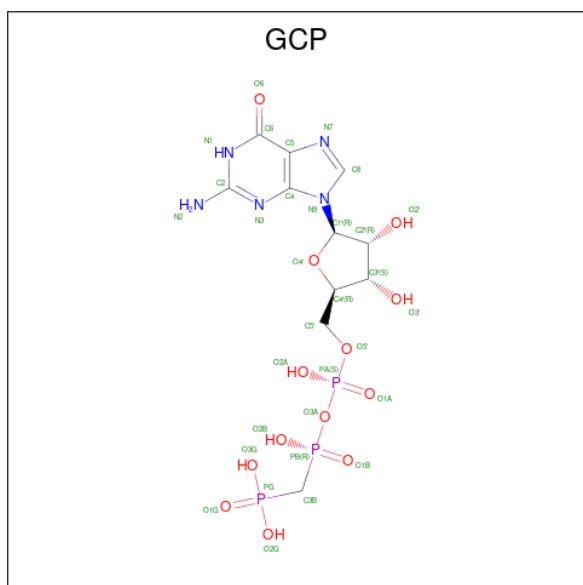
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Mol	Chain	Residues	Atoms		AltConf
86	jj	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 88 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

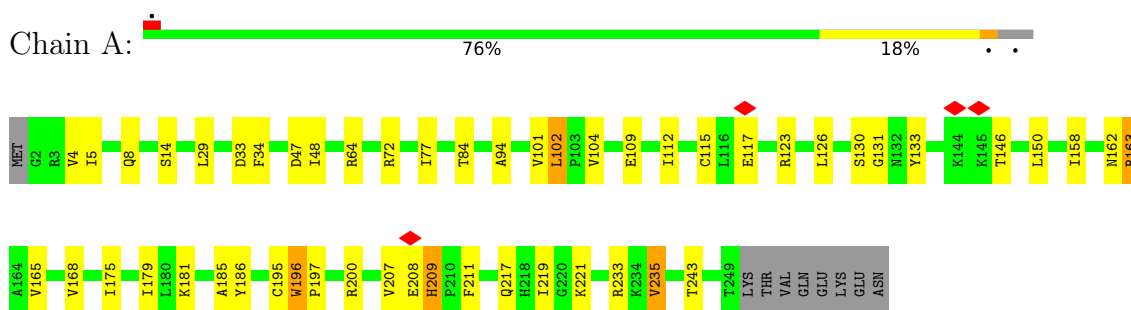


Mol	Chain	Residues	Atoms					AltConf
88	jj	1	Total	C	N	O	P	0
			32	11	5	13	3	

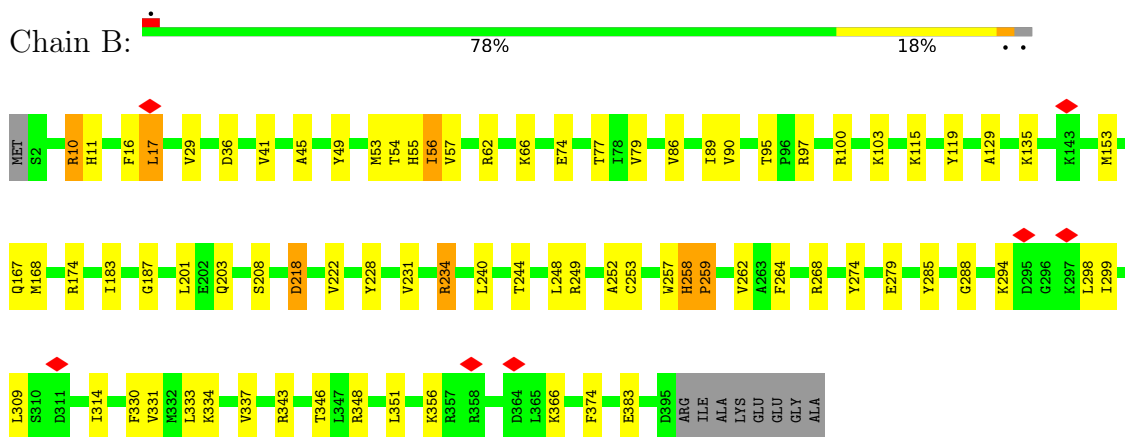
3 Residue-property plots

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

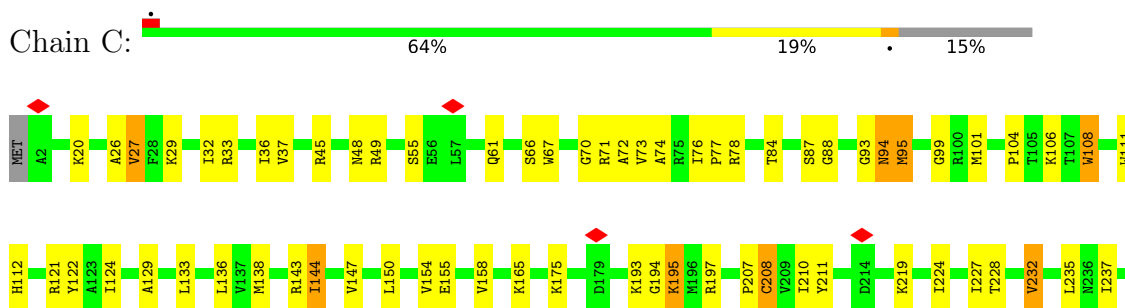
• Molecule 1: uL2



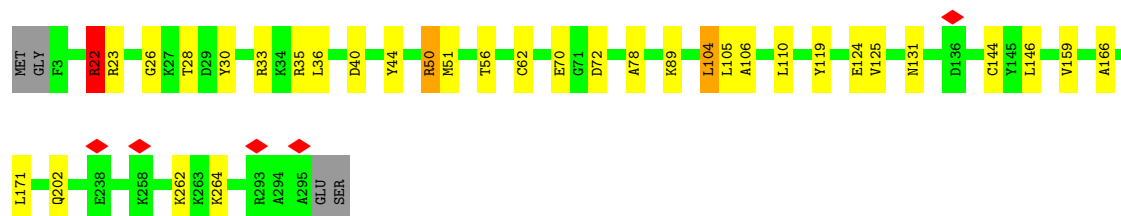
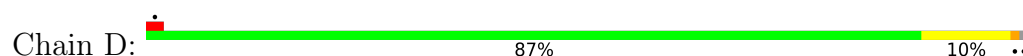
• Molecule 2: uL3



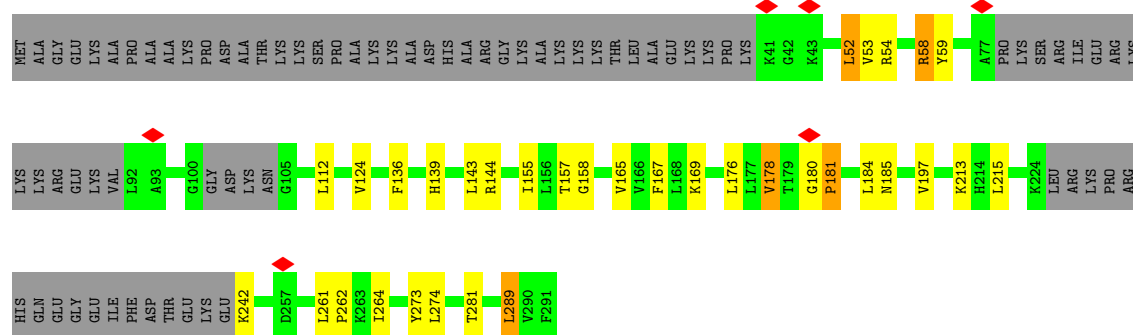
• Molecule 3: uL4



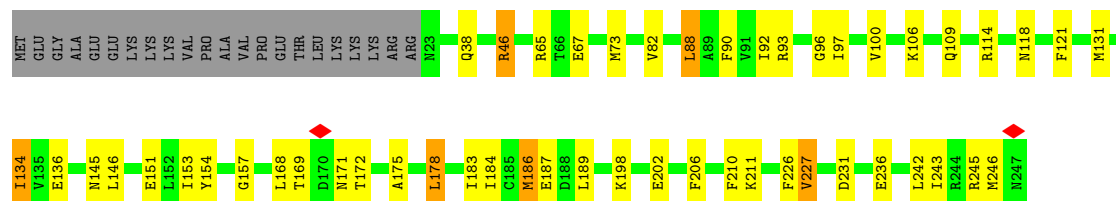
- Molecule 4: 60S ribosomal protein L5



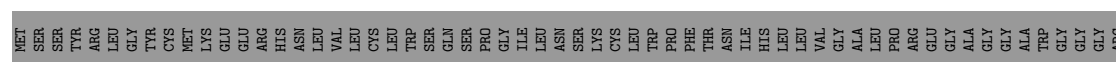
- Molecule 5: 60S ribosomal protein L6

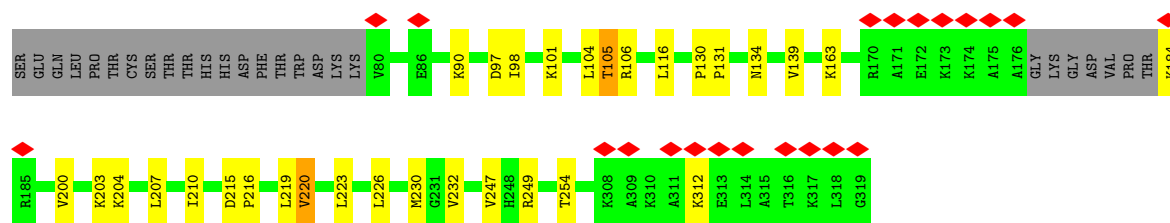


- Molecule 6: uL30

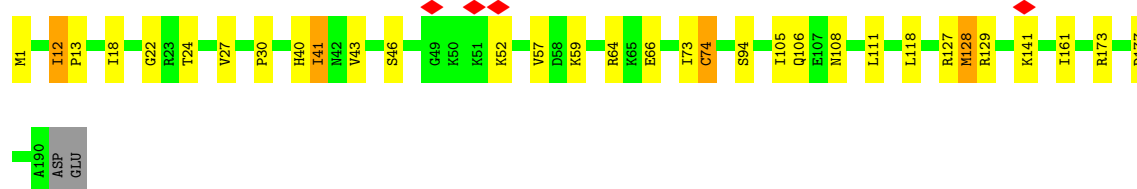
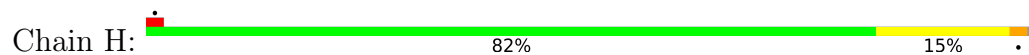


- Molecule 7: eL8

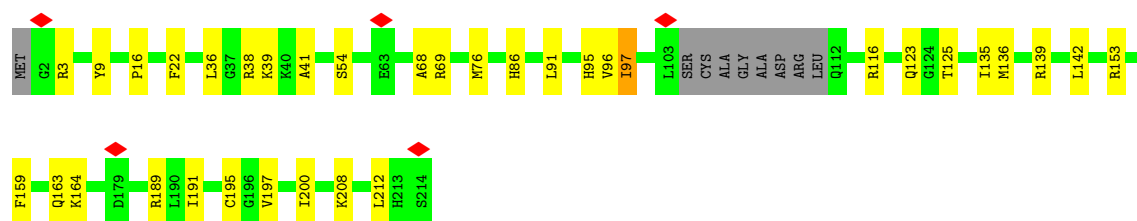
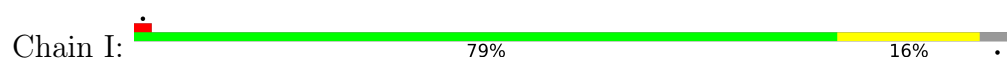




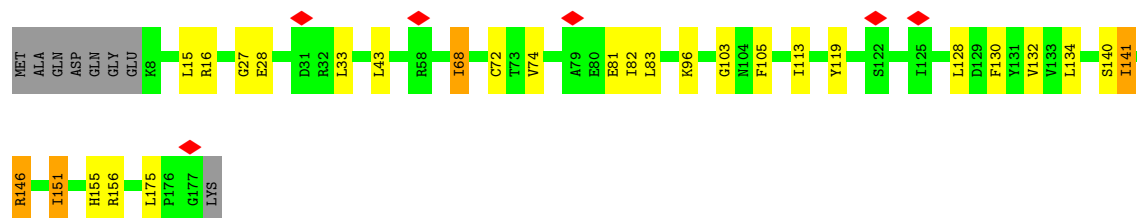
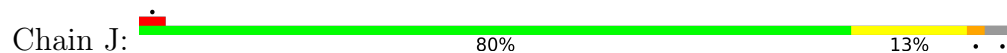
• Molecule 8: uL6



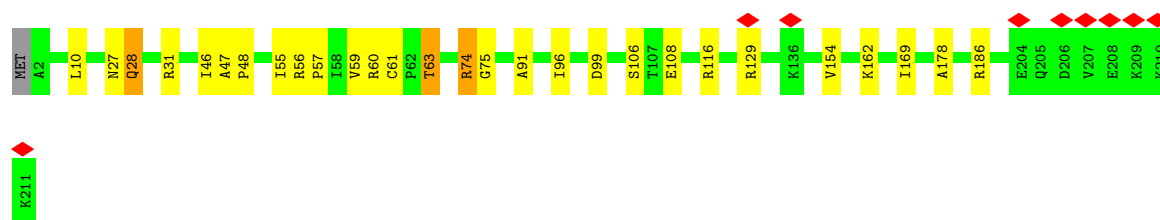
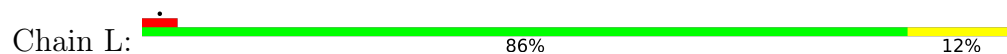
• Molecule 9: Ribosomal protein L10 (Predicted)



• Molecule 10: uL5

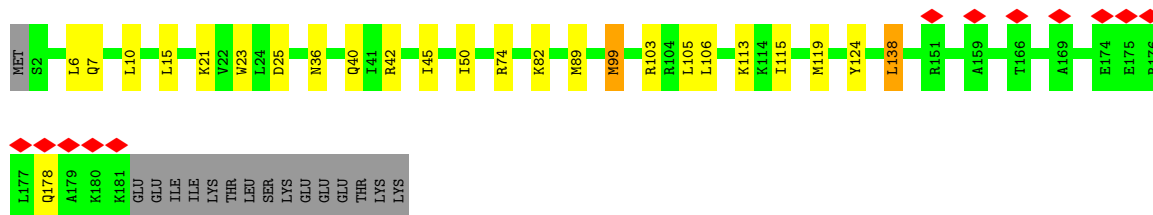
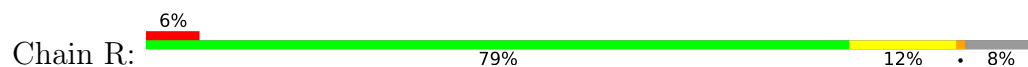


• Molecule 11: eL13

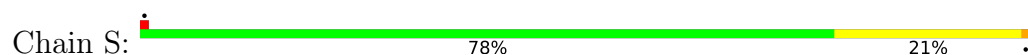




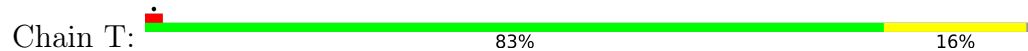
• Molecule 17: eL19



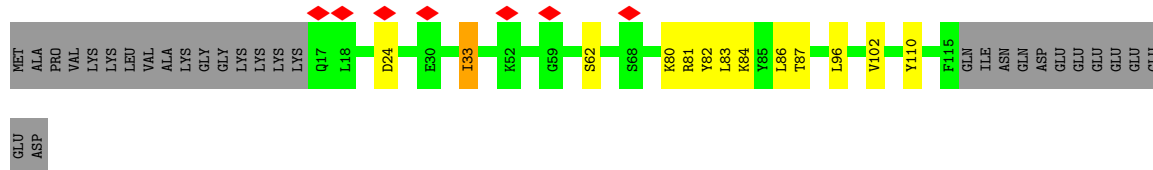
• Molecule 18: eL20



• Molecule 19: eL21



• Molecule 20: eL22

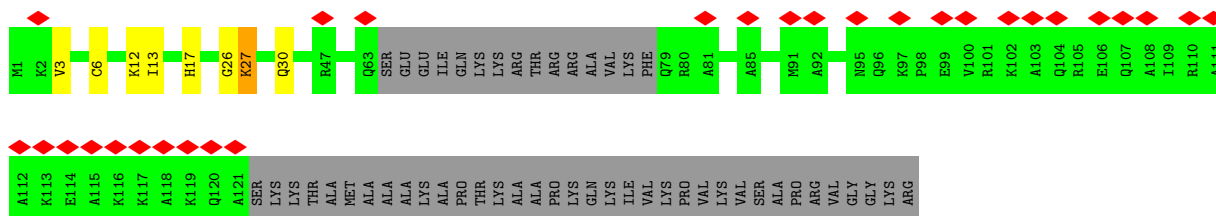


• Molecule 21: eL14

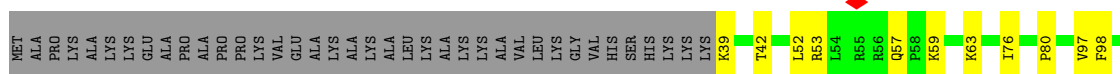




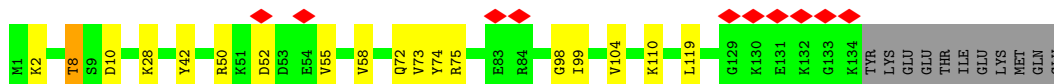
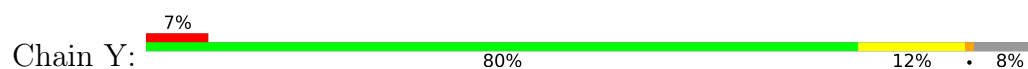
- Molecule 22: eL24



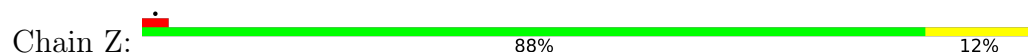
- Molecule 23: eL23



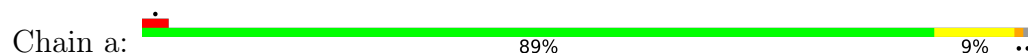
- Molecule 24: uL24



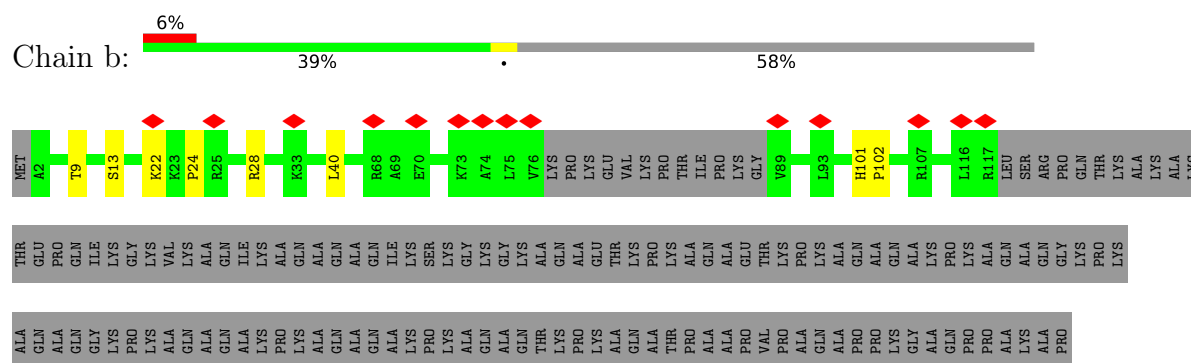
- Molecule 25: 60S ribosomal protein L27



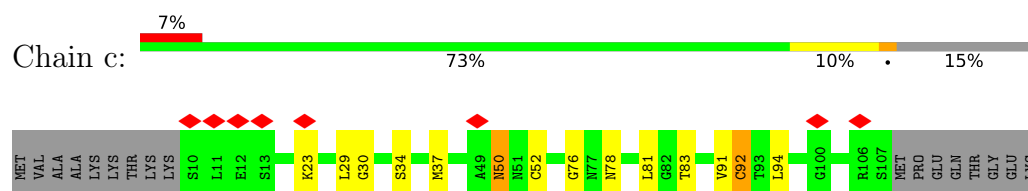
- Molecule 26: uL15



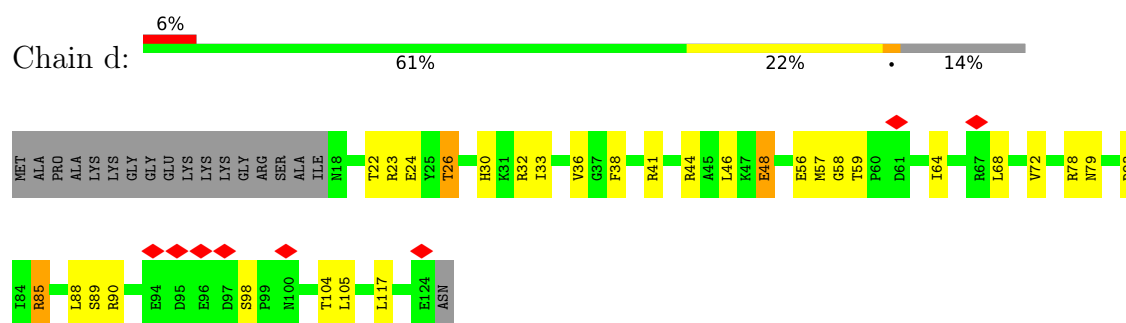
- Molecule 27: eL29



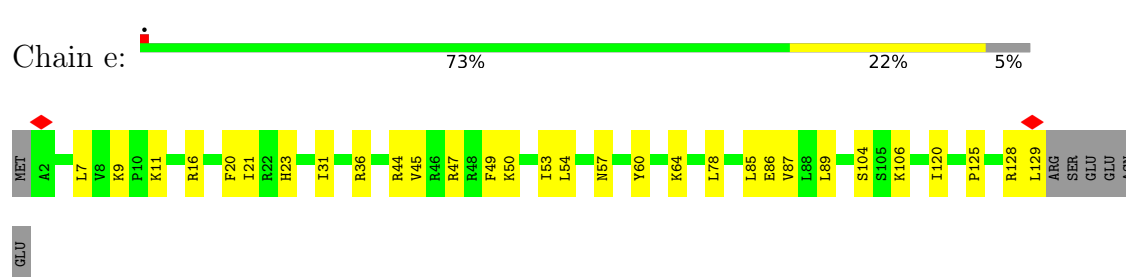
- Molecule 28: eL30



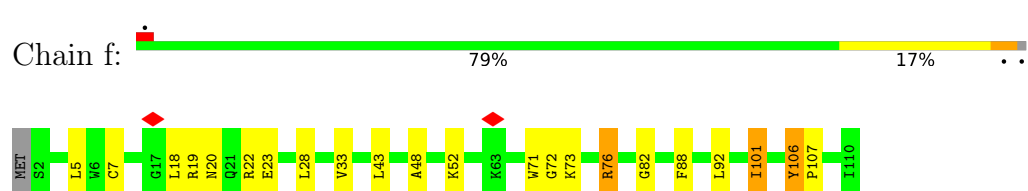
- Molecule 29: eL31



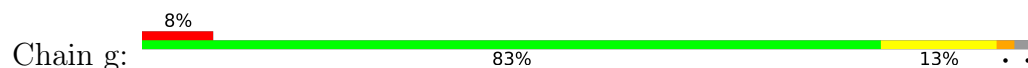
- Molecule 30: eL32

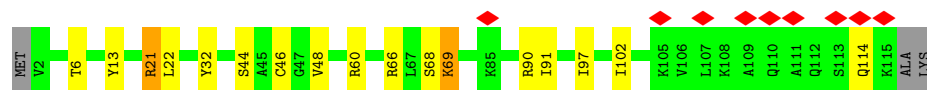


- Molecule 31: eL33

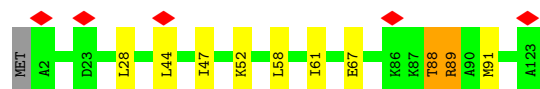
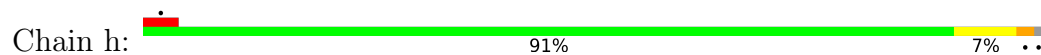


- Molecule 32: eL34

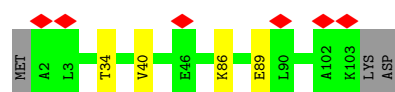




• Molecule 33: uL29



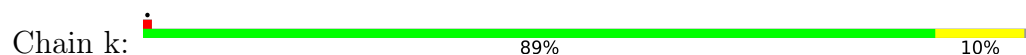
• Molecule 34: 60S ribosomal protein L36



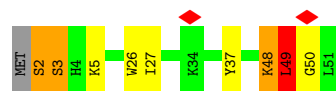
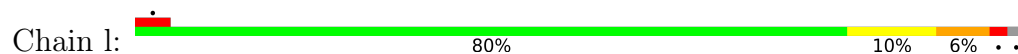
• Molecule 35: eL37



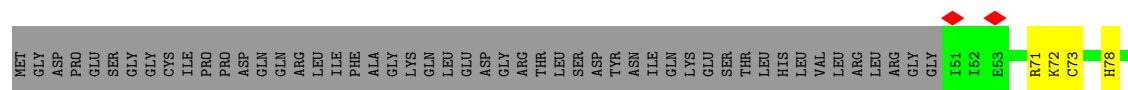
• Molecule 36: eL38



• Molecule 37: eL39

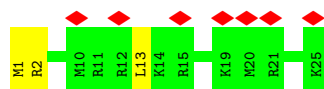
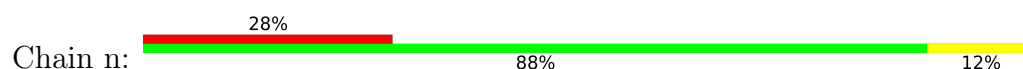


• Molecule 38: eL40

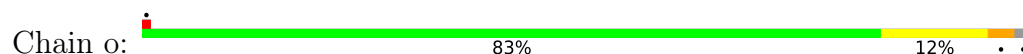




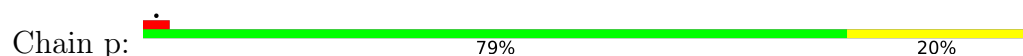
• Molecule 39: eL41



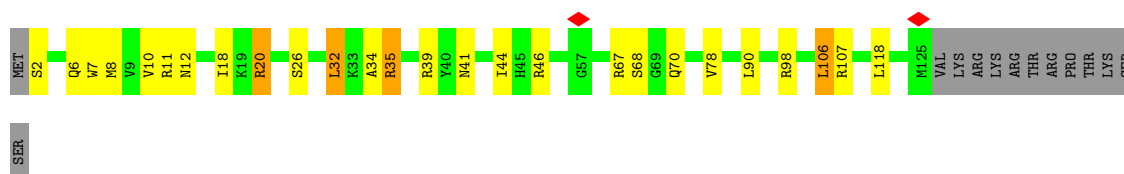
• Molecule 40: eL42



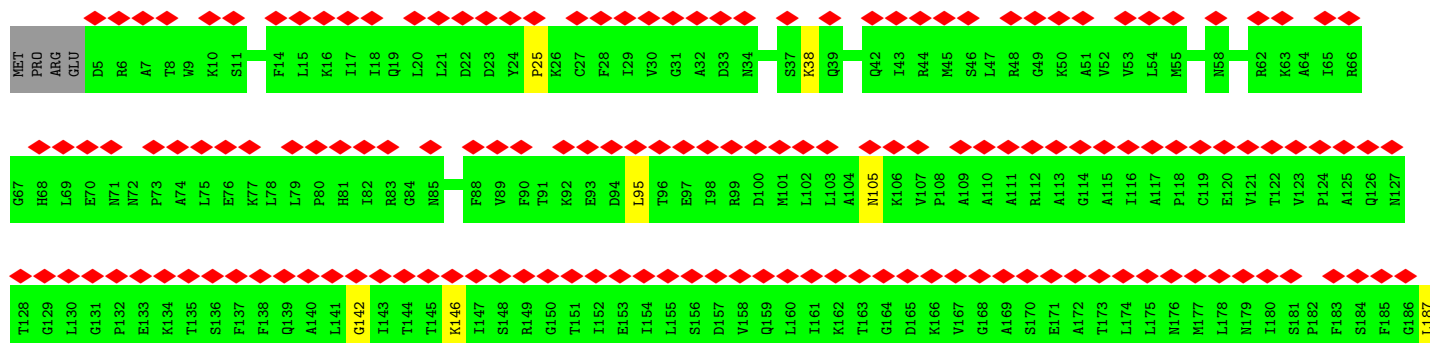
• Molecule 41: eL43



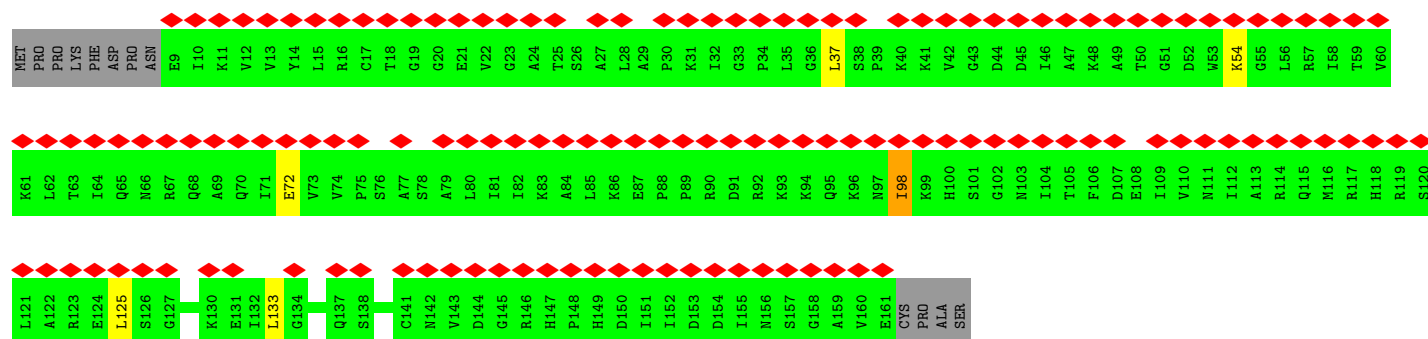
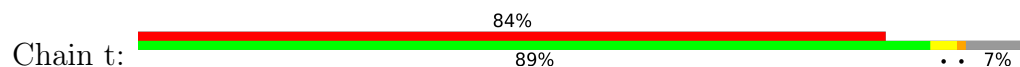
• Molecule 42: eL28



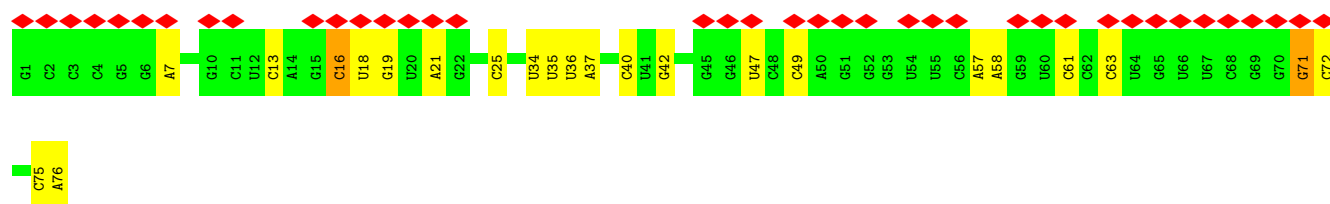
• Molecule 43: uL10



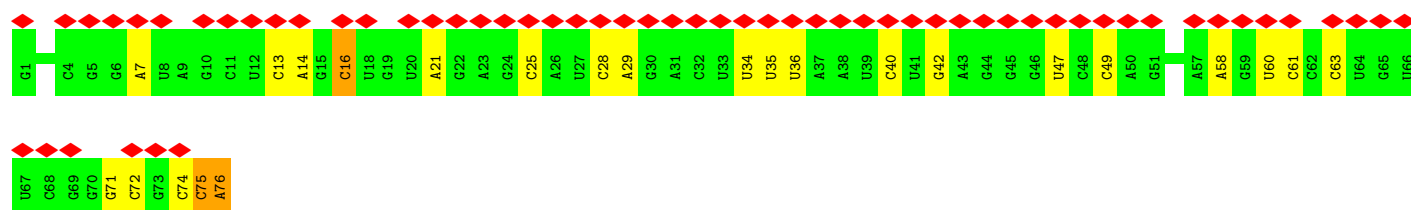
- Molecule 44: uL11



- Molecule 45: tRNA



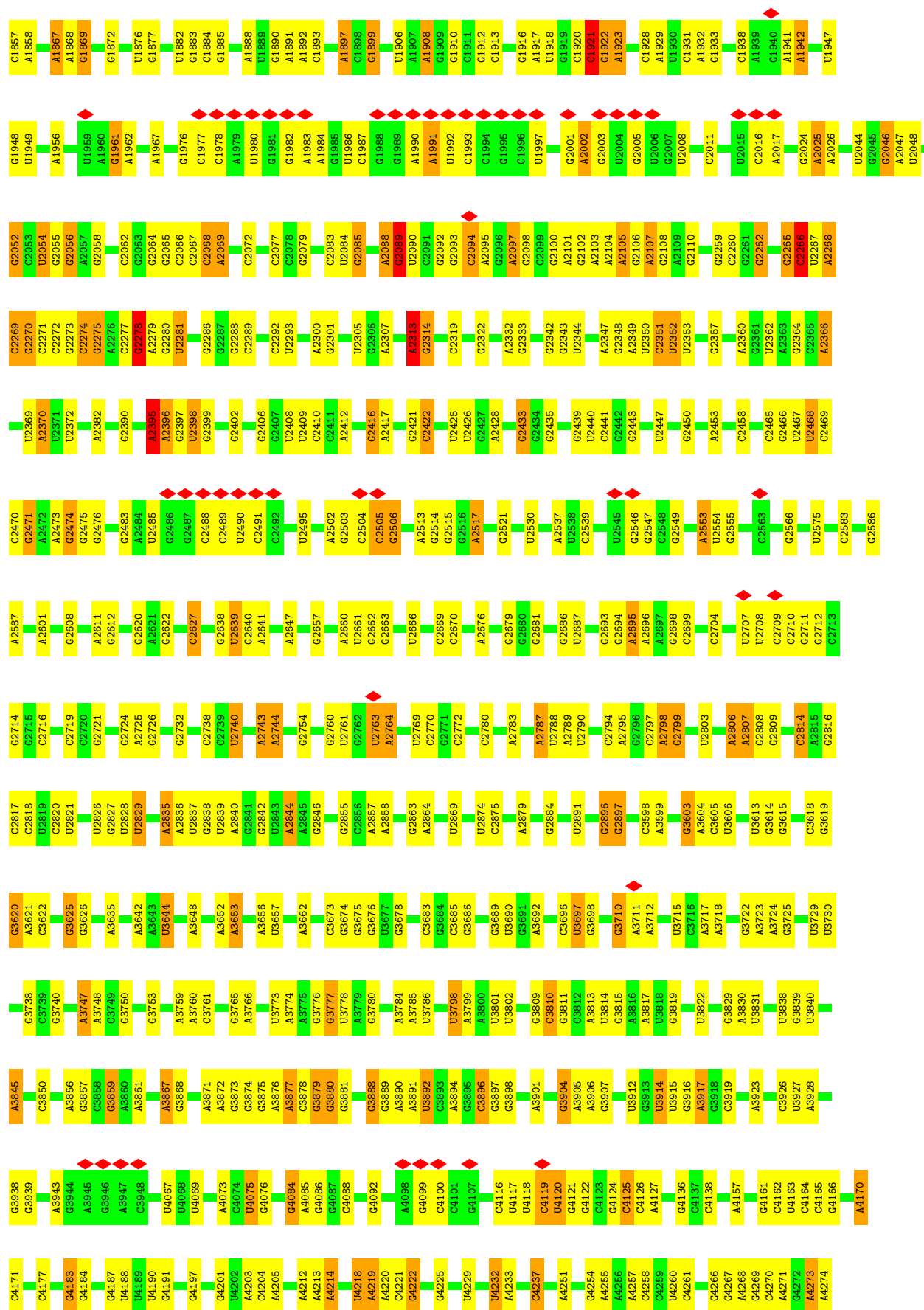
- Molecule 45: tRNA

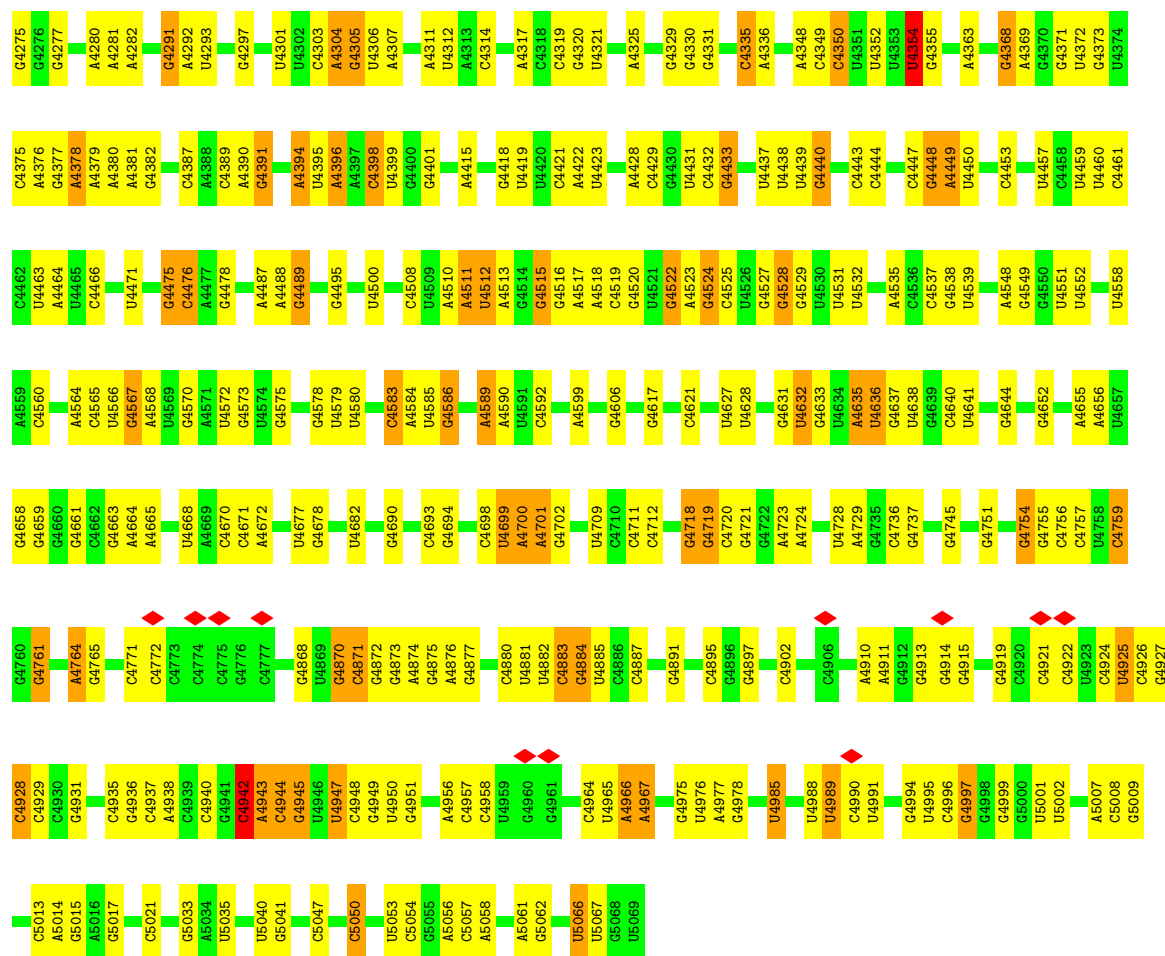


- Molecule 46: 28S ribosomal RNA









• Molecule 47: 5S ribosomal RNA



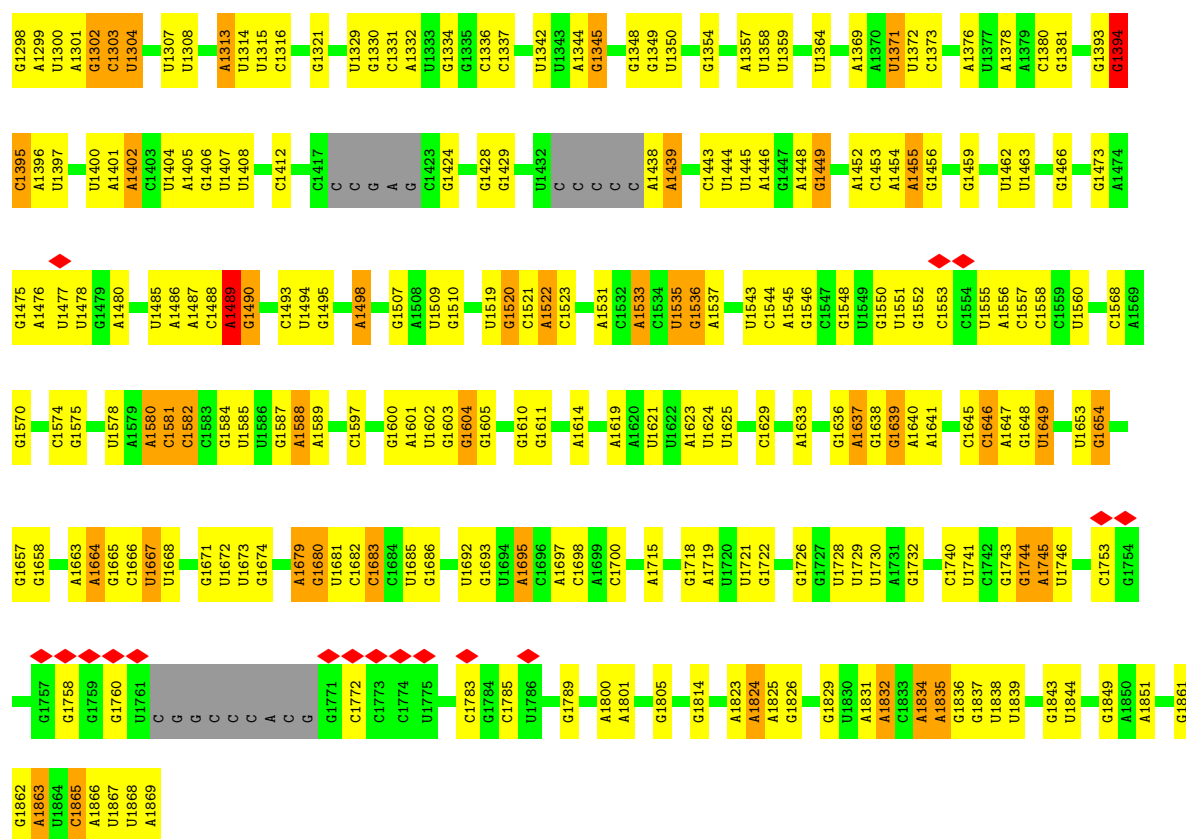
• Molecule 48: 5.8S ribosomal RNA



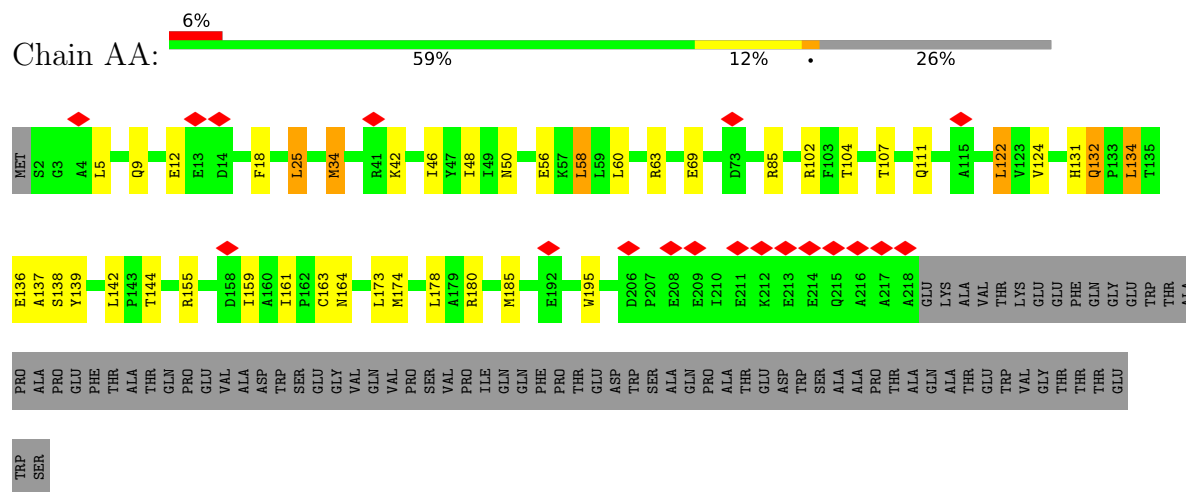
• Molecule 49: 18S ribosomal RNA



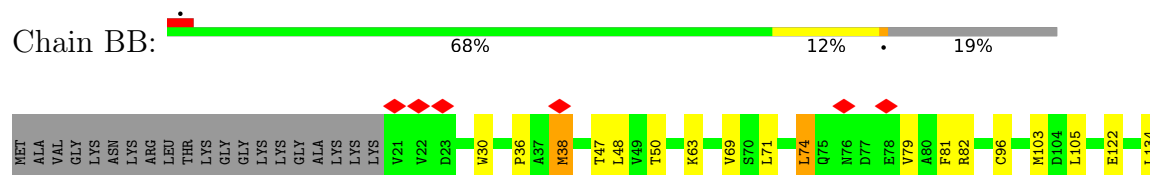


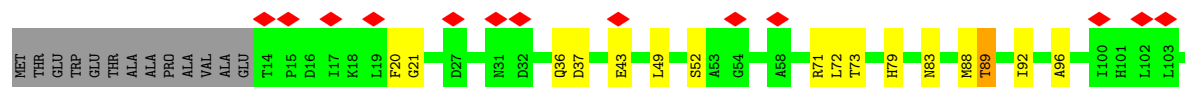
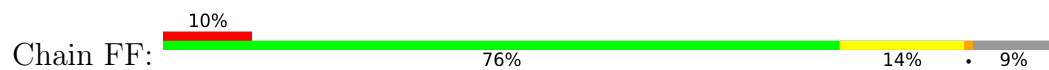
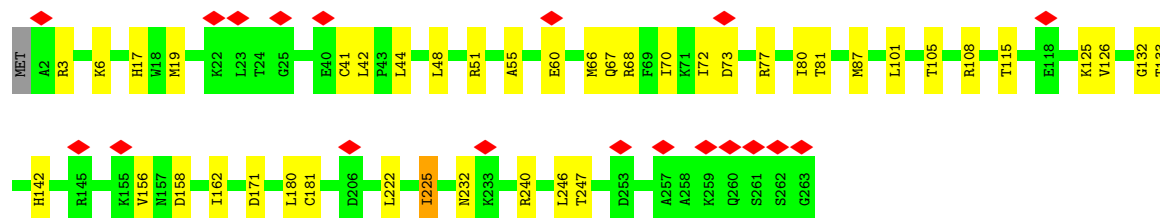
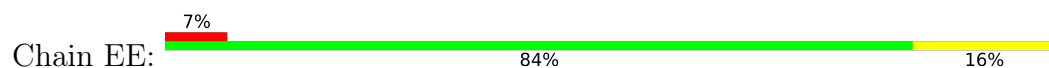
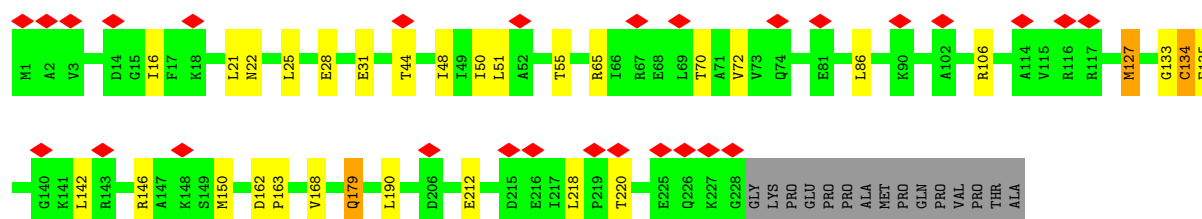
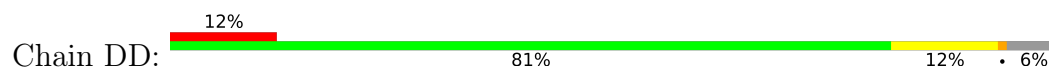
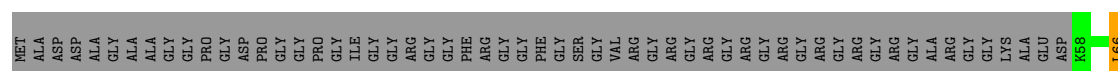


• Molecule 50: uS2



• Molecule 51: 40S ribosomal protein S3a

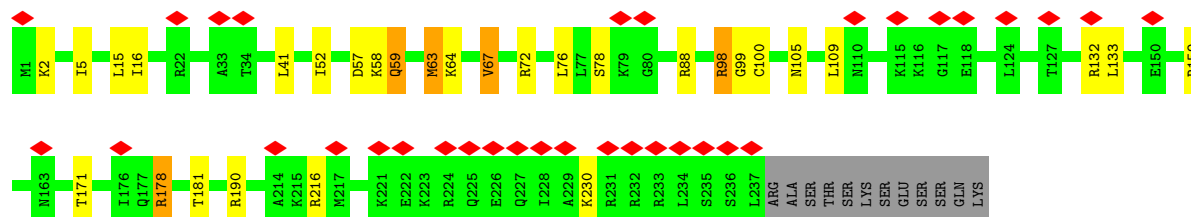






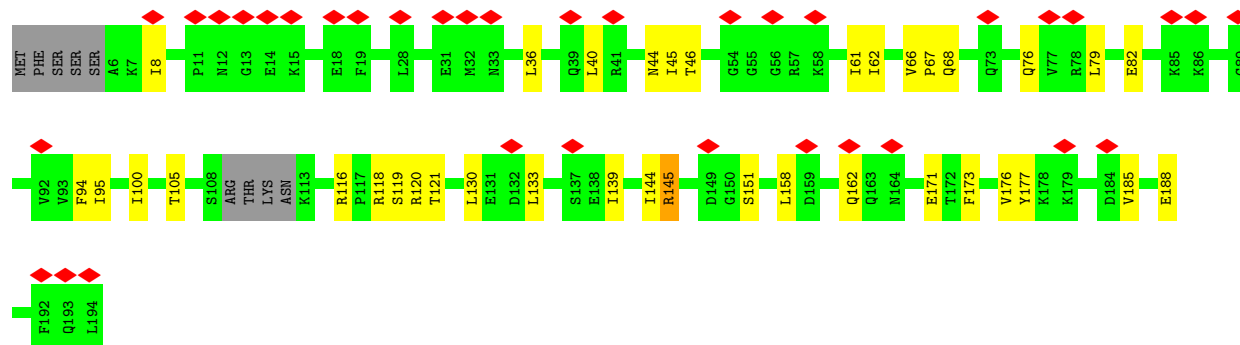
- Molecule 56: 40S ribosomal protein S6

Chain GG: 13% 83% 10% • 5%



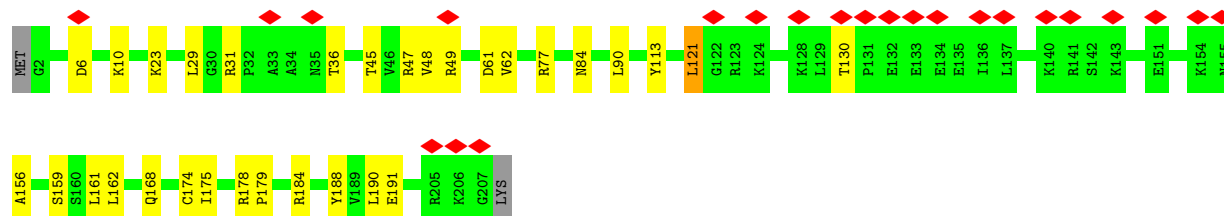
- Molecule 57: eS7

Chain HH: 18% 76% 19% • 5%



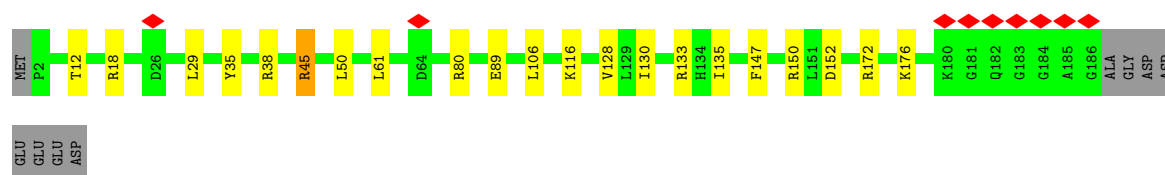
- Molecule 58: eS8

Chain II: 11% 84% 14%

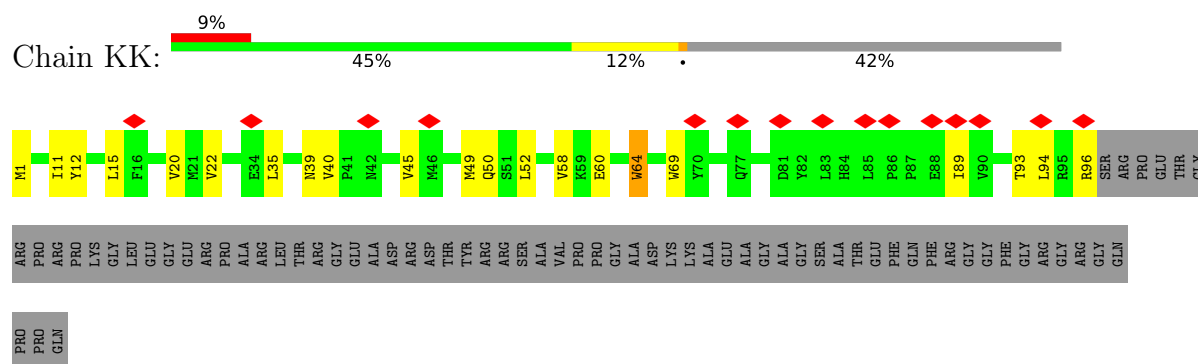


- Molecule 59: Ribosomal protein S9 (Predicted)

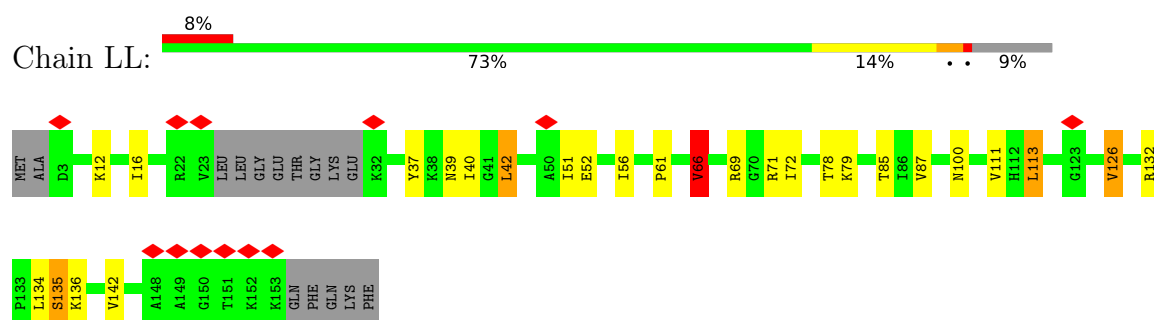
Chain JJ: 5% 85% 10% • 5%



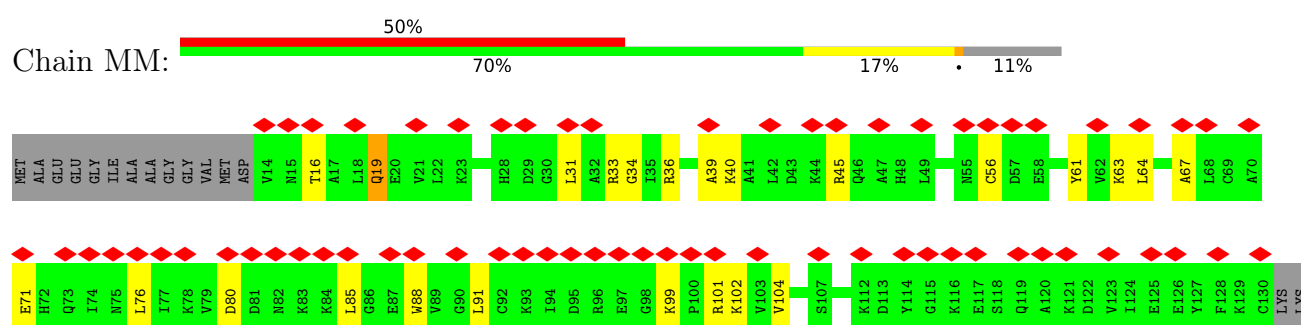
- Molecule 60: eS10



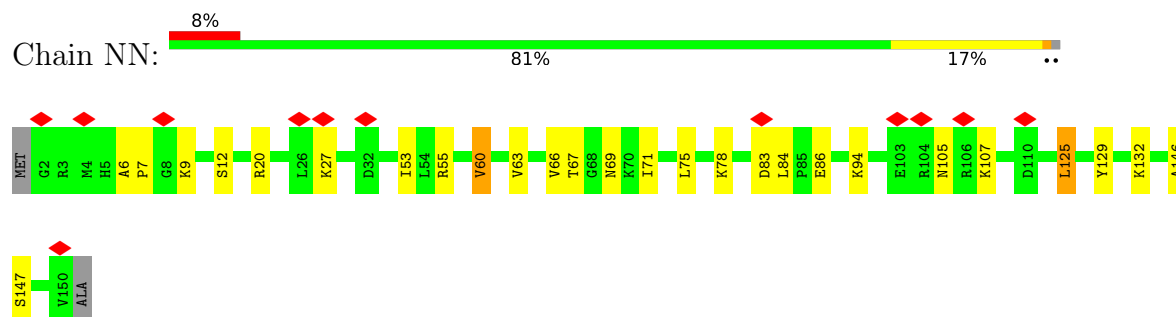
- Molecule 61: uS17



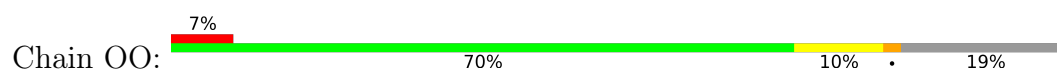
- Molecule 62: 40S ribosomal protein S12

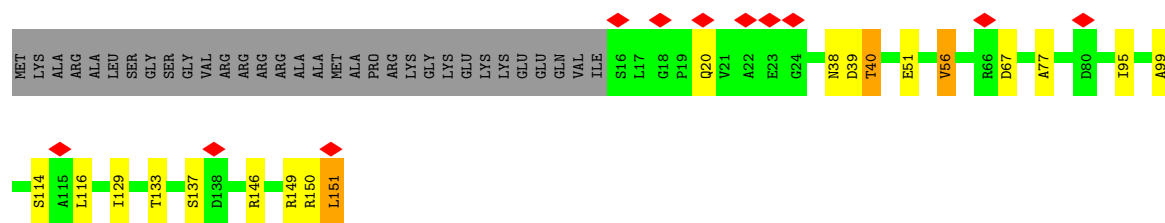


- Molecule 63: uS15

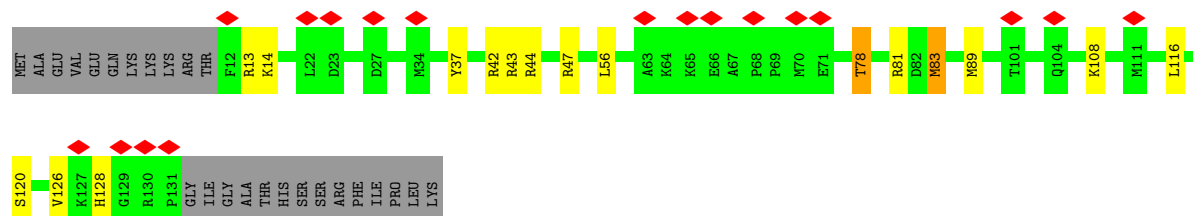
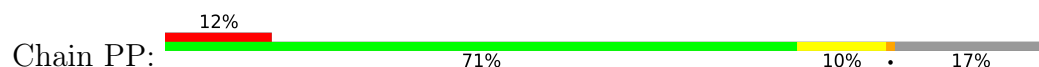


- Molecule 64: uS11

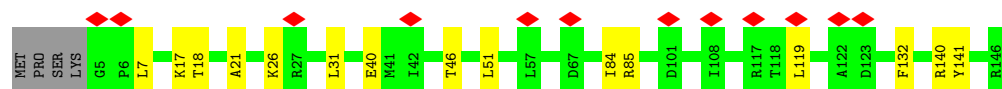
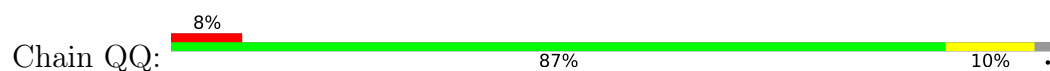




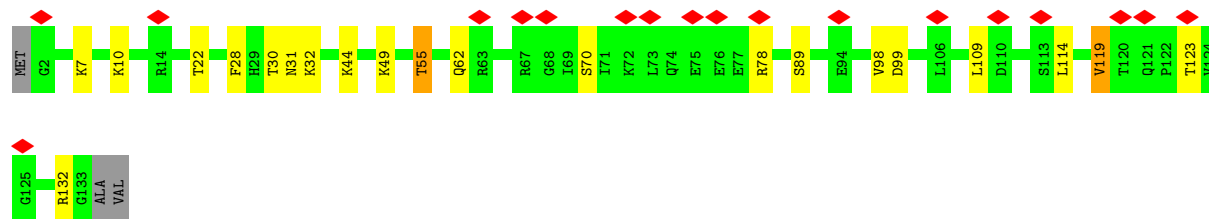
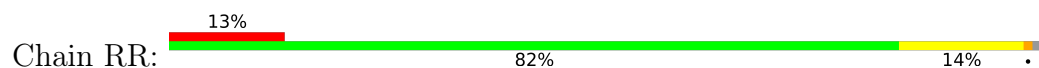
• Molecule 65: uS19



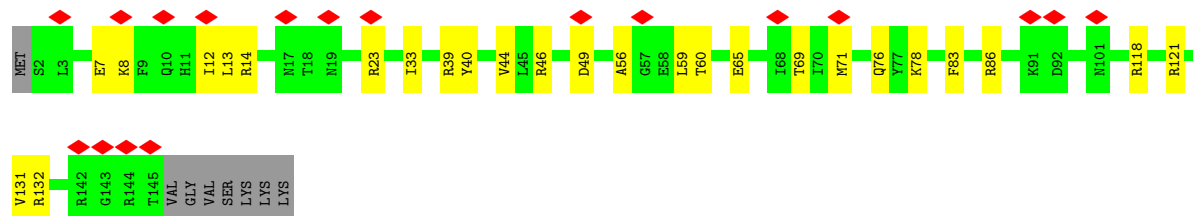
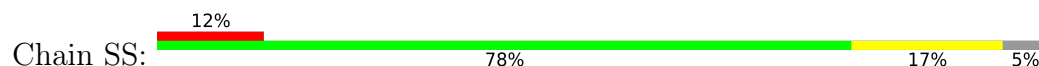
• Molecule 66: uS9



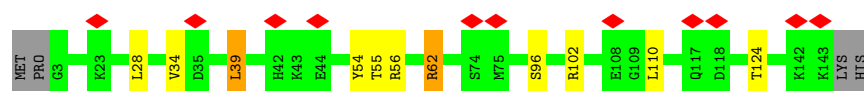
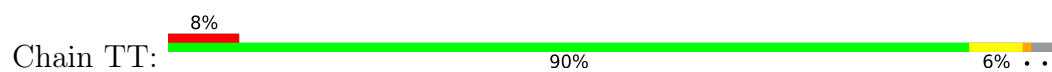
• Molecule 67: eS17



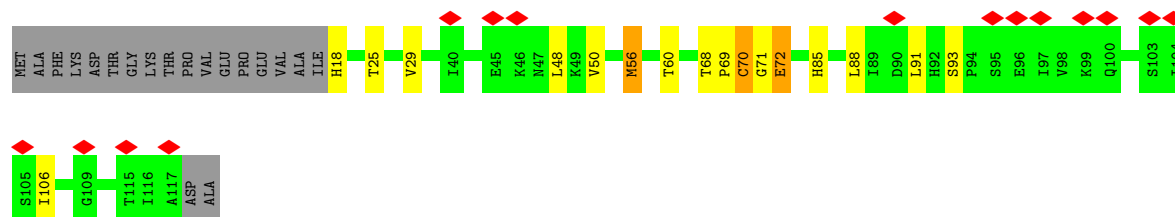
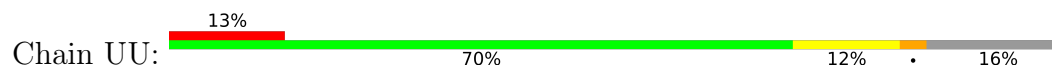
• Molecule 68: uS13



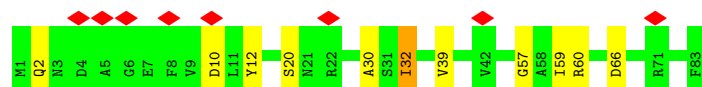
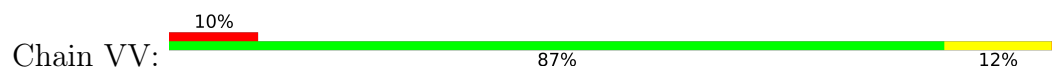
• Molecule 69: eS19



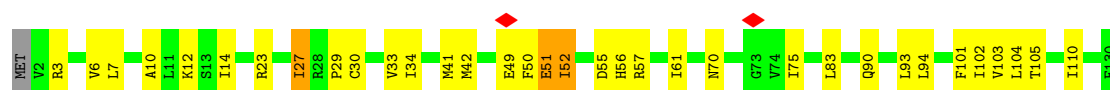
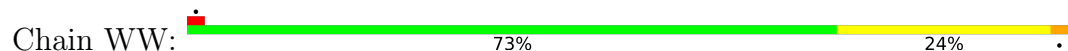
• Molecule 70: uS10



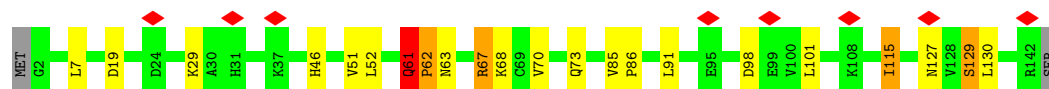
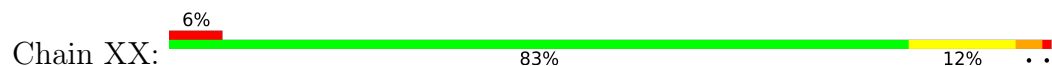
• Molecule 71: eS21



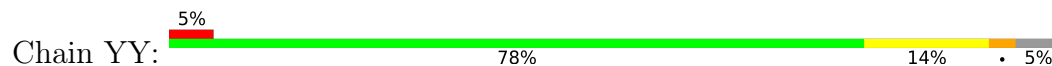
• Molecule 72: uS8



• Molecule 73: uS12

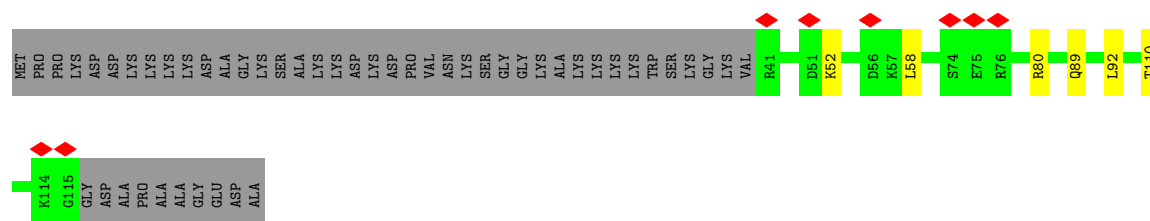


• Molecule 74: eS24

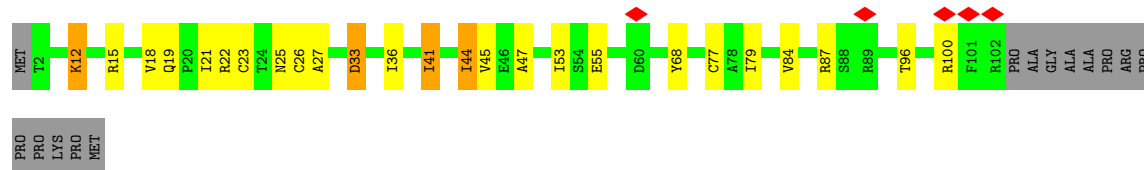


• Molecule 75: eS25

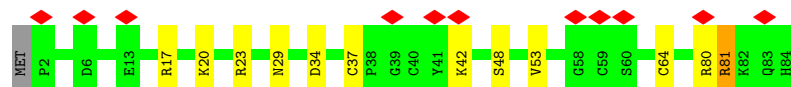
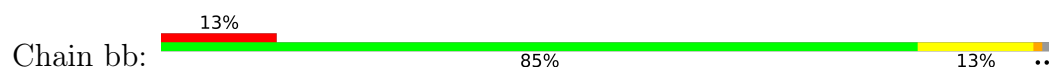




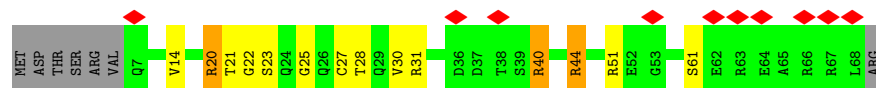
- Molecule 76: eS26



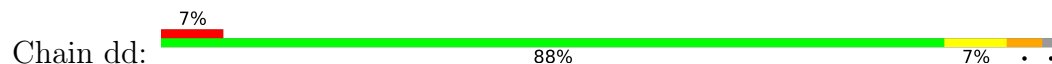
- Molecule 77: 40S ribosomal protein S27



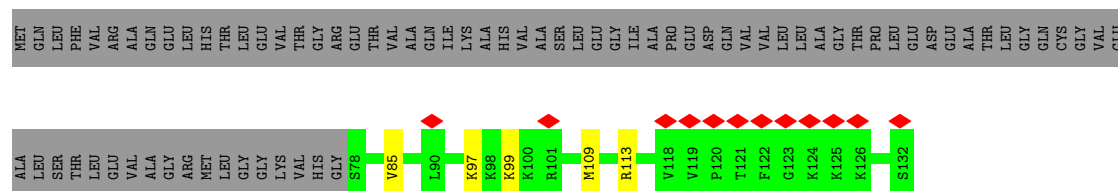
- Molecule 78: eS28



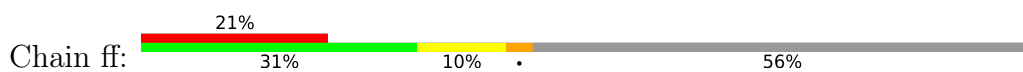
- Molecule 79: uS14



- Molecule 80: eS30



- Molecule 81: eS31

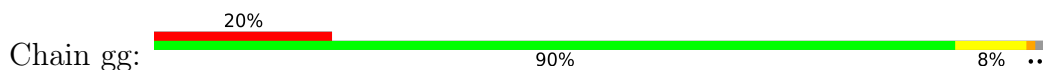


MET GLN ILE PHE VAL LYS THR LEU THR LEU GLY LYS THR ILE THR LEU GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS ALA ILE GLN ASP GLU GLY ILE PRO PRO ASP GLN ARG LEU PHE ALA LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU ARG LEU ARG GLY ALA LYS ARG LYS K83 S84 Y85 T86 T87 K90 N91 K92 H93 K94 R95 K96 K97 V98 K99 L100 A101 V102 Y105 V108 D109 E110 N111 G112 K113 I114 S115 E120 G121 P122 S123 D124 E125 G126

G127 A128 G129 V130 F131 M132 F136 D137 R138 H139 Y140 C141 G142 K143 C144 C145 L146 F150 ASN LYS PRO GLU ASP LYS

• Molecule 82: RACK1



MET T2 E3 Q4 L7 R8 L11 K12 G13 H14 N15 G16 W17 Q20 I21 A22 D29 M30 S35 R36 D37 K38 I41 K44 D48 E49 T50 G61 H64 S73 D74 G81 S82 L87 R99 R100 F101 V108 A112 S115 D116 Q119

G123 D126 N133 T134 L135 Q143 D144 G145 S146 S152 N159 S160 S161 C168 V198 T199 D203 C207 K212 L221 G224 L227 Q232 G233 D234 N244 T252 K257 I258 W259 I266 V267 D268 E269 L270 K271 Q272 E273 V274 I275 S276

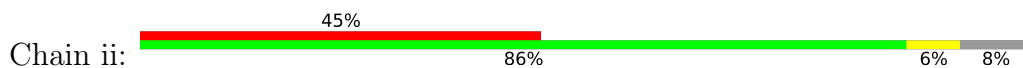
T277 S278 S279 T287 S288 L289 A293 D294 G295 Q296 T297 L298 T303 D304 N305 L306 V307 R308 T313 I314 GLY THR ARG

• Molecule 83: mRNA (polyadenylated)



A41 A42 A43 A44 A45 A46 A47 A48

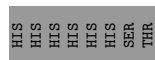
• Molecule 84: Protein pelota homolog



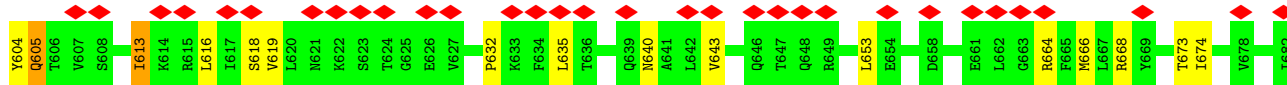
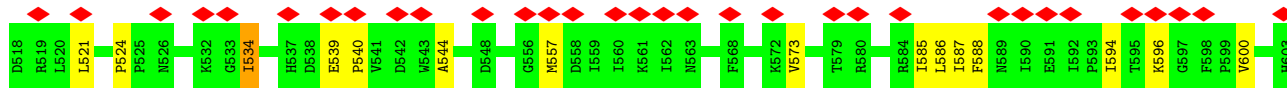
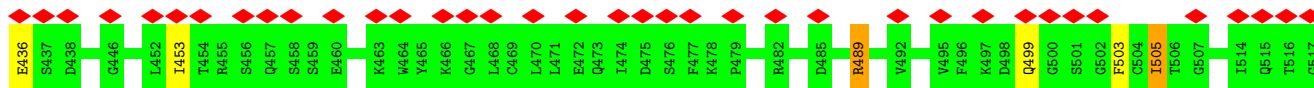
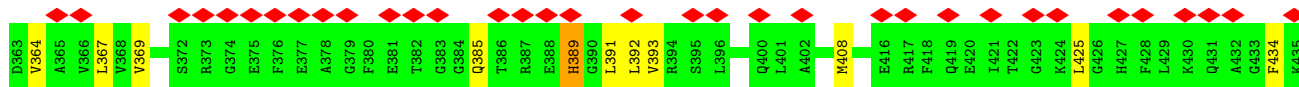
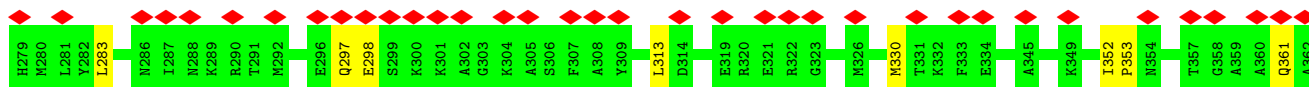
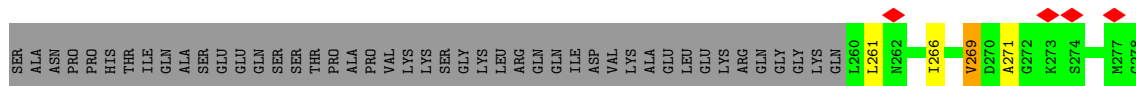
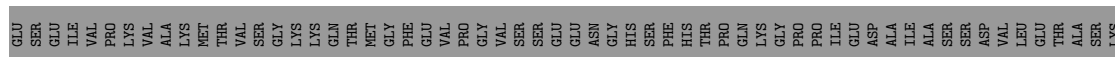
M1 R5 K6 N7 I8 E9 K10 D11 N12 A13 E22 P23 F24 D25 M26 W27 H28 Q34 D37 R40 A41 R45 K46 V47 Q48 T49 E50 S51 S52 T53 G54 S55 V56 G57 S58 N59 R62 T63 T64 L65 T66 L67 C68 V69 E70 A71 I72 D73 F74 S76 Q77 A78

C79 Q80 L81 R82 Q89 E90 N91 E92 Y93 Y94 K95 M96 G97 A98 Y99 H100 T101 I102 E103 L104 E105 P106 N107 R108 Q109 L112 Q116 W117 D118 E123 R124 T125 E126 Q127 P131 A132 W133 S134 A135 A139 E144 G145 I149 S155 M156 E164 V165 N166 K170

R171 K172 G173 N174 D179 R180 A181 E187 Q191 R195 H196 I197 H198 F199 D200 V201 V202 I205 A208 F212 E215 D219 Q223 Q224 V226 K227 T228 D229 N230 K231 L232 L233 L234 E235 N236 V243 S247 G248 H249 K250 Y251 S252 L253 C256 D259



Chain jj:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	0.572	Depositor
Minimum map value	-0.367	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	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 ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.59	0/1936	0.87	0/2596
2	B	0.60	0/3240	0.89	1/4339 (0.0%)
3	C	0.64	0/2937	0.93	2/3946 (0.1%)
4	D	0.51	0/2437	0.85	1/3264 (0.0%)
5	E	0.54	0/1762	0.86	0/2362
6	F	0.64	0/1911	0.92	0/2549
7	G	0.52	0/1910	0.88	2/2569 (0.1%)
8	H	0.55	0/1535	0.83	0/2063
9	I	0.56	0/1702	0.87	0/2272
10	J	0.51	0/1385	0.84	1/1852 (0.1%)
11	L	0.56	0/1733	0.90	1/2316 (0.0%)
12	M	0.56	0/1158	0.90	0/1547
13	N	0.57	0/1746	0.93	1/2338 (0.0%)
14	O	0.67	0/1662	0.97	3/2222 (0.1%)
15	P	0.61	0/1268	0.90	2/1700 (0.1%)
16	Q	0.63	0/1539	0.93	1/2054 (0.0%)
17	R	0.53	0/1524	0.88	0/2013
18	S	0.65	0/1501	0.90	1/2012 (0.0%)
19	T	0.55	0/1326	0.85	0/1770
20	U	0.51	0/823	0.80	0/1104
21	V	0.59	0/993	0.90	0/1332
22	W	0.54	0/873	0.81	0/1158
23	X	0.54	0/984	0.82	0/1323
24	Y	0.50	0/1132	0.86	1/1504 (0.1%)
25	Z	0.55	0/1130	0.81	0/1507
26	a	0.60	0/1191	0.93	1/1590 (0.1%)
27	b	0.54	0/861	0.92	0/1138
28	c	0.50	0/771	0.82	0/1034
29	d	0.58	0/903	0.87	1/1216 (0.1%)
30	e	0.65	1/1071 (0.1%)	0.90	0/1429
31	f	0.60	0/895	0.86	0/1198
32	g	0.58	0/916	0.86	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.50	0/1021	0.90	0/1348
34	i	0.50	0/841	0.87	0/1112
35	j	0.58	0/720	0.93	0/952
36	k	0.47	0/575	0.80	0/761
37	l	0.56	0/459	0.89	1/608 (0.2%)
38	m	0.53	0/435	0.86	0/575
39	n	0.47	0/240	0.85	0/305
40	o	0.50	0/864	0.80	0/1140
41	p	0.56	0/718	0.86	0/953
42	r	0.57	0/1010	0.91	0/1354
43	s	0.56	0/1530	0.74	0/2064
44	t	0.59	0/1174	0.82	0/1582
45	2	0.38	0/1777	0.73	1/2763 (0.0%)
45	3	0.37	0/1777	0.68	0/2763
46	5	0.44	3/84961 (0.0%)	0.85	182/132460 (0.1%)
47	7	0.42	0/2858	0.77	1/4455 (0.0%)
48	8	0.43	0/3581	0.82	4/5577 (0.1%)
49	9	0.42	0/40524	0.81	47/63134 (0.1%)
50	AA	0.56	0/1747	0.90	1/2374 (0.0%)
51	BB	0.47	0/1756	0.83	0/2350
52	CC	0.55	0/1753	0.93	1/2369 (0.0%)
53	DD	0.53	0/1796	0.83	0/2417
54	EE	0.53	0/2118	0.86	1/2849 (0.0%)
55	FF	0.53	0/1492	0.91	0/2005
56	GG	0.51	0/1946	0.84	0/2590
57	HH	0.52	0/1510	0.82	0/2022
58	II	0.58	0/1715	0.88	0/2287
59	JJ	0.52	0/1550	0.91	0/2069
60	KK	0.53	0/834	0.86	0/1125
61	LL	0.54	0/1195	0.82	0/1597
62	MM	0.54	0/918	0.83	0/1233
63	NN	0.52	0/1226	0.93	0/1649
64	OO	0.55	0/1029	0.97	1/1380 (0.1%)
65	PP	0.58	0/1017	0.90	0/1358
66	QQ	0.52	0/1146	0.86	0/1534
67	RR	0.53	0/1082	0.84	0/1452
68	SS	0.56	0/1208	0.89	0/1618
69	TT	0.53	0/1115	0.89	0/1493
70	UU	0.54	0/805	0.89	2/1081 (0.2%)
71	VV	0.54	0/643	0.93	0/860
72	WW	0.52	0/1051	0.91	0/1406
73	XX	0.53	0/1116	0.90	0/1490
74	YY	0.49	0/1028	0.80	0/1366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	ZZ	0.50	0/604	0.86	0/810
76	aa	0.54	0/828	0.92	0/1109
77	bb	0.53	0/665	0.86	0/891
78	cc	0.53	0/490	0.87	0/656
79	dd	0.54	0/470	0.78	1/623 (0.2%)
80	ee	0.49	0/447	0.84	0/587
81	ff	0.53	0/567	0.74	0/753
82	gg	0.50	0/2493	0.72	0/3394
83	hh	0.39	0/199	0.80	0/308
84	ii	0.52	0/2996	0.81	0/4050
85	jj	0.53	0/3352	0.79	1/4523 (0.0%)
All	All	0.49	4/237727 (0.0%)	0.85	263/348121 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3
4	D	0	1
11	L	0	1
31	f	0	1
37	l	0	1
46	5	0	2
72	WW	0	1
73	XX	0	1
All	All	0	11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	5	935	A	C5-C6	-7.09	1.26	1.41
46	5	922(A)	G	O3'-P	6.89	1.69	1.61
30	e	129	LEU	C-O	5.27	1.34	1.23
46	5	1411(B)	C	O3'-P	5.10	1.67	1.61

The worst 5 of 263 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	481	G	N1-C2-N2	-15.82	68.75	116.20
46	5	922	C	C2'-C3'-O3'	14.46	135.40	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	935	A	C5-C6-N6	-13.04	84.57	123.70
49	9	1835	A	C2'-C3'-O3'	11.37	126.56	109.50
46	5	1411	C	C2'-C3'-O3'	-10.88	97.38	113.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	16	PHE	Peptide
2	B	257	TRP	Peptide
2	B	259	PRO	Peptide
4	D	36	LEU	Peptide
11	L	46	ILE	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	28	0
2	B	3172	0	3310	34	0
3	C	2883	0	3053	55	0
4	D	2391	0	2424	15	0
5	E	1729	0	1887	18	0
6	F	1875	0	1995	27	0
7	G	1879	0	2027	12	0
8	H	1516	0	1597	16	0
9	I	1664	0	1712	15	0
10	J	1362	0	1399	14	0
11	L	1702	0	1820	14	0
12	M	1137	0	1211	18	0
13	N	1701	0	1749	27	0
14	O	1630	0	1778	32	0
15	P	1242	0	1274	15	0
16	Q	1515	0	1634	21	0
17	R	1508	0	1664	9	0
18	S	1462	0	1508	24	0
19	T	1298	0	1366	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	U	809	0	833	9	0
21	V	979	0	1039	13	0
22	W	860	0	903	4	0
23	X	967	0	1040	4	0
24	Y	1115	0	1205	6	0
25	Z	1107	0	1182	9	0
26	a	1162	0	1209	11	0
27	b	848	0	920	3	0
28	c	761	0	794	6	0
29	d	888	0	930	19	0
30	e	1053	0	1147	17	0
31	f	876	0	912	10	0
32	g	906	0	1001	7	0
33	h	1013	0	1147	5	0
34	i	830	0	916	1	0
35	j	705	0	738	7	0
36	k	569	0	637	2	0
37	l	447	0	480	6	0
38	m	429	0	466	3	0
39	n	239	0	289	0	0
40	o	851	0	920	9	0
41	p	708	0	758	14	0
42	r	994	0	1051	11	0
43	s	1507	0	1564	0	0
44	t	1160	0	1218	1	0
45	2	1593	0	811	5	0
45	3	1593	0	811	5	0
46	5	75972	0	38399	514	0
47	7	2558	0	1296	7	0
48	8	3208	0	1629	21	0
49	9	36249	0	18316	241	0
50	AA	1710	0	1708	17	0
51	BB	1729	0	1803	14	0
52	CC	1716	0	1806	15	0
53	DD	1768	0	1866	13	0
54	EE	2076	0	2177	15	0
55	FF	1471	0	1522	9	0
56	GG	1923	0	2089	15	0
57	HH	1488	0	1582	13	0
58	II	1686	0	1772	14	0
59	JJ	1525	0	1640	9	0
60	KK	810	0	836	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	LL	1175	0	1249	11	0
62	MM	908	0	939	39	0
63	NN	1202	0	1289	7	0
64	OO	1016	0	1039	9	0
65	PP	997	0	1045	7	0
66	QQ	1128	0	1195	7	0
67	RR	1068	0	1121	4	0
68	SS	1190	0	1249	10	0
69	TT	1097	0	1132	4	0
70	UU	795	0	862	5	0
71	VV	636	0	637	4	0
72	WW	1034	0	1080	17	0
73	XX	1098	0	1167	10	0
74	YY	1011	0	1083	7	0
75	ZZ	598	0	656	0	0
76	aa	814	0	864	12	0
77	bb	651	0	672	3	0
78	cc	488	0	514	22	0
79	dd	459	0	449	5	0
80	ee	443	0	492	0	0
81	ff	555	0	566	50	0
82	gg	2436	0	2393	9	0
83	hh	176	0	89	1	0
84	ii	2947	0	2957	10	0
85	jj	3292	0	3371	19	0
86	5	160	0	0	0	0
86	7	5	0	0	0	0
86	8	3	0	0	0	0
86	9	58	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	L	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	e	1	0	0	0	0
86	j	1	0	0	0	0
86	jj	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	g	1	0	0	1	0
87	j	1	0	0	0	0
87	m	1	0	0	2	0
87	o	1	0	0	0	0
87	p	1	0	0	2	0
88	jj	32	0	14	0	0
All	All	221912	0	166887	1509	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 4.

The worst 5 of 1509 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)
32:g:46:CYS:SG	87:g:200:ZN:ZN	1.19	1.32
46:5:3914:U:O4	46:5:4378:A:N1	1.60	1.32
49:9:1290:G:N7	81:ff:95:ARG:NH2	1.77	1.31
49:9:830:A:N1	49:9:844:U:O4	1.71	1.20
46:5:1929:A:N1	46:5:2054:U:O4	1.73	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%)	217 (88%)	25 (10%)	4 (2%)	7	37
2	B	392/403 (97%)	343 (88%)	47 (12%)	2 (0%)	24	60
3	C	360/425 (85%)	319 (89%)	32 (9%)	9 (2%)	4	29
4	D	291/297 (98%)	270 (93%)	18 (6%)	3 (1%)	12	45
5	E	208/291 (72%)	182 (88%)	25 (12%)	1 (0%)	24	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	223/247 (90%)	199 (89%)	20 (9%)	4 (2%)	6	34
7	G	229/319 (72%)	212 (93%)	16 (7%)	1 (0%)	30	65
8	H	188/192 (98%)	168 (89%)	18 (10%)	2 (1%)	11	44
9	I	201/214 (94%)	178 (89%)	23 (11%)	0	100	100
10	J	168/178 (94%)	156 (93%)	10 (6%)	2 (1%)	10	42
11	L	208/211 (99%)	185 (89%)	21 (10%)	2 (1%)	12	45
12	M	136/218 (62%)	126 (93%)	7 (5%)	3 (2%)	5	31
13	N	201/204 (98%)	180 (90%)	17 (8%)	4 (2%)	6	33
14	O	197/203 (97%)	176 (89%)	21 (11%)	0	100	100
15	P	151/184 (82%)	138 (91%)	11 (7%)	2 (1%)	9	41
16	Q	185/188 (98%)	163 (88%)	20 (11%)	2 (1%)	11	44
17	R	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
18	S	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	11	44
19	T	157/160 (98%)	141 (90%)	16 (10%)	0	100	100
20	U	97/128 (76%)	86 (89%)	9 (9%)	2 (2%)	5	32
21	V	129/140 (92%)	117 (91%)	10 (8%)	2 (2%)	7	37
22	W	102/157 (65%)	91 (89%)	10 (10%)	1 (1%)	12	45
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	8	38
26	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
27	b	100/245 (41%)	89 (89%)	10 (10%)	1 (1%)	12	45
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	87 (83%)	16 (15%)	2 (2%)	6	34
30	e	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	16	52
31	f	107/110 (97%)	96 (90%)	8 (8%)	3 (3%)	4	27
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	6	34
33	h	120/123 (98%)	112 (93%)	7 (6%)	1 (1%)	16	52
34	i	100/105 (95%)	91 (91%)	9 (9%)	0	100	100
35	j	84/97 (87%)	72 (86%)	11 (13%)	1 (1%)	10	42
36	k	67/70 (96%)	61 (91%)	5 (8%)	1 (2%)	8	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	l	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	5	32
38	m	50/102 (49%)	46 (92%)	3 (6%)	1 (2%)	6	33
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	89 (87%)	11 (11%)	2 (2%)	6	33
41	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
42	r	122/137 (89%)	103 (84%)	16 (13%)	3 (2%)	4	29
43	s	194/318 (61%)	173 (89%)	19 (10%)	2 (1%)	12	45
44	t	151/165 (92%)	135 (89%)	14 (9%)	2 (1%)	9	41
50	AA	215/295 (73%)	189 (88%)	23 (11%)	3 (1%)	9	39
51	BB	211/264 (80%)	194 (92%)	17 (8%)	0	100	100
52	CC	219/293 (75%)	202 (92%)	14 (6%)	3 (1%)	9	39
53	DD	226/243 (93%)	207 (92%)	18 (8%)	1 (0%)	30	65
54	EE	260/263 (99%)	245 (94%)	13 (5%)	2 (1%)	16	52
55	FF	181/204 (89%)	164 (91%)	14 (8%)	3 (2%)	7	36
56	GG	235/249 (94%)	221 (94%)	13 (6%)	1 (0%)	30	65
57	HH	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
58	II	204/208 (98%)	187 (92%)	17 (8%)	0	100	100
59	JJ	183/194 (94%)	172 (94%)	10 (6%)	1 (0%)	24	60
60	KK	94/165 (57%)	85 (90%)	8 (8%)	1 (1%)	11	44
61	LL	139/158 (88%)	119 (86%)	19 (14%)	1 (1%)	18	54
62	MM	115/132 (87%)	97 (84%)	18 (16%)	0	100	100
63	NN	147/151 (97%)	131 (89%)	16 (11%)	0	100	100
64	OO	134/168 (80%)	116 (87%)	17 (13%)	1 (1%)	18	54
65	PP	118/145 (81%)	103 (87%)	15 (13%)	0	100	100
66	QQ	140/146 (96%)	131 (94%)	8 (6%)	1 (1%)	18	54
67	RR	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	52
68	SS	142/152 (93%)	134 (94%)	6 (4%)	2 (1%)	9	39
69	TT	139/145 (96%)	130 (94%)	8 (6%)	1 (1%)	18	54
70	UU	98/119 (82%)	90 (92%)	7 (7%)	1 (1%)	12	45
71	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
72	WW	127/130 (98%)	112 (88%)	12 (9%)	3 (2%)	4	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	XX	139/143 (97%)	126 (91%)	10 (7%)	3 (2%)	5	31
74	YY	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
75	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
76	aa	99/115 (86%)	84 (85%)	13 (13%)	2 (2%)	6	33
77	bb	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	10	42
78	cc	60/69 (87%)	55 (92%)	4 (7%)	1 (2%)	7	36
79	dd	53/56 (95%)	44 (83%)	8 (15%)	1 (2%)	6	34
80	ee	53/133 (40%)	48 (91%)	5 (9%)	0	100	100
81	ff	66/156 (42%)	60 (91%)	4 (6%)	2 (3%)	3	26
82	gg	311/317 (98%)	281 (90%)	27 (9%)	3 (1%)	12	45
84	ii	370/403 (92%)	342 (92%)	28 (8%)	0	100	100
85	jj	423/710 (60%)	383 (90%)	35 (8%)	5 (1%)	10	42
All	All	12312/14488 (85%)	11148 (90%)	1047 (8%)	117 (1%)	15	45

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	254	GLU
7	G	105	THR
18	S	155	PRO
29	d	58	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/199 (96%)	176 (93%)	14 (7%)	13	36
2	B	342/348 (98%)	309 (90%)	33 (10%)	8	28
3	C	302/347 (87%)	278 (92%)	24 (8%)	11	35
4	D	247/250 (99%)	234 (95%)	13 (5%)	20	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	190/251 (76%)	177 (93%)	13 (7%)	14	39
6	F	196/215 (91%)	178 (91%)	18 (9%)	8	30
7	G	200/272 (74%)	186 (93%)	14 (7%)	14	38
8	H	169/171 (99%)	152 (90%)	17 (10%)	7	26
9	I	175/181 (97%)	162 (93%)	13 (7%)	13	36
10	J	143/149 (96%)	133 (93%)	10 (7%)	14	38
11	L	175/176 (99%)	167 (95%)	8 (5%)	24	47
12	M	117/161 (73%)	109 (93%)	8 (7%)	14	39
13	N	171/172 (99%)	159 (93%)	12 (7%)	14	38
14	O	171/173 (99%)	153 (90%)	18 (10%)	6	24
15	P	134/163 (82%)	127 (95%)	7 (5%)	21	44
16	Q	164/165 (99%)	146 (89%)	18 (11%)	6	23
17	R	159/175 (91%)	145 (91%)	14 (9%)	9	32
18	S	157/157 (100%)	146 (93%)	11 (7%)	14	38
19	T	139/140 (99%)	127 (91%)	12 (9%)	10	33
20	U	89/114 (78%)	87 (98%)	2 (2%)	45	65
21	V	101/107 (94%)	87 (86%)	14 (14%)	3	17
22	W	86/126 (68%)	85 (99%)	1 (1%)	63	73
23	X	106/134 (79%)	98 (92%)	8 (8%)	12	36
24	Y	124/135 (92%)	117 (94%)	7 (6%)	19	43
25	Z	117/118 (99%)	113 (97%)	4 (3%)	32	55
26	a	119/120 (99%)	114 (96%)	5 (4%)	26	49
27	b	84/184 (46%)	80 (95%)	4 (5%)	23	46
28	c	84/98 (86%)	77 (92%)	7 (8%)	10	33
29	d	98/110 (89%)	88 (90%)	10 (10%)	7	25
30	e	114/121 (94%)	104 (91%)	10 (9%)	9	32
31	f	88/89 (99%)	80 (91%)	8 (9%)	9	30
32	g	98/100 (98%)	89 (91%)	9 (9%)	8	30
33	h	109/110 (99%)	106 (97%)	3 (3%)	38	60
34	i	86/89 (97%)	83 (96%)	3 (4%)	32	54
35	j	73/80 (91%)	64 (88%)	9 (12%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	k	64/65 (98%)	60 (94%)	4 (6%)	16	41
37	l	47/48 (98%)	44 (94%)	3 (6%)	16	40
38	m	48/90 (53%)	45 (94%)	3 (6%)	16	41
39	n	24/24 (100%)	21 (88%)	3 (12%)	4	20
40	o	92/94 (98%)	87 (95%)	5 (5%)	20	44
41	p	74/75 (99%)	71 (96%)	3 (4%)	27	49
42	r	108/121 (89%)	96 (89%)	12 (11%)	6	23
43	s	164/258 (64%)	158 (96%)	6 (4%)	30	52
44	t	126/137 (92%)	122 (97%)	4 (3%)	34	56
50	AA	180/245 (74%)	159 (88%)	21 (12%)	5	21
51	BB	194/231 (84%)	177 (91%)	17 (9%)	9	32
52	CC	187/225 (83%)	170 (91%)	17 (9%)	9	30
53	DD	190/202 (94%)	174 (92%)	16 (8%)	10	33
54	EE	224/225 (100%)	205 (92%)	19 (8%)	10	33
55	FF	158/170 (93%)	144 (91%)	14 (9%)	9	31
56	GG	207/218 (95%)	191 (92%)	16 (8%)	12	35
57	HH	165/174 (95%)	146 (88%)	19 (12%)	5	22
58	II	178/180 (99%)	167 (94%)	11 (6%)	16	41
59	JJ	161/168 (96%)	149 (92%)	12 (8%)	12	36
60	KK	87/136 (64%)	81 (93%)	6 (7%)	14	39
61	LL	130/142 (92%)	116 (89%)	14 (11%)	6	24
62	MM	99/108 (92%)	87 (88%)	12 (12%)	5	21
63	NN	130/131 (99%)	114 (88%)	16 (12%)	4	20
64	OO	106/130 (82%)	98 (92%)	8 (8%)	12	36
65	PP	109/130 (84%)	101 (93%)	8 (7%)	13	37
66	QQ	117/121 (97%)	111 (95%)	6 (5%)	21	45
67	RR	119/121 (98%)	102 (86%)	17 (14%)	3	17
68	SS	125/132 (95%)	113 (90%)	12 (10%)	8	28
69	TT	111/115 (96%)	105 (95%)	6 (5%)	20	44
70	UU	92/107 (86%)	84 (91%)	8 (9%)	9	32
71	VV	67/67 (100%)	62 (92%)	5 (8%)	12	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	WW	112/113 (99%)	104 (93%)	8 (7%)	13	38
73	XX	113/115 (98%)	103 (91%)	10 (9%)	9	32
74	YY	107/112 (96%)	93 (87%)	14 (13%)	4	19
75	ZZ	66/103 (64%)	60 (91%)	6 (9%)	9	30
76	aa	88/98 (90%)	77 (88%)	11 (12%)	4	20
77	bb	75/76 (99%)	67 (89%)	8 (11%)	6	24
78	cc	55/62 (89%)	50 (91%)	5 (9%)	9	30
79	dd	48/49 (98%)	47 (98%)	1 (2%)	47	65
80	ee	46/106 (43%)	41 (89%)	5 (11%)	6	23
81	ff	61/140 (44%)	53 (87%)	8 (13%)	4	19
82	gg	272/275 (99%)	259 (95%)	13 (5%)	23	46
84	ii	326/353 (92%)	311 (95%)	15 (5%)	24	47
85	jj	358/608 (59%)	330 (92%)	28 (8%)	11	35
All	All	10727/12300 (87%)	9891 (92%)	836 (8%)	14	35

5 of 836 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	CC	78	LEU
58	II	190	LEU
84	ii	156	MET
52	CC	244	ILE
52	CC	66	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 173 such sidechains are listed below:

Mol	Chain	Res	Type
58	II	87	ASN
71	VV	47	ASN
60	KK	39	ASN
64	OO	32	HIS
75	ZZ	103	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	72/75 (96%)	17 (23%)	1 (1%)
45	3	72/75 (96%)	23 (31%)	1 (1%)
46	5	3511/3543 (99%)	949 (27%)	179 (5%)
47	7	119/120 (99%)	19 (15%)	3 (2%)
48	8	149/156 (95%)	40 (26%)	6 (4%)
49	9	1682/1869 (89%)	456 (27%)	88 (5%)
83	hh	7/8 (87%)	4 (57%)	0
All	All	5612/5846 (95%)	1508 (26%)	278 (4%)

5 of 1508 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	7	A
45	2	13	C
45	2	16	C
45	2	21	A
45	2	25	C

5 of 278 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	9	821	G
49	9	1114	U
49	9	1581	C
46	5	1986	U
46	5	1921	C

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 245 ligands modelled in this entry, 244 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	GCP	jj	700	86	32,34,34	1.40	7 (21%)	49,54,54	1.82	7 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	GCP	jj	700	86	-	3/19/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	jj	700	GCP	C5-C4	3.31	1.47	1.38
88	jj	700	GCP	PG-O2G	2.86	1.61	1.55
88	jj	700	GCP	PG-O3G	2.79	1.61	1.55
88	jj	700	GCP	C5-N7	-2.08	1.34	1.39
88	jj	700	GCP	C6-N1	-2.07	1.35	1.38

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	jj	700	GCP	C5-C4-N3	-6.19	118.54	128.39
88	jj	700	GCP	C2-N3-C4	5.22	121.30	112.30
88	jj	700	GCP	N9-C4-N3	4.45	134.86	125.95
88	jj	700	GCP	PB-O3A-PA	-3.57	120.71	132.37
88	jj	700	GCP	C6-C5-N7	3.37	136.43	130.29

There are no chirality outliers.

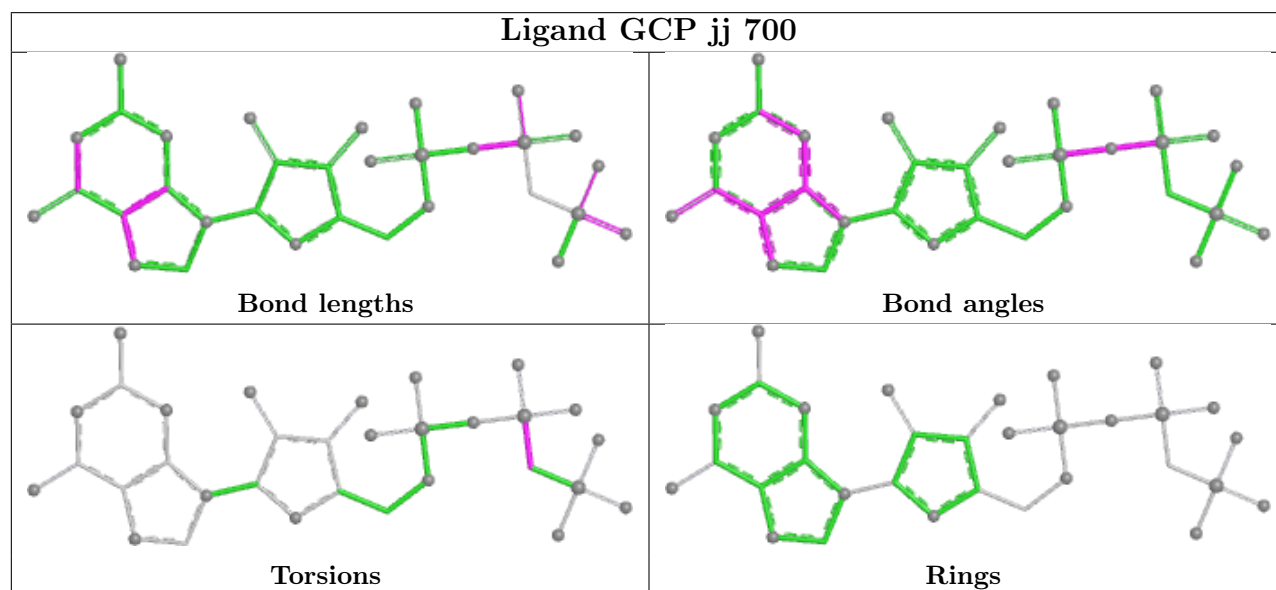
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	jj	700	GCP	PG-C3B-PB-O1B
88	jj	700	GCP	PG-C3B-PB-O3A
88	jj	700	GCP	PG-C3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	5	42
49	9	7
45	3	2
45	2	2

The worst 5 of 53 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.66
1	5	1252:C	O3'	1271:G	P	36.39
1	5	1405:C	O3'	1406:G	P	23.89
1	5	1219:G	O3'	1233:G	P	22.08
1	5	1406:G	O3'	1406(A):G	P	20.74

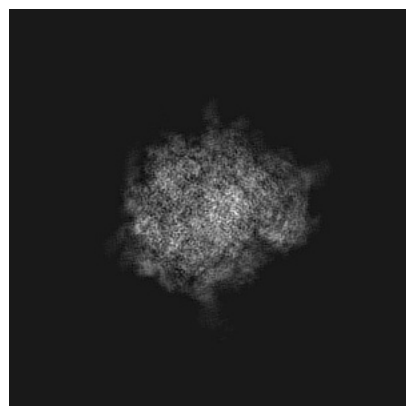
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4136. These allow visual inspection of the internal detail of the map and identification of artifacts.

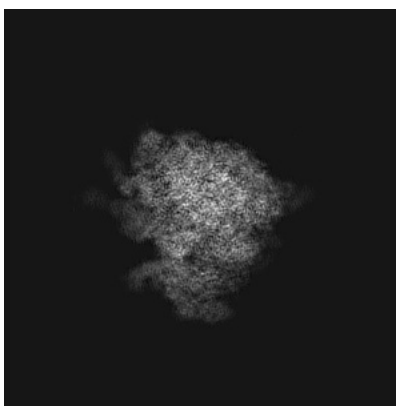
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

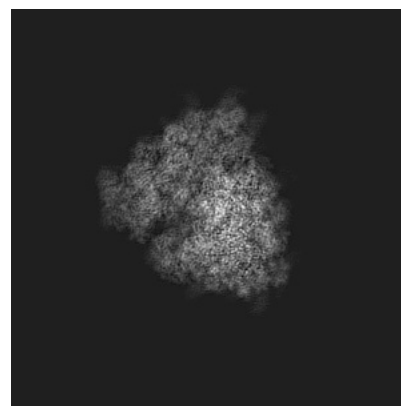
6.1.1 Primary map



X

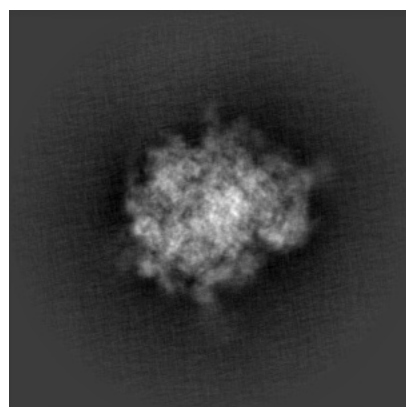


Y

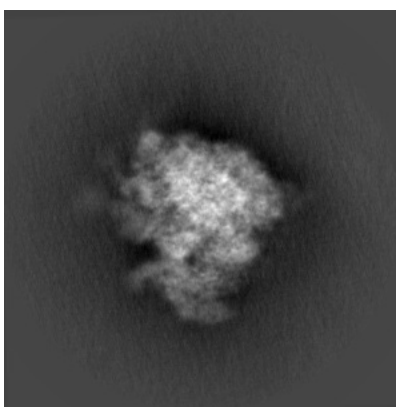


Z

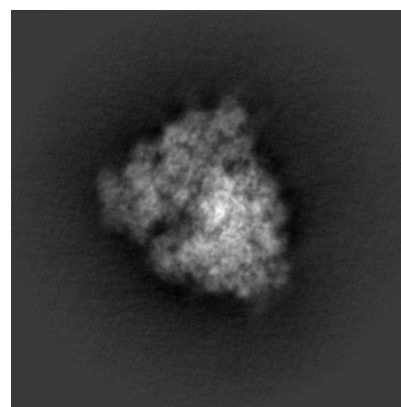
6.1.2 Raw map



X



Y

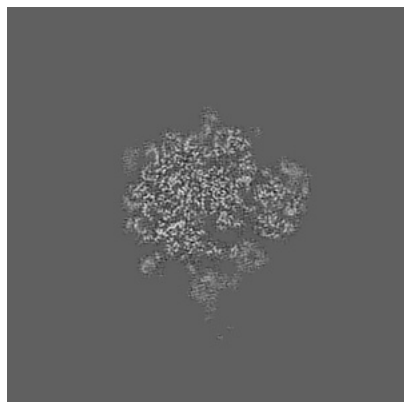


Z

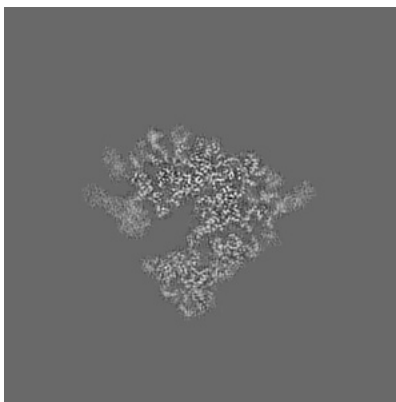
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

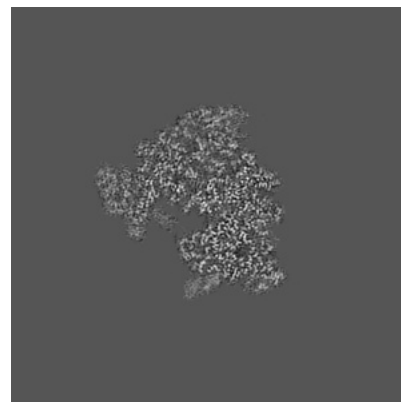
6.2.1 Primary map



X Index: 210

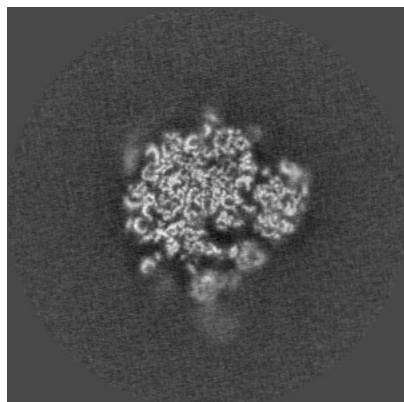


Y Index: 210

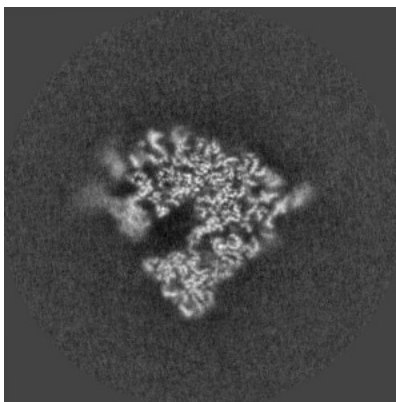


Z Index: 210

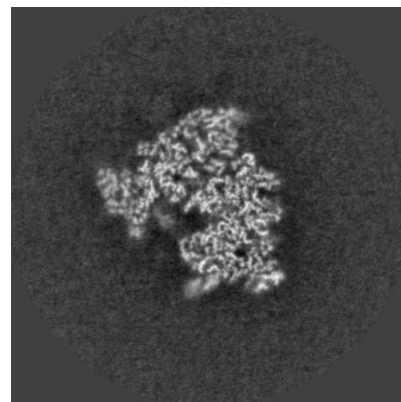
6.2.2 Raw map



X Index: 210



Y Index: 210

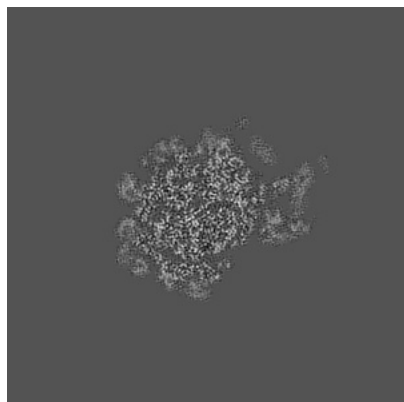


Z Index: 210

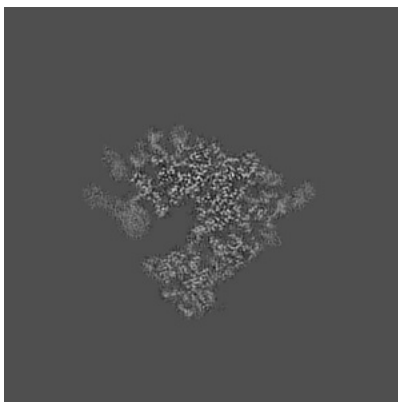
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

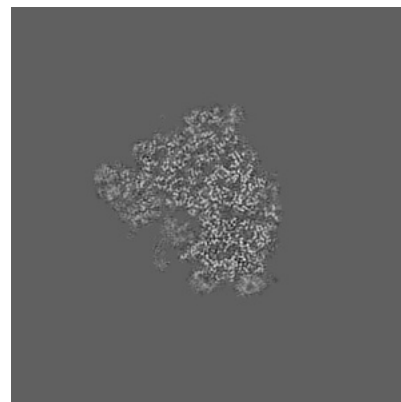
6.3.1 Primary map



X Index: 241

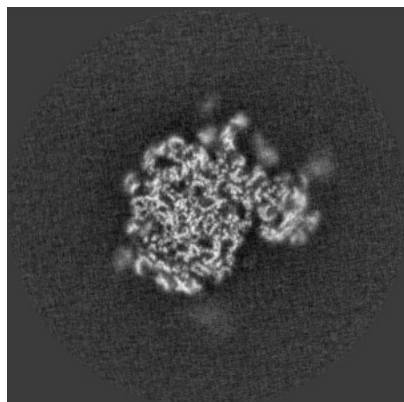


Y Index: 211

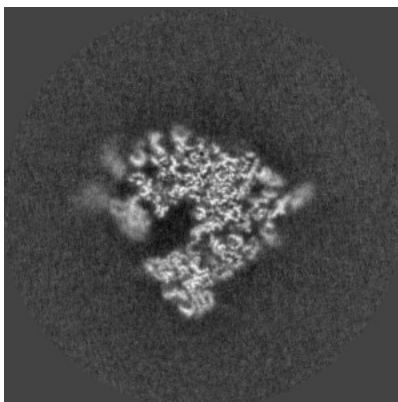


Z Index: 219

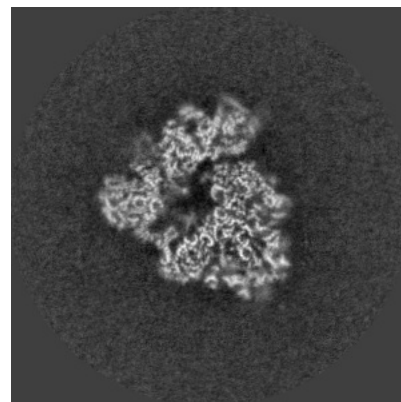
6.3.2 Raw map



X Index: 233



Y Index: 212

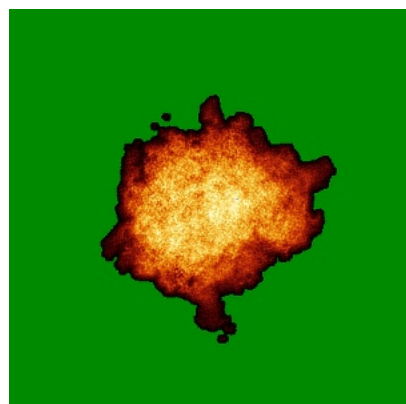


Z Index: 188

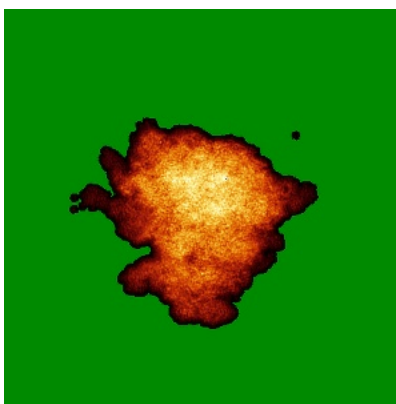
The images above show the largest variance slices of the map in three orthogonal directions.

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

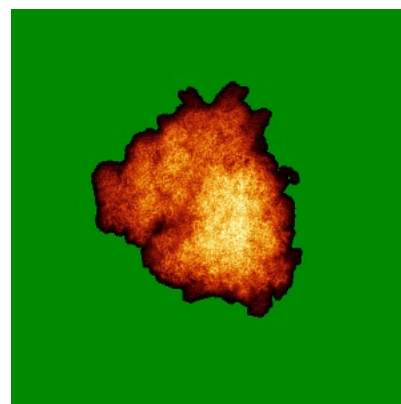
6.4.1 Primary map



X

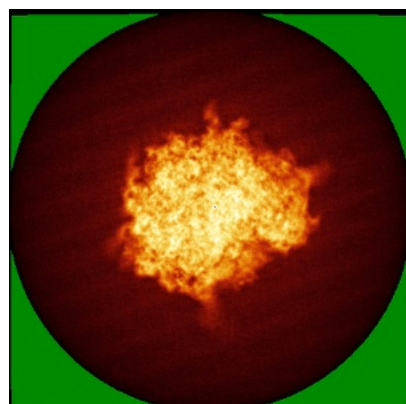


Y

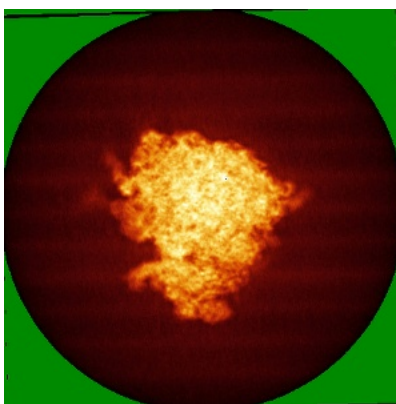


Z

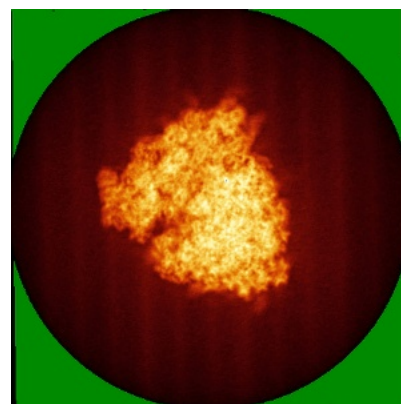
6.4.2 Raw map



X



Y

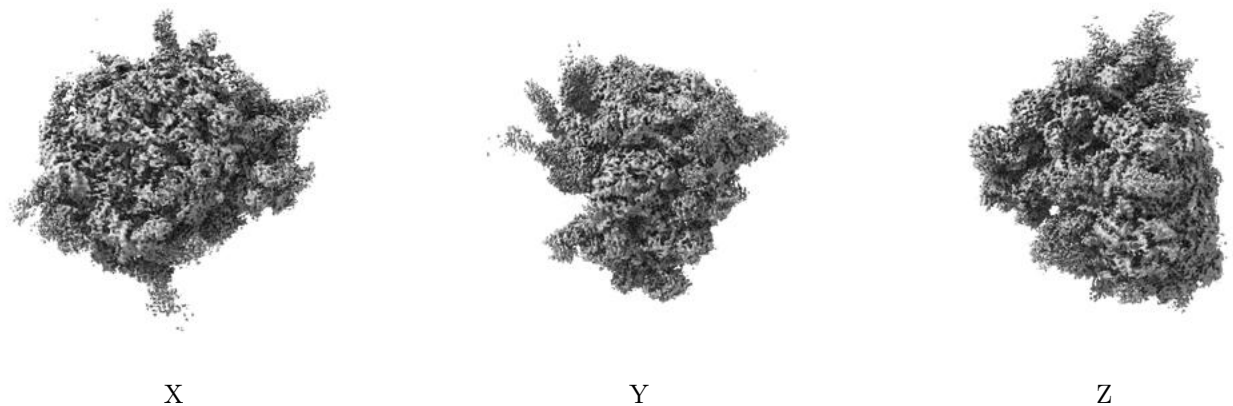


Z

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

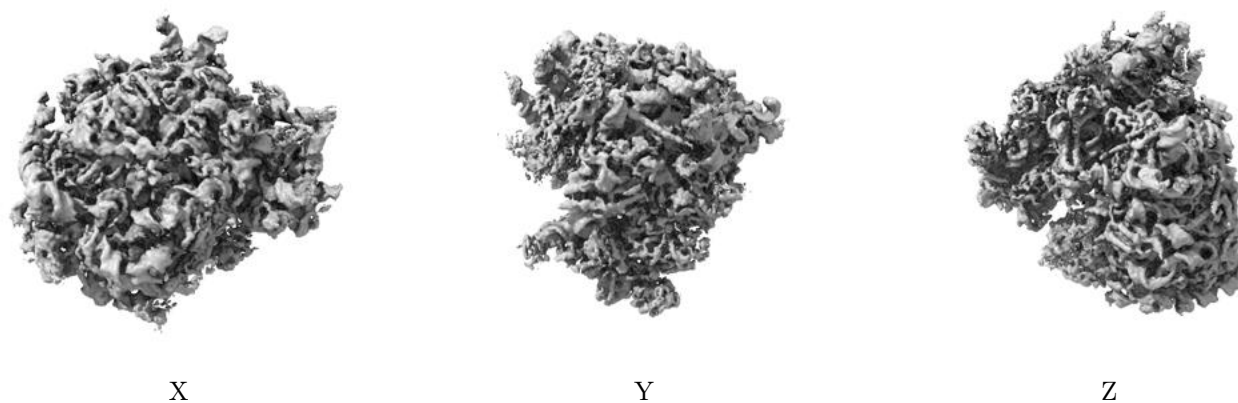
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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

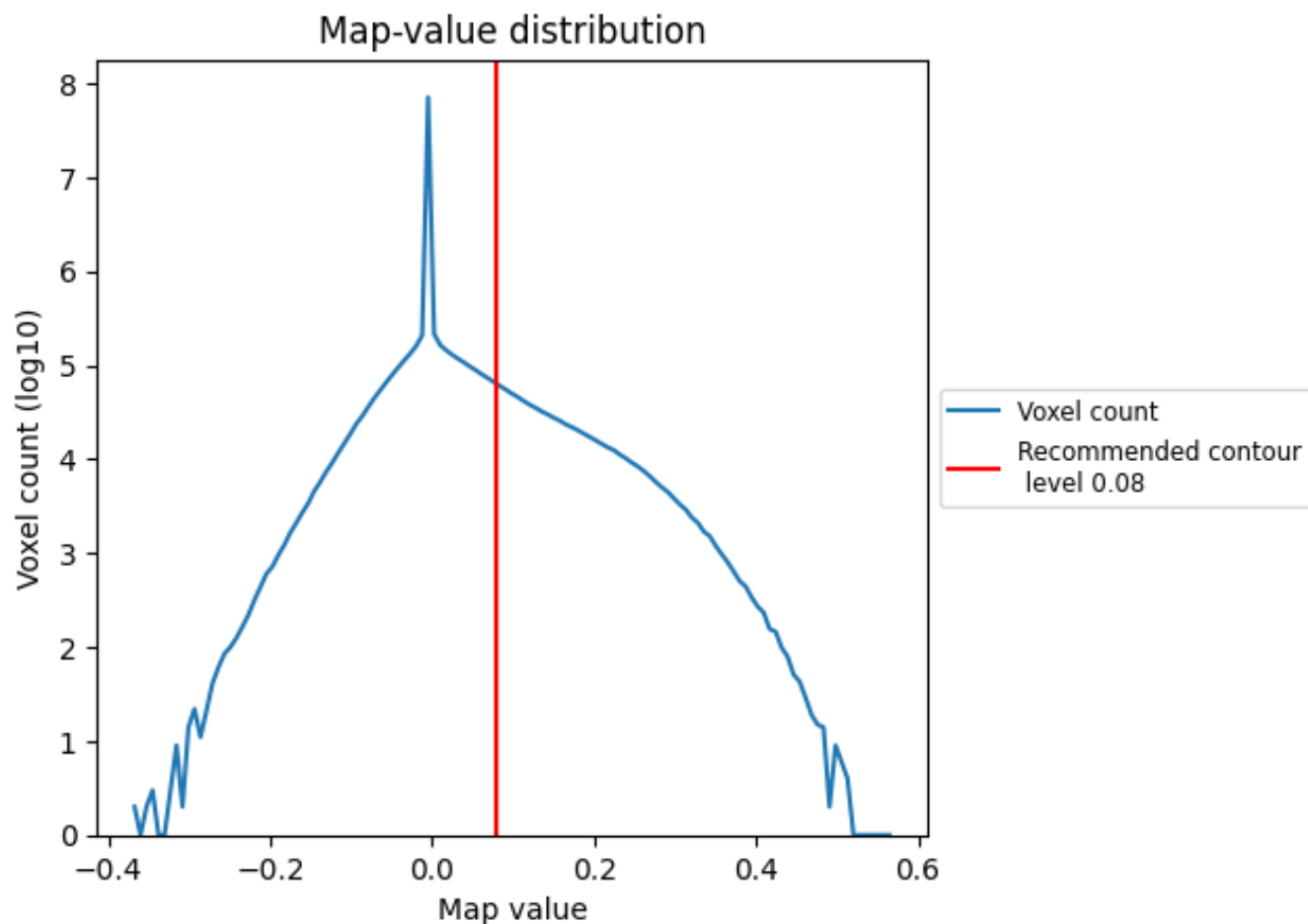
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

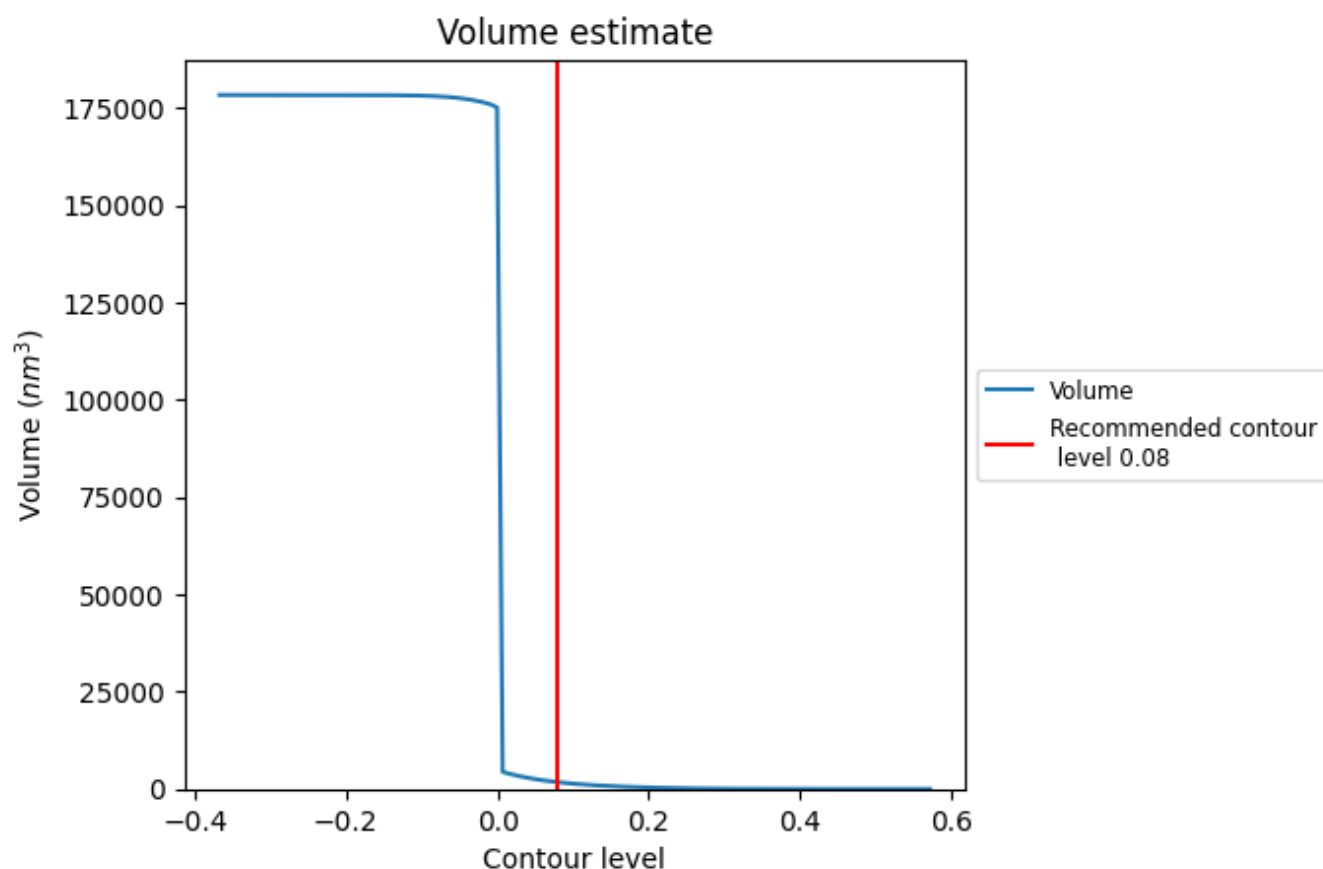
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

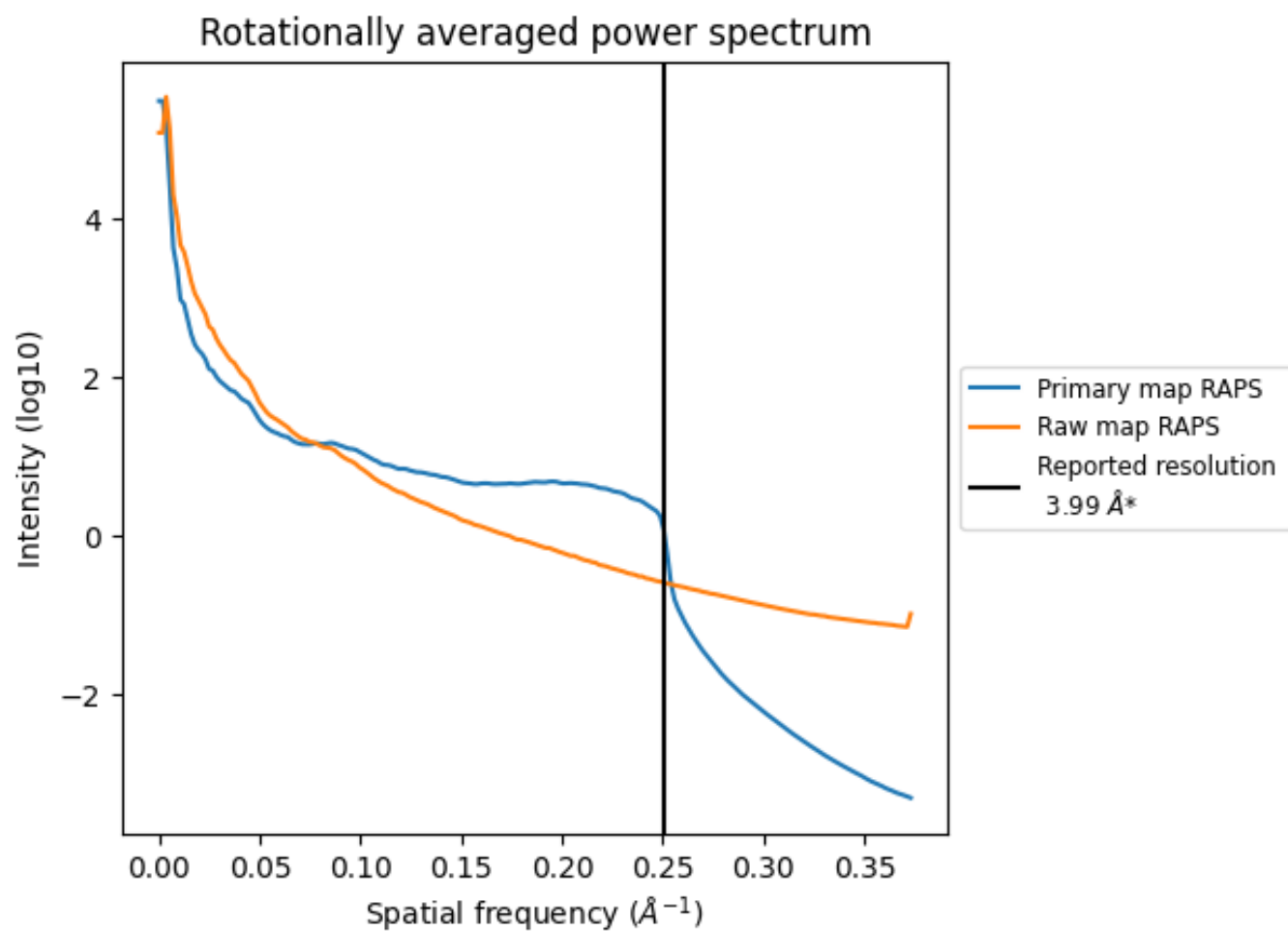
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1742 nm³; this corresponds to an approximate mass of 1573 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

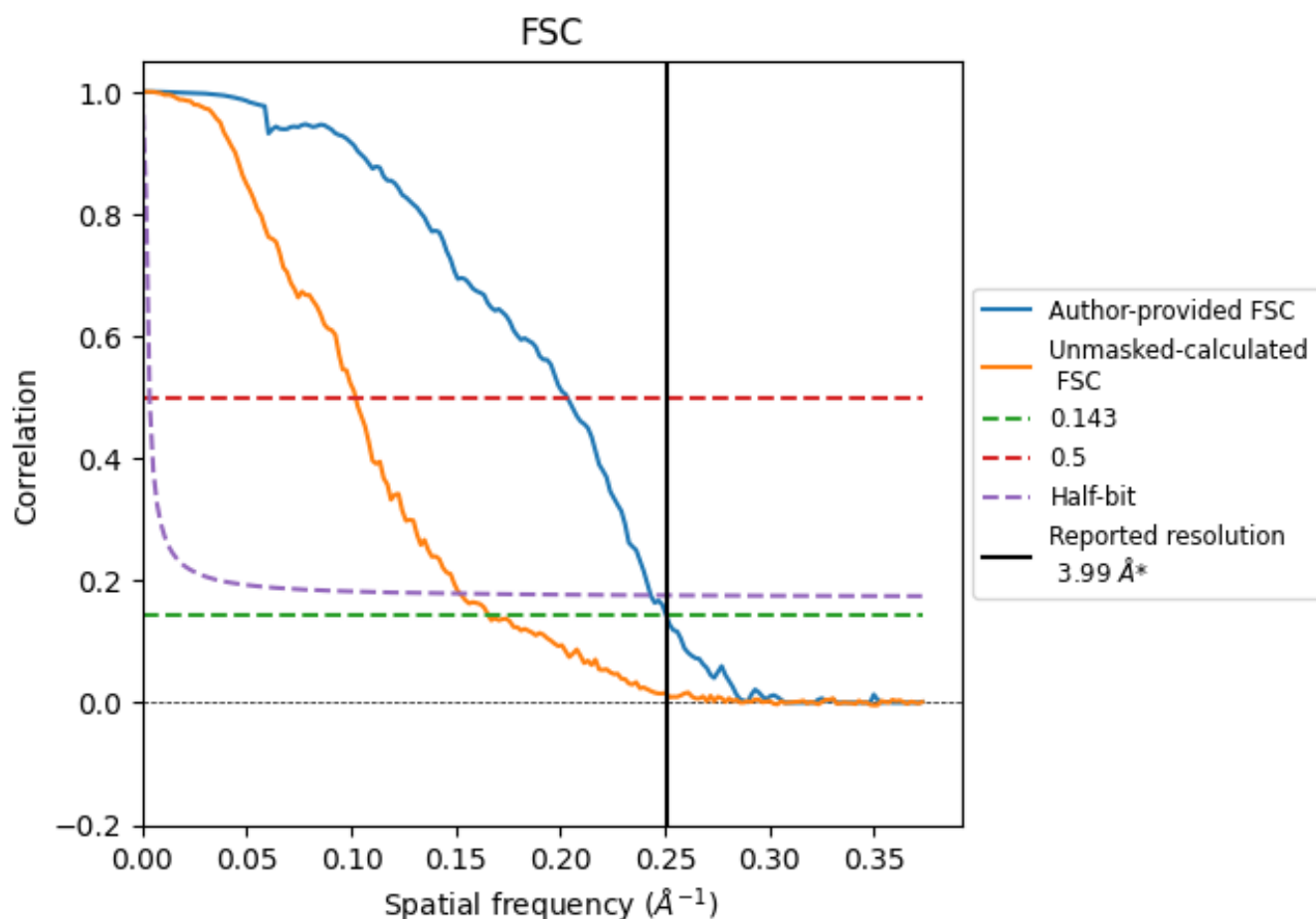


*Reported resolution corresponds to spatial frequency of 0.251 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.251 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

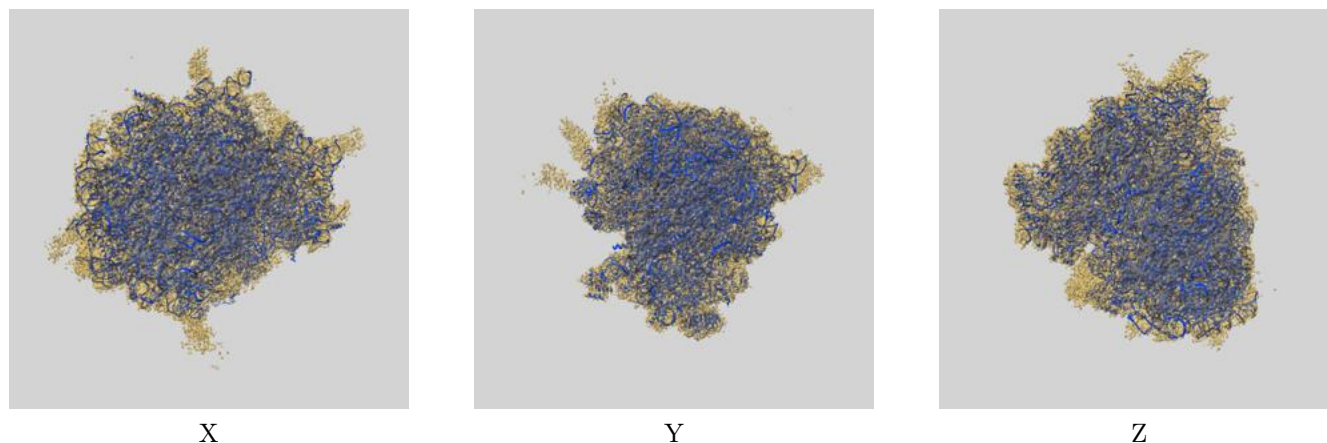
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.99	-	-
Author-provided FSC curve	3.99	4.92	4.11
Unmasked-calculated*	6.04	9.80	6.57

*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 6.04 differs from the reported value 3.99 by more than 10 %

9 Map-model fit [i](#)

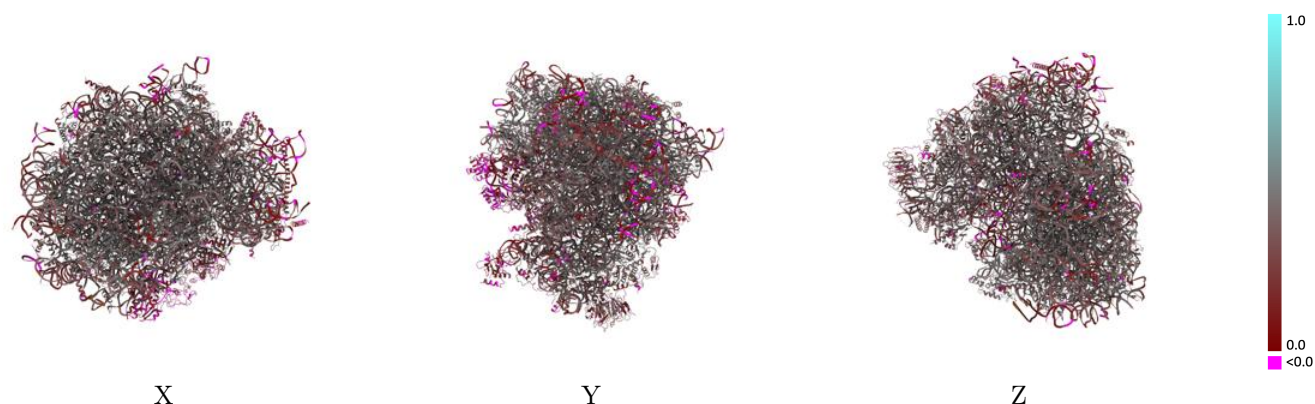
This section contains information regarding the fit between EMDB map EMD-4136 and PDB model 5LZY. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

9.1 Map-model overlay [i](#)



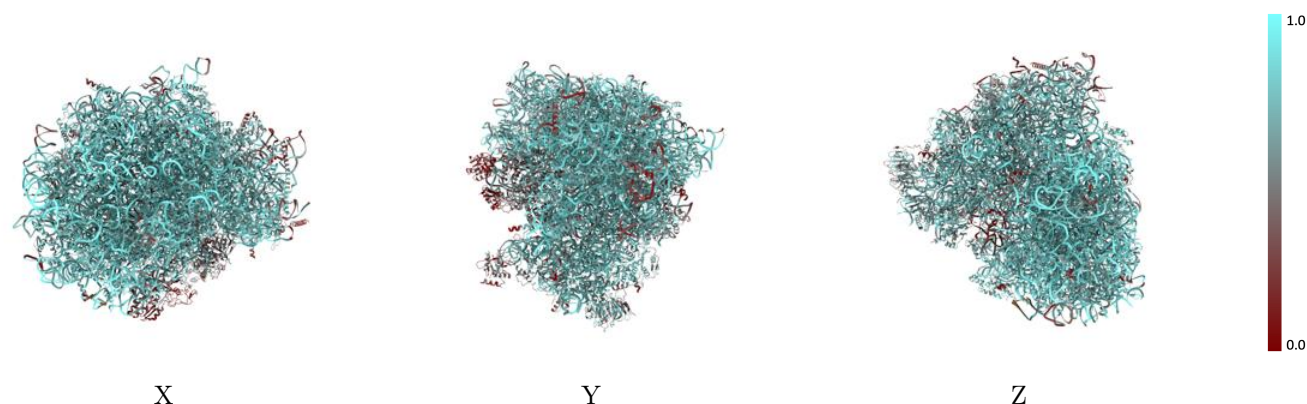
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



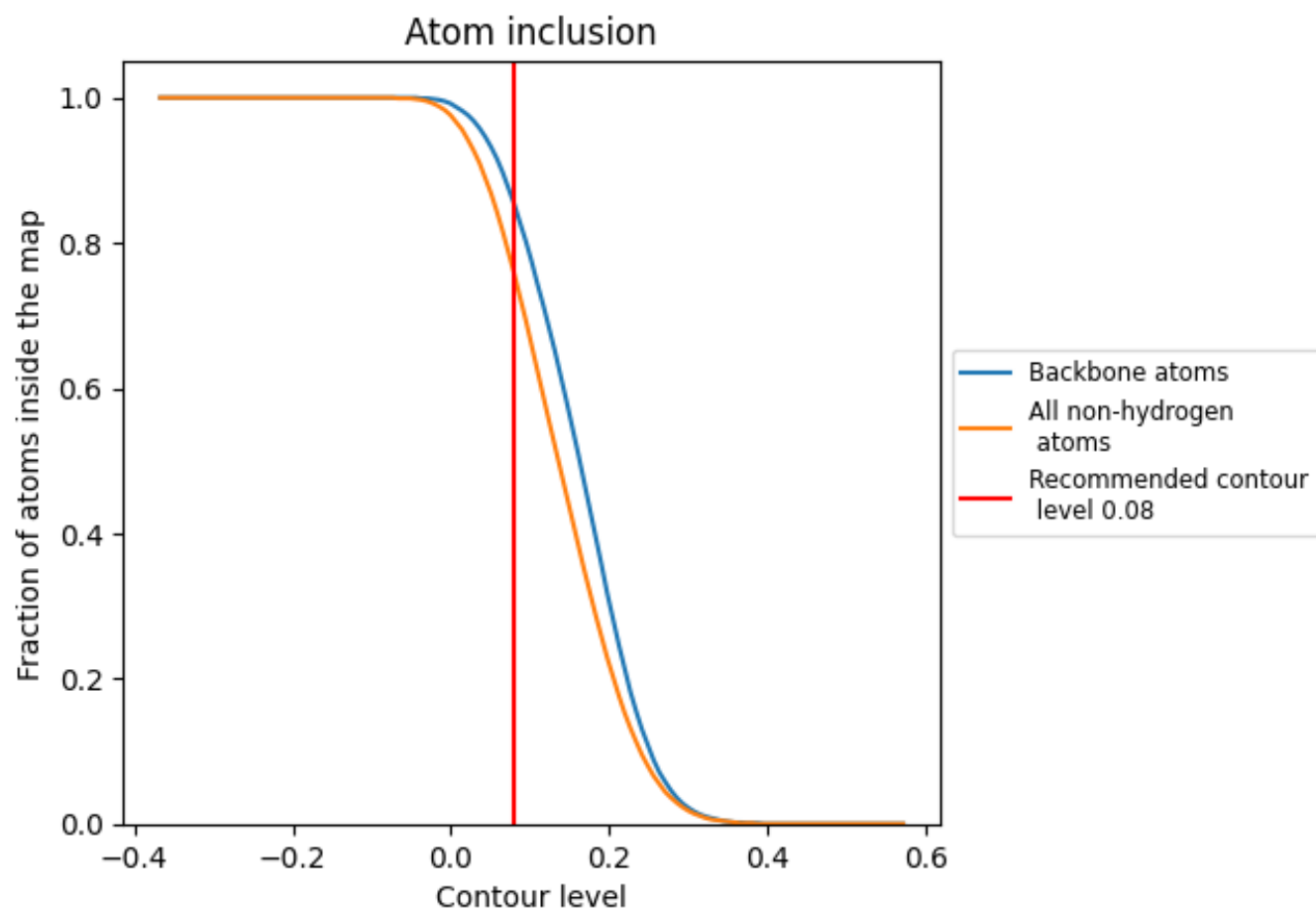
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 76% 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	 0.7590	 0.3670
2	 0.3860	 0.2510
3	 0.2810	 0.1410
5	 0.8450	 0.3750
7	 0.9170	 0.4170
8	 0.8630	 0.3820
9	 0.8180	 0.3540
A	 0.7560	 0.4430
AA	 0.6960	 0.3780
B	 0.7750	 0.4410
BB	 0.6840	 0.3840
C	 0.7700	 0.4310
CC	 0.7090	 0.3900
D	 0.7710	 0.3980
DD	 0.6230	 0.3390
E	 0.7560	 0.3940
EE	 0.6940	 0.3890
F	 0.7670	 0.4270
FF	 0.6580	 0.3620
G	 0.6990	 0.3670
GG	 0.6360	 0.3120
H	 0.7450	 0.4130
HH	 0.5930	 0.3230
I	 0.7430	 0.4230
II	 0.6720	 0.3650
J	 0.7140	 0.3820
JJ	 0.7110	 0.3740
KK	 0.6220	 0.2990
L	 0.7500	 0.4020
LL	 0.6920	 0.4060
M	 0.7640	 0.4050
MM	 0.3470	 0.1410
N	 0.7990	 0.4460
NN	 0.6870	 0.3910
O	 0.7840	 0.4380



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Chain	Atom inclusion	Q-score
OO	 0.7010	 0.3980
P	 0.7640	 0.4290
PP	 0.6240	 0.2960
Q	 0.7640	 0.4340
QQ	 0.6650	 0.3480
R	 0.7120	 0.3880
RR	 0.6360	 0.3440
S	 0.7810	 0.4380
SS	 0.6440	 0.3310
T	 0.7620	 0.4290
TT	 0.6540	 0.3400
U	 0.7000	 0.3690
UU	 0.6360	 0.3370
V	 0.7350	 0.4330
VV	 0.6860	 0.3800
W	 0.6010	 0.3290
WW	 0.7330	 0.4210
X	 0.7330	 0.4090
XX	 0.6960	 0.4160
Y	 0.7510	 0.3960
YY	 0.6760	 0.3510
Z	 0.7470	 0.4000
ZZ	 0.6360	 0.3230
a	 0.7900	 0.4340
aa	 0.7160	 0.4070
b	 0.6850	 0.3560
bb	 0.6510	 0.3640
c	 0.7330	 0.4000
cc	 0.6380	 0.3680
d	 0.7420	 0.4170
dd	 0.7290	 0.4040
e	 0.7620	 0.4390
ee	 0.6170	 0.3110
f	 0.7860	 0.4500
ff	 0.4310	 0.1380
g	 0.7300	 0.4080
gg	 0.5810	 0.2930
h	 0.7180	 0.3790
hh	 0.1420	 0.2150
i	 0.7440	 0.3980
ii	 0.4000	 0.2570
j	 0.8180	 0.4460

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Chain	Atom inclusion	Q-score
jj	 0.4570	 0.2400
k	 0.6930	 0.3710
l	 0.7490	 0.4290
m	 0.7520	 0.4210
n	 0.5870	 0.3820
o	 0.7410	 0.4220
p	 0.7270	 0.4160
r	 0.7950	 0.4450
s	 0.1820	 0.0620
t	 0.1330	 0.0300