



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 04:09 pm GMT

PDB ID : 6T59
EMDB ID : EMD-10380
Title : Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 and nascent chain-associated complex
Authors : Lin, Z.; Gasic, I.; Chandrasekaran, V.; Peters, N.; Shao, S.; Ramakrishnan, V.; Mitchison, T.J.; Hegde, R.S.
Deposited on : 2019-10-15
Resolution : 3.11 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

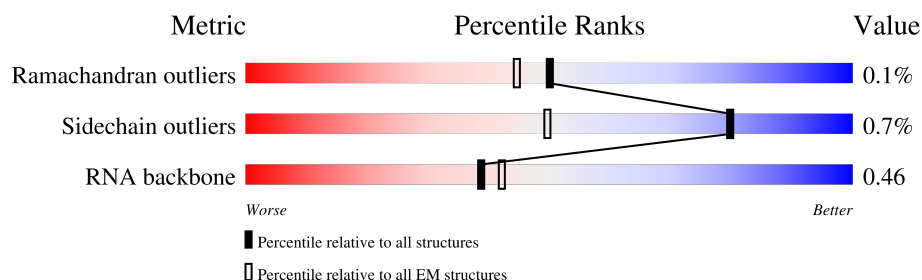
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	A3	257	<div> <div>85%</div> <div>96%</div> <div>••</div> </div>
2	B3	403	<div> <div>79%</div> <div>97%</div> <div>•</div> </div>
3	C3	425	<div> <div>68%</div> <div>84%</div> <div>• 15%</div> </div>
4	D3	297	<div> <div>70%</div> <div>99%</div> <div>•</div> </div>
5	E3	291	<div> <div>62%</div> <div>73%</div> <div>• 26%</div> </div>
6	F3	247	<div> <div>75%</div> <div>91%</div> <div>9%</div> </div>
7	G3	319	<div> <div>57%</div> <div>73%</div> <div>27%</div> </div>
8	H3	192	<div> <div>84%</div> <div>99%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
9	I3	214	
10	J3	178	
11	L3	211	
12	M3	218	
13	N3	204	
14	O3	203	
15	P3	184	
16	Q3	188	
17	R3	196	
18	S3	176	
19	T3	160	
20	U3	128	
21	V3	140	
22	W3	157	
23	X3	156	
24	Y3	145	
25	Z3	136	
26	a3	148	
27	b3	226	
28	c3	115	
29	d3	125	
30	e3	135	
31	f3	110	
32	g3	116	
33	h3	123	

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Mol	Chain	Length	Quality of chain
34	i3	105	<div>79%</div> <div>97%</div>
35	j3	97	<div>68%</div> <div>86%</div> <div>11%</div>
36	k3	70	<div>84%</div> <div>99%</div>
37	l3	51	<div>80%</div> <div>98%</div>
38	m3	102	<div>41%</div> <div>51%</div> <div>49%</div>
39	n3	25	<div>100%</div> <div>100%</div>
40	o3	106	<div>81%</div> <div>98%</div>
41	p3	92	<div>74%</div> <div>96%</div>
42	r3	137	<div>78%</div> <div>91%</div> <div>9%</div>
43	s3	318	<div>58%</div> <div>61%</div> <div>38%</div>
44	t3	165	<div>92%</div> <div>91%</div> <div>7%</div>
45	23	76	<div>99%</div> <div>82%</div> <div>18%</div>
46	54	3543	<div>73%</div> <div>76%</div> <div>24%</div>
47	74	120	<div>65%</div> <div>88%</div> <div>12%</div>
48	84	156	<div>68%</div> <div>76%</div> <div>21%</div>
49	NI	29	<div>90%</div> <div>97%</div>
50	NA	215	<div>25%</div> <div>25%</div> <div>75%</div>
51	NB	206	<div>28%</div> <div>28%</div> <div>72%</div>
52	TT	440	<div>92%</div> <div>96%</div>
53	1	64	<div>55%</div> <div>44%</div> <div>12%</div> <div>44%</div>

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 143047 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	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	B3	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
B3	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	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	D3	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
D3	1	MET	-	initiating methionine	UNP G1SYJ6

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E3	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	F3	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
F3	61	ARG	GLY	conflict	UNP G1TUB1
F3	93	ARG	GLY	conflict	UNP G1TUB1
F3	131	MET	VAL	conflict	UNP G1TUB1
F3	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J3	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	L3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M3	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	N3	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	O3	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	P3	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	Q3	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R3	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S3	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	T3	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	U3	102	Total	C	N	O	S	0	0
			834	534	146	152	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V3	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	W3	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X3	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y3	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	Z3	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	a3	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
a3	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b3	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	c3	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	d3	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	e3	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	f3	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	g3	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	h3	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	i3	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j3	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	k3	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k3	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l3	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	m3	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n3	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	o3	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	p3	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	r3	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	s3	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t3	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	23	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	54	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	74	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	84	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	NI	29	Total	C	N	O	0	0
			150	92	29	29		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	54	Total	C	N	O	S	0	0
			420	270	71	78	1		

- Molecule 51 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	58	Total	C	N	O	S	0	0
			444	278	76	88	2		

- Molecule 52 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	TT	426	Total	C	N	O	S	0	0
			3337	2097	580	647	13		

- Molecule 53 is a protein called Tubulin Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	36	Total	C	N	O	S	0	0
			292	184	51	55	2		

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	P3	2	Total	Mg	0
			2	2	
54	V3	1	Total	Mg	0
			1	1	
54	a3	1	Total	Mg	0
			1	1	
54	g3	1	Total	Mg	0
			1	1	
54	j3	1	Total	Mg	0
			1	1	
54	54	201	Total	Mg	0
			201	201	
54	74	7	Total	Mg	0
			7	7	
54	84	6	Total	Mg	0
			6	6	

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	g3	1	Total	Zn	0
			1	1	
55	j3	1	Total	Zn	0
			1	1	

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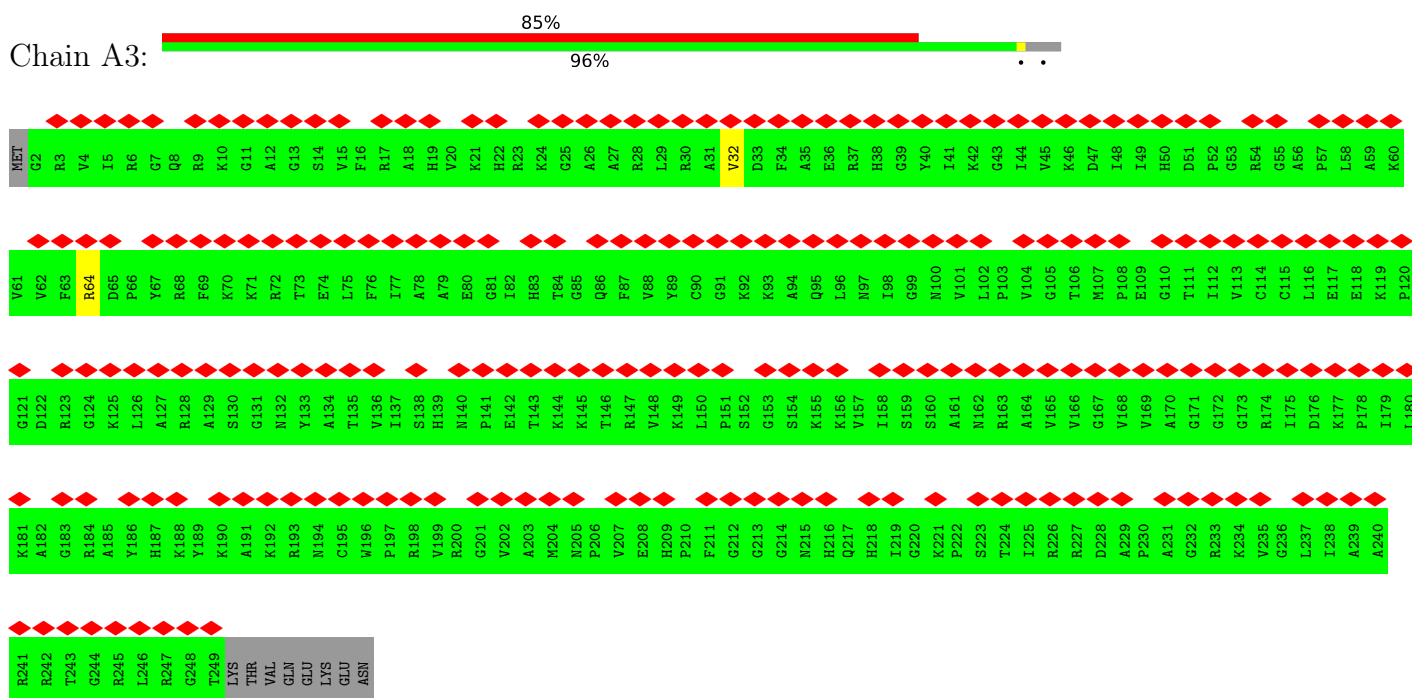
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Mol	Chain	Residues	Atoms		AltConf
55	m3	1	Total 1	Zn 1	0
55	o3	1	Total 1	Zn 1	0
55	p3	1	Total 1	Zn 1	0

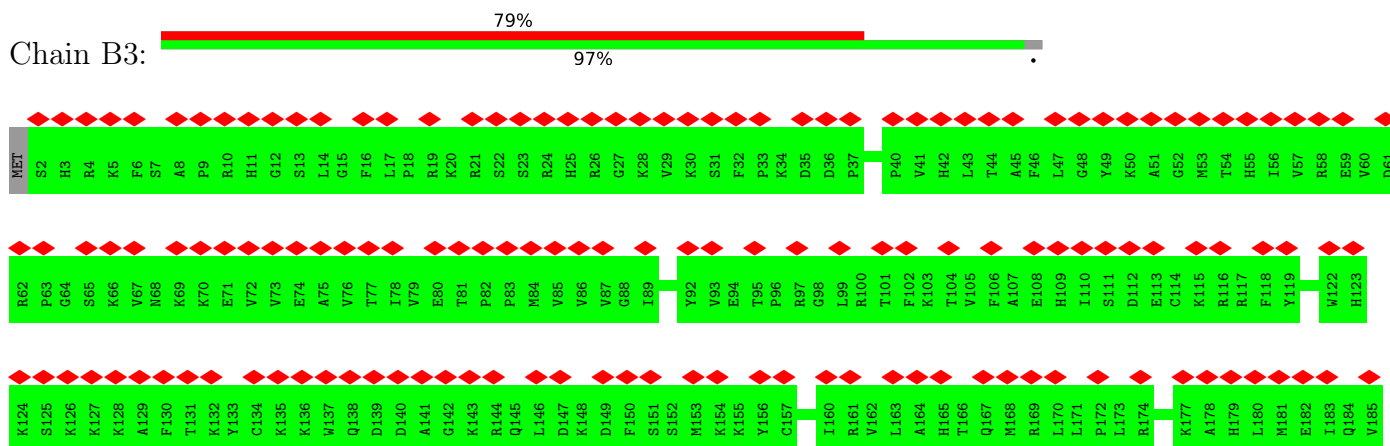
3 Residue-property plots

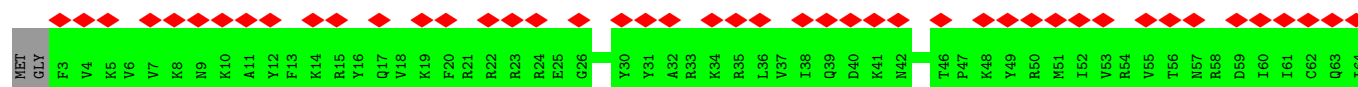
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

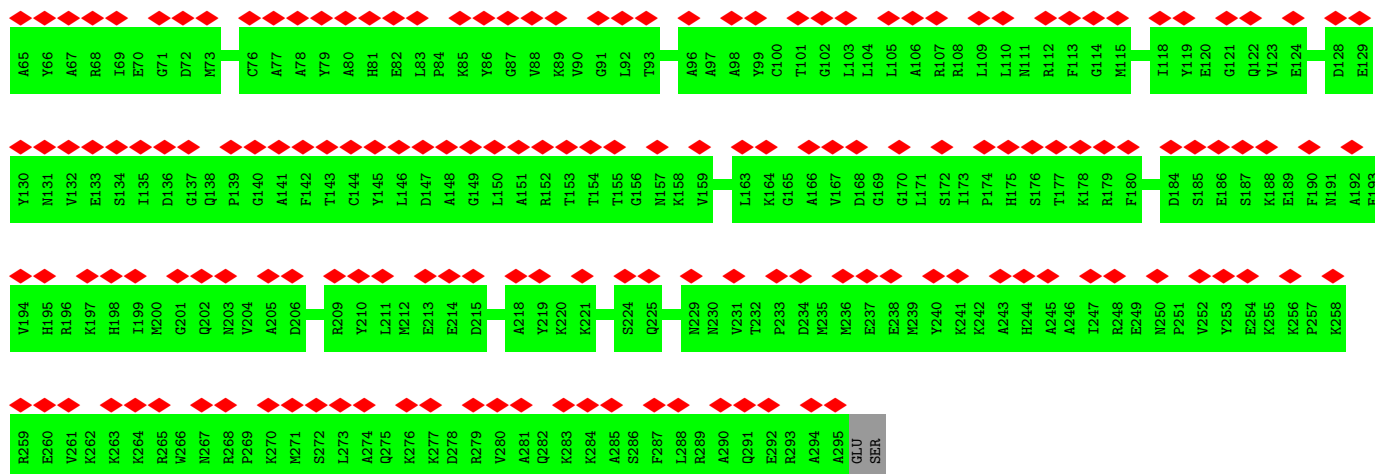
• Molecule 1: Ribosomal protein L8



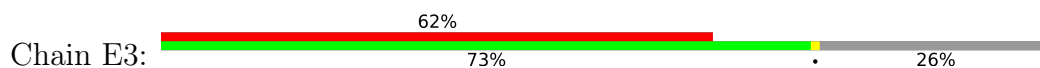
• Molecule 2: uL3



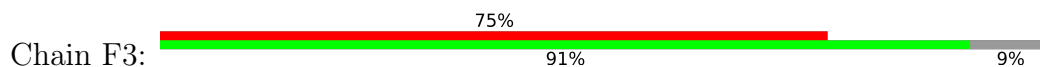


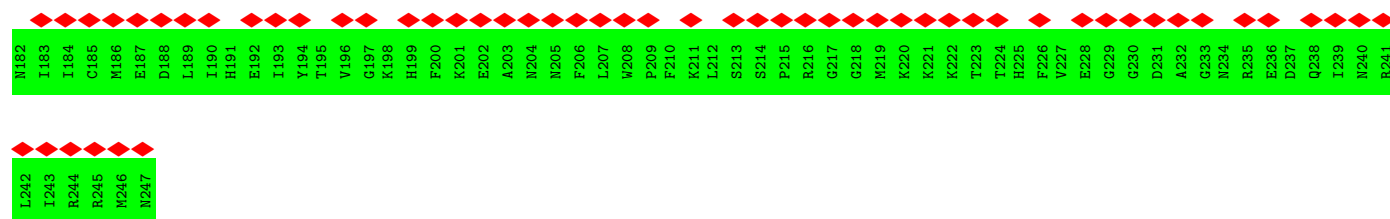


• Molecule 5: 60S ribosomal protein L6

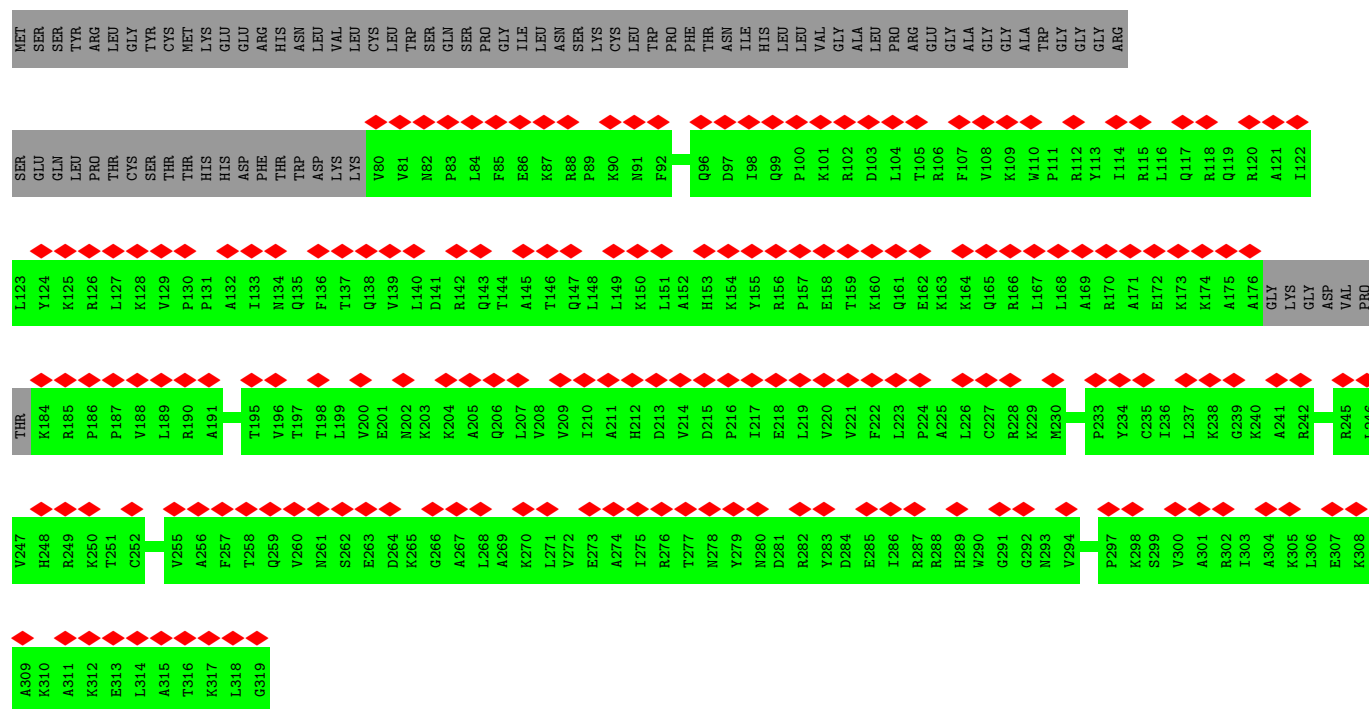
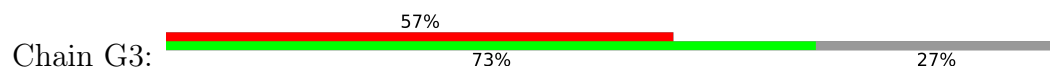


• Molecule 6: U130

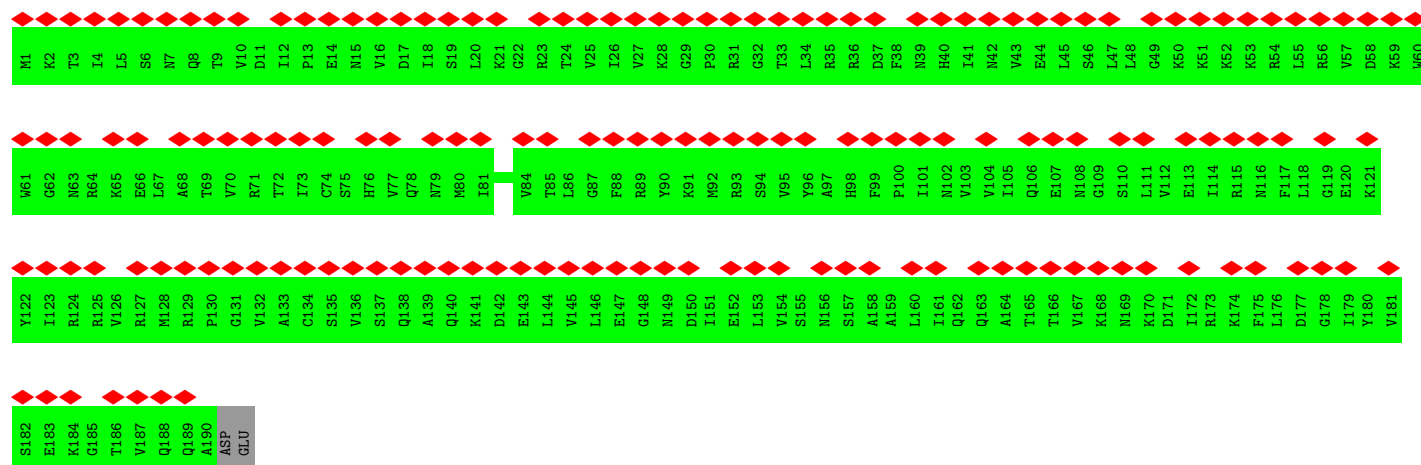
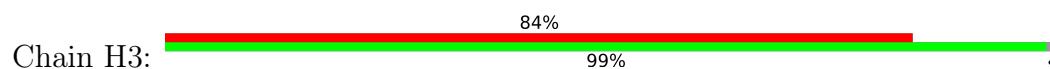




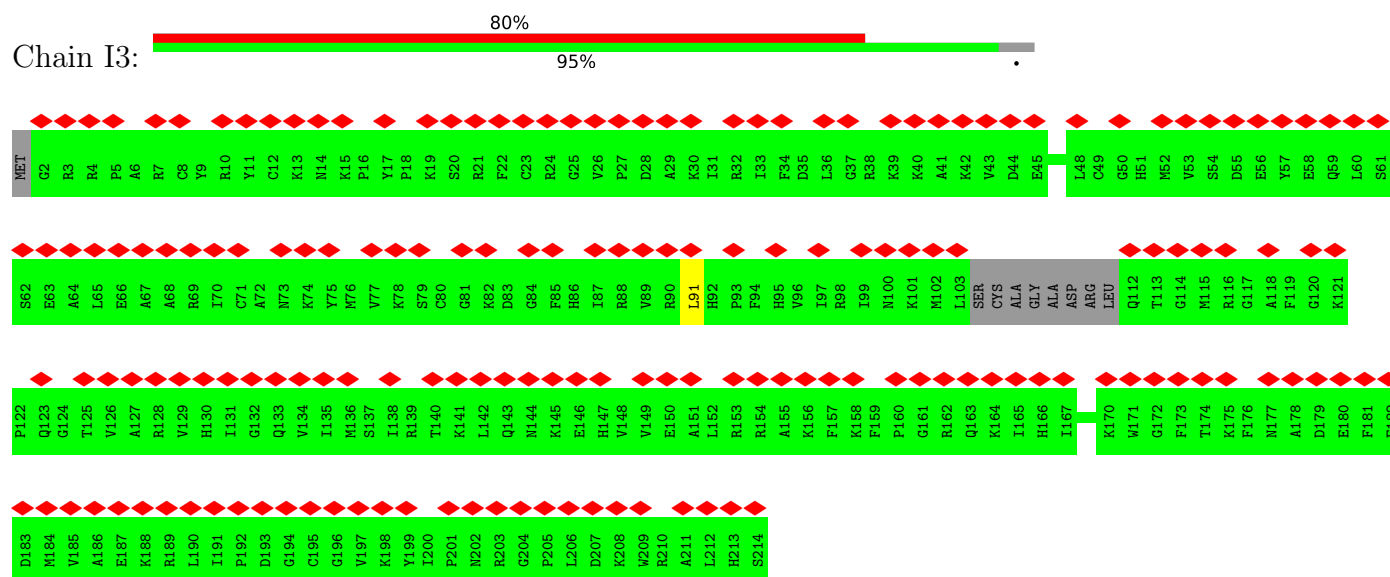
• Molecule 7: eL8



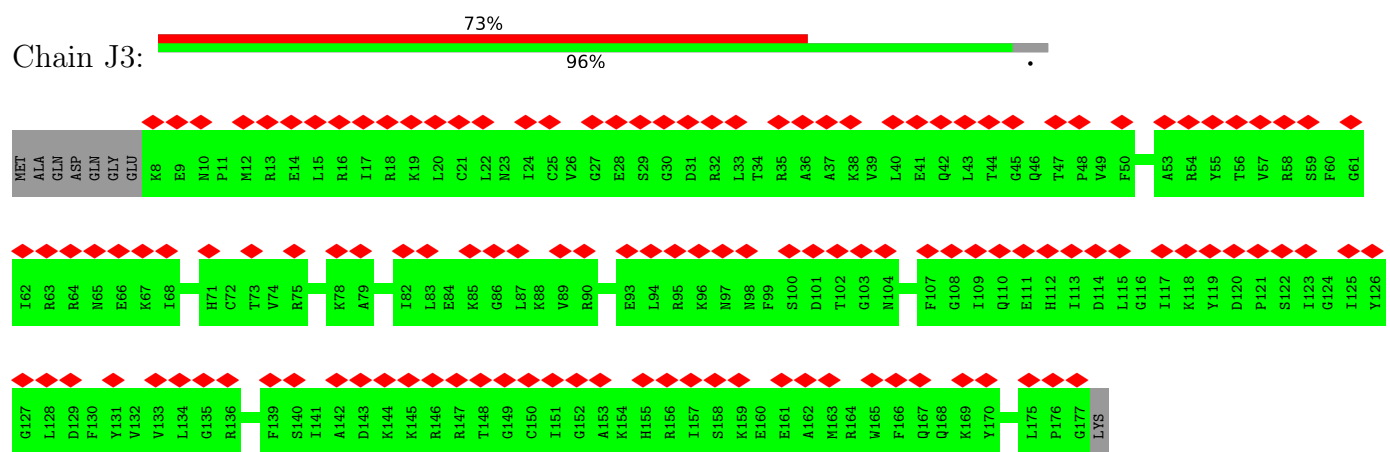
• Molecule 8: uL6



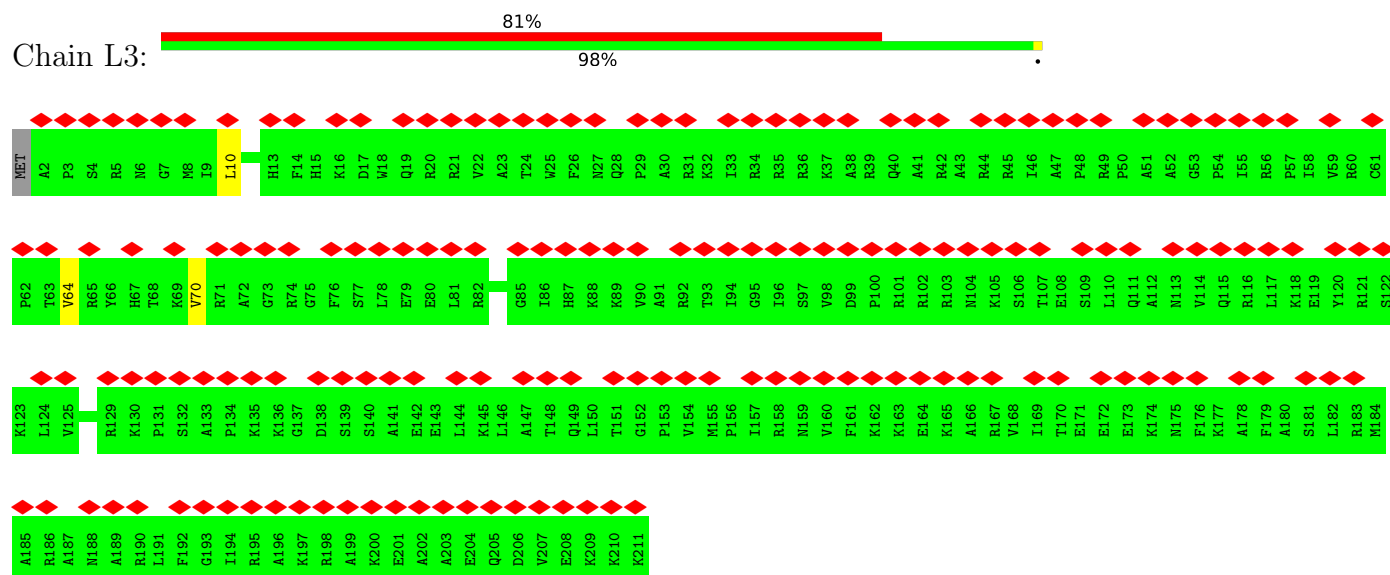
• Molecule 9: 60S ribosomal protein L10



• Molecule 10: Ribosomal protein L11

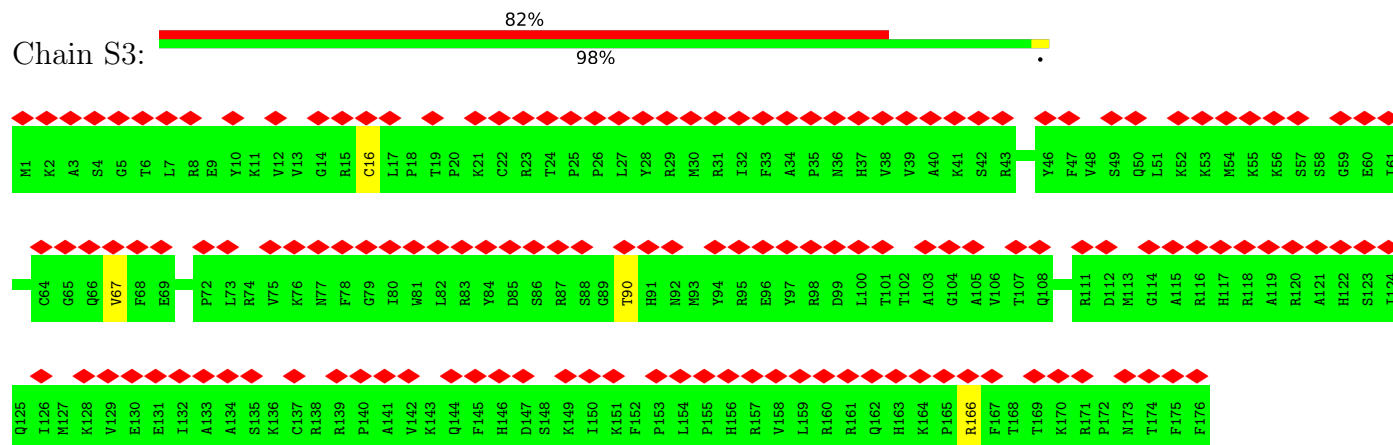


• Molecule 11: eL13

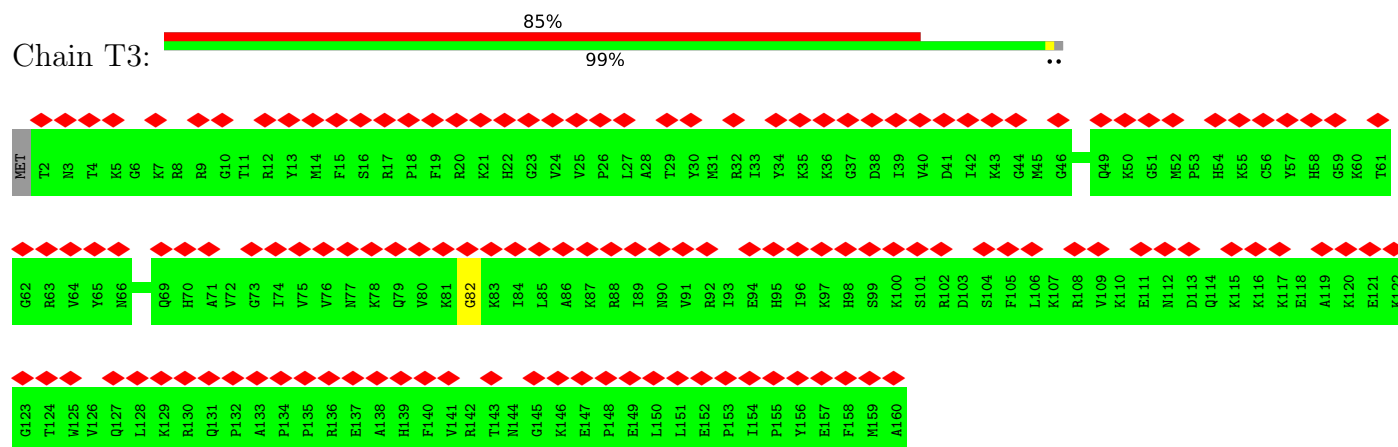


ILE
ILE
LYS
THR
LEU
SER
LYS
GLU
GLU
THR
LYS
LYS

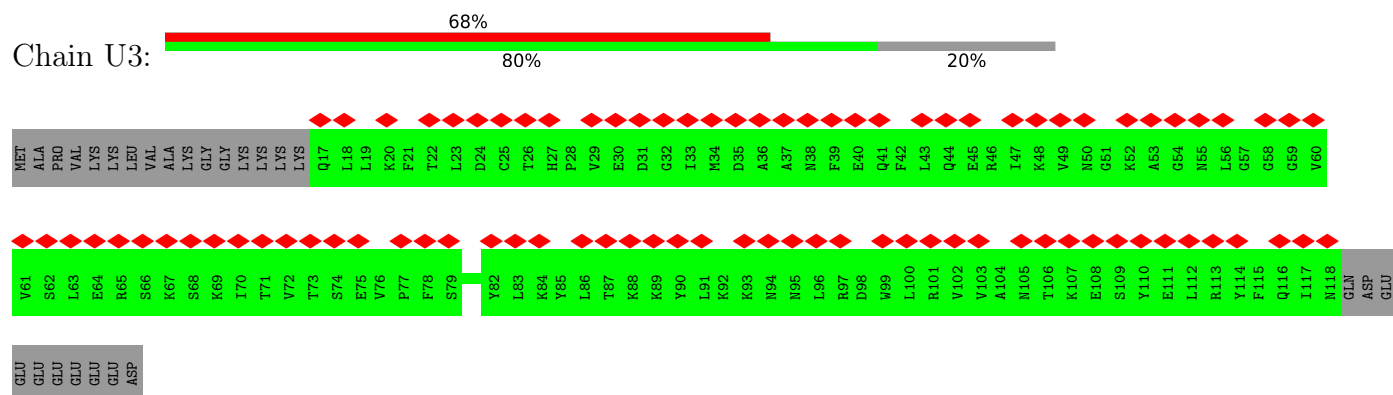
• Molecule 18: eL20



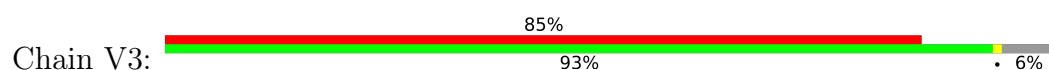
• Molecule 19: eL21



• Molecule 20: eL22

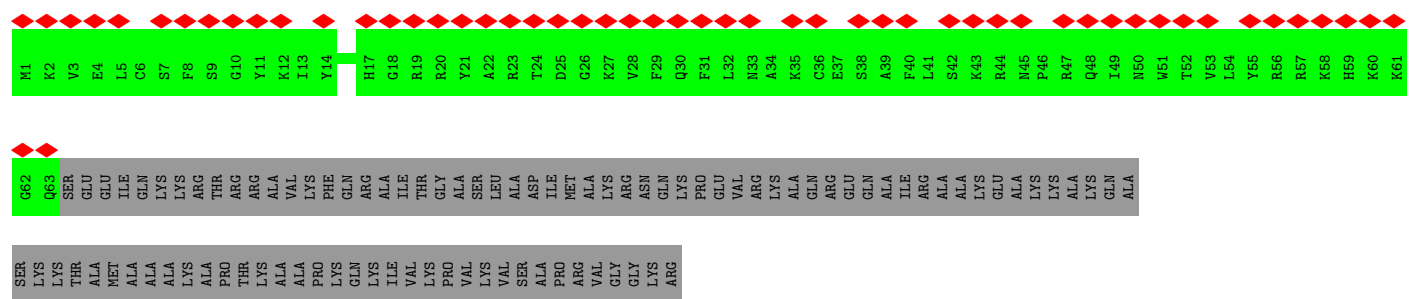


• Molecule 21: Ribosomal protein L23

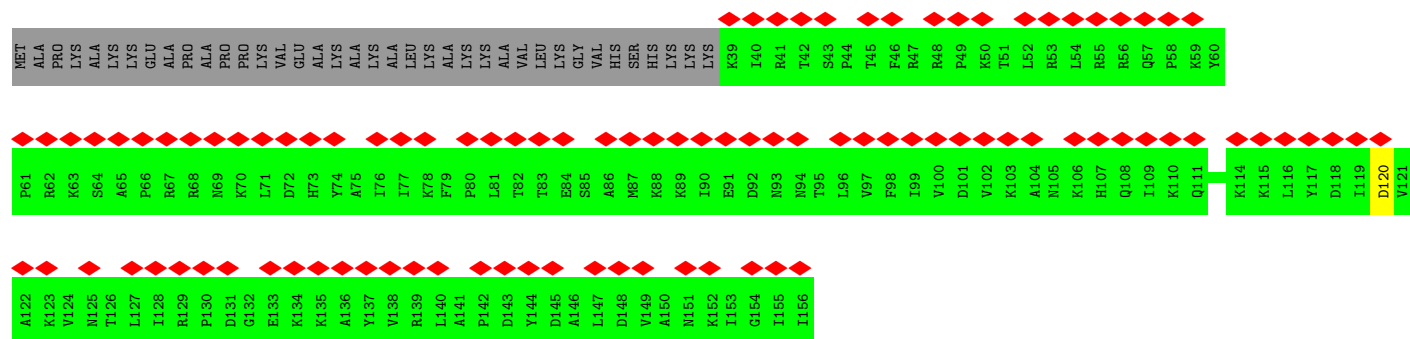
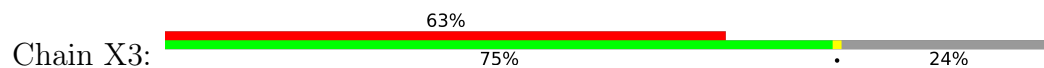




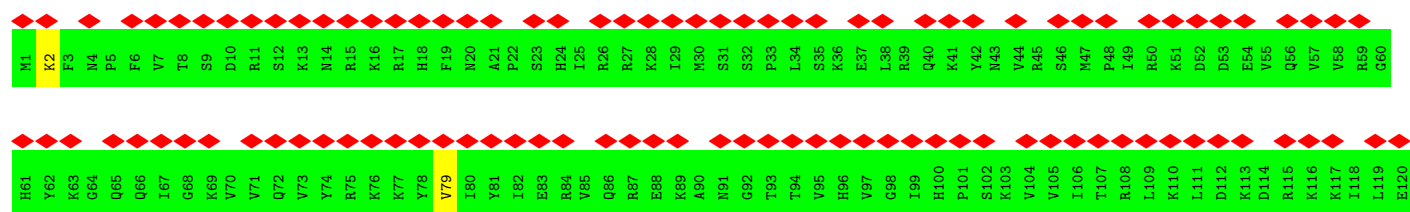
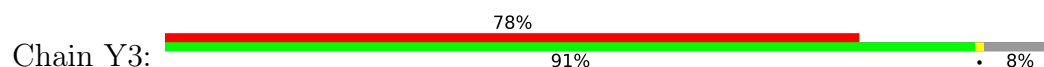
• Molecule 22: eL24

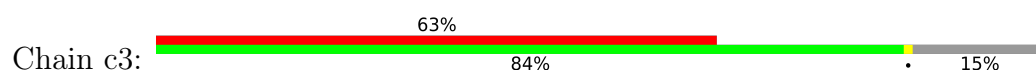


• Molecule 23: uL23

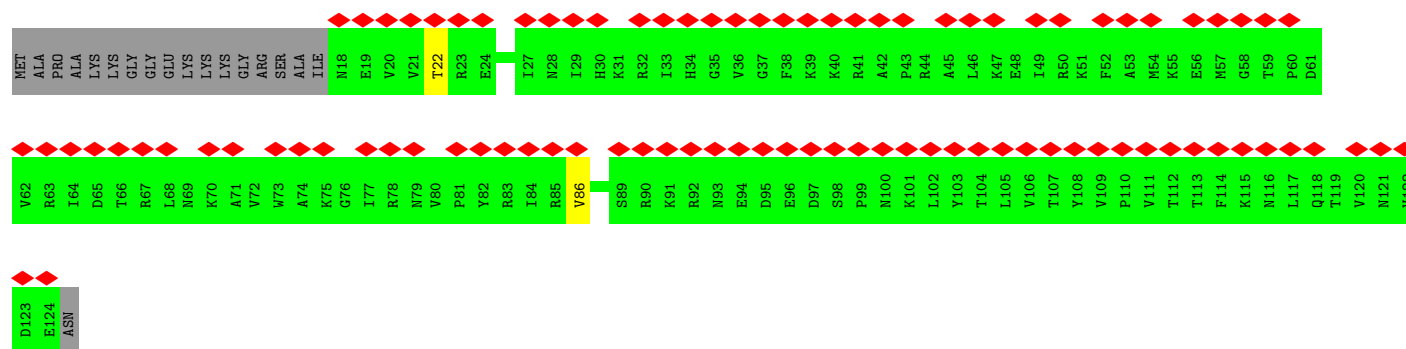
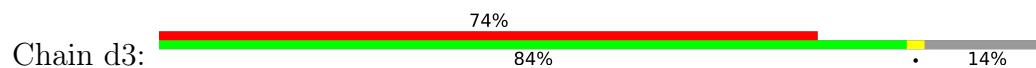


• Molecule 24: Ribosomal protein L26

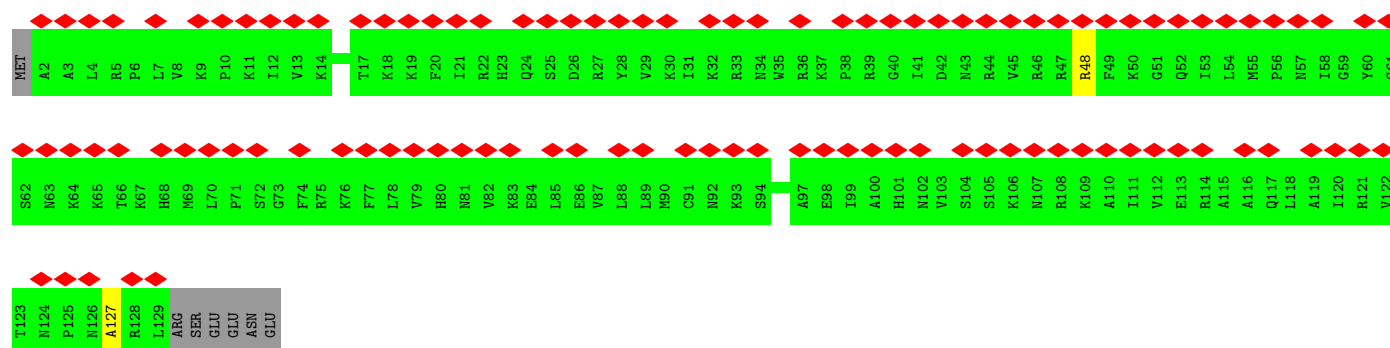
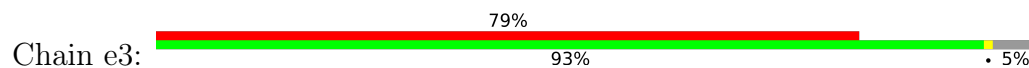




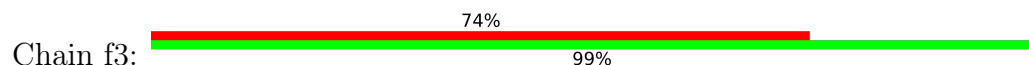
• Molecule 29: eL31



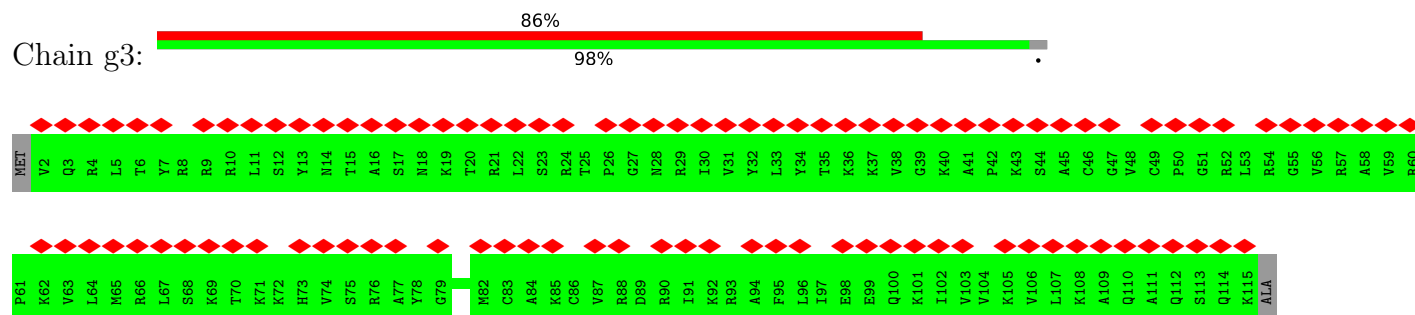
• Molecule 30: eL32



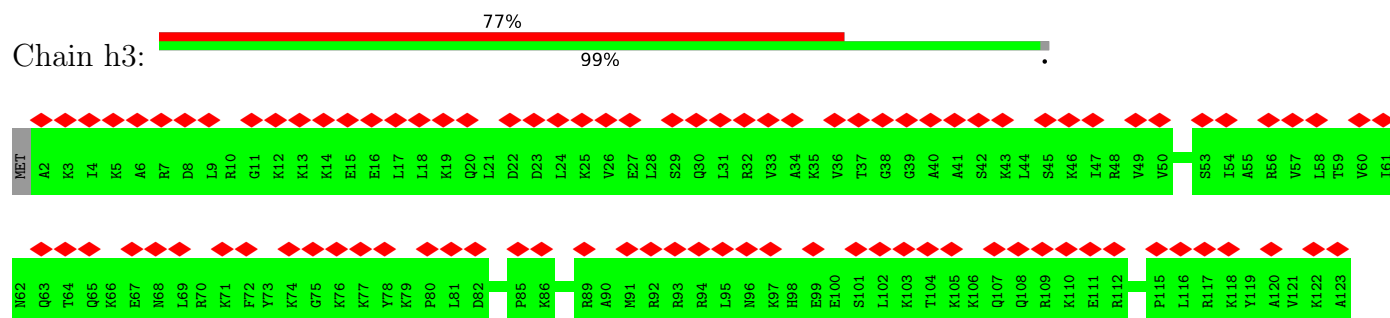
• Molecule 31: eL33



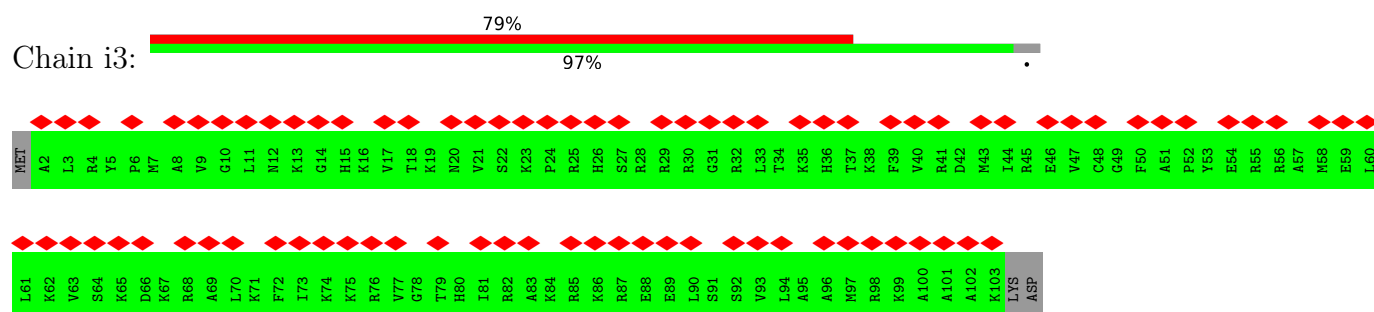
- Molecule 32: eL34



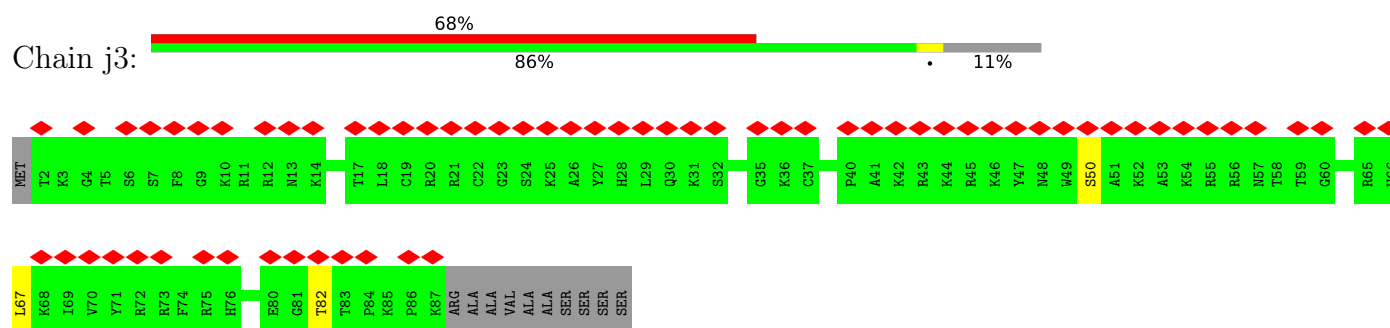
- Molecule 33: uL29



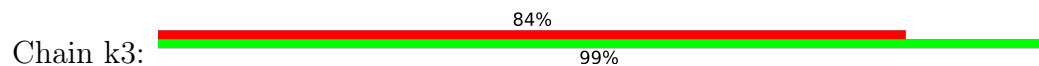
- Molecule 34: 60S ribosomal protein L36

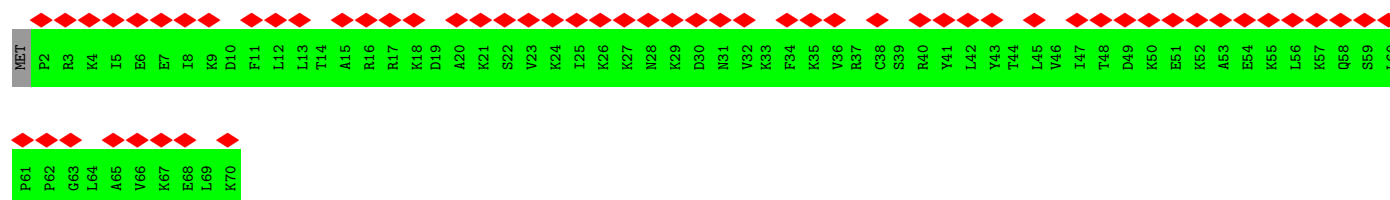


- Molecule 35: Ribosomal protein L37



- Molecule 36: eL38

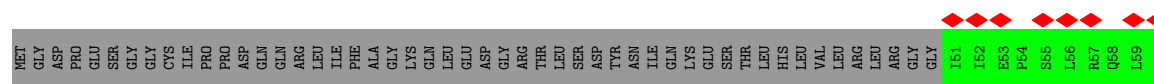
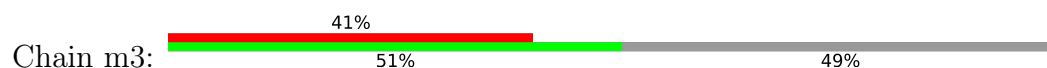




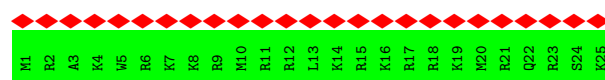
- Molecule 37: eL39



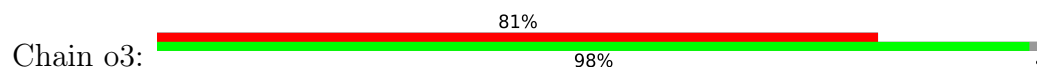
- Molecule 38: eL40



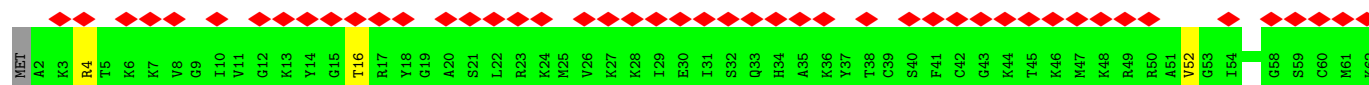
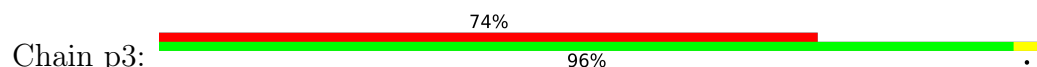
- Molecule 39: 60s ribosomal protein l41

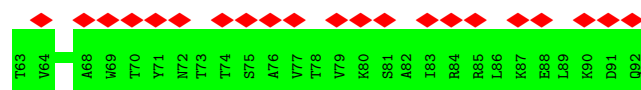


- Molecule 40: eL42

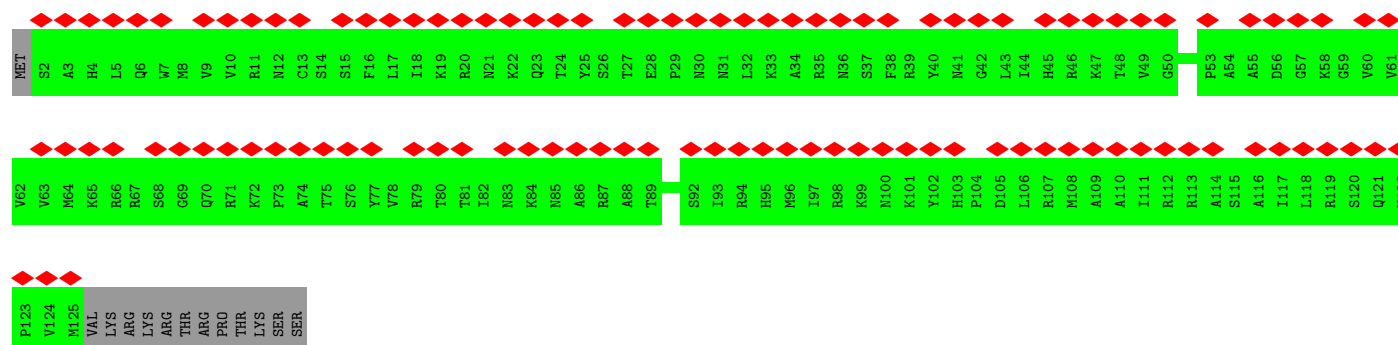
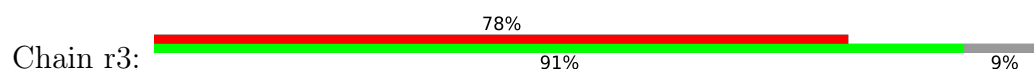


- Molecule 41: eL43

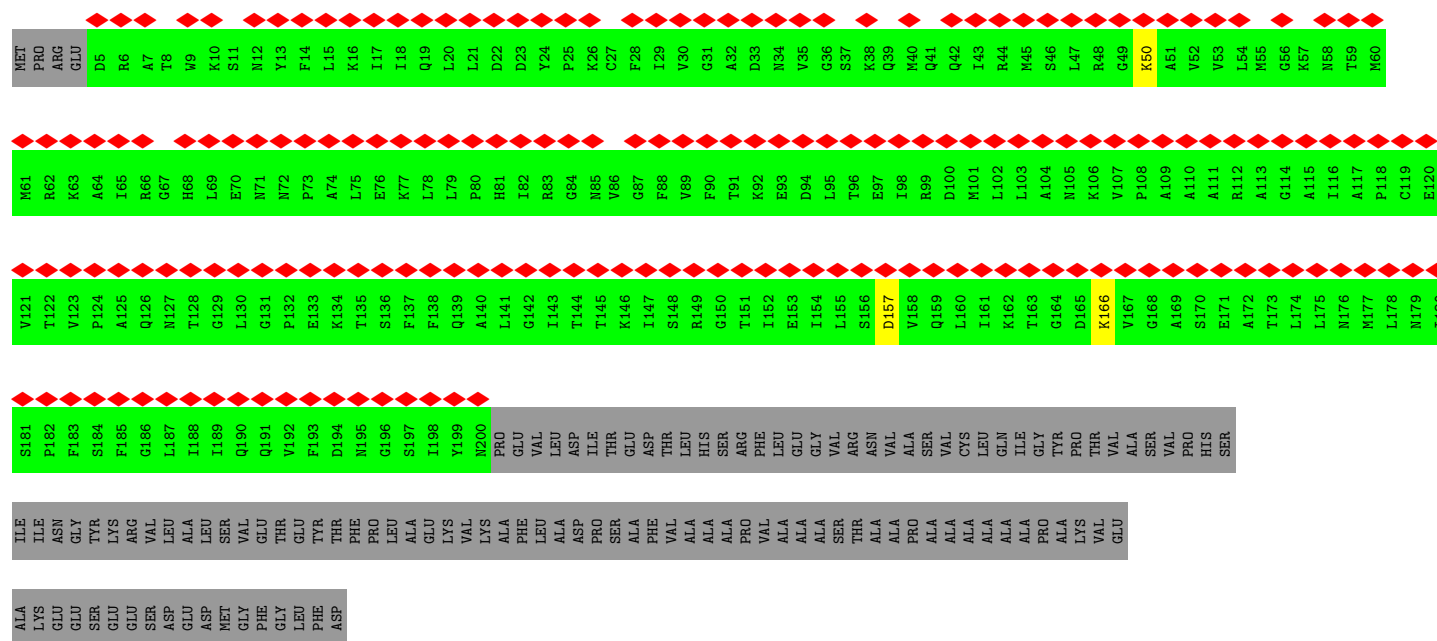




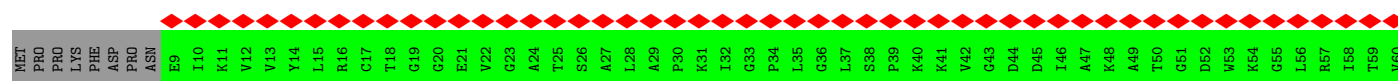
• Molecule 42: eL28

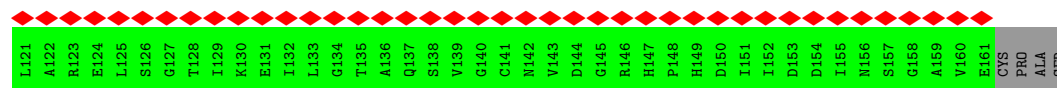


• Molecule 43: uL10

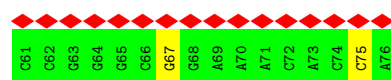
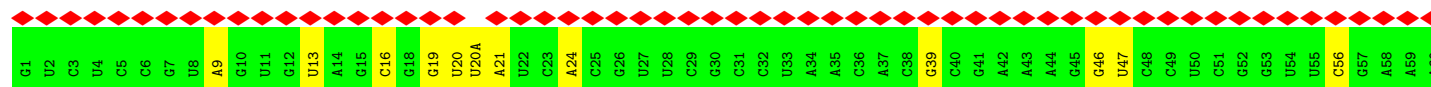
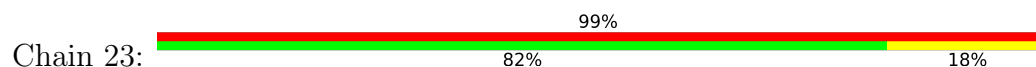


• Molecule 44: Ribosomal protein L12

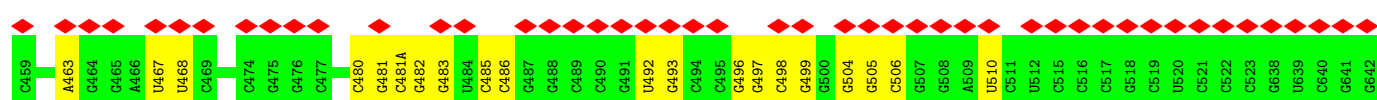
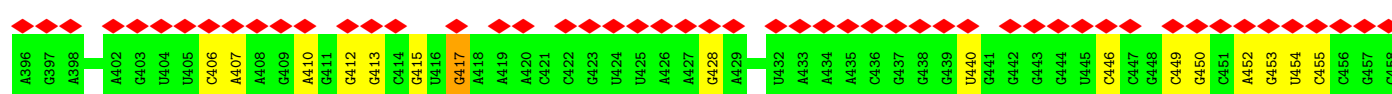
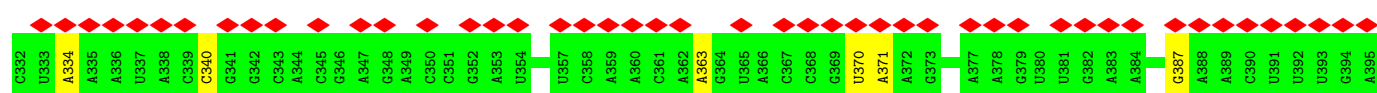
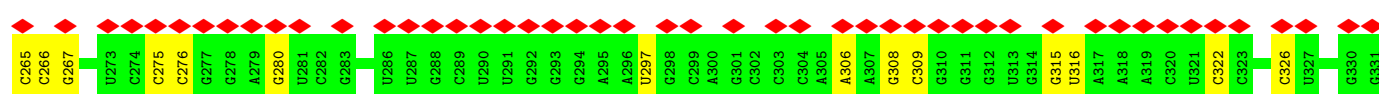
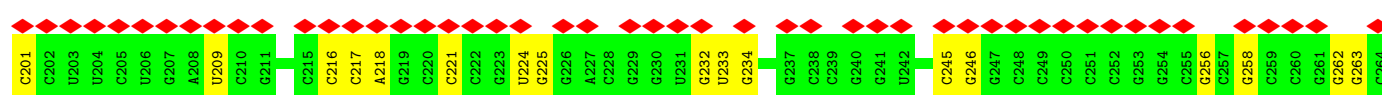
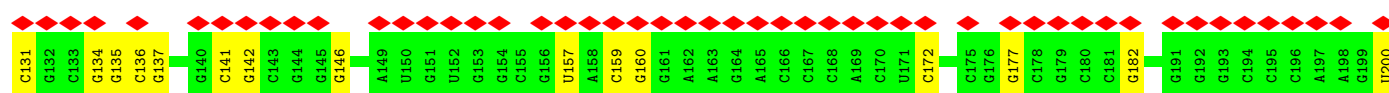
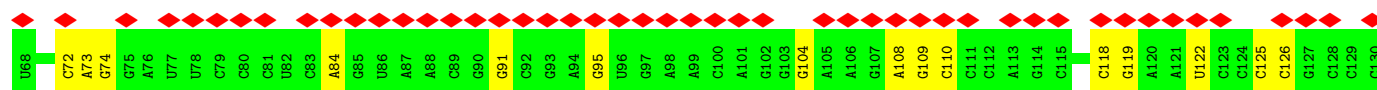
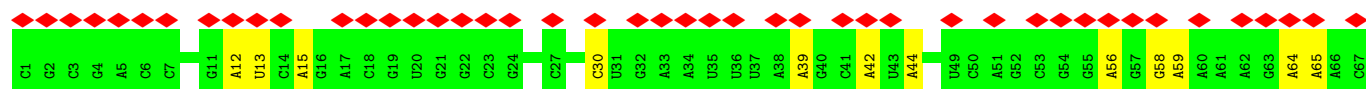
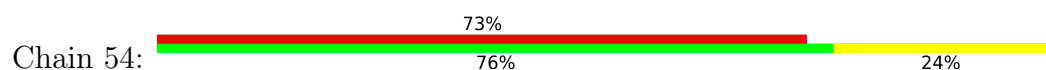


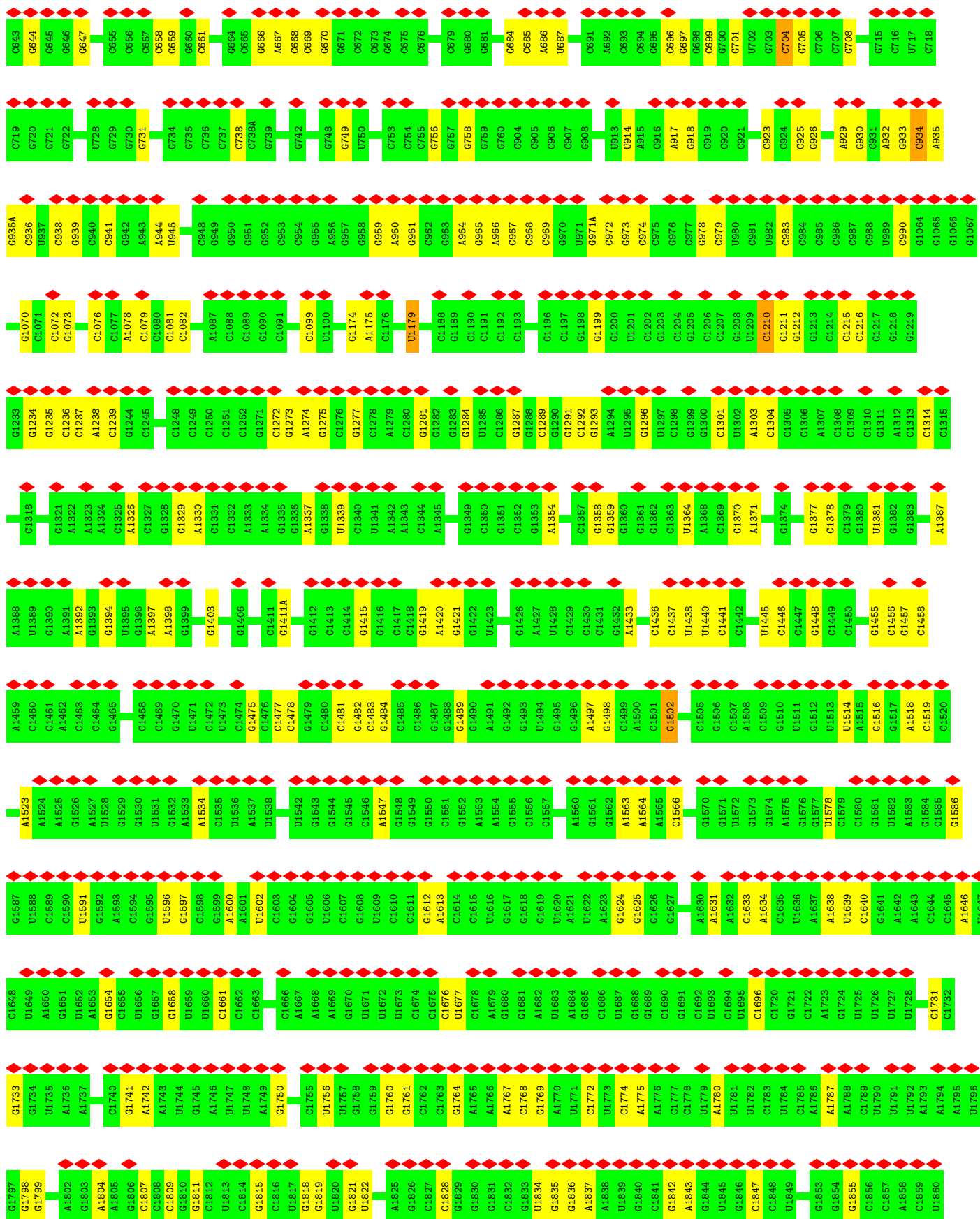


- Molecule 45: P-site tRNA



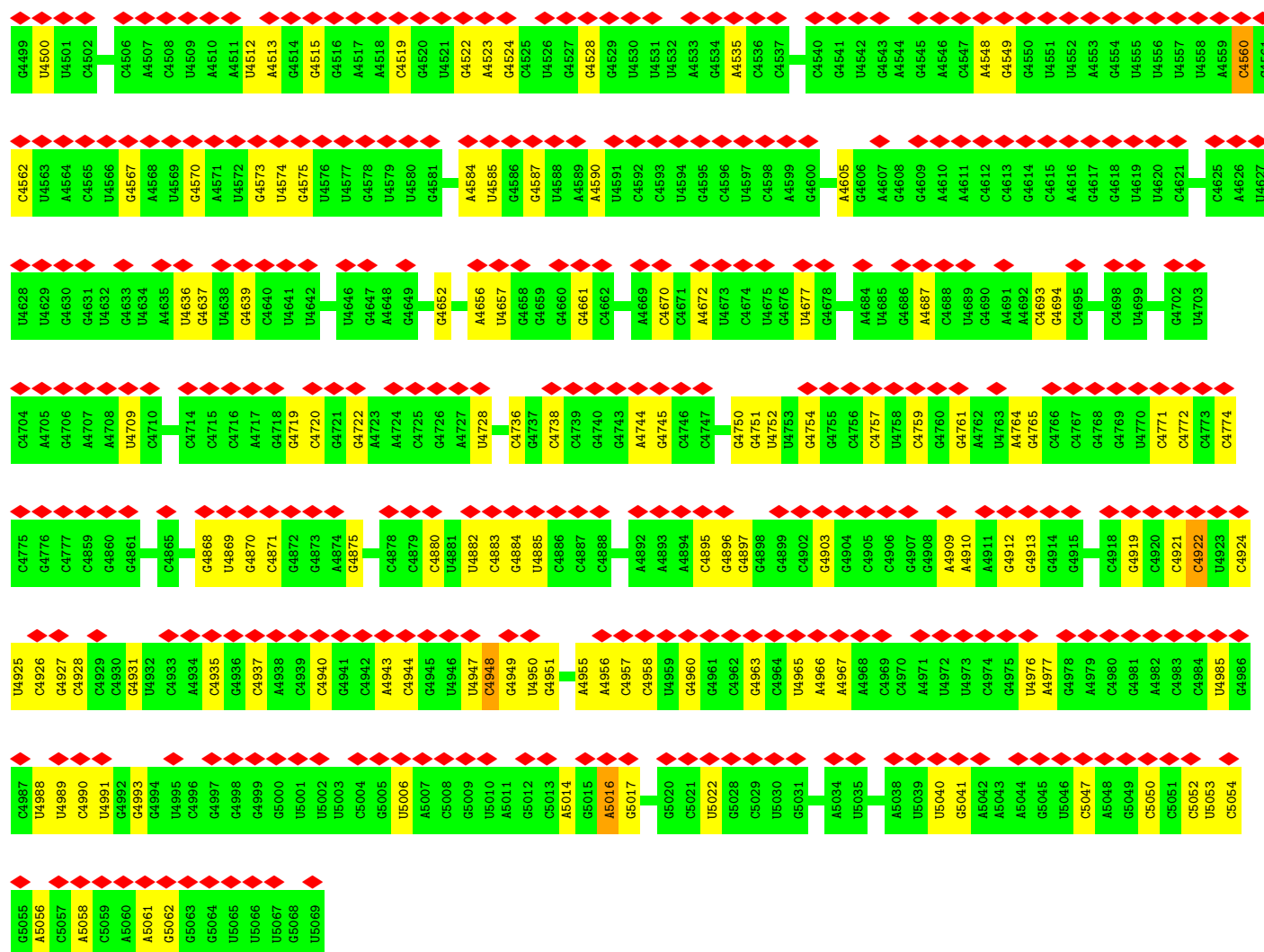
- Molecule 46: 28S ribosomal RNA



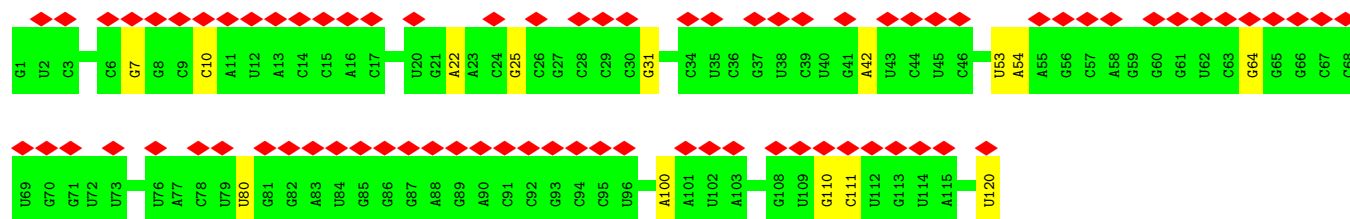
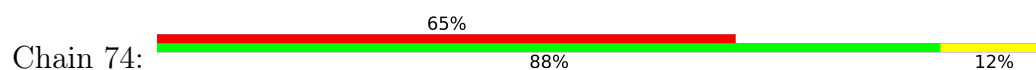


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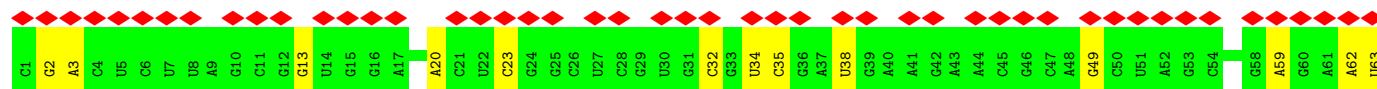
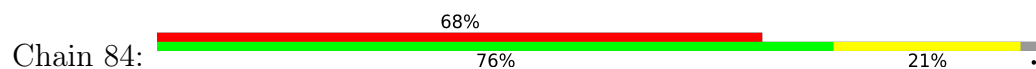
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U4302	U4303	U4304	U4305	U4306	U4307	U4308	U4309	U4313	U4314	U4315	U4316	U4317	U4318	U4319	U4320	U4324	U4325	U4326	U4327	U4328	U4329	U4330	U4331	U4332	U4333	U4334	U4335	U4336	U4337	U4338	U4339	U4340	U4341	U4342	U4343	U4344	U4345	U4346	U4347	U4348	U4349	U4350	U4351	U4352	U4353	U4354	U4355	U4356	U4357	U4358	U4359	U4360	U4361	U4362	U4363	U4364	U4365	U4366	U4367																																																																																																																																																																																																																																																																					
G4368	G4369	G4370	G4371	G4372	G4373	G4374	G4375	G4376	G4377	G4378	G4379	G4380	U4384	U4385	U4386	U4387	U4388	U4389	U4390	U4391	G4392	U4393	U4394	U4395	U4396	U4397	U4398	U4399	U4400	U4401	U4402	U4403	U4404	G4407	G4408	G4409	G4410	G4411	G4415	U4419	U4420	U4421	U4422	U4423	U4424	U4425	U4426	U4427	U4428	U4429	U4430	U4431	U4432	U4433	U4434	U4435																																																																																																																																																																																																																																																																								
U4169	U4170	U4171	U4172	U4173	U4174	U4175	U4176	U4177	U4178	U4182	U4183	U4184	U4185	U4186	U4187	U4188	U4189	U4190	U4191	U4192	U4193	U4194	U4195	U4196	U4197	U4198	U4199	U4200	U4201	U4202	U4203	U4204	U4205	U4206	U4207	U4208	U4211	U4212	U4215	U4216	U4217	U4218	U4219	U4220	U4221	U4222	U4223	U4224	U4225	U4226	U4227	U4228	U4229	U4230	U4231																																																																																																																																																																																																																																																																									
C4088	G4092	G4093	G4094	G4095	G4096	G4097	G4098	G4099	G4100	G4101	G4102	G4103	G4104	G4105	G4106	G4107	G4108	G4109	G4110	G4111	G4112	G4113	G4114	G4115	G4116	G4117	G4118	G4119	G4120	G4121	G4122	G4123	G4124	G4125	G4126	G4127	G4128	G4129	G4130	G4131	G4132	G4133	G4134	G4135	G4136	G4137	G4138	G4139	G4140	G4141	G4142	G4143	G4144	G4145	G4146	G4147	G4148	G4149																																																																																																																																																																																																																																																																						
A3908	C3909	C3910	C3911	U3914	U3915	U3916	U3917	U3918	U3919	U3920	U3921	U3922	U3923	U3924	U3925	U3926	U3927	U3928	U3929	U3930	U3931	U3932	U3933	U3934	C3937	C3938	U3939	U3940	U3941	U3942	U3943	G3946	U3947	U3948	U3949	U3950	U3951	U3952	U3953	U3954	U3955	U3956	U3957	U3958	U3959	U3960	U3961	U3962	U3963	U3964	U3965	U3966	U3967	U3968	U3969	U3970	U3971	U3972	U3973	U3974	U3975	U3976	U3977	U3978	U3979	U3980	U3981	U3982	U3983	U3984	U3985	U3986	U3987	U3988	U3989	U3990	U3991	U3992	U3993	U3994	U3995	U3996	U3997	U3998	U3999	U4000	U4001	U4002	U4003	U4004	U4005	U4006	U4007	U4008	U4009	U4010	U4011	U4012	U4013	U4014	U4015	U4016	U4017	U4018	U4019	U4020	U4021	U4022	U4023	U4024	U4025	U4026	U4027	U4028	U4029	U4030	U4031	U4032	U4033	U4034	U4035	U4036	U4037	U4038	U4039	U4040	U4041	U4042	U4043	U4044	U4045	U4046	U4047	U4048	U4049	U4050	U4051	U4052	U4053	U4054	U4055	U4056	U4057	U4058	U4059	U4060	U4061	U4062	U4063	U4064	U4065	U4066	U4067	U4068	U4069	U4070	U4071	U4072	U4073	U4074	U4075	U4076	U4077	U4078	U4079	U4080	U4081	U4082	U4083	U4084	U4085	U4086	U4087	U4088	U4089	U4090	U4091	U4092	U4093	U4094	U4095	U4096	U4097	U4098	U4099	U4100	U4101	U4102	U4103	U4104	U4105	U4106	U4107	U4108	U4109	U4110	U4111	U4112	U4113	U4114	U4115	U4116	U4117	U4118	U4119	U4120	U4121	U4122	U4123	U4124	U4125	U4126	U4127	U4128	U4129	U4130	U4131	U4132	U4133	U4134	U4135	U4136	U4137	U4138	U4139	U4140	U4141	U4142	U4143	U4144	U4145	U4146	U4147	U4148	U4149	U4150	U4151	U4152	U4153	U4154	U4155	U4156	U4157	U4158	U4159	U4160	U4161	U4162	U4163	U4164	U4165	U4166																																																																				
C3846	C3847	C3848	C3849	C3850	C3851	C3852	C3853	C3854	C3855	C3856	C3857	C3858	C3859	C3860	C3861	C3862	C3863	C3864	C3865	C3866	C3867	C3868	C3869	C3870	C3871	C3872	C3873	C3874	C3875	C3876	C3877	C3878	C3879	C3880	C3881	C3882	C3883	C3884	C3885	C3886	C3887	C3888	C3889	C3890	C3891	C3892	C3893	C3894	C3895	C3896	C3897	C3898	C3899	C3900	C3901	C3902	C3903	C3904	C3905	C3906	C3907	C3908	C3909	C3910	C3911	C3912	C3913	C3914	C3915	C3916	C3917	C3918	C3919	C3920	C3921	C3922	C3923	C3924	C3925	C3926	C3927	C3928	C3929	C3930	C3931	C3932	C3933	C3934	C3935	C3936	C3937	C3938	C3939	C3940	C3941	C3942	C3943	C3944	C3945	C3946	C3947	C3948	C3949	C3950	C3951	C3952	C3953	C3954	C3955	C3956	C3957	C3958	C3959	C3960	C3961	C3962	C3963	C3964	C3965	C3966	C3967	C3968	C3969	C3970	C3971	C3972	C3973	C3974	C3975	C3976	C3977	C3978	C3979	C3980	C3981	C3982	C3983	C3984	C3985	C3986	C3987	C3988	C3989	C3990	C3991	C3992	C3993	C3994	C3995	C3996	C3997	C3998	C3999	C4000	C4001	C4002	C4003	C4004	C4005	C4006	C4007	C4008	C4009	C4010	C4011	C4012	C4013	C4014	C4015	C4016	C4017	C4018	C4019	C4020	C4021	C4022	C4023	C4024	C4025	C4026	C4027	C4028	C4029	C4030	C4031	C4032	C4033	C4034	C4035	C4036	C4037	C4038	C4039	C4040	C4041	C4042	C4043	C4044	C4045	C4046	C4047	C4048	C4049	C4050	C4051	C4052	C4053	C4054	C4055	C4056	C4057	C4058	C4059	C4060	C4061	C4062	C4063	C4064	C4065	C4066	C4067	C4068	C4069	C4070	C4071	C4072	C4073	C4074	C4075	C4076	C4077	C4078	C4079	C4080	C4081	C4082	C4083	C4084	C4085	C4086	C4087	C4088	C4089	C4090	C4091	C4092	C4093	C4094	C4095	C4096	C4097	C4098	C4099	C4100	C4101	C4102	C4103	C4104	C4105	C4106	C4107	C4108	C4109	C4110	C4111	C4112	C4113	C4114	C4115	C4116	C4117	C4118	C4119	C4120	C4121	C4122	C4123	C4124	C4125	C4126	C4127	C4128	C4129	C4130	C4131	C4132	C4133	C4134	C4135	C4136	C4137	C4138	C4139	C4140	C4141	C4142	C4143	C4144	C4145	C4146	C4147	C4148	C4149	C4150	C4151	C4152	C4153	C4154	C4155	C4156	C4157	C4158	C4159	C4160	C4161	C4162	C4163	C4164	C4165	C4166
U3786	G3787	C3788	C3789	U3790	U3791	U3792	U3793	U3794	U3795	U3796	U3797	U3798	U3799	U3800	U3801	U3802	U3803	U3804	U3805	U3806	U3807	U3808	U3809	U3810	U3811	U3812	U3813	U3814	U3815	U3816	U3817	U3818	U3819	U3820	U3821	U3822	U3823	U3824	U3825	U3826	U3827	U3828	U3829	U3830	U3831	U3832	U3833	U3834	U3835	U3836	U3837	U3838	U3839	U3840	U3841	U3842	U3843	U3844	U3845																																																																																																																																																																																																																																																																					
G3725	A3726	A3727	U3728	U3729	U3730	U3731	U3732	U3733	U3734	U3735	U3736	U3737	U3738	U3739	U3740	U3741	U3742	U3743	U3744	U3745	U3746	U3747	U3748	U3749	U3750	U3751	U3752	U3753	U3754	U3755	U3756	U3757	U3758	U3759	U3760	U3761	U3762	U3763	U3764	U3765	U3766	U3767	U3768	U3769	U3770	U3771	U3772	U3773	U3774	U3775	U3776	U3777	U3778	U3779	U3780	U3781	U3782	U3783	U3784	U3785																																																																																																																																																																																																																																																																				
G3665	C3666	C3667	C3668	C3669	C3670	C3671	C3672	C3673	C3674	C3675	C3676	C3677	C3678	C3679	C3680	C3681	C3682	C3683	C3684	C3685	C3686	C3687	C3688	C3689	C3690	C3691	C3692	C3693	C3694	C3695	C3696	C3697	C3698	C3699	C3700	C3701	C3702	C3703	C3704	C3705	C3706	C3707	C3708	C3709	C3710	C3711	C3712	C3713	C3714	C3715	C3716	C3717	C3718	C3719	C3720	C3721	C3722	C3723	C3724																																																																																																																																																																																																																																																																					
C3605	U3606	U3607	U3608	U3609	U3610	U3611	U3612	U3613	U3614	U3615	U3616	U3617	U3618	U3619	U3620	U3621	U3622	U3623	U3624	U3625	U3626	U3627	U3628	U3629	U3630	U3631	U3632	U3633	U3634	U3635	U3636	U3637	U3638	U3639	U3640	U3641	U3642	U3643	U3644	U3645	U3646	U3647	U3648	U3649	U3650	U3651	U3652	U3653	U3654	U3655	U3656	U3657	U3658	U3659	U3660	U3661	U3662	U3663	U3664																																																																																																																																																																																																																																																																					
A2845	A2846	A2847	A2848	A2849	A2850	A2851	A2852	A2853	A2854	A2855	A2856	A2857	A2858	A2859	A2860	A2861	A2862	A2863	A2864	A2865	A2866	A2867	A2868	A2869	A2870	A2871	A2872	A2873	A2874	A2875	A2876	A2877	A2878	A2879	A2880	A2881	A2882	A2883	A2884	A2885	A2886	A2887	A2888	A2889	A2890	A2891	A2892	A2893	A2894	A2895	A2896	A2897	A2898	A2899	A2900	A2901	A2902	A2903	A2904	A2905	A2906	A2907	A2908	A2909	A2910	A2911	A2912	A2913	A2914	A2915	A2916	A2917	A2918	A2919	A2920	A2921	A2922	A2923	A2924	A2925	A2926	A2927	A2928	A2929	A2930	A2931	A2932	A2933	A2934	A2935	A2936	A2937	A2938	A2939	A2940	A2941	A2942	A2943	A2944	A2945	A2946	A2947	A2948	A2949	A2950	A2951	A2952	A2953	A2954	A2955	A2956	A2957	A29																																																																																																																																																																																																															

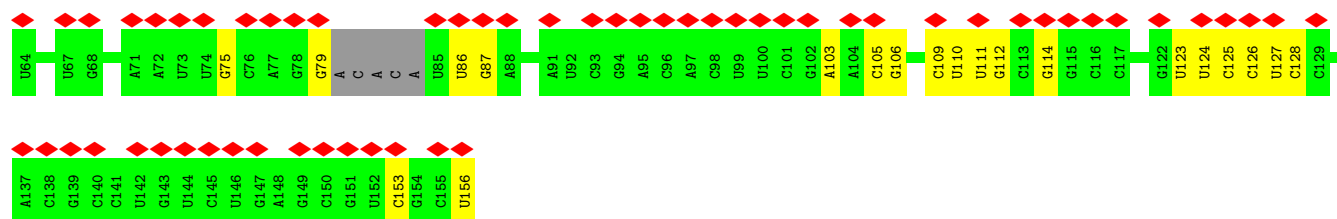


• Molecule 47: 5S ribosomal RNA



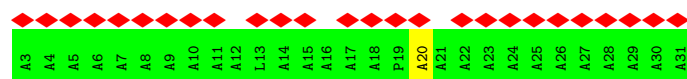
• Molecule 48: 5.8S ribosomal RNA





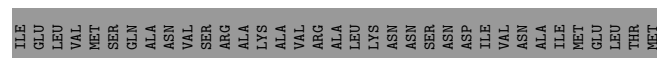
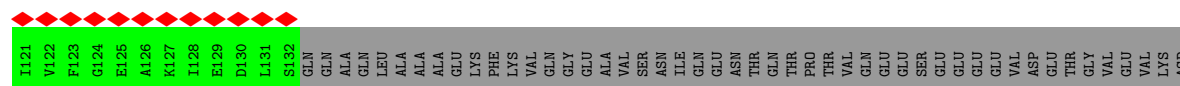
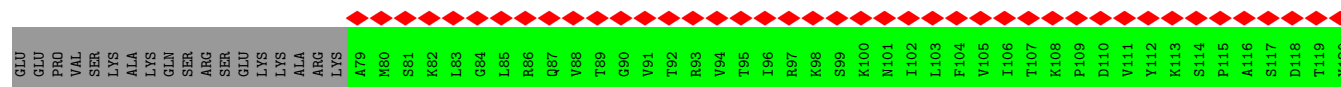
- Molecule 49: Nascent polypeptide-associated complex subunit alpha N-terminal region

Chain NI: 90%
97%



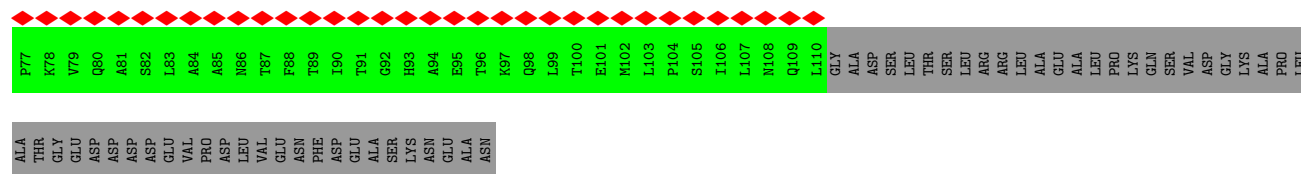
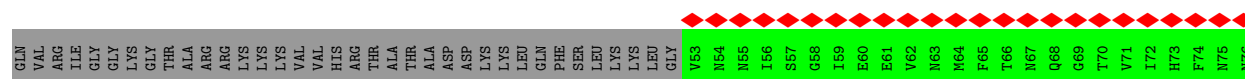
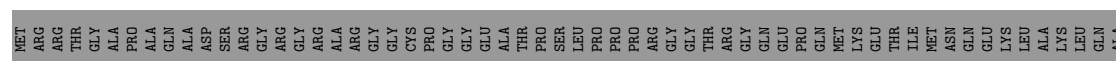
- Molecule 50: Nascent polypeptide-associated complex subunit alpha

Chain NA: 25%
25% 75%



- Molecule 51: Transcription factor BTF3

Chain NB: 28%
28% 72%



- Molecule 52: Tetratricopeptide repeat protein 5

Chain TT: 92%
96%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49626	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 ($e^-/\text{\AA}^2$)	48.36	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.694	Depositor
Minimum map value	-0.371	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (\AA)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.33, 1.33, 1.33	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

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	A3	0.63	0/1936	0.55	0/2596
2	B3	0.63	0/3240	0.56	0/4339
3	C3	0.61	0/2937	0.56	1/3946 (0.0%)
4	D3	0.60	0/2437	0.49	0/3264
5	E3	0.53	0/1762	0.55	0/2362
6	F3	0.66	0/1911	0.50	0/2549
7	G3	0.51	0/1910	0.50	0/2569
8	H3	0.54	0/1535	0.54	0/2063
9	I3	0.60	0/1702	0.53	1/2272 (0.0%)
10	J3	0.46	0/1385	0.52	0/1852
11	L3	0.54	0/1733	0.50	0/2316
12	M3	0.59	0/1158	0.49	0/1547
13	N3	0.70	0/1746	0.55	0/2338
14	O3	0.66	1/1662 (0.1%)	0.55	0/2222
15	P3	0.63	0/1268	0.55	1/1700 (0.1%)
16	Q3	0.64	0/1538	0.56	0/2054
17	R3	0.51	0/1310	0.52	0/1734
18	S3	0.69	0/1501	0.56	1/2012 (0.0%)
19	T3	0.64	0/1326	0.52	0/1770
20	U3	0.52	0/848	0.55	0/1138
21	V3	0.60	0/993	0.55	0/1332
22	W3	0.61	0/541	0.50	0/720
23	X3	0.54	0/984	0.50	0/1323
24	Y3	0.59	0/1132	0.52	0/1504
25	Z3	0.57	0/1130	0.52	0/1507
26	a3	0.68	0/1191	0.55	0/1590
27	b3	0.45	0/861	0.47	0/1138
28	c3	0.56	0/771	0.52	0/1034
29	d3	0.60	0/903	0.52	0/1216
30	e3	0.64	0/1071	0.57	0/1429
31	f3	0.73	0/895	0.61	0/1198
32	g3	0.59	0/916	0.55	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h3	0.52	0/1021	0.48	0/1348
34	i3	0.46	0/841	0.48	0/1112
35	j3	0.70	1/720 (0.1%)	0.56	0/952
36	k3	0.51	0/575	0.53	0/761
37	l3	0.62	0/459	0.55	0/608
38	m3	0.57	0/435	0.59	0/575
39	n3	0.28	0/240	0.43	0/305
40	o3	0.57	0/864	0.51	0/1140
41	p3	0.59	0/718	0.53	0/953
42	r3	0.61	0/1010	0.57	0/1354
43	s3	0.29	0/1530	0.49	0/2064
44	t3	0.27	0/1174	0.52	0/1582
45	23	0.41	0/1805	0.83	1/2809 (0.0%)
46	54	1.24	10/84976 (0.0%)	0.93	64/132520 (0.0%)
47	74	1.24	0/2858	0.87	0/4455
48	84	1.22	0/3581	0.87	0/5577
49	NI	0.31	0/150	0.63	0/209
50	NA	0.28	0/425	0.53	0/572
51	NB	0.28	0/450	0.52	0/612
52	TT	0.30	0/3402	0.46	0/4603
53	1	0.47	0/295	0.57	0/394
All	All	1.02	12/153762 (0.0%)	0.80	69/226359 (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
13	N3	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	54	1890	G	N9-C4	-7.84	1.31	1.38
46	54	978	G	N9-C4	-6.37	1.32	1.38
35	j3	50	SER	CA-CB	-6.22	1.43	1.52
46	54	1896	A	N9-C4	-6.03	1.34	1.37
46	54	1337	A	N9-C4	-5.72	1.34	1.37

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	54	1890	G	N3-C4-C5	9.26	133.23	128.60
46	54	978	G	N3-C4-C5	8.94	133.07	128.60
46	54	1890	G	N3-C4-N9	-8.64	120.81	126.00
46	54	2638	G	N3-C4-N9	-8.53	120.88	126.00
46	54	2638	G	N3-C4-C5	8.28	132.74	128.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	N3	76	PRO	Peptide
13	N3	78	GLY	Peptide

5.2 Too-close contacts [i](#)

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

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	A3	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	B3	392/403 (97%)	358 (91%)	34 (9%)	0	100	100
3	C3	360/425 (85%)	331 (92%)	29 (8%)	0	100	100
4	D3	291/297 (98%)	265 (91%)	26 (9%)	0	100	100
5	E3	208/291 (72%)	185 (89%)	23 (11%)	0	100	100
6	F3	223/247 (90%)	206 (92%)	17 (8%)	0	100	100
7	G3	229/319 (72%)	212 (93%)	17 (7%)	0	100	100
8	H3	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I3	201/214 (94%)	181 (90%)	20 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J3	168/178 (94%)	155 (92%)	13 (8%)	0	100	100
11	L3	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	25	56
12	M3	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N3	201/204 (98%)	185 (92%)	16 (8%)	0	100	100
14	O3	197/203 (97%)	185 (94%)	12 (6%)	0	100	100
15	P3	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
16	Q3	185/188 (98%)	170 (92%)	15 (8%)	0	100	100
17	R3	153/196 (78%)	142 (93%)	11 (7%)	0	100	100
18	S3	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	22	52
19	T3	157/160 (98%)	138 (88%)	18 (12%)	1 (1%)	22	52
20	U3	100/128 (78%)	89 (89%)	11 (11%)	0	100	100
21	V3	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
22	W3	61/157 (39%)	54 (88%)	7 (12%)	0	100	100
23	X3	116/156 (74%)	104 (90%)	12 (10%)	0	100	100
24	Y3	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z3	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a3	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	b3	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
28	c3	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d3	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e3	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	16	46
31	f3	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g3	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h3	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
34	i3	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j3	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
36	k3	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l3	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m3	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
39	n3	23/25 (92%)	23 (100%)	0	0	100	100
40	o3	102/106 (96%)	90 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	p3	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	r3	122/137 (89%)	111 (91%)	11 (9%)	0	100	100
43	s3	194/318 (61%)	167 (86%)	27 (14%)	0	100	100
44	t3	151/165 (92%)	121 (80%)	30 (20%)	0	100	100
49	NI	27/29 (93%)	15 (56%)	11 (41%)	1 (4%)	2	14
50	NA	52/215 (24%)	42 (81%)	10 (19%)	0	100	100
51	NB	56/206 (27%)	50 (89%)	6 (11%)	0	100	100
52	TT	424/440 (96%)	395 (93%)	29 (7%)	0	100	100
53	1	32/64 (50%)	17 (53%)	13 (41%)	2 (6%)	1	6
All	All	7271/8745 (83%)	6614 (91%)	650 (9%)	7 (0%)	50	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	1	4	ILE
11	L3	64	VAL
18	S3	166	ARG
30	e3	127	ALA
49	NI	20	ALA

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	A3	190/199 (96%)	188 (99%)	2 (1%)	70	83
2	B3	342/348 (98%)	340 (99%)	2 (1%)	84	91
3	C3	302/347 (87%)	300 (99%)	2 (1%)	81	90
4	D3	247/250 (99%)	247 (100%)	0	100	100
5	E3	190/251 (76%)	187 (98%)	3 (2%)	58	77
6	F3	196/215 (91%)	196 (100%)	0	100	100
7	G3	200/272 (74%)	200 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H3	169/171 (99%)	169 (100%)	0	100	100
9	I3	175/181 (97%)	175 (100%)	0	100	100
10	J3	143/149 (96%)	143 (100%)	0	100	100
11	L3	175/176 (99%)	173 (99%)	2 (1%)	70	83
12	M3	117/161 (73%)	117 (100%)	0	100	100
13	N3	171/172 (99%)	169 (99%)	2 (1%)	67	82
14	O3	171/173 (99%)	170 (99%)	1 (1%)	84	91
15	P3	134/163 (82%)	134 (100%)	0	100	100
16	Q3	164/164 (100%)	164 (100%)	0	100	100
17	R3	138/175 (79%)	137 (99%)	1 (1%)	81	90
18	S3	157/157 (100%)	155 (99%)	2 (1%)	65	80
19	T3	139/140 (99%)	139 (100%)	0	100	100
20	U3	92/114 (81%)	92 (100%)	0	100	100
21	V3	101/107 (94%)	100 (99%)	1 (1%)	73	85
22	W3	55/126 (44%)	55 (100%)	0	100	100
23	X3	106/134 (79%)	105 (99%)	1 (1%)	75	87
24	Y3	124/135 (92%)	122 (98%)	2 (2%)	58	77
25	Z3	117/118 (99%)	116 (99%)	1 (1%)	75	87
26	a3	119/120 (99%)	118 (99%)	1 (1%)	79	89
27	b3	84/172 (49%)	84 (100%)	0	100	100
28	c3	84/98 (86%)	83 (99%)	1 (1%)	67	82
29	d3	98/110 (89%)	96 (98%)	2 (2%)	50	72
30	e3	114/121 (94%)	113 (99%)	1 (1%)	75	87
31	f3	88/89 (99%)	88 (100%)	0	100	100
32	g3	98/99 (99%)	98 (100%)	0	100	100
33	h3	109/110 (99%)	109 (100%)	0	100	100
34	i3	86/89 (97%)	86 (100%)	0	100	100
35	j3	73/80 (91%)	71 (97%)	2 (3%)	40	65
36	k3	64/65 (98%)	64 (100%)	0	100	100
37	l3	47/48 (98%)	47 (100%)	0	100	100
38	m3	48/90 (53%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	n3	24/24 (100%)	24 (100%)	0	100	100
40	o3	92/94 (98%)	92 (100%)	0	100	100
41	p3	74/75 (99%)	71 (96%)	3 (4%)	26	55
42	r3	108/121 (89%)	108 (100%)	0	100	100
43	s3	164/258 (64%)	161 (98%)	3 (2%)	54	75
44	t3	126/137 (92%)	123 (98%)	3 (2%)	44	68
49	NI	2/2 (100%)	2 (100%)	0	100	100
50	NA	48/183 (26%)	48 (100%)	0	100	100
51	NB	51/165 (31%)	51 (100%)	0	100	100
52	TT	370/381 (97%)	367 (99%)	3 (1%)	79	89
53	1	32/53 (60%)	26 (81%)	6 (19%)	1	5
All	All	6318/7382 (86%)	6271 (99%)	47 (1%)	80	90

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	j3	82	THR
44	t3	83	LYS
41	p3	4	ARG
43	s3	50	LYS
44	t3	114	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
18	S3	37	HIS
27	b3	61	ASN
18	S3	92	ASN
22	W3	50	ASN
32	g3	114	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	23	74/76 (97%)	13 (17%)	0
46	54	3516/3543 (99%)	822 (23%)	58 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	74	119/120 (99%)	14 (11%)	0
48	84	149/156 (95%)	32 (21%)	1 (0%)
All	All	3858/3895 (99%)	881 (22%)	59 (1%)

5 of 881 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	23	9	A
45	23	13	U
45	23	16	C
45	23	19	G
45	23	20(A)	U

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	54	1455	G
46	54	4925	U
46	54	2266	C
46	54	4921	C
46	54	4354	U

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 225 ligands modelled in this entry, 225 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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	54	27
45	23	1

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	54	2113:G	O3'	2258:C	P	40.63
1	54	1252:C	O3'	1271:G	P	37.10
1	54	1219:G	O3'	1233:G	P	19.39
1	54	3948:C	O3'	4065:G	P	18.92
1	54	4138:C	O3'	4146:G	P	18.16

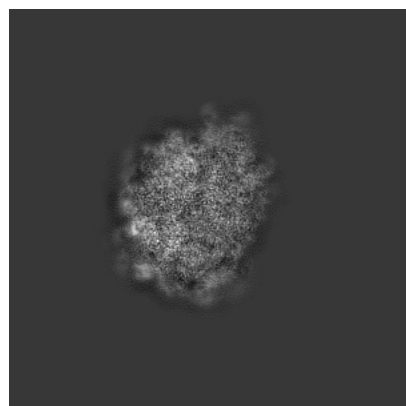
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10380. These allow visual inspection of the internal detail of the map and identification of artifacts.

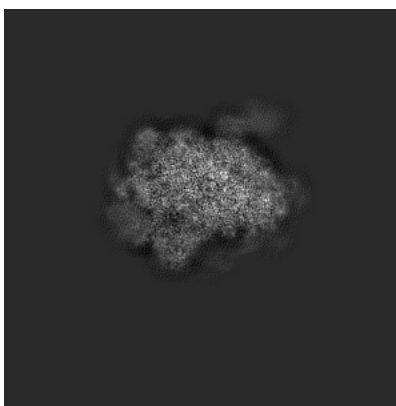
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

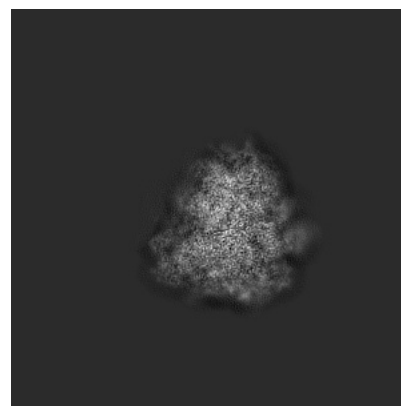
6.1.1 Primary map



X

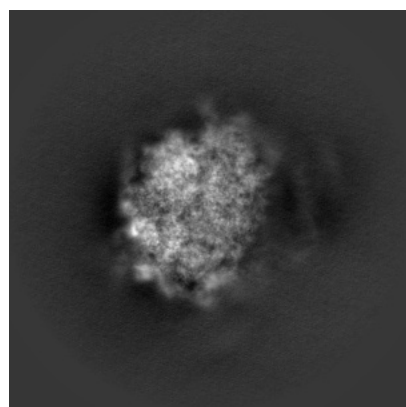


Y

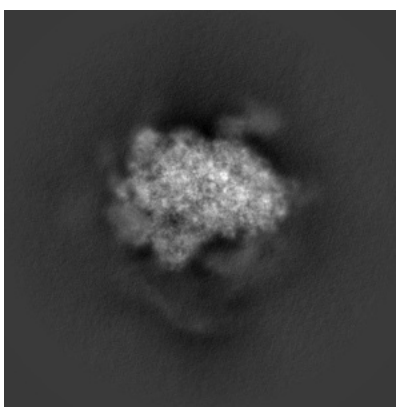


Z

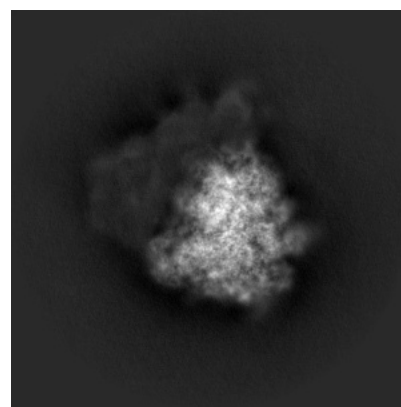
6.1.2 Raw map



X



Y

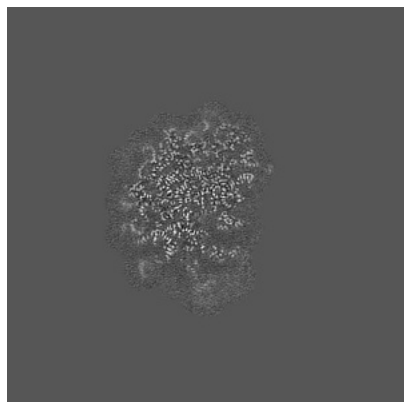


Z

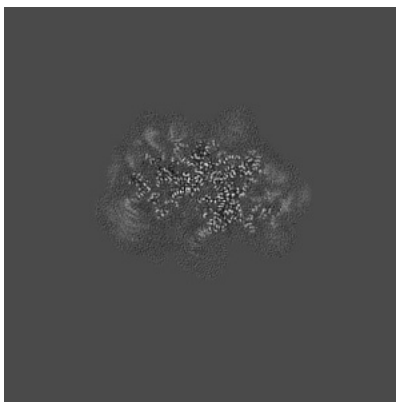
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

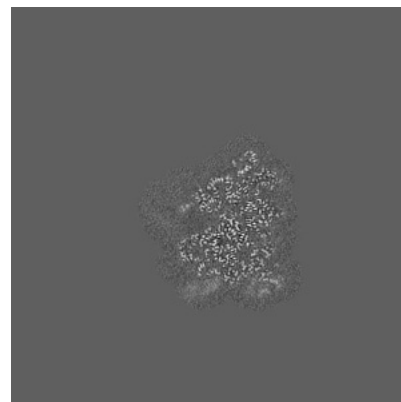
6.2.1 Primary map



X Index: 200

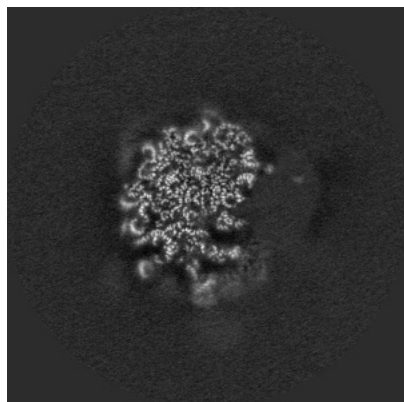


Y Index: 200

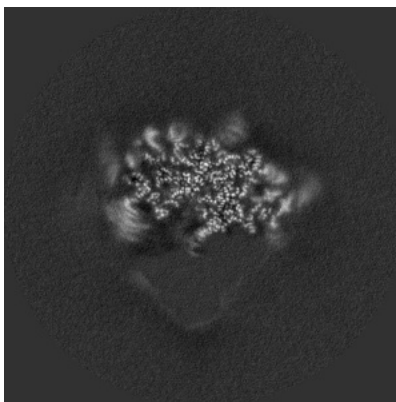


Z Index: 200

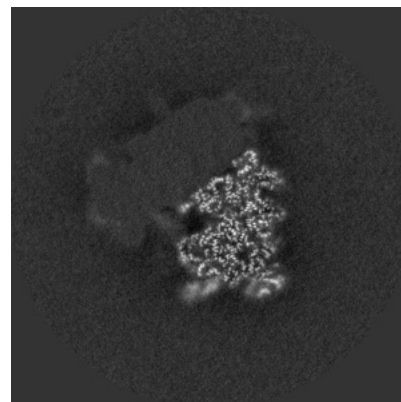
6.2.2 Raw map



X Index: 200



Y Index: 200

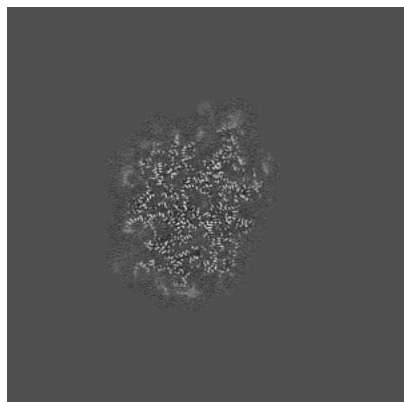


Z Index: 200

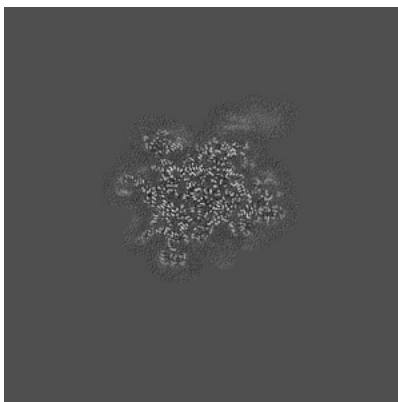
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

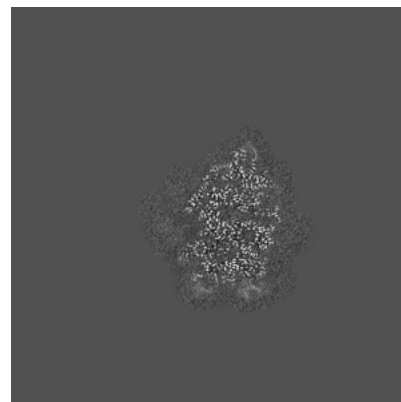
6.3.1 Primary map



X Index: 218

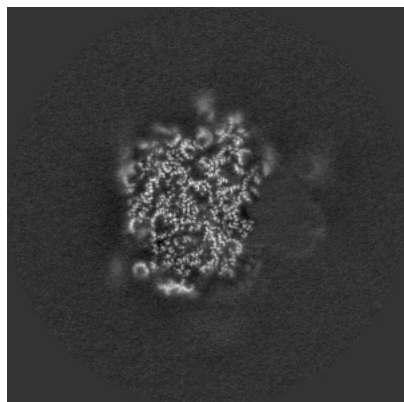


Y Index: 161

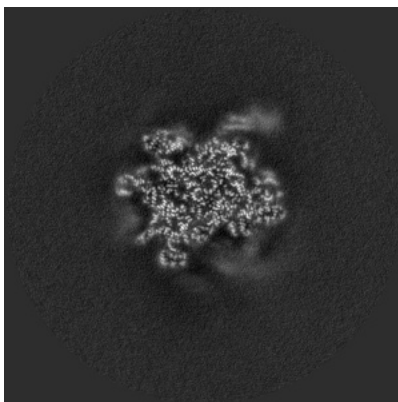


Z Index: 208

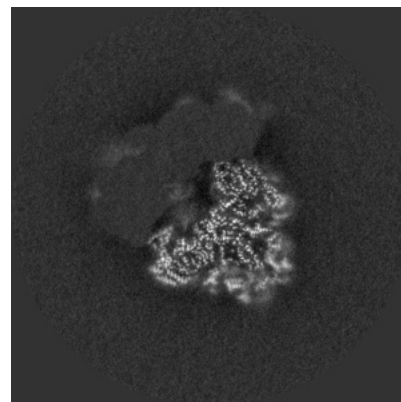
6.3.2 Raw map



X Index: 215



Y Index: 161

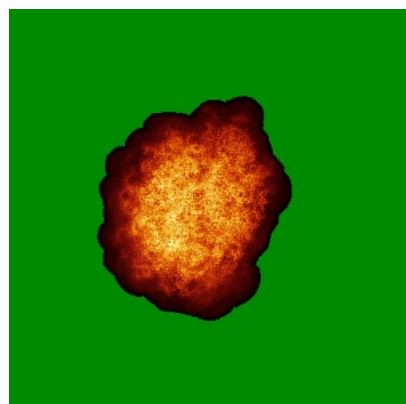


Z Index: 176

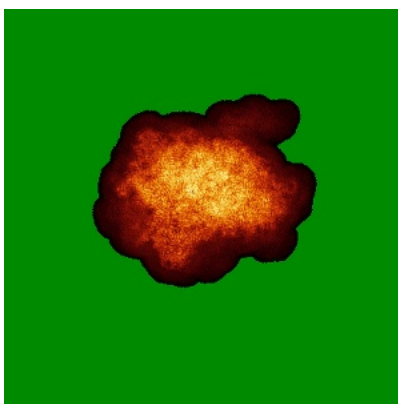
The images above show the largest variance slices of the map in three orthogonal directions.

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

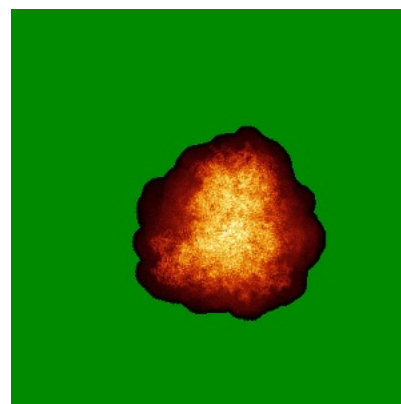
6.4.1 Primary map



X

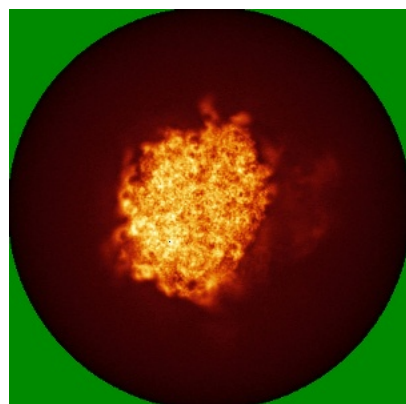


Y

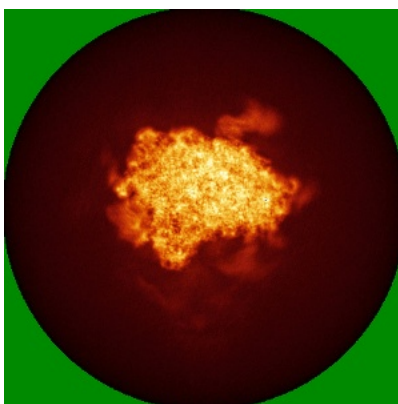


Z

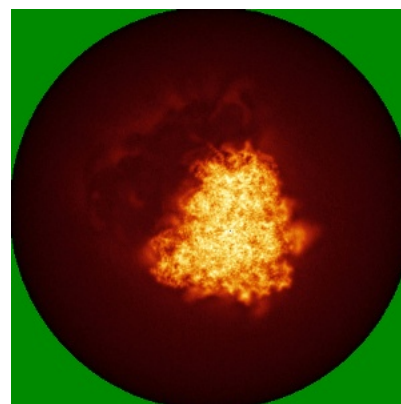
6.4.2 Raw map



X



Y

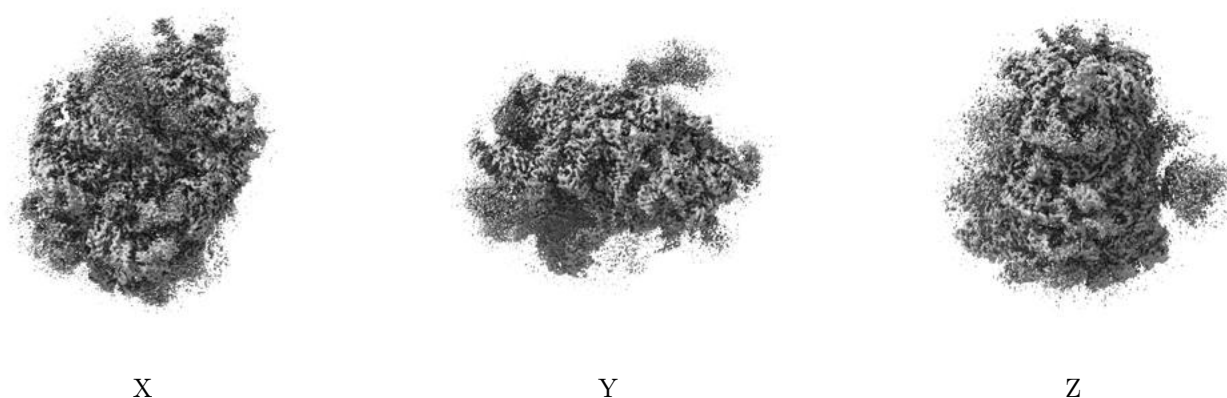


Z

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.

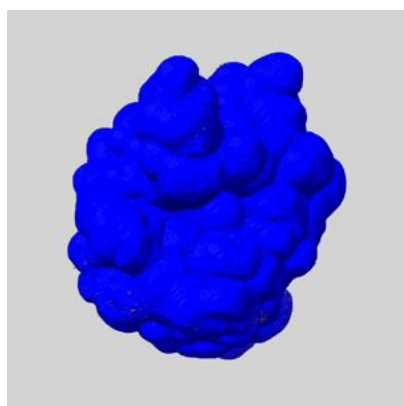
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

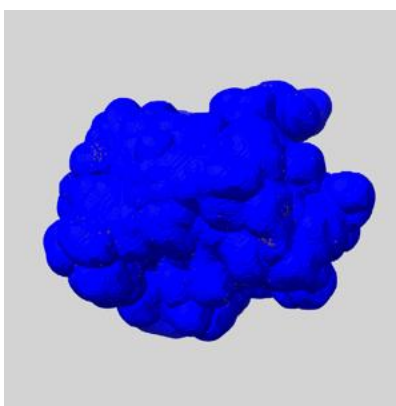
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

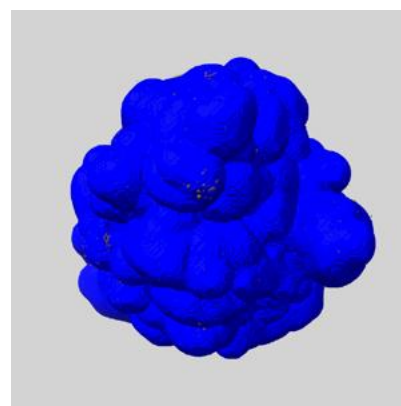
6.6.1 emd_10380_msk_1.map [i](#)



X



Y

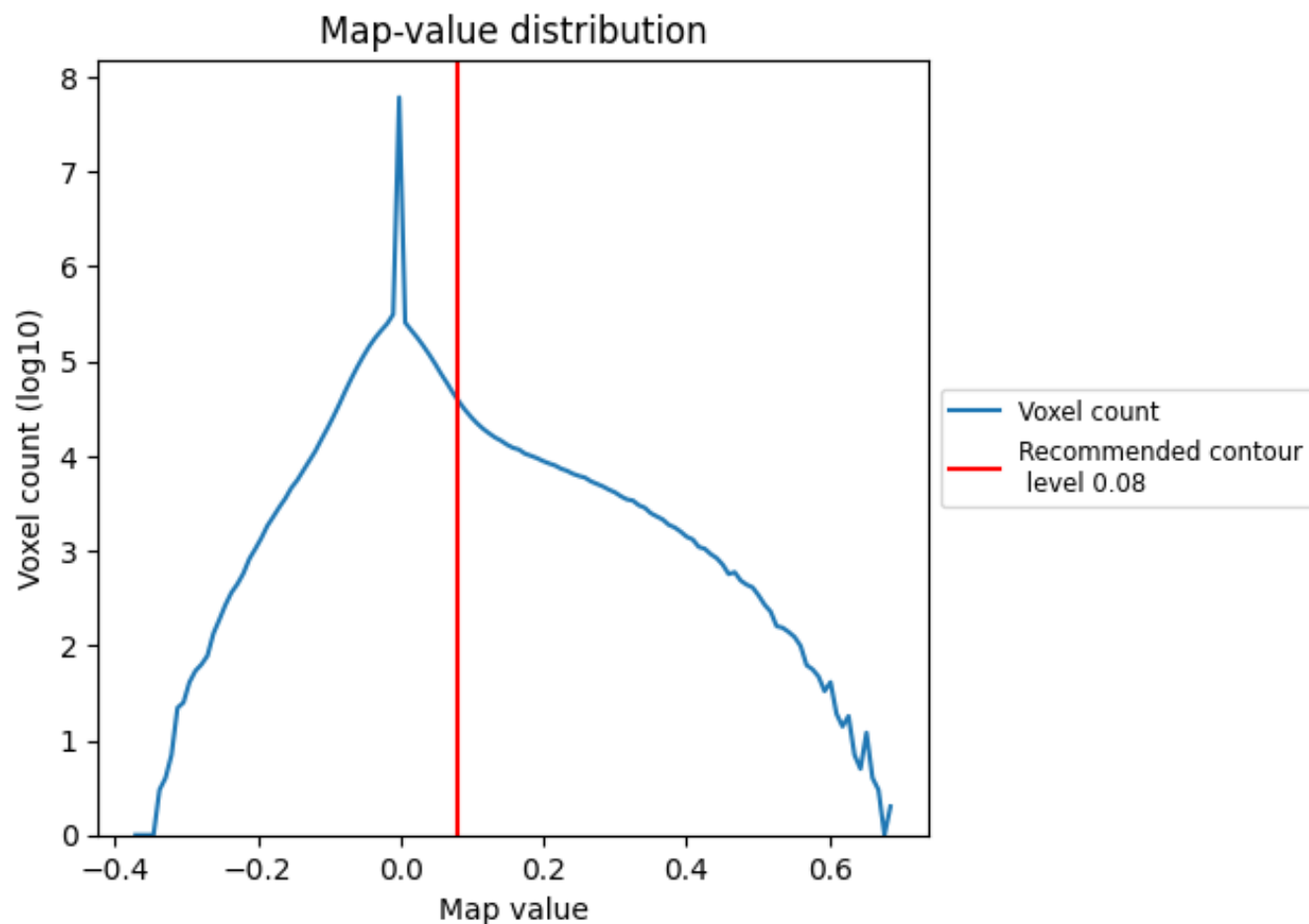


Z

7 Map analysis [i](#)

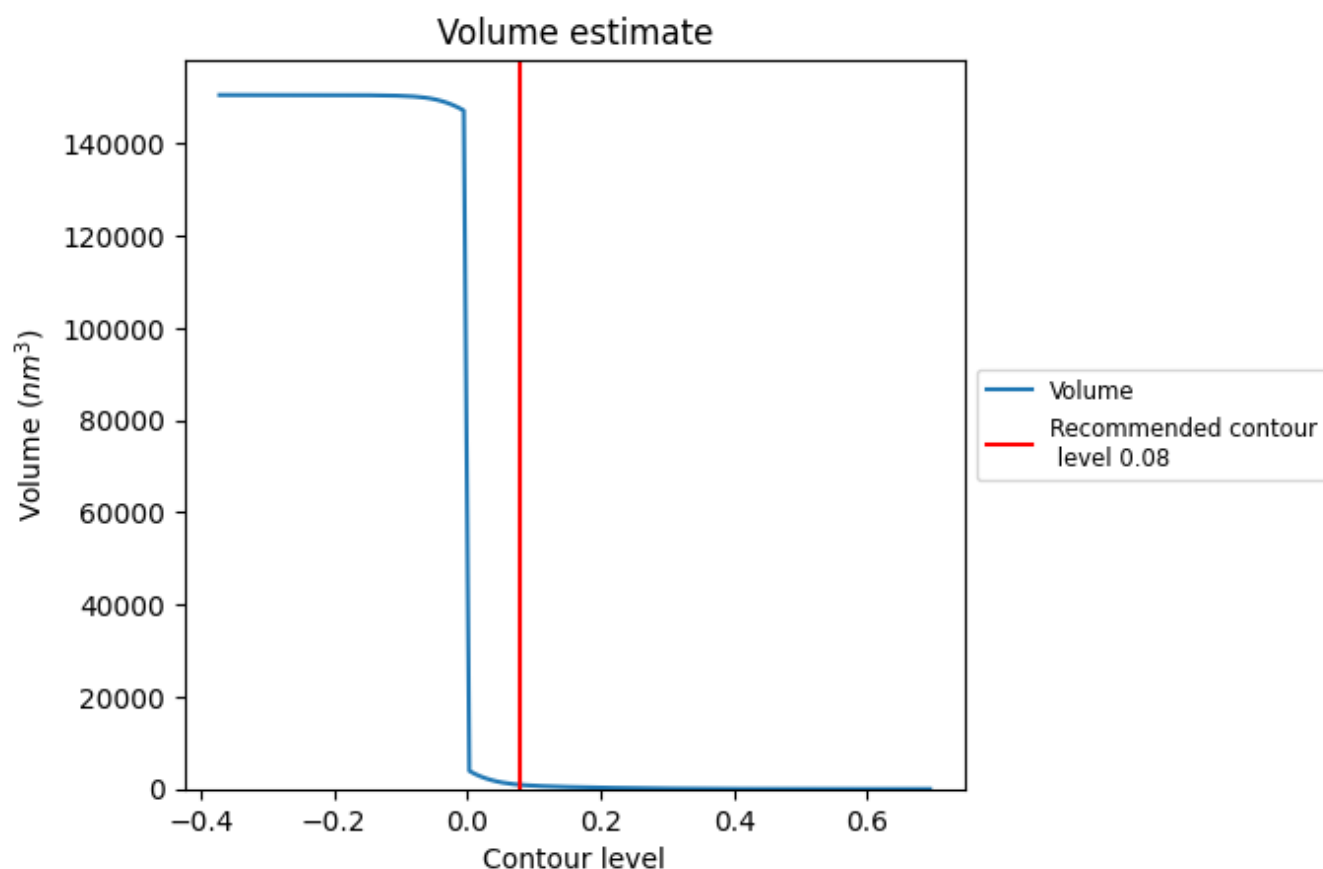
This section contains the results of statistical analysis of the map.

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.

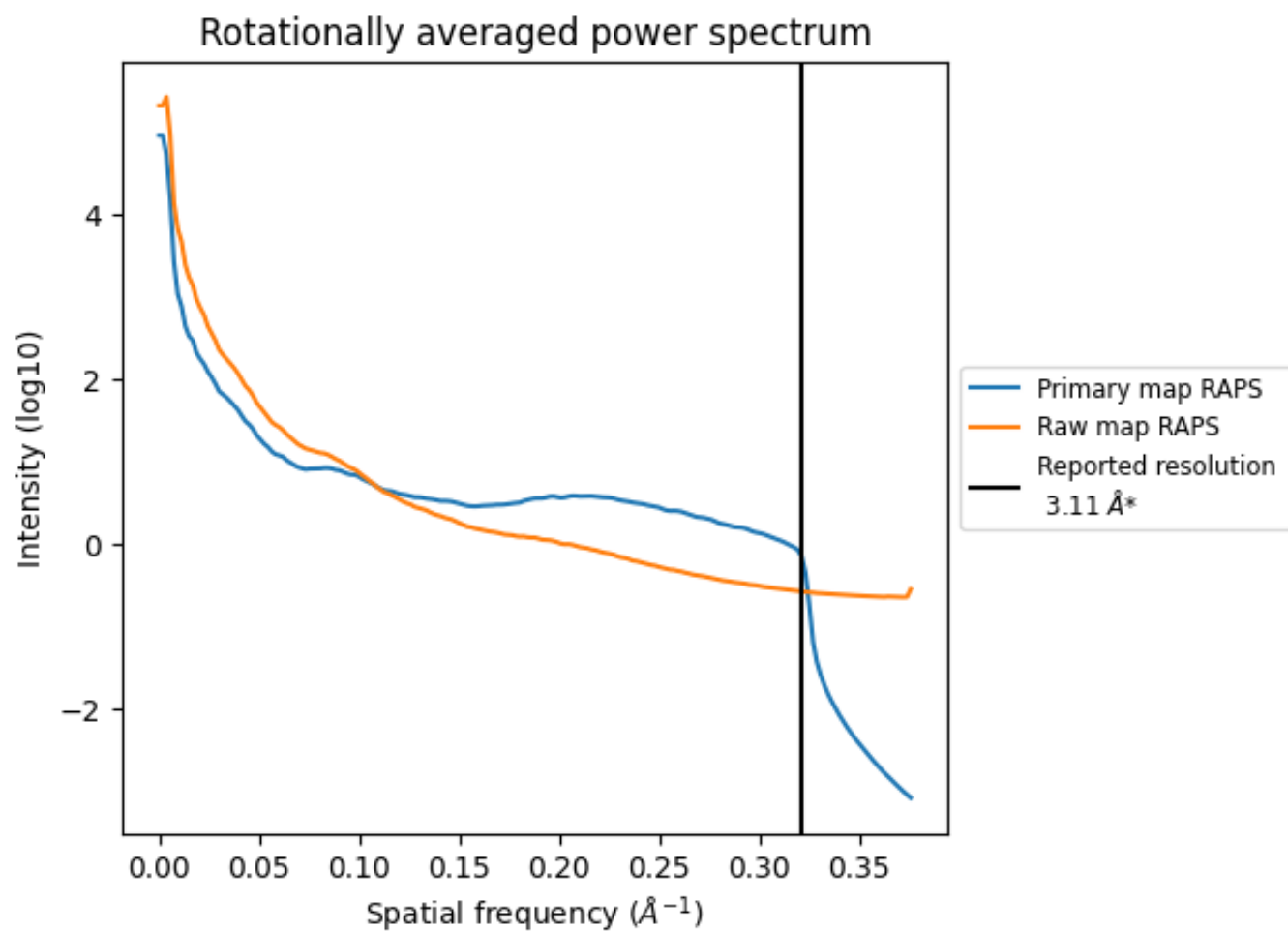
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 897 nm^3 ; this corresponds to an approximate mass of 810 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 ⓘ

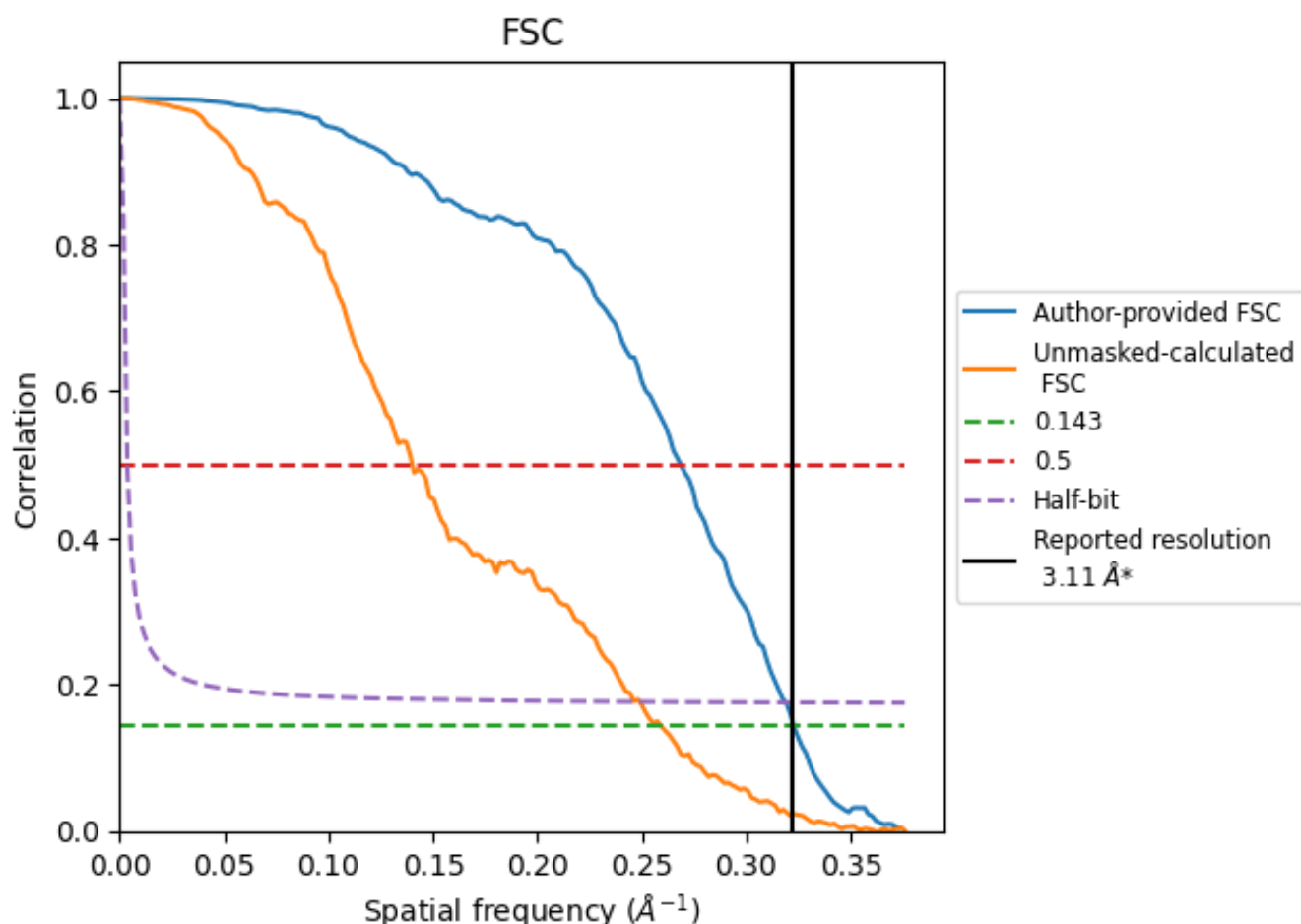


*Reported resolution corresponds to spatial frequency of 0.322 Å⁻¹

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 0.322 Å⁻¹

8.2 Resolution estimates [i](#)

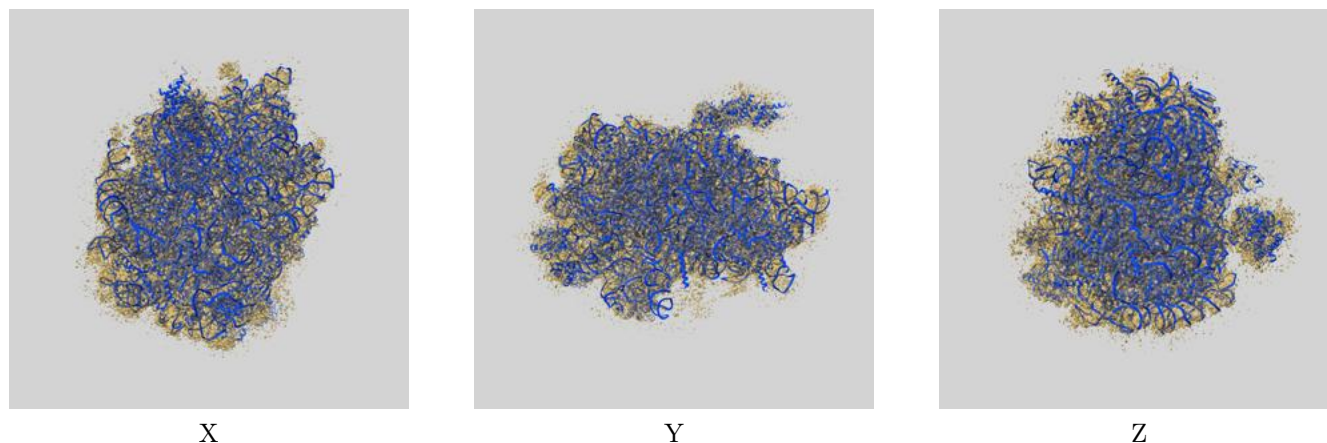
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.11	-	-
Author-provided FSC curve	3.10	3.72	3.14
Unmasked-calculated*	3.86	7.14	4.02

*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 3.86 differs from the reported value 3.11 by more than 10 %

9 Map-model fit [i](#)

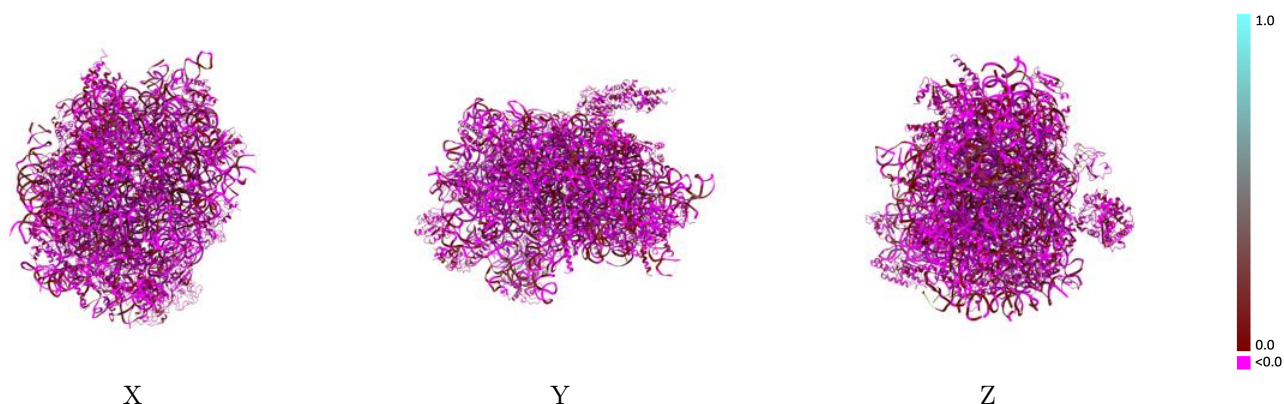
This section contains information regarding the fit between EMDB map EMD-10380 and PDB model 6T59. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



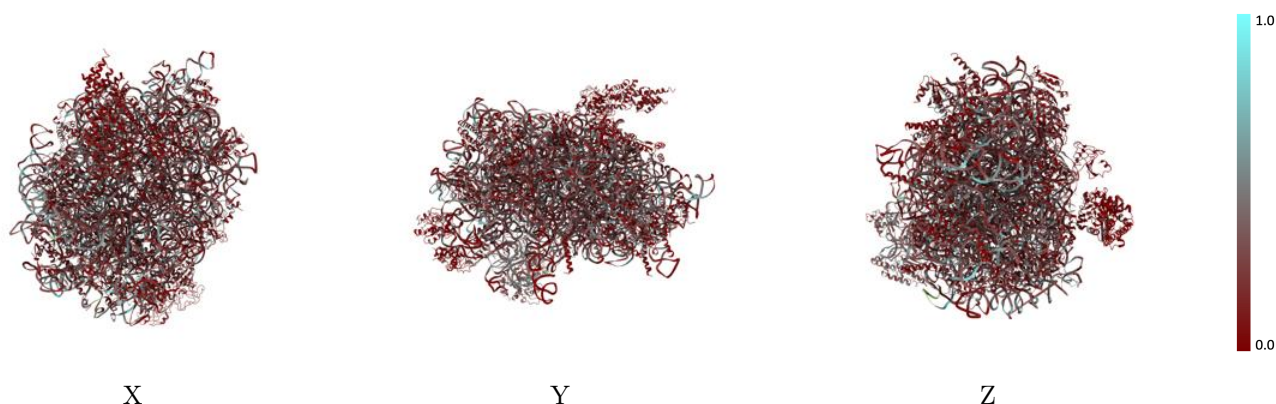
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



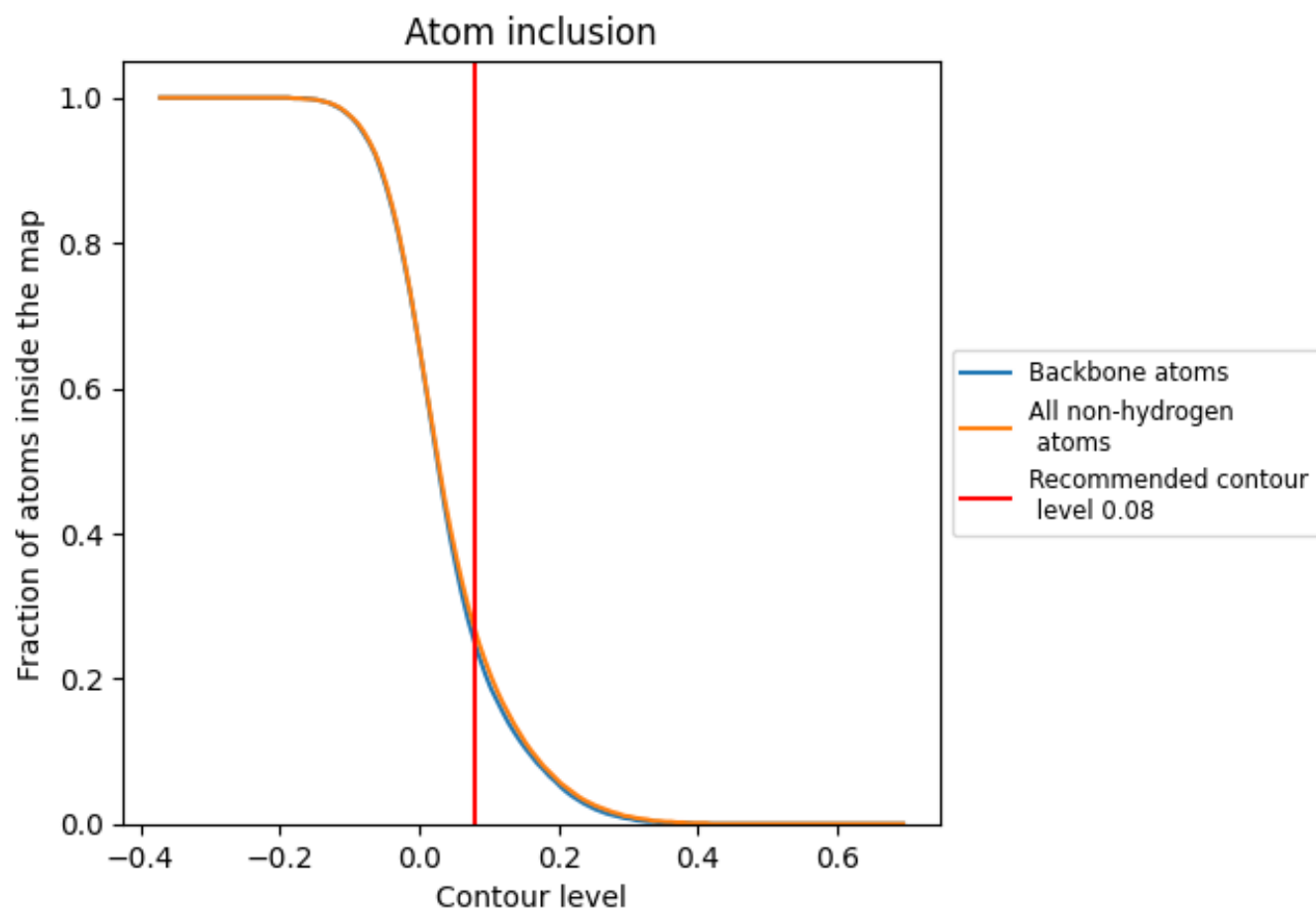
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 25% of all backbone atoms, 27% 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	 0.2670	 -0.0680
1	 0.0460	 0.0020
23	 0.0730	 -0.0110
54	 0.3170	 -0.0600
74	 0.3820	 -0.1130
84	 0.3300	 -0.0320
A3	 0.1850	 -0.1380
B3	 0.2070	 -0.0910
C3	 0.2270	 -0.0980
D3	 0.2970	 -0.0630
E3	 0.2210	 -0.0940
F3	 0.2230	 -0.1080
G3	 0.2170	 -0.0680
H3	 0.1930	 -0.0940
I3	 0.2320	 -0.0920
J3	 0.2410	 -0.0470
L3	 0.2320	 -0.0770
M3	 0.2550	 -0.1010
N3	 0.2200	 -0.1120
NA	 0.0560	 0.0400
NB	 0.0220	 0.0230
NI	 0.1530	 -0.1020
O3	 0.2320	 -0.0910
P3	 0.1900	 -0.1070
Q3	 0.1930	 -0.1340
R3	 0.2200	 -0.0660
S3	 0.2570	 -0.0880
T3	 0.2250	 -0.1000
TT	 0.0900	 -0.0270
U3	 0.1740	 -0.0630
V3	 0.1680	 -0.1160
W3	 0.1850	 -0.0880
X3	 0.1820	 -0.0520
Y3	 0.1860	 -0.0900
Z3	 0.2130	 -0.0630



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Chain	Atom inclusion	Q-score
a3	 0.2390	 -0.1140
b3	 0.1890	 -0.0920
c3	 0.2510	 -0.0690
d3	 0.1770	 -0.0770
e3	 0.1940	 -0.1160
f3	 0.2200	 -0.1000
g3	 0.1850	 -0.0740
h3	 0.2060	 -0.0630
i3	 0.2410	 -0.0720
j3	 0.2370	 -0.0720
k3	 0.1690	 -0.0380
l3	 0.2180	 -0.0780
m3	 0.2020	 -0.1270
n3	 0.0320	 -0.0910
o3	 0.1900	 -0.1030
p3	 0.2470	 -0.0540
r3	 0.1910	 -0.1180
s3	 0.0700	 -0.0170
t3	 0.0580	 0.0140