



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:06 am GMT

PDB ID : 6FRK
EMDB ID : EMD-4300
Title : Structure of a prehandover mammalian ribosomal SRP and SRP receptor targeting complex
Authors : Kobayashi, K.; Jomaa, A.; Ban, N.
Deposited on : 2018-02-16
Resolution : 3.70 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:

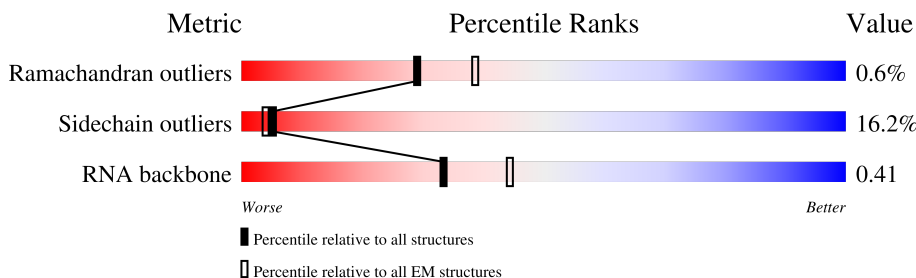
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.70 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.




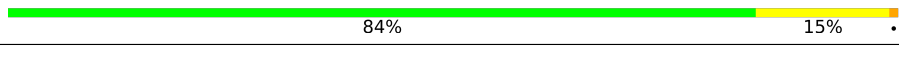
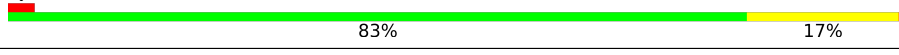




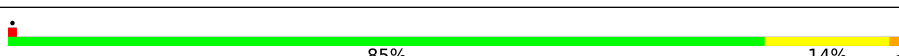
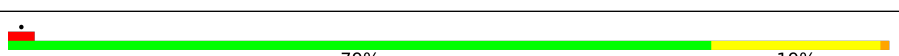

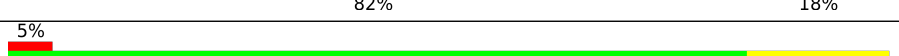
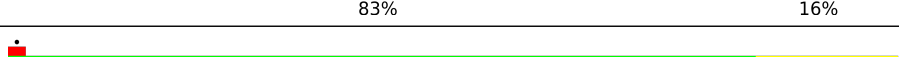
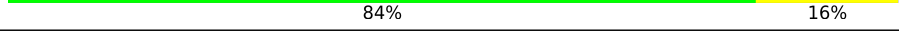



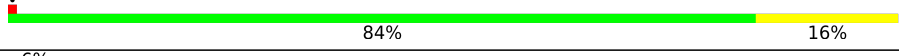



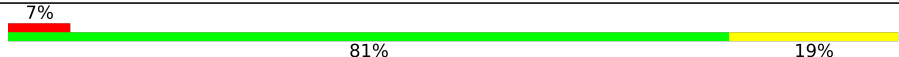

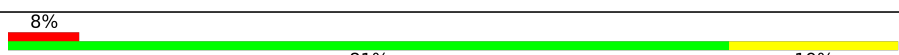
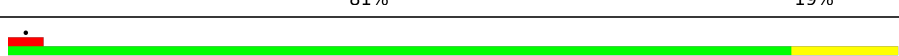

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	299	
2	2	76	
3	3	125	
4	4	163	
5	5	3658	
6	6	202	
7	7	120	
8	8	156	




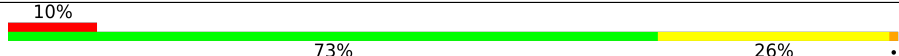
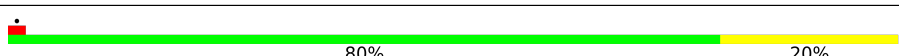
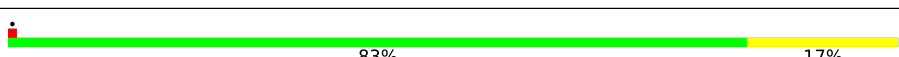
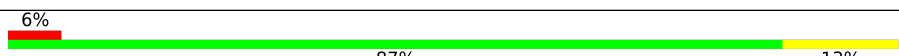
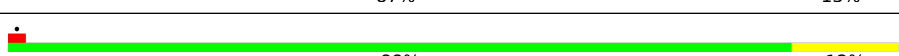
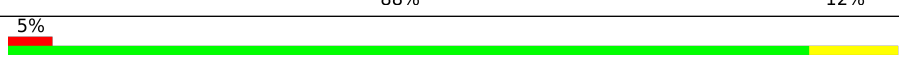

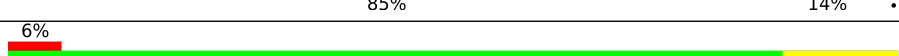
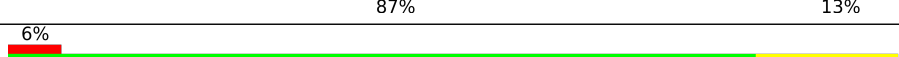

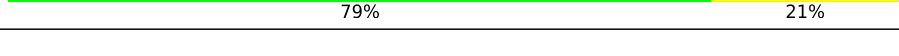
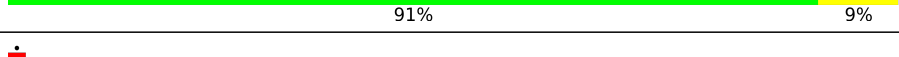


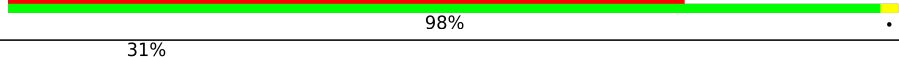
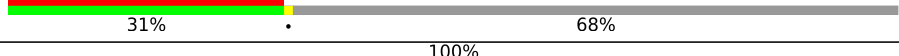
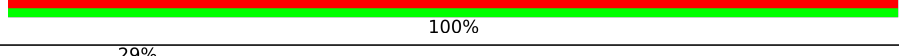

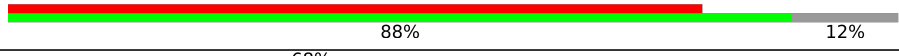



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Mol	Chain	Length	Quality of chain
9	A	244	 82% 18%
10	B	394	 84% 15%
11	C	367	 83% 17%
12	D	292	 79% 20%
13	E	236	 11% 74% 25%
14	F	225	 84% 16%
15	G	238	 8% 82% 18%
16	H	190	 85% 14%
17	I	213	 79% 19%
18	J	170	 5% 82% 18%
19	L	210	 5% 83% 16%
20	M	138	 84% 16%
21	N	203	 85% 15%
22	O	201	 89% 11%
23	P	153	 84% 16%
24	Q	187	 84% 16%
25	R	180	 6% 81% 19%
26	S	175	 81% 19%
27	T	159	 82% 17%
28	U	99	 7% 81% 19%
29	V	131	 85% 15%
30	W	63	 8% 81% 19%
31	X	119	 88% 12%
32	Y	134	 84% 16%
33	Z	135	 83% 17%

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Mol	Chain	Length	Quality of chain
34	a	147	
35	b	75	
36	c	94	
37	d	107	
38	e	128	
39	f	109	
40	g	114	
41	h	122	
42	i	102	
43	j	86	
44	k	69	
45	l	50	
46	m	52	
47	n	23	
48	o	104	
49	p	91	
50	q	105	
51	r	605	
52	t	11	
53	u	568	
54	v	213	
55	w	74	
56	x	504	
57	y	657	
58	z	110	

2 Entry composition [i](#)

There are 62 unique types of molecules in this entry. The entry contains 159957 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 RNA chain called Canis lupus familiaris RNA, 7SL, cytoplasmic 1 (RN7SL1), SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	258	5534	2463	1012	1801	258	0	0

- Molecule 2 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	76	1616	723	290	528	75	0	0

- Molecule 3 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	125	1001	622	206	168	5	0	0

- Molecule 4 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	163	1238	773	230	230	5	0	0

- Molecule 5 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	5	3658	78406	34911	14352	25486	3657	0	0

- Molecule 6 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	202	1556	989	272	286	9	0	0

- Molecule 7 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 8 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	8	156	3314	1480	585	1094	155	0	0

- Molecule 9 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	A	244	1868	1171	382	309	6	0	0

- Molecule 10 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	B	394	3147	2005	591	538	13	0	0

- Molecule 11 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	367	2919	1836	582	486	15	0	0

- Molecule 12 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D	292	2380	1508	434	426	12	0	0

- Molecule 13 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	236	1904	1219	364	316	5	0	0

- Molecule 14 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 15 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	238	Total	C	N	O	S	0	0
			1912	1218	368	322	4		

- Molecule 16 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 17 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 18 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 19 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 20 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 21 is a protein called Ribosomal protein L15.

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

- Molecule 22 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 23 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 24 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 25 is a protein called Ribosomal protein eL19.

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

- Molecule 26 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 27 is a protein called Ribosomal protein eL21.

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

- Molecule 28 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	U	99	808	518	141	147	2	0	0

- Molecule 29 is a protein called Ribosomal protein L23.

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

- Molecule 30 is a protein called Ribosomal protein eL24.

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

- Molecule 31 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	X	119	976	624	183	168	1	0	0

- Molecule 32 is a protein called Ribosomal protein uL24.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

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

- Molecule 34 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	a	147	1163	735	239	185	4	0	0

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 36 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 37 is a protein called Ribosomal protein eL31.

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

- Molecule 38 is a protein called Ribosomal protein eL32.

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

- Molecule 39 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 40 is a protein called Ribosomal protein eL34.

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

- Molecule 41 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 42 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 44 is a protein called Ribosomal protein eL38.

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

- Molecule 45 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 46 is a protein called Ribosomal protein eL40.

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

- Molecule 47 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 48 is a protein called Ribosomal protein eL42.

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

- Molecule 49 is a protein called Ribosomal protein eL43.

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

- Molecule 50 is a protein called Signal recognition particle subunit SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	q	105	844	534	152	152	6	0	0

- Molecule 51 is a protein called Signal recognition particle subunit SRP72,Signal recognition particle subunit SRP72,Signal recognition particle subunit SRP72.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	r	195	1540	970	274	291	5	1	0

- Molecule 52 is a protein called Signal sequence.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
52	t	11	88	66	11	11	0	0

- Molecule 53 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	u	218	1819	1151	335	325	8	0	0

- Molecule 54 is a protein called SRP receptor beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	v	188	1486	943	259	279	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	59	MET	-	initiating methionine	UNP G1STG2

- Molecule 55 is a protein called Signal recognition particle 9 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	w	74	607	386	106	110	5	0	0

- Molecule 56 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	x	374	2915	1848	495	550	22	0	0

- Molecule 57 is a protein called SRP receptor alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	y	424	3298	2093	572	615	18	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	-19	HIS	-	expression tag	UNP G1TCX6
y	-18	HIS	-	expression tag	UNP G1TCX6
y	-17	HIS	-	expression tag	UNP G1TCX6
y	-16	HIS	-	expression tag	UNP G1TCX6
y	-15	HIS	-	expression tag	UNP G1TCX6
y	-14	HIS	-	expression tag	UNP G1TCX6
y	-13	ASP	-	expression tag	UNP G1TCX6
y	-12	TYR	-	expression tag	UNP G1TCX6
y	-11	ASP	-	expression tag	UNP G1TCX6
y	-10	ILE	-	expression tag	UNP G1TCX6
y	-9	PRO	-	expression tag	UNP G1TCX6
y	-8	THR	-	expression tag	UNP G1TCX6
y	-7	THR	-	expression tag	UNP G1TCX6
y	-6	GLU	-	expression tag	UNP G1TCX6
y	-5	ASN	-	expression tag	UNP G1TCX6
y	-4	LEU	-	expression tag	UNP G1TCX6
y	-3	TYR	-	expression tag	UNP G1TCX6
y	-2	PHE	-	expression tag	UNP G1TCX6
y	-1	GLN	-	expression tag	UNP G1TCX6
y	0	GLY	-	expression tag	UNP G1TCX6

- Molecule 58 is a protein called Signal recognition particle 14 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	76	Total	C	N	O	S	0	0
			604	384	105	111	4		

- Molecule 59 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	5	119	Total	Mg	0
			119	119	
59	7	5	Total	Mg	0
			5	5	
59	8	3	Total	Mg	0
			3	3	
59	P	1	Total	Mg	0
			1	1	
59	V	1	Total	Mg	0
			1	1	
59	g	1	Total	Mg	0
			1	1	
59	v	1	Total	Mg	0
			1	1	
59	x	1	Total	Mg	0
			1	1	
59	y	1	Total	Mg	0
			1	1	

- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

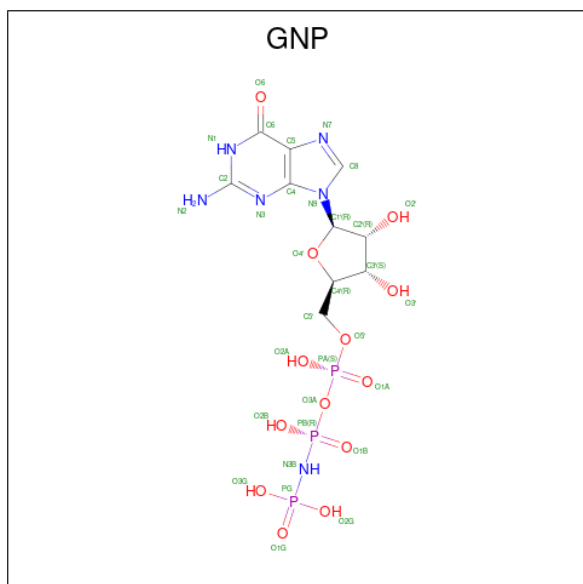
Mol	Chain	Residues	Atoms		AltConf
60	j	1	Total	Zn	0
			1	1	
60	m	1	Total	Zn	0
			1	1	
60	o	1	Total	Zn	0
			1	1	

- Molecule 61 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
61	v	1	32	10	5	14	3	0

- Molecule 62 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).

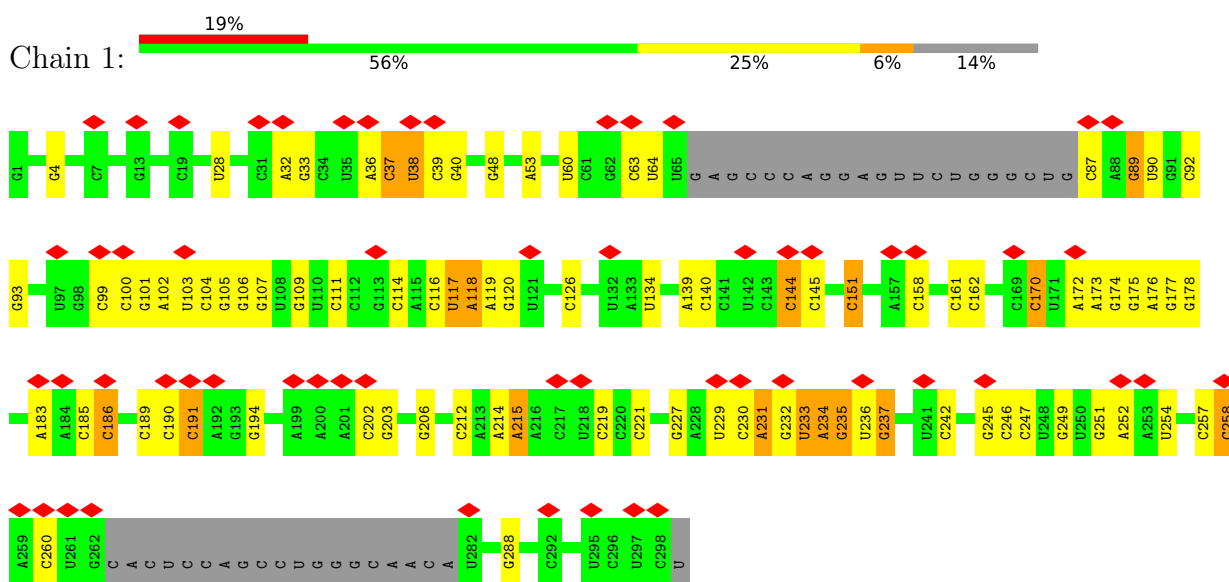


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
62	x	1	32	10	6	13	3	0
62	y	1	32	10	6	13	3	0

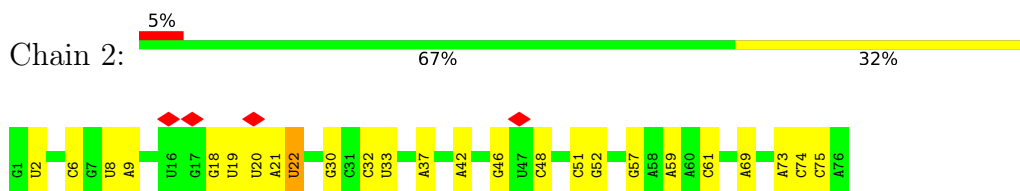
3 Residue-property plots [i](#)

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

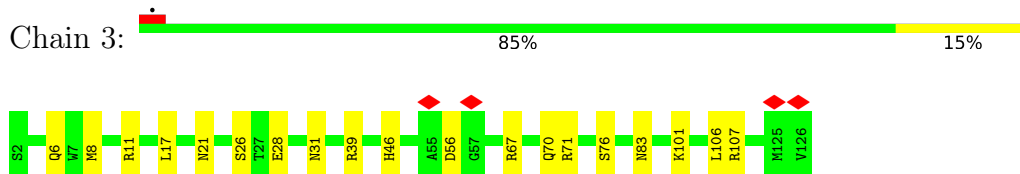
- Molecule 1: *Canis lupus familiaris* RNA, 7SL, cytoplasmic 1 (RN7SL1), SRP RNA



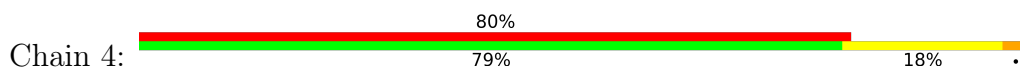
- Molecule 2: tRNA

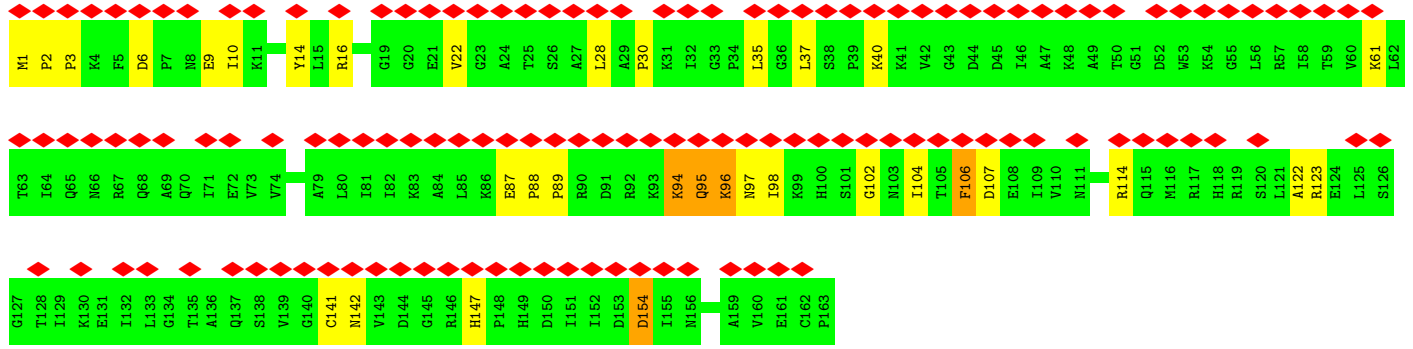


- Molecule 3: Ribosomal protein eL28

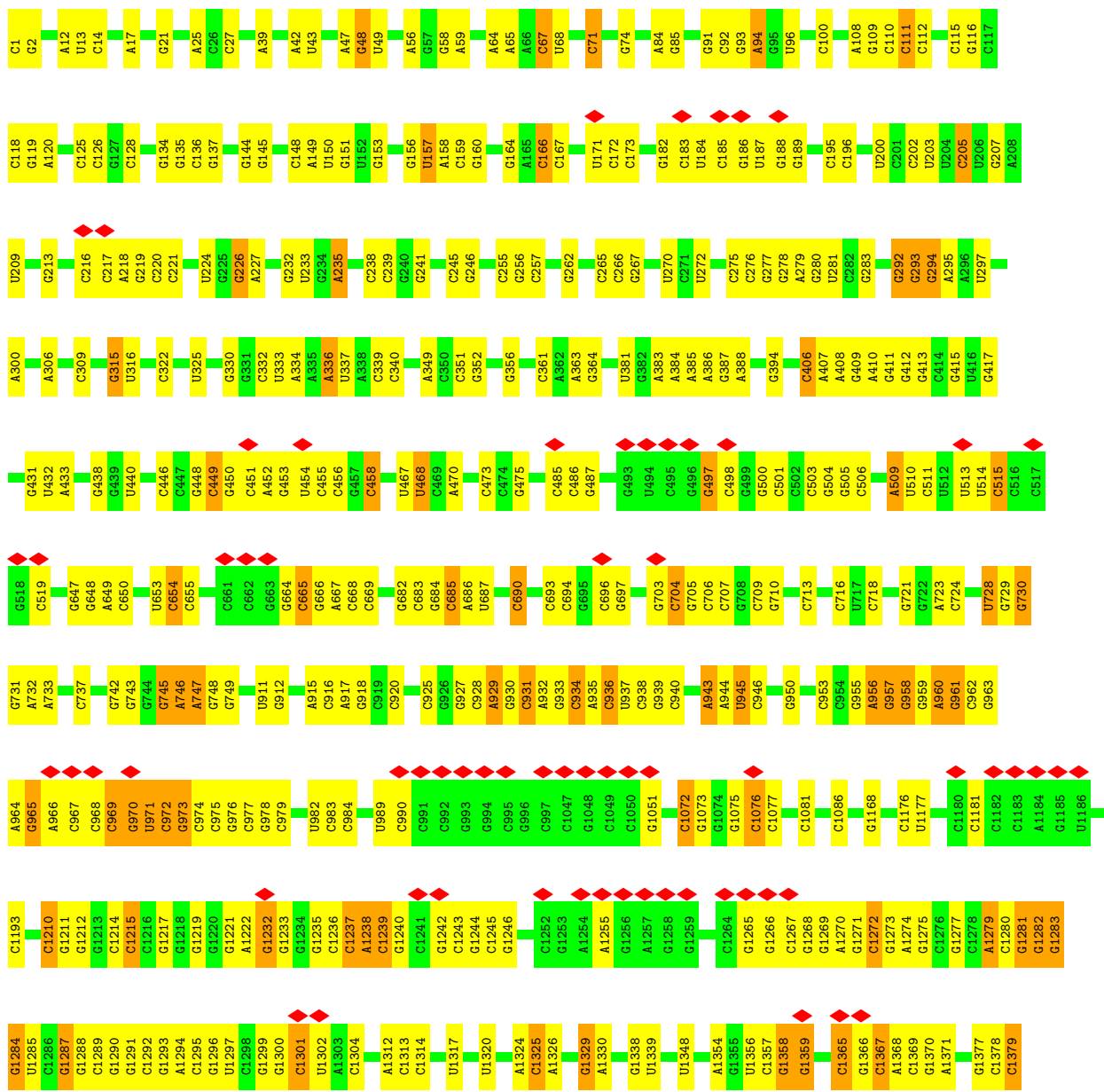


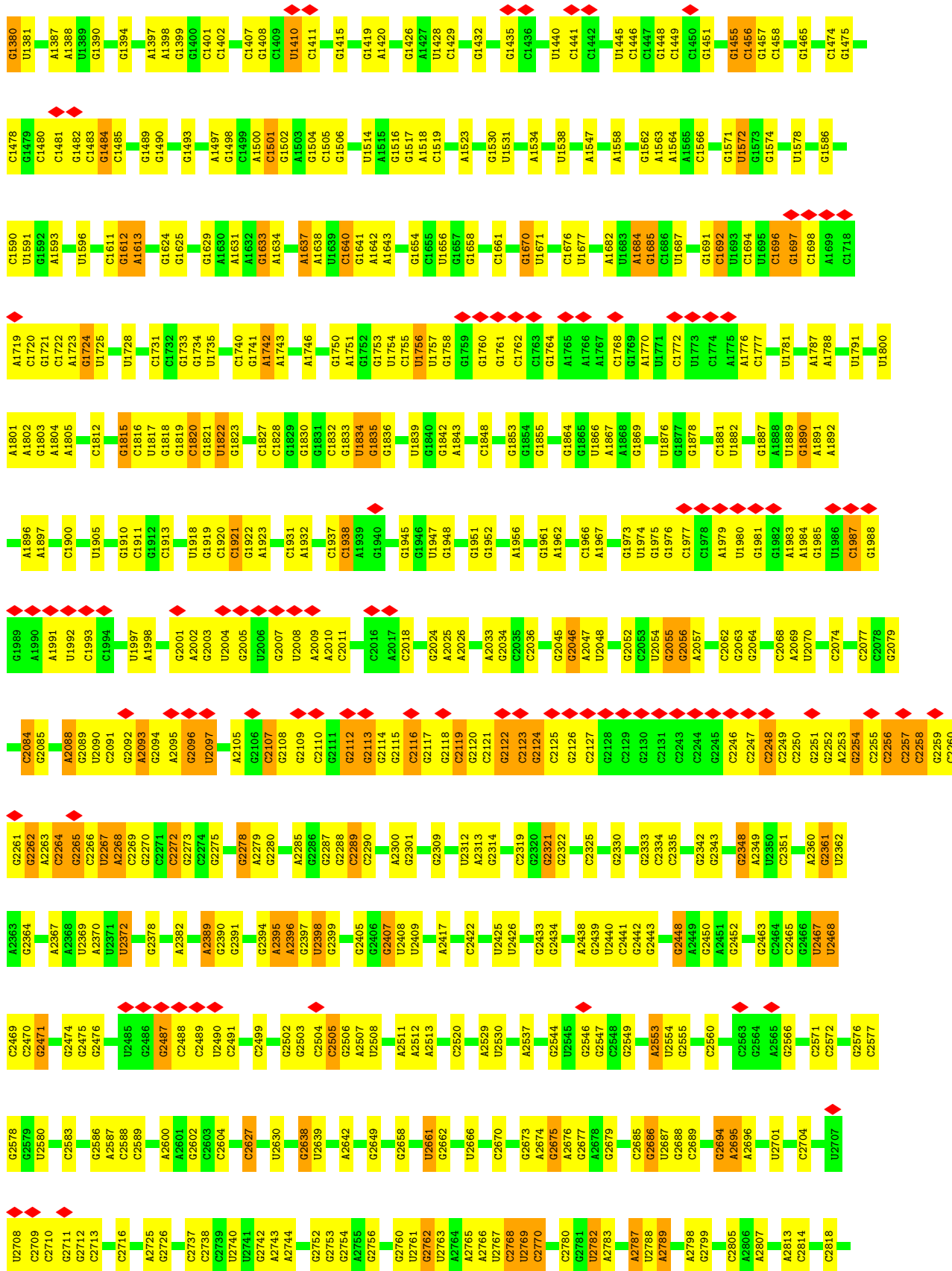
- Molecule 4: Ribosomal protein L12

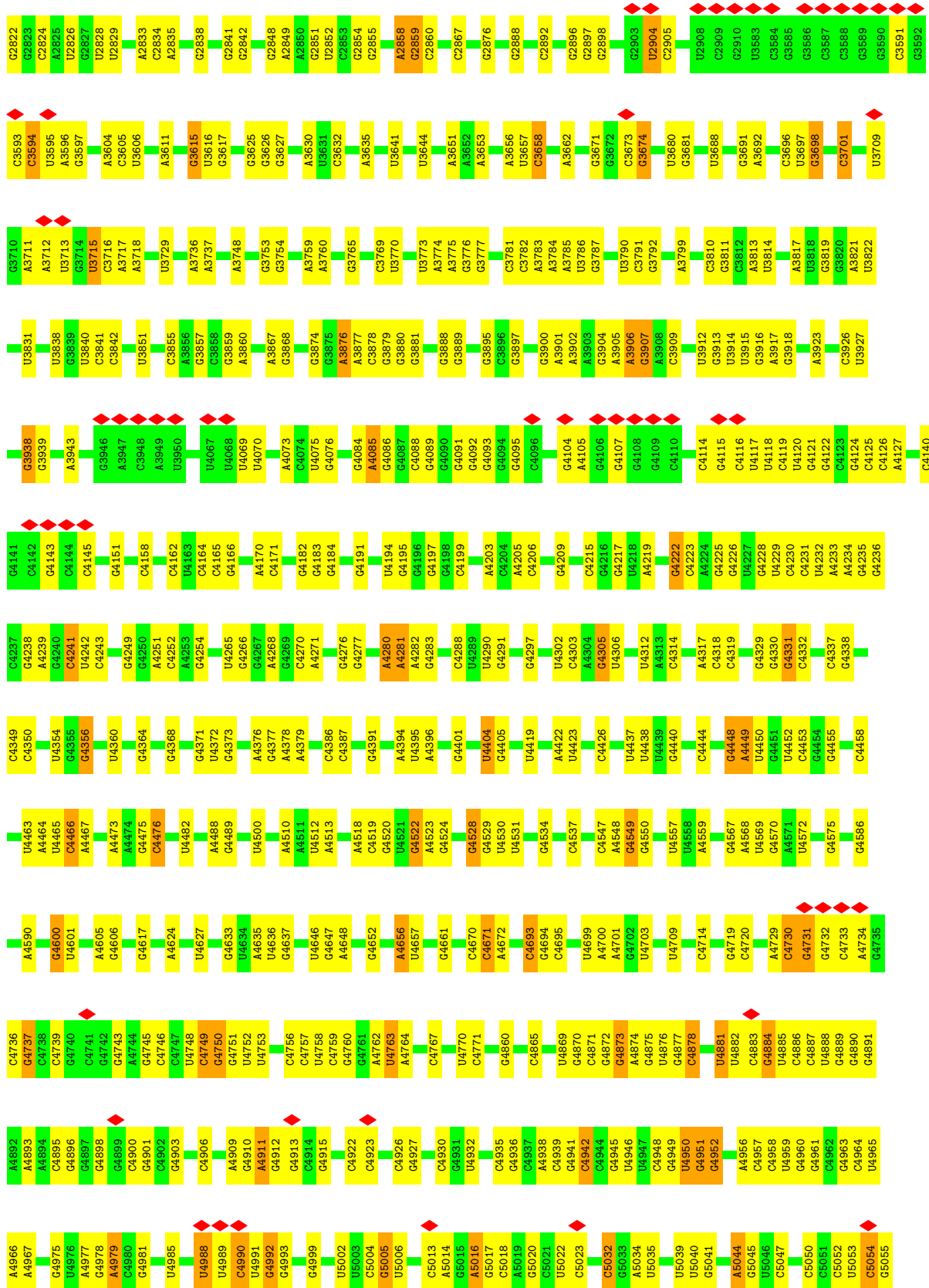


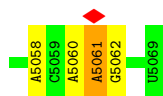


• Molecule 5: 28S ribosomal RNA

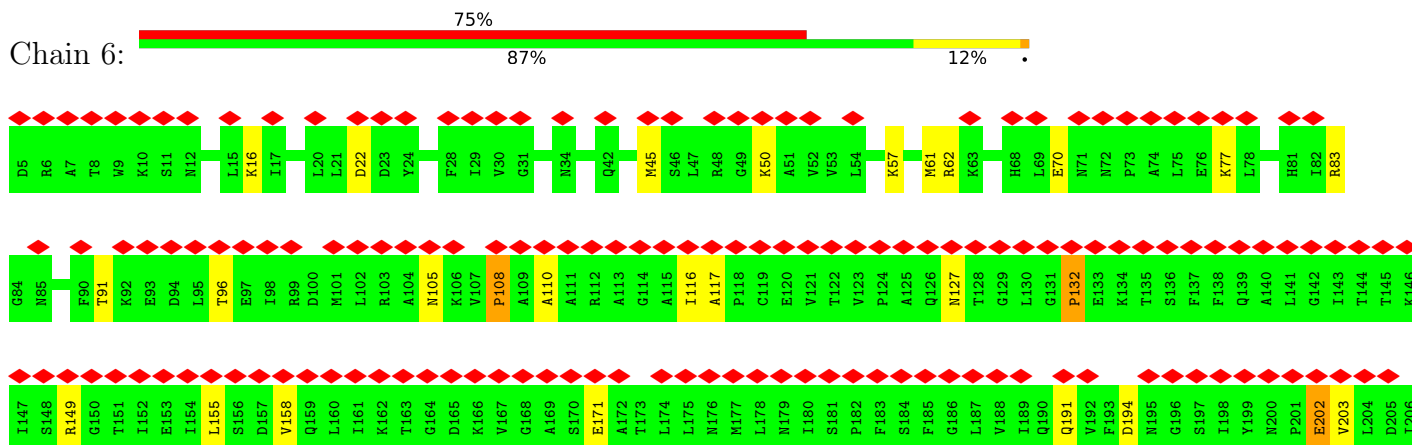




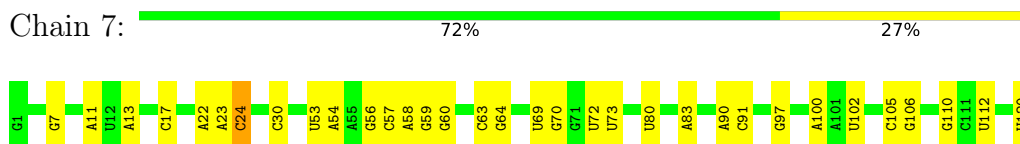




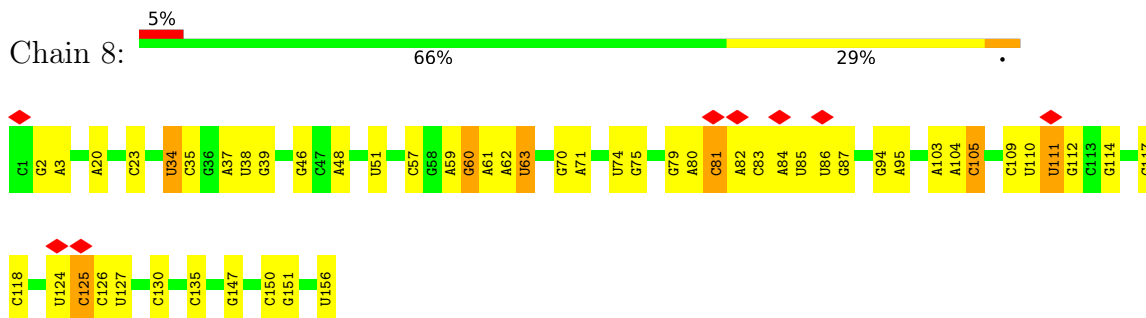
- Molecule 6: 60S acidic ribosomal protein P0



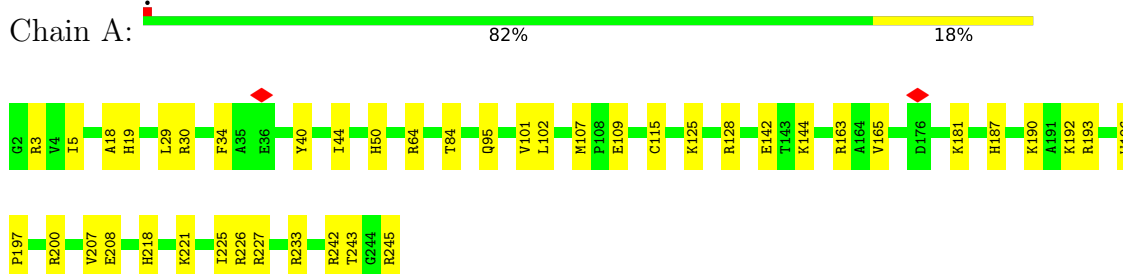
- Molecule 7: 5S ribosomal RNA



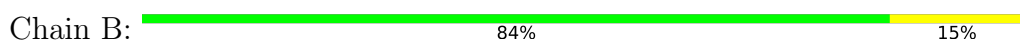
- Molecule 8: 5.8S ribosomal RNA

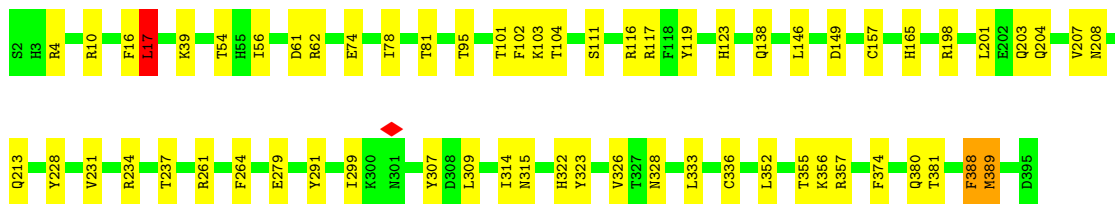


- Molecule 9: Ribosomal protein L8

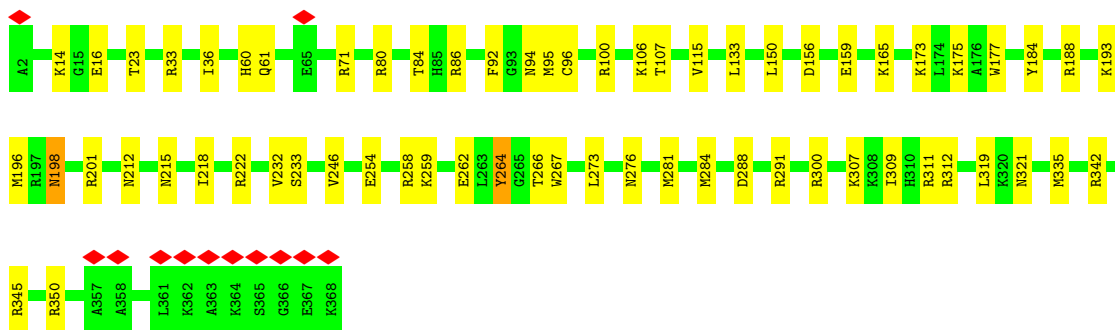
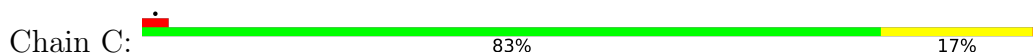


- Molecule 10: Ribosomal protein uL3

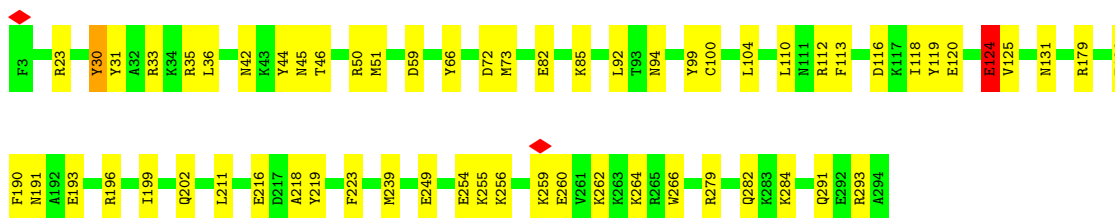
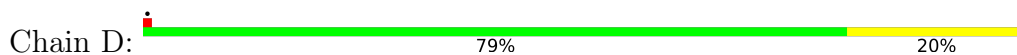




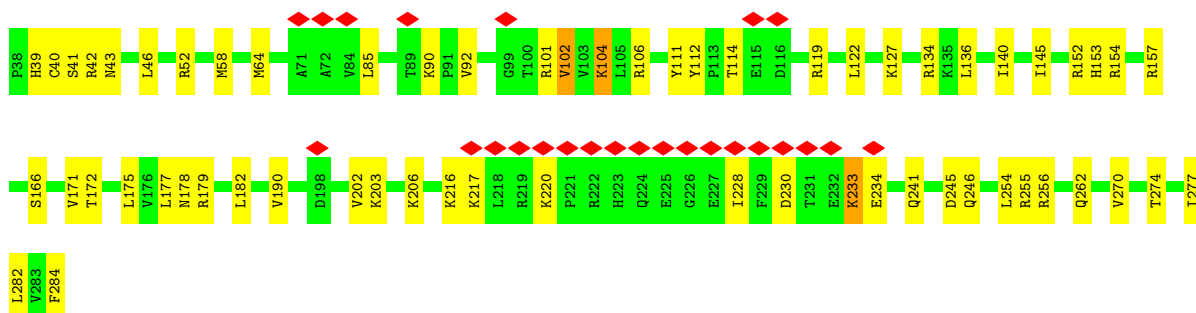
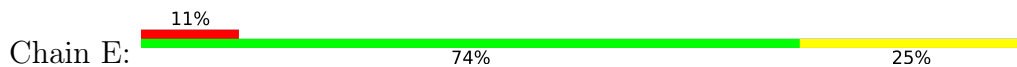
• Molecule 11: Ribosomal protein uL4



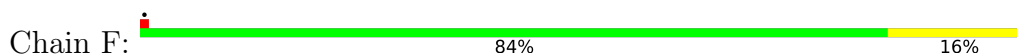
• Molecule 12: Ribosomal protein uL18

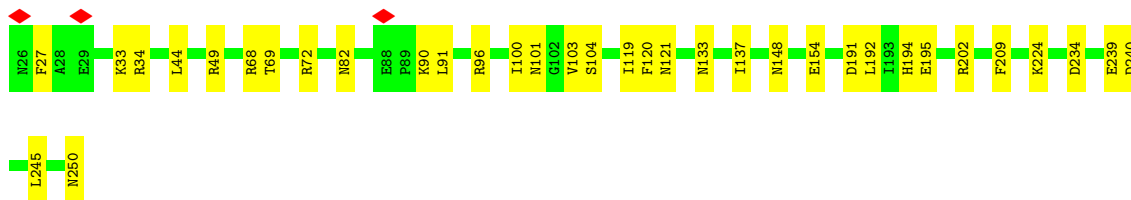


• Molecule 13: Ribosomal protein eL6

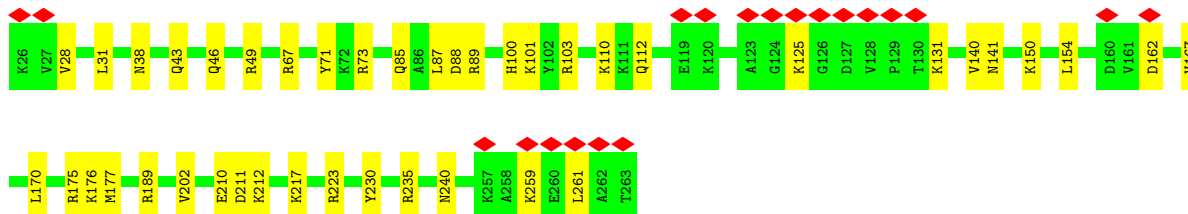
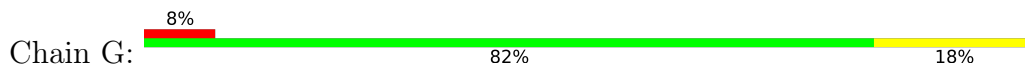


• Molecule 14: Ribosomal protein uL30

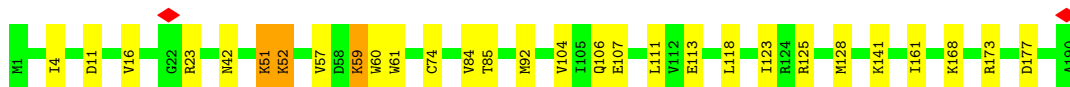
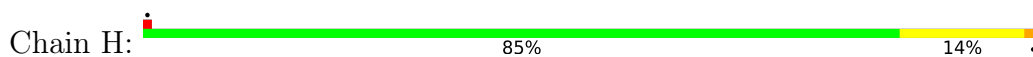




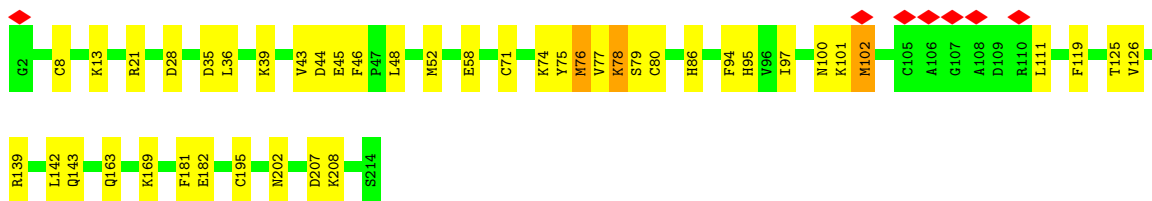
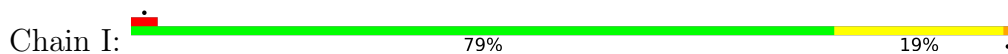
• Molecule 15: Ribosomal protein eL8



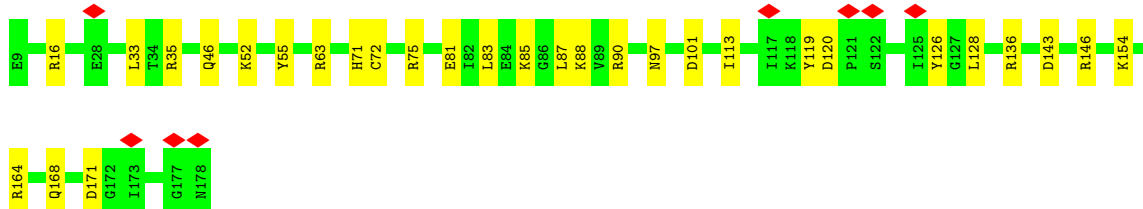
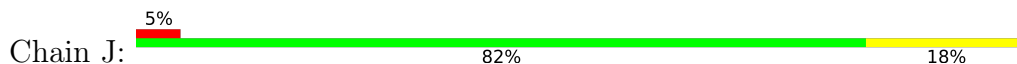
• Molecule 16: Ribosomal protein uL6



• Molecule 17: Ribosomal protein uL16

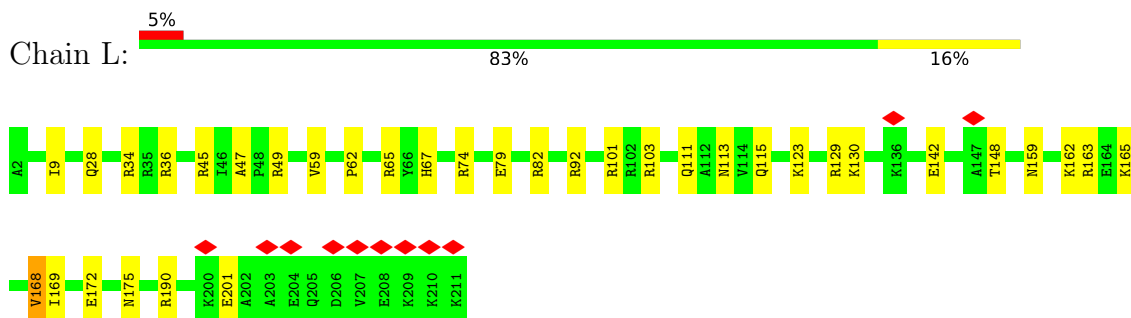


• Molecule 18: Ribosomal protein uL5

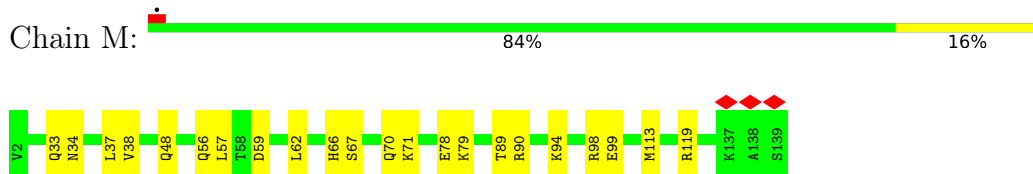


• Molecule 19: Ribosomal protein eL13

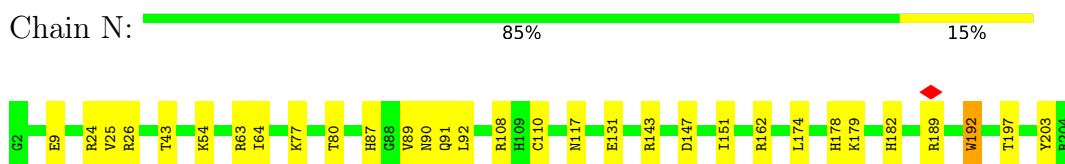




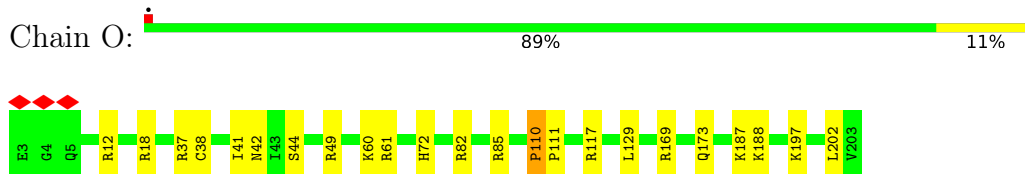
• Molecule 20: Ribosomal protein eL14



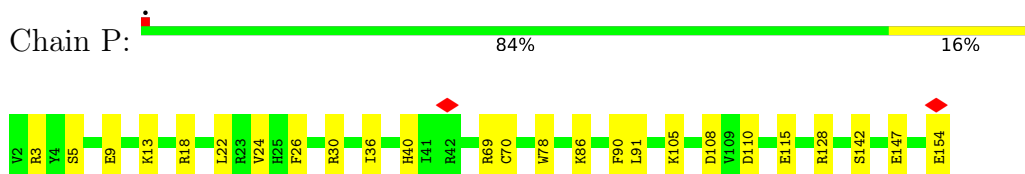
• Molecule 21: Ribosomal protein L15



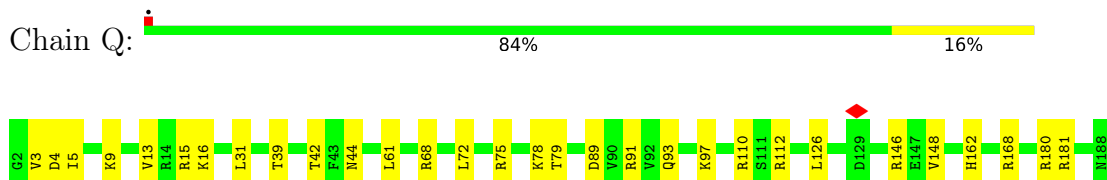
• Molecule 22: Ribosomal protein uL13



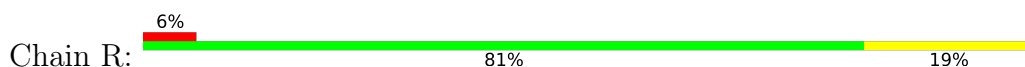
• Molecule 23: Ribosomal protein uL22



• Molecule 24: Ribosomal protein eL18

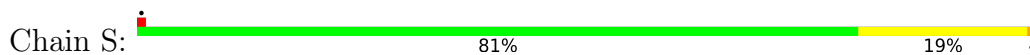


• Molecule 25: Ribosomal protein eL19

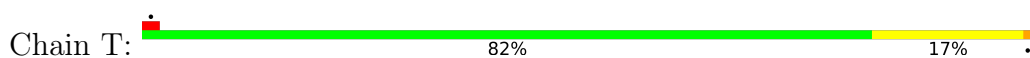




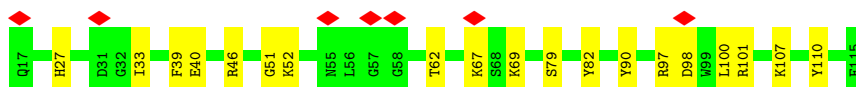
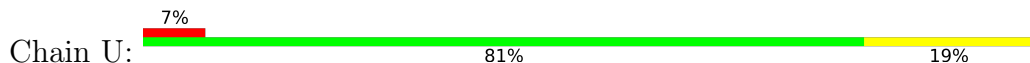
• Molecule 26: Ribosomal protein eL20



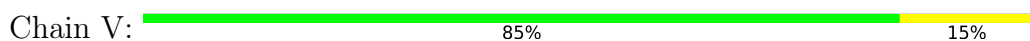
• Molecule 27: Ribosomal protein eL21



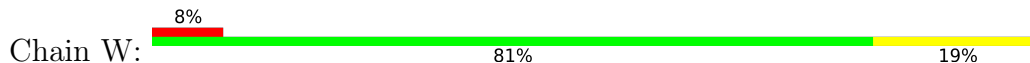
• Molecule 28: Ribosomal protein eL22



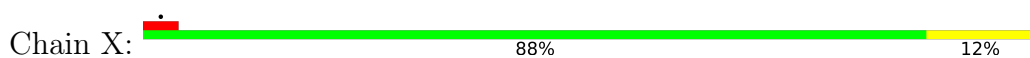
• Molecule 29: Ribosomal protein L23



• Molecule 30: Ribosomal protein eL24

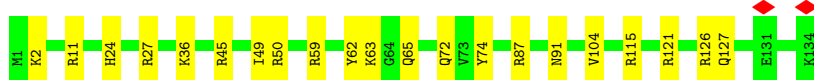
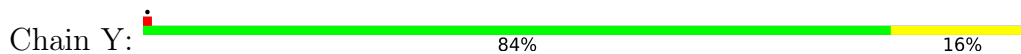


• Molecule 31: Ribosomal protein uL23

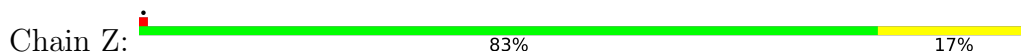




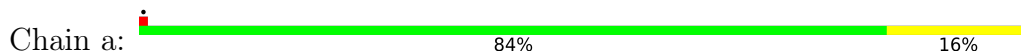
- Molecule 32: Ribosomal protein uL24



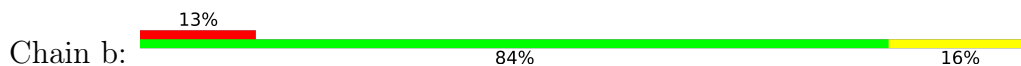
- Molecule 33: 60S ribosomal protein L27



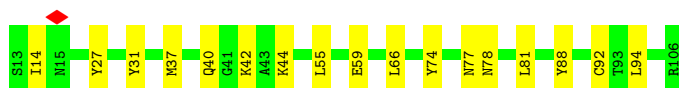
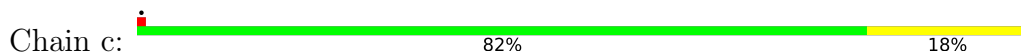
- Molecule 34: Ribosomal protein uL15



- Molecule 35: 60S ribosomal protein L29




- Molecule 36: Ribosomal protein eL30



- Molecule 37: Ribosomal protein eL31




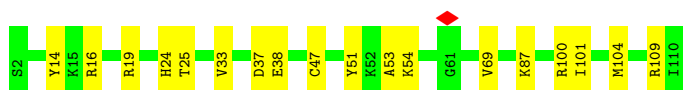
- Molecule 38: Ribosomal protein eL32

Chain e:  80% 20%




• Molecule 39: Ribosomal protein eL33

Chain f:  83% 17%




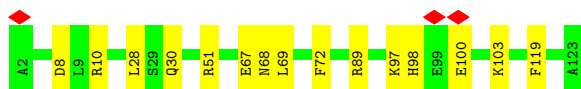
• Molecule 40: Ribosomal protein eL34

Chain g:  6% 87% 13%




• Molecule 41: Ribosomal protein uL29

Chain h:  88% 12%




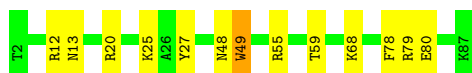
• Molecule 42: Ribosomal protein eL36

Chain i:  5% 90% 10%




• Molecule 43: Ribosomal protein L37

Chain j:  85% 14%

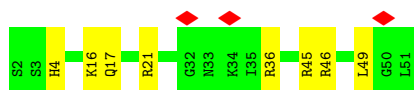
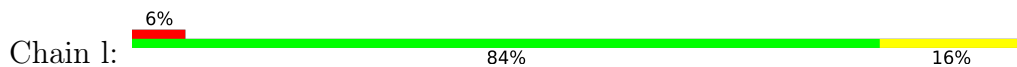


• Molecule 44: Ribosomal protein eL38

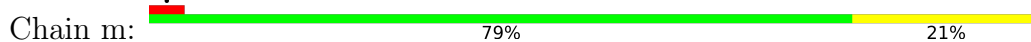
Chain k:  6% 87% 13%



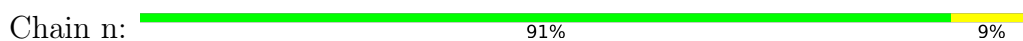
• Molecule 45: Ribosomal protein eL39



• Molecule 46: Ribosomal protein eL40



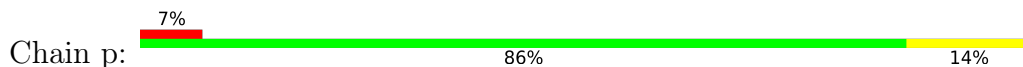
• Molecule 47: Ribosomal protein eL41



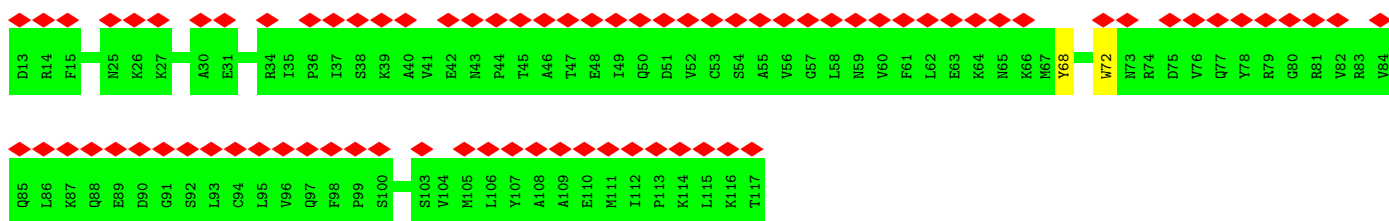
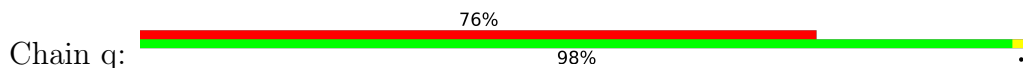
• Molecule 48: Ribosomal protein eL42

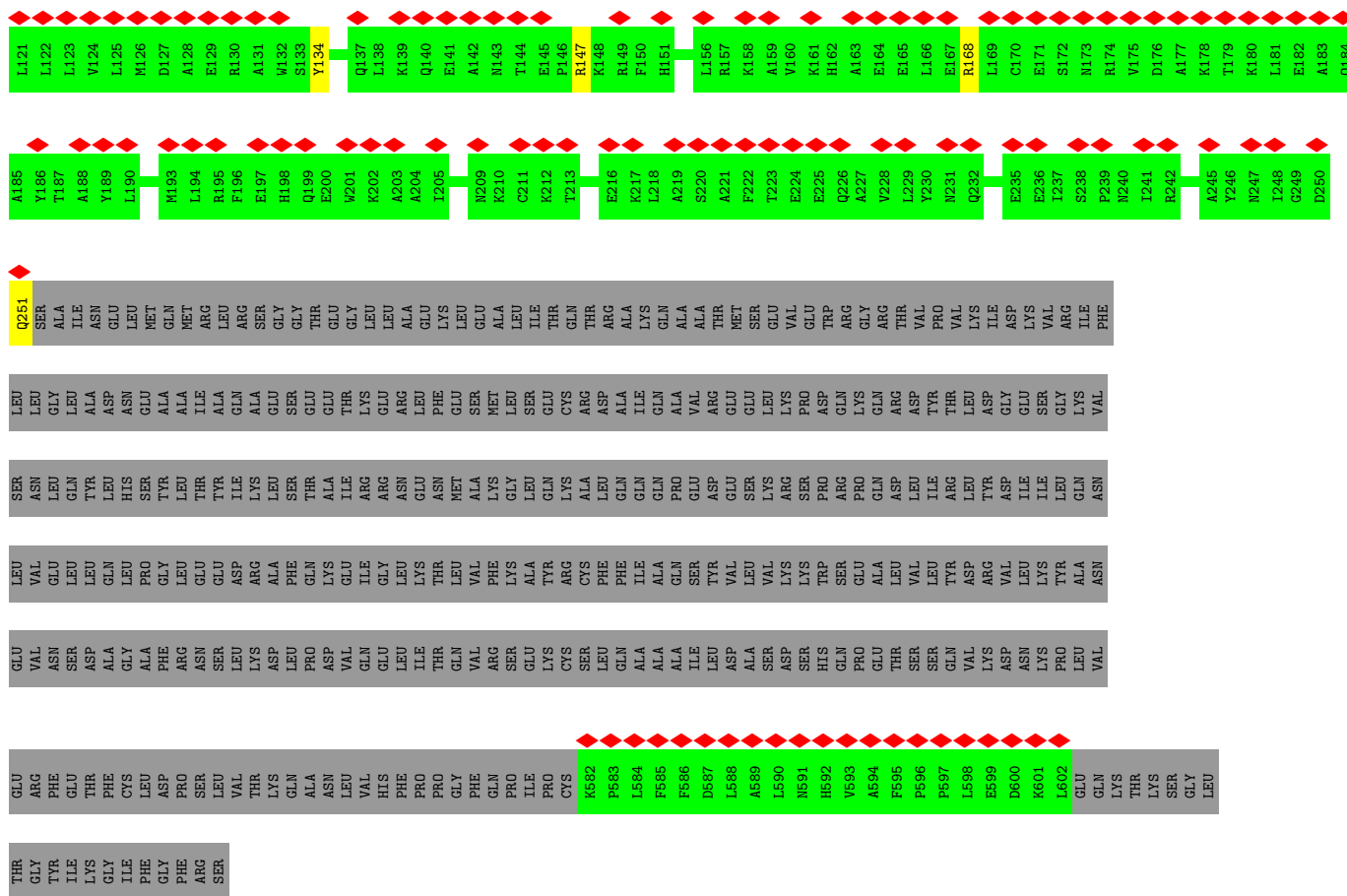


• Molecule 49: Ribosomal protein eL43



• Molecule 50: Signal recognition particle subunit SRP19





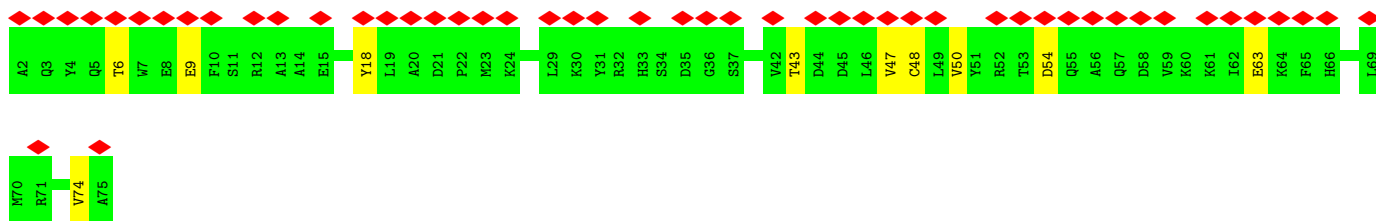
• Molecule 54: SRP receptor beta subunit

Chain v:

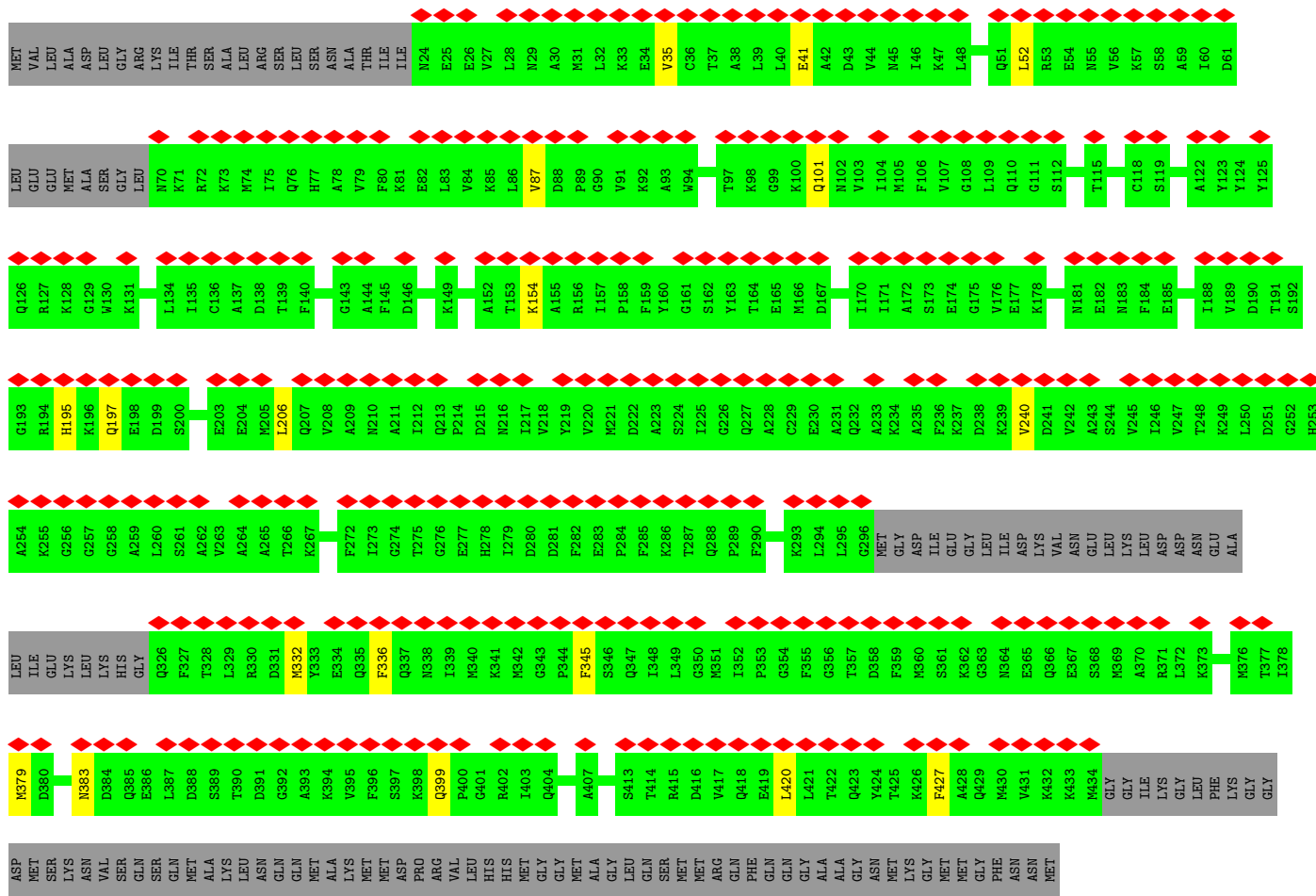


• Molecule 55: Signal recognition particle 9 kDa protein

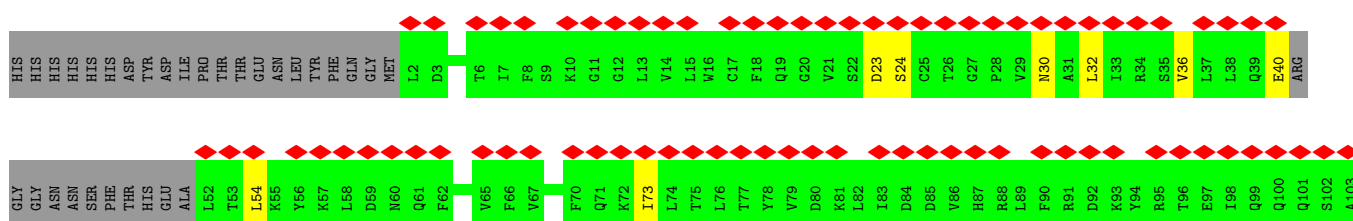
Chain w:

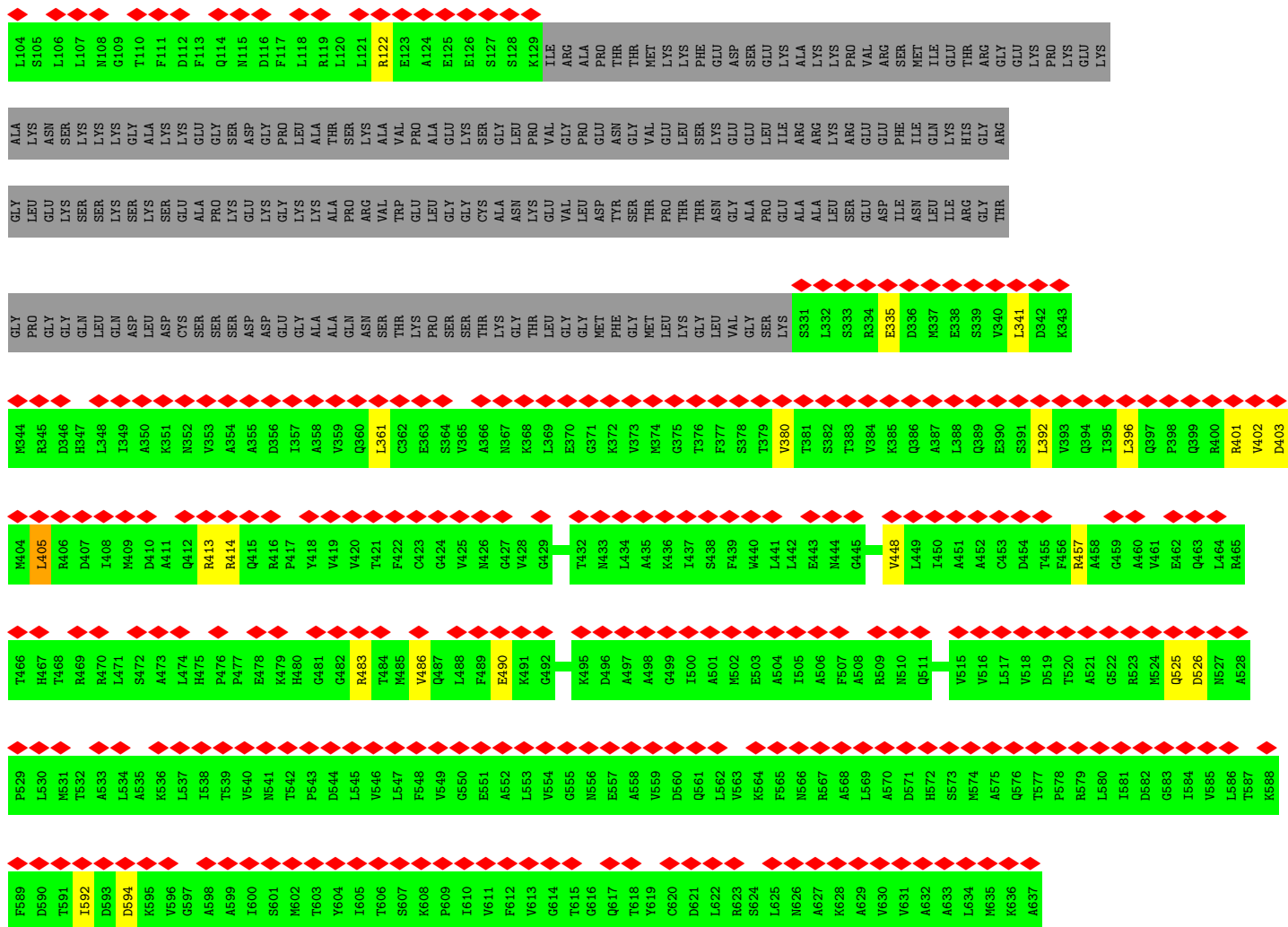


• Molecule 56: Signal recognition particle 54 kDa protein

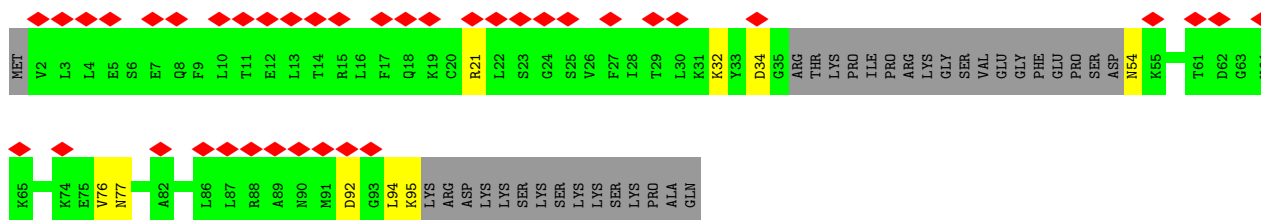


• Molecule 57: SRP receptor alpha subunit





• Molecule 58: Signal recognition particle 14 kDa protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45800	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.504	Depositor
Minimum map value	-0.309	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.064	Depositor
Map size (\AA)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.39, 1.39, 1.39	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	1	0.61	0/6188	1.36	72/9649 (0.7%)
2	2	0.35	0/1805	0.98	3/2809 (0.1%)
3	3	0.40	0/1017	0.63	0/1365
4	4	0.39	0/1257	0.75	3/1697 (0.2%)
5	5	0.54	10/87705 (0.0%)	1.28	692/136813 (0.5%)
6	6	0.28	0/1580	0.53	0/2133
7	7	0.46	0/2858	1.11	5/4455 (0.1%)
8	8	0.54	0/3701	1.26	18/5766 (0.3%)
9	A	0.43	0/1906	0.63	0/2556
10	B	0.41	0/3214	0.61	1/4308 (0.0%)
11	C	0.40	0/2973	0.60	1/3990 (0.0%)
12	D	0.39	0/2426	0.59	0/3252
13	E	0.37	0/1941	0.70	0/2601
14	F	0.41	0/1905	0.58	0/2539
15	G	0.35	0/1944	0.56	0/2618
16	H	0.37	0/1537	0.60	0/2066
17	I	0.37	0/1753	0.58	0/2343
18	J	0.33	0/1382	0.56	0/1849
19	L	0.37	0/1734	0.57	0/2318
20	M	0.38	0/1152	0.55	0/1539
21	N	0.40	0/1746	0.61	1/2338 (0.0%)
22	O	0.40	0/1684	0.55	0/2251
23	P	0.38	0/1268	0.60	1/1701 (0.1%)
24	Q	0.41	0/1530	0.59	0/2041
25	R	0.34	0/1524	0.56	0/2013
26	S	0.43	0/1493	0.60	0/2002
27	T	0.38	0/1326	0.59	1/1770 (0.1%)
28	U	0.32	0/822	0.57	0/1103
29	V	0.49	1/993 (0.1%)	0.56	0/1332
30	W	0.40	0/541	0.57	0/720
31	X	0.35	0/993	0.57	0/1334
32	Y	0.42	0/1132	0.57	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.39	0/1130	0.59	0/1507
34	a	0.41	0/1192	0.61	0/1591
35	b	0.38	0/620	0.53	0/819
36	c	0.37	0/742	0.60	0/996
37	d	0.45	0/903	0.61	0/1216
38	e	0.41	0/1071	0.61	0/1429
39	f	0.43	0/895	0.64	0/1198
40	g	0.39	0/916	0.58	0/1220
41	h	0.39	0/1023	0.54	0/1350
42	i	0.35	0/843	0.54	0/1115
43	j	0.43	0/721	0.65	1/953 (0.1%)
44	k	0.36	0/575	0.61	0/761
45	l	0.35	0/454	0.52	0/599
46	m	0.34	0/435	0.57	0/575
47	n	0.46	0/223	0.54	0/284
48	o	0.34	0/864	0.63	0/1140
49	p	0.39	0/718	0.60	0/953
50	q	0.49	0/858	0.57	0/1156
51	r	0.38	0/1442	0.55	0/1947
52	t	0.43	0/87	0.77	0/118
53	u	0.35	0/1853	0.53	1/2485 (0.0%)
54	v	0.44	0/1504	0.57	0/2020
55	w	0.29	0/617	0.51	0/829
56	x	0.41	0/2959	0.53	1/3971 (0.0%)
57	y	0.42	0/3344	0.56	0/4514
58	z	0.28	0/608	0.45	0/808
All	All	0.49	11/171627 (0.0%)	1.07	801/252329 (0.3%)

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
1	1	1	0
3	3	0	1
4	4	0	10
6	6	0	6
9	A	0	2
10	B	0	2
11	C	0	1
12	D	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	E	0	14
16	H	0	2
17	I	0	2
19	L	0	1
20	M	0	1
22	O	0	1
26	S	0	3
39	f	0	2
48	o	0	1
All	All	1	53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	5	4941	G	P-O5'	8.48	1.68	1.59
29	V	10	SER	C-N	8.11	1.47	1.33
5	5	960	A	N9-C4	7.54	1.42	1.37
5	5	149	A	N9-C4	-6.67	1.33	1.37
5	5	1890	G	N9-C4	-6.59	1.32	1.38

The worst 5 of 801 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	3594	C	C6-N1-C2	-11.99	115.51	120.30
5	5	960	A	C2-N3-C4	11.22	116.21	110.60
5	5	1890	G	N3-C4-C5	11.11	134.16	128.60
5	5	2036	C	N3-C2-O2	-10.97	114.22	121.90
5	5	960	A	C5-C6-N1	10.40	122.90	117.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	118	A	C1'

5 of 53 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	76	SER	Peptide
4	4	87	GLU	Peptide
4	4	88	PRO	Peptide
4	4	89	PRO	Peptide
4	4	94	LYS	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	
3	3	123/125 (98%)	109 (89%)	14 (11%)	0	100	100
4	4	161/163 (99%)	108 (67%)	46 (29%)	7 (4%)	2	24
6	6	200/202 (99%)	158 (79%)	40 (20%)	2 (1%)	15	51
9	A	242/244 (99%)	203 (84%)	38 (16%)	1 (0%)	34	69
10	B	392/394 (100%)	334 (85%)	55 (14%)	3 (1%)	19	56
11	C	365/367 (100%)	317 (87%)	46 (13%)	2 (0%)	29	66
12	D	290/292 (99%)	252 (87%)	36 (12%)	2 (1%)	22	59
13	E	232/236 (98%)	171 (74%)	56 (24%)	5 (2%)	6	37
14	F	223/225 (99%)	202 (91%)	21 (9%)	0	100	100
15	G	236/238 (99%)	209 (89%)	27 (11%)	0	100	100
16	H	188/190 (99%)	164 (87%)	21 (11%)	3 (2%)	9	43
17	I	211/213 (99%)	188 (89%)	19 (9%)	4 (2%)	8	40
18	J	168/170 (99%)	145 (86%)	23 (14%)	0	100	100
19	L	208/210 (99%)	175 (84%)	30 (14%)	3 (1%)	11	45
20	M	136/138 (99%)	118 (87%)	17 (12%)	1 (1%)	22	59
21	N	201/203 (99%)	179 (89%)	21 (10%)	1 (0%)	29	66
22	O	199/201 (99%)	186 (94%)	11 (6%)	2 (1%)	15	51
23	P	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
24	Q	185/187 (99%)	164 (89%)	21 (11%)	0	100	100
25	R	178/180 (99%)	160 (90%)	18 (10%)	0	100	100
26	S	173/175 (99%)	151 (87%)	20 (12%)	2 (1%)	13	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	T	157/159 (99%)	138 (88%)	18 (12%)	1 (1%)	25	62
28	U	97/99 (98%)	83 (86%)	13 (13%)	1 (1%)	15	51
29	V	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
30	W	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
31	X	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
32	Y	132/134 (98%)	120 (91%)	12 (9%)	0	100	100
33	Z	133/135 (98%)	119 (90%)	14 (10%)	0	100	100
34	a	145/147 (99%)	122 (84%)	23 (16%)	0	100	100
35	b	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
36	c	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
37	d	105/107 (98%)	89 (85%)	15 (14%)	1 (1%)	15	51
38	e	126/128 (98%)	116 (92%)	10 (8%)	0	100	100
39	f	107/109 (98%)	94 (88%)	13 (12%)	0	100	100
40	g	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
41	h	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
42	i	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
43	j	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
44	k	67/69 (97%)	54 (81%)	13 (19%)	0	100	100
45	l	48/50 (96%)	38 (79%)	10 (21%)	0	100	100
46	m	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
47	n	21/23 (91%)	21 (100%)	0	0	100	100
48	o	102/104 (98%)	87 (85%)	13 (13%)	2 (2%)	7	39
49	p	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
50	q	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
51	r	172/605 (28%)	156 (91%)	15 (9%)	1 (1%)	25	62
52	t	9/11 (82%)	9 (100%)	0	0	100	100
53	u	214/568 (38%)	207 (97%)	7 (3%)	0	100	100
54	v	182/213 (85%)	174 (96%)	8 (4%)	0	100	100
55	w	72/74 (97%)	63 (88%)	9 (12%)	0	100	100
56	x	368/504 (73%)	361 (98%)	7 (2%)	0	100	100
57	y	418/657 (64%)	389 (93%)	26 (6%)	3 (1%)	22	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	z	72/110 (66%)	71 (99%)	1 (1%)	0	100	100
All	All	8339/9666 (86%)	7392 (89%)	900 (11%)	47 (1%)	29	62

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	4	96	LYS
4	4	106	PHE
10	B	389	MET
13	E	153	HIS
16	H	60	TRP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	109/109 (100%)	91 (84%)	18 (16%)	2	14
4	4	136/136 (100%)	117 (86%)	19 (14%)	3	20
6	6	170/170 (100%)	148 (87%)	22 (13%)	4	22
9	A	187/187 (100%)	147 (79%)	40 (21%)	1	7
10	B	335/335 (100%)	275 (82%)	60 (18%)	2	11
11	C	305/305 (100%)	243 (80%)	62 (20%)	1	8
12	D	246/247 (100%)	188 (76%)	58 (24%)	1	5
13	E	209/209 (100%)	164 (78%)	45 (22%)	1	7
14	F	194/194 (100%)	159 (82%)	35 (18%)	1	11
15	G	204/206 (99%)	162 (79%)	42 (21%)	1	7
16	H	169/169 (100%)	142 (84%)	27 (16%)	2	15
17	I	180/180 (100%)	139 (77%)	41 (23%)	1	6
18	J	143/143 (100%)	113 (79%)	30 (21%)	1	7
19	L	176/176 (100%)	144 (82%)	32 (18%)	1	11
20	M	116/116 (100%)	96 (83%)	20 (17%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	N	171/171 (100%)	141 (82%)	30 (18%)	2	12
22	O	172/172 (100%)	151 (88%)	21 (12%)	5	24
23	P	134/134 (100%)	110 (82%)	24 (18%)	2	11
24	Q	163/163 (100%)	133 (82%)	30 (18%)	1	10
25	R	159/159 (100%)	125 (79%)	34 (21%)	1	7
26	S	156/156 (100%)	126 (81%)	30 (19%)	1	9
27	T	139/139 (100%)	112 (81%)	27 (19%)	1	9
28	U	89/89 (100%)	71 (80%)	18 (20%)	1	8
29	V	101/101 (100%)	83 (82%)	18 (18%)	2	12
30	W	55/55 (100%)	43 (78%)	12 (22%)	1	6
31	X	107/107 (100%)	93 (87%)	14 (13%)	4	22
32	Y	124/124 (100%)	103 (83%)	21 (17%)	2	13
33	Z	117/117 (100%)	94 (80%)	23 (20%)	1	8
34	a	119/119 (100%)	96 (81%)	23 (19%)	1	9
35	b	63/63 (100%)	51 (81%)	12 (19%)	1	9
36	c	79/79 (100%)	62 (78%)	17 (22%)	1	7
37	d	98/98 (100%)	69 (70%)	29 (30%)	0	2
38	e	114/114 (100%)	88 (77%)	26 (23%)	1	6
39	f	88/88 (100%)	72 (82%)	16 (18%)	1	11
40	g	98/98 (100%)	83 (85%)	15 (15%)	2	17
41	h	109/109 (100%)	94 (86%)	15 (14%)	3	21
42	i	86/86 (100%)	76 (88%)	10 (12%)	5	27
43	j	73/73 (100%)	60 (82%)	13 (18%)	2	12
44	k	64/64 (100%)	55 (86%)	9 (14%)	3	20
45	l	47/47 (100%)	39 (83%)	8 (17%)	2	13
46	m	48/48 (100%)	37 (77%)	11 (23%)	1	6
47	n	22/22 (100%)	20 (91%)	2 (9%)	9	36
48	o	92/92 (100%)	67 (73%)	25 (27%)	0	3
49	p	74/74 (100%)	61 (82%)	13 (18%)	2	12
50	q	92/94 (98%)	90 (98%)	2 (2%)	52	72
51	r	158/503 (31%)	153 (97%)	5 (3%)	39	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	t	11/11 (100%)	11 (100%)	0	100	100
53	u	192/498 (39%)	186 (97%)	6 (3%)	40	65
54	v	165/183 (90%)	164 (99%)	1 (1%)	86	93
55	w	66/66 (100%)	56 (85%)	10 (15%)	3	17
56	x	317/420 (76%)	300 (95%)	17 (5%)	22	54
57	y	360/550 (66%)	332 (92%)	28 (8%)	12	42
58	z	69/100 (69%)	60 (87%)	9 (13%)	4	22
All	All	7270/8268 (88%)	6095 (84%)	1175 (16%)	5	15

5 of 1175 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	d	103	TYR
57	y	341	LEU
38	e	95	TYR
37	d	101	LYS
45	l	17	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 202 such sidechains are listed below:

Mol	Chain	Res	Type
28	U	27	HIS
36	c	40	GLN
57	y	397	GLN
30	W	30	GLN
33	Z	79	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	255/299 (85%)	71 (27%)	11 (4%)
2	2	74/76 (97%)	23 (31%)	1 (1%)
5	5	3644/3658 (99%)	1236 (33%)	185 (5%)
7	7	119/120 (99%)	27 (22%)	2 (1%)
8	8	155/156 (99%)	46 (29%)	6 (3%)
All	All	4247/4309 (98%)	1403 (33%)	205 (4%)

5 of 1403 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	G
1	1	28	U
1	1	32	A
1	1	33	G
1	1	36	A

5 of 205 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	5	2123	C
5	5	2661	U
8	8	34	U
5	5	2256	C
5	5	2361	G

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 139 ligands modelled in this entry, 136 are monoatomic - leaving 3 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
62	GNP	x	601	59	29,34,34	1.65	8 (27%)	33,54,54	2.13	6 (18%)
62	GNP	y	701	59	29,34,34	1.52	7 (24%)	33,54,54	2.22	8 (24%)
61	GTP	v	302	59,54	26,34,34	1.05	2 (7%)	32,54,54	1.64	8 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	GNP	x	601	59	-	2/14/38/38	0/3/3/3
62	GNP	y	701	59	-	8/14/38/38	0/3/3/3
61	GTP	v	302	59,54	-	0/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	x	601	GNP	PG-O1G	4.49	1.53	1.46
62	x	601	GNP	PB-O3A	3.57	1.63	1.59
62	y	701	GNP	C6-N1	3.56	1.39	1.33
62	y	701	GNP	PB-O3A	3.44	1.63	1.59
61	v	302	GTP	C5-C6	-3.42	1.40	1.47

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	y	701	GNP	C5-C6-N1	-8.63	111.63	123.43
62	x	601	GNP	C5-C6-N1	-8.47	111.84	123.43
62	y	701	GNP	C2-N1-C6	6.05	125.54	115.93
62	x	601	GNP	C2-N1-C6	5.94	125.36	115.93
61	v	302	GTP	C5-C6-N1	3.79	120.65	113.95

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

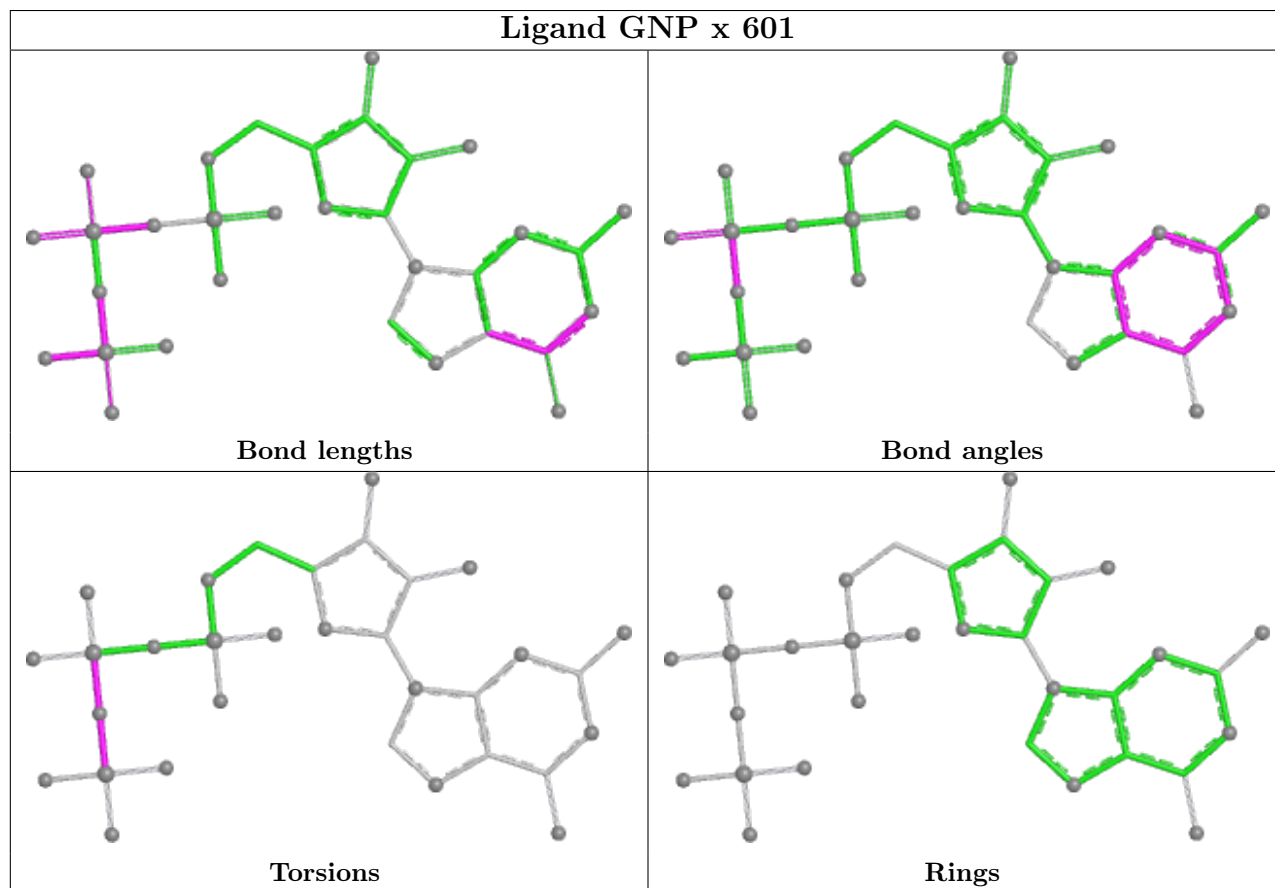
Mol	Chain	Res	Type	Atoms
62	x	601	GNP	PB-N3B-PG-O1G
62	x	601	GNP	PG-N3B-PB-O1B
62	y	701	GNP	PB-N3B-PG-O1G
62	y	701	GNP	PG-N3B-PB-O1B
62	y	701	GNP	C5'-O5'-PA-O3A

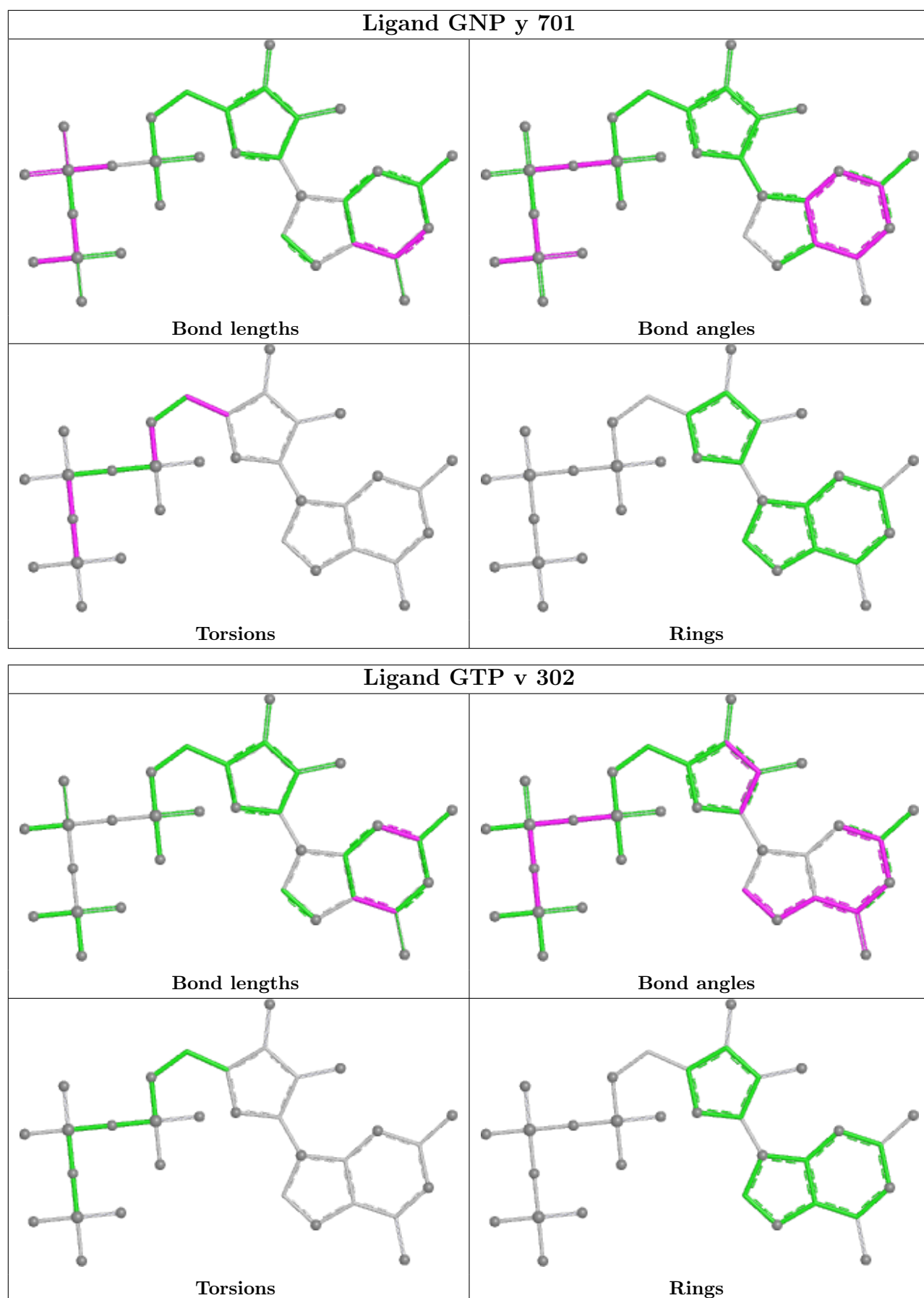
There are no ring outliers.

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
5	5	13
13	E	1
2	2	1

The worst 5 of 15 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	24.42
1	5	4776:G	O3'	4859:C	P	17.73
1	5	757:G	O3'	906:C	P	17.30
1	5	519:C	O3'	642:G	P	16.88
1	5	2910:G	O3'	3583:U	P	16.78

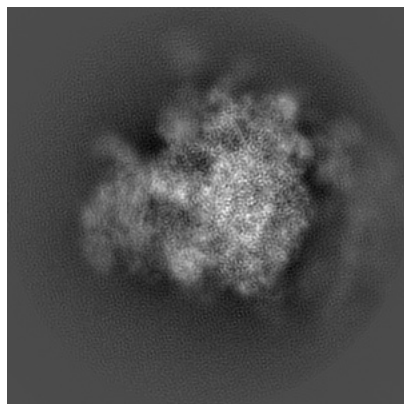
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4300. These allow visual inspection of the internal detail of the map and identification of artifacts.

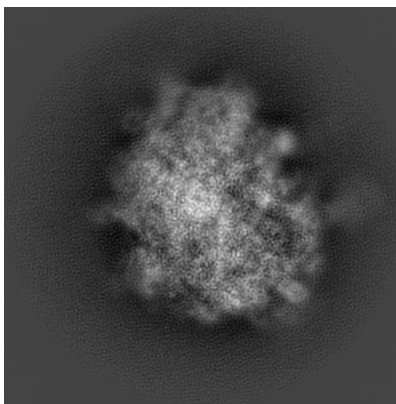
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

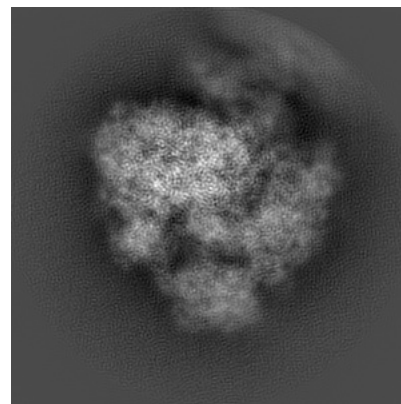
6.1.1 Primary map



X

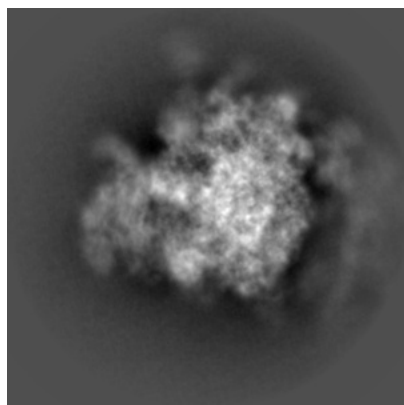


Y

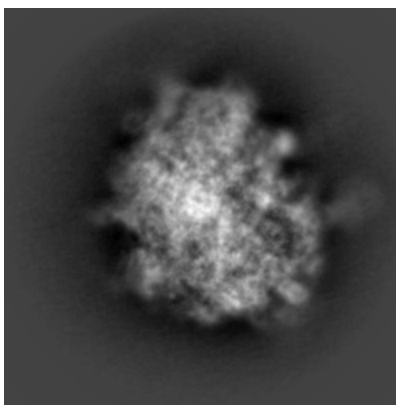


Z

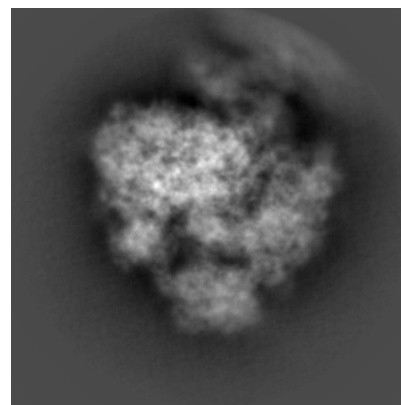
6.1.2 Raw map



X



Y

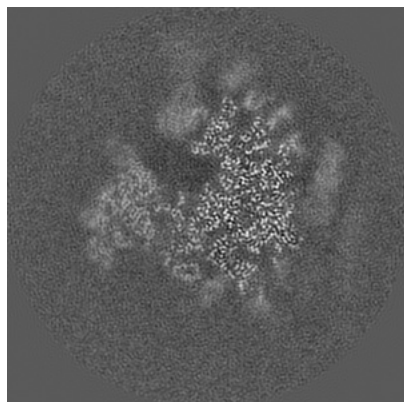


Z

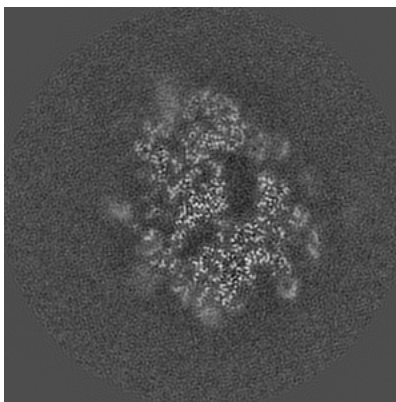
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

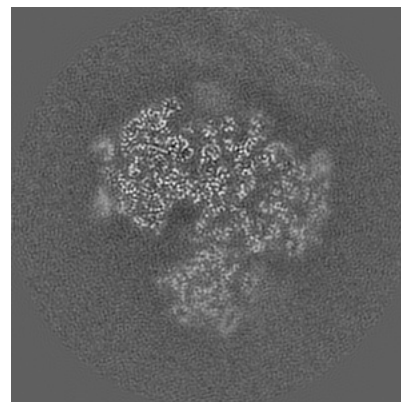
6.2.1 Primary map



X Index: 160

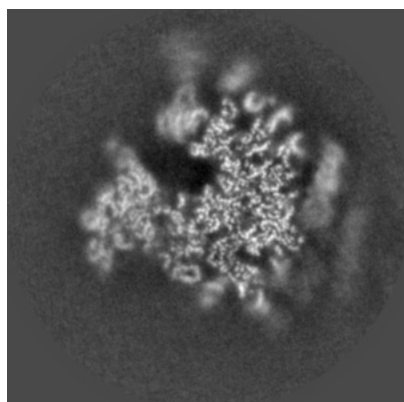


Y Index: 160

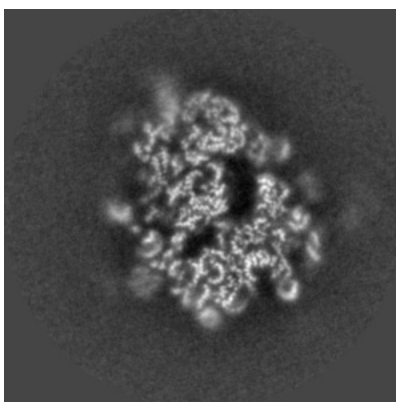


Z Index: 160

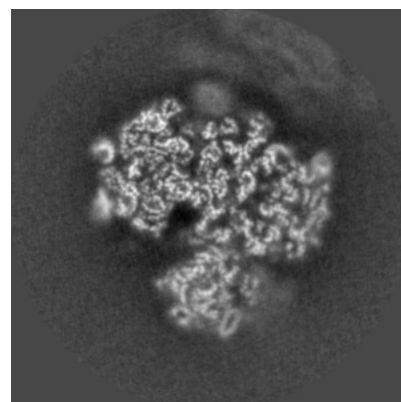
6.2.2 Raw map



X Index: 160



Y Index: 160

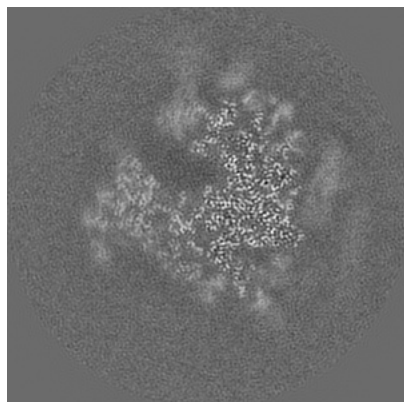


Z Index: 160

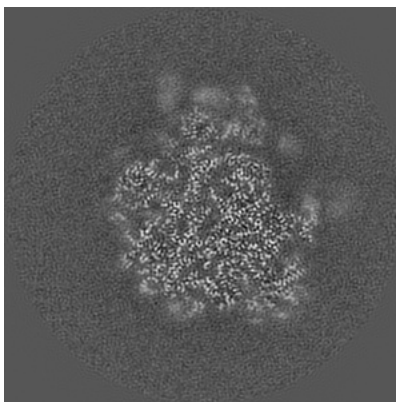
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

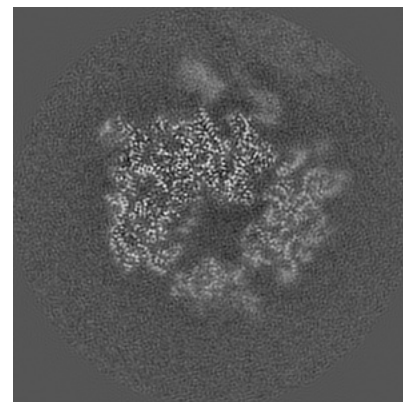
6.3.1 Primary map



X Index: 158

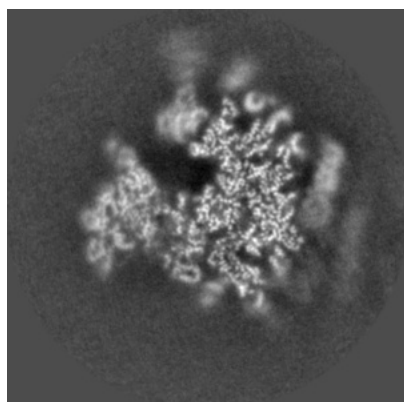


Y Index: 192

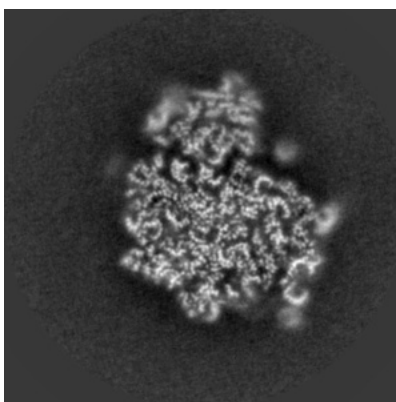


Z Index: 181

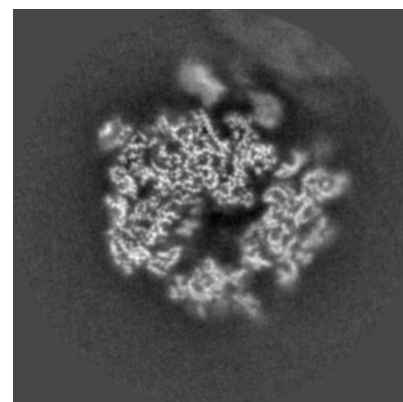
6.3.2 Raw map



X Index: 161



Y Index: 177

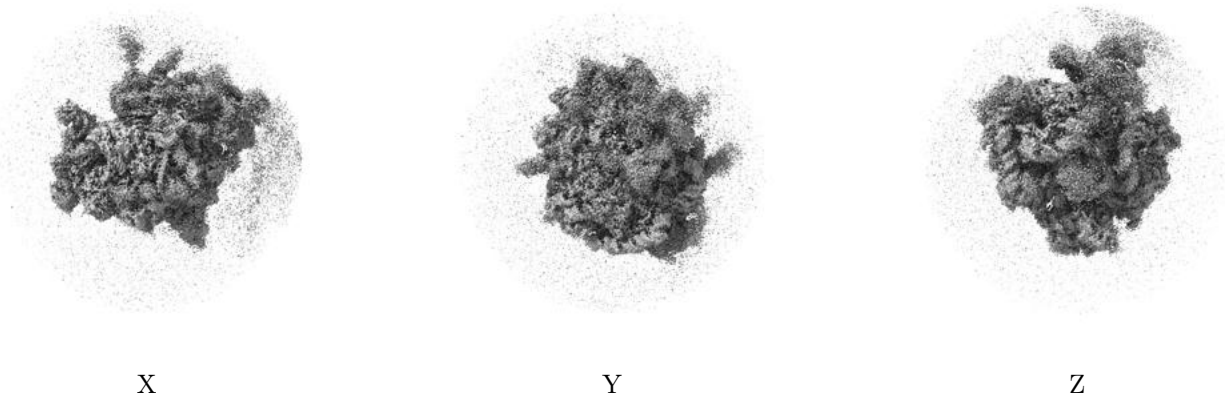


Z Index: 180

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

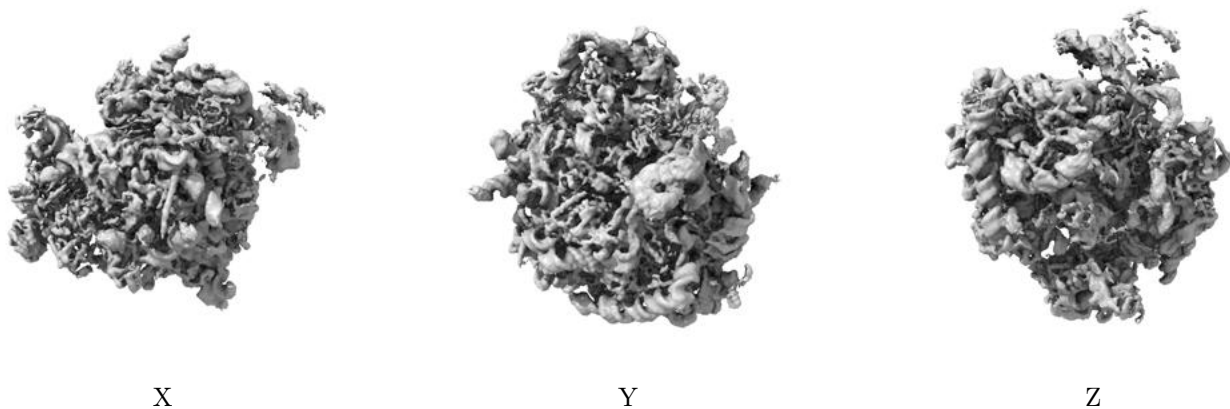
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.064. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

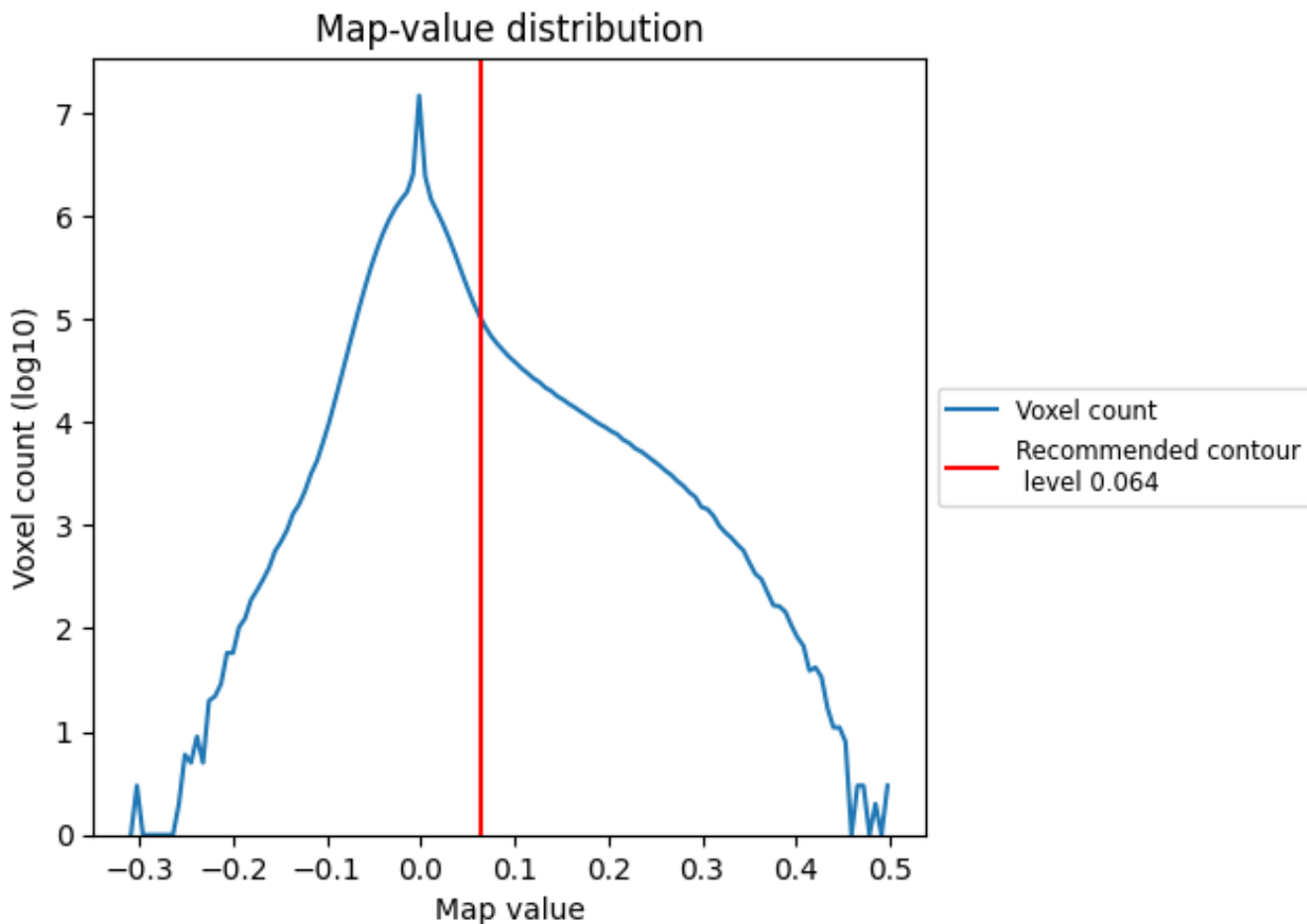
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

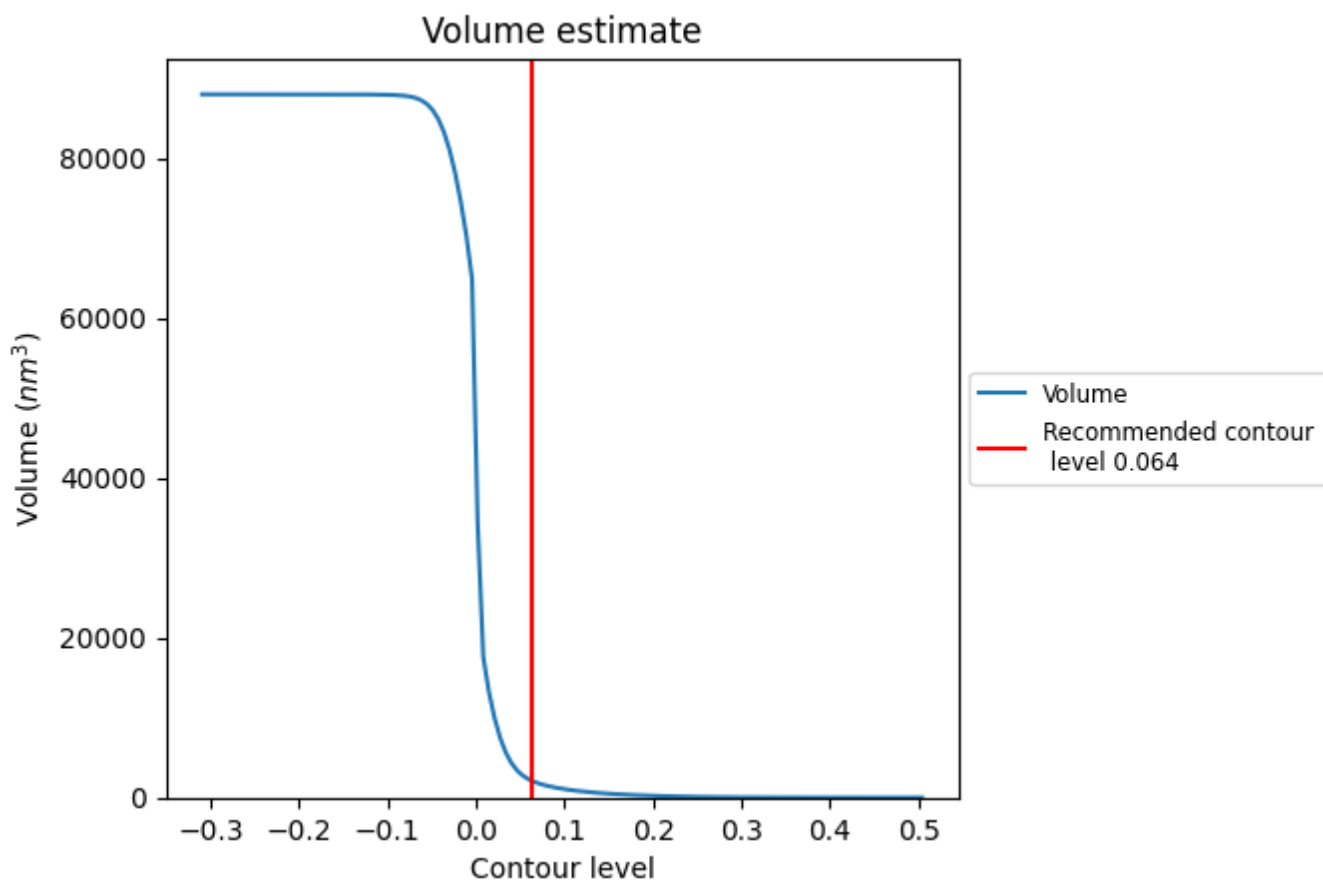
This section contains the results of statistical analysis of the map.

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.

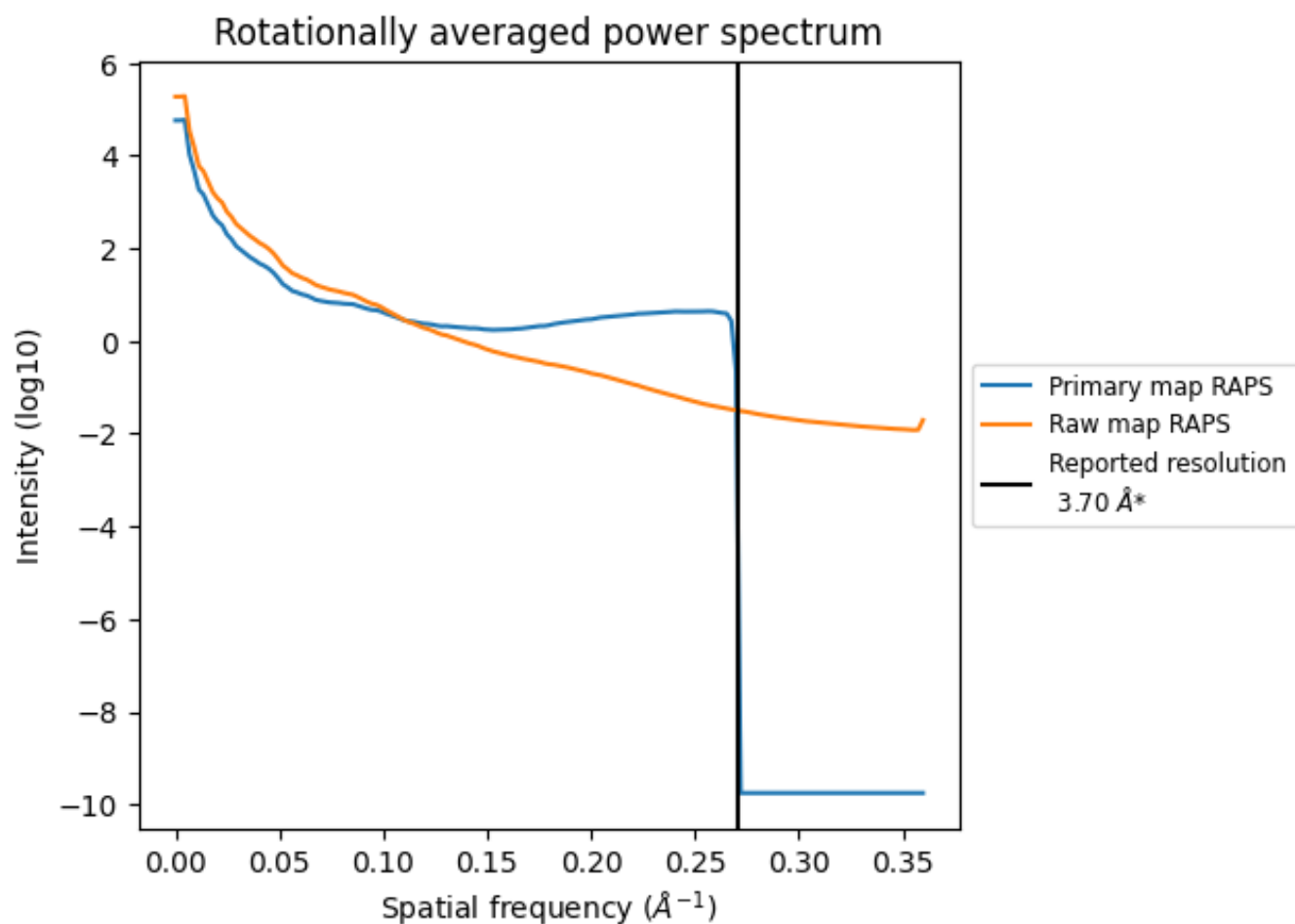
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2065 nm³; this corresponds to an approximate mass of 1865 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

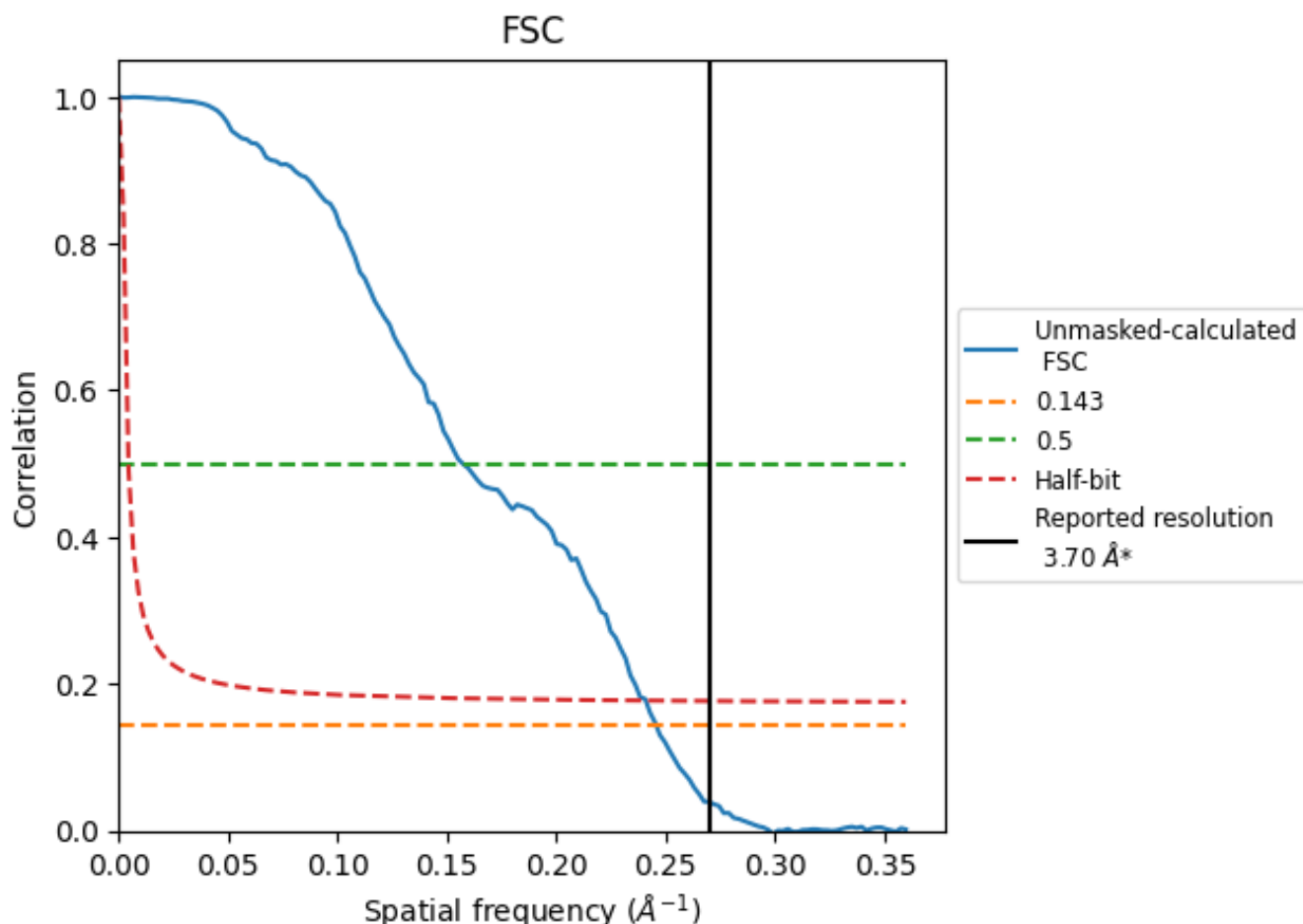


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

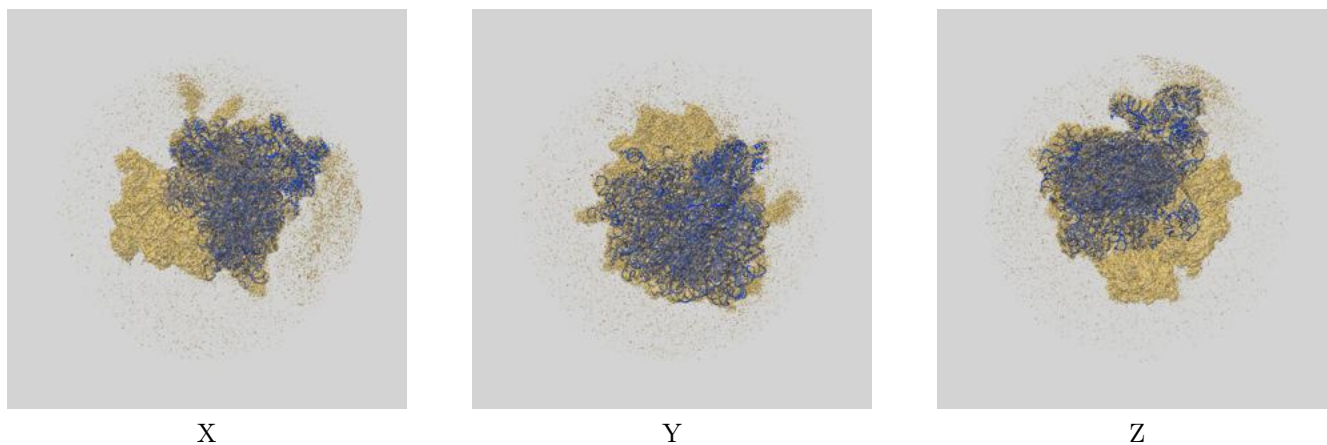
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	6.37	4.15

*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 4.07 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

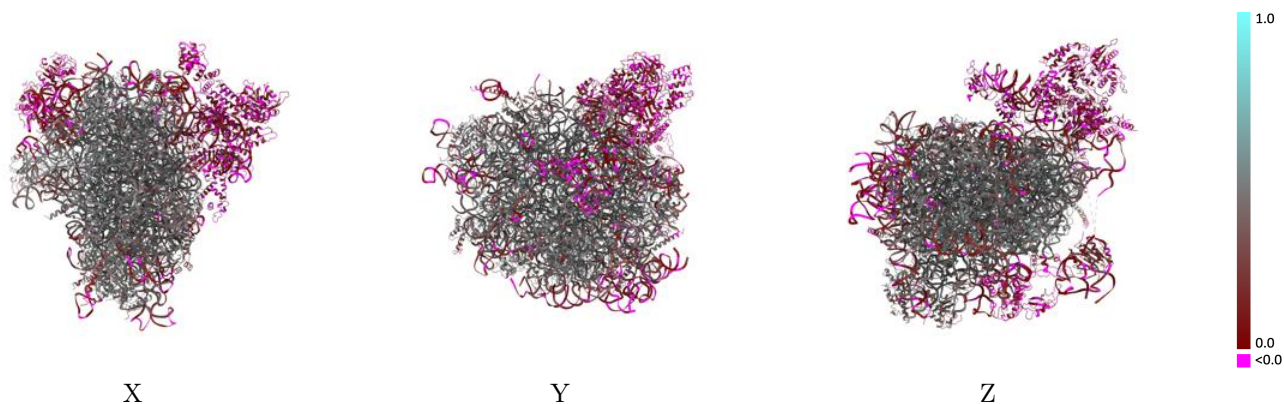
This section contains information regarding the fit between EMDB map EMD-4300 and PDB model 6FRK. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



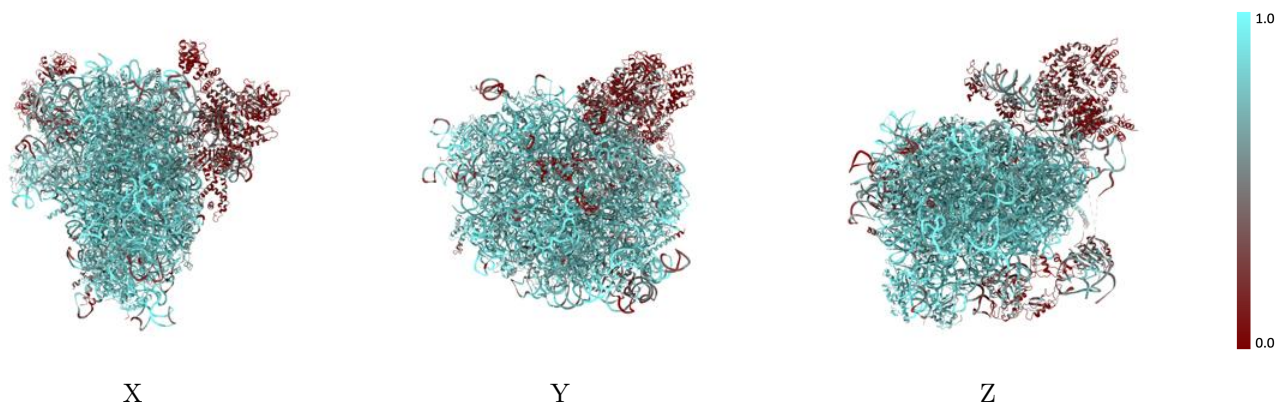
The images above show the 3D surface view of the map at the recommended contour level 0.064 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



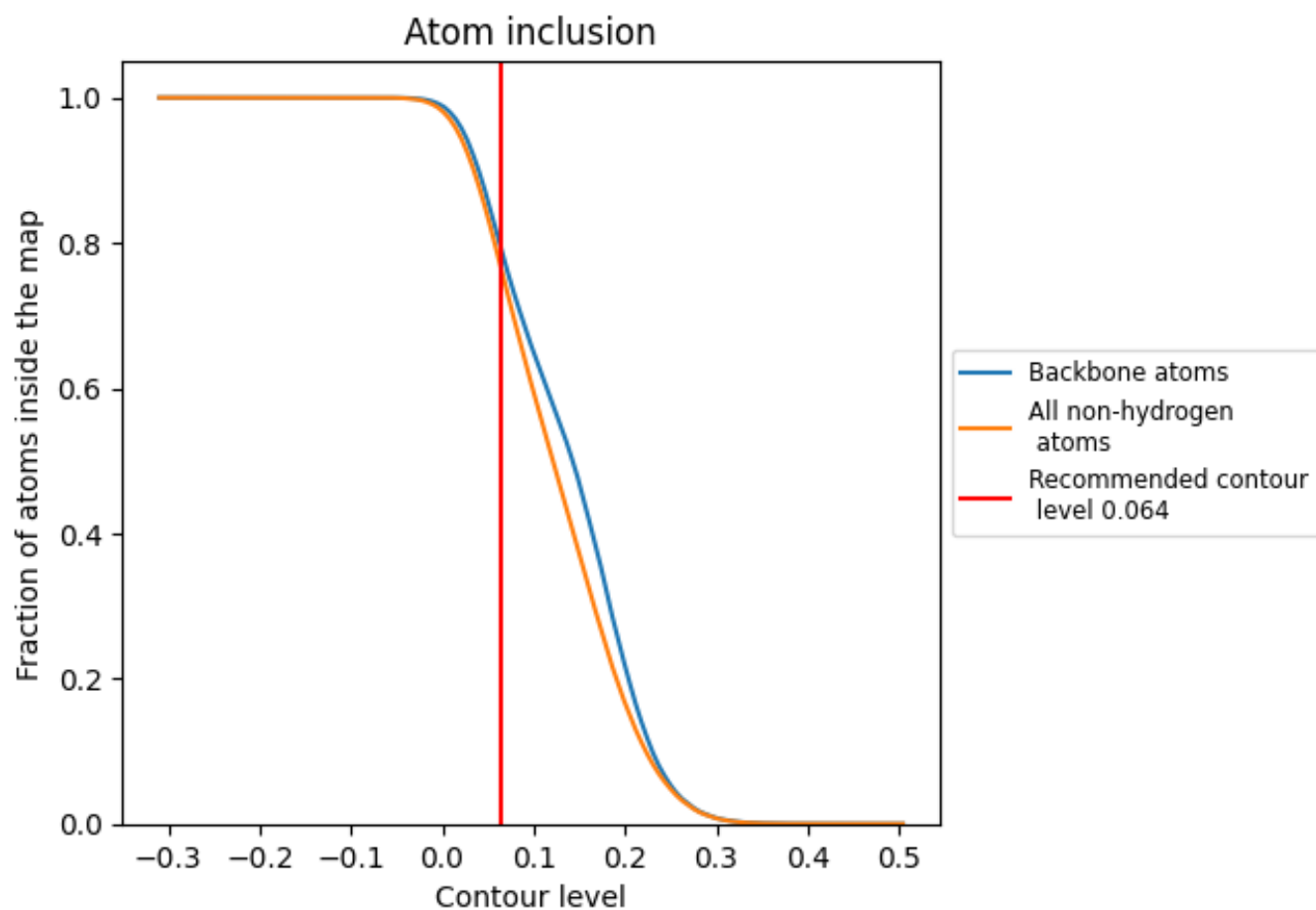
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.064).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 77% 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 (0.064) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7668	 0.3630
1	 0.5636	 0.0980
2	 0.7580	 0.3260
3	 0.8247	 0.4660
4	 0.1842	 0.0010
5	 0.8614	 0.3770
6	 0.2343	 0.0670
7	 0.9668	 0.4490
8	 0.8815	 0.3960
A	 0.8113	 0.4860
B	 0.7969	 0.4720
C	 0.8108	 0.4630
D	 0.8463	 0.4260
E	 0.7546	 0.3860
F	 0.8091	 0.4620
G	 0.7621	 0.4150
H	 0.8054	 0.4640
I	 0.7901	 0.4540
J	 0.7786	 0.4030
L	 0.7913	 0.4260
M	 0.8551	 0.4590
N	 0.8481	 0.4890
O	 0.8083	 0.4660
P	 0.7920	 0.4850
Q	 0.8150	 0.4780
R	 0.7370	 0.4040
S	 0.8414	 0.4830
T	 0.8100	 0.4690
U	 0.7063	 0.3710
V	 0.7693	 0.4790
W	 0.7485	 0.4350
X	 0.7629	 0.4450
Y	 0.8126	 0.4540
Z	 0.8276	 0.4370
a	 0.8707	 0.4870



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Chain	Atom inclusion	Q-score
b	 0.7306	 0.3950
c	 0.8154	 0.4460
d	 0.7048	 0.4350
e	 0.8220	 0.4760
f	 0.8492	 0.4890
g	 0.7747	 0.4510
h	 0.7790	 0.4280
i	 0.7982	 0.4230
j	 0.8576	 0.4810
k	 0.6786	 0.3830
l	 0.7683	 0.4710
m	 0.8029	 0.4590
n	 0.7363	 0.4400
o	 0.7736	 0.4430
p	 0.7602	 0.4670
q	 0.2293	 0.0270
r	 0.0863	 0.0610
t	 0.0455	 -0.0330
u	 0.2603	 0.0510
v	 0.1668	 0.0640
w	 0.3395	 0.2040
x	 0.2299	 0.1160
y	 0.1927	 0.0840
z	 0.4074	 0.2630