wwPDB EM Validation Summary Report (i)

Jun 13, 2022 – 08:06 pm BST

PDB ID	:	7QGR
EMDB ID	:	EMD-13958
Title	:	Structure of the SmrB-bound E. coli disome - collided 70S ribosome
Authors	:	Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2021-12-09
Resolution	:	5.70 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

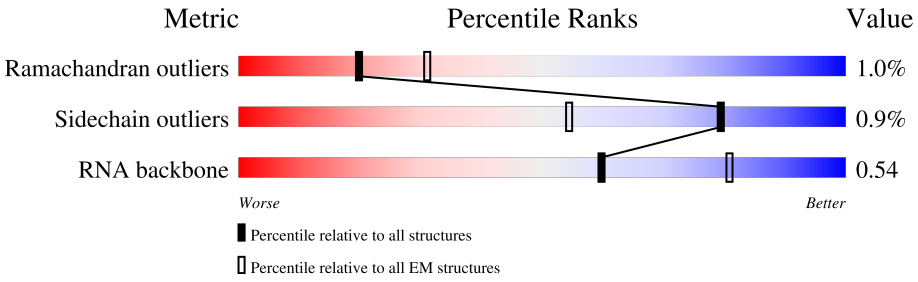
EMDB validation analysis	:	0.0.1.dev8
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.70 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 <=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	O	120	25% 77% 19%
2	P	273	72% 87% 10%
3	Q	209	65% 93% 7%
4	R	201	59% 95%
5	S	179	85% 98%
6	T	177	87% 98%
7	V	142	93% 98%
8	W	142	49% 95% 5%

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Mol	Chain	Length	Quality of chain
9	X	123	80% 95%
10	Y	144	65% 89% 8%
11	Z	136	60% 90% 9%
12	a	127	59% 83% 10% 6%
13	b	117	72% 94% 5%
14	c	115	76% 92% 5%
15	d	118	51% 88% 10%
16	e	103	73% 95%
17	f	110	71% 97%
18	g	100	70% 90% 7%
19	h	104	56% 94%
20	i	94	45% 100%
21	j	85	18% 82% 5% 12%
22	k	78	59% 92% 6%
23	l	63	70% 94% 6%
24	m	59	46% 95%
25	n	57	42% 82% 16%
26	o	55	69% 85% 5% 9%
27	p	46	57% 87% 13%
28	q	65	46% 88% 9%
29	r	55	49% 60% 9% 31%
30	N	2903	15% 66% 29% 5%
31	L	70	77% 76% 23%
32	C	223	60% 60% 40%
33	U	149	99% 98%

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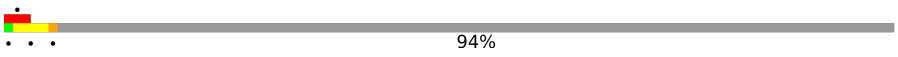
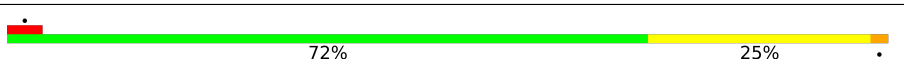
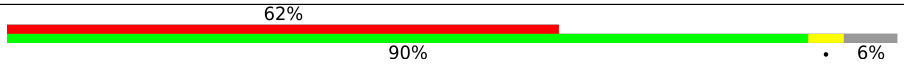
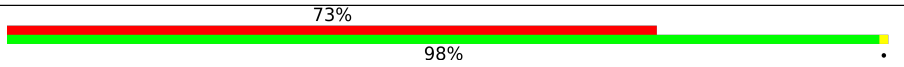
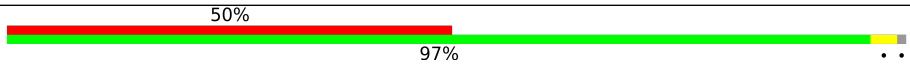
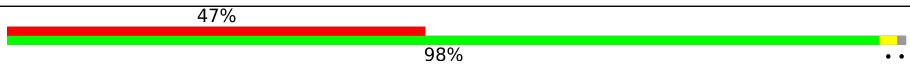
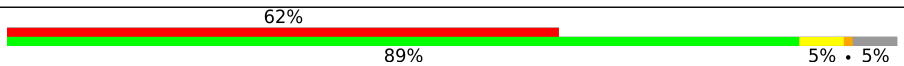
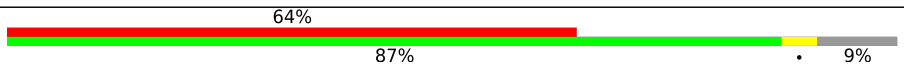
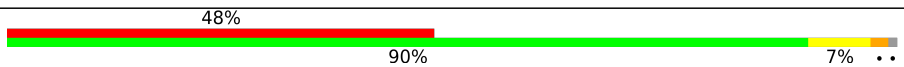
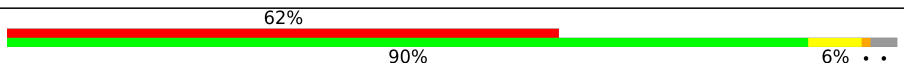
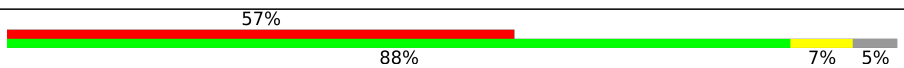
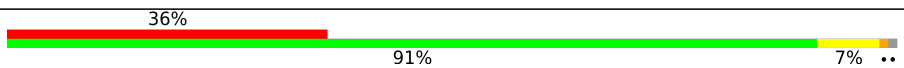
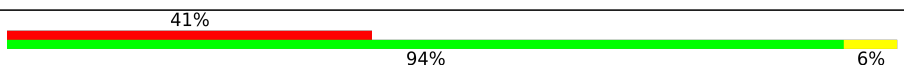
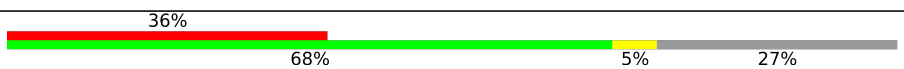
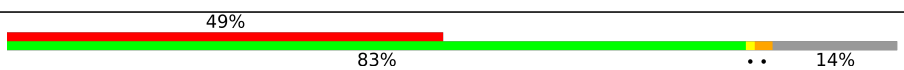
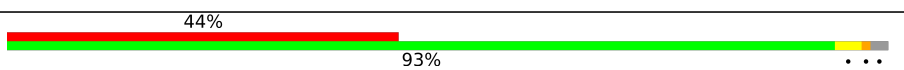
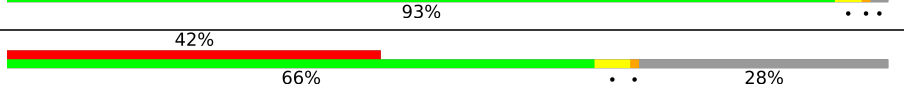
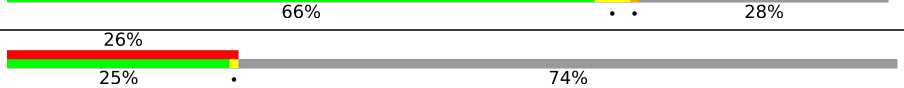
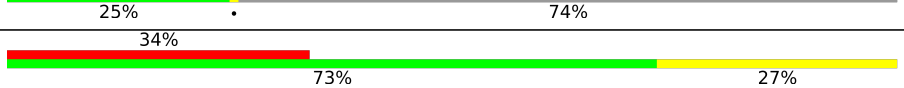
Mol	Chain	Length	Quality of chain
34	M	75	
35	x	692	
36	0	1539	
37	1	239	
38	2	218	
39	3	206	
40	4	162	
41	5	131	
42	6	152	
43	7	130	
44	8	130	
45	9	103	
46	A	129	
47	B	124	
48	D	118	
49	E	101	
50	F	89	
51	G	82	
52	H	84	
53	I	75	
54	J	92	
55	K	87	
56	s	71	
57	t	557	
58	u	73	

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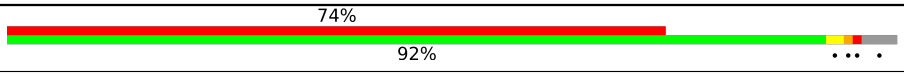
Mol	Chain	Length	Quality of chain
59	v	182	

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 149850 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	O	118	2529	1126	464	821	118	0	0

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	P	271	2082	1288	423	364	7	0	0

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	Q	209	1564	979	288	293	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	R	201	1552	974	283	290	5	0	0

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	S	177	1397	891	249	251	6	0	0

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	T	176	1322	832	243	245	2	0	0

- Molecule 7 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	X	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	a	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	conflict	UNP A0A829CNM8

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	b	116	Total 891	C 552	N 178	O 161	0	0

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	c	114	Total 915	C 573	N 179	O 162	S 1	0	0

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	d	117	Total 946	C 604	N 192	O 150	0	0

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e	103	Total 815	C 516	N 153	O 144	S 2	0	0

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	f	110	Total 857	C 532	N 166	O 156	S 3	0	0

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	g	93	Total 738	C 466	N 139	O 131	S 2	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	conflict	UNP A0A829CFV1

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	h	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	i	94	Total 752	C 479	N 137	O 133	S 3	0	0

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	j	75	Total 568	C 353	N 113	O 101	S 1	0	0

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	k	77	Total 624	C 388	N 129	O 105	S 2	0	0

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	63	Total 508	C 313	N 99	O 94	S 2	0	0

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	m	58	Total 448	C 281	N 87	O 78	S 2	0	0

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	n	56	Total 443	C 269	N 94	O 79	S 1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	o	50	Total 409	C 263	N 75	O 71	0	0

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	p	46	Total 376	C 228	N 90	O 56	S 2	0	0

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	q	64	Total 503	C 323	N 105	O 73	S 2	0	0

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	38	Total 301	C 185	N 65	O 47	S 4	0	0

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	2897	Total 62215	C 27754	N 11448	O 20115	P 2898	1	0

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L	54	Total 415	C 256	N 75	O 78	S 6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	conflict	UNP A0A1X3HZV8

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	C	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	U	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 34 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	75	Total	C	N	O	P	0	0
			1594	711	281	527	75		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	x	44	Total	C	N	O	P	0	0
			928	416	160	308	44		

- Molecule 36 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	0	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	218	Total	C	N	O	S	0	0
			1699	1078	303	311	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	conflict	UNP A0A377C6M5

- Molecule 41 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	101	SER	PRO	conflict	UNP P02358

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	conflict	UNP A0A1Z3UZ18

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	ALA	PRO	conflict	UNP A0A829AF87

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	D	114	Total	C	N	O	S	0	0
			877	543	175	156	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	VAL	MET	conflict	UNP A0A7U9IV78

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	E	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	ALA	GLU	conflict	UNP A0A090BZT4

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	G	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	H	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	2	ALA	THR	conflict	UNP A0A829A8C6

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	I	55	Total	C	N	O	0	0
			455	288	86	81		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	15	THR	ALA	conflict	UNP A0A376I7P4
I	58	ALA	CYS	conflict	UNP A0A376I7P4

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	J	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	82	TYR	GLY	conflict	UNP S1EA57
J	83	TYR	HIS	conflict	UNP S1EA57

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	K	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	LEU	MET	conflict	UNP P0A7U7

- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	s	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 57 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	t	143	Total	C	N	O	0	0
			704	418	143	143		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	241	VAL	ILE	conflict	UNP A0A829CYC5

- Molecule 58 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	73	Total	C	N	O	P	0	0
			1561	695	279	514	73		

- Molecule 59 is a protein called UPF0115 protein YfcN.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	v	175	Total	C	N	O	S	0	0
			1256	796	226	229	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	99	ALA	ASP	conflict	UNP Q6KCY1
v	101	ALA	HIS	conflict	UNP Q6KCY1

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	u	2	Total	Mg	0
			2	2	

- Molecule 61 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
61	u	1	Total	K	0
			1	1	

- Molecule 62 is water.

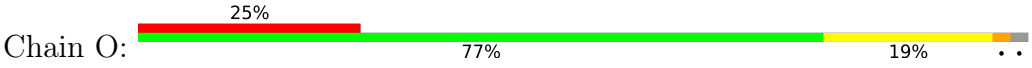
Mol	Chain	Residues	Atoms		AltConf
62	u	9	Total	O	0
			9	9	

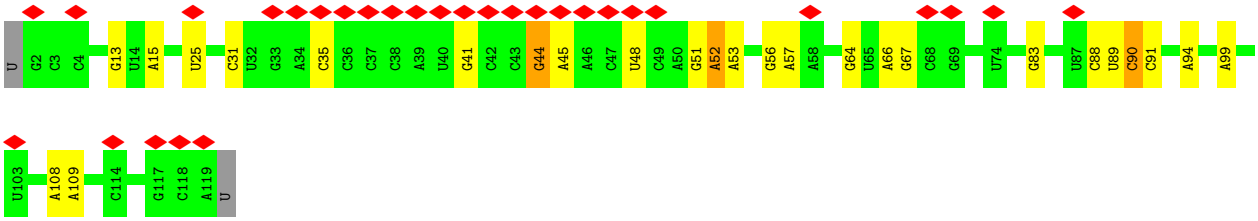
3 Residue-property plots (i)

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: 5S rRNA

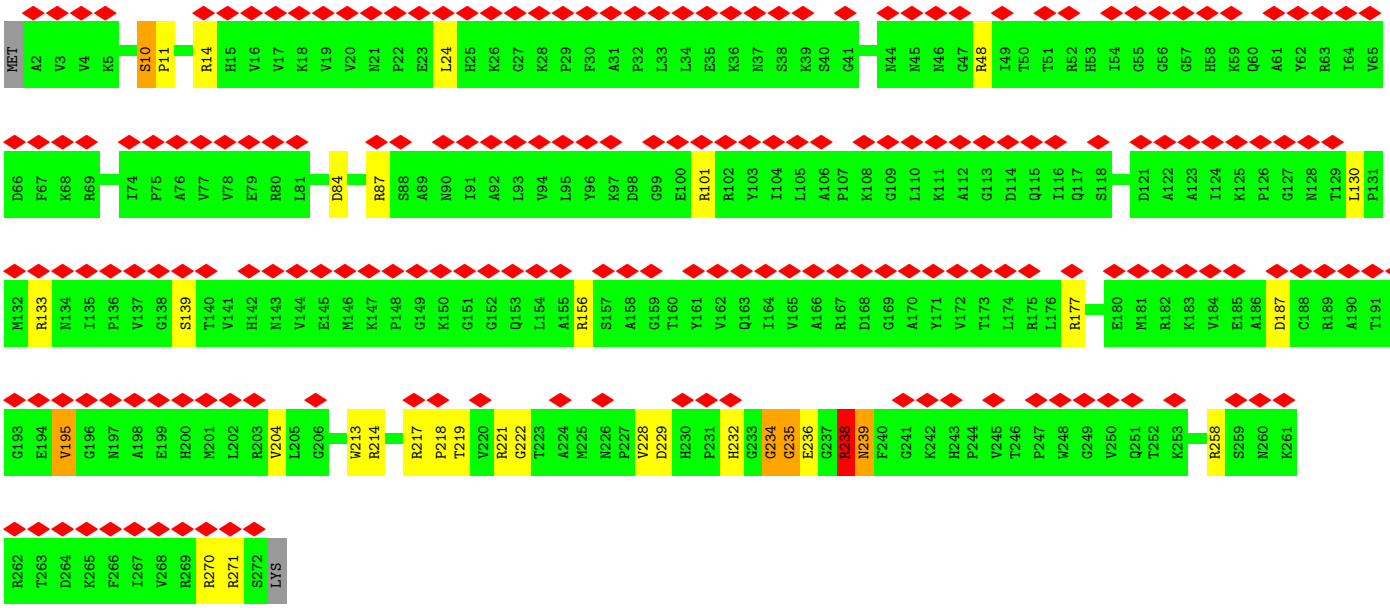
Chain O:





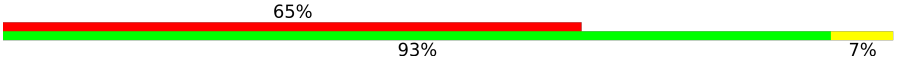
• Molecule 2: 50S ribosomal protein L2

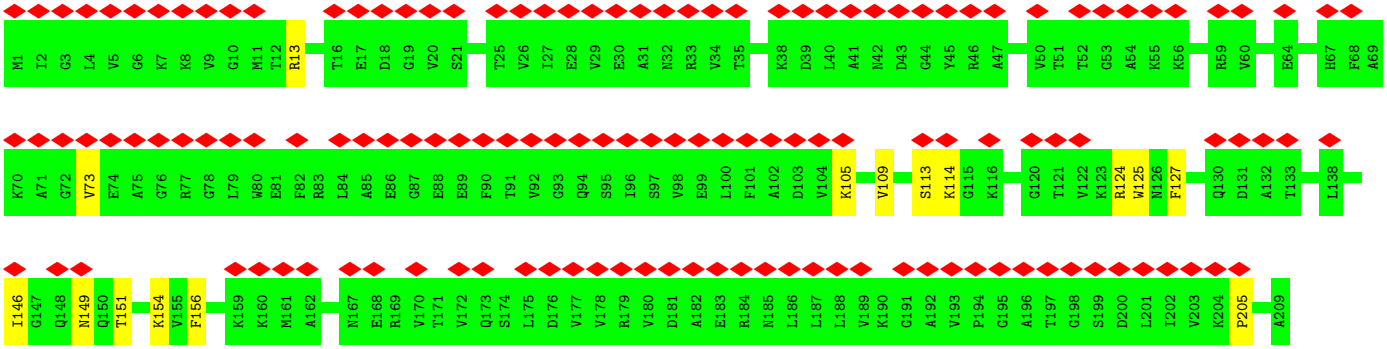
Chain P:



• Molecule 3: 50S ribosomal protein L3

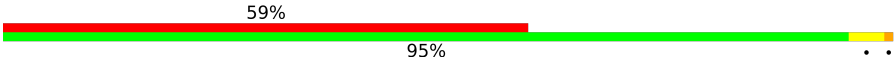
Chain Q:

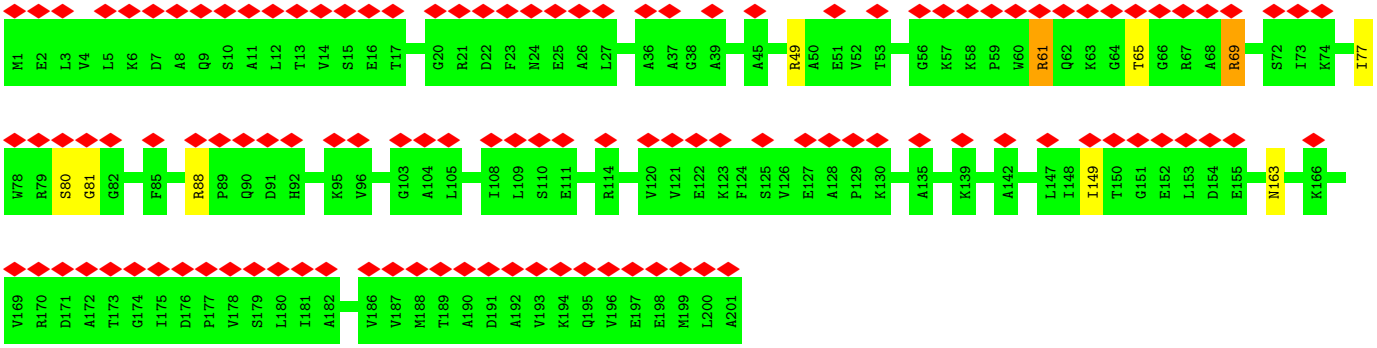




• Molecule 4: 50S ribosomal protein L4

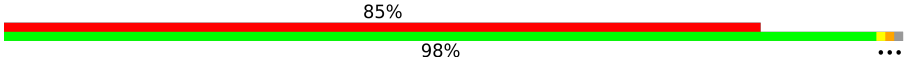
Chain R:

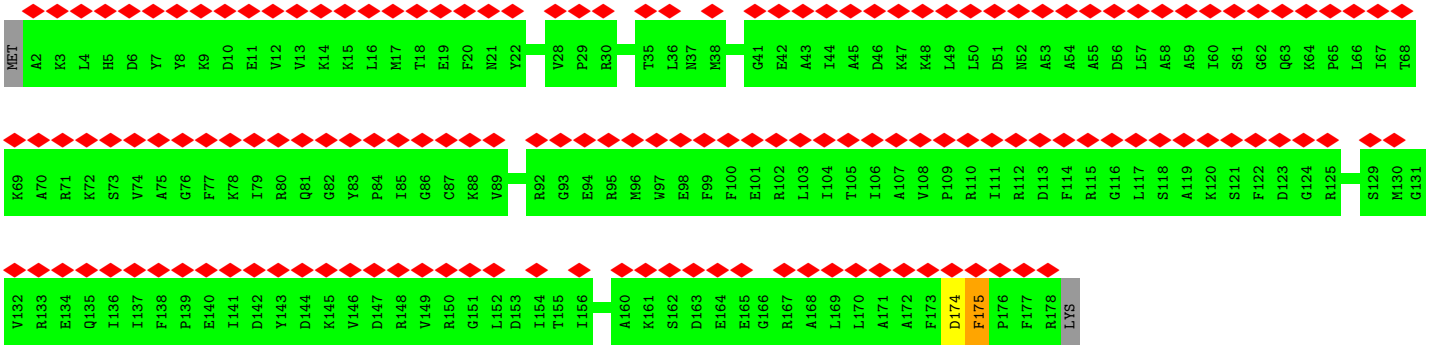




• Molecule 5: 50S ribosomal protein L5

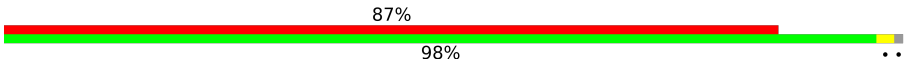
Chain S:

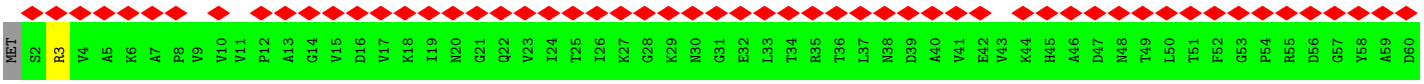


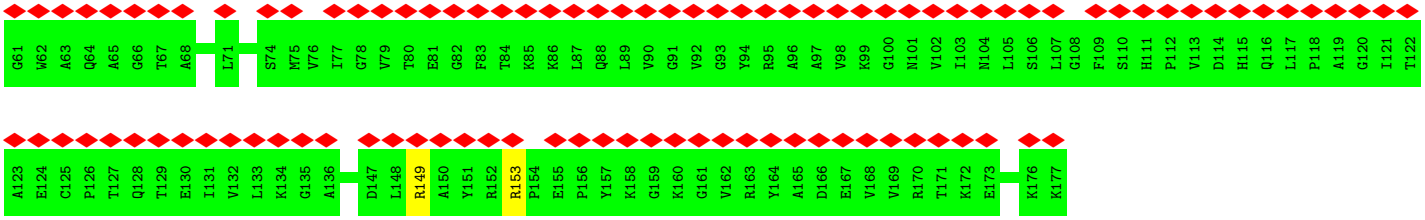


• Molecule 6: 50S ribosomal protein L6

Chain T:

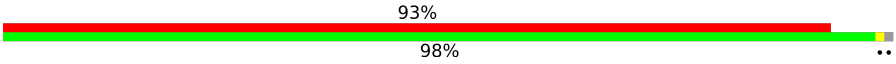


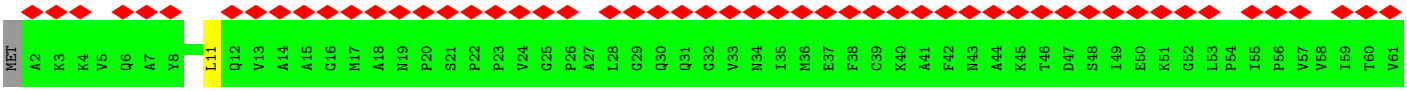




• Molecule 7: 50S ribosomal protein L11

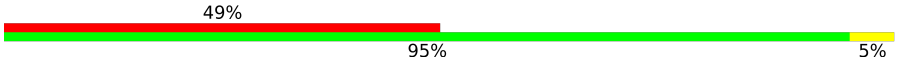
Chain V:

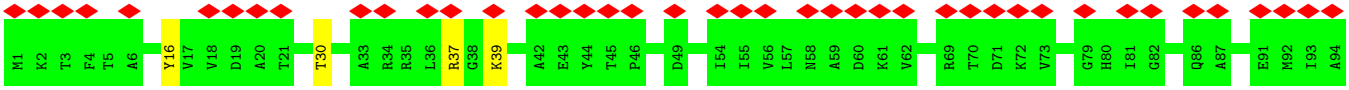




• Molecule 8: 50S ribosomal protein L13

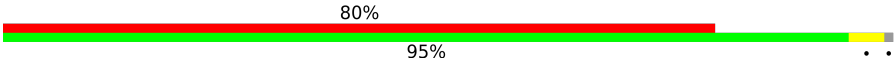
Chain W:

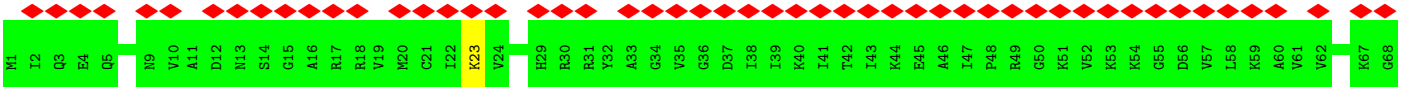


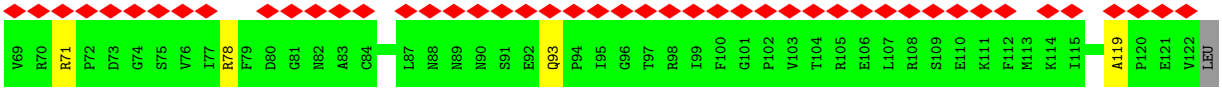


• Molecule 9: 50S ribosomal protein L14

Chain X:

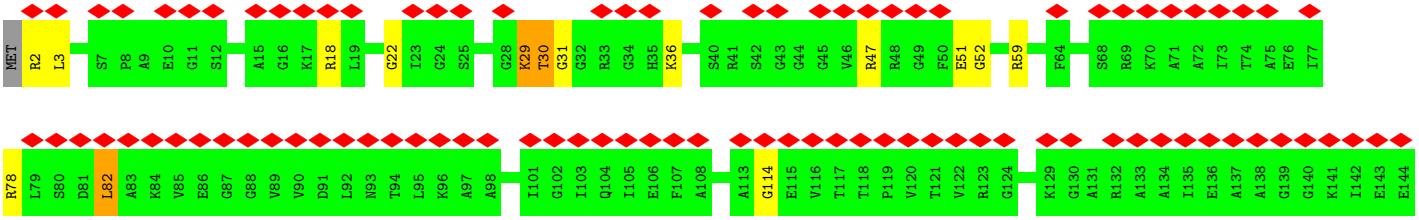






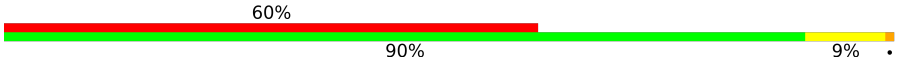
• Molecule 10: 50S ribosomal protein L15

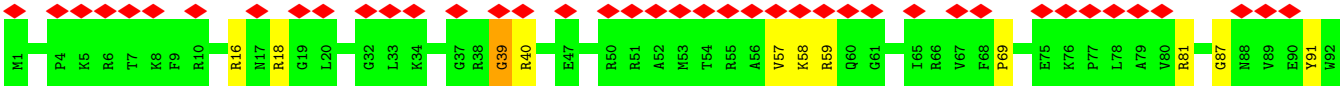
Chain Y:

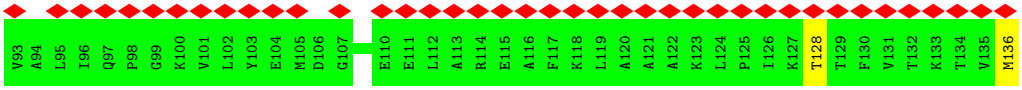


• Molecule 11: 50S ribosomal protein L16

Chain Z:

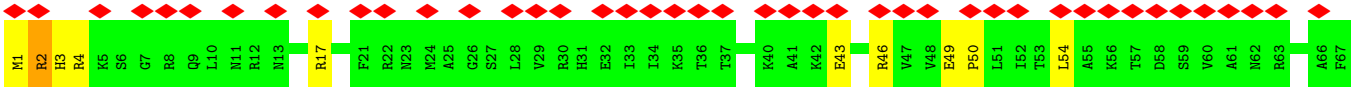






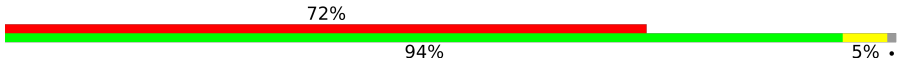
• Molecule 12: 50S ribosomal protein L17

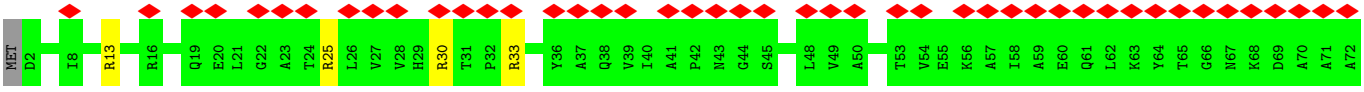
Chain a:

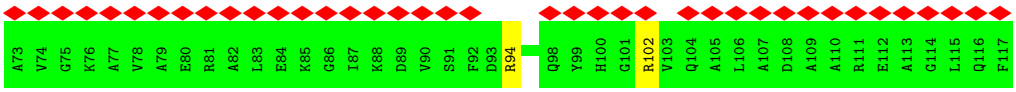


• Molecule 13: 50S ribosomal protein L18

Chain b:

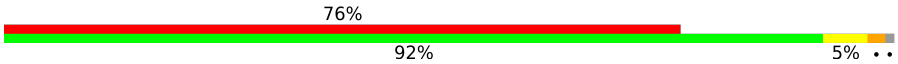


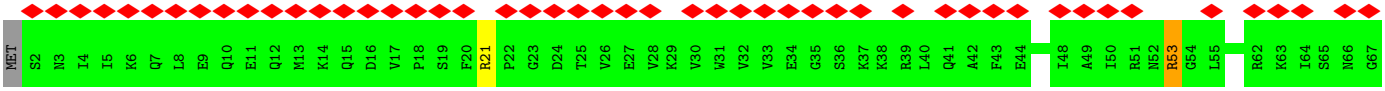


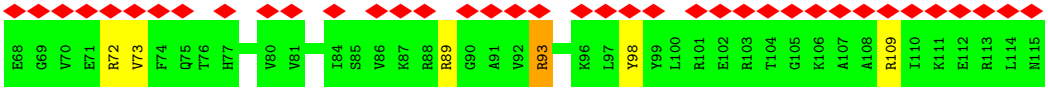


• Molecule 14: 50S ribosomal protein L19

Chain c:

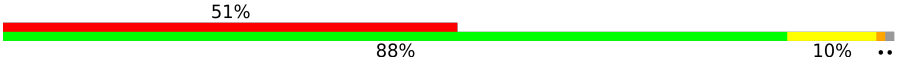


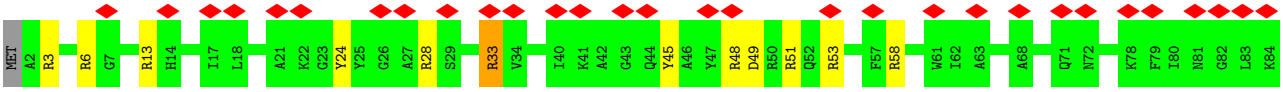


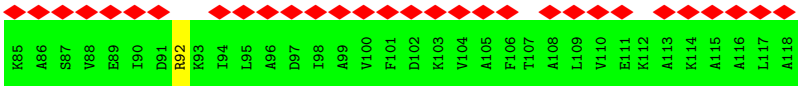


• Molecule 15: 50S ribosomal protein L20

Chain d:

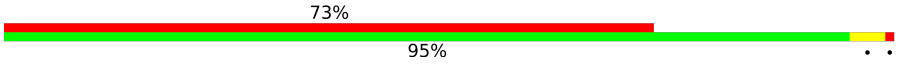


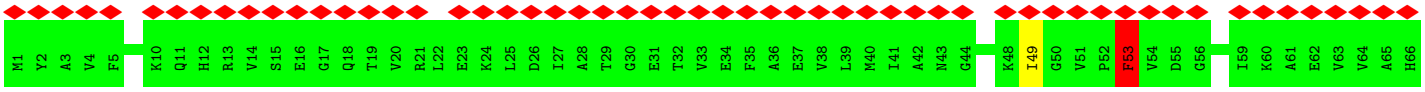


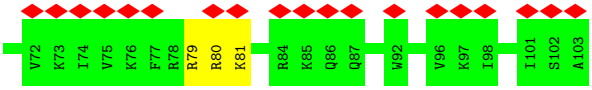


• Molecule 16: 50S ribosomal protein L21

Chain e:

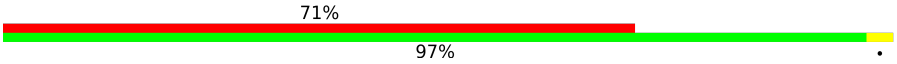


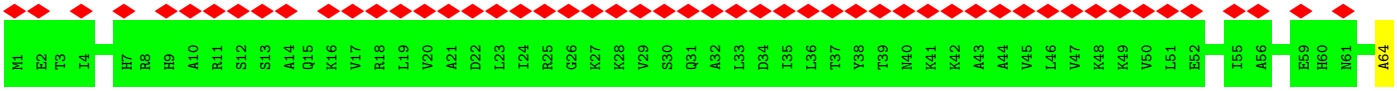


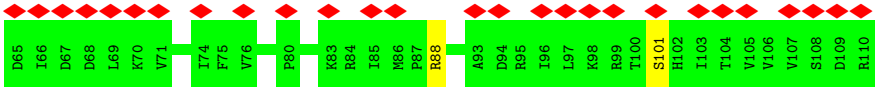


• Molecule 17: 50S ribosomal protein L22

Chain f:

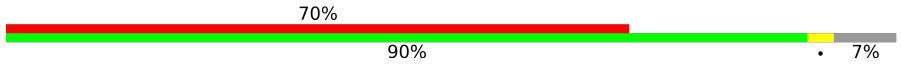


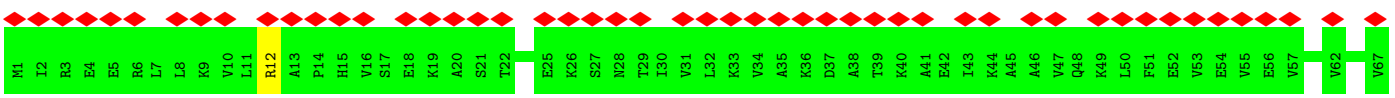


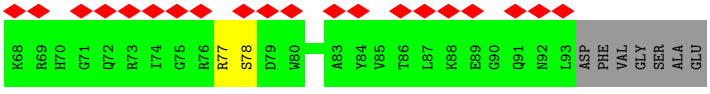


• Molecule 18: 50S ribosomal protein L23

Chain g:

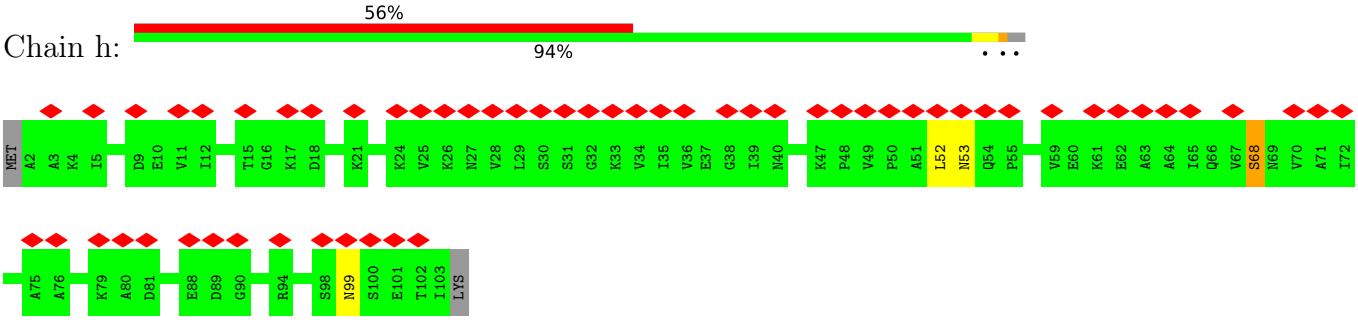






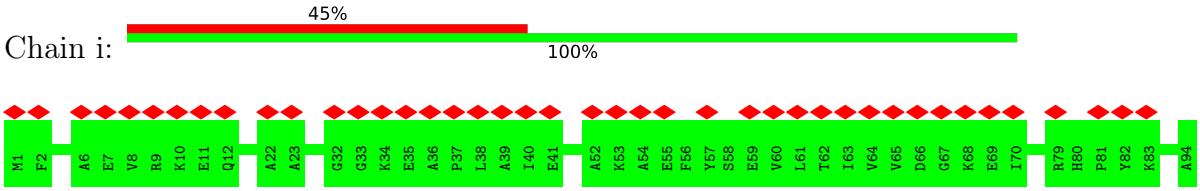
• Molecule 19: 50S ribosomal protein L24

Chain h:



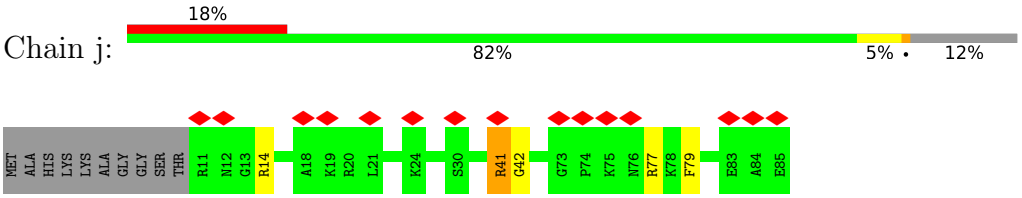
• Molecule 20: 50S ribosomal protein L25

Chain i:



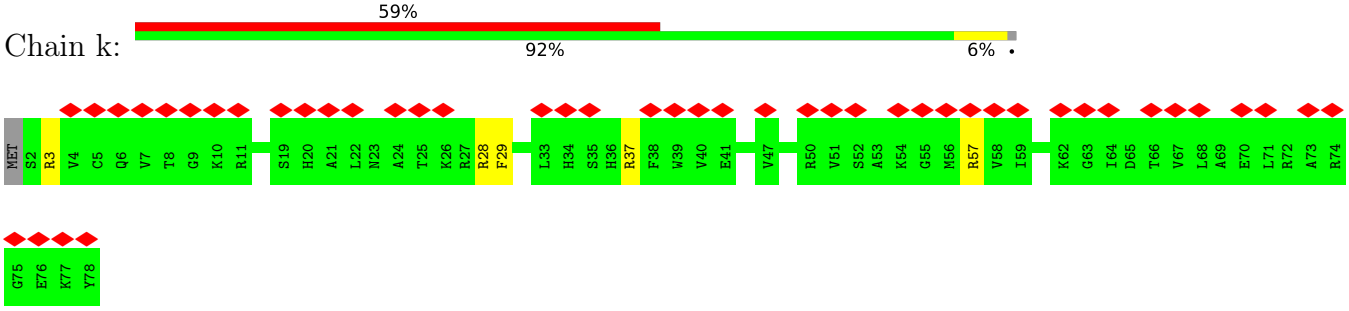
• Molecule 21: 50S ribosomal protein L27

Chain j:



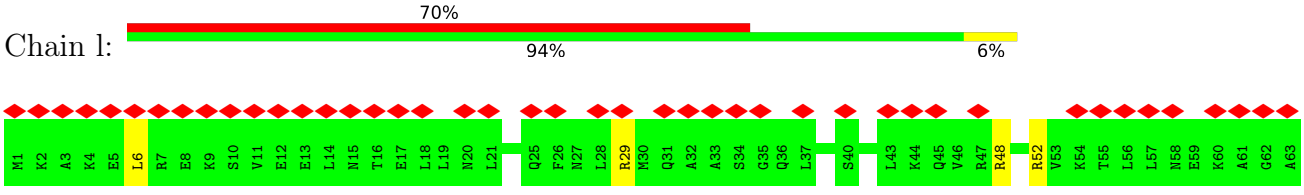
• Molecule 22: 50S ribosomal protein L28

Chain k:



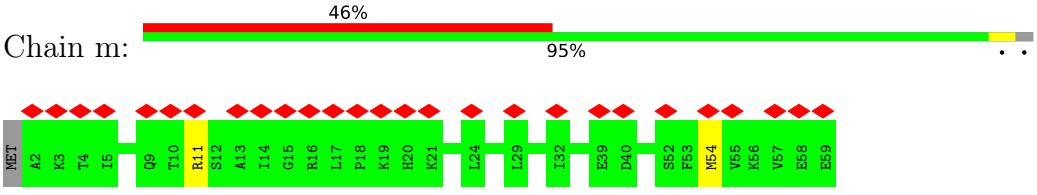
• Molecule 23: 50S ribosomal protein L29

Chain l:



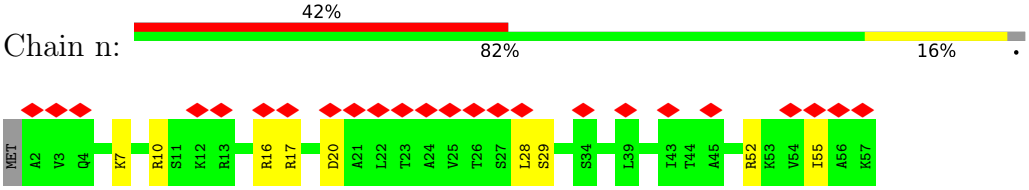
• Molecule 24: 50S ribosomal protein L30

Chain m:



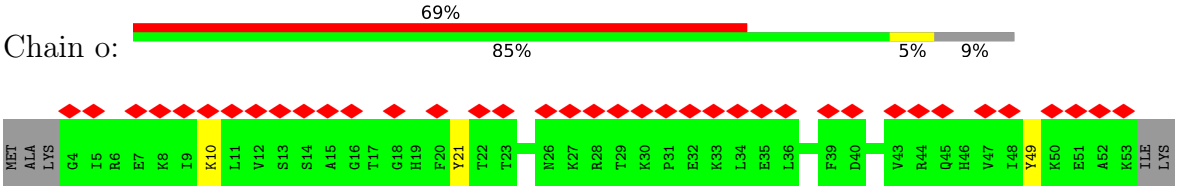
• Molecule 25: 50S ribosomal protein L32

Chain n:



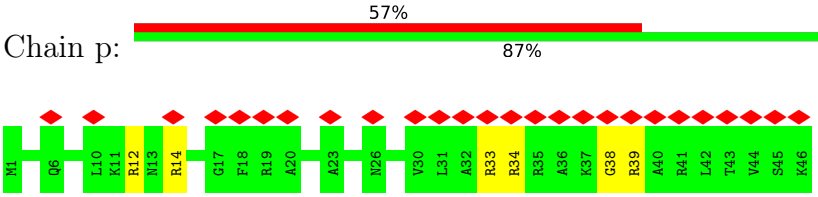
• Molecule 26: 50S ribosomal protein L33

Chain o:



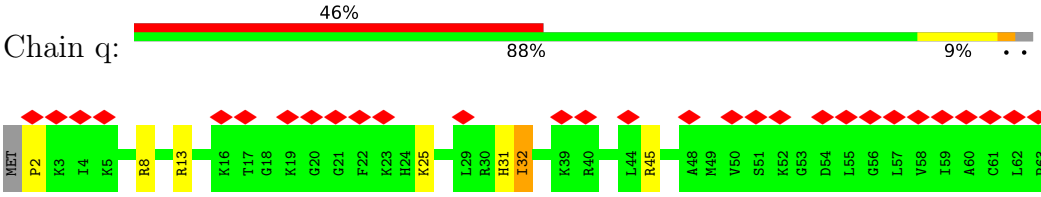
• Molecule 27: 50S ribosomal protein L34

Chain p:



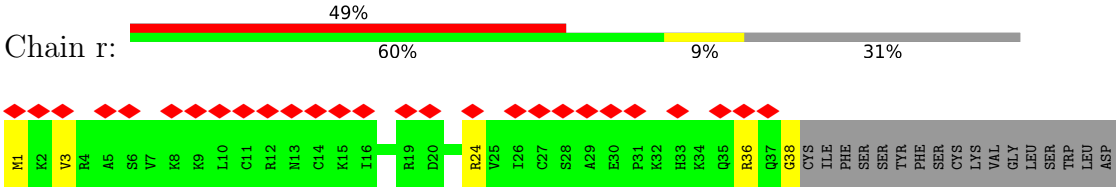
• Molecule 28: 50S ribosomal protein L35

Chain q:



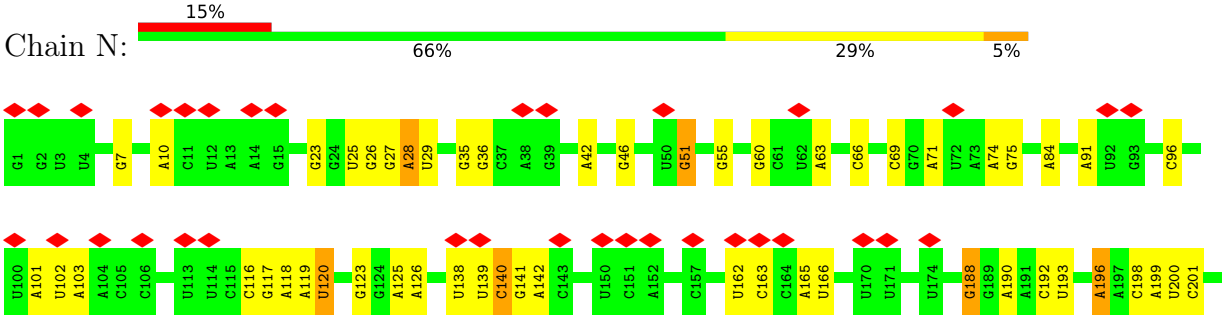
• Molecule 29: 50S ribosomal protein L36

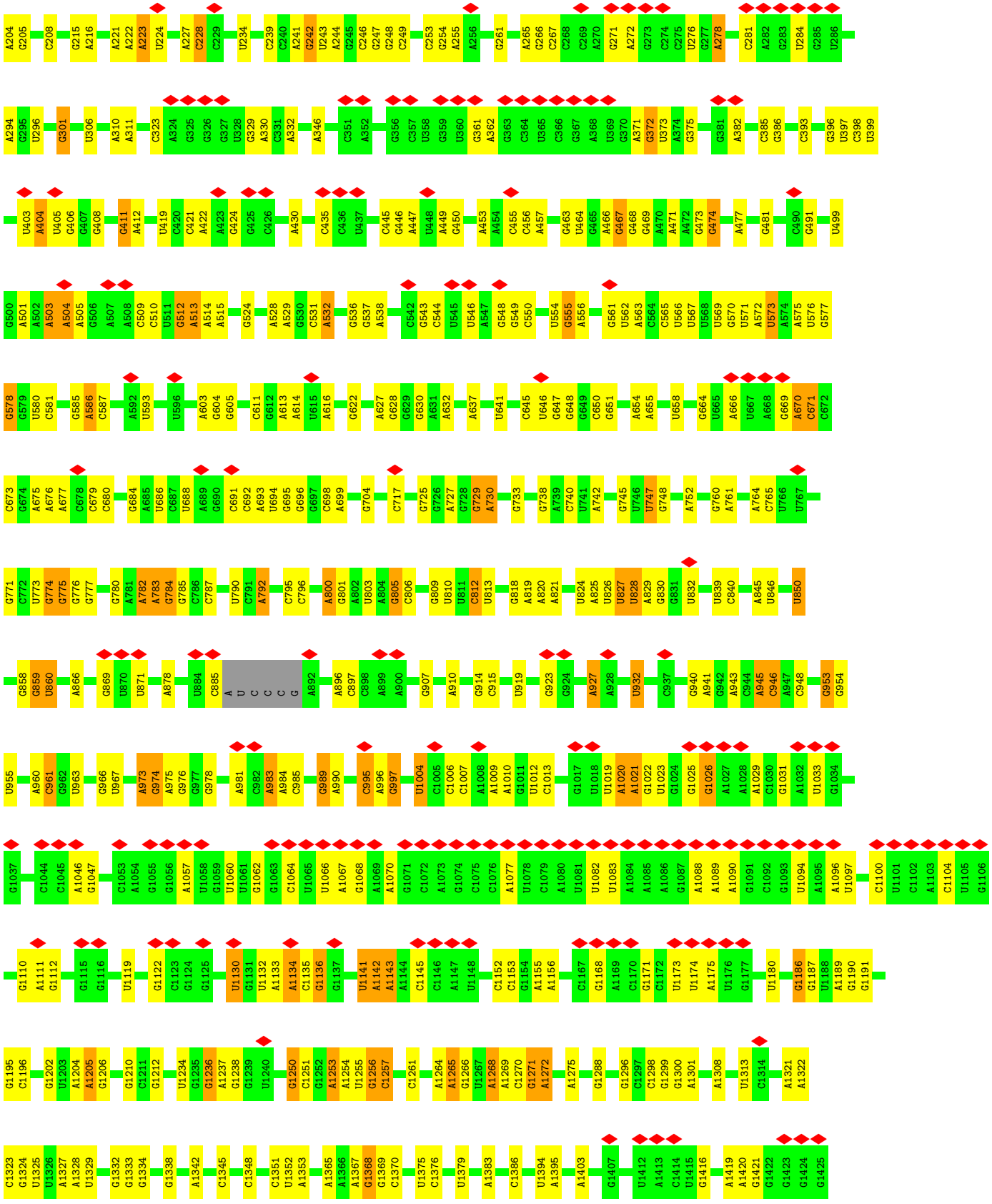
Chain r:

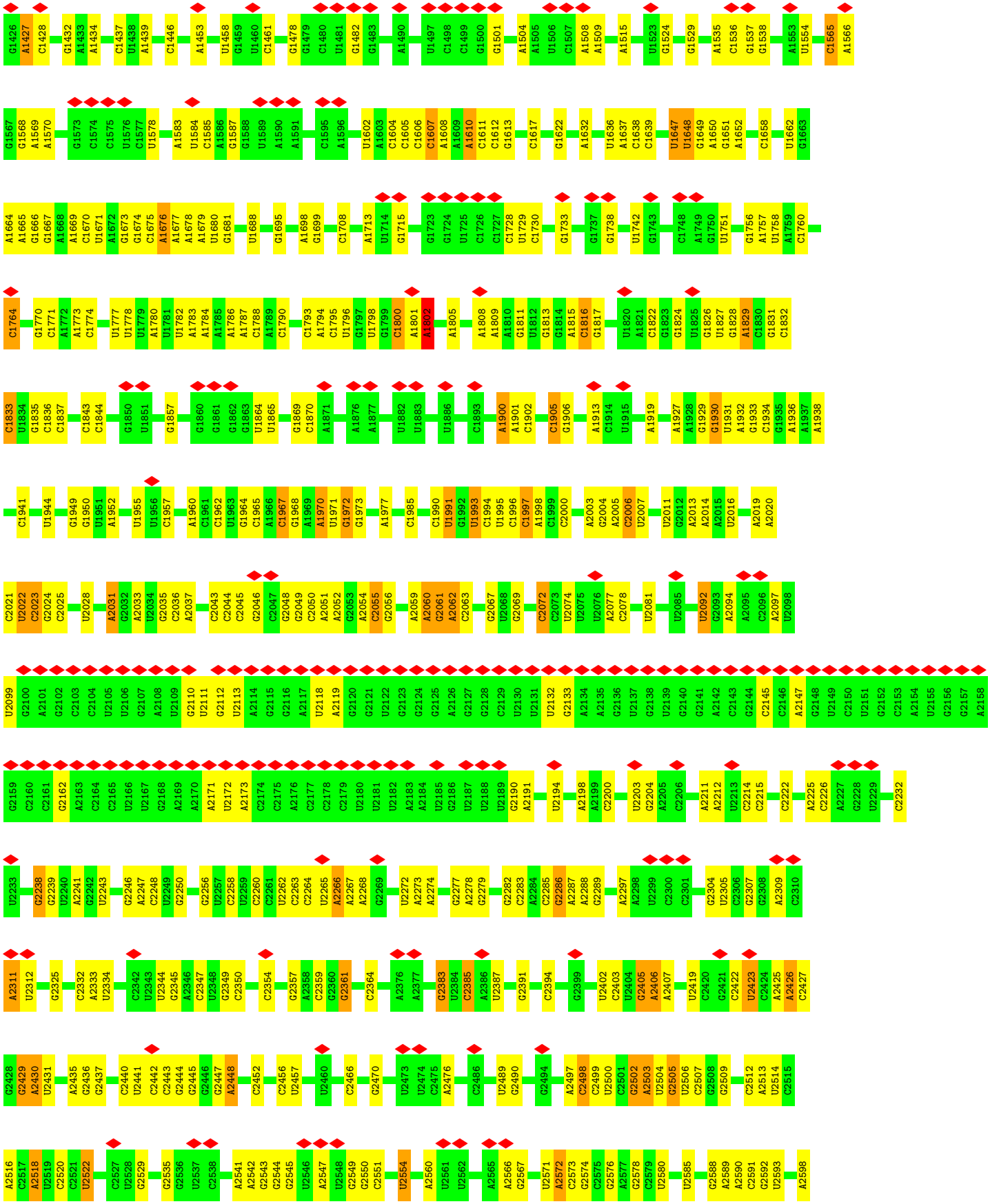


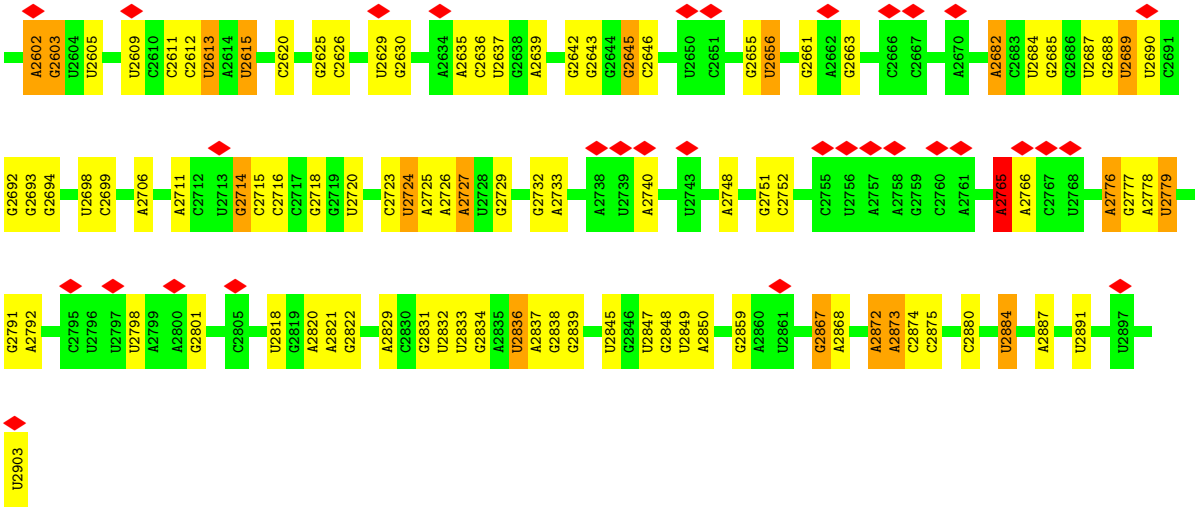
• Molecule 30: 23S rRNA

Chain N:



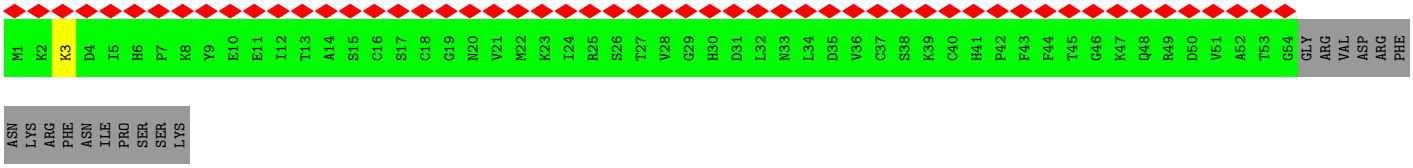

A204 G205 C208 G215 A216 A221 A222 A223 U224 A227 C228 C229 U234 C239 C240 A241 G242 U243 A244 G245 C246 G247 G248 C249 C253 G254 A255 A256 G261 A265 G266 C267 C268 C269 A270 G271 A272 G273 C274 C275 U276 G277 A278 C281 A282 G283 U284 G285 U286
A294 G295 U296 G301 U306 A310 A311 C323 A324 G325 G326 G327 U328 G329 A330 C331 A332 A346 C351 A352 G356 C357 U358 G359 U360 G361 A362 G363 C364 U365 C366 G367 A368 U369 G370 A371 G372 U373 A374 G375 G381 A382 C385 G386 C393 G396 U397 C398 U399
U403 A404 U405 G406 G407 G408 G411 A412 U419 C420 C421 A422 A423 G424 G425 C426 A430 C435 C436 U437 C445 G446 A447 U448 A449 G450 A453 A454 C455 C456 A457 G463 U464 G465 A466 G467 G468 G469 A470 A471 A472 G473 G474 A477 G481 C490 G491 U499
G500 A501 A502 A503 A504 A505 G506 A507 A508 C509 C510 U511 G512 A513 A514 A515 G524 A528 A529 G530 C531 A532 G536 G537 A538 C542 G543 C544 U545 U546 A547 G548 G549 C550 U554 G585 A556 G561 U562 A563 C564 C565 U566 U567 U568 U569 G570 U571 A572 U573 A574 A575 U576 G577
G578 G579 U580 C581 G585 A586 C587 A592 U593 U596 A603 G604 G605 C611 G612 A613 A614 U615 A616 G622 A627 G628 G629 G630 A631 A632 A637 U641 C645 U646 G647 G648 G649 C650 G651 A654 A655 U658 G664 U665 A666 U667 A668 G669 A670 C671 C672
C673 G674 A675 A676 A677 C678 C679 C680 G684 A685 U686 C687 U688 A689 G690 C691 C692 A693 U694 G695 G696 G697 C698 A699 G704 C717 G725 G726 A727 G728 G729 A730 G733 G738 A739 C740 U741 A742 G745 U746 U747 G748 A752 G760 A761 A764 C765 U766 U767
G771 C772 U773 G774 G775 G776 G777 G780 A781 A782 A783 G784 G785 C786 C787 U790 C791 A792 C795 C796 A800 G801 A802 U803 A804 G805 C806 G809 U810 U811 C812 U813 G818 A819 A820 A821 U824 A825 U826 U827 U828 A829 G830 G831 U832 U839 C840 A845 U846 U850
G858 G859 U860 A866 G869 U870 U871 A878 U884 C885 A U C C C G A892 A896 C897 C898 A899 A900 C907 A910 G914 C915 U919 G923 G924 A927 A928 U932 C937 G940 A941 G942 A943 C944 A945 C946 A947 C948 G953 G954
U955 A960 C961 G962 U963 G966 U967 A973 G974 A975 G976 G977 G978 A981 C982 A983 A984 C985 G989 A990 C995 A996 G997 U1004 C1005 C1006 C1007 A1008 A1009 A1010 G1011 U1012 C1013 G1017 U1018 U1019 A1020 A1021 G1022 U1023 G1024 G1025 G1026 A1027 A1028 A1029 C1030 G1031 A1032 U1033 G1034
G1037 C1044 C1045 A1046 G1047 C1053 A1054 G1055 G1056 A1057 U1058 G1059 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075 C1076 A1077 U1078 C1079 A1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 A1089 A1090 G1091 C1092 G1093 U1094 A1095 A1096 U1097 C1100 U1101 C1102 A1103 C1104 U1105 G1106
G1110 A1111 G1112 G1115 G1116 U1119 G1122 C1123 G1124 G1125 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 U1141 A1142 A1143 A1144 C1145 C1146 A1147 U1148 C1152 C1153 G1154 A1155 A1156 C1167 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 U1180 G1186 G1187 U1188 A1189 G1190 G1191
G1195 C1196 G1202 U1203 A1204 A1205 G1206 G1210 C1211 G1212 U1234 G1235 G1236 A1237 G1238 G1239 U1240 G1250 C1251 G1252 A1253 A1254 U1255 G1256 C1257 C1261 A1264 A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 A1275 G1288 G1296 C1297 C1298 G1299 G1300 A1301 A1308 U1313 C1314 A1321 A1322
C1323 G1324 U1325 U1326 A1327 A1328 U1329 G1332 G1333 G1334 G1338 A1342 C1345 C1348 C1351 U1352 A1353 A1365 A1366 A1367 G1368 G1369 C1370 U1375 C1376 U1379 A1383 C1386 U1394 A1395 A1403 G1407 U1412 A1413 C1414 U1415 G1416 A1419 A1420 G1421 G1422 G1423 G1424 G1425





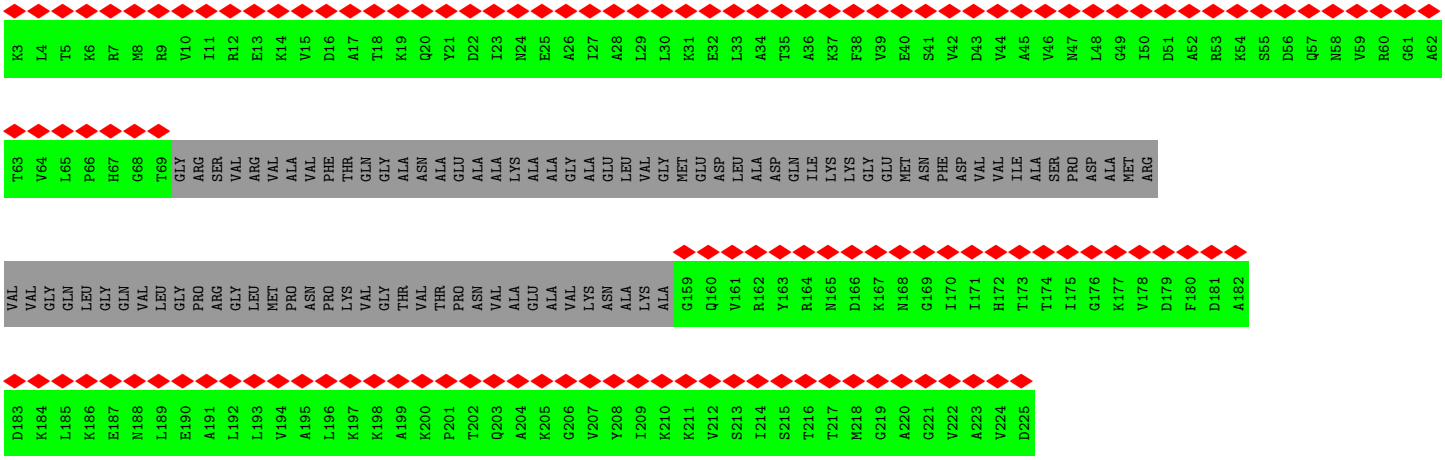
• Molecule 31: 50S ribosomal protein L31

Chain L:



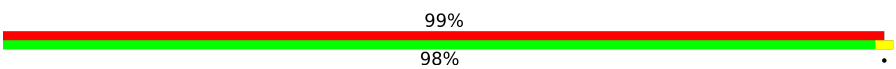
• Molecule 32: 50S ribosomal protein L1

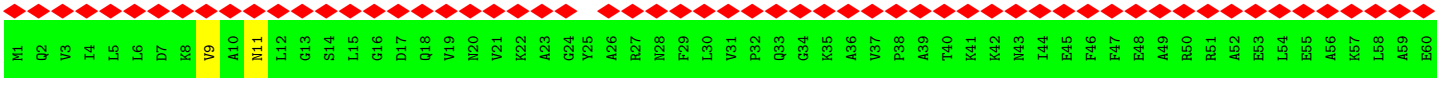
Chain C:

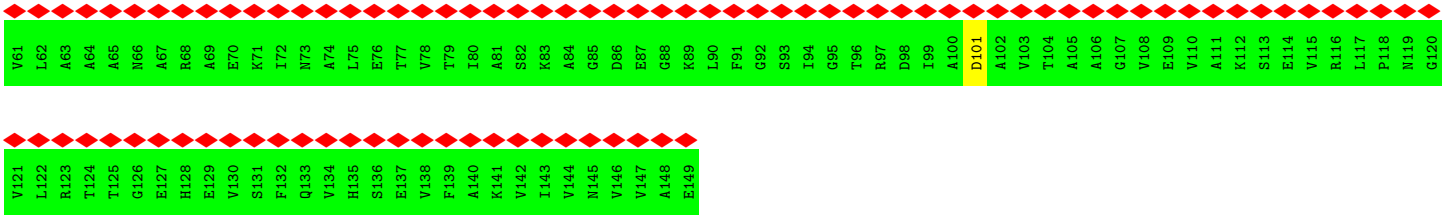


• Molecule 33: 50S ribosomal protein L9

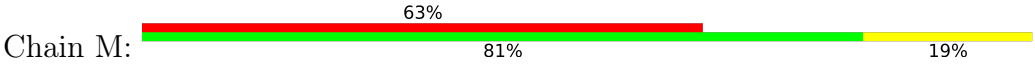
Chain U:

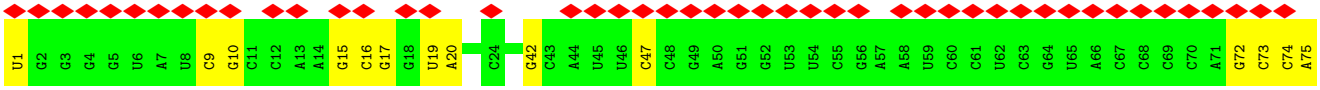




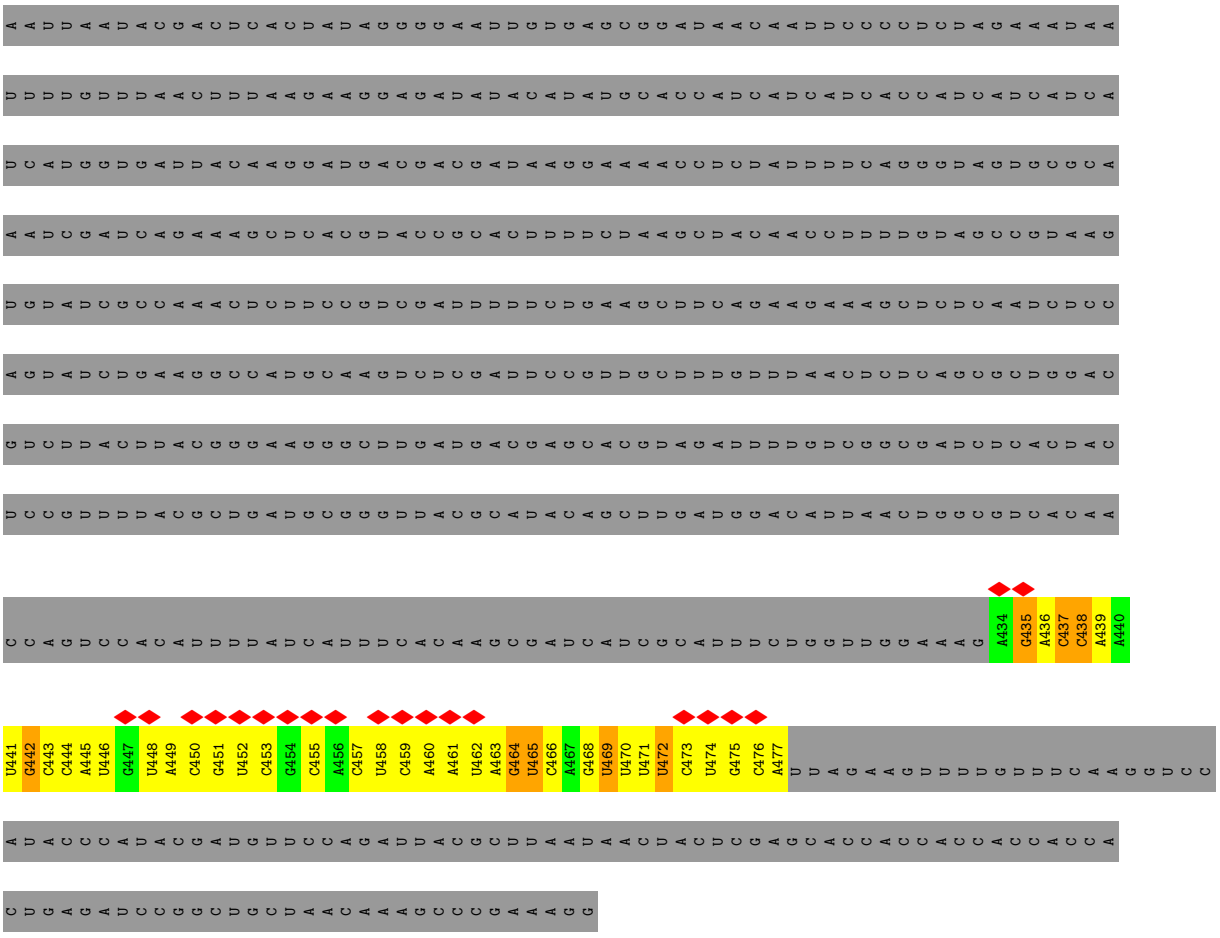


• Molecule 34: P-site tRNA

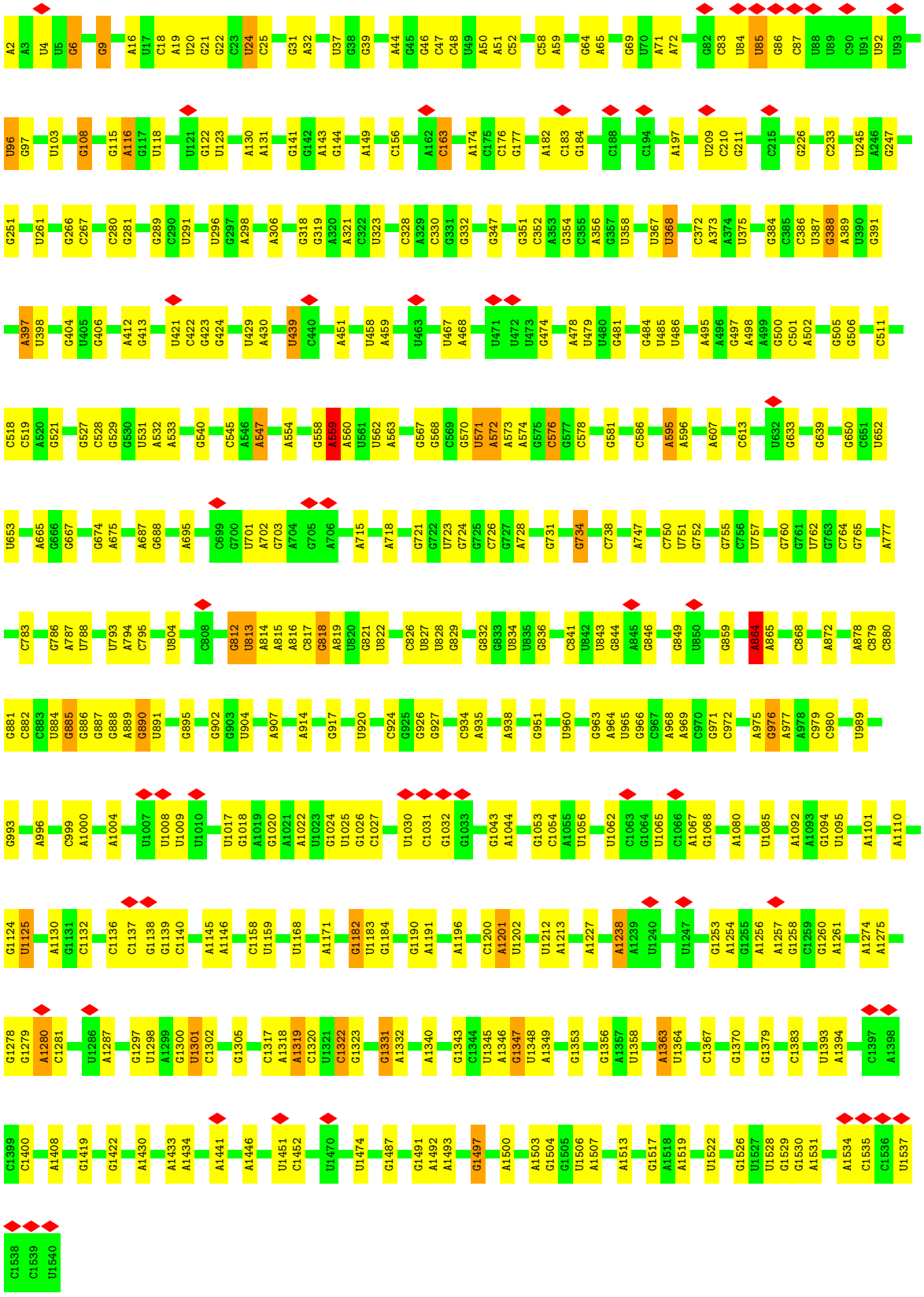




• Molecule 35: mRNA

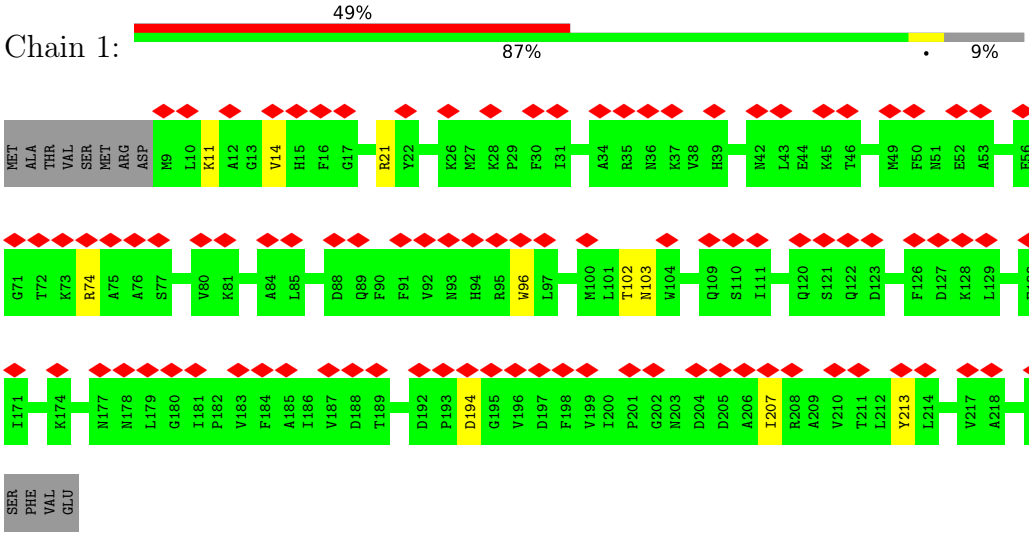


• Molecule 36: 16S rRNA



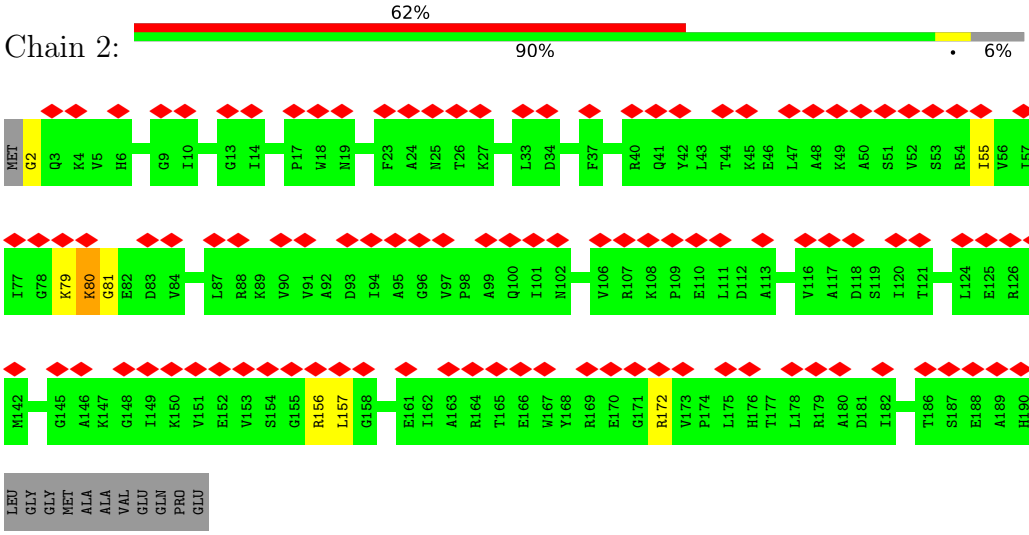
• Molecule 37: 30S ribosomal protein S2

Chain 1:



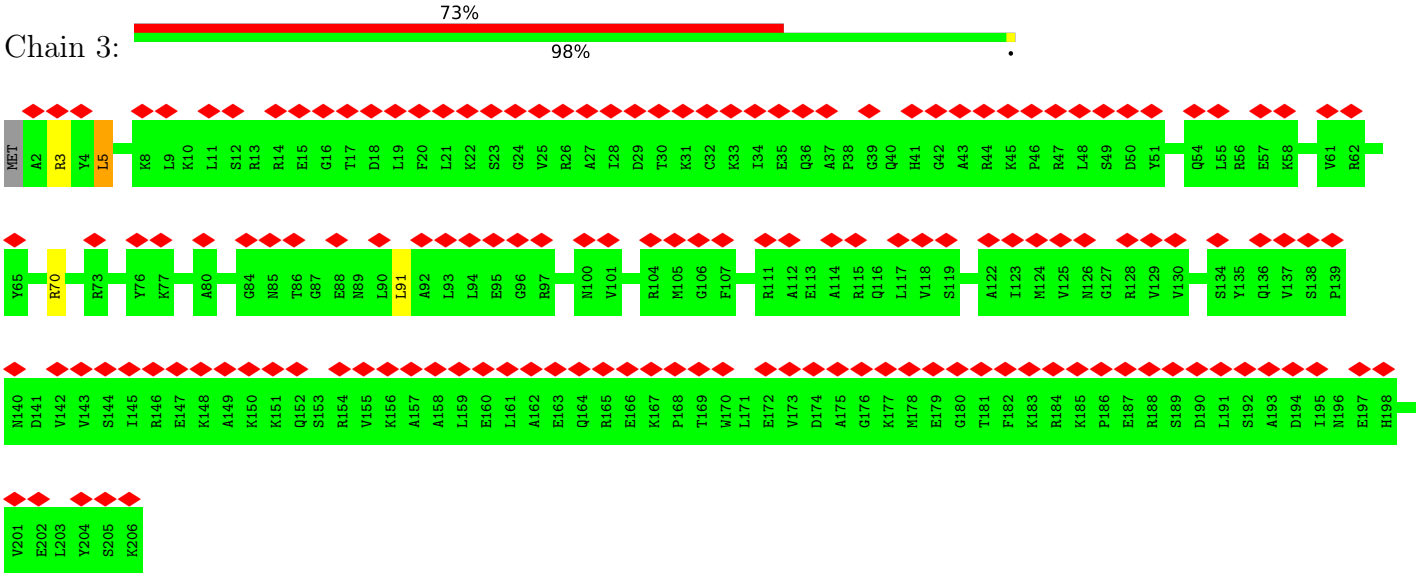
• Molecule 38: 30S ribosomal protein S3

Chain 2:



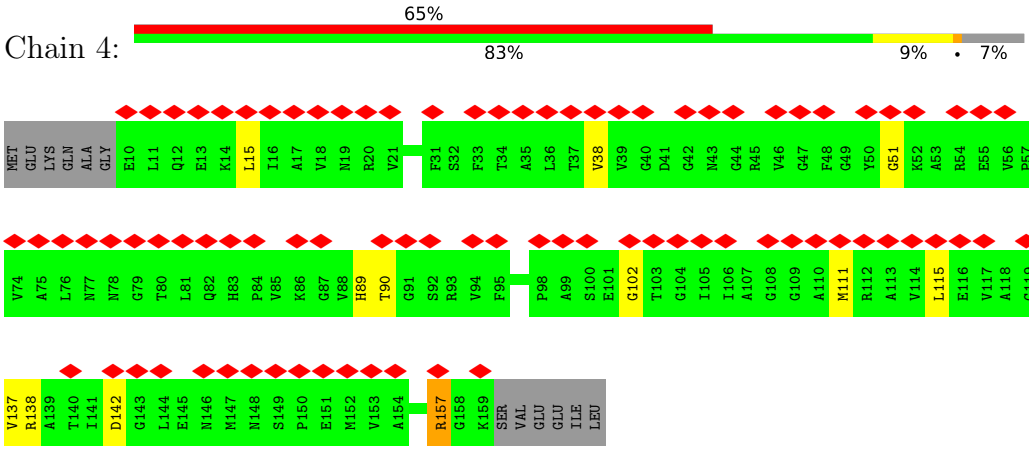
• Molecule 39: 30S ribosomal protein S4

Chain 3:



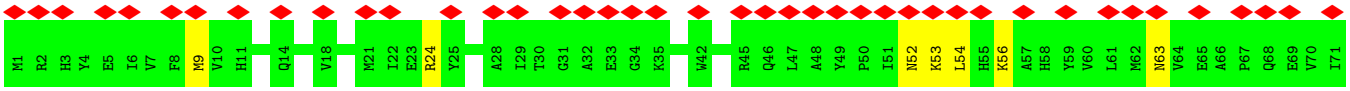
• Molecule 40: 30S ribosomal protein S5

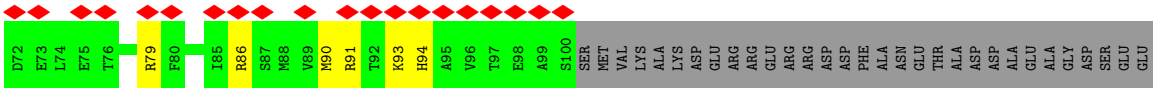
Chain 4:



• Molecule 41: 30S ribosomal protein S6, non-modified isoform

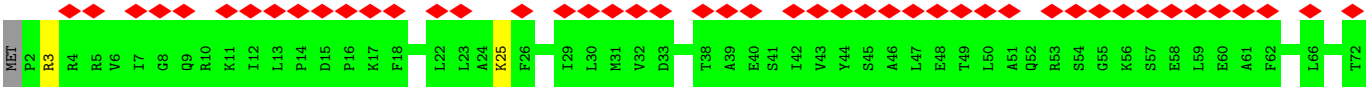
Chain 5:

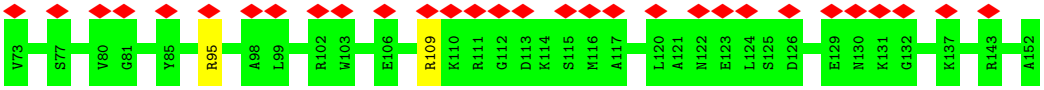




• Molecule 42: 30S ribosomal protein S7

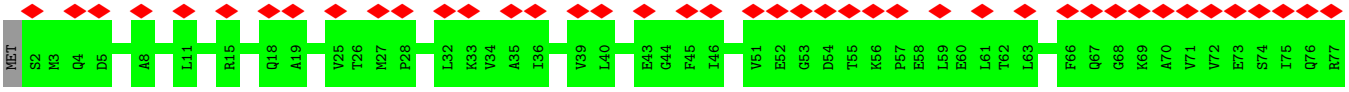
Chain 6:

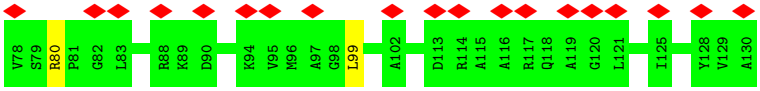




• Molecule 43: 30S ribosomal protein S8

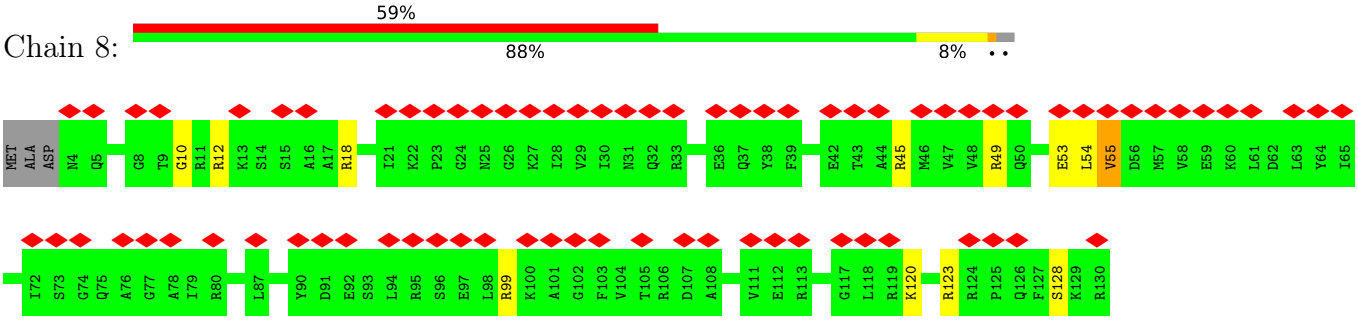
Chain 7:





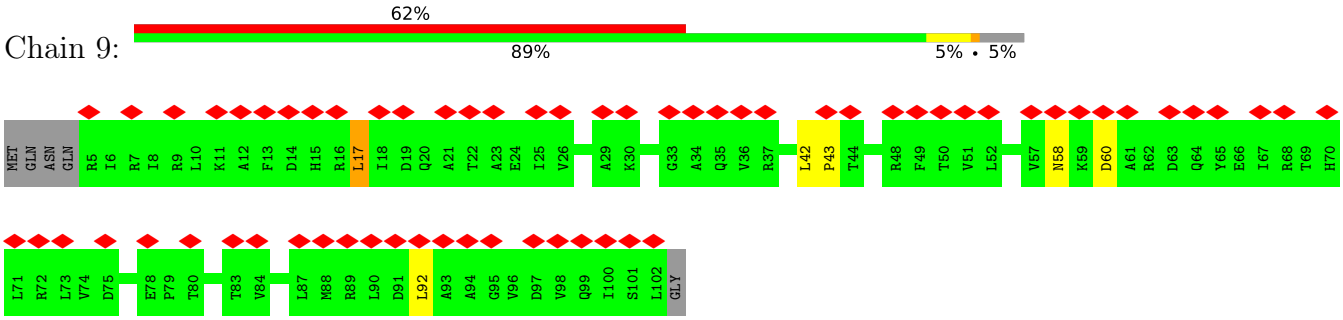
• Molecule 44: 30S ribosomal protein S9

Chain 8:



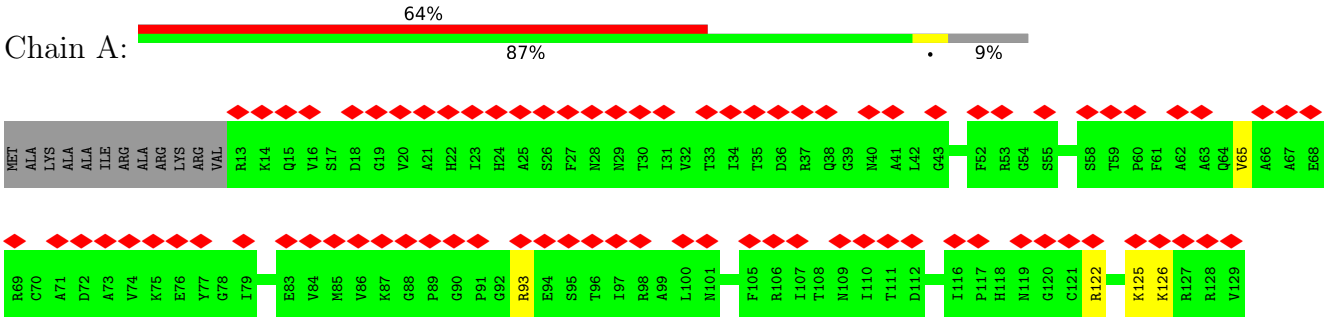
• Molecule 45: 30S ribosomal protein S10

Chain 9:



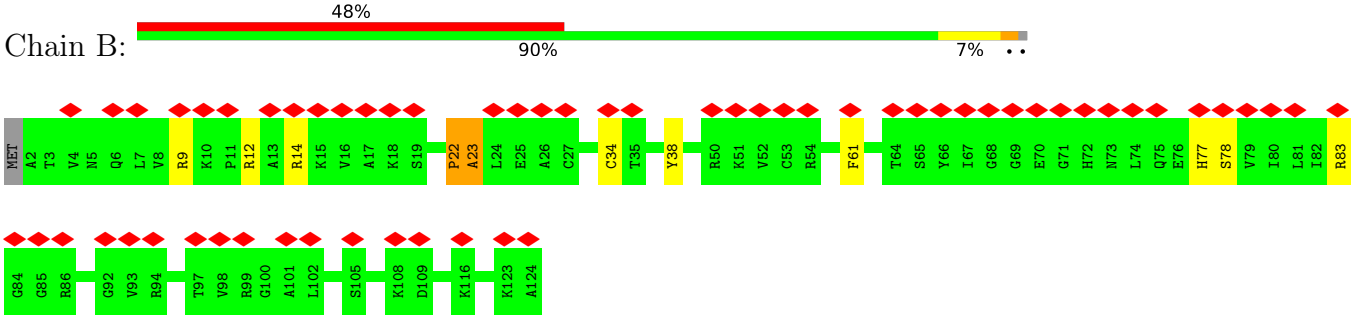
• Molecule 46: 30S ribosomal protein S11

Chain A:



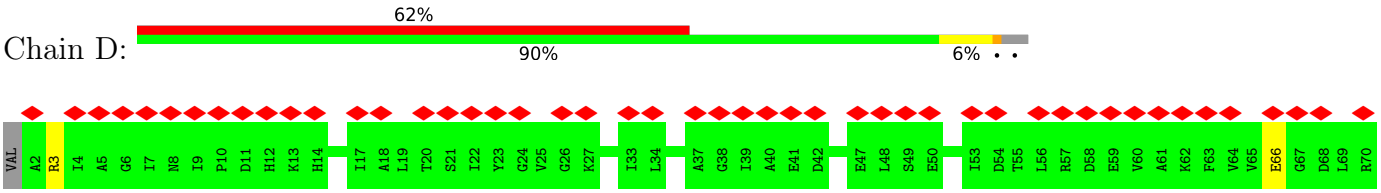
• Molecule 47: 30S ribosomal protein S12

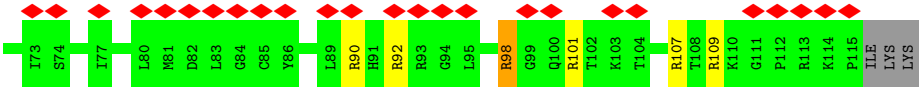
Chain B:



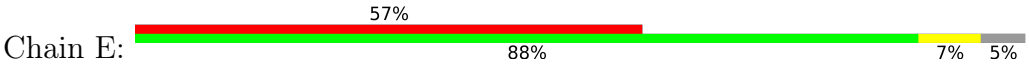
• Molecule 48: 30S ribosomal protein S13

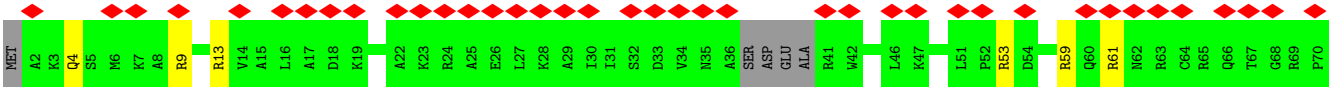
Chain D:

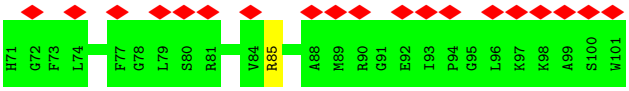




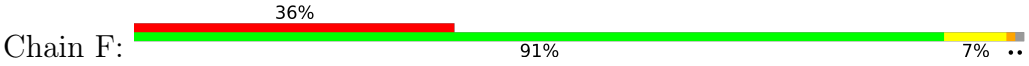
• Molecule 49: 30S ribosomal protein S14

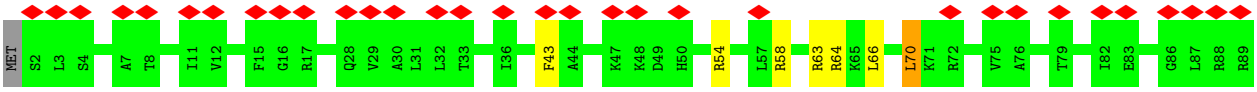




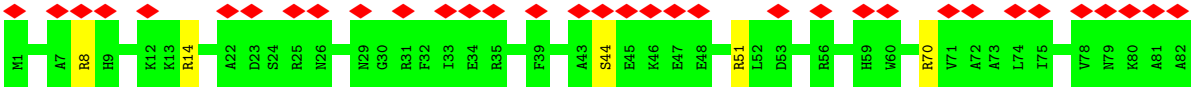


• Molecule 50: 30S ribosomal protein S15

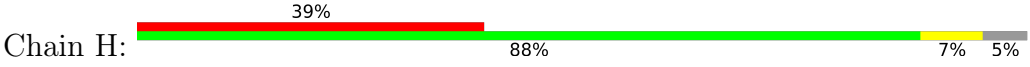


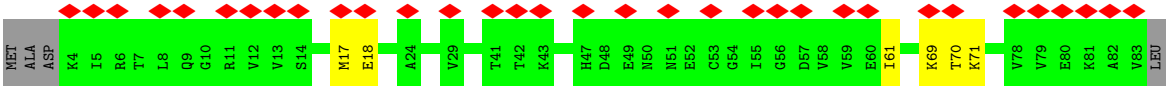


• Molecule 51: 30S ribosomal protein S16

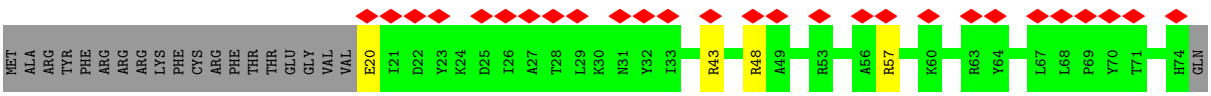


• Molecule 52: 30S ribosomal protein S17

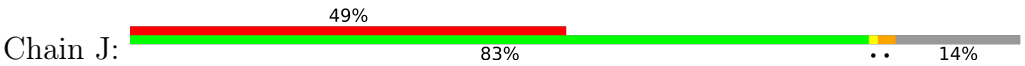


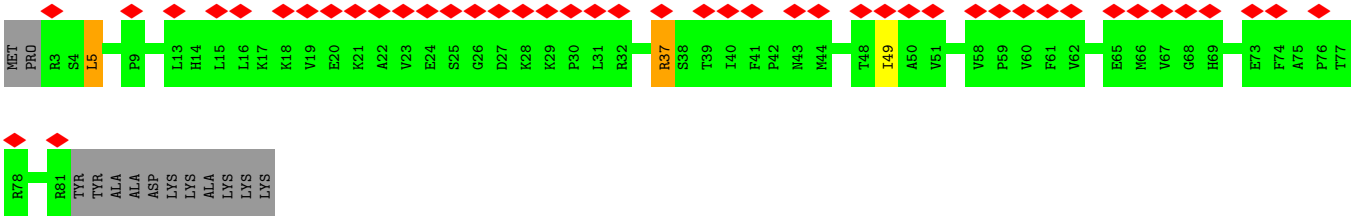


• Molecule 53: 30S ribosomal protein S18



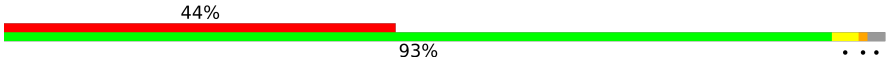
• Molecule 54: 30S ribosomal protein S19

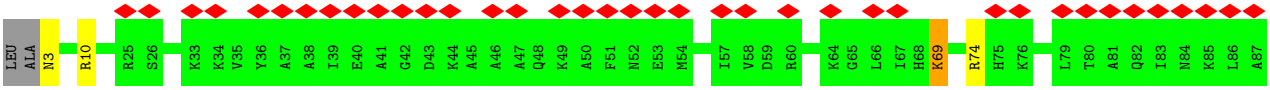




• Molecule 55: 30S ribosomal protein S20

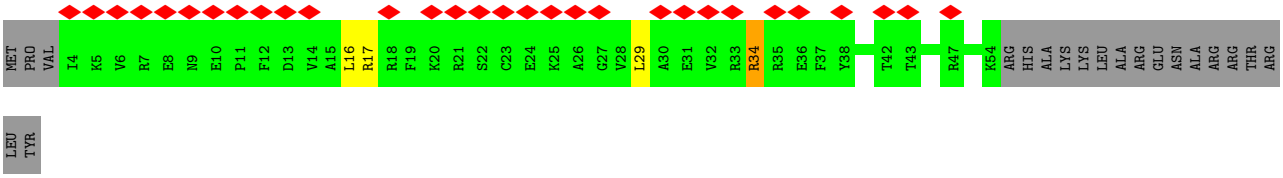
Chain K:





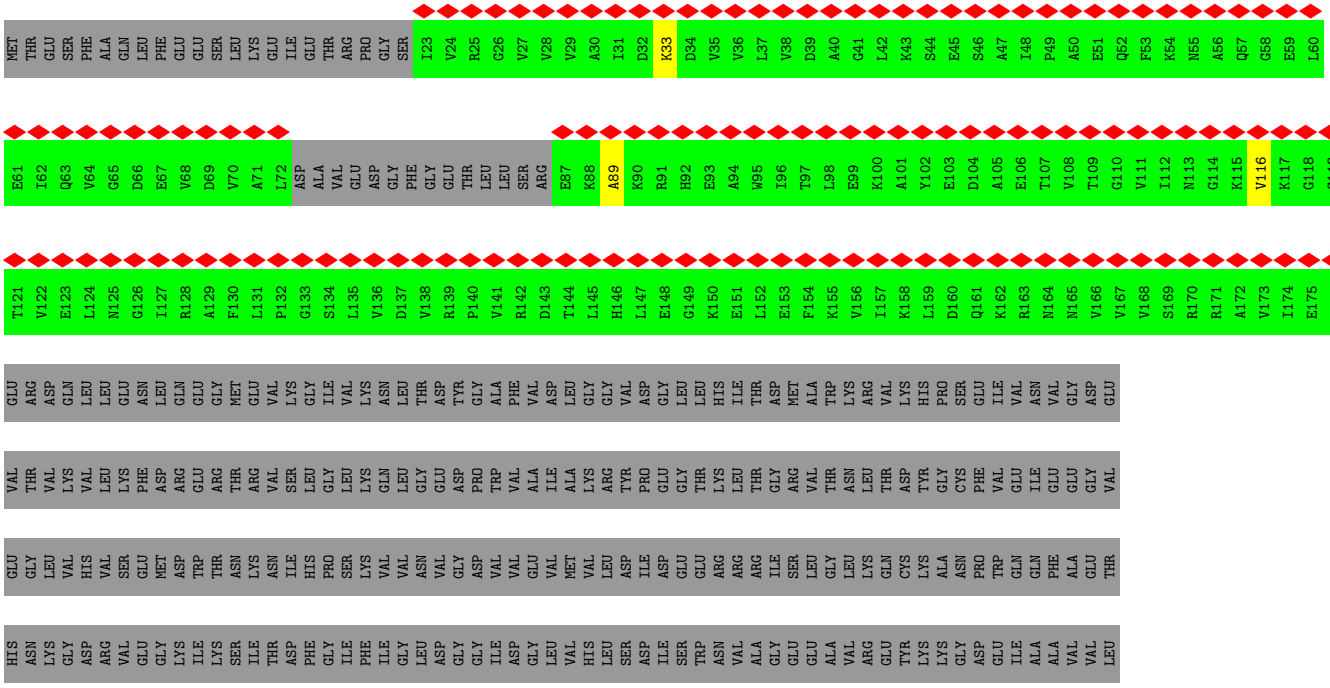
• Molecule 56: 30S ribosomal protein S21

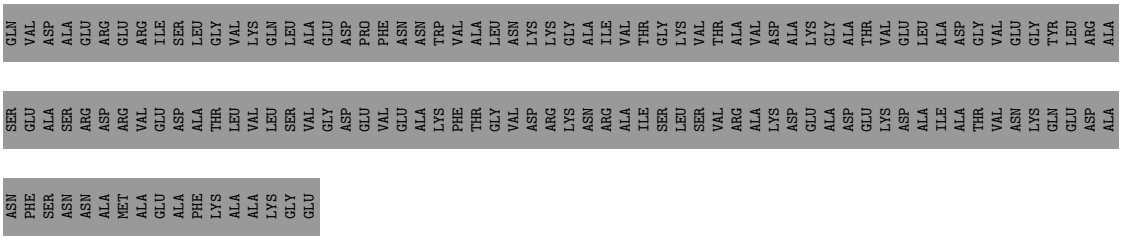
Chain s:



• Molecule 57: 30S ribosomal protein S1

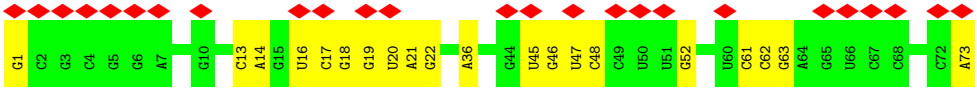
Chain t:





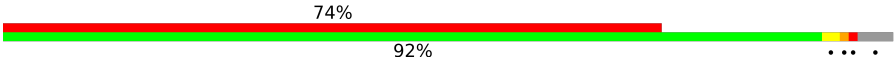
- Molecule 58: A-site tRNA

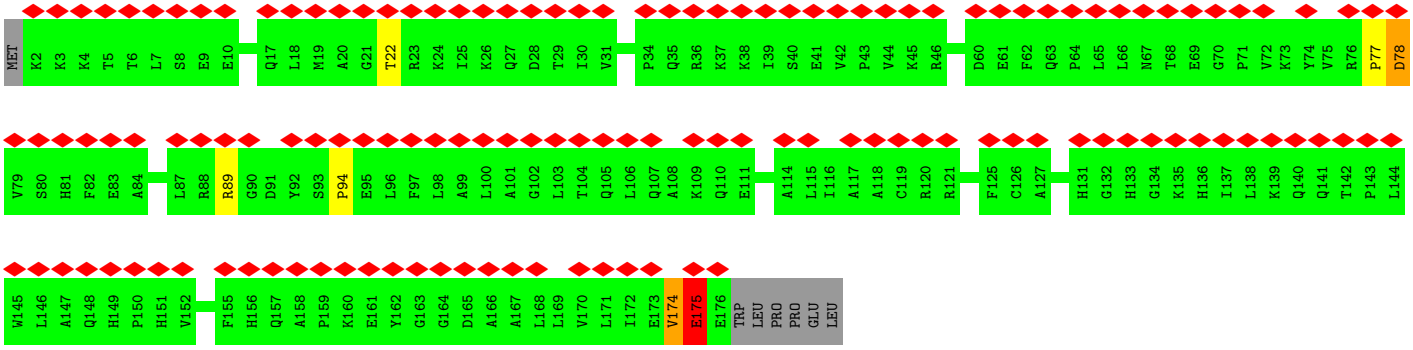
Chain u:



- Molecule 59: UPF0115 protein YfcN

Chain v:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32412	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	42.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.070	Depositor
Minimum map value	-0.867	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	847.19995, 847.19995, 847.19995	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.412, 1.412, 1.412	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, K

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	O	0.80	1/2828 (0.0%)	0.88	6/4410 (0.1%)
2	P	1.41	22/2121 (1.0%)	1.32	27/2852 (0.9%)
3	Q	1.18	3/1585 (0.2%)	1.13	8/2134 (0.4%)
4	R	0.97	3/1571 (0.2%)	1.02	9/2113 (0.4%)
5	S	0.67	0/1420	0.85	0/1907
6	T	0.67	0/1342	0.83	4/1816 (0.2%)
7	V	0.53	0/1045	0.66	0/1410
8	W	1.10	3/1151 (0.3%)	1.10	7/1551 (0.5%)
9	X	1.15	0/947	1.20	5/1268 (0.4%)
10	Y	1.30	3/1053 (0.3%)	1.38	12/1403 (0.9%)
11	Z	1.13	2/1092 (0.2%)	1.19	6/1460 (0.4%)
12	a	1.27	3/973 (0.3%)	1.30	9/1301 (0.7%)
13	b	0.84	2/901 (0.2%)	1.08	8/1209 (0.7%)
14	c	1.09	3/927 (0.3%)	1.19	7/1240 (0.6%)
15	d	1.32	4/959 (0.4%)	1.37	15/1278 (1.2%)
16	e	1.08	2/828 (0.2%)	1.08	3/1107 (0.3%)
17	f	1.02	1/864 (0.1%)	1.09	1/1156 (0.1%)
18	g	0.91	0/744	1.01	1/994 (0.1%)
19	h	0.82	1/787 (0.1%)	0.89	0/1051
20	i	0.79	0/765	0.87	0/1025
21	j	1.21	2/575 (0.3%)	1.29	7/762 (0.9%)
22	k	1.09	1/634 (0.2%)	1.15	5/848 (0.6%)
23	l	0.71	0/509	1.04	4/677 (0.6%)
24	m	0.87	0/452	1.08	2/605 (0.3%)
25	n	1.16	2/449 (0.4%)	1.42	7/599 (1.2%)
26	o	1.31	7/416 (1.7%)	0.97	1/554 (0.2%)
27	p	1.38	3/379 (0.8%)	1.76	7/498 (1.4%)
28	q	1.15	1/512 (0.2%)	1.26	6/676 (0.9%)
29	r	1.16	1/302 (0.3%)	1.35	5/397 (1.3%)
30	N	1.24	517/69681 (0.7%)	1.04	339/108706 (0.3%)
31	L	0.60	0/422	0.78	0/565
32	C	0.28	0/1034	0.52	0/1387

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	U	0.29	0/1122	0.58	0/1515
34	M	0.63	3/1779 (0.2%)	0.83	2/2768 (0.1%)
35	x	0.87	8/1035 (0.8%)	1.12	6/1608 (0.4%)
36	0	0.97	133/36966 (0.4%)	0.93	105/57666 (0.2%)
37	1	0.81	2/1729 (0.1%)	0.93	4/2330 (0.2%)
38	2	0.85	1/1651 (0.1%)	0.95	4/2225 (0.2%)
39	3	0.76	0/1664	0.99	5/2227 (0.2%)
40	4	1.11	1/1118 (0.1%)	1.22	7/1504 (0.5%)
41	5	0.90	1/835 (0.1%)	1.03	3/1128 (0.3%)
42	6	0.66	0/1195	0.95	6/1602 (0.4%)
43	7	0.88	0/988	0.99	2/1326 (0.2%)
44	8	0.86	0/1033	1.13	6/1375 (0.4%)
45	9	0.74	0/796	1.01	3/1077 (0.3%)
46	A	0.86	1/892 (0.1%)	1.03	3/1205 (0.2%)
47	B	1.09	3/968 (0.3%)	1.22	7/1300 (0.5%)
48	D	0.85	1/886 (0.1%)	1.11	9/1186 (0.8%)
49	E	0.86	0/784	1.15	7/1043 (0.7%)
50	F	0.94	0/717	1.14	8/959 (0.8%)
51	G	0.94	0/658	1.16	5/884 (0.6%)
52	H	0.82	0/657	1.02	0/881
53	I	0.98	1/462 (0.2%)	1.10	2/621 (0.3%)
54	J	0.81	0/652	1.05	3/877 (0.3%)
55	K	0.89	0/670	1.06	3/888 (0.3%)
56	s	1.07	1/430 (0.2%)	1.25	4/570 (0.7%)
57	t	0.34	0/702	0.44	0/973
58	u	0.66	1/1744 (0.1%)	0.86	0/2716
59	v	0.68	3/1282 (0.2%)	0.67	3/1746 (0.2%)
All	All	1.08	747/162683 (0.5%)	1.02	718/243159 (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
2	P	0	3
3	Q	0	1
5	S	0	2
7	V	0	1
10	Y	0	2
11	Z	0	2
19	h	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	q	0	1
30	N	0	6
36	0	0	5
37	1	0	2
38	2	0	2
40	4	0	5
41	5	0	2
44	8	0	4
46	A	0	1
47	B	0	2
52	H	0	2
54	J	0	1
55	K	0	1
56	s	0	1
59	v	0	3
All	All	0	50

The worst 5 of 747 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2873	A	C6-N1	-20.36	1.21	1.35
30	N	2765	A	C6-N1	-18.72	1.22	1.35
30	N	2502	G	P-OP2	16.57	1.77	1.49
30	N	503	A	C6-N1	-15.29	1.24	1.35
30	N	1156	A	P-OP2	15.23	1.74	1.49

The worst 5 of 718 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	N	2506[A]	U	OP1-P-O3'	17.16	142.95	105.20
30	N	2506[B]	U	OP1-P-O3'	17.16	142.95	105.20
27	p	39	ARG	NE-CZ-NH1	16.07	128.33	120.30
27	p	39	ARG	NE-CZ-NH2	-14.77	112.92	120.30
34	M	73	C	O3'-P-O5'	14.34	131.24	104.00

There are no chirality outliers.

5 of 50 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	P	195	VAL	Peptide
2	P	234	GLY	Peptide

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Mol	Chain	Res	Type	Group
2	P	238	ARG	Peptide
3	Q	151	THR	Peptide
5	S	174	ASP	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
2	P	269/273 (98%)	247 (92%)	18 (7%)	4 (2%)	10 45
3	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	29 69
4	R	199/201 (99%)	191 (96%)	8 (4%)	0	100 100
5	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	25 65
6	T	174/177 (98%)	165 (95%)	9 (5%)	0	100 100
7	V	139/142 (98%)	112 (81%)	27 (19%)	0	100 100
8	W	140/142 (99%)	136 (97%)	4 (3%)	0	100 100
9	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	9 42
10	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	5 30
11	Z	134/136 (98%)	118 (88%)	11 (8%)	5 (4%)	3 25
12	a	118/127 (93%)	102 (86%)	14 (12%)	2 (2%)	9 42
13	b	114/117 (97%)	108 (95%)	6 (5%)	0	100 100
14	c	112/115 (97%)	104 (93%)	8 (7%)	0	100 100
15	d	115/118 (98%)	115 (100%)	0	0	100 100
16	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	15 54
17	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	17 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
18	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	6 35
19	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	7 37
20	i	92/94 (98%)	89 (97%)	3 (3%)	0	100 100
21	j	73/85 (86%)	71 (97%)	2 (3%)	0	100 100
22	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	12 48
23	l	61/63 (97%)	56 (92%)	5 (8%)	0	100 100
24	m	56/59 (95%)	52 (93%)	4 (7%)	0	100 100
25	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	8 38
26	o	48/55 (87%)	45 (94%)	3 (6%)	0	100 100
27	p	44/46 (96%)	40 (91%)	4 (9%)	0	100 100
28	q	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	9 43
29	r	36/55 (66%)	35 (97%)	1 (3%)	0	100 100
31	L	52/70 (74%)	44 (85%)	7 (14%)	1 (2%)	8 38
32	C	130/223 (58%)	123 (95%)	7 (5%)	0	100 100
33	U	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	11 46
37	1	216/239 (90%)	188 (87%)	27 (12%)	1 (0%)	29 69
38	2	204/218 (94%)	186 (91%)	16 (8%)	2 (1%)	15 54
39	3	203/206 (98%)	182 (90%)	21 (10%)	0	100 100
40	4	148/162 (91%)	116 (78%)	30 (20%)	2 (1%)	11 46
41	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1 16
42	6	149/152 (98%)	139 (93%)	10 (7%)	0	100 100
43	7	127/130 (98%)	121 (95%)	6 (5%)	0	100 100
44	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	9 43
45	9	96/103 (93%)	84 (88%)	9 (9%)	3 (3%)	4 27
46	A	115/129 (89%)	102 (89%)	13 (11%)	0	100 100
47	B	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	9 42
48	D	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	17 56
49	E	92/101 (91%)	77 (84%)	14 (15%)	1 (1%)	14 51
50	F	86/89 (97%)	81 (94%)	5 (6%)	0	100 100
51	G	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	12 48
52	H	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	3 24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
53	I	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	8 38
54	J	77/92 (84%)	73 (95%)	4 (5%)	0	100 100
55	K	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	13 49
56	s	49/71 (69%)	40 (82%)	9 (18%)	0	100 100
57	t	139/557 (25%)	115 (83%)	21 (15%)	3 (2%)	6 35
59	v	173/182 (95%)	168 (97%)	3 (2%)	2 (1%)	13 49
All	All	6111/6981 (88%)	5521 (90%)	528 (9%)	62 (1%)	20 54

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	239	ASN
10	Y	36	LYS
11	Z	58	LYS
16	e	53	PHE
25	n	55	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	P	216/218 (99%)	215 (100%)	1 (0%)	88 93
3	Q	164/164 (100%)	161 (98%)	3 (2%)	59 77
4	R	165/165 (100%)	161 (98%)	4 (2%)	49 69
5	S	145/150 (97%)	145 (100%)	0	100 100
6	T	137/138 (99%)	137 (100%)	0	100 100
7	V	109/110 (99%)	108 (99%)	1 (1%)	78 87
8	W	116/116 (100%)	116 (100%)	0	100 100
9	X	103/104 (99%)	103 (100%)	0	100 100
10	Y	102/103 (99%)	102 (100%)	0	100 100
11	Z	109/109 (100%)	108 (99%)	1 (1%)	78 87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	a	100/102 (98%)	97 (97%)	3 (3%)	41 63
13	b	86/87 (99%)	86 (100%)	0	100 100
14	c	98/100 (98%)	95 (97%)	3 (3%)	40 62
15	d	89/90 (99%)	88 (99%)	1 (1%)	73 84
16	e	84/84 (100%)	82 (98%)	2 (2%)	49 69
17	f	93/93 (100%)	93 (100%)	0	100 100
18	g	80/85 (94%)	80 (100%)	0	100 100
19	h	83/85 (98%)	82 (99%)	1 (1%)	71 83
20	i	78/78 (100%)	78 (100%)	0	100 100
21	j	56/63 (89%)	55 (98%)	1 (2%)	59 77
22	k	67/68 (98%)	67 (100%)	0	100 100
23	l	55/55 (100%)	55 (100%)	0	100 100
24	m	48/49 (98%)	48 (100%)	0	100 100
25	n	47/48 (98%)	46 (98%)	1 (2%)	53 72
26	o	45/49 (92%)	45 (100%)	0	100 100
27	p	38/38 (100%)	38 (100%)	0	100 100
28	q	51/52 (98%)	49 (96%)	2 (4%)	32 56
29	r	34/50 (68%)	34 (100%)	0	100 100
31	L	48/63 (76%)	48 (100%)	0	100 100
32	C	110/174 (63%)	110 (100%)	0	100 100
33	U	114/114 (100%)	113 (99%)	1 (1%)	78 87
37	1	179/198 (90%)	177 (99%)	2 (1%)	73 84
38	2	170/178 (96%)	169 (99%)	1 (1%)	86 92
39	3	172/173 (99%)	171 (99%)	1 (1%)	86 92
40	4	113/123 (92%)	110 (97%)	3 (3%)	44 65
41	5	87/112 (78%)	86 (99%)	1 (1%)	73 84
42	6	124/125 (99%)	123 (99%)	1 (1%)	81 89
43	7	104/105 (99%)	104 (100%)	0	100 100
44	8	105/107 (98%)	104 (99%)	1 (1%)	76 86
45	9	86/90 (96%)	85 (99%)	1 (1%)	71 83
46	A	90/98 (92%)	89 (99%)	1 (1%)	73 84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
47	B	103/104 (99%)	103 (100%)	0	100 100
48	D	91/96 (95%)	90 (99%)	1 (1%)	73 84
49	E	79/83 (95%)	79 (100%)	0	100 100
50	F	75/77 (97%)	74 (99%)	1 (1%)	69 82
51	G	65/65 (100%)	65 (100%)	0	100 100
52	H	74/77 (96%)	73 (99%)	1 (1%)	67 80
53	I	48/66 (73%)	48 (100%)	0	100 100
54	J	70/80 (88%)	68 (97%)	2 (3%)	42 64
55	K	65/66 (98%)	65 (100%)	0	100 100
56	s	44/61 (72%)	43 (98%)	1 (2%)	50 70
59	v	108/156 (69%)	108 (100%)	0	100 100
All	All	4922/5244 (94%)	4879 (99%)	43 (1%)	79 87

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	3	5	LEU
45	9	17	LEU
40	4	15	LEU
41	5	9	MET
48	D	98	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
33	U	28	ASN
41	5	55	HIS
33	U	43	ASN
41	5	3	HIS
44	8	32	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	O	117/120 (97%)	21 (17%)	1 (0%)
30	N	2894/2903 (99%)	521 (18%)	34 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	M	74/75 (98%)	11 (14%)	0
35	x	43/692 (6%)	34 (79%)	0
36	0	1538/1539 (99%)	280 (18%)	21 (1%)
58	u	72/73 (98%)	19 (26%)	0
All	All	4738/5402 (87%)	886 (18%)	56 (1%)

5 of 886 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	O	13	G
1	O	25	U
1	O	31	C
1	O	35	C
1	O	41	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	N	2286	G
36	0	1528	U
36	0	64	G
36	0	1491	G
36	0	1190	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 3 ligands modelled in this entry, 3 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)

There are no chain breaks in this entry.

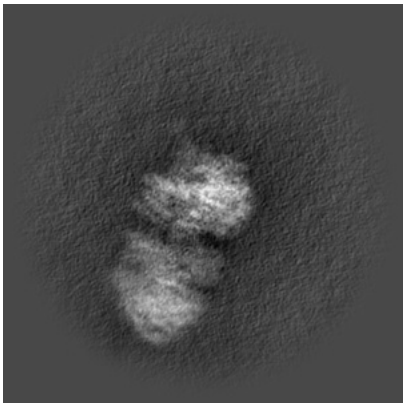
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13958. These allow visual inspection of the internal detail of the map and identification of artifacts.

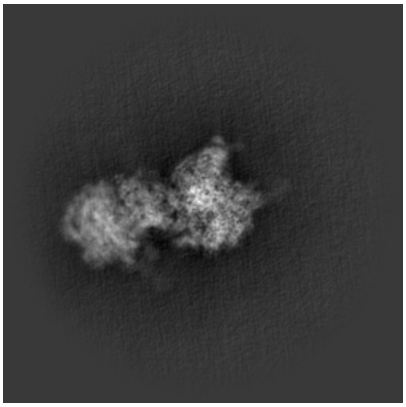
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

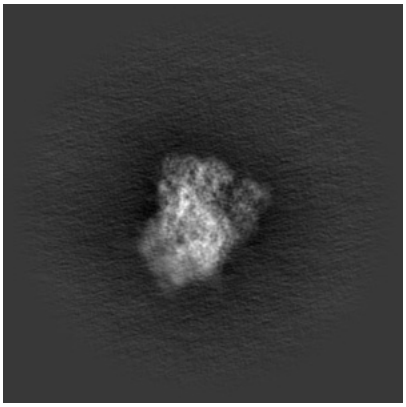
6.1.1 Primary map



X



Y

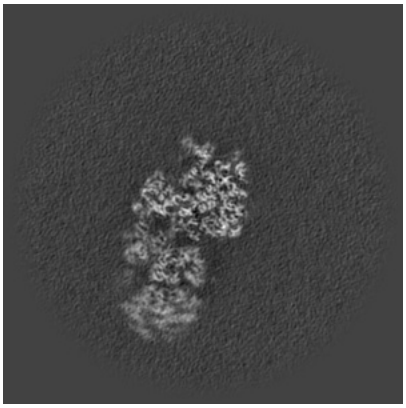


Z

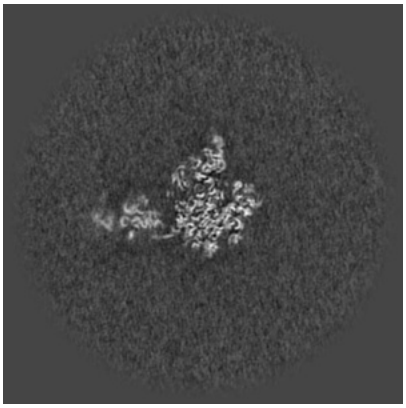
The images above show the map projected in three orthogonal directions.

6.2 Central slices

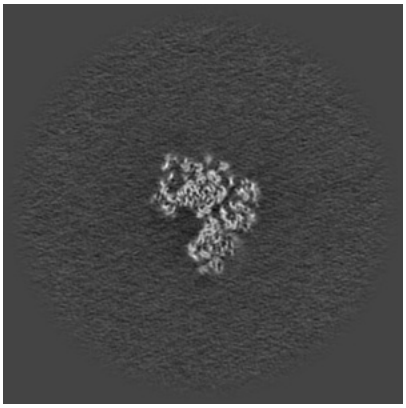
6.2.1 Primary map



X Index: 300



Y Index: 300

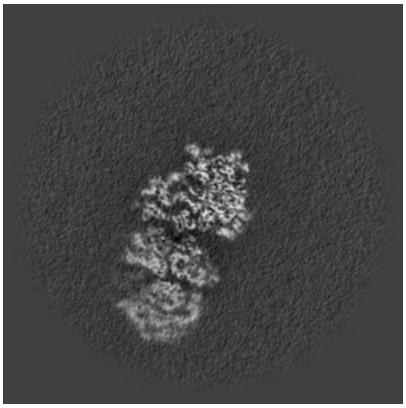


Z Index: 300

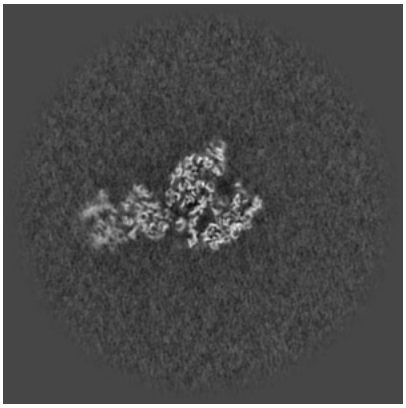
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

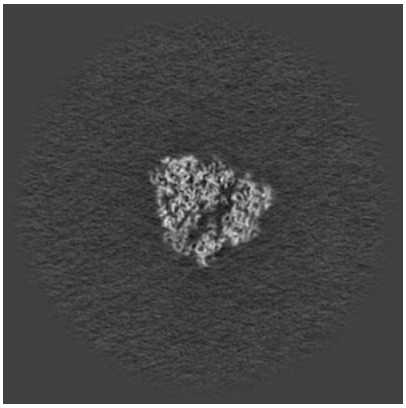
6.3.1 Primary map



X Index: 293



Y Index: 289



Z Index: 321

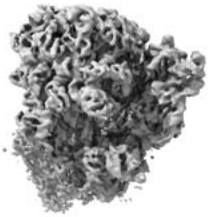
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

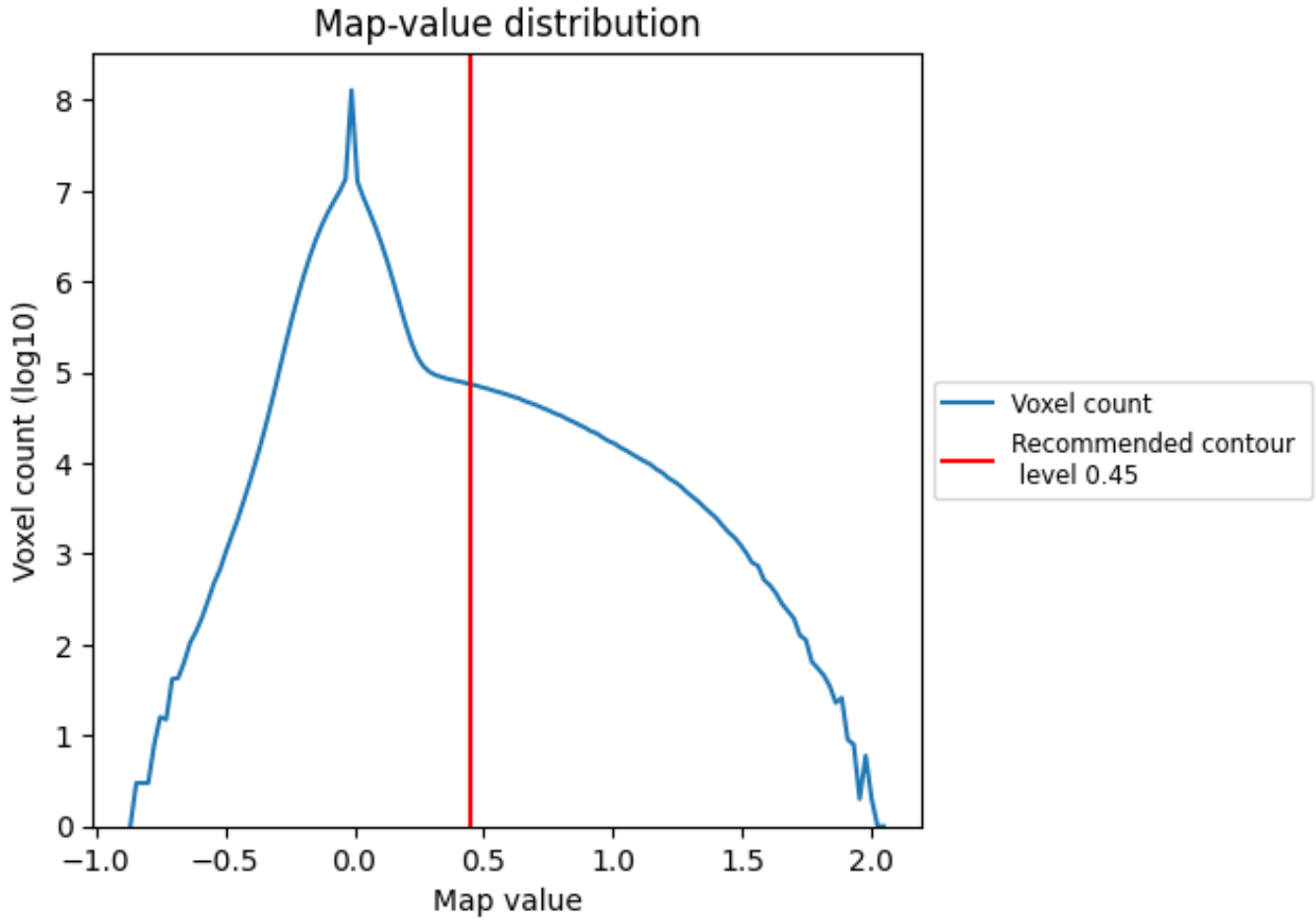
6.5 Mask visualisation (i)

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

7 Map analysis

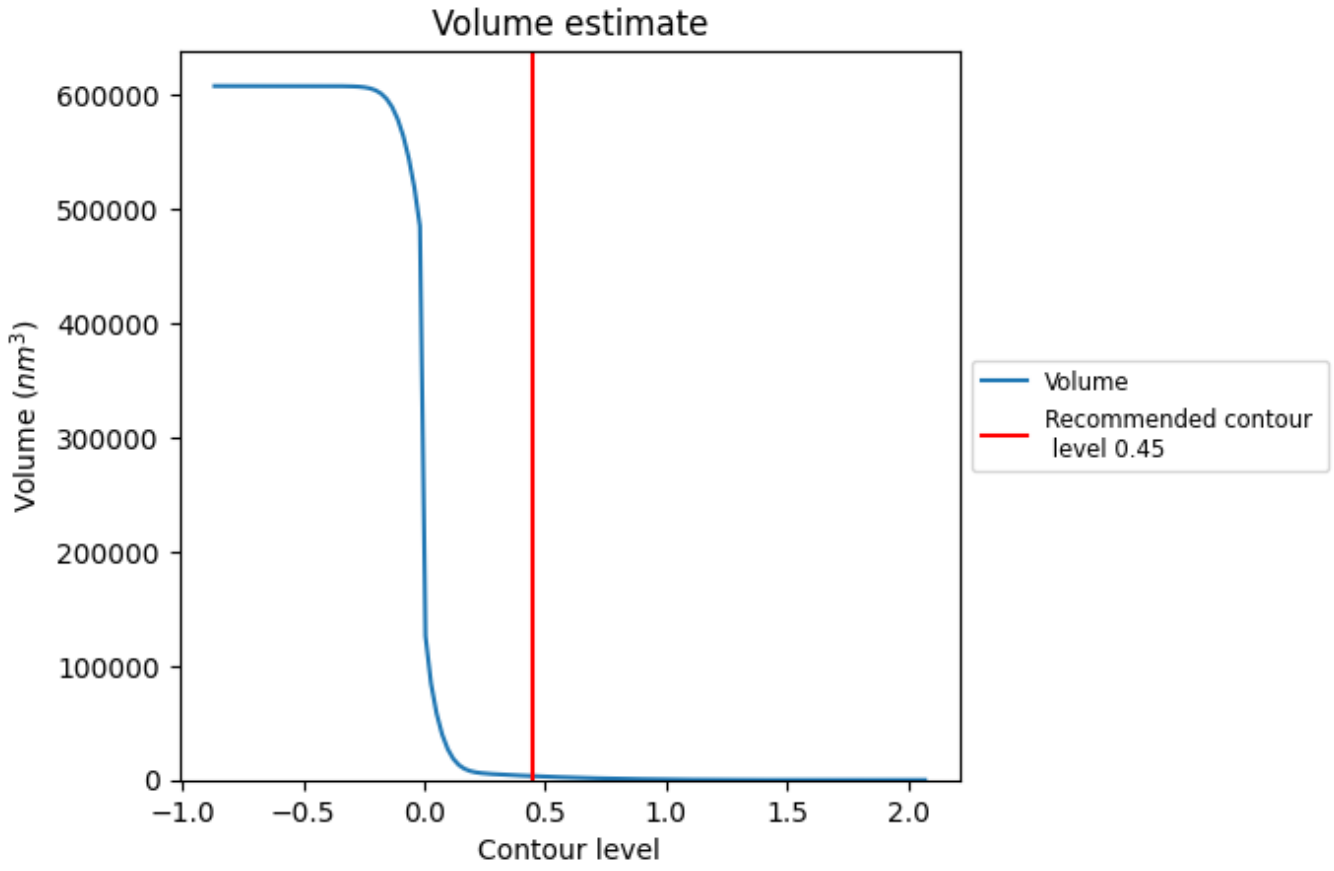
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

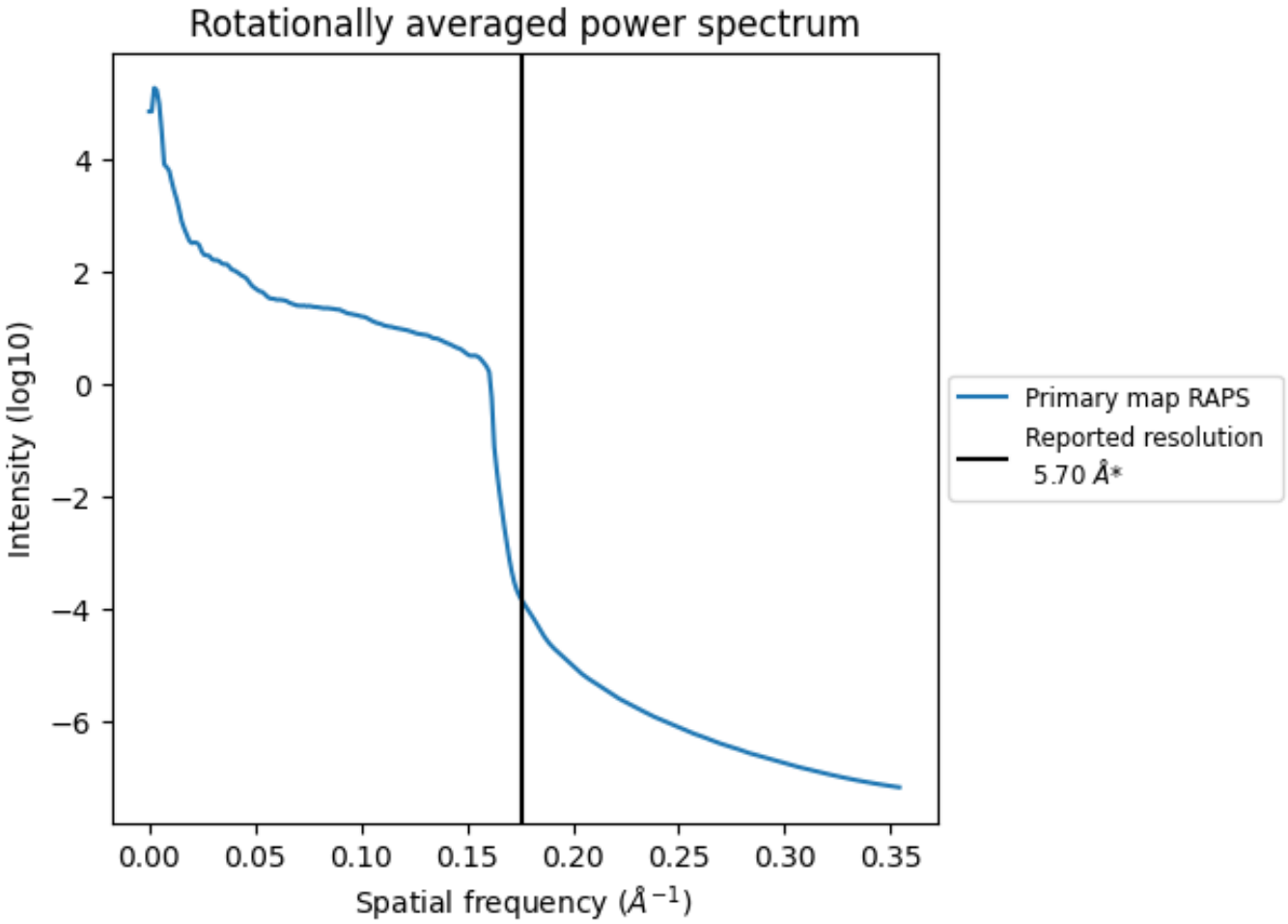
7.2 Volume estimate (i)



The volume at the recommended contour level is 3383 nm^3; this corresponds to an approximate mass of 3056 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 0.175 Å^{-1}

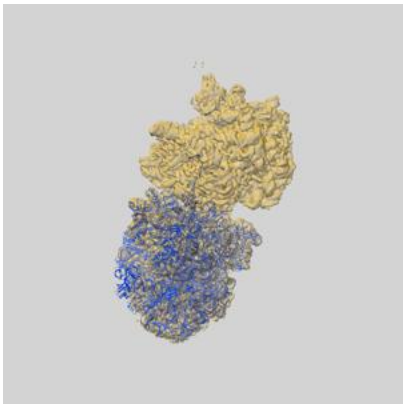
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

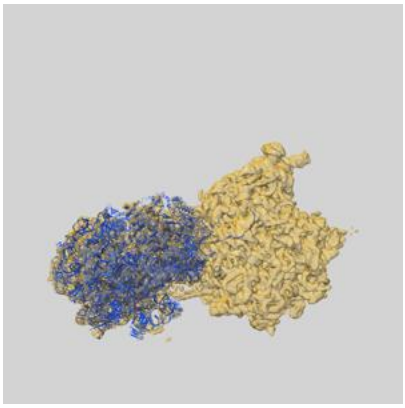
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13958 and PDB model 7QGR. Per-residue inclusion information can be found in section 3 on page 17.

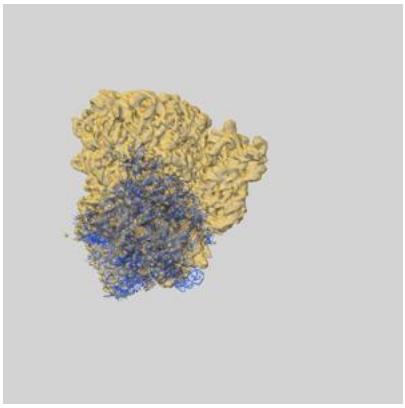
9.1 Map-model overlay



X



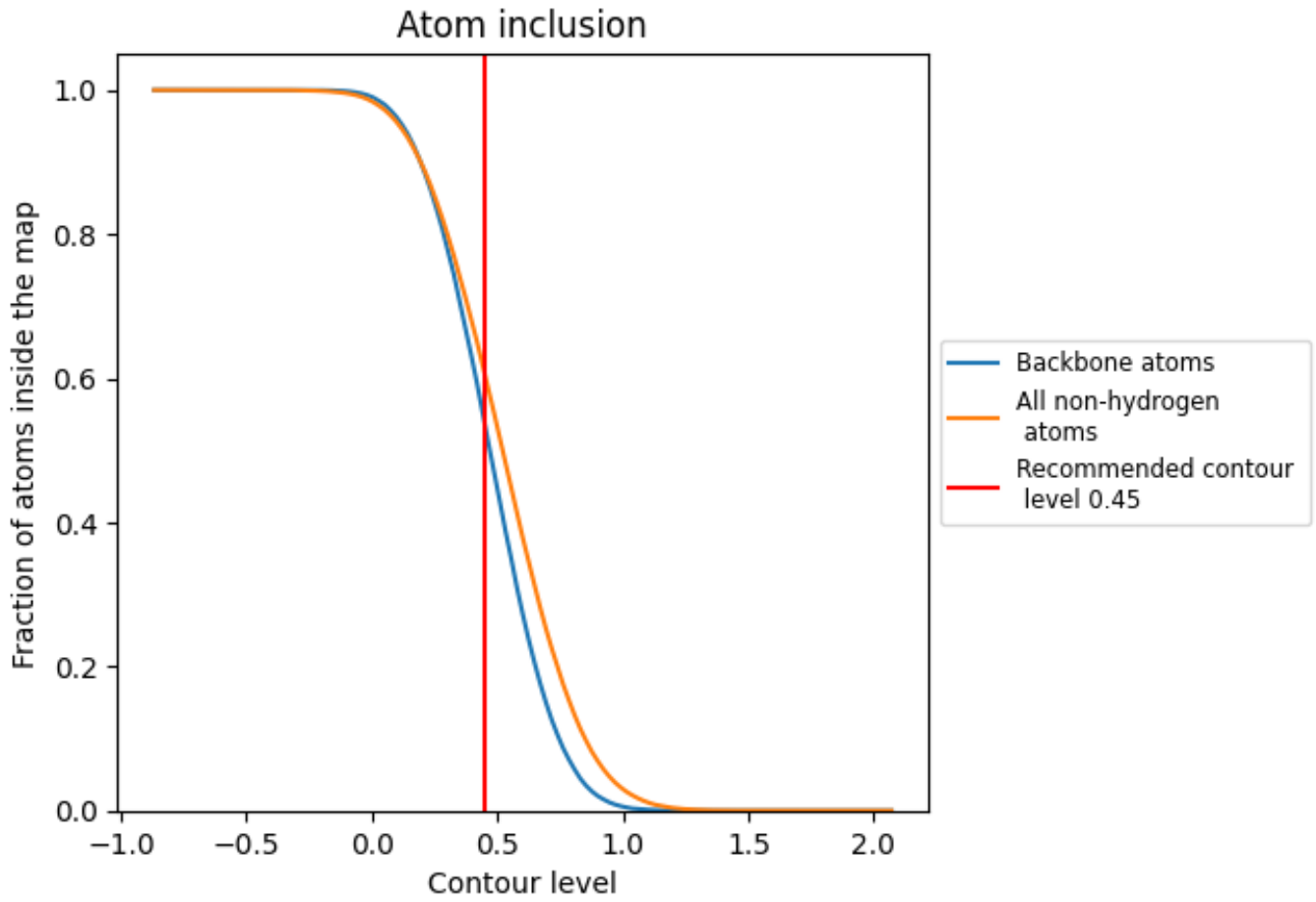
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45 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 Atom inclusion (i)



At the recommended contour level, 54% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.