



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:20 AM UTC

PDB ID : 6DNC / pdb_00006dnc
EMDB ID : EMD-7970
Title : E.coli RF1 bound to E.coli 70S ribosome in response to UAU sense A-site codon
Authors : Svidritskiy, E.; Demo, G.; Korostelev, A.A.
Deposited on : 2018-06-06
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:

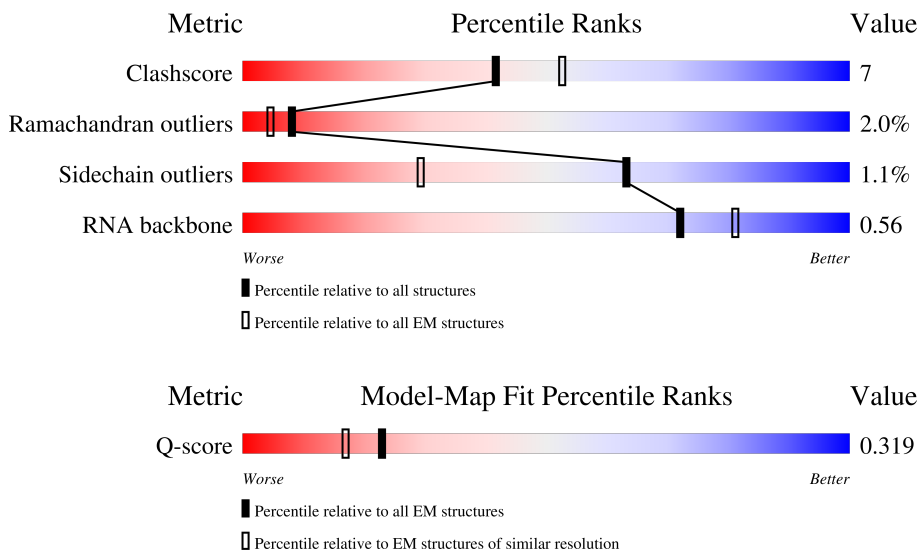
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	A	1539	
2	B	2903	
3	C	120	

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Mol	Chain	Length	Quality of chain
4	D	77	47% 45% 49% 5%
4	LA	77	30% 69% 27%
5	E	234	94% 68% 24% 6%
6	F	273	56% 79% 20%
7	G	209	45% 80% 19%
8	H	201	52% 80% 18%
9	I	179	61% 74% 23%
10	J	177	58% 80% 18%
11	K	149	86% 64% 34%
12	L	165	79% 48% 27% 21%
13	M	142	98% 64% 30% 6%
14	N	142	42% 82% 17%
15	O	123	68% 79% 17%
16	P	144	53% 81% 17%
17	Q	136	70% 88% 11%
18	R	127	27% 62% 29% 6%
19	S	117	29% 79% 19%
20	T	115	57% 77% 23%
21	U	118	24% 79% 19%
22	V	103	44% 75% 22%
23	W	110	47% 81% 17%
24	X	100	41% 85% 7% 7%
25	Y	104	40% 81% 16%
26	Z	94	35% 85% 14%
27	AA	85	38% 73% 15% 12%

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Mol	Chain	Length	Quality of chain
28	BA	78	46% 90% 9%
29	CA	63	35% 81% 17%
30	DA	59	41% 78% 20%
31	EA	70	90% 70% 24% 6%
32	FA	57	42% 79% 19%
33	GA	55	69% 89% 9%
34	HA	46	46% 72% 26%
35	IA	65	46% 82% 15%
36	JA	38	66% 74% 21% 5%
37	KA	27	41% 41% 30% 30%
38	MA	362	94% 70% 21% 5%
39	OA	241	65% 76% 14% 7%
40	PA	233	82% 66% 20% 12%
41	QA	206	60% 74% 24%
42	RA	167	51% 66% 25% 6%
43	SA	131	33% 47% 24% 24%
44	TA	156	57% 90% 6%
45	UA	130	47% 80% 18%
46	VA	130	52% 71% 25%
47	WA	103	79% 60% 30% 5% 5%
48	XA	129	53% 72% 16% 10%
49	YA	124	78% 66% 25% 7%
50	ZA	118	52% 71% 24%
51	AB	102	62% 51% 25% 19%
52	BB	89	40% 80% 18%

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Mol	Chain	Length	Quality of chain
53	CB	82	
54	DB	84	
55	EB	75	
56	FB	92	
57	GB	87	
58	HB	71	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 152438 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1539	33012	14725	6052	10697	1538	0	0

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	2903	62318	27801	11468	20147	2902	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	747	C	U	conflict	GB 1036415628
B	1847	G	A	conflict	GB 1036415628

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	120	A	-	expression tag	GB 1370526515

- Molecule 4 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	D	77	1640	732	297	535	76	0	0
4	LA	77	1640	732	297	535	76	0	0

- Molecule 5 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	220	1637	1023	298	310	6	0	0

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	209	1565	979	288	294	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	177	1410	899	249	256	6	0	0

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	176	1323	832	243	246	2	0	0

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 13 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 14 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 15 is a protein called 50S ribosomal protein L14.

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

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 17 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 18 is a protein called 50S ribosomal protein L17.

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

- Molecule 19 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	S	116	892	552	178	162	0	0

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	114	917	574	179	163	1	0	0

- Molecule 21 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	U	117	947	604	192	151	0	0

- Molecule 22 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	103	816	516	153	145	2	0	0

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

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

- Molecule 25 is a protein called 50S ribosomal protein L24.

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

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 32 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 33 is a protein called 50S ribosomal protein L33.

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

- Molecule 34 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	HA	46	377	228	90	57	2	0	0

- Molecule 35 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	IA	64	504	323	105	74	2	0	0

- Molecule 36 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	JA	38	302	185	65	48	4	0	0

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	KA	19	412	186	83	125	18	0	0

- Molecule 38 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	MA	344	2714	1656	507	538	13	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	361	LEU	-	expression tag	UNP B7MKB3
MA	362	GLU	-	expression tag	UNP B7MKB3

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	OA	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

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

- Molecule 41 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	QA	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	RA	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

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

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	UA	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	VA	127	1022	634	206	179	3	0	0

- Molecule 47 is a protein called 30S ribosomal protein S10.

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

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	XA	116	869	535	173	158	3	0	0

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	YA	123	955	590	196	165	4	0	0

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	ZA	114	883	546	178	156	3	0	0

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	AB	101	810	502	165	140	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	35	ALA	-	insertion	UNP B7MCS2

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CB	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 54 is a protein called 30S ribosomal protein S17.

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

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EB	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

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

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GB	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

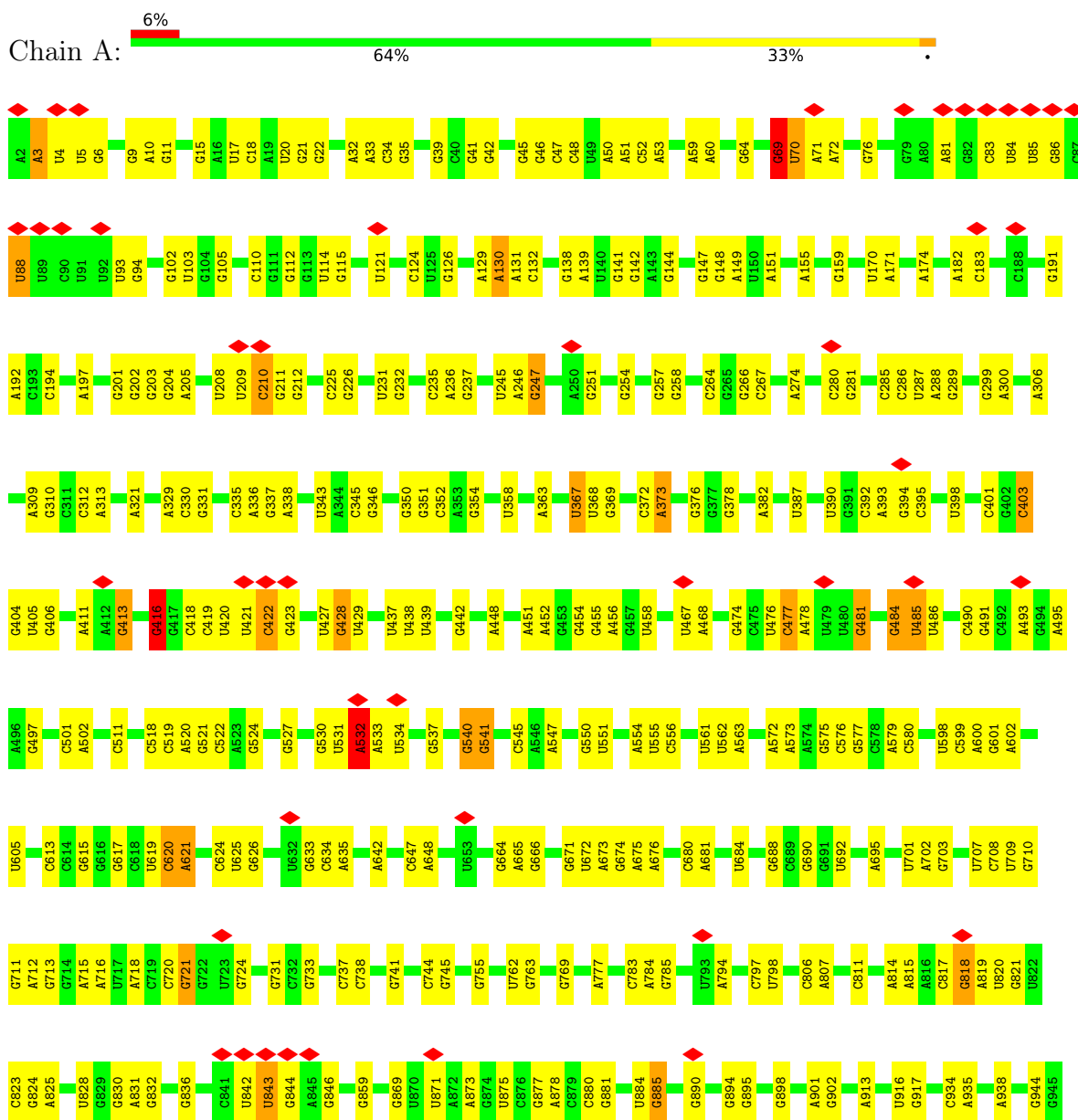
- Molecule 58 is a protein called 30S ribosomal protein S21.

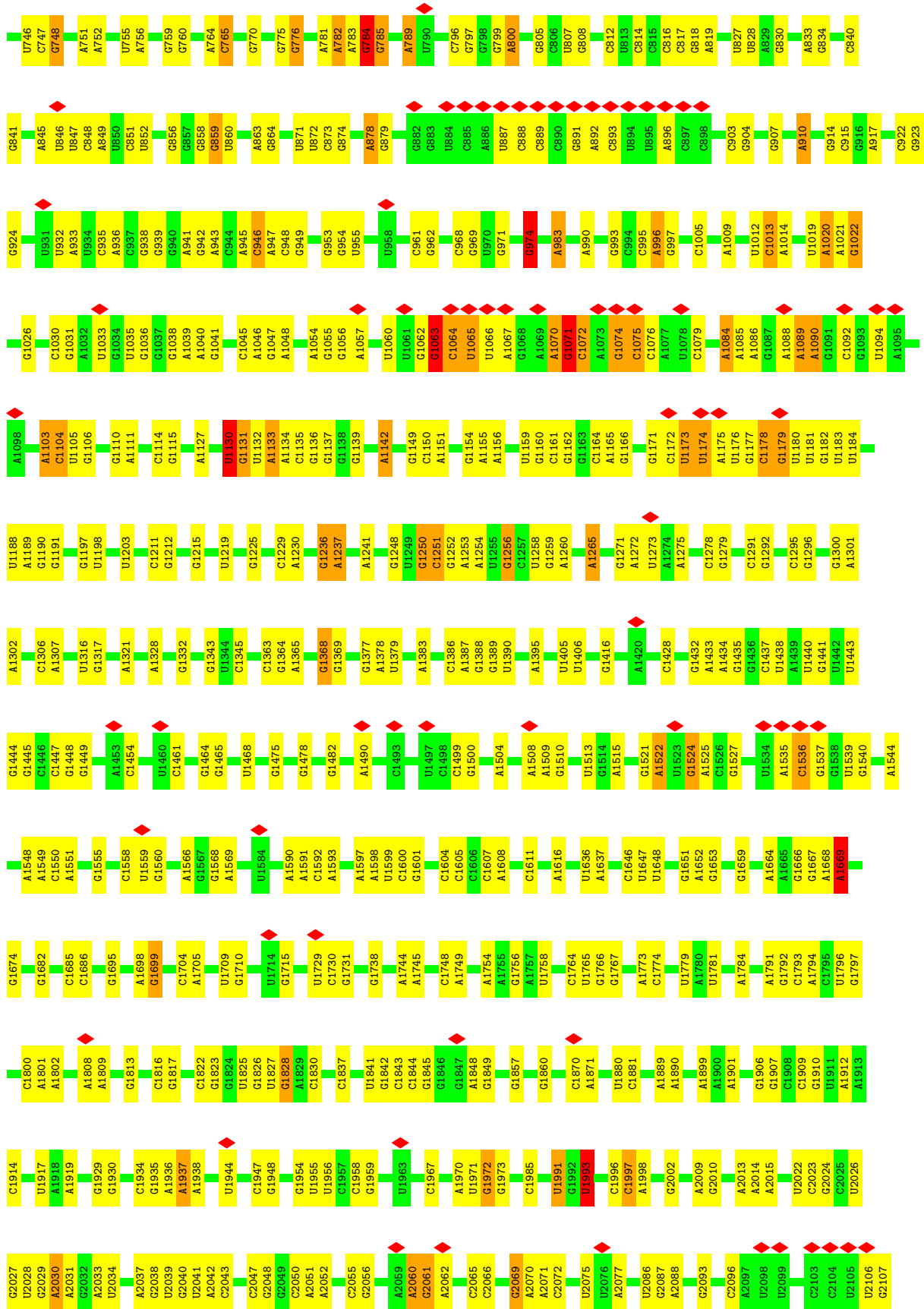
Mol	Chain	Residues	Atoms					AltConf	Trace
58	HB	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

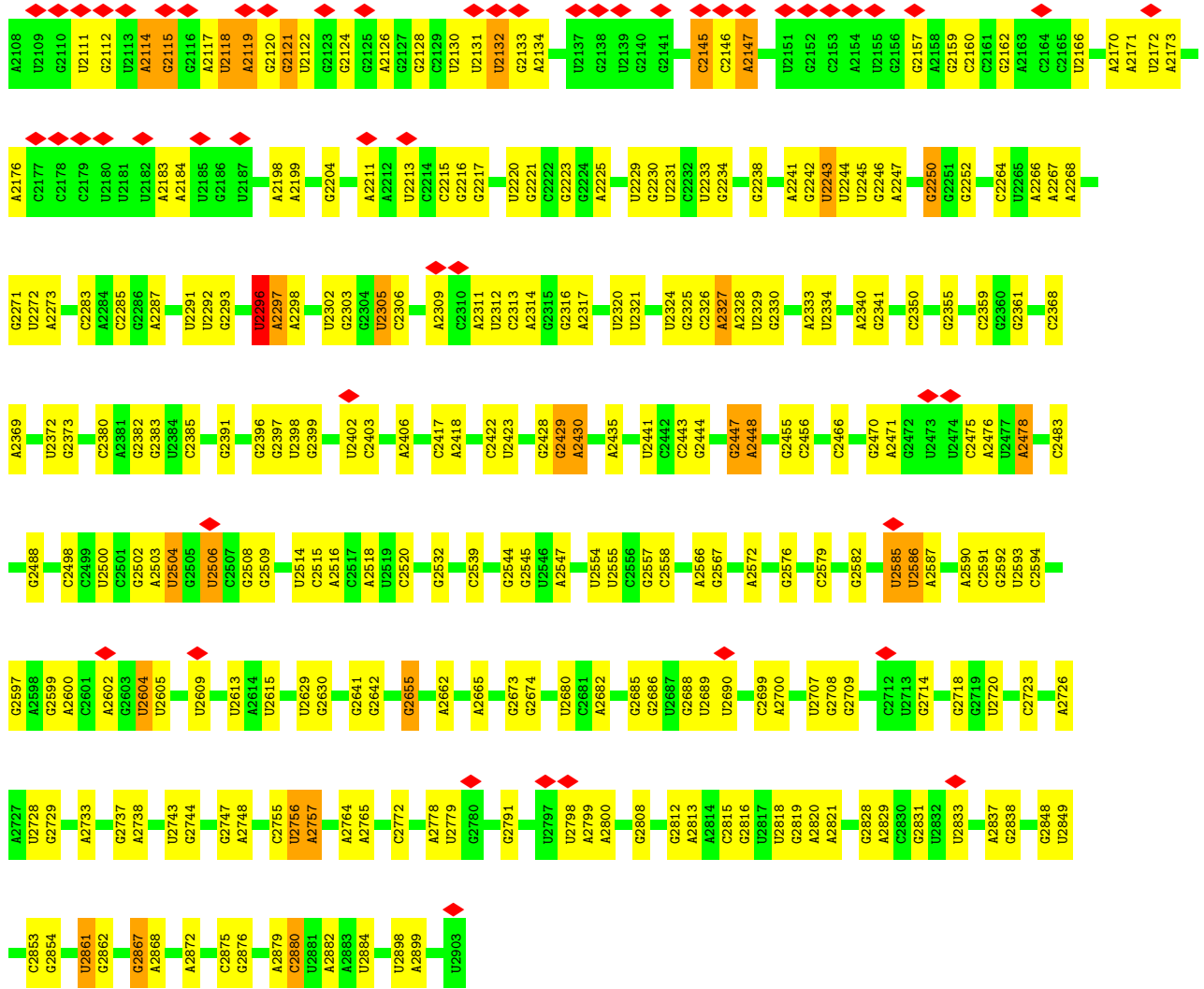
3 Residue-property plots [i](#)

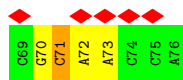
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

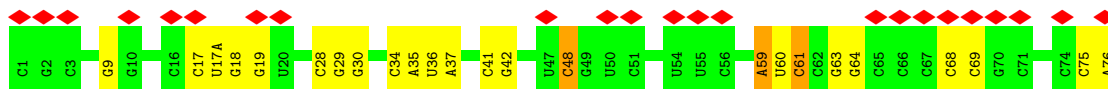








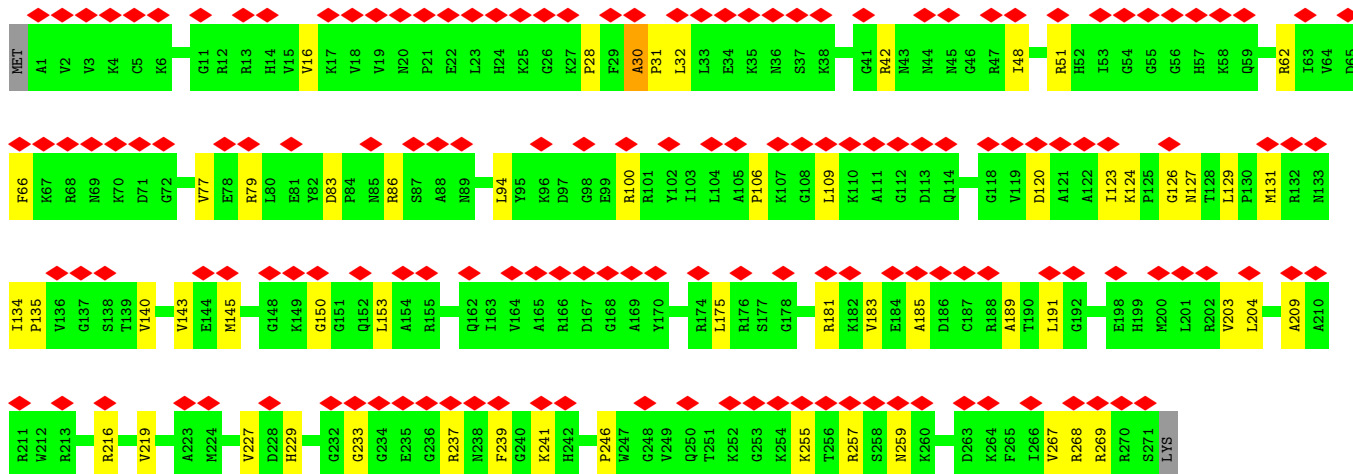
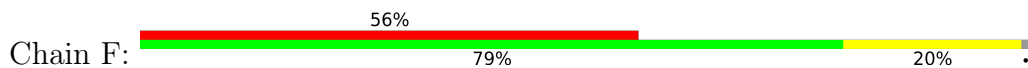
• Molecule 4: tRNA(fMet)



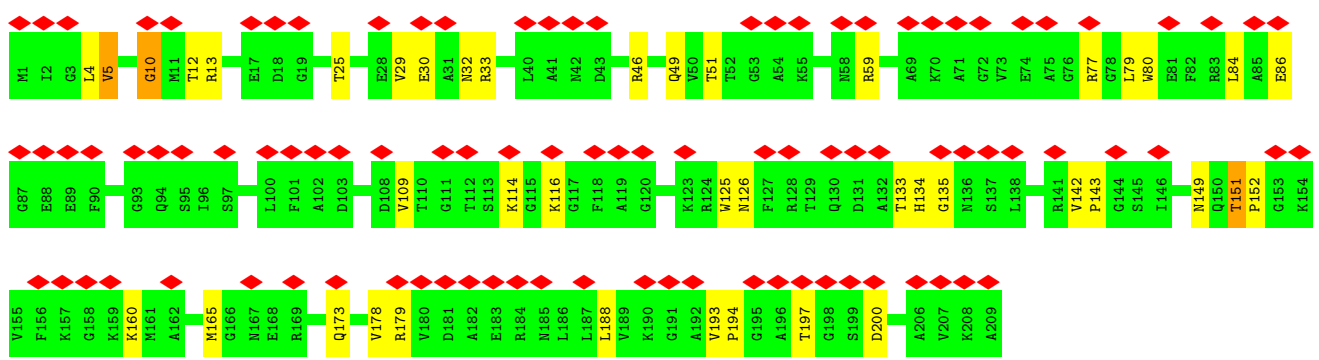
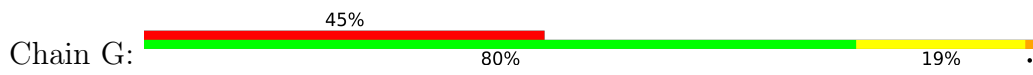
• Molecule 5: 50S ribosomal protein L1



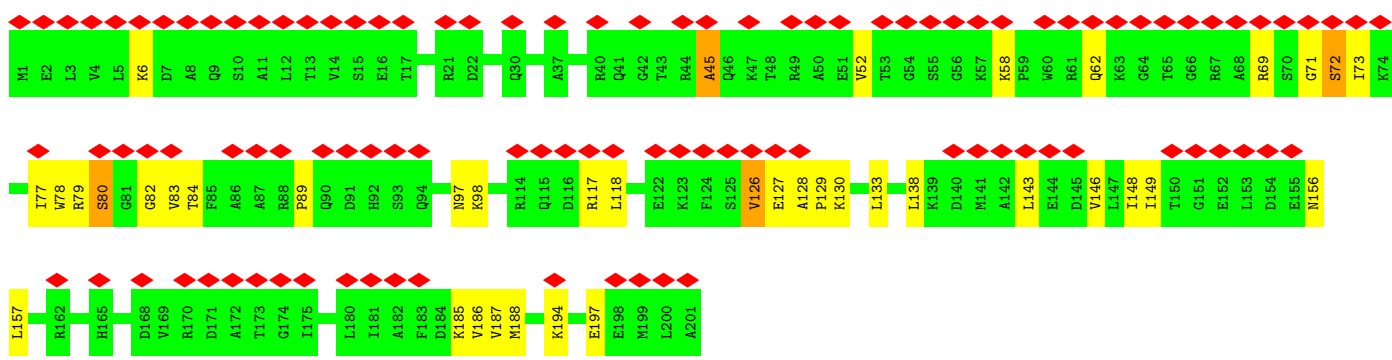
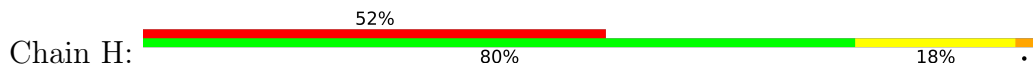
• Molecule 6: 50S ribosomal protein L2



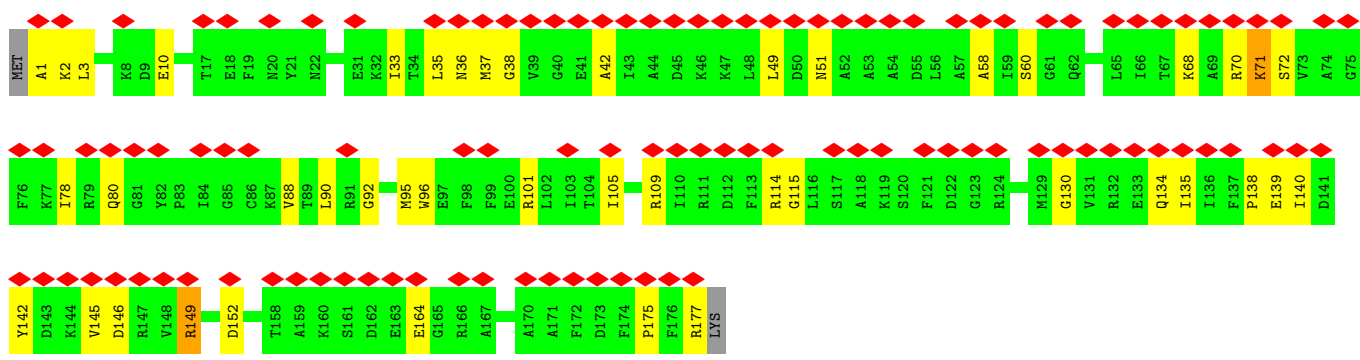
• Molecule 7: 50S ribosomal protein L3



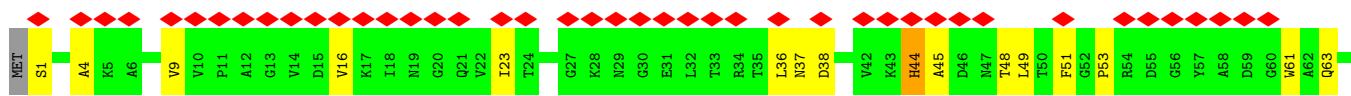
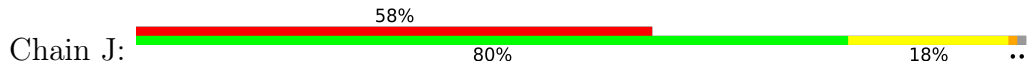
• Molecule 8: 50S ribosomal protein L4

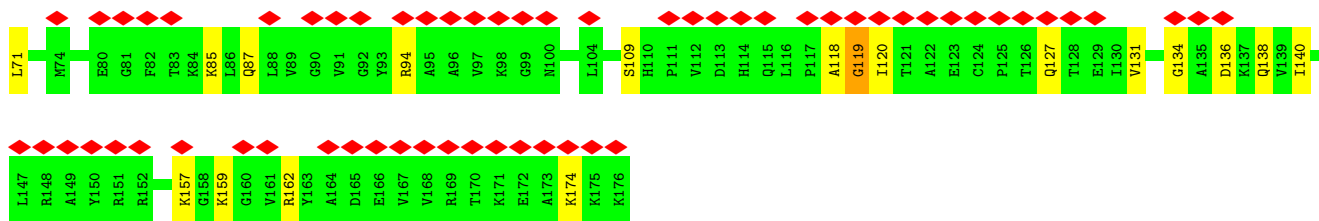


• Molecule 9: 50S ribosomal protein L5

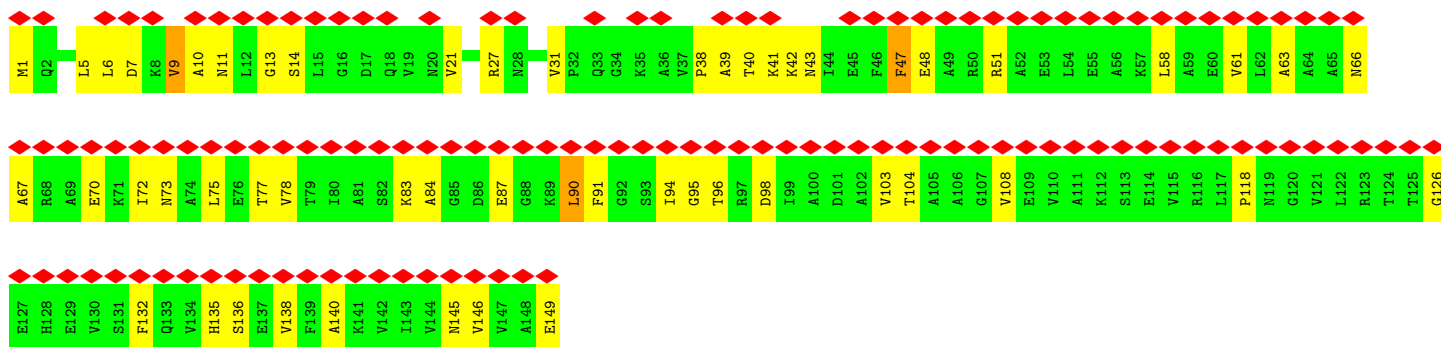
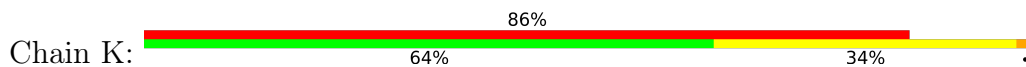


• Molecule 10: 50S ribosomal protein L6

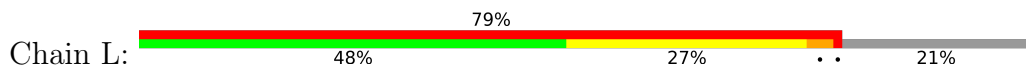




• Molecule 11: 50S ribosomal protein L9



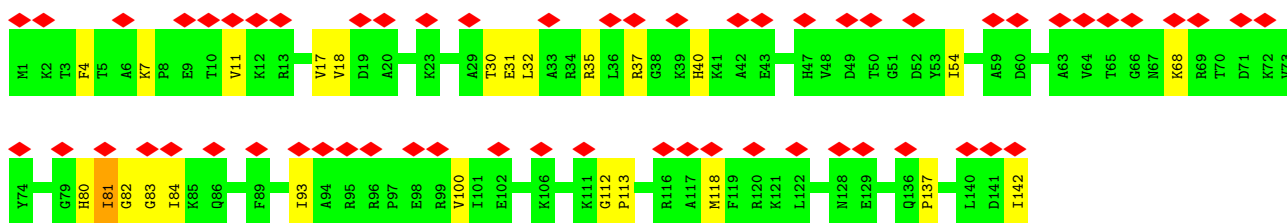
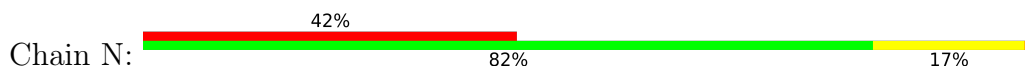
• Molecule 12: 50S ribosomal protein L10



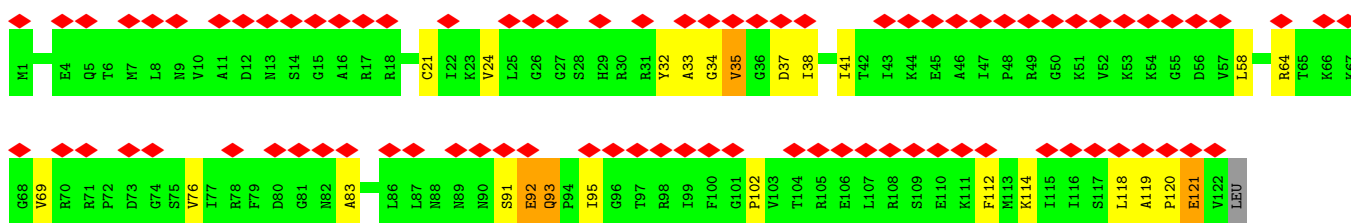
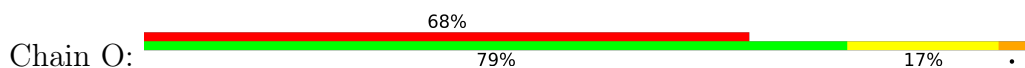
• Molecule 13: 50S ribosomal protein L11



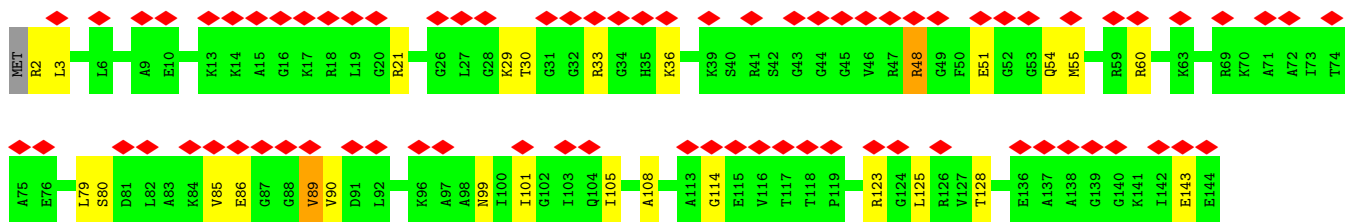
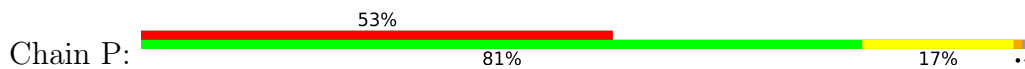
• Molecule 14: 50S ribosomal protein L13



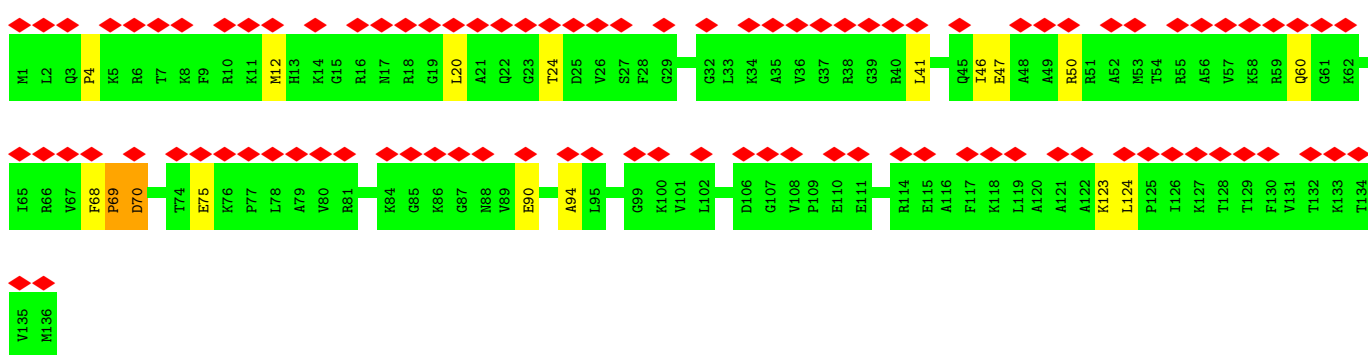
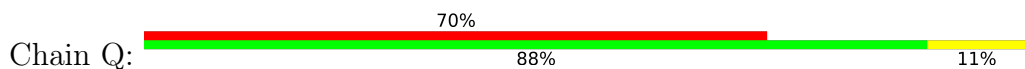
• Molecule 15: 50S ribosomal protein L14



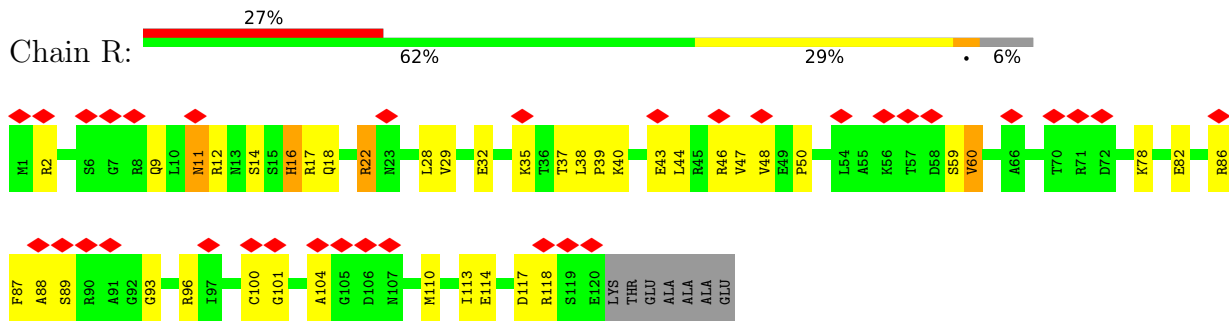
• Molecule 16: 50S ribosomal protein L15



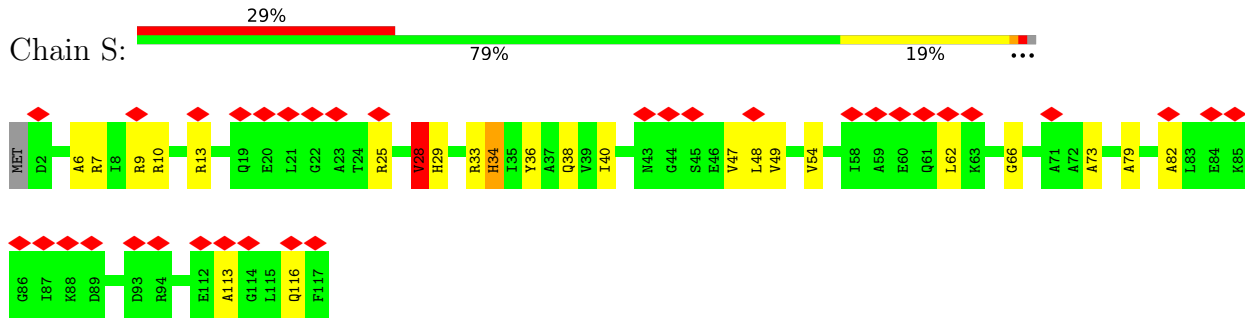
• Molecule 17: 50S ribosomal protein L16



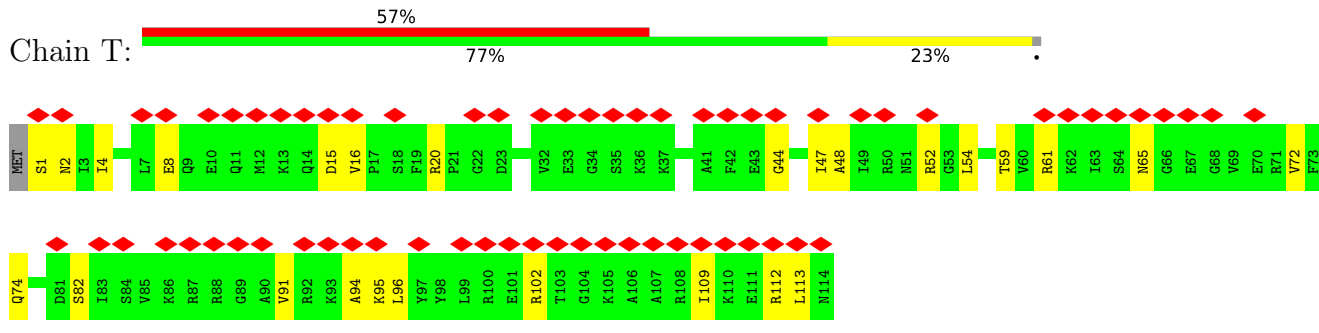
• Molecule 18: 50S ribosomal protein L17



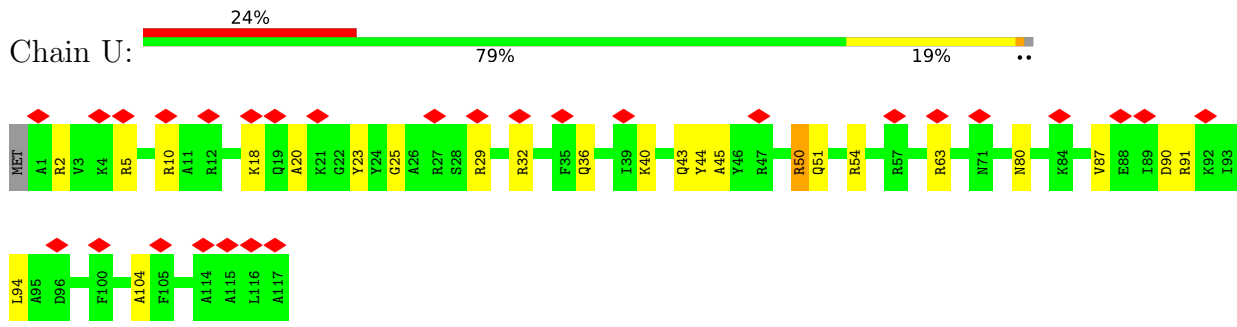
• Molecule 19: 50S ribosomal protein L18



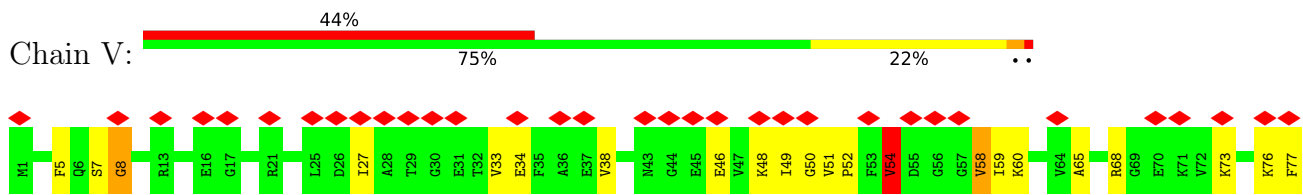
• Molecule 20: 50S ribosomal protein L19



• Molecule 21: 50S ribosomal protein L20

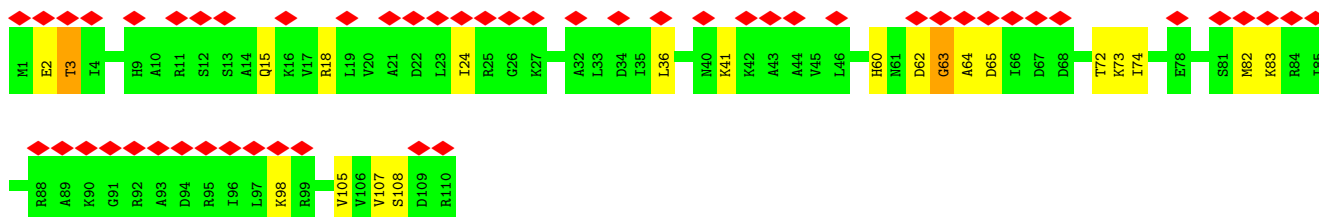
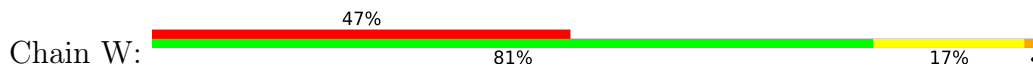


• Molecule 22: 50S ribosomal protein L21

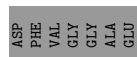
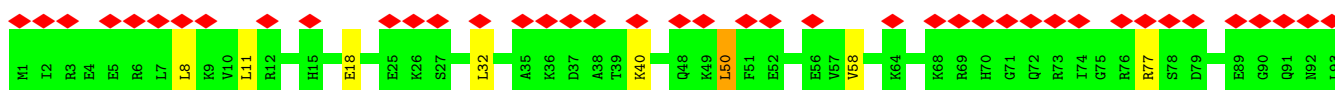
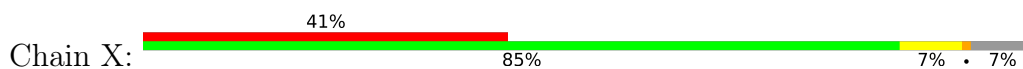




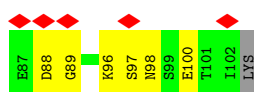
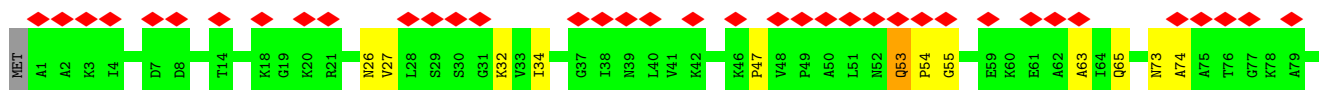
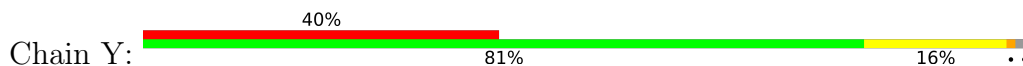
- Molecule 23: 50S ribosomal protein L22



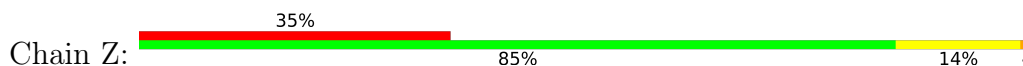
- Molecule 24: 50S ribosomal protein L23



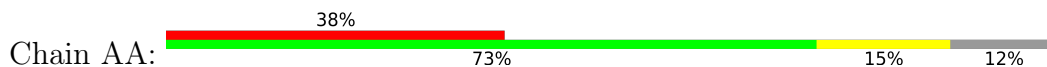
- Molecule 25: 50S ribosomal protein L24

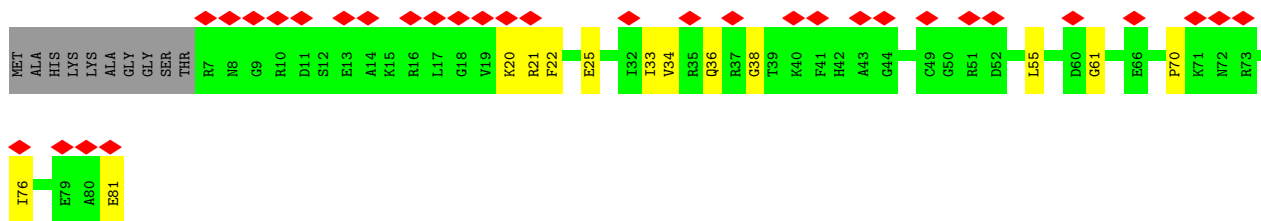


- Molecule 26: 50S ribosomal protein L25

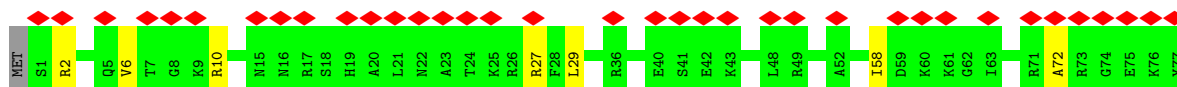
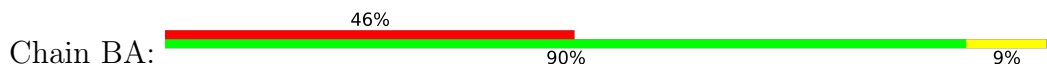


- Molecule 27: 50S ribosomal protein L27

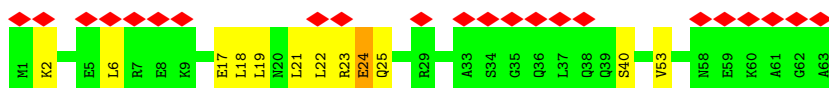
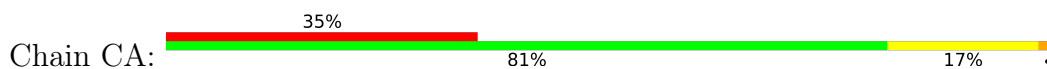




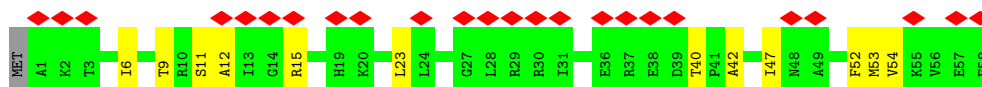
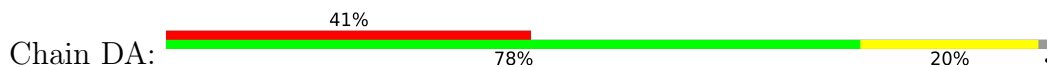
- Molecule 28: 50S ribosomal protein L28



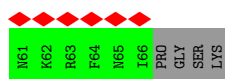
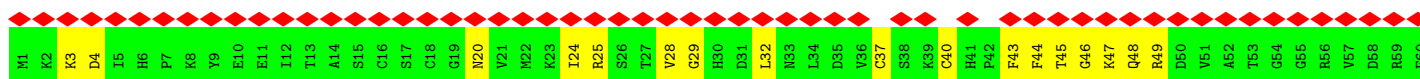
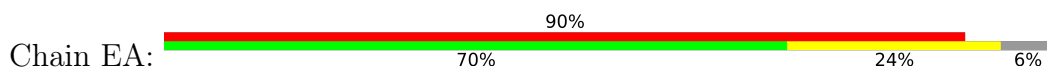
- Molecule 29: 50S ribosomal protein L29



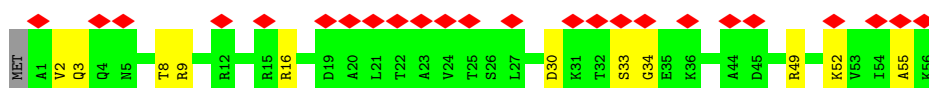
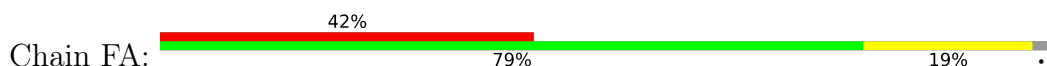
- Molecule 30: 50S ribosomal protein L30



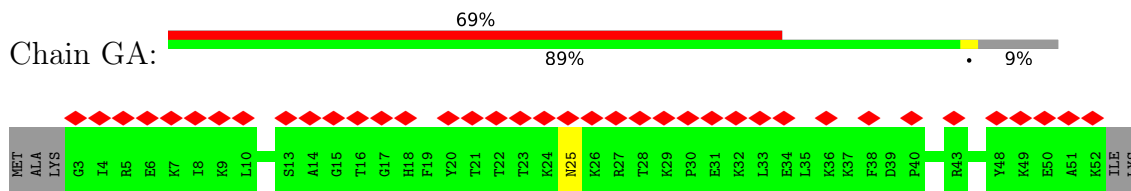
- Molecule 31: 50S ribosomal protein L31



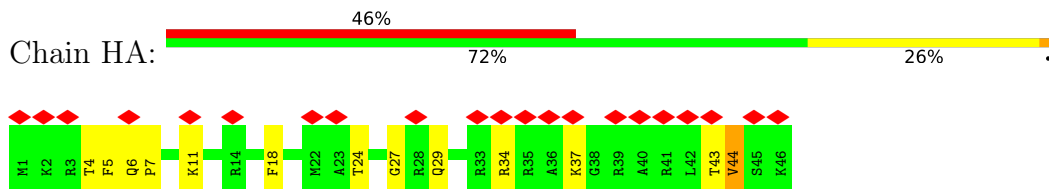
- Molecule 32: 50S ribosomal protein L32



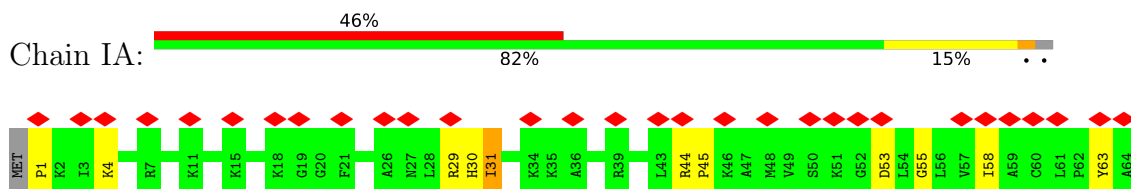
- Molecule 33: 50S ribosomal protein L33



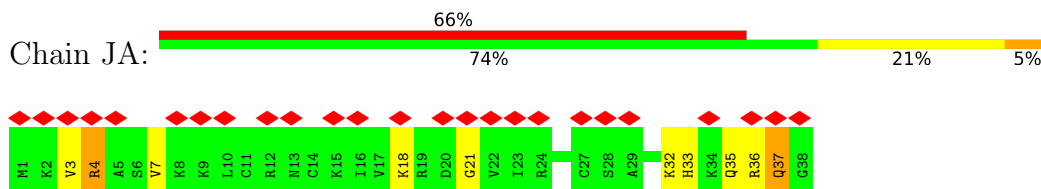
• Molecule 34: 50S ribosomal protein L34



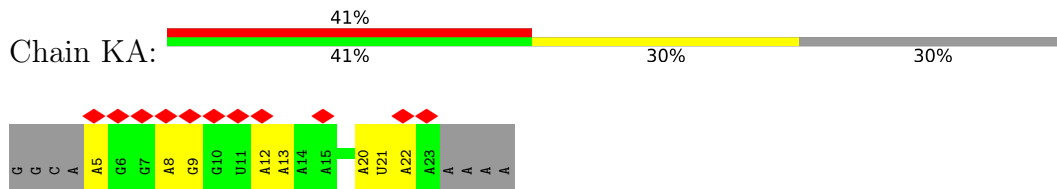
• Molecule 35: 50S ribosomal protein L35



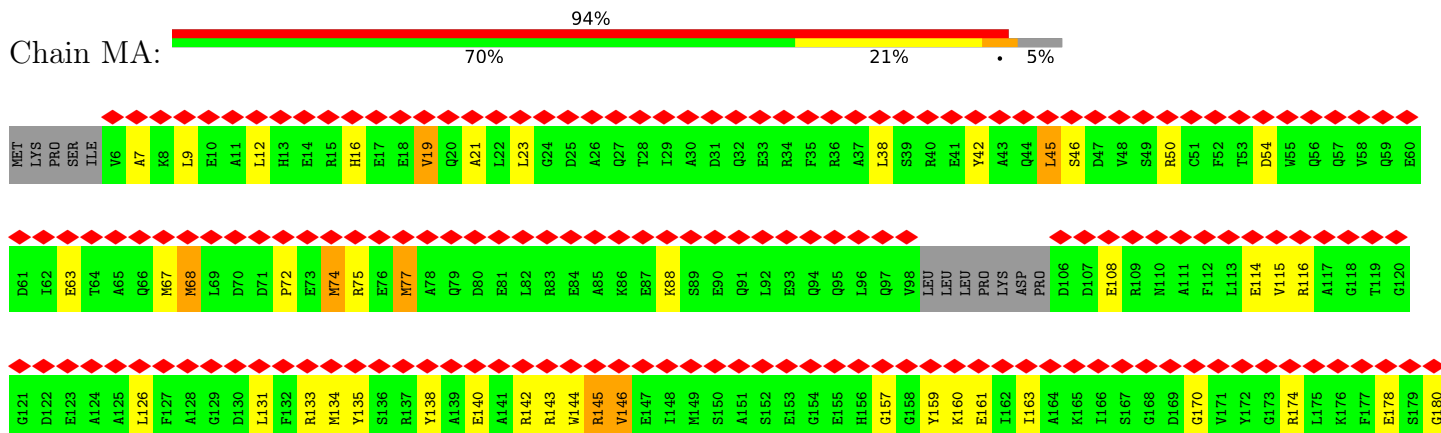
• Molecule 36: 50S ribosomal protein L36

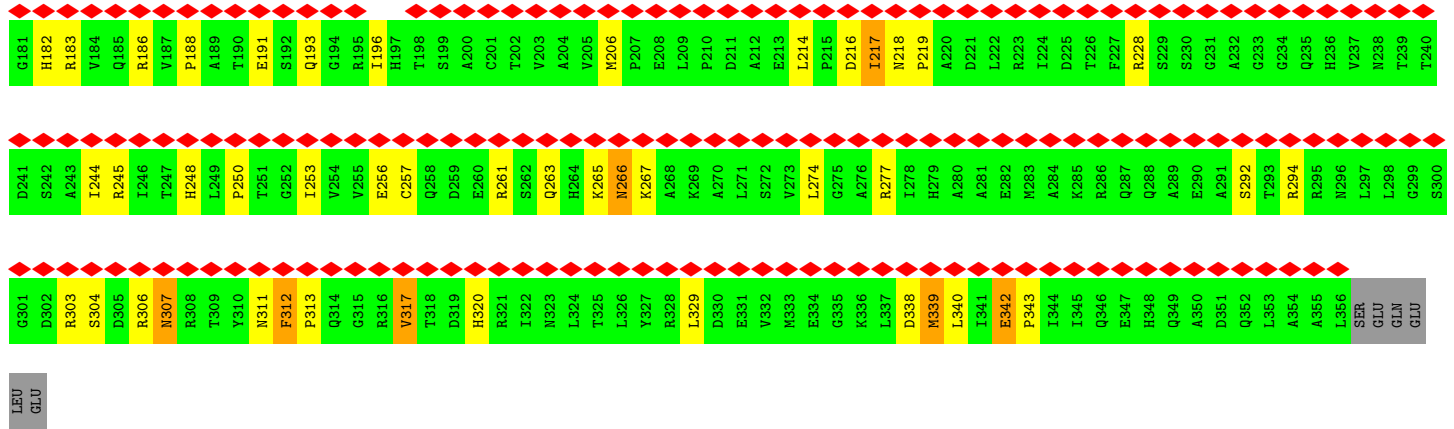


• Molecule 37: mRNA

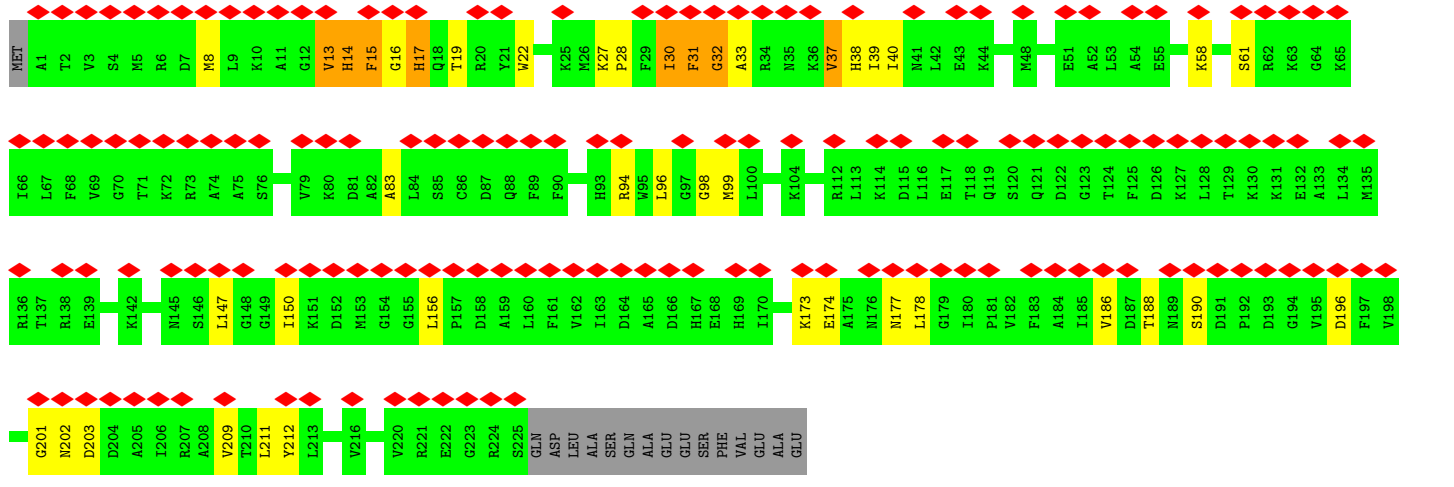
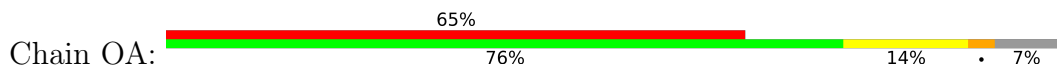


• Molecule 38: Peptide chain release factor 1

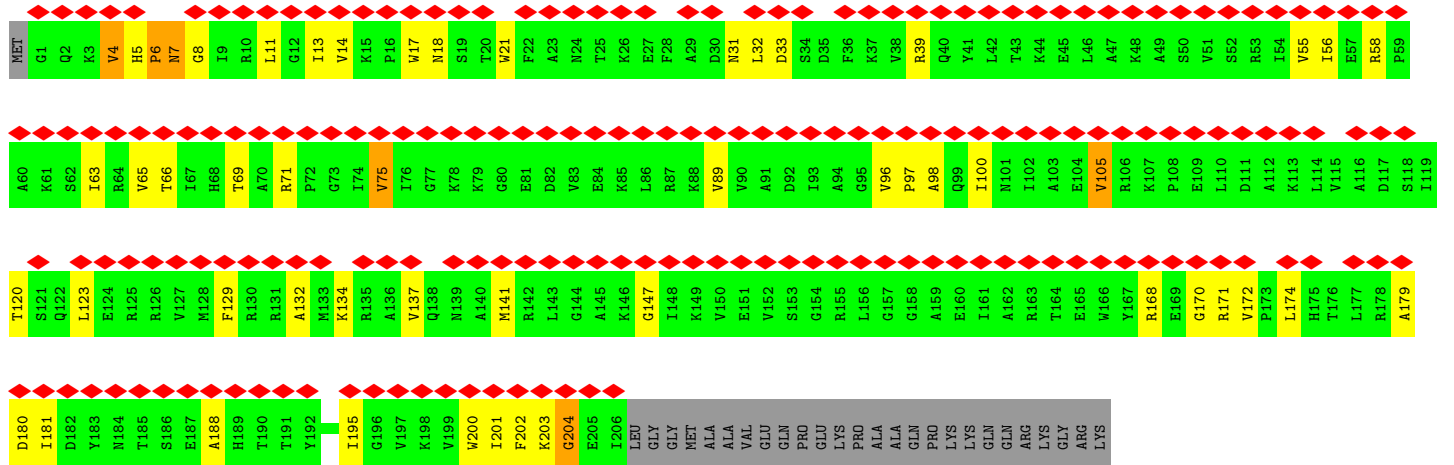
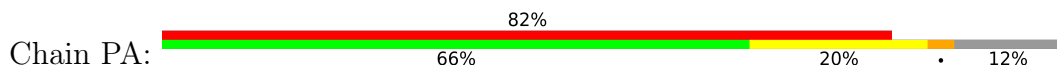




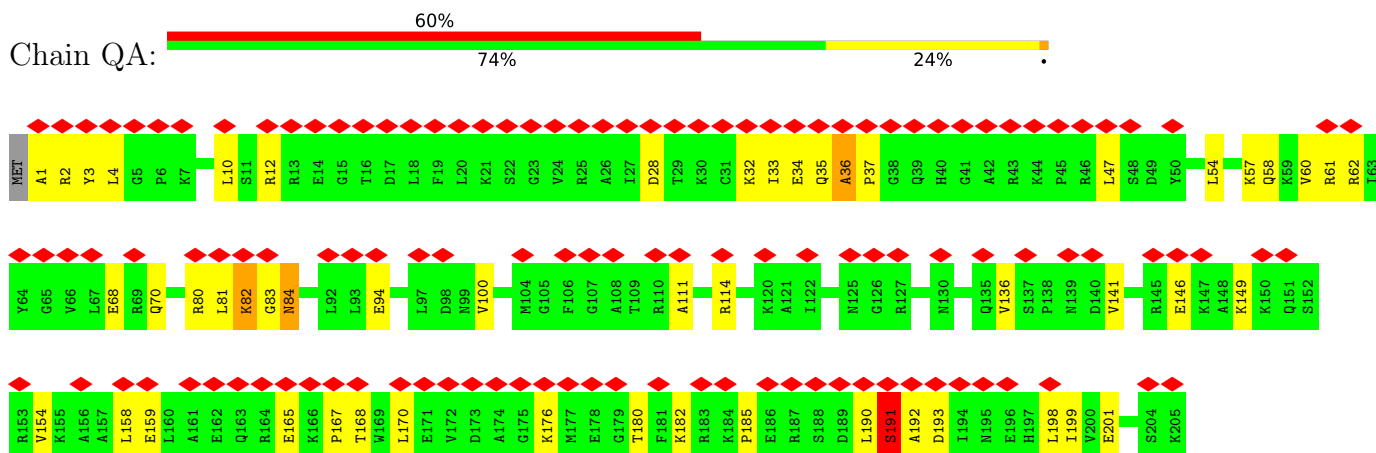
• Molecule 39: 30S ribosomal protein S2



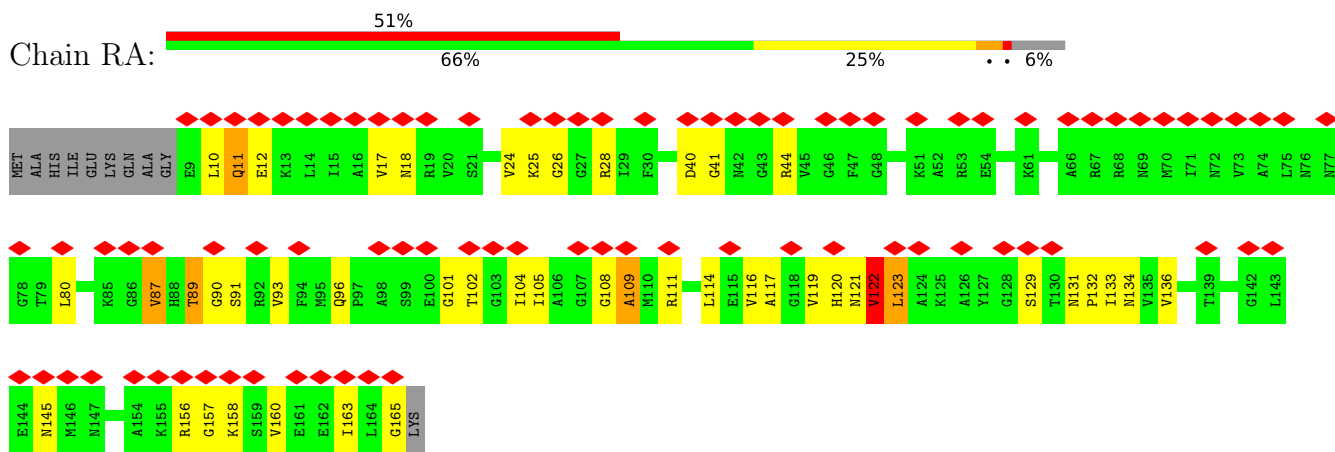
• Molecule 40: 30S ribosomal protein S3



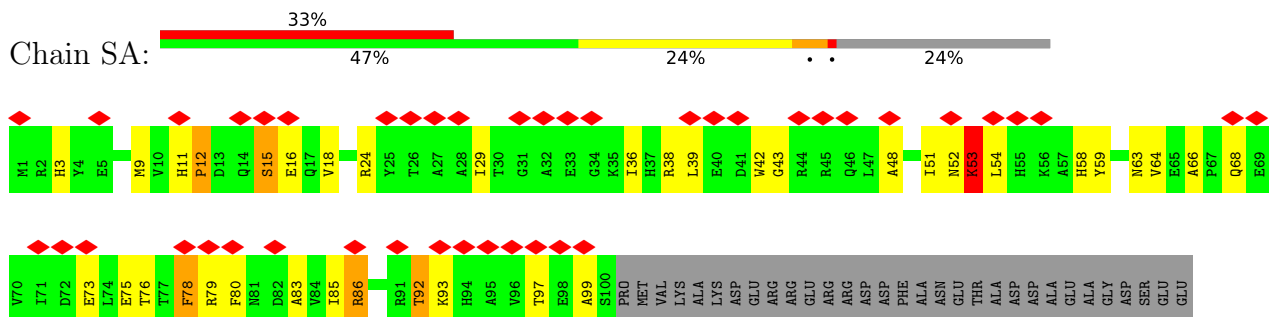
• Molecule 41: 30S ribosomal protein S4



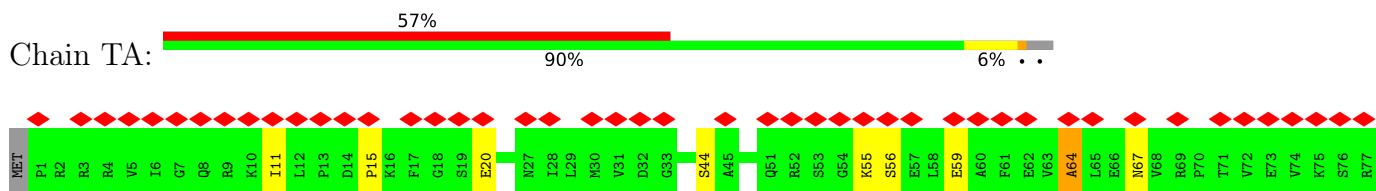
• Molecule 42: 30S ribosomal protein S5

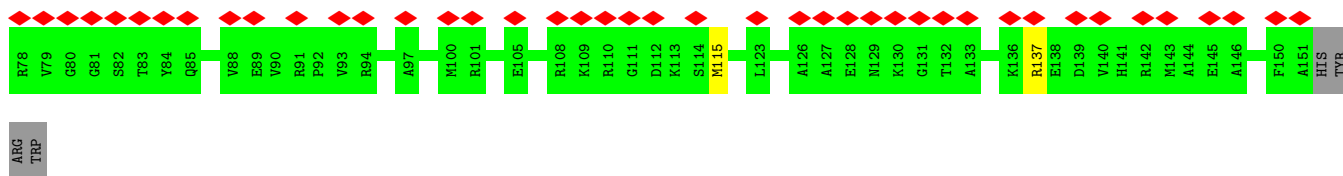


• Molecule 43: 30S ribosomal protein S6

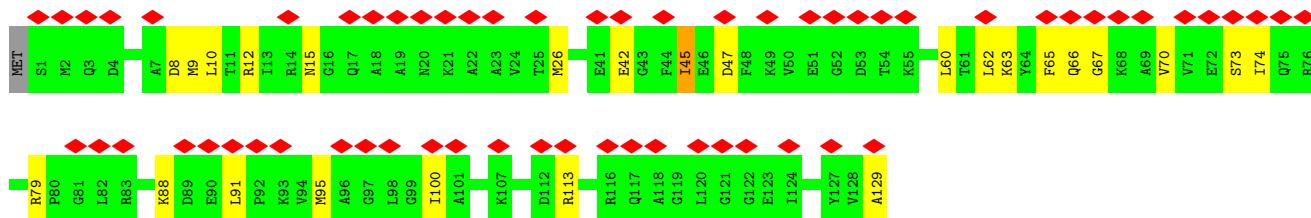
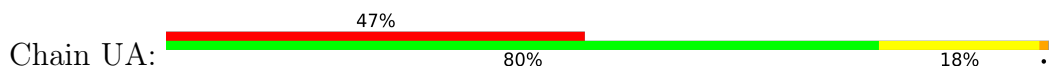


• Molecule 44: 30S ribosomal protein S7

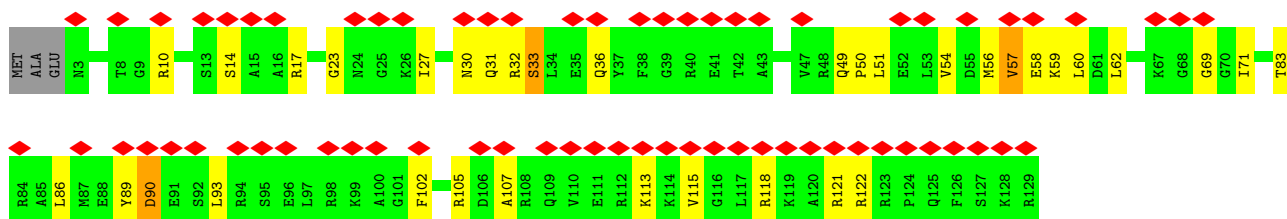
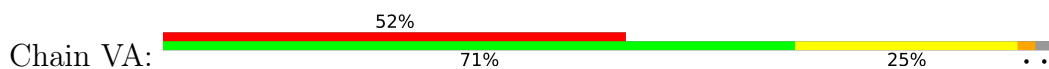




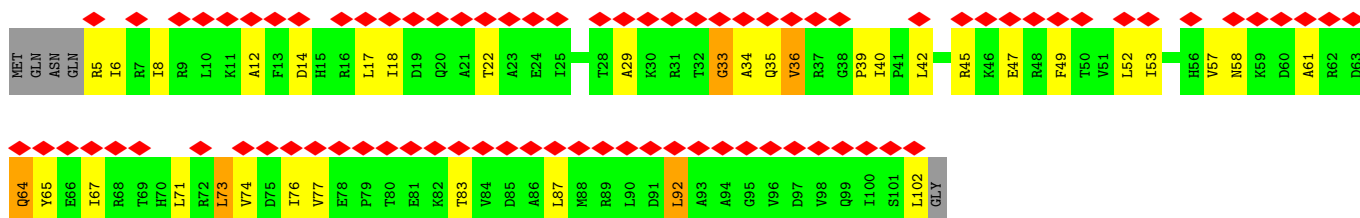
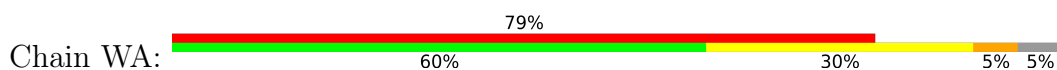
• Molecule 45: 30S ribosomal protein S8



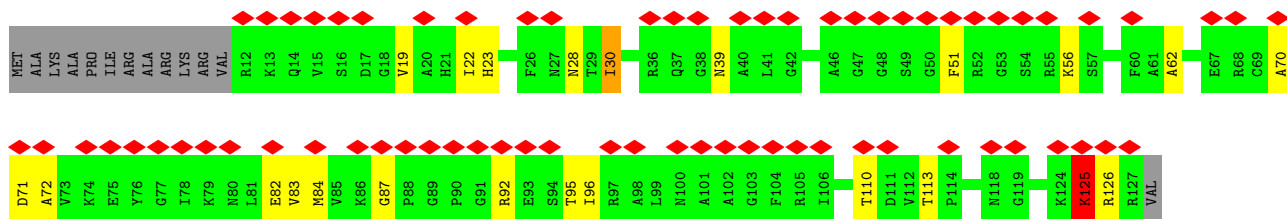
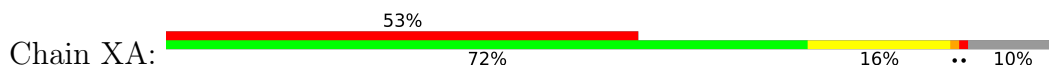
• Molecule 46: 30S ribosomal protein S9



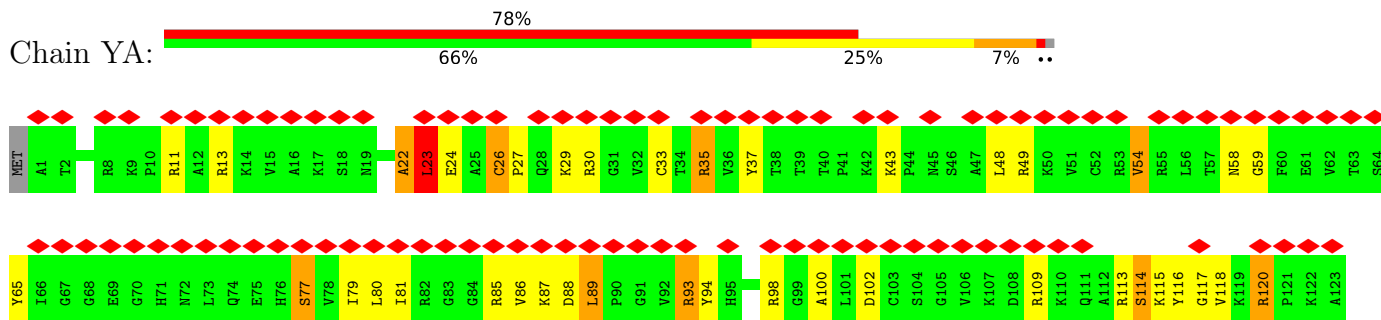
• Molecule 47: 30S ribosomal protein S10



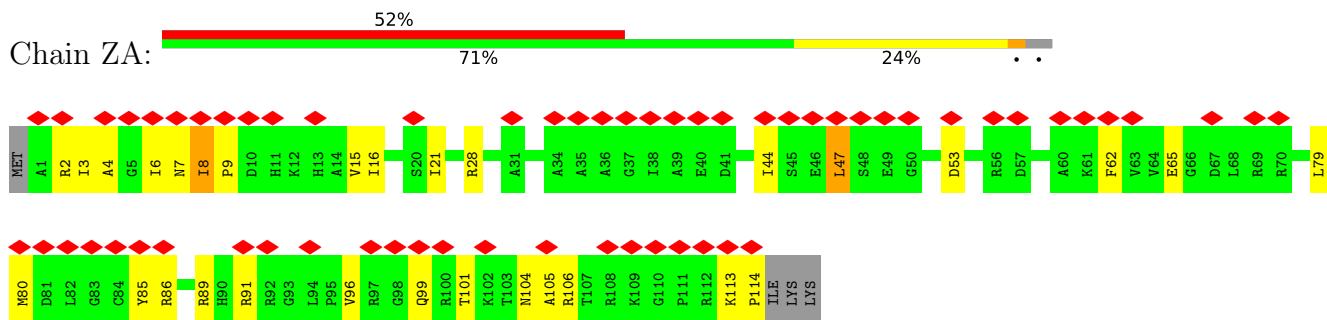
• Molecule 48: 30S ribosomal protein S11



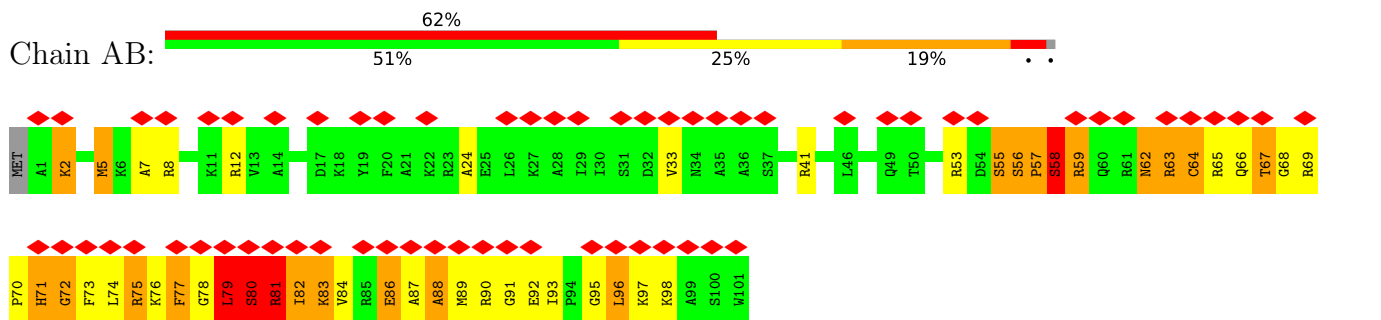
• Molecule 49: 30S ribosomal protein S12



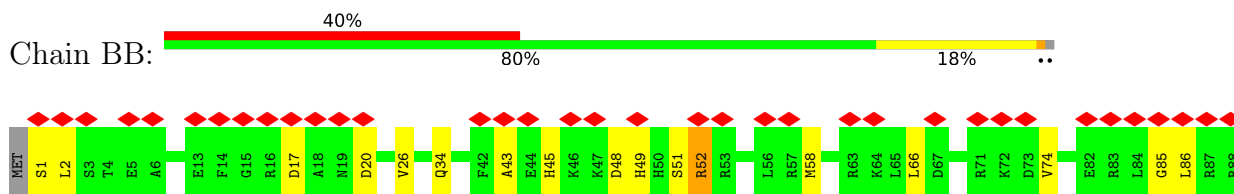
• Molecule 50: 30S ribosomal protein S13



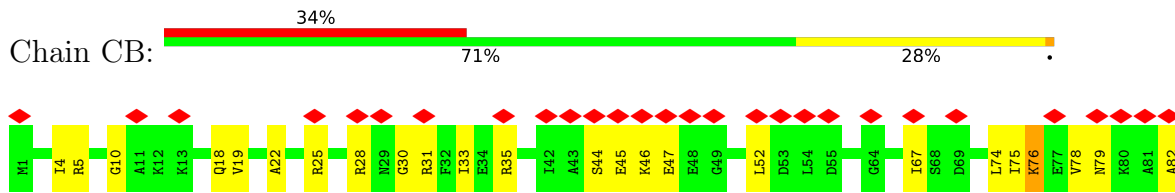
• Molecule 51: 30S ribosomal protein S14



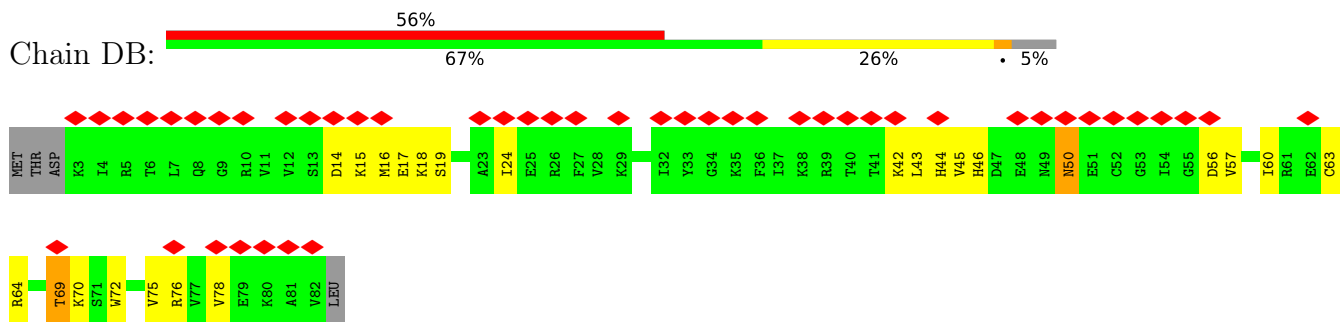
• Molecule 52: 30S ribosomal protein S15



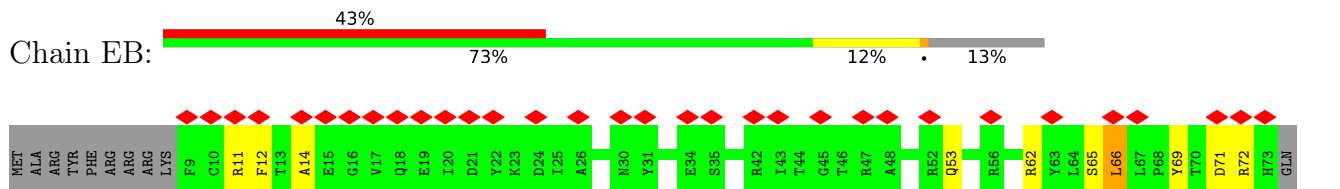
• Molecule 53: 30S ribosomal protein S16



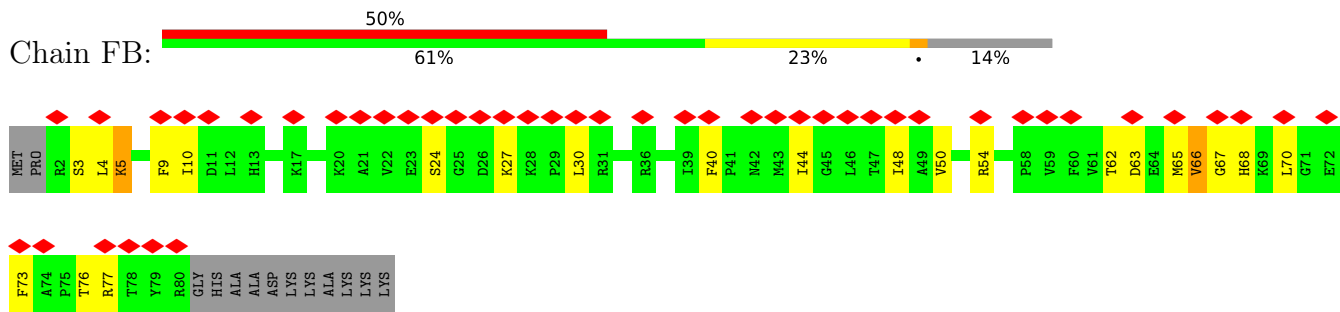
• Molecule 54: 30S ribosomal protein S17



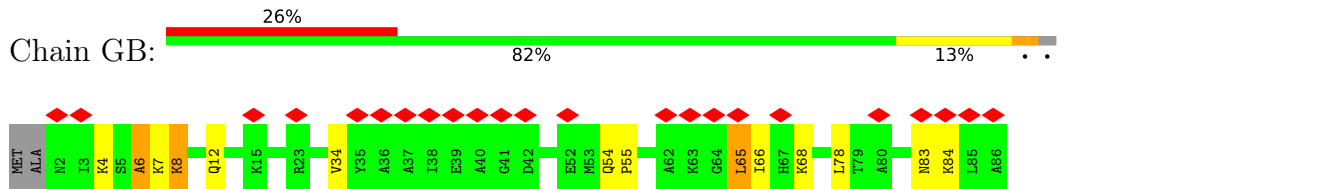
• Molecule 55: 30S ribosomal protein S18



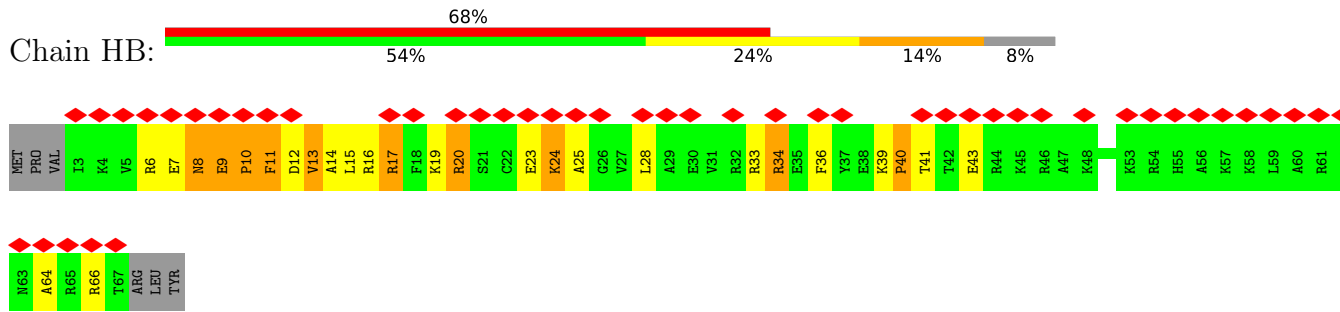
• Molecule 56: 30S ribosomal protein S19



• Molecule 57: 30S ribosomal protein S20



• Molecule 58: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	639088	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.5	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	22000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.659	Depositor
Minimum map value	-3.226	Depositor
Average map value	-0.215	Depositor
Map value standard deviation	1.283	Depositor
Recommended contour level	7	Depositor
Map size (Å)	444.96, 444.96, 444.96	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.927, 0.927, 0.927	Depositor

5 Model quality i

5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/36963	0.58	9/57662 (0.0%)
2	B	0.44	0/69797	0.59	21/108890 (0.0%)
3	C	0.44	0/2872	0.59	2/4479 (0.0%)
4	D	0.46	0/1832	0.52	0/2855
4	LA	0.45	0/1832	0.51	0/2855
5	E	0.46	0/1652	0.98	8/2227 (0.4%)
6	F	0.42	0/2121	1.04	8/2852 (0.3%)
7	G	0.42	0/1586	0.97	3/2134 (0.1%)
8	H	0.43	0/1571	0.98	3/2113 (0.1%)
9	I	0.45	0/1434	0.98	5/1926 (0.3%)
10	J	0.43	0/1343	0.95	2/1816 (0.1%)
11	K	0.55	0/1122	1.12	9/1515 (0.6%)
12	L	0.63	0/1001	1.24	13/1350 (1.0%)
13	M	0.59	0/1046	1.15	11/1410 (0.8%)
14	N	0.39	0/1152	0.90	4/1551 (0.3%)
15	O	0.41	0/947	0.99	2/1268 (0.2%)
16	P	0.39	0/1054	0.94	1/1403 (0.1%)
17	Q	0.42	0/1093	0.99	2/1460 (0.1%)
18	R	0.46	0/973	1.06	7/1301 (0.5%)
19	S	0.44	0/902	0.94	2/1209 (0.2%)
20	T	0.37	0/929	0.99	5/1242 (0.4%)
21	U	0.45	0/960	1.09	3/1278 (0.2%)
22	V	0.41	0/829	1.02	5/1107 (0.5%)
23	W	0.43	0/864	1.03	3/1156 (0.3%)
24	X	0.43	0/744	0.90	3/994 (0.3%)
25	Y	0.40	0/787	0.93	4/1051 (0.4%)
26	Z	0.37	0/766	0.87	3/1025 (0.3%)
27	AA	0.37	0/582	0.91	1/769 (0.1%)
28	BA	0.39	0/635	0.98	1/848 (0.1%)
29	CA	0.44	0/510	1.09	5/677 (0.7%)
30	DA	0.40	0/453	0.89	1/605 (0.2%)
31	EA	0.49	0/531	1.04	3/709 (0.4%)
32	FA	0.38	0/450	0.91	0/599
33	GA	0.38	0/416	0.83	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	HA	0.45	0/380	0.99	3/498 (0.6%)
35	IA	0.42	0/513	0.91	0/676
36	JA	0.51	0/303	1.07	1/397 (0.3%)
37	KA	0.43	0/464	0.60	0/723
38	MA	1.04	5/2751 (0.2%)	1.09	14/3703 (0.4%)
39	OA	0.70	2/1787 (0.1%)	1.32	13/2408 (0.5%)
40	PA	0.57	2/1651 (0.1%)	1.02	8/2225 (0.4%)
41	QA	0.44	0/1665	1.02	8/2227 (0.4%)
42	RA	0.55	1/1169 (0.1%)	1.16	12/1573 (0.8%)
43	SA	0.51	0/835	1.16	11/1128 (1.0%)
44	TA	0.42	0/1195	0.95	2/1602 (0.1%)
45	UA	0.41	0/989	0.96	2/1326 (0.2%)
46	VA	0.46	0/1034	1.02	2/1375 (0.1%)
47	WA	0.46	0/796	0.99	4/1077 (0.4%)
48	XA	0.45	0/885	0.97	3/1195 (0.3%)
49	YA	0.46	0/969	1.21	13/1300 (1.0%)
50	ZA	0.54	0/892	1.02	3/1193 (0.3%)
51	AB	1.14	10/822 (1.2%)	1.51	19/1095 (1.7%)
52	BB	0.44	0/722	1.05	5/964 (0.5%)
53	CB	0.44	0/659	1.02	2/884 (0.2%)
54	DB	0.36	0/657	0.87	1/881 (0.1%)
55	EB	0.47	0/544	0.95	2/731 (0.3%)
56	FB	0.46	0/652	0.93	1/877 (0.1%)
57	GB	0.39	0/671	0.96	6/888 (0.7%)
58	HB	0.53	0/550	1.21	7/728 (1.0%)
All	All	0.47	20/165304 (0.0%)	0.74	291/246564 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	10
2	B	0	33
3	C	0	1
4	D	0	1
All	All	0	45

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	OA	31	PHE	C-O	12.17	1.37	1.23
38	MA	77	MET	SD-CE	10.12	2.04	1.79
51	AB	63	ARG	CA-C	9.89	1.65	1.52
51	AB	71	HIS	CA-C	8.77	1.62	1.52
38	MA	67	MET	SD-CE	8.61	2.01	1.79

The worst 5 of 291 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	OA	32	GLY	N-CA-C	29.47	145.52	111.63
38	MA	342	GLU	CA-C-N	-16.08	101.59	119.28
38	MA	342	GLU	C-N-CA	-16.08	101.59	119.28
49	YA	22	ALA	N-CA-C	-12.41	97.25	111.03
39	OA	31	PHE	CA-C-N	-12.18	102.70	122.92

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	G	Sidechain
1	A	350	G	Sidechain
1	A	416	G	Sidechain
1	A	532	A	Sidechain
1	A	563	A	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	33012	0	16618	277	0
2	B	62318	0	31346	529	0
3	C	2568	0	1303	25	0
4	D	1640	0	837	28	0
4	LA	1640	0	837	15	0
5	E	1637	0	1719	40	0
6	F	2082	0	2157	36	0
7	G	1565	0	1616	33	0
8	H	1552	0	1619	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I	1410	0	1447	26	0
10	J	1323	0	1374	22	0
11	K	1111	0	1148	25	0
12	L	988	0	1025	41	0
13	M	1032	0	1088	33	0
14	N	1129	0	1162	17	0
15	O	938	0	1012	16	0
16	P	1045	0	1117	16	0
17	Q	1074	0	1157	12	0
18	R	960	0	1000	27	0
19	S	892	0	923	16	0
20	T	917	0	965	16	0
21	U	947	0	1022	21	0
22	V	816	0	839	18	0
23	W	857	0	922	13	0
24	X	738	0	807	5	0
25	Y	779	0	834	8	0
26	Z	753	0	780	9	0
27	AA	575	0	592	8	0
28	BA	625	0	655	3	0
29	CA	509	0	543	5	0
30	DA	449	0	491	7	0
31	EA	522	0	524	9	0
32	FA	444	0	461	8	0
33	GA	409	0	440	1	0
34	HA	377	0	418	8	0
35	IA	504	0	574	11	0
36	JA	302	0	343	10	0
37	KA	412	0	207	7	0
38	MA	2714	0	2636	63	0
39	OA	1756	0	1787	27	0
40	PA	1624	0	1699	37	0
41	QA	1643	0	1710	35	0
42	RA	1156	0	1199	25	0
43	SA	817	0	808	23	0
44	TA	1181	0	1240	4	0
45	UA	979	0	1034	14	0
46	VA	1022	0	1070	23	0
47	WA	786	0	828	25	0
48	XA	869	0	878	16	0
49	YA	955	0	1019	30	0
50	ZA	883	0	944	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	AB	810	0	852	59	0
52	BB	714	0	737	7	0
53	CB	649	0	666	18	0
54	DB	648	0	691	14	0
55	EB	535	0	552	7	0
56	FB	637	0	665	16	0
57	GB	665	0	714	6	0
58	HB	544	0	579	18	0
All	All	152438	0	104230	1709	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1709 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:77:MET:CE	38:MA:77:MET:SD	2.04	1.45
39:OA:32:GLY:O	39:OA:38:HIS:HA	1.51	1.08
39:OA:33:ALA:HA	39:OA:37:VAL:O	1.52	1.08
12:L:119:PRO:CD	12:L:120:ALA:H	1.63	1.03
51:AB:73:PHE:HA	51:AB:78:GLY:HA2	1.07	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	218/234 (93%)	185 (85%)	32 (15%)	1 (0%)	24	56
6	F	269/273 (98%)	229 (85%)	40 (15%)	0	100	100
7	G	207/209 (99%)	177 (86%)	27 (13%)	3 (1%)	9	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	199/201 (99%)	176 (88%)	19 (10%)	4 (2%)	6	32
9	I	175/179 (98%)	150 (86%)	23 (13%)	2 (1%)	11	42
10	J	174/177 (98%)	151 (87%)	20 (12%)	3 (2%)	7	34
11	K	147/149 (99%)	123 (84%)	19 (13%)	5 (3%)	3	25
12	L	129/165 (78%)	88 (68%)	34 (26%)	7 (5%)	1	16
13	M	139/142 (98%)	114 (82%)	21 (15%)	4 (3%)	3	26
14	N	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	50
15	O	120/123 (98%)	97 (81%)	20 (17%)	3 (2%)	4	29
16	P	141/144 (98%)	120 (85%)	19 (14%)	2 (1%)	9	37
17	Q	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8	36
18	R	118/127 (93%)	92 (78%)	24 (20%)	2 (2%)	7	34
19	S	114/117 (97%)	103 (90%)	8 (7%)	3 (3%)	4	28
20	T	112/115 (97%)	92 (82%)	19 (17%)	1 (1%)	14	45
21	U	115/118 (98%)	101 (88%)	13 (11%)	1 (1%)	14	45
22	V	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	6	32
23	W	108/110 (98%)	90 (83%)	15 (14%)	3 (3%)	4	27
24	X	91/100 (91%)	81 (89%)	10 (11%)	0	100	100
25	Y	100/104 (96%)	80 (80%)	17 (17%)	3 (3%)	3	26
26	Z	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
27	AA	73/85 (86%)	65 (89%)	8 (11%)	0	100	100
28	BA	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
29	CA	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	35
30	DA	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	EA	64/70 (91%)	52 (81%)	11 (17%)	1 (2%)	7	35
32	FA	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
33	GA	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
34	HA	44/46 (96%)	34 (77%)	9 (20%)	1 (2%)	5	30
35	IA	62/65 (95%)	50 (81%)	11 (18%)	1 (2%)	7	35
36	JA	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
38	MA	340/362 (94%)	292 (86%)	45 (13%)	3 (1%)	14	45
39	OA	223/241 (92%)	202 (91%)	19 (8%)	2 (1%)	14	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	PA	204/233 (88%)	177 (87%)	25 (12%)	2 (1%)	12	43
41	QA	203/206 (98%)	174 (86%)	21 (10%)	8 (4%)	2	21
42	RA	155/167 (93%)	121 (78%)	27 (17%)	7 (4%)	2	18
43	SA	98/131 (75%)	73 (74%)	20 (20%)	5 (5%)	1	17
44	TA	149/156 (96%)	125 (84%)	21 (14%)	3 (2%)	6	32
45	UA	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	7	35
46	VA	125/130 (96%)	98 (78%)	23 (18%)	4 (3%)	3	25
47	WA	96/103 (93%)	73 (76%)	19 (20%)	4 (4%)	2	20
48	XA	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	45
49	YA	121/124 (98%)	96 (79%)	19 (16%)	6 (5%)	1	17
50	ZA	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	34
51	AB	99/102 (97%)	64 (65%)	25 (25%)	10 (10%)	0	6
52	BB	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	5	30
53	CB	80/82 (98%)	63 (79%)	16 (20%)	1 (1%)	9	38
54	DB	78/84 (93%)	63 (81%)	12 (15%)	3 (4%)	2	22
55	EB	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
56	FB	77/92 (84%)	63 (82%)	14 (18%)	0	100	100
57	GB	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
58	HB	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	10
All	All	6412/6790 (94%)	5417 (84%)	868 (14%)	127 (2%)	8	32

5 of 127 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	83	VAL
9	I	2	LYS
10	J	119	GLY
11	K	9	VAL
11	K	10	ALA

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	
5	E	171/181 (94%)	170 (99%)	1 (1%)	78	79
6	F	216/218 (99%)	214 (99%)	2 (1%)	70	75
7	G	164/164 (100%)	164 (100%)	0	100	100
8	H	165/165 (100%)	162 (98%)	3 (2%)	51	67
9	I	148/150 (99%)	147 (99%)	1 (1%)	76	77
10	J	137/138 (99%)	137 (100%)	0	100	100
11	K	114/114 (100%)	112 (98%)	2 (2%)	51	67
12	L	100/123 (81%)	97 (97%)	3 (3%)	36	57
13	M	109/110 (99%)	108 (99%)	1 (1%)	70	75
14	N	116/116 (100%)	116 (100%)	0	100	100
15	O	103/104 (99%)	103 (100%)	0	100	100
16	P	102/103 (99%)	99 (97%)	3 (3%)	37	57
17	Q	109/109 (100%)	108 (99%)	1 (1%)	70	75
18	R	100/104 (96%)	100 (100%)	0	100	100
19	S	86/87 (99%)	83 (96%)	3 (4%)	32	54
20	T	99/100 (99%)	97 (98%)	2 (2%)	48	64
21	U	89/90 (99%)	89 (100%)	0	100	100
22	V	84/84 (100%)	83 (99%)	1 (1%)	63	72
23	W	93/93 (100%)	92 (99%)	1 (1%)	65	73
24	X	80/84 (95%)	80 (100%)	0	100	100
25	Y	83/85 (98%)	82 (99%)	1 (1%)	63	72
26	Z	78/78 (100%)	78 (100%)	0	100	100
27	AA	57/63 (90%)	57 (100%)	0	100	100
28	BA	67/68 (98%)	66 (98%)	1 (2%)	57	68
29	CA	55/55 (100%)	55 (100%)	0	100	100
30	DA	48/49 (98%)	48 (100%)	0	100	100
31	EA	59/62 (95%)	59 (100%)	0	100	100
32	FA	47/48 (98%)	46 (98%)	1 (2%)	47	64
33	GA	45/49 (92%)	45 (100%)	0	100	100
34	HA	38/38 (100%)	38 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	IA	51/52 (98%)	51 (100%)	0	100	100
36	JA	34/34 (100%)	34 (100%)	0	100	100
38	MA	284/302 (94%)	278 (98%)	6 (2%)	47	64
39	OA	186/199 (94%)	186 (100%)	0	100	100
40	PA	170/190 (90%)	165 (97%)	5 (3%)	37	57
41	QA	172/173 (99%)	171 (99%)	1 (1%)	78	79
42	RA	119/126 (94%)	116 (98%)	3 (2%)	42	61
43	SA	87/112 (78%)	86 (99%)	1 (1%)	65	73
44	TA	124/129 (96%)	124 (100%)	0	100	100
45	UA	104/105 (99%)	104 (100%)	0	100	100
46	VA	105/107 (98%)	105 (100%)	0	100	100
47	WA	86/90 (96%)	85 (99%)	1 (1%)	63	72
48	XA	89/99 (90%)	88 (99%)	1 (1%)	65	73
49	YA	103/104 (99%)	100 (97%)	3 (3%)	37	57
50	ZA	92/96 (96%)	91 (99%)	1 (1%)	65	73
51	AB	83/84 (99%)	79 (95%)	4 (5%)	23	48
52	BB	76/77 (99%)	76 (100%)	0	100	100
53	CB	65/65 (100%)	64 (98%)	1 (2%)	57	68
54	DB	74/78 (95%)	73 (99%)	1 (1%)	59	70
55	EB	56/65 (86%)	56 (100%)	0	100	100
56	FB	70/79 (89%)	69 (99%)	1 (1%)	59	70
57	GB	65/66 (98%)	64 (98%)	1 (2%)	57	68
58	HB	55/61 (90%)	53 (96%)	2 (4%)	31	54
All	All	5312/5525 (96%)	5253 (99%)	59 (1%)	63	73

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	MA	217	ILE
56	FB	66	VAL
40	PA	71	ARG
54	DB	69	THR
51	AB	58	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
21	U	43	GLN
49	YA	58	ASN
30	DA	48	ASN
49	YA	19	ASN
55	EB	51	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	223 (14%)	5 (0%)
2	B	2902/2903 (99%)	387 (13%)	8 (0%)
3	C	119/120 (99%)	18 (15%)	1 (0%)
37	KA	18/27 (66%)	3 (16%)	0
4	D	76/77 (98%)	10 (13%)	0
4	LA	76/77 (98%)	8 (10%)	0
All	All	4729/4743 (99%)	649 (13%)	14 (0%)

5 of 649 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	6	G
1	A	9	G
1	A	22	G
1	A	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1020	A
2	B	1130	U
3	C	66	A
2	B	2326	C
2	B	2756	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

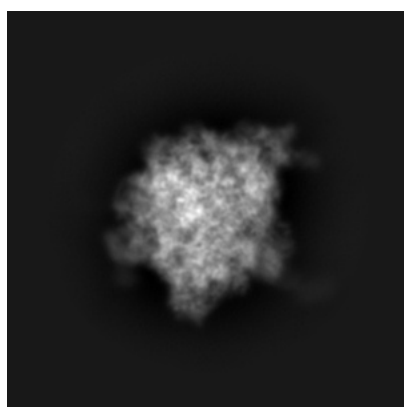
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7970. These allow visual inspection of the internal detail of the map and identification of artifacts.

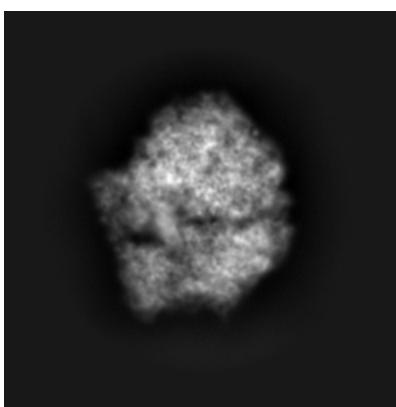
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

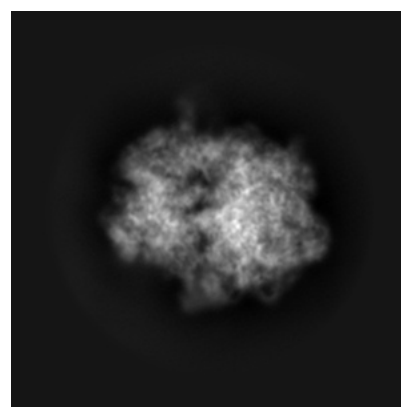
6.1.1 Primary map



X



Y

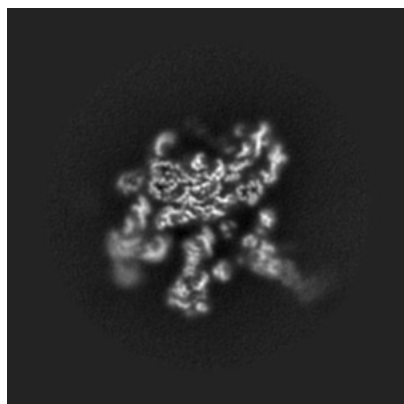


Z

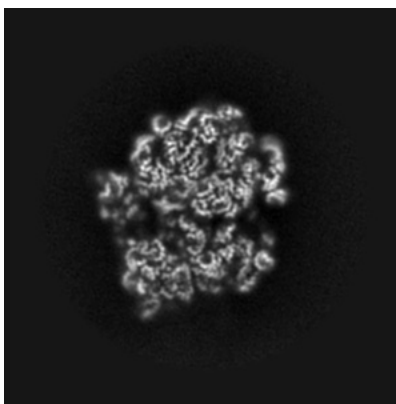
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

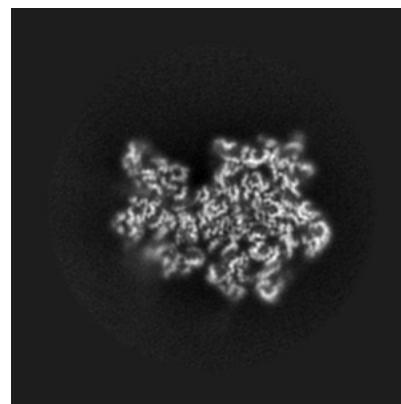
6.2.1 Primary map



X Index: 240



Y Index: 240

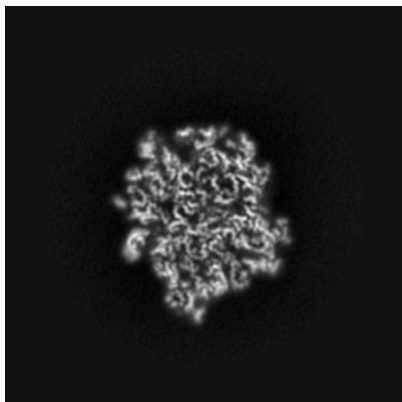


Z Index: 240

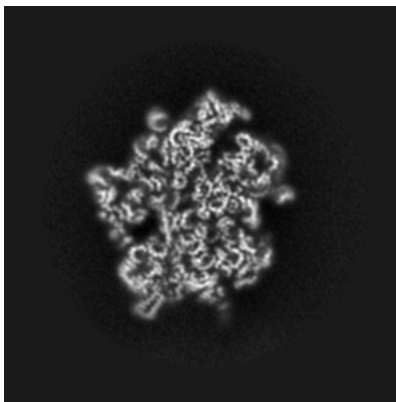
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

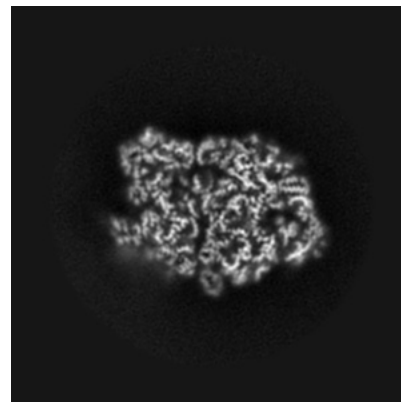
6.3.1 Primary map



X Index: 275



Y Index: 230

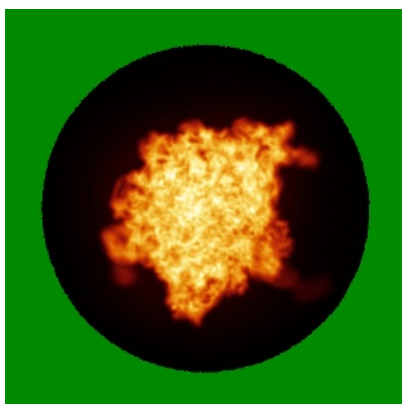


Z Index: 272

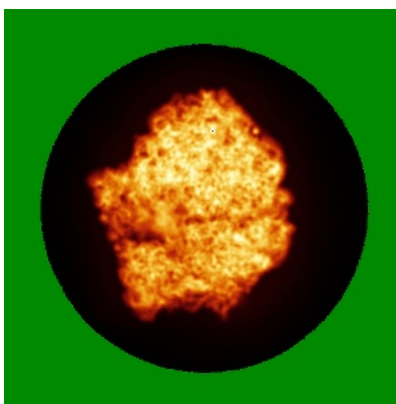
The images above show the largest variance slices of the map in three orthogonal directions.

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

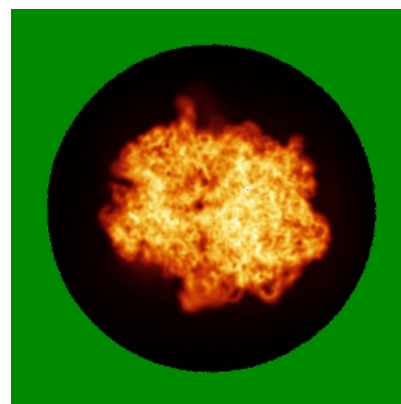
6.4.1 Primary map



X



Y

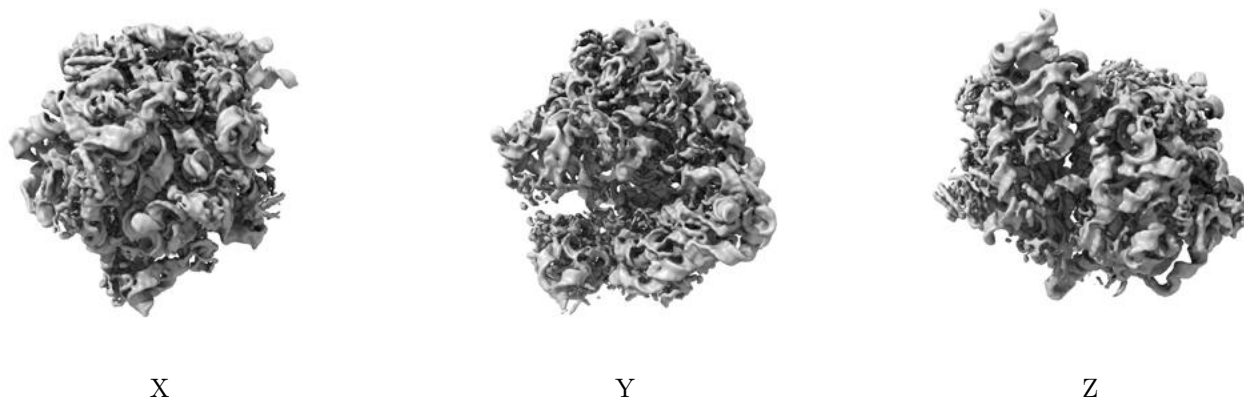


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

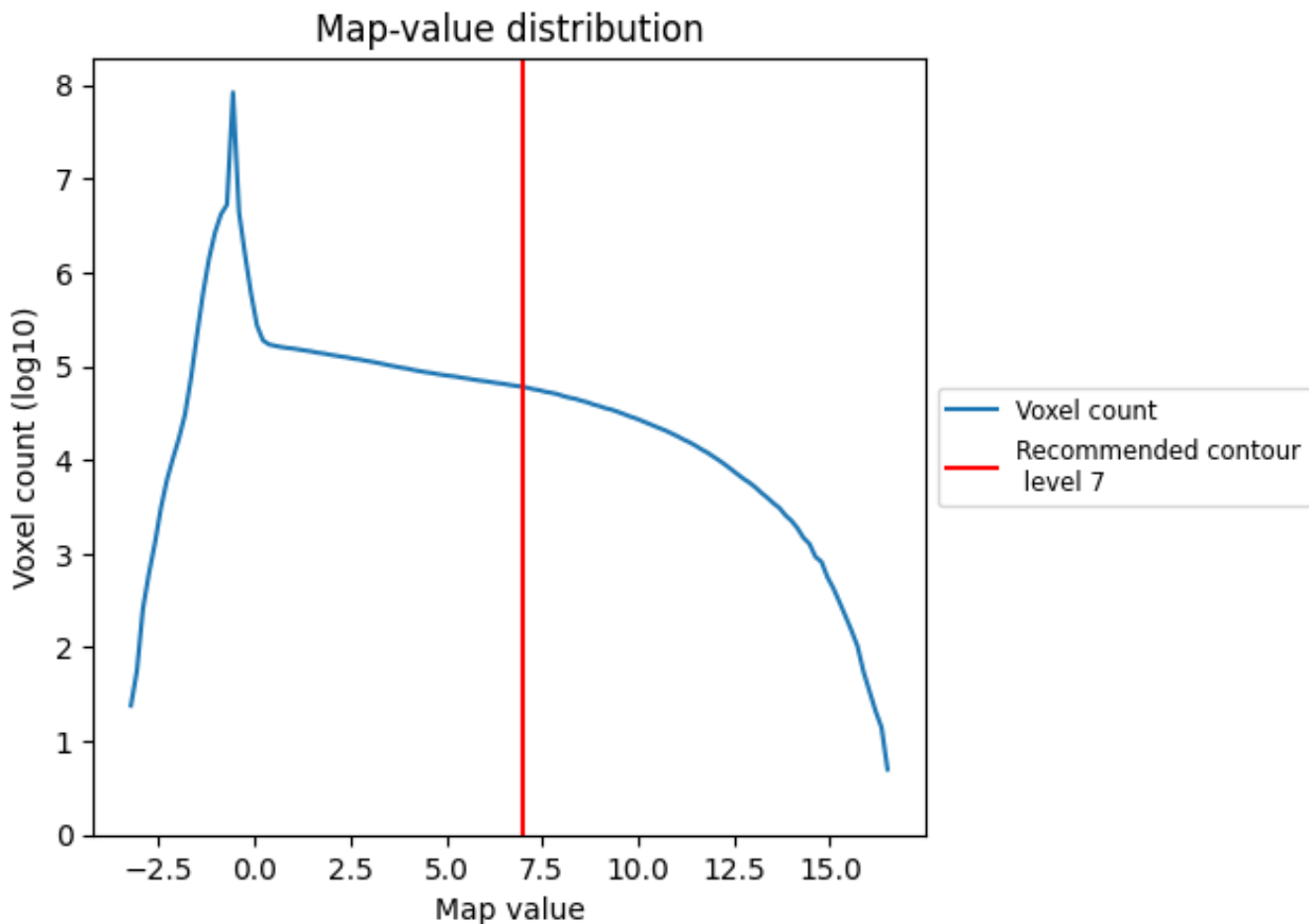
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

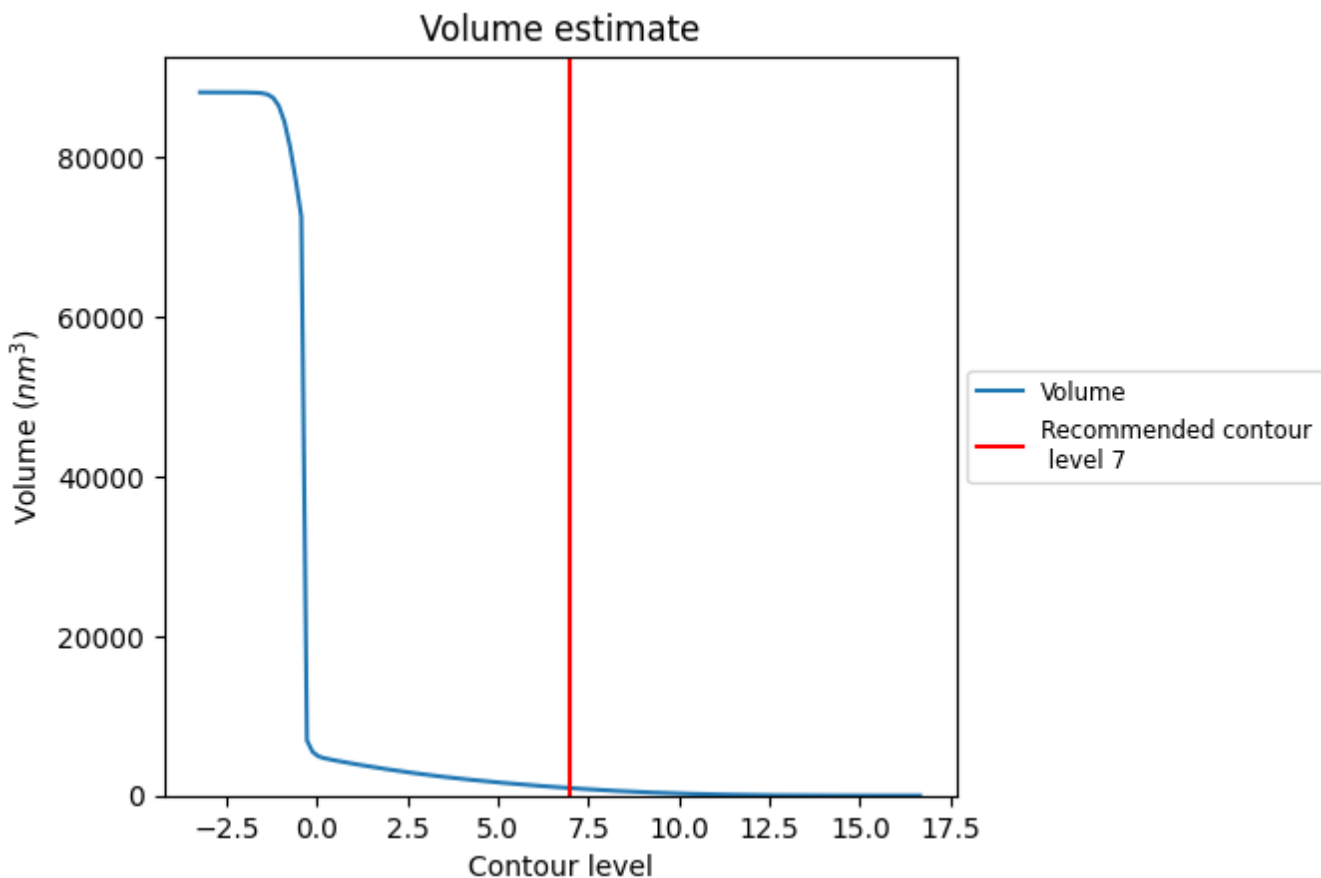
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

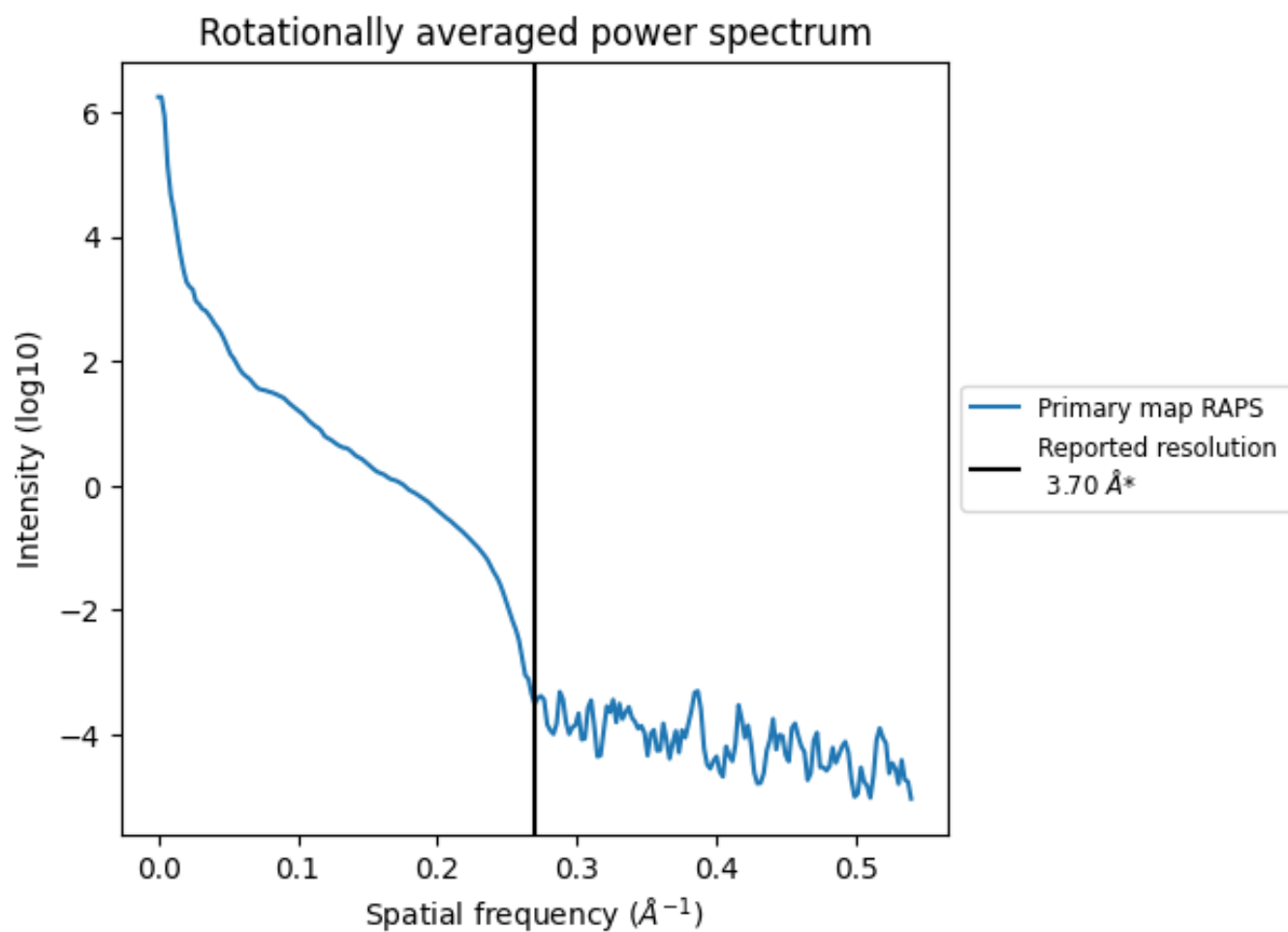
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 936 nm³; this corresponds to an approximate mass of 845 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\AA^{-1}

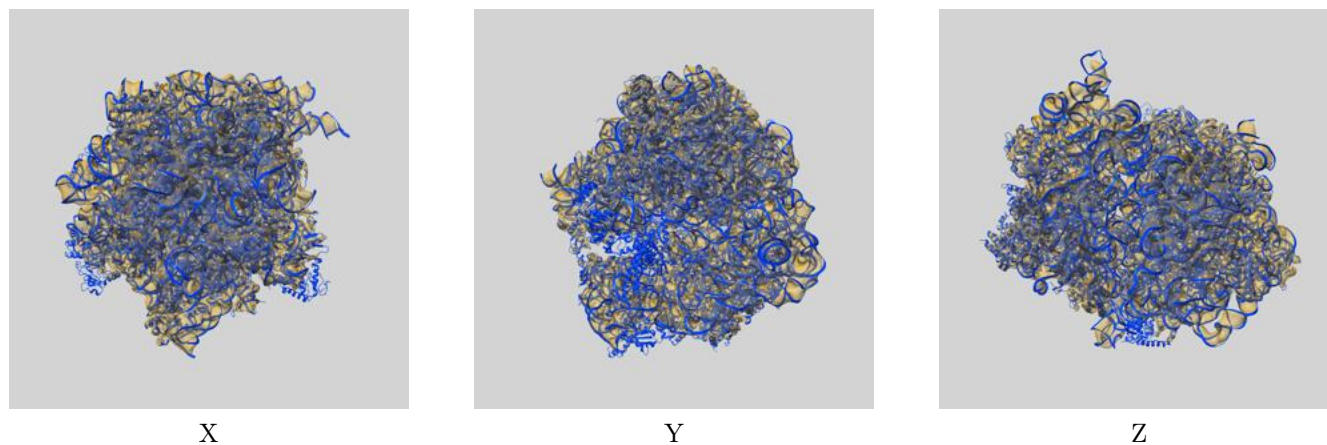
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

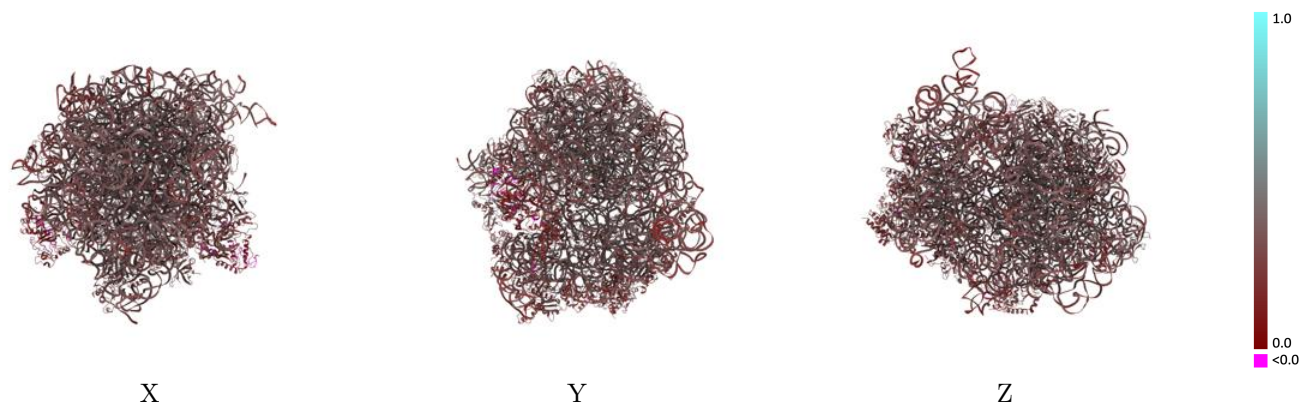
This section contains information regarding the fit between EMDB map EMD-7970 and PDB model 6DNC. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



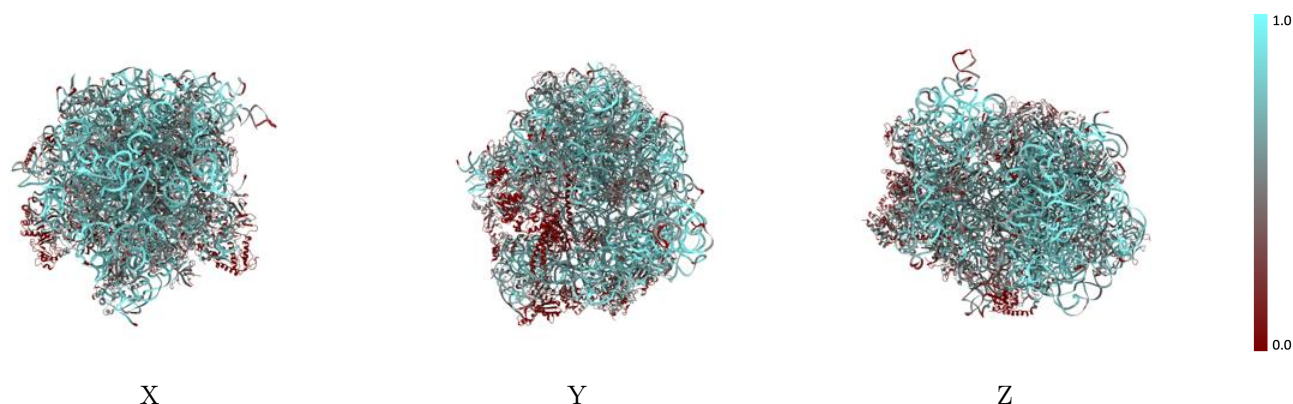
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



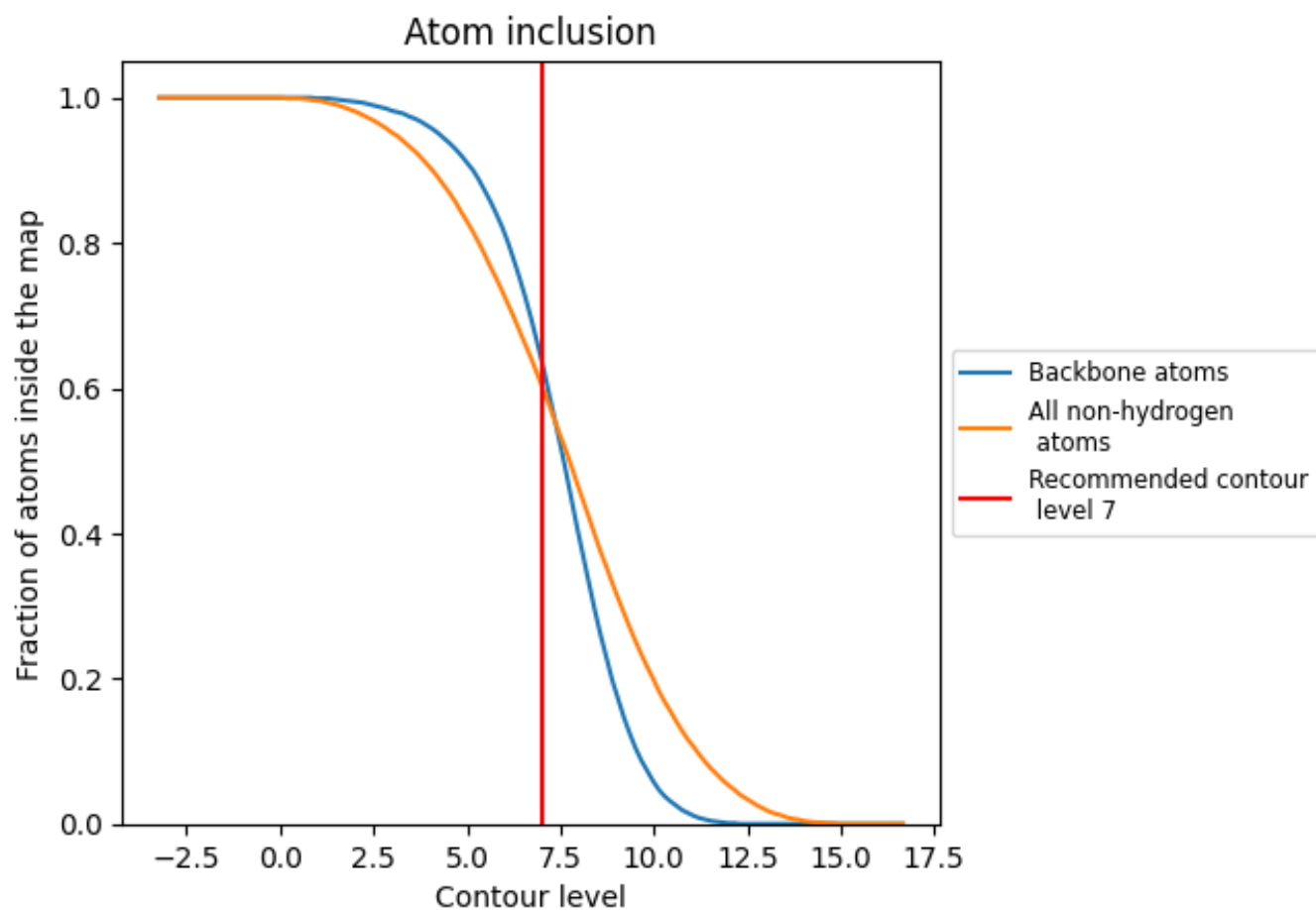
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 60% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6040	 0.3190
A	 0.7440	 0.3290
AA	 0.4360	 0.3360
AB	 0.3150	 0.2550
B	 0.7630	 0.3420
BA	 0.4260	 0.3190
BB	 0.4300	 0.2740
C	 0.7690	 0.3270
CA	 0.4530	 0.2410
CB	 0.4560	 0.3080
D	 0.4010	 0.2220
DA	 0.4440	 0.3190
DB	 0.3560	 0.3130
E	 0.0040	 0.1350
EA	 0.0940	 0.2490
EB	 0.3600	 0.2780
F	 0.3770	 0.3440
FA	 0.4320	 0.3270
FB	 0.3250	 0.2970
G	 0.3990	 0.3420
GA	 0.2240	 0.3180
GB	 0.4740	 0.2640
H	 0.3780	 0.3140
HA	 0.4250	 0.3150
HB	 0.2300	 0.2130
I	 0.3470	 0.2760
IA	 0.4170	 0.3420
J	 0.3140	 0.2970
JA	 0.3660	 0.3080
K	 0.1190	 0.2550
KA	 0.3810	 0.3090
L	 0.0020	 0.1020
LA	 0.4850	 0.3190
M	 0.0160	 0.1590
MA	 0.0200	 0.2600



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Chain	Atom inclusion	Q-score
N	0.4490	0.3170
O	0.2970	0.3400
OA	0.3040	0.2650
P	0.3970	0.3280
PA	0.1240	0.2940
Q	0.3170	0.3280
QA	0.3230	0.2600
R	0.4970	0.3190
RA	0.3870	0.3040
S	0.5030	0.3030
SA	0.4150	0.2940
T	0.3590	0.3270
TA	0.3160	0.2630
U	0.5050	0.2980
UA	0.4080	0.3040
V	0.4250	0.3390
VA	0.3750	0.2720
W	0.4160	0.3190
WA	0.1850	0.2790
X	0.4150	0.3190
XA	0.3560	0.3180
Y	0.4030	0.3140
YA	0.2300	0.3170
Z	0.4400	0.3110
ZA	0.3580	0.2690