Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 03:54 PM EST

PDB ID	:	8ESR
EMDB ID	:	EMD-24422
Title	:	Ytm1 associated nascent 60S ribosome (-fkbp39) State 2
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-14
Resolution	:	3.20 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

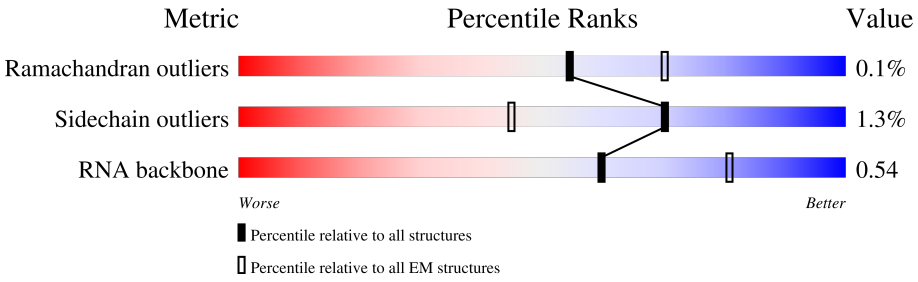
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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	1	3497	47% 14% 39%
2	2	165	76% 15% 9%
3	6	300	16% 11% 74%
4	7	707	16% 16% 84%
5	8	51	43% 57%
6	A	295	8% 68% 31%
7	B	388	85% 14%
8	C	363	98%

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Mol	Chain	Length	Quality of chain
9	D	578	28% 72% 28%
10	E	195	9% 78% 20%
11	F	250	84% 14%
12	G	259	79% 20%
13	H	190	95%
14	I	747	44% 55% 45%
15	J	333	18% 35% 65%
16	K	373	11% 66% 33%
17	L	208	55% 44%
18	M	134	93% 7%
19	N	201	82% 18%
20	O	197	99%
21	P	187	7% 78% 20%
22	Q	187	71% 29%
23	R	193	13% 58% 42%
24	S	176	6% 93% 5%
25	U	117	54% 84% 16%
26	V	139	9% 94% 5%
27	W	241	58% 89% 11%
28	X	141	94% 6%
29	Y	126	98%
30	Z	136	16% 99%
31	a	148	64% 34%
32	b	642	23% 56% 44%
33	c	117	44% 80% 20%

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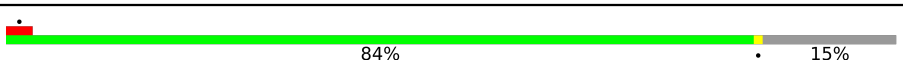
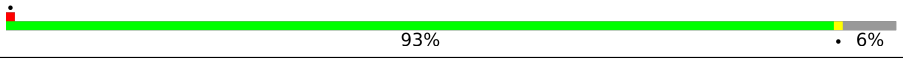
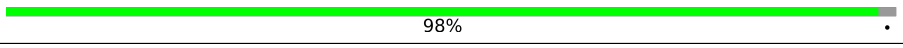
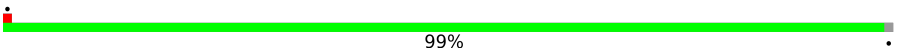
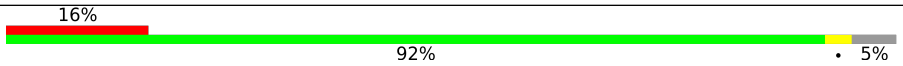
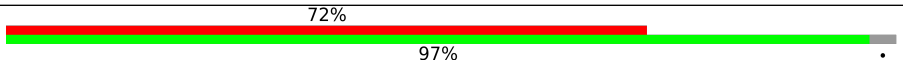
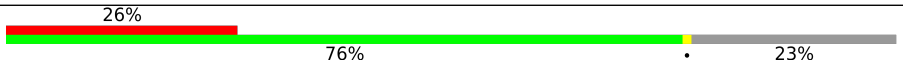
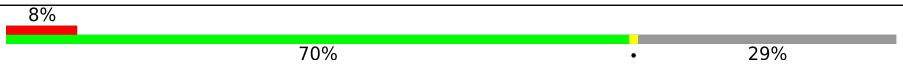
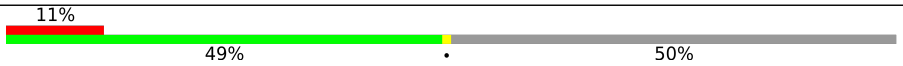
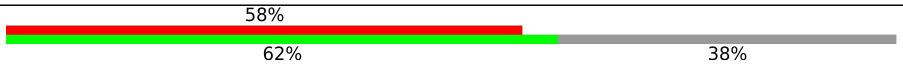
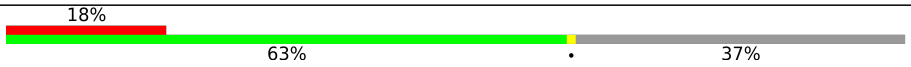
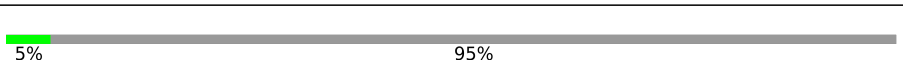
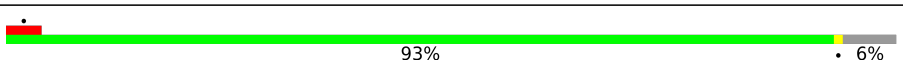
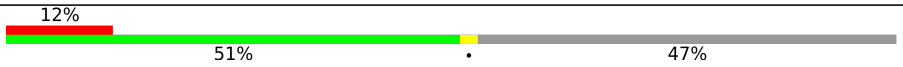
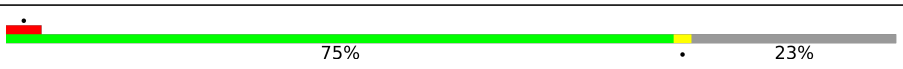
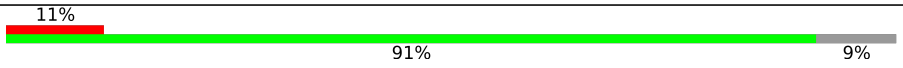
Mol	Chain	Length	Quality of chain
34	d	113	
35	e	127	
36	f	108	
37	g	112	
38	h	122	
39	i	99	
40	j	91	
41	k	74	
42	l	180	
43	m	740	
44	n	607	
45	o	276	
46	p	440	
47	q	608	
48	r	260	
49	s	470	
50	t	249	
51	u	192	
52	v	209	
53	w	802	
54	y	244	
55	z	117	
56	T	160	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 116762 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 RNA (2142-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2143	45883	20493	8324	14923	2143	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1741	C	U	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	150	3189	1427	564	1048	150	0	0

- Molecule 3 is a RNA chain called RNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	79	1674	751	288	556	79	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	137	C	U	conflict	GB 157310483
6	146	G	U	conflict	GB 157310483

- Molecule 4 is a protein called Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	7	110	548	328	110	110	0	0

- Molecule 5 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	8	22	Total	C	N	O	0	0
			187	119	40	28		

- Molecule 6 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	204	Total	C	N	O	S	0	0
			1652	1057	295	293	7		

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	335	Total	C	N	O	S	0	0
			2662	1687	492	474	9		

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 9 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	418	Total	C	N	O	S	0	0
			3320	2140	570	599	11		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	156	Total	C	N	O	S	0	0
			1213	777	226	207	3		

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	214	Total	C	N	O	S	0	0
			1745	1124	320	298	3		

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	206	Total	C	N	O	S	0	0
			1607	1030	294	280	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 14 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	409	Total	C	N	O	0	0
			2032	1214	409	409		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	607	LYS	LEU	conflict	UNP O94288

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	J	115	Total	C	N	O	0	0
			574	344	115	115		

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	250	Total	C	N	O	S	0	0
			1964	1256	336	366	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	165	Total	C	N	O	S	0	0
			1392	872	289	228	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	149	Total	C	N	O	S	0	0
			1168	742	216	207	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	133	Total	C	N	O	S	0	0
			1032	650	199	182	1		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	112	Total	C	N	O	S	0	0
			729	445	148	133	3		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	167	Total	C	N	O	S	0	0
			1401	905	262	229	5		

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	U	98	Total 484	C 288	N 98	O 98	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	132	Total 991	C 625	N 182	O 176	S 8	0	0

- Molecule 27 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	W	215	Total 1057	C 627	N 215	O 215	0	0

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	132	Total 1044	C 664	N 194	O 185	S 1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	125	Total 998	C 622	N 201	O 173	S 2	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Z	134	Total 662	C 393	N 134	O 135	0	0

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	a	97	Total 762	C 483	N 145	O 134	0	0

- Molecule 32 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	359	Total 1780	C 1062	N 359	O 359	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	c	94	Total 462	C 274	N 94	O 94	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	96	Total 801	C 507	N 158	O 133	S 3	0	0

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	119	Total 953	C 597	N 193	O 158	S 5	0	0

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total 839	C 534	N 162	O 140	S 3	0	0

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	g	97	Total 478	C 284	N 97	O 97	0	0

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	h	121	Total 999	C 629	N 194	O 176	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	85	Total	C	N	O	S	0	0
			696	431	148	116	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 42 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	l	174	Total	C	N	O	0	0
			860	512	174	174		

- Molecule 43 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	572	Total	C	N	O	S	0	0
			4526	2883	790	842	11		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	432	Total	C	N	O	S	0	0
			3517	2262	606	637	12		

- Molecule 45 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	137	Total	C	N	O	S	0	0
			1138	732	213	187	6		

- Molecule 46 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	p	275	Total	C	N	O	0	0
			1357	807	275	275		

- Molecule 47 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	q	260	Total	C	N	O	0	0
			1282	762	260	260		

- Molecule 48 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	165	Total	C	N	O	S	0	0
			1081	653	223	204	1		

- Molecule 49 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	s	23	Total	C	N	O	0	0
			193	117	44	32		

- Molecule 50 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	235	Total	C	N	O	S	0	0
			1948	1242	367	334	5		

- Molecule 51 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	101	Total	C	N	O	S	0	0
			714	448	143	116	7		

- Molecule 52 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 53 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	180	Total	C	N	O	S	0	0
			1462	910	276	270	6		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	y	223	Total	C	N	O	0	0
			1097	651	223	223		

- Molecule 55 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	z	35	Total	C	N	O	0	0
			292	183	63	46		

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	T	18	Total	C	N	O	0	0
			138	87	24	27		

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

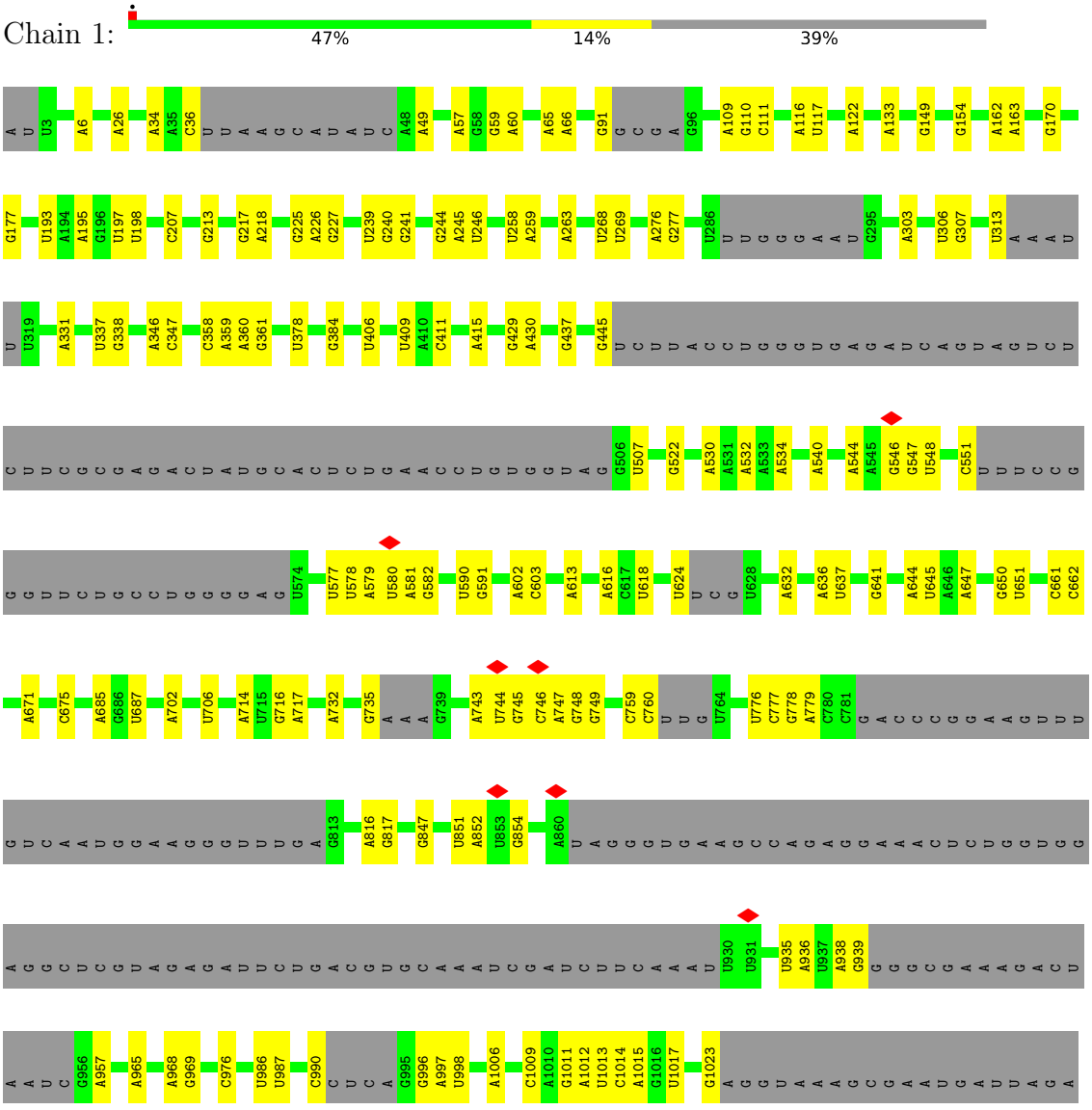
Mol	Chain	Residues	Atoms		AltConf
57	j	1	Total	Zn	0
			1	1	

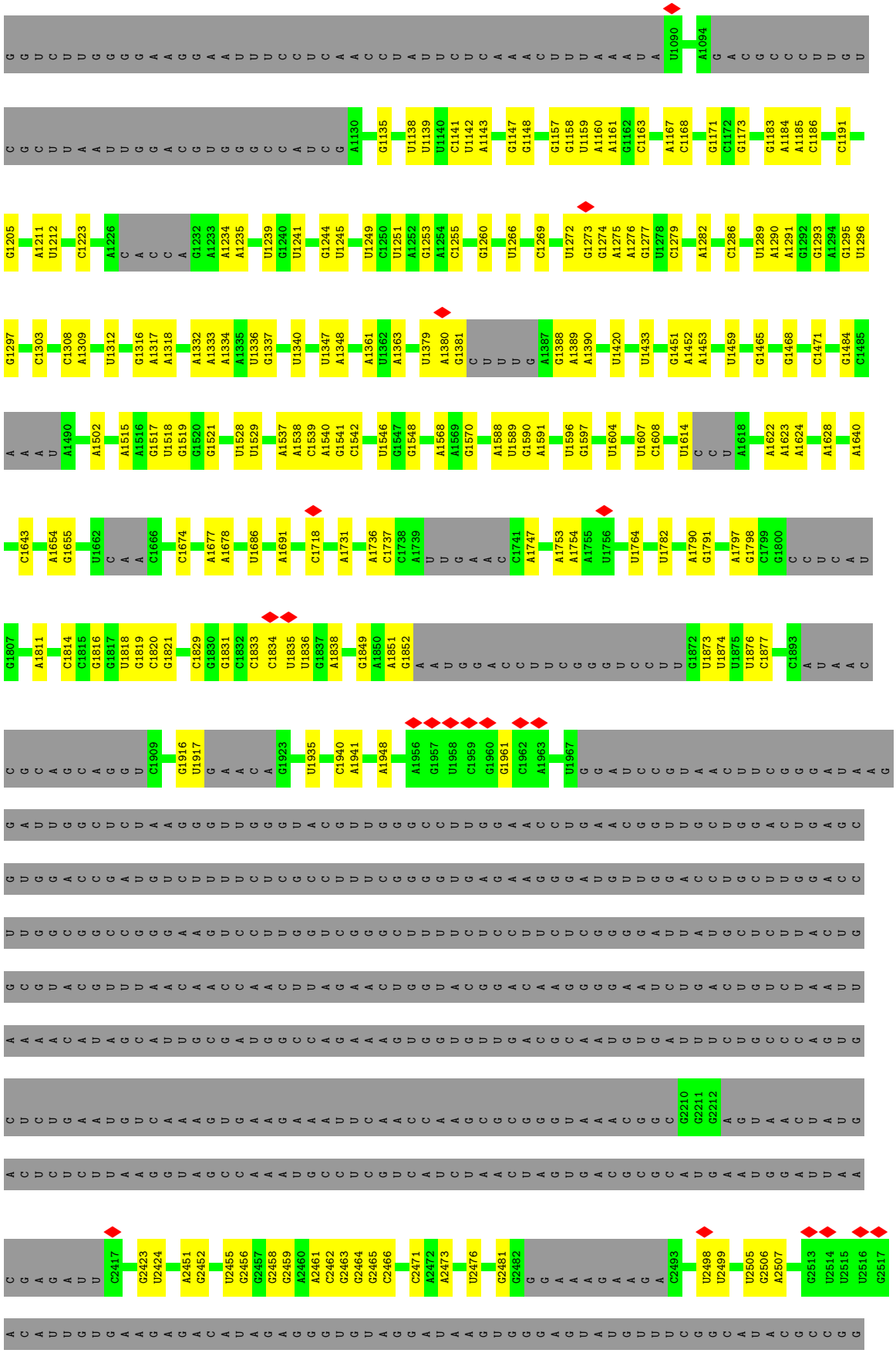
3 Residue-property plots (i)

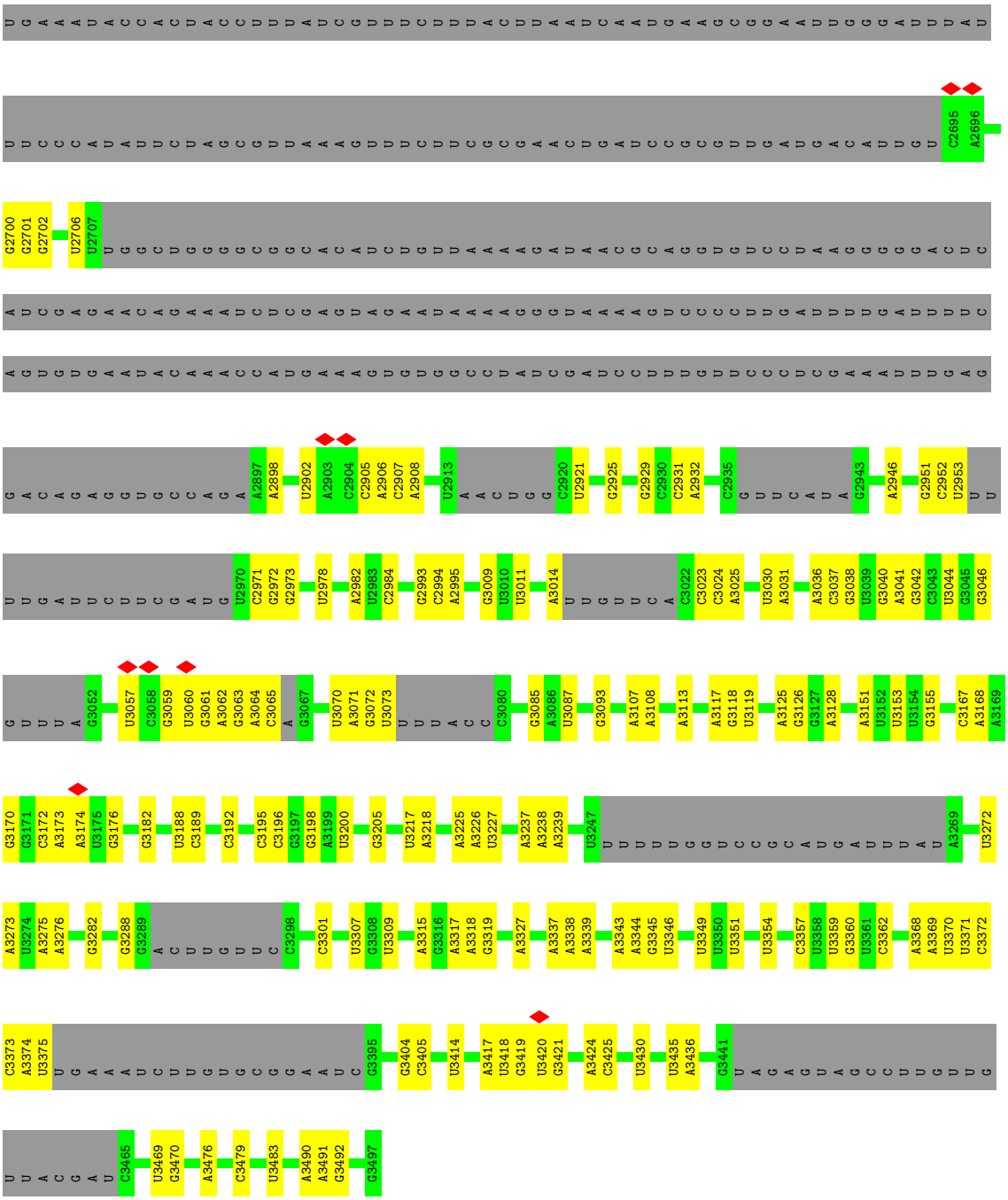
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (2142-MER)

Chain 1:

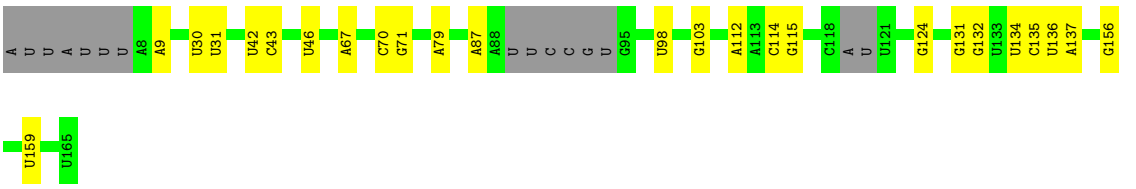






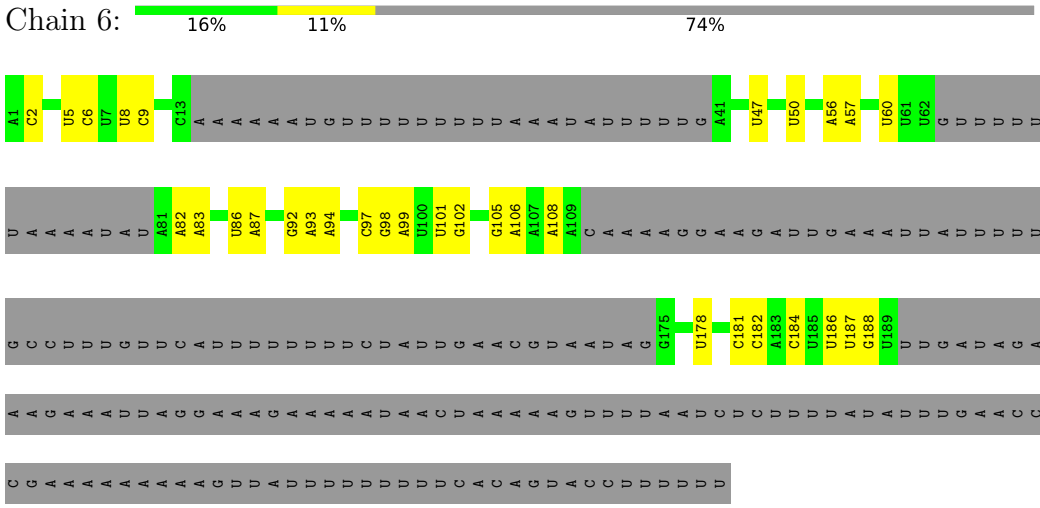
• Molecule 2: RNA (150-MER)

Chain 2:



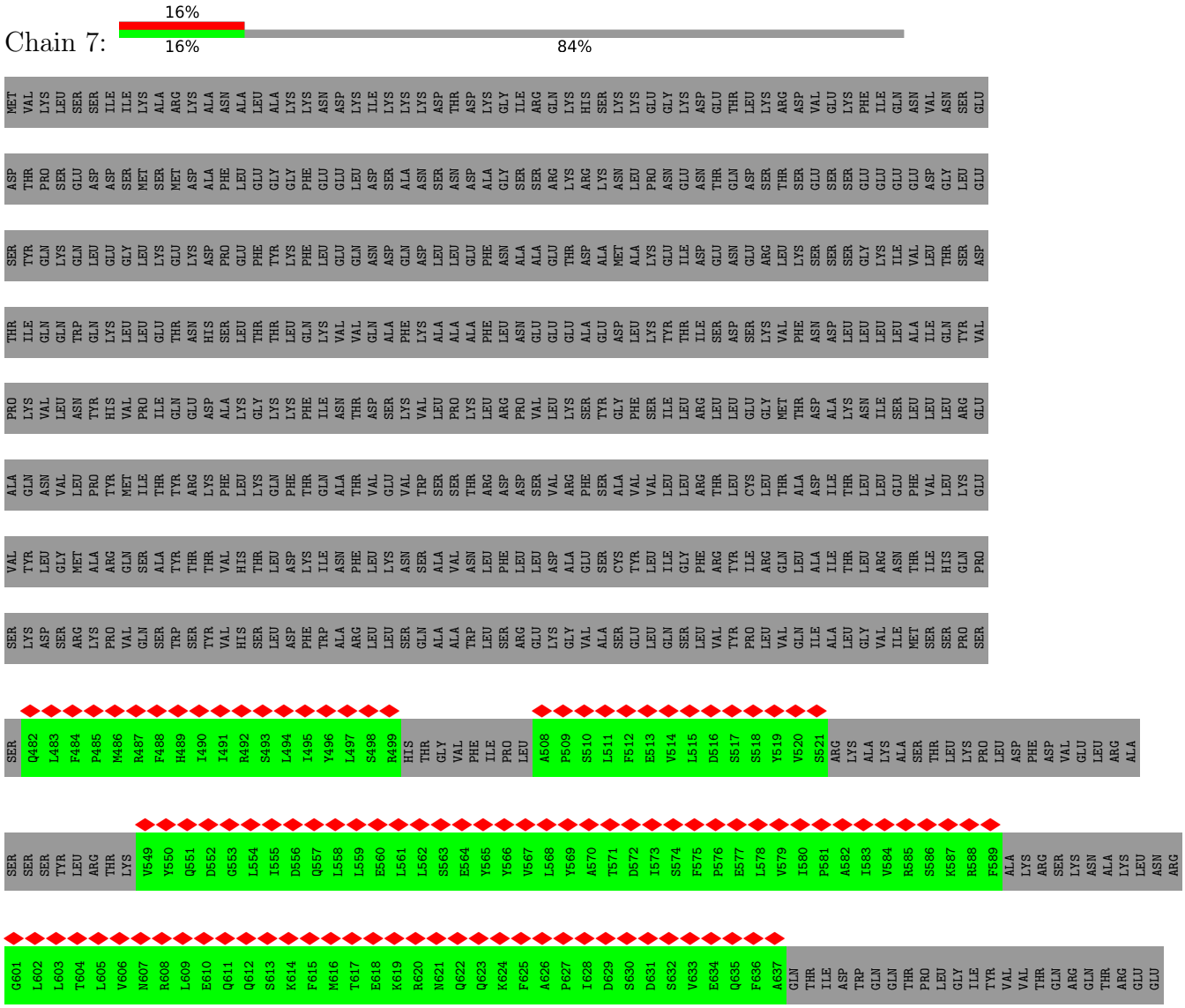
• Molecule 3: RNA (79-MER)

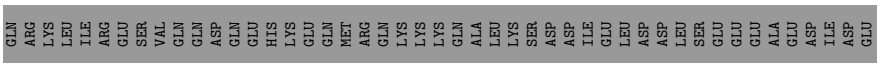
Chain 6:



• Molecule 4: Noc2

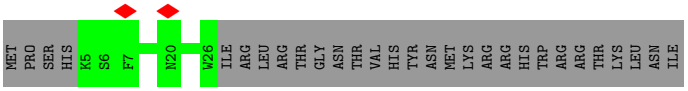
Chain 7:





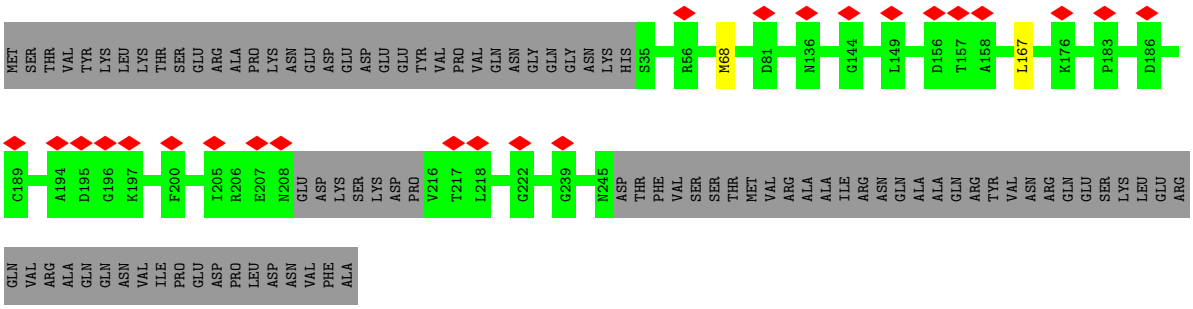
• Molecule 5: 60S ribosomal protein L39

Chain 8:



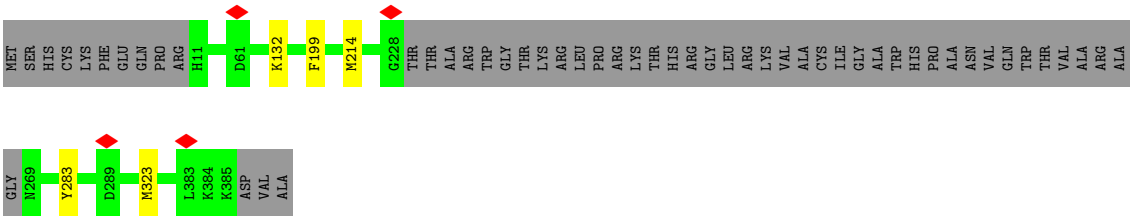
• Molecule 6: Ribosome biogenesis protein brx1

Chain A:



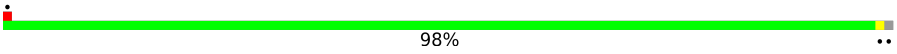
• Molecule 7: 60S ribosomal protein L3-A

Chain B:



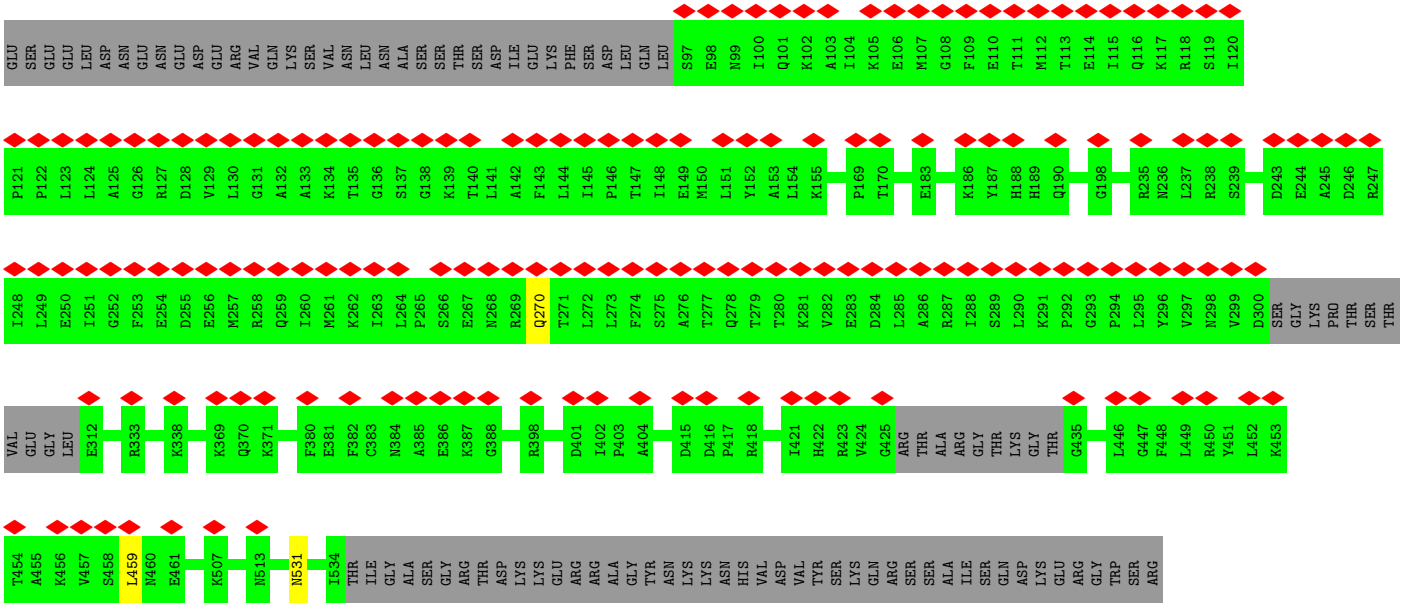
• Molecule 8: 60S ribosomal protein L4-B

Chain C:

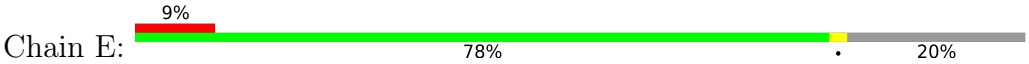


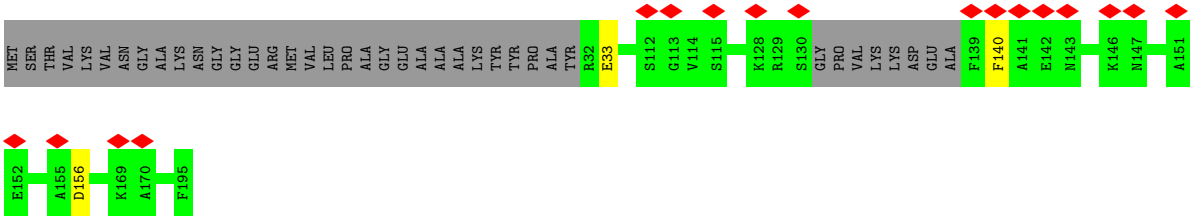
• Molecule 9: ATP-dependent RNA helicase has1

Chain D:

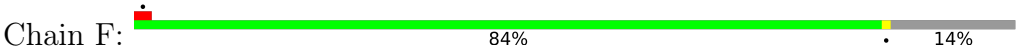


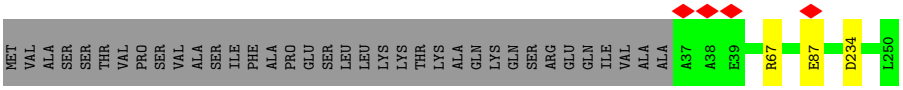
• Molecule 10: 60S ribosomal protein L6



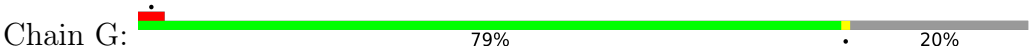


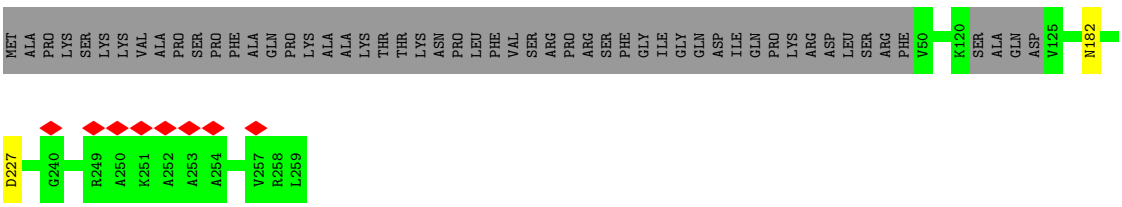
• Molecule 11: 60S ribosomal protein L7-B





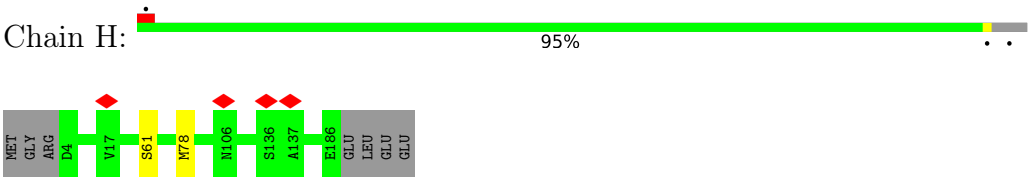
• Molecule 12: 60S ribosomal protein L8





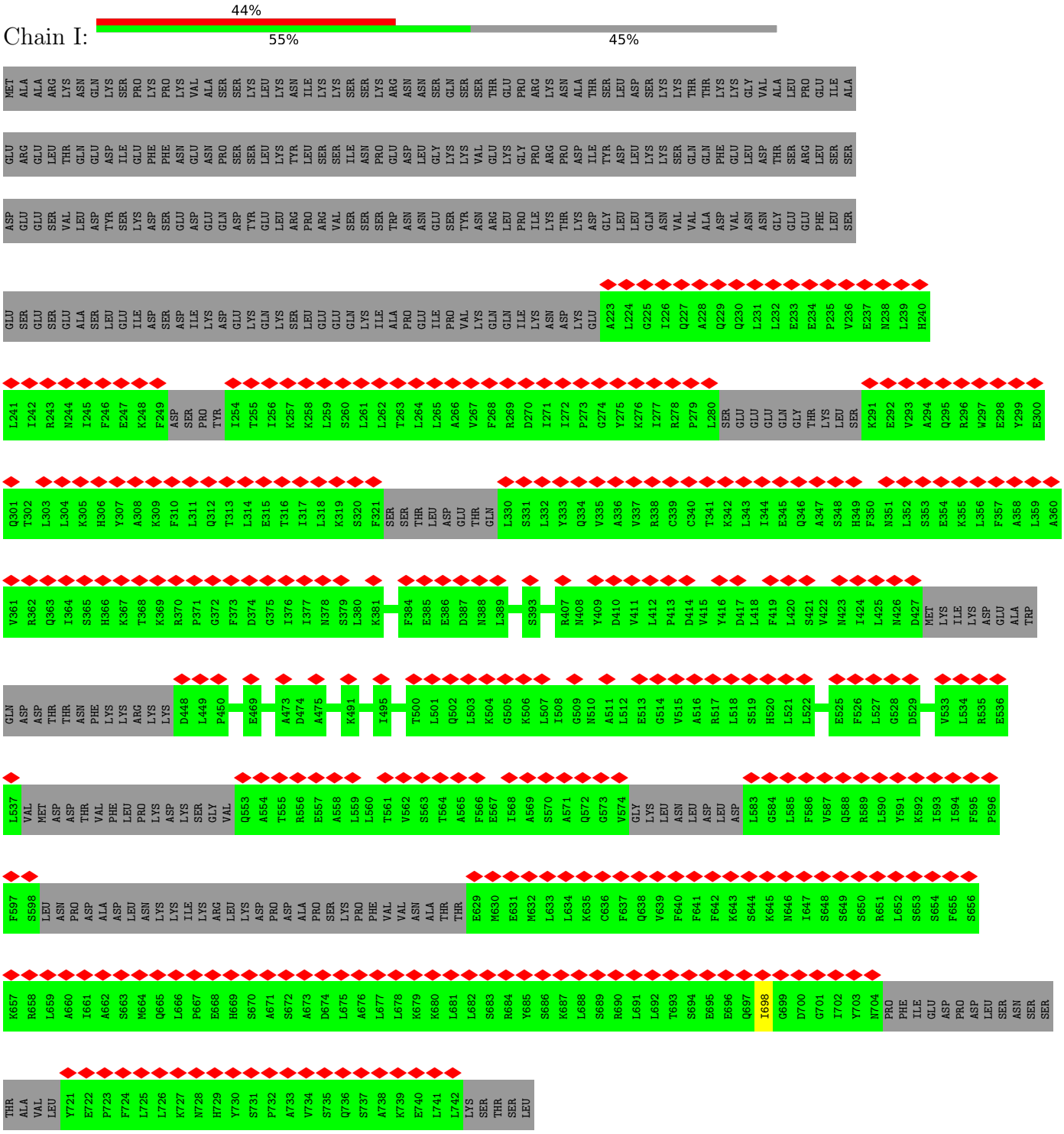
• Molecule 13: 60S ribosomal protein L9-A

Chain H:



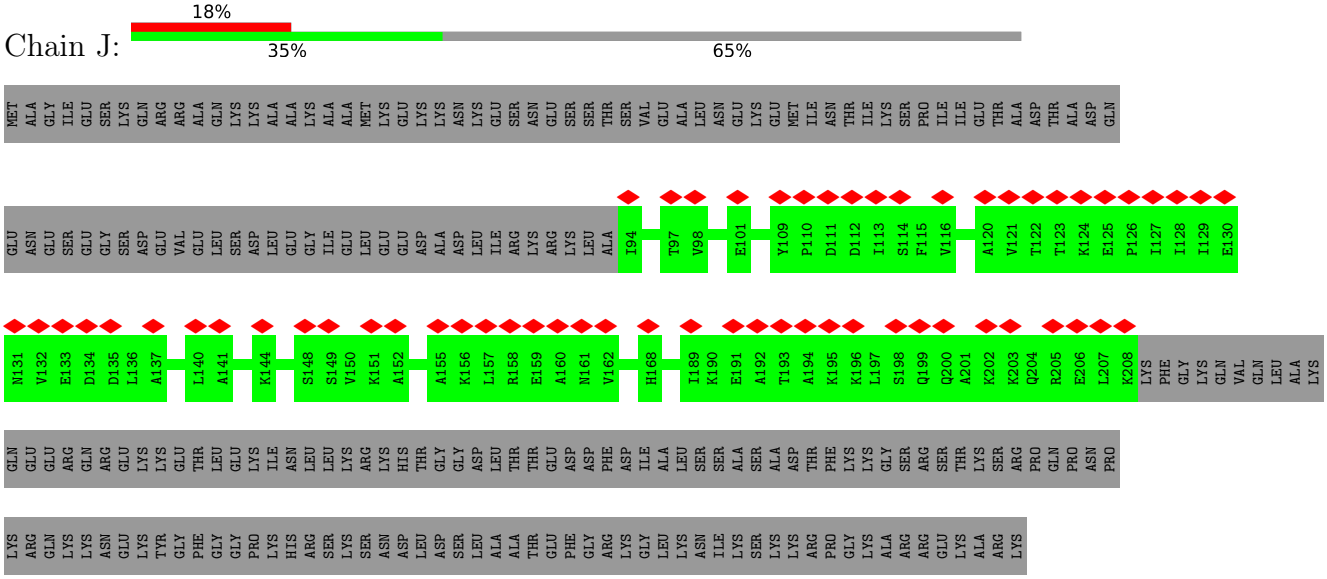
• Molecule 14: Nucleolar complex-associated protein 3

Chain I:



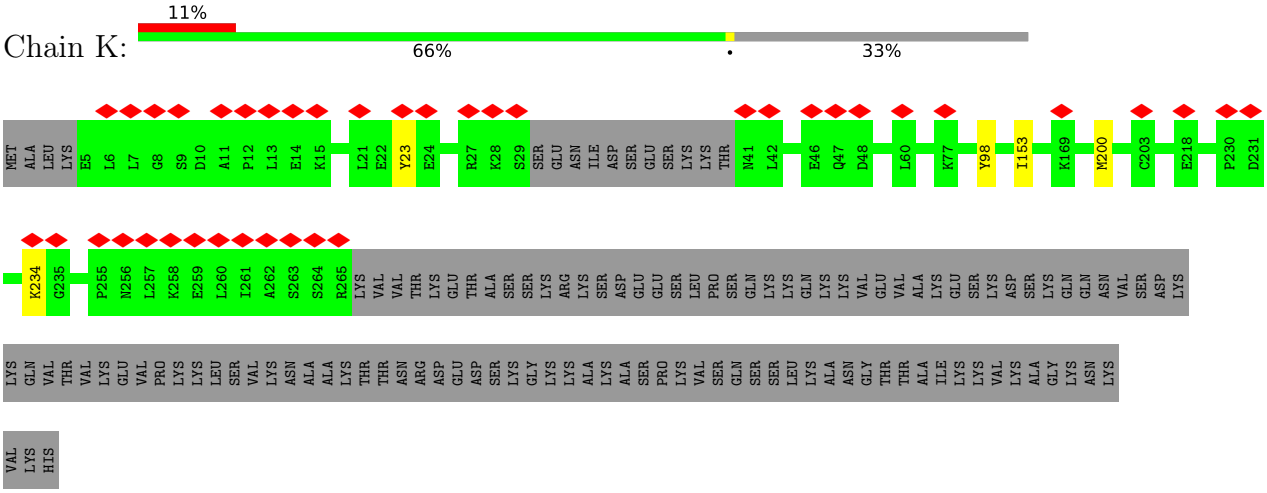
• Molecule 15: Probable rRNA-processing protein ebp2

Chain J:



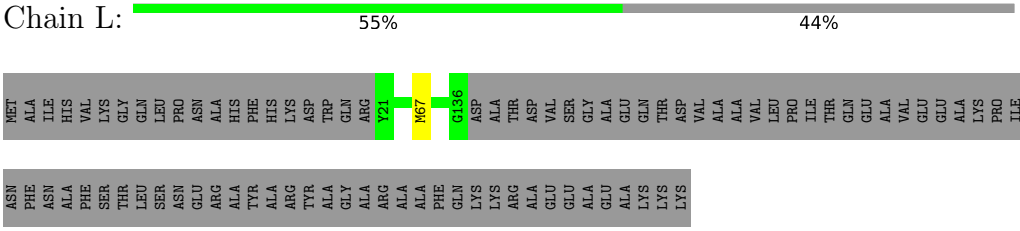
• Molecule 16: Putative ribosome biogenesis protein C8F11.04

Chain K:



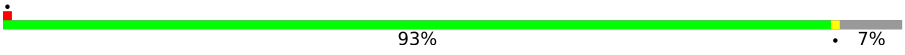
• Molecule 17: 60S ribosomal protein L13

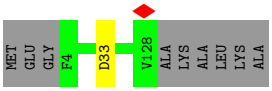
Chain L:



• Molecule 18: 60S ribosomal protein L14

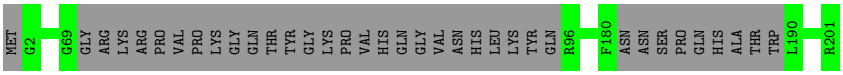
Chain M:





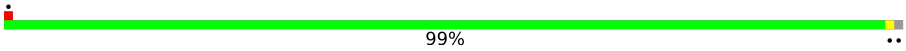
• Molecule 19: 60S ribosomal protein L15-A

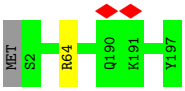
Chain N:



• Molecule 20: 60S ribosomal protein L16-B

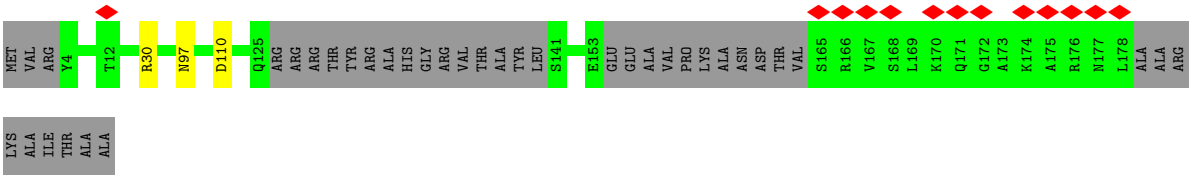
Chain O:





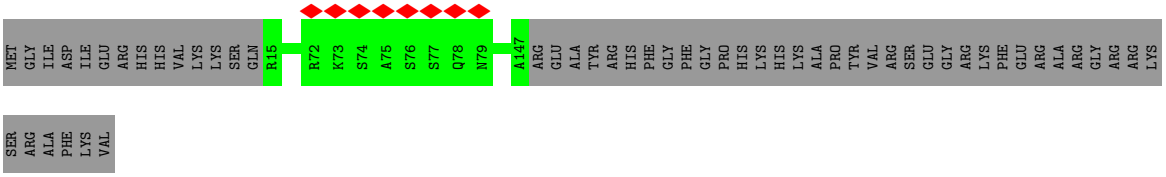
• Molecule 21: 60S ribosomal protein L17-A

Chain P:



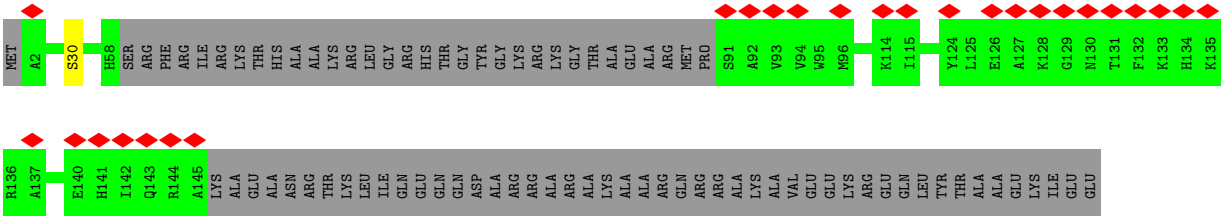
• Molecule 22: 60S ribosomal protein L18-A

Chain Q:



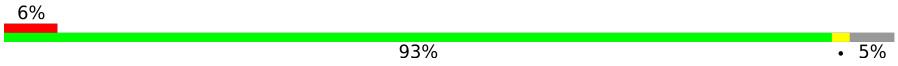
• Molecule 23: 60S ribosomal protein L19-A

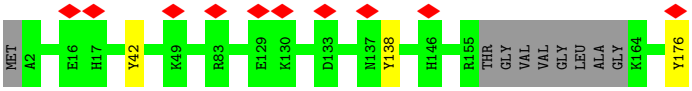
Chain R:



• Molecule 24: 60S ribosomal protein L20-A

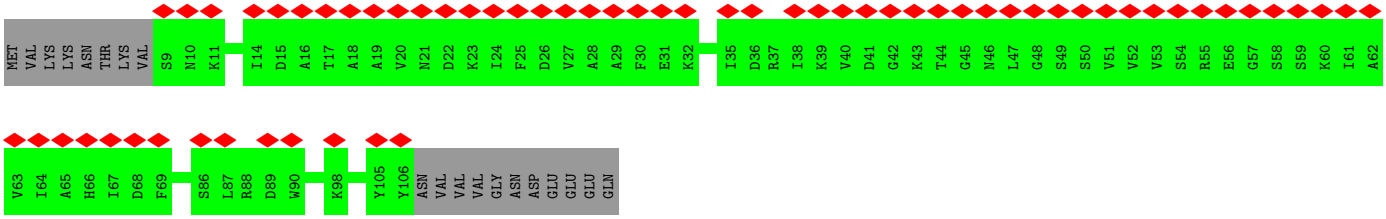
Chain S:





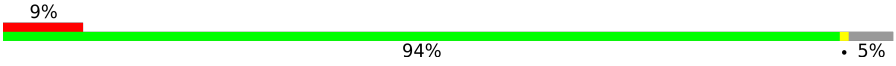
• Molecule 25: 60S ribosomal protein L22

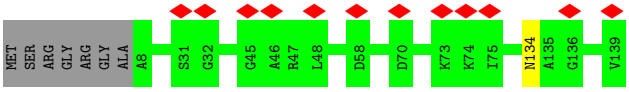
Chain U:



• Molecule 26: 60S ribosomal protein L23-A

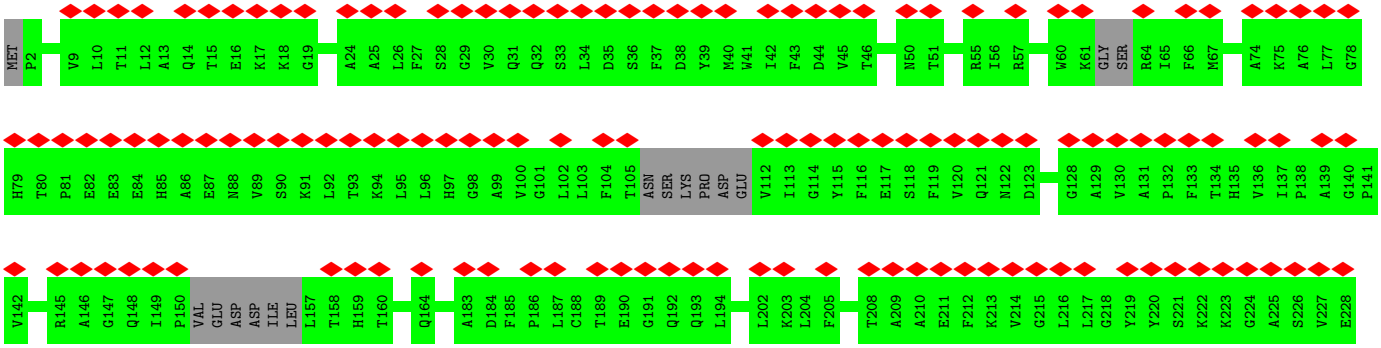
Chain V:





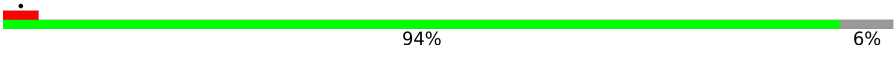
• Molecule 27: Ribosome assembly factor mrt4

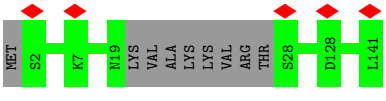
Chain W:



• Molecule 28: 60S ribosomal protein L25-A

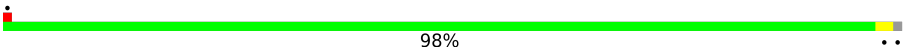
Chain X:

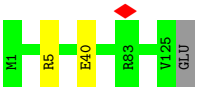




• Molecule 29: 60S ribosomal protein L26

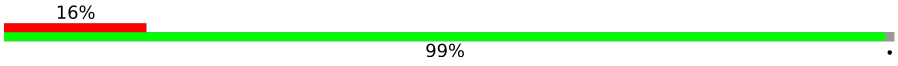
Chain Y:

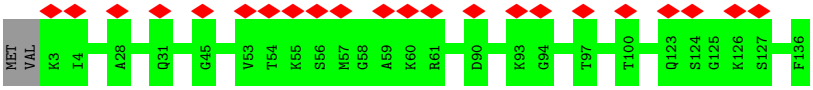




• Molecule 30: 60S ribosomal protein L27-A

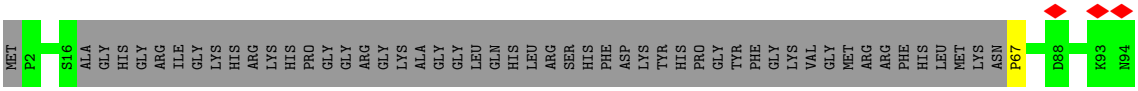
Chain Z:

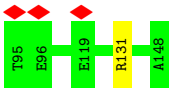




• Molecule 31: 60S ribosomal protein L28-A

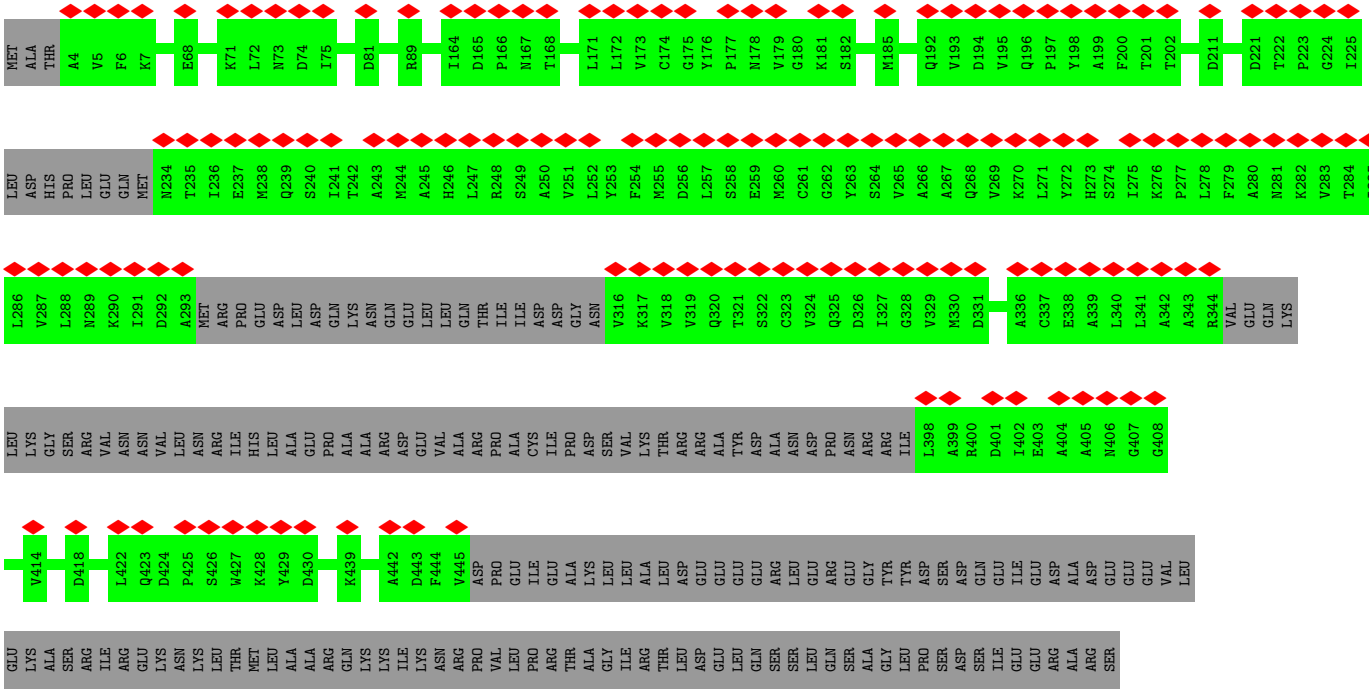
Chain a:

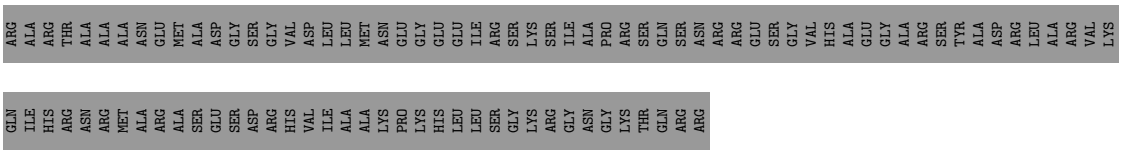




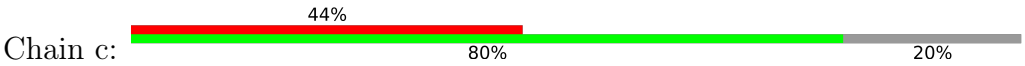
• Molecule 32: Probable nucleolar GTP-binding protein 1

Chain b:

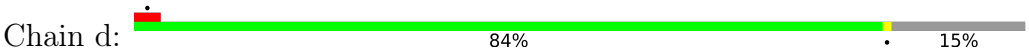


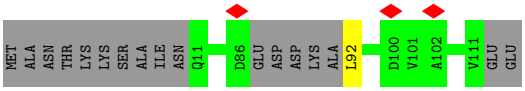


• Molecule 33: 60S ribosomal protein L30-2

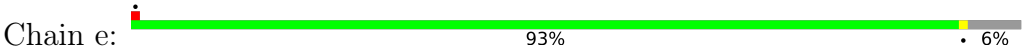


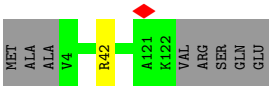
• Molecule 34: 60S ribosomal protein L31





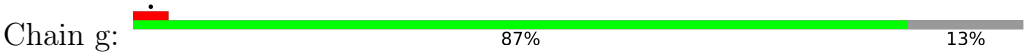
• Molecule 35: 60S ribosomal protein L32-A

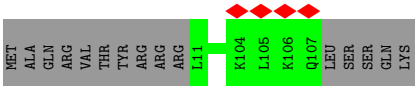




• Molecule 36: 60S ribosomal protein L33-B

• Molecule 37: 60S ribosomal protein L34-A

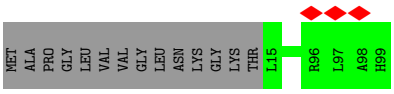




• Molecule 38: 60S ribosomal protein L35

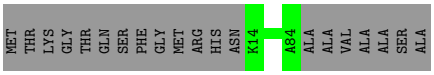
• Molecule 39: 60S ribosomal protein L36-B

Chain i:



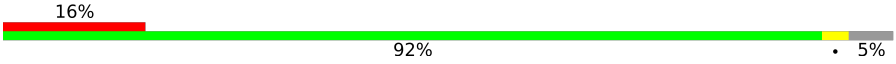
• Molecule 40: 60S ribosomal protein L37-B

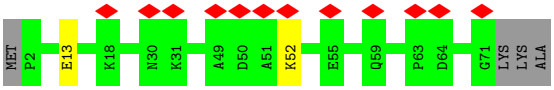
Chain j:



• Molecule 41: 60S ribosomal protein L38-1

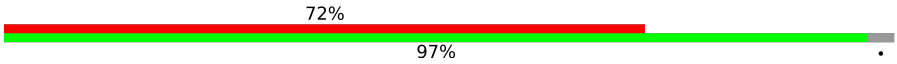
Chain k:

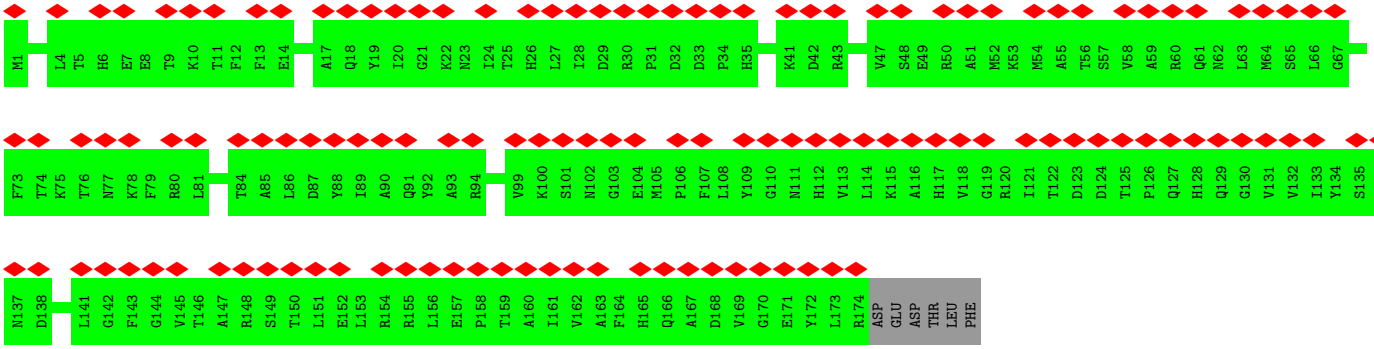




• Molecule 42: 60S ribosome subunit biogenesis protein nip7

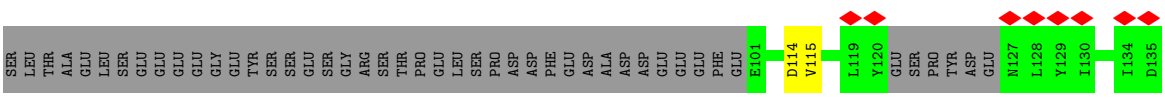
Chain l:

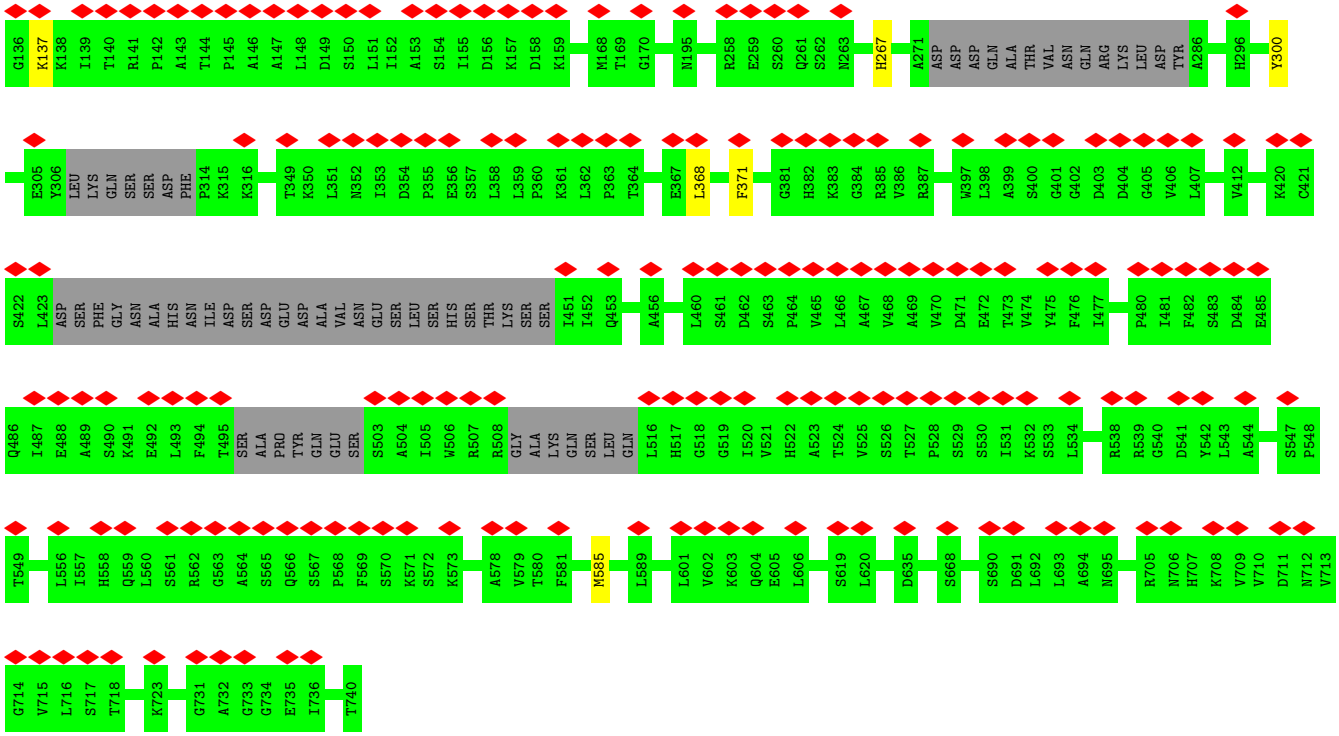




• Molecule 43: Ribosome biogenesis protein erb1

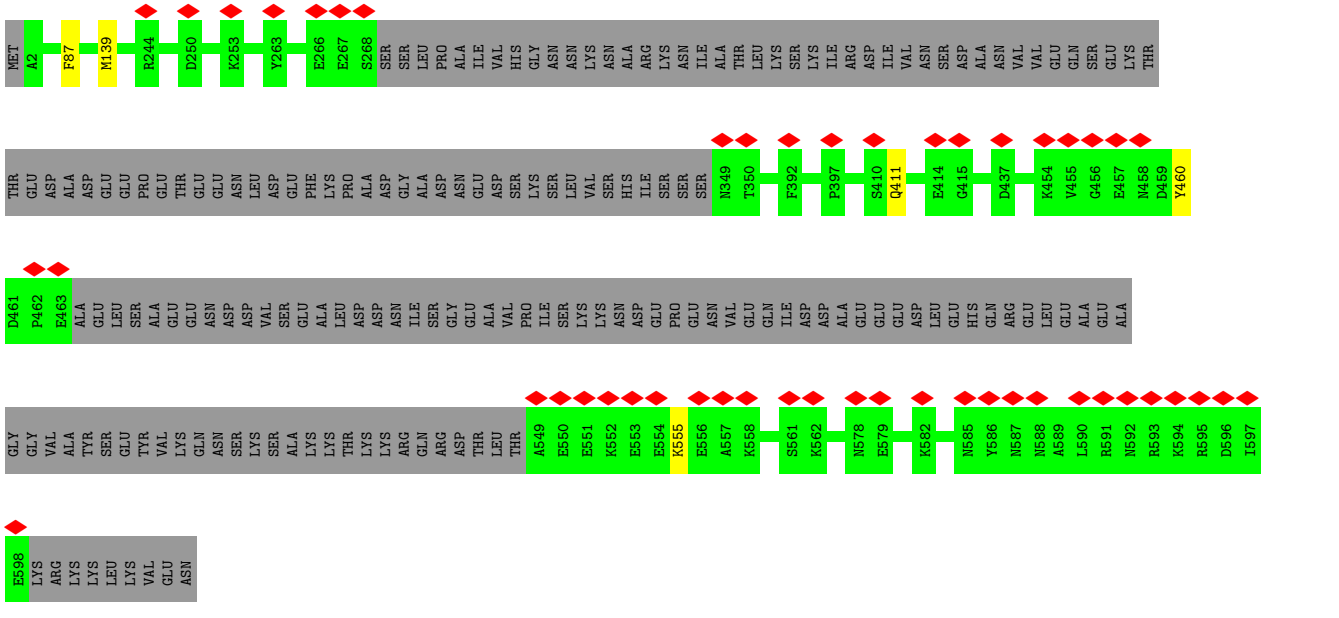
Chain m:





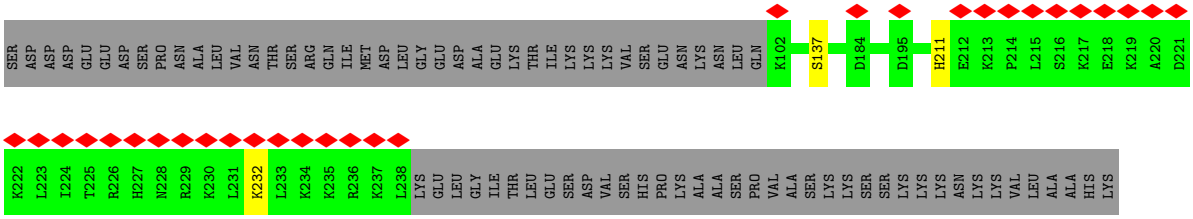
• Molecule 44: Pescadillo homolog

Chain n:



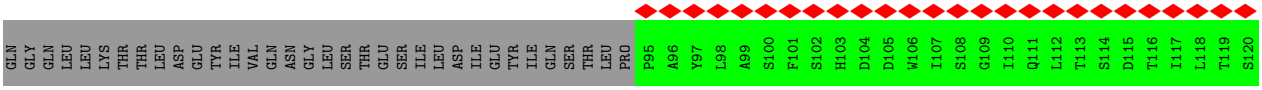
• Molecule 45: Uncharacterized RNA-binding protein C1827.05c

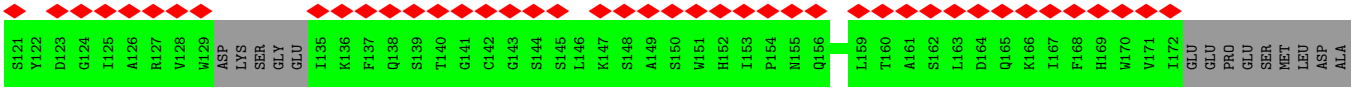
Chain o:

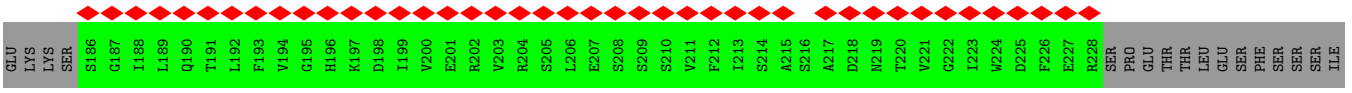


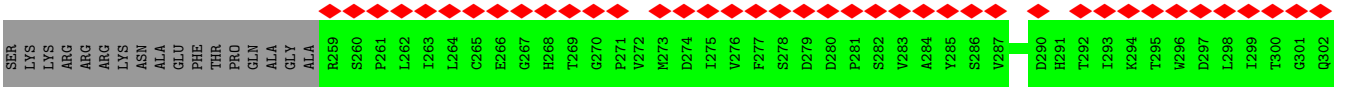
• Molecule 46: Ribosome biogenesis protein ytm1

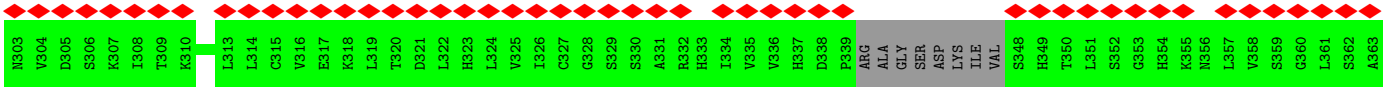
Chain p:

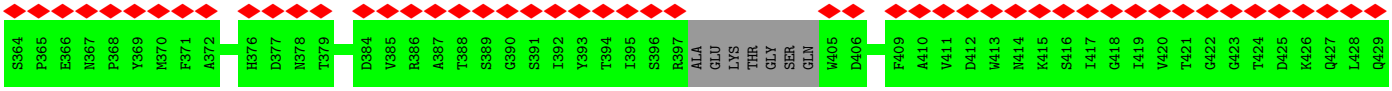


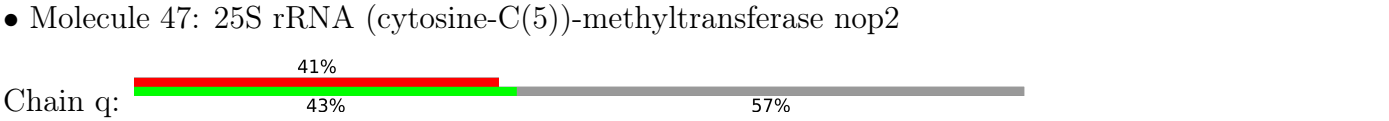


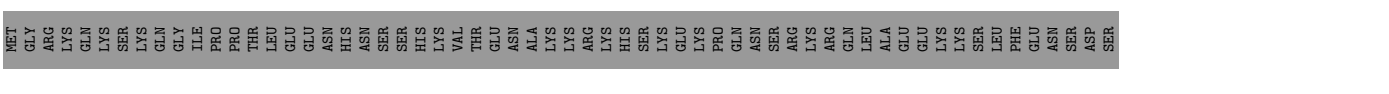


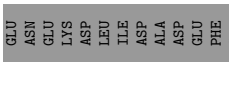






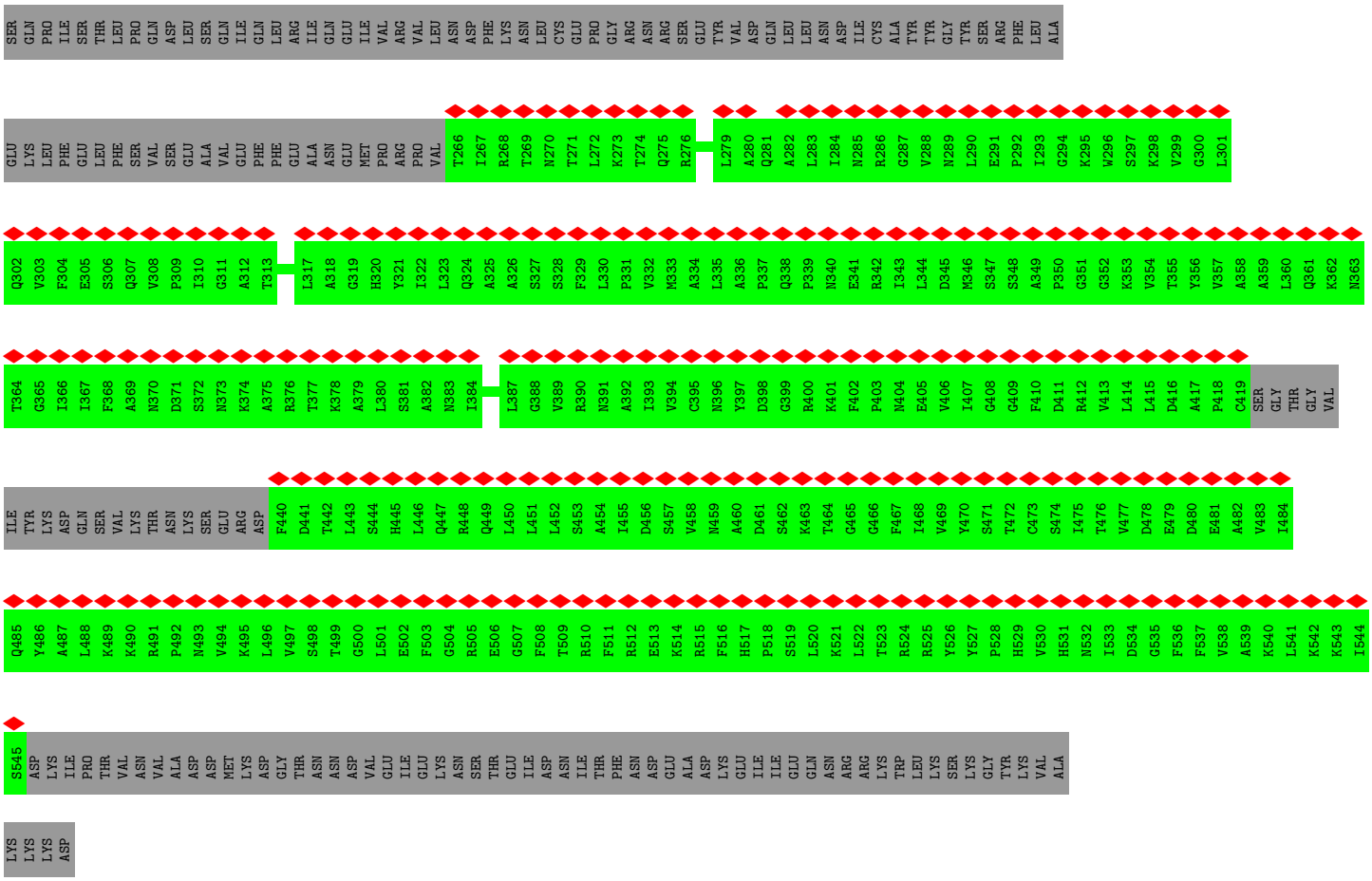






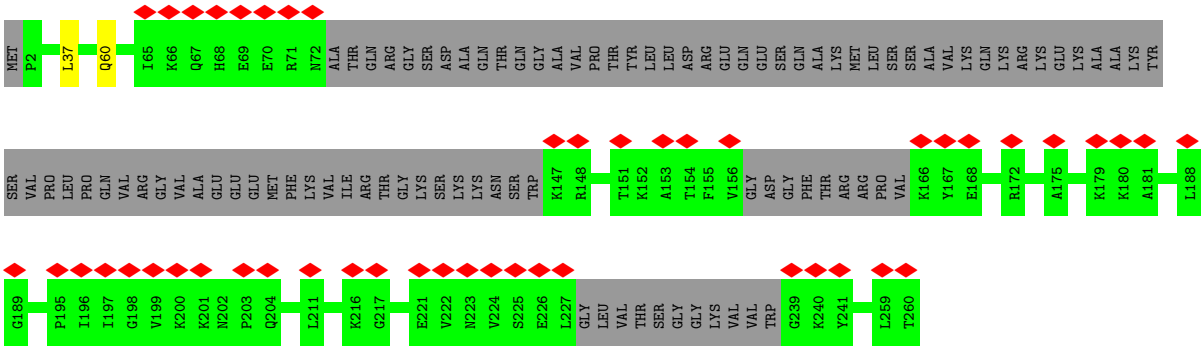
• Molecule 47: 25S rRNA (cytosine-C(5))-methyltransferase nop2

Chain q:



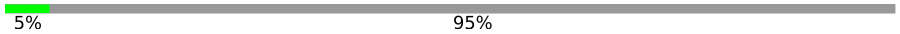
• Molecule 48: Ribosome biogenesis protein nsa2

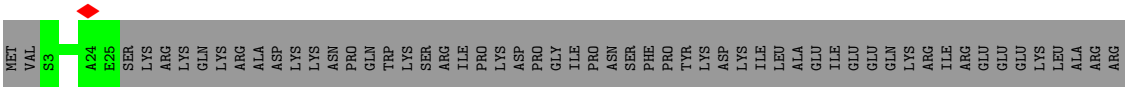
Chain r:

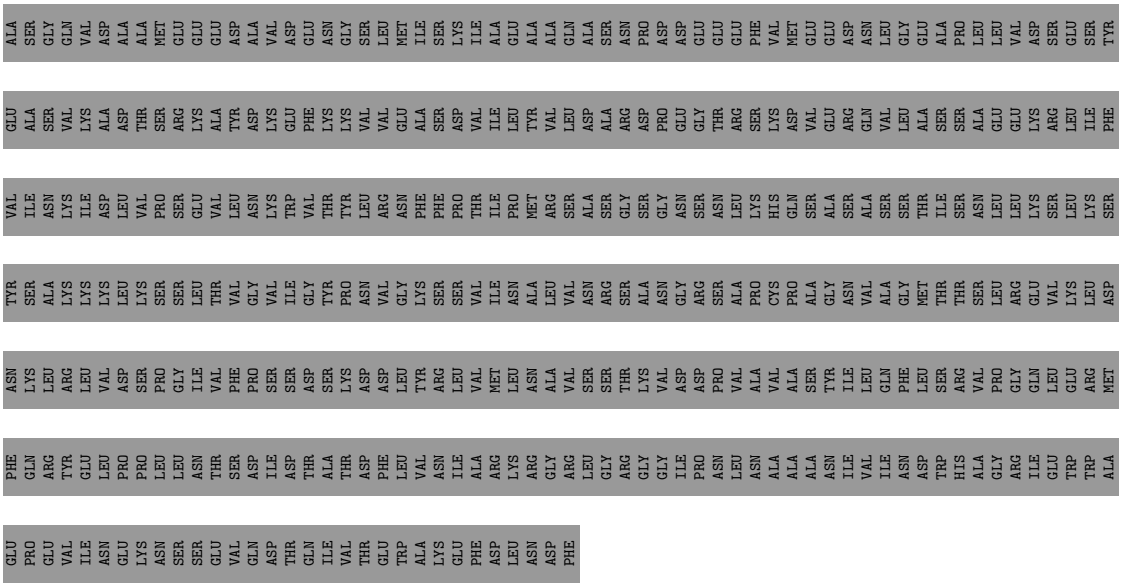


• Molecule 49: GTPase grn1

Chain s:

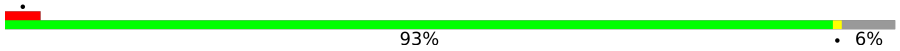


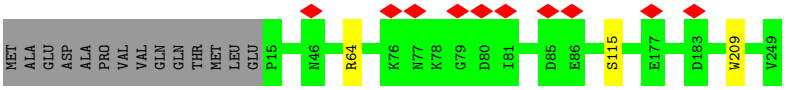




• Molecule 50: 60S ribosomal protein L7-A

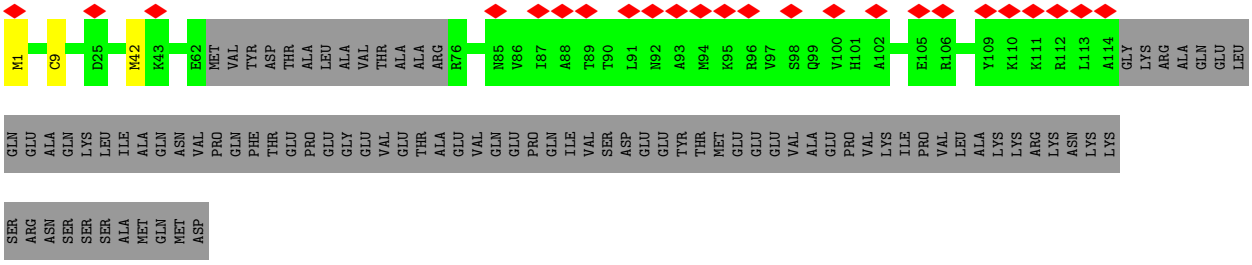
Chain t:





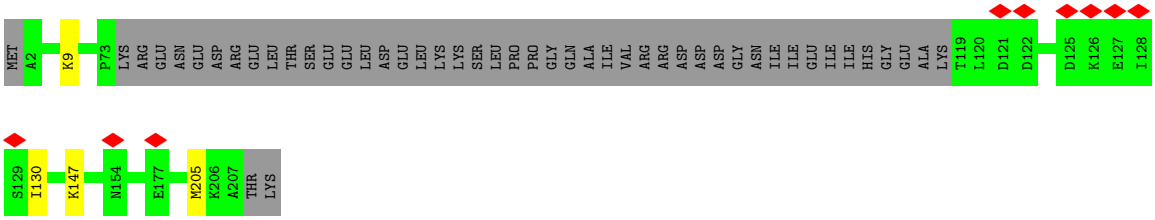
• Molecule 51: Ribosome biogenesis protein rlp24

Chain u:



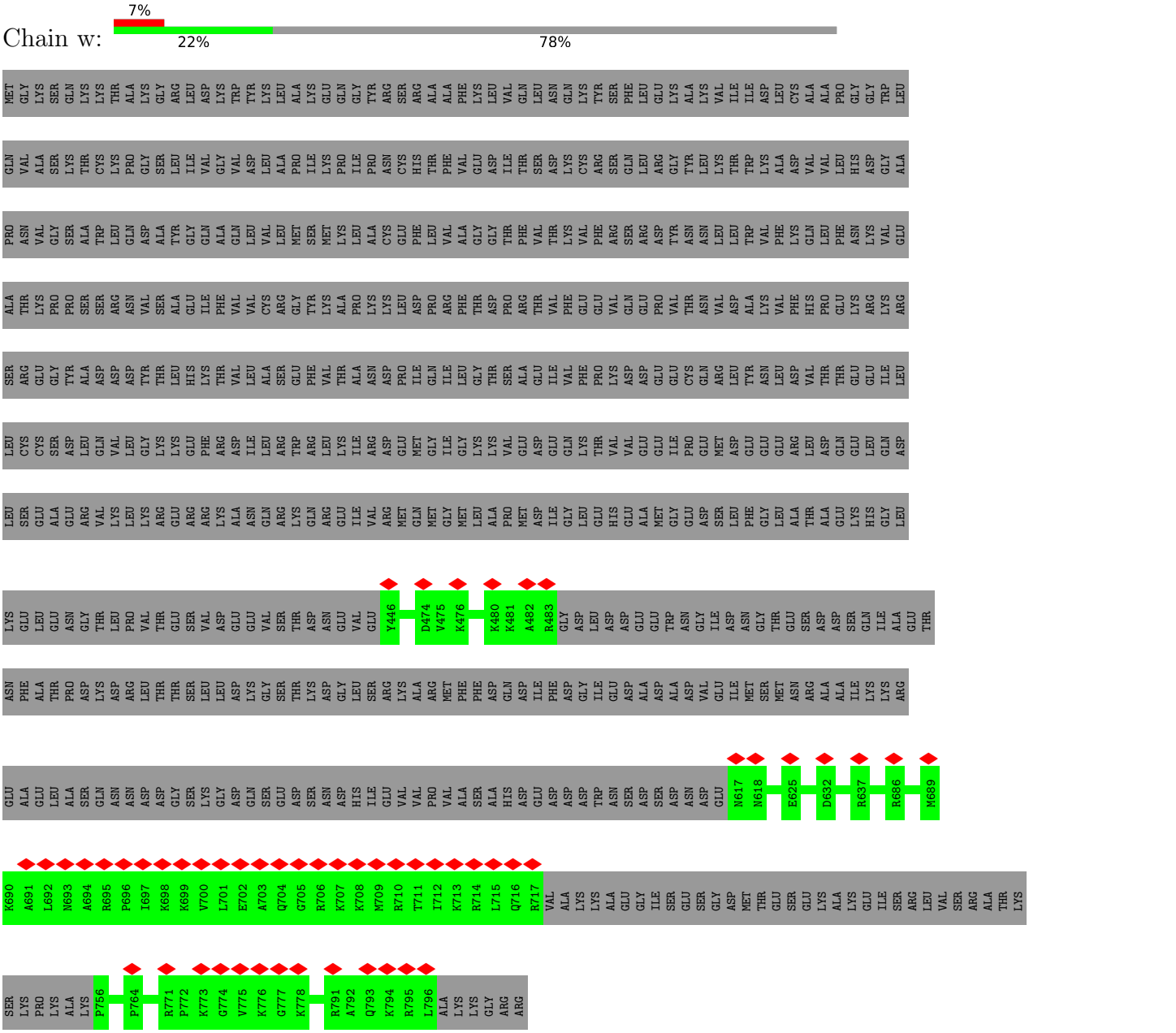
• Molecule 52: Nucleolar protein 16

Chain v:



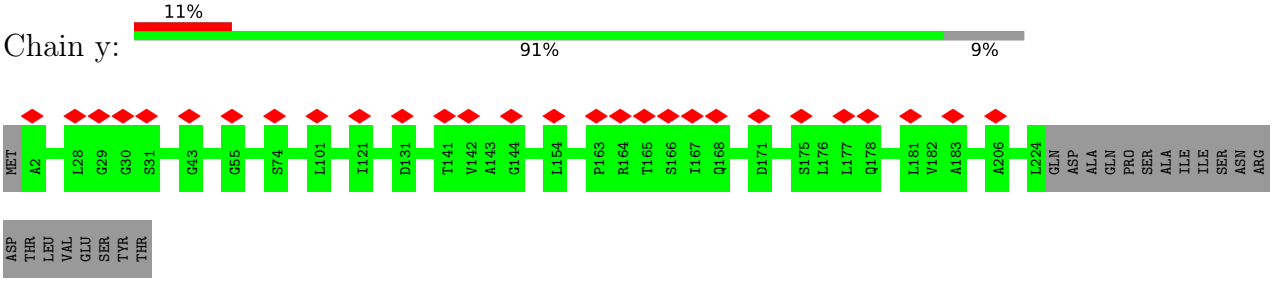
• Molecule 53: AdoMet-dependent rRNA methyltransferase spb1

Chain w:



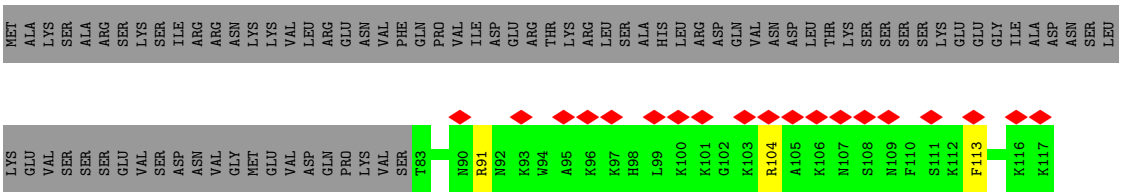
• Molecule 54: Eukaryotic translation initiation factor 6

Chain y:

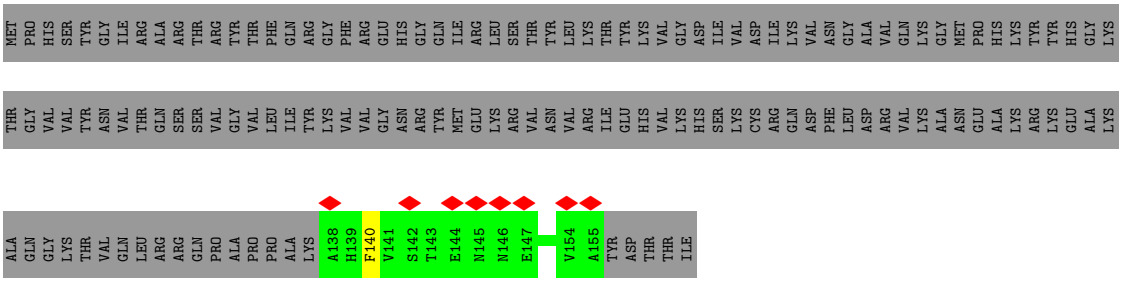


• Molecule 55: UPF0642 protein C32H8.05

Chain z:



• Molecule 56: 60S ribosomal protein L21-A



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.568	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.19	0/51332	0.72	0/79942
2	2	0.23	0/3563	0.72	0/5543
3	6	0.18	0/1868	0.71	0/2898
4	7	0.23	0/544	0.33	0/754
5	8	0.25	0/191	0.49	0/254
6	A	0.25	0/1686	0.52	0/2272
7	B	0.24	0/2715	0.52	0/3647
8	C	0.25	0/2848	0.50	0/3842
9	D	0.25	0/3381	0.46	0/4559
10	E	0.26	0/1235	0.53	0/1663
11	F	0.25	0/1781	0.48	0/2389
12	G	0.26	0/1629	0.49	0/2192
13	H	0.26	0/1470	0.54	0/1982
14	I	0.23	0/2023	0.34	0/2810
15	J	0.23	0/573	0.34	0/800
16	K	0.26	0/1999	0.50	0/2702
17	L	0.26	0/960	0.57	0/1288
18	M	0.23	0/1024	0.49	0/1375
19	N	0.26	0/1420	0.56	0/1897
20	O	0.25	0/1588	0.49	0/2128
21	P	0.26	0/1188	0.51	0/1590
22	Q	0.24	0/1043	0.54	0/1401
23	R	0.24	0/732	0.47	0/992
24	S	0.25	0/1437	0.54	0/1929
25	U	0.23	0/483	0.42	0/671
26	V	0.26	0/1007	0.58	0/1357
27	W	0.23	0/1053	0.43	0/1457
28	X	0.26	0/1060	0.50	0/1422
29	Y	0.25	0/1008	0.56	0/1341
30	Z	0.24	0/661	0.40	0/917
31	a	0.25	0/775	0.58	1/1047 (0.1%)
32	b	0.23	0/1776	0.37	0/2471

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c	0.24	0/461	0.39	0/639
34	d	0.25	0/815	0.58	0/1094
35	e	0.26	0/967	0.55	0/1289
36	f	0.25	0/859	0.52	0/1152
37	g	0.24	0/477	0.41	0/662
38	h	0.25	0/1008	0.50	0/1340
39	i	0.24	0/703	0.55	0/931
40	j	0.26	0/575	0.57	0/761
41	k	0.27	0/570	0.56	0/762
42	l	0.24	0/859	0.43	0/1195
43	m	0.24	0/4644	0.50	0/6313
44	n	0.25	0/3598	0.46	0/4845
45	o	0.26	0/1163	0.56	0/1552
46	p	0.24	0/1351	0.44	0/1871
47	q	0.24	0/1280	0.42	0/1778
48	r	0.30	0/1086	0.57	0/1457
49	s	0.23	0/192	0.60	0/248
50	t	0.24	0/1979	0.51	0/2645
51	u	0.29	0/729	0.56	0/981
52	v	0.25	0/1319	0.49	0/1769
53	w	0.25	0/1478	0.52	0/1967
54	y	0.24	0/1096	0.45	0/1522
55	z	0.25	0/297	0.49	0/388
56	T	0.25	0/142	0.46	0/196
All	All	0.22	0/123701	0.62	1/178889 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	a	67	PRO	N-CA-CB	5.88	110.36	103.30

There are no chirality outliers.

There are no planarity outliers.

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	
4	7	102/707 (14%)	101 (99%)	1 (1%)	0	100	100
5	8	20/51 (39%)	20 (100%)	0	0	100	100
6	A	200/295 (68%)	194 (97%)	6 (3%)	0	100	100
7	B	331/388 (85%)	318 (96%)	13 (4%)	0	100	100
8	C	357/363 (98%)	342 (96%)	15 (4%)	0	100	100
9	D	412/578 (71%)	401 (97%)	11 (3%)	0	100	100
10	E	152/195 (78%)	142 (93%)	10 (7%)	0	100	100
11	F	212/250 (85%)	205 (97%)	7 (3%)	0	100	100
12	G	202/259 (78%)	196 (97%)	4 (2%)	2 (1%)	15	54
13	H	181/190 (95%)	173 (96%)	8 (4%)	0	100	100
14	I	391/747 (52%)	382 (98%)	8 (2%)	1 (0%)	41	74
15	J	113/333 (34%)	112 (99%)	1 (1%)	0	100	100
16	K	246/373 (66%)	232 (94%)	13 (5%)	1 (0%)	34	69
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
19	N	159/201 (79%)	158 (99%)	1 (1%)	0	100	100
20	O	194/197 (98%)	188 (97%)	6 (3%)	0	100	100
21	P	143/187 (76%)	139 (97%)	4 (3%)	0	100	100
22	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
23	R	108/193 (56%)	107 (99%)	1 (1%)	0	100	100
24	S	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
25	U	96/117 (82%)	93 (97%)	3 (3%)	0	100	100
26	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
27	W	207/241 (86%)	196 (95%)	11 (5%)	0	100	100
28	X	128/141 (91%)	124 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	Y	123/126 (98%)	117 (95%)	6 (5%)	0	100	100
30	Z	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
31	a	93/148 (63%)	92 (99%)	1 (1%)	0	100	100
32	b	351/642 (55%)	346 (99%)	5 (1%)	0	100	100
33	c	92/117 (79%)	92 (100%)	0	0	100	100
34	d	92/113 (81%)	91 (99%)	1 (1%)	0	100	100
35	e	117/127 (92%)	114 (97%)	3 (3%)	0	100	100
36	f	104/108 (96%)	99 (95%)	5 (5%)	0	100	100
37	g	95/112 (85%)	92 (97%)	3 (3%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	83/99 (84%)	83 (100%)	0	0	100	100
40	j	69/91 (76%)	68 (99%)	1 (1%)	0	100	100
41	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
42	l	172/180 (96%)	170 (99%)	2 (1%)	0	100	100
43	m	558/740 (75%)	529 (95%)	28 (5%)	1 (0%)	47	79
44	n	426/607 (70%)	415 (97%)	11 (3%)	0	100	100
45	o	135/276 (49%)	129 (96%)	6 (4%)	0	100	100
46	p	263/440 (60%)	257 (98%)	6 (2%)	0	100	100
47	q	256/608 (42%)	252 (98%)	4 (2%)	0	100	100
48	r	157/260 (60%)	157 (100%)	0	0	100	100
49	s	21/470 (4%)	18 (86%)	3 (14%)	0	100	100
50	t	233/249 (94%)	221 (95%)	12 (5%)	0	100	100
51	u	97/192 (50%)	94 (97%)	3 (3%)	0	100	100
52	v	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	25	64
53	w	174/802 (22%)	170 (98%)	4 (2%)	0	100	100
54	y	221/244 (91%)	218 (99%)	3 (1%)	0	100	100
55	z	33/117 (28%)	31 (94%)	1 (3%)	1 (3%)	4	28
56	T	16/160 (10%)	16 (100%)	0	0	100	100
All	All	9072/14419 (63%)	8795 (97%)	270 (3%)	7 (0%)	54	83

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
52	v	130	ILE
12	G	227	ASP
16	K	153	ILE
12	G	182	ASN
55	z	104	ARG
43	m	115	VAL
14	I	698	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	
5	8	19/47 (40%)	19 (100%)	0	100	100
6	A	184/266 (69%)	182 (99%)	2 (1%)	73	88
7	B	284/326 (87%)	279 (98%)	5 (2%)	59	82
8	C	296/297 (100%)	293 (99%)	3 (1%)	76	90
9	D	362/505 (72%)	359 (99%)	3 (1%)	81	93
10	E	128/155 (83%)	125 (98%)	3 (2%)	50	78
11	F	180/210 (86%)	177 (98%)	3 (2%)	60	83
12	G	167/212 (79%)	167 (100%)	0	100	100
13	H	164/170 (96%)	162 (99%)	2 (1%)	71	88
16	K	223/333 (67%)	219 (98%)	4 (2%)	59	82
17	L	97/167 (58%)	96 (99%)	1 (1%)	76	90
18	M	108/113 (96%)	107 (99%)	1 (1%)	78	91
19	N	145/176 (82%)	145 (100%)	0	100	100
20	O	161/162 (99%)	160 (99%)	1 (1%)	86	94
21	P	121/149 (81%)	118 (98%)	3 (2%)	47	77
22	Q	114/159 (72%)	114 (100%)	0	100	100
23	R	51/162 (32%)	50 (98%)	1 (2%)	55	80
24	S	149/154 (97%)	146 (98%)	3 (2%)	55	80
26	V	103/107 (96%)	102 (99%)	1 (1%)	76	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	X	114/122 (93%)	114 (100%)	0	100	100
29	Y	110/111 (99%)	108 (98%)	2 (2%)	59	82
31	a	81/122 (66%)	80 (99%)	1 (1%)	71	88
34	d	88/102 (86%)	87 (99%)	1 (1%)	73	88
35	e	101/107 (94%)	100 (99%)	1 (1%)	76	90
36	f	89/91 (98%)	89 (100%)	0	100	100
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	74/84 (88%)	74 (100%)	0	100	100
40	j	58/71 (82%)	58 (100%)	0	100	100
41	k	63/66 (96%)	61 (97%)	2 (3%)	39	71
43	m	504/659 (76%)	497 (99%)	7 (1%)	67	86
44	n	378/532 (71%)	373 (99%)	5 (1%)	69	87
45	o	123/246 (50%)	120 (98%)	3 (2%)	49	77
48	r	63/224 (28%)	61 (97%)	2 (3%)	39	71
49	s	21/409 (5%)	21 (100%)	0	100	100
50	t	211/223 (95%)	208 (99%)	3 (1%)	67	86
51	u	55/168 (33%)	52 (94%)	3 (6%)	21	57
52	v	138/181 (76%)	135 (98%)	3 (2%)	52	79
53	w	158/697 (23%)	158 (100%)	0	100	100
55	z	31/107 (29%)	29 (94%)	2 (6%)	17	51
56	T	16/139 (12%)	15 (94%)	1 (6%)	18	52
All	All	5638/8438 (67%)	5566 (99%)	72 (1%)	70	87

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	A	68	MET
6	A	167	LEU
7	B	132	LYS
7	B	199	PHE
7	B	214	MET
7	B	283	TYR
7	B	323	MET
8	C	36	LEU
8	C	122	TYR

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Mol	Chain	Res	Type
8	C	345	SER
9	D	270	GLN
9	D	459	LEU
9	D	531	ASN
10	E	33	GLU
10	E	140	PHE
10	E	156	ASP
11	F	67	ARG
11	F	87	GLU
11	F	234	ASP
13	H	61	SER
13	H	78	MET
16	K	23	TYR
16	K	98	TYR
16	K	200	MET
16	K	234	LYS
17	L	67	MET
18	M	33	ASP
20	O	64	ARG
21	P	30	ARG
21	P	97	ASN
21	P	110	ASP
23	R	30	SER
24	S	42	TYR
24	S	138	TYR
24	S	176	TYR
26	V	134	ASN
29	Y	5	ARG
29	Y	40	GLU
31	a	131	ARG
34	d	92	LEU
35	e	42	ARG
41	k	13	GLU
41	k	52	LYS
43	m	114	ASP
43	m	137	LYS
43	m	267	HIS
43	m	300	TYR
43	m	368	LEU
43	m	371	PHE
43	m	585	MET
44	n	87	PHE

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Mol	Chain	Res	Type
44	n	139	MET
44	n	411	GLN
44	n	460	TYR
44	n	555	LYS
45	o	137	SER
45	o	211	HIS
45	o	232	LYS
48	r	37	LEU
48	r	60	GLN
50	t	64	ARG
50	t	115	SER
50	t	209	TRP
51	u	1	MET
51	u	9	CYS
51	u	42	MET
52	v	9	LYS
52	v	147	LYS
52	v	205	MET
55	z	91	ARG
55	z	113	PHE
56	T	140	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
6	A	97	ASN
7	B	279	ASN
8	C	323	ASN
9	D	367	HIS
9	D	370	GLN
9	D	531	ASN
16	K	177	GLN
41	k	59	GLN
44	n	190	GLN
44	n	408	HIS
44	n	411	GLN
45	o	187	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2100/3497 (60%)	496 (23%)	21 (1%)
2	2	147/165 (89%)	24 (16%)	1 (0%)
3	6	75/300 (25%)	32 (42%)	0
All	All	2322/3962 (58%)	552 (23%)	22 (0%)

All (552) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	6	A
1	1	26	A
1	1	34	A
1	1	36	C
1	1	49	A
1	1	57	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	91	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	122	A
1	1	133	A
1	1	149	G
1	1	154	G
1	1	162	A
1	1	163	A
1	1	170	G
1	1	177	G
1	1	193	U
1	1	195	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	213	G
1	1	217	G
1	1	218	A
1	1	225	G
1	1	226	A
1	1	227	G

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Mol	Chain	Res	Type
1	1	239	U
1	1	240	G
1	1	241	G
1	1	244	G
1	1	245	A
1	1	246	U
1	1	258	U
1	1	259	A
1	1	263	A
1	1	268	U
1	1	269	U
1	1	276	A
1	1	277	G
1	1	303	A
1	1	306	U
1	1	307	G
1	1	313	U
1	1	331	A
1	1	337	U
1	1	338	G
1	1	346	A
1	1	347	C
1	1	358	C
1	1	359	A
1	1	360	A
1	1	361	G
1	1	378	U
1	1	384	G
1	1	406	U
1	1	409	U
1	1	411	C
1	1	415	A
1	1	429	G
1	1	430	A
1	1	437	G
1	1	445	G
1	1	507	U
1	1	522	G
1	1	530	A
1	1	532	A
1	1	534	A
1	1	540	A

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Mol	Chain	Res	Type
1	1	544	A
1	1	546	G
1	1	547	G
1	1	548	U
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	590	U
1	1	591	G
1	1	602	A
1	1	603	C
1	1	613	A
1	1	616	A
1	1	618	U
1	1	624	U
1	1	632	A
1	1	636	A
1	1	637	U
1	1	641	G
1	1	645	U
1	1	647	A
1	1	650	G
1	1	651	U
1	1	661	C
1	1	662	C
1	1	671	A
1	1	675	C
1	1	685	A
1	1	687	U
1	1	702	A
1	1	706	U
1	1	714	A
1	1	716	G
1	1	717	A
1	1	732	A
1	1	735	G
1	1	743	A
1	1	744	U

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Mol	Chain	Res	Type
1	1	745	G
1	1	746	C
1	1	747	A
1	1	748	G
1	1	749	G
1	1	760	C
1	1	776	U
1	1	777	C
1	1	778	G
1	1	779	A
1	1	817	G
1	1	847	G
1	1	851	U
1	1	852	A
1	1	854	G
1	1	935	U
1	1	936	A
1	1	938	A
1	1	939	G
1	1	957	A
1	1	965	A
1	1	968	A
1	1	969	G
1	1	976	C
1	1	986	U
1	1	987	U
1	1	990	C
1	1	997	A
1	1	998	U
1	1	1006	A
1	1	1009	C
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1014	C
1	1	1015	A
1	1	1017	U
1	1	1023	G
1	1	1135	G
1	1	1138	U
1	1	1139	U
1	1	1141	C

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Mol	Chain	Res	Type
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1148	G
1	1	1157	G
1	1	1158	G
1	1	1159	U
1	1	1160	A
1	1	1161	A
1	1	1163	C
1	1	1167	A
1	1	1168	C
1	1	1171	G
1	1	1173	G
1	1	1184	A
1	1	1185	A
1	1	1186	C
1	1	1191	C
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1234	A
1	1	1235	A
1	1	1239	U
1	1	1241	U
1	1	1244	G
1	1	1245	U
1	1	1249	U
1	1	1251	U
1	1	1253	G
1	1	1255	C
1	1	1260	G
1	1	1266	U
1	1	1269	C
1	1	1272	U
1	1	1273	G
1	1	1274	G
1	1	1275	A
1	1	1276	A
1	1	1277	G
1	1	1279	C

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Mol	Chain	Res	Type
1	1	1282	A
1	1	1286	C
1	1	1289	U
1	1	1290	A
1	1	1291	A
1	1	1293	G
1	1	1295	G
1	1	1296	U
1	1	1297	G
1	1	1303	C
1	1	1308	C
1	1	1309	A
1	1	1312	U
1	1	1316	G
1	1	1317	A
1	1	1318	A
1	1	1332	A
1	1	1333	A
1	1	1334	A
1	1	1336	U
1	1	1337	G
1	1	1340	U
1	1	1347	U
1	1	1348	A
1	1	1361	A
1	1	1363	A
1	1	1379	U
1	1	1380	A
1	1	1381	G
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1420	U
1	1	1433	U
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1459	U
1	1	1465	G
1	1	1468	G
1	1	1471	C
1	1	1484	G

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Mol	Chain	Res	Type
1	1	1502	A
1	1	1515	A
1	1	1517	G
1	1	1518	U
1	1	1519	G
1	1	1521	G
1	1	1528	U
1	1	1529	U
1	1	1537	A
1	1	1538	A
1	1	1539	C
1	1	1541	G
1	1	1542	C
1	1	1546	U
1	1	1548	G
1	1	1568	A
1	1	1570	G
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1591	A
1	1	1596	U
1	1	1597	G
1	1	1604	U
1	1	1607	U
1	1	1608	C
1	1	1614	U
1	1	1622	A
1	1	1623	A
1	1	1624	A
1	1	1628	A
1	1	1640	A
1	1	1643	C
1	1	1654	A
1	1	1655	G
1	1	1674	C
1	1	1677	A
1	1	1678	A
1	1	1686	U
1	1	1691	A
1	1	1718	C
1	1	1731	A

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Mol	Chain	Res	Type
1	1	1736	A
1	1	1737	C
1	1	1747	A
1	1	1753	A
1	1	1754	A
1	1	1764	U
1	1	1782	U
1	1	1790	A
1	1	1791	G
1	1	1797	A
1	1	1798	G
1	1	1811	A
1	1	1814	C
1	1	1816	G
1	1	1818	U
1	1	1819	G
1	1	1820	C
1	1	1821	G
1	1	1829	C
1	1	1831	G
1	1	1833	C
1	1	1834	C
1	1	1835	U
1	1	1836	U
1	1	1838	A
1	1	1849	G
1	1	1852	G
1	1	1873	U
1	1	1874	U
1	1	1876	U
1	1	1877	C
1	1	1917	U
1	1	1935	U
1	1	1940	C
1	1	1941	A
1	1	1948	A
1	1	1961	G
1	1	2423	G
1	1	2424	U
1	1	2451	A
1	1	2452	G
1	1	2455	U

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Mol	Chain	Res	Type
1	1	2456	G
1	1	2458	G
1	1	2459	G
1	1	2461	A
1	1	2462	C
1	1	2463	G
1	1	2464	G
1	1	2465	G
1	1	2466	C
1	1	2471	C
1	1	2473	A
1	1	2476	U
1	1	2481	G
1	1	2498	U
1	1	2499	U
1	1	2505	U
1	1	2506	G
1	1	2507	A
1	1	2700	G
1	1	2701	G
1	1	2702	G
1	1	2706	U
1	1	2898	A
1	1	2902	U
1	1	2905	C
1	1	2906	A
1	1	2907	C
1	1	2908	A
1	1	2921	U
1	1	2925	G
1	1	2929	G
1	1	2931	C
1	1	2932	A
1	1	2946	A
1	1	2952	C
1	1	2953	U
1	1	2971	C
1	1	2972	G
1	1	2973	G
1	1	2978	U
1	1	2982	A
1	1	2984	C

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Mol	Chain	Res	Type
1	1	2993	G
1	1	2994	C
1	1	2995	A
1	1	3009	G
1	1	3011	U
1	1	3014	A
1	1	3023	C
1	1	3024	C
1	1	3025	A
1	1	3030	U
1	1	3031	A
1	1	3036	A
1	1	3037	C
1	1	3038	G
1	1	3040	G
1	1	3041	A
1	1	3042	G
1	1	3044	U
1	1	3046	G
1	1	3057	U
1	1	3059	G
1	1	3060	U
1	1	3061	G
1	1	3062	A
1	1	3063	G
1	1	3064	A
1	1	3065	C
1	1	3071	A
1	1	3072	G
1	1	3073	U
1	1	3085	G
1	1	3087	U
1	1	3093	G
1	1	3107	A
1	1	3108	A
1	1	3113	A
1	1	3117	A
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3126	G
1	1	3128	A

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Mol	Chain	Res	Type
1	1	3151	A
1	1	3153	U
1	1	3155	G
1	1	3167	C
1	1	3168	A
1	1	3170	G
1	1	3172	C
1	1	3173	A
1	1	3174	A
1	1	3176	G
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3192	C
1	1	3195	C
1	1	3196	C
1	1	3198	G
1	1	3200	U
1	1	3205	G
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3237	A
1	1	3238	A
1	1	3239	A
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A
1	1	3282	G
1	1	3288	G
1	1	3301	C
1	1	3307	U
1	1	3309	U
1	1	3315	A
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3327	A
1	1	3337	A
1	1	3338	A

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Mol	Chain	Res	Type
1	1	3339	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3349	U
1	1	3351	U
1	1	3354	U
1	1	3357	C
1	1	3359	U
1	1	3360	G
1	1	3362	C
1	1	3368	A
1	1	3369	A
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3374	A
1	1	3375	U
1	1	3404	G
1	1	3405	C
1	1	3414	U
1	1	3417	A
1	1	3418	U
1	1	3419	G
1	1	3420	U
1	1	3421	G
1	1	3424	A
1	1	3425	C
1	1	3430	U
1	1	3435	U
1	1	3436	A
1	1	3469	U
1	1	3470	G
1	1	3476	A
1	1	3479	C
1	1	3483	U
1	1	3490	A
1	1	3491	A
1	1	3492	G
2	2	9	A

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Mol	Chain	Res	Type
2	2	30	U
2	2	31	U
2	2	42	U
2	2	43	C
2	2	46	U
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	87	A
2	2	98	U
2	2	103	G
2	2	112	A
2	2	114	C
2	2	115	G
2	2	124	G
2	2	132	G
2	2	134	U
2	2	135	C
2	2	136	U
2	2	137	A
2	2	156	G
2	2	159	U
3	6	2	C
3	6	5	U
3	6	6	C
3	6	8	U
3	6	9	C
3	6	47	U
3	6	50	U
3	6	56	A
3	6	57	A
3	6	60	U
3	6	82	A
3	6	83	A
3	6	86	U
3	6	87	A
3	6	92	G
3	6	93	A
3	6	94	A
3	6	97	C
3	6	98	G

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Mol	Chain	Res	Type
3	6	99	A
3	6	101	U
3	6	102	G
3	6	105	G
3	6	106	A
3	6	108	A
3	6	178	U
3	6	181	C
3	6	182	C
3	6	184	C
3	6	186	U
3	6	187	U
3	6	188	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	359	A
1	1	360	A
1	1	644	A
1	1	661	C
1	1	759	C
1	1	816	A
1	1	996	G
1	1	1159	U
1	1	1183	G
1	1	1272	U
1	1	1380	A
1	1	1540	A
1	1	1851	A
1	1	1916	G
1	1	2951	G
1	1	2952	C
1	1	3024	C
1	1	3041	A
1	1	3070	U
1	1	3217	U
1	1	3337	A
2	2	131	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	3315:A	O3'	3316:G	P	3.15

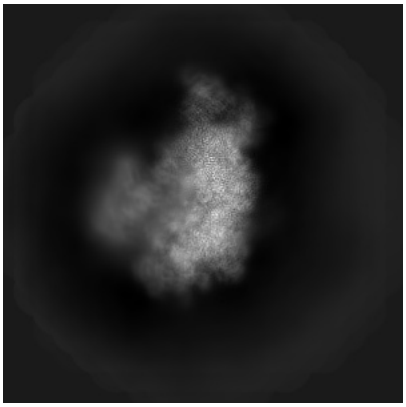
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24422. These allow visual inspection of the internal detail of the map and identification of artifacts.

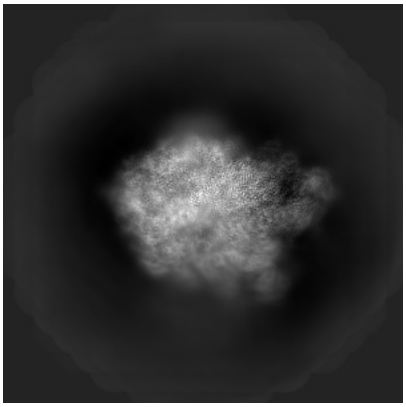
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

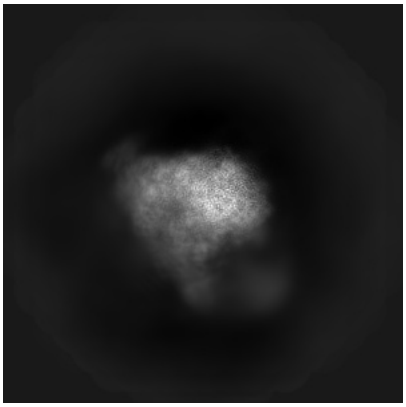
6.1.1 Primary map



X



Y

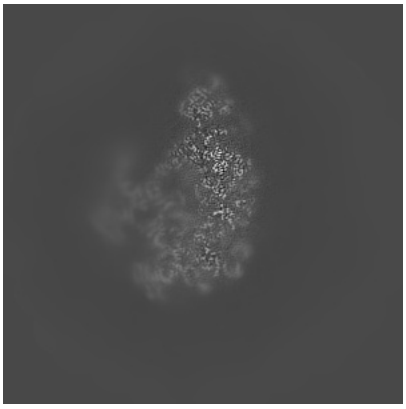


Z

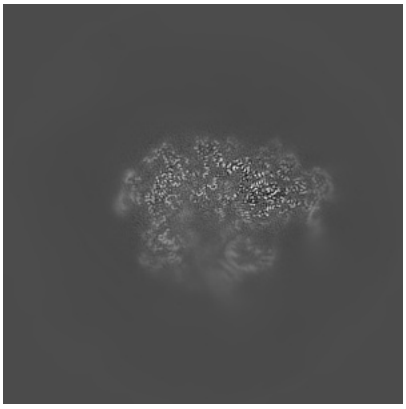
The images above show the map projected in three orthogonal directions.

6.2 Central slices

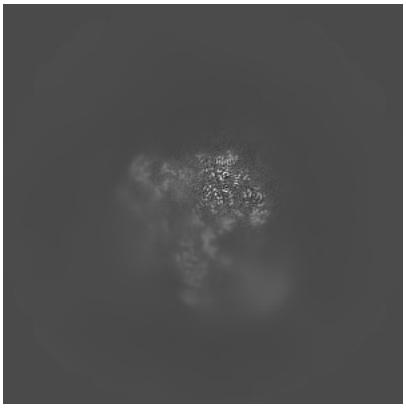
6.2.1 Primary map



X Index: 256



Y Index: 256

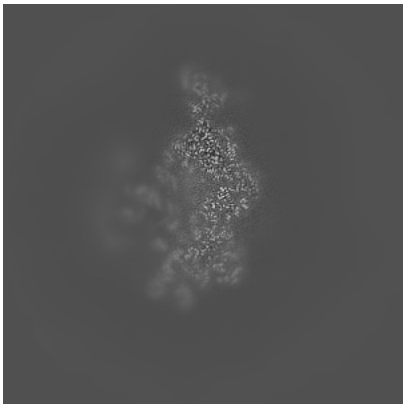


Z Index: 256

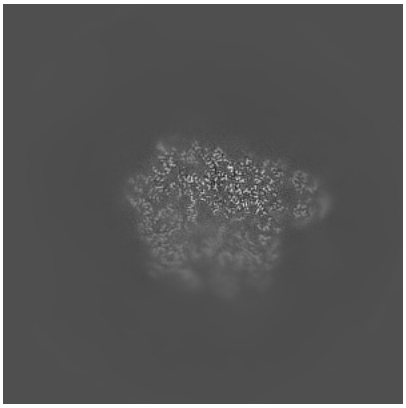
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

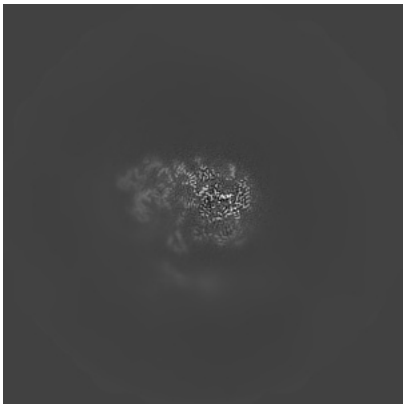
6.3.1 Primary map



X Index: 271



Y Index: 273



Z Index: 314

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

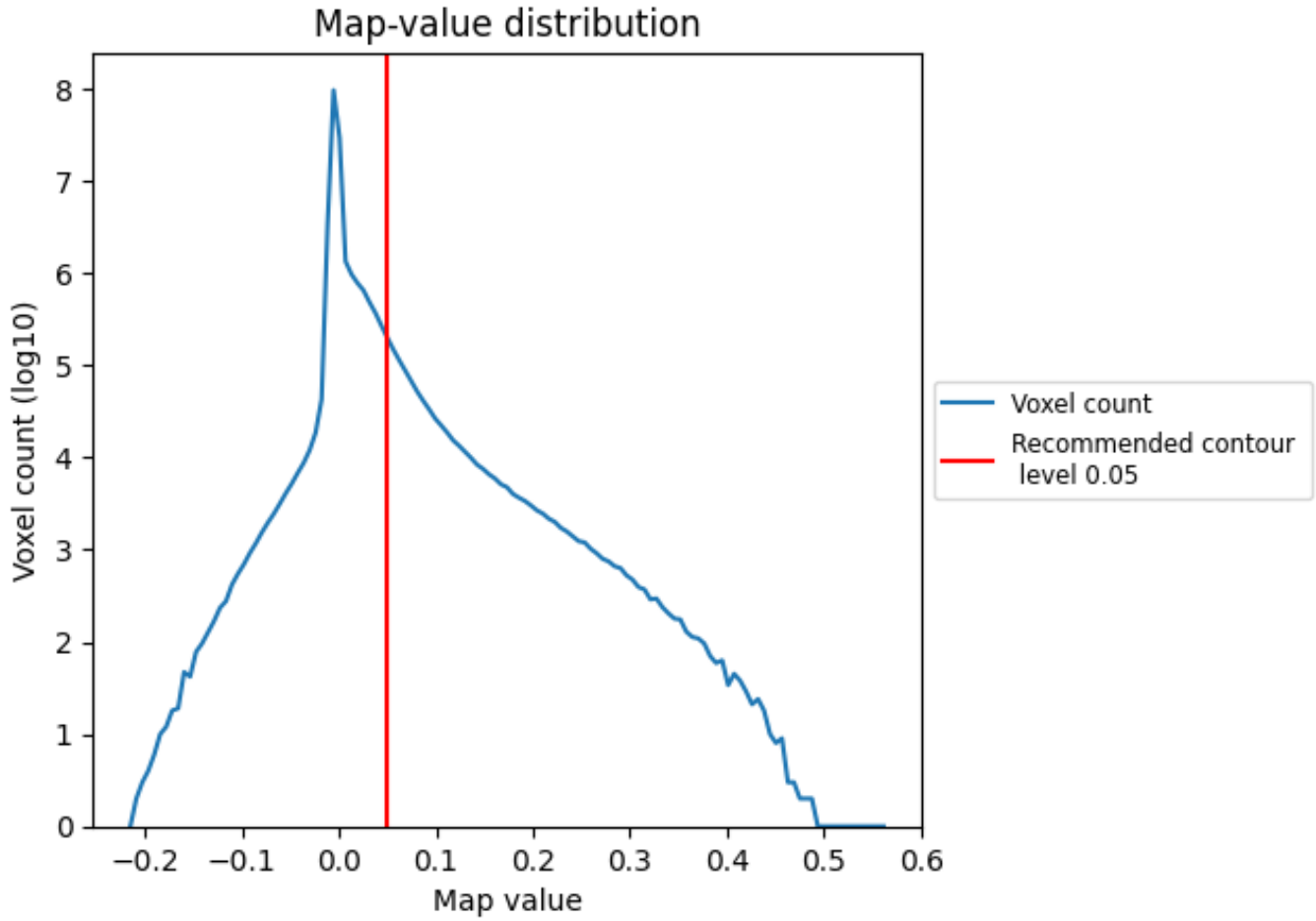
6.5 Mask visualisation (i)

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

7 Map analysis

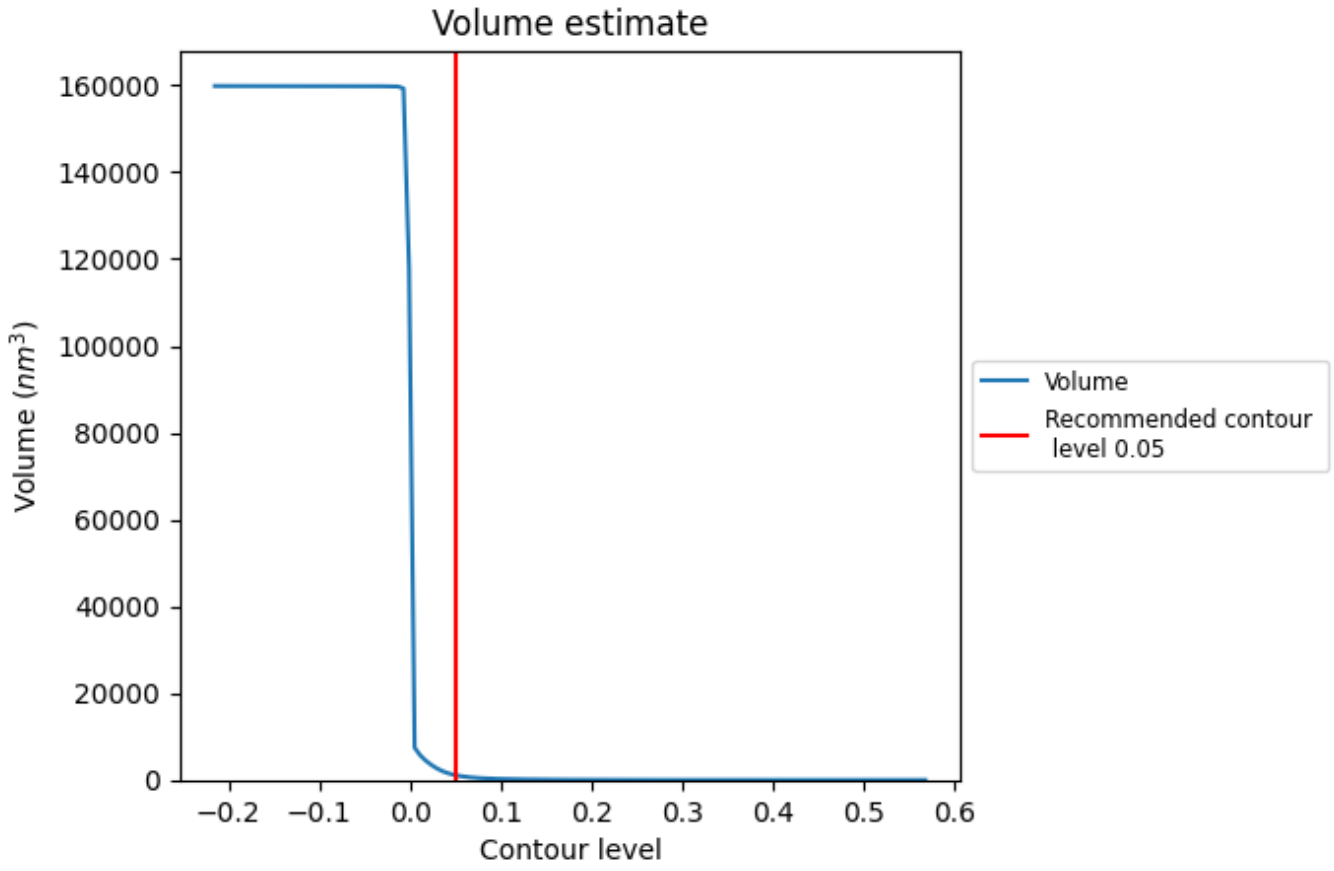
This section contains the results of statistical analysis of the map.

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.

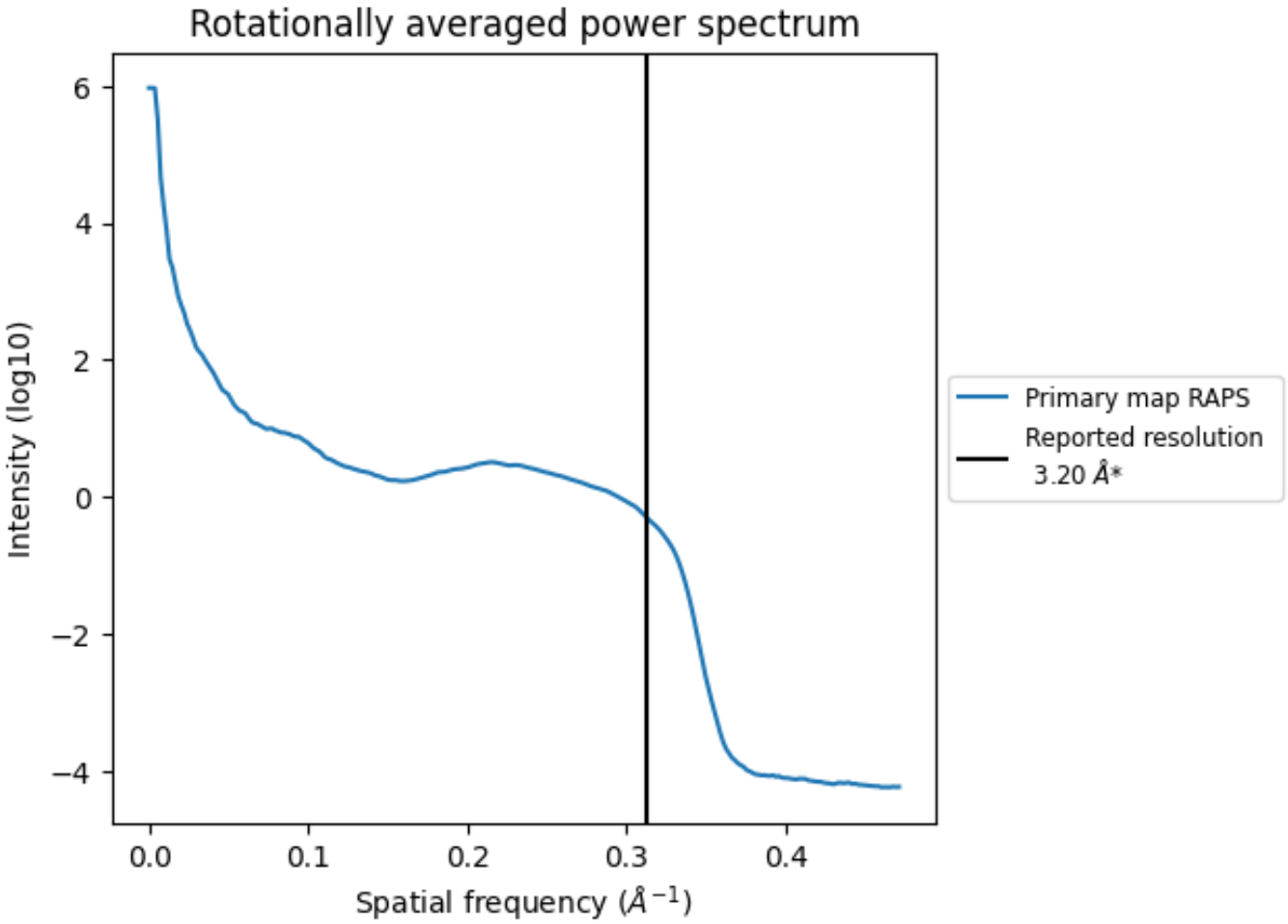
7.2 Volume estimate



The volume at the recommended contour level is 1113 nm^3; this corresponds to an approximate mass of 1006 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 0.312 Å^{-1}

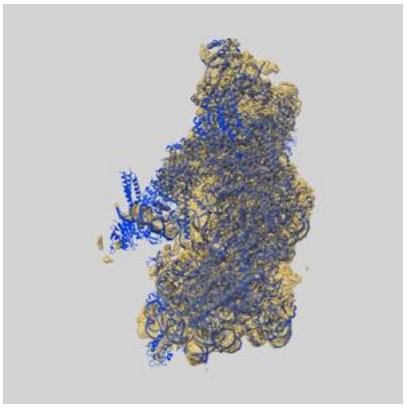
8 Fourier-Shell correlation (i)

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

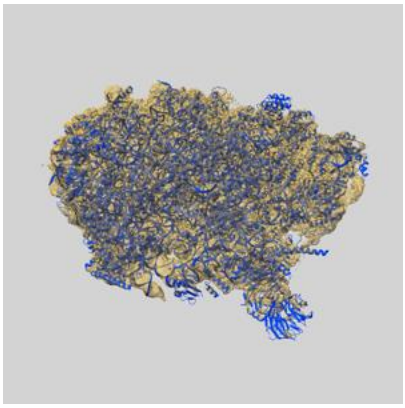
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24422 and PDB model 8ESR. Per-residue inclusion information can be found in section 3 on page 14.

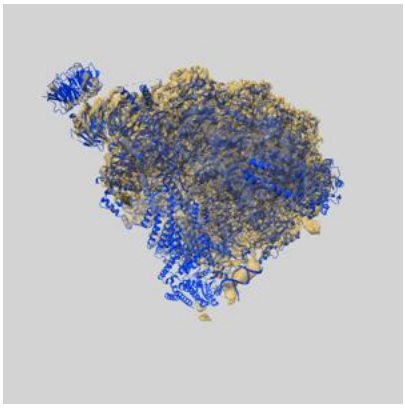
9.1 Map-model overlay



X



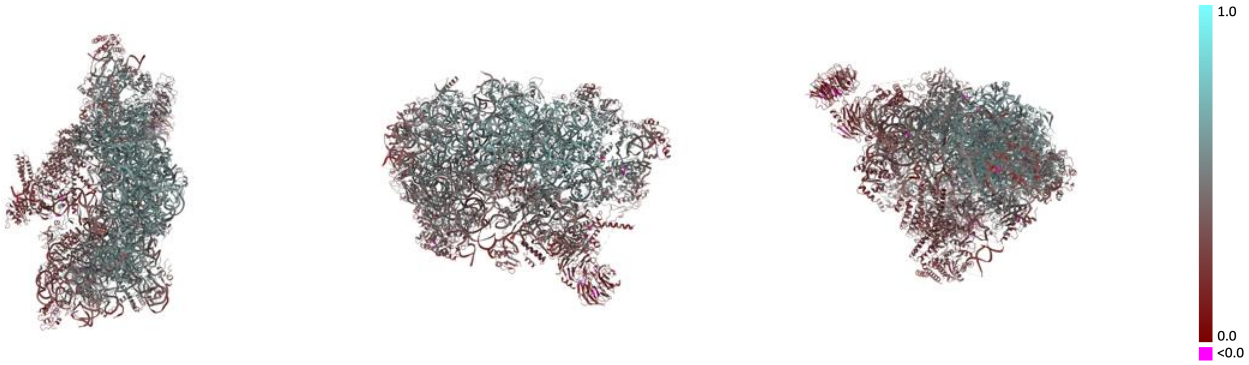
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

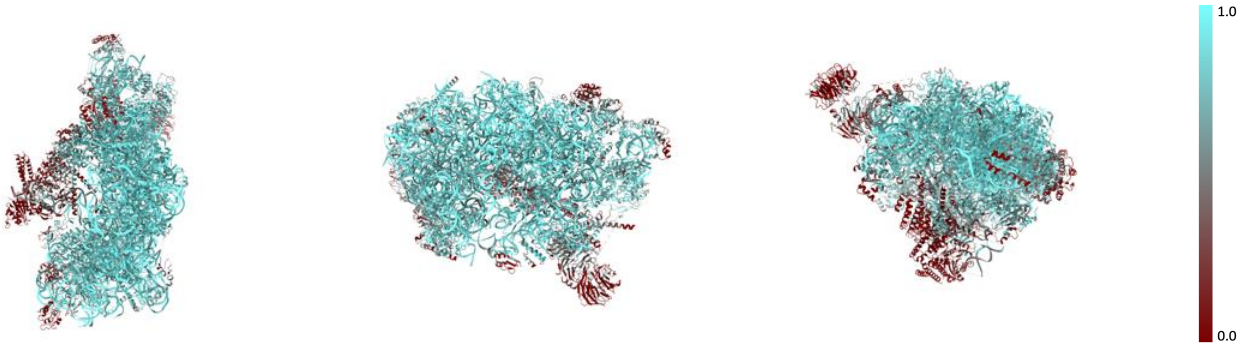
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

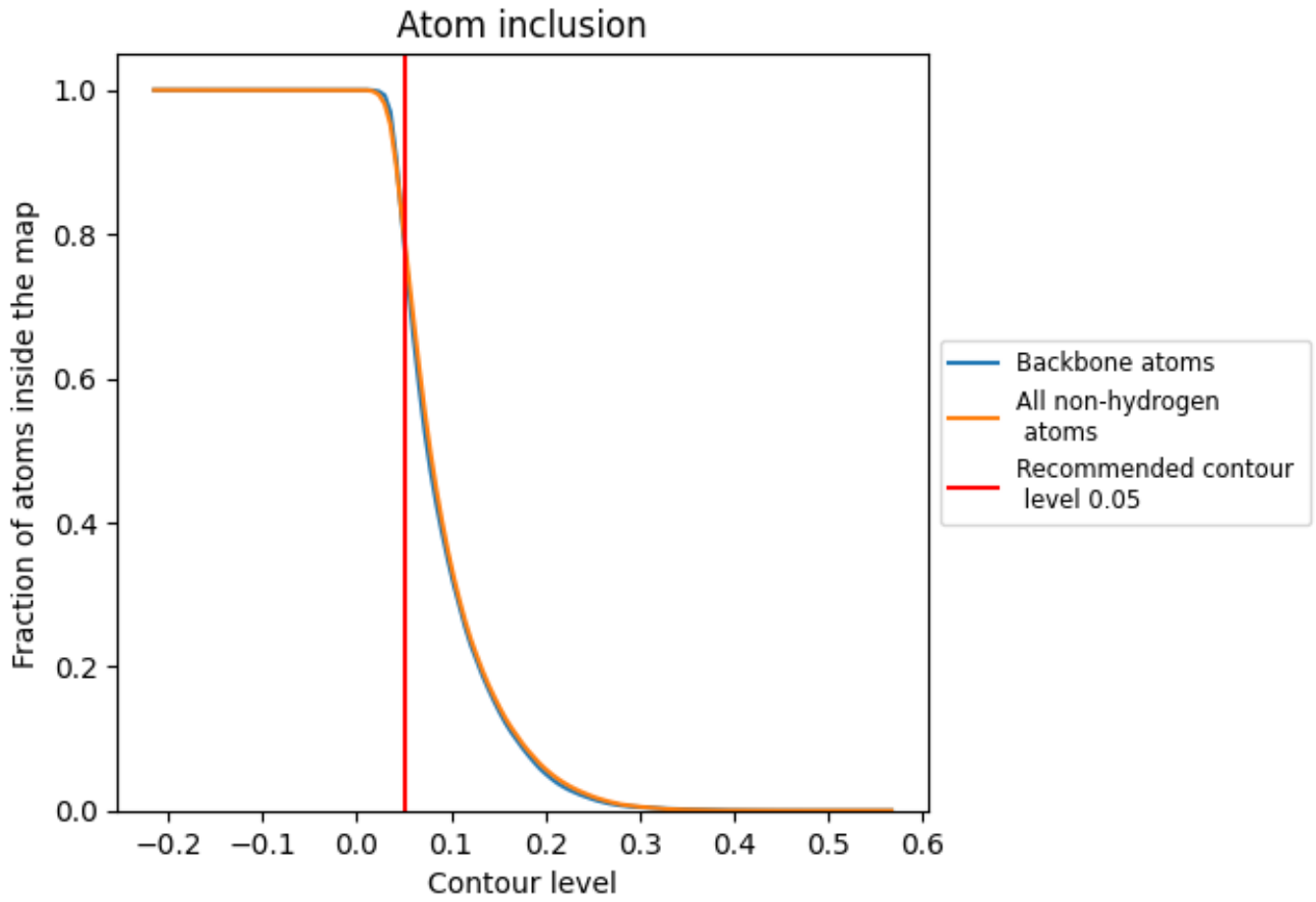
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7998	0.4400
1	0.9349	0.4440
2	0.9790	0.5630
6	0.8865	0.4240
7	0.0000	0.2620
8	0.7333	0.4100
A	0.6941	0.3800
B	0.8776	0.4640
C	0.9424	0.5670
D	0.4979	0.4460
E	0.7718	0.4590
F	0.8942	0.5070
G	0.8964	0.5620
H	0.7999	0.4020
I	0.1924	0.3030
J	0.4617	0.3280
K	0.6686	0.4160
L	0.9744	0.5950
M	0.8690	0.4500
N	0.9902	0.6090
O	0.9050	0.4940
P	0.8412	0.5050
Q	0.8852	0.5220
R	0.7291	0.3660
S	0.8118	0.4390
T	0.4493	0.3560
U	0.3223	0.2920
V	0.6939	0.3970
W	0.3377	0.2720
X	0.8907	0.5290
Y	0.9252	0.5570
Z	0.7462	0.3650
a	0.8011	0.5060
b	0.5360	0.3310
c	0.4329	0.2760

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Continued from previous page...

Chain	Atom inclusion	Q-score
d	0.8044	0.4260
e	0.9347	0.5520
f	0.9620	0.5560
g	0.8870	0.4270
h	0.9151	0.5640
i	0.9158	0.5410
j	0.9852	0.5950
k	0.6582	0.3760
l	0.2779	0.2860
m	0.5501	0.3440
n	0.7587	0.4360
o	0.6793	0.4390
p	0.0877	0.2130
q	0.0468	0.2600
r	0.6304	0.3590
s	0.7268	0.3880
t	0.8068	0.4680
u	0.6997	0.3320
v	0.8524	0.5330
w	0.5592	0.3930
y	0.7912	0.3600
z	0.3930	0.2780