Full wwPDB EM Validation Report (i)

Feb 8, 2023 – 01:21 pm GMT

PDB ID	:	6ELZ
EMDB ID	:	EMD-3891
Title	:	State E (TAP-Flag-Ytm1 E80A) - Visualizing the assembly pathway of nucleolar pre-60S ribosomes
Authors	:	Kater, L.; Cheng, J.; Barrio-Garcia, C.; Hurt, E.; Beckmann, R.
Deposited on	:	2017-09-30
Resolution	:	3.30 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 (i) 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 (i)) were used in the production of this report:

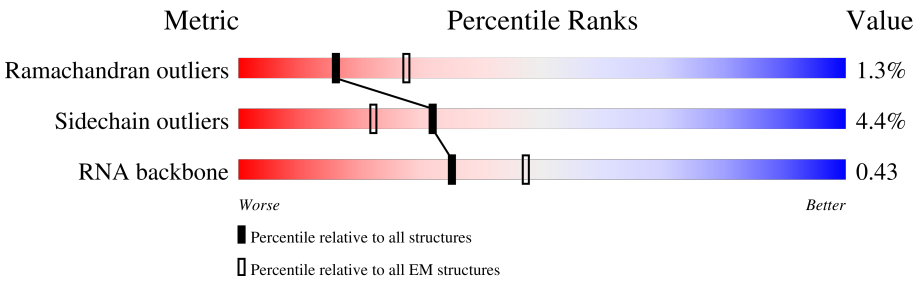
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.30 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	3396	8% 50% 22% 28%
2	2	158	• 77% 23% •
3	6	232	6% 15% 13% 72%
4	L	199	• 55% 6% 39%
5	N	204	• 82% 8% 9%
6	Q	186	8% 68% • 28%
7	R	189	23% 60% • 37%
8	S	172	16% 91% 7% ••

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Mol	Chain	Length	Quality of chain
9	T	160	34% 32% 66%
10	U	121	50% 80% 19%
11	Z	136	23% 95%
12	c	105	50% 88% 5% 8%
13	d	113	24% 89% 5%
14	e	130	92% 5%
15	f	107	94% 5%
16	g	121	15% 84% 8% 7%
17	i	100	25% 73% 9% 17%
18	j	88	73% 10% 17%
19	k	78	46% 91% 8%
20	O	199	72% 24%
21	V	137	19% 96%
22	a	149	29% 52% 46%
23	P	184	19% 96%
24	X	142	13% 94% 5%
25	Y	127	8% 97%
26	h	120	8% 93% 5%
27	F	244	7% 87% 9%
28	B	387	8% 82% 6% 12%
29	C	362	8% 95%
30	H	191	8% 95% 5%
31	A	291	13% 66% 32%
32	K	376	32% 67% 32%
33	m	807	28% 77% 20%

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Mol	Chain	Length	Quality of chain
34	D	505	16% 37% 62%
35	W	236	44% 94% 5%
36	l	181	41% 93%
37	b	647	31% 62% 35%
38	o	220	21% 59% 40%
39	n	605	12% 65% 32%
40	r	261	26% 66% 33%
41	s	520	7% 93%
42	t	322	24% 86% 10%
43	y	245	24% 89% 8%
44	z	106	41% 52% 48%
45	p	460	61% 63% 35%
46	q	618	35% 49% 49%
47	u	199	21% 55% 42%
48	v	231	7% 55% 44%
49	w	841	24% 50% 48%
50	I	663	34% 63% 35%
51	J	427	19% 33% 66%
52	E	176	14% 82% 6% 11%
53	G	256	6% 66% 6% 28%
54	M	138	7% 92% 7%

2 Entry composition (i)

There are 55 unique types of molecules in this entry. The entry contains 134887 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2457	52595	23485	9508	17146	2456	0	0

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called Internal transcribed spacer 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	65	1370	614	228	463	65	0	0

- Molecule 4 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	L	122	998	628	209	161	0	0

- Molecule 5 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	N	186	1587	994	333	259	1	0	0

- Molecule 6 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	Q	134	1035	659	196	179	1	0	0

- Molecule 7 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	R	120	964	610	194	160	0	0

- Molecule 8 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	S	170	1432	922	265	242	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	T	55	422	259	85	77	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	U	98	778	505	127	146	0	0

- Molecule 11 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	Z	135	1092	710	202	180	0	0

- Molecule 12 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	c	97	743	479	124	139	1	0	0

- Molecule 13 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	d	107	873	553	165	154	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	e	125	1009	641	203	164	1	0	0

- Molecule 15 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	f	106	850	540	165	144	1	0	0

- Molecule 16 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	g	112	881	546	179	152	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	i	83	658	408	135	113	2	0	0

- Molecule 18 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	j	73	580	353	126	96	5	0	0

- Molecule 19 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	k	77	612	391	115	106	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	197	1555	1003	289	262	1	0	0

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	134	993	623	187	176	7	0	0

- Molecule 22 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	a	81	626	408	108	110	0	0

- Molecule 23 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	P	183	1442	896	287	259	0	0

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	141	1100	705	196	197	2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	Y	126	993	625	192	176	0	0

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	h	119	969	615	186	167	1	0	0

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	F	222	1784	1151	324	308	1	0	0

- Molecule 28 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	B	341	2702	1715	501	480	6	0	0

- Molecule 29 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	C	359	2731	1720	518	490	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	H	190	1510	957	273	276	4	0	0

- Molecule 31 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	A	198	1623	1043	284	290	6	0	0

- Molecule 32 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	K	257	2073	1337	341	392	3	0	0

- Molecule 33 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	m	645	5223	3322	907	979	15	0	0

- Molecule 34 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	D	194	1590	1030	268	287	5	0	0

- Molecule 35 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	W	232	1870	1184	321	360	5	0	0

- Molecule 36 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	l	174	1377	887	242	241	7	0	0

- Molecule 37 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	b	421	3410	2180	585	627	18	0	0

- Molecule 38 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	o	133	1107	716	198	189	4	0	0

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	n	411	3369	2179	585	592	13	0	0

- Molecule 40 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	r	176	1438	906	279	248	5	0	0

- Molecule 41 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	s	36	301	184	69	46	2	0	0

- Molecule 42 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	t	290	2328	1472	431	422	3	0	0

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	y	225	1701	1056	295	343	7	0	0

- Molecule 44 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	z	55	444	273	88	83	0	0

- Molecule 45 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	p	298	2321	1448	410	457	6	0	0

- Molecule 46 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	q	317	2485	1591	429	455	10	0	0

- Molecule 47 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	u	116	976	612	200	155	9	0	0

- Molecule 48 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	v	130	1087	678	211	195	3	0	0

- Molecule 49 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	w	436	3511	2235	628	630	18	0	0

- Molecule 50 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	I	433	3470	2217	591	645	17	0	1

- Molecule 51 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	J	145	1215	759	225	228	3	0	0

- Molecule 52 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	E	156	1239	800	222	216	1	0	0

- Molecule 53 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	G	184	1438	930	249	257	2	0	0

- Molecule 54 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	M	136	1053	675	199	177	2	0	0

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

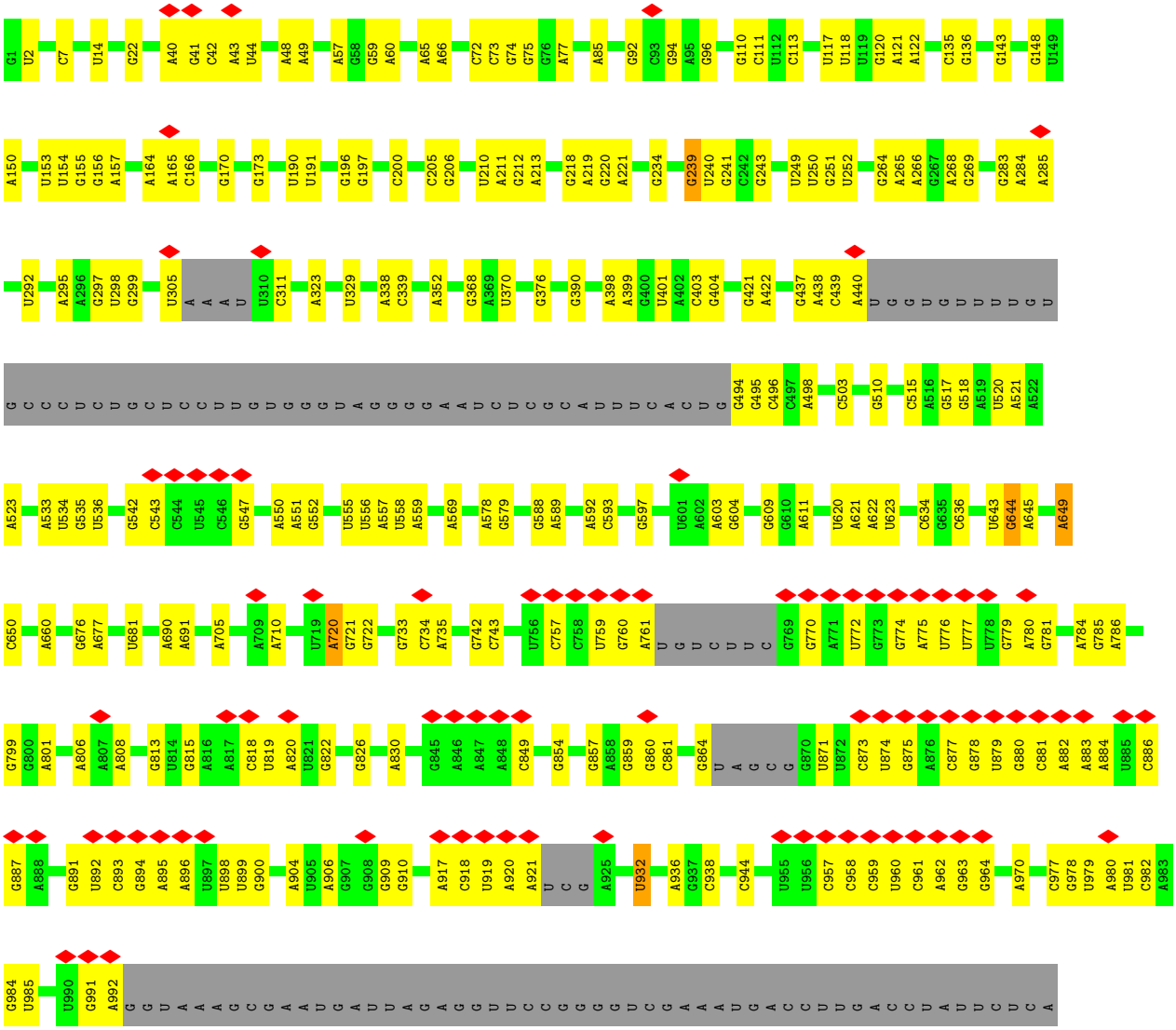
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
55	j	1	1	1	0

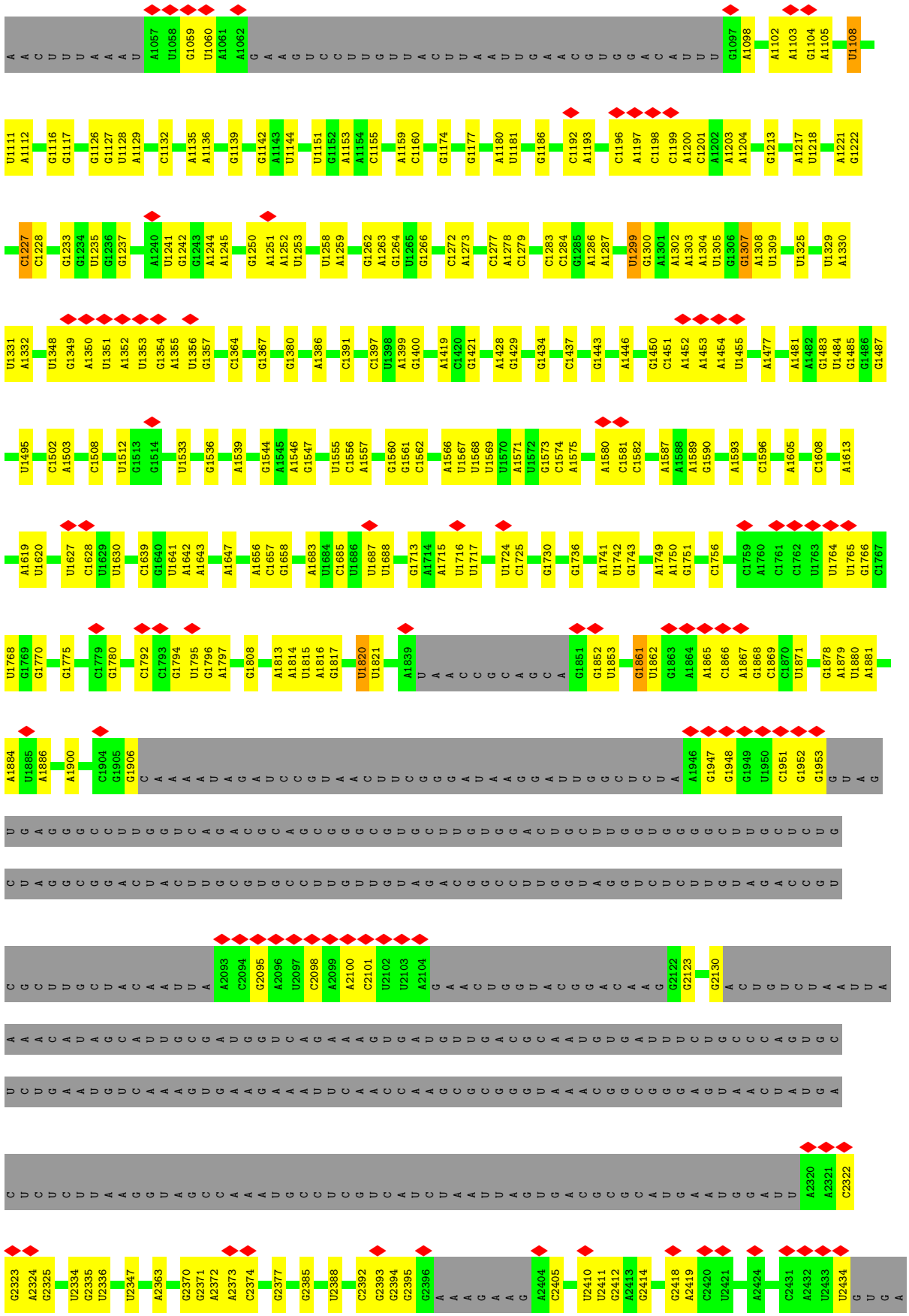
3 Residue-property plots (i)

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

- Molecule 1: 25S ribosomal RNA

Chain 1:

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C1227 C1228 G1233 G1234 U1235 G1236 G1237 A1240 U1241 G1242 G1243 A1244 A1245 G1250 A1251 A1252 U1253 U1258 A1259 G1262 A1263 G1264 U1265 G1266 C1272 A1273 C1277 A1278 C1279 C1283 C1284 G1285 A1286 A1287 U1299 G1300 A1301 A1302 A1303 A1304 U1305 G1306 G1307 A1308 U1309 U1325 U1329 A1330
U1331 A1332 U1348 G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 C1364 G1367 G1380 A1386 C1391 C1397 U1398 A1399 G1400 A1419 C1420 G1421 A1428 G1429 G1434 C1437 G1443 A1446 G1450 C1451 A1452 A1453 A1454 U1455 A1477 A1481 A1482 G1483 U1484 G1485 G1486 G1487
U1495 C1502 A1503 C1508 U1512 G1513 G1514 U1533 G1536 A1539 G1544 A1545 A1546 G1547 U1555 C1556 A1557 G1560 G1561 C1562 A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1573 C1574 A1575 A1580 C1581 C1582 A1587 A1588 A1589 G1590 A1593 C1596 A1605 C1608 A1613
A1619 U1620 U1627 C1628 U1629 U1630 C1639 G1640 U1641 A1642 A1643 A1647 A1656 C1657 G1658 A1683 U1684 C1685 U1686 U1687 U1688 G1713 A1714 A1715 U1716 U1717 U1724 C1725 G1730 G1736 A1741 U1742 G1743 A1749 A1750 G1751 C1756 C1759 A1760 C1761 C1762 U1763 U1764 U1765 G1766 C1767
U1768 G1769 G1770 G1775 C1779 G1780 C1792 C1793 G1794 U1795 G1796 A1797 G1808 A1813 A1814 U1815 A1816 G1817 U1820 U1821 A1839 U A A C C G C A G C A G1851 G1852 U1853 G1861 U1862 G1863 A1864 A1865 C1866 A1867 G1868 C1869 C1870 U1871 G1878 A1879 U1880 A1881
A1884 U1885 A1886 A1900 C1904 G1905 G1906 C A A A A U A G A U C C G U A A C U U C G G G A U A A A G G G A U U G C U C U A A1946 G1947 G1948 G1949 U1950 C1951 G1952 G1953 G U A G
U G A G G G C C U U G G A C A A C U U U G C A G C C U G G U G G C U U G C U G U G G G G C U U G A G C U C U C U G
C U U A G G C C G G U A A C U U U G C C G U G C C G G U U G G G C C U G U G G G A C U U G U G A C U C C U G U
C G G C U U G C U A A C A A U U A G U G C C G G G A A A A C U G G G C C U G U G G G A C U U G G G C U U G C U G
A A A A C A U A U G G C A U U A A G G U C A G U G A A A G U G A U U G U U G A C C G G G C U G G G U A A A C U G
U C U G A U A U G U C A U A A A G U G A A G A A U C A A G U G A A U G U U G A A A C G G A C U G G U A A C U A U G A
C U C U C U U A A G G U G U U C A A G U G C C U U C C U G U G U U C G G U A A A C U G G U A A A U U G
A2320 A2321 C2322
G2323 A2324 G2325 U2334 G2335 U2336 U2347 A2363 G2370 G2371 A2372 A2373 C2374 G2377 G2385 U2388 C2392 G2393 G2394 G2395 G2396 A A A G A A G A2404 C2405 U2410 U2411 G2412 A2413 G2414 G2418 A2419 C2420 U2421 A2424 C2431 A2432 U2433 U2434 G U G A
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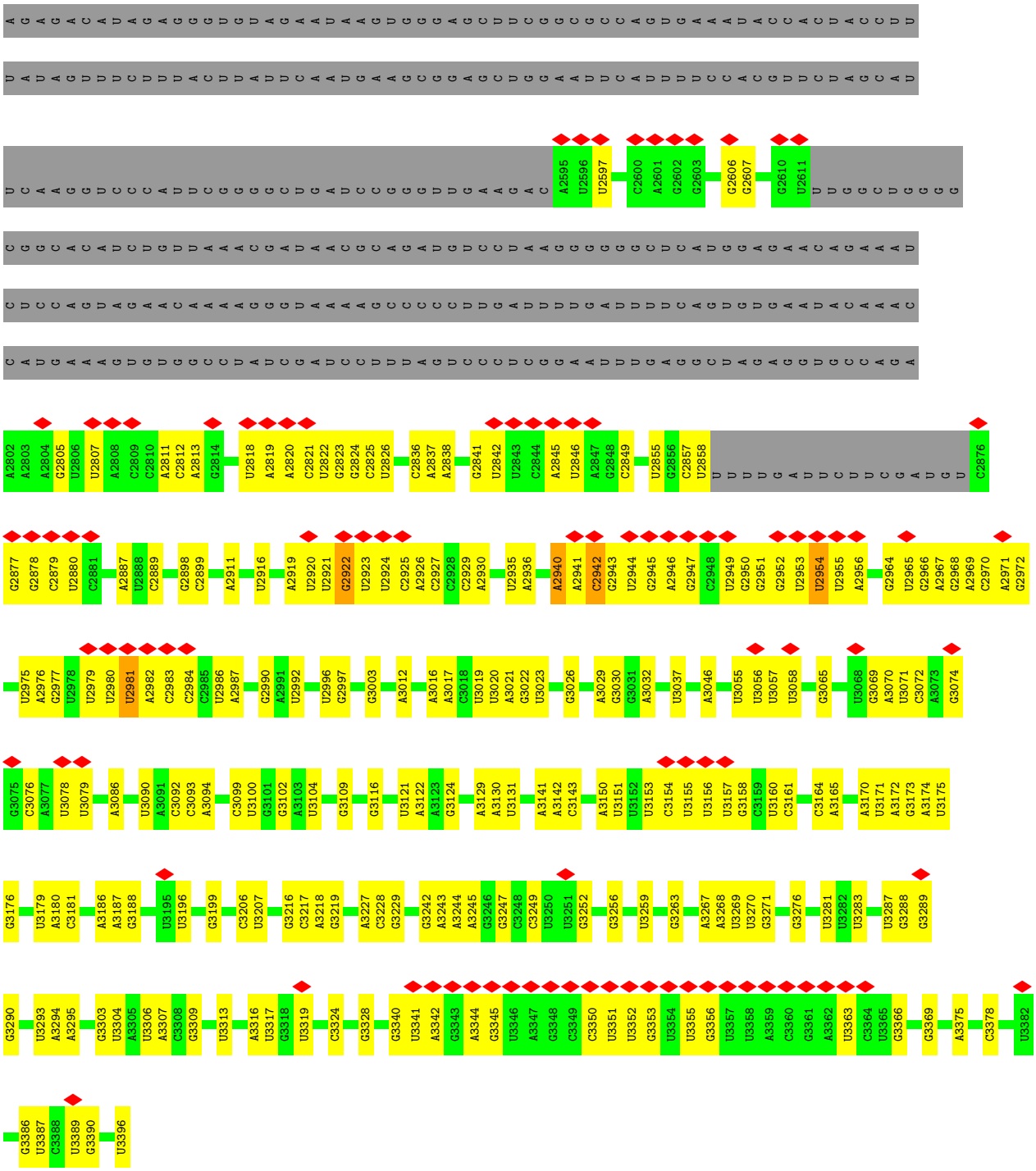
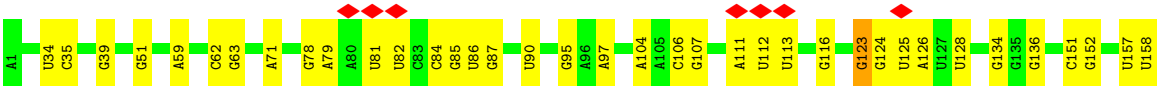


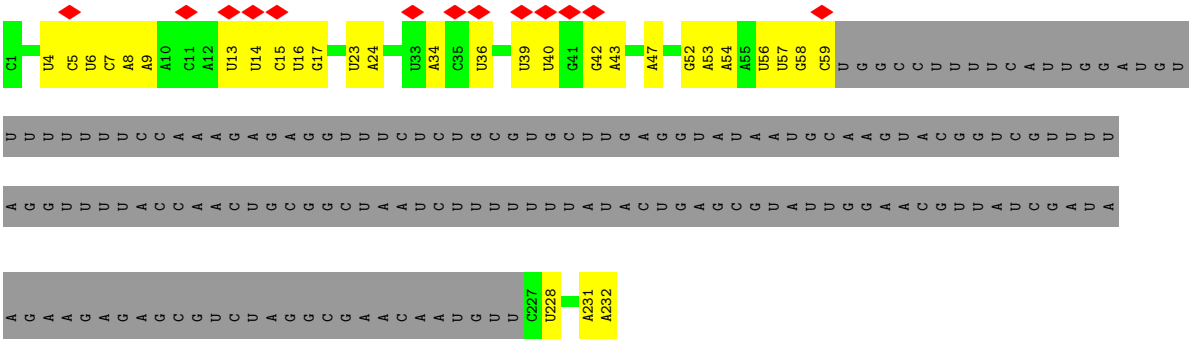
• Molecule 2: 5.8S ribosomal RNA

Chain 2:



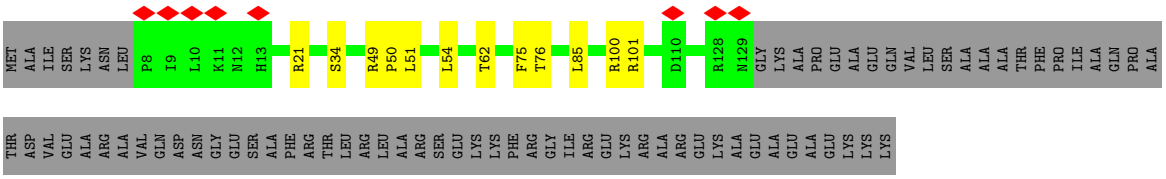
• Molecule 3: Internal transcribed spacer 2

Chain 6: 6% 15% 13% 72%



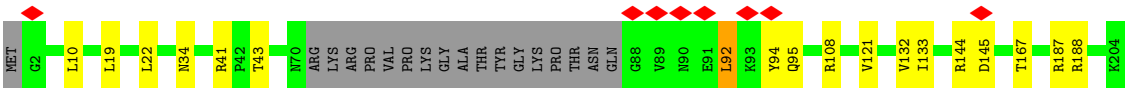
- Molecule 4: 60S ribosomal protein L13-A

Chain L: 55% 6% 39%



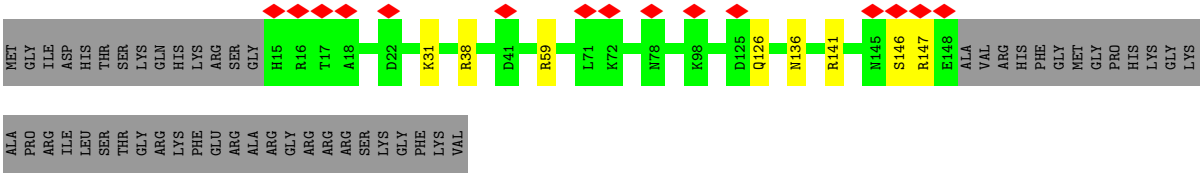
- Molecule 5: 60S ribosomal protein L15-A

Chain N: 82% 8% 9%



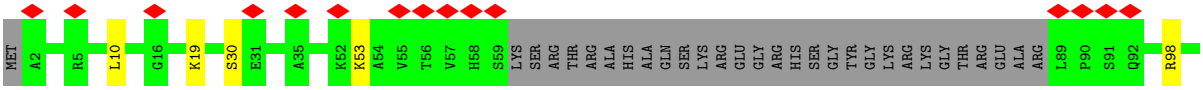
- Molecule 6: 60S ribosomal protein L18-A

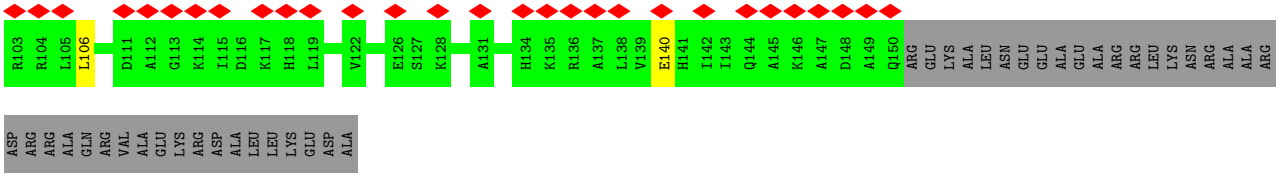
Chain Q: 8% 68% 28%



- Molecule 7: 60S ribosomal protein L19-A

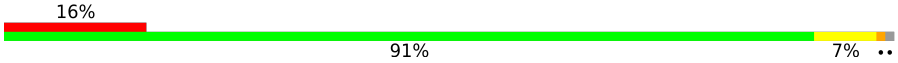
Chain R: 23% 60% 37%

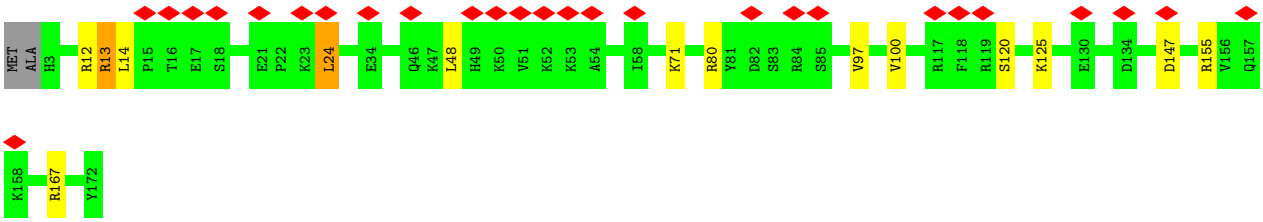




• Molecule 8: 60S ribosomal protein L20-A

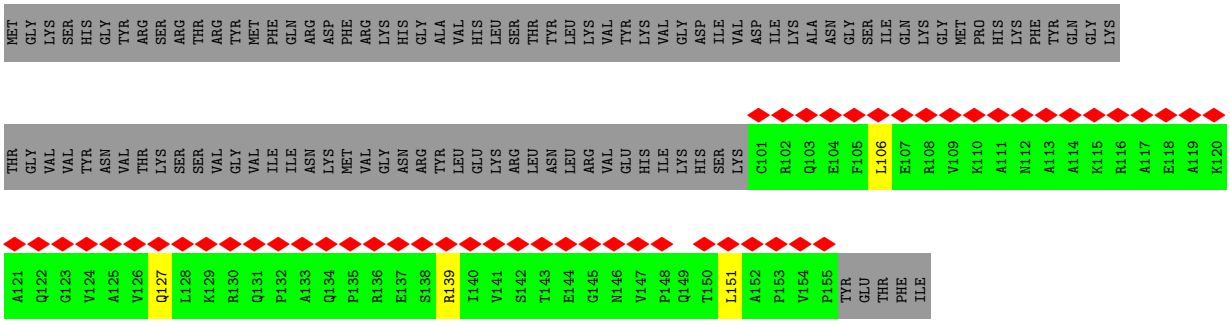
Chain S:





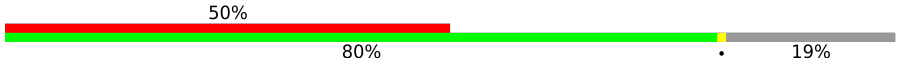
• Molecule 9: 60S ribosomal protein L21-A

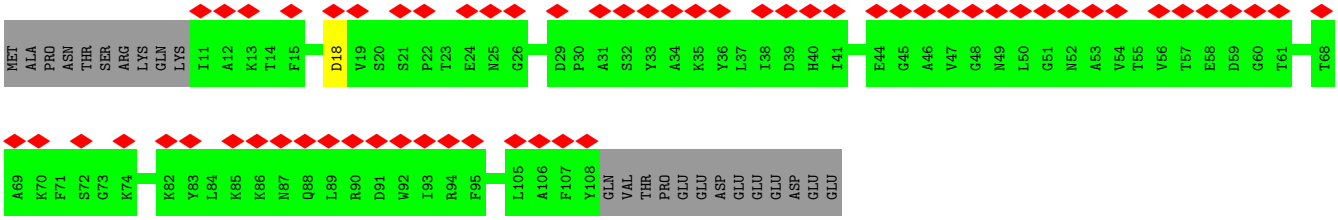
Chain T:



• Molecule 10: 60S ribosomal protein L22-A

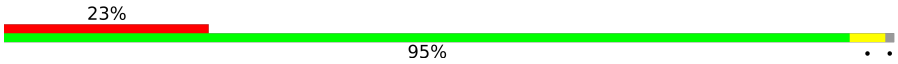
Chain U:

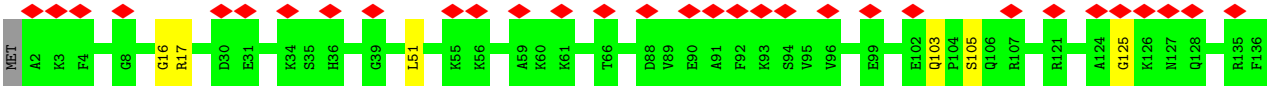




• Molecule 11: 60S ribosomal protein L27-A

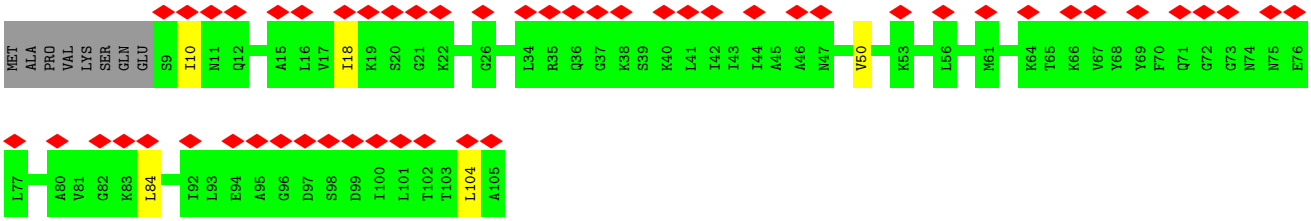
Chain Z:





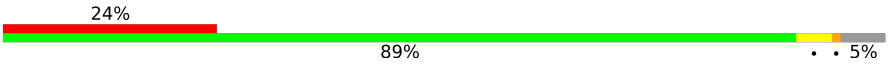
• Molecule 12: 60S ribosomal protein L30

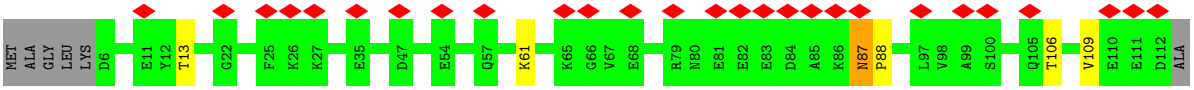
Chain c:



- Molecule 13: 60S ribosomal protein L31-A

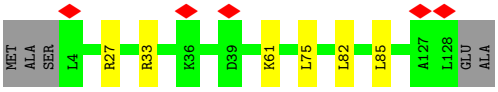
Chain d:





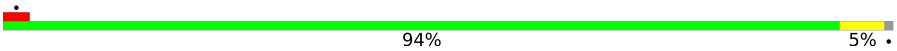
- Molecule 14: 60S ribosomal protein L32

Chain e:



- Molecule 15: 60S ribosomal protein L33-A

Chain f:

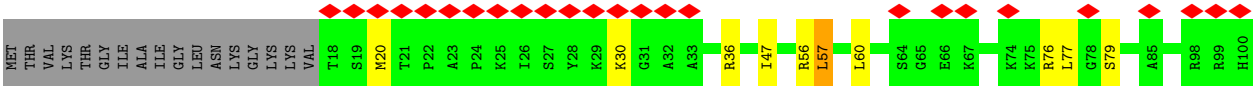


- Molecule 16: 60S ribosomal protein L34-A

Chain g:

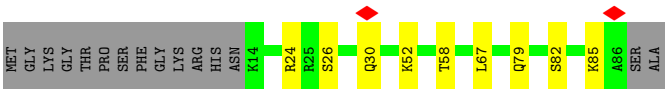
- Molecule 17: 60S ribosomal protein L36-A

Chain i:



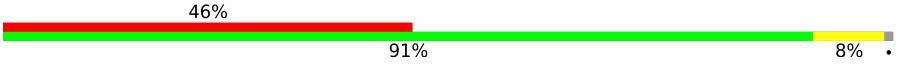
- Molecule 18: 60S ribosomal protein L37-A

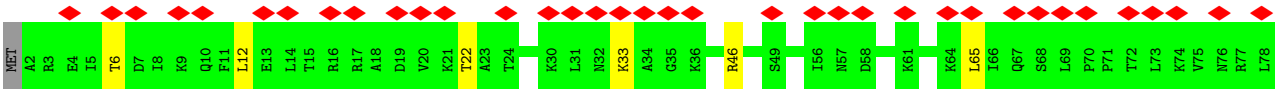
Chain j:



- Molecule 19: 60S ribosomal protein L38

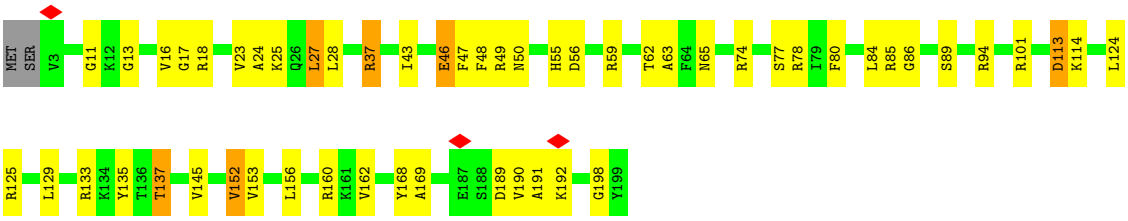
Chain k:





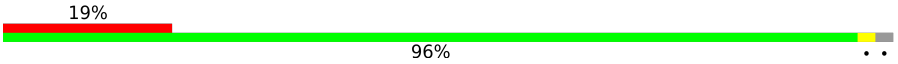
- Molecule 20: 60S ribosomal protein L16-A

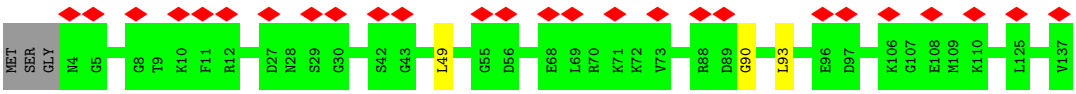
Chain O:



- Molecule 21: 60S ribosomal protein L23-A

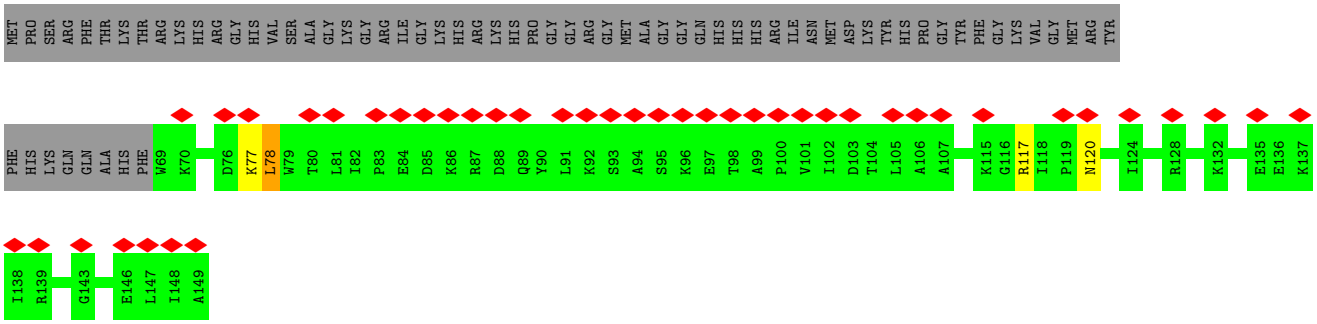
Chain V:





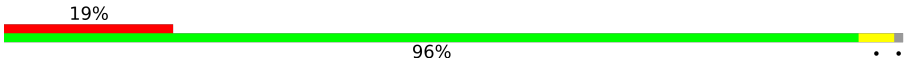
- Molecule 22: 60S ribosomal protein L28

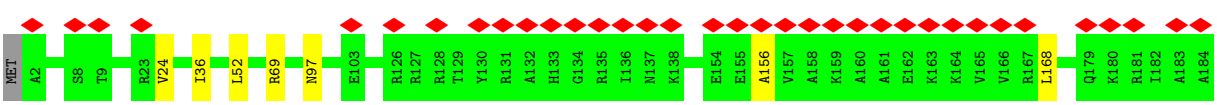
Chain a:



- Molecule 23: 60S ribosomal protein L17-A

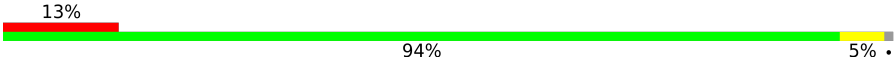
Chain P:

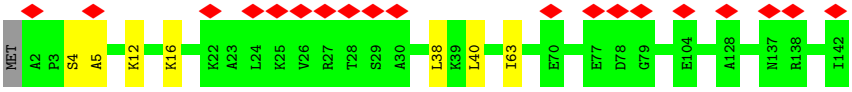




- Molecule 24: 60S ribosomal protein L25

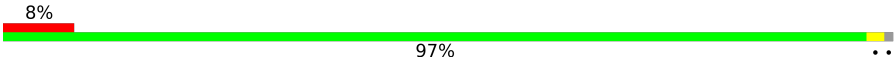
Chain X:

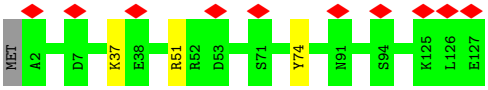




- Molecule 25: 60S ribosomal protein L26-A

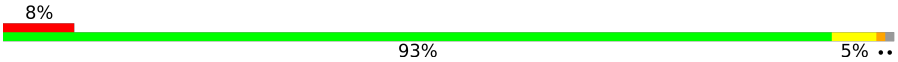
Chain Y:

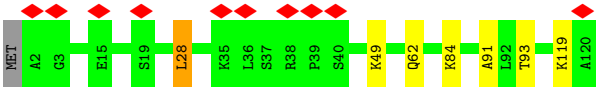




- Molecule 26: 60S ribosomal protein L35-A

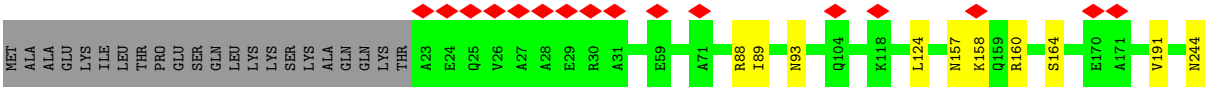
Chain h:





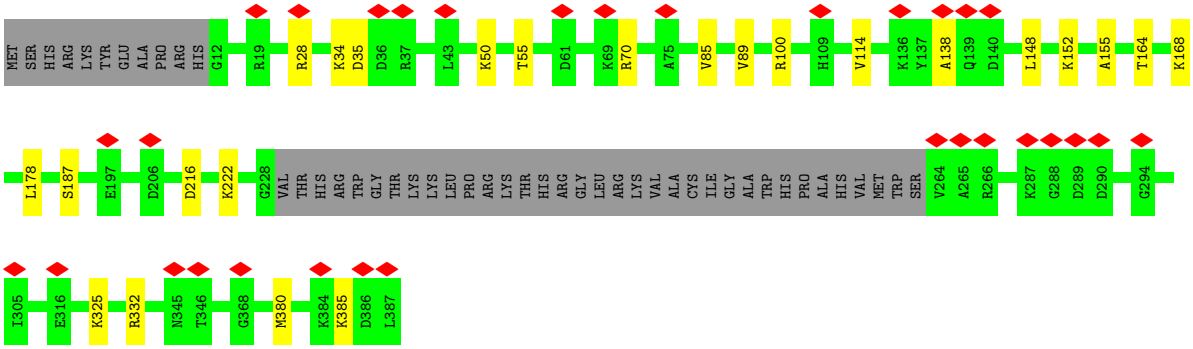
- Molecule 27: 60S ribosomal protein L7-A

Chain F:



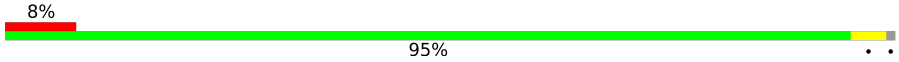
- Molecule 28: 60S ribosomal protein L3

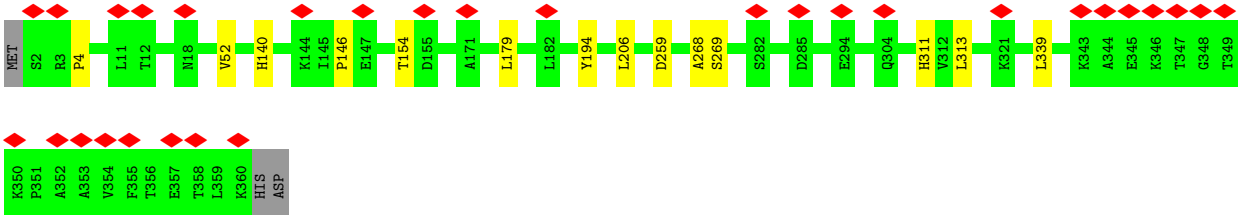
Chain B:



- Molecule 29: 60S ribosomal protein L4-A

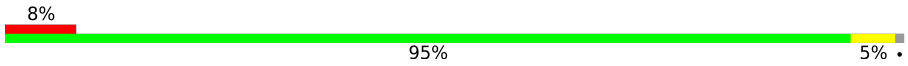
Chain C:

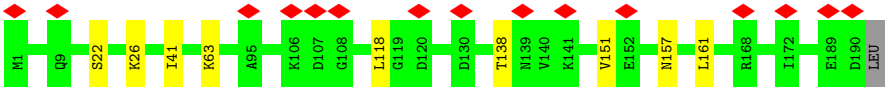




- Molecule 30: 60S ribosomal protein L9-A

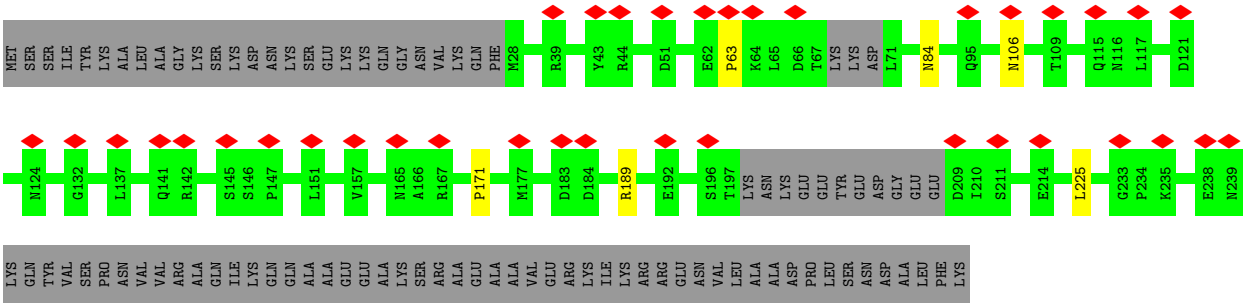
Chain H:





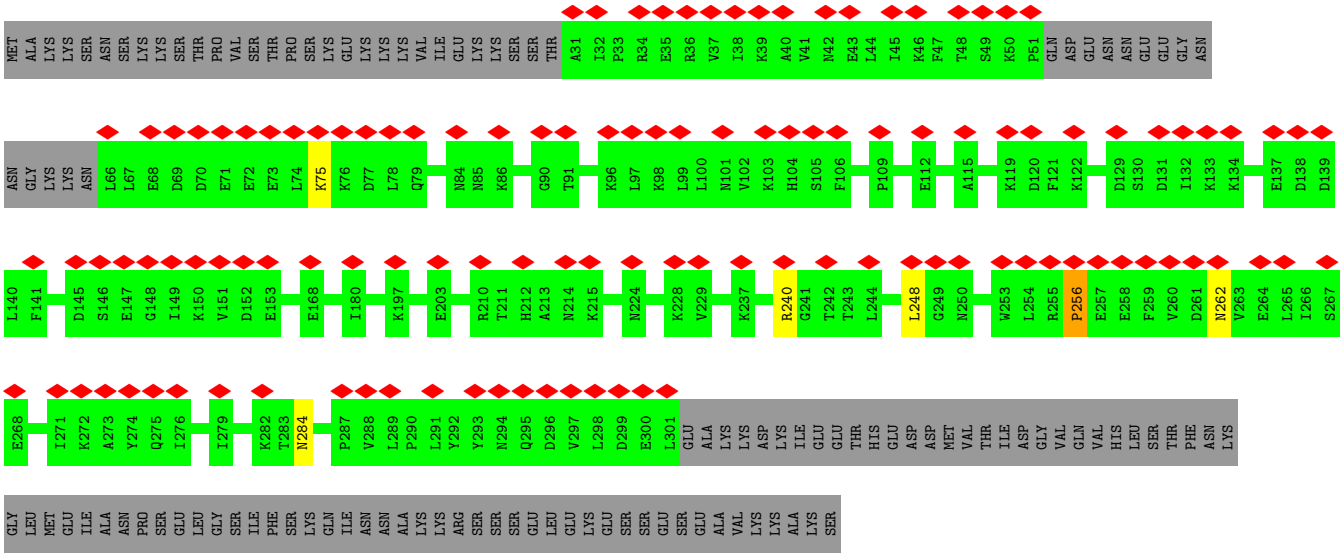
- Molecule 31: Ribosome biogenesis protein BRX1

Chain A:



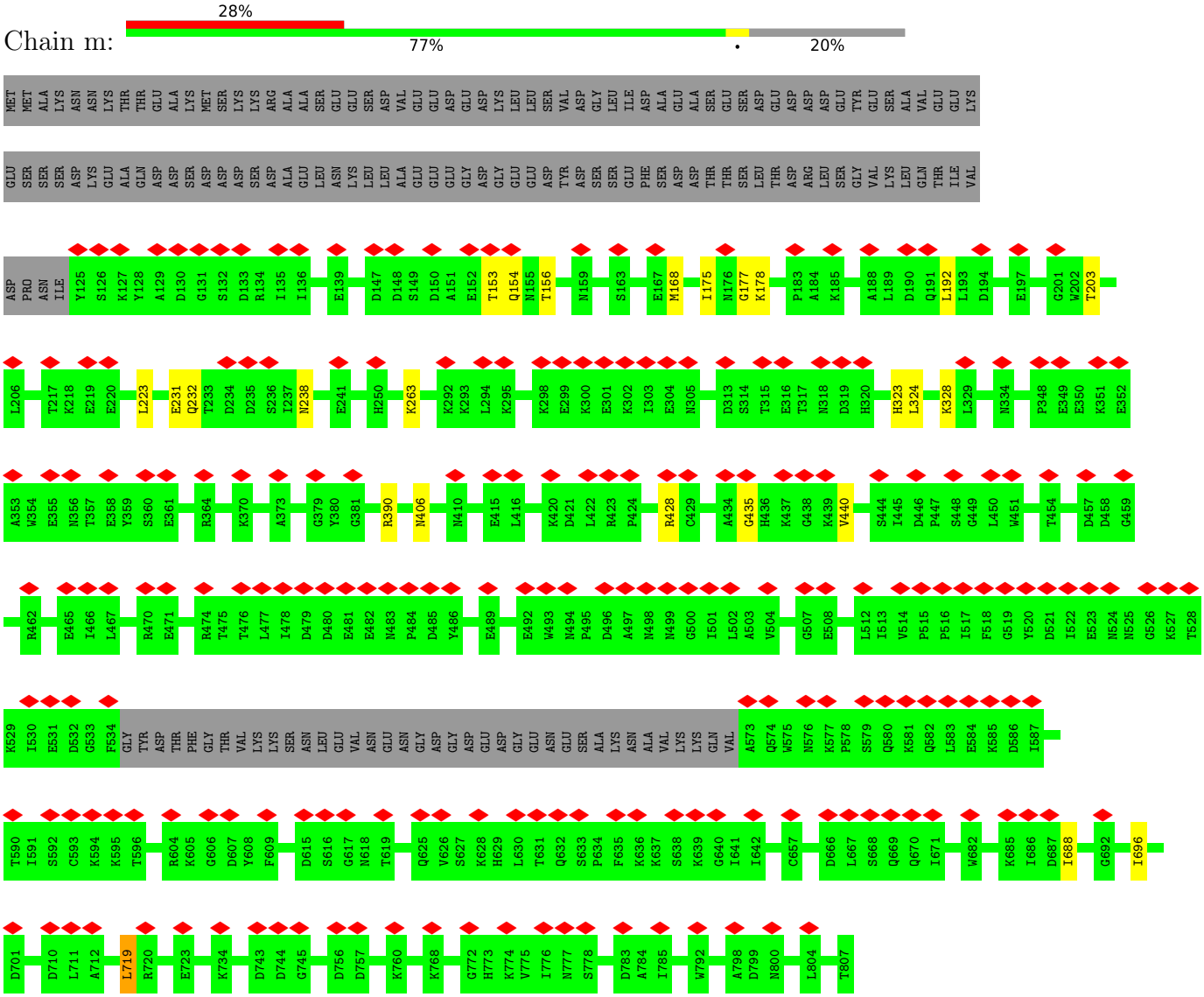
- Molecule 32: Proteasome-interacting protein CIC1

Chain K:



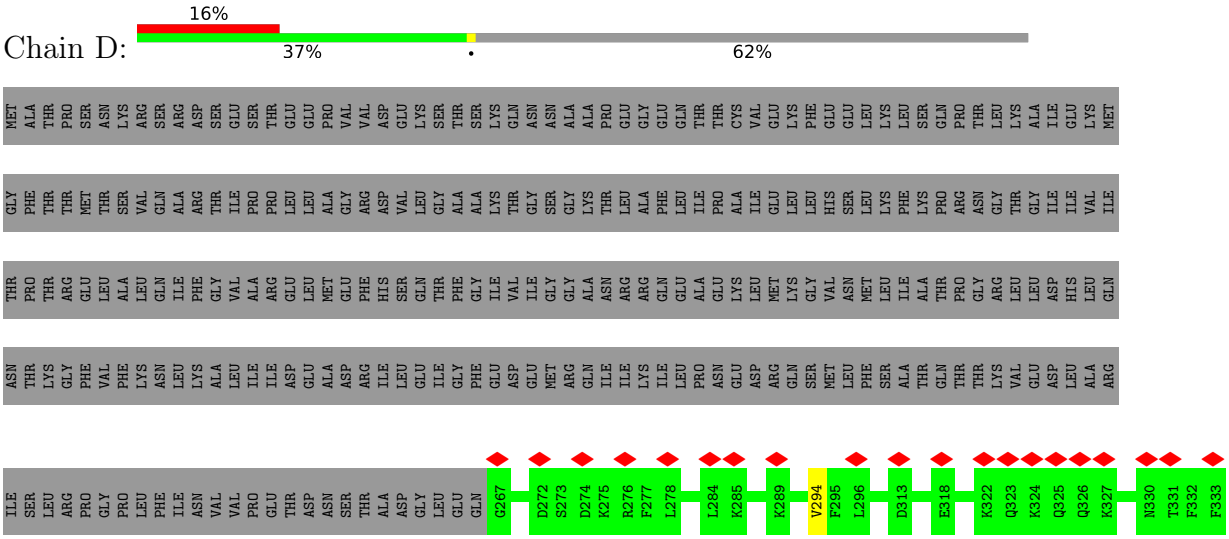
- Molecule 33: Ribosome biogenesis protein ERB1

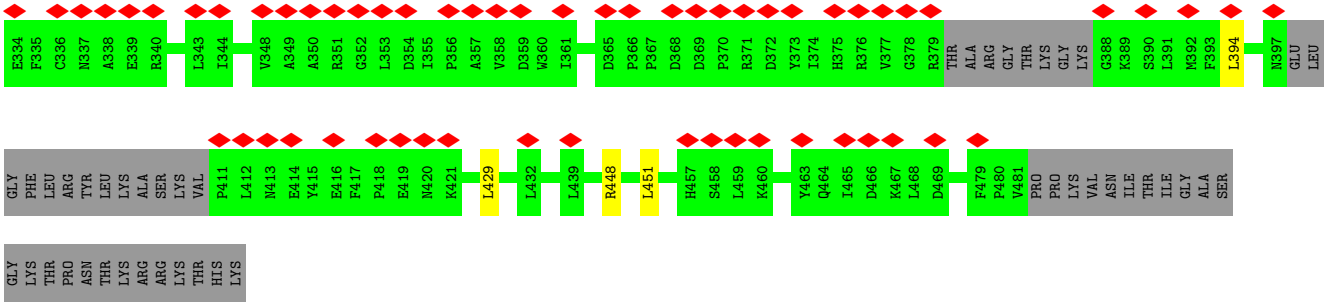
Chain m:



• Molecule 34: ATP-dependent RNA helicase HAS1

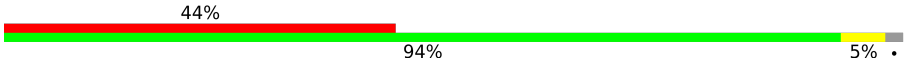
Chain D:

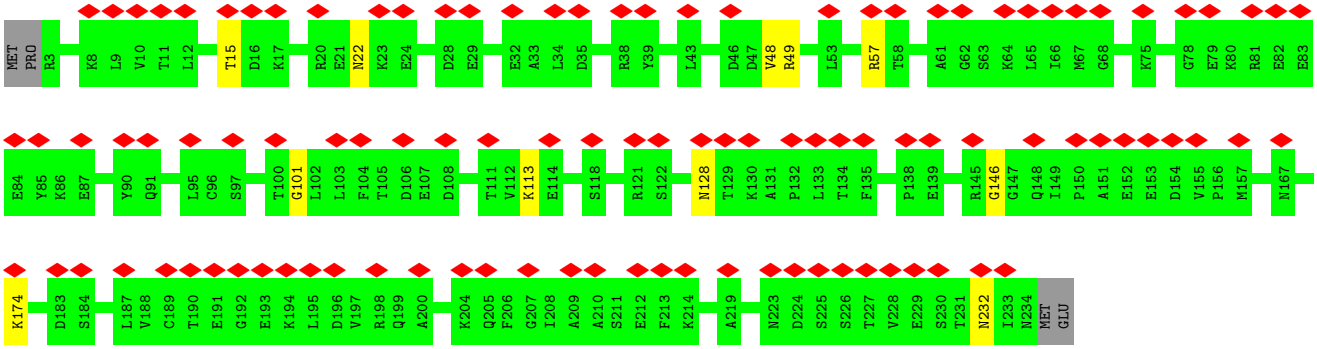




- Molecule 35: Ribosome assembly factor MRT4

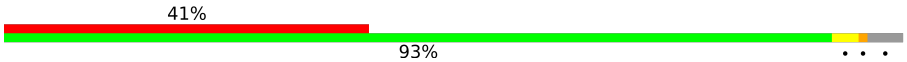
Chain W:

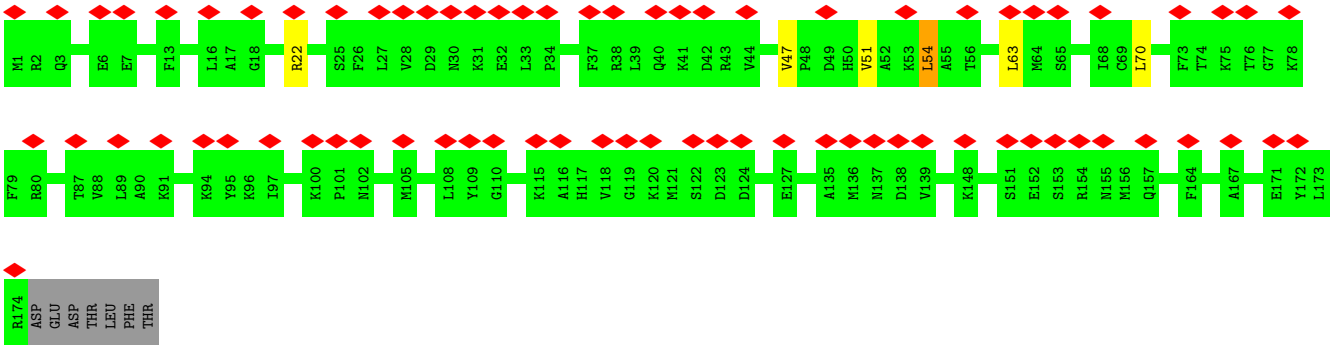




- Molecule 36: 60S ribosome subunit biogenesis protein NIP7

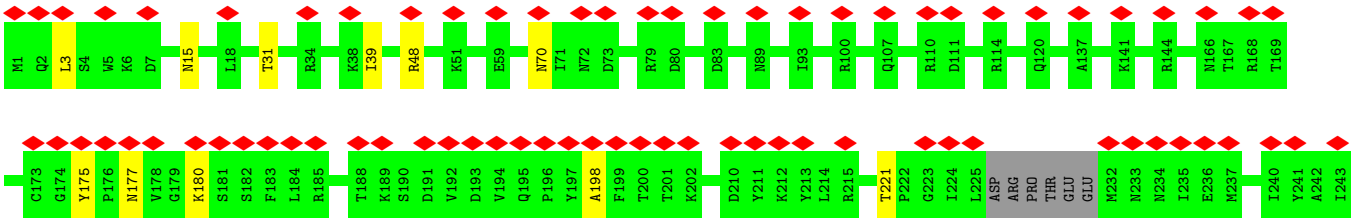
Chain l:

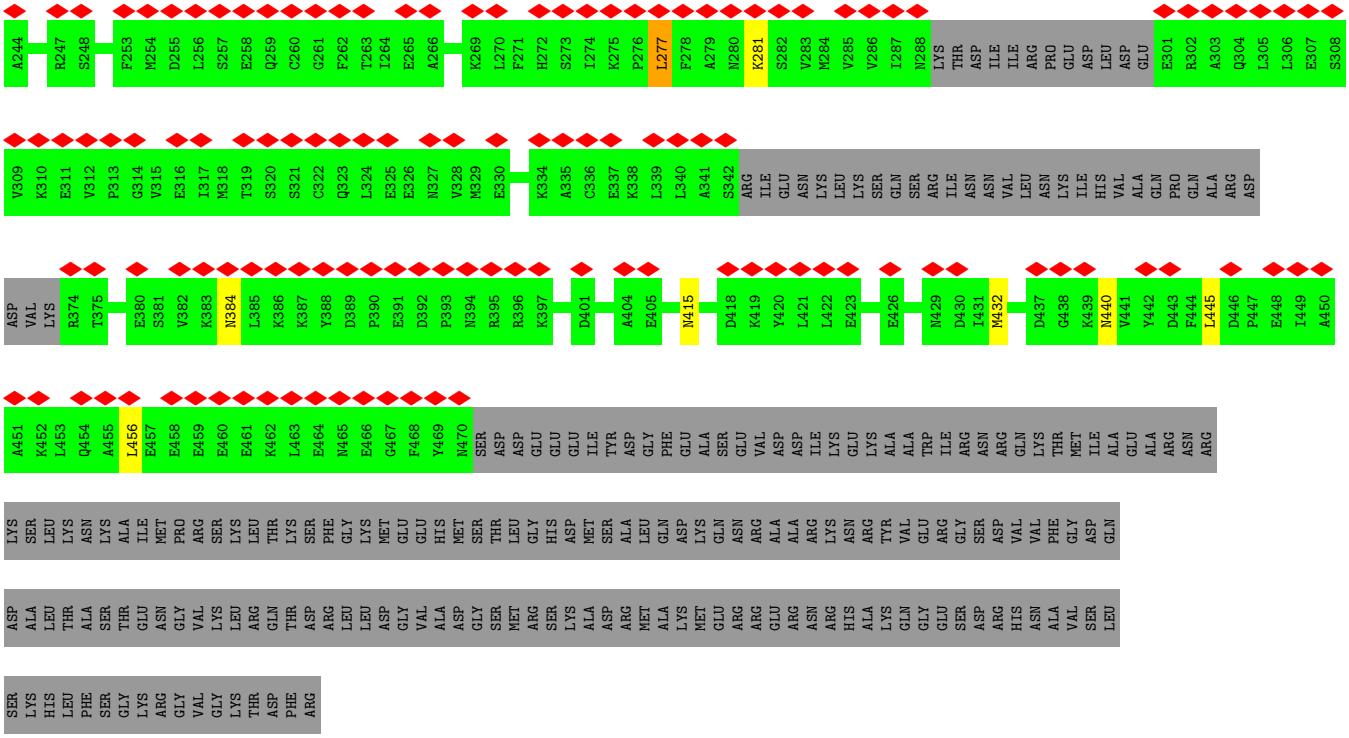




- Molecule 37: Nucleolar GTP-binding protein 1

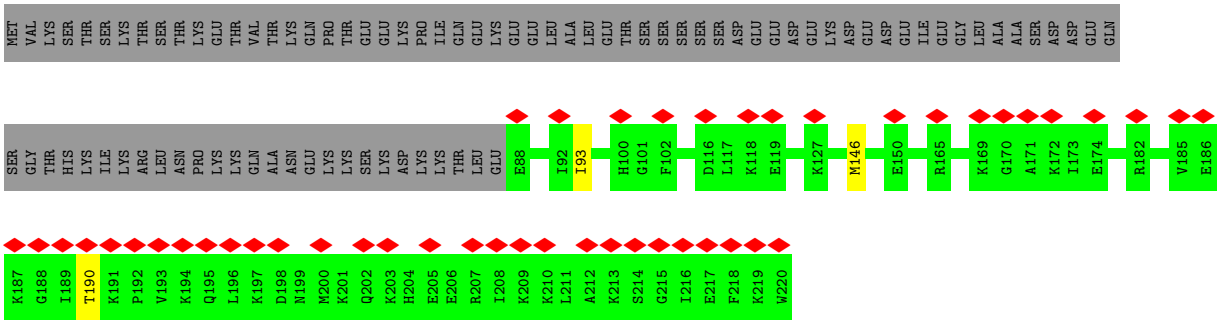
Chain b:





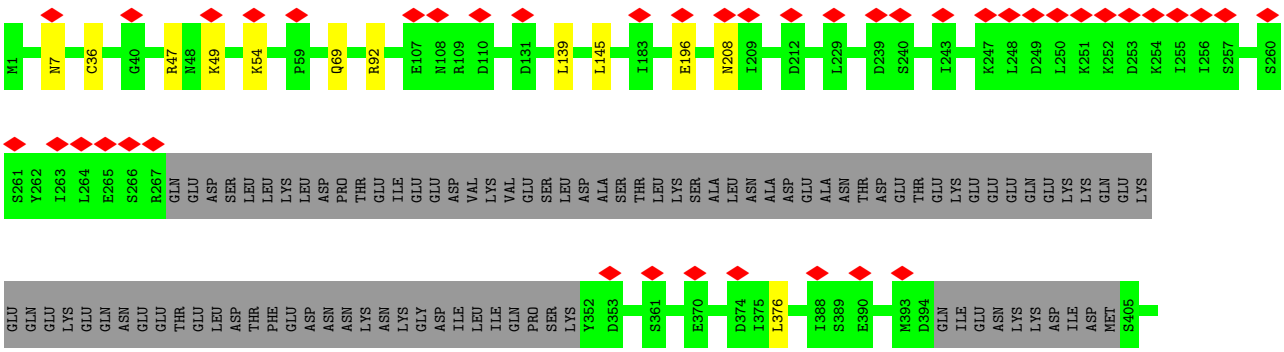
- Molecule 38: Ribosome biogenesis protein 15

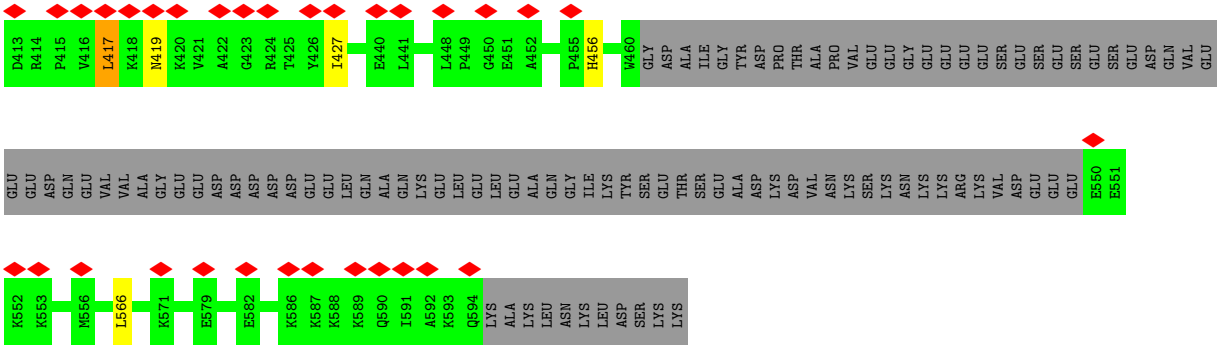
Chain o:



- Molecule 39: Pescadillo homolog

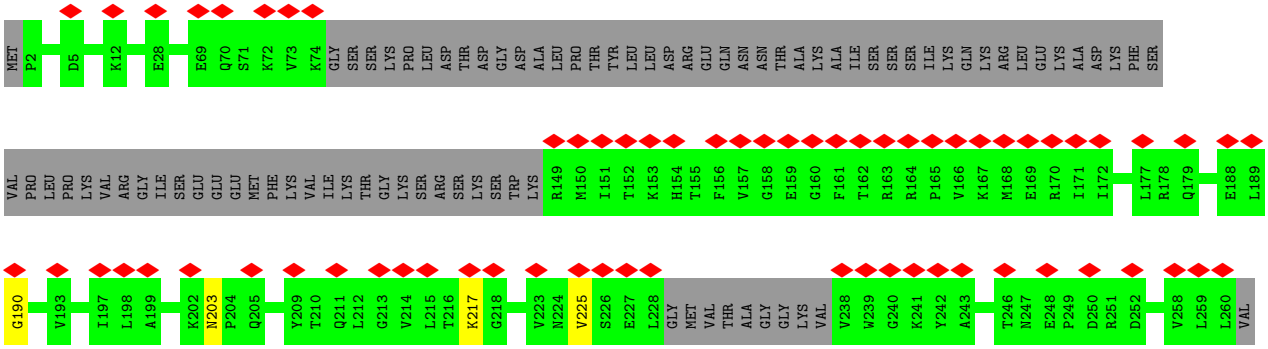
Chain n:





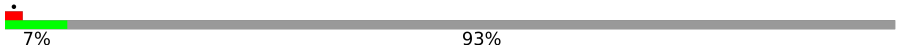
• Molecule 40: Ribosome biogenesis protein NSA2

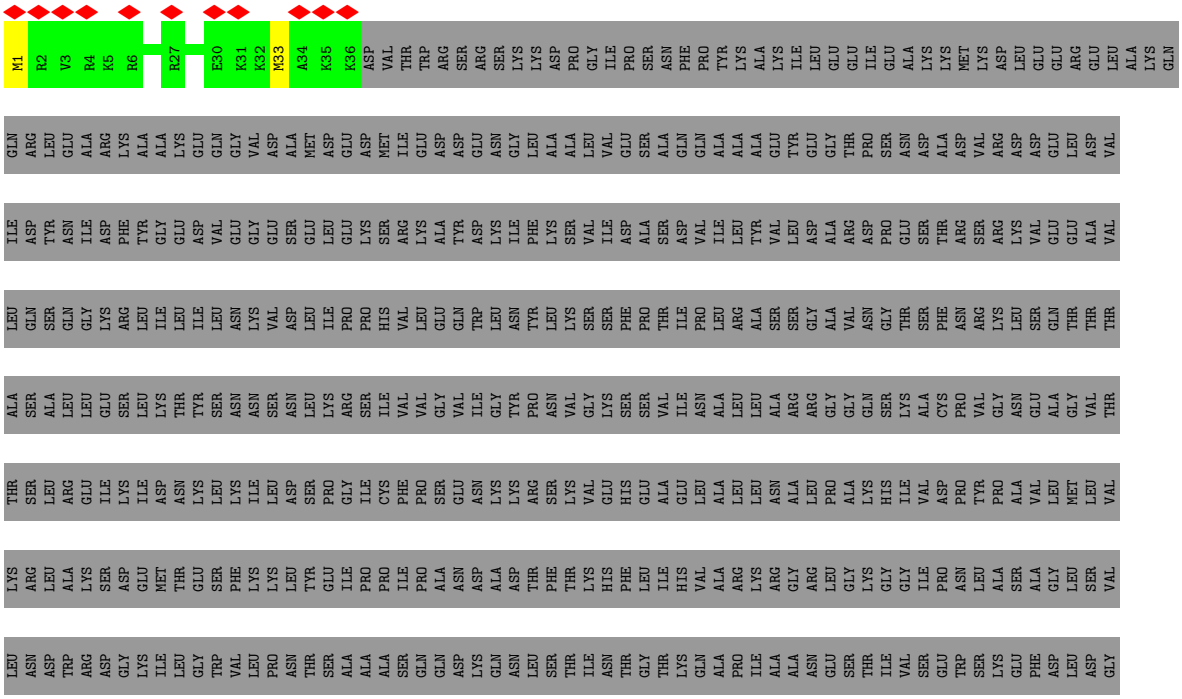
Chain r:



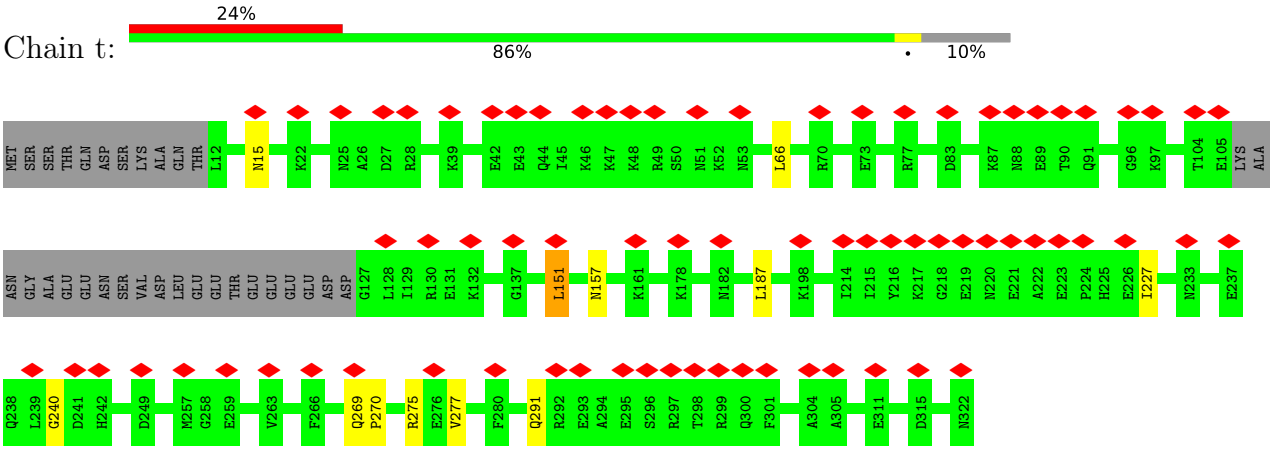
• Molecule 41: Nuclear GTP-binding protein NUG1

Chain s:

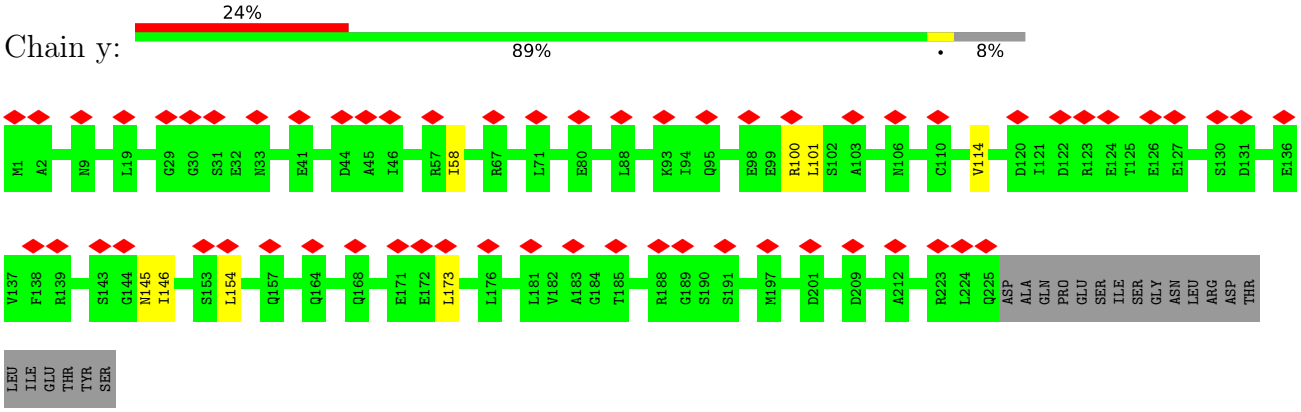




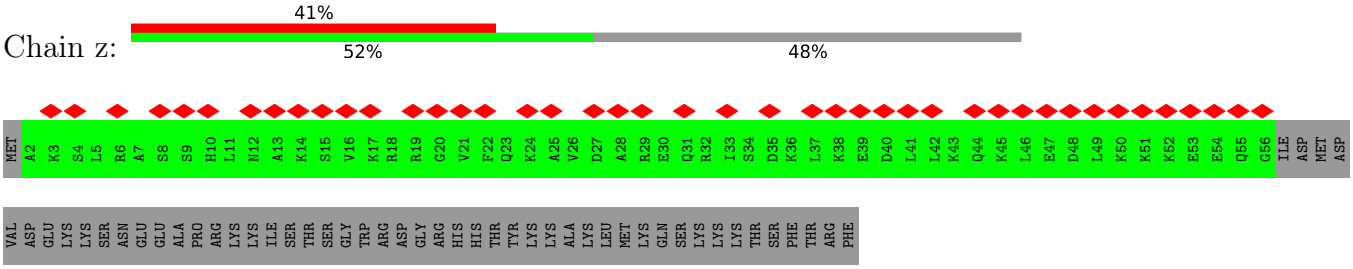
• Molecule 42: Ribosome biogenesis protein RLP7



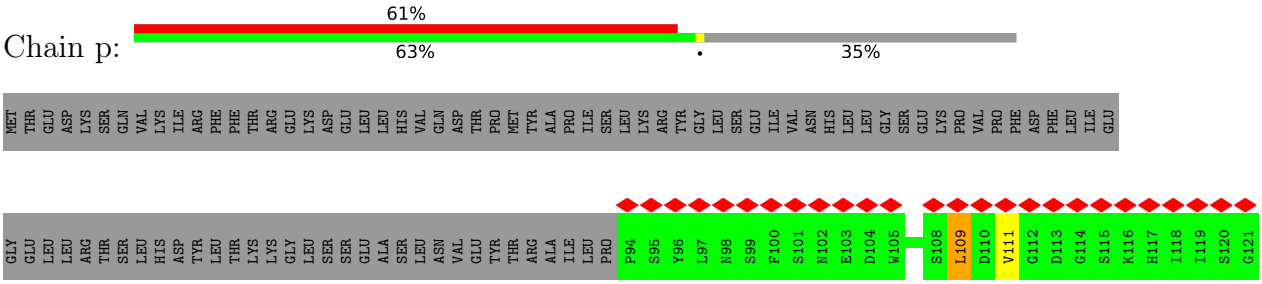
• Molecule 43: Eukaryotic translation initiation factor 6



• Molecule 44: UPF0642 protein YBL028C



• Molecule 45: Ribosome biogenesis protein YTM1



S122 Y123 D124 G125 I126 V127 R128 T129 W130 D131 L132 S133 G134 N135 V136 Q137 K138 Q139 Y140 S141 G142 H143 S144 G145 P146 I147 R148 A149 V150 K151 Y152 I153 S154 N155 T156 R157 L158 V159 S160 A161 G162 N163 D164 R165 T166 L167 R168 L169 W170 K171 T172 K173 N174 ASP ASP LEU LYS LEU THR SER

GLN GLN GLN ALA GLN GLU ASP ASP ASP ASP GLU VAL ASN ILE GLU D197 G198 K199 T200 L201 A202 I203 L204 E205 G206 H207 K208 A209 P210 V211 V212 S213 I214 D215 V216 S217 D218 N219 S220 R221 T222 L223 S224 A225 S226 Y227 D228 N229 S230 I231 G232 F233 W234 S235 T236 I237 Y238 K239 E240 M241

T242 V243 V244 ASP PRO LEU GLU ASP ILE ASN ASN PRO ASN ASN LYS ILE SER THR ALA ALA ARG LYS ARG ARG LYS LEU THR MET LYS ASP GLY THR ILE R275 R276 R277 A278 P279 L280 S281 L282 L283 E284 S285 H286 T287 A288 P289 V290 E291 Q292 V293 I294 F295 D296 S297 T298 D299 N300 T301

V302 G303 Y304 S305 V306 S307 Q308 D309 H310 T311 I312 K313 T314 W315 D316 L317 V318 T319 A320 R321 C322 I323 D324 T325 R326 T327 T328 S329 Y330 S331 L332 L333 S334 I335 A336 Q337 L338 S339 T340 L341 N342 L343 L344 A345 C346 G347 S348 S349 A350 R351 H352 I353 T354 L355 H356 D357 P358 R359 VAL GLY

ALA SER SER LYS VAL T367 Q368 Q369 Q370 L371 I372 G373 H374 K375 N376 F377 V378 S379 S380 L381 D382 T383 C384 P385 E386 N387 E388 Y389 I390 L391 C392 S393 G394 S395 H396 D397 G398 T399 V400 K401 V402 W403 D404 V405 R406 S407 T408 S409 P410 M411 Y412 T413 I414 T415 R416 E417 D418 K419 S420 VAL

GLN LYS G424 V425 N426 D427 K428 V429 F430 A431 V432 K433 W434 A435 E436 K437 V438 G439 I440 I441 S442 A443 G444 Q445 D446 K447 K448 I449 Q450 I451 N452 K453 GLY ASP ASN ILE PHE LYS ASN

- Molecule 46: 25S rRNA (cytosine(2870)-C(5))-methyltransferase

Chain q: 35% 49% · 49%

MET GLY SER ARG ARG HIS LYS ASN LYS GLN ALA ALA PRO PRO THR LEU GLU GLU PHE GLN ALA ARG LYS GLU LYS LYS ALA ASN ARG LYS LEU GLU LYS GLY LYS ARG PRO SER THR THR GLN GLY ASP GLU VAL SER ASP ARG LYS LYS LYS LYS SER LYS PRO PHE LYS LYS SER ARG

LYS GLU GLU GLU GLU VAL VAL GLU GLU ASP ASP LYS ASP LEU PRO GLU VAL ASP LEU GLU GLU GLU LEU SER LYS ALA ARG LYS SER LEU PHE ASP ASP GLU GLU GLU ASP ASP ASP GLU ALA GLY LEU LEU VAL ASP GLU GLU LEU LYS ASP GLU PHE ASP LEU GLU GLN GLU TYR ASP TYR ASP GLU ASP

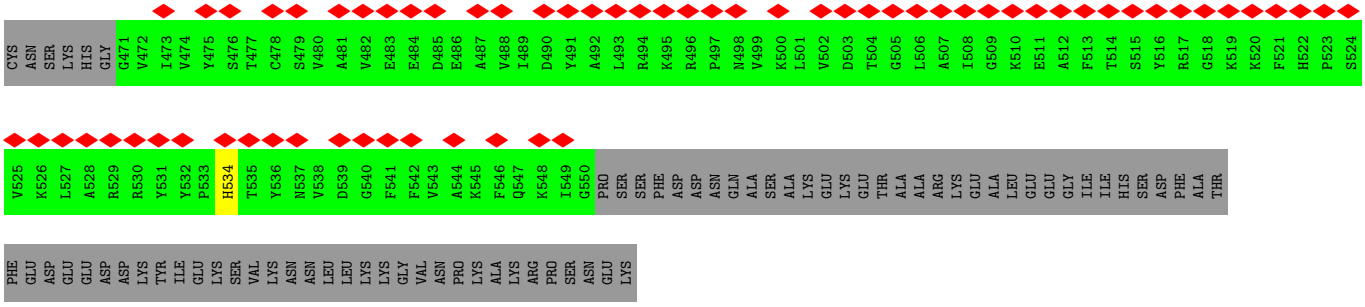
GLU ASP ASN ASP ALA HIS PRO ILE PHE SER ASP ASP ASP ASP GLU ALA ASP LEU GLU GLU LEU ASN ALA GLN ASN MET GLU ALA LEU SER LYS LYS LEU ASP GLU GLU GLU GLU ALA GLU GLU ALA GLU GLU ALA GLU MET GLU LEU VAL GLU ALA GLU ASN MET GLN PRO ARG ALA ASP ILE

LEU PRO THR GLU GLU GLN GLU GLU MET MET ALA GLN GLU THR PRO ASN LEU THR SER THR ARG THR ARG MET ILE GLU ILE VAL LYS VAL LEU GLU ASN PHE LYS THR LEU GLY ALA GLU GLY ARG SER ARG GLY GLU Y227 V228 D229 R230 L231 L232 K233 D234 I235 C236 E237 Y238 F239 G240

Y241 T242 P243 F244 L245 A246 E247 K248 L249 F250 N251 L252 F253 S254 P255 A256 E257 A258 M259 E260 F261 F262 E263 A264 N265 E266 I267 A268 R269 P270 I271 T272 I273 R274 T280 R281 R282 R283 D284 L285 A286 Q287 N291 R292 G293 V294 N295 L296 Q297 P298 I299 G300 S301 W302 T303 K304 V305 G306

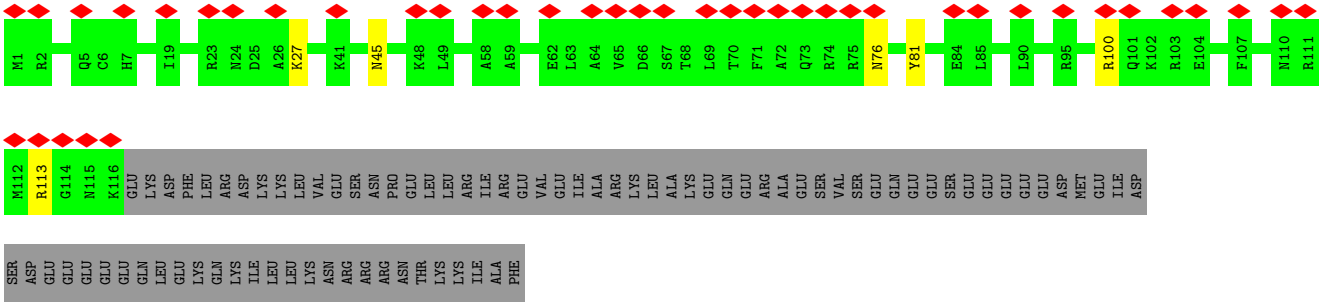
L307 Q308 I309 F310 D311 S312 Q313 V314 P315 I316 G317 A318 Y322 L329 Q330 A331 A332 S333 S334 V338 H344 E345 N346 E347 R348 D351 M352 A353 A354 A355 P356 G357 G358 K359 M366 M367 K368 N369 T370 G371 A375 A376 D377 A378 N379 K380 S381 K384 I387 N397

T398 I399 M402 Y403 D404 A405 R406 E407 F408 P409 K410 V411 I412 F415 D421 A422 P423 C424 S425 G426 T427 G428 V429 I430 G431 K432 D433 Q434 S435 V436 K437 V438 S439 R440 T441 E442 K443 D444 F445 I446 Q447 I448 P449 H450 L451 Q452 K453 Q454 L455 L456 L457 S458 D461 S462 V463 ASP



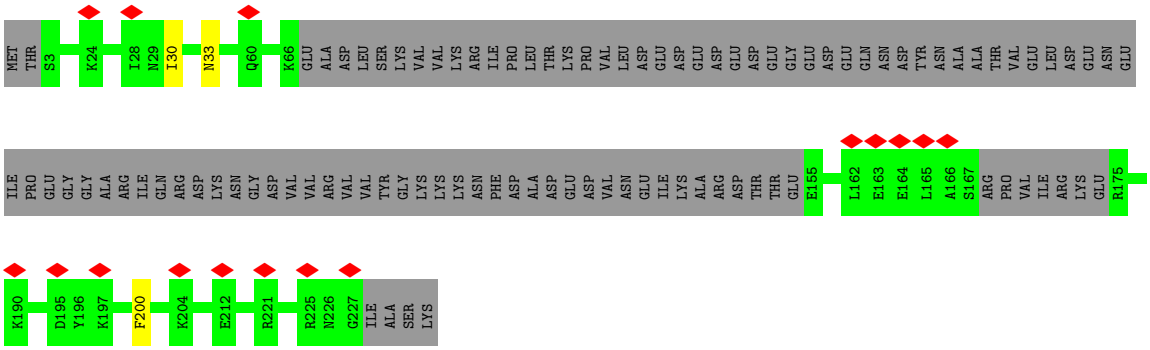
- Molecule 47: Ribosome biogenesis protein RLP24

Chain u:



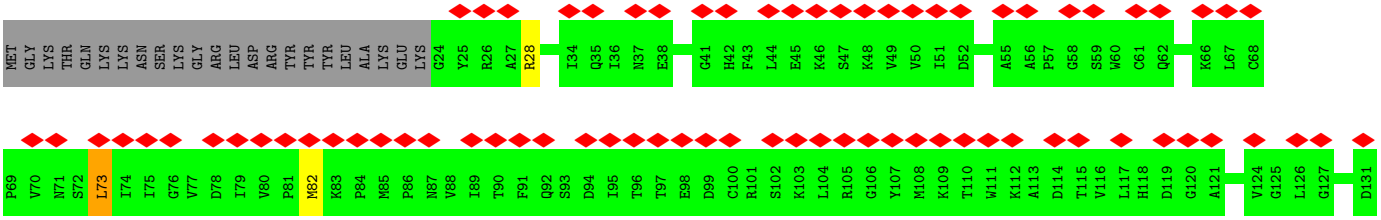
- Molecule 48: Nucleolar protein 16

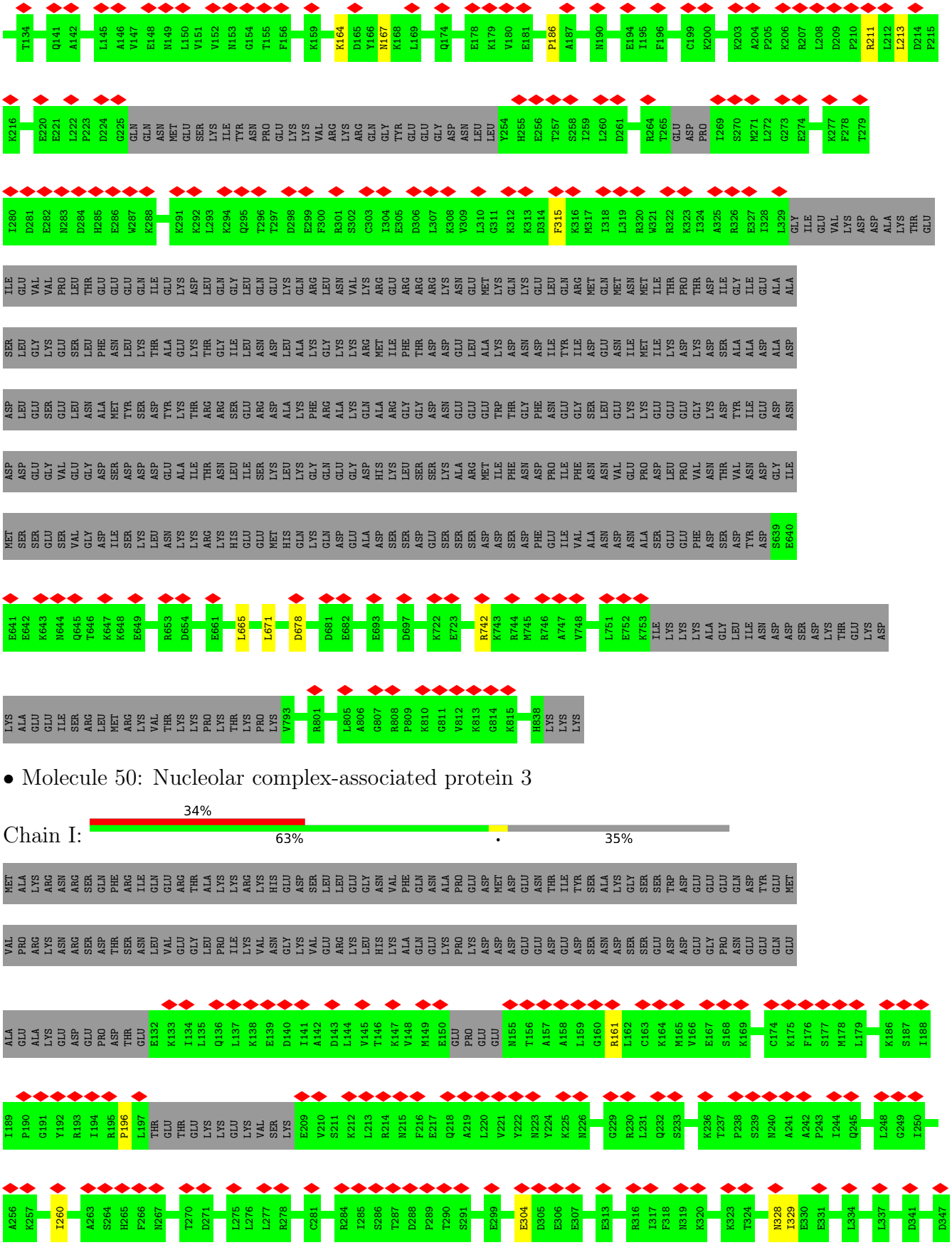
Chain v:

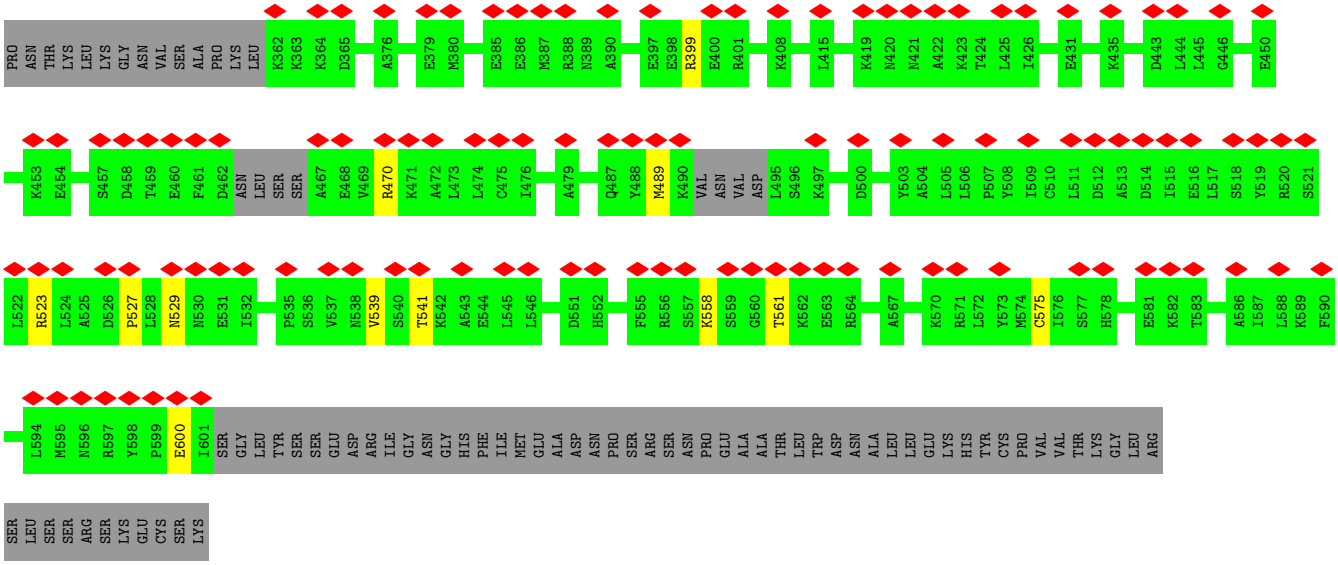


- Molecule 49: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

Chain w:

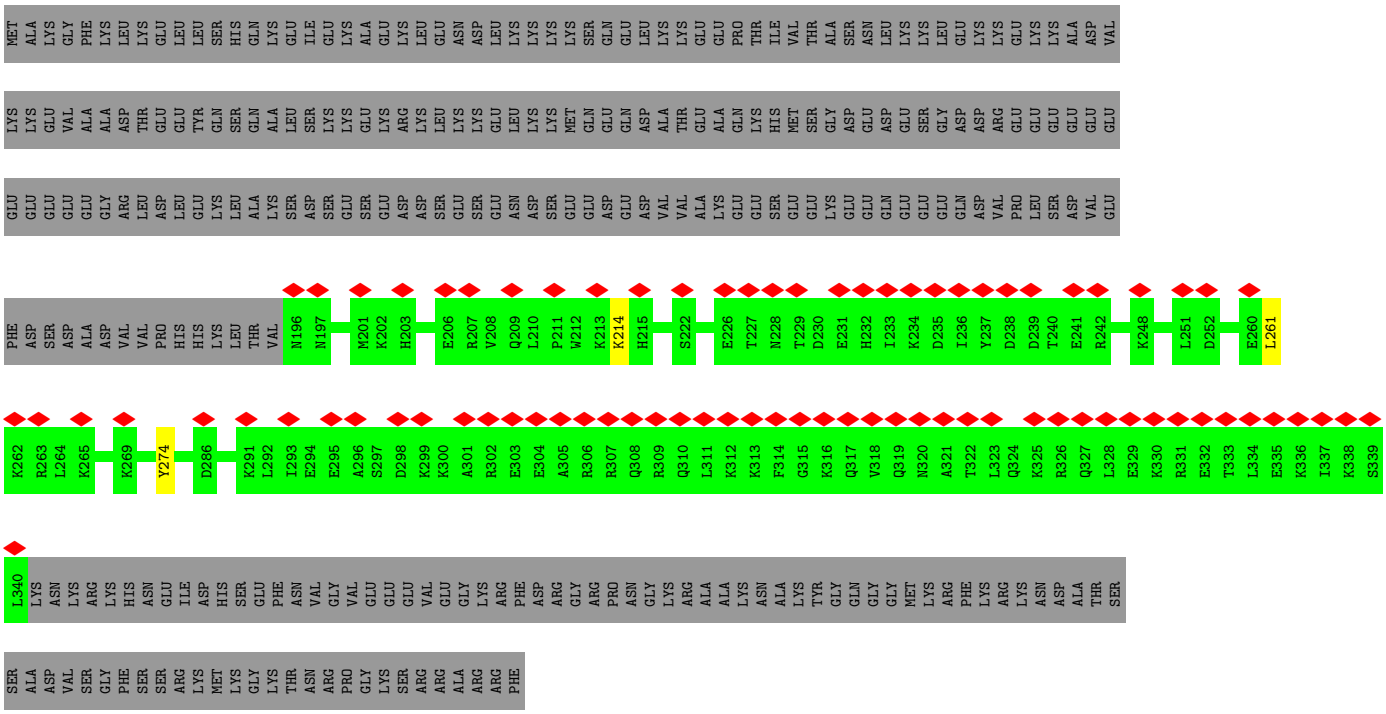



T134
Q141 A142
L145 A146 V147 E148 N149 L150 V151 V152 N153 G154 T155 F156
K159
K164
D165 Y166
N167
K168 L169
Q174
E178 K179 V180 E181
P186
A187
N190
E194 I195 F196
C199 K200
K203 A204 P205 K206 R207 L208 D209 P210 R211 L212 L213 D214 P215
K216
E220 E221 L222 P223 D224 G225
GLN GLN ASN MET GLU SER LYS ILE TYR ASN PRO GLU LYS LYS VAL ARG LYS ARG GLN GLY TYR GLU GLU GLY ASP ASN LEU LEU
Y254 H255 E256 T257 S258 I259 L260 D261
R264 T265
GLU ASP PRO
I269 S270 M271 L272 G273 E274
K277 F278 T279
I280 D281 E282 N283 D284 H285 E286 W287 K288
K291 K292 L293 K294 Q295 T296 T297 D298 E299 F300 R301 S302 C303 I304 E305 D306 L307 K308 V309 L310 G311 K312 K313 D314
F315
K316 M317 I318 L319 R320 W321 R322 K323 I324 A325 R326 E327 I328 L329
GLY ILE GLU VAL LYS ASP ASP ALA LYS THR GLU
ILE GLU VAL VAL PRO LEU THR GLU GLU GLU GLN ILE GLU LYS ASP LEU GLN GLY LEU GLN GLU LYS GLN LYS GLN ARG LEU ASN VAL LYS ARG GLU ARG ARG ARG LYS ASN GLU MET LYS GLN LYS GLU LEU GLN ARG MET GLN MET ASN MET ILE THR PRO THR ASP ILE GLY ILE GLU ALA ALA
SER LEU GLY LYS GLU SER LEU PHE ASN LEU LYS THR ALA GLU LYS THR GLY ILE LEU ASN ASP LEU ALA LYS GLY GLY LYS LYS ARG MET ILE PHE THR ASP ASP GLU LEU ALA LYS ASP ASN ASP ILE TYR ILE ASP GLU ASN ILE MET ILE LYS ASP LYS ASP SER ALA ALA ASP ALA ASP
ASP LEU GLU SER GLU LEU ASN ALA MET TYR SER ASP TYR LYS THR ARG ARG SER GLU ARG ASP ALA LYS PHE ARG ALA LYS GLN ALA ARG GLY GLY ASP ASN GLU GLU GLU GLU TRP THR GLY PHE ASN GLU GLY SER LEU GLU GLU LYS LYS GLU GLU GLU GLY LYS ASP TYR ILE GLU ASP ASN
ASP ASP GLU GLY VAL GLU GLY ASP SER ASP ASP ASP GLU ALA ILE THR ASN LEU ILE SER LYS LEU LYS GLY GLN GLU GLY ASP HIS LYS LEU SER SER LYS ASN ARG MET ILE PHE ASN ASP PRO ILE PHE ASN ASN VAL GLU PRO ASP LEU PRO VAL ASN THR VAL ASN ASP GLY ILE
MET SER SER GLU SER VAL GLY ASP ILE SER LYS LEU ASN LYS LYS LYS ARG LYS HIS GLU GLU MET HIS GLN LYS GLN ASP GLU ALA ASP SER SER ASP GLU SER SER SER ASP ASP SER ASP PHE GLU ILE VAL ALA ASN ASP ASN ALA SER GLU GLU PHE ASP SER ASP TYR ASP
S639 E640
E641 E642 K643 N644 Q645 T646 K647 K648 E649
R653 D654
E661
L665
L671
D678
D681 E682
E693
D697
K722 E723
R742
K743 R744 M745 R746 A747 V748
L751 E752 K753
ILE LYS LYS LYS ALA GLY LEU ILE ASN ASP ASP SER ASP LYS THR GLU LYS ASP
LYS ALA GLU GLU ILE SER ARG LEU MET ARG LYS VAL THR LYS LYS PRO LYS THR LYS PRO LYS
V793
R801
L805 A806
G807
R808 P809 K810 G811 V812 K813 G814 K815
H838
LYS LYS LYS
• Molecule 50: Nucleolar complex-associated protein 3
Chain I:
34%
63%
35%
MET ALA LYS ARG ASN ARG SER GLN PHE ARG ILE GLN GLU ARG THR ALA LYS LYS ARG LYS HIS GLU ASP SER LEU LEU GLU GLY ASN VAL PHE GLN ASN ALA PRO GLU ASP MET ASP GLU ASN THR ILE TYR SER ALA LYS GLY SER SER TRP ASP GLU GLU GLU GLN ASP TYR GLU MET
VAL PRO ARG LYS ASN ARG SER ASP THR SER ASN LEU VAL GLU GLY LEU PRO ILE LYS VAL ASN GLY LYS VAL GLU ARG LYS LEU HIS LYS ALA GLN GLU LYS PRO LYS ASP ASP ASP GLU GLU ASP GLU ASP SER ASN ASP SER SER GLU ASP ASP GLU GLY PRO ASN GLU GLU GLN GLU
ALA GLU ALA LYS GLU ASP GLU PRO ASP THR GLU
E132 K133 I134 L135 Q136 L137 K138 E139 D140 I141 A142 D143 L144 V145 T146 K147 V148 M149 E150
GLU PRO GLU GLU
N155 T156 A157 A158 L159 G160
R161 L162 C163 K164 M165 V166 E167 S168 K169
C174 K175 F176 S177 M178 L179
K186 S187 I188
I189 P190 G191 Y192 R193 I194 R195 P196 L197
THR GLU THR GLU LYS LYS GLU LYS VAL SER LYS
E209 V210 S211 K212 L213 R214 N215 F216 E217 Q218 A219 L220 V221 Y222 N223 Y224 K225 N226
G229 R230 L231 Q232 S233
K236 T237 P238 S239 N240 A241 A242 P243 I244 Q245
L248 G249 I250
A256 K257
I260
A263 S264 H265 F266 N267
T270 D271
L275 L276 L277 R278
C281
R284 I285 S286 T287 D288 P289 T290 S291
E299
E304 D305 E306 E307
E313
R316 I317 F318 N319 K320
K323 T324
N328 I329 E330 E331
L334
L337
D341
D347



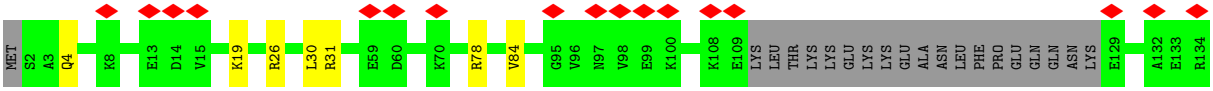
- Molecule 51: rRNA-processing protein EBP2

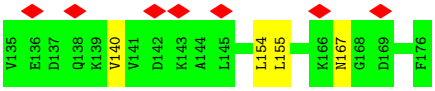
Chain J:



- Molecule 52: 60S ribosomal protein L6-A

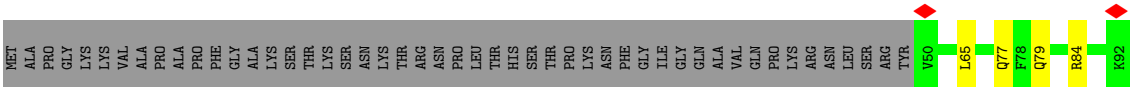
Chain E:

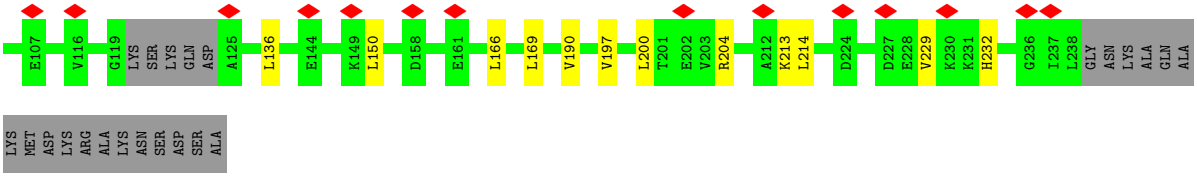




• Molecule 53: 60S ribosomal protein L8-A

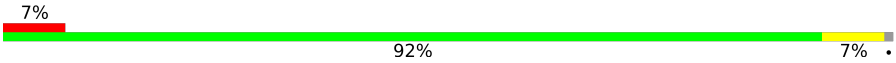
Chain G:

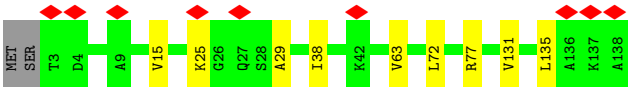




• Molecule 54: 60S ribosomal protein L14-A

Chain M:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	112099	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.521	Depositor
Minimum map value	-0.290	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	455.28, 455.28, 455.28	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	0.26	2/58862 (0.0%)	0.70	18/91746 (0.0%)
2	2	0.25	0/3746	0.67	1/5832 (0.0%)
3	6	0.27	0/1527	0.75	0/2371
4	L	0.39	0/1016	0.70	0/1363
5	N	0.38	0/1619	0.69	0/2166
6	Q	0.40	0/1050	0.68	0/1419
7	R	0.38	0/977	0.66	0/1310
8	S	0.41	0/1468	0.64	0/1973
9	T	0.41	0/427	0.70	0/576
10	U	0.45	0/794	0.59	0/1076
11	Z	0.41	0/1118	0.65	0/1497
12	c	0.42	0/751	0.63	0/1008
13	d	0.38	0/887	0.64	1/1191 (0.1%)
14	e	0.38	0/1030	0.65	1/1379 (0.1%)
15	f	0.37	0/868	0.63	0/1168
16	g	0.37	0/891	0.65	0/1191
17	i	0.40	0/665	0.76	1/884 (0.1%)
18	j	0.39	0/592	0.68	0/785
19	k	0.39	0/618	0.66	0/826
20	O	0.28	0/1585	0.44	0/2128
21	V	0.39	0/1008	0.63	0/1356
22	a	0.41	0/637	0.63	0/862
23	P	0.38	0/1464	0.62	0/1965
24	X	0.39	0/1116	0.64	1/1503 (0.1%)
25	Y	0.37	0/1004	0.66	0/1341
26	h	0.37	0/978	0.63	1/1301 (0.1%)
27	F	0.40	0/1821	0.63	0/2451
28	B	0.41	0/2756	0.66	0/3702
29	C	0.38	0/2782	0.64	1/3766 (0.0%)
30	H	0.38	0/1531	0.60	0/2062
31	A	0.40	0/1663	0.67	0/2248
32	K	0.42	0/2107	0.65	0/2845

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	m	0.40	0/5356	0.65	1/7264 (0.0%)
34	D	0.44	0/1626	0.65	0/2193
35	W	0.42	0/1902	0.64	0/2564
36	l	0.42	0/1407	0.66	1/1896 (0.1%)
37	b	0.42	0/3474	0.63	1/4683 (0.0%)
38	o	0.42	0/1129	0.65	0/1502
39	n	0.40	0/3441	0.61	1/4625 (0.0%)
40	r	0.37	0/1462	0.60	0/1952
41	s	0.32	0/301	0.60	0/386
42	t	0.39	0/2355	0.65	0/3158
43	y	0.40	0/1722	0.62	0/2343
44	z	0.36	0/445	0.62	0/585
45	p	0.42	0/2362	0.67	1/3200 (0.0%)
46	q	0.44	0/2536	0.64	0/3433
47	u	0.41	0/996	0.61	0/1324
48	v	0.38	0/1100	0.59	0/1456
49	w	0.40	0/3571	0.63	2/4789 (0.0%)
50	I	0.41	0/3515	0.63	0/4725
51	J	0.39	0/1232	0.62	0/1642
52	E	0.39	0/1260	0.66	0/1694
53	G	0.41	0/1463	0.70	0/1978
54	M	0.38	0/1068	0.63	0/1438
All	All	0.34	2/143081 (0.0%)	0.67	32/206121 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	N	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2981	U	C1'-N1	5.54	1.57	1.48
1	1	2942	C	C1'-N1	5.06	1.56	1.48

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	649	A	C2'-C3'-O3'	8.32	127.80	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	932	U	N1-C1'-C2'	7.62	123.90	114.00
33	m	719	LEU	CA-CB-CG	7.58	132.74	115.30
17	i	57	LEU	CA-CB-CG	7.46	132.46	115.30
37	b	277	LEU	CA-CB-CG	6.73	130.77	115.30
45	p	109	LEU	CA-CB-CG	6.72	130.75	115.30
1	1	1227	C	C2'-C3'-O3'	6.68	124.39	113.70
1	1	644	G	C2'-C3'-O3'	6.41	123.95	113.70
36	l	54	LEU	CA-CB-CG	6.25	129.67	115.30
1	1	2922	G	C2'-C3'-O3'	6.25	123.69	113.70
39	n	417	LEU	CA-CB-CG	6.10	129.32	115.30
14	e	82	LEU	CA-CB-CG	6.03	129.18	115.30
2	2	123	G	C2'-C3'-O3'	5.95	123.21	113.70
29	C	313	LEU	CA-CB-CG	5.85	128.75	115.30
1	1	1307	G	C2'-C3'-O3'	5.81	123.00	113.70
1	1	239	G	C2'-C3'-O3'	5.79	122.97	113.70
1	1	292	U	O4'-C1'-N1	5.59	112.67	108.20
49	w	213	LEU	CA-CB-CG	5.59	128.15	115.30
1	1	2954	U	C2'-C3'-O3'	5.54	122.57	113.70
26	h	28	LEU	CA-CB-CG	5.46	127.86	115.30
1	1	221	A	O4'-C1'-N9	5.35	112.48	108.20
49	w	73	LEU	CA-CB-CG	5.26	127.41	115.30
1	1	1203	A	N9-C1'-C2'	5.22	120.78	114.00
1	1	1299	U	N1-C1'-C2'	-5.19	106.29	112.00
1	1	720	A	C2'-C3'-O3'	5.14	121.93	113.70
1	1	2940	A	C4'-C3'-O3'	5.12	123.24	113.00
1	1	1861	G	C2'-C3'-O3'	5.12	121.89	113.70
1	1	1299	U	C5'-C4'-O4'	5.10	115.22	109.10
13	d	87	ASN	C-N-CD	-5.10	109.38	120.60
24	X	40	LEU	CA-CB-CG	5.06	126.93	115.30
1	1	1820	U	C2'-C3'-O3'	5.02	121.72	113.70
1	1	1108	U	O4'-C1'-N1	5.00	112.20	108.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	N	92	LEU	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L	119/199 (60%)	107 (90%)	8 (7%)	4 (3%)	3	22
5	N	182/204 (89%)	166 (91%)	13 (7%)	3 (2%)	9	36
6	Q	132/186 (71%)	123 (93%)	9 (7%)	0	100	100
7	R	116/189 (61%)	109 (94%)	6 (5%)	1 (1%)	17	48
8	S	168/172 (98%)	151 (90%)	13 (8%)	4 (2%)	6	28
9	T	53/160 (33%)	46 (87%)	6 (11%)	1 (2%)	8	34
10	U	96/121 (79%)	90 (94%)	6 (6%)	0	100	100
11	Z	133/136 (98%)	117 (88%)	13 (10%)	3 (2%)	6	29
12	c	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
13	d	105/113 (93%)	96 (91%)	7 (7%)	2 (2%)	8	34
14	e	123/130 (95%)	120 (98%)	3 (2%)	0	100	100
15	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
16	g	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
17	i	81/100 (81%)	68 (84%)	12 (15%)	1 (1%)	13	42
18	j	71/88 (81%)	67 (94%)	3 (4%)	1 (1%)	11	38
19	k	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	12	40
20	O	195/199 (98%)	125 (64%)	38 (20%)	32 (16%)	0	1
21	V	132/137 (96%)	123 (93%)	8 (6%)	1 (1%)	19	51
22	a	79/149 (53%)	72 (91%)	5 (6%)	2 (2%)	5	27
23	P	179/184 (97%)	164 (92%)	14 (8%)	1 (1%)	25	57
24	X	139/142 (98%)	122 (88%)	15 (11%)	2 (1%)	11	38
25	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
26	h	117/120 (98%)	108 (92%)	6 (5%)	3 (3%)	5	27
27	F	220/244 (90%)	204 (93%)	11 (5%)	5 (2%)	6	29
28	B	337/387 (87%)	293 (87%)	38 (11%)	6 (2%)	8	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	C	357/362 (99%)	317 (89%)	33 (9%)	7 (2%)	7	32
30	H	188/191 (98%)	173 (92%)	14 (7%)	1 (0%)	29	61
31	A	192/291 (66%)	174 (91%)	16 (8%)	2 (1%)	15	46
32	K	253/376 (67%)	231 (91%)	20 (8%)	2 (1%)	19	51
33	m	641/807 (79%)	576 (90%)	58 (9%)	7 (1%)	14	45
34	D	188/505 (37%)	167 (89%)	21 (11%)	0	100	100
35	W	230/236 (98%)	214 (93%)	14 (6%)	2 (1%)	17	48
36	l	170/181 (94%)	156 (92%)	14 (8%)	0	100	100
37	b	413/647 (64%)	387 (94%)	24 (6%)	2 (0%)	29	61
38	o	131/220 (60%)	121 (92%)	9 (7%)	1 (1%)	19	51
39	n	403/605 (67%)	372 (92%)	29 (7%)	2 (0%)	29	61
40	r	170/261 (65%)	149 (88%)	20 (12%)	1 (1%)	25	57
41	s	34/520 (6%)	33 (97%)	1 (3%)	0	100	100
42	t	286/322 (89%)	260 (91%)	20 (7%)	6 (2%)	7	31
43	y	223/245 (91%)	211 (95%)	11 (5%)	1 (0%)	34	66
44	z	53/106 (50%)	53 (100%)	0	0	100	100
45	p	288/460 (63%)	262 (91%)	24 (8%)	2 (1%)	22	54
46	q	313/618 (51%)	270 (86%)	36 (12%)	7 (2%)	6	30
47	u	114/199 (57%)	107 (94%)	6 (5%)	1 (1%)	17	48
48	v	124/231 (54%)	118 (95%)	6 (5%)	0	100	100
49	w	426/841 (51%)	389 (91%)	37 (9%)	0	100	100
50	I	421/663 (64%)	380 (90%)	35 (8%)	6 (1%)	11	38
51	J	143/427 (34%)	135 (94%)	8 (6%)	0	100	100
52	E	152/176 (86%)	132 (87%)	20 (13%)	0	100	100
53	G	180/256 (70%)	166 (92%)	12 (7%)	2 (1%)	14	45
54	M	134/138 (97%)	124 (92%)	9 (7%)	1 (1%)	22	54
All	All	9512/13782 (69%)	8630 (91%)	756 (8%)	126 (1%)	16	40

All (126) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L	51	LEU
5	N	145	ASP

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Mol	Chain	Res	Type
8	S	13	ARG
11	Z	103	GLN
19	k	33	LYS
20	O	28	LEU
20	O	47	PHE
20	O	48	PHE
20	O	62	THR
20	O	63	ALA
20	O	86	GLY
20	O	89	SER
20	O	113	ASP
20	O	114	LYS
20	O	137	THR
20	O	145	VAL
20	O	162	VAL
20	O	189	ASP
21	V	90	GLY
26	h	91	ALA
27	F	160	ARG
28	B	34	LYS
28	B	222	LYS
29	C	4	PRO
29	C	140	HIS
29	C	339	LEU
33	m	231	GLU
38	o	190	THR
42	t	227	ILE
42	t	269	GLN
50	I	558	LYS
4	L	50	PRO
5	N	144	ARG
11	Z	125	GLY
13	d	87	ASN
17	i	30	LYS
20	O	13	GLY
20	O	16	VAL
20	O	17	GLY
20	O	27	LEU
20	O	77	SER
20	O	190	VAL
20	O	191	ALA
20	O	198	GLY

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Mol	Chain	Res	Type
27	F	191	VAL
28	B	35	ASP
28	B	138	ALA
29	C	269	SER
30	H	22	SER
33	m	177	GLY
33	m	232	GLN
33	m	328	LYS
42	t	277	VAL
46	q	300	GLY
46	q	427	THR
46	q	429	VAL
54	M	29	ALA
4	L	62	THR
4	L	75	PHE
7	R	53	LYS
20	O	11	GLY
20	O	168	TYR
20	O	169	ALA
20	O	192	LYS
22	a	77	LYS
24	X	4	SER
26	h	119	LYS
27	F	157	ASN
27	F	158	LYS
27	F	164	SER
28	B	187	SER
31	A	171	PRO
33	m	406	ASN
37	b	198	ALA
47	u	81	TYR
50	I	541	THR
53	G	232	HIS
5	N	94	TYR
8	S	24	LEU
9	T	127	GLN
18	j	85	LYS
20	O	24	ALA
20	O	37	ARG
20	O	85	ARG
20	O	152	VAL
22	a	78	LEU

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Mol	Chain	Res	Type
23	P	156	ALA
24	X	5	ALA
26	h	84	LYS
28	B	155	ALA
29	C	268	ALA
31	A	63	PRO
32	K	284	ASN
33	m	154	GLN
33	m	435	GLY
42	t	240	GLY
42	t	270	PRO
46	q	317	GLY
50	I	600	GLU
8	S	14	LEU
13	d	88	PRO
29	C	311	HIS
32	K	256	PRO
37	b	432	MET
39	n	196	GLU
39	n	456	HIS
42	t	151	LEU
45	p	351	ARG
45	p	418	ASP
50	I	527	PRO
50	I	561	THR
53	G	79	GLN
20	O	46	GLU
46	q	268	ALA
20	O	43	ILE
35	W	146	GLY
46	q	269	ARG
11	Z	16	GLY
29	C	146	PRO
35	W	101	GLY
50	I	196	PRO
8	S	167	ARG
40	r	190	GLY
43	y	58	ILE
46	q	423	PRO
20	O	153	VAL

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	
4	L	101/159 (64%)	93 (92%)	8 (8%)	12	37
5	N	161/176 (92%)	146 (91%)	15 (9%)	9	30
6	Q	110/151 (73%)	102 (93%)	8 (7%)	14	41
7	R	101/154 (66%)	95 (94%)	6 (6%)	19	49
8	S	155/156 (99%)	143 (92%)	12 (8%)	13	38
9	T	44/137 (32%)	41 (93%)	3 (7%)	16	44
10	U	85/107 (79%)	84 (99%)	1 (1%)	71	83
11	Z	115/116 (99%)	112 (97%)	3 (3%)	46	71
12	c	81/88 (92%)	76 (94%)	5 (6%)	18	47
13	d	94/97 (97%)	90 (96%)	4 (4%)	29	59
14	e	108/111 (97%)	103 (95%)	5 (5%)	27	58
15	f	90/91 (99%)	85 (94%)	5 (6%)	21	52
16	g	95/103 (92%)	85 (90%)	10 (10%)	7	25
17	i	69/82 (84%)	60 (87%)	9 (13%)	4	17
18	j	60/71 (84%)	52 (87%)	8 (13%)	4	17
19	k	68/69 (99%)	63 (93%)	5 (7%)	13	40
20	O	160/162 (99%)	132 (82%)	28 (18%)	2	8
21	V	103/105 (98%)	101 (98%)	2 (2%)	57	77
22	a	66/119 (56%)	63 (96%)	3 (4%)	27	58
23	P	145/146 (99%)	139 (96%)	6 (4%)	30	61
24	X	117/118 (99%)	113 (97%)	4 (3%)	37	65
25	Y	109/110 (99%)	106 (97%)	3 (3%)	43	70
26	h	104/105 (99%)	100 (96%)	4 (4%)	33	62
27	F	186/205 (91%)	181 (97%)	5 (3%)	44	71
28	B	284/323 (88%)	266 (94%)	18 (6%)	18	47
29	C	286/289 (99%)	280 (98%)	6 (2%)	53	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	H	170/171 (99%)	162 (95%)	8 (5%)	26	57
31	A	185/263 (70%)	181 (98%)	4 (2%)	52	74
32	K	238/346 (69%)	233 (98%)	5 (2%)	53	75
33	m	582/723 (80%)	564 (97%)	18 (3%)	40	67
34	D	175/440 (40%)	170 (97%)	5 (3%)	42	69
35	W	209/213 (98%)	200 (96%)	9 (4%)	29	59
36	l	149/156 (96%)	143 (96%)	6 (4%)	31	61
37	b	377/573 (66%)	360 (96%)	17 (4%)	27	58
38	o	118/199 (59%)	116 (98%)	2 (2%)	60	78
39	n	371/548 (68%)	356 (96%)	15 (4%)	31	61
40	r	156/229 (68%)	153 (98%)	3 (2%)	57	77
41	s	32/445 (7%)	30 (94%)	2 (6%)	18	47
42	t	259/287 (90%)	252 (97%)	7 (3%)	44	71
43	y	193/211 (92%)	186 (96%)	7 (4%)	35	63
44	z	48/95 (50%)	48 (100%)	0	100	100
45	p	265/413 (64%)	260 (98%)	5 (2%)	57	77
46	q	268/535 (50%)	262 (98%)	6 (2%)	52	74
47	u	101/180 (56%)	96 (95%)	5 (5%)	24	55
48	v	116/205 (57%)	113 (97%)	3 (3%)	46	71
49	w	383/745 (51%)	371 (97%)	12 (3%)	40	67
50	I	393/602 (65%)	381 (97%)	12 (3%)	40	67
51	J	133/383 (35%)	130 (98%)	3 (2%)	50	73
52	E	134/153 (88%)	123 (92%)	11 (8%)	11	36
53	G	150/208 (72%)	136 (91%)	14 (9%)	9	30
54	M	107/109 (98%)	99 (92%)	8 (8%)	13	39
All	All	8409/11982 (70%)	8036 (96%)	373 (4%)	32	59

All (373) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	21	ARG
4	L	34	SER
4	L	49	ARG

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Mol	Chain	Res	Type
4	L	54	LEU
4	L	76	THR
4	L	85	LEU
4	L	100	ARG
4	L	101	ARG
5	N	10	LEU
5	N	19	LEU
5	N	22	LEU
5	N	34	ASN
5	N	41	ARG
5	N	43	THR
5	N	92	LEU
5	N	95	GLN
5	N	108	ARG
5	N	121	VAL
5	N	132	VAL
5	N	133	ILE
5	N	167	THR
5	N	187	ARG
5	N	188	ARG
6	Q	31	LYS
6	Q	38	ARG
6	Q	59	ARG
6	Q	126	GLN
6	Q	136	ASN
6	Q	141	ARG
6	Q	146	SER
6	Q	147	ARG
7	R	10	LEU
7	R	19	LYS
7	R	30	SER
7	R	98	ARG
7	R	106	LEU
7	R	140	GLU
8	S	12	ARG
8	S	13	ARG
8	S	24	LEU
8	S	48	LEU
8	S	71	LYS
8	S	80	ARG
8	S	97	VAL
8	S	100	VAL

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Mol	Chain	Res	Type
8	S	120	SER
8	S	125	LYS
8	S	147	ASP
8	S	155	ARG
9	T	106	LEU
9	T	139	ARG
9	T	151	LEU
10	U	18	ASP
11	Z	17	ARG
11	Z	51	LEU
11	Z	105	SER
12	c	10	ILE
12	c	18	ILE
12	c	50	VAL
12	c	84	LEU
12	c	104	LEU
13	d	13	THR
13	d	61	LYS
13	d	106	THR
13	d	109	VAL
14	e	27	ARG
14	e	33	ARG
14	e	61	LYS
14	e	75	LEU
14	e	85	LEU
15	f	49	ILE
15	f	59	VAL
15	f	60	ARG
15	f	81	VAL
15	f	107	ILE
16	g	10	ARG
16	g	16	ARG
16	g	29	ILE
16	g	44	CYS
16	g	49	SER
16	g	51	LEU
16	g	55	SER
16	g	59	PRO
16	g	83	ASN
16	g	108	GLN
17	i	20	MET
17	i	36	ARG

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Mol	Chain	Res	Type
17	i	47	ILE
17	i	56	ARG
17	i	57	LEU
17	i	60	LEU
17	i	76	ARG
17	i	77	LEU
17	i	79	SER
18	j	24	ARG
18	j	26	SER
18	j	30	GLN
18	j	52	LYS
18	j	58	THR
18	j	67	LEU
18	j	79	GLN
18	j	82	SER
19	k	6	THR
19	k	12	LEU
19	k	22	THR
19	k	46	ARG
19	k	65	LEU
20	O	18	ARG
20	O	23	VAL
20	O	25	LYS
20	O	27	LEU
20	O	37	ARG
20	O	46	GLU
20	O	49	ARG
20	O	50	ASN
20	O	55	HIS
20	O	56	ASP
20	O	59	ARG
20	O	65	ASN
20	O	74	ARG
20	O	78	ARG
20	O	80	PHE
20	O	84	LEU
20	O	94	ARG
20	O	101	ARG
20	O	113	ASP
20	O	124	LEU
20	O	125	ARG
20	O	129	LEU

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Mol	Chain	Res	Type
20	O	133	ARG
20	O	135	TYR
20	O	137	THR
20	O	152	VAL
20	O	156	LEU
20	O	160	ARG
21	V	49	LEU
21	V	93	LEU
22	a	78	LEU
22	a	117	ARG
22	a	120	ASN
23	P	24	VAL
23	P	36	ILE
23	P	52	LEU
23	P	69	ARG
23	P	97	ASN
23	P	168	LEU
24	X	12	LYS
24	X	16	LYS
24	X	38	LEU
24	X	63	ILE
25	Y	37	LYS
25	Y	51	ARG
25	Y	74	TYR
26	h	28	LEU
26	h	49	LYS
26	h	62	GLN
26	h	93	THR
27	F	88	ARG
27	F	89	ILE
27	F	93	ASN
27	F	124	LEU
27	F	244	ASN
28	B	28	ARG
28	B	50	LYS
28	B	55	THR
28	B	70	ARG
28	B	85	VAL
28	B	89	VAL
28	B	100	ARG
28	B	114	VAL
28	B	148	LEU

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Mol	Chain	Res	Type
28	B	152	LYS
28	B	164	THR
28	B	168	LYS
28	B	178	LEU
28	B	216	ASP
28	B	325	LYS
28	B	332	ARG
28	B	380	MET
28	B	385	LYS
29	C	52	VAL
29	C	154	THR
29	C	179	LEU
29	C	194	TYR
29	C	206	LEU
29	C	259	ASP
30	H	26	LYS
30	H	41	ILE
30	H	63	LYS
30	H	118	LEU
30	H	138	THR
30	H	151	VAL
30	H	157	ASN
30	H	161	LEU
31	A	84	ASN
31	A	106	ASN
31	A	189	ARG
31	A	225	LEU
32	K	75	LYS
32	K	240	ARG
32	K	248	LEU
32	K	256	PRO
32	K	262	ASN
33	m	153	THR
33	m	156	THR
33	m	168	MET
33	m	175	ILE
33	m	178	LYS
33	m	192	LEU
33	m	203	THR
33	m	223	LEU
33	m	238	ASN
33	m	263	LYS

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Mol	Chain	Res	Type
33	m	323	HIS
33	m	324	LEU
33	m	390	ARG
33	m	428	ARG
33	m	440	VAL
33	m	688	ILE
33	m	696	ILE
33	m	719	LEU
34	D	294	VAL
34	D	394	LEU
34	D	429	LEU
34	D	448	ARG
34	D	451	LEU
35	W	15	THR
35	W	22	ASN
35	W	48	VAL
35	W	49	ARG
35	W	57	ARG
35	W	113	LYS
35	W	128	ASN
35	W	174	LYS
35	W	232	ASN
36	l	22	ARG
36	l	47	VAL
36	l	51	VAL
36	l	54	LEU
36	l	63	LEU
36	l	70	LEU
37	b	3	LEU
37	b	15	ASN
37	b	31	THR
37	b	39	ILE
37	b	48	ARG
37	b	70	ASN
37	b	175	TYR
37	b	177	ASN
37	b	180	LYS
37	b	221	THR
37	b	277	LEU
37	b	281	LYS
37	b	384	ASN
37	b	415	ASN

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Mol	Chain	Res	Type
37	b	440	ASN
37	b	445	LEU
37	b	456	LEU
38	o	93	ILE
38	o	146	MET
39	n	7	ASN
39	n	36	CYS
39	n	47	ARG
39	n	49	LYS
39	n	54	LYS
39	n	69	GLN
39	n	92	ARG
39	n	139	LEU
39	n	145	LEU
39	n	208	ASN
39	n	376	LEU
39	n	417	LEU
39	n	419	ASN
39	n	427	ILE
39	n	566	LEU
40	r	203	ASN
40	r	217	LYS
40	r	225	VAL
41	s	1	MET
41	s	33	MET
42	t	15	ASN
42	t	66	LEU
42	t	151	LEU
42	t	157	ASN
42	t	187	LEU
42	t	275	ARG
42	t	291	GLN
43	y	100	ARG
43	y	101	LEU
43	y	114	VAL
43	y	145	ASN
43	y	146	ILE
43	y	154	LEU
43	y	173	LEU
45	p	109	LEU
45	p	111	VAL
45	p	165	ARG

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Mol	Chain	Res	Type
45	p	167	LEU
45	p	326	ARG
46	q	273	ILE
46	q	274	ARG
46	q	280	THR
46	q	282	ARG
46	q	299	ILE
46	q	534	HIS
47	u	27	LYS
47	u	45	ASN
47	u	76	ASN
47	u	100	ARG
47	u	113	ARG
48	v	30	ILE
48	v	33	ASN
48	v	200	PHE
49	w	28	ARG
49	w	73	LEU
49	w	82	MET
49	w	164	LYS
49	w	167	ASN
49	w	186	PRO
49	w	211	ARG
49	w	315	PHE
49	w	665	LEU
49	w	671	LEU
49	w	678	ASP
49	w	742	ARG
50	I	161	ARG
50	I	260	ILE
50	I	304	GLU
50	I	328	ASN
50	I	329	ILE
50	I	399	ARG
50	I	470	ARG
50	I	489	MET
50	I	523	ARG
50	I	529	ASN
50	I	539	VAL
50	I	575	CYS
51	J	214	LYS
51	J	261	LEU

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Mol	Chain	Res	Type
51	J	274	TYR
52	E	4	GLN
52	E	19	LYS
52	E	26	ARG
52	E	30	LEU
52	E	31	ARG
52	E	78	ARG
52	E	84	VAL
52	E	140	VAL
52	E	154	LEU
52	E	155	LEU
52	E	167	ASN
53	G	65	LEU
53	G	77	GLN
53	G	84	ARG
53	G	136	LEU
53	G	150	LEU
53	G	166	LEU
53	G	169	LEU
53	G	190	VAL
53	G	197	VAL
53	G	200	LEU
53	G	204	ARG
53	G	213	LYS
53	G	214	LEU
53	G	229	VAL
54	M	15	VAL
54	M	25	LYS
54	M	38	ILE
54	M	63	VAL
54	M	72	LEU
54	M	77	ARG
54	M	131	VAL
54	M	135	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
4	L	12	ASN
4	L	37	ASN
4	L	120	GLN
5	N	34	ASN

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Mol	Chain	Res	Type
5	N	37	HIS
5	N	95	GLN
6	Q	58	ASN
6	Q	73	GLN
6	Q	136	ASN
7	R	92	GLN
8	S	89	ASN
11	Z	57	HIS
15	f	42	GLN
19	k	40	GLN
20	O	26	GLN
20	O	31	GLN
20	O	42	ASN
20	O	50	ASN
20	O	65	ASN
20	O	72	HIS
20	O	122	GLN
21	V	98	ASN
22	a	120	ASN
23	P	34	GLN
23	P	37	ASN
23	P	96	GLN
24	X	111	ASN
26	h	59	ASN
27	F	209	ASN
28	B	182	GLN
28	B	184	ASN
28	B	279	ASN
28	B	345	ASN
29	C	48	GLN
29	C	87	GLN
29	C	114	ASN
29	C	291	ASN
30	H	58	HIS
31	A	73	GLN
31	A	75	ASN
31	A	150	GLN
31	A	175	HIS
32	K	42	ASN
32	K	262	ASN
33	m	232	GLN
33	m	238	ASN

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Mol	Chain	Res	Type
33	m	629	HIS
33	m	748	HIS
34	D	310	ASN
35	W	128	ASN
35	W	205	GLN
35	W	232	ASN
36	l	50	HIS
36	l	82	HIS
36	l	112	HIS
37	b	70	ASN
37	b	78	HIS
37	b	217	GLN
37	b	415	ASN
38	o	113	GLN
39	n	73	HIS
39	n	164	ASN
39	n	419	ASN
39	n	437	ASN
40	r	4	ASN
42	t	51	ASN
42	t	238	GLN
43	y	9	ASN
43	y	11	ASN
45	p	139	GLN
45	p	337	GLN
45	p	452	ASN
46	q	447	GLN
47	u	45	ASN
47	u	76	ASN
48	v	33	ASN
48	v	39	ASN
49	w	118	HIS
49	w	130	GLN
49	w	137	GLN
49	w	167	ASN
49	w	276	ASN
49	w	694	ASN
50	I	155	ASN
50	I	335	ASN
50	I	344	HIS
50	I	596	ASN
51	J	215	HIS

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Mol	Chain	Res	Type
51	J	220	HIS
51	J	221	GLN
52	E	4	GLN
53	G	95	ASN
53	G	137	ASN
54	M	56	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2439/3396 (71%)	742 (30%)	70 (2%)
2	2	157/158 (99%)	35 (22%)	3 (1%)
3	6	63/232 (27%)	30 (47%)	2 (3%)
All	All	2659/3786 (70%)	807 (30%)	75 (2%)

All (807) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	14	U
1	1	22	G
1	1	40	A
1	1	41	G
1	1	42	C
1	1	43	A
1	1	44	U
1	1	48	A
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	72	C
1	1	73	C
1	1	74	G
1	1	75	G
1	1	77	A
1	1	85	A
1	1	92	G

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Mol	Chain	Res	Type
1	1	94	G
1	1	96	G
1	1	110	G
1	1	111	C
1	1	113	C
1	1	117	U
1	1	118	U
1	1	120	G
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G
1	1	143	G
1	1	148	G
1	1	150	A
1	1	154	U
1	1	155	G
1	1	156	G
1	1	157	A
1	1	164	A
1	1	165	A
1	1	166	C
1	1	170	G
1	1	173	G
1	1	190	U
1	1	191	U
1	1	196	G
1	1	197	G
1	1	200	C
1	1	205	C
1	1	206	G
1	1	210	U
1	1	211	A
1	1	212	G
1	1	213	A
1	1	218	G
1	1	219	A
1	1	220	G
1	1	234	G
1	1	240	U
1	1	241	G
1	1	243	G

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Mol	Chain	Res	Type
1	1	249	U
1	1	250	U
1	1	251	G
1	1	252	U
1	1	264	G
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	283	G
1	1	284	A
1	1	285	A
1	1	295	A
1	1	298	U
1	1	299	G
1	1	305	U
1	1	311	C
1	1	323	A
1	1	329	U
1	1	338	A
1	1	339	C
1	1	352	A
1	1	368	G
1	1	370	U
1	1	376	G
1	1	390	G
1	1	398	A
1	1	399	A
1	1	401	U
1	1	403	C
1	1	404	G
1	1	421	G
1	1	422	A
1	1	437	G
1	1	438	A
1	1	439	C
1	1	440	A
1	1	495	G
1	1	496	C
1	1	498	A
1	1	503	C
1	1	510	G

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Mol	Chain	Res	Type
1	1	515	C
1	1	517	G
1	1	518	G
1	1	520	U
1	1	521	A
1	1	523	A
1	1	533	A
1	1	534	U
1	1	535	G
1	1	536	U
1	1	542	G
1	1	543	C
1	1	547	G
1	1	550	A
1	1	551	A
1	1	552	G
1	1	555	U
1	1	556	U
1	1	557	A
1	1	558	U
1	1	559	A
1	1	569	A
1	1	578	A
1	1	579	G
1	1	589	A
1	1	592	A
1	1	593	C
1	1	597	G
1	1	603	A
1	1	604	G
1	1	609	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	622	A
1	1	623	U
1	1	634	C
1	1	636	C
1	1	643	U
1	1	644	G
1	1	645	A
1	1	649	A

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Mol	Chain	Res	Type
1	1	650	C
1	1	660	A
1	1	676	G
1	1	677	A
1	1	681	U
1	1	690	A
1	1	691	A
1	1	705	A
1	1	710	A
1	1	720	A
1	1	721	G
1	1	722	G
1	1	733	G
1	1	734	C
1	1	735	A
1	1	742	G
1	1	743	C
1	1	757	C
1	1	759	U
1	1	760	G
1	1	761	A
1	1	770	G
1	1	772	U
1	1	774	G
1	1	775	A
1	1	776	U
1	1	777	U
1	1	779	G
1	1	780	A
1	1	781	G
1	1	784	A
1	1	785	G
1	1	786	A
1	1	799	G
1	1	801	A
1	1	806	A
1	1	808	A
1	1	813	G
1	1	815	G
1	1	818	C
1	1	819	U
1	1	820	A

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Mol	Chain	Res	Type
1	1	822	G
1	1	826	G
1	1	830	A
1	1	849	C
1	1	854	G
1	1	857	G
1	1	859	G
1	1	860	G
1	1	861	C
1	1	864	G
1	1	871	U
1	1	874	U
1	1	875	G
1	1	877	C
1	1	878	G
1	1	879	U
1	1	880	G
1	1	881	C
1	1	882	A
1	1	883	A
1	1	884	A
1	1	886	C
1	1	887	G
1	1	891	G
1	1	892	U
1	1	893	C
1	1	894	G
1	1	895	A
1	1	896	A
1	1	898	U
1	1	899	U
1	1	900	G
1	1	904	A
1	1	906	A
1	1	909	G
1	1	910	G
1	1	918	C
1	1	919	U
1	1	920	A
1	1	921	A
1	1	932	U
1	1	936	A

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Mol	Chain	Res	Type
1	1	938	C
1	1	944	C
1	1	957	C
1	1	958	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	962	A
1	1	963	G
1	1	964	G
1	1	970	A
1	1	977	C
1	1	978	G
1	1	979	U
1	1	980	A
1	1	981	U
1	1	982	C
1	1	984	G
1	1	985	U
1	1	991	G
1	1	992	A
1	1	1059	G
1	1	1060	U
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1105	A
1	1	1108	U
1	1	1111	U
1	1	1112	A
1	1	1116	G
1	1	1117	G
1	1	1126	G
1	1	1127	G
1	1	1129	A
1	1	1132	C
1	1	1135	A
1	1	1136	A
1	1	1139	G
1	1	1142	G
1	1	1144	U
1	1	1151	U

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Mol	Chain	Res	Type
1	1	1153	A
1	1	1155	C
1	1	1159	A
1	1	1160	C
1	1	1174	G
1	1	1177	G
1	1	1180	A
1	1	1181	U
1	1	1186	G
1	1	1192	C
1	1	1193	A
1	1	1196	C
1	1	1197	A
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1201	C
1	1	1204	A
1	1	1213	G
1	1	1217	A
1	1	1218	U
1	1	1221	A
1	1	1222	G
1	1	1227	C
1	1	1228	C
1	1	1233	G
1	1	1235	U
1	1	1237	G
1	1	1241	U
1	1	1242	G
1	1	1244	A
1	1	1245	A
1	1	1250	G
1	1	1251	A
1	1	1252	A
1	1	1253	U
1	1	1258	U
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1264	G
1	1	1266	G

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Mol	Chain	Res	Type
1	1	1272	C
1	1	1273	A
1	1	1277	C
1	1	1278	A
1	1	1279	C
1	1	1283	C
1	1	1284	C
1	1	1286	A
1	1	1287	A
1	1	1299	U
1	1	1300	G
1	1	1302	A
1	1	1303	A
1	1	1304	A
1	1	1305	U
1	1	1307	G
1	1	1308	A
1	1	1309	U
1	1	1325	U
1	1	1330	A
1	1	1331	U
1	1	1332	A
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1355	A
1	1	1356	U
1	1	1357	G
1	1	1364	C
1	1	1367	G
1	1	1380	G
1	1	1386	A
1	1	1391	C
1	1	1397	C
1	1	1399	A
1	1	1400	G
1	1	1419	A
1	1	1421	G

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Mol	Chain	Res	Type
1	1	1429	G
1	1	1434	G
1	1	1437	C
1	1	1443	G
1	1	1446	A
1	1	1450	G
1	1	1452	A
1	1	1453	A
1	1	1454	A
1	1	1455	U
1	1	1477	A
1	1	1481	A
1	1	1483	G
1	1	1484	U
1	1	1485	G
1	1	1487	G
1	1	1495	U
1	1	1503	A
1	1	1508	C
1	1	1512	U
1	1	1533	U
1	1	1536	G
1	1	1539	A
1	1	1544	G
1	1	1546	A
1	1	1547	G
1	1	1555	U
1	1	1556	C
1	1	1557	A
1	1	1560	G
1	1	1561	G
1	1	1562	C
1	1	1566	A
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1573	G
1	1	1574	C
1	1	1575	A
1	1	1580	A
1	1	1581	C

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Mol	Chain	Res	Type
1	1	1582	C
1	1	1587	A
1	1	1589	A
1	1	1590	G
1	1	1593	A
1	1	1596	C
1	1	1605	A
1	1	1608	C
1	1	1613	A
1	1	1619	A
1	1	1620	U
1	1	1627	U
1	1	1628	C
1	1	1630	U
1	1	1639	C
1	1	1641	U
1	1	1642	A
1	1	1643	A
1	1	1647	A
1	1	1656	A
1	1	1657	C
1	1	1658	G
1	1	1683	A
1	1	1685	C
1	1	1687	U
1	1	1688	U
1	1	1713	G
1	1	1715	A
1	1	1716	U
1	1	1717	U
1	1	1724	U
1	1	1725	C
1	1	1730	G
1	1	1736	G
1	1	1741	A
1	1	1742	U
1	1	1743	G
1	1	1749	A
1	1	1750	A
1	1	1751	G
1	1	1756	C
1	1	1764	U

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Mol	Chain	Res	Type
1	1	1765	U
1	1	1766	G
1	1	1768	U
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1792	C
1	1	1794	G
1	1	1795	U
1	1	1796	G
1	1	1797	A
1	1	1808	G
1	1	1813	A
1	1	1814	A
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1820	U
1	1	1821	U
1	1	1852	G
1	1	1853	U
1	1	1862	U
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1868	G
1	1	1869	C
1	1	1871	U
1	1	1878	G
1	1	1879	A
1	1	1880	U
1	1	1881	A
1	1	1884	A
1	1	1886	A
1	1	1900	A
1	1	1906	G
1	1	1947	G
1	1	1948	G
1	1	1951	C
1	1	1952	G
1	1	1953	G
1	1	2095	G

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Mol	Chain	Res	Type
1	1	2098	C
1	1	2100	A
1	1	2101	C
1	1	2123	G
1	1	2130	G
1	1	2322	C
1	1	2323	G
1	1	2324	A
1	1	2325	G
1	1	2334	U
1	1	2335	G
1	1	2336	U
1	1	2347	U
1	1	2363	A
1	1	2370	G
1	1	2371	G
1	1	2372	A
1	1	2373	A
1	1	2374	C
1	1	2377	G
1	1	2385	G
1	1	2388	U
1	1	2392	C
1	1	2393	G
1	1	2394	G
1	1	2395	G
1	1	2405	C
1	1	2410	U
1	1	2411	U
1	1	2412	G
1	1	2414	G
1	1	2418	G
1	1	2419	A
1	1	2434	U
1	1	2597	U
1	1	2606	G
1	1	2607	G
1	1	2805	G
1	1	2807	U
1	1	2811	A
1	1	2812	C
1	1	2813	A

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Mol	Chain	Res	Type
1	1	2818	U
1	1	2819	A
1	1	2820	A
1	1	2821	C
1	1	2822	U
1	1	2823	G
1	1	2824	G
1	1	2825	C
1	1	2826	U
1	1	2836	C
1	1	2837	A
1	1	2838	A
1	1	2841	G
1	1	2842	U
1	1	2845	A
1	1	2846	U
1	1	2849	C
1	1	2855	U
1	1	2857	C
1	1	2858	U
1	1	2877	G
1	1	2878	G
1	1	2879	C
1	1	2880	U
1	1	2887	A
1	1	2889	C
1	1	2898	G
1	1	2899	C
1	1	2911	A
1	1	2916	U
1	1	2919	A
1	1	2920	U
1	1	2921	U
1	1	2922	G
1	1	2923	U
1	1	2924	U
1	1	2925	C
1	1	2926	A
1	1	2927	C
1	1	2929	C
1	1	2930	A
1	1	2935	U

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Mol	Chain	Res	Type
1	1	2936	A
1	1	2941	A
1	1	2942	C
1	1	2943	G
1	1	2944	U
1	1	2945	G
1	1	2946	A
1	1	2947	G
1	1	2949	U
1	1	2950	G
1	1	2951	G
1	1	2952	G
1	1	2953	U
1	1	2954	U
1	1	2955	U
1	1	2956	A
1	1	2964	G
1	1	2965	U
1	1	2966	G
1	1	2967	A
1	1	2968	G
1	1	2969	A
1	1	2970	C
1	1	2971	A
1	1	2972	G
1	1	2975	U
1	1	2976	A
1	1	2977	G
1	1	2979	U
1	1	2980	U
1	1	2981	U
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2987	A
1	1	2990	G
1	1	2992	U
1	1	2996	U
1	1	2997	G
1	1	3003	G
1	1	3012	A
1	1	3017	A

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Mol	Chain	Res	Type
1	1	3019	U
1	1	3020	U
1	1	3021	A
1	1	3022	G
1	1	3023	U
1	1	3026	G
1	1	3029	A
1	1	3030	G
1	1	3032	A
1	1	3037	U
1	1	3046	A
1	1	3056	U
1	1	3057	U
1	1	3058	U
1	1	3065	G
1	1	3069	G
1	1	3070	A
1	1	3071	U
1	1	3072	C
1	1	3074	G
1	1	3076	C
1	1	3078	U
1	1	3079	U
1	1	3086	A
1	1	3090	U
1	1	3092	C
1	1	3093	C
1	1	3094	A
1	1	3099	C
1	1	3100	U
1	1	3102	G
1	1	3104	U
1	1	3109	G
1	1	3116	G
1	1	3122	A
1	1	3124	G
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3141	A
1	1	3142	A
1	1	3143	C

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Mol	Chain	Res	Type
1	1	3150	A
1	1	3151	U
1	1	3153	U
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3158	G
1	1	3160	U
1	1	3161	C
1	1	3164	C
1	1	3165	A
1	1	3170	A
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3175	U
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3186	A
1	1	3187	A
1	1	3188	G
1	1	3196	U
1	1	3199	G
1	1	3206	C
1	1	3207	U
1	1	3216	G
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3227	A
1	1	3228	C
1	1	3229	G
1	1	3242	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3249	C
1	1	3252	G

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Mol	Chain	Res	Type
1	1	3256	G
1	1	3259	U
1	1	3263	G
1	1	3268	A
1	1	3269	U
1	1	3270	U
1	1	3271	G
1	1	3276	G
1	1	3281	U
1	1	3283	U
1	1	3287	U
1	1	3288	G
1	1	3289	G
1	1	3290	G
1	1	3293	U
1	1	3294	A
1	1	3295	A
1	1	3303	G
1	1	3304	U
1	1	3306	U
1	1	3307	A
1	1	3309	G
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3319	U
1	1	3324	C
1	1	3328	G
1	1	3341	U
1	1	3342	A
1	1	3344	A
1	1	3345	G
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3353	G
1	1	3355	U
1	1	3356	G
1	1	3363	U
1	1	3366	G
1	1	3369	G
1	1	3375	A

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Mol	Chain	Res	Type
1	1	3378	C
1	1	3386	G
1	1	3387	U
1	1	3390	G
1	1	3396	U
2	2	34	U
2	2	35	C
2	2	39	G
2	2	51	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	71	A
2	2	78	G
2	2	79	A
2	2	81	U
2	2	82	U
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	97	A
2	2	104	A
2	2	106	C
2	2	107	G
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	126	A
2	2	128	U
2	2	134	G
2	2	136	G
2	2	151	C
2	2	152	G
2	2	157	U
2	2	158	U
3	6	4	U
3	6	5	C

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Mol	Chain	Res	Type
3	6	6	U
3	6	7	C
3	6	8	A
3	6	9	A
3	6	13	U
3	6	14	U
3	6	15	C
3	6	16	U
3	6	17	G
3	6	23	U
3	6	24	A
3	6	34	A
3	6	36	U
3	6	39	U
3	6	40	U
3	6	42	G
3	6	43	A
3	6	47	A
3	6	52	G
3	6	53	A
3	6	54	A
3	6	56	U
3	6	57	U
3	6	58	G
3	6	59	C
3	6	228	U
3	6	231	A
3	6	232	A

All (75) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	40	A
1	1	153	U
1	1	154	U
1	1	165	A
1	1	239	G
1	1	297	G
1	1	376	G
1	1	494	G
1	1	518	G
1	1	533	A

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Mol	Chain	Res	Type
1	1	556	U
1	1	557	A
1	1	588	G
1	1	644	G
1	1	649	A
1	1	720	A
1	1	734	C
1	1	818	C
1	1	873	C
1	1	878	G
1	1	899	U
1	1	917	A
1	1	978	G
1	1	1102	A
1	1	1103	A
1	1	1104	G
1	1	1128	U
1	1	1159	A
1	1	1227	C
1	1	1241	U
1	1	1299	U
1	1	1302	A
1	1	1307	G
1	1	1329	U
1	1	1331	U
1	1	1355	A
1	1	1428	A
1	1	1451	C
1	1	1481	A
1	1	1502	C
1	1	1574	C
1	1	1581	C
1	1	1641	U
1	1	1716	U
1	1	1813	A
1	1	1820	U
1	1	1861	G
1	1	1947	G
1	1	2323	G
1	1	2837	A
1	1	2857	C
1	1	2878	G

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Mol	Chain	Res	Type
1	1	2922	G
1	1	2940	A
1	1	2946	A
1	1	2954	U
1	1	2986	U
1	1	3016	A
1	1	3055	U
1	1	3093	C
1	1	3116	G
1	1	3121	U
1	1	3171	U
1	1	3218	A
1	1	3228	C
1	1	3267	A
1	1	3269	U
1	1	3340	G
1	1	3350	C
1	1	3389	U
2	2	85	G
2	2	112	U
2	2	123	G
3	6	16	U
3	6	56	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 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	2
36	l	1
4	L	1
23	P	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	l	135:ALA	C	136:MET	N	6.21
1	1	1792:C	O3'	1793:C	P	5.60
1	L	8:PRO	C	9:ILE	N	4.88
1	1	966:U	O3'	967:A	P	4.55
1	P	131:ARG	C	132:ALA	N	3.63

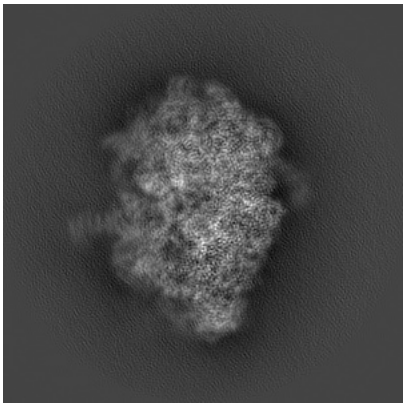
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-3891. These allow visual inspection of the internal detail of the map and identification of artifacts.

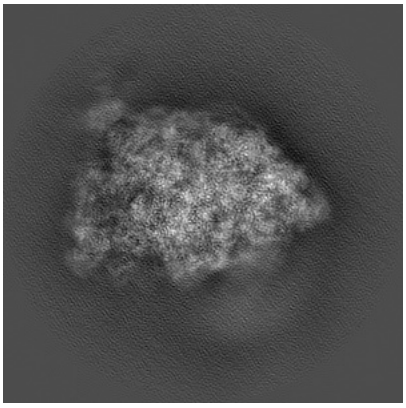
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

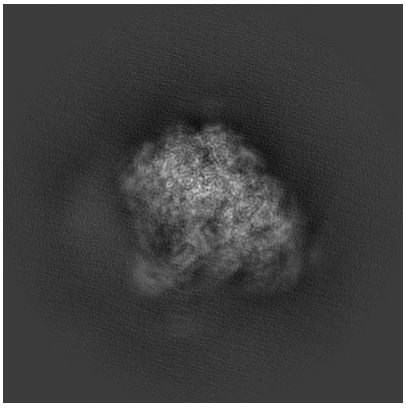
6.1.1 Primary map



X



Y

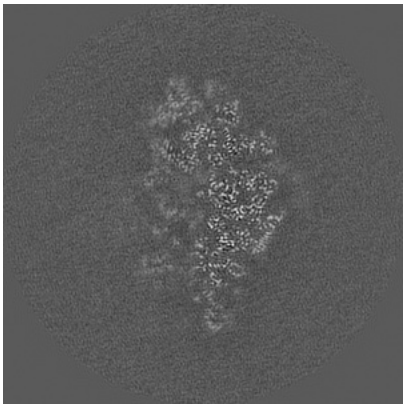


Z

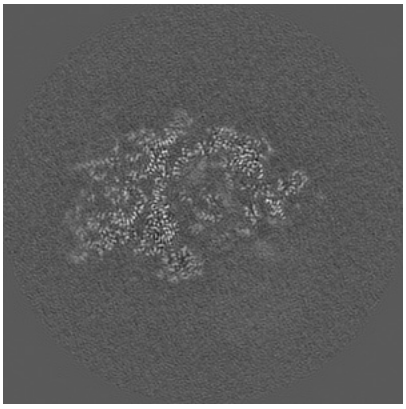
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

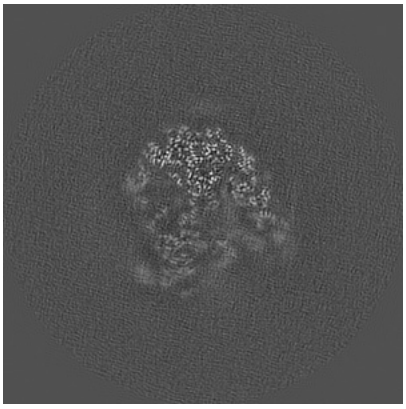
6.2.1 Primary map



X Index: 210



Y Index: 210

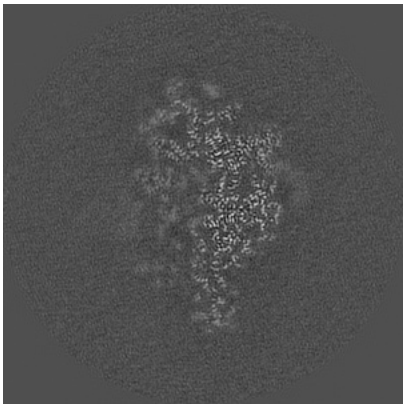


Z Index: 210

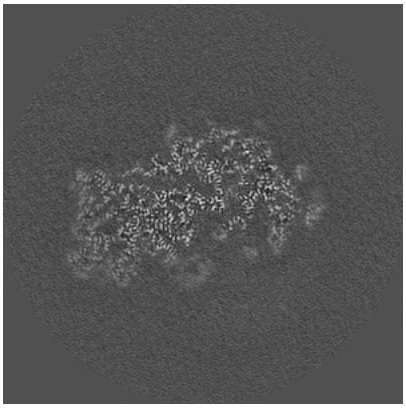
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

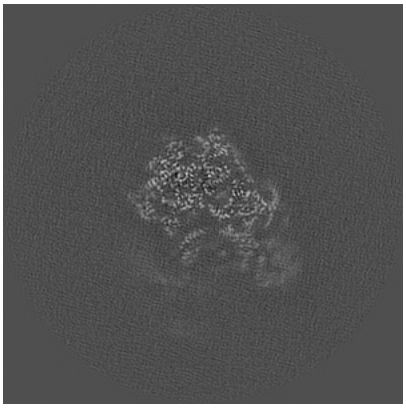
6.3.1 Primary map



X Index: 216



Y Index: 227



Z Index: 172

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

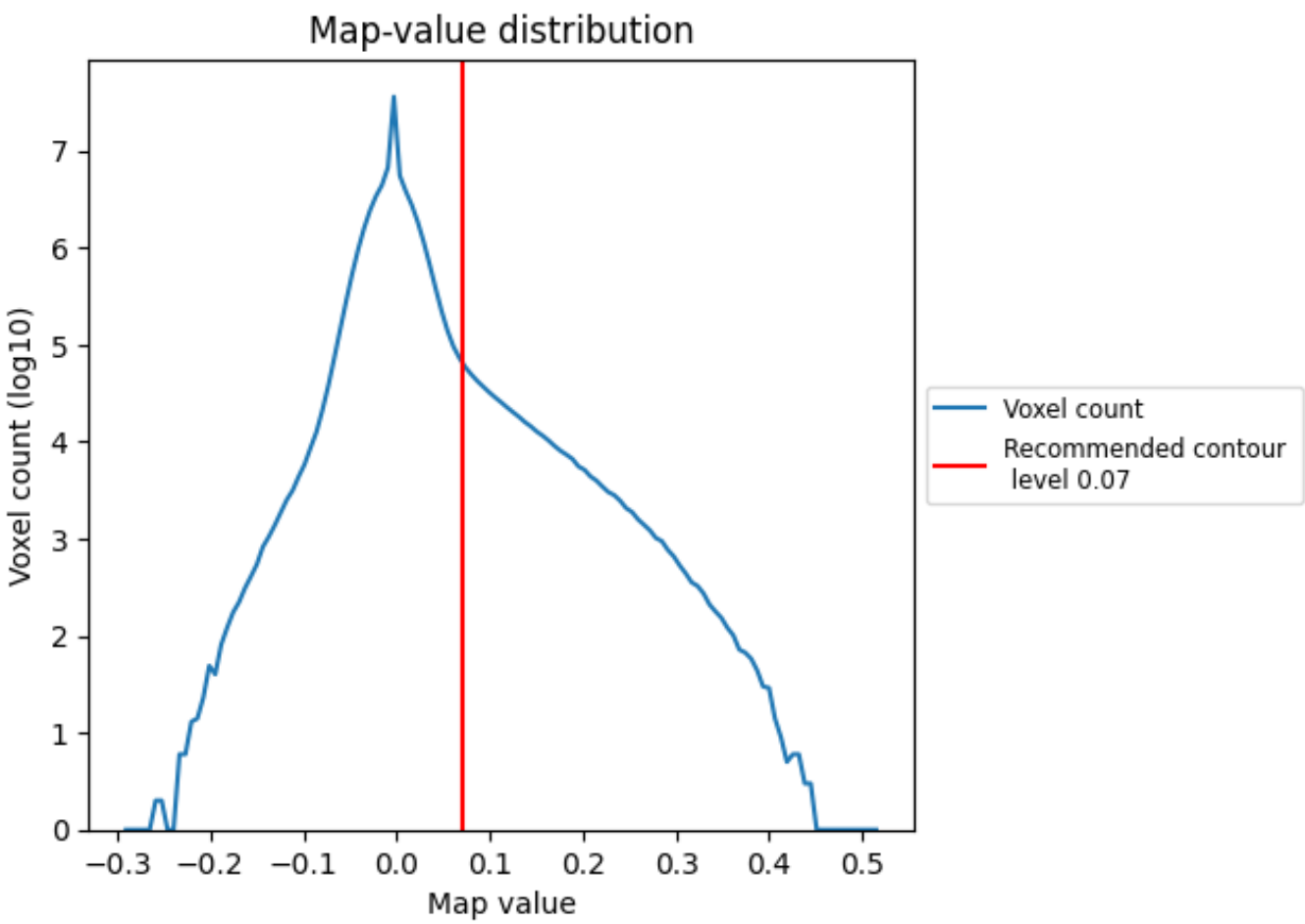
6.5 Mask visualisation (i)

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

7 Map analysis (i)

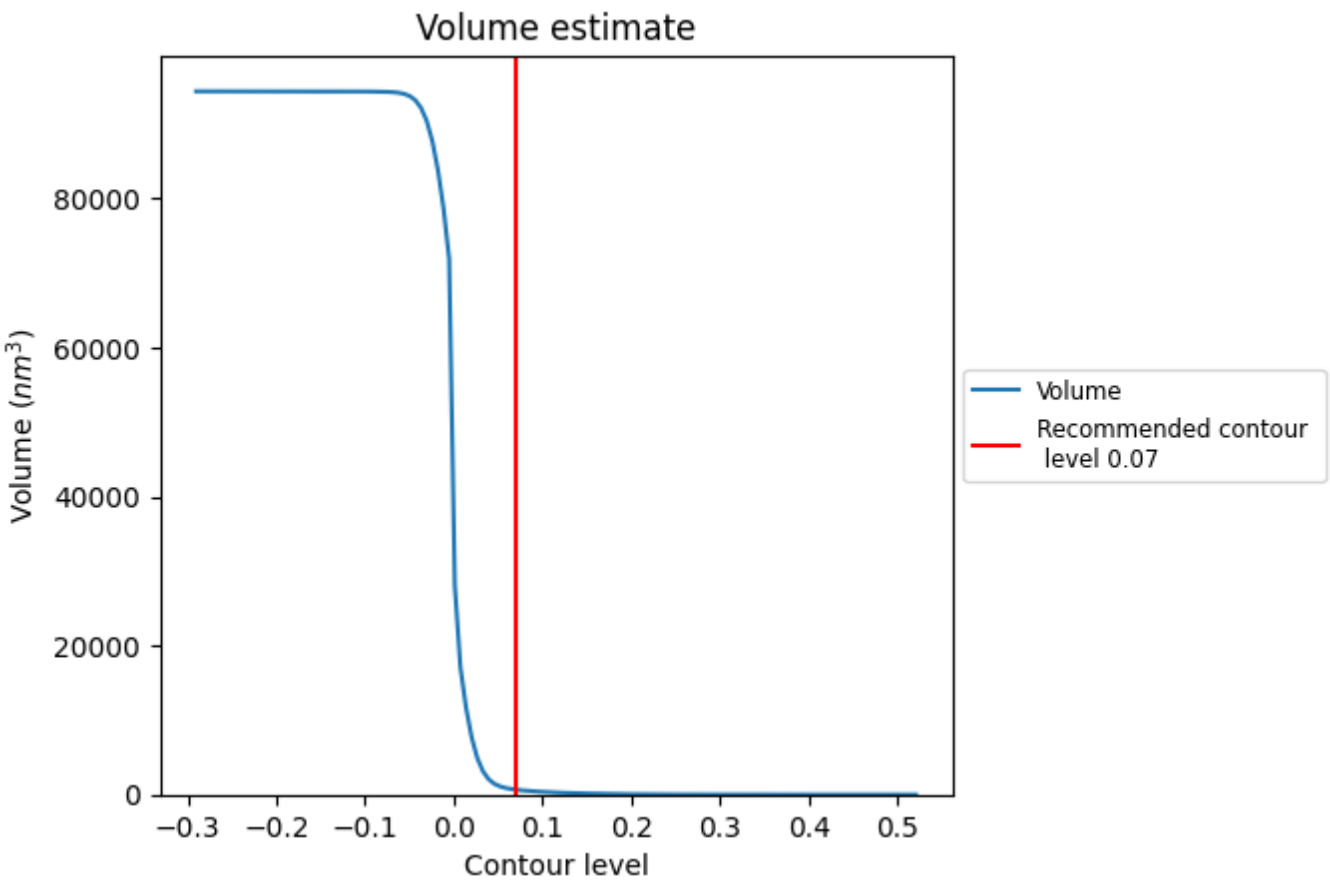
This section contains the results of statistical analysis of the map.

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.

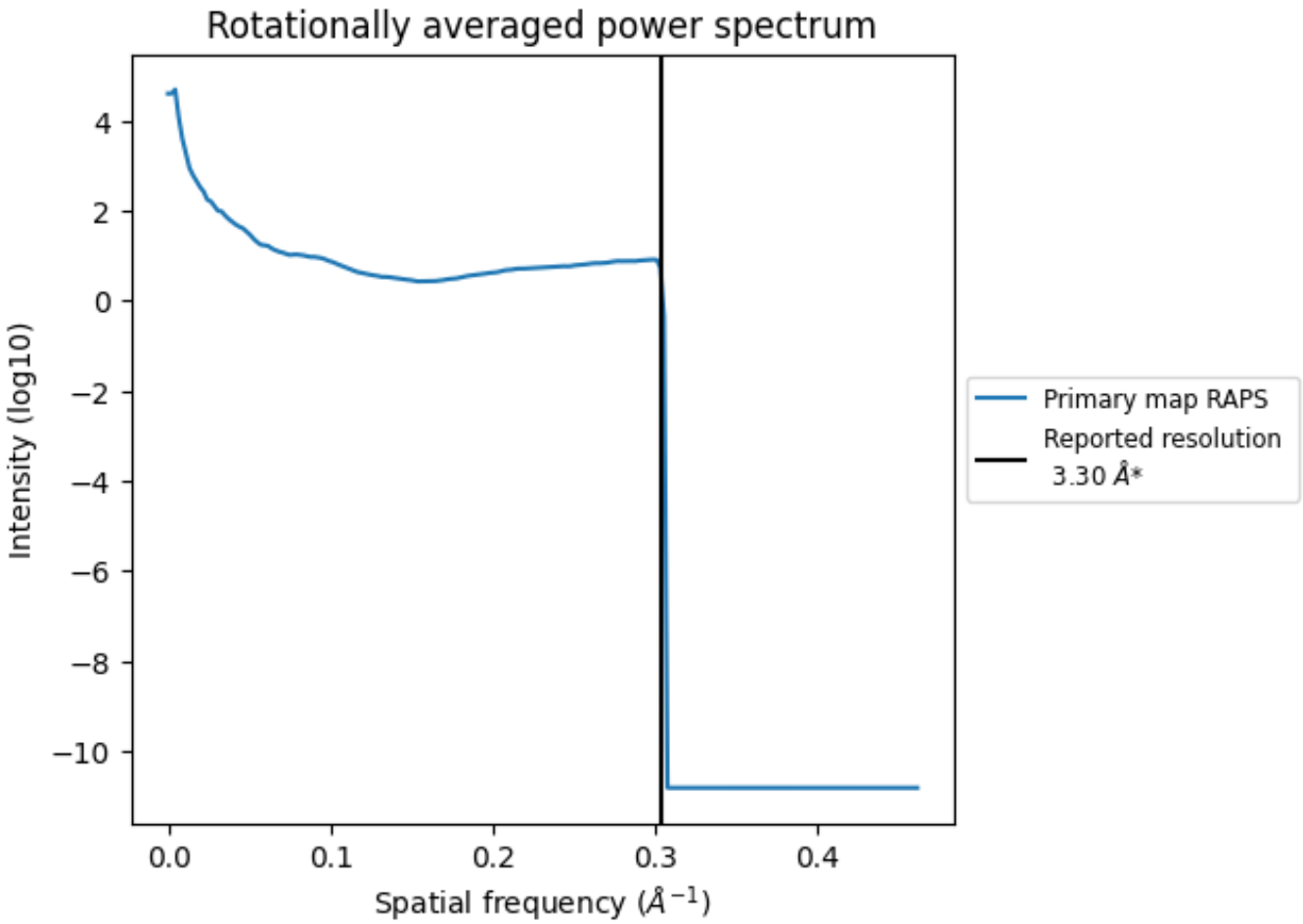
7.2 Volume estimate (i)



The volume at the recommended contour level is 662 nm^3; this corresponds to an approximate mass of 598 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)

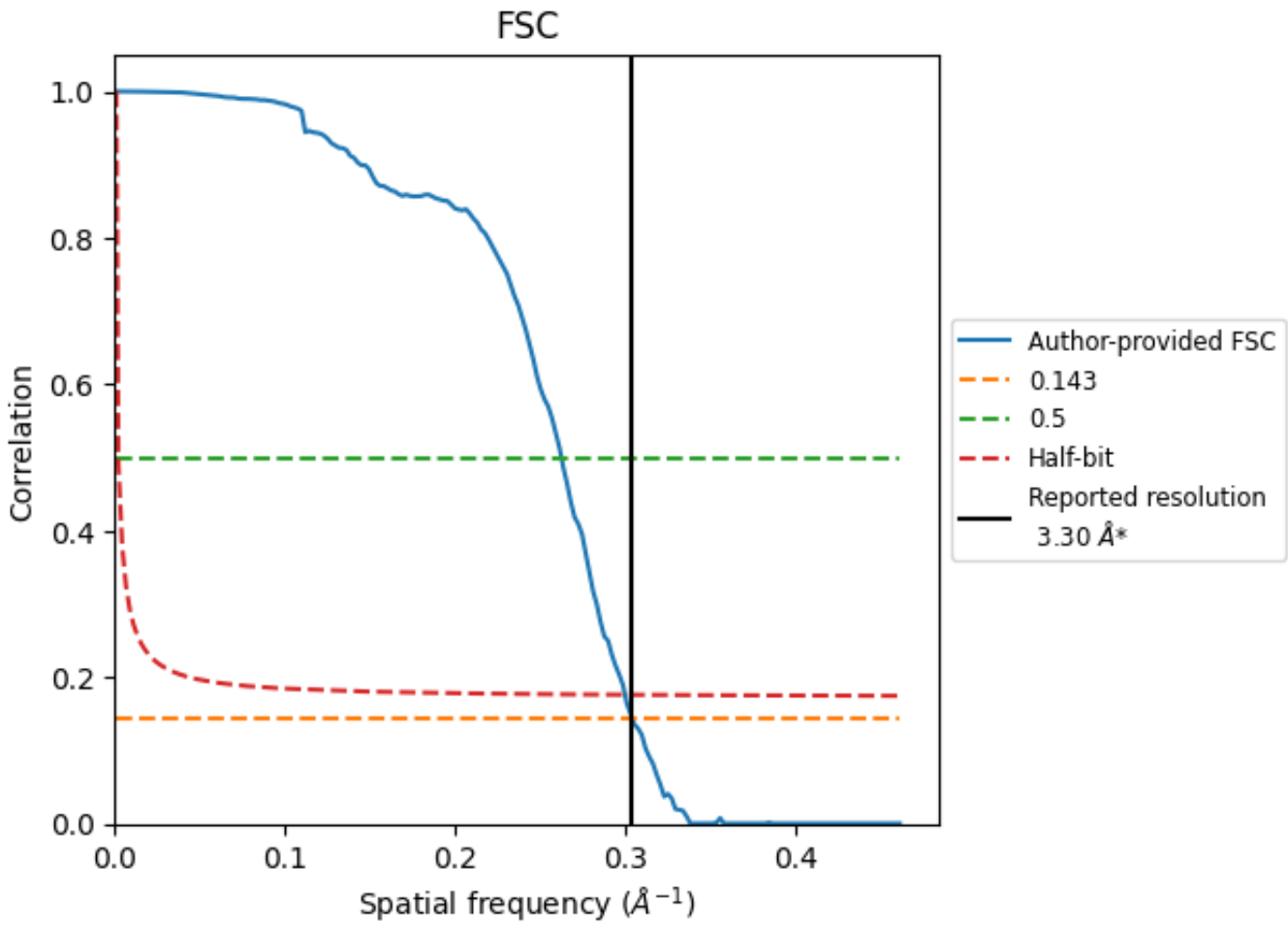


*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

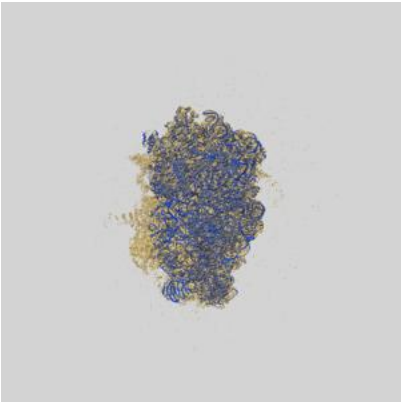
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.29	3.81	3.33
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

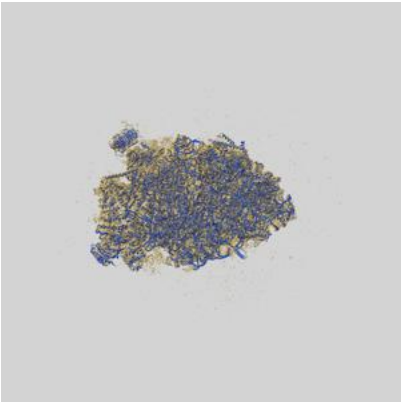
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-3891 and PDB model 6ELZ. Per-residue inclusion information can be found in section 3 on page 13.

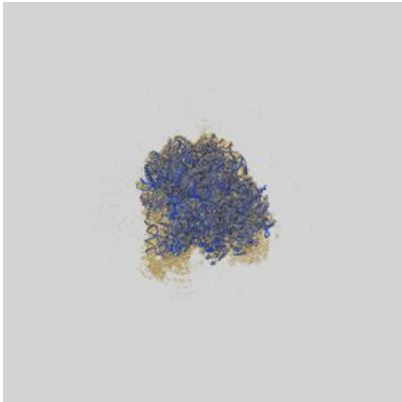
9.1 Map-model overlay (i)



X



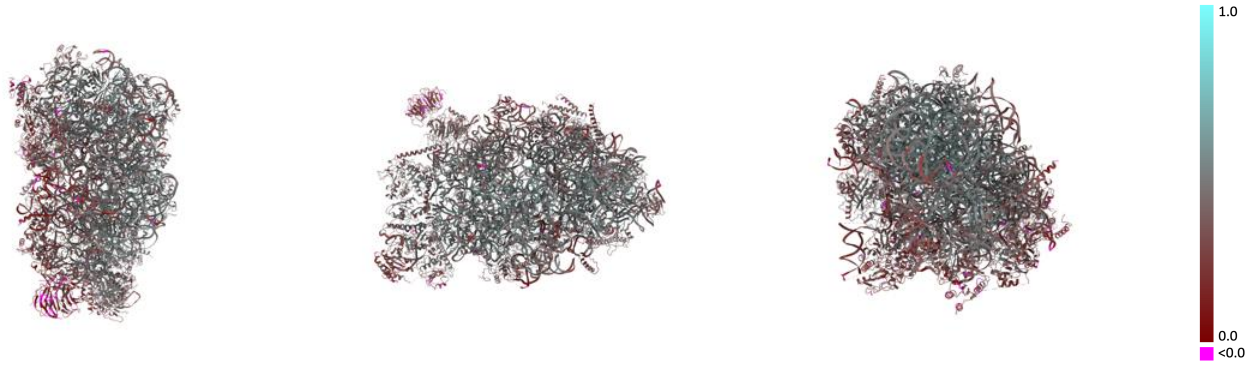
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07 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.

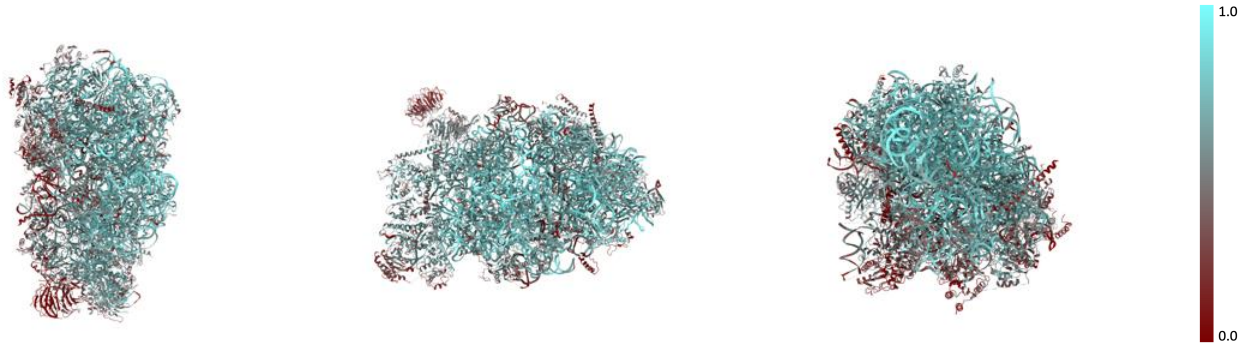
9.2 Q-score mapped to coordinate model (i)



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.

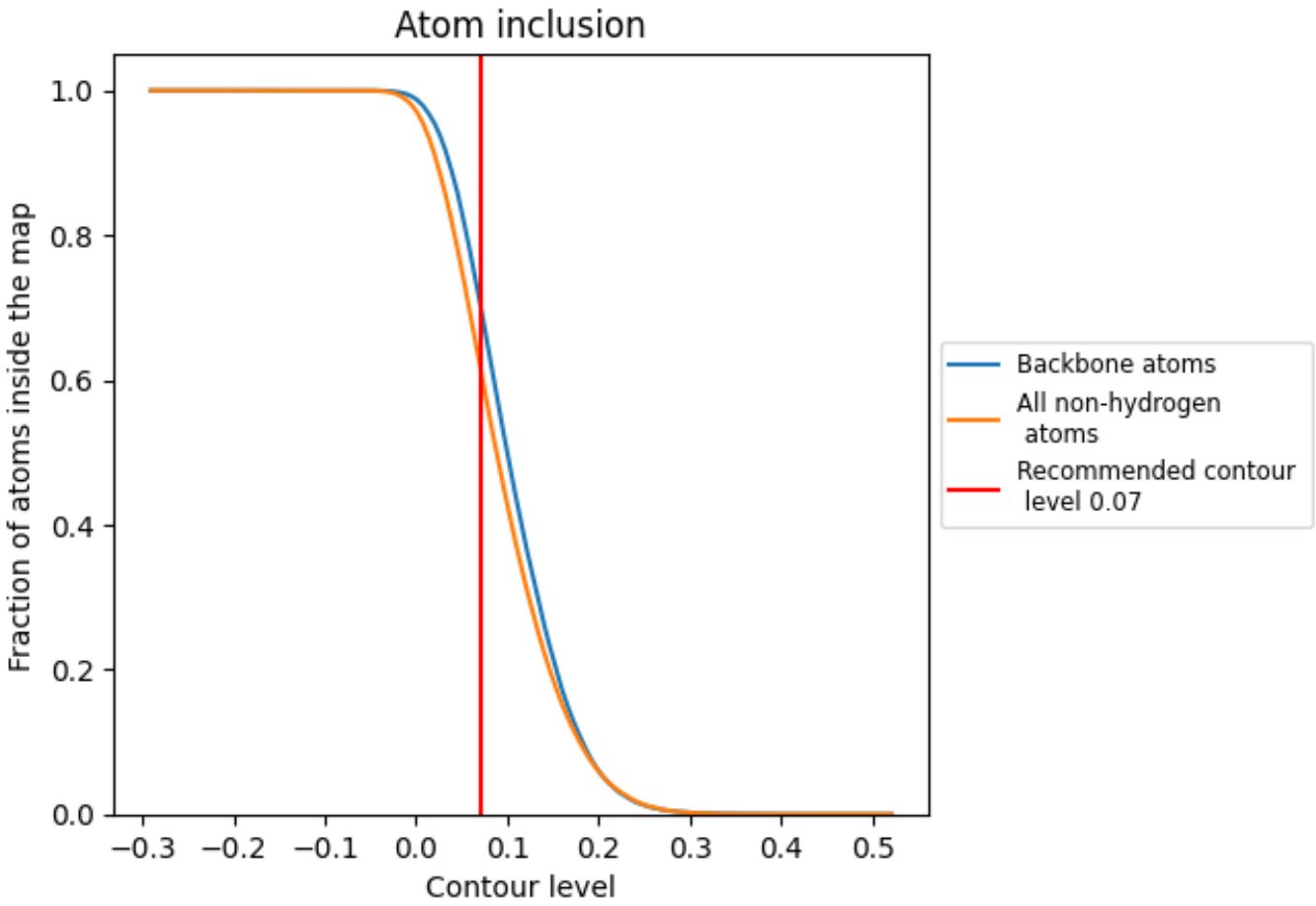
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.07).

9.4 Atom inclusion (i)



At the recommended contour level, 71% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6207	0.4140
1	0.7352	0.4370
2	0.8357	0.5050
6	0.6277	0.3820
A	0.5842	0.4050
B	0.6707	0.4390
C	0.7145	0.4860
D	0.4698	0.3600
E	0.6356	0.4550
F	0.6866	0.4660
G	0.6780	0.4760
H	0.6660	0.4790
I	0.3953	0.3330
J	0.3860	0.3260
K	0.4157	0.3330
L	0.7109	0.4840
M	0.6949	0.4880
N	0.7753	0.5280
O	0.7801	0.5250
P	0.6383	0.4320
Q	0.6465	0.4450
R	0.4941	0.3330
S	0.6335	0.4590
T	0.0585	0.2390
U	0.3076	0.2610
V	0.5862	0.4250
W	0.4401	0.3520
X	0.6568	0.4540
Y	0.7143	0.4770
Z	0.5359	0.3570
a	0.4039	0.3420
b	0.4125	0.3440
c	0.3995	0.3100
d	0.5537	0.4020
e	0.7070	0.5100

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Chain	Atom inclusion	Q-score
f	0.7674	0.5370
g	0.6068	0.4100
h	0.6607	0.4800
i	0.5190	0.3550
j	0.7935	0.5330
k	0.4591	0.3270
l	0.4371	0.3620
m	0.5001	0.3630
n	0.6012	0.4280
o	0.5032	0.3730
p	0.1297	0.1550
q	0.2686	0.2930
r	0.4557	0.4030
s	0.4983	0.4580
t	0.5312	0.3940
u	0.5187	0.3490
v	0.6277	0.4400
w	0.4276	0.3650
y	0.5347	0.3550
z	0.2442	0.3400