



wwPDB EM Validation Summary Report ⓘ

May 14, 2026 – 05:13 PM EDT

PDB ID : 9N78 / pdb_00009n78
EMDB ID : EMD-49088
Title : SSU processome maturation and disassembly, State L
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 4.17 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

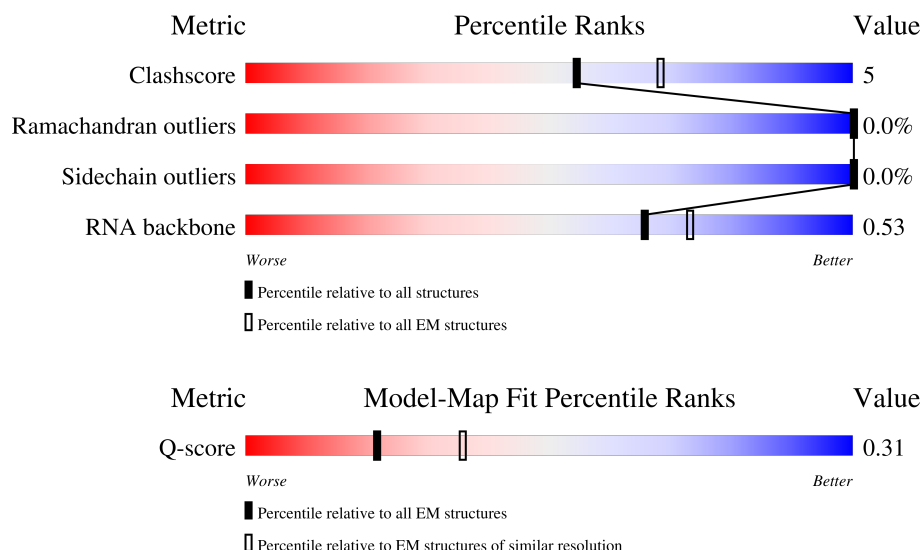
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.17 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5438 (3.67 - 4.67)

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

Mol	Chain	Length	Quality of chain
1	L0	700	5% . 93%
2	L1	1803	12% 53% 19% 26%
3	L2	334	7% 46% 11% 41%

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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LS	594	
24	NA	593	
25	NB	610	
26	ND	214	
27	NF	151	
28	NG	137	

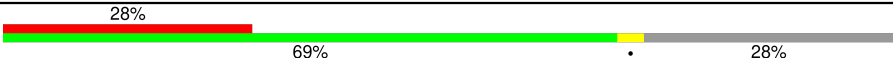
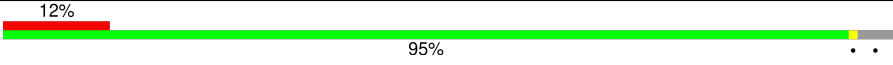
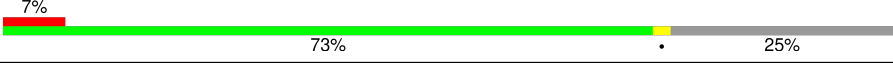
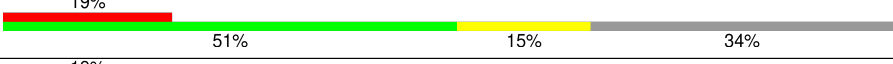
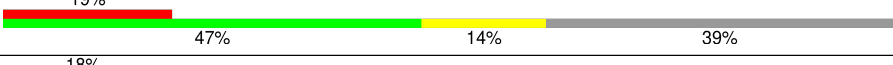
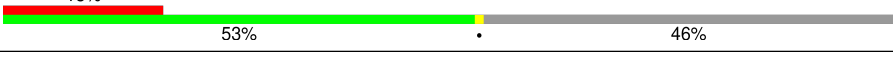
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Mol	Chain	Length	Quality of chain
29	NL	318	
30	NM	255	
31	NP	144	
32	NQ	82	
33	NS	1267	
34	NV	733	
35	OH	143	
36	OU	152	
37	SA	504	
38	SB	511	
39	SC	327	
39	SD	327	
40	SE	126	
40	SF	126	
41	SG	573	
42	SH	367	
43	SI	1183	
44	SJ	252	
44	SK	252	
45	SL	189	
46	SM	290	
47	SP	2493	
48	SQ	217	
49	SR	145	
50	SS	899	

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Mol	Chain	Length	Quality of chain
51	ST	810	
52	SU	552	
53	SV	206	
54	SW	274	
55	SY	250	
56	SZ	483	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 149183 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 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	50	Total	C	N	O	P	0	0
			1068	477	190	351	50		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1342	Total	C	N	O	P	0	0
			28628	12798	5106	9382	1342		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	196	Total	C	N	O	P	0	0
			4165	1861	721	1386	197		

- Molecule 4 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	106	Total	C	N	O	S	0	0
			862	545	159	156	2		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	244	Total	C	N	O	S	0	0
			1936	1239	359	335	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	197	Total	C	N	O	S	0	0
			1558	975	291	289	3		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	216	Total	C	N	O	S	0	0
			1740	1094	335	308	3		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	178	Total	C	N	O	S	0	0
			1427	918	251	258			

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	170	Total	C	N	O	S	0	0
			1348	836	269	241	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	181	Total	C	N	O	S	0	0
			1470	930	285	254	1		

- Molecule 11 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	128	Total	C	N	O	S	0	0
			642	386	128	128			

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	137	Total	C	N	O	S	0	0
			1112	714	212	183	3		

- Molecule 13 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LF	130	Total	C	N	O	0	0
			1046	662	204	180		

- Molecule 15 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	LG	62	Total	C	N	O	0	0
			309	185	62	62		

- Molecule 16 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	744	Total	C	N	O	S	0	0
			5941	3794	1006	1126	15		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	600	Total	C	N	O	S	0	0
			3792	2375	679	733	5		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	453	Total	C	N	O	S	0	0
			3579	2262	634	673	10		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	132	Total	C	N	O	S	0	0
			1068	681	185	199	3		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	163	Total	C	N	O	S	0	0
			1291	808	235	245	3		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	LM	1196	Total	C	N	O	0	0
			6011	3619	1196	1196		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	663	Total	C	N	O	S	0	0
			5263	3333	913	995	22		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LS	362	Total	C	N	O	S	0	0
			2829	1793	509	518	9		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	NA	183	Total	C	N	O	S	0	0
			1269	778	227	263	1		

- Molecule 25 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	NB	240	Total	C	N	O	S	0	0
			1470	900	288	281	1		

- Molecule 26 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	ND	74	Total	C	N	O	0	0
			564	351	115	98		

- Molecule 27 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	NF	141	Total	C	N	O	S	0	0
			1135	725	214	194	2		

- Molecule 28 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	NG	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 29 is a protein called Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	NL	272	Total	C	N	O	S	0	0
			2180	1393	387	387	13		

- Molecule 30 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	NM	229	Total	C	N	O	S	0	0
			1828	1156	339	329	4		

- Molecule 31 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	NP	134	Total	C	N	O		0	0
			666	398	134	134			

- Molecule 32 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	NQ	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 33 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	NS	105	Total	C	N	O	S	0	0
			879	547	175	156	1		

- Molecule 34 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	NV	16	Total	C	N	O	0	0
			126	80	28	18		

- Molecule 35 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	OH	120	Total	C	N	O	0	0
			594	354	120	120		

- Molecule 36 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	OU	56	Total	C	N	O	0	0
			278	166	56	56		

- Molecule 37 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SA	397	Total	C	N	O	S	1	0
			3100	1964	534	593	9		

- Molecule 38 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SB	403	Total	C	N	O	S	0	0
			3099	1960	524	606	9		

- Molecule 39 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SC	240	Total	C	N	O	S	1	0
			1865	1181	335	339	10		
39	SD	238	Total	C	N	O	S	0	0
			1850	1171	333	336	10		

- Molecule 40 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
40	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SG	459	Total	C	N	O	S	0	0
			3672	2331	645	686	10		

- Molecule 42 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SH	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 43 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SI	763	Total	C	N	O	S	0	0
			6187	3967	1103	1089	28		

- Molecule 44 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SJ	213	Total	C	N	O		0	0
			1074	648	213	213			
44	SK	229	Total	C	N	O		0	0
			1160	702	229	229			

- Molecule 45 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SL	148	Total	C	N	O	S	0	0
			1171	750	209	202	10		

- Molecule 46 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SM	219	Total	C	N	O	S	0	0
			1756	1107	325	318	6		

- Molecule 47 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SP	1852	Total	C	N	O	S	0	0
			15102	9753	2498	2804	47		

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SQ	97	Total	C	N	O	S	0	0
			836	526	155	152	3		

- Molecule 49 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SR	134	Total	C	N	O	S	0	0
			1052	668	204	178	2		

- Molecule 50 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SS	117	Total	C	N	O	S	0	0
			992	610	195	177	10		

- Molecule 51 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ST	584	Total	C	N	O	S	0	0
			3341	2039	656	643	3		

- Molecule 52 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SU	532	Total	C	N	O	0	0
			2703	1639	532	532		

- Molecule 53 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SV	155	Total	C	N	O	0	0
			852	512	176	164		

- Molecule 54 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SW	182	Total	C	N	O	S	0	0
			1444	923	262	255	4		

- Molecule 55 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SY	152	Total	C	N	O	S	0	0
			1287	801	250	231	5		

- Molecule 56 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SZ	259	Total	C	N	O	0	0
			1314	796	259	259		

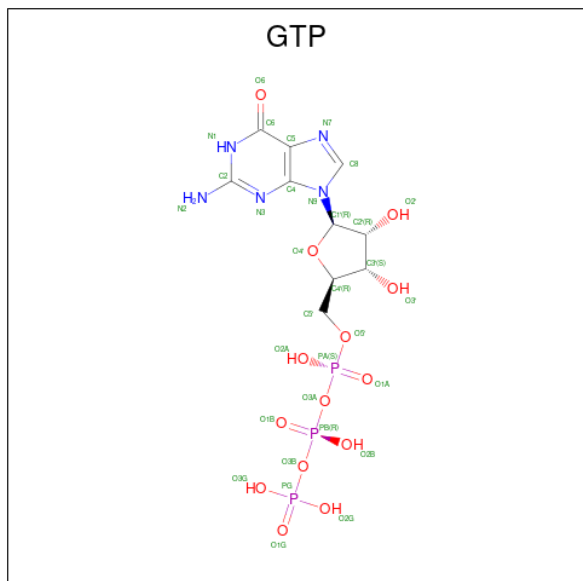
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	L1	46	Total	Mg	0
			46	46	
57	SI	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	NQ	1	Total	Zn	0
			1	1	
58	SL	1	Total	Zn	0
			1	1	

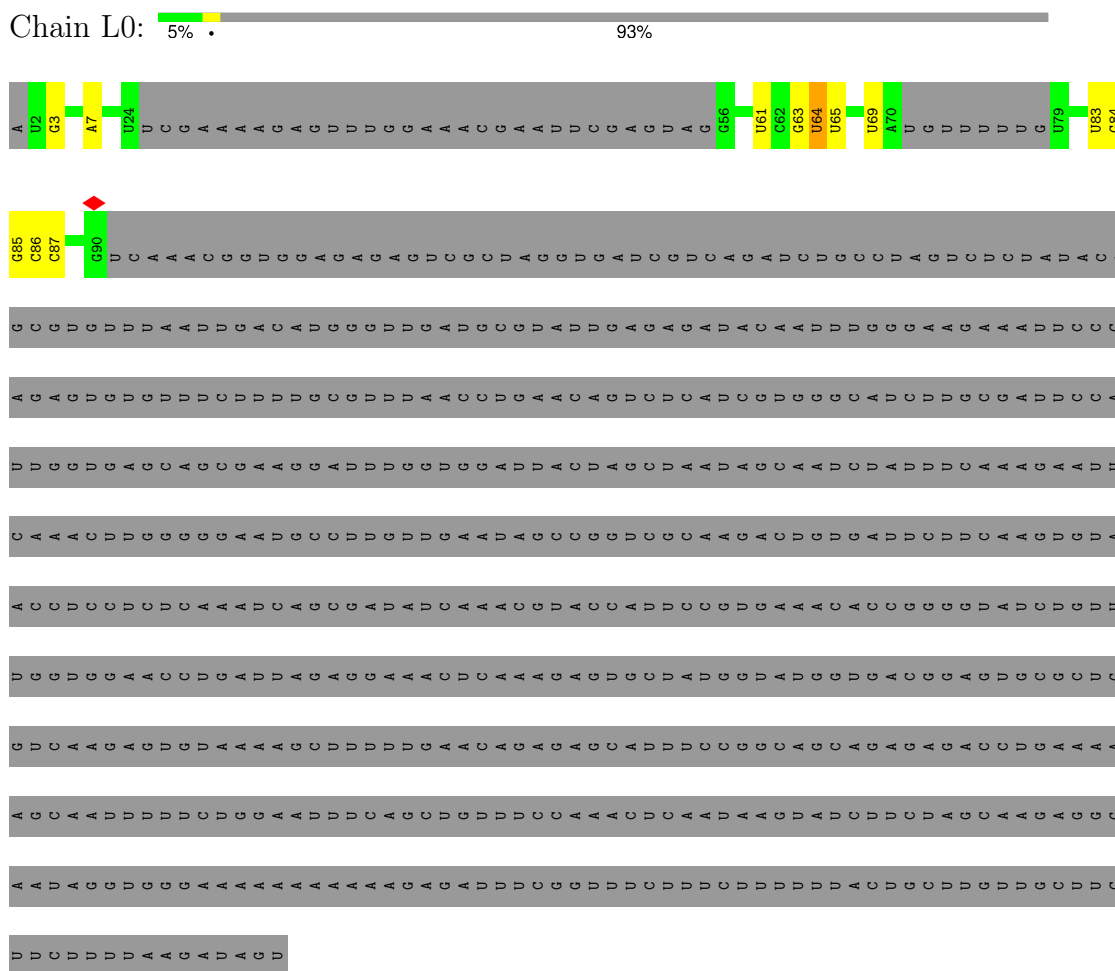
- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



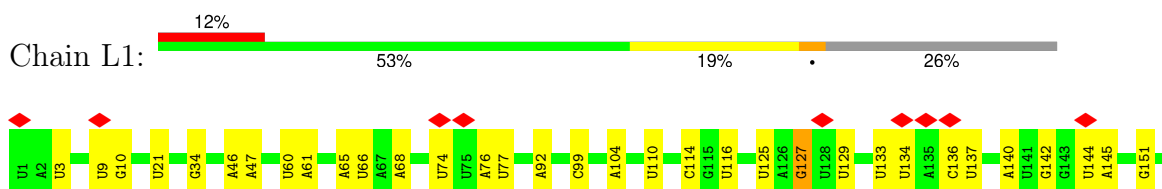
3 Residue-property plots

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.

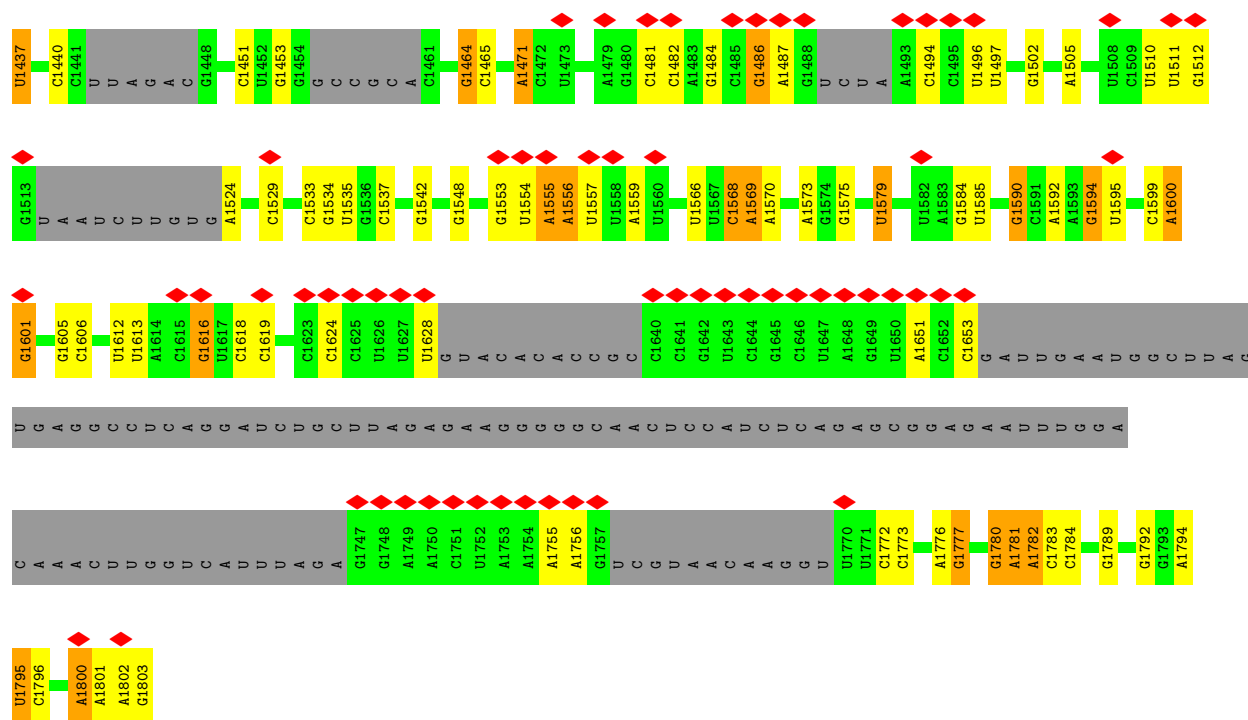
• Molecule 1: 5'ETS rRNA



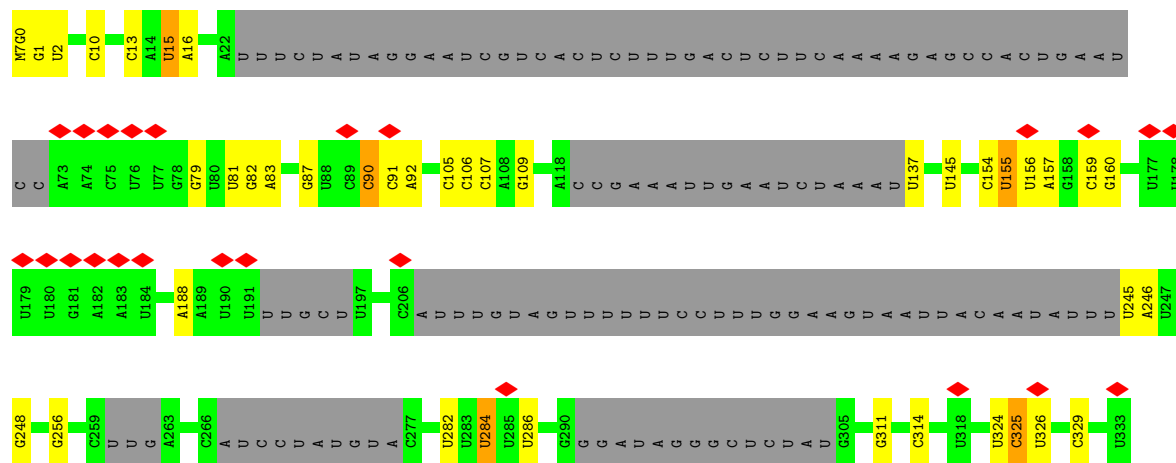
• Molecule 2: 18S rRNA



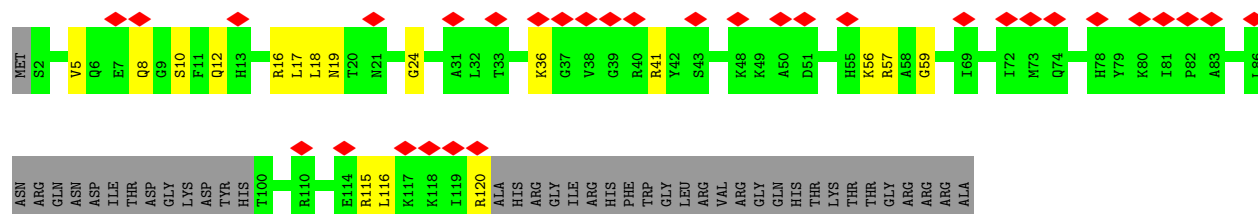




• Molecule 3: U3 snoRNA

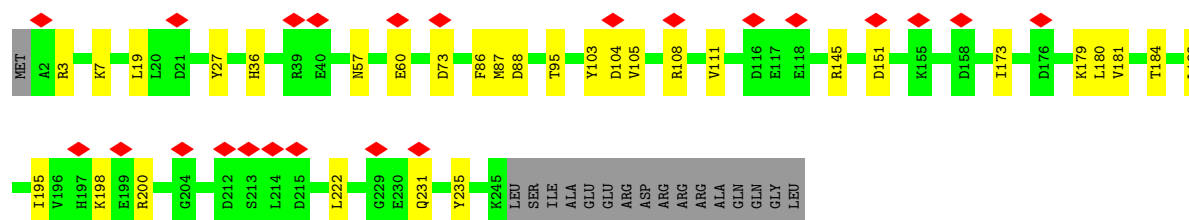


• Molecule 4: 40S ribosomal protein S18-A

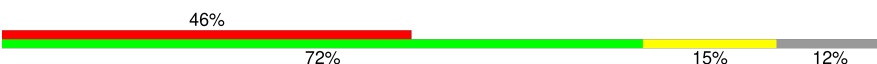


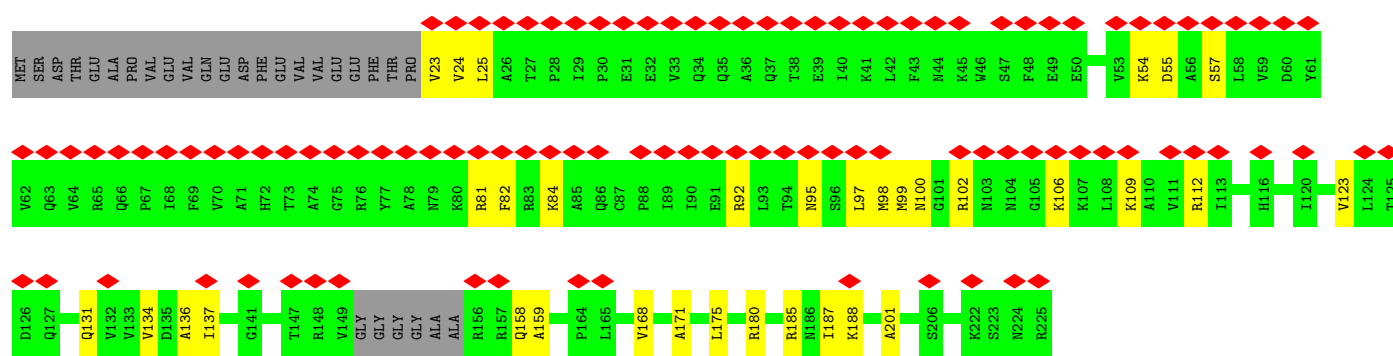
- Molecule 5: 40S ribosomal protein S4-A

Chain L4: 



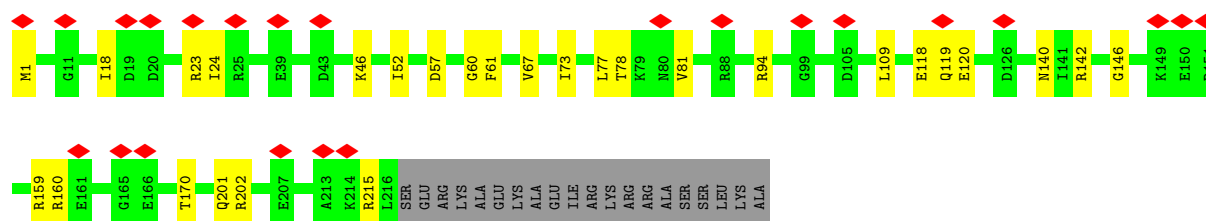
- Molecule 6: 40S ribosomal protein S5

Chain L5: 



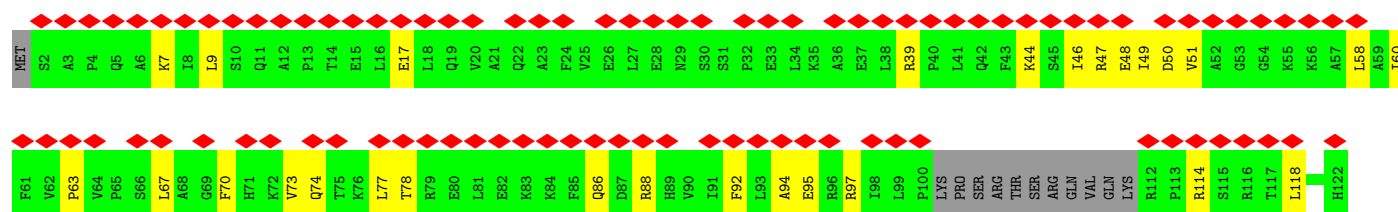
- Molecule 7: 40S ribosomal protein S6-A

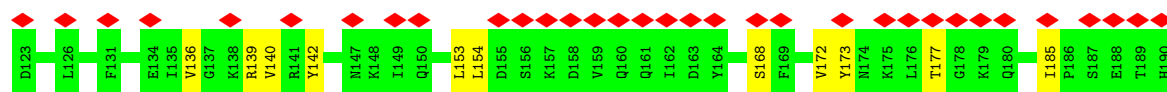
Chain L6: 



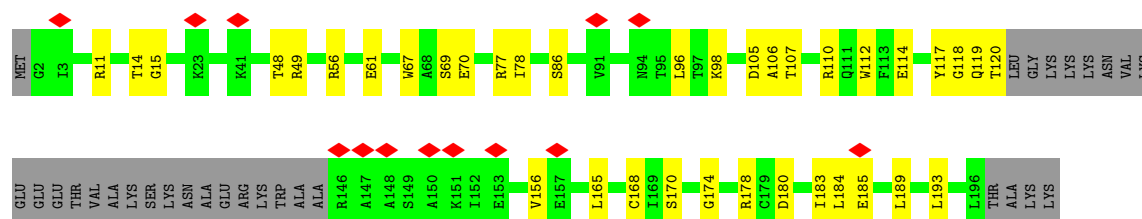
- Molecule 8: 40S ribosomal protein S7-A

Chain L7: 

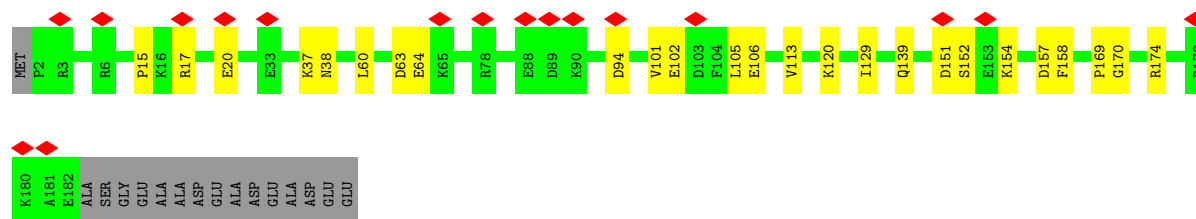
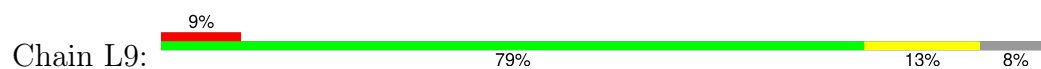




- Molecule 9: 40S ribosomal protein S8-A



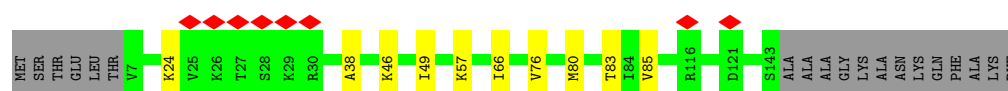
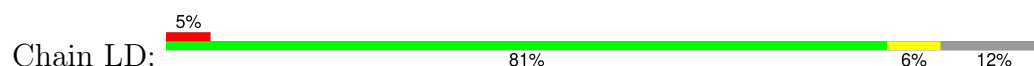
- Molecule 10: 40S ribosomal protein S9-A



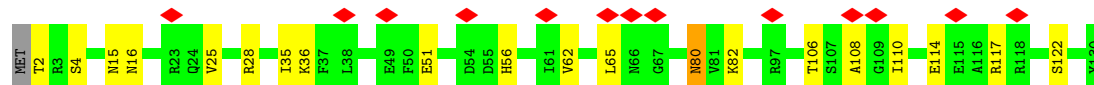
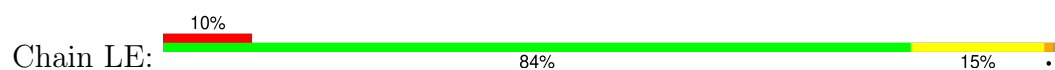
- Molecule 11: 40S ribosomal protein S16-A



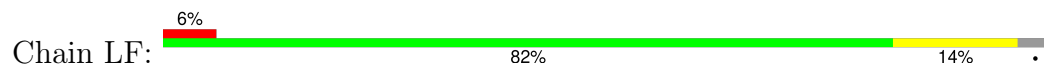
- Molecule 12: 40S ribosomal protein S11-A



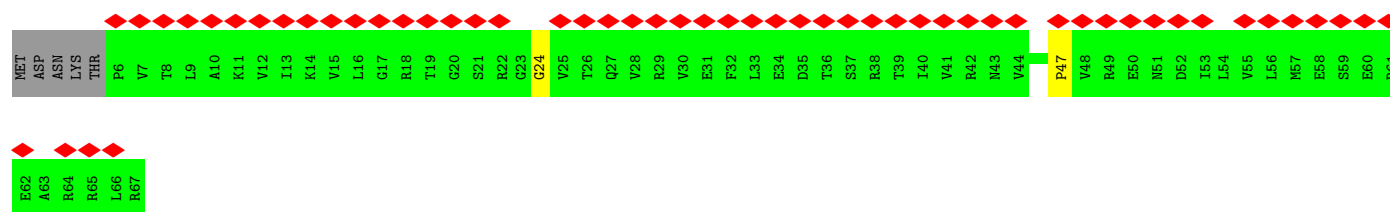
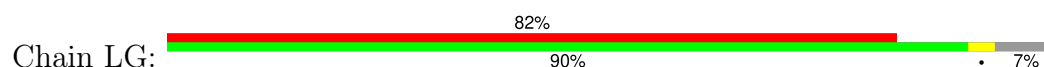
- Molecule 13: 40S ribosomal protein S22-A



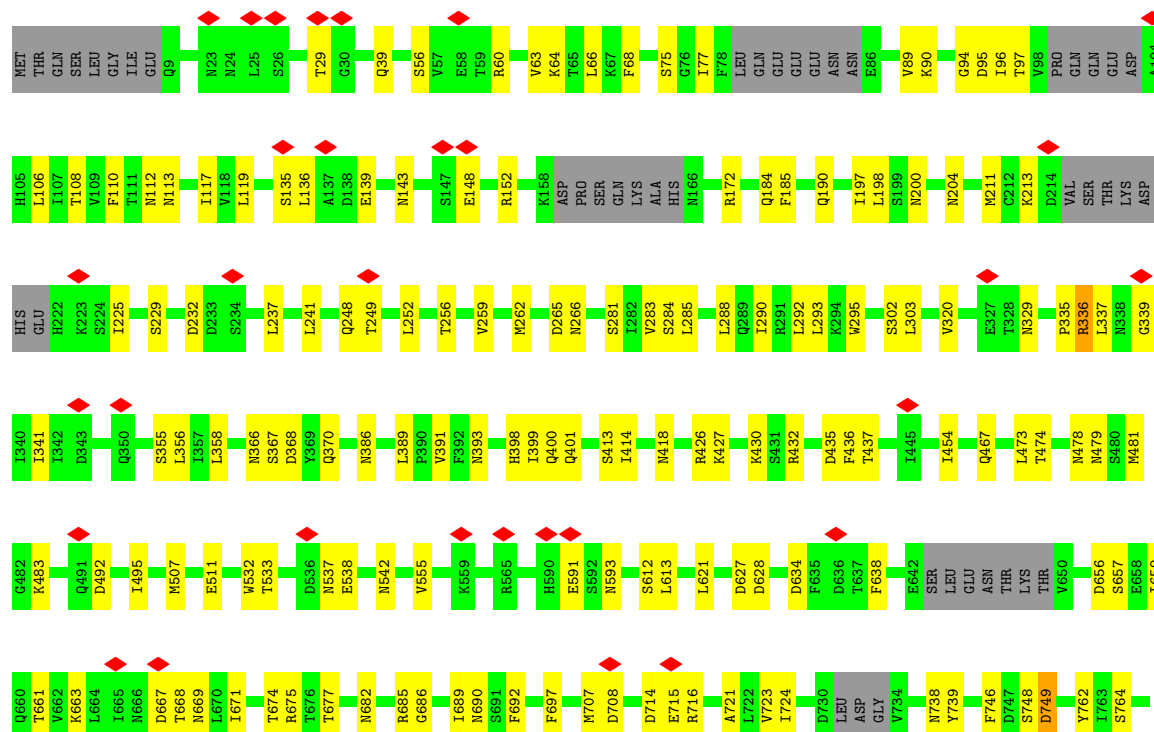
- Molecule 14: 40S ribosomal protein S24-A



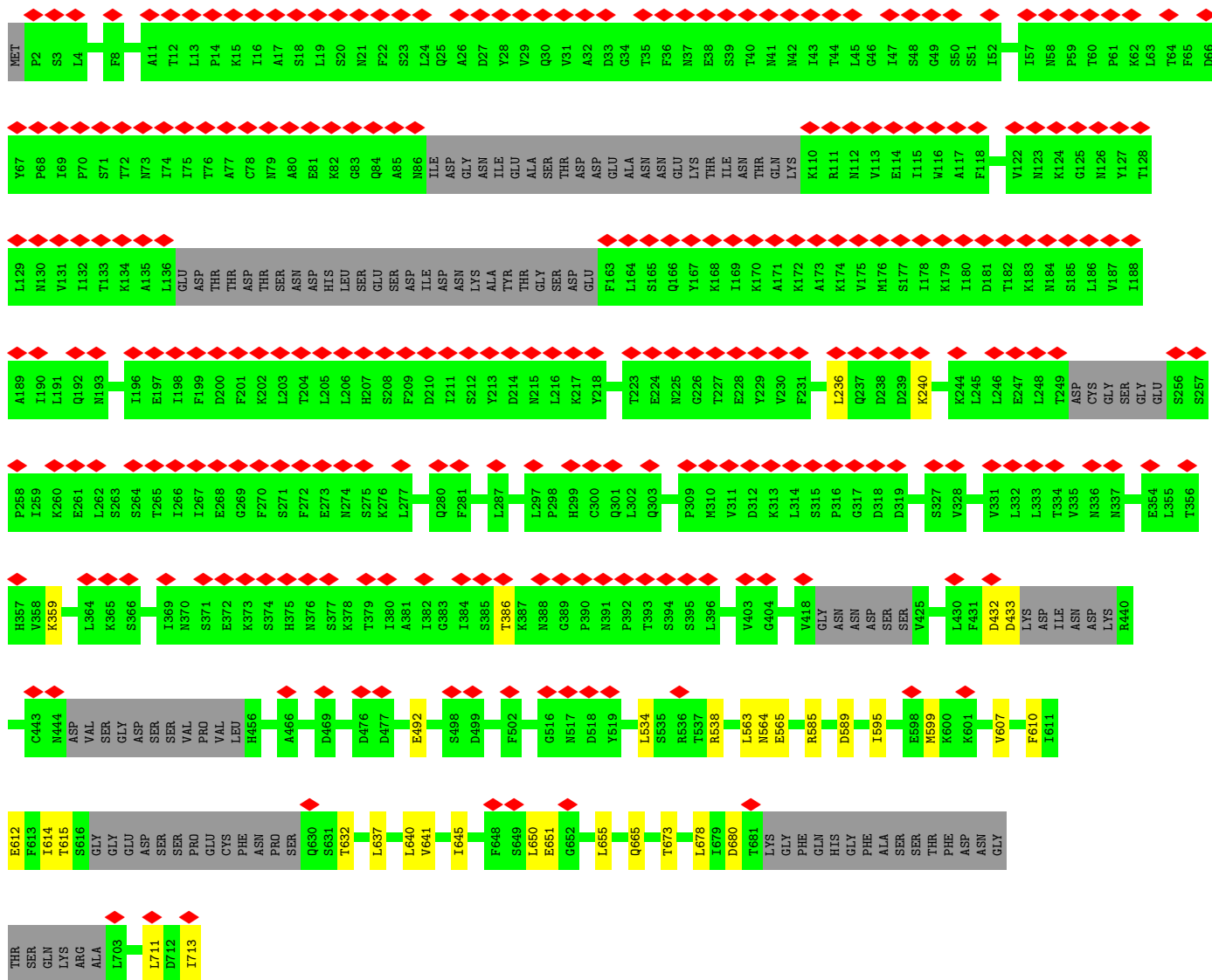
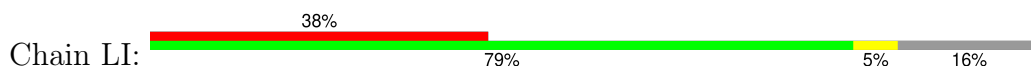
- Molecule 15: 40S ribosomal protein S28-A



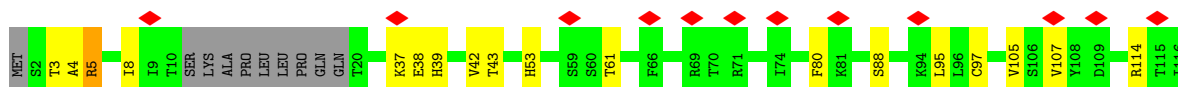
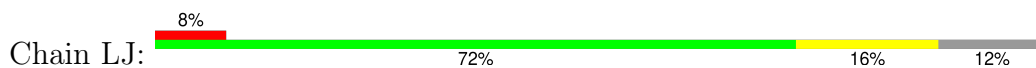
- Molecule 16: NET1-associated nuclear protein 1

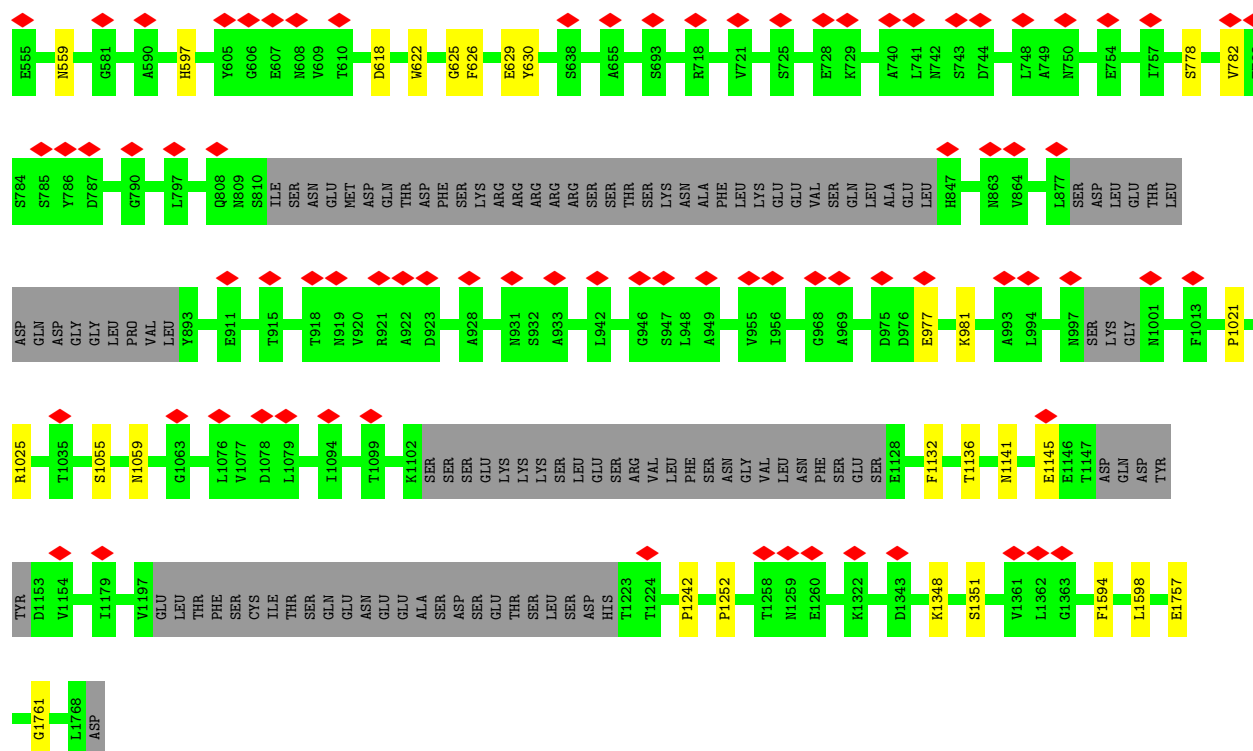


- Molecule 17: U3 small nucleolar RNA-associated protein 8



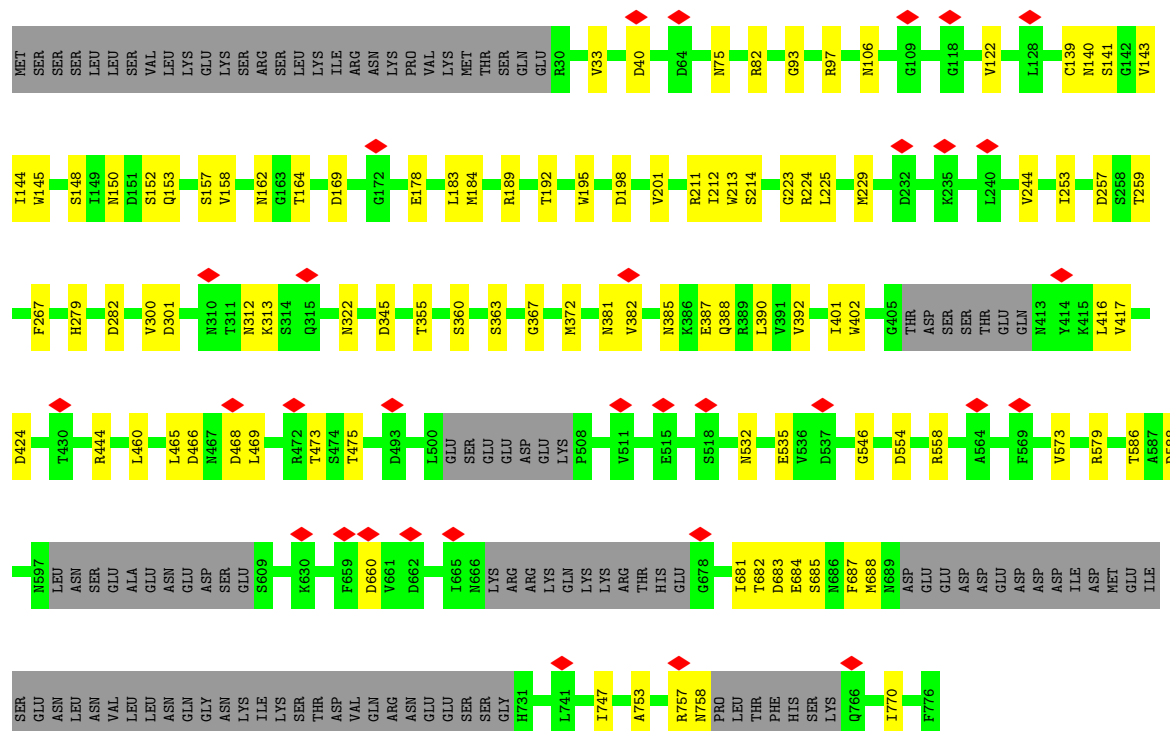
- Molecule 18: U3 small nucleolar RNA-associated protein 15



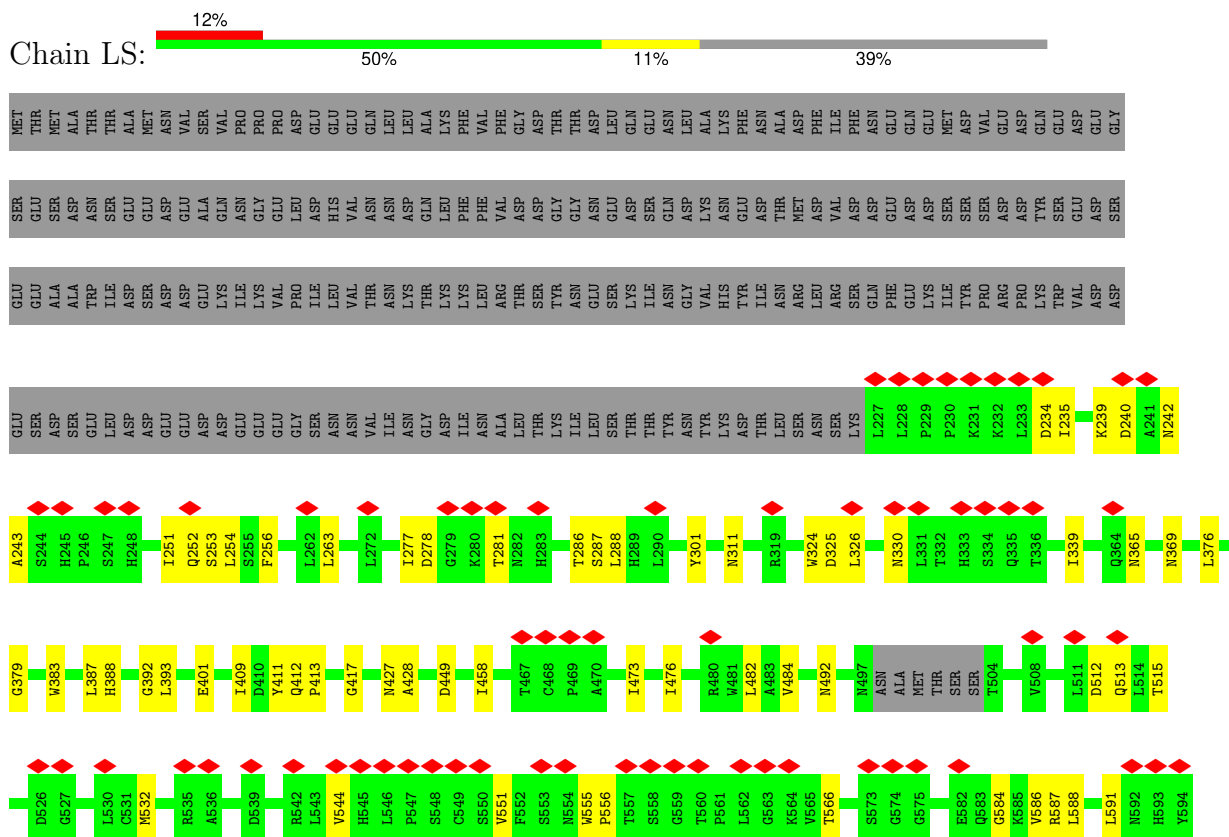


- Molecule 22: U3 small nucleolar RNA-associated protein 4

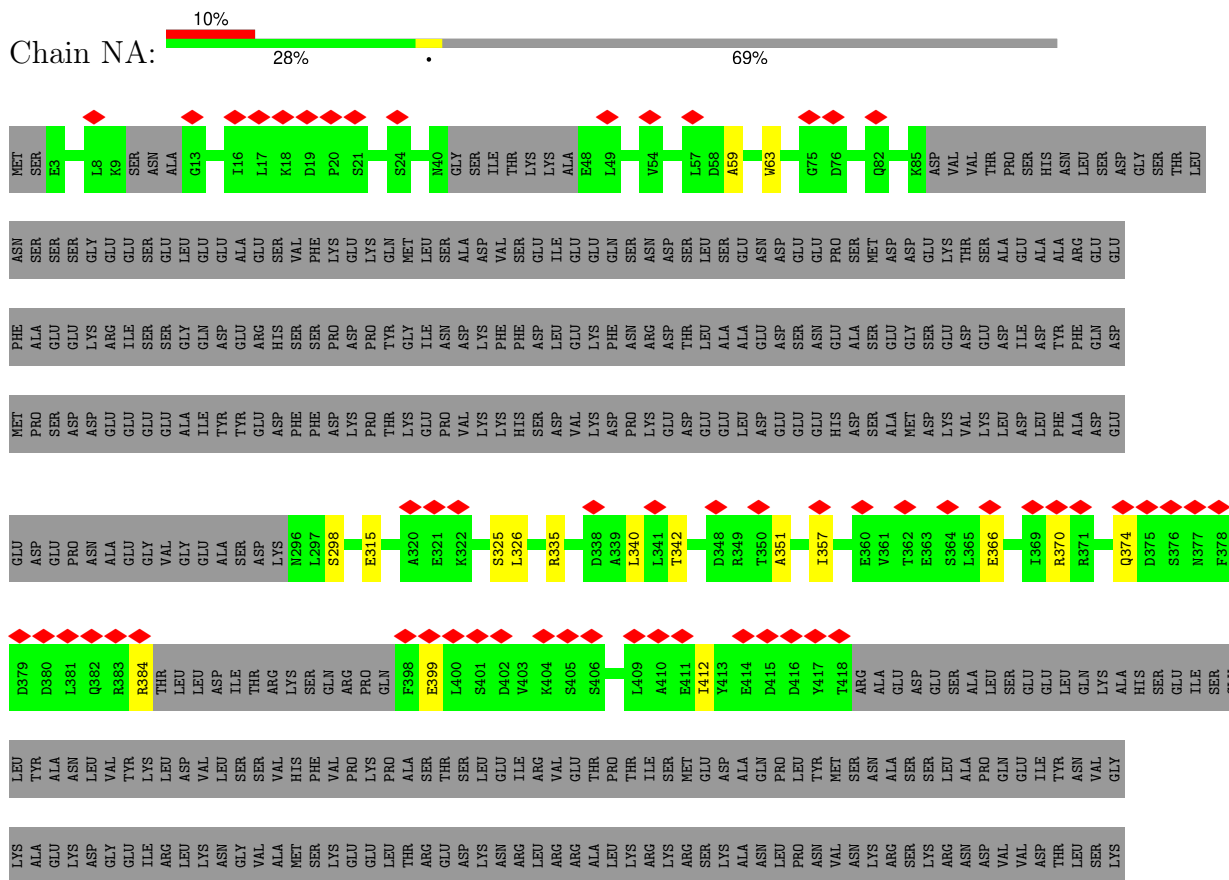
Chain LN: 73% 13% 15%



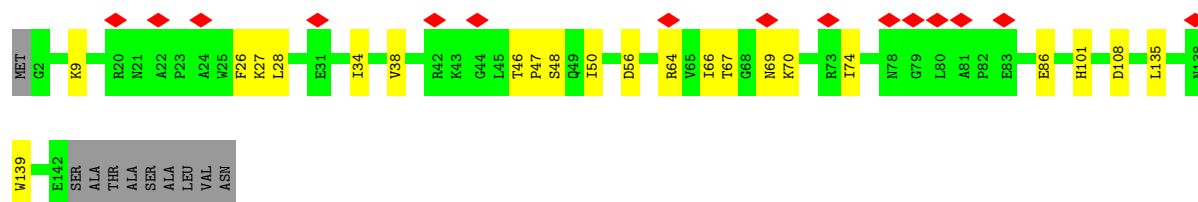
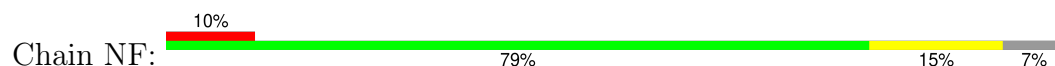
- Molecule 23: U3 small nucleolar RNA-associated protein 18



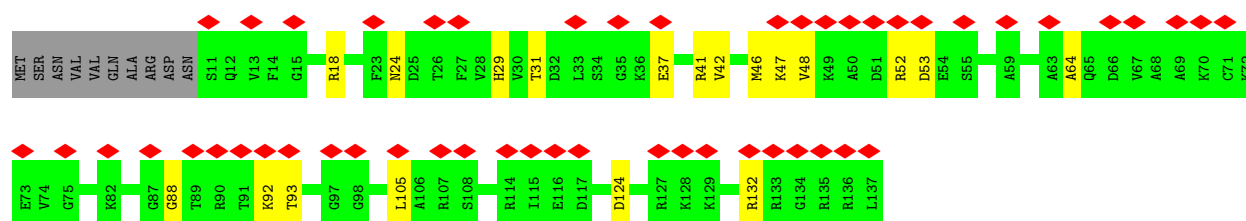
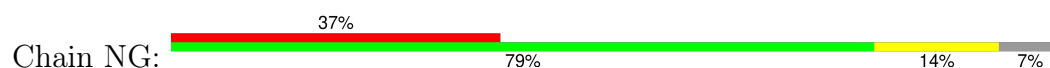
- Molecule 24: U3 small nucleolar RNA-associated protein MPP10



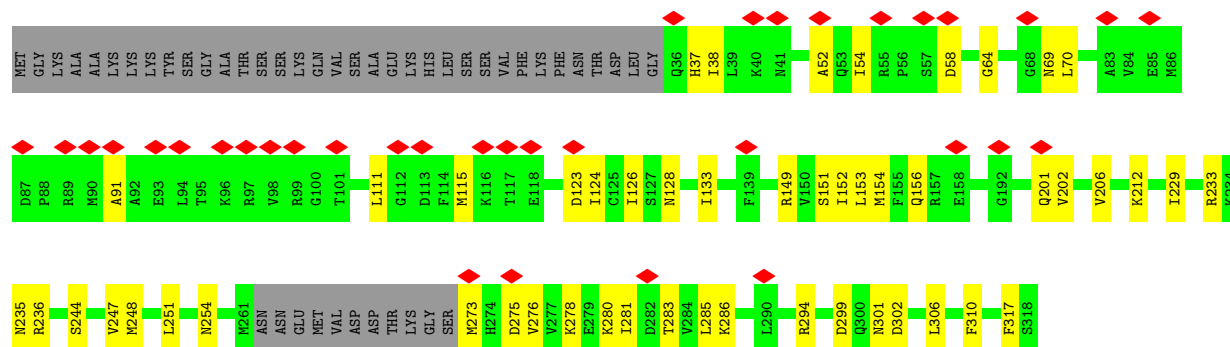
- Molecule 27: 40S ribosomal protein S13



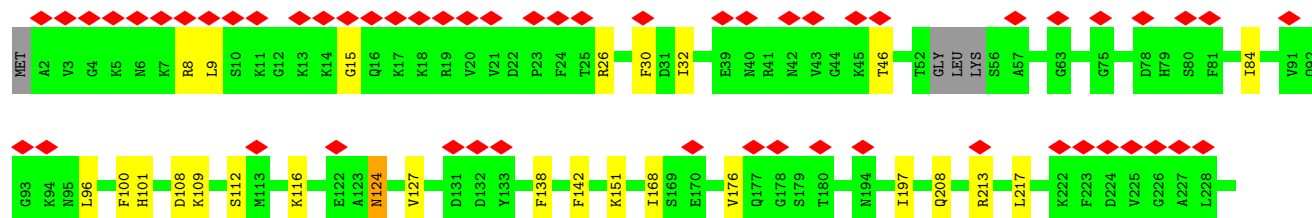
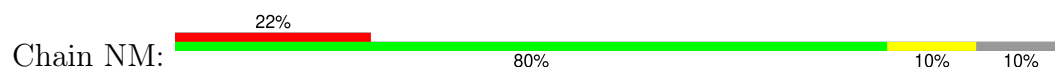
- Molecule 28: 40S ribosomal protein S14-A



- Molecule 29: Dimethyladenosine transferase



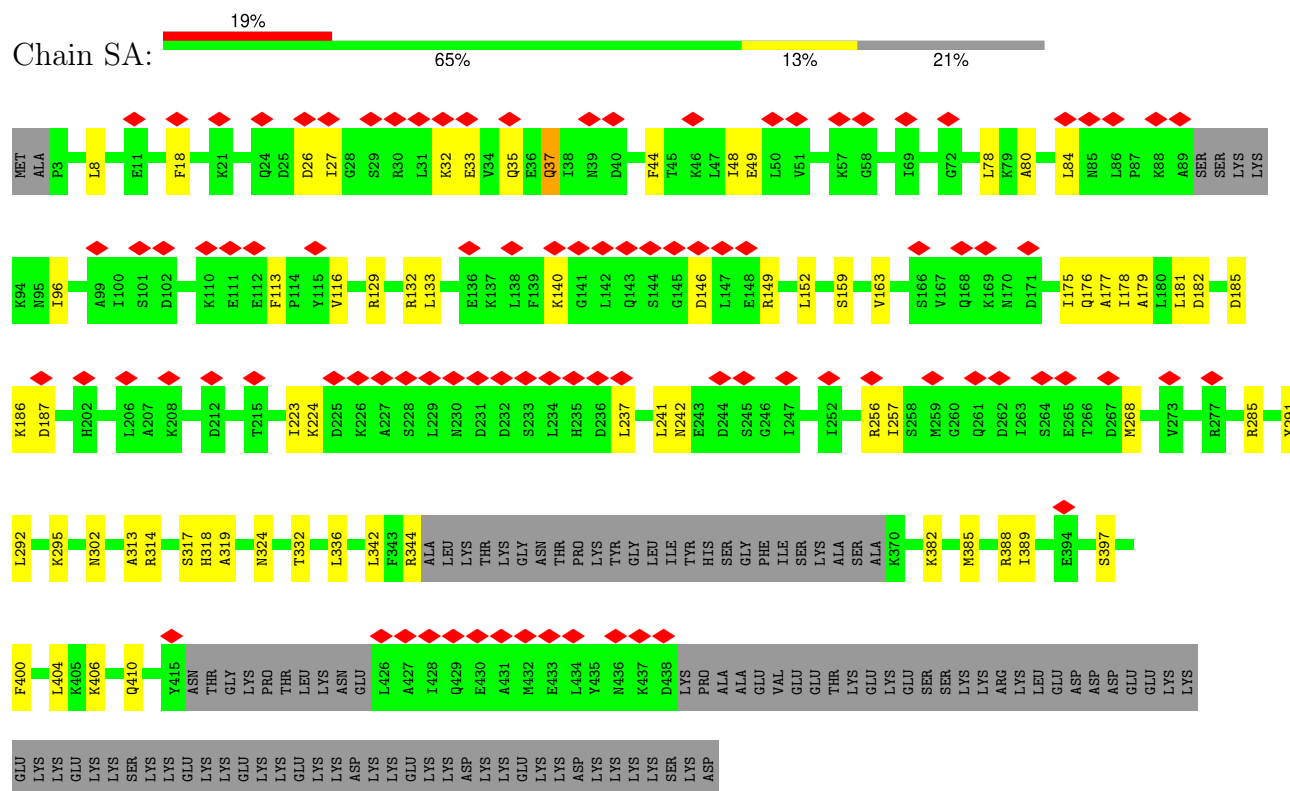
- Molecule 30: Small ribosomal subunit protein eS1A





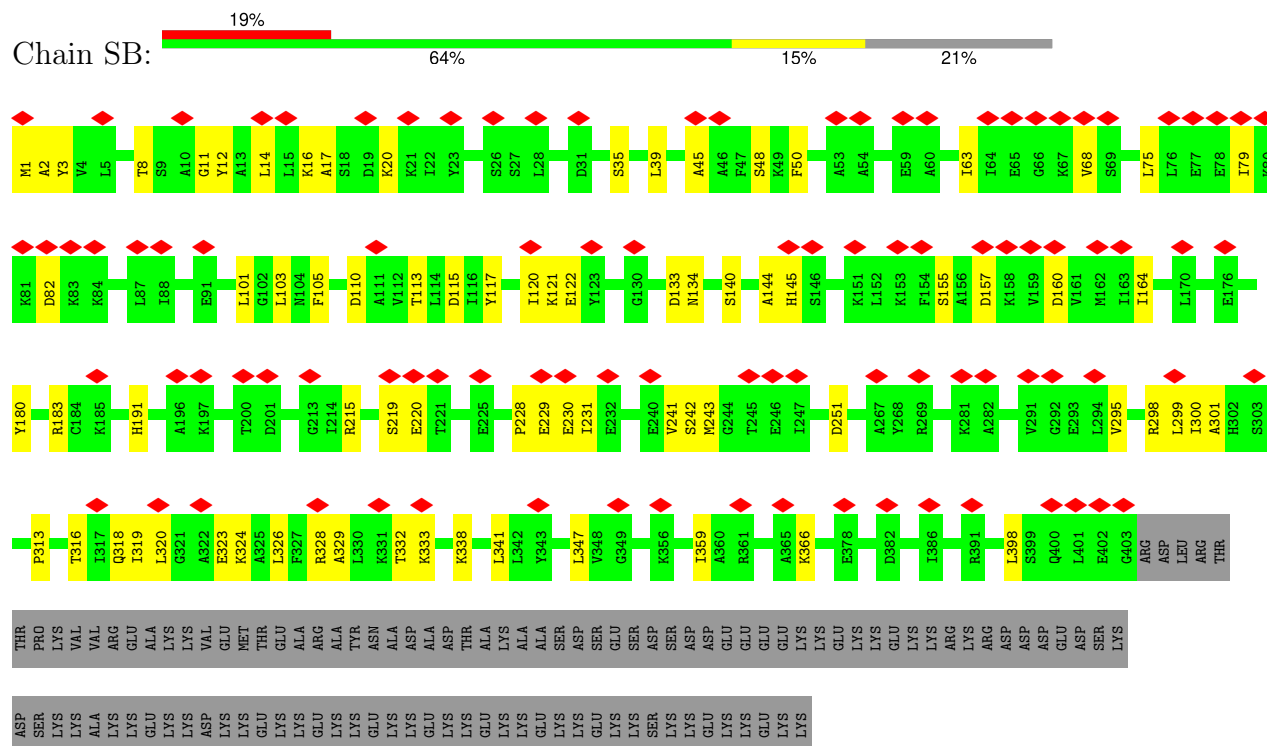
- Molecule 37: Nucleolar protein 56

Chain SA:

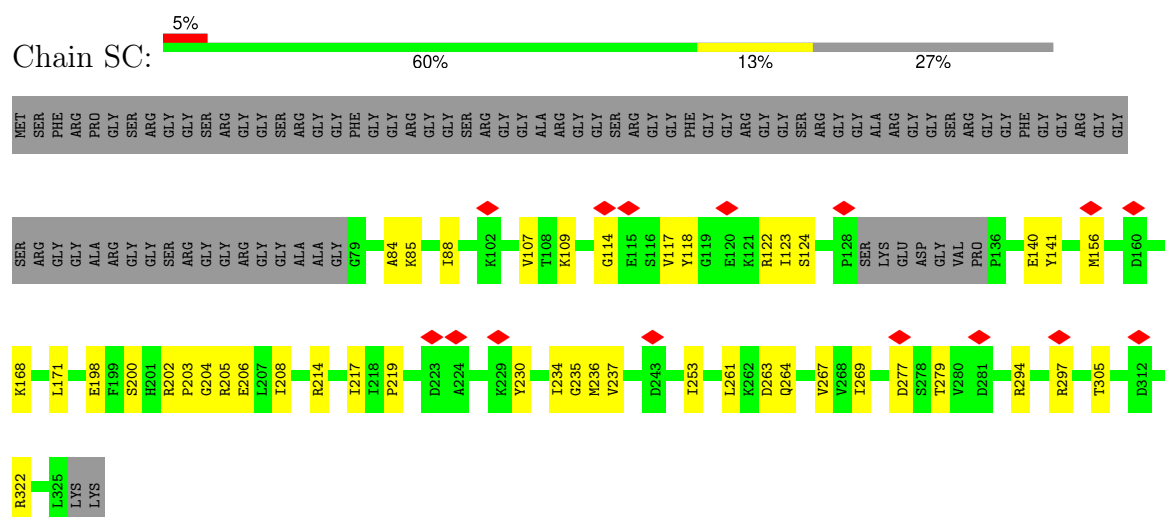


- Molecule 38: Nucleolar protein 58

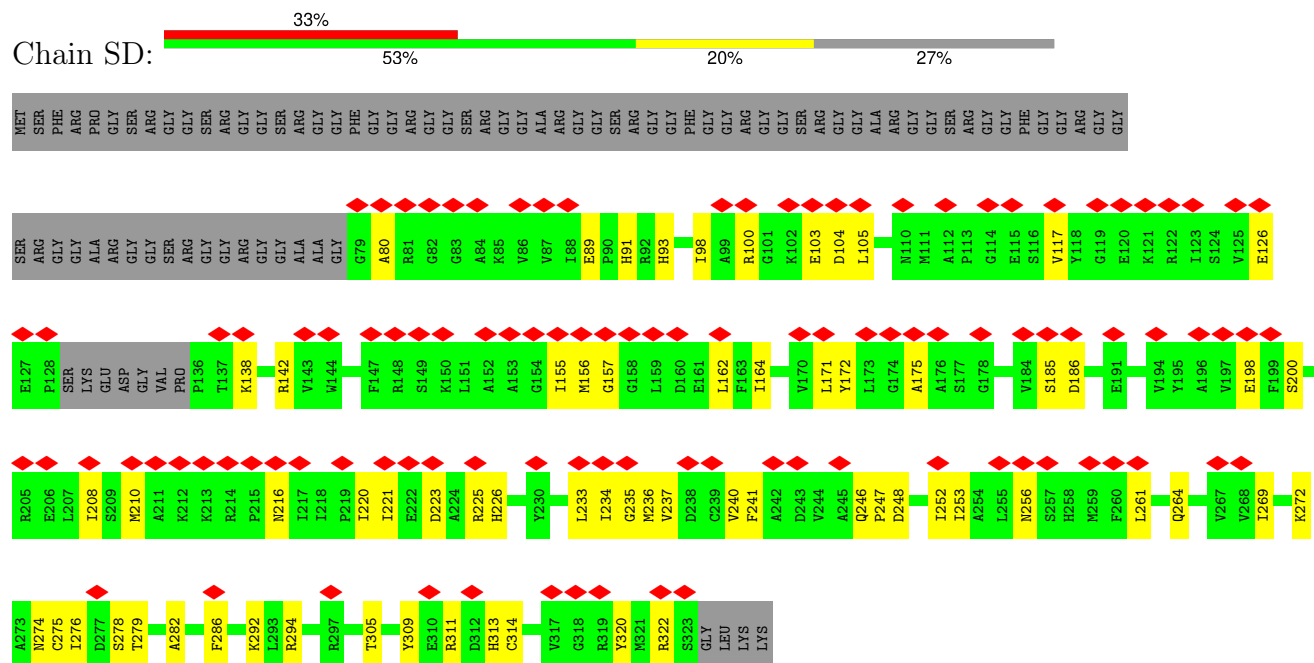
Chain SB:



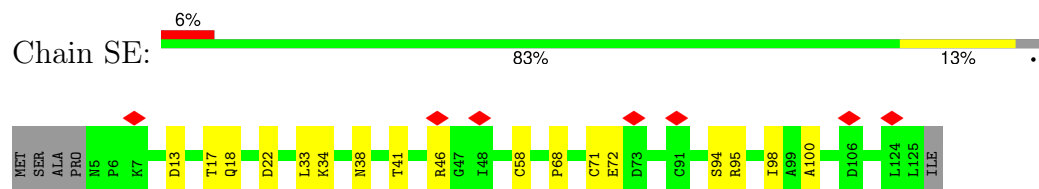
- Molecule 39: rRNA 2'-O-methyltransferase fibrillar



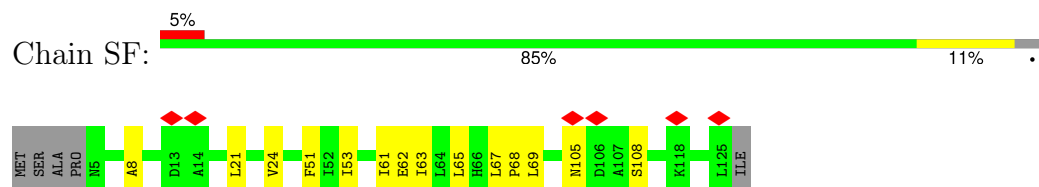
- Molecule 39: rRNA 2'-O-methyltransferase fibrillar



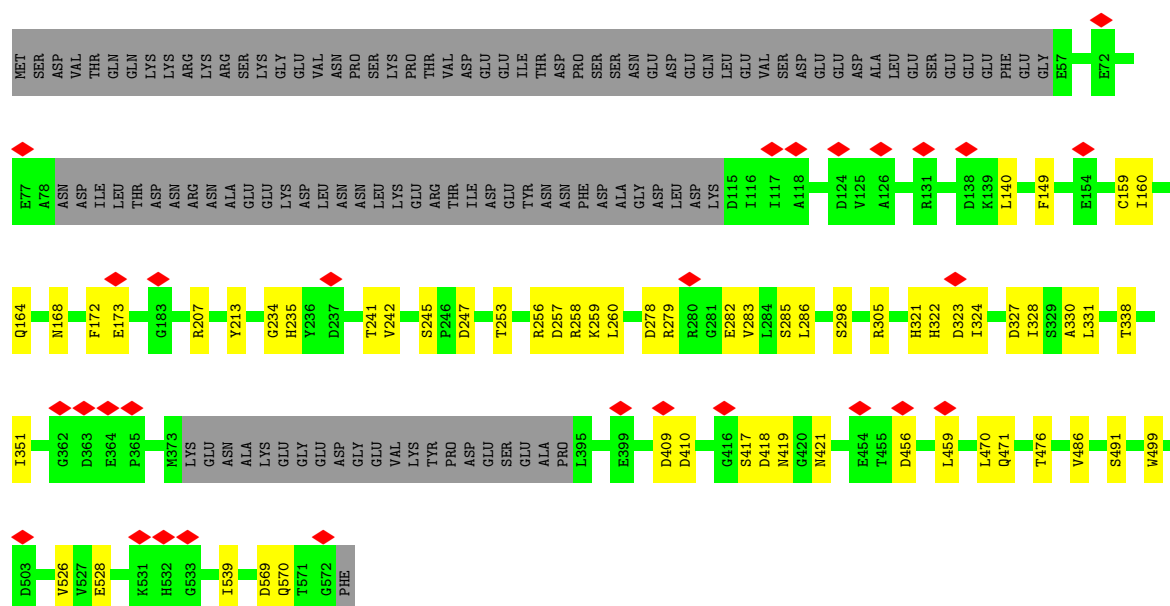
- Molecule 40: 13 kDa ribonucleoprotein-associated protein



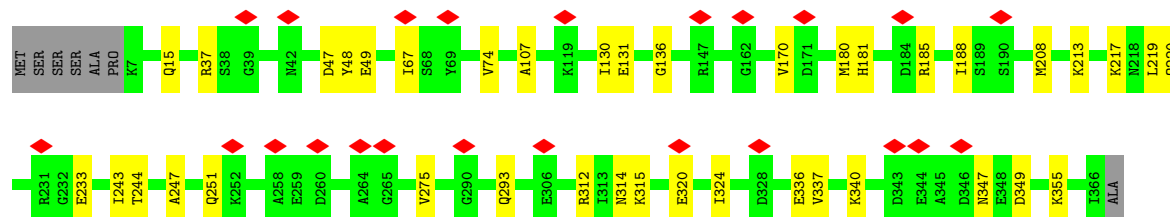
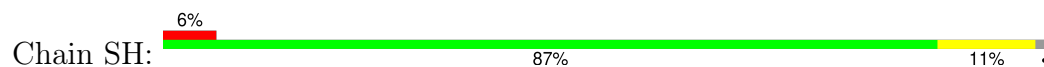
- Molecule 40: 13 kDa ribonucleoprotein-associated protein



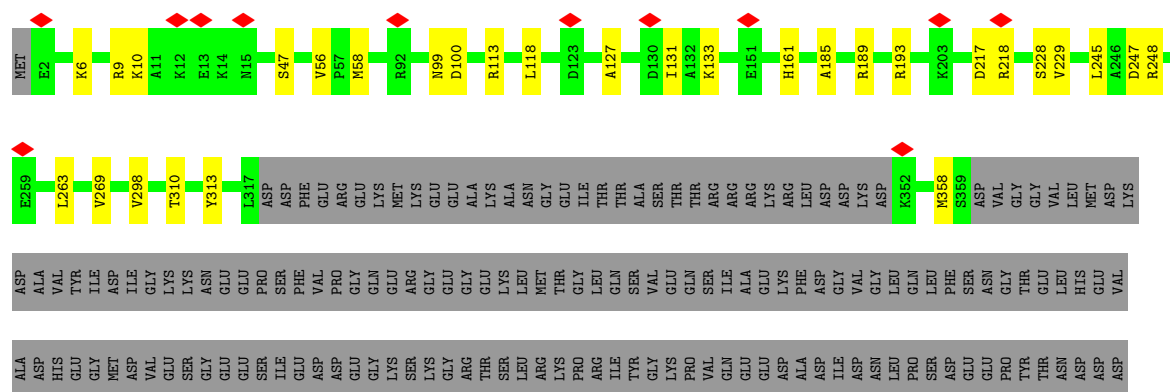
• Molecule 41: Ribosomal RNA-processing protein 9

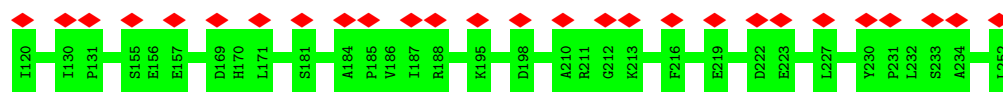


• Molecule 42: RNA 3'-terminal phosphate cyclase-like protein



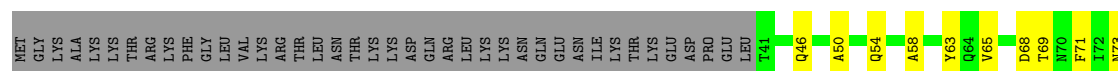
• Molecule 43: Ribosome biogenesis protein BMS1





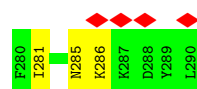
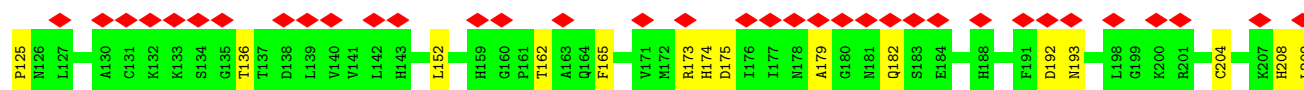
• Molecule 45: rRNA-processing protein FCF1

Chain SL: 59% 19% 22%



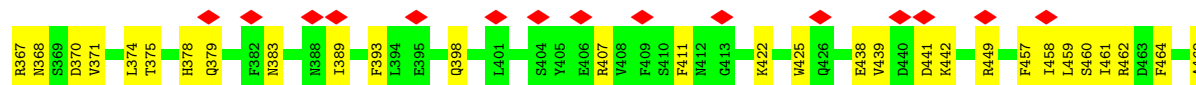
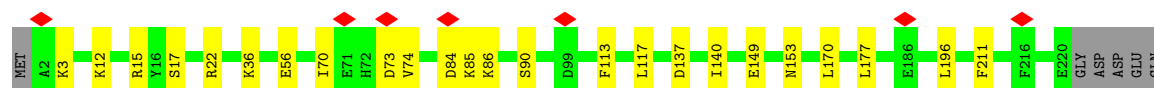
• Molecule 46: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 39% 61% 14% 24%

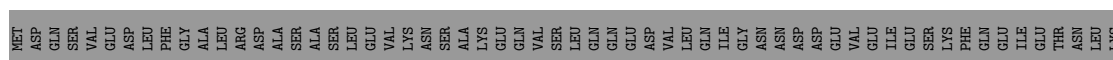


• Molecule 47: U3 small nucleolar RNA-associated protein 20

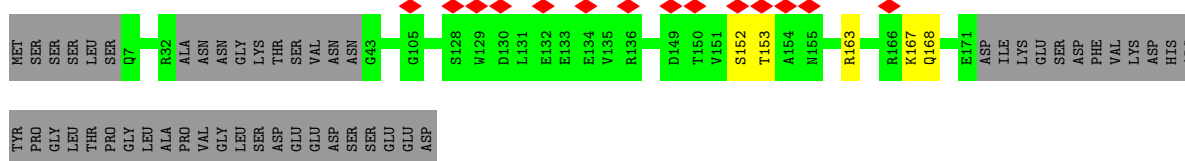
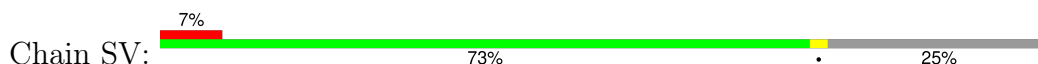
Chain SP: 31% 64% 10% 26%



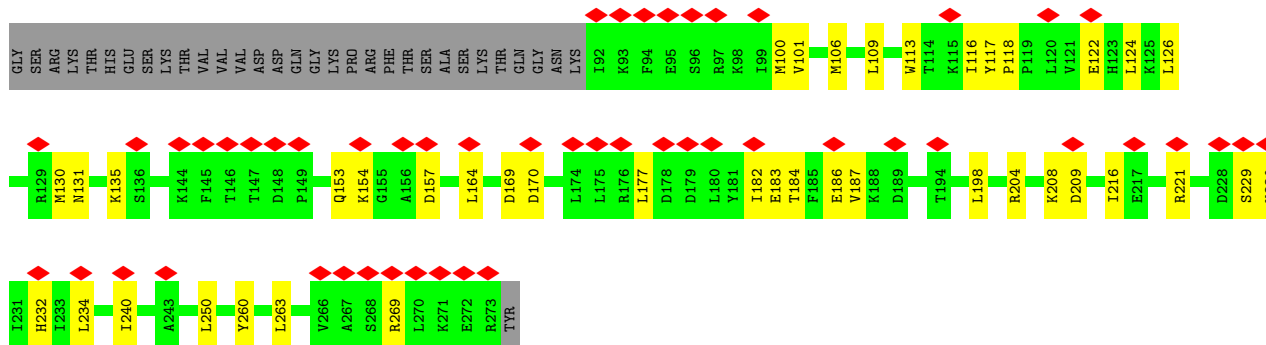
V1553	P1554	L1555	D1496	E1497	T1558	L1559	R1560	L1561	V1562	R1563	ASP	GLY	ALA	GLU	SER	LYS	LEU	T1571	L1572	S1573	K1574	F1575	P1576	S1577	N1578	L1579	D1580	E1581	P1582	S1583	N1584	K1584	A1585	L1586	K1587	Q1588	E1589	L1590	Y1591	L1594	S1595	K1596	I1597	L1598	G1599	T1600	R1601	D1602	D1603	E1604	T1605	L1606	I1606	I1607	E1608	R1609	E1614	A1615	L1616
V1493	F1494	S1495	D1436	D1437	E1498	R1499	Y1500	R1501	N1502	I1503	G1504	M1505	E1506	T1507	Q1508	I1509	A1510	I1511	G1512	G1513	L1514	A1515	Q1516	H1517	M1518	S1519	W1520	N1521	Q1522	Y1523	K1524	A1525	L1526	R1527	K1528	GLU	ASP	ASP	ALA	SER	N1535	N1536	L1537	K1549	R1556	L1561	E1569	S1570	L1571	M1575	D1593	R1597	Y1598	E1599	E1602				
D1433	F1434	E1435	D1436	M1437	A1438	I1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	E1447	A1448	D1449	F1450	F1451	T1452	M1453	V1454	N1455	H1456	I1457	Q1458	L1459	H1460	R1461	R1462	Q1463	R1464	A1465	I1466	K1467	L1468	L1469	G1470	E1471	H1472	A1473	H1474	Q1475	L1476	L1477	D1478	N1479	S1480	L1481	S1482	H1483	Y1484	L1485	I1486	P1487	N1488	T1489	E1490	H1491	Y1492
K1373	F1374	I1375	D1376	F1377	I1378	N1379	E1380	K1381	P1382	N1383	L1384	N1385	E1386	A1387	S1388	K1389	S1390	I1391	G1392	M1393	L1394	K1395	D1396	I1397	L1398	L1399	P1400	M1401	L1402	R1403	L1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	H1413	Q1414	S1415	E1416	Y1417	V1418	S1419	V1420	L1421	S1422	Y1423	M1424	V1425	K1426	N1427	T1428	K1429	Y1430	F1431	T1432
S1310	Y1311	S1312	SER	SER	ARG	MET	H1317	E1318	Y1319	D1320	F1321	P1322	R1323	L1324	L1325	S1326	G1330	L1331	I1332	E1333	D1334	G1335	L1336	K1337	S1338	Y1339	P1340	E1341	L1342	E1343	W1344	L1345	P1346	L1347	L1348	F1349	T1350	F1351	L1352	H1353	F1354	I1355	N1356	L1357	K1358	E1359	E1360	L1361	A1362	L1363	S1364	T1365	S1366	H1369	A1370	L1371	M1372		
I1250	V1251	F1252	N1253	Y1254	N1255	C1256	S1257	I1258	S1259	D1260	I1261	E1262	E1263	L1264	Y1265	T1266	I1267	N1268	S1269	S1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	N1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	I1289	E1290	L1291	G1292	R1293	K1294	V1295	P1296	E1297	L1298	E1299	S1300	I1301	S1302	K1303	L1304	V1305	A1306	D1307	N1309	
L1185	Y1186	V1187	K1188	L1189	S1190	D1191	S1192	N1193	S1194	I1195	F1198	L1201	L1202	V1203	S1204	G1209	F1210	I1211	Q1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	L1220	I1221	S1222	L1223	L1224	I1225	S1226	I1227	L1228	K1229	GLY	L1230	L1231	L1232	L1233	L1234	L1235	L1236	L1237	L1238	L1239	L1240	Q1241	K1242	L1243	L1244	K1245	L1246	L1247	K1248	L1249		
Y1119	Q1120	F1121	L1122	D1125	E1126	F1127	A1130	T1131	A1132	L1133	M1134	D1135	T1136	I1137	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	G1148	I1151	E1152	A1153	A1154	D1155	S1156	I1157	L1158	R1159	N1160	P1161	V1162	M1163	D1164	D1165	H1166	Y1167	V1168	D1169	L1170	I1174	C1175	T1176	S1177	L1178	L1179	K1180	L1181	L1182	P1183	S1184					
M997	R1012	L1017	N1020	S1021	L1037	D1038	T1039	E1040	S1041	T1042	E1043	E1044	R1048	K1049	M1050	F1066	E1067	F1068	T1072	F1073	D1074	W1075	S1076	T1077	S1078	M1079	E1080	D1081	V1087	K1088	F1089	R1090	I1091	S1092	H1093	F1094	S1095	D1096	E1097	N1098	L1099	Q1100	Q1101	R1107	L1108	F1109	A1113	L1118											
Q866	K867	L868	L881	N882	L891	D894	F897	I901	T902	T903	F904	L905	Q911	A915	E916	M922	Y924	R943	S951	F956	K957	K958	F964	A968	S969	E970	R971	L972	D973	Y974	Y976	N980	N985	S986	S987	K988	A989	K992	R995	R996																			
R735	K749	Y750	N754	R764	I772	L773	M782	L783	Q787	Y788	A789	D795	K805	T806	Y807	L808	Y809	M810	T811	A812	R817	V818	I819	E825	V826	D827	R828	F831	K833	T834	L835	K839	N840	I841	E849	S886	S887	K888	A889	D864	V865																		
L603	L607	L610	Q611	V615	L618	L619	I625	L632	A635	R636	I640	R641	I642	K643	G646	A647	E648	G668	T671	D683	A694	F703	I704	K705	L706	F707	D708	E709	N710	Q711	N712	L713	D714	Q717	P718	L719	L720	E721	D722	G723	A724	N725	K726																
E469	N471	F486	K487	Y488	S489	K490	L491	Q492	N493	E495	L496	L497	L501	A509	K516	D517	L522	L523	K524	Y525	R526	H527	K528	GLU	ASP	ASP	ALA	SER	N535	N536	L537	K549	R556	L561	E569	S570	L571	M575	D593	R597	Y598	E599	E602																



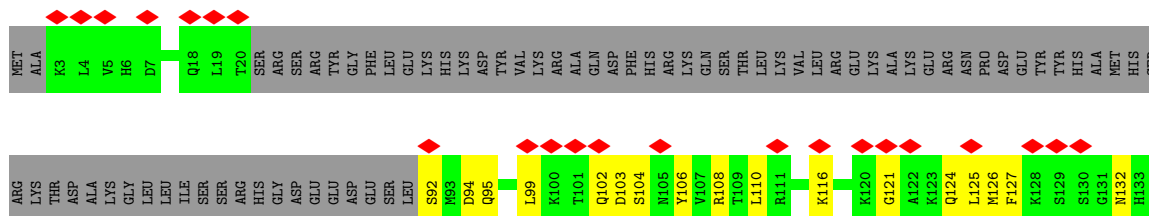
- Molecule 53: Regulator of rDNA transcription protein 14

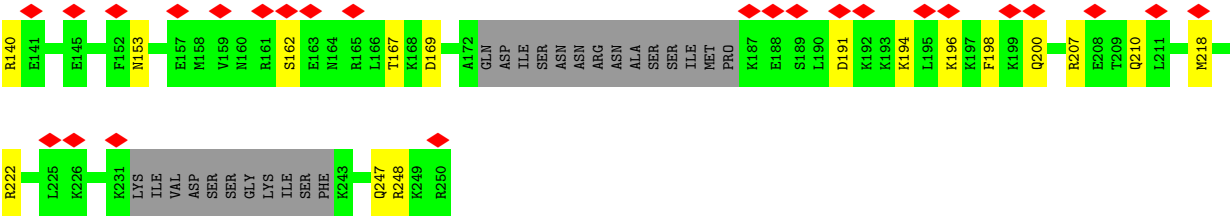


- Molecule 54: Pre-rRNA-processing protein PNO1

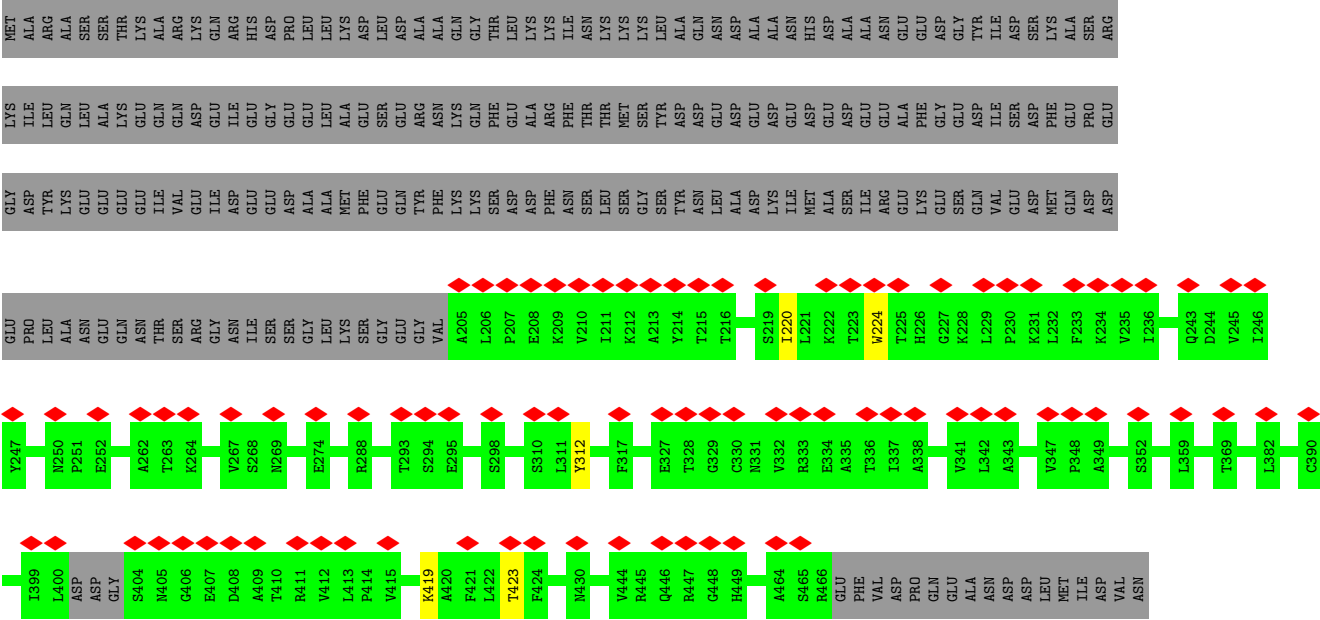


- Molecule 55: U3 small nucleolar RNA-associated protein 11





• Molecule 56: Essential nuclear protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10725	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 ($e^-/\text{\AA}^2$)	61.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.637	Depositor
Minimum map value	0.000	Depositor
Average map value	0.089	Depositor
Map value standard deviation	0.157	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	535.75195, 535.75195, 535.75195	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.063, 1.063, 1.063	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: M7G, MG, ZN, GTP

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	L0	0.11	0/1192	0.23	0/1851
2	L1	0.13	0/32012	0.27	0/49844
3	L2	0.12	0/4613	0.25	0/7165
4	L3	0.15	0/872	0.37	0/1173
5	L4	0.17	0/1977	0.36	0/2664
6	L5	0.18	0/1575	0.35	0/2127
7	L6	0.16	0/1764	0.35	0/2359
8	L7	0.17	0/1451	0.44	0/1956
9	L8	0.19	0/1371	0.41	0/1833
10	L9	0.18	0/1495	0.45	1/2003 (0.0%)
11	LC	0.18	0/647	0.43	0/903
12	LD	0.15	0/1138	0.33	0/1533
13	LE	0.18	0/1039	0.38	0/1395
14	LF	0.16	0/1060	0.37	0/1412
15	LG	0.17	0/310	0.37	0/430
16	LH	0.17	0/6063	0.41	2/8217 (0.0%)
17	LI	0.15	0/3835	0.37	0/5263
18	LJ	0.15	0/3654	0.35	0/4959
19	LK	0.14	0/1085	0.32	0/1463
20	LL	0.14	0/1307	0.35	0/1770
21	LM	0.13	0/6036	0.34	2/8445 (0.0%)
22	LN	0.15	0/5359	0.33	0/7255
23	LS	0.16	0/2895	0.34	0/3930
24	NA	0.17	0/1276	0.42	0/1725
25	NB	0.13	0/1477	0.31	0/2006
26	ND	0.18	0/568	0.44	0/755
27	NF	0.15	0/1158	0.33	0/1559
28	NG	0.13	0/952	0.32	0/1279
29	NL	0.16	0/2222	0.38	0/3003
30	NM	0.12	0/1853	0.31	0/2484
31	NP	0.13	0/669	0.34	0/928
32	NQ	0.14	0/605	0.37	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	NS	0.16	0/885	0.35	0/1162
34	NV	0.13	0/126	0.31	0/160
35	OH	0.09	0/595	0.28	0/827
36	OU	0.11	0/278	0.32	0/386
37	SA	0.15	0/3146	0.33	0/4240
38	SB	0.16	0/3136	0.36	0/4226
39	SC	0.18	0/1903	0.38	0/2567
39	SD	0.18	0/1885	0.40	0/2543
40	SE	0.21	0/928	0.45	0/1262
40	SF	0.17	0/928	0.36	0/1262
41	SG	0.14	0/3744	0.31	0/5040
42	SH	0.14	0/2832	0.33	0/3825
43	SI	0.16	0/6321	0.34	0/8504
44	SJ	0.40	1/1080 (0.1%)	0.60	3/1508 (0.2%)
44	SK	0.15	0/1170	0.37	0/1639
45	SL	0.17	0/1193	0.37	0/1611
46	SM	0.16	0/1792	0.36	0/2425
47	SP	0.16	0/15404	0.35	2/20833 (0.0%)
48	SQ	0.19	0/853	0.45	0/1139
49	SR	0.18	0/1069	0.40	0/1427
50	SS	0.15	0/1002	0.37	0/1318
51	ST	0.14	0/3361	0.35	0/4615
52	SU	0.22	1/2726 (0.0%)	0.41	3/3825 (0.1%)
53	SV	0.13	0/854	0.34	0/1175
54	SW	0.14	0/1470	0.33	0/1980
55	SY	0.20	0/1297	0.42	0/1708
56	SZ	0.14	0/1326	0.33	0/1859
All	All	0.15	2/154834 (0.0%)	0.34	13/217572 (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
16	LH	0	1
18	LJ	0	1
46	SM	0	1
47	SP	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	SJ	231	PRO	CG-CD	-11.54	1.11	1.50
52	SU	487	PRO	CG-CD	-8.30	1.22	1.50

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	SJ	231	PRO	N-CD-CG	-14.52	81.43	103.20
47	SP	1346	PRO	CA-N-CD	-10.88	96.76	112.00
52	SU	487	PRO	N-CD-CG	-10.82	86.98	103.20
44	SJ	231	PRO	CA-CB-CG	-8.35	88.63	104.50
44	SJ	231	PRO	CA-N-CD	-8.18	100.54	112.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	LH	336	ARG	Sidechain
18	LJ	5	ARG	Sidechain
46	SM	99	ARG	Sidechain
47	SP	1403	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L0	1068	0	539	7	0
2	L1	28628	0	14422	167	0
3	L2	4165	0	2110	26	0
4	L3	862	0	900	16	0
5	L4	1936	0	2019	26	0
6	L5	1558	0	1629	27	0
7	L6	1740	0	1835	20	0
8	L7	1427	0	1499	29	0
9	L8	1348	0	1366	33	0
10	L9	1470	0	1554	16	0
11	LC	642	0	328	1	0
12	LD	1112	0	1179	6	0
13	LE	1022	0	1060	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	LF	1046	0	1114	15	0
15	LG	309	0	145	2	0
16	LH	5941	0	5912	110	0
17	LI	3792	0	2859	29	0
18	LJ	3579	0	3580	65	0
19	LK	1068	0	1120	14	0
20	LL	1291	0	1315	28	0
21	LM	6011	0	2758	13	0
22	LN	5263	0	5270	68	0
23	LS	2829	0	2833	41	0
24	NA	1269	0	1055	18	0
25	NB	1470	0	1107	6	0
26	ND	564	0	587	14	0
27	NF	1135	0	1197	16	0
28	NG	941	0	979	16	0
29	NL	2180	0	2257	40	0
30	NM	1828	0	1926	20	0
31	NP	666	0	345	3	0
32	NQ	595	0	611	13	0
33	NS	879	0	940	12	0
34	NV	126	0	146	1	0
35	OH	594	0	298	1	0
36	OU	278	0	135	1	0
37	SA	3100	0	3084	55	0
38	SB	3099	0	3205	59	0
39	SC	1865	0	1908	39	0
39	SD	1850	0	1889	56	0
40	SE	916	0	964	12	0
40	SF	916	0	964	9	0
41	SG	3672	0	3690	37	0
42	SH	2781	0	2878	30	0
43	SI	6187	0	6364	86	0
44	SJ	1074	0	514	1	0
44	SK	1160	0	570	1	0
45	SL	1171	0	1229	28	0
46	SM	1756	0	1765	35	0
47	SP	15102	0	15321	177	0
48	SQ	836	0	840	16	0
49	SR	1052	0	1120	17	0
50	SS	992	0	1033	19	0
51	ST	3341	0	2155	22	0
52	SU	2703	0	1302	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	SV	852	0	476	4	0
54	SW	1444	0	1526	31	0
55	SY	1287	0	1368	31	0
56	SZ	1314	0	649	3	0
57	L1	46	0	0	0	0
57	SI	1	0	0	0	0
58	NQ	1	0	0	0	0
58	SL	1	0	0	0	0
59	SI	32	0	12	0	0
All	All	149183	0	123755	1389	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1389 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:NL:229:ILE:HD13	29:NL:247:VAL:HG21	1.42	1.02
8:L7:67:LEU:HD22	8:L7:94:ALA:HB2	1.41	1.02
2:L1:976:G:H1	2:L1:1023:A:HO2'	1.18	0.86
16:LH:435:ASP:O	16:LH:762:TYR:OH	1.94	0.85
27:NF:48:SER:OG	27:NF:86:GLU:OE2	1.94	0.85

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L3	102/146 (70%)	100 (98%)	2 (2%)	0	100	100
5	L4	242/261 (93%)	238 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	L5	193/225 (86%)	186 (96%)	7 (4%)	0	100	100
7	L6	214/236 (91%)	209 (98%)	5 (2%)	0	100	100
8	L7	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
9	L8	166/200 (83%)	163 (98%)	3 (2%)	0	100	100
10	L9	179/197 (91%)	177 (99%)	2 (1%)	0	100	100
11	LC	126/143 (88%)	121 (96%)	5 (4%)	0	100	100
12	LD	135/156 (86%)	132 (98%)	3 (2%)	0	100	100
13	LE	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
14	LF	128/135 (95%)	127 (99%)	1 (1%)	0	100	100
15	LG	60/67 (90%)	58 (97%)	2 (3%)	0	100	100
16	LH	730/896 (82%)	704 (96%)	25 (3%)	1 (0%)	48	82
17	LI	582/713 (82%)	574 (99%)	8 (1%)	0	100	100
18	LJ	447/513 (87%)	441 (99%)	6 (1%)	0	100	100
19	LK	130/575 (23%)	130 (100%)	0	0	100	100
20	LL	157/643 (24%)	156 (99%)	1 (1%)	0	100	100
21	LM	1182/1769 (67%)	1165 (99%)	17 (1%)	0	100	100
22	LN	649/776 (84%)	631 (97%)	18 (3%)	0	100	100
23	LS	358/594 (60%)	349 (98%)	9 (2%)	0	100	100
24	NA	173/593 (29%)	172 (99%)	1 (1%)	0	100	100
25	NB	228/610 (37%)	226 (99%)	2 (1%)	0	100	100
26	ND	70/214 (33%)	69 (99%)	1 (1%)	0	100	100
27	NF	139/151 (92%)	138 (99%)	1 (1%)	0	100	100
28	NG	125/137 (91%)	121 (97%)	4 (3%)	0	100	100
29	NL	268/318 (84%)	264 (98%)	4 (2%)	0	100	100
30	NM	225/255 (88%)	224 (100%)	1 (0%)	0	100	100
31	NP	130/144 (90%)	127 (98%)	3 (2%)	0	100	100
32	NQ	77/82 (94%)	76 (99%)	1 (1%)	0	100	100
33	NS	99/1267 (8%)	98 (99%)	1 (1%)	0	100	100
34	NV	12/733 (2%)	12 (100%)	0	0	100	100
35	OH	118/143 (82%)	118 (100%)	0	0	100	100
36	OU	54/152 (36%)	54 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	SA	390/504 (77%)	386 (99%)	4 (1%)	0	100	100
38	SB	401/511 (78%)	394 (98%)	7 (2%)	0	100	100
39	SC	237/327 (72%)	235 (99%)	2 (1%)	0	100	100
39	SD	234/327 (72%)	230 (98%)	4 (2%)	0	100	100
40	SE	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
40	SF	119/126 (94%)	116 (98%)	3 (2%)	0	100	100
41	SG	453/573 (79%)	445 (98%)	8 (2%)	0	100	100
42	SH	358/367 (98%)	351 (98%)	7 (2%)	0	100	100
43	SI	749/1183 (63%)	735 (98%)	14 (2%)	0	100	100
44	SJ	207/252 (82%)	206 (100%)	1 (0%)	0	100	100
44	SK	225/252 (89%)	219 (97%)	6 (3%)	0	100	100
45	SL	146/189 (77%)	140 (96%)	6 (4%)	0	100	100
46	SM	217/290 (75%)	215 (99%)	2 (1%)	0	100	100
47	SP	1832/2493 (74%)	1806 (99%)	26 (1%)	0	100	100
48	SQ	95/217 (44%)	94 (99%)	1 (1%)	0	100	100
49	SR	130/145 (90%)	128 (98%)	2 (2%)	0	100	100
50	SS	111/899 (12%)	110 (99%)	1 (1%)	0	100	100
51	ST	562/810 (69%)	557 (99%)	5 (1%)	0	100	100
52	SU	524/552 (95%)	519 (99%)	5 (1%)	0	100	100
53	SV	151/206 (73%)	148 (98%)	3 (2%)	0	100	100
54	SW	180/274 (66%)	177 (98%)	3 (2%)	0	100	100
55	SY	144/250 (58%)	141 (98%)	3 (2%)	0	100	100
56	SZ	255/483 (53%)	250 (98%)	5 (2%)	0	100	100
All	All	15638/24720 (63%)	15372 (98%)	265 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LH	749	ASP

5.3.2 Protein sidechains ⓘ

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	L3	96/129 (74%)	96 (100%)	0	100	100
5	L4	208/222 (94%)	208 (100%)	0	100	100
6	L5	170/191 (89%)	170 (100%)	0	100	100
7	L6	185/201 (92%)	185 (100%)	0	100	100
8	L7	158/170 (93%)	158 (100%)	0	100	100
9	L8	137/161 (85%)	137 (100%)	0	100	100
10	L9	156/166 (94%)	156 (100%)	0	100	100
11	LC	6/119 (5%)	6 (100%)	0	100	100
12	LD	124/137 (90%)	124 (100%)	0	100	100
13	LE	110/111 (99%)	109 (99%)	1 (1%)	70	75
14	LF	109/113 (96%)	109 (100%)	0	100	100
15	LG	2/60 (3%)	2 (100%)	0	100	100
16	LH	684/826 (83%)	684 (100%)	0	100	100
17	LI	244/657 (37%)	244 (100%)	0	100	100
18	LJ	400/454 (88%)	400 (100%)	0	100	100
19	LK	124/533 (23%)	124 (100%)	0	100	100
20	LL	145/574 (25%)	145 (100%)	0	100	100
21	LM	32/1633 (2%)	32 (100%)	0	100	100
22	LN	603/713 (85%)	603 (100%)	0	100	100
23	LS	315/529 (60%)	315 (100%)	0	100	100
24	NA	104/535 (19%)	104 (100%)	0	100	100
25	NB	80/538 (15%)	80 (100%)	0	100	100
26	ND	57/196 (29%)	57 (100%)	0	100	100
27	NF	121/128 (94%)	121 (100%)	0	100	100
28	NG	96/105 (91%)	96 (100%)	0	100	100
29	NL	245/283 (87%)	245 (100%)	0	100	100
30	NM	203/224 (91%)	202 (100%)	1 (0%)	81	81
31	NP	5/116 (4%)	5 (100%)	0	100	100
32	NQ	68/71 (96%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	NS	94/1140 (8%)	94 (100%)	0	100	100
34	NV	12/671 (2%)	12 (100%)	0	100	100
35	OH	2/119 (2%)	2 (100%)	0	100	100
36	OU	1/135 (1%)	1 (100%)	0	100	100
37	SA	328/435 (75%)	326 (99%)	2 (1%)	78	80
38	SB	334/433 (77%)	334 (100%)	0	100	100
39	SC	200/240 (83%)	200 (100%)	0	100	100
39	SD	198/240 (82%)	198 (100%)	0	100	100
40	SE	100/104 (96%)	100 (100%)	0	100	100
40	SF	100/104 (96%)	100 (100%)	0	100	100
41	SG	399/503 (79%)	399 (100%)	0	100	100
42	SH	307/312 (98%)	307 (100%)	0	100	100
43	SI	670/1039 (64%)	670 (100%)	0	100	100
44	SJ	9/222 (4%)	9 (100%)	0	100	100
44	SK	12/222 (5%)	12 (100%)	0	100	100
45	SL	131/169 (78%)	131 (100%)	0	100	100
46	SM	194/258 (75%)	194 (100%)	0	100	100
47	SP	1725/2307 (75%)	1724 (100%)	1 (0%)	88	88
48	SQ	91/200 (46%)	91 (100%)	0	100	100
49	SR	113/120 (94%)	113 (100%)	0	100	100
50	SS	104/808 (13%)	104 (100%)	0	100	100
51	ST	125/732 (17%)	125 (100%)	0	100	100
52	SU	27/506 (5%)	27 (100%)	0	100	100
53	SV	20/192 (10%)	20 (100%)	0	100	100
54	SW	159/238 (67%)	159 (100%)	0	100	100
55	SY	146/234 (62%)	146 (100%)	0	100	100
56	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	10602/22002 (48%)	10597 (100%)	5 (0%)	100	100

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	LE	80	ASN

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Mol	Chain	Res	Type
30	NM	124	ASN
37	SA	37[A]	GLN
37	SA	37[B]	GLN
47	SP	787	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
37	SA	183	GLN
43	SI	276	HIS
49	SR	18	HIS
37	SA	318	HIS
41	SG	570	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	47/700 (6%)	7 (14%)	0
2	L1	1322/1803 (73%)	274 (20%)	10 (0%)
3	L2	187/334 (55%)	23 (12%)	1 (0%)
All	All	1556/2837 (54%)	304 (19%)	11 (0%)

5 of 304 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	7	A
1	L0	61	U
1	L0	63	G
1	L0	64	U
1	L0	83	U

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	1082	C
2	L1	1555	A
3	L2	156	U
2	L1	1568	C
2	L1	793	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 50 ligands modelled in this entry, 49 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	GTP	SI	2001	57	33,34,34	1.83	4 (12%)	50,54,54	1.49	6 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	GTP	SI	2001	57	-	1/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	SI	2001	GTP	C5-N7	6.66	1.52	1.39
59	SI	2001	GTP	C8-N9	-4.31	1.27	1.37
59	SI	2001	GTP	C4-N9	-3.84	1.28	1.38
59	SI	2001	GTP	C4-N3	2.27	1.39	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SI	2001	GTP	C8-N9-C4	7.24	119.59	106.03
59	SI	2001	GTP	N9-C4-N3	2.73	131.41	125.95
59	SI	2001	GTP	C1'-N9-C8	-2.51	119.61	126.73
59	SI	2001	GTP	C6-C5-N7	2.47	134.79	130.29
59	SI	2001	GTP	C5-C4-N9	-2.14	101.82	105.66

There are no chirality outliers.

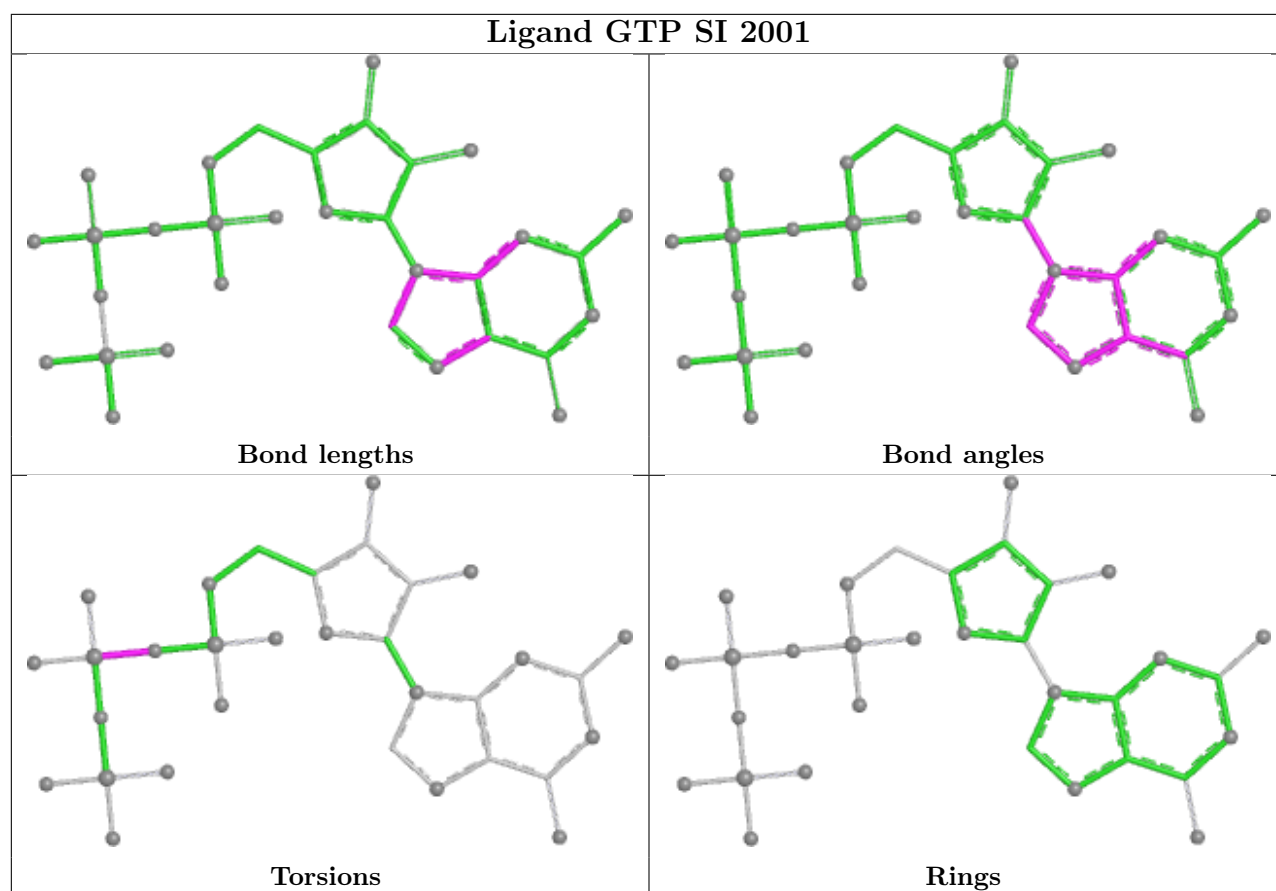
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	SI	2001	GTP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

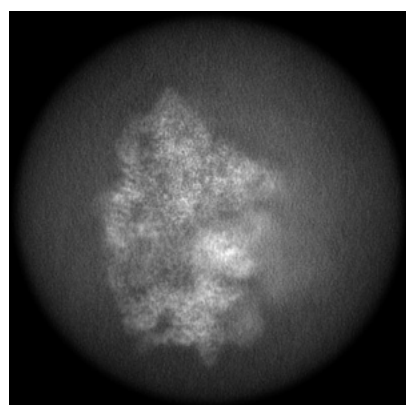
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49088. These allow visual inspection of the internal detail of the map and identification of artifacts.

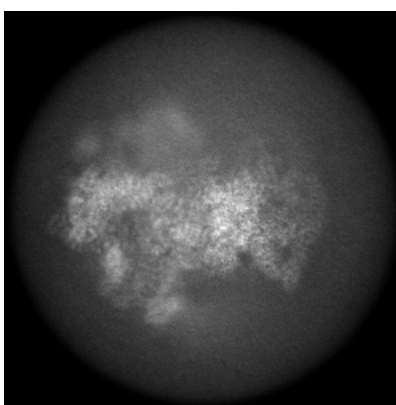
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

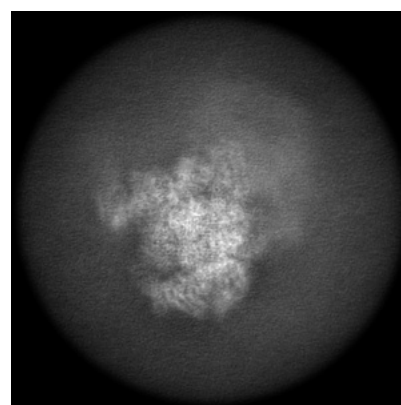
6.1.1 Primary map



X



Y

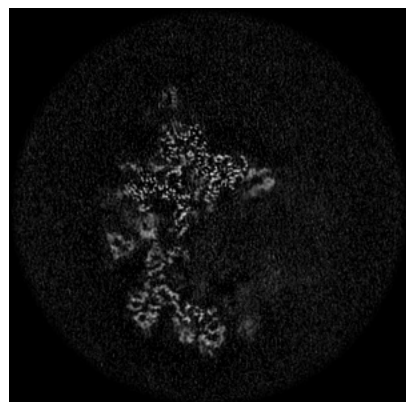


Z

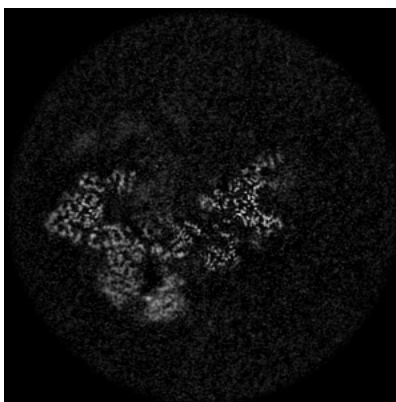
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

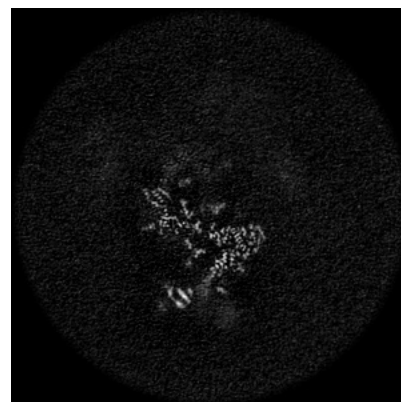
6.2.1 Primary map



X Index: 252



Y Index: 252

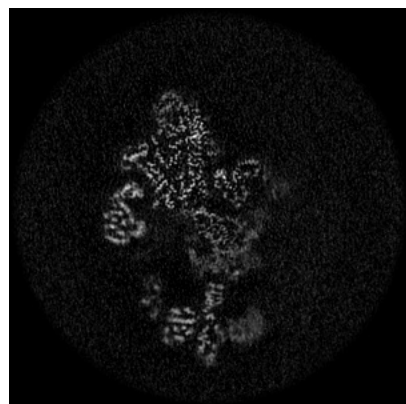


Z Index: 252

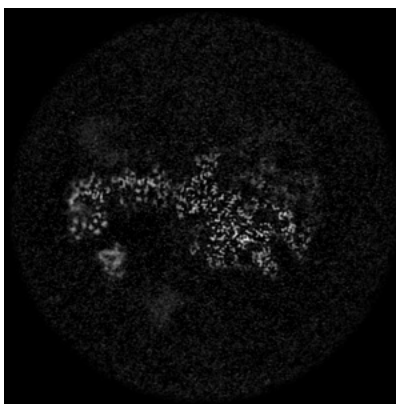
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

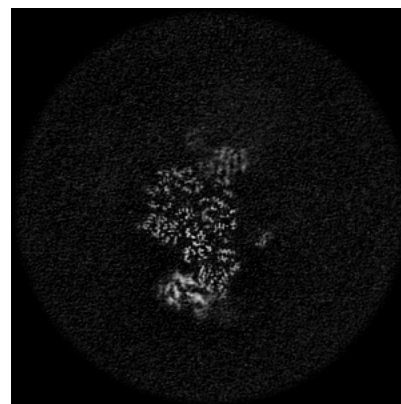
6.3.1 Primary map



X Index: 226



Y Index: 217

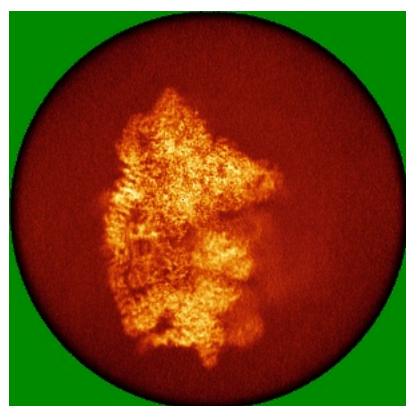


Z Index: 270

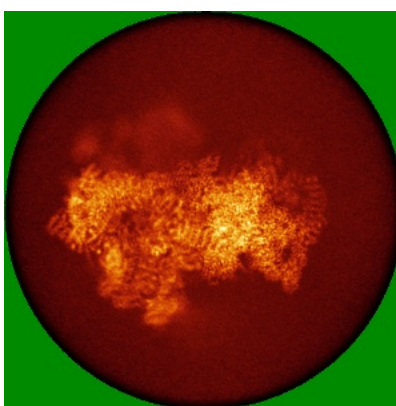
The images above show the largest variance slices of the map in three orthogonal directions.

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

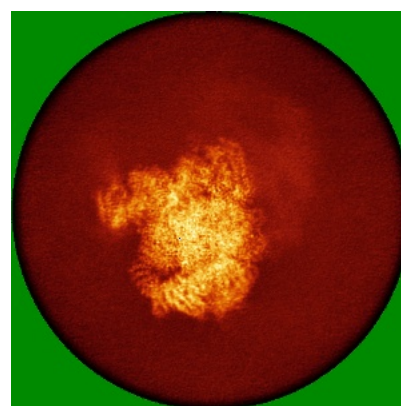
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

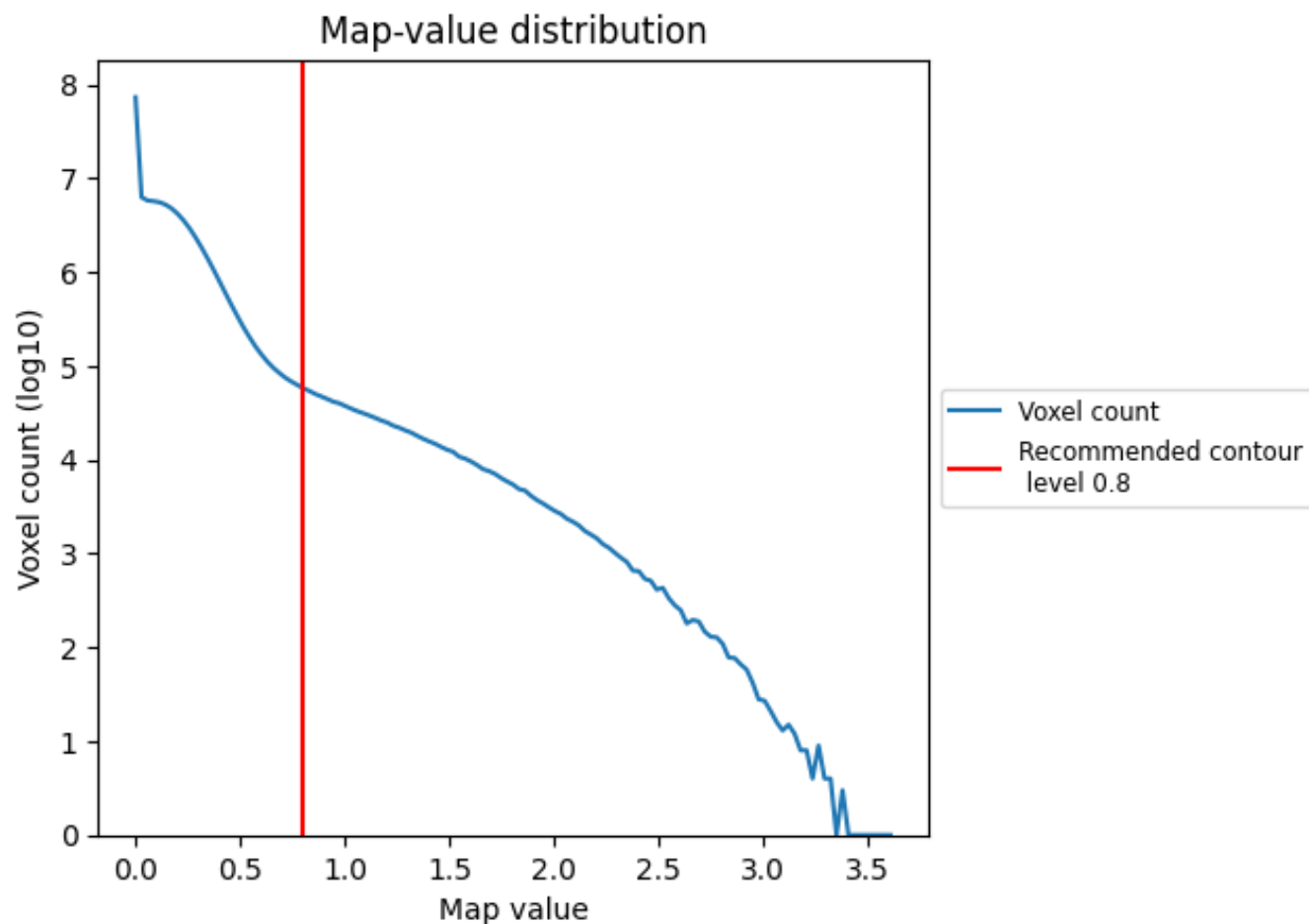
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

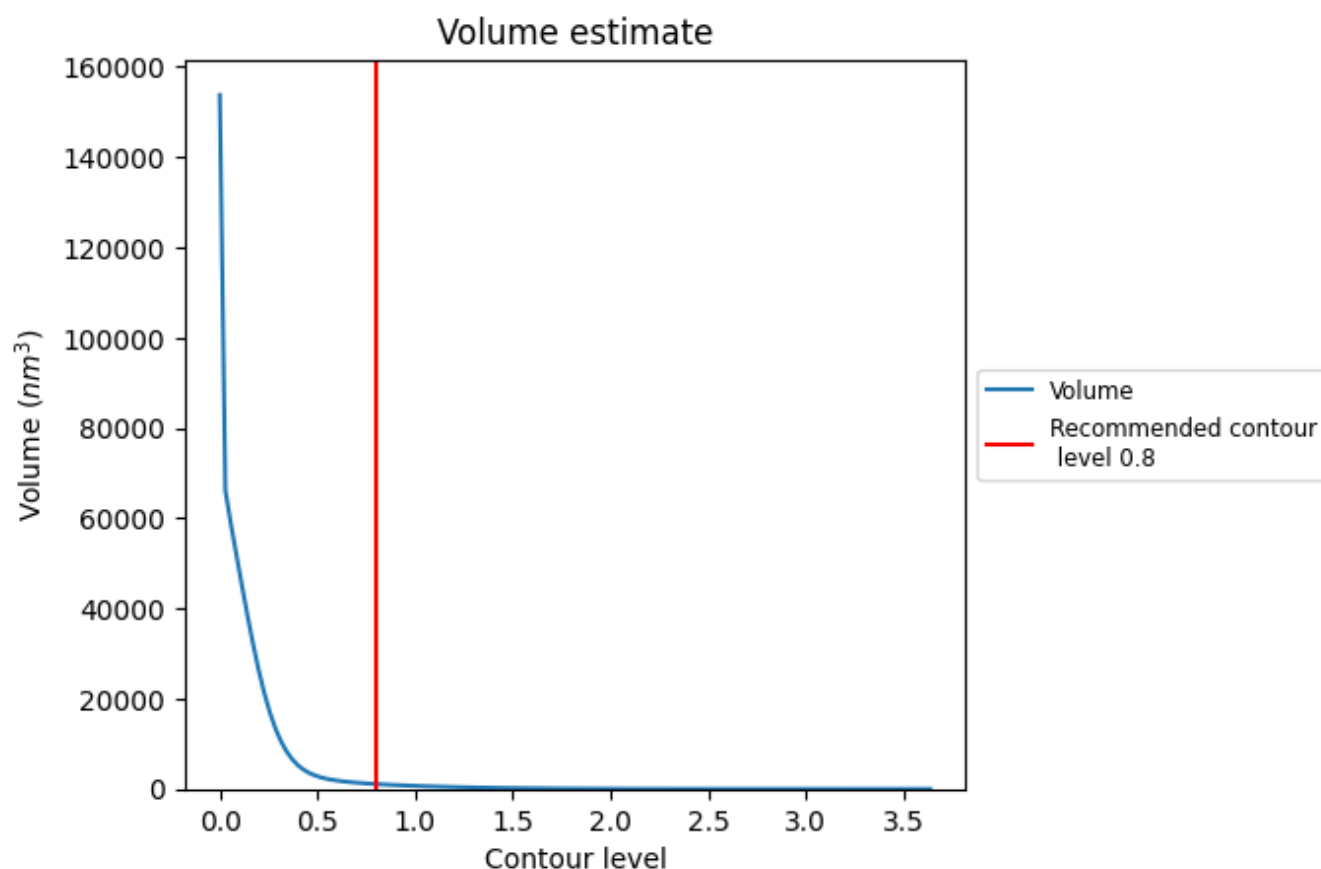
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

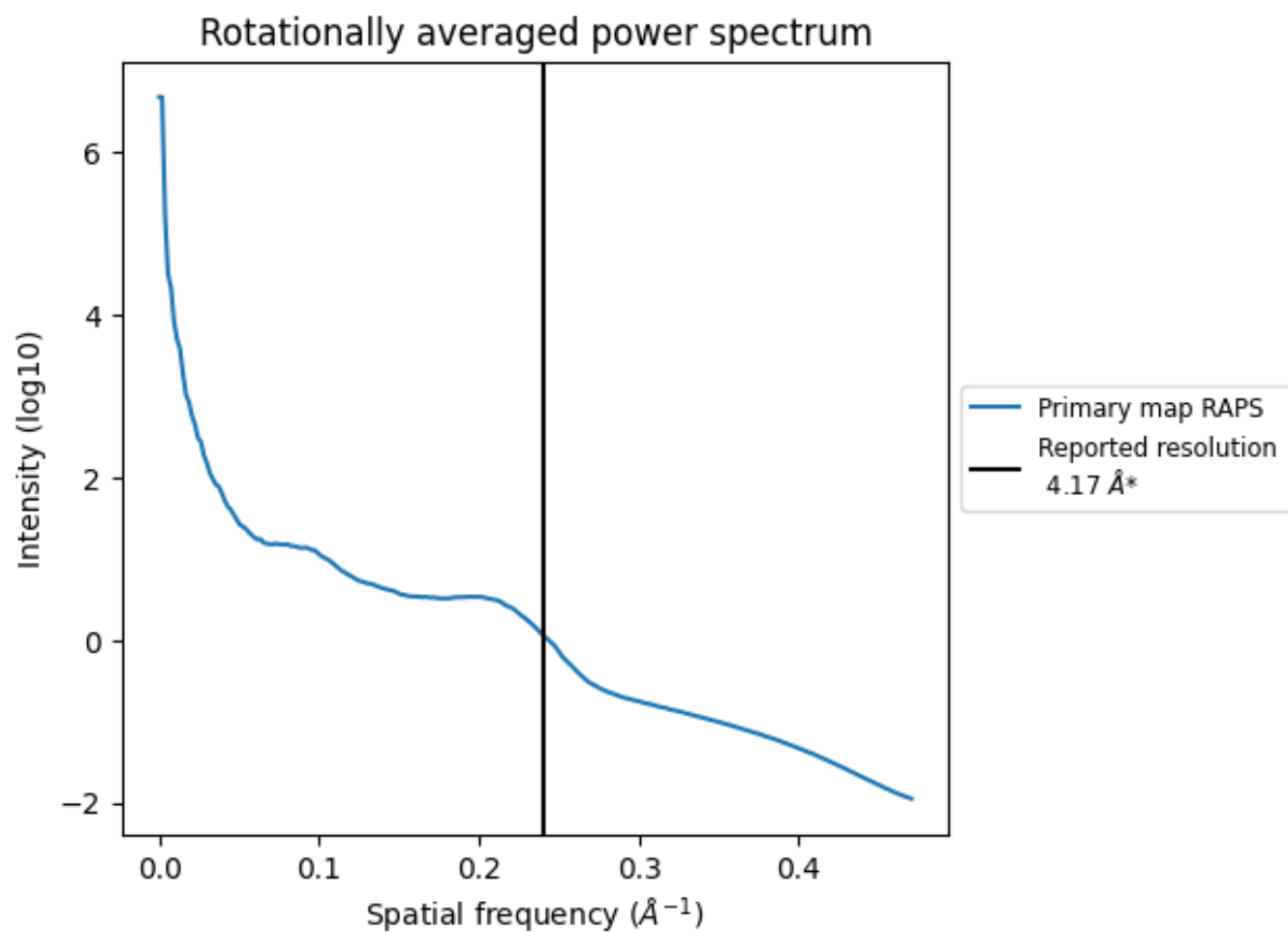
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1087 nm³; this corresponds to an approximate mass of 982 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.240 $\text{\AA}^{-1}$

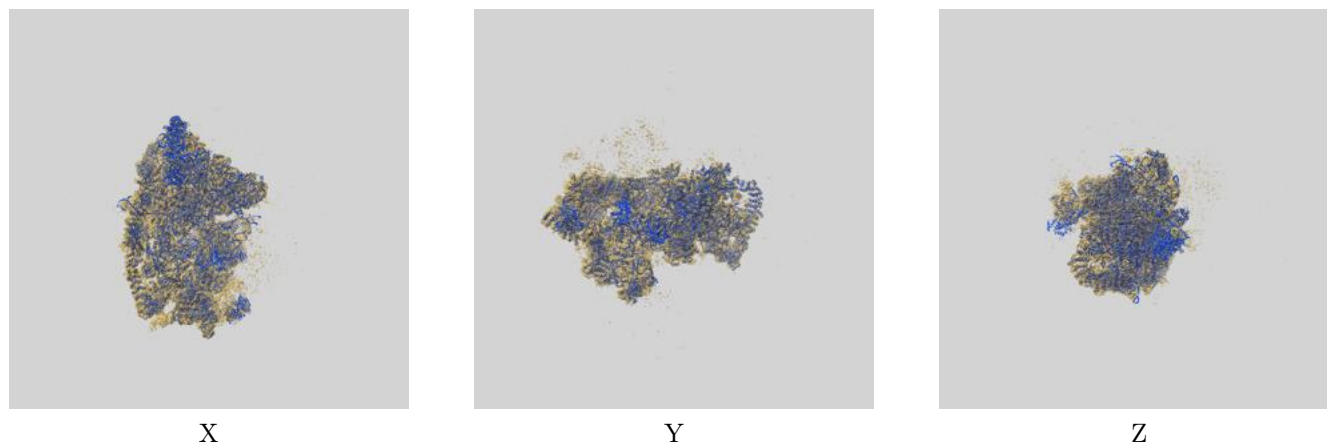
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

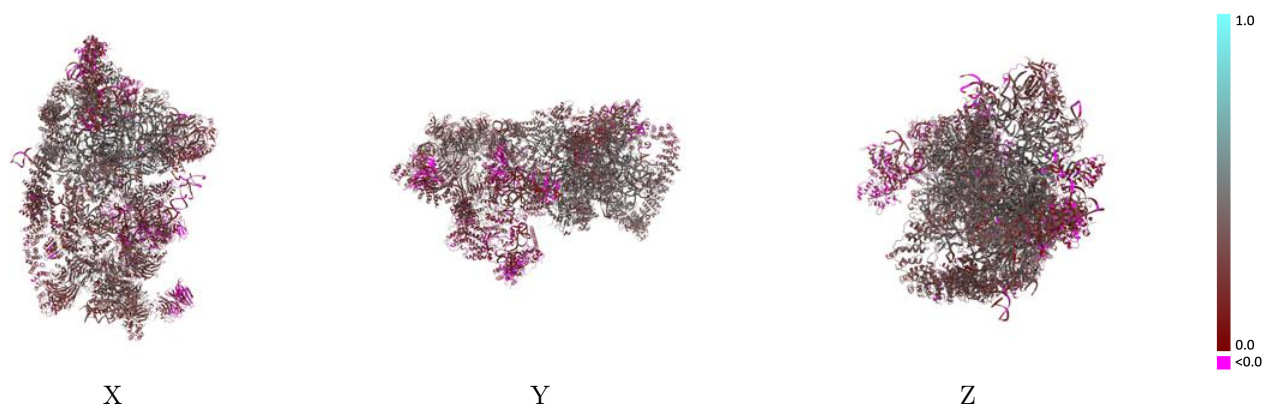
This section contains information regarding the fit between EMDB map EMD-49088 and PDB model 9N78. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



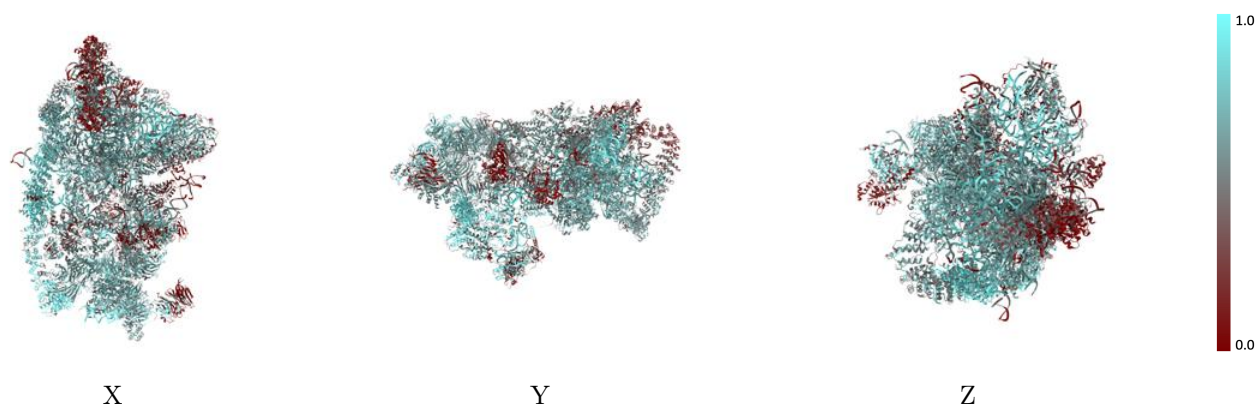
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



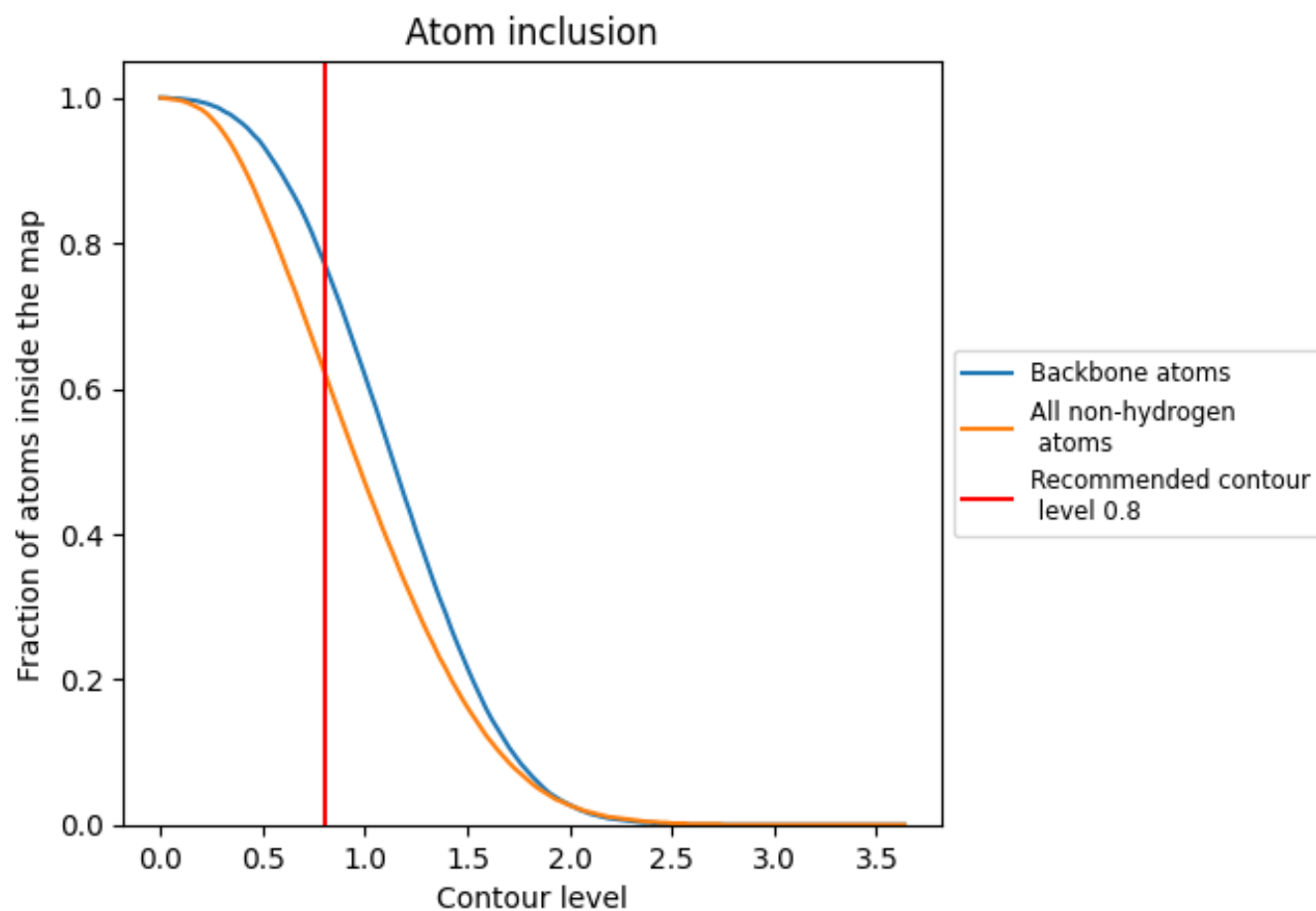
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 62% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6230	 0.3100
L0	 0.9070	 0.3180
L1	 0.7350	 0.3270
L2	 0.7790	 0.3120
L3	 0.4990	 0.2560
L4	 0.6320	 0.4400
L5	 0.3610	 0.1700
L6	 0.6530	 0.4080
L7	 0.2700	 0.2040
L8	 0.6690	 0.3700
L9	 0.6800	 0.4260
LC	 0.0090	 0.0310
LD	 0.6730	 0.4450
LE	 0.6060	 0.4240
LF	 0.7170	 0.3960
LG	 0.0940	 0.0250
LH	 0.6850	 0.3310
LI	 0.4710	 0.1830
LJ	 0.6510	 0.2770
LK	 0.6330	 0.2250
LL	 0.6420	 0.2720
LM	 0.8600	 0.2720
LN	 0.6830	 0.3150
LS	 0.5810	 0.3140
NA	 0.5220	 0.3020
NB	 0.6950	 0.3060
ND	 0.5520	 0.2540
NF	 0.6540	 0.3970
NG	 0.4770	 0.2650
NL	 0.6110	 0.3850
NM	 0.5240	 0.2680
NP	 0.2280	 0.1920
NQ	 0.5490	 0.3670
NS	 0.5400	 0.3560
NV	 0.3360	 0.3740



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Chain	Atom inclusion	Q-score
OH	 0.0370	 0.0450
OU	 0.0070	 0.0390
SA	 0.5420	 0.3080
SB	 0.5330	 0.2670
SC	 0.6570	 0.4210
SD	 0.4430	 0.2630
SE	 0.6400	 0.3160
SF	 0.6710	 0.4190
SG	 0.6900	 0.4040
SH	 0.6580	 0.4050
SI	 0.6570	 0.4060
SJ	 0.7020	 0.1620
SK	 0.7140	 0.2220
SL	 0.6890	 0.4440
SM	 0.3860	 0.2910
SP	 0.4370	 0.2940
SQ	 0.5820	 0.3690
SR	 0.6570	 0.4330
SS	 0.5380	 0.3660
ST	 0.5400	 0.1880
SU	 0.8140	 0.2270
SV	 0.8090	 0.3150
SW	 0.4890	 0.2490
SY	 0.4850	 0.2940
SZ	 0.6300	 0.1080