



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2024 – 09:53 AM JST

PDB ID : 6LQP
EMDB ID : EMD-0949
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State A)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 3.20 Å (reported)
Based on initial model : 6KE6

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:

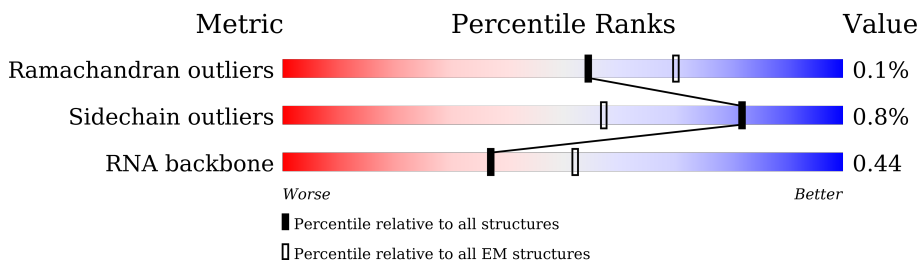
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



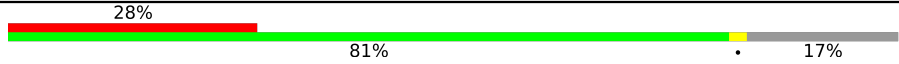







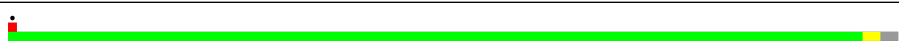

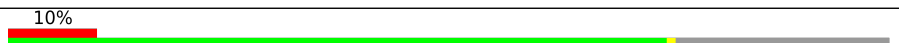

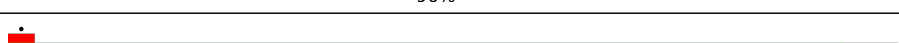
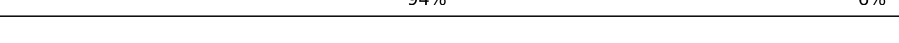
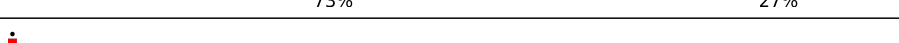
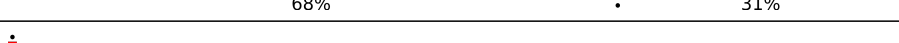
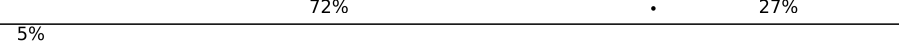
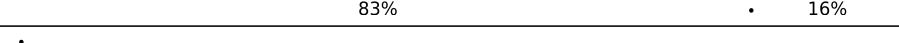
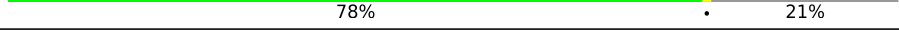
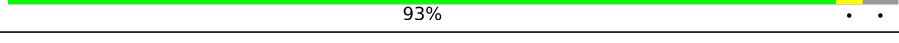
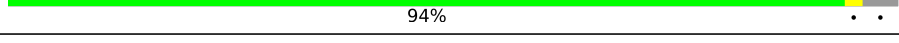




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	3A	333	
2	5A	700	
3	SA	1808	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	

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Mol	Chain	Length	Quality of chain
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	

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Mol	Chain	Length	Quality of chain
32	AF	513	95%
33	AG	896	91% 8%
34	B1	923	89% 10%
35	B2	943	88% 10%
36	B3	817	89% 7%
37	B8	594	80% 20%
38	BE	939	91% 8%
39	B6	440	84% 15% 14%
40	5B	214	27% 72%
41	5C	554	95%
42	5D	250	92% 6%
43	5E	593	34% 66%
44	5F	183	97%
45	5G	290	96%
46	5H	610	22% 78%
47	5I	489	93% 6%
48	5J	217	70% 30% 11%
49	5K	189	92% 7%
50	RA	707	47% 52% 12%
51	RB	357	36% 62% 6%
52	RC	316	88% 12% 14%
53	RE	1237	86% 13% 11%
54	RF	297	79% 19% 27%
55	RG	252	84% 14% 9%
55	RH	252	90% 9%

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Mol	Chain	Length	Quality of chain
56	RI	274	92% 8%
57	RJ	1183	66% 33%
58	RK	367	96%
59	RL	1056	24% 76% 24%
59	RM	1056	57% 72% 27%
60	RN	810	11% 74% 25%
61	RO	552	9% 94% 5%
62	RP	2493	63% 84% 15%
63	RQ	899	25% 75%
64	RS	483	34% 52% 48%
65	RT	326	52% 48%
66	RV	346	54% 45%
67	RW	206	31% 69%
68	RY	534	7% 93%
69	X1	347	5% 18% 82%

2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 232186 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 U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	3A	175	3711	1661	648	1227	175	0	0

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	523	11163	4988	1984	3668	523	0	0

- Molecule 3 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1325	28258	12629	5035	9269	1325	0	0

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SC	230	1830	1156	335	335	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SF	229	1815	1161	331	320	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SG	213	1669	1045	307	314	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	SH	167	1327	834	256	235	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SI	165	1321	853	226	242		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	SJ	166	1324	824	262	236	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	SK	171	1388	879	268	240	1	0	0

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	SM	123	997	641	189	164	3	0	0

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	SN	119	865	545	151	167	2	0	0

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	SO	134	1087	698	202	186	1	0	0

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	SP	118	868	536	164	165	3	0	0

- Molecule 15 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	SR	125	973	625	174	174		0	0

- Molecule 16 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	ST	117	964	610	184	168	2	0	0

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	SX	127	1003	640	183	177	3	0	0

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	SY	103	786	503	144	137	2	0	0

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	SZ	102	809	517	148	144		0	0

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Sc	80	603	377	109	112	5	0	0

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
22	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
26	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	A5	514	3976	2520	688	755	13	0	0

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	A8	548	3307	2054	608	642	3	0	0

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	A9	128	939	594	173	170	2	0	0

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AE	1534	9955	6242	1771	1923	19	0	0

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	AF	493	3911	2462	702	735	12	0	0

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	AG	826	6570	4181	1111	1259	19	0	0

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	B1	834	6635	4223	1140	1253	19	0	0

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	B2	851	6723	4294	1133	1269	27	0	0

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	B3	757	5919	3769	993	1130	27	0	0

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	B8	477	3764	2387	662	705	10	0	0

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	BE	865	6810	4322	1175	1292	21	0	0

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	B6	374	2800	1782	501	505	12	0	0

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	5B	60	495	310	101	84	0	0

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	5C	535	4237	2656	762	807	12	0	0

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	5H	136	Total	C	N	O	0	0
			1065	658	211	196		

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	5K	175	1403	896	256	241	10	0	0

- Molecule 50 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	RA	338	2709	1713	463	524	9	0	0

- Molecule 51 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	RB	134	1108	664	227	214	3	0	0

- Molecule 52 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	RC	278	2207	1408	391	395	13	0	0

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	RE	1079	8716	5666	1437	1589	24	0	0

- Molecule 54 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	RF	241	1963	1253	335	367	8	0	0

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	RG	216	1701	1079	296	315	11	0	0
55	RH	230	1799	1142	313	333	11	0	0

- Molecule 56 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	RI	252	2045	1309	362	366	8	0	0

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	RJ	796	6379	4086	1136	1128	29	0	0

- Molecule 58 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	RL	805	4539	2760	885	887	7	0	0
59	RM	766	3779	2247	766	766		0	0

- Molecule 60 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	RN	607	4529	2861	820	837	11	0	0

- Molecule 61 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	RO	525	3766	2412	646	696	12	0	0

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	RP	2109	12176	7486	2292	2382	16	0	0

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	RQ	226	1651	1023	313	313	2	0	0

- Molecule 64 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	RS	251	2051	1340	349	359	3	0	0

- Molecule 65 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	RT	171	1357	864	249	240	4	0	0

- Molecule 66 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	RV	190	1448	891	290	264	3	0	0

- Molecule 67 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
67	RW	63	381	234	69	78	0	0

- Molecule 68 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
68	RY	37	299	191	48	60	0	0

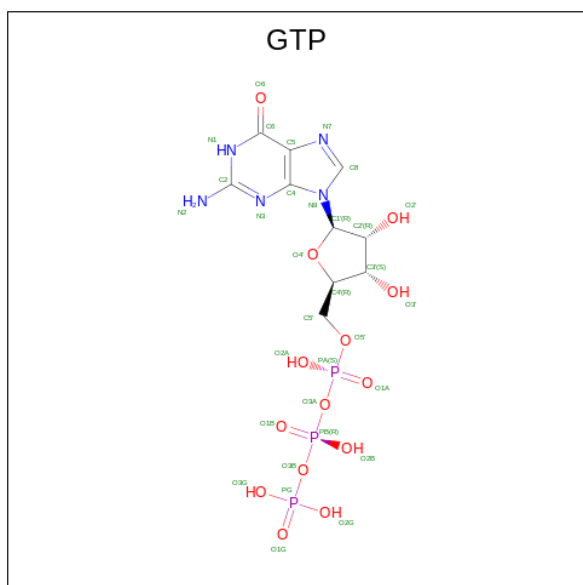
- Molecule 69 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
69	X1	61	305	183	61	61	0	0

- Molecule 70 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
70	Sc	1	Total	Zn	0
			1	1	
70	5K	1	Total	Zn	0
			1	1	

- Molecule 71 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
71	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

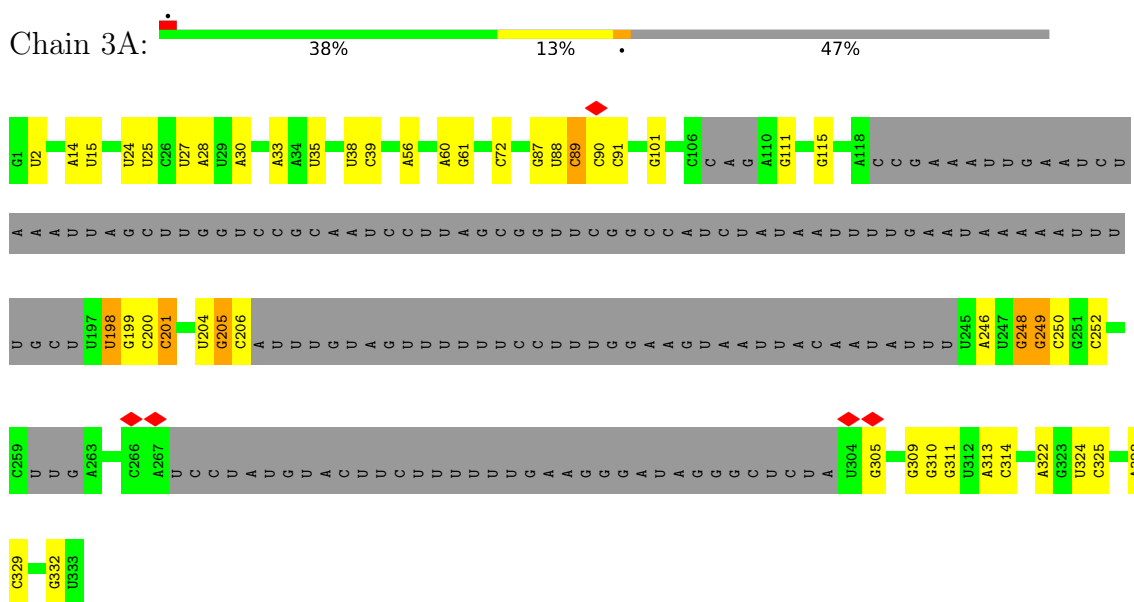
- Molecule 72 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	RJ	1	Total	Mg	0
			1	1	

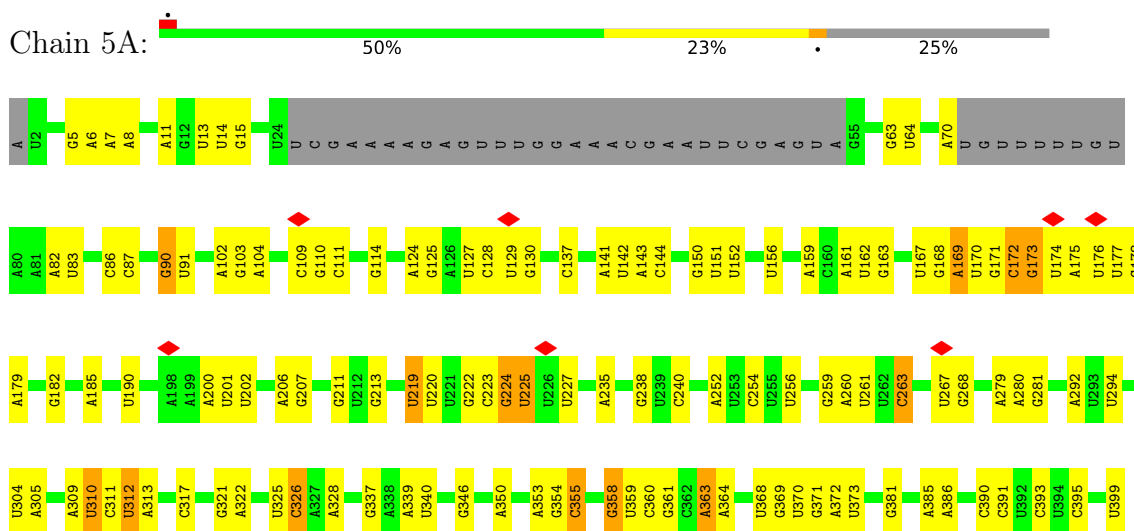
3 Residue-property plots

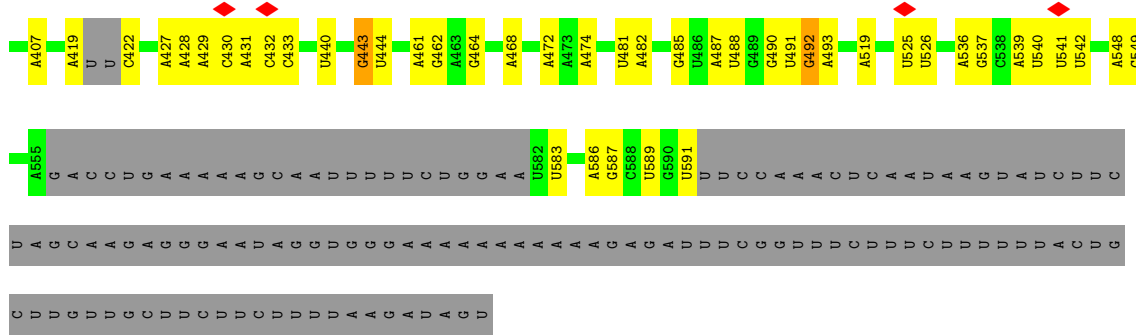
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U3 snoRNA

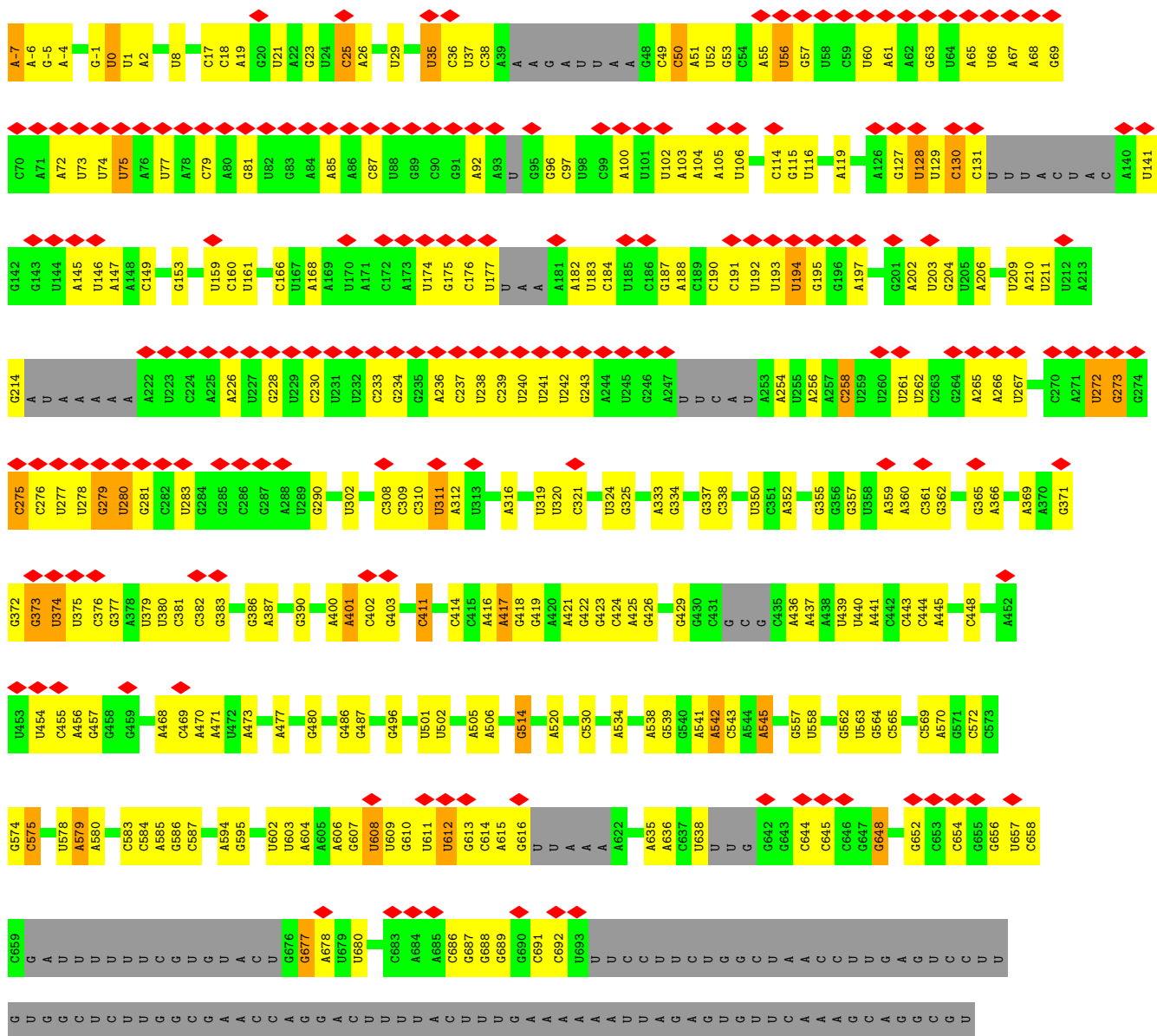


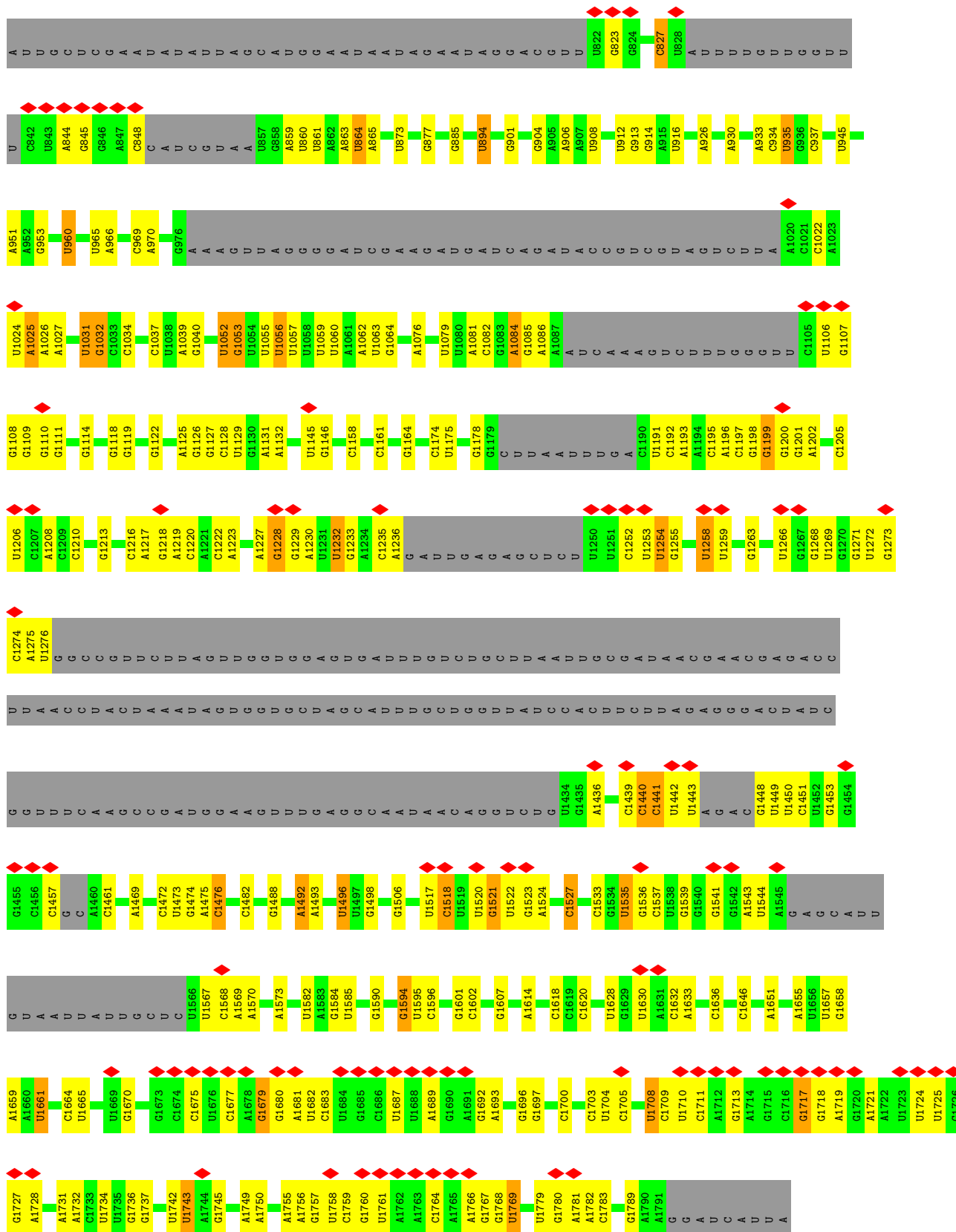
- Molecule 2: 5' ETS



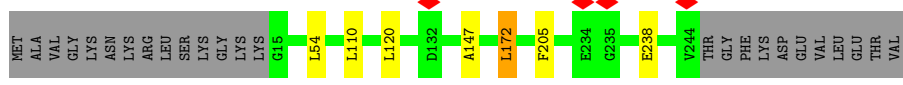
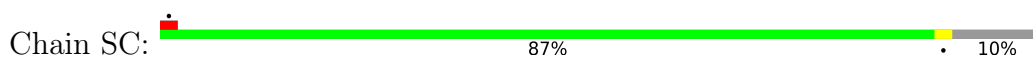


• Molecule 3: 18S pre-rRNA

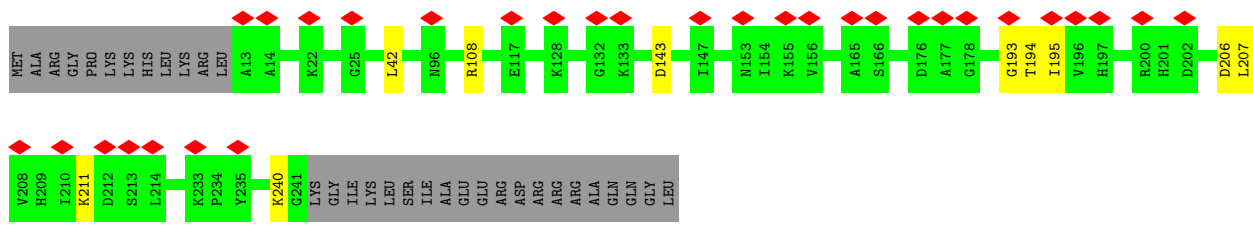
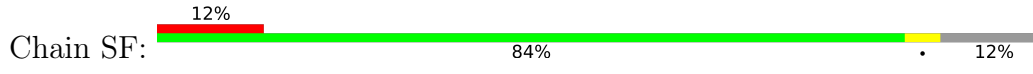




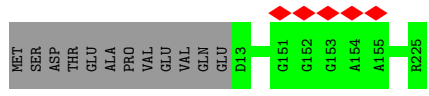
• Molecule 4: 40S ribosomal protein S1-A



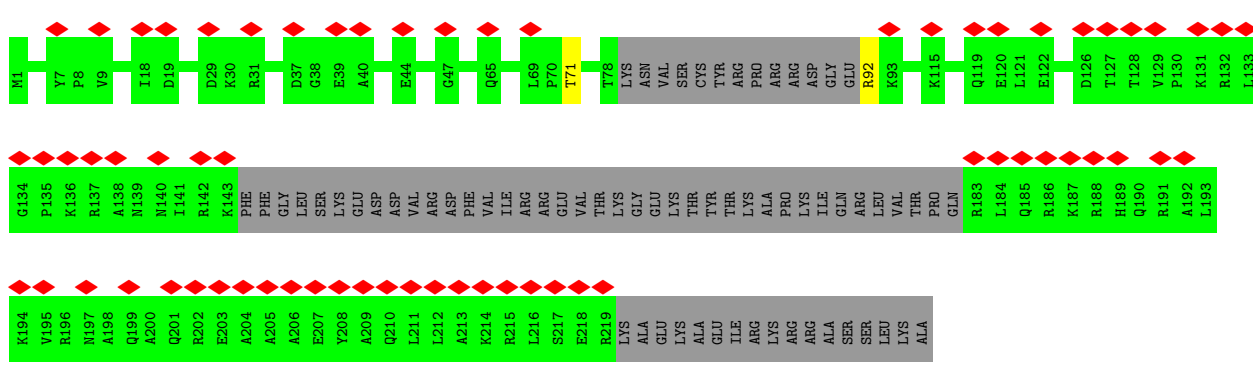
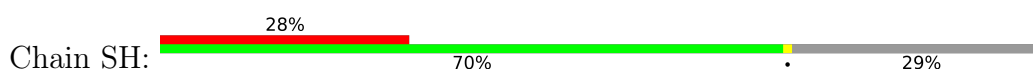
• Molecule 5: 40S ribosomal protein S4-A



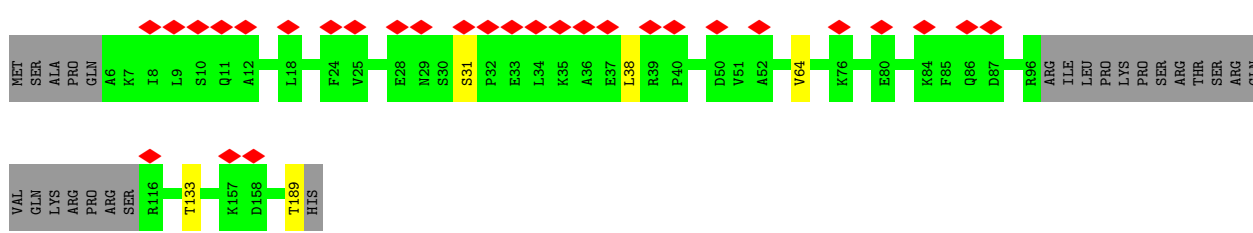
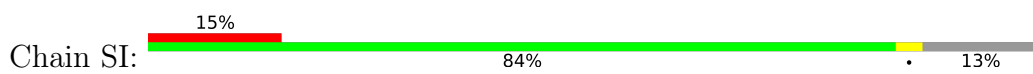
• Molecule 6: 40S ribosomal protein S5



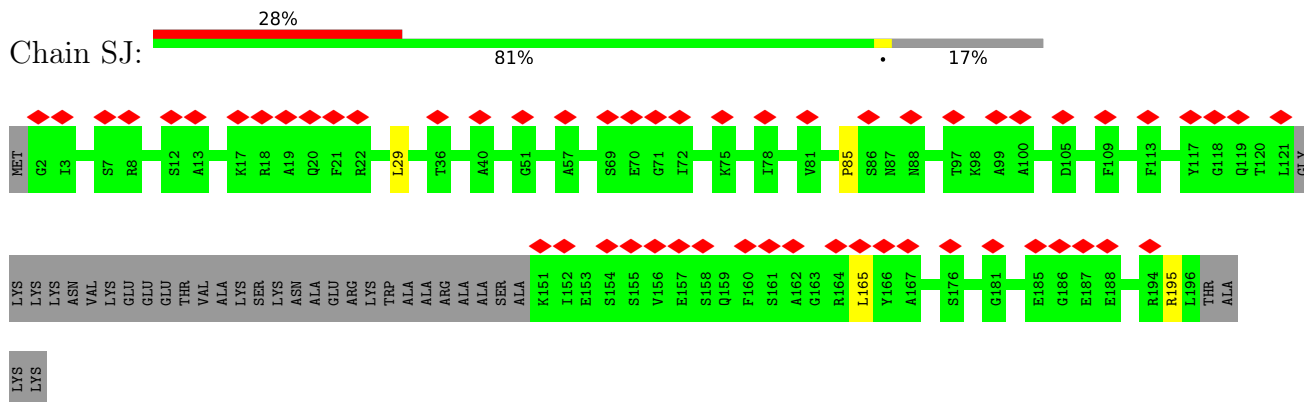
• Molecule 7: 40S ribosomal protein S6-A



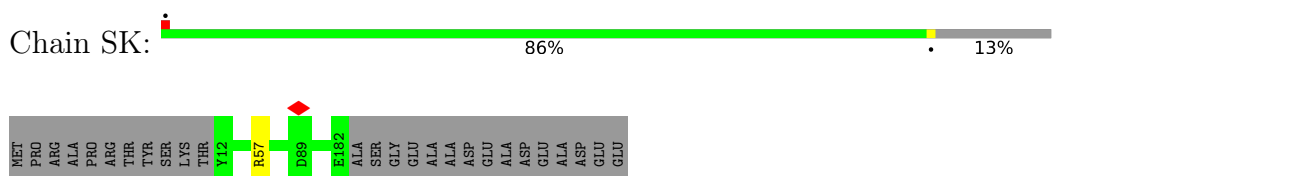
• Molecule 8: 40S ribosomal protein S7-A



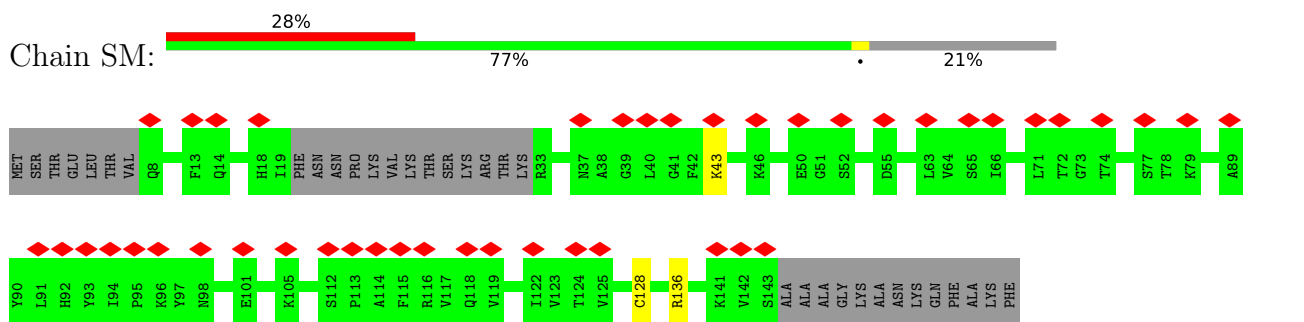
• Molecule 9: 40S ribosomal protein S8-A



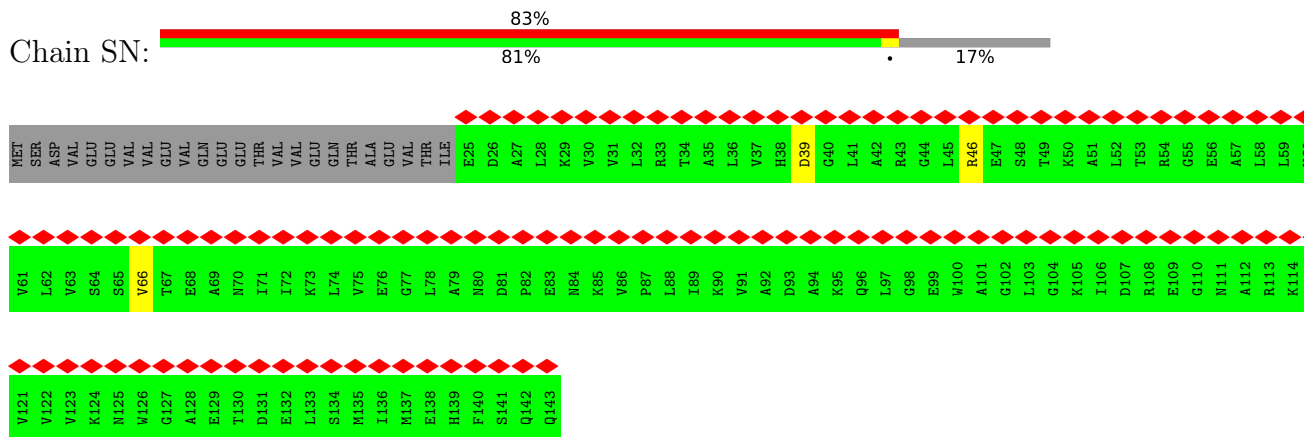
• Molecule 10: 40S ribosomal protein S9-A



• Molecule 11: 40S ribosomal protein S11-A



• Molecule 12: 40S ribosomal protein S12

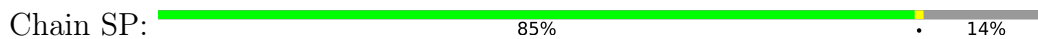


• Molecule 13: 40S ribosomal protein S13

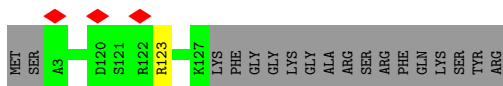
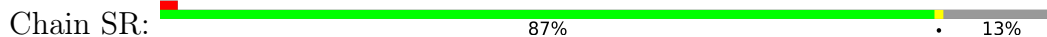




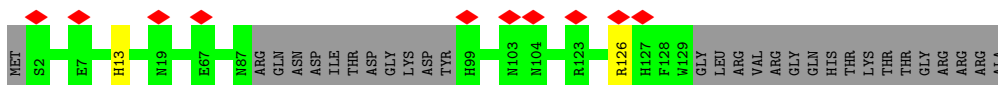
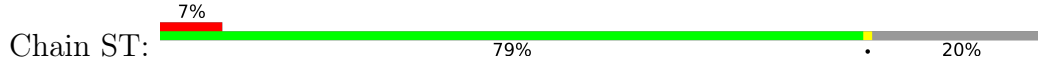
- Molecule 14: 40S ribosomal protein S14-A



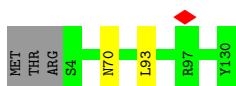
- Molecule 15: 40S ribosomal protein S16-A



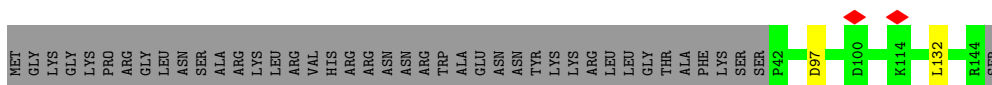
- Molecule 16: 40S ribosomal protein S18-A



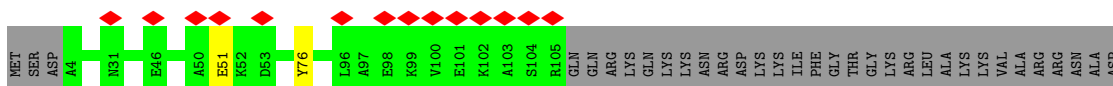
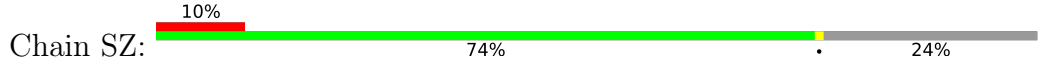
- Molecule 17: 40S ribosomal protein S22-B



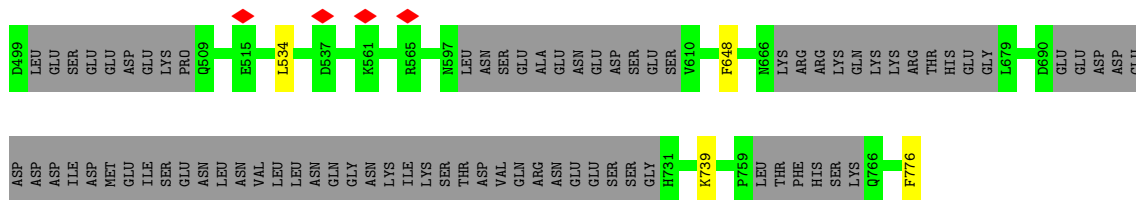
- Molecule 18: 40S ribosomal protein S23-A



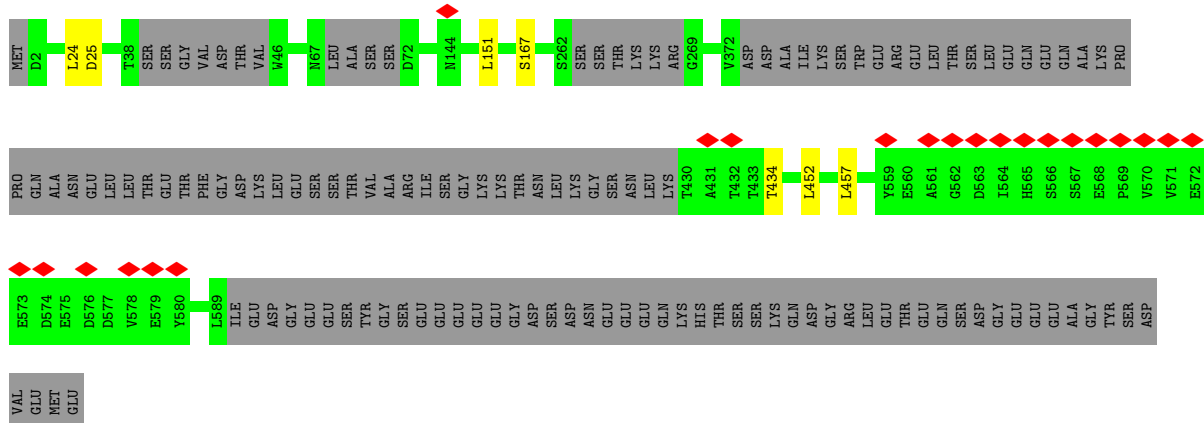
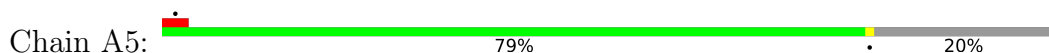
- Molecule 19: 40S ribosomal protein S24-A



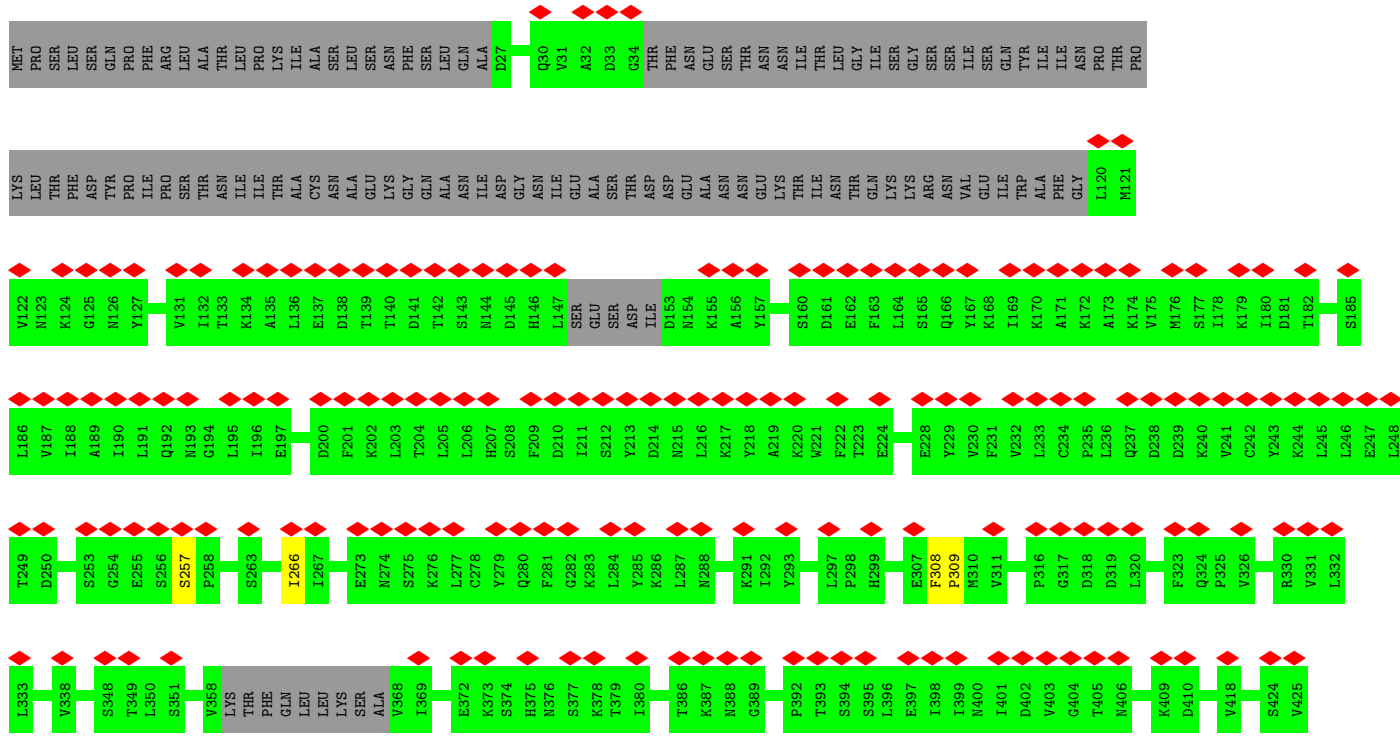
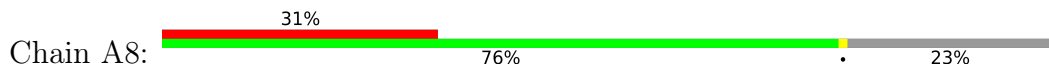
- Molecule 20: 40S ribosomal protein S27-A

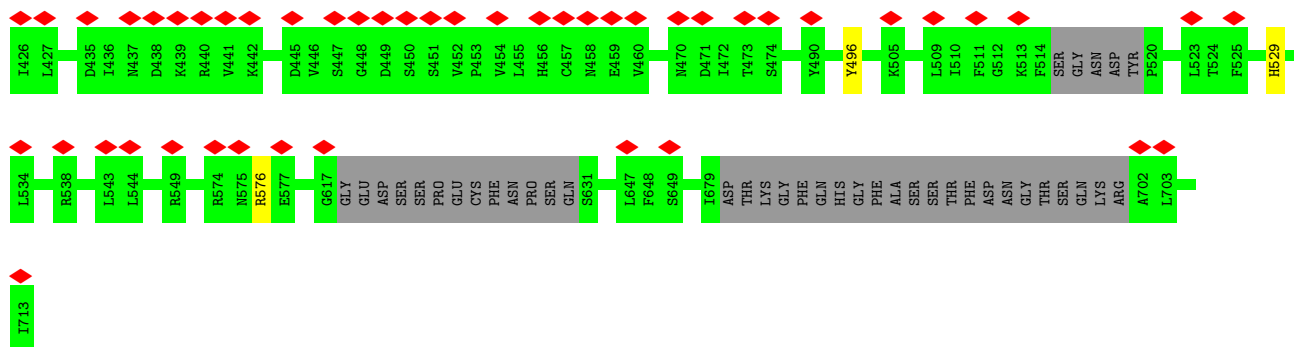


• Molecule 28: U3 small nucleolar RNA-associated protein 5

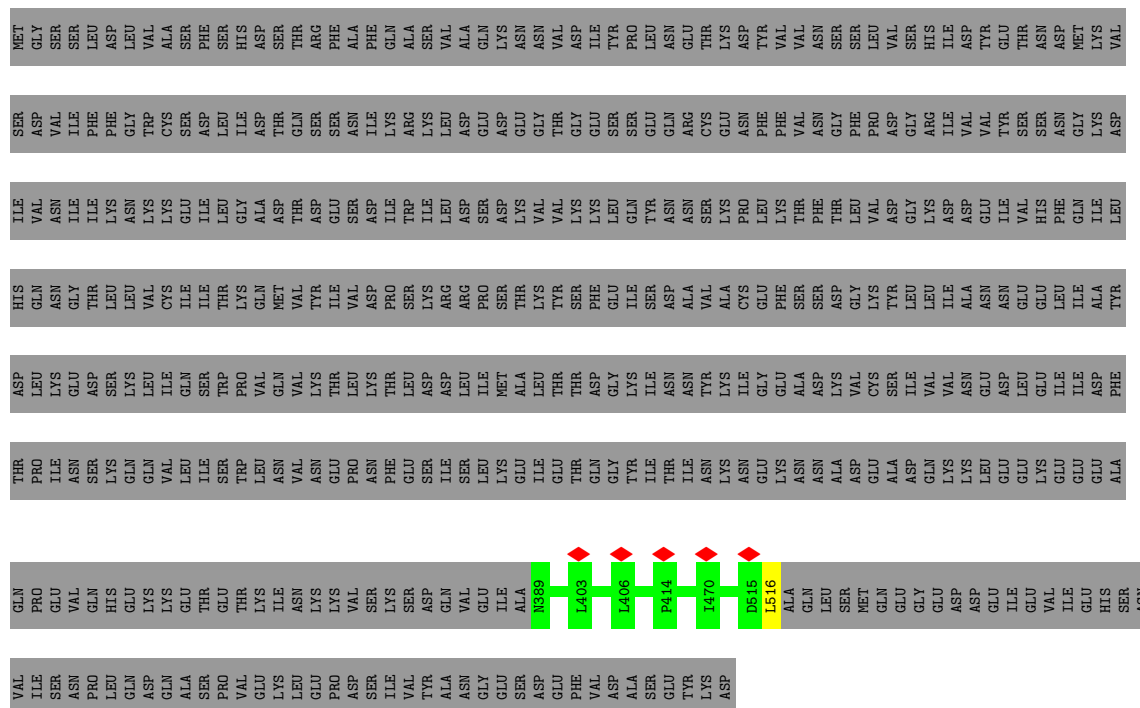


• Molecule 29: U3 small nucleolar RNA-associated protein 8

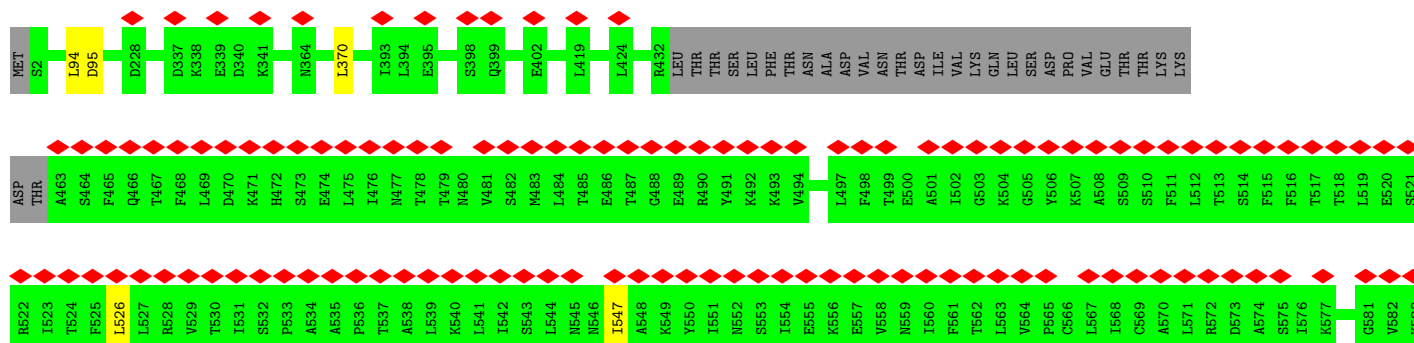
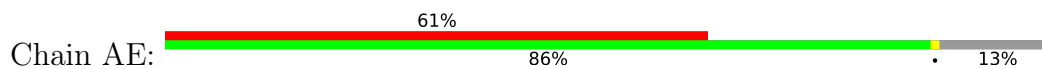




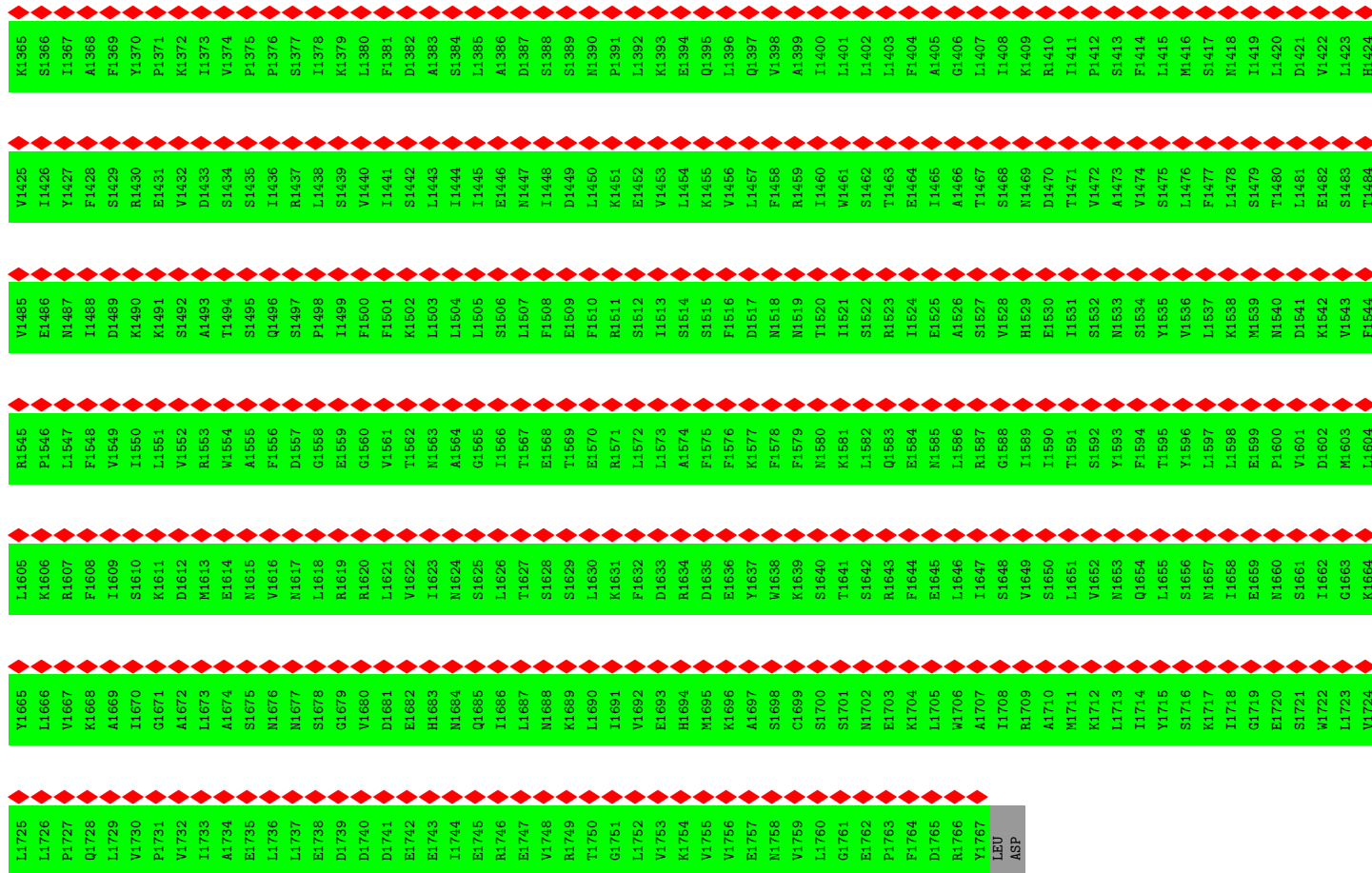
- Molecule 30: U3 small nucleolar RNA-associated protein 9



- Molecule 31: U3 small nucleolar RNA-associated protein 10

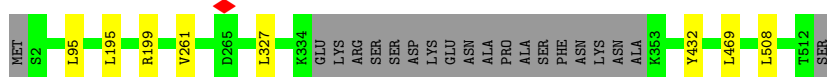


I1305	S1306	Q1307	V1308	I1309	L1310	M1311	T1312	M1313	T1314	A1315	L1316	V1317	S1318	K1319	Y1320	G1326	S1327	I1328	L1329	T1330	Q1331	A1332	L1333	T1334	L1335	A1336	T1337	I1338	K1339	V1340	S1341	S1342	D1343	M1344	T1345	E1346	V1347	K1348	I1349	M1350	S1351	L1352	A1353	L1354	I1355	T1356	M1357	C1358	V1359	Q1360	V1361	L1362	G1363	V1364					
E1245	F1246	V1247	M1248	A1249	V1250	L1251	P1252	L1253	L1254	S1255	T1256	S1257	T1258	M1259	E1260	D1261	I1262	R1263	Y1264	H1265	L1266	T1267	L1268	V1269	I1270	G1271	S1272	K1273	E1274	E1275	L1276	E1277	I1278	G1279	E1280	A1281	I1282	P1283	I1284	V1285	M1286	M1287	V1288	M1289	K1290	V1291	L1292	L1293	D1294	R1295	M1296	P1297	L1298	E1299	S1300	K1301	S1302	V1303	V1304
THR	LEU	GLU	GLY	LEU	PHE	ILE	ASN	ASN	THR	VAL	LEU	ASN	ASN	THR	GLU	THR	THR	ASP	GLN	D1150	Y1151	Y1152	D1153	V1154	R1155	R1156	M1157	L1158	R1159	L1160	K1161	V1162	Y1163	S1164	V1165	L1166	LEU	ASP	GLU	THR	SER	D1172	K1173	K1174	L1175	T1176	R1177	M1178	T1179	R1180	GLU	GLU	PHE	GLY	PRO	V1243	D1244		
A1065	R1066	I1067	L1068	I1069	E1070	F1071	ILE	ASN	ALA	LEU	VAL	ASN	LEU	H1080	I1081	M1082	E1083	E1084	L1085	S1086	G1087	M1088	M1089	D1090	L1091	L1092	I1094	I1095	K1096	L1097	L1098	T1099	S1100	K1101	K1102	S1103	S1104	S1105	E1106	K1107	K1108	K1109	S1110	L1111	E1112	S1113	R1114	VAL	LEU	PHE	SER	ASN	GLY	VAL	ASN	PHE			
E1005	M1006	GLU	PHE	LEU	LEU	SER	PHE	THR	THR	ALA	LEU	GLN	H1019	V1020	P1021	R1022	H1023	R1024	R1025	V1026	K1027	L1028	F1029	S1030	T1031	L1032	ILE	LYS	THR	LEU	ASP	PRO	V1039	K1040	A1041	L1042	G1043	S1044	F1045	L1046	F1047	L1048	I1049	ALA	GLN	GLN	TVR	SER	SER	ALA	L1057	V1058	M1059	F1060	K1061	I1062	G1063	E1064	
I945	G946	S947	L948	ALA	THR	LEU	SER	SER	E954	V955	I956	L957	H958	S959	V960	M961	P962	I963	F964	T965	F966	M967	G968	ALA	HIS	SER	ILE	GLN	ASP	GLU	PHE	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	P992	A993	L994	I995	K996	N997	S998	K999	G1000	N1001	K940	I1002	K1003	E1004					
G987	G888	L889	F890	V891	L892	Y893	A894	Q895	E896	T897	L898	I899	CYS	THR	LEU	ASN	ALA	GLU	ILE	Y908	L909	K910	E911	H912	G913	C914	T915	E916	L917	D918	N919	V920	ALA	ASP	ILE	THR	ILE	THR	VAL	VAL	ALA	ARG	ASN	SER	A933	P935	Q936	V937	Q938	N939	THR	L941	L942	L943	V944				
ARG	ARG	R827	S828	S829	T830	S831	K832	N833	A834	F835	L836	K837	E838	E839	V840	SER	GLN	LEU	ALA	GLU	HIS	LEU	ARG	LYS	LEU	THR	ILE	LEU	GLU	A857	L858	D859	K860	V861	N863	V864	G865	F866	E867	K868	LEU	LEU	PHE	THR	LEU	LEU	SER	ASN	SER	ASN	GLU	ASP	MET	GLN	THR	PHE	SER	LYS	ARG
R645	M646	E647	K648	V649	F650	L651	M652	F653	M654	A655	M656	Q657	A658	L659	L660	I661	P662	S663	P664	Y665	A666	K667	T668	V669	L670	L671	D672	M673	L674	M675	K676	S677	P678	T679	Y680	A681	S682	S683	Y684	S685	S686	L687	F688	E689	E690	F691	I692	S693	H694	Y695	L696	I697	M698	R699	S700	V701	W702	E703	K704
K684	I685	L686	S687	L688	I689	A690	K691	R692	P693	S694	T695	K696	H697	Y698	F699	L600	S601	D602	K603	L604	Y605	G606	E607	M608	V609	T610	L611	P612	M615	P616	K617	D618	S619	E620	A621	W622	L623	S624	G625	F626	L627	M628	E629	Y630	V631	T632	E633	M634	Y635	D636	I637	S638	R639	I640	T642	P643	K644		
S705	C706	I707	A708	N709	K710	T711	N712	F713	E714	H715	F716	E717	R718	S719	L720	I721	N722	L723	V724	S725	P726	K727	E728	K729	Q730	S731	F732	M733	I734	D735	F736	V737	L738	S739	A740	L741	N742	S743	D744	Y745	E746	Q747	L748	A749	N750	I751	A752	A753	H754	R755	L756	I757	S758	I759	F760	A761	S762	L763	N764
N765	A766	Q767	K768	L769	K770	I771	V772	Q773	E774	I775	V776	D777	S778	S779	S780	N781	N782	E783	S784	S785	Y786	D787	T788	K729	Q730	S731	F732	M733	I734	D735	F736	V737	L738	S739	A740	L741	N742	S743	D744	Y745	E746	Q747	L748	A749	N750	I751	A752	A753	H754	R755	L756	I757	S758	I759	F760	A761	S762	L763	N764



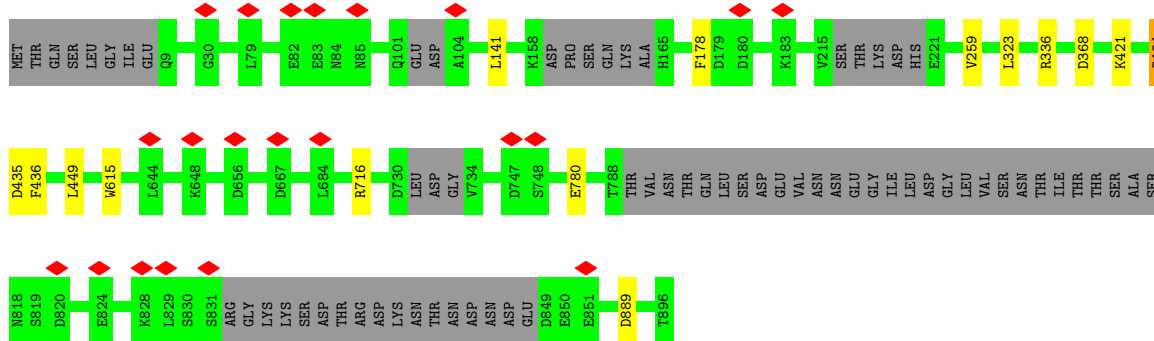
• Molecule 32: U3 small nucleolar RNA-associated protein 15

Chain AF:  95%

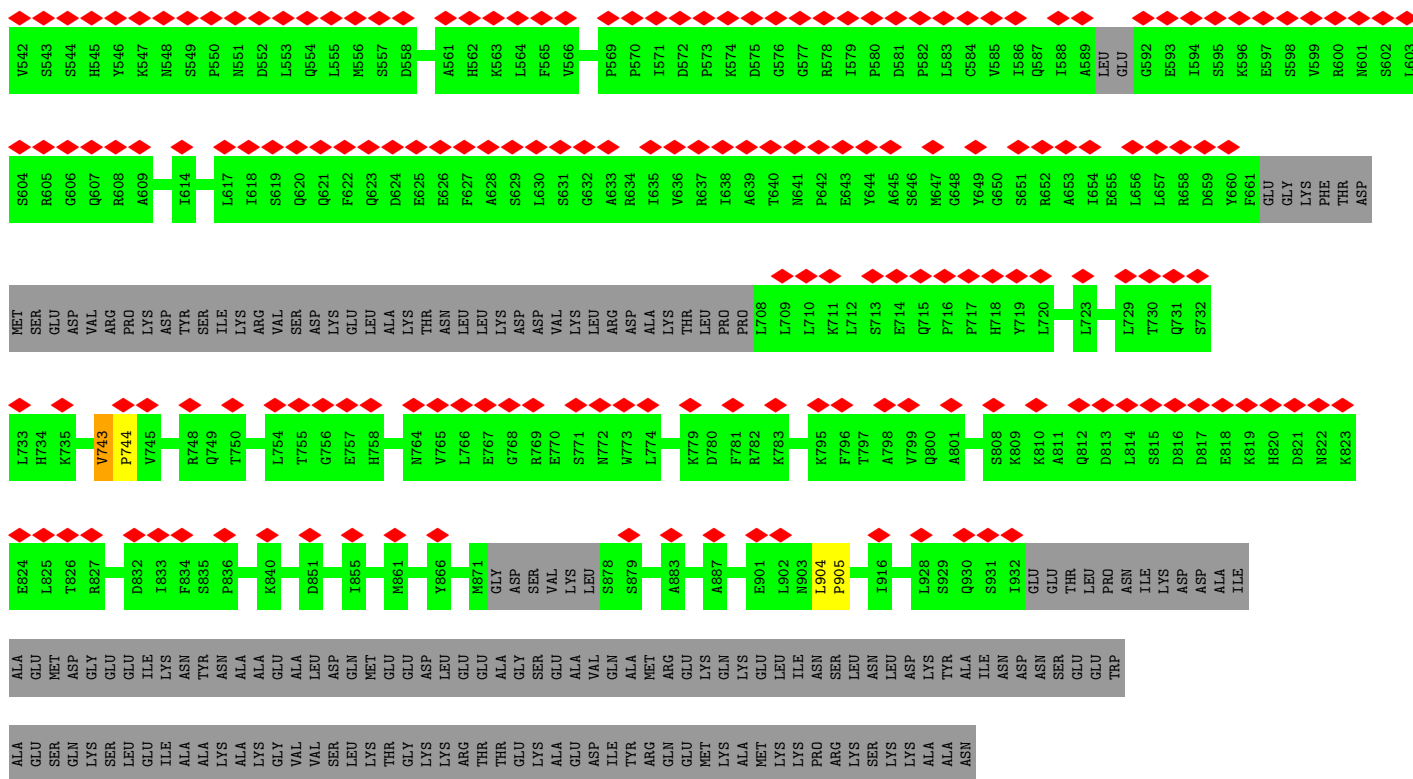


• Molecule 33: NET1-associated nuclear protein 1

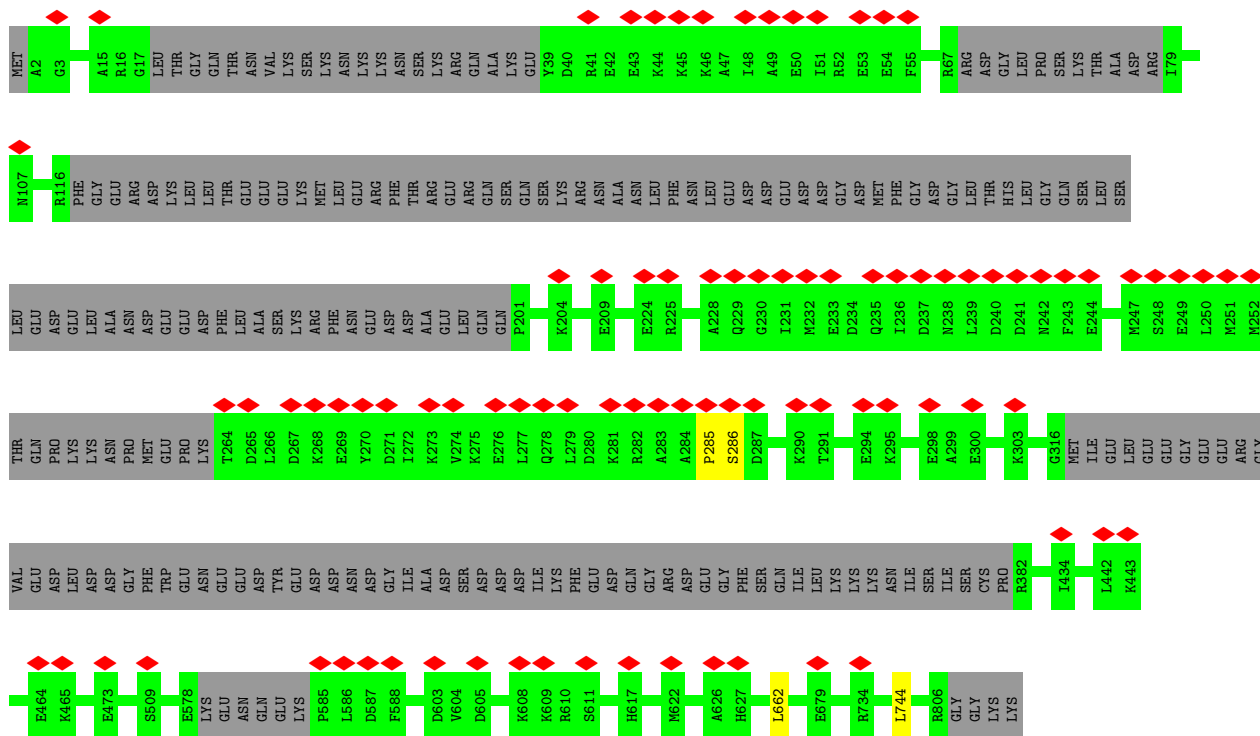
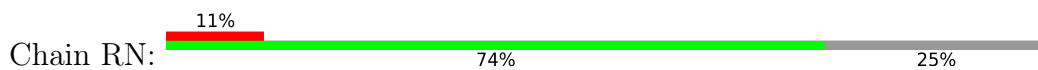
Chain AG:  91%



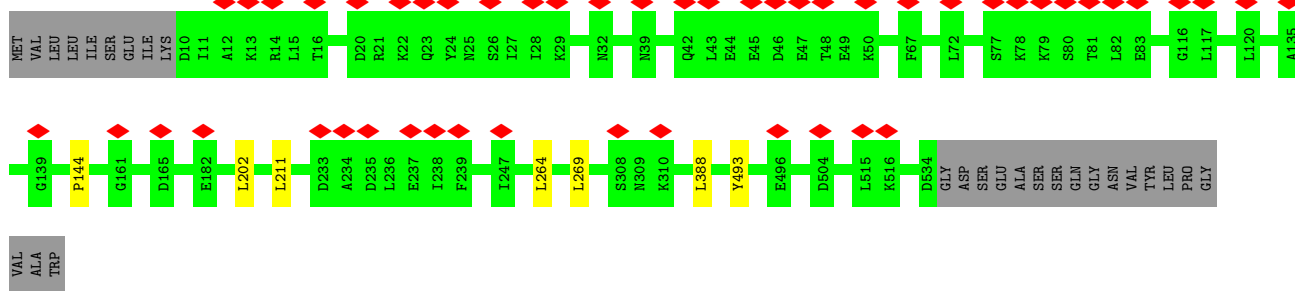
• Molecule 34: Periodic tryptophan protein 2



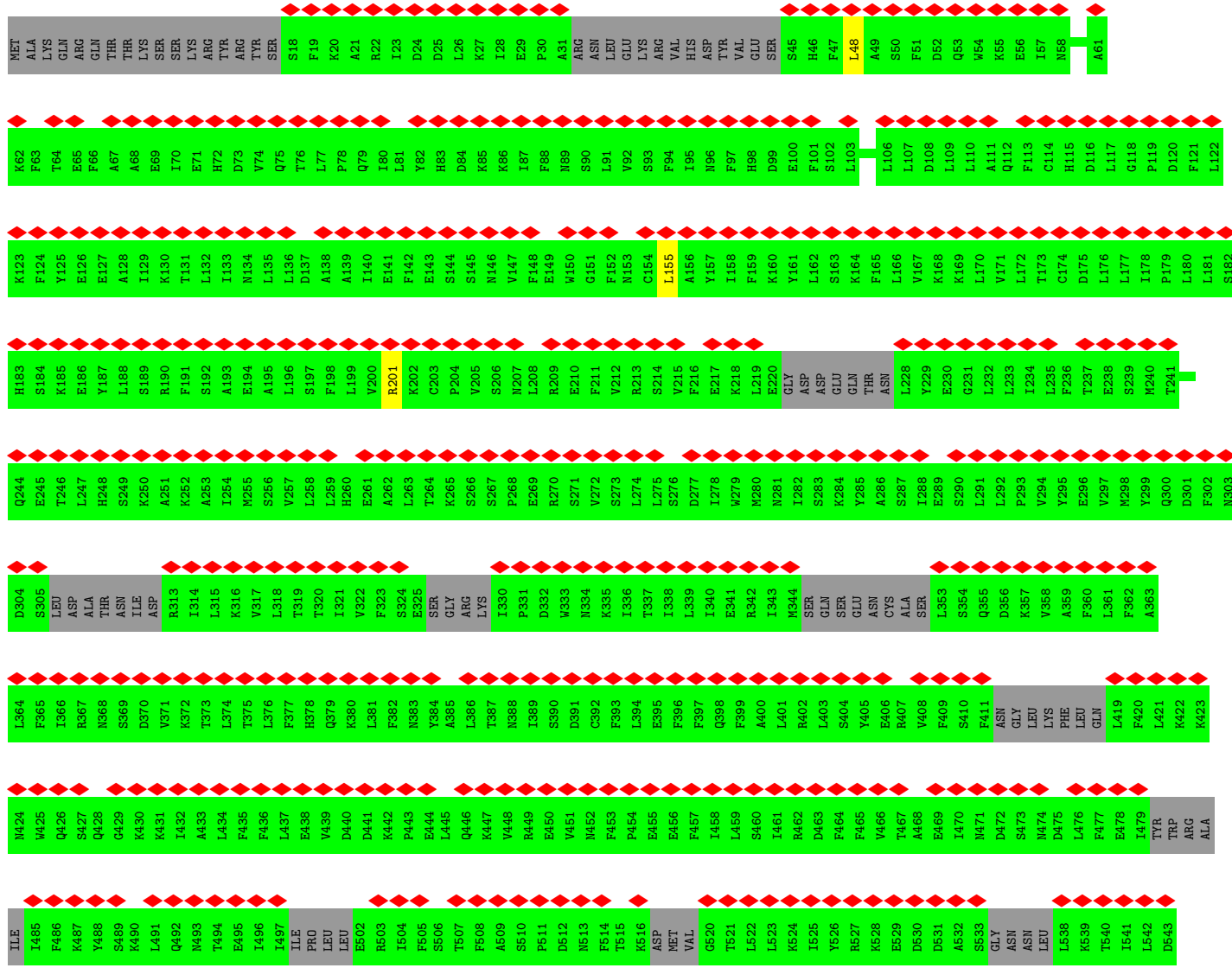
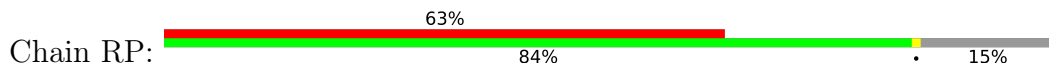
• Molecule 60: Nucleolar complex protein 14



• Molecule 61: Nucleolar complex protein 4

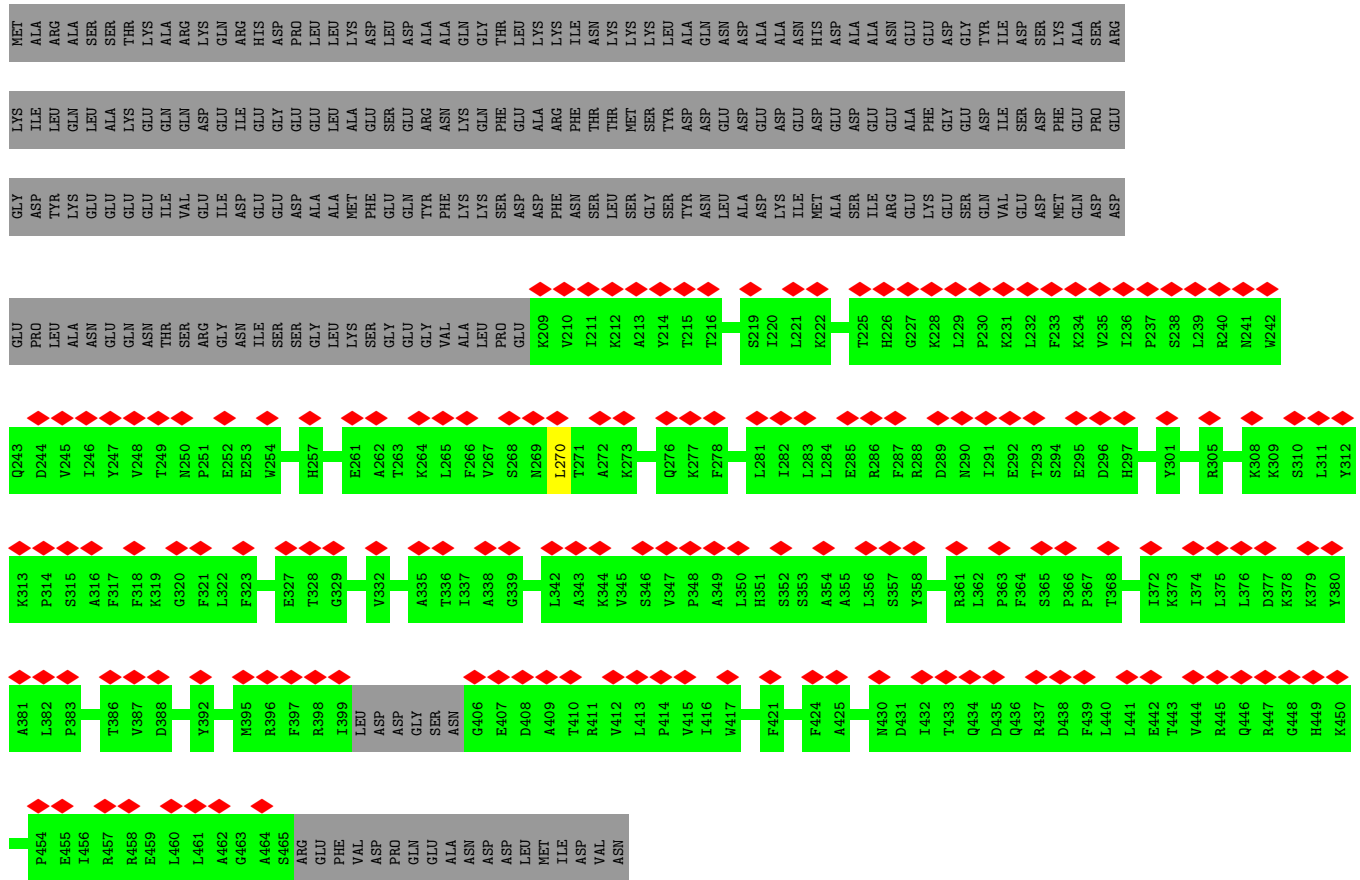


• Molecule 62: U3 small nucleolar RNA-associated protein 20

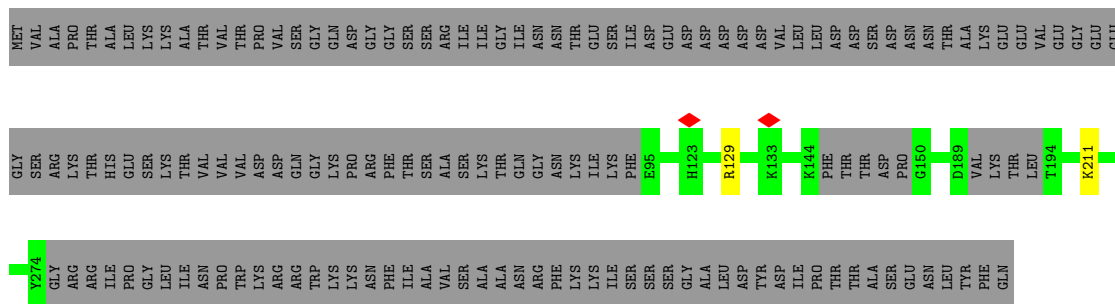


K1303	L1304	V1305	A1306	D1307	L1308	M1309	S1310	Y1311	S1312	S1313	S1314	M1315	M1316	H1317	E1318	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	LEU	ILE	GLU	ASP	GLY	TYR	LYS	SER	SER	GLU	LEU	TRP	PRO	LEU	LEU	PHE	THR	PHE	LEU	HIS	PHE	ILE	ASN	ASN	LYS	GLU	LEU	ALA					
K1242	I1243	L1244	K1245	I1246	L1247	K1248	L1249	I1250	V1251	F1252	N1253	Y1254	N1255	C1256	S1257	W1258	S1259	D1260	I1261	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	S1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	L1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	I1289	E1290	R1293	K1294	P1296	E1297	L1298	S1300	I1301	S1302				
L1122	Y1123	Y1124	D1125	E1126	F1127	A1128	T1129	A1130	T1131	A1132	L1133	M1134	D1135	T1136	I1137	S1138	N1139	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	G1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	R1159	N1160	V1161	N1163	D1164	L1165	H1166	Y1167	V1168	L1169	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	L1238	S1239	T1240	I1181	
L1182	P1183	S1184	L1185	Y1186	W1187	K1188	L1189	S1190	D1191	S1192	M1193	I1195	S1196	T1197	F1198	L1199	M200	L1201	L1202	V1203	S1204	I1205	T1206	E1207	M208	G1209	F1210	I1211	Q1212	D1213	A1214	D1215	V1216	R1217	S1218	L1219	L1220	I1221	S1222	L1224	I1225	S1226	I1227	L1228	K1229	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	L1238	S1239	T1240	I1181				
K1242	I1243	L1244	K1245	I1246	L1247	K1248	L1249	I1250	V1251	F1252	N1253	Y1254	N1255	C1256	S1257	W1258	S1259	D1260	I1261	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	S1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	L1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	I1289	E1290	R1293	K1294	P1296	E1297	L1298	S1300	I1301	S1302				
K664	Y665	G668	L669	L670	I609	L610	Q611	G612	M613	Q614	V615	P616	D617	L618	L619	S620	S621	G622	M623	V624	I625	E626	E627	I628	P629	L630	T631	L632	Q633	N634	A635	R636	D637	L638	T639	I640	R641	L642	K643	ASN	VAL	GLY	ALA	GLU	PHE	GLY	LYS	T652	K653	T654	D655	K656	L657	R658	S659	S660	F661	F662	A724	N725
K664	Y665	G668	L669	L670	I609	L610	Q611	G612	M613	Q614	V615	P616	D617	L618	L619	S620	S621	G622	M623	V624	I625	E626	E627	I628	P629	L630	T631	L632	Q633	N634	A635	R636	D637	L638	T639	I640	R641	L642	K643	ASN	VAL	GLY	ALA	GLU	PHE	GLY	LYS	T652	K653	T654	D655	K656	L657	R658	S659	S660	F661	F662	A724	N725
K726	V727	L728	W729	D730	S731	D732	V733	W734	R735	L736	R737	D738	T739	I740	F743	S744	H745	I746	W747	S748	T752	Q753	N754	T755	S756	I757	I758	S759	T760	T761	I762	E763	R764	R765	G766	N767	Y770	P771	I772	L773	I774	R775	N776	Q777	A778	L779	K780	V781	M782	L783	S784	I785	F786	Q787	V788	A789				
E790	M791	H792	F793	W794	D795	I796	A797	R798	F799	V800	V801	M802	D803	F804	K805	T806	Y807	K808	D809	E810	E811	D812	M813	E814	M815	R816	R817	V818	I819	T820	G821	S822	E825	V826	D827	R828	M829	V830	F831	L832	K833	T834	S836	K837	F838	K839	N840	I841	K842	N843	V844	V845	S846	A847	T848	E849	L850			
H851	D852	H853	L854	M855	V856	L858	G859	S860	R861	M862	T863	D864	V865	Q866	L868	A869	L870	D871	A872	L873	L874	A875	V876	K877	M878	P879	T880	L881	M882	K883	V884	R885	D886	N887	L888	K889	N890	L891	D892	D893	D894	T895	L896	F897	K898	D899	E900	I901	T902	N903	F904	L905	T906	E907	N908	G909	S910			
Q911	S912	I913	K914	A915	E916	D917	E918	K919	V920	V921	M922	P923	Y924	R927	I928	Q931	A932	A933	Q934	V935	P936	P937	T938	S939	G940	Q941	K942	R943	S944	R945	K946	I947	A948	V949	I950	S951	L953	P954	N955	I961	F964	S969	E970	D973	V974	N975	Y976	F977	F978	G979	N980	S981								
H982	Q983	I984	N985	S986	S987	K988	A989	T990	L991	R995	T998	G999	F1000	V1001	N1002	I1003	V1004	M1005	S1006	T1007	V1010	V1022	L1023	Q1024	P1025	S1029	I1030	A1031	M1032	A1033	Y1034	I1035	V1036	L1037	D1038	T1039	E1040	S1041	T1042	E1043	V1044	H1046	L1047	R1048	K1049	M1050	A1051	P1116	S1117	L1118	Y1119	Q1120	F1121	Q1057						
G1058	L1059	K1060	C1061	L1062	S1063	S1064	V1065	F1066	V1069	G1070	M1071	F1072	D1074	S1076	T1077	S1078	D1081	A1084	V1087	K1088	P1089	R1090	I1091	S1092	H1093	F1094	S1095	D1096	E1097	M1098	L1099	Q1100	Q1101	F1102	S1104	L1105	L1106	R1107	L1108	F1109	Y1111	V1112	W1113	H1114	M1115	P1116	S1117	L1118	Y1119	Q1120	F1121									
L1122	Y1123	Y1124	D1125	E1126	F1127	A1128	T1129	A1130	T1131	A1132	L1133	M1134	D1135	T1136	I1137	S1138	N1139	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	G1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	R1159	N1160	V1161	N1163	D1164	L1165	H1166	Y1167	V1168	L1169	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	L1238	S1239	T1240	I1181	
L1182	P1183	S1184	L1185	Y1186	W1187	K1188	L1189	S1190	D1191	S1192	M1193	I1195	S1196	T1197	F1198	L1199	M200	L1201	L1202	V1203	S1204	I1205	T1206	E1207	M208	G1209	F1210	I1211	Q1212	D1213	A1214	D1215	V1216	R1217	S1218	L1219	L1220	I1221	S1222	L1224	I1225	S1226	I1227	L1228	K1229	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	L1238	S1239	T1240	I1181				
K1242	I1243	L1244	K1245	I1246	L1247	K1248	L1249	I1250	V1251	F1252	N1253	Y1254	N1255	C1256	S1257	W1258	S1259	D1260	I1261	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	S1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	L1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	I1289	E1290	R1293	K1294	P1296	E1297	L1298	S1300	I1301	S1302				

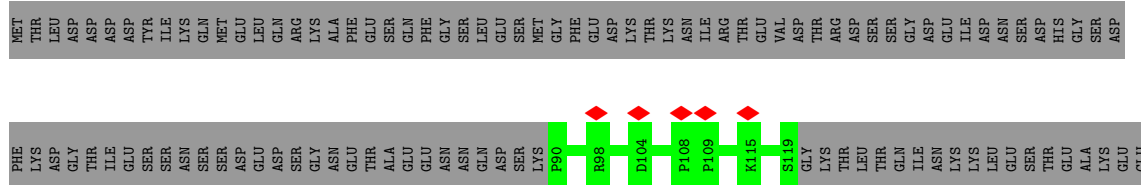
LEU	ARG	THR	ASN	ALA	SER	HIS	ILE	LEU	PHE	LYS	THR	ILE	D1376	F1377	I1378	N1379	E1380	K1381	P1382	N1383	L1384	N1385	E1386	A1387	S1388	K1389	I1390	S1392	M1393	L1394	K1395	D1396	I1397	L1398	L1399	P1400	N1401	I1402	R1403	I1404	G1405	L1406	R1407	D1408	S1409	I1410	E1411	E1412	V1413	GLN	GLU	TYR	VAL	SER	V1420	L1421	S1422
Y1423	M1424	V1425	K1426	N1427	T1428	K1429	Y1430	F1431	T1432	D1433	F1434	E1435	D1436	I1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	E1447	D1448	PHE	THR	THR	ASN	VAL	ASN	HIS	ILE	GLN	LEU	HIS	R1461	R1462	Q1463	A1465	I1466	K1467	R1468	L1469	D1470	S1471	I1472	A1473	H1474	Q1475	L1476	K1477	D1478	N1479	S1480	I1481	S1482	H1483	
Y1484	L1485	I1486	M1488	I1489	H1491	Y1492	F1493	V1494	S1495	D1496	D1497	E1498	R1499	Y1500	R1501	I1502	I1503	G1504	M1505	E1506	T1507	I1508	I1509	A1510	I1511	G1512	G1513	L1514	Q1515	PRO	H1517	M1518	S1519	W1520	M1521	K1524	A1525	L1526	L1527	R1528	R1529	Y1530	I1531	S1532	M1533	L1534	K1535	T1536	K1537	P1538	N1539	Q1540	I1541	K1542	Q1543	A1544	
V1545	Q1546	L1547	I1548	VAL	GLN	SER	LEU	PRO	VAL	LEU	ARG	GLU	T1558	I1561	V1562	G1565	A1566	E1567	S1568	K1569	L1570	T1571	L1572	S1573	K1574	F1575	F1576	S1577	ASN	LEU	ASP	GLU	PRO	LEU	PRO	LEU	THR	LEU	TYR	PRO	THR	LEU	LYS	ILE	GLY	THR	ARG	ASP	GLU	THR	ILE						
ILE	E1608	R1609	M1610	P1611	I1612	A1613	E1614	A1615	L1616	V1617	N1618	I1619	V1620	L1621	G1622	L1623	T1624	N1625	D1626	D1627	I1628	T1629	M1630	F1631	L1632	P1633	S1634	I1635	L1636	T1637	M1638	I1639	C1640	Q1641	V1642	L1643	R1644	S1645	E1648	E1649	L1650	R1651	D1652	A1653	V1654	G1659	S1662	L1670	V1671	F1672	E1676	A1679					
K1682	R1683	G1684	S1685	Q1686	I1687	H1688	Y1692	Y1696	K1706	H1707	S1708	D1709	L1710	S1713	M1716	I1717	E1723	G1727	F1728	A1729	G1730	E1731	K1732	K1733	D1734	S1735	E1736	N1737	I1738	H1739	T1740	L1741	V1742	K1743	E1744	I1745	K1746	K1749	Y1751	D1752	A1753	G1754	L1757	M1760	I1761	S1762	L1763	T1764									
E1765	F1766	G1767	T1768	L1769	L1770	R1780	I1781	N1782	L1783	R1784	N1785	L1792	L1793	R1794	L1797	H1802	M1803	S1804	E1809	K1813	C1814	C1815	E1821	S1822	MET	SER	ASN	ASN	PRO	GLN	ILE	PRO	LYS	LYS	VAL	VAL	ASP	GLN	ASP	GLU	LYS	GLU	ASP	PHE	PHE	VAL	VAL	ASN	LEU								
GLU	SER	LYS	THR	TYR	ILE	ASN	ASN	S1961	L1962	D1974	R1982	H1983	A1984	S1985	F1986	L1987	T1988	H1991	L1992	E1993	I1996	R1900	D1901	L1904	S1905	E1906	M1907	E1908	D1925	F1926	D1928	S1927	E1929	S1930	S1931	E1932	S1950	L1963	H1969	T1970	D1971	S1972	T1973	L1974	K1975	D1976											
E1992	R1995	I2011	M2012	L2013	P2014	E2015	L2016	Y2017	D2018	K2033	Y2044	L2047	M2048	E2049	Q2051	Q2052	S2053	K2054	L2057	E2058	Q2060	F2061	Y2065	L2082	L2085	I2086	K2089	ALA	P2092	A2093	S2096	K2097	L2098	S2099	F2103	L2104	A2105	N2112	D2113	D2114	A2115	A2122															
S2123	V2124	L2125	I2126	L2130	L2133	E2134	N2135	K2136	D2137	L2138	E2139	I2140	V2141	E2142	K2143	A2147	TRP	LEU	LYS	GLN	VAL	D2153	M2154	A2155	S2156	F2157	L2162	L2163	T2164	Y2165	K2166	V2167	L2171	L2172	S2171	I2172	G2173	F2174	H2176	T2177	I2178	E2179	L2180	L2183	K2186	R2187	I2188	D2189	TYR	ILE	LEU						
SER	ASP	THR	SER	VAL	GLY	SER	GLU	HIS	GLN	TRP	ASP	THR	F2213	S2214	S2215	I2216	S2222	V2223	Y2224	K2225	H2226	G2227	PHE	LYS	ASP	ILE	V2232	D2233	G2234	L2235	L2236	T2237	C2238	L2239	L2240	Y2241	P2242	H2243	S2244	W2245	W2246	ARG	GLN	SER	ALA	A2251	N2252	L2253	V2254	H2255	Q2256						
L2257	I2258	A2259	N2260	K2261	D2262	K2263	L2264	E2265	I2266	S2267	L2268	T2269	ASN	LEU	GLU	ILE	F2275	I2276	A2277	T2278	R2279	I2280	L2281	H2282	Q2283	L2284	G2285	A2286	P2287	S2288	I2289	P2290	GLU	ASN	LEU	A2294	N2295	V2296	S2297	L2298	K2299	T2300	L2301	V2302	S2305	L2306	L2307	W2308	K2309	V2310	Q2311	ARG	THR	PRO	PHE	ILE	MET
ASP	VAL	SER	LYS	GLN	T2323	E2325	D2326	L2327	K2328	S2329	T2330	T2331	A2332	L2333	D2334	Y2335	M2336	V2337	T2338	R2339	ILE	GLY	G2342	L2343	I2344	R2345	S2346	D2347	E2348	H2349	K2350	M2351	D2352	S2353	F2354	M2355	S2356	K2357	ALA	CYS	ILE	GLN	LEU	A2365	L2366	L2367	V2368	Q2369	V2370	L2371	D2372	E2373	D2374	E2375	V2376	I2377	



• Molecule 65: Pno1



• Molecule 66: Protein FAF1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	71230	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.246	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	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: MG, GTP, 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	3A	0.92	0/4141	1.17	24/6433 (0.4%)
2	5A	0.84	0/12485	1.11	48/19449 (0.2%)
3	SA	0.71	0/31590	1.16	247/49182 (0.5%)
4	SC	0.47	0/1856	0.73	5/2490 (0.2%)
5	SF	0.35	0/1854	0.66	1/2504 (0.0%)
6	SG	0.53	0/1690	0.64	0/2285
7	SH	0.31	0/1341	0.60	0/1789
8	SI	0.38	0/1341	0.67	1/1806 (0.1%)
9	SJ	0.31	0/1347	0.59	1/1801 (0.1%)
10	SK	0.47	0/1410	0.60	0/1888
11	SM	0.31	0/1020	0.58	0/1374
12	SN	0.32	0/873	0.73	1/1185 (0.1%)
13	SO	0.45	0/1109	0.62	0/1495
14	SP	0.49	0/879	0.68	0/1186
15	SR	0.58	0/990	0.73	1/1335 (0.1%)
16	ST	0.38	0/980	0.63	0/1319
17	SX	0.51	0/1020	0.66	1/1371 (0.1%)
18	SY	0.54	0/798	0.67	1/1065 (0.1%)
19	SZ	0.43	0/822	0.64	0/1103
20	Sc	0.44	0/613	0.65	0/828
21	Sd	0.54	0/499	0.66	0/670
22	3B	0.59	0/1901	0.66	1/2567 (0.0%)
22	3C	0.44	0/1796	0.62	1/2424 (0.0%)
23	3D	0.44	0/2891	0.63	3/3895 (0.1%)
24	3E	0.41	0/3059	0.62	3/4153 (0.1%)
25	3F	0.42	0/3715	0.64	2/5001 (0.0%)
26	3G	0.52	0/928	0.76	1/1262 (0.1%)
26	3H	0.47	0/928	0.69	2/1262 (0.2%)
27	A4	0.47	0/5321	0.66	5/7207 (0.1%)
28	A5	0.48	0/4044	0.68	5/5493 (0.1%)
29	A8	0.30	0/3328	0.61	0/4565
30	A9	0.31	0/951	0.58	1/1287 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.37	0/10049	0.56	6/13737 (0.0%)
32	AF	0.53	0/3993	0.67	4/5413 (0.1%)
33	AG	0.47	0/6699	0.65	3/9077 (0.0%)
34	B1	0.64	0/6780	0.68	7/9175 (0.1%)
35	B2	0.43	0/6853	0.67	3/9256 (0.0%)
36	B3	0.39	0/6014	0.69	7/8137 (0.1%)
37	B8	0.58	0/3848	0.66	4/5218 (0.1%)
38	BE	0.57	0/6948	0.66	7/9391 (0.1%)
39	B6	0.45	0/2849	0.58	1/3853 (0.0%)
40	5B	0.34	0/499	0.62	0/659
41	5C	0.58	0/4321	0.68	5/5832 (0.1%)
42	5D	0.50	0/1998	0.66	3/2644 (0.1%)
43	5E	0.47	0/1665	0.64	1/2233 (0.0%)
44	5F	0.66	0/1559	0.73	2/2097 (0.1%)
45	5G	0.56	0/2337	0.66	1/3148 (0.0%)
46	5H	0.45	0/1074	0.56	0/1422
47	5I	0.61	0/3844	0.66	2/5174 (0.0%)
48	5J	0.42	0/1302	0.54	0/1728
49	5K	0.56	0/1426	0.66	1/1917 (0.1%)
50	RA	0.34	0/2769	0.67	1/3753 (0.0%)
51	RB	0.38	0/1121	0.62	0/1487
52	RC	0.46	0/2245	0.60	0/3021
53	RE	0.38	0/8924	0.62	6/12070 (0.0%)
54	RF	0.34	0/2004	0.63	2/2697 (0.1%)
55	RG	0.39	0/1727	0.68	2/2329 (0.1%)
55	RH	0.42	0/1828	0.61	0/2470
56	RI	0.46	0/2080	0.65	0/2797
57	RJ	0.50	0/6514	0.60	1/8768 (0.0%)
58	RK	0.44	0/2832	0.65	3/3825 (0.1%)
59	RL	0.29	0/4549	0.50	0/6241
59	RM	0.25	0/3765	0.47	0/5218
60	RN	0.36	0/4591	0.58	2/6187 (0.0%)
61	RO	0.38	0/3849	0.62	5/5261 (0.1%)
62	RP	0.28	0/12230	0.51	5/16819 (0.0%)
63	RQ	0.46	0/1678	0.58	0/2282
64	RS	0.33	0/2104	0.67	1/2854 (0.0%)
65	RT	0.42	0/1379	0.63	1/1853 (0.1%)
66	RV	0.47	0/1456	0.63	2/1937 (0.1%)
67	RW	0.34	0/385	0.50	0/529
68	RY	0.29	0/307	0.51	0/415
All	All	0.53	0/239915	0.77	443/334598 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
13	SO	0	1
14	SP	0	1
16	ST	0	1
19	SZ	0	1
20	Sc	0	1
23	3D	0	3
24	3E	0	1
25	3F	0	1
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	1
29	A8	0	4
33	AG	0	2
34	B1	0	3
35	B2	0	9
36	B3	0	11
38	BE	0	1
41	5C	0	2
42	5D	0	1
43	5E	0	1
44	5F	0	1
45	5G	0	1
47	5I	0	2
50	RA	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
57	RJ	0	2
58	RK	0	1
59	RL	0	1
59	RM	0	1
60	RN	0	1
61	RO	0	1
62	RP	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
63	RQ	0	1
66	RV	0	2
All	All	0	79

There are no bond length outliers.

The worst 5 of 443 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	861	U	C2-N1-C1'	10.60	130.42	117.70
3	SA	376	C	N1-C2-O2	10.43	125.16	118.90
3	SA	1174	C	N1-C2-O2	10.35	125.11	118.90
44	5F	13	LEU	CA-CB-CG	10.29	138.96	115.30
3	SA	1034	C	C5-C6-N1	10.00	126.00	121.00

There are no chirality outliers.

5 of 79 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	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	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	34	69
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
13	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
14	SP	116/137 (85%)	99 (85%)	16 (14%)	1 (1%)	17	56
15	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
16	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
17	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
18	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
19	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	15	54
20	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
21	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
23	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
24	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
25	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	47	79
26	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	58
26	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
27	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
28	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
29	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	34	69
30	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
31	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
32	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
33	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	51	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
35	B2	839/943 (89%)	749 (89%)	88 (10%)	2 (0%)	47	79
36	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	41	74
37	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
38	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
39	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	487 (92%)	43 (8%)	1 (0%)	47	79
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	29	67
44	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
45	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
46	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
47	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
48	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
49	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
50	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
51	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	19	58
52	RC	276/316 (87%)	259 (94%)	17 (6%)	0	100	100
53	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
54	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
55	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
55	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
56	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
57	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	51	83
58	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
59	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	41	74
59	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	29	67
60	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	47	79
61	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
62	RP	2043/2493 (82%)	1815 (89%)	227 (11%)	1 (0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
64	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
65	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
66	RV	184/346 (53%)	165 (90%)	19 (10%)	0	100	100
67	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
68	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	24979/33626 (74%)	22503 (90%)	2452 (10%)	24 (0%)	54	83

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
59	RM	905	PRO
19	SZ	51	GLU

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	SC	203/224 (91%)	201 (99%)	2 (1%)	76	90
5	SF	196/222 (88%)	190 (97%)	6 (3%)	40	72
6	SG	180/191 (94%)	180 (100%)	0	100	100
7	SH	139/201 (69%)	137 (99%)	2 (1%)	67	86
8	SI	146/170 (86%)	145 (99%)	1 (1%)	84	94
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	65	85
10	SK	147/166 (89%)	146 (99%)	1 (1%)	84	94
11	SM	110/137 (80%)	108 (98%)	2 (2%)	59	82
12	SN	88/119 (74%)	86 (98%)	2 (2%)	50	78
13	SO	117/128 (91%)	116 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	SP	90/105 (86%)	90 (100%)	0	100	100
15	SR	105/119 (88%)	105 (100%)	0	100	100
16	ST	105/129 (81%)	104 (99%)	1 (1%)	76	90
17	SX	108/111 (97%)	107 (99%)	1 (1%)	78	91
18	SY	85/120 (71%)	84 (99%)	1 (1%)	71	88
19	SZ	85/113 (75%)	85 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	201 (100%)	0	100	100
22	3C	190/240 (79%)	187 (98%)	3 (2%)	62	84
23	3D	296/435 (68%)	293 (99%)	3 (1%)	76	90
24	3E	262/433 (60%)	261 (100%)	1 (0%)	91	95
25	3F	396/503 (79%)	394 (100%)	2 (0%)	88	95
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	591/713 (83%)	584 (99%)	7 (1%)	71	88
28	A5	433/574 (75%)	432 (100%)	1 (0%)	93	98
29	A8	174/657 (26%)	173 (99%)	1 (1%)	86	94
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	705 (100%)	3 (0%)	91	95
32	AF	437/454 (96%)	433 (99%)	4 (1%)	78	91
33	AG	750/826 (91%)	740 (99%)	10 (1%)	69	87
34	B1	730/812 (90%)	726 (100%)	4 (0%)	88	95
35	B2	736/832 (88%)	731 (99%)	5 (1%)	84	94
36	B3	665/719 (92%)	655 (98%)	10 (2%)	65	85
37	B8	421/529 (80%)	420 (100%)	1 (0%)	93	98
38	BE	757/819 (92%)	754 (100%)	3 (0%)	91	95
39	B6	251/414 (61%)	247 (98%)	4 (2%)	62	84
40	5B	57/196 (29%)	55 (96%)	2 (4%)	36	69
41	5C	465/480 (97%)	463 (100%)	2 (0%)	91	95
42	5D	221/234 (94%)	219 (99%)	2 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	5E	185/535 (35%)	184 (100%)	1 (0%)	88	95
44	5F	171/172 (99%)	170 (99%)	1 (1%)	86	94
45	5G	251/258 (97%)	249 (99%)	2 (1%)	81	93
46	5H	107/538 (20%)	107 (100%)	0	100	100
47	5I	416/443 (94%)	414 (100%)	2 (0%)	88	95
48	5J	140/200 (70%)	140 (100%)	0	100	100
49	5K	157/169 (93%)	157 (100%)	0	100	100
50	RA	303/636 (48%)	300 (99%)	3 (1%)	76	90
51	RB	117/315 (37%)	114 (97%)	3 (3%)	46	76
52	RC	231/289 (80%)	230 (100%)	1 (0%)	91	95
53	RE	984/1125 (88%)	979 (100%)	5 (0%)	88	95
54	RF	221/274 (81%)	219 (99%)	2 (1%)	78	91
55	RG	195/222 (88%)	193 (99%)	2 (1%)	76	90
55	RH	206/222 (93%)	204 (99%)	2 (1%)	76	90
56	RI	235/256 (92%)	235 (100%)	0	100	100
57	RJ	683/1039 (66%)	676 (99%)	7 (1%)	76	90
58	RK	307/312 (98%)	303 (99%)	4 (1%)	69	87
59	RL	164/934 (18%)	162 (99%)	2 (1%)	71	88
60	RN	422/732 (58%)	422 (100%)	0	100	100
61	RO	329/506 (65%)	328 (100%)	1 (0%)	92	96
62	RP	499/2307 (22%)	493 (99%)	6 (1%)	71	88
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	55	80
64	RS	225/424 (53%)	225 (100%)	0	100	100
65	RT	148/282 (52%)	146 (99%)	2 (1%)	67	86
66	RV	141/304 (46%)	141 (100%)	0	100	100
67	RW	22/192 (12%)	22 (100%)	0	100	100
68	RY	31/482 (6%)	30 (97%)	1 (3%)	39	71
All	All	18233/29007 (63%)	18093 (99%)	140 (1%)	82	93

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	RJ	566	ARG

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Mol	Chain	Res	Type
57	RJ	1128	LYS
62	RP	1770	LEU
33	AG	259	VAL
33	AG	141	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 304 such sidechains are listed below:

Mol	Chain	Res	Type
53	RE	537	ASN
62	RP	1686	GLN
53	RE	1033	ASN
57	RJ	289	HIS
65	RT	218	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	1304/1808 (72%)	498 (38%)	19 (1%)
All	All	1991/2841 (70%)	703 (35%)	32 (1%)

5 of 703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1197	C
3	SA	1521	G
2	5A	536	A
2	5A	492	G
3	SA	1594	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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
71	GTP	RJ	1201	72	26,34,34	0.94	2 (7%)	32,54,54	0.92	0

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
71	GTP	RJ	1201	72	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	RJ	1201	GTP	C5-C6	-2.47	1.42	1.47
71	RJ	1201	GTP	C8-N7	-2.05	1.31	1.35

There are no bond angle outliers.

There are no chirality outliers.

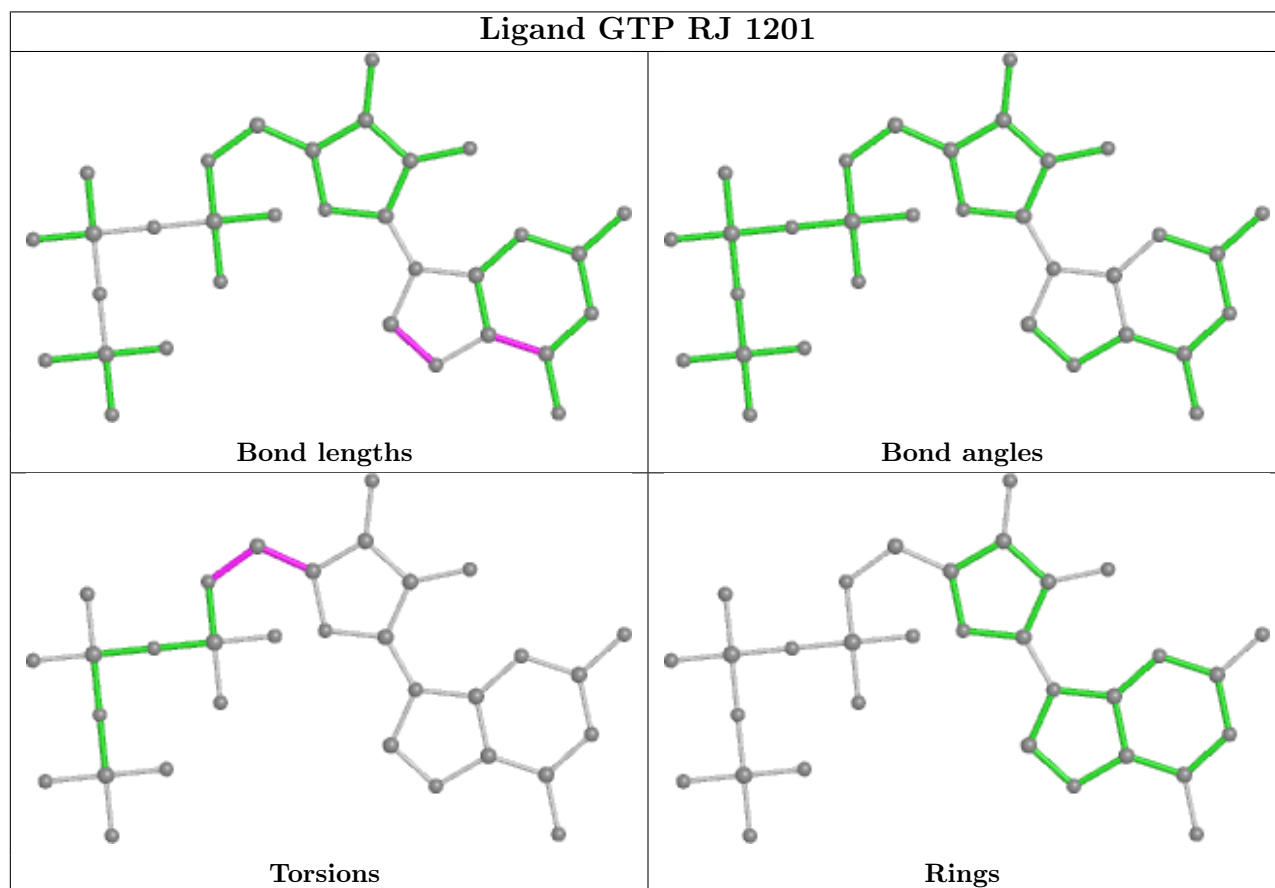
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RJ	1201	GTP	O4'-C4'-C5'-O5'
71	RJ	1201	GTP	C3'-C4'-C5'-O5'
71	RJ	1201	GTP	C4'-C5'-O5'-PA

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.

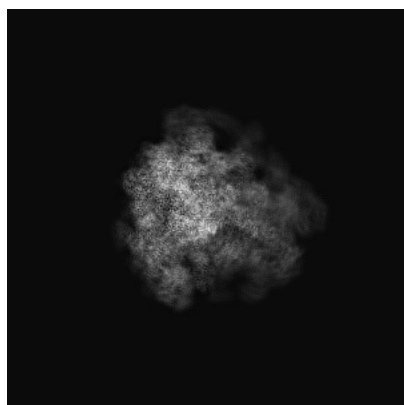
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0949. These allow visual inspection of the internal detail of the map and identification of artifacts.

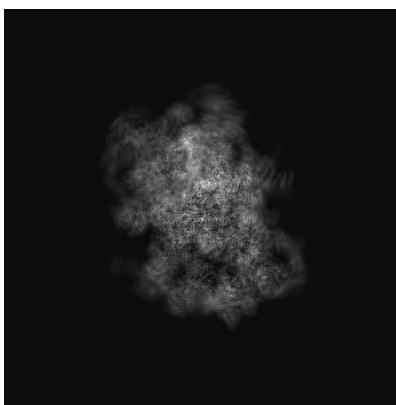
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

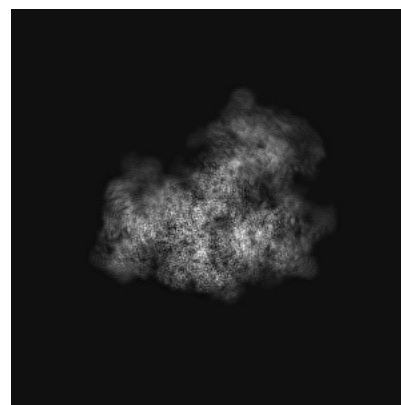
6.1.1 Primary map



X



Y

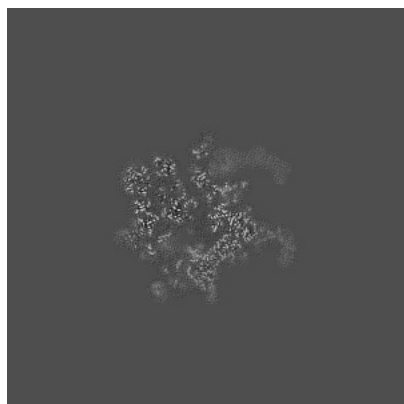


Z

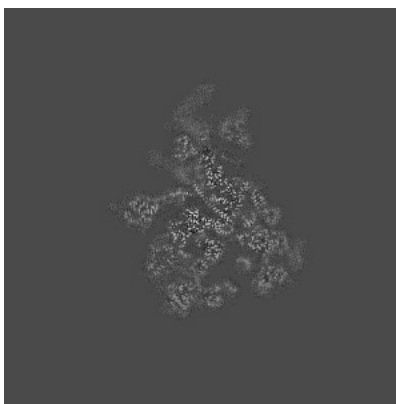
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

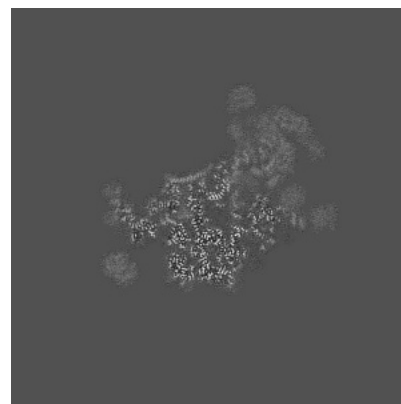
6.2.1 Primary map



X Index: 224



Y Index: 224

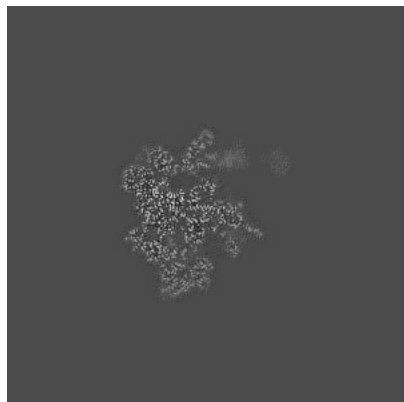


Z Index: 224

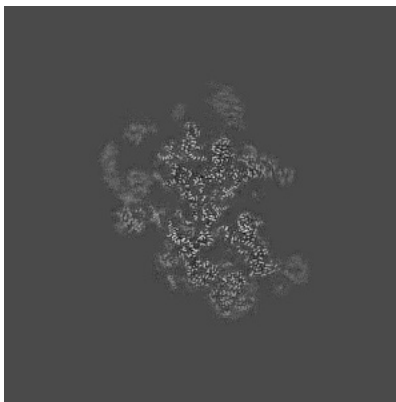
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

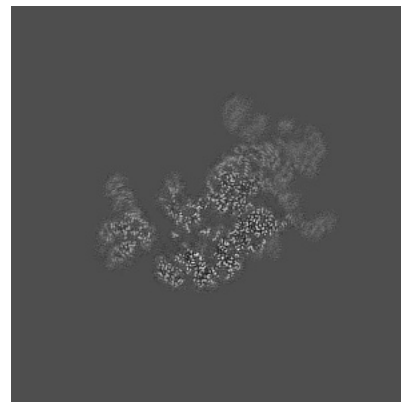
6.3.1 Primary map



X Index: 212



Y Index: 196

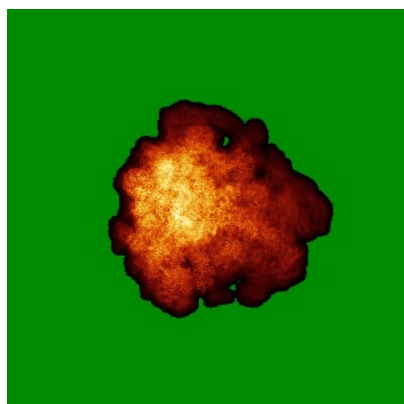


Z Index: 242

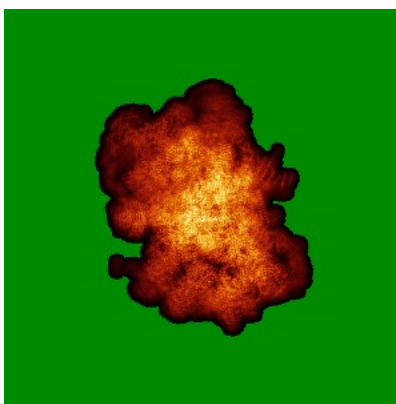
The images above show the largest variance slices of the map in three orthogonal directions.

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

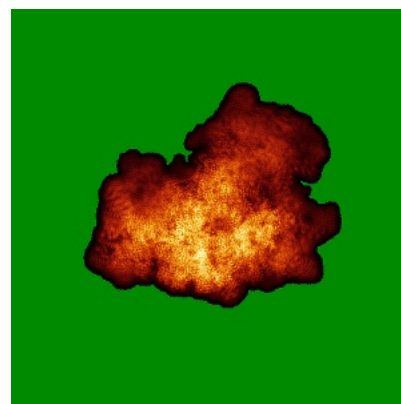
6.4.1 Primary map



X



Y

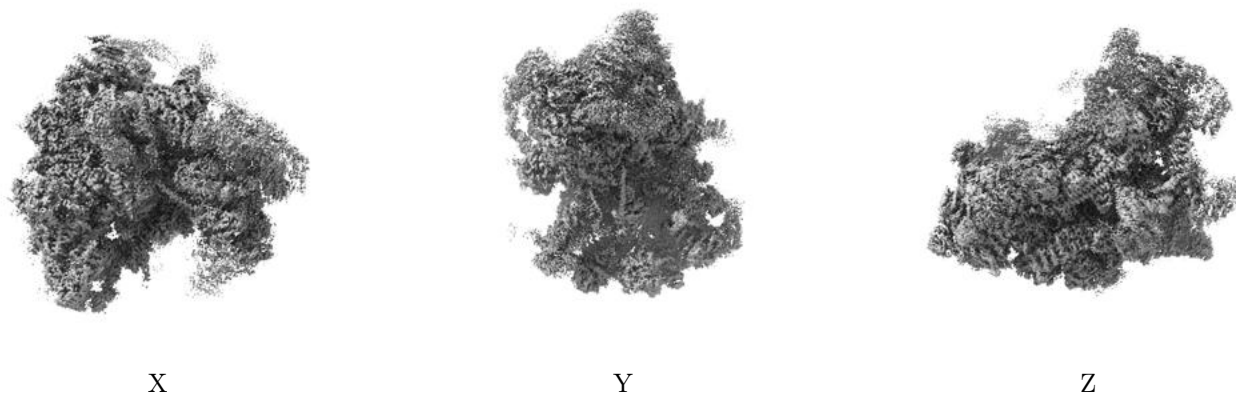


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

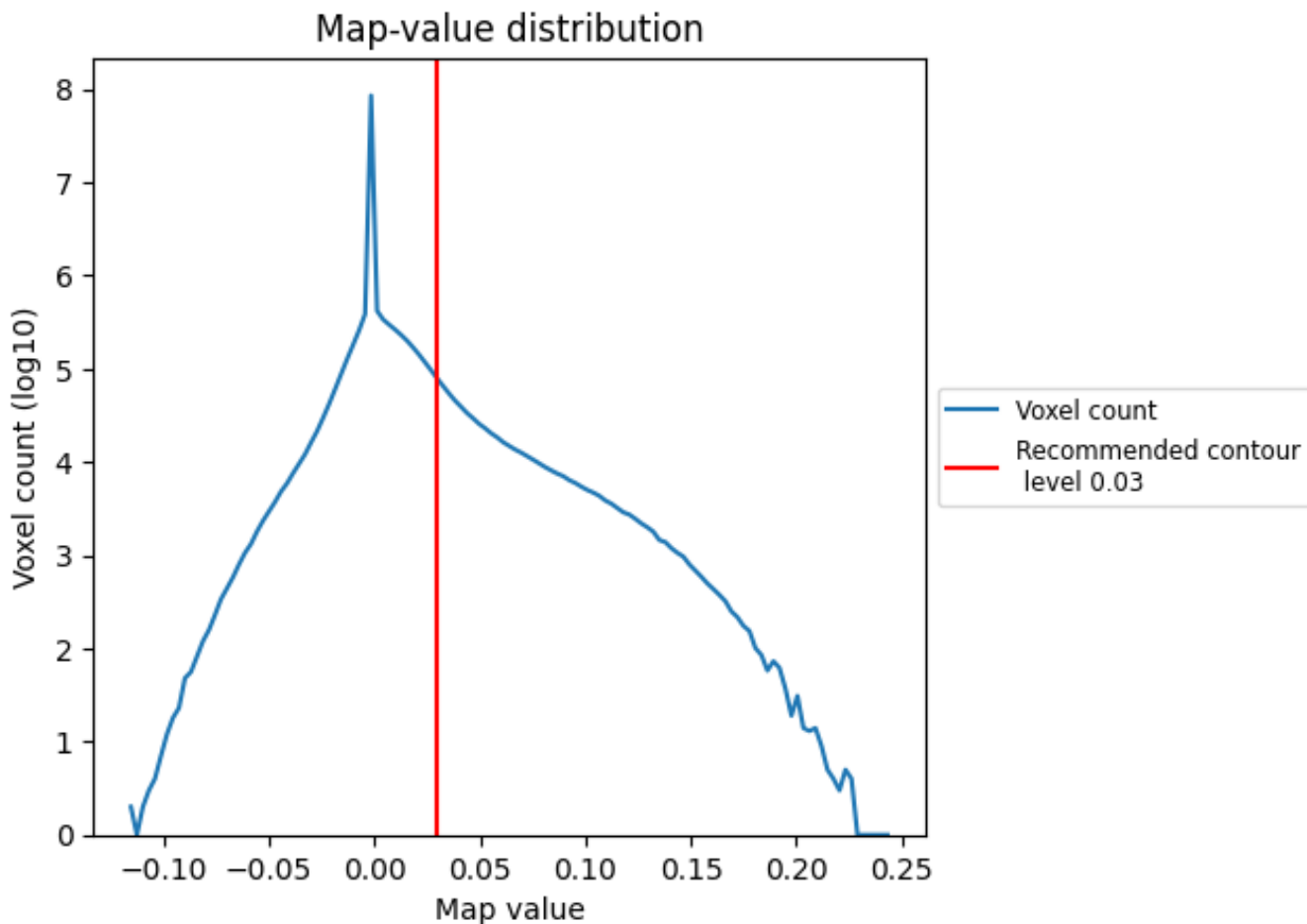
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

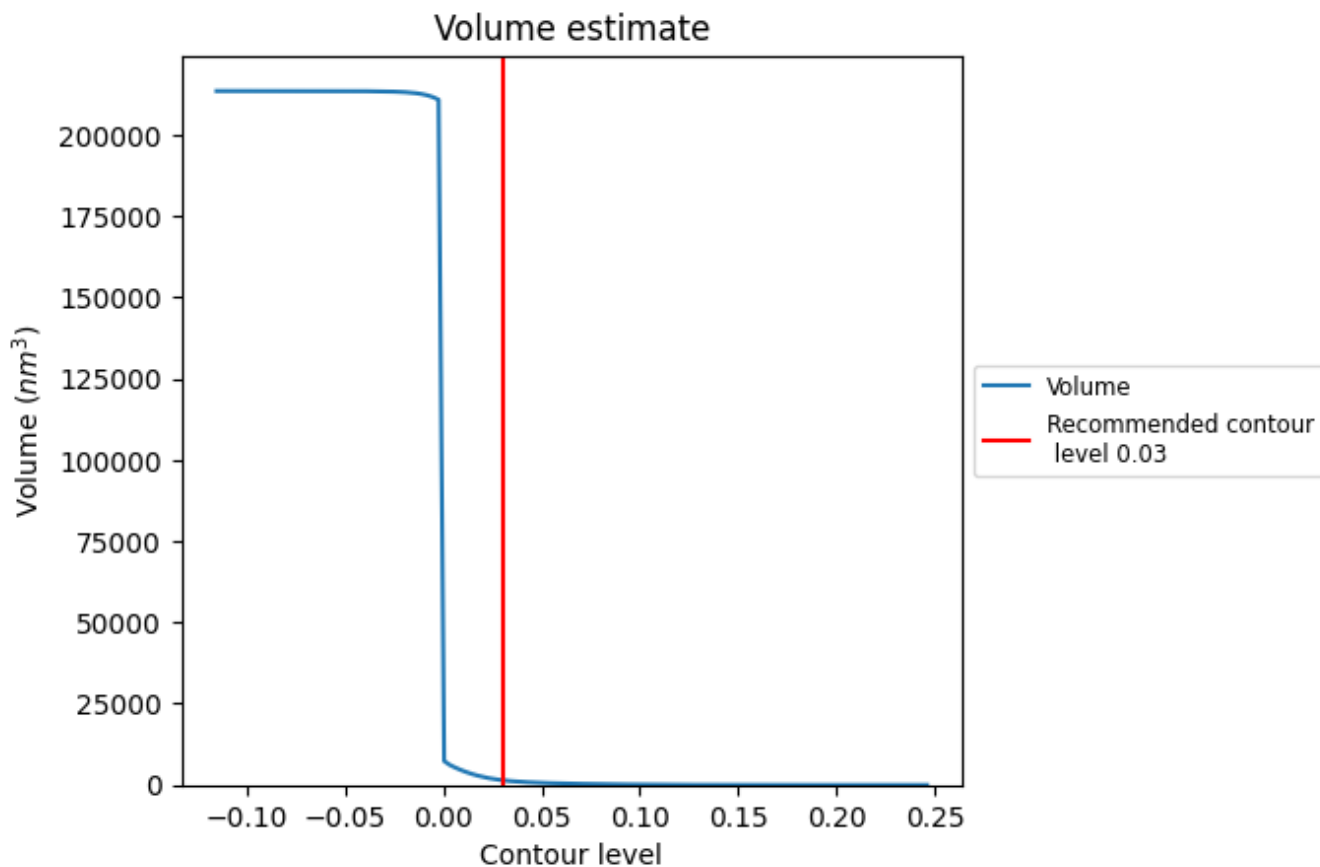
This section contains the results of statistical analysis of the map.

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.

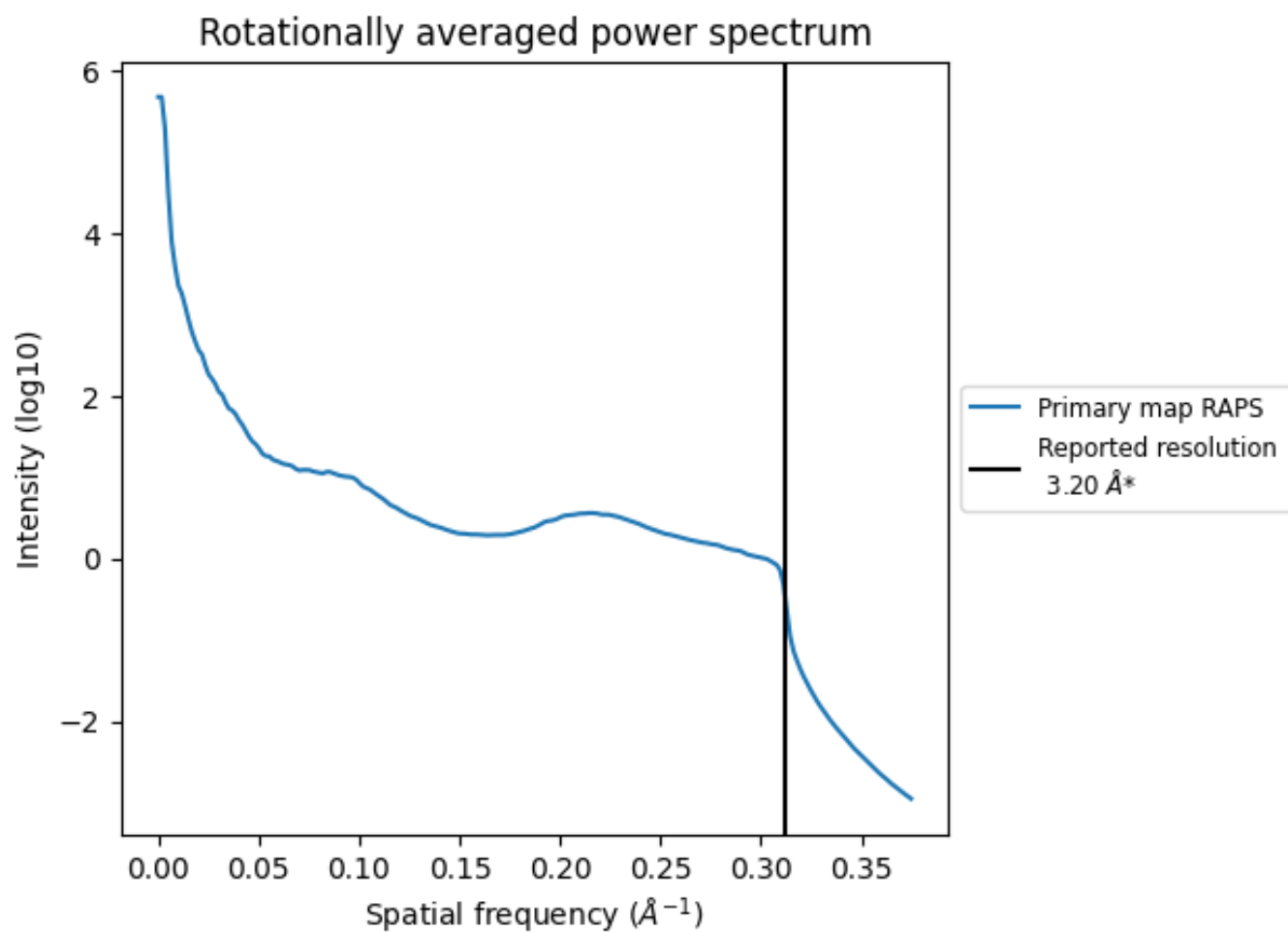
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1466 nm³; this corresponds to an approximate mass of 1324 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

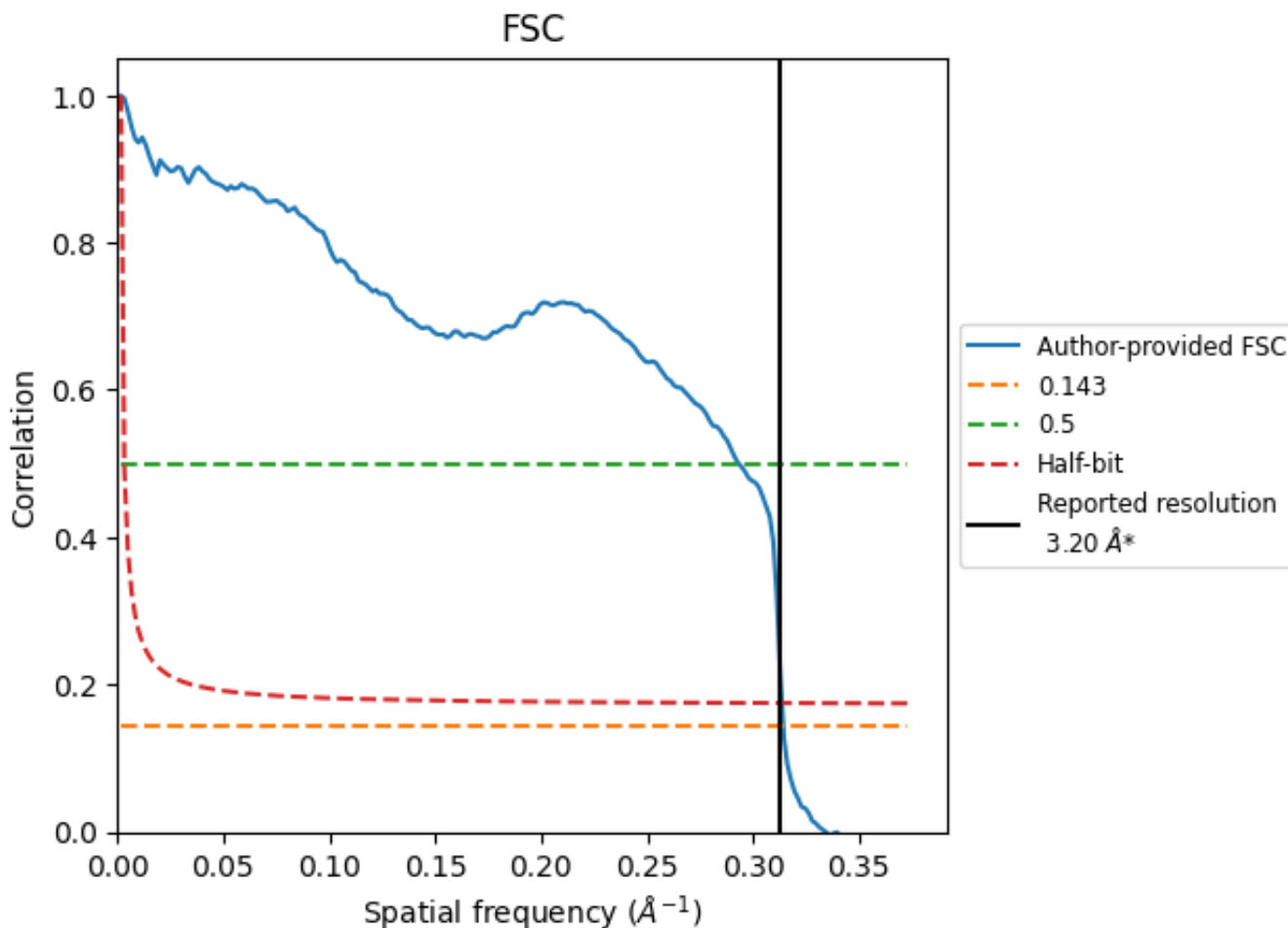


*Reported resolution corresponds to spatial frequency of 0.312\AA^{-1}

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

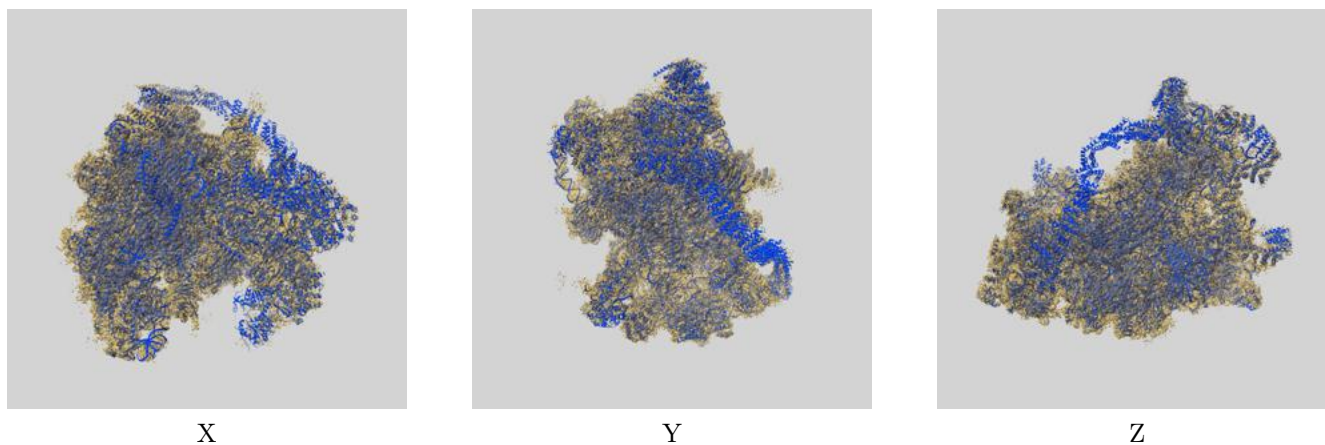
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.41	3.19
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

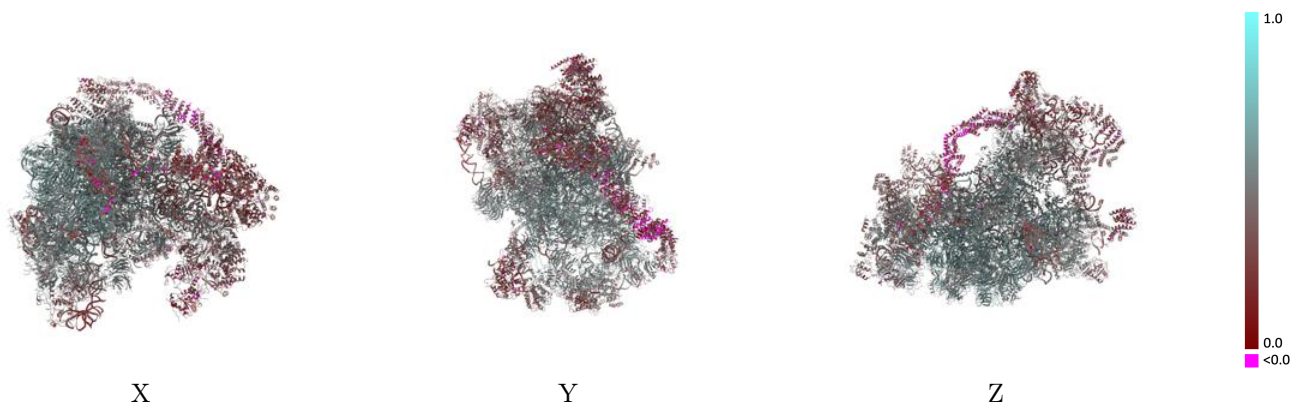
This section contains information regarding the fit between EMDB map EMD-0949 and PDB model 6LQP. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



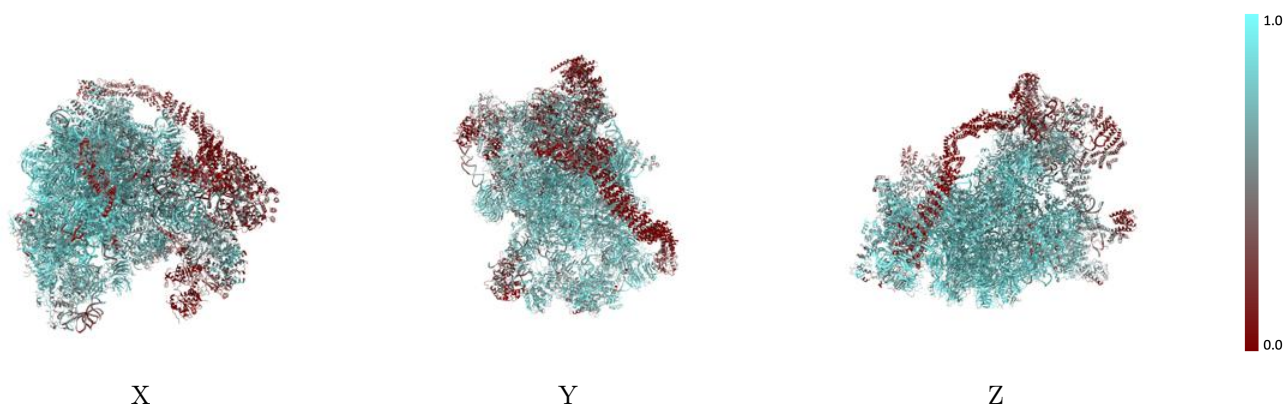
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



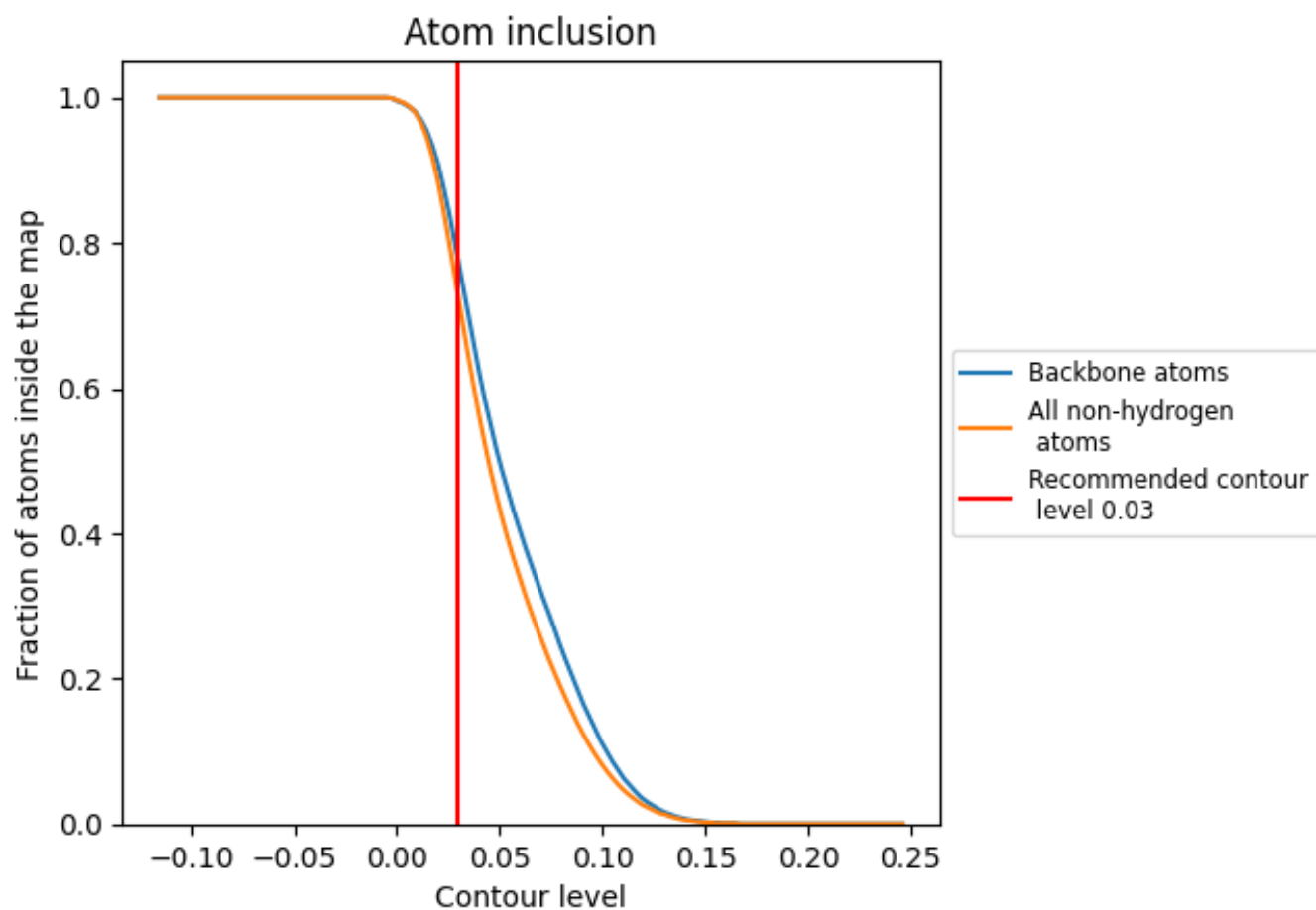
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4710
3A	 0.9050	 0.5090
3B	 0.8850	 0.5680
3C	 0.7980	 0.5000
3D	 0.8130	 0.5140
3E	 0.7920	 0.4870
3F	 0.7810	 0.4970
3G	 0.8710	 0.5540
3H	 0.8270	 0.5340
5A	 0.8940	 0.4880
5B	 0.7230	 0.4830
5C	 0.8960	 0.5750
5D	 0.8260	 0.5310
5E	 0.8190	 0.5440
5F	 0.9230	 0.5830
5G	 0.8720	 0.5680
5H	 0.8170	 0.5270
5I	 0.8990	 0.5770
5J	 0.7060	 0.5110
5K	 0.8810	 0.5670
A4	 0.8400	 0.5160
A5	 0.8530	 0.5350
A8	 0.5490	 0.3710
A9	 0.7580	 0.4200
AE	 0.3280	 0.3250
AF	 0.8920	 0.5540
AG	 0.8330	 0.5210
B1	 0.9100	 0.5770
B2	 0.8170	 0.5040
B3	 0.7660	 0.4720
B6	 0.7450	 0.4690
B8	 0.8980	 0.5670
BE	 0.9110	 0.5760
RA	 0.5410	 0.4120
RB	 0.6400	 0.4590



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Chain	Atom inclusion	Q-score
RC	 0.7470	 0.5120
RE	 0.6650	 0.4410
RF	 0.5400	 0.4040
RG	 0.6890	 0.4530
RH	 0.8230	 0.5330
RI	 0.8460	 0.5290
RJ	 0.8370	 0.5370
RK	 0.8320	 0.5310
RL	 0.5790	 0.4100
RM	 0.2390	 0.3000
RN	 0.6800	 0.4410
RO	 0.7590	 0.4580
RP	 0.3010	 0.3170
RQ	 0.7450	 0.5040
RS	 0.3360	 0.2730
RT	 0.8270	 0.5200
RV	 0.8290	 0.5350
RW	 0.7040	 0.4960
RY	 0.4400	 0.3860
SA	 0.7270	 0.4210
SC	 0.8170	 0.5370
SF	 0.6230	 0.4190
SG	 0.8590	 0.5590
SH	 0.4570	 0.4220
SI	 0.6410	 0.4510
SJ	 0.5160	 0.3740
SK	 0.8580	 0.5550
SM	 0.4930	 0.3660
SN	 0.0400	 0.2760
SO	 0.8530	 0.5380
SP	 0.8680	 0.5470
SR	 0.8980	 0.5690
ST	 0.6950	 0.4700
SX	 0.8400	 0.5470
SY	 0.8750	 0.5630
SZ	 0.6750	 0.4650
Sc	 0.8620	 0.5520
Sd	 0.8600	 0.5610
X1	 0.6560	 0.4480