wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 29, 2021 – 04:52 pm GMT

PDB ID	:	7OSM
Title	:	Intermediate translocation complex of 80 S.cerevisiae ribosome with eEF2 and ligands
Authors	:	Djumagulov, M.; Jenner, L.; Rozov, A.; Demeshkina, N.; Yusupov, M.; Yusupova, G.
Deposited on	:	2021-06-09
Resolution	:	3.00 Å(reported)

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

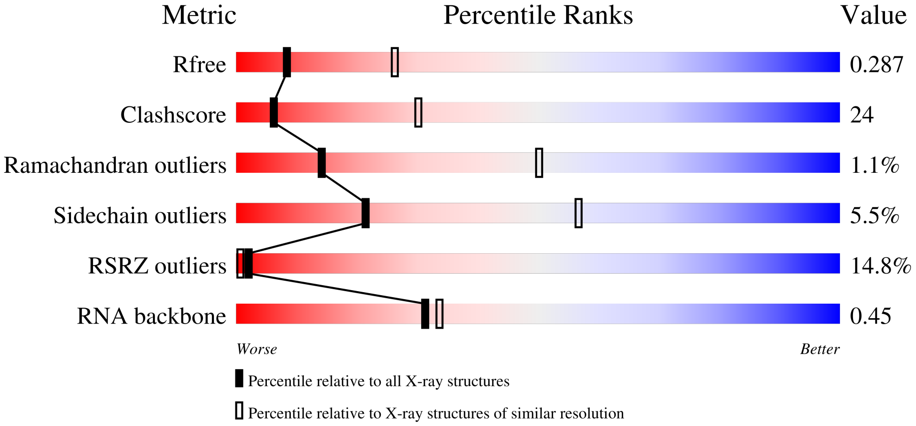
MolProbity	:	4.02b-467
Mogul	:	1.8.4 (270009), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

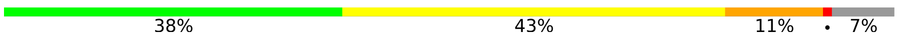
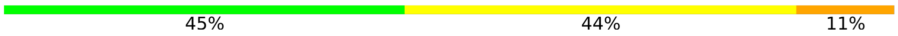
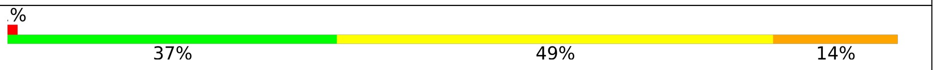
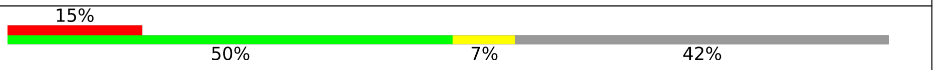
The reported resolution of this entry is 3.00 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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

Mol	Chain	Length	Quality of chain
1	25S	3396	
2	AB	121	
3	58S	158	
4	uL10	312	

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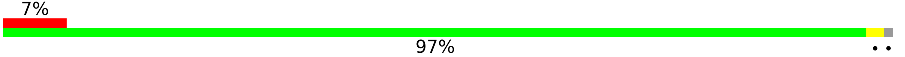
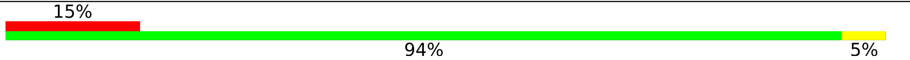
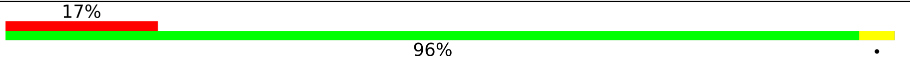
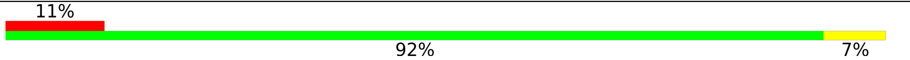
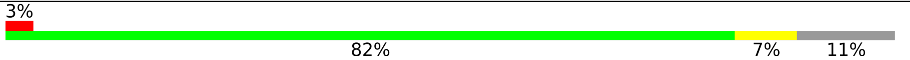
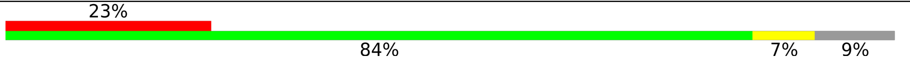
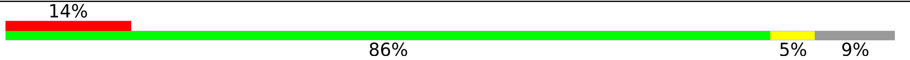
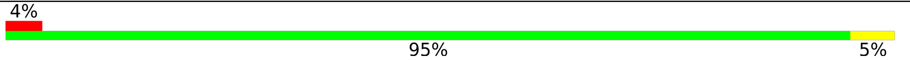
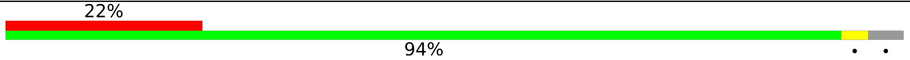
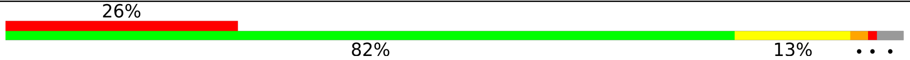
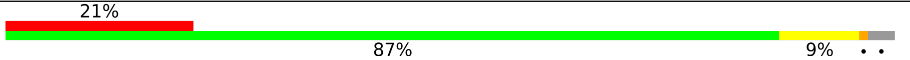
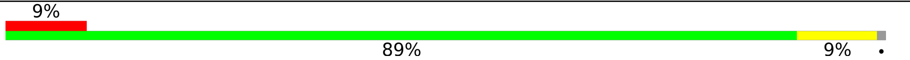
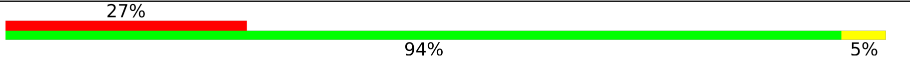
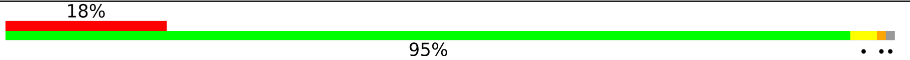
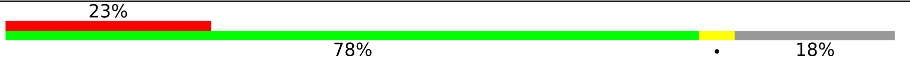
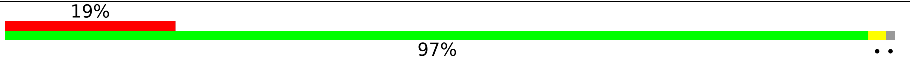
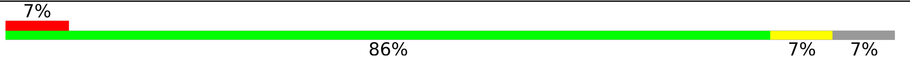
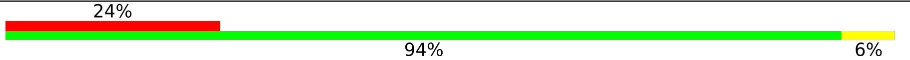
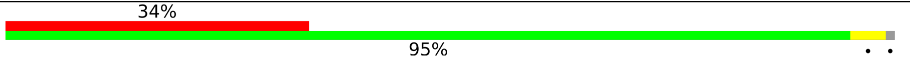
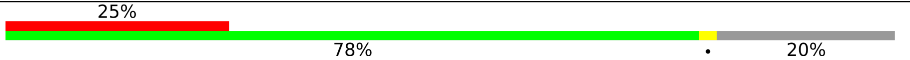
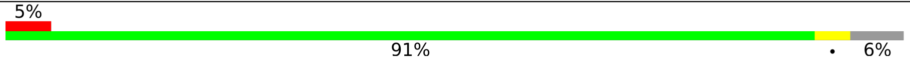
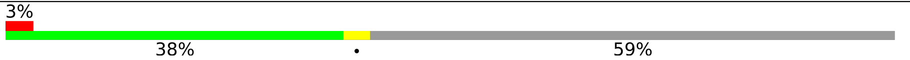
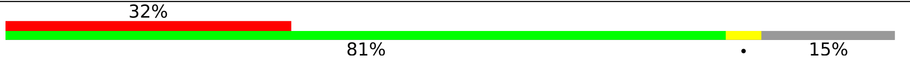
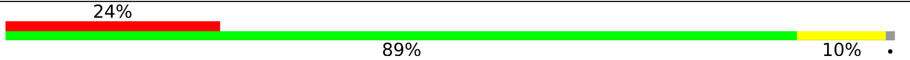
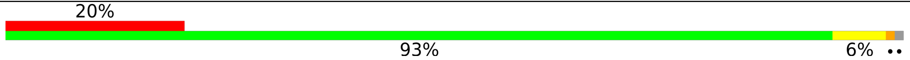
Mol	Chain	Length	Quality of chain
5	uL2	254	
6	uL3	387	
7	uL4	362	
8	uL18	297	
9	eL6	176	
10	uL30	244	
11	eL8	256	
12	uL6	191	
13	uL16	221	
14	uL5	174	
15	eL13	199	
16	eL14	138	
17	eL15	204	
18	uL13	199	
19	uL22	184	
20	eL18	186	
21	eL19	189	
22	eL20	172	
23	eL21	160	
24	eL22	121	
25	uL14	137	
26	eL24	155	
27	uL23	142	
28	uL24	127	
29	eL27	136	

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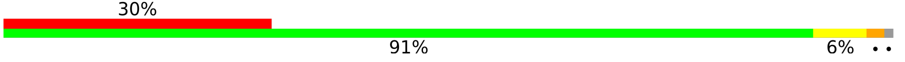
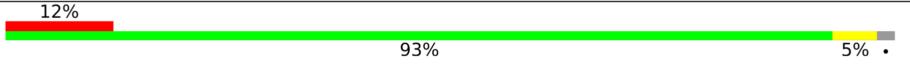
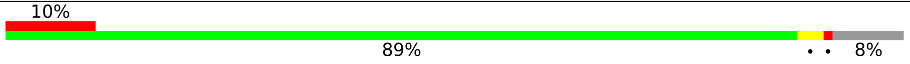
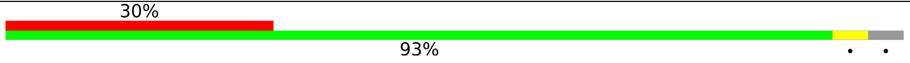
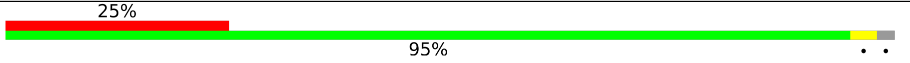
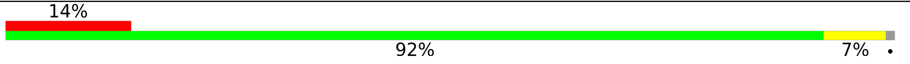
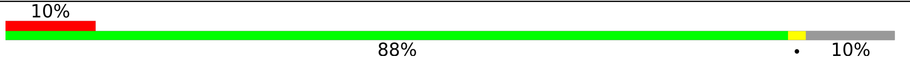
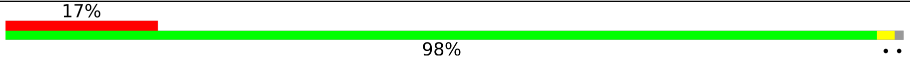
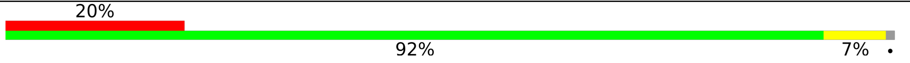
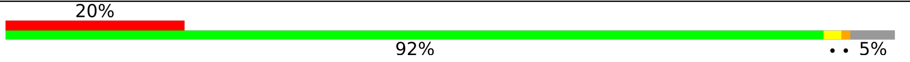
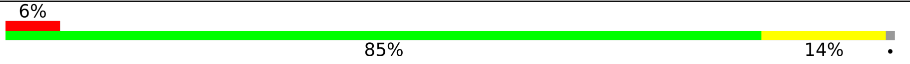
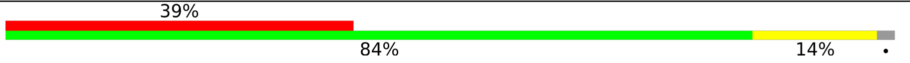
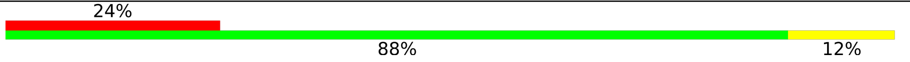
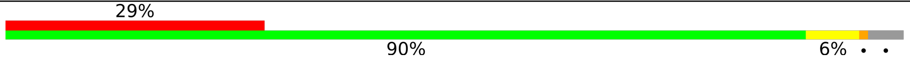
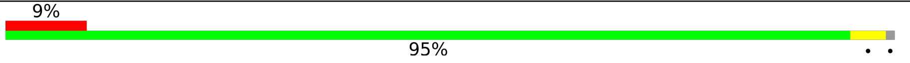
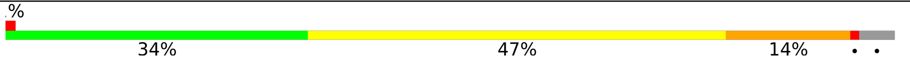
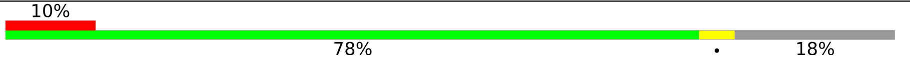
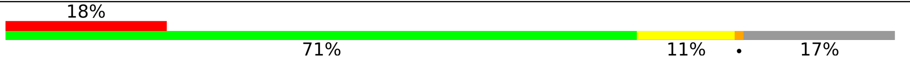
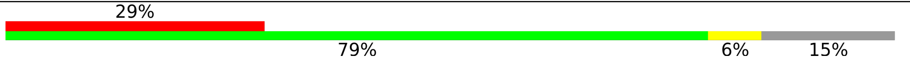
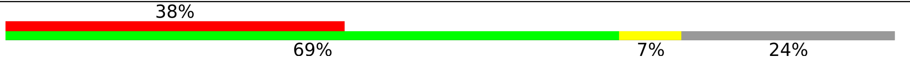
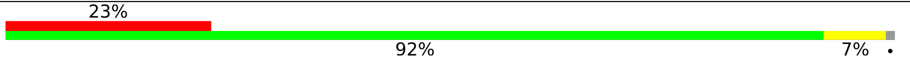
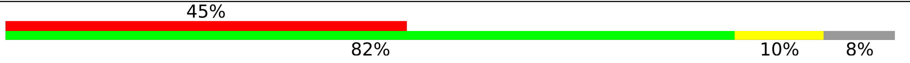
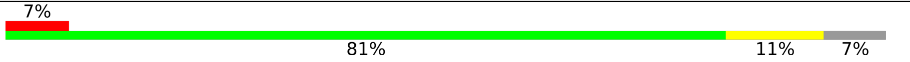
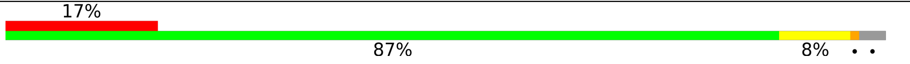
Mol	Chain	Length	Quality of chain
30	uL15	149	
31	eL29	59	
32	eL30	105	
33	eL31	113	
34	eL32	130	
35	eL33	107	
36	eL34	121	
37	uL29	120	
38	eL36	100	
39	eL37	88	
40	eL38	78	
41	eL39	51	
42	eL40	128	
43	eL41	25	
44	eL42	106	
45	eL43	92	
46	18S	1798	
47	uS2	252	
48	eS1	255	
49	uS5	254	
50	uS3	240	
51	eS4	261	
52	uS7	225	
53	eS6	236	
54	eS7	190	

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Mol	Chain	Length	Quality of chain
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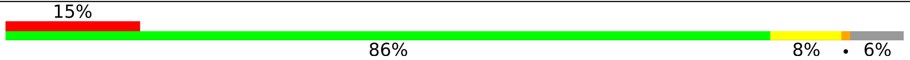
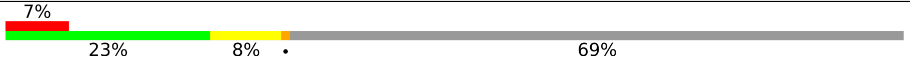
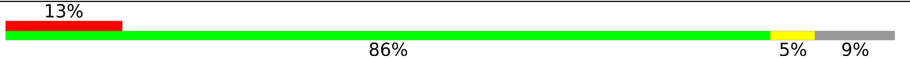
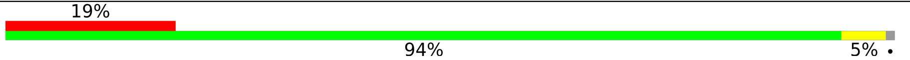
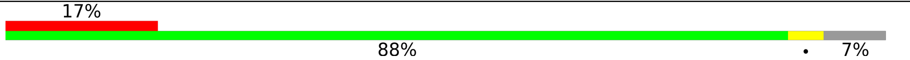
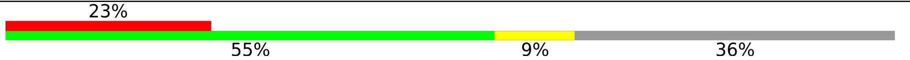
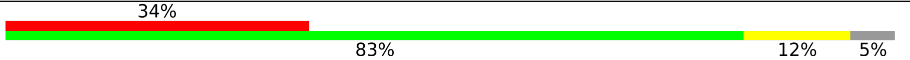
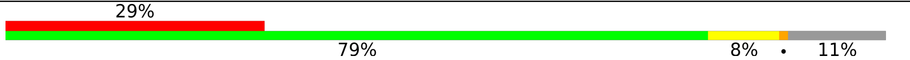
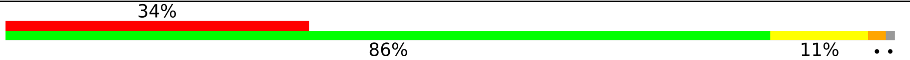
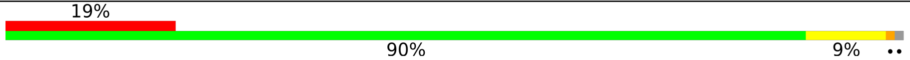
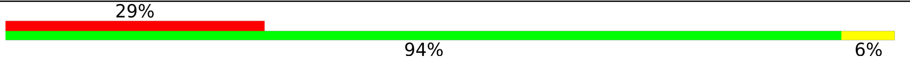
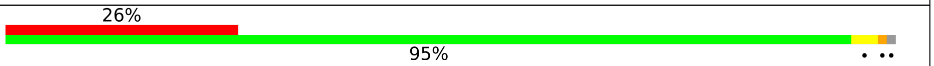
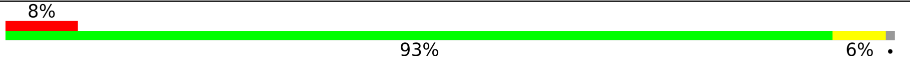
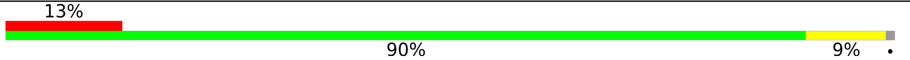
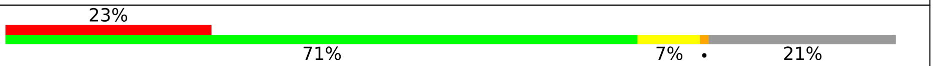
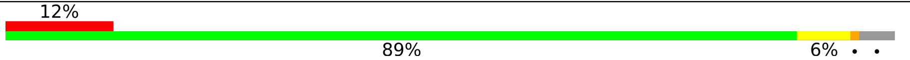
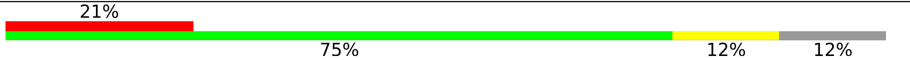
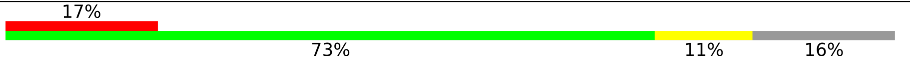
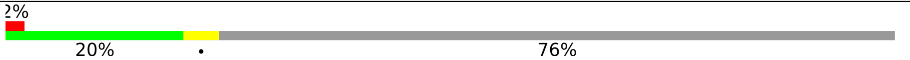
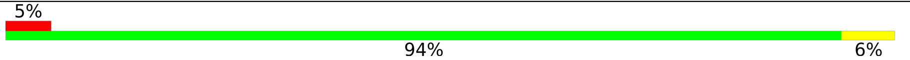
56	uS4	197	
57	eS10	105	
58	uS17	156	
59	uS15	151	
60	uS11	137	
61	uS19	142	
62	uS9	143	
63	eS17	136	
64	uS13	146	
65	eS19	144	
66	uS10	121	
67	eS21	87	
68	uS8	130	
69	uS12	145	
70	eS24	135	
71	eS25	108	
72	eS26	119	
73	eS27	82	
74	eS28	67	
75	uS14	56	
76	eS30	63	
77	RACK	319	
78	eS31	152	
79	eEF2	842	

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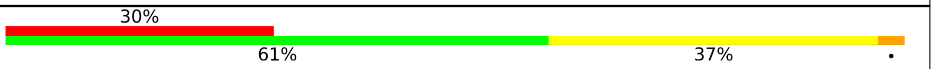
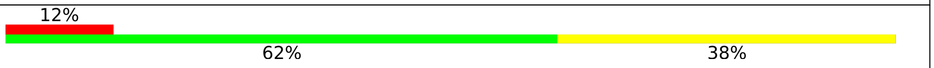
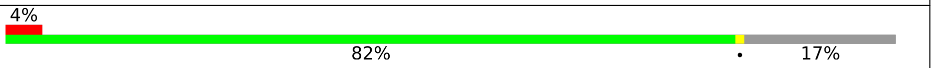
Mol	Chain	Length	Quality of chain
80	ASIT	76	
81	PSIT	77	
82	mRNA	8	
83	uL11	165	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
84	MG	18S	1825	-	-	-	X
84	MG	18S	1886	-	-	-	X
84	MG	18S	1896	-	-	-	X
84	MG	18S	1899	-	-	-	X
84	MG	25S	3438	-	-	-	X
84	MG	25S	3472	-	-	-	X
84	MG	25S	3484	-	-	-	X
84	MG	25S	3488	-	-	-	X
84	MG	25S	3515	-	-	-	X
84	MG	25S	3532	-	-	-	X
84	MG	25S	3534	-	-	-	X
84	MG	25S	3547	-	-	-	X
84	MG	25S	3567	-	-	-	X
84	MG	25S	3578	-	-	-	X
84	MG	25S	3600	-	-	-	X
84	MG	25S	3615	-	-	-	X
84	MG	25S	3633	-	-	-	X
84	MG	25S	3649	-	-	-	X
84	MG	25S	3656	-	-	-	X
84	MG	25S	3687	-	-	-	X
84	MG	25S	3702	-	-	-	X
84	MG	25S	3714	-	-	-	X
84	MG	PSIT	102	-	-	-	X
84	MG	eL30	201	-	-	-	X
84	MG	eL42	201	-	-	-	X

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 207073 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	25S	3162	Total	C	N	O	P	0	0	0
			67633	30210	12192	22069	3162			

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	58S	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			

- Molecule 4 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	uL10	180	Total	C	N	O	S	0	0	0
			1397	898	239	257	3			

- Molecule 5 is a protein called 60S ribosomal protein L2-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	uL2	252	Total	C	N	O	S	0	0	0
			1914	1191	388	334	1			

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	uL3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			

- Molecule 7 is a protein called BJ4_G0008850.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	uL4	361	2748	1729	522	494	3	0	0	0

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	uL18	296	2375	1501	414	458	2	0	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	eL6	156	1239	800	222	216	1	0	0	0

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	uL30	222	1784	1151	324	308	1	0	0	0

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	eL8	233	1804	1151	323	327	3	0	0	0

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	uL6	191	1518	963	274	277	4	0	0	0

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	uL16	213	1732	1096	329	301	6	0	0	0

- Molecule 14 is a protein called BJ4_G0027750.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	uL5	169	1353	847	253	249	4	0	0	0

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
15	eL13	193	1543	962	315	266	0	0	0

- Molecule 16 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
16	eL14	136	1053	675	199	177	2	0	0	0

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
17	eL15	203	1720	1077	361	281	1	0	0	0

- Molecule 18 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
18	uL13	197	1555	1003	289	262	1	0	0	0

- Molecule 19 is a protein called BJ4_G0005750.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
19	uL22	151	1195	745	233	217	0	0	0

- Molecule 20 is a protein called BJ4_G0033900.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
20	eL18	185	1441	908	290	241	2	0	0	0

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	eL19	176	Total 1423	C 875	N 308	O 240	0	0	0

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	eL20	172	Total 1445	C 930	N 267	O 244	S 4	0	0	0

- Molecule 23 is a protein called BJ4_G0003770.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	eL21	159	Total 1276	C 805	N 246	O 221	S 4	0	0	0

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	eL22	97	Total 770	C 499	N 126	O 145	0	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	uL14	129	Total 963	C 607	N 180	O 169	S 7	0	0	0

- Molecule 26 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	eL24	63	Total 521	C 336	N 102	O 82	S 1	0	0	0

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	uL23	120	Total 959	C 617	N 168	O 172	S 2	0	0	0

- Molecule 28 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
28	uL24	126	Total 993	C 625	N 192	O 176	0	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
29	eL27	135	Total 1092	C 710	N 202	O 180	0	0	0

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	uL15	148	Total 1173	C 749	N 231	O 190	S 3	0	0	0

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
31	eL29	58	Total 462	C 289	N 100	O 73	0	0	0

- Molecule 32 is a protein called BJ4_G0020000.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	eL30	97	Total 742	C 479	N 124	O 138	S 1	0	0	0

- Molecule 33 is a protein called BJ4_G0008090.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	eL31	109	Total 883	C 559	N 167	O 156	S 1	0	0	0

- Molecule 34 is a protein called HN1_G0013350.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	eL32	127	Total 1020	C 647	N 205	O 167	S 1	0	0	0

- Molecule 35 is a protein called BJ4_G0025510.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
35	eL33	106	850	540	165	144	1	0	0	0

- Molecule 36 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
36	eL34	109	861	533	175	149	4	0	0	0

- Molecule 37 is a protein called BJ4_G0044250.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
37	uL29	119	969	615	186	167	1	0	0	0

- Molecule 38 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
38	eL36	99	771	481	156	132	2	0	0	0

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
39	eL37	84	665	405	145	110	5	0	0	0

- Molecule 40 is a protein called BJ4_G0032190.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
40	eL38	77	612	391	115	106	0	0	0

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
41	eL39	50	436	272	97	65	2	0	0	0

- Molecule 42 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
42	eL40	52	417	259	86	67	5	0	0	0

- Molecule 43 is a protein called eL41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
43	eL41	25	233	142	63	27	1	0	0	0

- Molecule 44 is a protein called BJ4_G0001880.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
44	eL42	102	819	514	166	134	5	0	0	0

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
45	eL43	91	694	429	138	121	6	0	0	0

- Molecule 46 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
46	18S	1732	36918	16504	6551	12131	1732	0	0	0

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
47	uS2	206	1577	1014	278	283	2	0	0	0

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
48	eS1	212	1689	1073	303	309	4	0	0	0

- Molecule 49 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	uS5	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			

- Molecule 50 is a protein called BJ4_G0045400.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	uS3	183	Total	C	N	O	S	0	0	0
			1412	893	260	253	6			

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	eS4	258	Total	C	N	O	S	0	0	0
			2056	1308	387	358	3			

- Molecule 52 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	uS7	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	eS6	219	Total	C	N	O	S	0	0	0
			1766	1108	341	314	3			

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
54	eS7	184	Total	C	N	O	0	0	0
			1481	951	265	265			

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	eS8	184	Total	C	N	O	S	0	0	0
			1457	906	291	258	2			

- Molecule 56 is a protein called BJ4_G0026100.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
56	uS4	185	1494	943	289	261	1	0	0	0

- Molecule 57 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
57	eS10	33	300	199	46	55	0	0	0

- Molecule 58 is a protein called 40S ribosomal protein S11-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
58	uS17	142	1146	735	217	191	3	0	0	0

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
59	uS15	150	1192	759	224	207	2	0	0	0

- Molecule 60 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
60	uS11	127	891	545	182	163	1	0	0	0

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
61	uS19	91	732	469	138	120	5	0	0	0

- Molecule 62 is a protein called BJ4_G0008010.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
62	uS9	136	1069	686	195	188	0	0	0

- Molecule 63 is a protein called BJ4_G0020710.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
63	eS17	121	Total	C	N	O	S	0	0	0
			961	599	182	178	2			

- Molecule 64 is a protein called 40S ribosomal protein S18-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	uS13	145	Total	C	N	O	S	0	0	0
			1192	743	237	210	2			

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
65	eS19	143	Total	C	N	O	S	0	0	0
			1112	694	208	208	2			

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	uS10	30	Total	C	N	O	S	0	0	0
			245	155	44	45	1			

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	eS21	87	Total	C	N	O	S	0	0	0
			684	420	125	137	2			

- Molecule 68 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	uS8	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	uS12	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			

- Molecule 70 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
70	eS24	134	1073	676	208	189	0	0	0

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
71	eS25	70	563	360	104	99	0	0	0

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
72	eS26	94	750	462	157	126	5	0	0	0

- Molecule 73 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
73	eS27	79	590	370	104	111	5	0	0	0

- Molecule 74 is a protein called eS28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
74	eS28	63	497	306	99	91	1	0	0	0

- Molecule 75 is a protein called HLJ1_G0030400.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
75	uS14	49	404	249	86	65	4	0	0	0

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
76	eS30	53	427	269	88	69	1	0	0	0

- Molecule 77 is a protein called BJ4_G0022010.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
77	RACK	318	2436	1541	418	469	8	0	0	0

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
78	eS31	36	276	173	54	45	4	0	0	0

- Molecule 79 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
79	eEF2	842	6569	4173	1126	1239	31	0	0	0

- Molecule 80 is a RNA chain called PHE tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
80	ASIT	76	1636	734	291	536	75	0	0	0

- Molecule 81 is a RNA chain called FMET tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
81	PSIT	77	1644	732	298	537	77	0	0	0

- Molecule 82 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
82	mRNA	8	169	76	29	56	8	0	0	0

- Molecule 83 is a protein called 60S ribosomal protein L12-B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
83	uL11	137	673	399	137	137	0	0	0

- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
84	25S	317	Total Mg 324 324	0	7
84	AB	5	Total Mg 5 5	0	0
84	58S	7	Total Mg 7 7	0	0
84	uL2	3	Total Mg 3 3	0	0
84	uL3	1	Total Mg 1 1	0	0
84	uL18	2	Total Mg 2 2	0	0
84	uL16	1	Total Mg 1 1	0	0
84	eL15	1	Total Mg 1 1	0	0
84	uL22	1	Total Mg 1 1	0	0
84	eL18	1	Total Mg 1 1	0	0
84	eL20	1	Total Mg 1 1	0	0
84	uL14	1	Total Mg 1 1	0	0
84	eL30	2	Total Mg 2 2	0	0
84	eL31	1	Total Mg 1 1	0	0
84	eL32	1	Total Mg 1 1	0	0
84	eL33	1	Total Mg 1 1	0	0
84	eL40	1	Total Mg 1 1	0	0
84	eL41	1	Total Mg 1 1	0	0
84	eL42	2	Total Mg 2 2	0	0
84	18S	122	Total Mg 122 122	0	0
84	eS1	1	Total Mg 1 1	0	0
84	eS4	3	Total Mg 3 3	0	0

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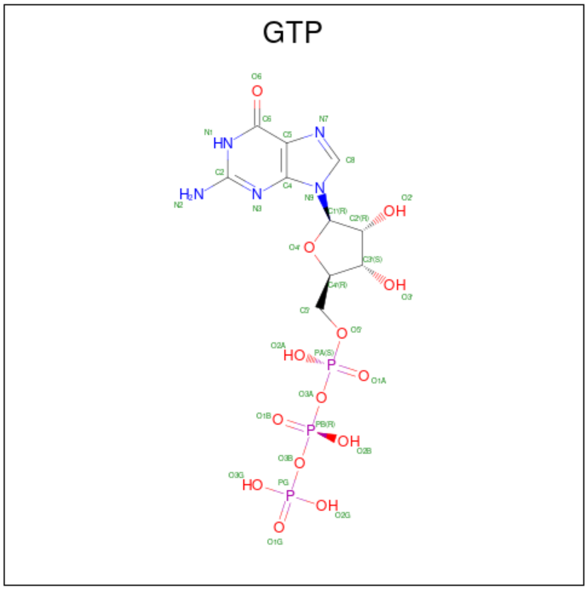
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
84	eS6	2	Total Mg 2 2	0	0
84	uS15	1	Total Mg 1 1	0	0
84	uS19	1	Total Mg 1 1	0	0
84	uS12	3	Total Mg 3 3	0	0
84	eS26	1	Total Mg 1 1	0	0
84	uS14	1	Total Mg 1 1	0	0
84	eEF2	6	Total Mg 6 6	0	0
84	ASIT	1	Total Mg 1 1	0	0
84	PSIT	6	Total Mg 6 6	0	0
84	mRNA	1	Total Mg 1 1	0	0

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
85	eL34	1	Total Zn 1 1	0	0
85	eL37	1	Total Zn 1 1	0	0
85	eL40	1	Total Zn 1 1	0	0
85	eL42	1	Total Zn 1 1	0	0
85	eL43	1	Total Zn 1 1	0	0
85	eS26	1	Total Zn 1 1	0	0
85	uS14	1	Total Zn 1 1	0	0
85	eS31	1	Total Zn 1 1	0	0

- Molecule 86 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



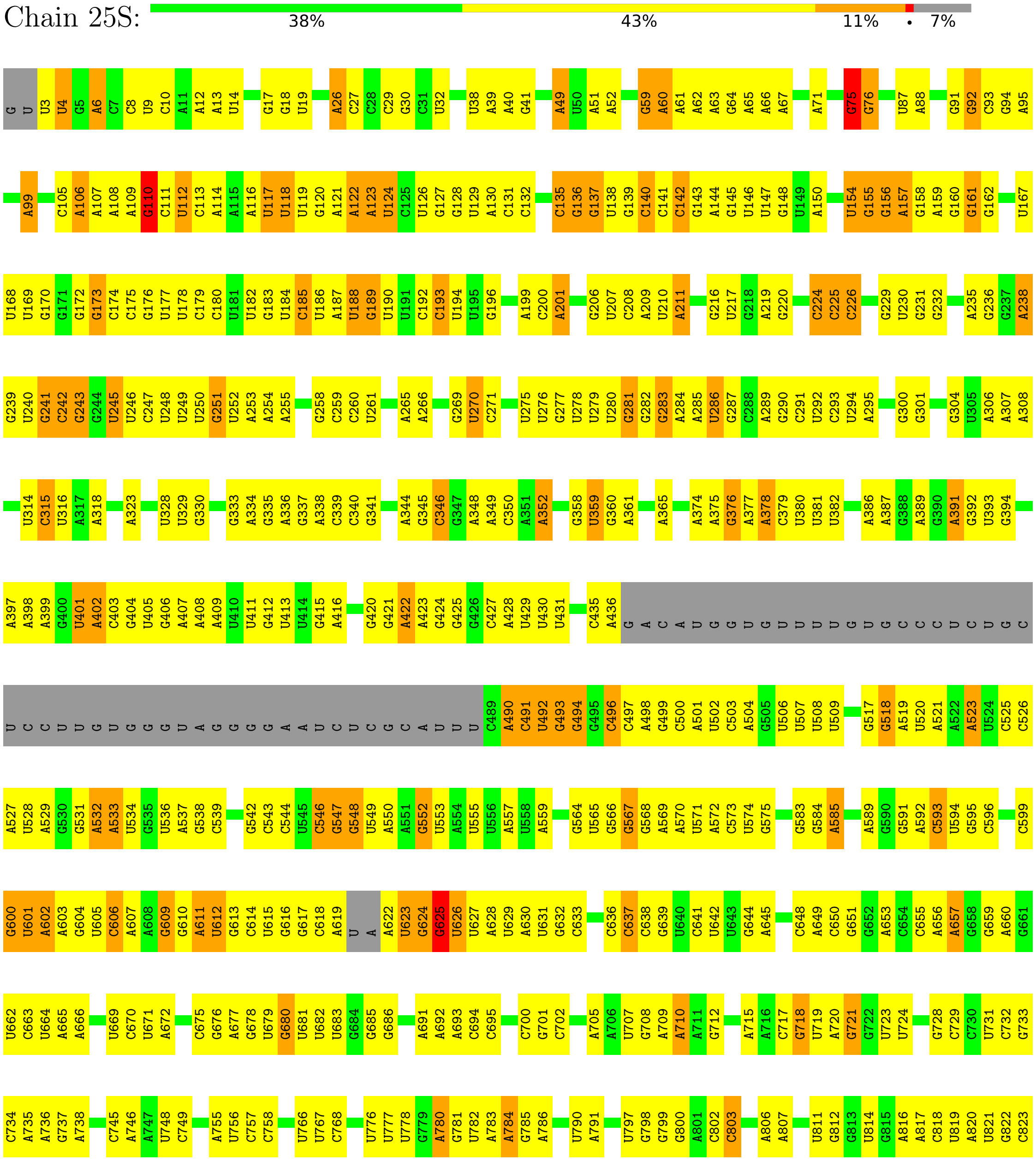
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
86	eEF2	1	32	10	5	14	3	0	0

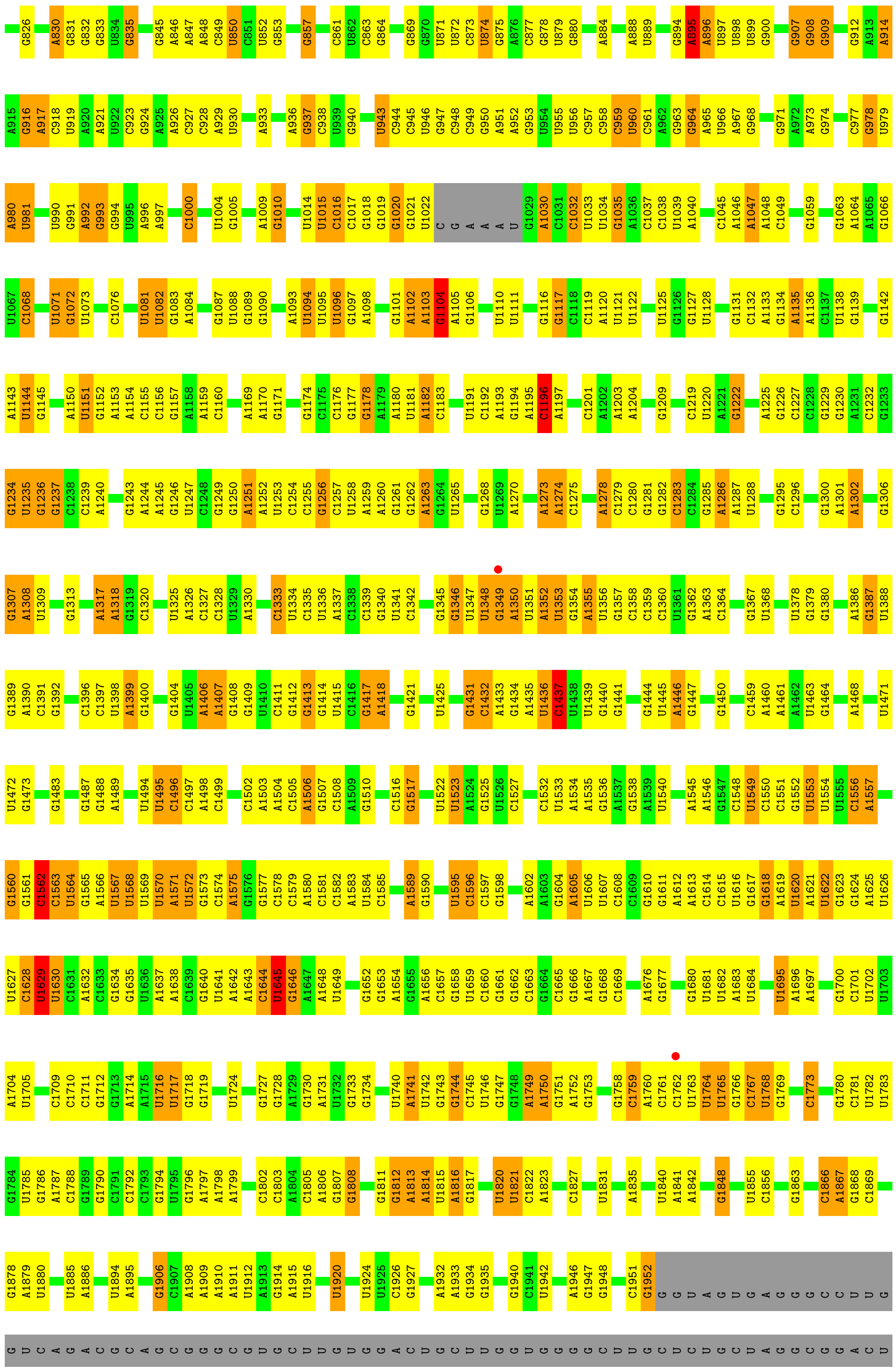
3 Residue-property plots ⓘ

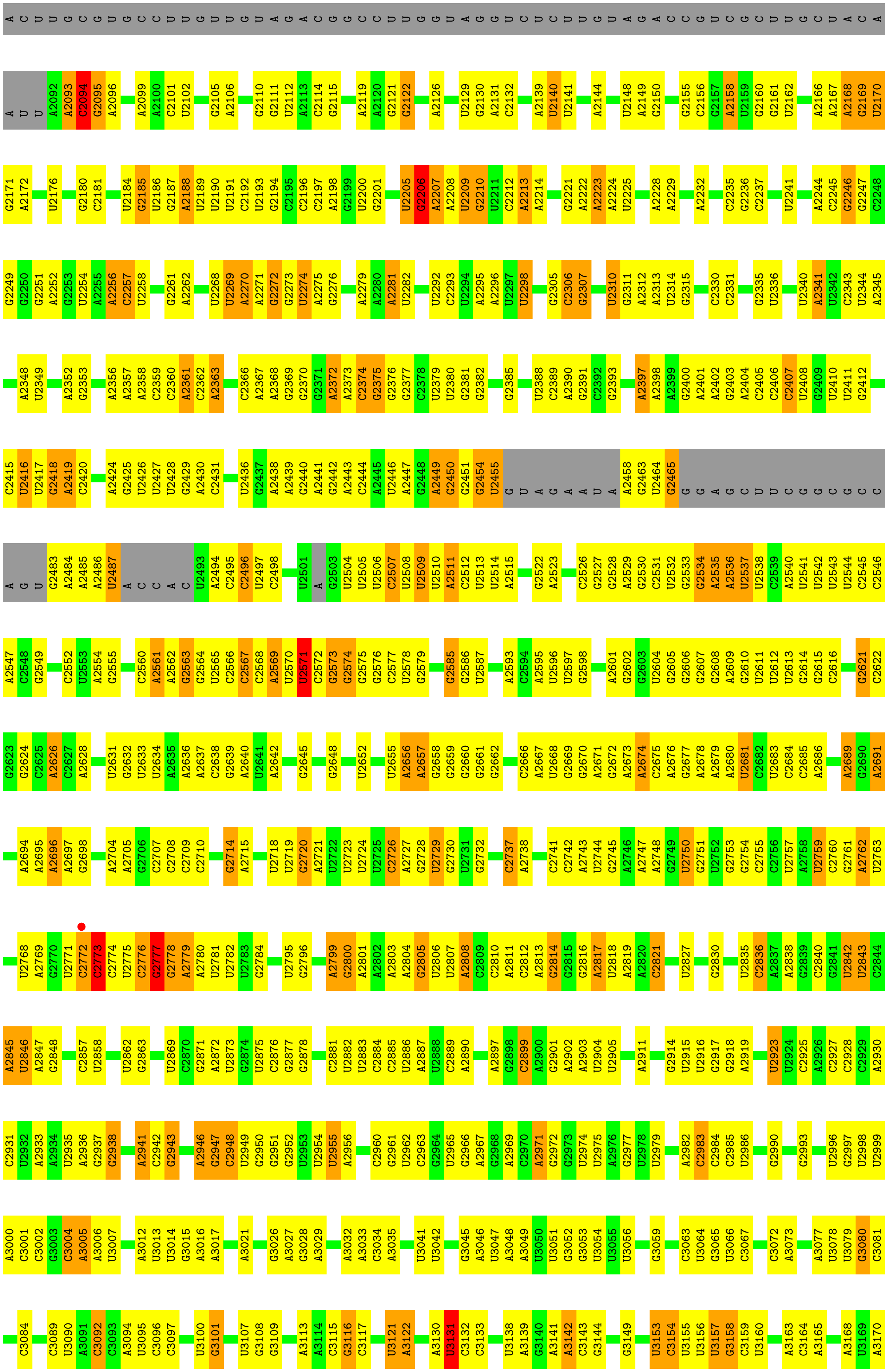
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

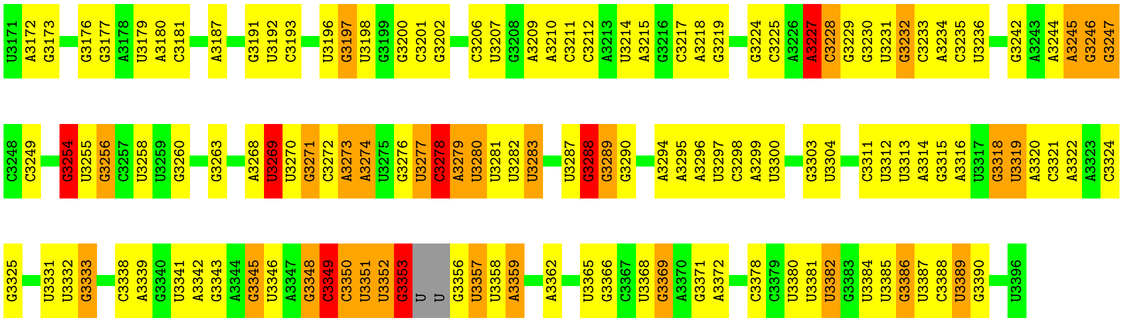
- Molecule 1: 25S rRNA

Chain 25S:

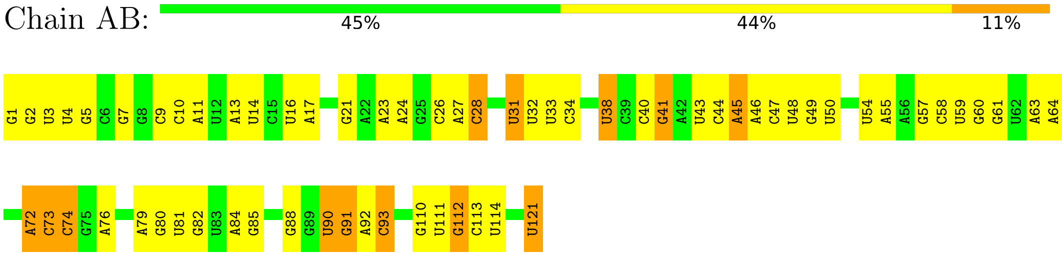




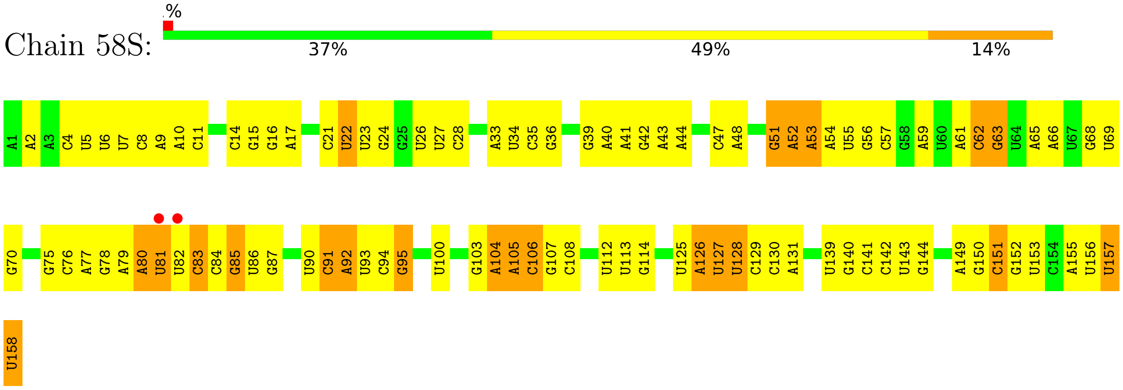

A C U U G C G U G C C U U G U U G U A G A C G G C C U U G G U A G G U C U C U U G U A G A C C G U C G C U U G C U A C A
A U U A2092 A2093 C2094 G2095 A2096 A2099 A2100 C2101 U2102 G2105 A2106 G2110 G2111 U2112 A2113 C2114 G2115 A2119 A2120 G2121 G2122 A2126 U2129 G2130 A2131 C2132 A2139 U2140 U2141 A2144 U2148 A2149 G2150 G2155 C2156 G2157 A2158 U2159 G2160 G2161 U2162 A2166 A2167 A2168 G2169 U2170
G2171 A2172 U2176 G2180 C2181 U2184 G2185 U2186 G2187 A2188 U2189 U2190 U2191 C2192 U2193 G2194 C2195 C2196 C2197 A2198 G2199 U2200 G2201 U2205 G2206 A2207 A2208 U2209 G2210 U2211 C2212 A2213 A2214 G2221 A2222 A2223 A2224 U2225 A2228 A2229 A2232 C2235 G2236 C2237 U2241 A2244 C2245 G2246 G2247 C2248
G2249 G2250 G2251 A2252 G2253 U2254 A2255 A2256 C2257 U2258 G2261 A2262 U2268 U2269 A2270 A2271 G2272 G2273 U2274 A2275 G2276 A2279 A2280 A2281 U2282 U2292 C2293 U2294 A2295 A2296 U2297 U2298 G2305 C2306 G2307 U2310 G2311 A2312 A2313 U2314 G2315 C2330 C2331 G2335 U2336 U2340 A2341 U2342 C2343 U2344 A2345
A2348 U2349 A2352 G2353 A2356 A2357 A2358 C2359 C2360 A2361 C2362 A2363 C2366 A2367 A2368 G2369 G2370 G2371 A2372 A2373 C2374 G2375 G2376 G2377 C2378 U2379 U2380 G2381 G2382 G2385 U2388 C2389 A2390 G2391 C2392 G2393 A2397 A2398 A2399 G2400 A2401 A2402 G2403 A2404 C2405 C2406 C2407 U2408 G2409 U2410 U2411 G2412
C2415 U2416 U2417 G2418 A2419 C2420 A2424 G2425 U2426 U2427 U2428 G2429 A2430 C2431 U2436 G2437 A2438 A2439 G2440 A2441 G2442 A2443 C2444 A2445 U2446 A2447 G2448 A2449 G2450 G2451 G2454 U2455 G U A G A A U A A2458 G2463 U2464 G2465 G G A G C U U C G G C G C C
A G U G2483 A2484 A2485 A2486 U2487 A C C A C U2493 A2494 C2495 C2496 U2497 C2498 U2501 A G2503 U2504 U2505 U2506 C2507 U2508 U2509 U2510 A2511 C2512 U2513 U2514 A2515 G2522 A2523 C2526 G2527 G2528 A2529 G2530 C2531 U2532 G2533 G2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2545 C2546
A2547 C2548 G2549 C2552 U2553 A2554 G2555 C2560 A2561 A2562 G2563 G2564 U2565 C2566 C2567 C2568 A2569 U2570 U2571 C2572 G2573 G2574 G2575 G2576 C2577 U2578 G2579 G2585 G2586 U2587 A2593 C2594 A2595 U2596 U2597 G2598 A2601 G2602 G2603 U2604 G2605 G2606 G2607 G2608 A2609 G2610 U2611 U2612 U2613 G2614 G2615 C2616 G2621 C2622
G2623 G2624 C2625 A2626 C2627 A2628 U2631 G2632 U2633 U2634 A2635 A2636 A2637 C2638 G2639 A2640 U2641 A2642 G2645 G2648 U2652 U2655 A2656 A2657 G2658 G2659 G2660 G2661 G2662 C2666 A2667 U2668 G2669 G2670 A2671 G2672 A2673 A2674 C2675 A2676 G2677 A2678 A2679 A2680 U2681 C2682 U2683 C2684 C2685 A2686 A2689 G2690 A2691
A2694 A2695 A2696 A2697 G2698 A2704 A2705 G2706 C2707 C2708 C2709 C2710 G2714 A2715 U2718 U2719 G2720 A2721 U2722 U2723 U2724 U2725 C2726 A2727 G2728 U2729 G2730 U2731 G2732 C2737 A2738 C2741 C2742 A2743 U2744 G2745 A2746 A2747 A2748 G2749 U2750 G2751 U2752 G2753 G2754 C2755 C2756 U2757 A2758 U2759 C2760 G2761 A2762 U2763
●
U2768 A2769 G2770 U2771 C2772 C2773 C2774 U2775 C2776 G2777 G2778 A2779 A2780 U2781 U2782 U2783 G2784 U2795 G2796 A2799 G2800 A2801 A2802 A2803 A2804 G2805 U2806 U2807 A2808 C2809 C2810 A2811 C2812 A2813 G2814 G2815 G2816 A2817 U2818 A2819 A2820 C2821 U2827 G2830 U2835 C2836 A2837 A2838 G2839 C2840 G2841 U2842 U2843 C2844
A2845 U2846 A2847 G2848 C2857 U2858 U2862 G2863 U2869 C2870 G2871 A2872 U2873 G2874 U2875 C2876 G2877 G2878 C2881 U2882 U2883 C2884 C2885 U2886 A2887 U2888 C2889 A2890 A2897 G2898 C2899 A2900 G2901 A2902 A2903 U2904 U2905 A2911 G2914 U2915 U2916 G2917 G2918 A2919 U2923 U2924 C2925 A2926 C2927 C2928 C2929 A2930
C2931 U2932 A2933 A2934 U2935 A2936 G2937 G2938 A2941 C2942 G2943 A2946 G2947 C2948 U2949 G2950 G2951 G2952 U2953 U2954 U2955 A2956 C2960 G2961 U2962 C2963 G2964 U2965 G2966 A2967 G2968 A2969 C2970 A2971 G2972 G2973 U2974 U2975 A2976 G2977 U2978 U2979 A2982 C2983 C2984 C2985 U2986 G2990 G2993 U2996 G2997 U2998 U2999
A3000 C3001 C3002 G3003 C3004 A3005 A3006 U3007 A3012 U3013 U3014 G3015 A3016 A3017 A3021 G3026 A3027 G3028 A3029 A3032 A3033 C3034 A3035 U3041 U3042 G3045 A3046 U3047 A3048 A3049 U3050 U3051 G3052 G3053 U3054 U3055 U3056 G3059 C3063 U3064 G3065 U3066 C3067 C3072 A3073 A3077 U3078 U3079 G3080 C3081
C3084 C3089 U3090 A3091 C3092 C3093 A3094 U3095 C3096 C3097 U3100 G3101 U3107 G3108 G3109 A3113 A3114 C3115 G3116 C3117 U3121 A3122 A3130 U3131 C3132 C3133 U3138 A3139 G3140 A3141 A3142 C3143 G3144 G3149 U3153 C3154 U3155 U3156 U3157 G3158 C3159 U3160 A3163 C3164 A3165 A3168 U3169 A3170



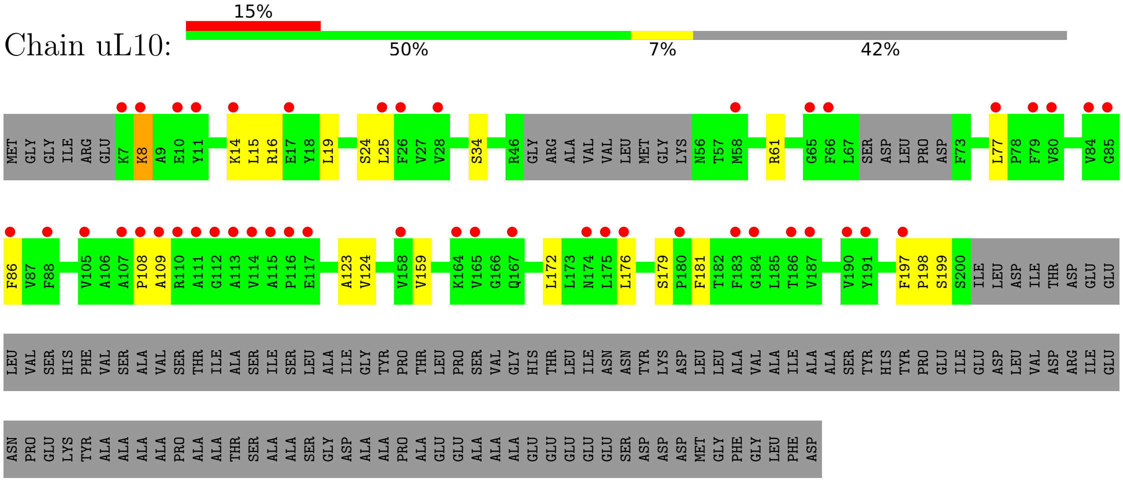
- Molecule 2: 5S rRNA



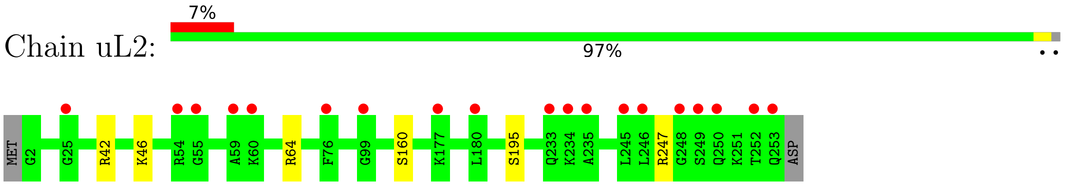
- Molecule 3: 5.8S rRNA



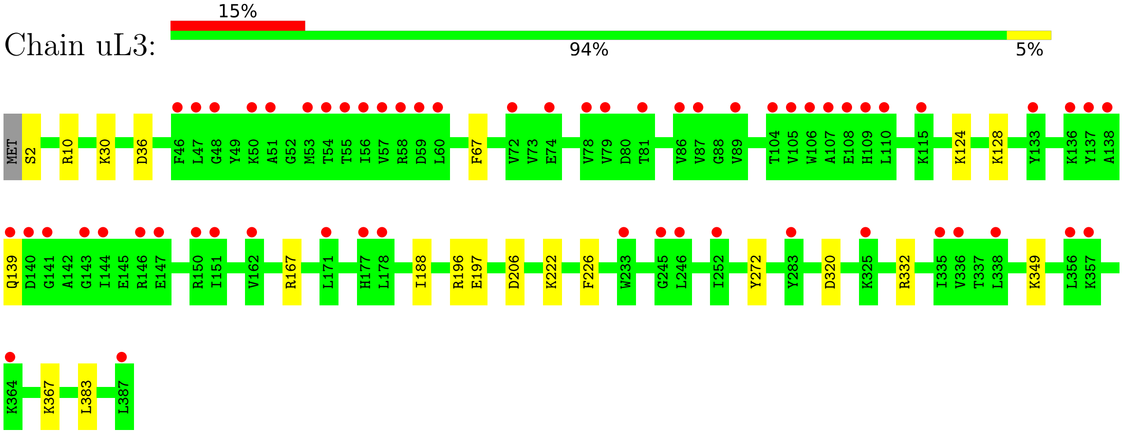
- Molecule 4: 60S acidic ribosomal protein P0



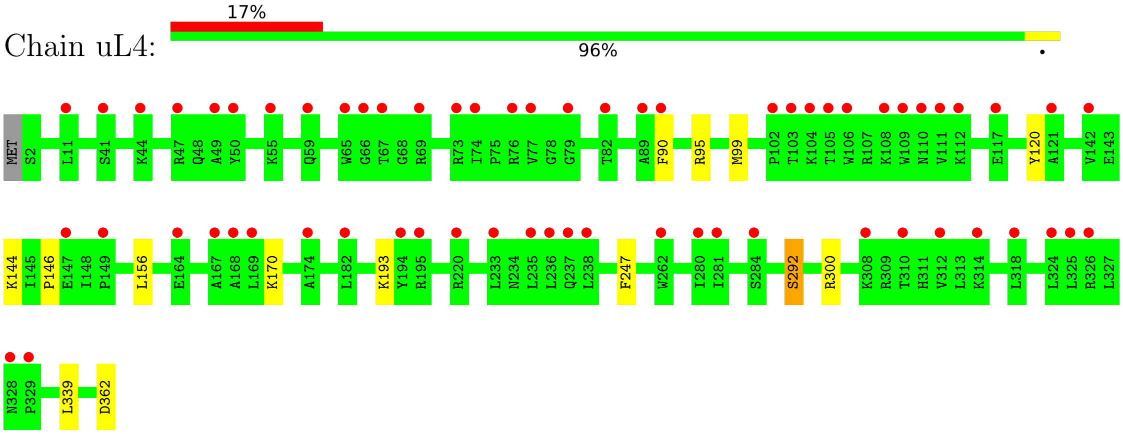
- Molecule 5: 60S ribosomal protein L2-B



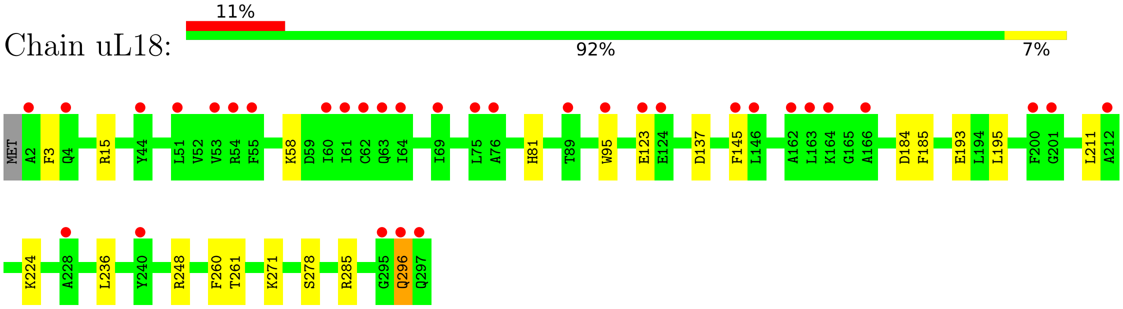
• Molecule 6: 60S ribosomal protein L3



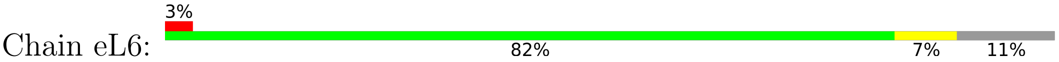
• Molecule 7: BJ4_G0008850.mRNA.1.CDS.1

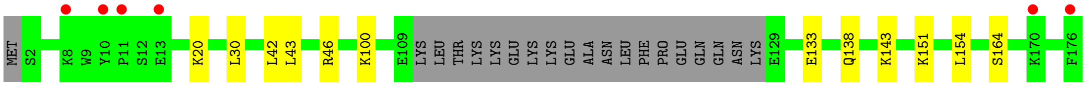


• Molecule 8: 60S ribosomal protein L5



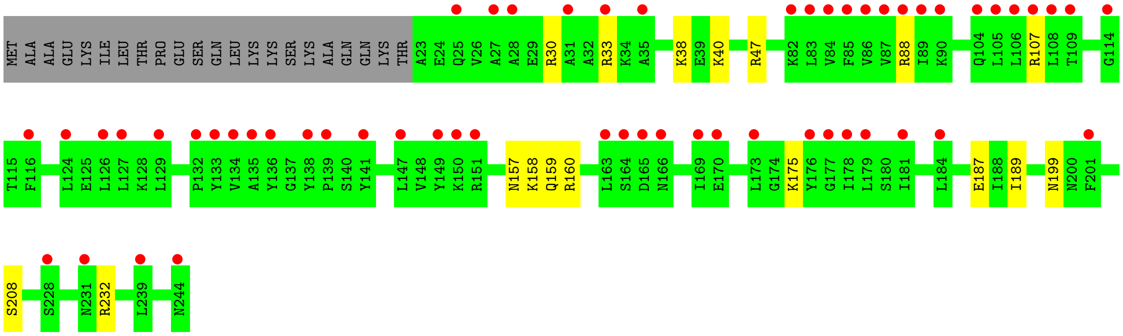
• Molecule 9: 60S ribosomal protein L6





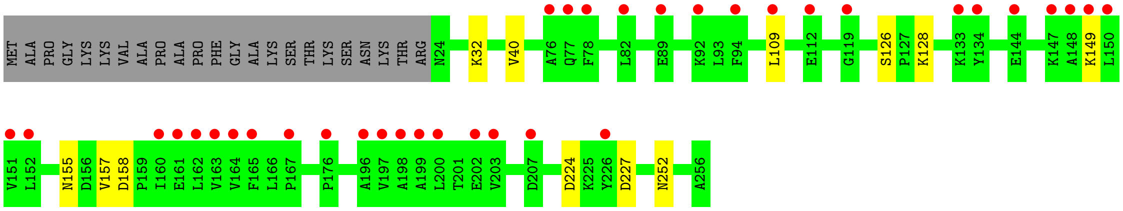
- Molecule 10: 60S ribosomal protein L7-A

Chain uL30:



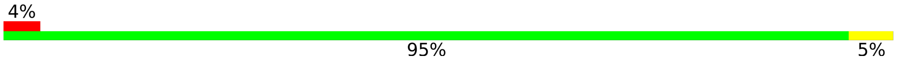
- Molecule 11: 60S ribosomal protein L8-A

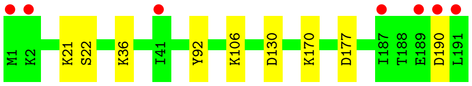
Chain eL8:



- Molecule 12: 60S ribosomal protein L9-A

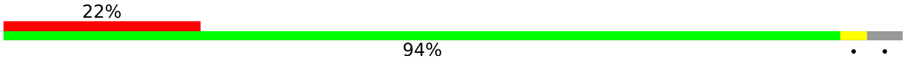
Chain uL6:

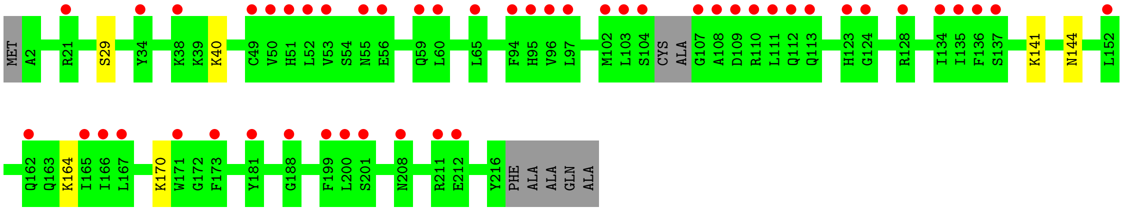




- Molecule 13: 60S ribosomal protein L10

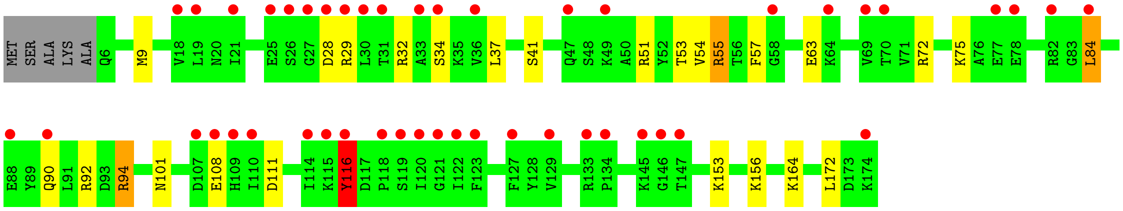
Chain uL16:





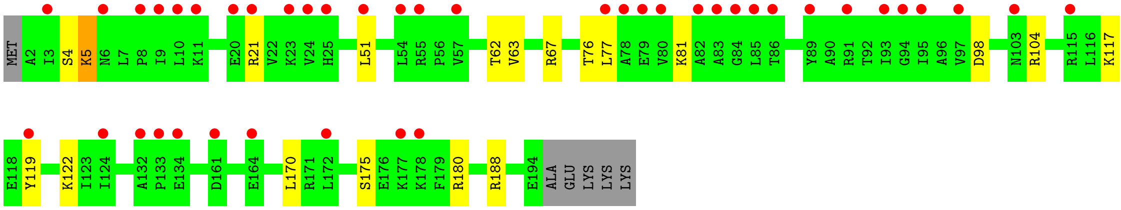
- Molecule 14: BJ4_G0027750.mRNA.1.CDS.1

Chain uL5:



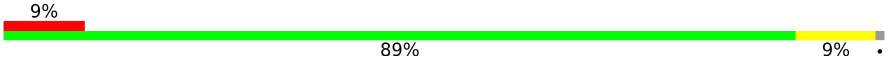
- Molecule 15: 60S ribosomal protein L13

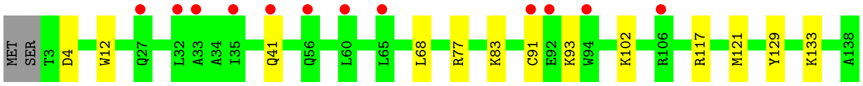
Chain eL13:



- Molecule 16: 60S ribosomal protein L14-A

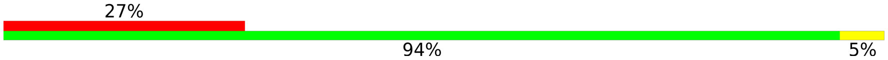
Chain eL14:

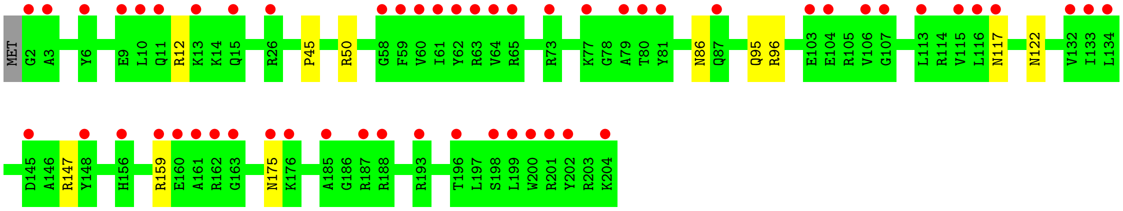




- Molecule 17: 60S ribosomal protein L15-A

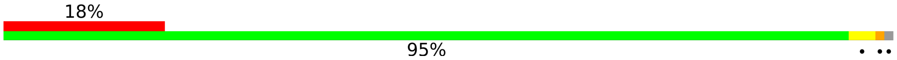
Chain eL15:

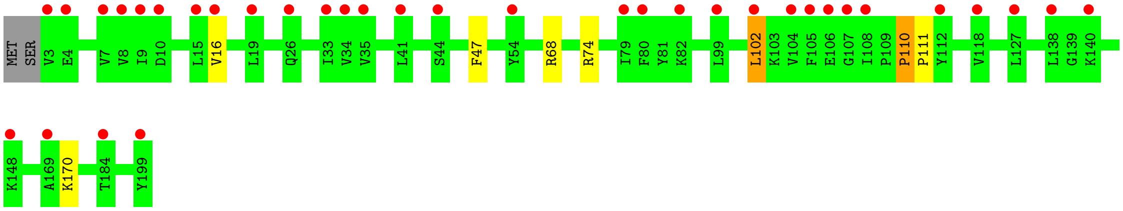




- Molecule 18: 60S ribosomal protein L16-A

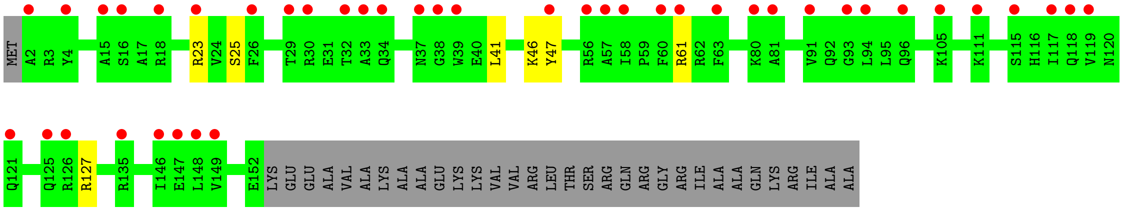
Chain uL13:





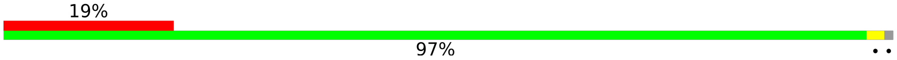
- Molecule 19: BJ4_G0005750.mRNA.1.CDS.1

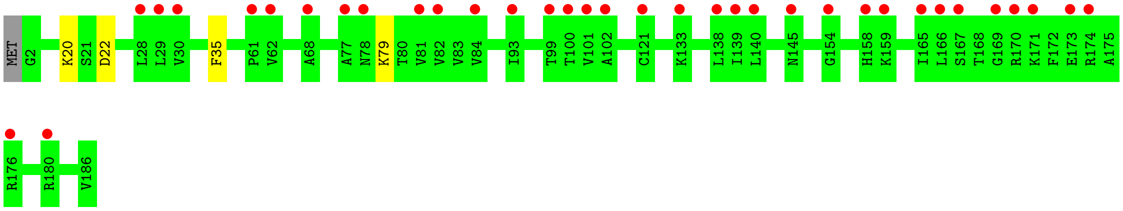
Chain uL22:



- Molecule 20: BJ4_G0033900.mRNA.1.CDS.1

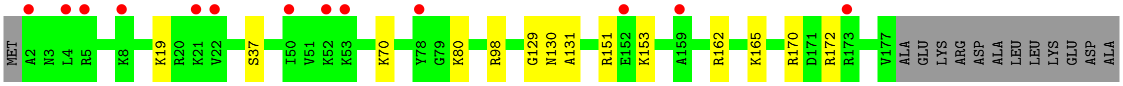
Chain eL18:





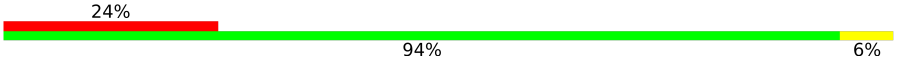
- Molecule 21: 60S ribosomal protein L19-A

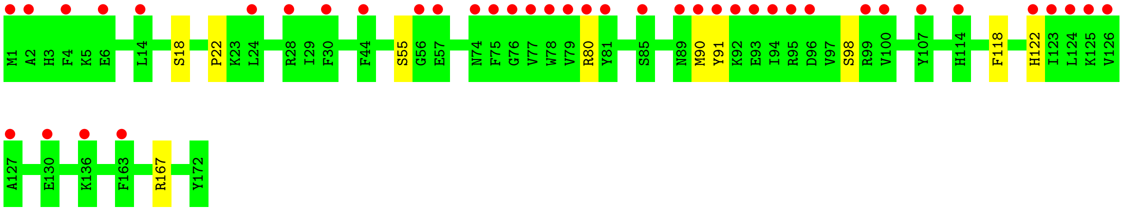
Chain eL19:



- Molecule 22: 60S ribosomal protein L20

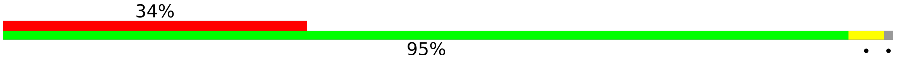
Chain eL20:

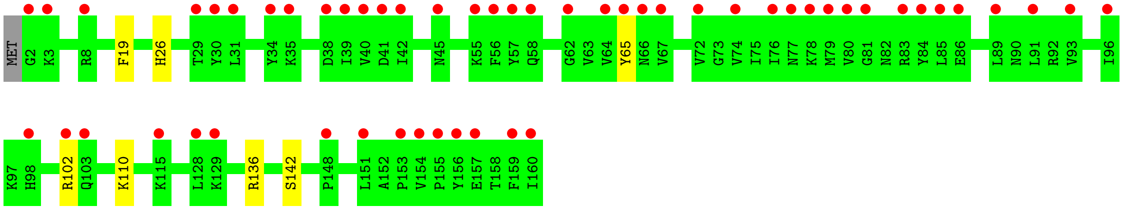




- Molecule 23: BJ4_G0003770.mRNA.1.CDS.1

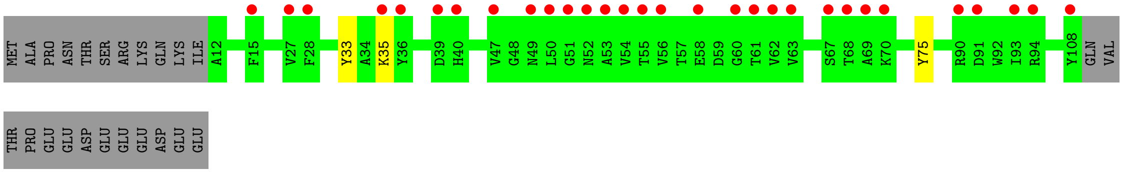
Chain eL21:





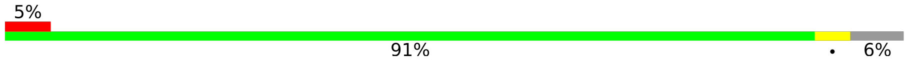
- Molecule 24: 60S ribosomal protein L22-A

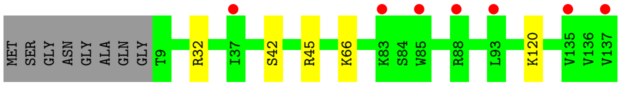
Chain eL22:



- Molecule 25: 60S ribosomal protein L23-B

Chain uL14:



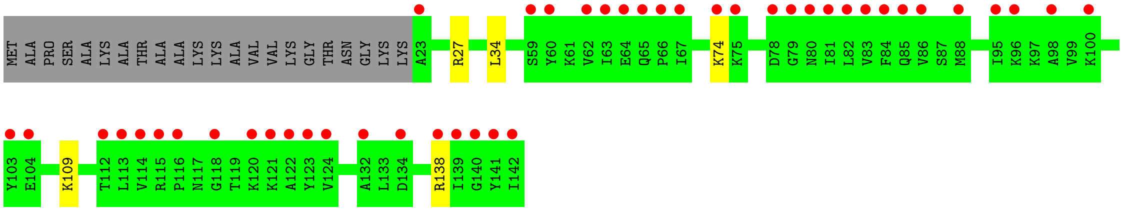


- Molecule 26: 60S ribosomal protein L24-A

Chain eL24:

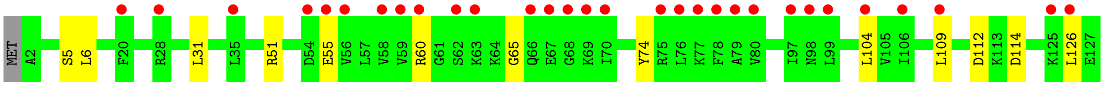
- Molecule 27: 60S ribosomal protein L25

Chain uL23:



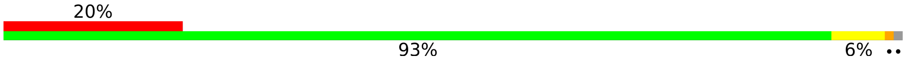
- Molecule 28: 60S ribosomal protein L26-A

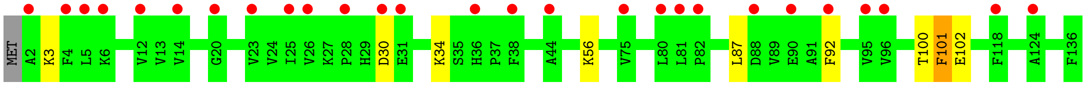
Chain uL24:



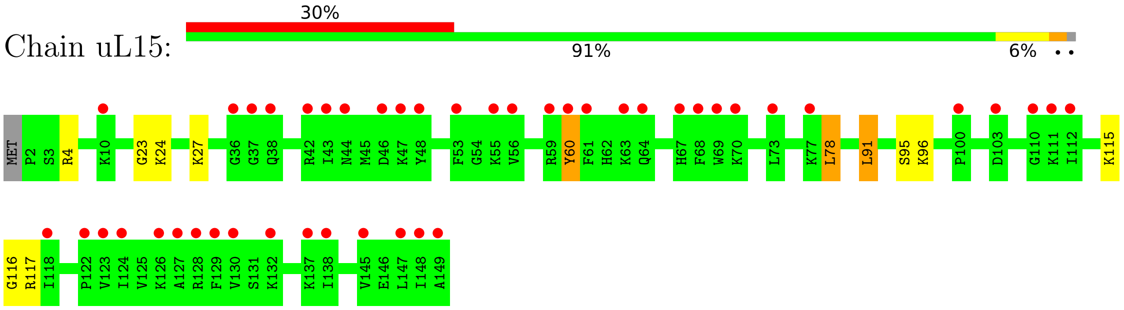
- Molecule 29: 60S ribosomal protein L27

Chain eL27:

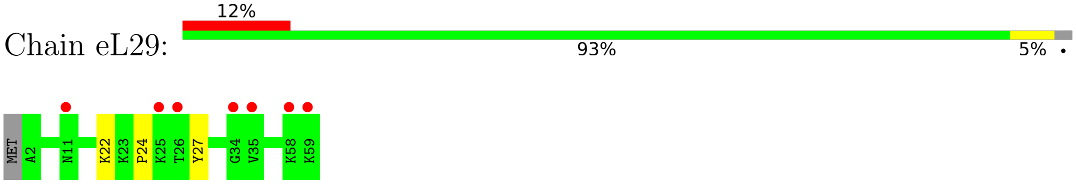




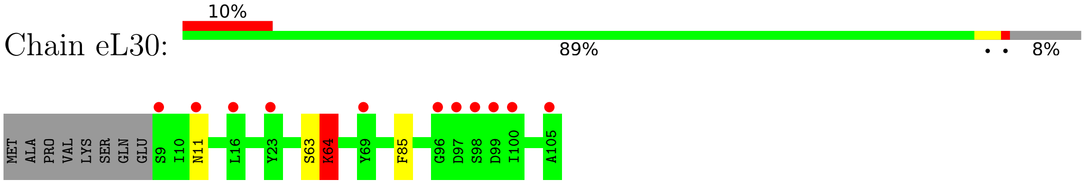
- Molecule 30: 60S ribosomal protein L28



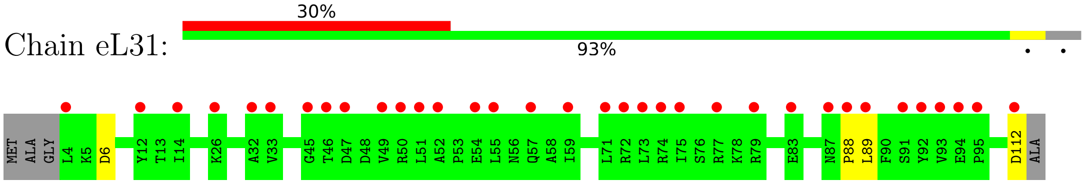
- Molecule 31: 60S ribosomal protein L29



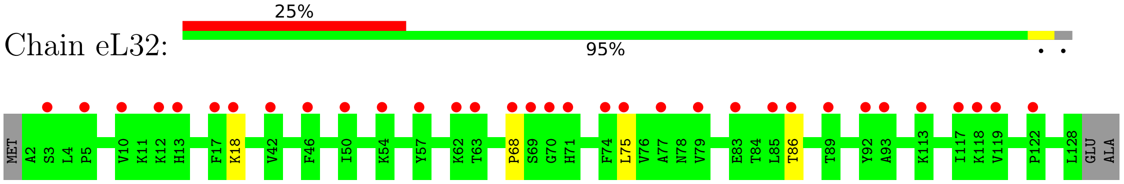
- Molecule 32: BJ4_G0020000.mRNA.1.CDS.1



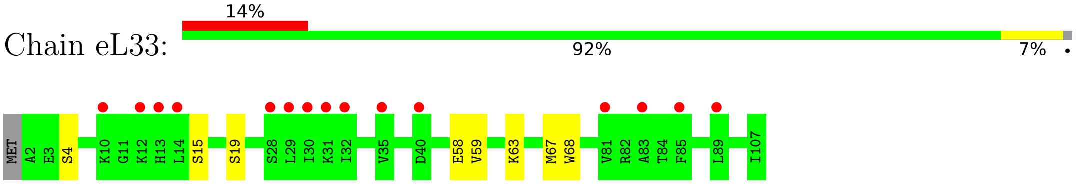
- Molecule 33: BJ4_G0008090.mRNA.1.CDS.1



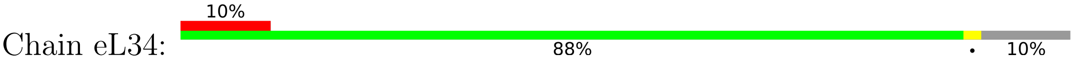
- Molecule 34: HN1_G0013350.mRNA.1.CDS.1

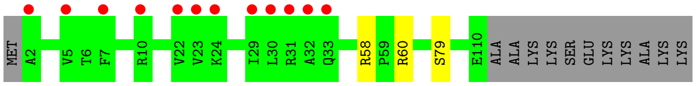


- Molecule 35: BJ4_G0025510.mRNA.1.CDS.1



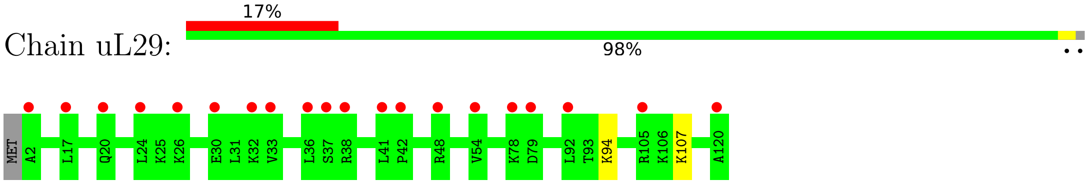
- Molecule 36: 60S ribosomal protein L34-A





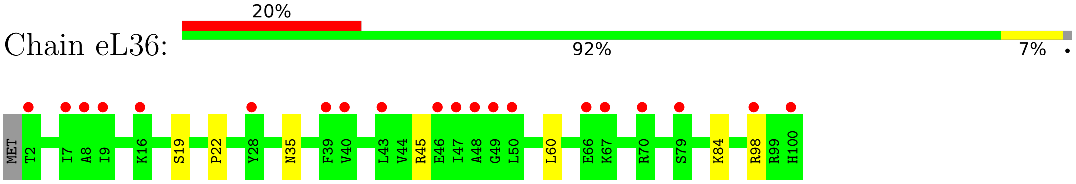
- Molecule 37: BJ4_G0044250.mRNA.1.CDS.1

Chain uL29:



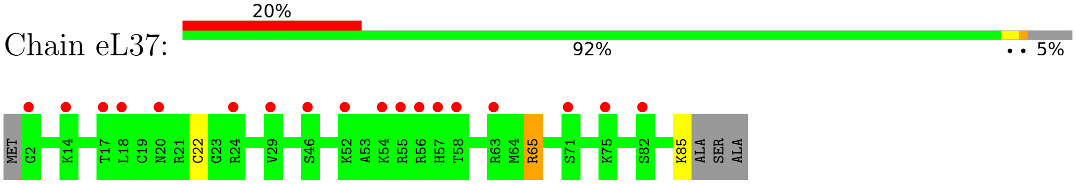
- Molecule 38: 60S ribosomal protein L36-A

Chain eL36:



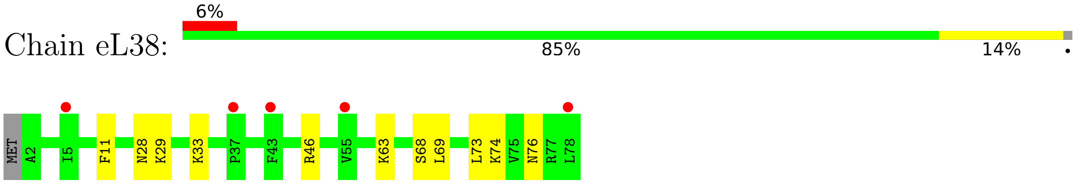
- Molecule 39: Ribosomal protein L37

Chain eL37:



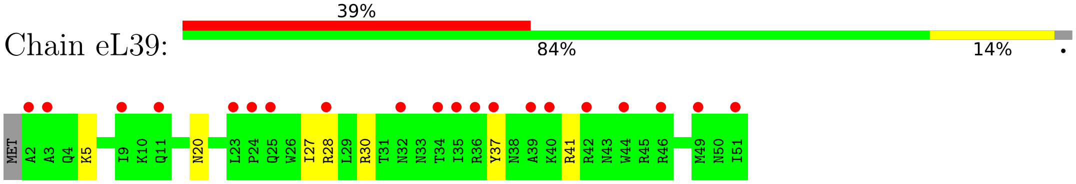
- Molecule 40: BJ4_G0032190.mRNA.1.CDS.1

Chain eL38:



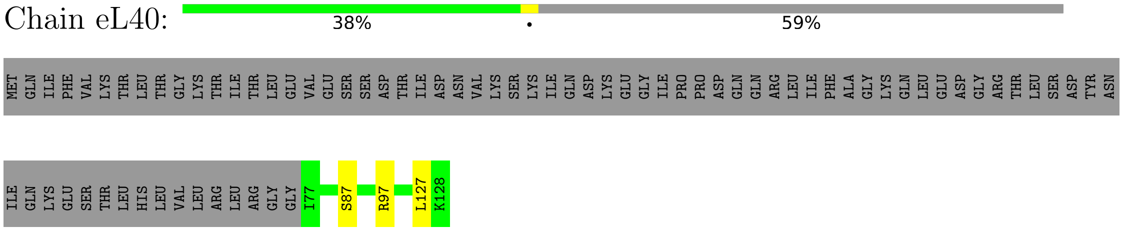
- Molecule 41: 60S ribosomal protein L39

Chain eL39:



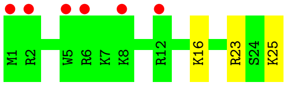
- Molecule 42: Ubiquitin

Chain eL40:



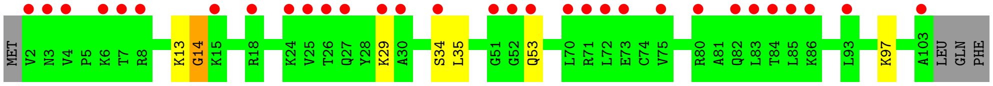
- Molecule 43: eL41

Chain eL41:



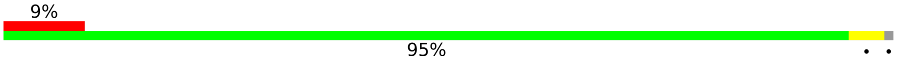
- Molecule 44: BJ4_G0001880.mRNA.1.CDS.1

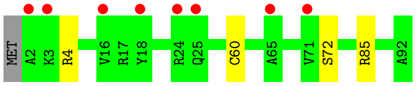
Chain eL42:



- Molecule 45: 60S ribosomal protein L43-A

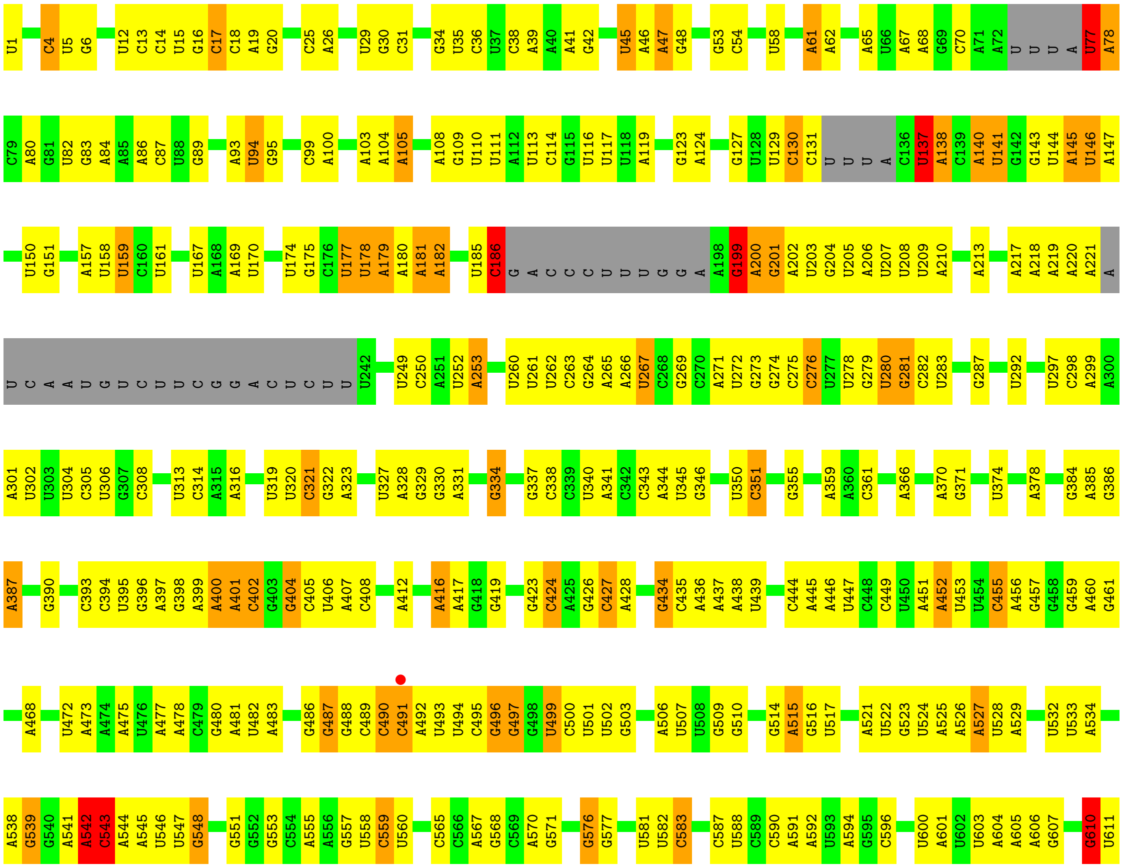
Chain eL43:

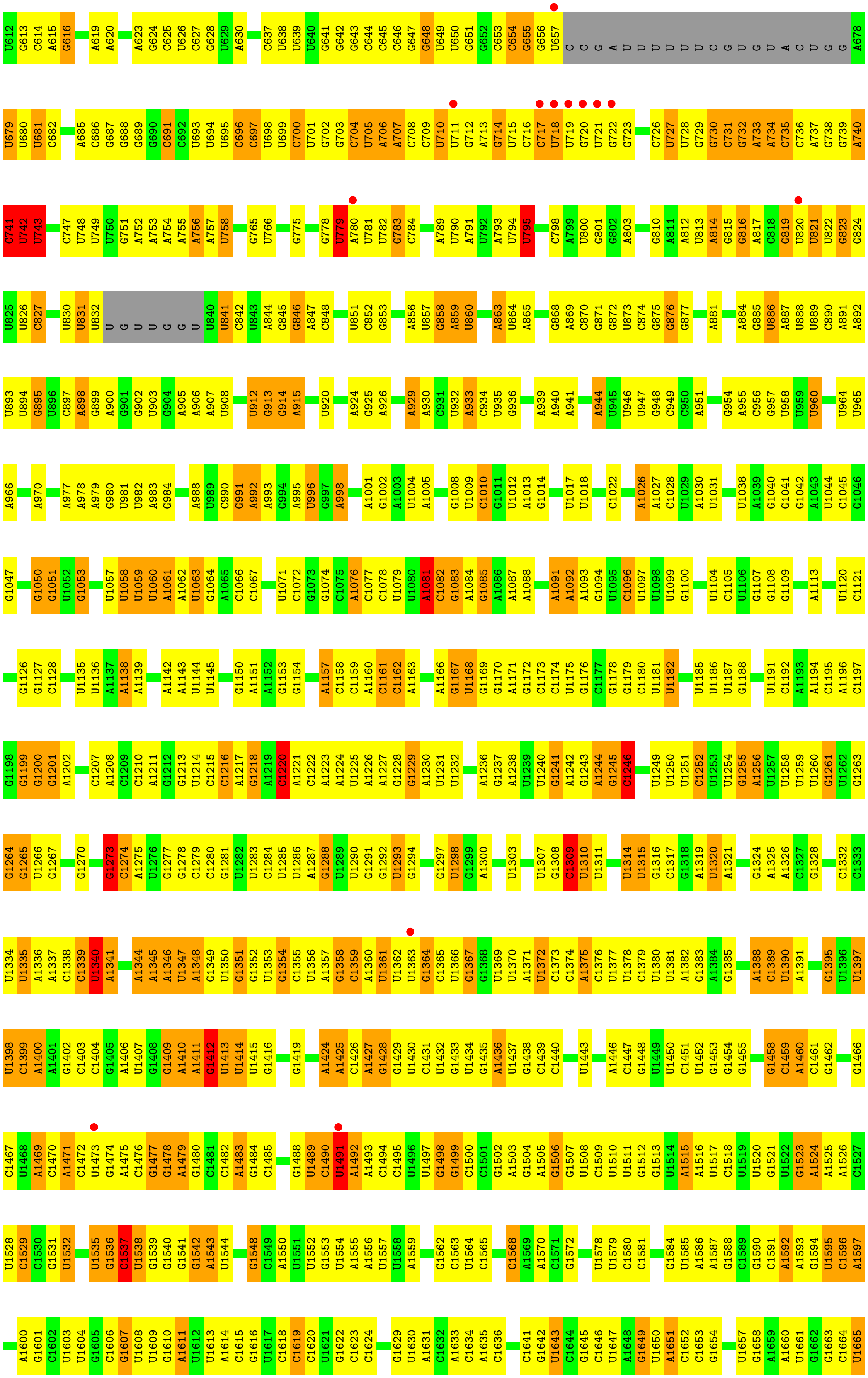




- Molecule 46: 18S rRNA

Chain 18S:

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U679 U680 U681 C682 A685 C686 G687 G688 G689 G690 C691 C692 U693 U694 U695 C696 C697 U698 U699 C700 U701 C702 G703 C704 U705 A706 A707 C708 C709 U710 U711 G712 A713 G714 U715 C716 C717 U718 U719 G720 U721 G722 G723 C726 U727 U728 G729 G730 C731 G732 A733 A734 C735 C736 A737 G738 G739 A740
C741 U742 U743 C747 U748 U749 U750 G751 A752 A753 A754 A755 A756 A757 U758 G765 U766 G775 G778 U779 A780 U781 U782 G783 C784 A789 U790 A791 U792 A793 U794 U795 C798 A799 U800 G801 G802 A803 G810 A811 A812 U813 A814 G815 G816 A817 C818 G819 U820 U821 U822 G823 G824
U825 U826 C827 U830 U831 U832 U G U U G G U U840 U841 C842 U843 A844 G845 G846 A847 C848 U851 C852 G853 A856 U857 G858 A859 U860 A863 U864 A865 G868 A869 C870 G871 G872 U873 C874 G875 G876 G877 A881 A884 G885 U886 A887 U888 U889 C890 A891 A892
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A966 A970 A977 A978 A979 G980 U981 U982 A983 G984 A988 U989 C990 G991 A992 A993 G994 A995 U996 G997 A998 A1001 G1002 A1003 U1004 A1005 G1008 U1009 C1010 G1011 U1012 A1013 G1014 U1017 U1018 C1022 A1026 A1027 C1028 U1029 A1030 U1031 U1038 A1039 G1040 G1041 G1042 A1043 U1044 C1045 G1046
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G1264 G1265 U1266 G1267 G1270 G1273 C1274 A1275 U1276 G1277 G1278 C1279 C1280 G1281 U1282 U1283 C1284 U1285 U1286 A1287 G1288 U1289 U1290 G1291 G1292 U1293 G1294 G1297 U1298 G1299 A1300 U1303 G1307 G1308 C1309 U1310 U1311 U1314 U1315 G1316 C1317 G1318 A1319 U1320 A1321 G1324 A1325 A1326 C1327 G1328 C1332 C1333
U1334 U1335 A1336 A1337 C1338 C1339 U1340 A1341 A1344 A1345 A1346 U1347 A1348 G1349 U1350 G1351 G1352 U1353 G1354 C1355 U1356 A1357 G1358 C1359 A1360 U1361 U1362 U1363 G1364 C1365 U1366 G1367 G1368 U1369 U1370 A1371 U1372 C1373 C1374 A1375 C1376 U1377 U1378 C1379 U1380 U1381 A1382 G1383 A1384 G1385 A1388 C1389 U1390 A1391 G1395 U1396 U1397
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C1467 U1468 A1469 C1470 A1471 C1472 U1473 G1474 A1475 C1476 G1477 G1478 A1479 G1480 C1481 C1482 A1483 G1484 C1485 G1488 U1489 C1490 U1491 A1492 A1493 C1494 C1495 U1496 U1497 G1498 G1499 C1500 C1501 G1502 A1503 G1504 A1505 G1506 G1507 U1508 C1509 U1510 U1511 G1512 G1513 U1514 A1515 A1516 U1517 C1518 U1519 U1520 G1521 U1522 G1523 A1524 A1525 A1526 C1527
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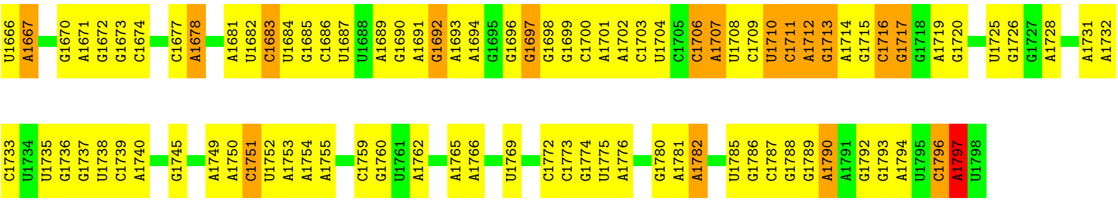
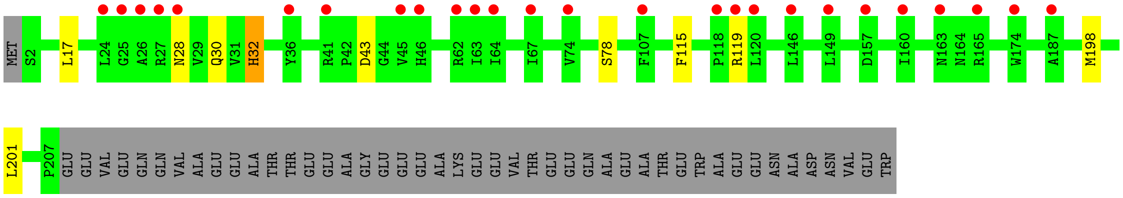


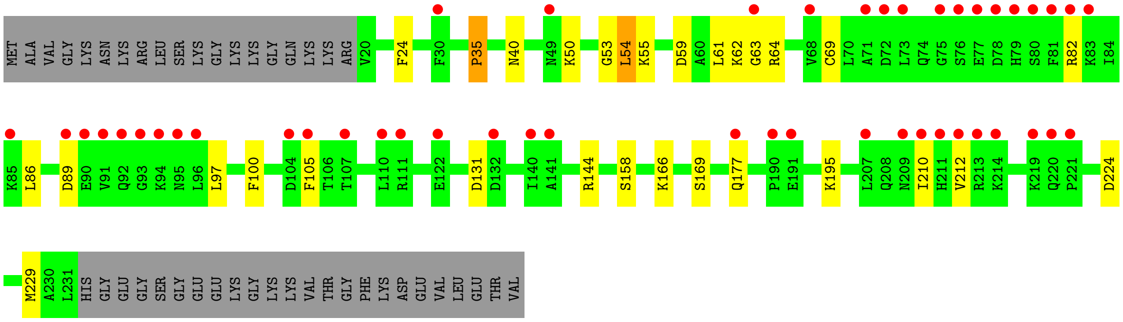
- Molecule 47: 40S ribosomal protein S0

Chain uS2:



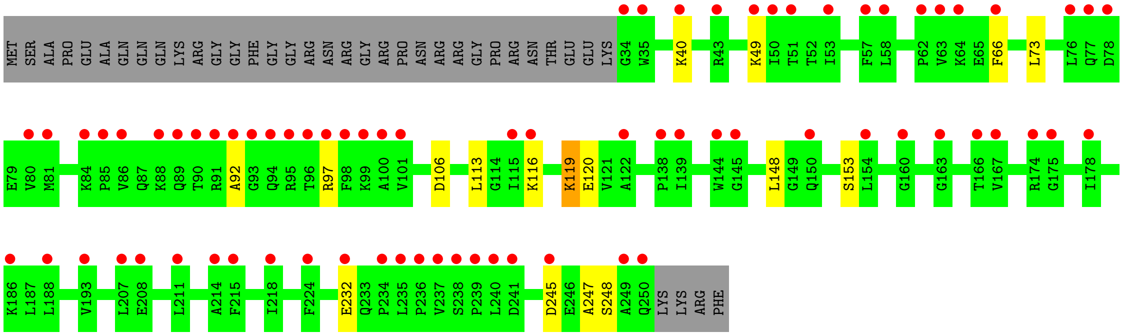
- Molecule 48: 40S ribosomal protein S1

Chain eS1:



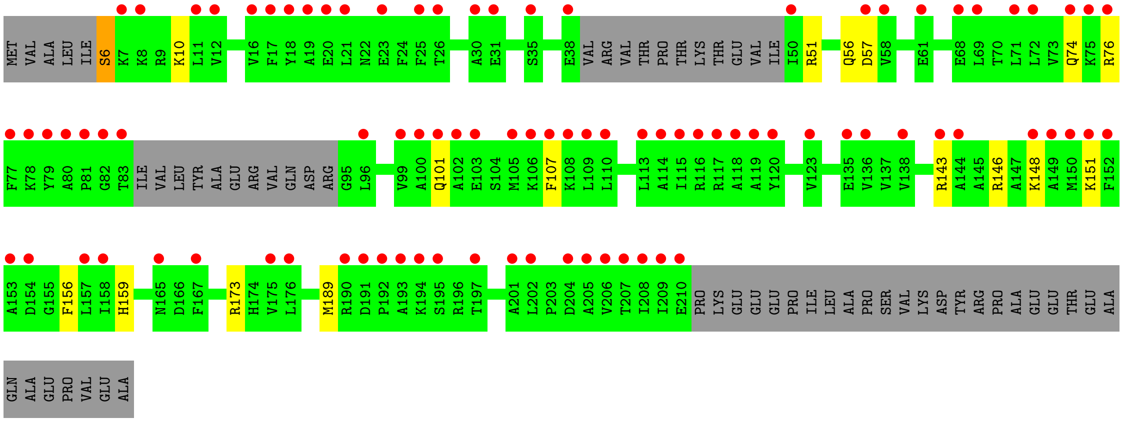
- Molecule 49: 40S ribosomal protein S2

Chain uS5:



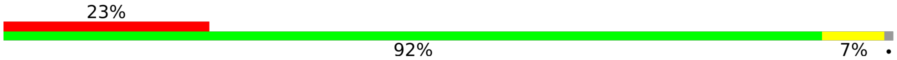
- Molecule 50: BJ4_G0045400.mRNA.1.CDS.1

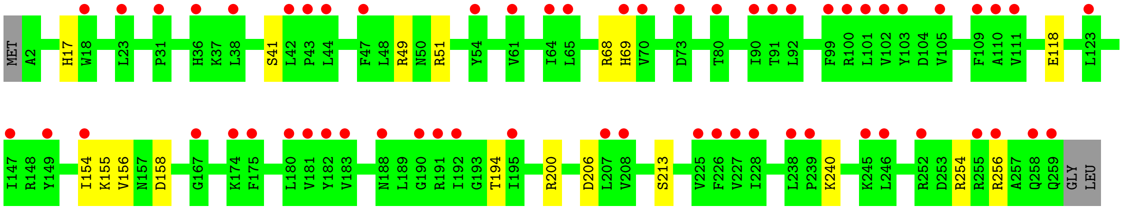
Chain uS3:



- Molecule 51: 40S ribosomal protein S4

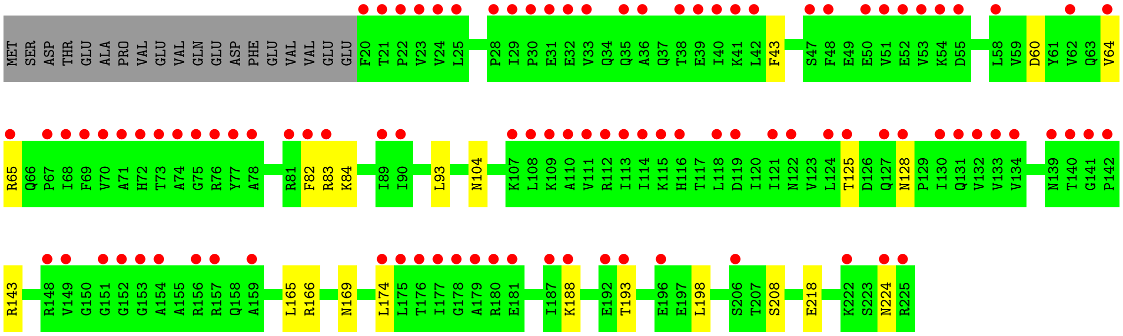
Chain eS4:





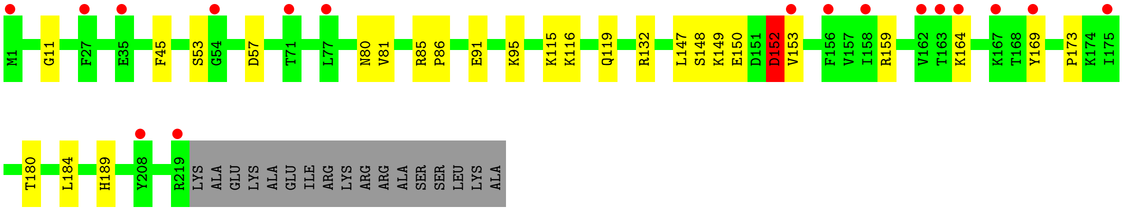
- Molecule 52: Rps5p

Chain uS7:



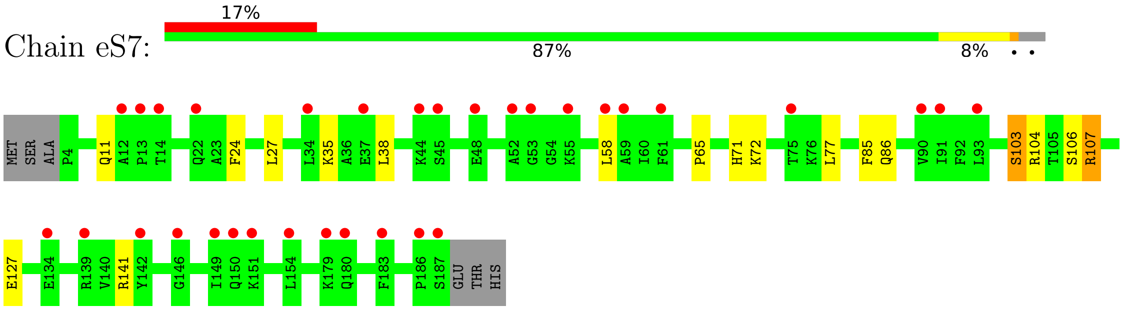
- Molecule 53: 40S ribosomal protein S6

Chain eS6:



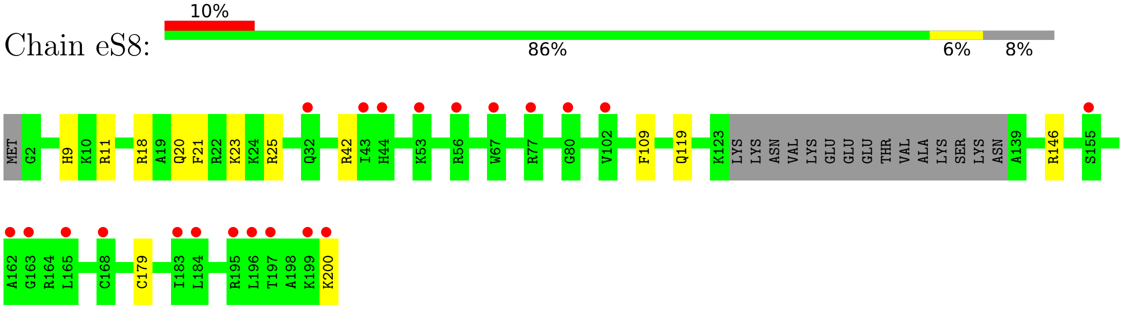
- Molecule 54: 40S ribosomal protein S7

Chain eS7:



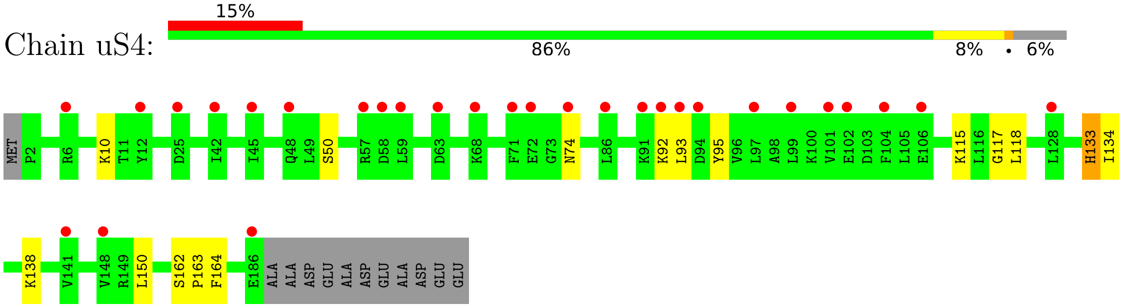
- Molecule 55: 40S ribosomal protein S8

Chain eS8:



- Molecule 56: BJ4_G0026100.mRNA.1.CDS.1

Chain uS4:

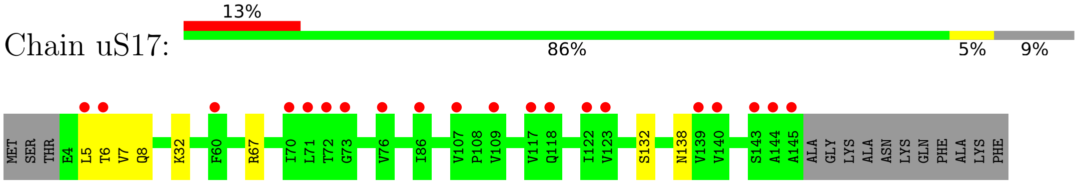


- Molecule 57: 40S ribosomal protein S10-A

Chain eS10:

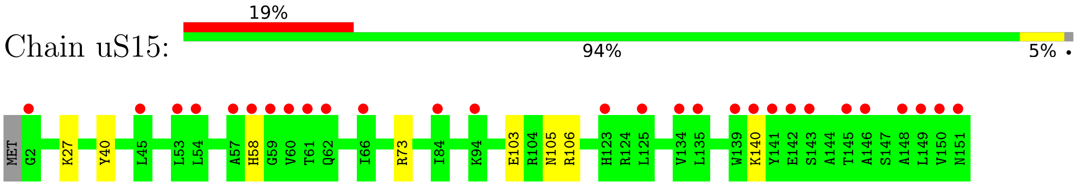
- Molecule 58: 40S ribosomal protein S11-B

Chain uS17:



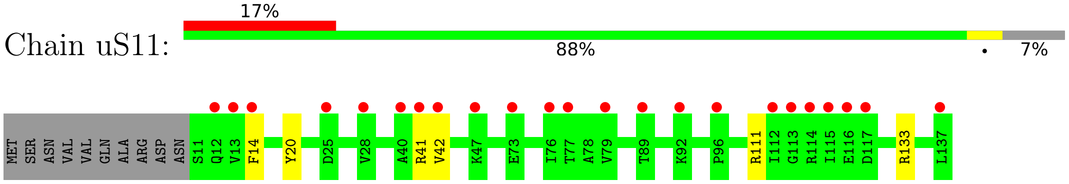
- Molecule 59: 40S ribosomal protein S13

Chain uS15:



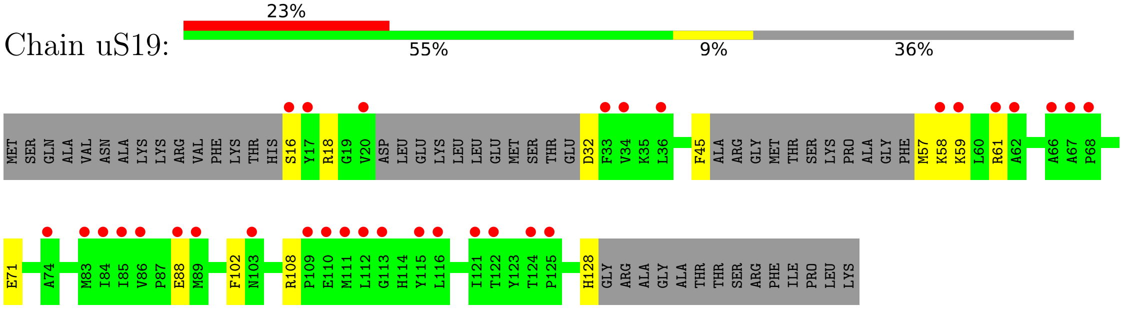
- Molecule 60: 40S ribosomal protein S14-A

Chain uS11:



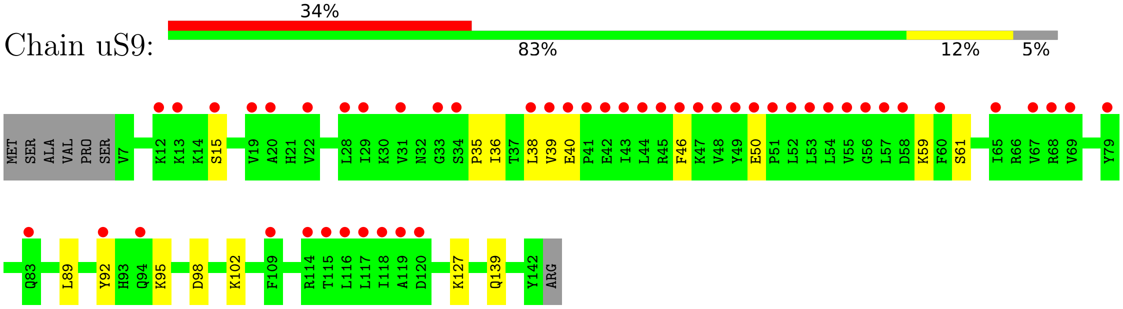
- Molecule 61: 40S ribosomal protein S15

Chain uS19:



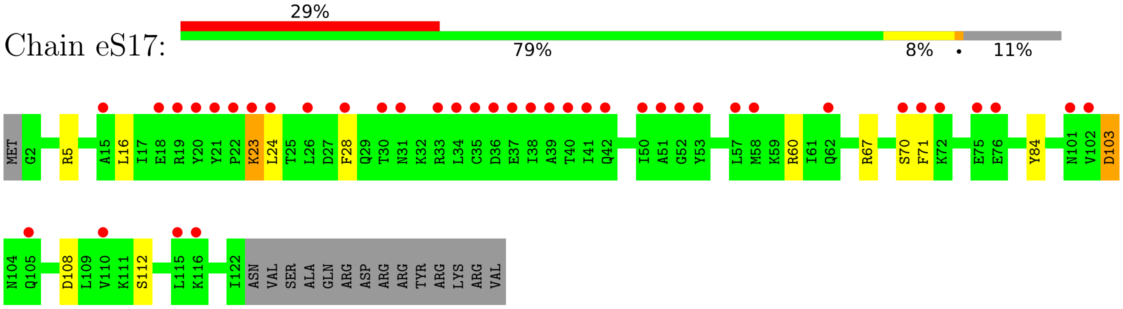
- Molecule 62: BJ4_G0008010.mRNA.1.CDS.1

Chain uS9:



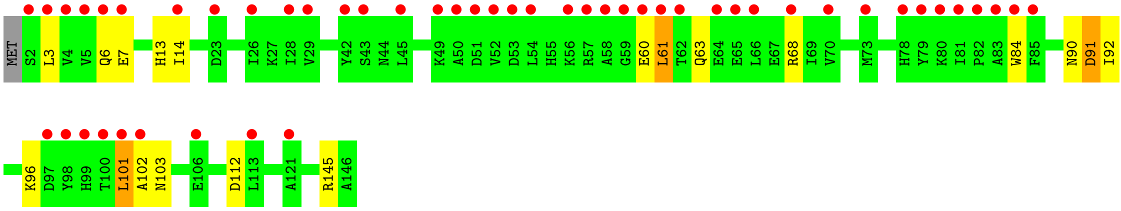
- Molecule 63: BJ4_G0020710.mRNA.1.CDS.1

Chain eS17:



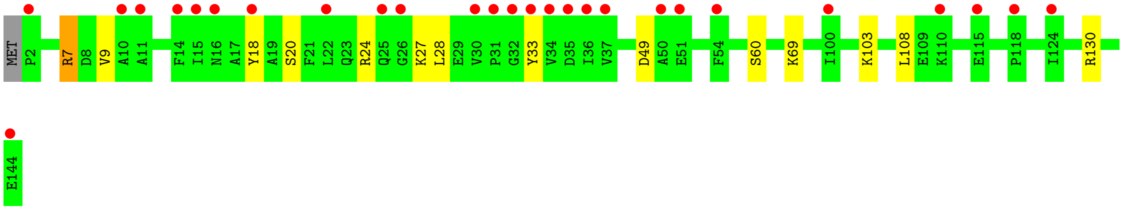
- Molecule 64: 40S ribosomal protein S18-B

Chain uS13:



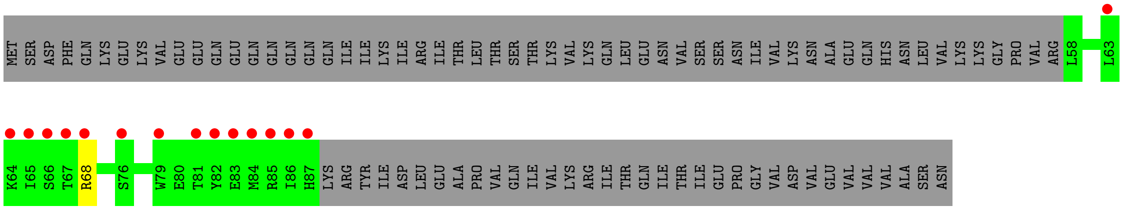
- Molecule 65: 40S ribosomal protein S19-A

Chain eS19:



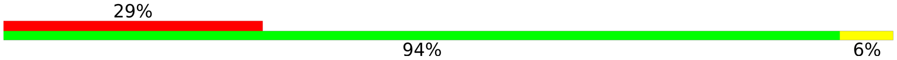
- Molecule 66: 40S ribosomal protein S20

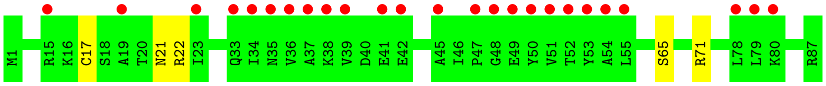
Chain uS10:



- Molecule 67: 40S ribosomal protein S21

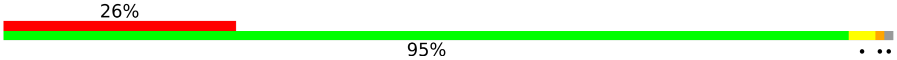
Chain eS21:

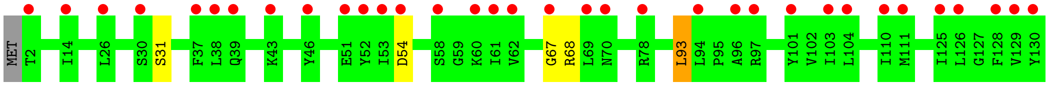




- Molecule 68: 40S ribosomal protein S22-A

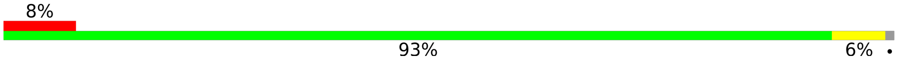
Chain uS8:

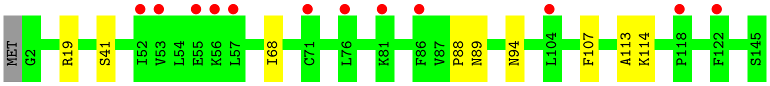




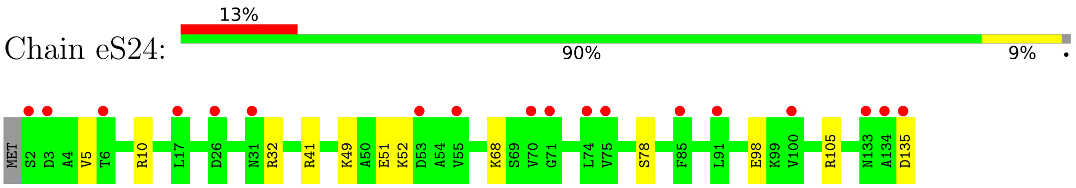
- Molecule 69: 40S ribosomal protein S23

Chain uS12:

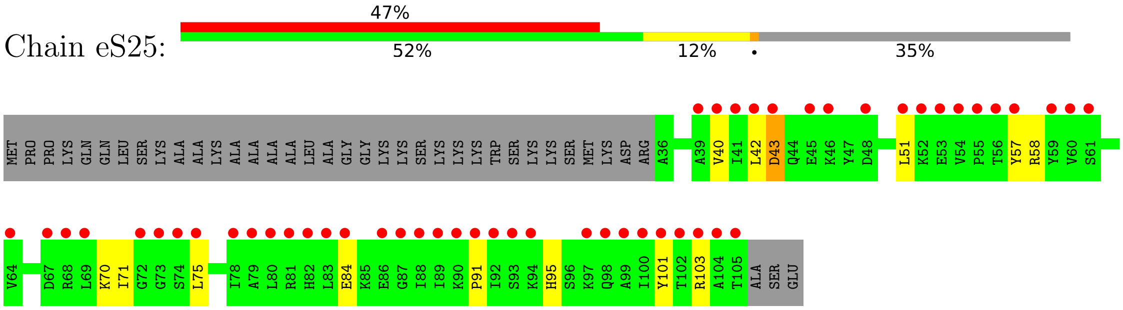




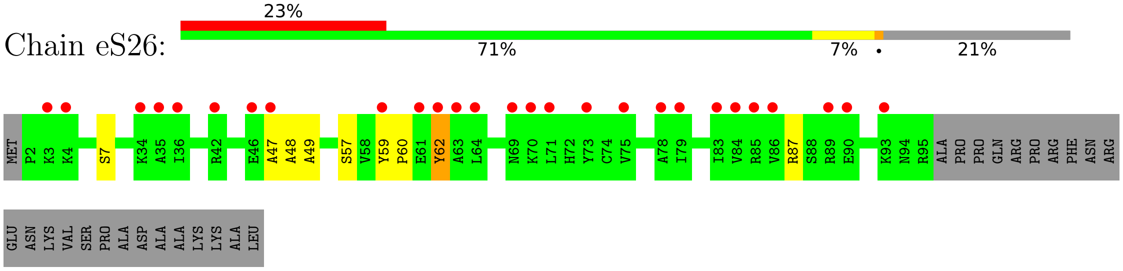
- Molecule 70: 40S ribosomal protein S24



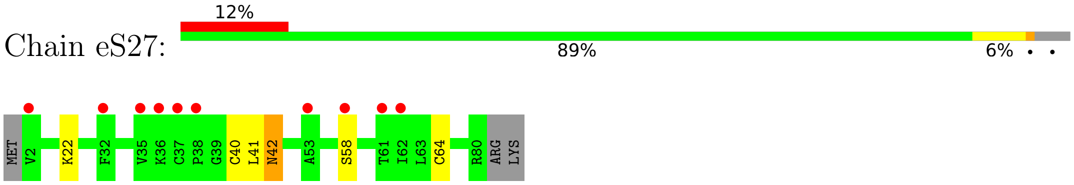
- Molecule 71: 40S ribosomal protein S25



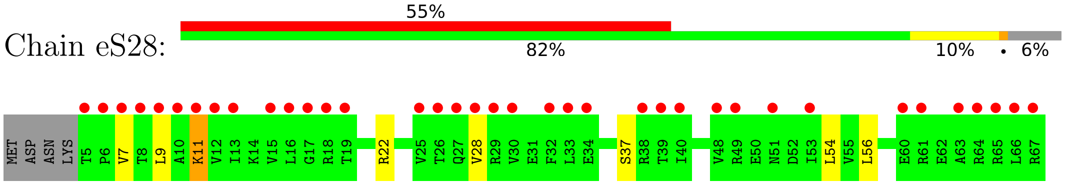
- Molecule 72: 40S ribosomal protein S26



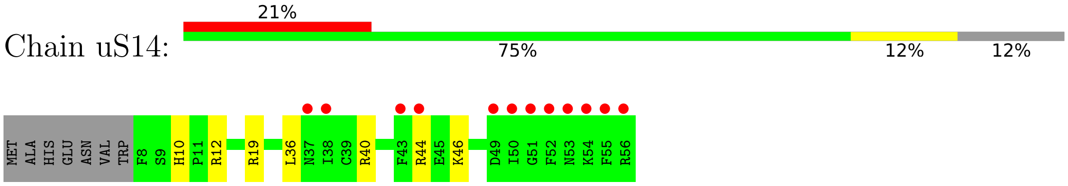
- Molecule 73: 40S ribosomal protein S27-A



- Molecule 74: eS28

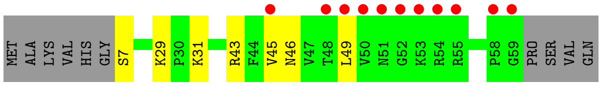


- Molecule 75: HLJ1_G0030400.mRNA.1.CDS.1



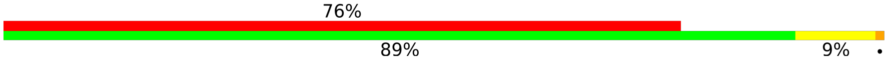
- Molecule 76: 40S ribosomal protein S30

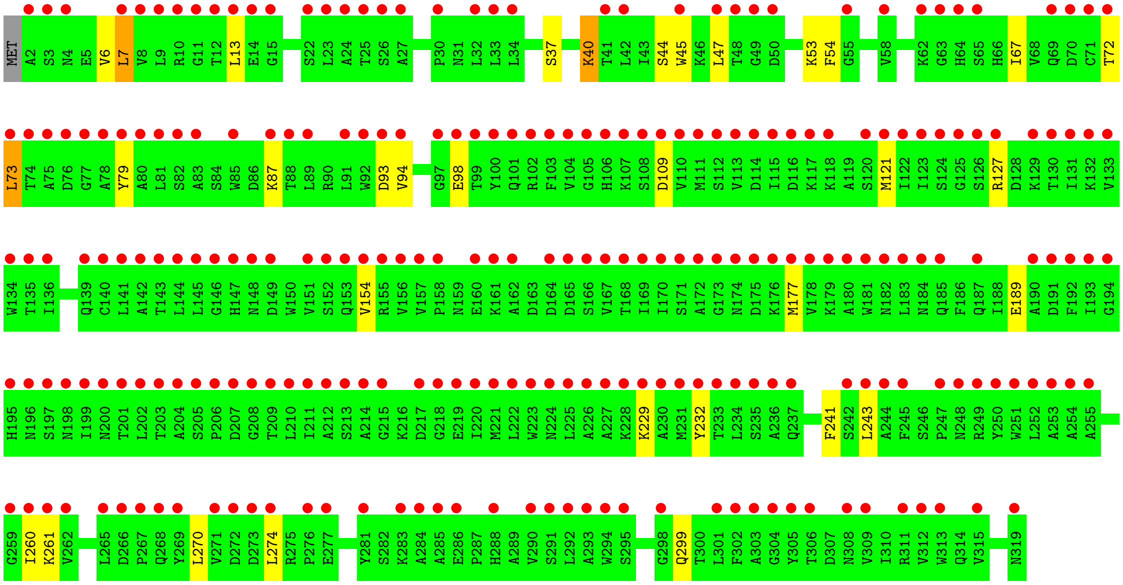
Chain eS30:



- Molecule 77: BJ4_G0022010.mRNA.1.CDS.1

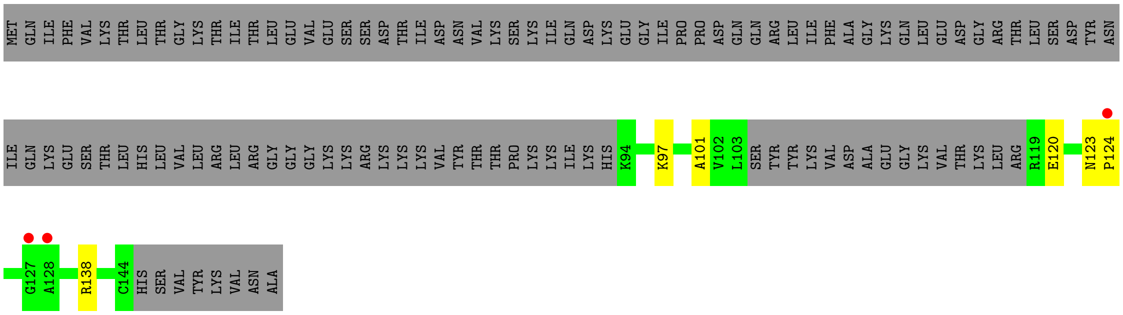
Chain RACK:





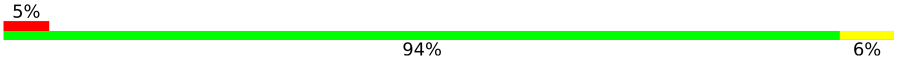
- Molecule 78: Ubiquitin-40S ribosomal protein S31

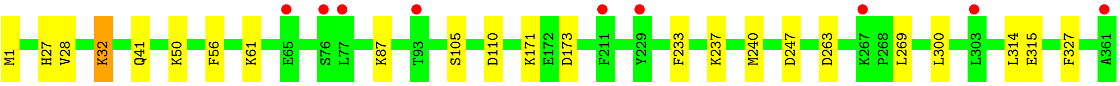
Chain eS31:

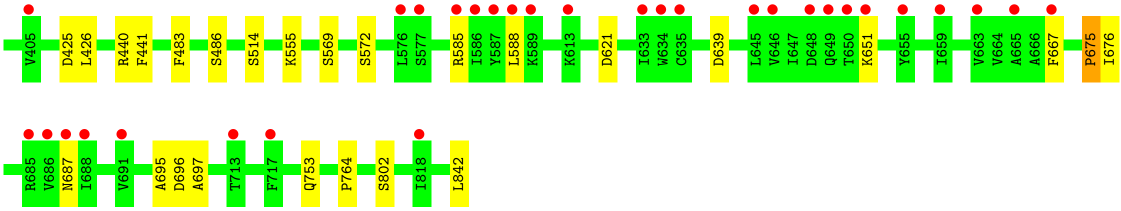


- Molecule 79: Elongation factor 2

Chain eEF2:

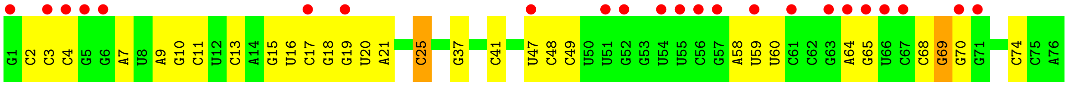






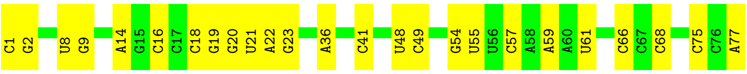
- Molecule 80: PHE tRNA

Chain ASIT:



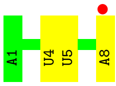
- Molecule 81: FMET tRNA

Chain PSIT:



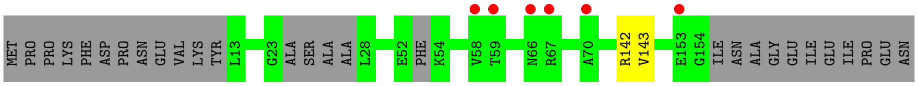
- Molecule 82: MRNA

Chain mRNA:



- Molecule 83: 60S ribosomal protein L12-B

Chain uL11:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	233.49Å 299.85Å 513.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	149.93 – 3.00 212.57 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (149.93-3.00) 90.5 (212.57-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.56 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.19rc4_4035	Depositor
R, R_{free}	0.228 , 0.284 0.227 , 0.287	Depositor DCC
R_{free} test set	2000 reflections (0.28%)	wwPDB-VP
Wilson B-factor (Å^2)	88.5	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	207073	wwPDB-VP
Average B, all atoms (Å^2)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.16% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: DDE, YG, GTP, MG, 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	25S	0.29	0/75698	0.95	140/118002 (0.1%)
2	AB	0.27	0/2883	0.91	2/4491 (0.0%)
3	58S	0.25	0/3746	0.86	2/5832 (0.0%)
4	uL10	0.51	0/1421	0.94	5/1921 (0.3%)
5	uL2	0.29	0/1948	0.56	0/2617
6	uL3	0.29	0/3146	0.53	0/4228
7	uL4	0.33	0/2800	0.67	1/3790 (0.0%)
8	uL18	0.38	1/2425 (0.0%)	0.65	4/3271 (0.1%)
9	eL6	0.41	0/1260	0.77	3/1694 (0.2%)
10	uL30	0.31	0/1821	0.64	1/2451 (0.0%)
11	eL8	0.37	0/1836	0.67	1/2481 (0.0%)
12	uL6	0.34	0/1539	0.60	0/2073
13	uL16	0.32	0/1767	0.55	0/2368
14	uL5	0.84	7/1374 (0.5%)	1.10	12/1842 (0.7%)
15	eL13	0.35	0/1568	0.68	3/2106 (0.1%)
16	eL14	0.41	0/1068	0.70	2/1438 (0.1%)
17	eL15	0.30	0/1757	0.54	0/2354
18	uL13	0.45	2/1585 (0.1%)	0.64	3/2128 (0.1%)
19	uL22	0.29	0/1218	0.55	1/1641 (0.1%)
20	eL18	0.32	0/1465	0.60	0/1965
21	eL19	0.35	1/1440 (0.1%)	0.60	1/1921 (0.1%)
22	eL20	0.30	0/1481	0.55	0/1990
23	eL21	0.31	0/1300	0.54	0/1743
24	eL22	0.43	0/786	0.81	1/1065 (0.1%)
25	uL14	0.29	0/978	0.56	0/1316
26	eL24	0.27	0/533	0.46	0/707
27	uL23	0.33	0/974	0.66	1/1314 (0.1%)
28	uL24	0.45	0/1004	0.95	5/1341 (0.4%)
29	eL27	0.37	0/1118	0.62	1/1497 (0.1%)
30	uL15	0.43	0/1204	0.74	3/1612 (0.2%)
31	eL29	0.28	0/473	0.55	0/629
32	eL30	0.35	0/750	0.59	1/1008 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	eL31	0.40	1/897 (0.1%)	0.67	1/1205 (0.1%)
34	eL32	0.30	0/1041	0.66	1/1394 (0.1%)
35	eL33	0.31	0/868	0.57	0/1168
36	eL34	0.26	0/871	0.52	0/1164
37	uL29	0.33	0/978	0.64	0/1301
38	eL36	0.34	0/778	0.65	1/1034 (0.1%)
39	eL37	0.29	0/680	0.58	0/901
40	eL38	0.36	0/618	0.78	1/826 (0.1%)
41	eL39	0.30	0/443	0.72	1/588 (0.2%)
42	eL40	0.27	0/423	0.47	0/562
43	eL41	0.23	0/234	0.50	0/300
44	eL42	0.30	0/831	0.63	1/1097 (0.1%)
45	eL43	0.26	0/701	0.54	0/934
46	18S	0.31	2/41291 (0.0%)	0.97	94/64331 (0.1%)
47	uS2	0.36	0/1617	0.68	3/2215 (0.1%)
48	eS1	0.53	0/1714	1.03	6/2308 (0.3%)
49	uS5	0.37	0/1665	0.73	5/2263 (0.2%)
50	uS3	0.55	2/1429 (0.1%)	0.74	1/1913 (0.1%)
51	eS4	0.31	0/2097	0.61	0/2823
52	uS7	0.53	0/1629	0.94	4/2202 (0.2%)
53	eS6	0.46	1/1790 (0.1%)	0.78	2/2393 (0.1%)
54	eS7	0.41	0/1506	0.75	1/2028 (0.0%)
55	eS8	0.32	0/1482	0.63	1/1980 (0.1%)
56	uS4	0.36	0/1519	0.71	3/2035 (0.1%)
57	eS10	0.60	0/309	1.13	4/416 (1.0%)
58	uS17	0.31	0/1172	0.56	1/1580 (0.1%)
59	uS15	0.33	0/1215	0.58	0/1638
60	uS11	0.35	0/901	0.69	0/1217
61	uS19	0.38	0/747	0.71	1/1002 (0.1%)
62	uS9	0.46	0/1088	0.86	3/1459 (0.2%)
63	eS17	0.55	0/971	0.87	2/1303 (0.2%)
64	uS13	0.46	0/1211	0.95	3/1628 (0.2%)
65	eS19	0.51	1/1130 (0.1%)	0.78	4/1517 (0.3%)
66	uS10	0.42	0/250	0.70	1/336 (0.3%)
67	eS21	0.33	0/693	0.65	0/935
68	uS8	0.27	0/1038	0.59	1/1395 (0.1%)
69	uS12	0.28	0/1139	0.55	0/1518
70	eS24	0.34	0/1087	0.57	0/1449
71	eS25	0.74	2/571 (0.4%)	1.09	3/768 (0.4%)
72	eS26	0.37	0/761	0.66	0/1016
73	eS27	0.43	1/600 (0.2%)	0.86	2/813 (0.2%)
74	eS28	0.50	1/499 (0.2%)	0.92	2/670 (0.3%)
75	uS14	0.37	0/412	0.65	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
76	eS30	0.31	0/433	0.78	1/575 (0.2%)
77	RACK	0.61	1/2489 (0.0%)	1.05	11/3389 (0.3%)
78	eS31	0.48	0/279	0.93	0/369
79	eEF2	0.32	0/6673	0.62	4/9032 (0.0%)
80	ASIT	0.28	0/1784	0.97	3/2780 (0.1%)
81	PSIT	0.42	1/1836 (0.1%)	1.08	3/2859 (0.1%)
82	mRNA	0.17	0/188	0.70	0/290
83	uL11	0.24	0/670	0.48	0/926
All	All	0.34	24/221614 (0.0%)	0.86	368/325225 (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	uL10	0	4
6	uL3	0	1
10	uL30	0	2
11	eL8	0	2
12	uL6	0	1
14	uL5	0	5
15	eL13	0	1
18	uL13	0	1
20	eL18	0	1
21	eL19	0	1
22	eL20	0	1
25	uL14	0	1
28	uL24	0	1
29	eL27	0	3
30	uL15	0	4
31	eL29	0	1
35	eL33	0	1
38	eL36	0	1
40	eL38	0	1
41	eL39	0	2
44	eL42	0	1
47	uS2	0	2
48	eS1	0	8
49	uS5	0	4
51	eS4	0	2
52	uS7	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	eS6	0	6
54	eS7	0	5
56	uS4	0	3
57	eS10	0	4
58	uS17	0	1
59	uS15	0	2
60	uS11	0	1
62	uS9	0	1
63	eS17	0	3
64	uS13	0	5
65	eS19	0	3
68	uS8	0	1
69	uS12	0	1
70	eS24	0	2
71	eS25	0	3
72	eS26	0	5
74	eS28	0	2
77	RACK	0	7
78	eS31	0	2
79	eEF2	0	5
83	uL11	0	1
All	All	0	120

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	uL5	29	ARG	CG-CD	11.86	1.81	1.51
81	PSIT	1	C	OP3-P	-10.54	1.48	1.61
14	uL5	29	ARG	CB-CG	8.89	1.76	1.52
18	uL13	170	LYS	CE-NZ	8.76	1.71	1.49
50	uS3	10	LYS	CD-CE	7.40	1.69	1.51

The worst 5 of 368 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	eS1	61	LEU	CB-CG-CD1	20.84	146.43	111.00
46	18S	94	U	C2-N3-C4	15.29	136.18	127.00
18	uL13	170	LYS	CD-CE-NZ	-13.49	80.67	111.70
46	18S	1390	U	O5'-P-OP2	-12.89	94.10	105.70
46	18S	1389	C	C2-N1-C1'	12.35	132.39	118.80

There are no chirality outliers.

5 of 120 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	uL10	108	PRO	Peptide
4	uL10	123	ALA	Peptide
4	uL10	198	PRO	Peptide
4	uL10	8	LYS	Peptide
6	uL3	349	LYS	Peptide

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	25S	67633	0	33994	1260	0
2	AB	2579	0	1304	41	0
3	58S	3353	0	1695	68	0
4	uL10	1397	0	0	0	0
5	uL2	1914	0	2283	0	0
6	uL3	3075	0	3336	0	0
7	uL4	2748	0	2859	0	0
8	uL18	2375	0	0	0	0
9	eL6	1239	0	1326	0	0
10	uL30	1784	0	0	0	0
11	eL8	1804	0	1877	0	0
12	uL6	1518	0	1587	0	0
13	uL16	1732	0	0	0	0
14	uL5	1353	0	1383	0	0
15	eL13	1543	0	0	0	0
16	eL14	1053	0	0	0	0
17	eL15	1720	0	0	0	0
18	uL13	1555	0	0	0	0
19	uL22	1195	0	0	0	0
20	eL18	1441	0	0	0	0
21	eL19	1423	0	0	0	0
22	eL20	1445	0	0	0	0
23	eL21	1276	0	0	0	0
24	eL22	770	0	0	0	0
25	uL14	963	0	0	0	0
26	eL24	521	0	0	0	0
27	uL23	959	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	uL24	993	0	0	0	0
29	eL27	1092	0	0	0	0
30	uL15	1173	0	0	0	0
31	eL29	462	0	0	0	0
32	eL30	742	0	0	0	1
33	eL31	883	0	0	0	0
34	eL32	1020	0	0	0	0
35	eL33	850	0	0	0	0
36	eL34	861	0	0	0	0
37	uL29	969	0	0	0	0
38	eL36	771	0	0	0	0
39	eL37	665	0	0	0	0
40	eL38	612	0	0	0	0
41	eL39	436	0	0	0	0
42	eL40	417	0	0	0	0
43	eL41	233	0	0	0	0
44	eL42	819	0	0	0	0
45	eL43	694	0	0	0	0
46	18S	36918	0	18578	736	1
47	uS2	1577	0	1567	0	0
48	eS1	1689	0	1874	0	0
49	uS5	1635	0	1723	0	0
50	uS3	1412	0	1473	0	0
51	eS4	2056	0	2140	0	0
52	uS7	1609	0	1675	0	0
53	eS6	1766	0	1859	0	0
54	eS7	1481	0	1572	0	0
55	eS8	1457	0	1488	0	0
56	uS4	1494	0	1573	0	0
57	eS10	300	0	0	0	0
58	uS17	1146	0	0	0	0
59	uS15	1192	0	0	0	0
60	uS11	891	0	0	0	0
61	uS19	732	0	0	0	0
62	uS9	1069	0	1126	0	0
63	eS17	961	0	0	0	0
64	uS13	1192	0	0	0	0
65	eS19	1112	0	0	0	0
66	uS10	245	0	0	0	0
67	eS21	684	0	0	0	0
68	uS8	1021	0	1060	0	0
69	uS12	1121	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	eS24	1073	0	0	0	0
71	eS25	563	0	0	0	0
72	eS26	750	0	0	0	0
73	eS27	590	0	0	0	0
74	eS28	497	0	0	0	0
75	uS14	404	0	0	0	0
76	eS30	427	0	0	0	0
77	RACK	2436	0	0	0	0
78	eS31	276	0	0	0	0
79	eEF2	6569	0	0	0	0
80	ASIT	1636	0	0	0	0
81	PSIT	1644	0	0	0	0
82	mRNA	169	0	0	0	0
83	uL11	673	0	0	0	0
84	18S	122	0	0	0	0
84	25S	324	0	0	0	0
84	58S	7	0	0	0	0
84	AB	5	0	0	0	0
84	ASIT	1	0	0	0	0
84	PSIT	6	0	0	0	0
84	eEF2	6	0	0	0	0
84	eL15	1	0	0	0	0
84	eL18	1	0	0	0	0
84	eL20	1	0	0	0	0
84	eL30	2	0	0	0	0
84	eL31	1	0	0	0	0
84	eL32	1	0	0	0	0
84	eL33	1	0	0	0	0
84	eL40	1	0	0	0	0
84	eL41	1	0	0	0	0
84	eL42	2	0	0	0	0
84	eS1	1	0	0	0	0
84	eS26	1	0	0	0	0
84	eS4	3	0	0	0	0
84	eS6	2	0	0	0	0
84	mRNA	1	0	0	0	0
84	uL14	1	0	0	0	0
84	uL16	1	0	0	0	0
84	uL18	2	0	0	0	0
84	uL2	3	0	0	0	0
84	uL22	1	0	0	0	0
84	uL3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	uS12	3	0	0	0	0
84	uS14	1	0	0	0	0
84	uS15	1	0	0	0	0
84	uS19	1	0	0	0	0
85	eL34	1	0	0	0	0
85	eL37	1	0	0	0	0
85	eL40	1	0	0	0	0
85	eL42	1	0	0	0	0
85	eL43	1	0	0	0	0
85	eS26	1	0	0	0	0
85	eS31	1	0	0	0	0
85	uS14	1	0	0	0	0
86	eEF2	32	0	0	0	0
All	All	207073	0	89352	2085	1

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 24.

The worst 5 of 2085 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)
1:25S:3321:C:O2	1:25S:3386:G:N2	1.98	0.95
46:18S:1397:U:H3'	46:18S:1398:U:H5"	1.46	0.94
1:25S:1352:A:H4'	1:25S:1353:U:H5'	1.50	0.93
1:25S:547:G:H2'	1:25S:548:G:C8	2.04	0.93
1:25S:3348:G:H1	1:25S:3357:U:H3	1.20	0.90

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:eL30:64:LYS:NZ	46:18S:273:G:O3'[3_455]	2.07	0.13

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	uL10	174/312 (56%)	127 (73%)	42 (24%)	5 (3%)	4	24
5	uL2	250/254 (98%)	230 (92%)	20 (8%)	0	100	100
6	uL3	384/387 (99%)	336 (88%)	47 (12%)	1 (0%)	41	76
7	uL4	359/362 (99%)	307 (86%)	50 (14%)	2 (1%)	25	64
8	uL18	294/297 (99%)	260 (88%)	33 (11%)	1 (0%)	41	76
9	eL6	152/176 (86%)	127 (84%)	25 (16%)	0	100	100
10	uL30	220/244 (90%)	199 (90%)	19 (9%)	2 (1%)	17	55
11	eL8	231/256 (90%)	200 (87%)	29 (13%)	2 (1%)	17	55
12	uL6	189/191 (99%)	162 (86%)	26 (14%)	1 (0%)	29	68
13	uL16	209/221 (95%)	185 (88%)	24 (12%)	0	100	100
14	uL5	167/174 (96%)	125 (75%)	37 (22%)	5 (3%)	4	24
15	eL13	191/199 (96%)	152 (80%)	34 (18%)	5 (3%)	5	27
16	eL14	134/138 (97%)	118 (88%)	16 (12%)	0	100	100
17	eL15	201/204 (98%)	173 (86%)	27 (13%)	1 (0%)	29	68
18	uL13	195/199 (98%)	182 (93%)	10 (5%)	3 (2%)	10	42
19	uL22	149/184 (81%)	134 (90%)	15 (10%)	0	100	100
20	eL18	183/186 (98%)	153 (84%)	30 (16%)	0	100	100
21	eL19	174/189 (92%)	157 (90%)	15 (9%)	2 (1%)	14	50
22	eL20	170/172 (99%)	155 (91%)	15 (9%)	0	100	100
23	eL21	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	25	64
24	eL22	95/121 (78%)	83 (87%)	12 (13%)	0	100	100
25	uL14	127/137 (93%)	122 (96%)	5 (4%)	0	100	100
26	eL24	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
27	uL23	118/142 (83%)	94 (80%)	24 (20%)	0	100	100
28	uL24	124/127 (98%)	107 (86%)	17 (14%)	0	100	100
29	eL27	133/136 (98%)	110 (83%)	21 (16%)	2 (2%)	10	42
30	uL15	146/149 (98%)	127 (87%)	16 (11%)	3 (2%)	7	33
31	eL29	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
32	eL30	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	14	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	eL31	107/113 (95%)	93 (87%)	13 (12%)	1 (1%)	17	55
34	eL32	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	9	40
35	eL33	104/107 (97%)	99 (95%)	4 (4%)	1 (1%)	15	53
36	eL34	107/121 (88%)	101 (94%)	6 (6%)	0	100	100
37	uL29	117/120 (98%)	101 (86%)	16 (14%)	0	100	100
38	eL36	97/100 (97%)	75 (77%)	20 (21%)	2 (2%)	7	33
39	eL37	82/88 (93%)	72 (88%)	9 (11%)	1 (1%)	13	48
40	eL38	75/78 (96%)	59 (79%)	15 (20%)	1 (1%)	12	45
41	eL39	48/51 (94%)	40 (83%)	8 (17%)	0	100	100
42	eL40	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
43	eL41	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
44	eL42	100/106 (94%)	77 (77%)	22 (22%)	1 (1%)	15	53
45	eL43	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
47	uS2	204/252 (81%)	165 (81%)	38 (19%)	1 (0%)	29	68
48	eS1	210/255 (82%)	150 (71%)	54 (26%)	6 (3%)	4	24
49	uS5	215/254 (85%)	185 (86%)	28 (13%)	2 (1%)	17	55
50	uS3	177/240 (74%)	138 (78%)	36 (20%)	3 (2%)	9	39
51	eS4	256/261 (98%)	219 (86%)	34 (13%)	3 (1%)	13	48
52	uS7	204/225 (91%)	149 (73%)	52 (26%)	3 (2%)	10	42
53	eS6	217/236 (92%)	176 (81%)	34 (16%)	7 (3%)	4	22
54	eS7	182/190 (96%)	145 (80%)	34 (19%)	3 (2%)	9	40
55	eS8	180/200 (90%)	149 (83%)	29 (16%)	2 (1%)	14	50
56	uS4	183/197 (93%)	151 (82%)	28 (15%)	4 (2%)	6	31
57	eS10	29/105 (28%)	19 (66%)	9 (31%)	1 (3%)	3	20
58	uS17	140/156 (90%)	116 (83%)	22 (16%)	2 (1%)	11	43
59	uS15	148/151 (98%)	127 (86%)	20 (14%)	1 (1%)	22	60
60	uS11	125/137 (91%)	102 (82%)	22 (18%)	1 (1%)	19	57
61	uS19	85/142 (60%)	60 (71%)	23 (27%)	2 (2%)	6	29
62	uS9	134/143 (94%)	98 (73%)	32 (24%)	4 (3%)	4	24
63	eS17	119/136 (88%)	91 (76%)	26 (22%)	2 (2%)	9	39
64	uS13	143/146 (98%)	110 (77%)	26 (18%)	7 (5%)	2	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	eS19	141/144 (98%)	106 (75%)	35 (25%)	0	100	100
66	uS10	28/121 (23%)	25 (89%)	3 (11%)	0	100	100
67	eS21	85/87 (98%)	66 (78%)	19 (22%)	0	100	100
68	uS8	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	19	57
69	uS12	142/145 (98%)	129 (91%)	9 (6%)	4 (3%)	5	25
70	eS24	132/135 (98%)	117 (89%)	15 (11%)	0	100	100
71	eS25	68/108 (63%)	40 (59%)	25 (37%)	3 (4%)	2	15
72	eS26	92/119 (77%)	72 (78%)	16 (17%)	4 (4%)	2	15
73	eS27	77/82 (94%)	62 (80%)	14 (18%)	1 (1%)	12	45
74	eS28	61/67 (91%)	44 (72%)	17 (28%)	0	100	100
75	uS14	47/56 (84%)	42 (89%)	5 (11%)	0	100	100
76	eS30	51/63 (81%)	31 (61%)	18 (35%)	2 (4%)	3	17
77	RACK	316/319 (99%)	202 (64%)	111 (35%)	3 (1%)	17	55
78	eS31	32/152 (21%)	13 (41%)	17 (53%)	2 (6%)	1	7
79	eEF2	839/842 (100%)	717 (86%)	114 (14%)	8 (1%)	15	53
83	uL11	131/165 (79%)	97 (74%)	33 (25%)	1 (1%)	19	57
All	All	11582/13056 (89%)	9666 (84%)	1787 (15%)	129 (1%)	14	50

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	uL10	109	ALA
4	uL10	199	SER
7	uL4	339	LEU
10	uL30	159	GLN
15	eL13	63	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	uL10	152/254 (60%)	142 (93%)	10 (7%)	16	49
5	uL2	193/196 (98%)	187 (97%)	6 (3%)	40	75
6	uL3	320/323 (99%)	301 (94%)	19 (6%)	19	54
7	uL4	288/289 (100%)	276 (96%)	12 (4%)	30	66
8	uL18	244/245 (100%)	226 (93%)	18 (7%)	13	44
9	eL6	134/153 (88%)	124 (92%)	10 (8%)	13	43
10	uL30	186/205 (91%)	174 (94%)	12 (6%)	17	50
11	eL8	187/208 (90%)	180 (96%)	7 (4%)	34	70
12	uL6	171/171 (100%)	164 (96%)	7 (4%)	30	67
13	uL16	183/187 (98%)	177 (97%)	6 (3%)	38	73
14	uL5	147/150 (98%)	135 (92%)	12 (8%)	11	39
15	eL13	154/159 (97%)	143 (93%)	11 (7%)	14	46
16	eL14	107/109 (98%)	96 (90%)	11 (10%)	7	28
17	eL15	175/176 (99%)	165 (94%)	10 (6%)	20	56
18	uL13	160/162 (99%)	156 (98%)	4 (2%)	47	79
19	uL22	122/146 (84%)	116 (95%)	6 (5%)	25	61
20	eL18	150/151 (99%)	147 (98%)	3 (2%)	55	83
21	eL19	143/154 (93%)	134 (94%)	9 (6%)	18	51
22	eL20	156/156 (100%)	147 (94%)	9 (6%)	20	55
23	eL21	136/137 (99%)	130 (96%)	6 (4%)	28	65
24	eL22	84/107 (78%)	82 (98%)	2 (2%)	49	79
25	uL14	101/105 (96%)	97 (96%)	4 (4%)	31	68
26	eL24	55/129 (43%)	51 (93%)	4 (7%)	14	44
27	uL23	104/118 (88%)	100 (96%)	4 (4%)	33	69
28	uL24	109/110 (99%)	101 (93%)	8 (7%)	14	44
29	eL27	115/116 (99%)	111 (96%)	4 (4%)	36	71
30	uL15	118/119 (99%)	112 (95%)	6 (5%)	24	60
31	eL29	46/47 (98%)	44 (96%)	2 (4%)	29	66
32	eL30	81/88 (92%)	78 (96%)	3 (4%)	34	70
33	eL31	94/97 (97%)	92 (98%)	2 (2%)	53	82
34	eL32	109/111 (98%)	108 (99%)	1 (1%)	78	92
35	eL33	90/91 (99%)	84 (93%)	6 (7%)	16	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	eL34	94/103 (91%)	91 (97%)	3 (3%)	39	74
37	uL29	104/105 (99%)	102 (98%)	2 (2%)	57	84
38	eL36	81/82 (99%)	78 (96%)	3 (4%)	34	70
39	eL37	69/71 (97%)	66 (96%)	3 (4%)	29	66
40	eL38	68/69 (99%)	60 (88%)	8 (12%)	5	22
41	eL39	45/46 (98%)	41 (91%)	4 (9%)	9	35
42	eL40	47/116 (40%)	44 (94%)	3 (6%)	17	51
43	eL41	23/23 (100%)	20 (87%)	3 (13%)	4	19
44	eL42	87/91 (96%)	82 (94%)	5 (6%)	20	56
45	eL43	71/72 (99%)	67 (94%)	4 (6%)	21	56
47	uS2	164/210 (78%)	159 (97%)	5 (3%)	41	75
48	eS1	189/224 (84%)	175 (93%)	14 (7%)	13	44
49	uS5	176/205 (86%)	168 (96%)	8 (4%)	27	64
50	uS3	145/195 (74%)	132 (91%)	13 (9%)	9	35
51	eS4	220/222 (99%)	207 (94%)	13 (6%)	19	54
52	uS7	173/191 (91%)	163 (94%)	10 (6%)	20	55
53	eS6	188/201 (94%)	175 (93%)	13 (7%)	15	48
54	eS7	165/170 (97%)	154 (93%)	11 (7%)	16	49
55	eS8	146/161 (91%)	136 (93%)	10 (7%)	16	48
56	uS4	158/166 (95%)	151 (96%)	7 (4%)	28	65
57	eS10	32/98 (33%)	30 (94%)	2 (6%)	18	51
58	uS17	127/137 (93%)	123 (97%)	4 (3%)	40	75
59	uS15	127/128 (99%)	122 (96%)	5 (4%)	32	69
60	uS11	81/105 (77%)	77 (95%)	4 (5%)	25	61
61	uS19	77/118 (65%)	67 (87%)	10 (13%)	4	19
62	uS9	113/119 (95%)	104 (92%)	9 (8%)	12	40
63	eS17	105/124 (85%)	97 (92%)	8 (8%)	13	43
64	uS13	128/129 (99%)	121 (94%)	7 (6%)	21	57
65	eS19	115/116 (99%)	107 (93%)	8 (7%)	15	47
66	uS10	28/114 (25%)	28 (100%)	0	100	100
67	eS21	74/74 (100%)	69 (93%)	5 (7%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	uS8	110/111 (99%)	107 (97%)	3 (3%)	44	77
69	uS12	119/120 (99%)	115 (97%)	4 (3%)	37	72
70	eS24	112/113 (99%)	102 (91%)	10 (9%)	9	35
71	eS25	61/89 (68%)	56 (92%)	5 (8%)	11	39
72	eS26	81/101 (80%)	80 (99%)	1 (1%)	71	90
73	eS27	68/71 (96%)	65 (96%)	3 (4%)	28	65
74	eS28	56/60 (93%)	52 (93%)	4 (7%)	14	46
75	uS14	43/49 (88%)	36 (84%)	7 (16%)	2	11
76	eS30	46/54 (85%)	42 (91%)	4 (9%)	10	37
77	RACK	259/262 (99%)	241 (93%)	18 (7%)	15	48
78	eS31	30/135 (22%)	28 (93%)	2 (7%)	16	49
79	eEF2	714/714 (100%)	680 (95%)	34 (5%)	25	62
All	All	9733/10833 (90%)	9200 (94%)	533 (6%)	21	57

5 of 533 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
73	eS27	64	CYS
76	eS30	29	LYS
73	eS27	58	SER
79	eEF2	514	SER
26	eL24	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	25S	3151/3396 (92%)	726 (23%)	22 (0%)
2	AB	120/121 (99%)	21 (17%)	1 (0%)
3	58S	157/158 (99%)	37 (23%)	1 (0%)
46	18S	1726/1798 (95%)	510 (29%)	23 (1%)
80	ASIT	75/76 (98%)	30 (40%)	2 (2%)
81	PSIT	76/77 (98%)	21 (27%)	0
82	mRNA	7/8 (87%)	3 (42%)	0
All	All	5312/5634 (94%)	1348 (25%)	49 (0%)

5 of 1348 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	25S	4	U
1	25S	6	A
1	25S	14	U
1	25S	17	G
1	25S	26	A

5 of 49 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	18S	199	G
46	18S	1082	C
46	18S	487	G
46	18S	781	U
46	18S	1244	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 515 ligands modelled in this entry, 514 are monoatomic - leaving 1 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	25S	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	25S	2458:A	O3’	2463:G	P	18.22

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	25S	3162/3396 (93%)	-0.53	3 (0%) 95 89	62, 101, 192, 285	0
2	AB	121/121 (100%)	-0.54	0 100 100	50, 108, 139, 149	0
3	58S	158/158 (100%)	-0.52	2 (1%) 77 51	94, 113, 157, 214	0
4	uL10	180/312 (57%)	1.07	46 (25%) 0 0	109, 163, 192, 199	0
5	uL2	252/254 (99%)	0.23	19 (7%) 14 4	65, 81, 107, 190	0
6	uL3	386/387 (99%)	0.70	59 (15%) 2 1	66, 96, 124, 166	0
7	uL4	361/362 (99%)	0.77	63 (17%) 1 0	79, 123, 153, 163	0
8	uL18	296/297 (99%)	0.49	33 (11%) 5 1	88, 126, 161, 176	0
9	eL6	156/176 (88%)	-0.09	6 (3%) 40 16	103, 138, 165, 183	0
10	uL30	222/244 (90%)	1.20	57 (25%) 0 0	82, 105, 156, 197	0
11	eL8	233/256 (91%)	0.62	36 (15%) 2 1	95, 127, 186, 210	0
12	uL6	191/191 (100%)	0.05	7 (3%) 41 17	73, 103, 127, 167	0
13	uL16	213/221 (96%)	1.02	49 (23%) 0 0	76, 99, 130, 152	0
14	uL5	169/174 (97%)	1.30	46 (27%) 0 0	105, 160, 186, 197	0
15	eL13	193/199 (96%)	1.10	42 (21%) 0 0	82, 129, 161, 181	0
16	eL14	136/138 (98%)	0.31	12 (8%) 10 3	96, 122, 157, 179	0
17	eL15	203/204 (99%)	1.31	55 (27%) 0 0	74, 101, 118, 131	0
18	uL13	197/199 (98%)	0.84	35 (17%) 1 0	74, 97, 148, 160	0
19	uL22	151/184 (82%)	1.34	42 (27%) 0 0	74, 107, 136, 142	0
20	eL18	185/186 (99%)	0.92	35 (18%) 1 0	88, 117, 136, 156	0
21	eL19	176/189 (93%)	0.38	13 (7%) 14 4	69, 98, 166, 192	0
22	eL20	172/172 (100%)	1.22	41 (23%) 0 0	86, 104, 123, 142	0
23	eL21	159/160 (99%)	1.39	54 (33%) 0 0	80, 101, 172, 186	0
24	eL22	97/121 (80%)	1.42	30 (30%) 0 0	119, 146, 172, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
25	uL14	129/137 (94%)	0.44	7 (5%) 25 9	62, 85, 103, 110	0
26	eL24	63/155 (40%)	0.30	5 (7%) 12 4	77, 92, 117, 136	0
27	uL23	120/142 (84%)	1.63	45 (37%) 0 0	96, 117, 142, 157	0
28	uL24	126/127 (99%)	1.08	30 (23%) 0 0	106, 136, 161, 170	0
29	eL27	135/136 (99%)	0.82	27 (20%) 1 0	93, 114, 142, 158	0
30	uL15	148/149 (99%)	1.29	45 (30%) 0 0	77, 112, 146, 154	0
31	eL29	58/59 (98%)	0.54	7 (12%) 4 1	82, 116, 156, 186	0
32	eL30	97/105 (92%)	0.75	11 (11%) 5 1	86, 104, 148, 154	0
33	eL31	109/113 (96%)	1.56	34 (31%) 0 0	80, 111, 179, 189	0
34	eL32	127/130 (97%)	1.15	33 (25%) 0 0	84, 120, 161, 165	0
35	eL33	106/107 (99%)	0.69	15 (14%) 2 1	89, 108, 154, 182	0
36	eL34	109/121 (90%)	0.24	12 (11%) 5 2	77, 96, 144, 167	0
37	uL29	119/120 (99%)	0.78	20 (16%) 1 0	102, 128, 155, 167	0
38	eL36	99/100 (99%)	0.99	20 (20%) 1 0	102, 124, 148, 197	0
39	eL37	84/88 (95%)	1.03	18 (21%) 0 0	68, 98, 127, 149	0
40	eL38	77/78 (98%)	-0.00	5 (6%) 18 5	102, 130, 154, 159	0
41	eL39	50/51 (98%)	1.83	20 (40%) 0 0	91, 109, 133, 144	0
42	eL40	52/128 (40%)	-0.36	0 100 100	75, 90, 112, 119	0
43	eL41	25/25 (100%)	1.20	6 (24%) 0 0	88, 102, 112, 117	0
44	eL42	102/106 (96%)	1.28	31 (30%) 0 0	75, 106, 134, 165	0
45	eL43	91/92 (98%)	0.35	8 (8%) 10 3	67, 85, 106, 124	0
46	18S	1732/1798 (96%)	-0.62	14 (0%) 86 65	65, 110, 249, 326	0
47	uS2	206/252 (81%)	0.51	26 (12%) 3 1	92, 123, 160, 173	0
48	eS1	212/255 (83%)	1.04	47 (22%) 0 0	87, 141, 189, 206	0
49	uS5	217/254 (85%)	1.61	74 (34%) 0 0	80, 105, 146, 187	0
50	uS3	183/240 (76%)	2.39	90 (49%) 0 0	106, 152, 188, 200	0
51	eS4	258/261 (98%)	1.20	60 (23%) 0 0	72, 99, 123, 189	0
52	uS7	206/225 (91%)	2.42	101 (49%) 0 0	137, 179, 204, 219	0
53	eS6	219/236 (92%)	0.10	17 (7%) 13 4	78, 125, 163, 187	0
54	eS7	184/190 (96%)	0.70	32 (17%) 1 0	88, 140, 196, 210	0
55	eS8	184/200 (92%)	0.55	21 (11%) 5 1	72, 104, 155, 192	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
56	uS4	185/197 (93%)	0.85	29 (15%) 2 1	83, 108, 147, 200	0
57	eS10	33/105 (31%)	0.95	7 (21%) 0 0	155, 179, 188, 192	0
58	uS17	142/156 (91%)	0.60	20 (14%) 2 1	65, 89, 149, 163	0
59	uS15	150/151 (99%)	1.09	28 (18%) 1 0	74, 98, 127, 144	0
60	uS11	127/137 (92%)	0.93	23 (18%) 1 0	78, 124, 157, 168	0
61	uS19	91/142 (64%)	1.30	32 (35%) 0 0	139, 167, 193, 202	0
62	uS9	136/143 (95%)	2.00	49 (36%) 0 0	119, 174, 201, 204	0
63	eS17	121/136 (88%)	1.89	40 (33%) 0 0	122, 161, 189, 198	0
64	uS13	145/146 (99%)	1.32	50 (34%) 0 0	126, 161, 194, 210	0
65	eS19	143/144 (99%)	0.75	27 (18%) 1 0	130, 160, 185, 195	0
66	uS10	30/121 (24%)	1.91	15 (50%) 0 0	111, 123, 158, 161	0
67	eS21	87/87 (100%)	1.37	25 (28%) 0 0	91, 111, 161, 168	0
68	uS8	129/130 (99%)	1.13	34 (26%) 0 0	73, 88, 103, 114	0
69	uS12	144/145 (99%)	0.36	12 (8%) 11 3	66, 87, 113, 128	0
70	eS24	134/135 (99%)	0.74	18 (13%) 3 1	86, 115, 175, 191	0
71	eS25	70/108 (64%)	4.57	51 (72%) 0 0	171, 203, 214, 218	0
72	eS26	94/119 (78%)	1.31	27 (28%) 0 0	77, 97, 158, 175	0
73	eS27	79/82 (96%)	0.71	10 (12%) 3 1	85, 107, 173, 178	0
74	eS28	63/67 (94%)	3.26	37 (58%) 0 0	141, 182, 207, 214	0
75	uS14	49/56 (87%)	1.00	12 (24%) 0 0	115, 133, 146, 150	0
76	eS30	53/63 (84%)	1.06	11 (20%) 1 0	94, 120, 186, 189	0
77	RACK	318/319 (99%)	4.97	242 (76%) 0 0	186, 211, 224, 230	0
78	eS31	36/152 (23%)	-0.04	3 (8%) 11 3	151, 195, 204, 213	0
79	eEF2	841/842 (99%)	0.14	40 (4%) 30 11	77, 112, 148, 178	0
80	ASIT	75/76 (98%)	1.37	23 (30%) 0 0	114, 197, 233, 248	0
81	PSIT	77/77 (100%)	-0.63	0 100 100	81, 162, 191, 199	0
82	mRNA	8/8 (100%)	0.64	1 (12%) 3 1	115, 121, 141, 160	0
83	uL11	137/165 (83%)	-0.33	6 (4%) 34 13	115, 144, 157, 168	0
All	All	17093/18690 (91%)	0.53	2538 (14%) 2 1	50, 114, 195, 326	0

The worst 5 of 2538 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
77	RACK	231	MET	24.4
77	RACK	144	LEU	20.6
77	RACK	72	THR	18.9
77	RACK	204	ALA	17.9
77	RACK	230	ALA	17.7

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
79	DDE	eEF2	699	20/21	0.92	0.48	102,119,130,134	0
80	YG	ASIT	37	39/40	0.93	0.18	102,130,141,141	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
84	MG	18S	1834	1/1	0.21	0.29	123,123,123,123	0
84	MG	25S	3483	1/1	0.27	0.31	105,105,105,105	0
84	MG	18S	1842	1/1	0.29	0.23	97,97,97,97	0
84	MG	eL33	201	1/1	0.40	0.34	109,109,109,109	0
84	MG	18S	1902	1/1	0.41	0.27	115,115,115,115	0
84	MG	18S	1886	1/1	0.43	0.43	108,108,108,108	0
84	MG	25S	3580	1/1	0.45	0.33	85,85,85,85	0
84	MG	25S	3645	1/1	0.47	0.37	104,104,104,104	0
84	MG	25S	3633	1/1	0.47	0.46	95,95,95,95	0
84	MG	25S	3600	1/1	0.48	0.52	100,100,100,100	0
84	MG	25S	3506	1/1	0.48	0.18	96,96,96,96	0
84	MG	18S	1899	1/1	0.49	0.40	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
84	MG	25S	3679	1/1	0.49	0.33	105,105,105,105	0
84	MG	eS4	303	1/1	0.50	0.22	96,96,96,96	0
84	MG	25S	3515	1/1	0.51	0.54	122,122,122,122	0
84	MG	25S	3707	1/1	0.55	0.17	78,78,78,78	0
84	MG	18S	1920	1/1	0.55	0.20	82,82,82,82	0
84	MG	25S	3656	1/1	0.55	0.59	128,128,128,128	0
84	MG	25S	3547	1/1	0.56	0.55	109,109,109,109	0
84	MG	18S	1825	1/1	0.57	1.52	122,122,122,122	0
84	MG	eL42	201	1/1	0.57	0.60	110,110,110,110	0
84	MG	25S	3702	1/1	0.58	0.71	117,117,117,117	0
84	MG	18S	1912	1/1	0.59	0.22	92,92,92,92	0
84	MG	18S	1896	1/1	0.61	0.49	109,109,109,109	0
84	MG	25S	3663	1/1	0.61	0.25	97,97,97,97	0
84	MG	25S	3438	1/1	0.61	0.54	85,85,85,85	0
84	MG	18S	1911	1/1	0.64	0.19	93,93,93,93	0
84	MG	25S	3649	1/1	0.64	0.79	129,129,129,129	0
84	MG	25S	3644	1/1	0.64	0.23	88,88,88,88	0
84	MG	25S	3714	1/1	0.64	0.43	112,112,112,112	0
84	MG	25S	3668	1/1	0.65	0.28	87,87,87,87	0
84	MG	25S	3578	1/1	0.65	0.42	107,107,107,107	0
84	MG	eL42	202	1/1	0.66	0.20	90,90,90,90	0
84	MG	25S	3632	1/1	0.66	0.31	86,86,86,86	0
84	MG	uS12	201	1/1	0.66	0.30	101,101,101,101	0
84	MG	18S	1874	1/1	0.67	0.17	81,81,81,81	0
84	MG	25S	3534	1/1	0.68	0.97	86,86,86,86	0
84	MG	25S	3716	1/1	0.68	0.21	79,79,79,79	0
84	MG	25S	3472	1/1	0.68	0.44	82,82,82,82	0
84	MG	25S	3453	1/1	0.69	0.36	75,75,75,75	0
84	MG	18S	1872	1/1	0.69	0.22	90,90,90,90	0
84	MG	25S	3621	1/1	0.69	0.21	76,76,76,76	0
84	MG	mRNA	600	1/1	0.69	0.18	82,82,82,82	0
84	MG	25S	3498	1/1	0.70	0.17	97,97,97,97	0
84	MG	25S	3687	1/1	0.71	0.50	109,109,109,109	0
84	MG	25S	3689	1/1	0.71	0.26	121,121,121,121	0
84	MG	25S	3700	1/1	0.71	0.28	105,105,105,105	0
84	MG	18S	1922	1/1	0.71	0.25	91,91,91,91	0
84	MG	25S	3623	1/1	0.71	0.26	80,80,80,80	0
84	MG	eL41	101	1/1	0.71	0.12	70,70,70,70	0
84	MG	18S	1864	1/1	0.71	0.22	103,103,103,103	0
84	MG	25S	3695	1/1	0.72	0.25	95,95,95,95	0
84	MG	25S	3672	1/1	0.72	0.21	89,89,89,89	0
84	MG	25S	3488	1/1	0.72	0.42	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	18S	1850	1/1	0.73	0.15	77,77,77,77	0
84	MG	25S	3508	1/1	0.73	0.26	87,87,87,87	0
84	MG	uS12	202	1/1	0.73	0.33	84,84,84,84	0
84	MG	PSIT	101	1/1	0.73	0.14	87,87,87,87	0
84	MG	25S	3655	1/1	0.73	0.25	101,101,101,101	0
84	MG	eL31	201	1/1	0.74	0.26	93,93,93,93	0
84	MG	25S	3646	1/1	0.74	0.23	85,85,85,85	0
84	MG	25S	3504	1/1	0.74	0.37	91,91,91,91	0
84	MG	uS14	101	1/1	0.74	0.18	82,82,82,82	0
84	MG	25S	3532	1/1	0.74	0.42	73,73,73,73	0
84	MG	25S	3561	1/1	0.74	0.28	61,61,61,61	0
84	MG	eL15	301	1/1	0.75	0.23	83,83,83,83	0
84	MG	18S	1832	1/1	0.75	0.20	105,105,105,105	0
84	MG	25S	3693	1/1	0.75	0.23	84,84,84,84	0
84	MG	25S	3556	1/1	0.75	0.37	86,86,86,86	0
84	MG	18S	1900	1/1	0.75	0.23	72,72,72,72	0
84	MG	25S	3708	1/1	0.75	0.36	86,86,86,86	0
84	MG	25S	3696	1/1	0.75	0.35	87,87,87,87	0
84	MG	25S	3615	1/1	0.75	0.48	110,110,110,110	0
85	ZN	eS31	201	1/1	0.75	0.08	210,210,210,210	0
84	MG	25S	3610	1/1	0.76	0.27	78,78,78,78	0
84	MG	18S	1893	1/1	0.76	0.30	75,75,75,75	0
84	MG	eS4	302	1/1	0.76	0.25	83,83,83,83	0
84	MG	25S	3709	1/1	0.76	0.29	95,95,95,95	0
84	MG	25S	3503	1/1	0.76	0.29	92,92,92,92	0
84	MG	25S	3512	1/1	0.76	0.30	101,101,101,101	0
84	MG	18S	1901	1/1	0.76	0.37	115,115,115,115	0
84	MG	25S	3704	1/1	0.76	0.21	106,106,106,106	0
84	MG	25S	3567	1/1	0.76	0.53	108,108,108,108	0
84	MG	18S	1885	1/1	0.76	0.27	79,79,79,79	0
84	MG	25S	3564	1/1	0.77	0.27	105,105,105,105	0
84	MG	18S	1817	1/1	0.77	0.19	90,90,90,90	0
84	MG	ASIT	101	1/1	0.77	0.33	107,107,107,107	0
84	MG	25S	3566	1/1	0.77	0.29	77,77,77,77	0
84	MG	PSIT	105	1/1	0.77	0.24	100,100,100,100	0
84	MG	25S	3521	1/1	0.77	0.14	66,66,66,66	0
84	MG	25S	3484	1/1	0.77	0.41	87,87,87,87	0
84	MG	18S	1906	1/1	0.78	0.23	91,91,91,91	0
84	MG	eL30	201	1/1	0.78	0.62	81,81,81,81	0
84	MG	PSIT	102	1/1	0.78	0.48	86,86,86,86	0
84	MG	25S	3697	1/1	0.78	0.34	86,86,86,86	0
84	MG	25S	3526	1/1	0.78	0.34	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	18S	1881	1/1	0.78	0.18	85,85,85,85	0
84	MG	25S	3589	1/1	0.79	0.37	77,77,77,77	0
84	MG	25S	3607	1/1	0.79	0.35	90,90,90,90	0
84	MG	eS6	302	1/1	0.79	0.11	119,119,119,119	0
84	MG	18S	1919	1/1	0.79	0.23	92,92,92,92	0
84	MG	18S	1859	1/1	0.79	0.32	124,124,124,124	0
84	MG	18S	1821	1/1	0.79	0.17	135,135,135,135	0
84	MG	25S	3688	1/1	0.80	0.33	98,98,98,98	0
84	MG	25S	3586	1/1	0.80	0.41	83,83,83,83	0
84	MG	18S	1879	1/1	0.80	0.27	135,135,135,135	0
84	MG	PSIT	106	1/1	0.80	0.19	92,92,92,92	0
84	MG	58S	207	1/1	0.80	0.34	104,104,104,104	0
84	MG	uL18	301	1/1	0.80	0.30	109,109,109,109	0
84	MG	25S	3669	1/1	0.81	0.24	84,84,84,84	0
84	MG	25S	3518	1/1	0.81	0.55	95,95,95,95	0
84	MG	25S	3626	1/1	0.81	0.19	95,95,95,95	0
84	MG	eL18	201	1/1	0.81	0.25	89,89,89,89	0
84	MG	eEF2	906	1/1	0.81	0.34	110,110,110,110	0
84	MG	25S	3713[A]	1/1	0.81	0.39	55,55,55,55	1
84	MG	25S	3713[B]	1/1	0.81	0.39	72,72,72,72	1
84	MG	25S	3694	1/1	0.81	0.29	88,88,88,88	0
84	MG	18S	1892	1/1	0.81	0.20	88,88,88,88	0
84	MG	25S	3501	1/1	0.81	0.20	77,77,77,77	0
84	MG	18S	1853	1/1	0.81	0.31	70,70,70,70	0
84	MG	AB	202	1/1	0.81	0.32	73,73,73,73	0
84	MG	18S	1888	1/1	0.82	0.15	61,61,61,61	0
84	MG	25S	3590	1/1	0.82	0.45	93,93,93,93	0
84	MG	18S	1875	1/1	0.82	0.20	75,75,75,75	0
84	MG	25S	3636	1/1	0.82	0.47	95,95,95,95	0
84	MG	25S	3604	1/1	0.82	0.36	82,82,82,82	0
84	MG	25S	3622	1/1	0.82	1.65	78,78,78,78	0
84	MG	25S	3660	1/1	0.82	0.15	86,86,86,86	0
84	MG	25S	3591	1/1	0.83	0.19	99,99,99,99	0
84	MG	18S	1898	1/1	0.83	0.29	89,89,89,89	0
84	MG	25S	3490	1/1	0.83	0.20	80,80,80,80	0
84	MG	18S	1913	1/1	0.83	0.25	104,104,104,104	0
84	MG	25S	3516	1/1	0.83	0.23	68,68,68,68	0
84	MG	25S	3415	1/1	0.83	0.29	78,78,78,78	0
84	MG	18S	1866	1/1	0.83	0.33	66,66,66,66	0
84	MG	25S	3637	1/1	0.84	0.35	86,86,86,86	0
84	MG	eS6	301	1/1	0.84	0.06	137,137,137,137	0
84	MG	25S	3670	1/1	0.84	0.19	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	PSIT	103	1/1	0.84	0.22	125,125,125,125	0
84	MG	25S	3502	1/1	0.84	0.33	97,97,97,97	0
84	MG	25S	3698	1/1	0.84	0.20	82,82,82,82	0
84	MG	18S	1883	1/1	0.84	0.20	112,112,112,112	0
85	ZN	eL40	202	1/1	0.84	0.38	170,170,170,170	0
84	MG	18S	1851	1/1	0.84	0.11	82,82,82,82	0
84	MG	18S	1915	1/1	0.85	0.11	96,96,96,96	0
84	MG	eEF2	903	1/1	0.85	0.23	78,78,78,78	0
84	MG	25S	3692	1/1	0.85	0.36	88,88,88,88	0
84	MG	25S	3587	1/1	0.85	0.11	70,70,70,70	0
84	MG	18S	1814	1/1	0.85	0.40	88,88,88,88	0
84	MG	25S	3701	1/1	0.85	0.18	105,105,105,105	0
84	MG	25S	3674	1/1	0.86	0.13	102,102,102,102	0
84	MG	18S	1917	1/1	0.86	0.17	71,71,71,71	0
84	MG	25S	3715	1/1	0.86	0.52	97,97,97,97	0
84	MG	18S	1816	1/1	0.86	0.21	70,70,70,70	0
84	MG	25S	3677	1/1	0.86	0.29	85,85,85,85	0
84	MG	25S	3699	1/1	0.86	0.25	76,76,76,76	0
84	MG	25S	3410	1/1	0.86	0.25	57,57,57,57	0
84	MG	18S	1826	1/1	0.86	0.43	86,86,86,86	0
84	MG	uL3	401	1/1	0.86	0.35	60,60,60,60	0
84	MG	25S	3549	1/1	0.86	0.41	89,89,89,89	0
84	MG	25S	3550	1/1	0.86	0.17	82,82,82,82	0
84	MG	18S	1897	1/1	0.86	0.36	102,102,102,102	0
84	MG	25S	3552	1/1	0.86	0.43	97,97,97,97	0
84	MG	eEF2	904	1/1	0.86	0.31	82,82,82,82	0
84	MG	eL20	201	1/1	0.86	0.55	79,79,79,79	0
84	MG	18S	1852	1/1	0.86	0.31	71,71,71,71	0
84	MG	25S	3585	1/1	0.86	0.17	76,76,76,76	0
84	MG	25S	3477	1/1	0.86	0.23	74,74,74,74	0
84	MG	25S	3482	1/1	0.86	0.34	84,84,84,84	0
84	MG	18S	1908	1/1	0.86	0.17	81,81,81,81	0
84	MG	eL40	201	1/1	0.86	0.41	98,98,98,98	0
84	MG	25S	3588	1/1	0.86	0.29	78,78,78,78	0
84	MG	25S	3519	1/1	0.86	0.27	102,102,102,102	0
84	MG	18S	1914	1/1	0.86	0.22	85,85,85,85	0
84	MG	25S	3460	1/1	0.87	0.32	69,69,69,69	0
84	MG	25S	3647	1/1	0.87	0.44	98,98,98,98	0
84	MG	25S	3628	1/1	0.87	0.46	107,107,107,107	0
84	MG	25S	3640	1/1	0.87	0.41	107,107,107,107	0
84	MG	25S	3641	1/1	0.87	0.14	93,93,93,93	0
84	MG	25S	3717	1/1	0.87	0.12	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	18S	1828	1/1	0.87	0.28	83,83,83,83	0
84	MG	18S	1921	1/1	0.87	0.41	81,81,81,81	0
84	MG	25S	3466	1/1	0.87	0.47	75,75,75,75	0
84	MG	25S	3439	1/1	0.87	0.27	63,63,63,63	0
84	MG	18S	1839	1/1	0.87	0.54	85,85,85,85	0
84	MG	25S	3682	1/1	0.87	0.11	98,98,98,98	0
85	ZN	eL37	101	1/1	0.87	0.27	124,124,124,124	0
84	MG	25S	3685	1/1	0.87	0.38	99,99,99,99	0
85	ZN	eL43	101	1/1	0.87	0.30	124,124,124,124	0
84	MG	18S	1802	1/1	0.87	0.26	56,56,56,56	0
84	MG	25S	3538	1/1	0.88	0.33	79,79,79,79	0
84	MG	25S	3540	1/1	0.88	0.23	63,63,63,63	0
84	MG	25S	3681	1/1	0.88	0.64	113,113,113,113	0
84	MG	uS12	203	1/1	0.88	0.34	93,93,93,93	0
84	MG	25S	3665	1/1	0.88	0.33	87,87,87,87	0
84	MG	25S	3572	1/1	0.88	1.44	111,111,111,111	0
84	MG	18S	1831	1/1	0.88	0.21	114,114,114,114	0
84	MG	25S	3686	1/1	0.88	0.16	110,110,110,110	0
84	MG	25S	3652	1/1	0.88	0.34	67,67,67,67	0
84	MG	25S	3654	1/1	0.88	0.56	112,112,112,112	0
84	MG	18S	1841	1/1	0.88	0.19	87,87,87,87	0
84	MG	25S	3671	1/1	0.88	0.31	75,75,75,75	0
84	MG	18S	1891	1/1	0.88	0.33	133,133,133,133	0
84	MG	18S	1847	1/1	0.88	0.14	61,61,61,61	0
84	MG	58S	203	1/1	0.88	0.18	117,117,117,117	0
84	MG	58S	204	1/1	0.88	0.48	76,76,76,76	0
84	MG	25S	3456	1/1	0.88	0.10	73,73,73,73	0
84	MG	uL2	303	1/1	0.88	0.21	91,91,91,91	0
84	MG	25S	3625	1/1	0.88	0.92	96,96,96,96	0
84	MG	25S	3442	1/1	0.89	0.34	67,67,67,67	0
84	MG	25S	3440	1/1	0.89	0.32	82,82,82,82	0
84	MG	25S	3527	1/1	0.89	0.31	81,81,81,81	0
84	MG	25S	3496	1/1	0.89	0.32	75,75,75,75	0
84	MG	uL22	201	1/1	0.89	0.22	78,78,78,78	0
84	MG	25S	3486	1/1	0.89	0.24	57,57,57,57	0
84	MG	18S	1840	1/1	0.89	0.28	85,85,85,85	0
84	MG	18S	1873	1/1	0.89	0.20	85,85,85,85	0
84	MG	25S	3535	1/1	0.89	0.10	85,85,85,85	0
84	MG	25S	3499	1/1	0.89	0.21	78,78,78,78	0
84	MG	58S	206	1/1	0.89	0.29	87,87,87,87	0
84	MG	25S	3507	1/1	0.89	0.22	62,62,62,62	0
84	MG	25S	3462	1/1	0.90	0.33	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	25S	3505	1/1	0.90	0.19	71,71,71,71	0
84	MG	18S	1905	1/1	0.90	0.18	80,80,80,80	0
84	MG	25S	3617	1/1	0.90	0.48	103,103,103,103	0
84	MG	25S	3426	1/1	0.90	0.35	50,50,50,50	0
84	MG	18S	1909	1/1	0.90	0.21	94,94,94,94	0
84	MG	25S	3574	1/1	0.90	0.27	73,73,73,73	0
84	MG	25S	3489	1/1	0.90	0.16	110,110,110,110	0
84	MG	25S	3594	1/1	0.90	0.15	102,102,102,102	0
84	MG	18S	1815	1/1	0.90	0.28	63,63,63,63	0
84	MG	25S	3598	1/1	0.90	0.25	69,69,69,69	0
84	MG	25S	3468	1/1	0.90	0.23	91,91,91,91	0
84	MG	25S	3631	1/1	0.90	0.13	101,101,101,101	0
84	MG	18S	1822	1/1	0.90	0.37	75,75,75,75	0
84	MG	18S	1824	1/1	0.90	0.33	79,79,79,79	0
84	MG	25S	3421	1/1	0.90	0.28	81,81,81,81	0
84	MG	25S	3544	1/1	0.90	0.45	71,71,71,71	0
84	MG	18S	1869	1/1	0.90	0.19	75,75,75,75	0
84	MG	25S	3609	1/1	0.90	0.57	108,108,108,108	0
84	MG	25S	3514	1/1	0.91	0.63	89,89,89,89	0
84	MG	eS4	301	1/1	0.91	0.16	84,84,84,84	0
84	MG	18S	1806	1/1	0.91	0.36	60,60,60,60	0
84	MG	25S	3683	1/1	0.91	0.18	75,75,75,75	0
84	MG	25S	3684	1/1	0.91	0.12	91,91,91,91	0
84	MG	25S	3536	1/1	0.91	0.20	86,86,86,86	0
84	MG	18S	1857	1/1	0.91	0.10	97,97,97,97	0
84	MG	25S	3551	1/1	0.91	0.59	80,80,80,80	0
84	MG	18S	1818	1/1	0.91	0.39	87,87,87,87	0
84	MG	25S	3705	1/1	0.91	0.22	72,72,72,72	0
84	MG	25S	3627	1/1	0.91	0.14	84,84,84,84	0
84	MG	25S	3464	1/1	0.91	0.13	65,65,65,65	0
84	MG	18S	1907	1/1	0.91	0.17	82,82,82,82	0
84	MG	25S	3630	1/1	0.91	0.26	99,99,99,99	0
84	MG	25S	3614	1/1	0.91	0.29	105,105,105,105	0
84	MG	25S	3555	1/1	0.91	0.23	62,62,62,62	0
84	MG	25S	3452	1/1	0.91	0.42	79,79,79,79	0
84	MG	25S	3463	1/1	0.91	0.25	78,78,78,78	0
84	MG	18S	1882	1/1	0.91	0.14	75,75,75,75	0
84	MG	25S	3493	1/1	0.91	0.21	77,77,77,77	0
84	MG	25S	3680	1/1	0.91	0.12	78,78,78,78	0
84	MG	AB	201	1/1	0.91	0.36	102,102,102,102	0
84	MG	25S	3658	1/1	0.91	0.44	78,78,78,78	0
84	MG	AB	205	1/1	0.91	0.32	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	eS1	301	1/1	0.92	0.07	127,127,127,127	0
84	MG	25S	3635	1/1	0.92	0.13	80,80,80,80	0
84	MG	18S	1856	1/1	0.92	0.30	63,63,63,63	0
84	MG	25S	3542	1/1	0.92	0.14	98,98,98,98	0
84	MG	uL18	302	1/1	0.92	0.28	75,75,75,75	0
84	MG	18S	1860	1/1	0.92	0.22	79,79,79,79	0
84	MG	uS19	201	1/1	0.92	0.31	101,101,101,101	0
84	MG	25S	3543	1/1	0.92	0.23	81,81,81,81	0
84	MG	25S	3639	1/1	0.92	0.32	90,90,90,90	0
84	MG	25S	3520	1/1	0.92	0.08	82,82,82,82	0
84	MG	25S	3691	1/1	0.92	0.14	87,87,87,87	0
84	MG	25S	3558	1/1	0.92	0.24	64,64,64,64	0
84	MG	25S	3470	1/1	0.92	0.23	83,83,83,83	0
84	MG	25S	3563	1/1	0.92	0.24	82,82,82,82	0
84	MG	18S	1877	1/1	0.92	0.07	99,99,99,99	0
84	MG	25S	3548	1/1	0.92	0.14	79,79,79,79	0
84	MG	25S	3675	1/1	0.92	0.18	66,66,66,66	0
84	MG	25S	3629[A]	1/1	0.92	0.36	69,69,69,69	1
84	MG	25S	3629[B]	1/1	0.92	0.36	74,74,74,74	1
84	MG	18S	1884	1/1	0.92	0.28	83,83,83,83	0
84	MG	25S	3491	1/1	0.92	0.23	63,63,63,63	0
84	MG	25S	3467	1/1	0.92	0.20	69,69,69,69	0
84	MG	25S	3419	1/1	0.92	0.20	48,48,48,48	0
84	MG	25S	3620	1/1	0.92	0.32	85,85,85,85	0
84	MG	25S	3634	1/1	0.92	0.14	84,84,84,84	0
84	MG	25S	3471	1/1	0.93	0.25	64,64,64,64	0
84	MG	25S	3413	1/1	0.93	0.31	55,55,55,55	0
84	MG	25S	3459	1/1	0.93	0.43	77,77,77,77	0
84	MG	18S	1894	1/1	0.93	0.23	92,92,92,92	0
84	MG	25S	3619	1/1	0.93	0.14	83,83,83,83	0
84	MG	25S	3479	1/1	0.93	0.42	94,94,94,94	0
84	MG	eEF2	905	1/1	0.93	0.15	87,87,87,87	0
84	MG	AB	203	1/1	0.93	0.29	71,71,71,71	0
84	MG	25S	3581[A]	1/1	0.93	0.54	86,86,86,86	1
84	MG	25S	3581[B]	1/1	0.93	0.54	87,87,87,87	1
84	MG	25S	3602	1/1	0.93	0.27	64,64,64,64	0
84	MG	25S	3624	1/1	0.93	0.34	115,115,115,115	0
84	MG	25S	3487	1/1	0.93	0.43	72,72,72,72	0
84	MG	25S	3509	1/1	0.93	0.24	76,76,76,76	0
84	MG	25S	3494	1/1	0.93	0.28	78,78,78,78	0
84	MG	18S	1863	1/1	0.93	0.15	85,85,85,85	0
84	MG	25S	3513	1/1	0.93	0.09	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	uS15	201	1/1	0.93	0.14	63,63,63,63	0
84	MG	18S	1910	1/1	0.93	0.15	71,71,71,71	0
84	MG	AB	204	1/1	0.94	0.26	107,107,107,107	0
84	MG	25S	3522	1/1	0.94	0.10	67,67,67,67	0
84	MG	18S	1916	1/1	0.94	0.24	81,81,81,81	0
84	MG	18S	1819	1/1	0.94	0.33	62,62,62,62	0
84	MG	25S	3603	1/1	0.94	0.18	84,84,84,84	0
84	MG	25S	3458	1/1	0.94	0.35	68,68,68,68	0
84	MG	25S	3576	1/1	0.94	0.19	136,136,136,136	0
84	MG	18S	1880	1/1	0.94	0.06	74,74,74,74	0
84	MG	25S	3447	1/1	0.94	0.25	66,66,66,66	0
84	MG	25S	3510	1/1	0.94	0.52	91,91,91,91	0
84	MG	25S	3449	1/1	0.94	0.06	65,65,65,65	0
84	MG	25S	3553	1/1	0.94	0.34	82,82,82,82	0
84	MG	25S	3584	1/1	0.94	0.13	68,68,68,68	0
84	MG	18S	1833	1/1	0.94	0.10	105,105,105,105	0
84	MG	25S	3485	1/1	0.94	0.29	61,61,61,61	0
84	MG	18S	1835	1/1	0.94	0.21	79,79,79,79	0
84	MG	25S	3461[A]	1/1	0.94	0.45	68,68,68,68	1
84	MG	25S	3706	1/1	0.94	0.23	76,76,76,76	0
84	MG	25S	3461[B]	1/1	0.94	0.45	68,68,68,68	1
84	MG	eS26	201	1/1	0.94	0.33	52,52,52,52	0
84	MG	25S	3560	1/1	0.94	0.31	78,78,78,78	0
84	MG	25S	3412	1/1	0.94	0.40	59,59,59,59	0
84	MG	25S	3712	1/1	0.94	0.15	72,72,72,72	0
84	MG	25S	3562	1/1	0.94	0.25	57,57,57,57	0
84	MG	25S	3473	1/1	0.94	0.40	79,79,79,79	0
84	MG	25S	3653	1/1	0.94	0.79	72,72,72,72	0
84	MG	18S	1855	1/1	0.94	0.22	65,65,65,65	0
84	MG	25S	3592	1/1	0.94	0.14	111,111,111,111	0
84	MG	25S	3475	1/1	0.94	0.34	58,58,58,58	0
84	MG	18S	1803	1/1	0.94	0.18	54,54,54,54	0
84	MG	25S	3596	1/1	0.94	0.28	51,51,51,51	0
84	MG	18S	1862	1/1	0.94	0.14	62,62,62,62	0
85	ZN	eL34	201	1/1	0.94	0.11	120,120,120,120	0
84	MG	18S	1813	1/1	0.94	0.24	109,109,109,109	0
84	MG	25S	3403	1/1	0.94	0.30	54,54,54,54	0
84	MG	25S	3599	1/1	0.94	0.17	91,91,91,91	0
84	MG	25S	3445	1/1	0.94	0.24	72,72,72,72	0
86	GTP	eEF2	907	32/32	0.94	0.19	74,93,109,114	0
84	MG	25S	3424	1/1	0.95	0.33	61,61,61,61	0
84	MG	25S	3559	1/1	0.95	0.20	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	25S	3664	1/1	0.95	0.43	108,108,108,108	0
84	MG	25S	3711	1/1	0.95	0.18	94,94,94,94	0
84	MG	25S	3406	1/1	0.95	0.29	74,74,74,74	0
84	MG	25S	3666	1/1	0.95	0.29	85,85,85,85	0
84	MG	25S	3434	1/1	0.95	0.33	56,56,56,56	0
84	MG	25S	3642	1/1	0.95	0.17	91,91,91,91	0
84	MG	18S	1903	1/1	0.95	0.12	97,97,97,97	0
84	MG	eL30	202	1/1	0.95	0.22	69,69,69,69	0
84	MG	18S	1830	1/1	0.95	0.27	69,69,69,69	0
84	MG	25S	3437	1/1	0.95	0.23	64,64,64,64	0
84	MG	25S	3465	1/1	0.95	0.27	69,69,69,69	0
84	MG	25S	3420	1/1	0.95	0.27	58,58,58,58	0
84	MG	18S	1876	1/1	0.95	0.34	83,83,83,83	0
84	MG	25S	3673	1/1	0.95	0.14	63,63,63,63	0
84	MG	25S	3616	1/1	0.95	0.20	63,63,63,63	0
84	MG	18S	1836	1/1	0.95	0.15	86,86,86,86	0
84	MG	25S	3582	1/1	0.95	0.26	78,78,78,78	0
84	MG	25S	3618[A]	1/1	0.95	0.26	61,61,61,61	1
84	MG	25S	3618[B]	1/1	0.95	0.26	59,59,59,59	1
84	MG	18S	1805	1/1	0.95	0.36	73,73,73,73	0
84	MG	25S	3583	1/1	0.95	0.16	90,90,90,90	0
84	MG	18S	1811	1/1	0.95	0.14	58,58,58,58	0
84	MG	25S	3476	1/1	0.95	0.21	64,64,64,64	0
84	MG	25S	3418	1/1	0.95	0.33	50,50,50,50	0
84	MG	25S	3657	1/1	0.95	0.25	78,78,78,78	0
84	MG	25S	3571	1/1	0.95	0.34	118,118,118,118	0
84	MG	18S	1918	1/1	0.96	0.03	121,121,121,121	0
84	MG	18S	1808	1/1	0.96	0.27	65,65,65,65	0
84	MG	25S	3595	1/1	0.96	0.12	86,86,86,86	0
84	MG	18S	1846	1/1	0.96	0.18	63,63,63,63	0
84	MG	18S	1812	1/1	0.96	0.29	56,56,56,56	0
84	MG	uL2	301	1/1	0.96	0.32	64,64,64,64	0
84	MG	uL2	302	1/1	0.96	0.09	61,61,61,61	0
84	MG	18S	1889	1/1	0.96	0.11	58,58,58,58	0
84	MG	18S	1890	1/1	0.96	0.12	71,71,71,71	0
84	MG	25S	3435	1/1	0.96	0.22	71,71,71,71	0
84	MG	25S	3531	1/1	0.96	0.09	78,78,78,78	0
84	MG	25S	3511	1/1	0.96	0.24	80,80,80,80	0
84	MG	25S	3667	1/1	0.96	0.35	100,100,100,100	0
84	MG	25S	3436	1/1	0.96	0.36	69,69,69,69	0
84	MG	25S	3500	1/1	0.96	0.15	87,87,87,87	0
84	MG	25S	3416	1/1	0.96	0.44	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	18S	1861	1/1	0.96	0.32	54,54,54,54	0
84	MG	25S	3401	1/1	0.96	0.37	58,58,58,58	0
84	MG	eEF2	902	1/1	0.96	0.29	75,75,75,75	0
84	MG	25S	3478	1/1	0.96	0.34	79,79,79,79	0
84	MG	25S	3517	1/1	0.96	0.27	96,96,96,96	0
84	MG	25S	3450	1/1	0.96	0.17	62,62,62,62	0
84	MG	18S	1904	1/1	0.96	0.15	87,87,87,87	0
84	MG	18S	1867	1/1	0.96	0.34	92,92,92,92	0
84	MG	25S	3480	1/1	0.96	0.37	69,69,69,69	0
84	MG	18S	1870	1/1	0.96	0.24	88,88,88,88	0
84	MG	18S	1871	1/1	0.96	0.04	73,73,73,73	0
84	MG	25S	3451	1/1	0.96	0.30	51,51,51,51	0
84	MG	25S	3678	1/1	0.96	0.08	94,94,94,94	0
84	MG	25S	3407	1/1	0.96	0.48	61,61,61,61	0
84	MG	25S	3570	1/1	0.96	0.30	83,83,83,83	0
84	MG	58S	202	1/1	0.96	0.15	97,97,97,97	0
84	MG	25S	3495	1/1	0.96	0.25	84,84,84,84	0
85	ZN	eL42	203	1/1	0.96	0.15	113,113,113,113	0
84	MG	18S	1838	1/1	0.96	0.22	60,60,60,60	0
84	MG	25S	3523	1/1	0.96	0.12	80,80,80,80	0
84	MG	25S	3404	1/1	0.96	0.29	61,61,61,61	0
84	MG	25S	3643	1/1	0.97	0.09	69,69,69,69	0
84	MG	25S	3492	1/1	0.97	0.24	67,67,67,67	0
84	MG	25S	3573	1/1	0.97	0.35	74,74,74,74	0
84	MG	18S	1827	1/1	0.97	0.39	70,70,70,70	0
84	MG	25S	3429	1/1	0.97	0.30	72,72,72,72	0
84	MG	18S	1829	1/1	0.97	0.15	62,62,62,62	0
84	MG	25S	3597	1/1	0.97	0.20	62,62,62,62	0
84	MG	25S	3648	1/1	0.97	0.20	87,87,87,87	0
84	MG	25S	3710	1/1	0.97	0.24	100,100,100,100	0
84	MG	25S	3448	1/1	0.97	0.23	88,88,88,88	0
84	MG	25S	3554	1/1	0.97	0.26	74,74,74,74	0
84	MG	25S	3431	1/1	0.97	0.46	61,61,61,61	0
84	MG	25S	3601	1/1	0.97	0.13	72,72,72,72	0
84	MG	18S	1837	1/1	0.97	0.32	61,61,61,61	0
84	MG	25S	3432	1/1	0.97	0.39	67,67,67,67	0
84	MG	25S	3409	1/1	0.97	0.33	62,62,62,62	0
84	MG	25S	3539	1/1	0.97	0.28	55,55,55,55	0
84	MG	18S	1801	1/1	0.97	0.26	66,66,66,66	0
84	MG	25S	3427	1/1	0.97	0.41	67,67,67,67	0
84	MG	18S	1844	1/1	0.97	0.26	77,77,77,77	0
84	MG	25S	3541	1/1	0.97	0.20	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	18S	1804	1/1	0.97	0.21	71,71,71,71	0
84	MG	18S	1848	1/1	0.97	0.28	83,83,83,83	0
84	MG	eEF2	901	1/1	0.97	0.10	66,66,66,66	0
84	MG	18S	1849	1/1	0.97	0.20	60,60,60,60	0
84	MG	18S	1895	1/1	0.97	0.20	92,92,92,92	0
84	MG	25S	3690	1/1	0.97	0.22	66,66,66,66	0
84	MG	25S	3662	1/1	0.97	0.27	66,66,66,66	0
84	MG	25S	3444	1/1	0.97	0.24	77,77,77,77	0
84	MG	18S	1810	1/1	0.97	0.43	64,64,64,64	0
84	MG	18S	1854	1/1	0.97	0.40	80,80,80,80	0
84	MG	25S	3612	1/1	0.97	0.27	74,74,74,74	0
84	MG	25S	3613	1/1	0.97	0.15	87,87,87,87	0
84	MG	PSIT	104	1/1	0.97	0.17	104,104,104,104	0
84	MG	25S	3428	1/1	0.97	0.30	64,64,64,64	0
84	MG	25S	3524	1/1	0.97	0.29	89,89,89,89	0
84	MG	58S	205	1/1	0.97	0.21	93,93,93,93	0
84	MG	25S	3565	1/1	0.97	0.34	93,93,93,93	0
84	MG	25S	3638	1/1	0.97	0.09	83,83,83,83	0
84	MG	25S	3446[A]	1/1	0.97	0.38	70,70,70,70	1
84	MG	25S	3446[B]	1/1	0.97	0.38	73,73,73,73	1
84	MG	18S	1865	1/1	0.97	0.36	62,62,62,62	0
84	MG	25S	3528	1/1	0.97	0.12	75,75,75,75	0
84	MG	25S	3529	1/1	0.97	0.27	49,49,49,49	0
84	MG	18S	1843	1/1	0.98	0.23	72,72,72,72	0
84	MG	18S	1807	1/1	0.98	0.30	60,60,60,60	0
84	MG	25S	3423	1/1	0.98	0.22	65,65,65,65	0
84	MG	18S	1809	1/1	0.98	0.32	91,91,91,91	0
84	MG	18S	1887	1/1	0.98	0.13	49,49,49,49	0
84	MG	25S	3443	1/1	0.98	0.33	65,65,65,65	0
84	MG	25S	3433	1/1	0.98	0.34	45,45,45,45	0
84	MG	25S	3525	1/1	0.98	0.17	86,86,86,86	0
84	MG	25S	3455	1/1	0.98	0.32	44,44,44,44	0
84	MG	25S	3569	1/1	0.98	0.20	72,72,72,72	0
84	MG	25S	3402[A]	1/1	0.98	0.36	62,62,62,62	1
84	MG	25S	3497	1/1	0.98	0.35	84,84,84,84	0
84	MG	25S	3703	1/1	0.98	0.21	118,118,118,118	0
84	MG	25S	3457	1/1	0.98	0.46	86,86,86,86	0
84	MG	25S	3676	1/1	0.98	0.16	90,90,90,90	0
84	MG	18S	1820	1/1	0.98	0.23	77,77,77,77	0
84	MG	25S	3530	1/1	0.98	0.31	61,61,61,61	0
84	MG	uL16	301	1/1	0.98	0.17	77,77,77,77	0
84	MG	25S	3469	1/1	0.98	0.19	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
84	MG	25S	3417	1/1	0.98	0.30	59,59,59,59	0
84	MG	25S	3651	1/1	0.98	0.33	74,74,74,74	0
84	MG	25S	3577	1/1	0.98	0.26	76,76,76,76	0
84	MG	uL14	201	1/1	0.98	0.32	55,55,55,55	0
84	MG	25S	3533	1/1	0.98	0.30	55,55,55,55	0
84	MG	25S	3579	1/1	0.98	0.32	61,61,61,61	0
84	MG	25S	3411	1/1	0.98	0.28	75,75,75,75	0
84	MG	25S	3402[B]	1/1	0.98	0.36	64,64,64,64	1
84	MG	25S	3605	1/1	0.98	0.20	88,88,88,88	0
84	MG	25S	3557	1/1	0.98	0.38	83,83,83,83	0
84	MG	25S	3659	1/1	0.98	0.24	74,74,74,74	0
84	MG	25S	3408	1/1	0.98	0.24	68,68,68,68	0
84	MG	25S	3537	1/1	0.98	0.32	58,58,58,58	0
84	MG	25S	3611	1/1	0.98	0.09	64,64,64,64	0
84	MG	25S	3474	1/1	0.98	0.22	109,109,109,109	0
84	MG	25S	3430	1/1	0.98	0.32	92,92,92,92	0
85	ZN	eS26	202	1/1	0.98	0.15	79,79,79,79	0
85	ZN	uS14	102	1/1	0.98	0.10	139,139,139,139	0
84	MG	25S	3405	1/1	0.98	0.28	59,59,59,59	0
84	MG	58S	201	1/1	0.98	0.32	77,77,77,77	0
84	MG	25S	3454	1/1	0.99	0.25	78,78,78,78	0
84	MG	25S	3650	1/1	0.99	0.24	69,69,69,69	0
84	MG	25S	3545	1/1	0.99	0.08	81,81,81,81	0
84	MG	18S	1878	1/1	0.99	0.20	76,76,76,76	0
84	MG	18S	1858	1/1	0.99	0.24	73,73,73,73	0
84	MG	18S	1823	1/1	0.99	0.10	128,128,128,128	0
84	MG	25S	3546	1/1	0.99	0.24	59,59,59,59	0
84	MG	25S	3422	1/1	0.99	0.14	81,81,81,81	0
84	MG	25S	3425	1/1	0.99	0.24	64,64,64,64	0
84	MG	25S	3593	1/1	0.99	0.22	95,95,95,95	0
84	MG	18S	1845	1/1	0.99	0.17	66,66,66,66	0
84	MG	eL32	201	1/1	0.99	0.11	83,83,83,83	0
84	MG	25S	3481	1/1	0.99	0.19	87,87,87,87	0
84	MG	25S	3606	1/1	0.99	0.13	70,70,70,70	0
84	MG	18S	1868	1/1	0.99	0.17	70,70,70,70	0
84	MG	25S	3575	1/1	0.99	0.26	64,64,64,64	0
84	MG	25S	3608	1/1	0.99	0.17	71,71,71,71	0
84	MG	25S	3441	1/1	0.99	0.22	58,58,58,58	0
84	MG	25S	3661	1/1	0.99	0.28	53,53,53,53	0
84	MG	25S	3414	1/1	0.99	0.28	44,44,44,44	0
84	MG	25S	3568	1/1	0.99	0.14	69,69,69,69	0

6.5 Other polymers ⓘ

There are no such residues in this entry.