



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 09:47 AM EDT

PDB ID : 7OSA / pdb_00007osa
Title : Pre-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 : 2021-06-08
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

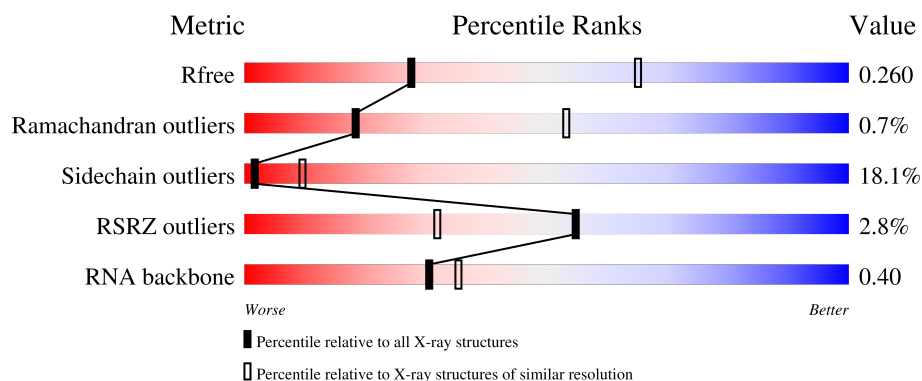
1 Overall quality at a glance

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}	180053	2672 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)
RNA backbone	3983	1109 (3.20-2.80)

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 $\leq 5\%$. 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% 74% 19% 6%
2	AB	121	 % 90% 10%
3	58S	753	 17% 79%
4	uL10	312	 6% 47% 16% 36%
5	uL2	254	 % 85% 12%

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Mol	Chain	Length	Quality of chain
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	135	
30	uL15	149	

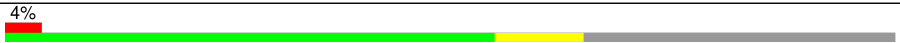
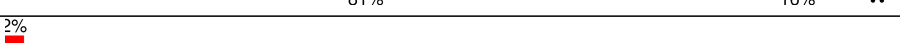
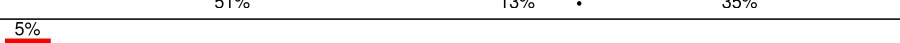
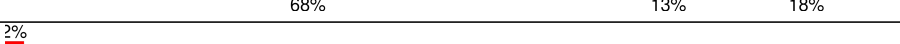
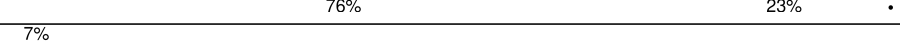
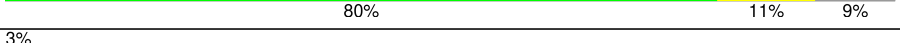
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Mol	Chain	Length	Quality of chain
31	eL29	59	
32	eL30	105	
33	eL31	113	
34	eL32	130	
35	eL33	107	
36	eL34	121	
37	uL29	120	
38	eL36	100	
39	eL37	88	
40	eL38	78	
41	eL39	51	
42	eL40	128	
43	eL41	25	
44	eL42	106	
45	eL43	92	
46	18S	1798	
47	uS2	252	
48	eS1	255	
49	uS5	254	
50	uS3	240	
51	eS4	261	
52	uS7	225	
53	eS6	236	
54	eS7	190	
55	eS8	200	

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Mol	Chain	Length	Quality of chain
56	uS4	197	
57	eS10	105	
58	uS17	156	
59	eS12	143	
60	uS15	151	
61	uS11	137	
62	uS19	142	
63	uS9	143	
64	eS17	136	
65	uS13	146	
66	eS19	144	
67	uS10	121	
68	eS21	87	
69	uS8	130	
70	uS12	145	
71	eS24	135	
72	eS25	108	
73	eS26	119	
74	eS27	82	
75	eS28	67	
76	uS14	56	
77	eS30	63	
78	RACK	319	
79	eS31	152	
80	eEF2	842	

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Mol	Chain	Length	Quality of chain
81	PSIT	77	
82	mRNA	3	
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	1808	-	-	-	X
84	MG	18S	1852	-	-	-	X
84	MG	18S	1854	-	-	-	X
84	MG	18S	1889	-	-	-	X
84	MG	25S	3401	-	-	-	X
84	MG	25S	3424	-	-	-	X
84	MG	25S	3452	-	-	-	X
84	MG	25S	3463	-	-	-	X
84	MG	25S	3473	-	-	-	X
84	MG	25S	3493	-	-	-	X
84	MG	25S	3510	-	-	-	X
84	MG	25S	3514	-	-	-	X
84	MG	25S	3515	-	-	-	X
84	MG	25S	3516	-	-	-	X
84	MG	25S	3520[A]	-	-	-	X
84	MG	25S	3520[B]	-	-	-	X
84	MG	25S	3525	-	-	-	X
84	MG	25S	3535	-	-	-	X
84	MG	25S	3543	-	-	-	X
84	MG	25S	3616	-	-	-	X
84	MG	25S	3641	-	-	-	X
84	MG	25S	3645	-	-	-	X
84	MG	25S	3673	-	-	-	X
84	MG	25S	3674	-	-	-	X
84	MG	25S	3686	-	-	-	X
84	MG	eEF2	903	-	-	-	X
84	MG	eL22	201	-	-	-	X

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 208056 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	3180	Total	C	N	O	P	0	0	0
			68026	30386	12274	22186	3180			

- Molecule 2 is a RNA chain called 5S.

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	199	Total	C	N	O	S	0	0	0
			1543	988	268	283	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	uL2	247	Total	C	N	O	S	0	0	0
			1878	1170	381	326	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
7	uL4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	eL8	229	Total	C	N	O	S	0	0	0
			1779	1138	319	319	3			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	uL16	210	Total	C	N	O	S	0	0	0
			1710	1088	322	294	6			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	uL22	154	Total	C	N	O		0	0	0
			1222	761	237	224				

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	eL19	174	Total	C	N	O			
			1409	867	304	238	0	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	eL20	172	Total	C	N	O	S		
			1445	930	267	244	4	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	C	N	O	S		
			1276	805	246	221	4	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	eL22	98	Total	C	N	O			
			778	505	127	146		0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	uL14	132	Total	C	N	O	S		
			981	617	184	173	7	0	0

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	uL23	121	Total	C	N	O	S		
			964	620	169	173	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	eL34	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			

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

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

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

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

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	eL37	85	Total	C	N	O	S	0	0	0
			670	408	146	111	5			

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

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

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

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

- Molecule 42 is a protein called Ubiquitin.

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

- Molecule 43 is a protein called eL41.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	eL42	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	18S	1717	Total	C	N	O	P	0	0	1
			36588	16356	6504	12011	1717			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	uS2	202	Total	C	N	O	S	0	0	0
			1555	1000	274	279	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	eS1	214	Total	C	N	O	S	0	0	0
			1703	1081	307	311	4			

- 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	214	Total	C	N	O	S	0	0	0
			1664	1054	303	301	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	223	Total	C	N	O	S	0	0	0
			1790	1123	346	318	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	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	eS10	96	Total	C	N	O	S	0	0	0
			772	499	126	145	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	uS17	141	Total	C	N	O	S	0	0	0
			1143	733	216	191	3			

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	eS12	124	Total	C	N	O	S	0	0	0
			890	560	156	172	2			

- Molecule 60 is a protein called 40S ribosomal protein S13.

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

- Molecule 61 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
62	uS19	117	Total	C	N	O	S	0	0	0
			924	587	171	159	7			

- Molecule 63 is a protein called BJ4_G0008010.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
63	uS9	135	Total	C	N	O			
			1062	681	194	187	0	0	0

- Molecule 64 is a protein called BJ4_G0020710.mRNA.1.CDS.1.

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

- Molecule 65 is a protein called 40S ribosomal protein S18-B.

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

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
67	uS10	79	Total	C	N	O	S		
			644	405	120	118	1	0	0

- Molecule 68 is a protein called 40S ribosomal protein S21.

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

- Molecule 69 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 70 is a protein called 40S ribosomal protein S23.

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

- Molecule 71 is a protein called 40S ribosomal protein S24.

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

- Molecule 72 is a protein called 40S ribosomal protein S25.

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

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	eS26	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			

- Molecule 74 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	eS27	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			

- Molecule 75 is a protein called eS28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	eS28	61	Total	C	N	O	S	0	0	0
			478	294	94	89	1			

- Molecule 76 is a protein called HLJ1_G0030400.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	uS14	51	Total	C	N	O	S	0	0	0
			420	262	84	70	4			

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	eS30	56	Total	C	N	O	S	0	0	0
			448	282	93	72	1			

- Molecule 78 is a protein called BJ4_G0022010.mRNA.1.CDS.1.

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

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	eS31	63	Total	C	N	O	S	0	0	0
			499	317	95	83	4			

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	eEF2	842	Total	C	N	O	S	0	0	0
			6559	4166	1124	1238	31			

- Molecule 81 is a RNA chain called Psite tRNA-Phe.

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

- Molecule 82 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	mRNA	3	Total	C	N	O	P	0	0	0
			65	29	12	21	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
83	uL11	137	Total	C	N	O		0	0	0
			672	398	137	137				

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
84	25S	332	Total Mg 335 335	0	3
84	AB	10	Total Mg 10 10	0	0
84	58S	9	Total Mg 9 9	0	0
84	uL2	2	Total Mg 2 2	0	0
84	uL3	1	Total Mg 1 1	0	0
84	uL16	2	Total Mg 2 2	0	0
84	uL13	2	Total Mg 2 2	0	0
84	uL22	1	Total Mg 1 1	0	0
84	eL19	1	Total Mg 1 1	0	0
84	eL22	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	eL32	2	Total Mg 2 2	0	0
84	eL37	1	Total Mg 1 1	0	0
84	eL39	1	Total Mg 1 1	0	0
84	eL41	1	Total Mg 1 1	0	0
84	eL42	1	Total Mg 1 1	0	0
84	18S	107	Total Mg 109 109	0	2
84	uS5	1	Total Mg 1 1	0	0
84	eS6	1	Total Mg 1 1	0	0
84	uS4	1	Total Mg 1 1	0	0
84	uS12	3	Total Mg 3 3	0	0

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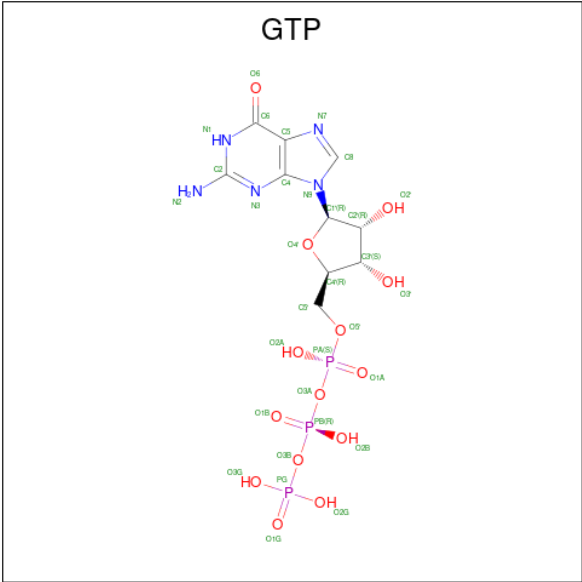
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
84	eS26	1	Total	Mg	0	0
			1	1		
84	eEF2	4	Total	Mg	0	0
			4	4		
84	PSIT	2	Total	Mg	0	0
			2	2		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 86 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

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.

Chain 25S:

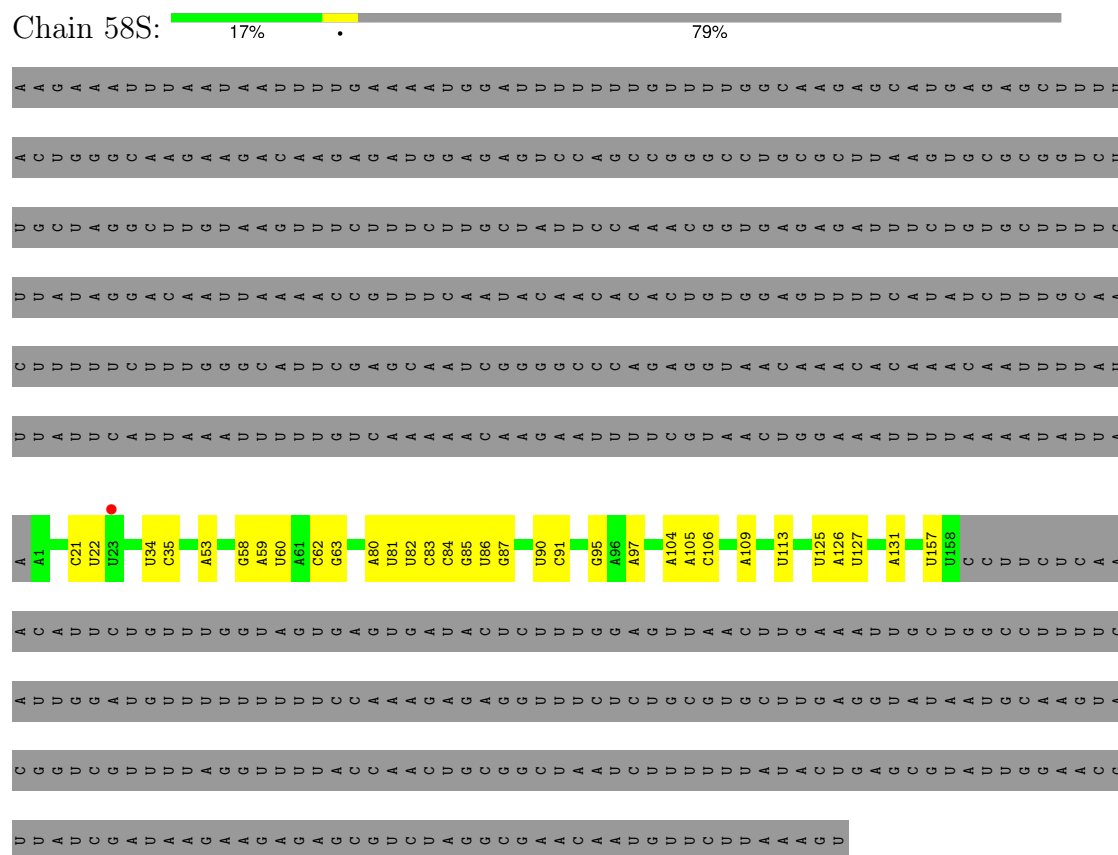
74% 19% 6%

Sequence positions (from left to right):

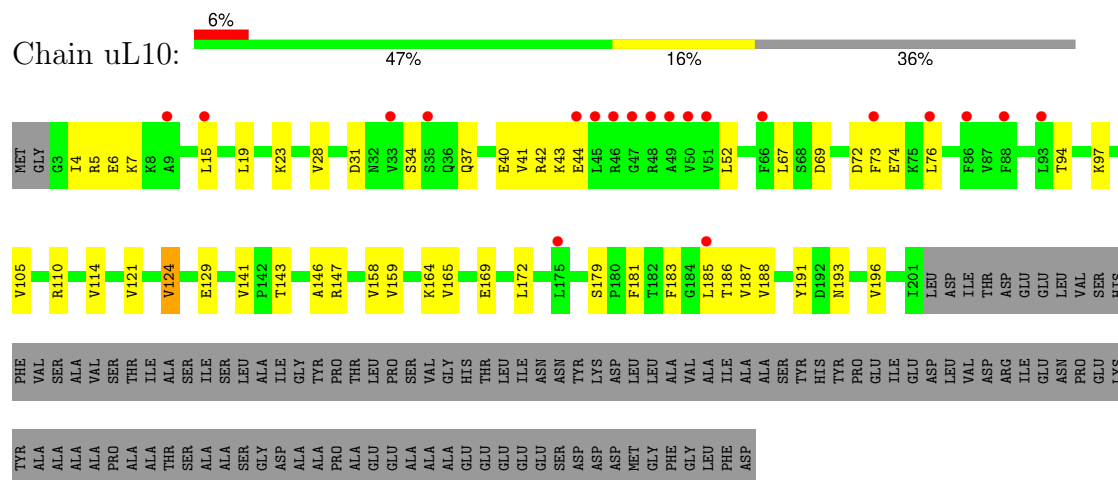
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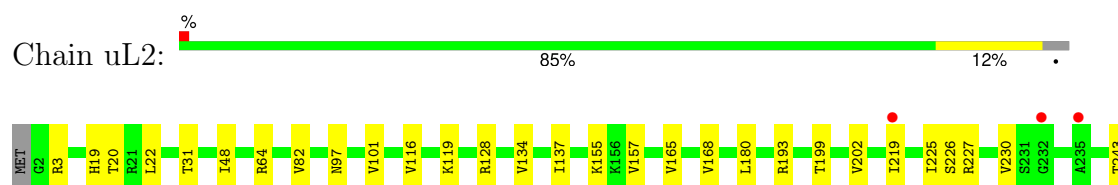
- Molecule 3: 5.8S rRNA

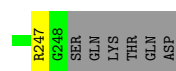


- Molecule 4: 60S acidic ribosomal protein P0

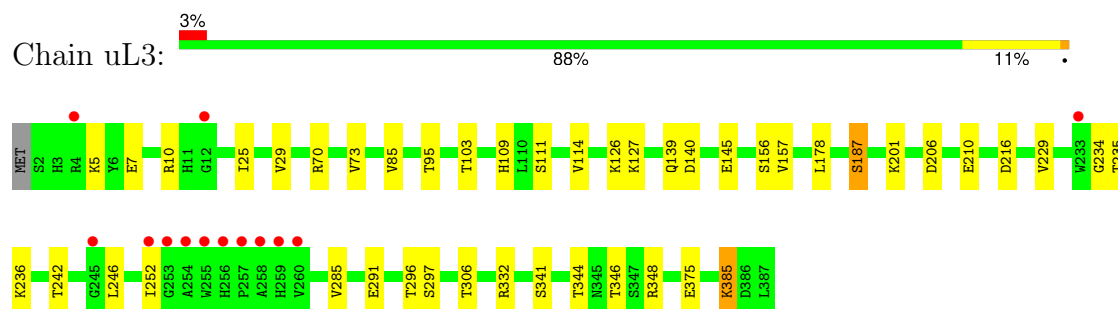


- Molecule 5: 60S ribosomal protein L2-B

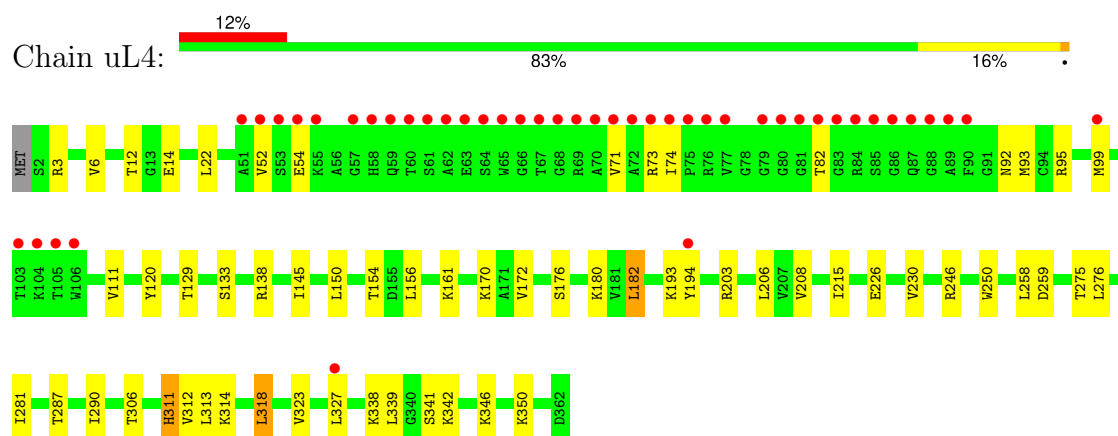




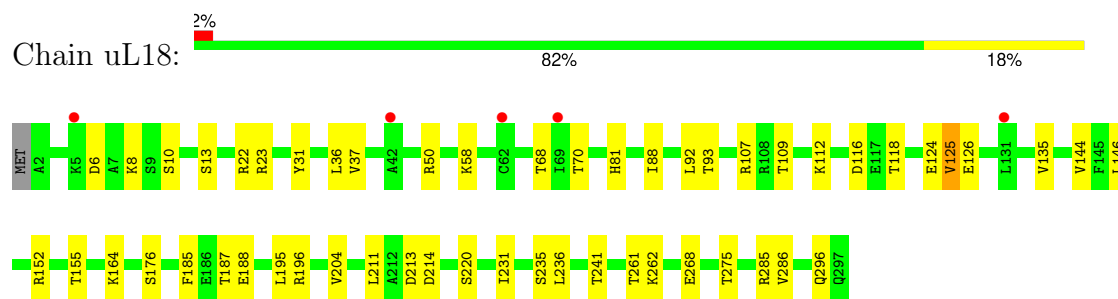
• Molecule 6: 60S ribosomal protein L3



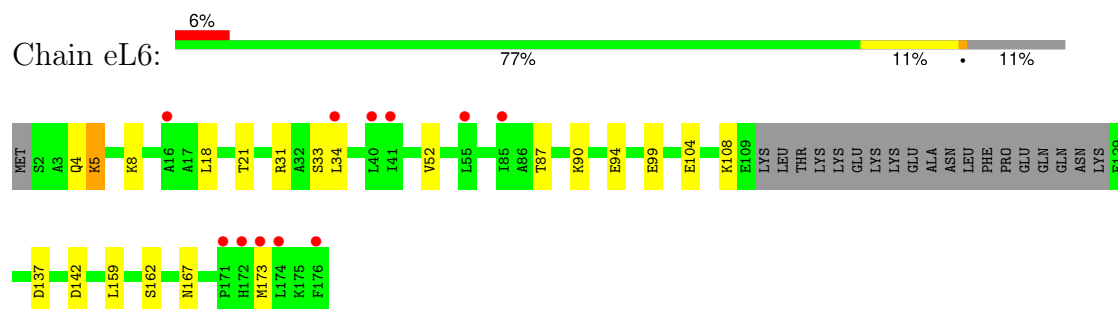
• Molecule 7: BJ4_G0008850.mRNA.1.CDS.1



• Molecule 8: 60S ribosomal protein L5



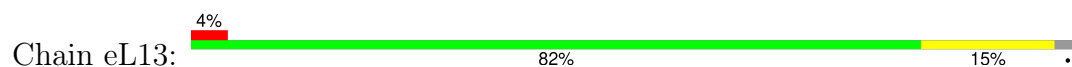
• Molecule 9: 60S ribosomal protein L6



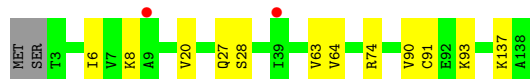
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| MET | SER | ALA | LVS | ALA | G6 | N7 | P8 | | L12 | E15 | V23 | D28 | R29 | L30 | T31 | S34 | L40 | V46 | Y52 | T56 | V71 | E77 | | L84 | R92 | D93 | R94 | N95 | I106 | D107 | E108 | H109 | | L112 | K115 | Y116 | V129 | M132 | R137 | S151 | T154 |
|-----|-----|-----|-----|-----|----|----|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|-----|-----|------|------|------|------|--|------|------|------|------|------|------|------|------|



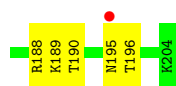
- Molecule 15: 60S ribosomal protein L13



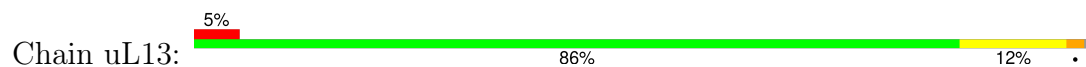
- Molecule 16: 60S ribosomal protein L14-A



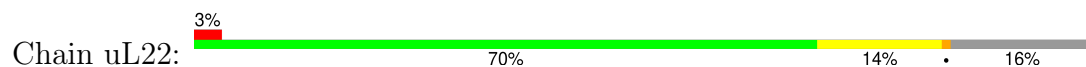
- Molecule 17: 60S ribosomal protein L15-A



- Molecule 18: 60S ribosomal protein L16-A

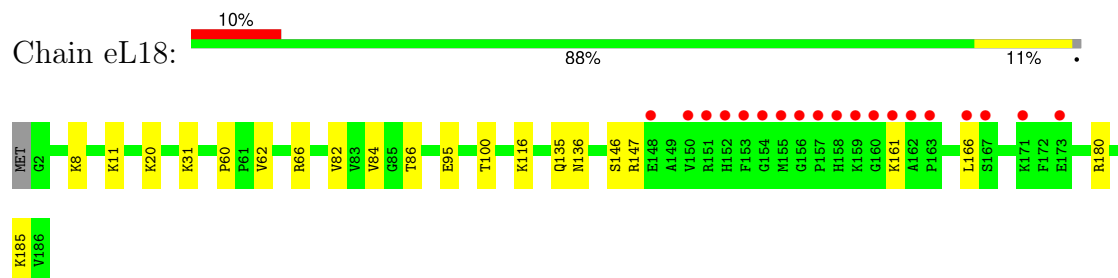


- Molecule 19: BJ4_G0005750.mRNA.1.CDS.1

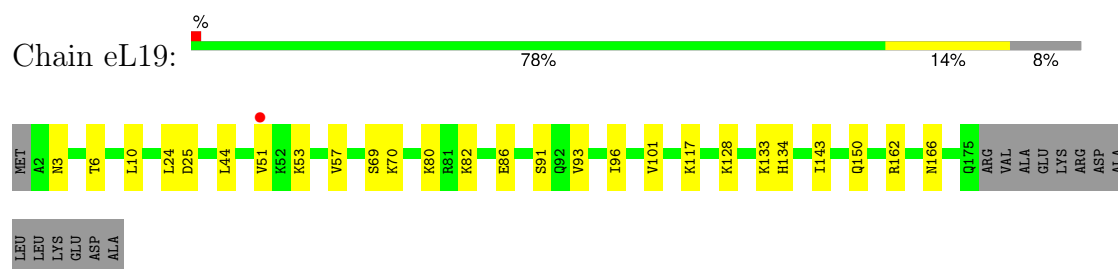


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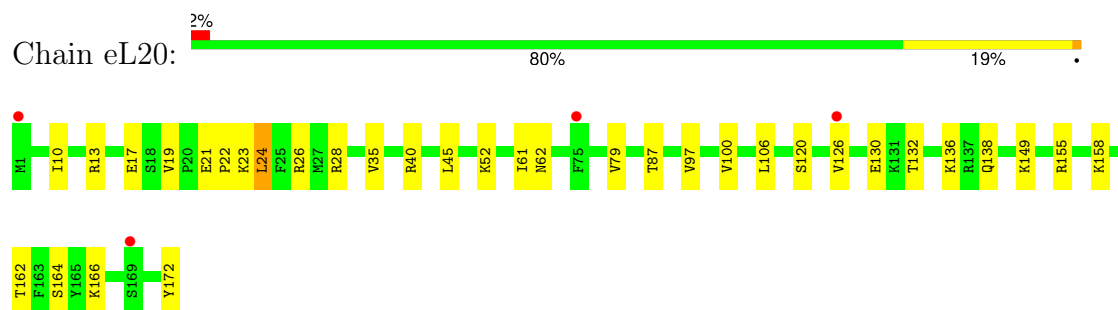
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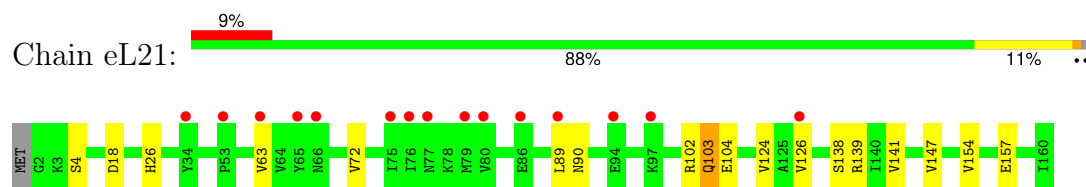
- Molecule 21: 60S ribosomal protein L19-A



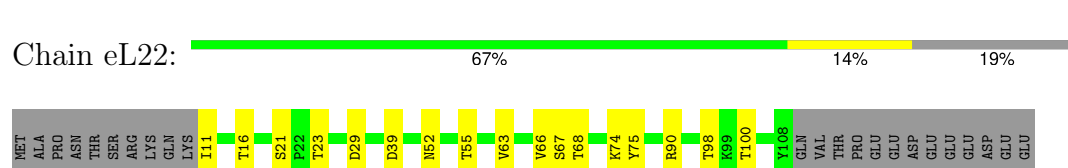
- Molecule 22: 60S ribosomal protein L20



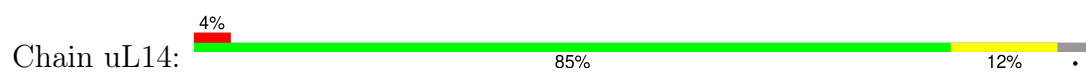
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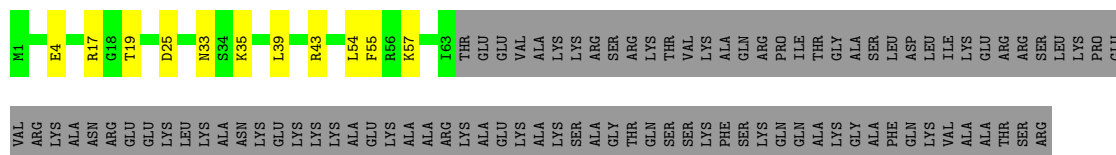
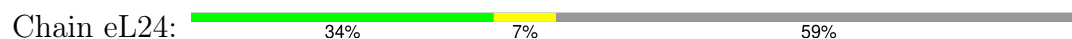
- Molecule 24: 60S ribosomal protein L22-A



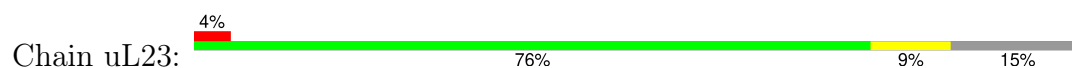
- Molecule 25: 60S ribosomal protein L23-B



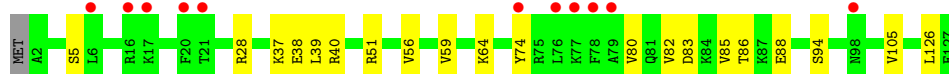
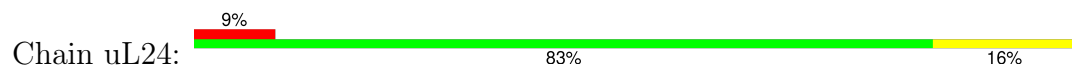
- Molecule 26: 60S ribosomal protein L24-A



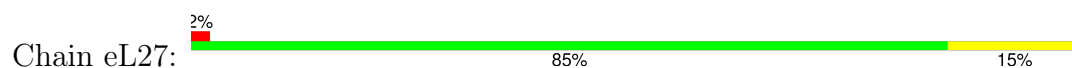
- Molecule 27: 60S ribosomal protein L25



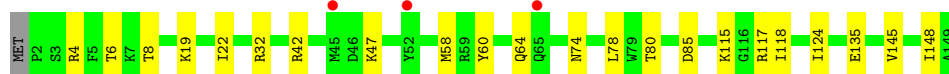
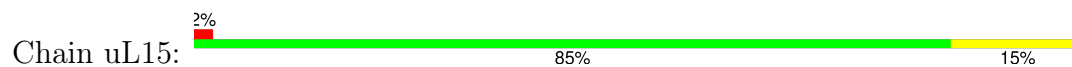
- Molecule 28: 60S ribosomal protein L26-A



- Molecule 29: 60S ribosomal protein L27



- Molecule 30: 60S ribosomal protein L28

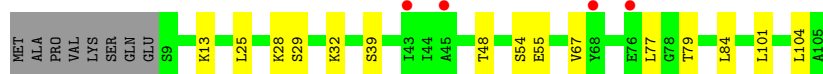
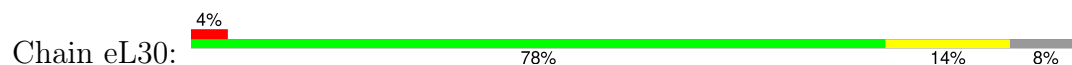


- Molecule 31: 60S ribosomal protein L29





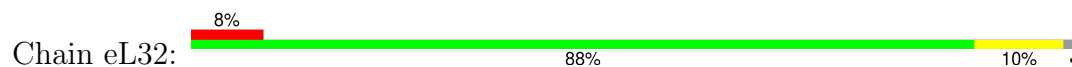
- Molecule 32: BJ4_G0020000.mRNA.1.CDS.1



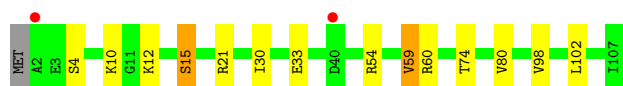
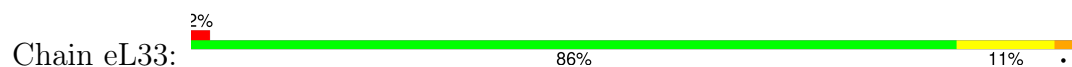
- Molecule 33: BJ4_G0008090.mRNA.1.CDS.1



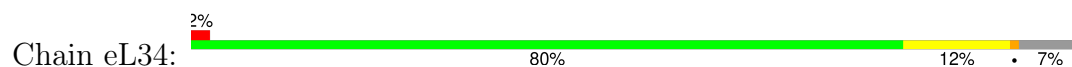
- Molecule 34: HN1_G0013350.mRNA.1.CDS.1



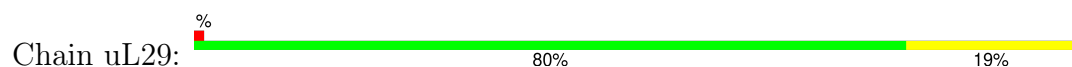
- Molecule 35: BJ4_G0025510.mRNA.1.CDS.1



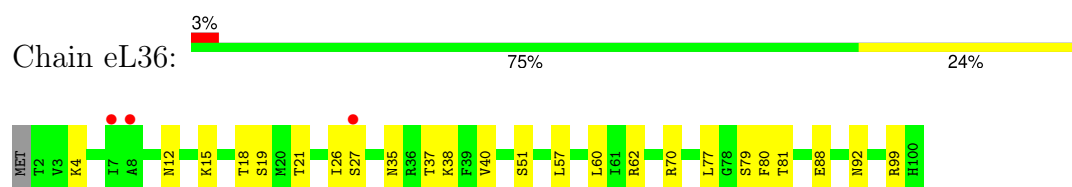
- Molecule 36: 60S ribosomal protein L34-A



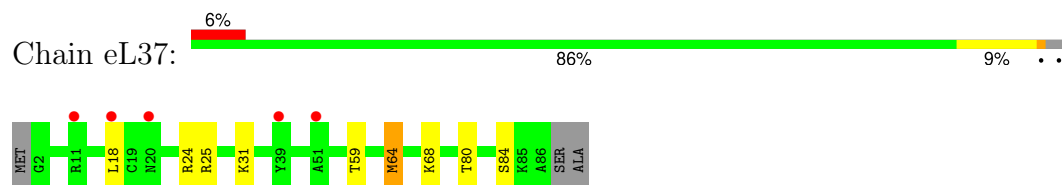
- Molecule 37: BJ4_G0044250.mRNA.1.CDS.1



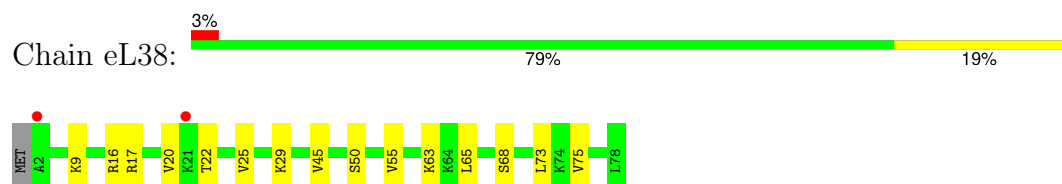
- Molecule 38: 60S ribosomal protein L36-A



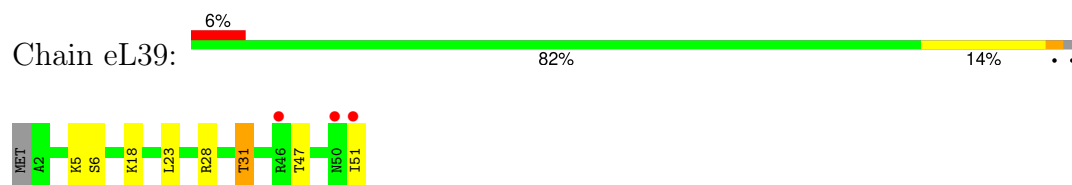
- Molecule 39: Ribosomal protein L37



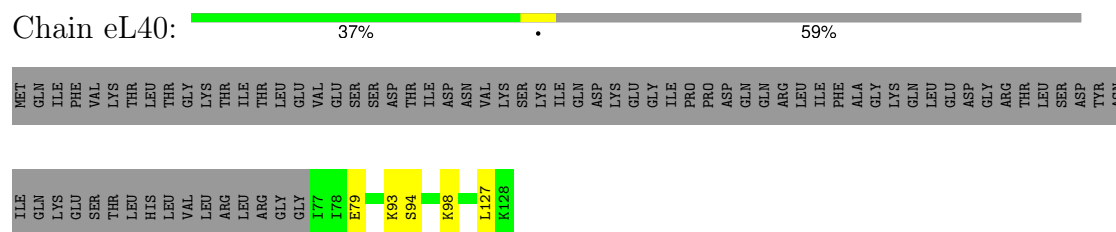
- Molecule 40: BJ4_G0032190.mRNA.1.CDS.1



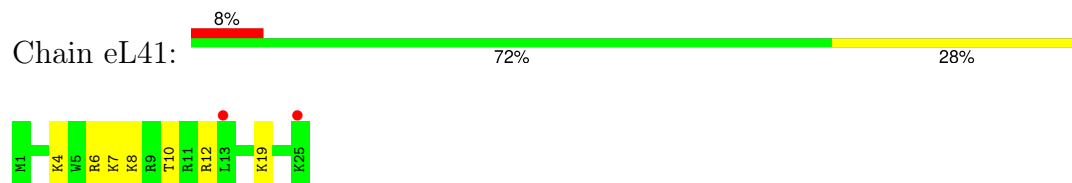
- Molecule 41: 60S ribosomal protein L39



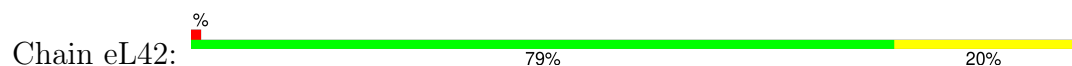
- Molecule 42: Ubiquitin



- Molecule 43: eL41

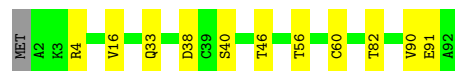


- Molecule 44: BJ4_G0001880.mRNA.1.CDS.1

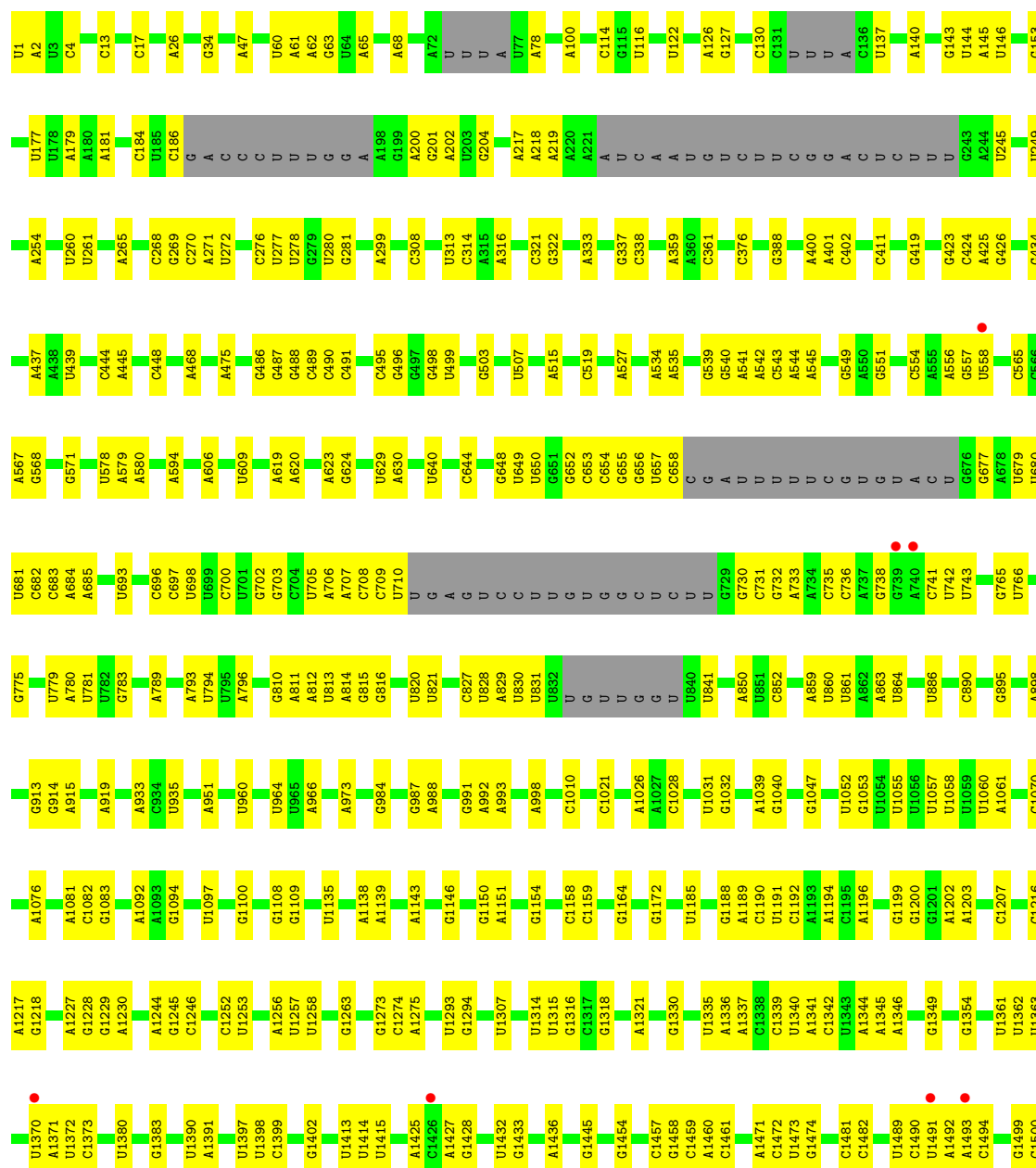
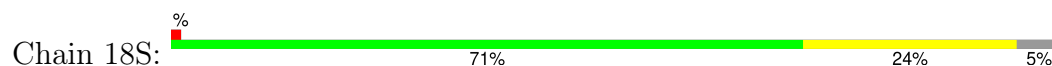


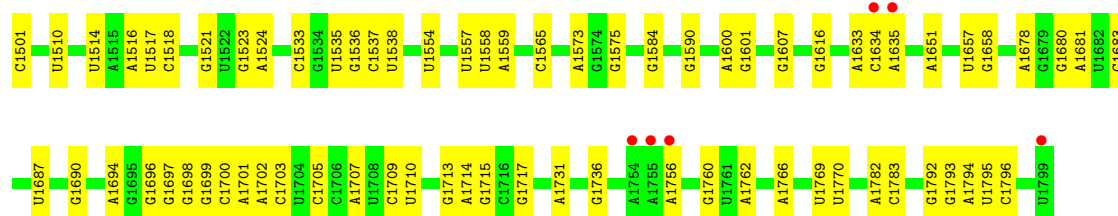


- Molecule 45: 60S ribosomal protein L43-A

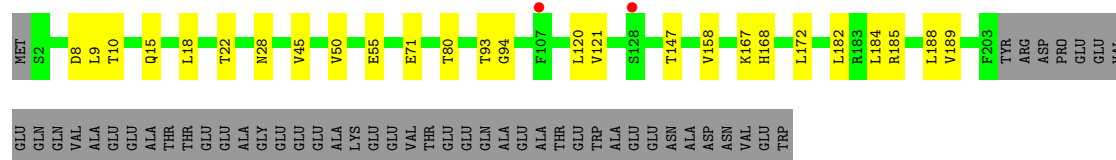
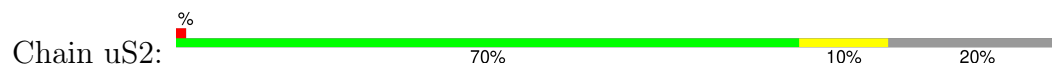


- Molecule 46: 18S rRNA

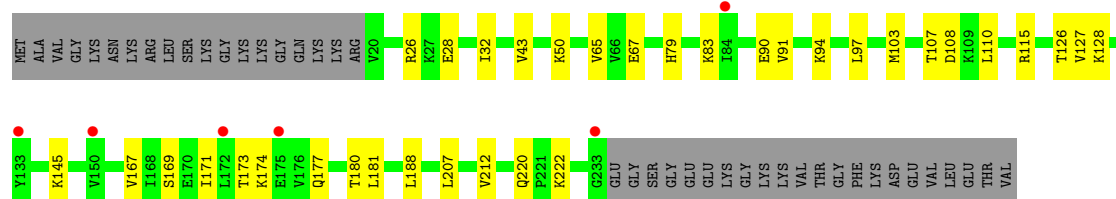
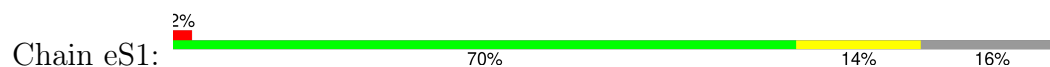




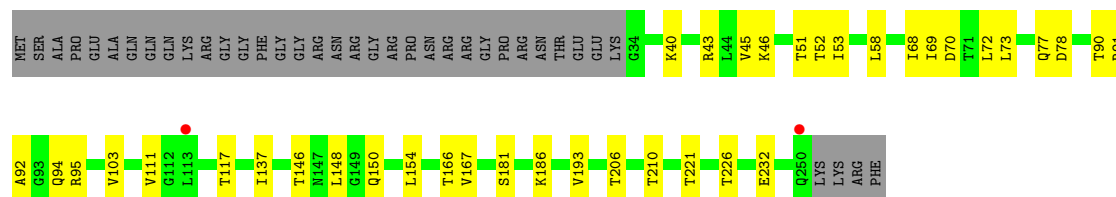
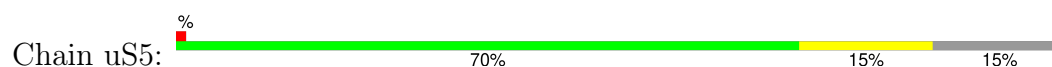
• Molecule 47: 40S ribosomal protein S0



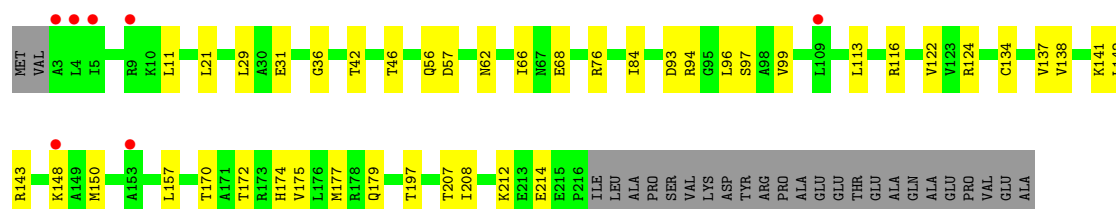
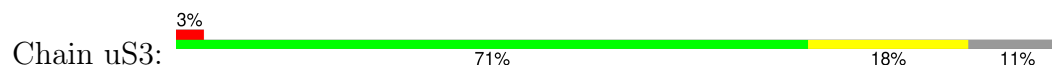
• Molecule 48: 40S ribosomal protein S1



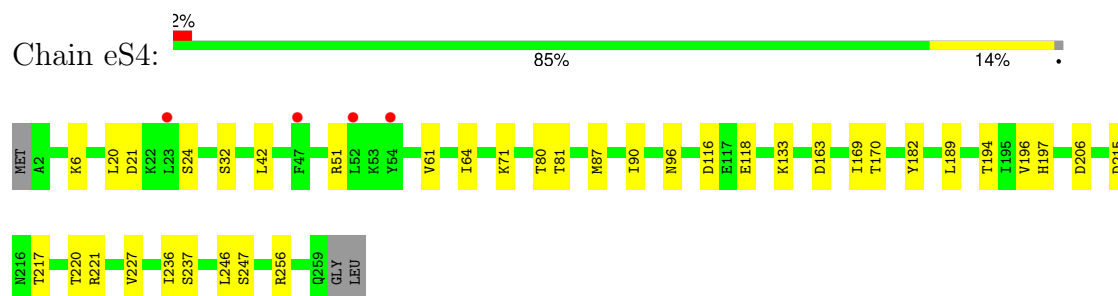
• Molecule 49: 40S ribosomal protein S2



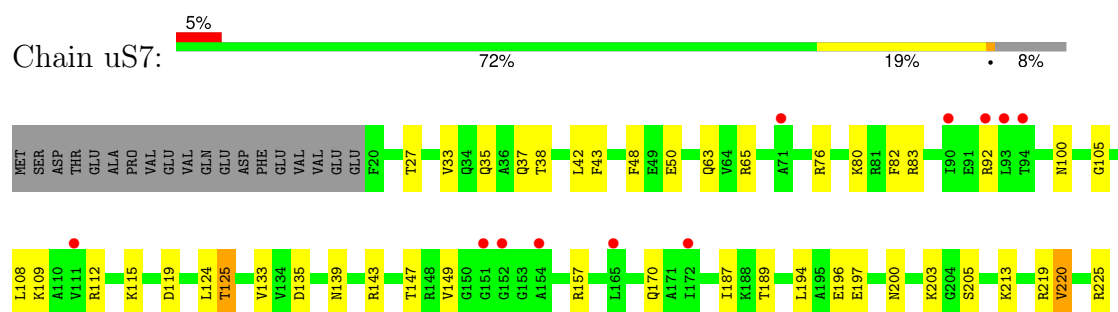
• Molecule 50: BJ4_G0045400.mRNA.1.CDS.1



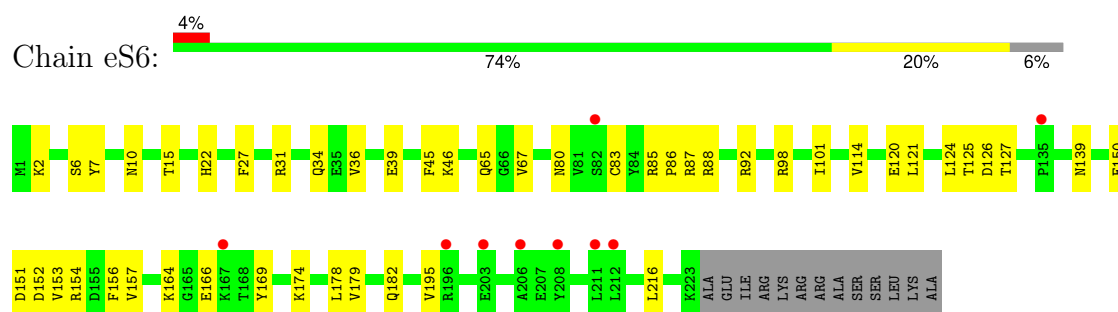
- Molecule 51: 40S ribosomal protein S4



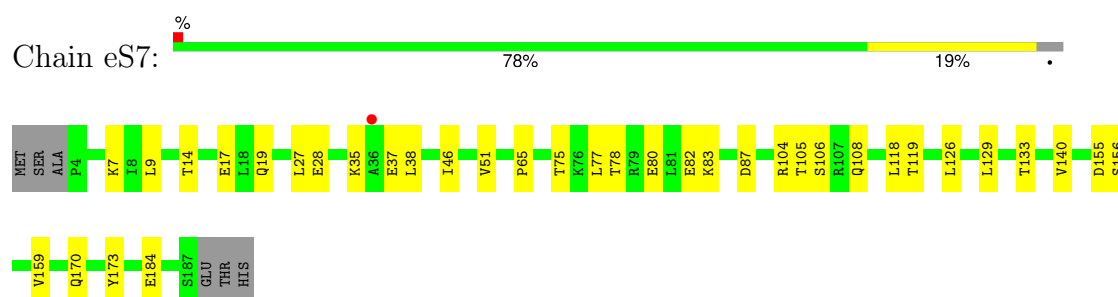
- Molecule 52: Rps5p



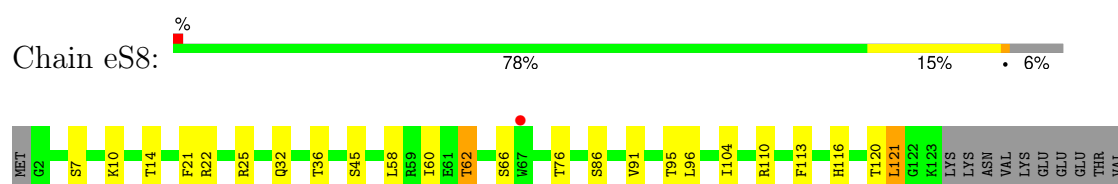
- Molecule 53: 40S ribosomal protein S6



- Molecule 54: 40S ribosomal protein S7



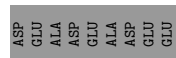
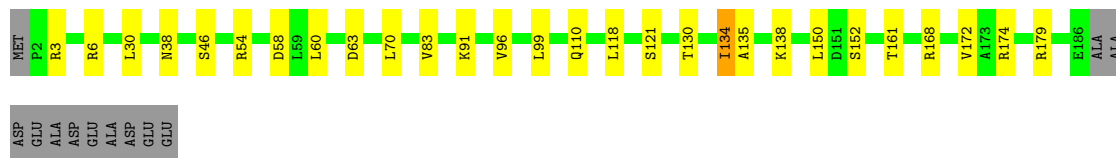
- Molecule 55: 40S ribosomal protein S8





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

Chain uS4: 80% 14% 6%



- Molecule 57: 40S ribosomal protein S10-A

Chain eS10: 73% 17% 9%



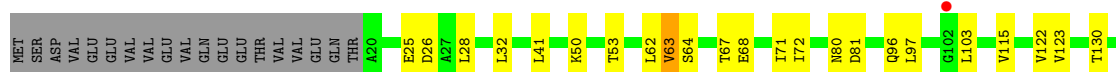
- Molecule 58: 40S ribosomal protein S11-B

Chain uS17: 76% 14% 10%



- Molecule 59: 40S ribosomal protein S12

Chain eS12: 68% 18% 13%



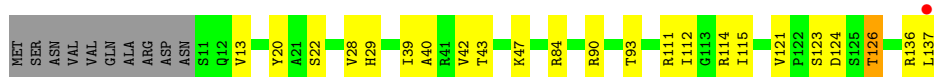
- Molecule 60: 40S ribosomal protein S13

Chain uS15: 77% 22% 1%

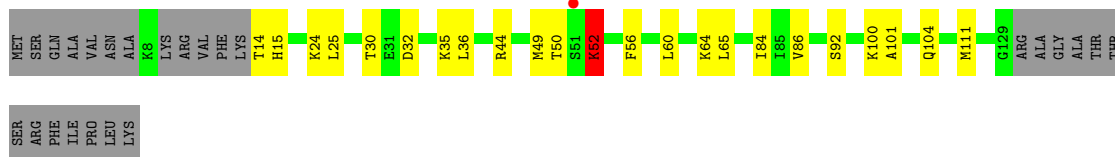


- Molecule 61: 40S ribosomal protein S14-A

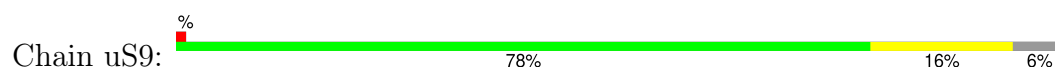
Chain uS11: 76% 16% 7%



- Molecule 62: 40S ribosomal protein S15



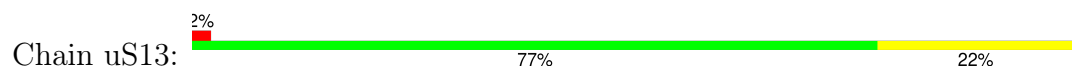
- Molecule 63: BJ4_G0008010.mRNA.1.CDS.1



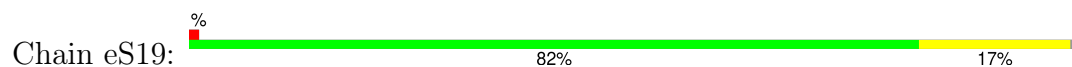
- Molecule 64: BJ4_G0020710.mRNA.1.CDS.1



- Molecule 65: 40S ribosomal protein S18-B

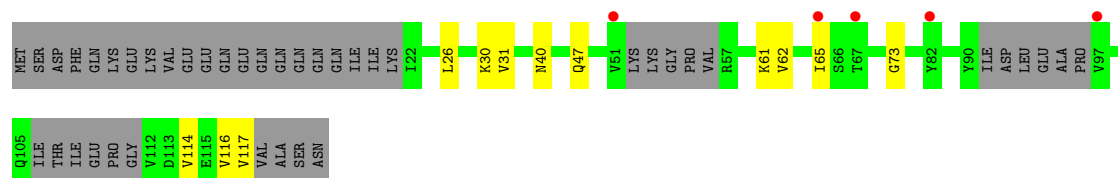


- Molecule 66: 40S ribosomal protein S19-A



- Molecule 67: 40S ribosomal protein S20





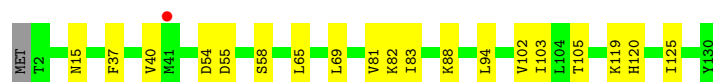
- Molecule 68: 40S ribosomal protein S21

Chain eS21: 80% 20%



- Molecule 69: 40S ribosomal protein S22-A

Chain uS8: 85% 15%



- Molecule 70: 40S ribosomal protein S23

Chain uS12: 87% 12%



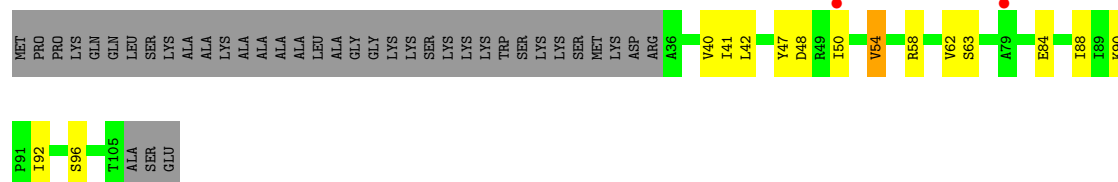
- Molecule 71: 40S ribosomal protein S24

Chain eS24: 81% 16% 7%



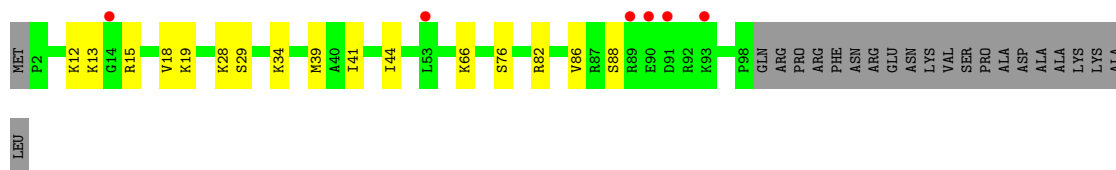
- Molecule 72: 40S ribosomal protein S25

Chain eS25: 51% 13% 35%

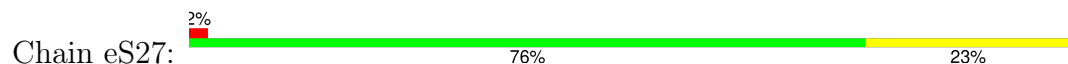


- Molecule 73: 40S ribosomal protein S26

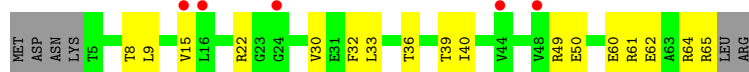
Chain eS26: 68% 13% 18%



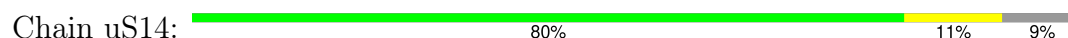
- Molecule 74: 40S ribosomal protein S27-A



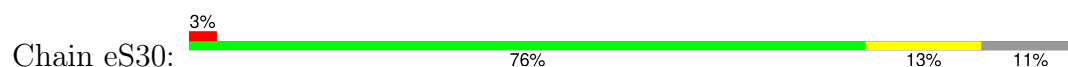
- Molecule 75: eS28



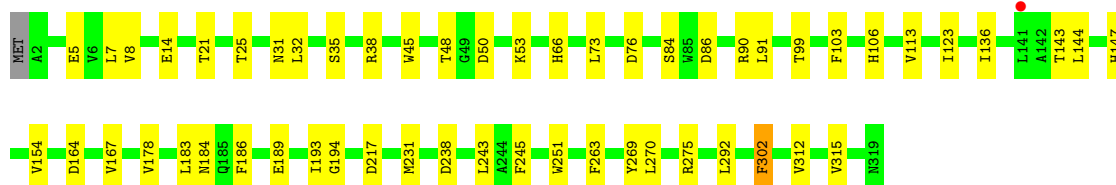
- Molecule 76: HLJ1_G0030400.mRNA.1.CDS.1



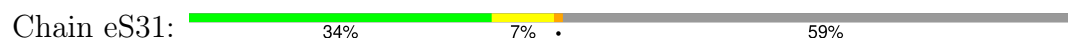
- Molecule 77: 40S ribosomal protein S30



- Molecule 78: BJ4_G0022010.mRNA.1.CDS.1



- Molecule 79: Ubiquitin-40S ribosomal protein S31



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	227.11Å 309.35Å 527.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	154.68 – 3.00 154.68 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (154.68-3.00) 94.8 (154.68-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.38 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.196 , 0.250 0.199 , 0.260	Depositor DCC
R_{free} test set	2000 reflections (0.24%)	wwPDB-VP
Wilson B-factor (Å ²)	98.2	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 120.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	208056	wwPDB-VP
Average B, all atoms (Å ²)	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	25S	0.44	0/76146	0.66	1/118714 (0.0%)
2	AB	0.58	1/2883 (0.0%)	0.64	2/4491 (0.0%)
3	58S	0.34	0/3746	0.54	0/5832
4	uL10	0.32	0/1570	0.61	2/2123 (0.1%)
5	uL2	0.51	0/1912	0.76	0/2569
6	uL3	0.51	0/3146	0.79	2/4228 (0.0%)
7	uL4	0.37	0/2800	0.68	2/3790 (0.1%)
8	uL18	0.37	0/2425	0.61	0/3271
9	eL6	0.37	0/1260	0.60	0/1694
10	uL30	0.44	0/1821	0.65	0/2451
11	eL8	0.47	1/1811 (0.1%)	0.63	1/2447 (0.0%)
12	uL6	0.45	0/1539	0.77	3/2073 (0.1%)
13	uL16	0.48	0/1746	0.65	0/2341
14	uL5	0.33	0/1374	0.58	0/1842
15	eL13	0.33	0/1568	0.60	1/2106 (0.0%)
16	eL14	0.40	0/1068	0.66	0/1438
17	eL15	0.40	0/1757	0.65	0/2354
18	uL13	0.52	0/1585	0.77	0/2128
19	uL22	0.43	0/1245	0.67	0/1676
20	eL18	0.47	1/1465 (0.1%)	0.69	1/1965 (0.1%)
21	eL19	0.44	0/1426	0.65	0/1901
22	eL20	0.45	0/1481	0.70	0/1990
23	eL21	0.46	0/1300	0.67	0/1743
24	eL22	0.36	0/794	0.58	0/1076
25	uL14	0.56	0/996	0.77	0/1340
26	eL24	0.47	0/533	0.77	0/707
27	uL23	0.40	0/979	0.57	0/1321
28	uL24	0.32	0/1004	0.53	0/1341
29	eL27	0.36	0/1118	0.60	0/1497
30	uL15	0.44	0/1204	0.70	0/1612
31	eL29	0.38	0/473	0.63	0/629
32	eL30	0.42	0/750	0.68	1/1008 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	eL31	0.42	0/897	0.71	1/1205 (0.1%)
34	eL32	0.41	0/1041	0.67	0/1394
35	eL33	0.48	0/868	0.72	0/1168
36	eL34	0.43	0/890	0.70	0/1189
37	uL29	0.34	0/978	0.56	0/1301
38	eL36	0.39	0/778	0.65	0/1034
39	eL37	0.46	0/685	0.80	2/908 (0.2%)
40	eL38	0.41	0/618	0.68	0/826
41	eL39	0.43	0/443	0.71	0/588
42	eL40	0.52	0/423	0.68	0/562
43	eL41	0.55	0/234	0.77	0/300
44	eL42	0.48	0/860	0.73	0/1136
45	eL43	0.49	0/701	0.76	0/934
46	18S	0.37	1/40923 (0.0%)	0.60	0/63757
47	uS2	0.37	0/1594	0.60	0/2182
48	eS1	0.35	0/1729	0.61	0/2328
49	uS5	0.38	0/1665	0.66	0/2263
50	uS3	0.34	0/1687	0.62	1/2269 (0.0%)
51	eS4	0.36	0/2097	0.69	0/2823
52	uS7	0.32	0/1629	0.62	0/2202
53	eS6	0.41	0/1814	0.74	3/2425 (0.1%)
54	eS7	0.30	0/1506	0.62	0/2028
55	eS8	0.57	1/1514 (0.1%)	0.68	0/2021
56	uS4	0.37	0/1519	0.68	2/2035 (0.1%)
57	eS10	0.31	0/789	0.68	1/1067 (0.1%)
58	uS17	0.43	0/1169	0.71	0/1576
59	eS12	0.29	0/898	0.69	0/1220
60	uS15	0.40	0/1215	0.70	1/1638 (0.1%)
61	uS11	0.44	0/901	0.81	2/1217 (0.2%)
62	uS19	0.36	0/943	0.61	0/1266
63	uS9	0.37	0/1081	0.68	0/1449
64	eS17	0.35	0/971	0.69	1/1303 (0.1%)
65	uS13	0.31	0/1211	0.56	0/1628
66	eS19	0.49	1/1130 (0.1%)	0.60	1/1517 (0.1%)
67	uS10	0.32	0/648	0.53	0/869
68	eS21	0.35	0/693	0.63	0/935
69	uS8	0.41	0/1038	0.67	1/1395 (0.1%)
70	uS12	0.50	0/1139	0.76	0/1518
71	eS24	0.33	0/1087	0.57	0/1449
72	eS25	0.32	0/571	0.78	1/768 (0.1%)
73	eS26	0.45	0/782	0.75	0/1047
74	eS27	0.34	0/620	0.60	0/838
75	eS28	0.34	0/480	0.57	0/645

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	uS14	0.35	0/429	0.62	0/569
77	eS30	0.40	0/456	0.67	0/607
78	RACK	0.33	0/2489	0.64	0/3389
79	eS31	0.34	0/508	0.74	0/677
80	eEF2	0.41	2/6685 (0.0%)	0.67	7/9050 (0.1%)
81	PSIT	0.28	0/1836	0.53	0/2859
82	mRNA	0.37	0/72	0.54	0/110
83	uL11	0.41	0/668	0.64	1/921 (0.1%)
All	All	0.42	8/222527 (0.0%)	0.65	41/326103 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	uL2	0	1
6	uL3	0	2
7	uL4	0	1
8	uL18	0	1
14	uL5	0	1
16	eL14	0	1
18	uL13	0	2
19	uL22	0	1
20	eL18	0	1
22	eL20	0	2
23	eL21	0	1
35	eL33	0	1
36	eL34	0	1
40	eL38	0	1
44	eL42	0	1
47	uS2	0	1
50	uS3	0	2
51	eS4	0	1
52	uS7	0	3
53	eS6	0	4
54	eS7	0	1
55	eS8	0	1
57	eS10	0	1
59	eS12	0	3
60	uS15	0	2
61	uS11	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
62	uS19	0	1
63	uS9	0	3
65	uS13	0	1
69	uS8	0	1
71	eS24	0	2
72	eS25	0	2
74	eS27	0	1
78	RACK	0	1
80	eEF2	0	1
83	uL11	0	1
All	All	0	53

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	1	G	O3'-P	-22.41	1.27	1.61
55	eS8	62	THR	C-N	-16.20	1.25	1.33
11	eL8	72	PRO	CA-C	13.79	1.61	1.52
66	eS19	46	PRO	CA-C	10.35	1.59	1.52
20	eL18	60	PRO	CA-C	9.26	1.56	1.51

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	eL8	72	PRO	O-C-N	14.14	127.80	121.15
12	uL6	59	ASN	CA-C-N	-10.10	113.01	122.80
12	uL6	59	ASN	C-N-CA	-10.10	113.01	122.80
80	eEF2	32	LYS	CA-C-N	9.75	133.89	120.63
80	eEF2	32	LYS	C-N-CA	9.75	133.89	120.63

There are no chirality outliers.

5 of 53 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	uL18	58	LYS	Peptide
5	uL2	19	HIS	Peptide
6	uL3	126	LYS	Peptide
6	uL3	385	LYS	Peptide
7	uL4	318	LEU	Peptide

5.2 Too-close contacts ⓘ

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

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	197/312 (63%)	153 (78%)	43 (22%)	1 (0%)	24	60
5	uL2	245/254 (96%)	221 (90%)	24 (10%)	0	100	100
6	uL3	384/387 (99%)	337 (88%)	44 (12%)	3 (1%)	16	50
7	uL4	359/362 (99%)	306 (85%)	50 (14%)	3 (1%)	16	50
8	uL18	294/297 (99%)	258 (88%)	35 (12%)	1 (0%)	36	70
9	eL6	152/176 (86%)	129 (85%)	22 (14%)	1 (1%)	18	53
10	uL30	220/244 (90%)	195 (89%)	24 (11%)	1 (0%)	24	60
11	eL8	227/256 (89%)	197 (87%)	28 (12%)	2 (1%)	14	48
12	uL6	189/191 (99%)	171 (90%)	17 (9%)	1 (0%)	24	60
13	uL16	206/221 (93%)	182 (88%)	24 (12%)	0	100	100
14	uL5	167/174 (96%)	143 (86%)	22 (13%)	2 (1%)	10	40
15	eL13	191/199 (96%)	167 (87%)	20 (10%)	4 (2%)	5	27
16	eL14	134/138 (97%)	122 (91%)	12 (9%)	0	100	100
17	eL15	201/204 (98%)	181 (90%)	17 (8%)	3 (2%)	8	35
18	uL13	195/199 (98%)	176 (90%)	15 (8%)	4 (2%)	5	27
19	uL22	152/184 (83%)	138 (91%)	14 (9%)	0	100	100
20	eL18	183/186 (98%)	158 (86%)	25 (14%)	0	100	100
21	eL19	172/189 (91%)	161 (94%)	10 (6%)	1 (1%)	21	56
22	eL20	170/172 (99%)	150 (88%)	19 (11%)	1 (1%)	21	56
23	eL21	157/160 (98%)	138 (88%)	18 (12%)	1 (1%)	21	56
24	eL22	96/121 (79%)	76 (79%)	19 (20%)	1 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	uL14	130/137 (95%)	118 (91%)	12 (9%)	0	100	100
26	eL24	61/155 (39%)	56 (92%)	5 (8%)	0	100	100
27	uL23	119/142 (84%)	108 (91%)	11 (9%)	0	100	100
28	uL24	124/127 (98%)	114 (92%)	10 (8%)	0	100	100
29	eL27	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
30	uL15	146/149 (98%)	124 (85%)	20 (14%)	2 (1%)	9	36
31	eL29	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
32	eL30	95/105 (90%)	88 (93%)	7 (7%)	0	100	100
33	eL31	107/113 (95%)	90 (84%)	16 (15%)	1 (1%)	14	48
34	eL32	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
35	eL33	104/107 (97%)	96 (92%)	7 (7%)	1 (1%)	12	45
36	eL34	110/121 (91%)	99 (90%)	10 (9%)	1 (1%)	14	48
37	uL29	117/120 (98%)	103 (88%)	14 (12%)	0	100	100
38	eL36	97/100 (97%)	78 (80%)	18 (19%)	1 (1%)	12	45
39	eL37	83/88 (94%)	74 (89%)	7 (8%)	2 (2%)	4	24
40	eL38	75/78 (96%)	65 (87%)	10 (13%)	0	100	100
41	eL39	48/51 (94%)	40 (83%)	7 (15%)	1 (2%)	5	27
42	eL40	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
43	eL41	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
44	eL42	103/106 (97%)	82 (80%)	21 (20%)	0	100	100
45	eL43	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	uS2	200/252 (79%)	170 (85%)	29 (14%)	1 (0%)	24	60
48	eS1	212/255 (83%)	175 (82%)	36 (17%)	1 (0%)	24	60
49	uS5	215/254 (85%)	187 (87%)	25 (12%)	3 (1%)	9	36
50	uS3	212/240 (88%)	178 (84%)	33 (16%)	1 (0%)	24	60
51	eS4	256/261 (98%)	221 (86%)	33 (13%)	2 (1%)	16	50
52	uS7	204/225 (91%)	161 (79%)	41 (20%)	2 (1%)	12	45
53	eS6	221/236 (94%)	173 (78%)	47 (21%)	1 (0%)	24	60
54	eS7	182/190 (96%)	147 (81%)	34 (19%)	1 (0%)	24	60
55	eS8	184/200 (92%)	159 (86%)	23 (12%)	2 (1%)	11	43
56	uS4	183/197 (93%)	154 (84%)	26 (14%)	3 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	eS10	94/105 (90%)	72 (77%)	21 (22%)	1 (1%)	11	43
58	uS17	139/156 (89%)	120 (86%)	19 (14%)	0	100	100
59	eS12	122/143 (85%)	82 (67%)	40 (33%)	0	100	100
60	uS15	148/151 (98%)	130 (88%)	17 (12%)	1 (1%)	18	53
61	uS11	125/137 (91%)	99 (79%)	23 (18%)	3 (2%)	4	24
62	uS19	114/142 (80%)	90 (79%)	22 (19%)	2 (2%)	6	31
63	uS9	133/143 (93%)	105 (79%)	28 (21%)	0	100	100
64	eS17	119/136 (88%)	92 (77%)	25 (21%)	2 (2%)	7	32
65	uS13	143/146 (98%)	118 (82%)	23 (16%)	2 (1%)	9	36
66	eS19	141/144 (98%)	113 (80%)	28 (20%)	0	100	100
67	uS10	71/121 (59%)	66 (93%)	4 (6%)	1 (1%)	9	36
68	eS21	85/87 (98%)	64 (75%)	21 (25%)	0	100	100
69	uS8	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
70	uS12	142/145 (98%)	125 (88%)	16 (11%)	1 (1%)	18	53
71	eS24	132/135 (98%)	112 (85%)	19 (14%)	1 (1%)	16	50
72	eS25	68/108 (63%)	53 (78%)	14 (21%)	1 (2%)	8	35
73	eS26	95/119 (80%)	76 (80%)	18 (19%)	1 (1%)	11	43
74	eS27	79/82 (96%)	64 (81%)	15 (19%)	0	100	100
75	eS28	59/67 (88%)	45 (76%)	14 (24%)	0	100	100
76	uS14	47/56 (84%)	41 (87%)	6 (13%)	0	100	100
77	eS30	54/63 (86%)	37 (68%)	16 (30%)	1 (2%)	6	30
78	RACK	316/319 (99%)	231 (73%)	83 (26%)	2 (1%)	21	56
79	eS31	61/152 (40%)	40 (66%)	19 (31%)	2 (3%)	3	17
80	eEF2	840/842 (100%)	721 (86%)	111 (13%)	8 (1%)	12	45
83	uL11	129/165 (78%)	98 (76%)	30 (23%)	1 (1%)	16	50
All	All	11938/13198 (90%)	10158 (85%)	1694 (14%)	86 (1%)	18	53

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	uL10	124	VAL
6	uL3	5	LYS
6	uL3	127	LYS

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Mol	Chain	Res	Type
11	eL8	157	VAL
14	uL5	95	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	168/254 (66%)	118 (70%)	50 (30%)	0	2
5	uL2	189/196 (96%)	160 (85%)	29 (15%)	3	14
6	uL3	319/323 (99%)	278 (87%)	41 (13%)	4	19
7	uL4	288/289 (100%)	229 (80%)	59 (20%)	1	7
8	uL18	244/245 (100%)	192 (79%)	52 (21%)	1	6
9	eL6	134/153 (88%)	113 (84%)	21 (16%)	2	13
10	uL30	186/205 (91%)	164 (88%)	22 (12%)	5	22
11	eL8	184/208 (88%)	146 (79%)	38 (21%)	1	7
12	uL6	171/171 (100%)	136 (80%)	35 (20%)	1	7
13	uL16	180/187 (96%)	156 (87%)	24 (13%)	4	18
14	uL5	147/150 (98%)	115 (78%)	32 (22%)	1	6
15	eL13	154/159 (97%)	129 (84%)	25 (16%)	2	12
16	eL14	107/109 (98%)	96 (90%)	11 (10%)	7	28
17	eL15	175/176 (99%)	151 (86%)	24 (14%)	3	17
18	uL13	160/162 (99%)	137 (86%)	23 (14%)	3	15
19	uL22	125/146 (86%)	99 (79%)	26 (21%)	1	7
20	eL18	150/151 (99%)	131 (87%)	19 (13%)	4	20
21	eL19	142/154 (92%)	117 (82%)	25 (18%)	2	10
22	eL20	156/156 (100%)	124 (80%)	32 (20%)	1	7
23	eL21	136/137 (99%)	119 (88%)	17 (12%)	4	20
24	eL22	85/107 (79%)	69 (81%)	16 (19%)	1	9
25	uL14	102/105 (97%)	86 (84%)	16 (16%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	eL24	55/129 (43%)	44 (80%)	11 (20%)	1	7
27	uL23	104/118 (88%)	91 (88%)	13 (12%)	4	20
28	uL24	109/110 (99%)	89 (82%)	20 (18%)	2	9
29	eL27	115/115 (100%)	95 (83%)	20 (17%)	2	10
30	uL15	118/119 (99%)	98 (83%)	20 (17%)	2	11
31	eL29	46/47 (98%)	38 (83%)	8 (17%)	2	10
32	eL30	81/88 (92%)	67 (83%)	14 (17%)	2	10
33	eL31	94/97 (97%)	82 (87%)	12 (13%)	4	19
34	eL32	109/111 (98%)	96 (88%)	13 (12%)	5	22
35	eL33	90/91 (99%)	76 (84%)	14 (16%)	2	13
36	eL34	95/103 (92%)	81 (85%)	14 (15%)	3	15
37	uL29	104/105 (99%)	81 (78%)	23 (22%)	1	5
38	eL36	81/82 (99%)	58 (72%)	23 (28%)	0	2
39	eL37	69/71 (97%)	62 (90%)	7 (10%)	7	29
40	eL38	68/69 (99%)	54 (79%)	14 (21%)	1	7
41	eL39	45/46 (98%)	37 (82%)	8 (18%)	2	10
42	eL40	47/116 (40%)	42 (89%)	5 (11%)	6	27
43	eL41	23/23 (100%)	16 (70%)	7 (30%)	0	1
44	eL42	90/91 (99%)	70 (78%)	20 (22%)	1	5
45	eL43	71/72 (99%)	60 (84%)	11 (16%)	2	13
47	uS2	163/210 (78%)	139 (85%)	24 (15%)	3	15
48	eS1	190/224 (85%)	156 (82%)	34 (18%)	2	10
49	uS5	176/205 (86%)	141 (80%)	35 (20%)	1	7
50	uS3	174/195 (89%)	135 (78%)	39 (22%)	1	5
51	eS4	220/222 (99%)	186 (84%)	34 (16%)	2	13
52	uS7	173/191 (91%)	131 (76%)	42 (24%)	1	4
53	eS6	189/201 (94%)	148 (78%)	41 (22%)	1	6
54	eS7	165/170 (97%)	131 (79%)	34 (21%)	1	7
55	eS8	150/161 (93%)	120 (80%)	30 (20%)	1	7
56	uS4	158/166 (95%)	133 (84%)	25 (16%)	2	13
57	eS10	77/98 (79%)	60 (78%)	17 (22%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	uS17	128/137 (93%)	106 (83%)	22 (17%)	2	11
59	eS12	88/119 (74%)	63 (72%)	25 (28%)	0	2
60	uS15	127/128 (99%)	98 (77%)	29 (23%)	1	5
61	uS11	81/105 (77%)	63 (78%)	18 (22%)	1	5
62	uS19	97/118 (82%)	75 (77%)	22 (23%)	1	5
63	uS9	112/119 (94%)	92 (82%)	20 (18%)	2	10
64	eS17	105/124 (85%)	80 (76%)	25 (24%)	1	4
65	uS13	128/129 (99%)	99 (77%)	29 (23%)	1	5
66	eS19	115/116 (99%)	91 (79%)	24 (21%)	1	7
67	uS10	76/114 (67%)	65 (86%)	11 (14%)	3	15
68	eS21	74/74 (100%)	57 (77%)	17 (23%)	1	5
69	uS8	110/111 (99%)	93 (84%)	17 (16%)	2	13
70	uS12	119/120 (99%)	102 (86%)	17 (14%)	3	16
71	eS24	112/113 (99%)	89 (80%)	23 (20%)	1	7
72	eS25	61/89 (68%)	49 (80%)	12 (20%)	1	8
73	eS26	83/101 (82%)	68 (82%)	15 (18%)	2	9
74	eS27	70/71 (99%)	52 (74%)	18 (26%)	0	3
75	eS28	54/60 (90%)	37 (68%)	17 (32%)	0	1
76	uS14	45/49 (92%)	39 (87%)	6 (13%)	4	18
77	eS30	48/54 (89%)	41 (85%)	7 (15%)	3	15
78	RACK	259/262 (99%)	207 (80%)	52 (20%)	1	7
79	eS31	54/135 (40%)	44 (82%)	10 (18%)	1	9
80	eEF2	715/715 (100%)	605 (85%)	110 (15%)	2	13
All	All	10012/10952 (91%)	8197 (82%)	1815 (18%)	2	9

5 of 1815 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	uS2	120	LEU
80	eEF2	525	SER
53	eS6	125	THR
80	eEF2	418	TYR
74	eS27	33	LEU

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	3174/3396 (93%)	644 (20%)	32 (1%)
2	AB	120/121 (99%)	10 (8%)	1 (0%)
3	58S	157/753 (20%)	32 (20%)	2 (1%)
46	18S	1709/1798 (95%)	430 (25%)	24 (1%)
81	PSIT	76/77 (98%)	23 (30%)	4 (5%)
82	mRNA	2/3 (66%)	0	0
All	All	5238/6148 (85%)	1139 (21%)	63 (1%)

5 of 1139 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	25S	16	A
1	25S	26	A
1	25S	30	G
1	25S	40	A
1	25S	43	A

5 of 63 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	25S	2954	U
46	18S	1491	U
46	18S	1	U
46	18S	1489	U
81	PSIT	20	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 504 ligands modelled in this entry, 503 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	GTP	eEF2	905	84	33,34,34	1.20	4 (12%)	50,54,54	1.87	12 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	GTP	eEF2	905	84	-	2/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	eEF2	905	GTP	PB-O3B	4.48	1.64	1.59
86	eEF2	905	GTP	C5-N7	-2.16	1.34	1.39
86	eEF2	905	GTP	C2-N3	2.03	1.38	1.33
86	eEF2	905	GTP	O4'-C4'	-2.00	1.40	1.45

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	eEF2	905	GTP	O3A-PB-O1B	-5.11	95.33	110.70
86	eEF2	905	GTP	C5-C4-N3	-4.73	120.86	128.39
86	eEF2	905	GTP	C2-N3-C4	4.55	120.14	112.30
86	eEF2	905	GTP	O2G-PG-O3B	3.67	116.95	104.64
86	eEF2	905	GTP	C2-N1-C6	-3.19	119.32	125.11

There are no chirality outliers.

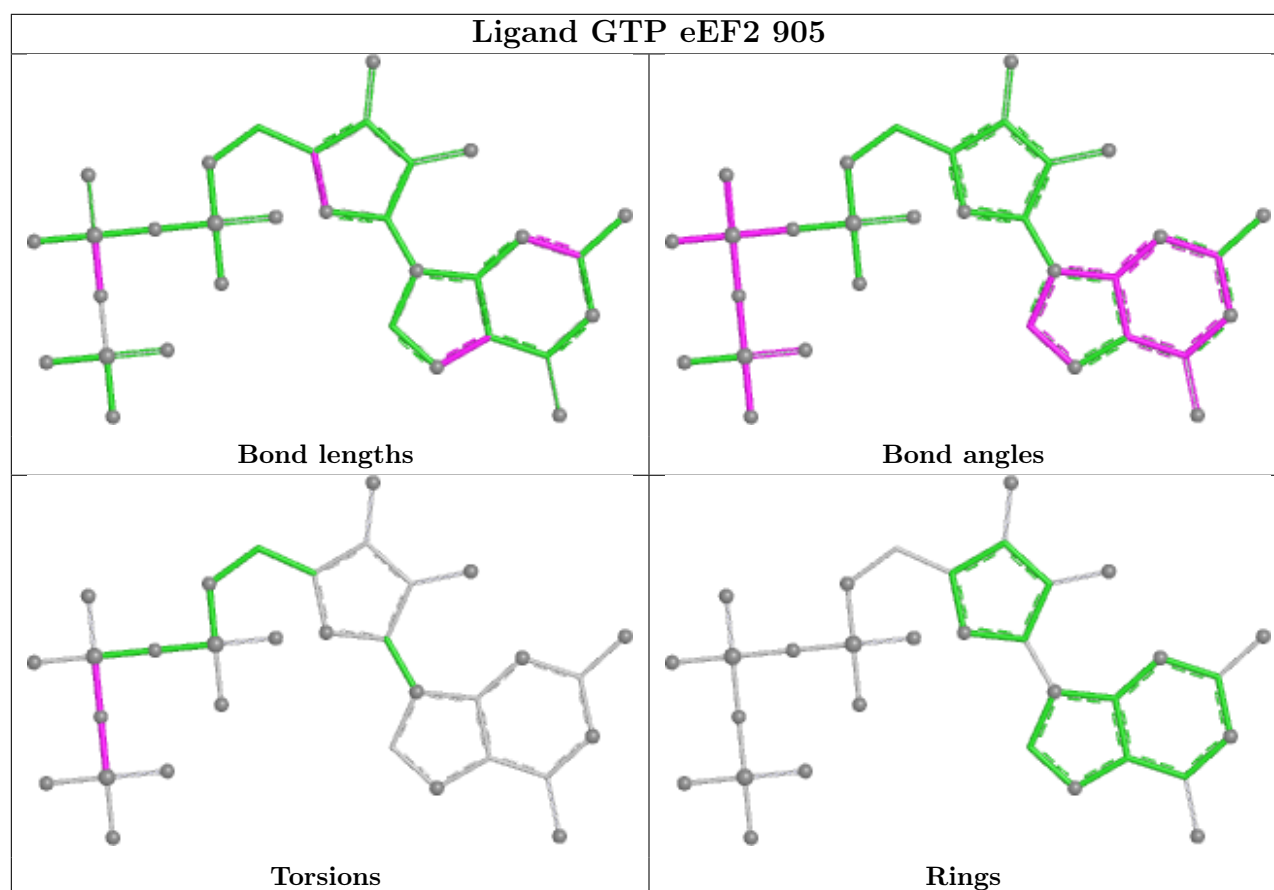
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	eEF2	905	GTP	PB-O3B-PG-O2G
86	eEF2	905	GTP	PG-O3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	18S	1
2	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	18S	1798:U	O3'	1799:U	P	2.81
1	AB	1:G	O3'	2:G	P	1.27

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	3180/3396 (93%)	-0.47	79 (2%) 58 35	63, 98, 191, 291	0
2	AB	121/121 (100%)	-0.93	1 (0%) 82 64	50, 106, 130, 137	0
3	58S	158/753 (20%)	-0.45	1 (0%) 85 69	94, 112, 155, 220	0
4	uL10	199/312 (63%)	0.37	20 (10%) 12 7	108, 158, 184, 198	0
5	uL2	247/254 (97%)	0.04	3 (1%) 76 55	66, 83, 105, 128	0
6	uL3	386/387 (99%)	-0.15	13 (3%) 48 27	64, 90, 116, 149	0
7	uL4	361/362 (99%)	0.53	45 (12%) 8 5	73, 117, 142, 153	0
8	uL18	296/297 (99%)	-0.29	5 (1%) 69 45	87, 126, 161, 193	0
9	eL6	156/176 (88%)	0.26	11 (7%) 22 11	94, 130, 164, 174	0
10	uL30	222/244 (90%)	0.07	6 (2%) 56 33	71, 95, 146, 201	0
11	eL8	229/256 (89%)	0.11	10 (4%) 39 21	98, 137, 184, 206	0
12	uL6	191/191 (100%)	-0.25	0 100 100	81, 99, 125, 166	0
13	uL16	210/221 (95%)	-0.30	0 100 100	74, 95, 131, 145	0
14	uL5	169/174 (97%)	-0.08	2 (1%) 76 55	97, 135, 157, 176	0
15	eL13	193/199 (96%)	0.03	7 (3%) 46 26	79, 129, 173, 189	0
16	eL14	136/138 (98%)	-0.10	2 (1%) 72 49	84, 103, 144, 159	0
17	eL15	203/204 (99%)	0.36	12 (5%) 28 14	78, 106, 125, 141	0
18	uL13	197/199 (98%)	0.07	9 (4%) 37 20	67, 85, 135, 156	0
19	uL22	154/184 (83%)	0.04	6 (3%) 43 24	75, 96, 121, 165	0
20	eL18	185/186 (99%)	0.29	19 (10%) 12 6	88, 113, 128, 142	0
21	eL19	174/189 (92%)	-0.20	1 (0%) 85 69	73, 99, 191, 198	0
22	eL20	172/172 (100%)	-0.21	4 (2%) 61 38	76, 92, 116, 138	0
23	eL21	159/160 (99%)	0.39	15 (9%) 14 7	80, 96, 162, 180	0
24	eL22	98/121 (80%)	-0.04	0 100 100	110, 149, 164, 175	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	uL14	132/137 (96%)	0.06	5 (3%) 44 24	67, 82, 110, 131	0
26	eL24	63/155 (40%)	-0.36	0 100 100	74, 88, 113, 134	0
27	uL23	121/142 (85%)	0.29	5 (4%) 41 23	95, 121, 144, 161	0
28	uL24	126/127 (99%)	0.34	11 (8%) 16 8	105, 129, 148, 157	0
29	eL27	135/135 (100%)	0.03	3 (2%) 62 39	95, 122, 144, 160	0
30	uL15	148/149 (99%)	0.12	3 (2%) 65 41	75, 113, 153, 162	0
31	eL29	58/59 (98%)	-0.08	4 (6%) 23 12	69, 120, 160, 179	0
32	eL30	97/105 (92%)	0.13	4 (4%) 41 23	92, 114, 160, 181	0
33	eL31	109/113 (96%)	-0.34	0 100 100	82, 100, 168, 181	0
34	eL32	127/130 (97%)	0.31	10 (7%) 18 10	78, 105, 131, 152	0
35	eL33	106/107 (99%)	0.04	2 (1%) 66 43	78, 97, 133, 145	0
36	eL34	112/121 (92%)	0.38	3 (2%) 56 33	81, 100, 174, 186	0
37	uL29	119/120 (99%)	-0.05	1 (0%) 82 64	108, 132, 151, 156	0
38	eL36	99/100 (99%)	0.15	3 (3%) 52 30	111, 131, 172, 188	0
39	eL37	85/88 (96%)	0.12	5 (5%) 28 14	70, 93, 138, 148	0
40	eL38	77/78 (98%)	-0.09	2 (2%) 57 34	108, 135, 162, 176	0
41	eL39	50/51 (98%)	-0.03	3 (6%) 27 14	84, 104, 129, 134	0
42	eL40	52/128 (40%)	-0.32	0 100 100	73, 85, 109, 128	0
43	eL41	25/25 (100%)	0.44	2 (8%) 18 9	81, 100, 119, 122	0
44	eL42	105/106 (99%)	-0.17	1 (0%) 79 59	73, 103, 147, 200	0
45	eL43	91/92 (98%)	-0.00	0 100 100	70, 85, 107, 116	0
46	18S	1717/1798 (95%)	-0.61	13 (0%) 82 64	71, 114, 238, 323	0
47	uS2	202/252 (80%)	0.01	2 (0%) 79 59	107, 128, 152, 171	0
48	eS1	214/255 (83%)	0.20	6 (2%) 55 32	93, 122, 163, 179	0
49	uS5	217/254 (85%)	-0.09	2 (0%) 81 61	89, 110, 141, 187	0
50	uS3	214/240 (89%)	-0.19	7 (3%) 49 28	115, 146, 186, 198	0
51	eS4	258/261 (98%)	-0.07	4 (1%) 70 47	93, 127, 151, 174	0
52	uS7	206/225 (91%)	0.15	11 (5%) 32 16	117, 152, 187, 196	0
53	eS6	223/236 (94%)	0.16	9 (4%) 42 23	92, 140, 176, 192	0
54	eS7	184/190 (96%)	-0.28	1 (0%) 87 72	102, 171, 215, 234	0
55	eS8	188/200 (94%)	-0.17	2 (1%) 78 57	87, 125, 172, 195	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
56	uS4	185/197 (93%)	0.10	0 100 100	100, 125, 160, 214	0
57	eS10	96/105 (91%)	-0.19	1 (1%) 79 59	136, 166, 201, 217	0
58	uS17	141/156 (90%)	-0.48	0 100 100	84, 108, 165, 191	0
59	eS12	124/143 (86%)	-0.07	2 (1%) 70 47	190, 209, 229, 238	0
60	uS15	150/151 (99%)	-0.07	1 (0%) 84 66	85, 116, 139, 146	0
61	uS11	127/137 (92%)	-0.07	1 (0%) 82 64	76, 113, 134, 162	0
62	uS19	117/142 (82%)	-0.06	1 (0%) 81 61	110, 146, 182, 200	0
63	uS9	135/143 (94%)	0.01	1 (0%) 84 66	101, 151, 185, 189	0
64	eS17	121/136 (88%)	-0.20	0 100 100	111, 150, 185, 191	0
65	uS13	145/146 (99%)	-0.16	3 (2%) 63 40	113, 144, 175, 192	0
66	eS19	143/144 (99%)	-0.34	1 (0%) 84 66	110, 152, 174, 195	0
67	uS10	79/121 (65%)	0.12	5 (6%) 26 13	100, 161, 204, 212	0
68	eS21	87/87 (100%)	-0.40	0 100 100	104, 122, 160, 173	0
69	uS8	129/130 (99%)	-0.36	1 (0%) 82 64	90, 105, 117, 123	0
70	uS12	144/145 (99%)	-0.12	2 (1%) 73 51	78, 91, 111, 139	0
71	eS24	134/135 (99%)	0.27	9 (6%) 24 12	96, 133, 171, 197	0
72	eS25	70/108 (64%)	0.11	2 (2%) 53 31	143, 169, 188, 198	0
73	eS26	97/119 (81%)	0.41	6 (6%) 26 14	84, 103, 168, 176	0
74	eS27	81/82 (98%)	0.24	2 (2%) 58 35	99, 122, 184, 194	0
75	eS28	61/67 (91%)	0.47	5 (8%) 17 9	121, 147, 188, 209	0
76	uS14	51/56 (91%)	-0.40	0 100 100	109, 123, 137, 145	0
77	eS30	56/63 (88%)	0.11	2 (3%) 46 26	94, 130, 199, 218	0
78	RACK	318/319 (99%)	-0.19	1 (0%) 90 79	158, 192, 208, 223	0
79	eS31	63/152 (41%)	-0.27	0 100 100	165, 193, 205, 207	0
80	eEF2	842/842 (100%)	-0.09	32 (3%) 44 24	82, 117, 153, 173	0
81	PSIT	77/77 (100%)	-0.01	4 (5%) 33 17	80, 152, 185, 191	0
82	mRNA	3/3 (100%)	0.11	0 100 100	119, 119, 130, 140	0
83	uL11	137/165 (83%)	0.29	7 (5%) 33 17	125, 139, 148, 157	0
All	All	17369/19346 (89%)	-0.16	484 (2%) 55 32	50, 116, 190, 323	0

The worst 5 of 484 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
80	eEF2	696	ASP	11.8
7	uL4	83	GLY	10.9
7	uL4	82	THR	10.6
7	uL4	70	ALA	9.3
7	uL4	69	ARG	9.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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	25S	3520[A]	1/1	-0.28	0.48	116,116,116,116	1
84	MG	25S	3520[B]	1/1	-0.28	0.48	110,110,110,110	1
84	MG	25S	3510	1/1	-0.26	0.41	134,134,134,134	0
84	MG	25S	3572	1/1	-0.06	0.36	129,129,129,129	0
84	MG	25S	3673	1/1	-0.03	0.59	94,94,94,94	0
84	MG	58S	406	1/1	0.11	0.25	126,126,126,126	0
84	MG	eL22	201	1/1	0.18	0.41	122,122,122,122	0
84	MG	25S	3660	1/1	0.23	0.37	121,121,121,121	0
84	MG	18S	1904	1/1	0.26	0.24	121,121,121,121	0
84	MG	25S	3525	1/1	0.28	0.41	124,124,124,124	0
84	MG	58S	407	1/1	0.28	0.32	117,117,117,117	0
84	MG	25S	3690	1/1	0.30	0.33	109,109,109,109	0
84	MG	25S	3691	1/1	0.35	0.32	117,117,117,117	0
84	MG	18S	1907	1/1	0.37	0.29	124,124,124,124	0
84	MG	18S	1873	1/1	0.41	0.31	116,116,116,116	0
84	MG	18S	1889	1/1	0.41	0.43	115,115,115,115	0
84	MG	25S	3635	1/1	0.43	0.18	140,140,140,140	0
84	MG	25S	3717	1/1	0.44	0.23	117,117,117,117	0
84	MG	eEF2	904	1/1	0.45	0.23	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
84	MG	25S	3732	1/1	0.47	0.30	132,132,132,132	0
84	MG	25S	3674	1/1	0.48	0.63	102,102,102,102	0
84	MG	25S	3489	1/1	0.48	0.27	120,120,120,120	0
84	MG	18S	1903	1/1	0.48	0.20	109,109,109,109	0
84	MG	25S	3545	1/1	0.49	0.29	111,111,111,111	0
84	MG	25S	3720	1/1	0.50	0.28	127,127,127,127	0
84	MG	25S	3726	1/1	0.52	0.27	121,121,121,121	0
84	MG	25S	3645	1/1	0.52	0.40	121,121,121,121	0
84	MG	AB	210	1/1	0.52	0.16	107,107,107,107	0
84	MG	25S	3718	1/1	0.53	0.23	102,102,102,102	0
84	MG	25S	3618[B]	1/1	0.53	0.35	89,89,89,89	1
84	MG	25S	3617	1/1	0.53	0.35	111,111,111,111	0
84	MG	25S	3618[A]	1/1	0.53	0.35	85,85,85,85	1
84	MG	18S	1868	1/1	0.53	0.11	97,97,97,97	0
84	MG	18S	1869	1/1	0.53	0.39	108,108,108,108	0
84	MG	25S	3679	1/1	0.55	0.31	108,108,108,108	0
84	MG	18S	1879	1/1	0.56	0.35	113,113,113,113	0
84	MG	uS4	201	1/1	0.56	0.28	117,117,117,117	0
84	MG	18S	1817	1/1	0.56	0.37	104,104,104,104	0
84	MG	18S	1891	1/1	0.59	0.18	136,136,136,136	0
84	MG	58S	409	1/1	0.59	0.13	121,121,121,121	0
84	MG	25S	3723	1/1	0.59	0.24	111,111,111,111	0
84	MG	25S	3700	1/1	0.59	0.39	105,105,105,105	0
84	MG	18S	1823	1/1	0.59	0.38	96,96,96,96	0
84	MG	18S	1865	1/1	0.59	0.20	100,100,100,100	0
84	MG	25S	3716	1/1	0.60	0.21	109,109,109,109	0
84	MG	25S	3658	1/1	0.60	0.24	101,101,101,101	0
84	MG	18S	1860	1/1	0.60	0.36	100,100,100,100	0
84	MG	25S	3659	1/1	0.61	0.32	115,115,115,115	0
84	MG	18S	1906	1/1	0.61	0.25	127,127,127,127	0
84	MG	25S	3580	1/1	0.61	0.32	106,106,106,106	0
84	MG	18S	1837	1/1	0.61	0.19	129,129,129,129	0
84	MG	18S	1808	1/1	0.61	0.41	90,90,90,90	0
84	MG	18S	1893	1/1	0.62	0.28	120,120,120,120	0
84	MG	25S	3719	1/1	0.62	0.34	113,113,113,113	0
84	MG	18S	1832[A]	1/1	0.62	0.26	100,100,100,100	1
84	MG	18S	1832[B]	1/1	0.62	0.26	103,103,103,103	1
84	MG	25S	3648	1/1	0.62	0.20	86,86,86,86	0
84	MG	25S	3639	1/1	0.62	0.24	107,107,107,107	0
84	MG	25S	3710	1/1	0.62	0.32	111,111,111,111	0
84	MG	25S	3672	1/1	0.63	0.32	111,111,111,111	0
84	MG	58S	404	1/1	0.63	0.13	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3500	1/1	0.63	0.30	110,110,110,110	0
84	MG	AB	209	1/1	0.64	0.17	109,109,109,109	0
84	MG	25S	3713	1/1	0.64	0.13	91,91,91,91	0
84	MG	25S	3493	1/1	0.64	0.54	86,86,86,86	0
84	MG	25S	3614	1/1	0.64	0.30	119,119,119,119	0
84	MG	25S	3452	1/1	0.65	0.44	96,96,96,96	0
84	MG	25S	3722	1/1	0.66	0.24	107,107,107,107	0
84	MG	25S	3524	1/1	0.66	0.34	96,96,96,96	0
84	MG	25S	3516	1/1	0.66	0.42	111,111,111,111	0
84	MG	25S	3646	1/1	0.66	0.30	92,92,92,92	0
84	MG	25S	3601	1/1	0.67	0.35	118,118,118,118	0
84	MG	25S	3652	1/1	0.67	0.19	111,111,111,111	0
84	MG	25S	3606	1/1	0.67	0.29	111,111,111,111	0
84	MG	25S	3654	1/1	0.68	0.23	110,110,110,110	0
84	MG	18S	1900	1/1	0.68	0.20	117,117,117,117	0
84	MG	25S	3535	1/1	0.68	0.41	99,99,99,99	0
84	MG	25S	3544	1/1	0.68	0.24	88,88,88,88	0
84	MG	25S	3615	1/1	0.68	0.22	93,93,93,93	0
84	MG	25S	3491	1/1	0.68	0.28	93,93,93,93	0
84	MG	25S	3694	1/1	0.68	0.30	115,115,115,115	0
84	MG	AB	204	1/1	0.68	0.21	111,111,111,111	0
84	MG	25S	3485	1/1	0.69	0.26	91,91,91,91	0
84	MG	18S	1902	1/1	0.69	0.08	102,102,102,102	0
84	MG	25S	3729	1/1	0.69	0.26	101,101,101,101	0
84	MG	18S	1806	1/1	0.69	0.40	83,83,83,83	0
84	MG	25S	3730	1/1	0.69	0.23	107,107,107,107	0
84	MG	25S	3552	1/1	0.69	0.34	92,92,92,92	0
84	MG	25S	3560	1/1	0.69	0.27	100,100,100,100	0
84	MG	18S	1894	1/1	0.69	0.23	115,115,115,115	0
84	MG	18S	1834[B]	1/1	0.70	0.21	108,108,108,108	1
84	MG	25S	3519	1/1	0.70	0.30	112,112,112,112	0
84	MG	25S	3444	1/1	0.70	0.35	93,93,93,93	0
84	MG	18S	1834[A]	1/1	0.70	0.21	102,102,102,102	1
84	MG	25S	3687	1/1	0.71	0.26	96,96,96,96	0
84	MG	25S	3616	1/1	0.71	0.42	112,112,112,112	0
84	MG	25S	3463	1/1	0.71	0.41	84,84,84,84	0
84	MG	25S	3641	1/1	0.71	0.52	98,98,98,98	0
84	MG	25S	3401	1/1	0.71	0.44	67,67,67,67	0
84	MG	25S	3424	1/1	0.71	0.42	92,92,92,92	0
84	MG	18S	1890	1/1	0.71	0.19	121,121,121,121	0
84	MG	uS5	301	1/1	0.71	0.17	109,109,109,109	0
84	MG	25S	3686	1/1	0.71	0.61	109,109,109,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
84	MG	18S	1815	1/1	0.71	0.27	97,97,97,97	0
84	MG	25S	3585	1/1	0.72	0.18	98,98,98,98	0
84	MG	25S	3640	1/1	0.72	0.40	98,98,98,98	0
84	MG	25S	3543	1/1	0.72	0.40	107,107,107,107	0
84	MG	eS6	301	1/1	0.72	0.23	110,110,110,110	0
84	MG	25S	3703	1/1	0.72	0.15	116,116,116,116	0
84	MG	eEF2	901	1/1	0.72	0.26	105,105,105,105	0
84	MG	18S	1875	1/1	0.72	0.16	117,117,117,117	0
84	MG	25S	3449	1/1	0.73	0.13	76,76,76,76	0
84	MG	25S	3430	1/1	0.73	0.31	96,96,96,96	0
84	MG	25S	3413	1/1	0.73	0.31	74,74,74,74	0
84	MG	18S	1882	1/1	0.73	0.32	114,114,114,114	0
84	MG	25S	3702	1/1	0.73	0.16	113,113,113,113	0
84	MG	25S	3490	1/1	0.74	0.28	110,110,110,110	0
84	MG	25S	3515	1/1	0.74	0.41	91,91,91,91	0
84	MG	18S	1822	1/1	0.74	0.15	96,96,96,96	0
84	MG	18S	1887	1/1	0.74	0.27	101,101,101,101	0
84	MG	18S	1861	1/1	0.74	0.13	96,96,96,96	0
84	MG	25S	3422	1/1	0.74	0.32	84,84,84,84	0
84	MG	25S	3542	1/1	0.74	0.24	73,73,73,73	0
84	MG	25S	3599	1/1	0.74	0.23	105,105,105,105	0
84	MG	18S	1871	1/1	0.74	0.20	113,113,113,113	0
84	MG	25S	3554	1/1	0.74	0.23	102,102,102,102	0
84	MG	18S	1854	1/1	0.75	0.46	100,100,100,100	0
84	MG	18S	1805	1/1	0.75	0.30	73,73,73,73	0
84	MG	25S	3534	1/1	0.75	0.22	92,92,92,92	0
84	MG	25S	3503	1/1	0.75	0.20	100,100,100,100	0
84	MG	25S	3692	1/1	0.75	0.35	102,102,102,102	0
84	MG	25S	3706	1/1	0.75	0.23	97,97,97,97	0
84	MG	25S	3676	1/1	0.75	0.28	96,96,96,96	0
84	MG	25S	3705	1/1	0.76	0.25	113,113,113,113	0
84	MG	25S	3541	1/1	0.76	0.32	110,110,110,110	0
84	MG	18S	1870	1/1	0.76	0.16	86,86,86,86	0
84	MG	18S	1821	1/1	0.76	0.23	108,108,108,108	0
84	MG	25S	3634	1/1	0.76	0.22	122,122,122,122	0
84	MG	58S	401	1/1	0.76	0.29	102,102,102,102	0
84	MG	18S	1895	1/1	0.76	0.21	111,111,111,111	0
84	MG	25S	3575	1/1	0.76	0.29	106,106,106,106	0
84	MG	25S	3540	1/1	0.76	0.23	81,81,81,81	0
84	MG	25S	3480	1/1	0.77	0.28	81,81,81,81	0
84	MG	18S	1836	1/1	0.77	0.29	91,91,91,91	0
84	MG	25S	3711	1/1	0.77	0.16	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	18S	1852	1/1	0.77	0.41	104,104,104,104	0
84	MG	18S	1880	1/1	0.77	0.30	101,101,101,101	0
84	MG	25S	3655	1/1	0.77	0.31	98,98,98,98	0
84	MG	25S	3513	1/1	0.77	0.34	104,104,104,104	0
84	MG	25S	3613	1/1	0.77	0.19	98,98,98,98	0
84	MG	25S	3502	1/1	0.77	0.27	77,77,77,77	0
84	MG	AB	202	1/1	0.77	0.29	109,109,109,109	0
84	MG	25S	3441	1/1	0.77	0.32	77,77,77,77	0
84	MG	eEF2	902	1/1	0.77	0.24	84,84,84,84	0
84	MG	eEF2	903	1/1	0.77	0.44	113,113,113,113	0
84	MG	25S	3563	1/1	0.77	0.18	100,100,100,100	0
84	MG	25S	3633	1/1	0.78	0.31	108,108,108,108	0
84	MG	18S	1892	1/1	0.78	0.19	104,104,104,104	0
84	MG	25S	3474	1/1	0.78	0.25	77,77,77,77	0
84	MG	18S	1863	1/1	0.78	0.25	79,79,79,79	0
84	MG	25S	3688	1/1	0.78	0.29	101,101,101,101	0
84	MG	AB	208	1/1	0.78	0.27	91,91,91,91	0
84	MG	25S	3458	1/1	0.78	0.32	82,82,82,82	0
84	MG	25S	3418	1/1	0.78	0.32	62,62,62,62	0
84	MG	25S	3731	1/1	0.78	0.16	92,92,92,92	0
84	MG	25S	3567	1/1	0.79	0.30	112,112,112,112	0
84	MG	18S	1843	1/1	0.79	0.25	110,110,110,110	0
84	MG	25S	3461	1/1	0.79	0.34	87,87,87,87	0
84	MG	25S	3557	1/1	0.79	0.26	82,82,82,82	0
84	MG	18S	1857	1/1	0.79	0.23	85,85,85,85	0
84	MG	25S	3667	1/1	0.79	0.22	91,91,91,91	0
84	MG	25S	3620	1/1	0.79	0.17	102,102,102,102	0
84	MG	18S	1828	1/1	0.79	0.25	101,101,101,101	0
84	MG	25S	3627	1/1	0.79	0.35	108,108,108,108	0
84	MG	25S	3632	1/1	0.79	0.20	105,105,105,105	0
84	MG	25S	3448	1/1	0.79	0.23	72,72,72,72	0
84	MG	25S	3433	1/1	0.79	0.39	70,70,70,70	0
84	MG	25S	3565	1/1	0.79	0.39	85,85,85,85	0
84	MG	25S	3517	1/1	0.80	0.18	88,88,88,88	0
84	MG	18S	1847	1/1	0.80	0.29	125,125,125,125	0
84	MG	25S	3409	1/1	0.80	0.36	82,82,82,82	0
84	MG	25S	3709	1/1	0.80	0.32	112,112,112,112	0
84	MG	25S	3682	1/1	0.80	0.18	102,102,102,102	0
84	MG	25S	3443	1/1	0.80	0.25	96,96,96,96	0
84	MG	25S	3473	1/1	0.80	0.52	94,94,94,94	0
84	MG	25S	3439	1/1	0.80	0.30	82,82,82,82	0
84	MG	25S	3574	1/1	0.80	0.23	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3514	1/1	0.80	0.44	91,91,91,91	0
84	MG	25S	3475	1/1	0.80	0.29	86,86,86,86	0
84	MG	58S	403	1/1	0.80	0.32	100,100,100,100	0
84	MG	25S	3670	1/1	0.80	0.25	90,90,90,90	0
84	MG	25S	3644	1/1	0.80	0.40	82,82,82,82	0
84	MG	25S	3447	1/1	0.80	0.34	80,80,80,80	0
84	MG	18S	1835	1/1	0.80	0.17	100,100,100,100	0
84	MG	25S	3536	1/1	0.80	0.24	66,66,66,66	0
84	MG	uL22	201	1/1	0.80	0.31	76,76,76,76	0
84	MG	18S	1883	1/1	0.80	0.26	87,87,87,87	0
84	MG	18S	1838	1/1	0.80	0.41	89,89,89,89	0
84	MG	18S	1804	1/1	0.81	0.38	85,85,85,85	0
84	MG	25S	3584	1/1	0.81	0.28	93,93,93,93	0
84	MG	25S	3708	1/1	0.81	0.18	94,94,94,94	0
84	MG	25S	3497	1/1	0.81	0.48	92,92,92,92	0
84	MG	25S	3421	1/1	0.81	0.31	79,79,79,79	0
84	MG	25S	3561	1/1	0.81	0.36	106,106,106,106	0
84	MG	18S	1862	1/1	0.81	0.18	102,102,102,102	0
84	MG	AB	207	1/1	0.81	0.32	102,102,102,102	0
84	MG	25S	3656	1/1	0.81	0.26	103,103,103,103	0
84	MG	25S	3715	1/1	0.81	0.26	102,102,102,102	0
84	MG	25S	3488	1/1	0.81	0.34	88,88,88,88	0
84	MG	18S	1905	1/1	0.81	0.26	93,93,93,93	0
84	MG	25S	3410	1/1	0.81	0.34	71,71,71,71	0
84	MG	25S	3505	1/1	0.81	0.41	96,96,96,96	0
84	MG	25S	3407	1/1	0.81	0.50	83,83,83,83	0
84	MG	25S	3403	1/1	0.81	0.30	72,72,72,72	0
84	MG	25S	3671	1/1	0.81	0.24	104,104,104,104	0
84	MG	uS12	201	1/1	0.81	0.15	92,92,92,92	0
84	MG	25S	3481	1/1	0.81	0.24	76,76,76,76	0
84	MG	uL13	202	1/1	0.81	0.16	112,112,112,112	0
84	MG	25S	3495	1/1	0.81	0.35	87,87,87,87	0
84	MG	25S	3583	1/1	0.81	0.58	99,99,99,99	0
84	MG	25S	3665	1/1	0.82	0.23	67,67,67,67	0
84	MG	25S	3693	1/1	0.82	0.43	106,106,106,106	0
84	MG	58S	408	1/1	0.82	0.18	101,101,101,101	0
84	MG	25S	3721	1/1	0.82	0.24	110,110,110,110	0
84	MG	18S	1839	1/1	0.82	0.23	94,94,94,94	0
84	MG	25S	3415	1/1	0.82	0.29	80,80,80,80	0
84	MG	18S	1845	1/1	0.82	0.26	90,90,90,90	0
84	MG	25S	3435	1/1	0.82	0.33	95,95,95,95	0
84	MG	18S	1851	1/1	0.82	0.20	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3701	1/1	0.82	0.15	88,88,88,88	0
84	MG	25S	3504	1/1	0.82	0.25	95,95,95,95	0
84	MG	25S	3494	1/1	0.82	0.15	88,88,88,88	0
84	MG	25S	3590	1/1	0.82	0.18	82,82,82,82	0
84	MG	25S	3647	1/1	0.82	0.26	93,93,93,93	0
84	MG	AB	201	1/1	0.82	0.21	101,101,101,101	0
84	MG	25S	3569	1/1	0.82	0.21	68,68,68,68	0
84	MG	25S	3455	1/1	0.82	0.44	74,74,74,74	0
84	MG	25S	3631	1/1	0.82	0.25	96,96,96,96	0
84	MG	25S	3685	1/1	0.82	0.15	87,87,87,87	0
84	MG	18S	1825	1/1	0.82	0.22	97,97,97,97	0
84	MG	25S	3604	1/1	0.82	0.35	82,82,82,82	0
84	MG	25S	3425	1/1	0.82	0.26	71,71,71,71	0
84	MG	25S	3610	1/1	0.82	0.24	111,111,111,111	0
84	MG	25S	3408	1/1	0.82	0.30	76,76,76,76	0
84	MG	25S	3576	1/1	0.82	0.27	94,94,94,94	0
84	MG	PSIT	101	1/1	0.82	0.26	94,94,94,94	0
84	MG	25S	3603	1/1	0.83	0.24	87,87,87,87	0
84	MG	25S	3509	1/1	0.83	0.25	92,92,92,92	0
84	MG	25S	3468	1/1	0.83	0.24	107,107,107,107	0
84	MG	25S	3546	1/1	0.83	0.16	75,75,75,75	0
84	MG	18S	1810	1/1	0.83	0.19	85,85,85,85	0
84	MG	25S	3683	1/1	0.83	0.27	109,109,109,109	0
84	MG	25S	3469	1/1	0.83	0.23	76,76,76,76	0
84	MG	25S	3472	1/1	0.83	0.21	96,96,96,96	0
84	MG	18S	1848	1/1	0.83	0.21	89,89,89,89	0
84	MG	25S	3440	1/1	0.83	0.24	85,85,85,85	0
84	MG	25S	3486	1/1	0.83	0.44	88,88,88,88	0
84	MG	18S	1884	1/1	0.83	0.13	109,109,109,109	0
84	MG	25S	3420	1/1	0.83	0.38	70,70,70,70	0
84	MG	25S	3518	1/1	0.83	0.22	80,80,80,80	0
84	MG	25S	3564	1/1	0.83	0.51	103,103,103,103	0
84	MG	25S	3507	1/1	0.83	0.32	95,95,95,95	0
84	MG	eL19	201	1/1	0.83	0.29	101,101,101,101	0
84	MG	25S	3508	1/1	0.83	0.30	99,99,99,99	0
84	MG	25S	3465	1/1	0.84	0.29	102,102,102,102	0
84	MG	25S	3588	1/1	0.84	0.16	93,93,93,93	0
84	MG	25S	3498	1/1	0.84	0.14	87,87,87,87	0
84	MG	25S	3649	1/1	0.84	0.41	93,93,93,93	0
84	MG	18S	1901	1/1	0.84	0.14	104,104,104,104	0
84	MG	25S	3651	1/1	0.84	0.22	92,92,92,92	0
84	MG	18S	1811	1/1	0.84	0.35	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
84	MG	18S	1840	1/1	0.84	0.48	97,97,97,97	0
84	MG	25S	3593	1/1	0.84	0.29	82,82,82,82	0
84	MG	18S	1877	1/1	0.84	0.22	102,102,102,102	0
84	MG	25S	3626	1/1	0.84	0.19	99,99,99,99	0
84	MG	25S	3581	1/1	0.84	0.14	71,71,71,71	0
84	MG	25S	3707	1/1	0.84	0.24	91,91,91,91	0
84	MG	AB	205	1/1	0.84	0.22	99,99,99,99	0
84	MG	AB	206	1/1	0.84	0.16	109,109,109,109	0
84	MG	25S	3547	1/1	0.84	0.13	79,79,79,79	0
84	MG	18S	1829	1/1	0.84	0.26	105,105,105,105	0
84	MG	25S	3450	1/1	0.84	0.34	77,77,77,77	0
84	MG	eL39	101	1/1	0.84	0.10	106,106,106,106	0
84	MG	eL41	101	1/1	0.84	0.44	92,92,92,92	0
84	MG	25S	3451	1/1	0.85	0.25	72,72,72,72	0
84	MG	eL42	201	1/1	0.85	0.31	112,112,112,112	0
84	MG	18S	1896	1/1	0.85	0.15	112,112,112,112	0
84	MG	25S	3684	1/1	0.85	0.20	79,79,79,79	0
84	MG	25S	3428	1/1	0.85	0.41	84,84,84,84	0
84	MG	25S	3608	1/1	0.85	0.20	107,107,107,107	0
84	MG	25S	3496	1/1	0.85	0.40	89,89,89,89	0
84	MG	25S	3724	1/1	0.85	0.14	76,76,76,76	0
84	MG	25S	3612	1/1	0.85	0.28	118,118,118,118	0
84	MG	25S	3586	1/1	0.85	0.25	101,101,101,101	0
84	MG	25S	3675	1/1	0.85	0.27	87,87,87,87	0
84	MG	25S	3636	1/1	0.85	0.19	88,88,88,88	0
84	MG	25S	3549	1/1	0.85	0.21	105,105,105,105	0
84	MG	uL16	301	1/1	0.85	0.25	85,85,85,85	0
84	MG	25S	3680	1/1	0.85	0.14	91,91,91,91	0
84	MG	25S	3695	1/1	0.85	0.27	100,100,100,100	0
84	MG	25S	3697	1/1	0.85	0.11	77,77,77,77	0
84	MG	25S	3698	1/1	0.85	0.26	74,74,74,74	0
84	MG	eL30	202	1/1	0.85	0.12	97,97,97,97	0
84	MG	25S	3650	1/1	0.85	0.35	103,103,103,103	0
84	MG	25S	3728	1/1	0.86	0.15	81,81,81,81	0
84	MG	18S	1898	1/1	0.86	0.10	103,103,103,103	0
84	MG	25S	3437	1/1	0.86	0.34	78,78,78,78	0
84	MG	18S	1827	1/1	0.86	0.23	94,94,94,94	0
84	MG	58S	402	1/1	0.86	0.15	106,106,106,106	0
84	MG	25S	3462	1/1	0.86	0.24	69,69,69,69	0
84	MG	25S	3417	1/1	0.86	0.33	65,65,65,65	0
84	MG	25S	3555	1/1	0.86	0.20	68,68,68,68	0
84	MG	18S	1856	1/1	0.86	0.23	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3582	1/1	0.86	0.32	91,91,91,91	0
84	MG	18S	1858	1/1	0.86	0.15	99,99,99,99	0
84	MG	25S	3663	1/1	0.86	0.18	92,92,92,92	0
84	MG	25S	3511	1/1	0.86	0.36	96,96,96,96	0
84	MG	25S	3522	1/1	0.86	0.15	90,90,90,90	0
84	MG	eS26	201	1/1	0.86	0.43	107,107,107,107	0
84	MG	25S	3668	1/1	0.86	0.16	64,64,64,64	0
84	MG	25S	3642	1/1	0.86	0.22	73,73,73,73	0
84	MG	18S	1867	1/1	0.86	0.27	90,90,90,90	0
84	MG	25S	3512	1/1	0.86	0.12	70,70,70,70	0
84	MG	25S	3712	1/1	0.86	0.35	91,91,91,91	0
84	MG	25S	3550	1/1	0.87	0.21	80,80,80,80	0
84	MG	25S	3579	1/1	0.87	0.34	101,101,101,101	0
84	MG	18S	1859	1/1	0.87	0.16	94,94,94,94	0
84	MG	25S	3681	1/1	0.87	0.17	88,88,88,88	0
84	MG	18S	1824	1/1	0.87	0.12	108,108,108,108	0
84	MG	25S	3484	1/1	0.87	0.34	97,97,97,97	0
84	MG	18S	1841	1/1	0.87	0.21	87,87,87,87	0
84	MG	25S	3657	1/1	0.87	0.18	72,72,72,72	0
84	MG	25S	3467	1/1	0.87	0.25	75,75,75,75	0
84	MG	25S	3630	1/1	0.87	0.10	88,88,88,88	0
84	MG	25S	3457	1/1	0.87	0.25	72,72,72,72	0
84	MG	18S	1849	1/1	0.87	0.14	94,94,94,94	0
84	MG	25S	3699	1/1	0.87	0.34	84,84,84,84	0
84	MG	25S	3419	1/1	0.87	0.30	68,68,68,68	0
84	MG	18S	1897	1/1	0.87	0.17	112,112,112,112	0
84	MG	25S	3598	1/1	0.87	0.20	71,71,71,71	0
84	MG	25S	3689	1/1	0.87	0.20	97,97,97,97	0
84	MG	PSIT	102	1/1	0.87	0.08	106,106,106,106	0
84	MG	25S	3533	1/1	0.88	0.19	92,92,92,92	0
84	MG	25S	3460	1/1	0.88	0.36	75,75,75,75	0
84	MG	uL2	301	1/1	0.88	0.48	92,92,92,92	0
84	MG	25S	3466	1/1	0.88	0.35	88,88,88,88	0
84	MG	25S	3571	1/1	0.88	0.20	84,84,84,84	0
84	MG	25S	3653	1/1	0.88	0.16	103,103,103,103	0
84	MG	25S	3442	1/1	0.88	0.31	69,69,69,69	0
84	MG	18S	1830	1/1	0.88	0.43	86,86,86,86	0
84	MG	25S	3591	1/1	0.88	0.08	75,75,75,75	0
84	MG	25S	3553	1/1	0.88	0.17	104,104,104,104	0
84	MG	25S	3414	1/1	0.88	0.35	67,67,67,67	0
84	MG	25S	3406	1/1	0.88	0.31	70,70,70,70	0
84	MG	25S	3470	1/1	0.88	0.22	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	18S	1802	1/1	0.88	0.25	75,75,75,75	0
84	MG	25S	3528	1/1	0.88	0.25	81,81,81,81	0
84	MG	25S	3529	1/1	0.88	0.09	80,80,80,80	0
84	MG	25S	3664	1/1	0.88	0.09	86,86,86,86	0
84	MG	18S	1874	1/1	0.88	0.17	102,102,102,102	0
84	MG	25S	3530	1/1	0.88	0.36	88,88,88,88	0
84	MG	18S	1809	1/1	0.88	0.53	79,79,79,79	0
84	MG	25S	3704	1/1	0.88	0.32	96,96,96,96	0
84	MG	25S	3666	1/1	0.88	0.28	62,62,62,62	0
84	MG	18S	1846	1/1	0.88	0.19	77,77,77,77	0
84	MG	18S	1813	1/1	0.88	0.34	69,69,69,69	0
84	MG	25S	3725	1/1	0.88	0.17	90,90,90,90	0
84	MG	25S	3532	1/1	0.88	0.28	97,97,97,97	0
84	MG	18S	1888	1/1	0.88	0.32	93,93,93,93	0
84	MG	25S	3727	1/1	0.88	0.14	90,90,90,90	0
84	MG	eL32	202	1/1	0.89	0.14	83,83,83,83	0
84	MG	25S	3416	1/1	0.89	0.31	69,69,69,69	0
84	MG	25S	3487	1/1	0.89	0.41	87,87,87,87	0
84	MG	18S	1826	1/1	0.89	0.31	87,87,87,87	0
84	MG	25S	3589	1/1	0.89	0.22	74,74,74,74	0
84	MG	58S	405	1/1	0.89	0.20	96,96,96,96	0
84	MG	25S	3506	1/1	0.89	0.17	95,95,95,95	0
84	MG	25S	3527	1/1	0.89	0.28	64,64,64,64	0
84	MG	18S	1831	1/1	0.89	0.23	99,99,99,99	0
84	MG	AB	203	1/1	0.89	0.26	86,86,86,86	0
84	MG	18S	1807	1/1	0.89	0.32	84,84,84,84	0
84	MG	25S	3456	1/1	0.89	0.16	77,77,77,77	0
84	MG	25S	3597	1/1	0.89	0.08	109,109,109,109	0
84	MG	25S	3538	1/1	0.89	0.10	81,81,81,81	0
84	MG	25S	3412	1/1	0.89	0.52	79,79,79,79	0
84	MG	25S	3479	1/1	0.89	0.44	87,87,87,87	0
84	MG	25S	3531[A]	1/1	0.89	0.20	66,66,66,66	1
84	MG	25S	3531[B]	1/1	0.89	0.20	66,66,66,66	1
84	MG	25S	3605	1/1	0.89	0.13	126,126,126,126	0
84	MG	eL32	201	1/1	0.89	0.10	88,88,88,88	0
84	MG	18S	1842	1/1	0.89	0.43	92,92,92,92	0
84	MG	uL16	302	1/1	0.90	0.14	75,75,75,75	0
84	MG	uL13	201	1/1	0.90	0.32	105,105,105,105	0
84	MG	25S	3637	1/1	0.90	0.10	81,81,81,81	0
84	MG	18S	1866	1/1	0.90	0.41	98,98,98,98	0
84	MG	25S	3471	1/1	0.90	0.29	79,79,79,79	0
84	MG	18S	1816	1/1	0.90	0.49	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
84	MG	25S	3445	1/1	0.90	0.16	70,70,70,70	0
84	MG	18S	1899	1/1	0.90	0.07	97,97,97,97	0
84	MG	25S	3621	1/1	0.90	0.22	80,80,80,80	0
84	MG	uL14	201	1/1	0.90	0.26	66,66,66,66	0
84	MG	25S	3623	1/1	0.90	0.22	101,101,101,101	0
84	MG	25S	3643	1/1	0.90	0.20	65,65,65,65	0
84	MG	25S	3677	1/1	0.90	0.11	91,91,91,91	0
84	MG	18S	1876	1/1	0.90	0.21	85,85,85,85	0
84	MG	eL37	101	1/1	0.90	0.21	85,85,85,85	0
84	MG	25S	3609	1/1	0.90	0.21	70,70,70,70	0
84	MG	25S	3594	1/1	0.90	0.08	79,79,79,79	0
84	MG	18S	1881	1/1	0.90	0.20	90,90,90,90	0
84	MG	25S	3454	1/1	0.90	0.32	73,73,73,73	0
84	MG	25S	3537	1/1	0.90	0.27	96,96,96,96	0
84	MG	25S	3523	1/1	0.90	0.16	112,112,112,112	0
84	MG	18S	1886	1/1	0.90	0.14	88,88,88,88	0
84	MG	25S	3436	1/1	0.90	0.41	74,74,74,74	0
84	MG	25S	3402	1/1	0.90	0.30	65,65,65,65	0
84	MG	25S	3551	1/1	0.90	0.28	74,74,74,74	0
84	MG	uL3	401	1/1	0.90	0.15	62,62,62,62	0
84	MG	25S	3476	1/1	0.90	0.23	80,80,80,80	0
84	MG	18S	1885	1/1	0.91	0.16	92,92,92,92	0
84	MG	25S	3629	1/1	0.91	0.17	101,101,101,101	0
84	MG	25S	3427	1/1	0.91	0.35	73,73,73,73	0
84	MG	25S	3602	1/1	0.91	0.09	81,81,81,81	0
84	MG	25S	3559	1/1	0.91	0.20	67,67,67,67	0
84	MG	25S	3570	1/1	0.91	0.21	58,58,58,58	0
84	MG	18S	1818	1/1	0.91	0.24	93,93,93,93	0
84	MG	25S	3661	1/1	0.91	0.20	81,81,81,81	0
84	MG	25S	3423	1/1	0.91	0.21	86,86,86,86	0
84	MG	25S	3539	1/1	0.91	0.09	95,95,95,95	0
84	MG	uS12	203	1/1	0.91	0.16	80,80,80,80	0
84	MG	25S	3429	1/1	0.91	0.19	77,77,77,77	0
84	MG	25S	3595	1/1	0.91	0.09	93,93,93,93	0
84	MG	25S	3622	1/1	0.91	0.14	82,82,82,82	0
84	MG	25S	3426	1/1	0.91	0.58	76,76,76,76	0
84	MG	25S	3714	1/1	0.91	0.18	91,91,91,91	0
84	MG	25S	3521	1/1	0.91	0.15	80,80,80,80	0
84	MG	25S	3587	1/1	0.91	0.11	95,95,95,95	0
84	MG	25S	3477	1/1	0.92	0.18	79,79,79,79	0
84	MG	18S	1872	1/1	0.92	0.14	105,105,105,105	0
84	MG	25S	3638	1/1	0.92	0.22	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3556	1/1	0.92	0.16	77,77,77,77	0
84	MG	25S	3432	1/1	0.92	0.22	83,83,83,83	0
84	MG	25S	3625	1/1	0.92	0.12	100,100,100,100	0
84	MG	18S	1820	1/1	0.92	0.23	91,91,91,91	0
84	MG	25S	3577	1/1	0.92	0.18	95,95,95,95	0
84	MG	25S	3578	1/1	0.92	0.16	67,67,67,67	0
84	MG	25S	3562	1/1	0.92	0.21	93,93,93,93	0
84	MG	18S	1801	1/1	0.92	0.18	76,76,76,76	0
84	MG	18S	1844	1/1	0.92	0.12	95,95,95,95	0
84	MG	25S	3596	1/1	0.93	0.23	105,105,105,105	0
84	MG	25S	3678	1/1	0.93	0.11	92,92,92,92	0
84	MG	25S	3446	1/1	0.93	0.22	80,80,80,80	0
84	MG	18S	1819	1/1	0.93	0.28	73,73,73,73	0
84	MG	25S	3624	1/1	0.93	0.38	103,103,103,103	0
84	MG	25S	3453	1/1	0.93	0.37	86,86,86,86	0
84	MG	18S	1803	1/1	0.93	0.20	75,75,75,75	0
84	MG	25S	3696	1/1	0.93	0.16	115,115,115,115	0
84	MG	18S	1864	1/1	0.93	0.09	116,116,116,116	0
84	MG	25S	3548	1/1	0.93	0.13	96,96,96,96	0
84	MG	25S	3600	1/1	0.93	0.16	74,74,74,74	0
84	MG	25S	3566	1/1	0.93	0.27	85,85,85,85	0
84	MG	25S	3499	1/1	0.93	0.34	87,87,87,87	0
84	MG	uS12	202	1/1	0.93	0.10	90,90,90,90	0
84	MG	25S	3558	1/1	0.93	0.39	89,89,89,89	0
84	MG	25S	3438	1/1	0.93	0.38	72,72,72,72	0
84	MG	25S	3464	1/1	0.93	0.22	80,80,80,80	0
84	MG	18S	1812	1/1	0.93	0.17	70,70,70,70	0
84	MG	25S	3411	1/1	0.93	0.21	73,73,73,73	0
84	MG	18S	1814	1/1	0.93	0.16	85,85,85,85	0
84	MG	18S	1853	1/1	0.93	0.12	77,77,77,77	0
84	MG	25S	3482	1/1	0.93	0.25	84,84,84,84	0
86	GTP	eEF2	905	32/32	0.93	0.10	83,95,105,109	0
84	MG	25S	3573	1/1	0.94	0.13	75,75,75,75	0
84	MG	25S	3611	1/1	0.94	0.13	92,92,92,92	0
84	MG	uL2	302	1/1	0.94	0.05	54,54,54,54	0
84	MG	25S	3501	1/1	0.94	0.20	83,83,83,83	0
84	MG	eL30	201	1/1	0.94	0.17	89,89,89,89	0
84	MG	25S	3662	1/1	0.94	0.14	89,89,89,89	0
84	MG	25S	3478	1/1	0.94	0.23	79,79,79,79	0
84	MG	18S	1850	1/1	0.94	0.16	79,79,79,79	0
84	MG	25S	3404	1/1	0.94	0.22	62,62,62,62	0
84	MG	25S	3459	1/1	0.94	0.23	62,62,62,62	0

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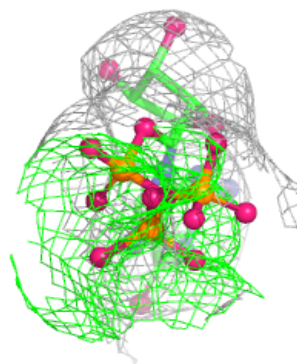
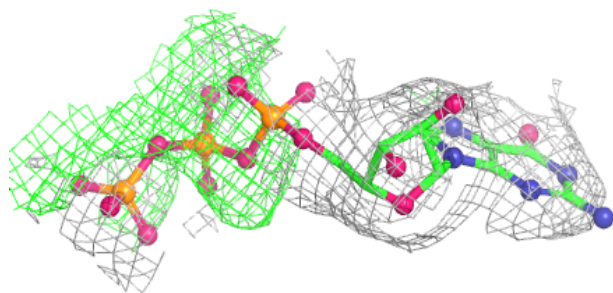
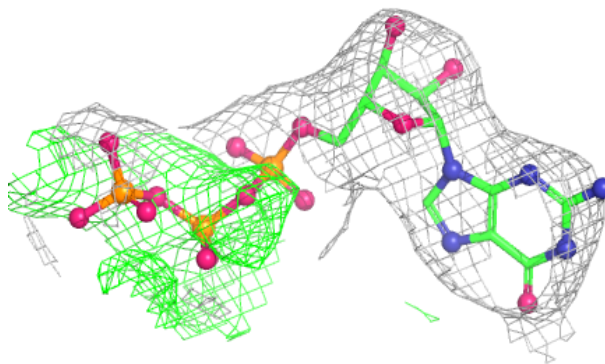
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	18S	1833	1/1	0.94	0.09	110,110,110,110	0
84	MG	25S	3619	1/1	0.95	0.12	85,85,85,85	0
84	MG	25S	3568	1/1	0.95	0.06	73,73,73,73	0
84	MG	18S	1855	1/1	0.95	0.12	93,93,93,93	0
85	ZN	eS31	201	1/1	0.95	0.06	206,206,206,206	0
84	MG	25S	3483	1/1	0.95	0.20	76,76,76,76	0
84	MG	18S	1878	1/1	0.96	0.13	87,87,87,87	0
84	MG	25S	3492	1/1	0.96	0.38	70,70,70,70	0
84	MG	25S	3434	1/1	0.96	0.21	61,61,61,61	0
84	MG	25S	3526	1/1	0.96	0.07	77,77,77,77	0
84	MG	25S	3405	1/1	0.96	0.26	57,57,57,57	0
84	MG	25S	3431	1/1	0.97	0.44	76,76,76,76	0
84	MG	25S	3628	1/1	0.97	0.06	105,105,105,105	0
84	MG	25S	3669	1/1	0.97	0.08	74,74,74,74	0
84	MG	25S	3607	1/1	0.98	0.09	78,78,78,78	0
85	ZN	eL42	202	1/1	0.99	0.03	130,130,130,130	0
85	ZN	uS14	101	1/1	0.99	0.03	114,114,114,114	0
84	MG	25S	3592	1/1	0.99	0.06	74,74,74,74	0
85	ZN	eL34	201	1/1	0.99	0.13	123,123,123,123	0
85	ZN	eS26	202	1/1	1.00	0.02	96,96,96,96	0
85	ZN	eL40	201	1/1	1.00	0.08	105,105,105,105	0
85	ZN	eL37	102	1/1	1.00	0.04	98,98,98,98	0
85	ZN	eL43	101	1/1	1.00	0.04	102,102,102,102	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GTP eEF2 905:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.