



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:02 AM UTC

PDB ID : 7OSM / pdb_00007osm
Title : Intermediate translocation complex of 80 S.cerevisiae ribosome with eEF2 and ligands
Authors : Djumagulov, M.; Jenner, L.; Rozov, A.; Demeshkina, N.; Yusupov, M.; Yusupova, G.
Deposited on : 2021-06-09
Resolution : 3.00 Å(reported)

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

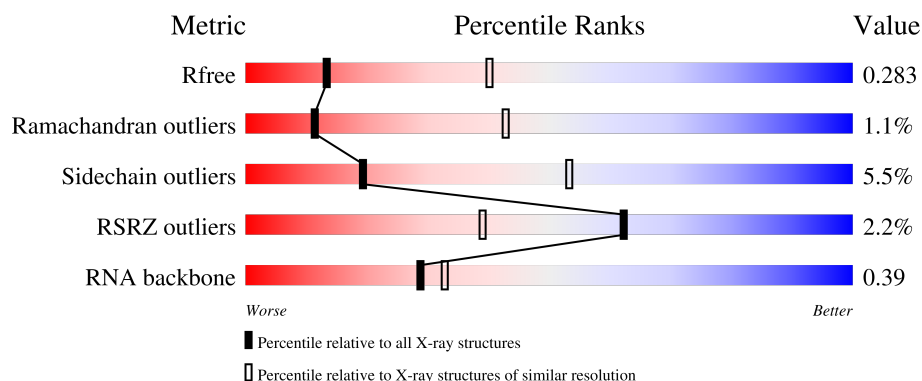
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

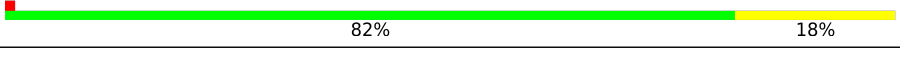
The reported resolution of this entry is 3.00 Å.

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	AB	121	
3	58S	158	
4	uL10	312	

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

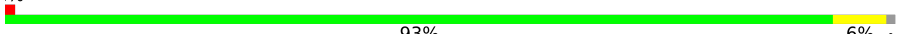
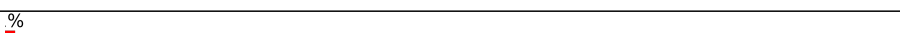
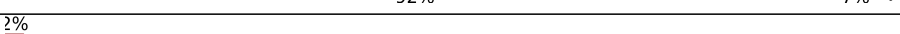
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Mol	Chain	Length	Quality of chain
30	uL15	149	
31	eL29	59	
32	eL30	105	
33	eL31	113	
34	eL32	130	
35	eL33	107	
36	eL34	121	
37	uL29	120	
38	eL36	100	
39	eL37	88	
40	eL38	78	
41	eL39	51	
42	eL40	128	
43	eL41	25	
44	eL42	106	
45	eL43	92	
46	18S	1798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

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Mol	Chain	Length	Quality of chain
55	eS8	200	
56	uS4	197	
57	eS10	105	
58	uS17	156	
59	uS15	151	
60	uS11	137	
61	uS19	142	
62	uS9	143	
63	eS17	136	
64	uS13	146	
65	eS19	144	
66	uS10	121	
67	eS21	87	
68	uS8	130	
69	uS12	145	
70	eS24	135	
71	eS25	108	
72	eS26	119	
73	eS27	82	
74	eS28	67	
75	uS14	56	
76	eS30	63	
77	RACK	319	
78	eS31	152	
79	eEF2	842	

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Mol	Chain	Length	Quality of chain
80	ASIT	76	 61%39%
81	PSIT	77	 3%73%27%
82	mRNA	8	 62%38%
83	uL11	165	 5%82%17%

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	25S	3461[A]	-	-	-	X
84	MG	25S	3461[B]	-	-	-	X
84	MG	eL40	201	-	-	-	X

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	233	Total	C	N	O	S	0	0	0
			1804	1151	323	327	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	213	Total	C	N	O	S	0	0	0
			1732	1096	329	301	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	151	Total	C	N	O		0	0	0
			1195	745	233	217				

- 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	176	Total	C	N	O			
			1423	875	308	240	0	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	eL20	172	Total	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	97	Total	C	N	O			
			770	499	126	145		0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	uL14	129	Total	C	N	O	S		
			963	607	180	169	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	120	Total	C	N	O	S		
			959	617	168	172	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	109	Total	C	N	O	S	0	0	0
			861	533	175	149	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	84	Total	C	N	O	S	0	0	0
			665	405	145	110	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	102	Total	C	N	O	S	0	0	0
			819	514	166	134	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	1732	Total	C	N	O	P	0	0	0
			36918	16504	6551	12131	1732			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	eS1	212	Total	C	N	O	S	0	0	0
			1689	1073	303	309	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	183	Total	C	N	O	S	0	0	0
			1412	893	260	253	6			

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

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

- Molecule 52 is a protein called Rps5p.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 74 is a protein called eS28.

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

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

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

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

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

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

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

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

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

- Molecule 79 is a protein called Elongation factor 2.

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

- Molecule 80 is a RNA chain called PHE tRNA.

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

- Molecule 81 is a RNA chain called FMET tRNA.

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	8	Total	C	N	O	P	0	0	0
			169	76	29	56	8			

- 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
			673	399	137	137			

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

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

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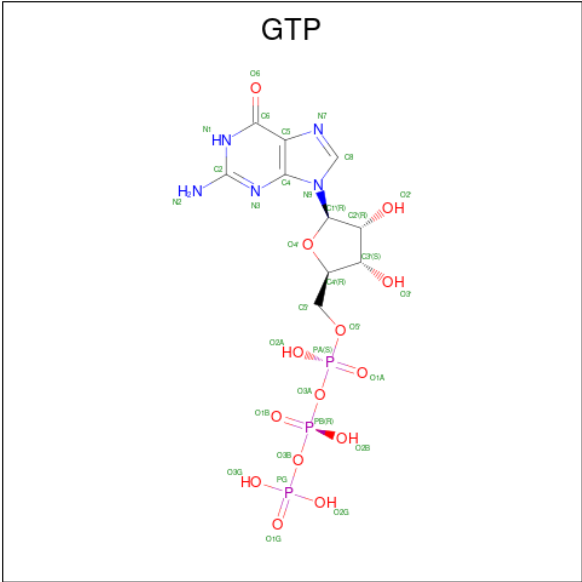
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
84	eS6	2	Total	Mg	0	0
			2	2		
84	uS15	1	Total	Mg	0	0
			1	1		
84	uS19	1	Total	Mg	0	0
			1	1		
84	uS12	3	Total	Mg	0	0
			3	3		
84	eS26	1	Total	Mg	0	0
			1	1		
84	uS14	1	Total	Mg	0	0
			1	1		
84	eEF2	6	Total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

- 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		

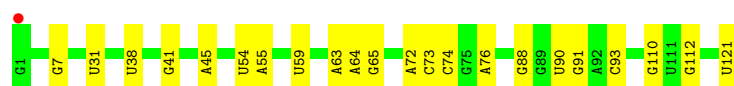
- Molecule 86 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



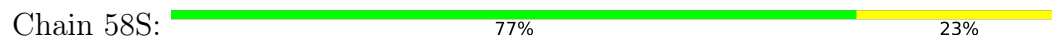
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
86	eEF2	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 2: 5S rRNA

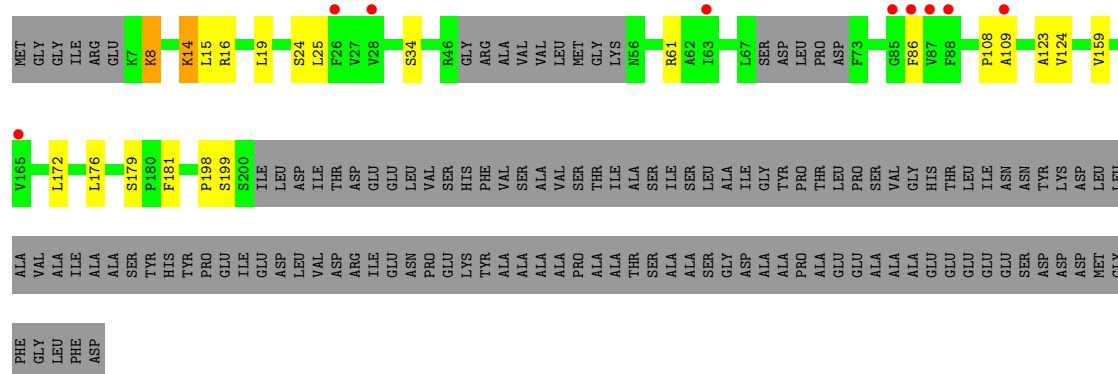




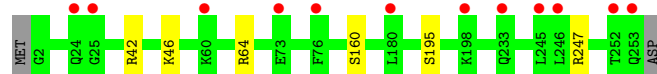
- Molecule 3: 5.8S rRNA



- Molecule 4: 60S acidic ribosomal protein P0



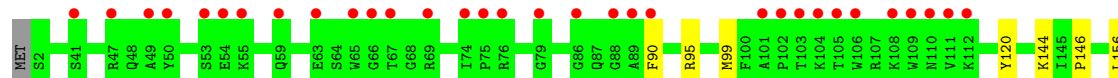
- Molecule 5: 60S ribosomal protein L2-B



- Molecule 6: 60S ribosomal protein L3



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





- Molecule 8: 60S ribosomal protein L5

Chain uL18: 93% 6%



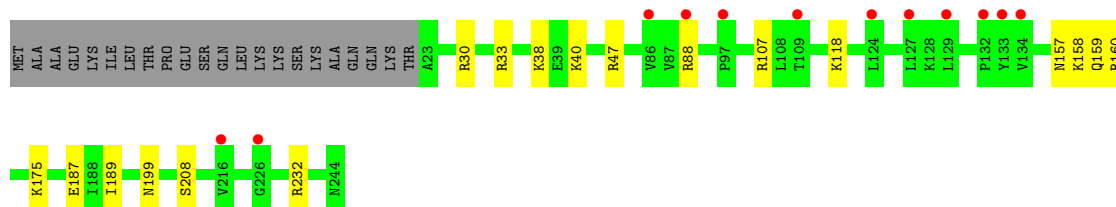
- Molecule 9: 60S ribosomal protein L6

Chain eL6: 8% 82% 6% 11%



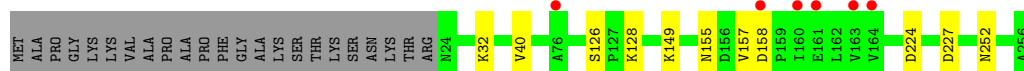
- Molecule 10: 60S ribosomal protein L7-A

Chain uL30: 5% 84% 7% 9%



- Molecule 11: 60S ribosomal protein L8-A

Chain eL8: 2% 87% 9%



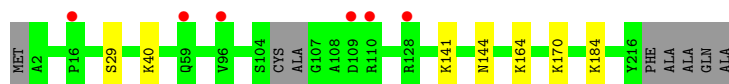
- Molecule 12: 60S ribosomal protein L9-A

Chain uL6: 95% 5%

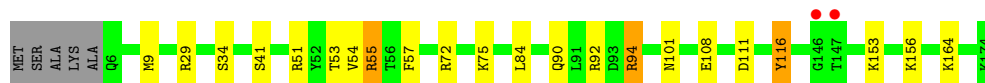
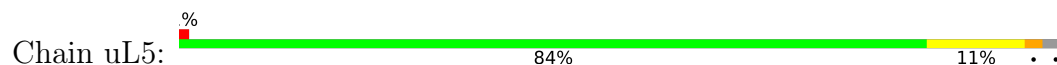


- Molecule 13: 60S ribosomal protein L10

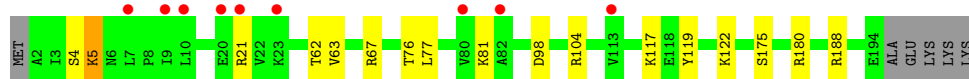
Chain uL16: 3% 93% 4%



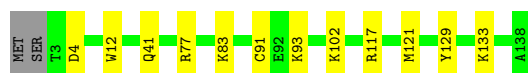
- Molecule 14: BJ4_G0027750.mRNA.1.CDS.1



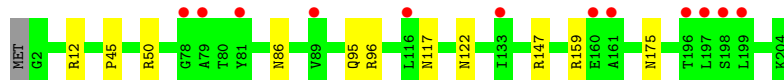
- Molecule 15: 60S ribosomal protein L13



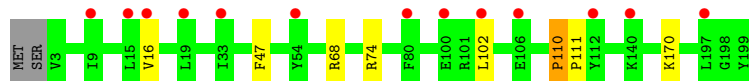
- Molecule 16: 60S ribosomal protein L14-A



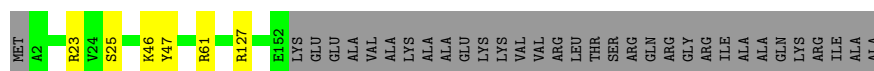
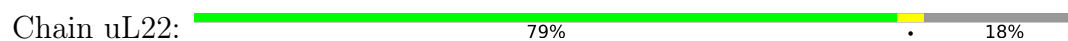
- Molecule 17: 60S ribosomal protein L15-A



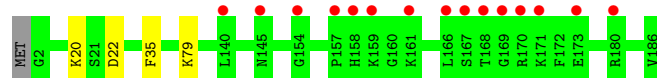
- Molecule 18: 60S ribosomal protein L16-A



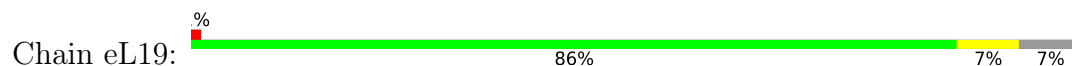
- Molecule 19: BJ4_G0005750.mRNA.1.CDS.1



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



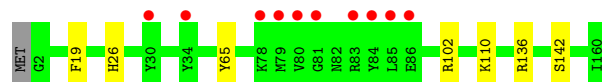
- Molecule 21: 60S ribosomal protein L19-A



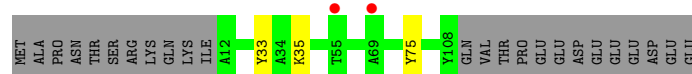
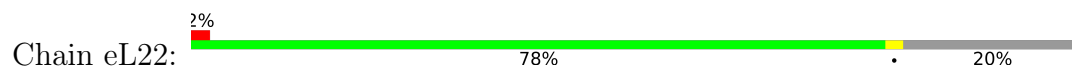
- Molecule 22: 60S ribosomal protein L20



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



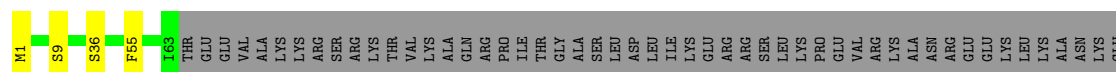
- Molecule 24: 60S ribosomal protein L22-A



- Molecule 25: 60S ribosomal protein L23-B

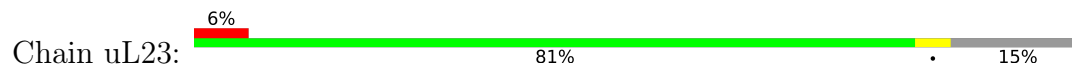


- Molecule 26: 60S ribosomal protein L24-A



LYS
LYS
LYS
ALA
GLU
LYS
LYS
ALA
ALA
ARG
LYS
ALA
GLU
LYS
LYS
LYS
SER
GLY
ALA
THR
GLN
SER
LYS
PHE
SER
LYS
GLN
GLN
ALA
LYS
GLY
ALA
PHE
GLN
LYS
VAL
ALA
ALA
THR
SER
ARG

- Molecule 27: 60S ribosomal protein L25



MET
ALA
PRO
SER
ALA
LYS
LYS
THR
ALA
LYS
LYS
VAL
VAL
LYS
GLY
THR
ASN
GLY
LYS
LYS
A23
L24
R27
K74
I81
I82
V83
F84
Q85
K109
G118
V124
R138
I142

- Molecule 28: 60S ribosomal protein L26-A



MET
A2
S5
L6
F20
F21
R51
E55
R60
Q65
Q66
Y74
F78
D112
K113
D114
E127

- Molecule 29: 60S ribosomal protein L27



MET
A2
K3
D30
E31
G32
S33
K34
S35
K56
L58
F92
T100
F101
E102
F136

- Molecule 30: 60S ribosomal protein L28



MET
P2
S3
R4
G23
K24
K27
N44
N45
D46
K47
Y48
H49
V56
Y60
F68
K77
L78
L91
S95
K96
G110
K111
I112
K115
G116
R117
A149

- Molecule 31: 60S ribosomal protein L29



MET
A2
K22
K23
P24
Y27
K59

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



MET
ALA
PRO
VAL
LYS
SER
GLN
GLU
S9
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I16
S63
K64
F85
D97
A105

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

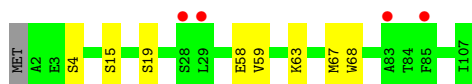




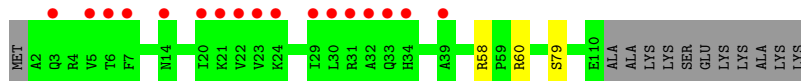
- Molecule 34: HN1_G0013350.mRNA.1.CDS.1



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



- Molecule 36: 60S ribosomal protein L34-A



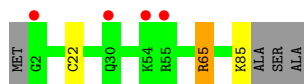
- Molecule 37: BJ4_G0044250.mRNA.1.CDS.1



- Molecule 38: 60S ribosomal protein L36-A



- Molecule 39: Ribosomal protein L37

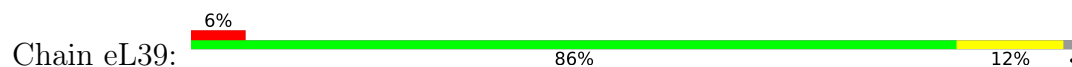


- Molecule 40: BJ4_G0032190.mRNA.1.CDS.1

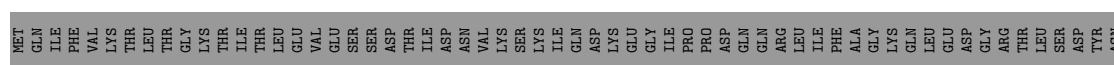




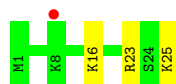
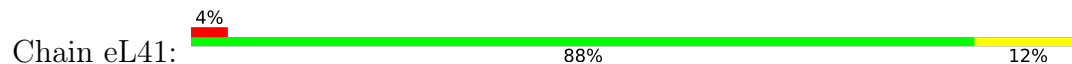
- Molecule 41: 60S ribosomal protein L39



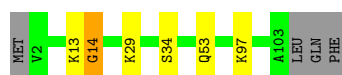
- Molecule 42: Ubiquitin



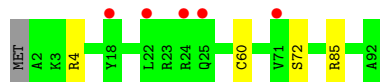
- Molecule 43: eL41



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



- Molecule 45: 60S ribosomal protein L43-A



- Molecule 46: 18S rRNA

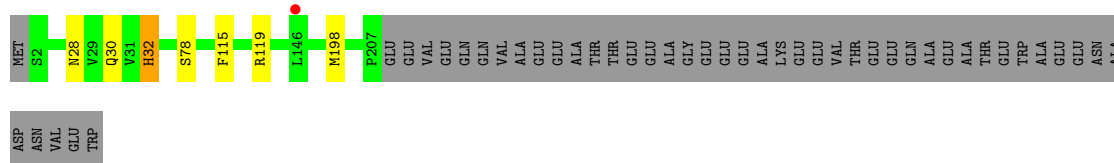


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G1713	C1472	A1360	G1255	G1150	U960	U820	C717	G649	G516	C402	A	U146
A1714	U1473	U1361	A1266	A1151	U964	U821	U718	U650	U517	G403	C	A147
G1715	G1474	U1362	U1267	G1152	U965	G823	U719	G651	A527	G404	U	U158
C1716	G1477	U1363	U1268	A1153	A966	G827	U721	G652	U528	A412	C	U159
G1717	C1478	G1364	U1269	G1154	A988	C827	G722	G653	A529	A416	U	G160
A1740	A1479	G1367	U1261	A1157	A988	U830	G723	G654	A534	U242		U161
C1618	C1482	U1370	G1261	C1158	G991	U831	U727	G655	A538	G419	U	U167
C1619	A1483	U1371	G1264	G1161	A992	U832	U728	G656	U539	G423	C	U168
G1622	U1489	U1372	G1265	C1162	A993	G	G729	U657	G540	A424	A	A169
A1631	C1490	A1375	G1270	G1167	U996	U	C730	C	A541	A425		U177
C1632	U1491	C1376	G1273	G1167	G997	U	C731	G	A542	U260		U178
A1633	A1492	G1377	G1274	G1170	A998	U	A732	A	C543	C427		U179
A1634	C1493	U1380	A1275	G1170	A998	U	A733	U	A544	A436		A180
A1635	C1494	G1385	A1275	U1182	C1010	U	C735	U	A545	G434		A181
C1636	G1499	G1385	U1285	U1182	C1010	U840	U743	U	G548	C435		A182
C1637	C1500	U1286	U1286	U1185	C1022	U841	G738	U	G551	A437		U185
U1643	G1506	A1287	G1288	U1191	A1026	G846	G739	C	G557	A437		C186
A1651	G1506	G1288	U1288	U1191	A1027	G846	A740	G	G558	U439		
U1657	A1515	U1293	U1293	C1192	C1028	A856	U742	U	A555	C444		C
G1658	A1516	U1298	U1298	A1194	A1030	G853	A756	U	G557	A445		C
U1665	U1517	U1307	U1307	C1195	U1031	A859	A757	A	C559	A452		C
U1666	U1520	U1307	U1307	A1196	U1031	U860	U758	U	C565	C455		U
A1667	G1523	G1308	U1308	G1199	G1040	A863	G765	G	C566	G459		U
A1678	A1524	C1309	U1310	G1201	U1051	G876	U766	G	A567	A468		G
A1681	U1532	U1314	U1314	G1202	U1052	A881	G775	U	G568	A476		A
U1682	U1535	U1315	G1316	C1207	U1057	U886	U779	C	G576	A477		G198
C1683	G1536	U1411	G1316	G1216	U1058	U886	A780	C	A579	U476		G199
U1684	C1537	U1412	U1320	A1217	U1059	G895	U781	C	A580	U477		A200
G1685	U1538	U1413	A1321	G1218	U1060	U896	U782	U	U581	A477		G201
C1686	U1538	U1414	A1321	A1219	A1061	C897	G783	U	U582	A315		A202
A1691	G1542	U1423	U1335	C1220	U1062	A898	C784	C	C583	A316		U203
G1692	A1543	A1424	U1336	A1076	U1063	U912	A789	C	A594	C321		G204
A1693	G1548	A1425	A1337	U1224	U1067	G913	A793	U	A606	G322		A217
A1694	C1549	C1426	C1338	U1225	U1068	G914	U794	C	G610	G488		A218
G1695	A1550	G1427	U1340	A1226	U1069	A915	U795	U	U611	C489		A219
G1696	U1557	U1432	A1341	A1227	G1082	U920	U796	U	G616	C490		A220
G1697	U1558	U1433	A1344	G1229	G1083	U920	C798	C	G616	U493		A221
G1698	A1559	G1433	A1345	A1238	G1085	A926	U803	C	G619	G496		A
G1699	C1563	A1436	A1346	G1241	A1091	A929	A803	U	A619	G497		U
C1700	U1701	C1447	A1348	A1242	A1092	A929	C810	C	A620	U499		A
A1702	C1568	G1458	G1351	G1243	A1093	A933	A811	U	A623	G361		U
C1703	A1569	C1459	G1351	A1244	U1097	C934	A812	U	G624	G366		U
G1706	A1570	A1480	G1354	G1245	G1100	U935	U813	U	A630	A387		U
A1707	A1592	A1469	C1355	C1246	A1113	A944	A814	C	A637	U507		U
U1710	A1597	C1470	G1358	U1249	A1113	A951	C815	C	A399	A400		G

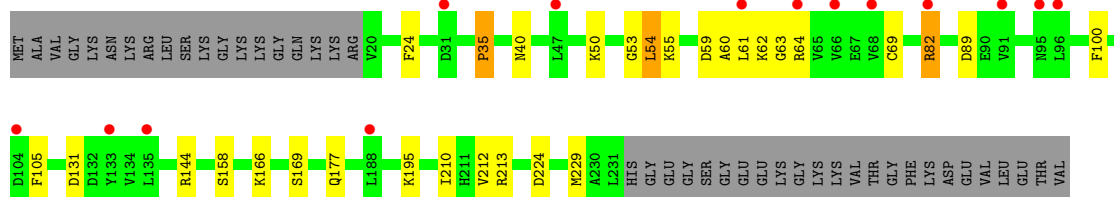
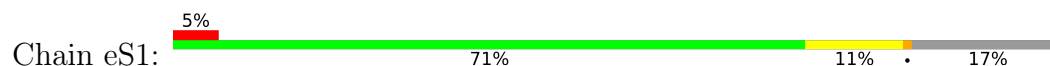
• Molecule 47: 40S ribosomal protein S0

Chain uS2:

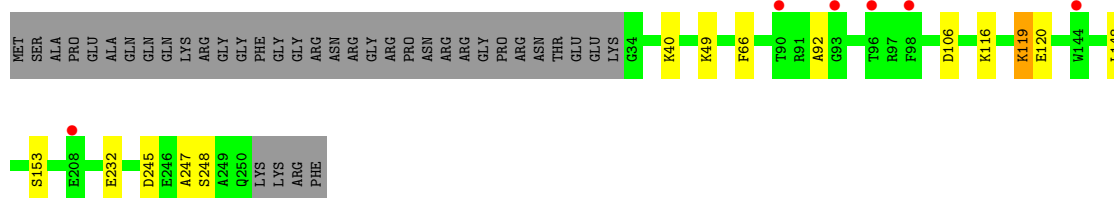
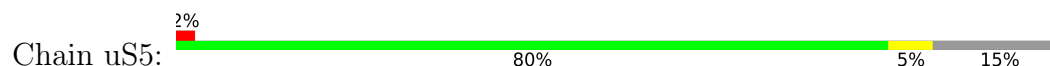




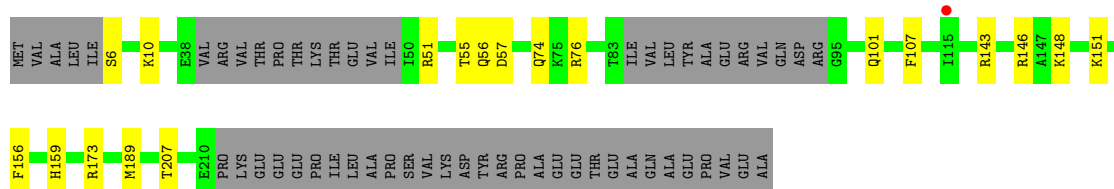
- Molecule 48: 40S ribosomal protein S1



- Molecule 49: 40S ribosomal protein S2



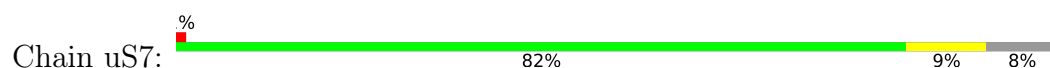
- Molecule 50: BJ4_G0045400.mRNA.1.CDS.1

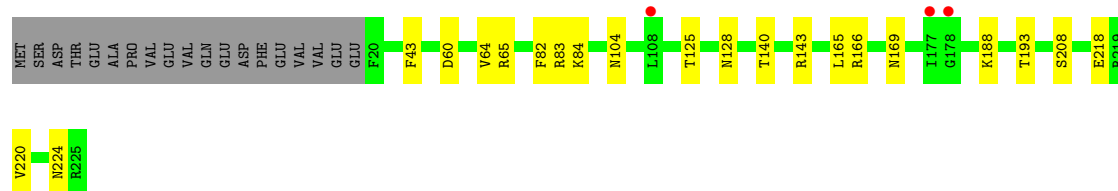


- Molecule 51: 40S ribosomal protein S4

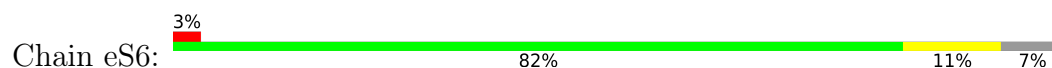


- Molecule 52: Rps5p





- Molecule 53: 40S ribosomal protein S6



- Molecule 54: 40S ribosomal protein S7



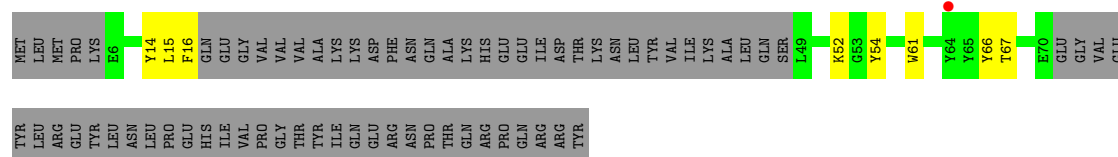
- Molecule 55: 40S ribosomal protein S8



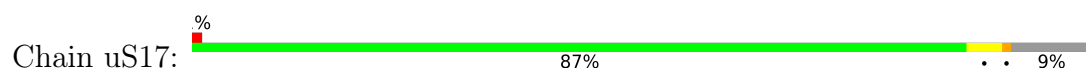
- Molecule 56: BJ4_G0026100.mRNA.1.CDS.1



- Molecule 57: 40S ribosomal protein S10-A



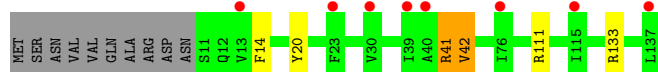
- Molecule 58: 40S ribosomal protein S11-B



- Molecule 59: 40S ribosomal protein S13



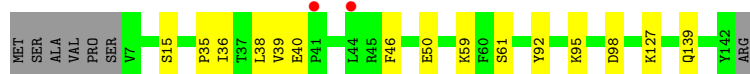
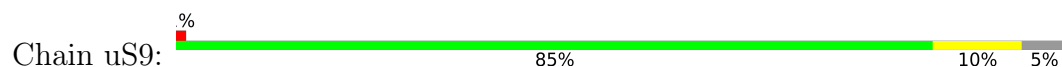
- Molecule 60: 40S ribosomal protein S14-A



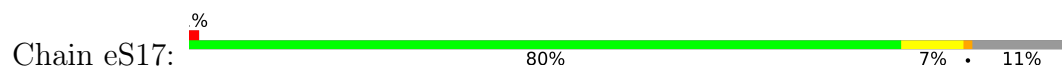
- Molecule 61: 40S ribosomal protein S15



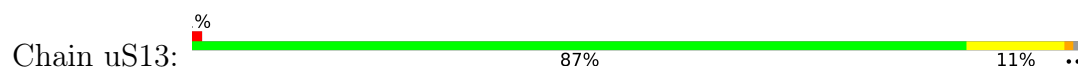
- Molecule 62: BJ4_G0008010.mRNA.1.CDS.1



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



- Molecule 64: 40S ribosomal protein S18-B





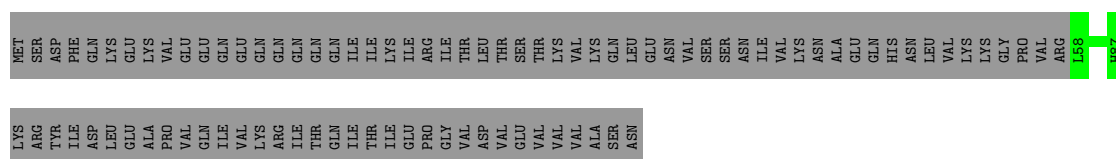
- Molecule 65: 40S ribosomal protein S19-A

Chain eS19: 92% 7% ..



- Molecule 66: 40S ribosomal protein S20

Chain uS10: 25% 75%



- Molecule 67: 40S ribosomal protein S21

Chain eS21: 94% 6%



- Molecule 68: 40S ribosomal protein S22-A

Chain uS8: 95% 5% .



- Molecule 69: 40S ribosomal protein S23

Chain uS12: 92% 7% .



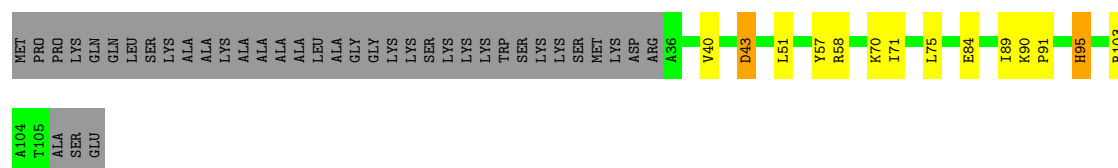
- Molecule 70: 40S ribosomal protein S24

Chain eS24: 90% 9% .



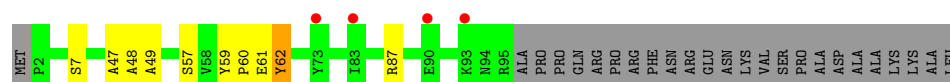
- Molecule 71: 40S ribosomal protein S25

Chain eS25: 

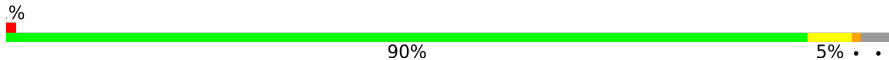


- Molecule 72: 40S ribosomal protein S26

Chain eS26: 



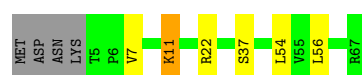
- Molecule 73: 40S ribosomal protein S27-A

Chain eS27: 



- Molecule 74: eS28

Chain eS28: 



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

Chain uS14: 

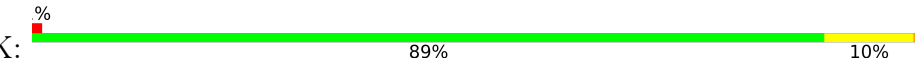


- Molecule 76: 40S ribosomal protein S30

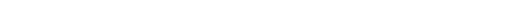
Chain eS30: 

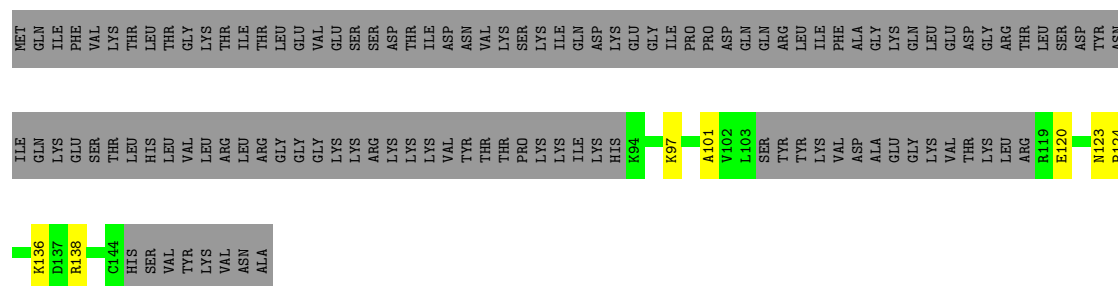


- Molecule 77: BJ4_G0022010.mRNA.1.CDS.1

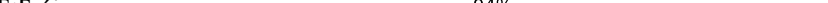
Chain RACK: 

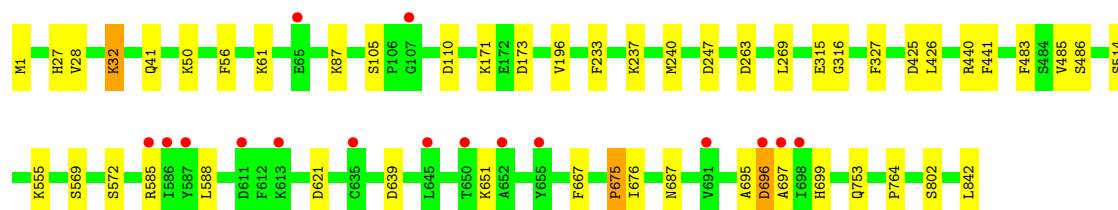
- Molecule 78: Ubiquitin-40S ribosomal protein S31

Chain eS31: 

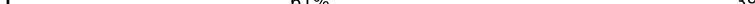


- Molecule 79: Elongation factor 2

Chain eEF2: 

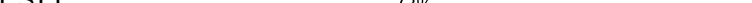


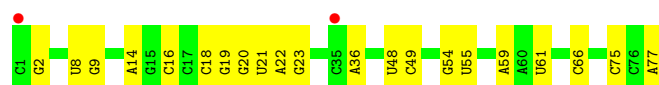
- Molecule 80: PHE tRNA

Chain ASIT: 

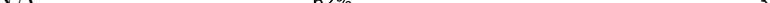


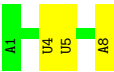
- Molecule 81: FMET tRNA

Chain PSIT: 

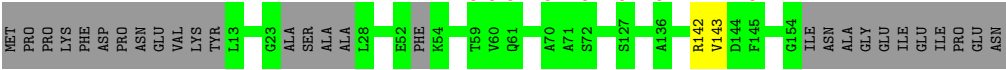
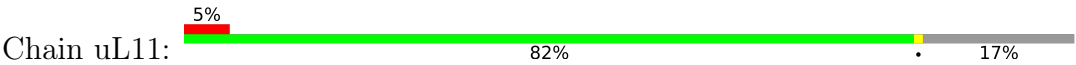


- Molecule 82: mRNA

Chain mRNA: 



• Molecule 83: 60S ribosomal protein L12-B



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	233.49Å 299.85Å 513.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	149.93 – 3.00 149.93 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (149.93-3.00) 90.5 (149.93-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.56 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.19rc4_4035	Depositor
R, R_{free}	0.228 , 0.284 0.228 , 0.283	Depositor DCC
R_{free} test set	2000 reflections (0.28%)	wwPDB-VP
Wilson B-factor (Å ²)	88.5	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 88.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	207073	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

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

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: YG, GTP, ZN, DDE, MG

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	0.16	0/75698	0.39	0/118002
2	AB	0.15	0/2883	0.35	0/4491
3	58S	0.15	0/3746	0.38	0/5832
4	uL10	0.46	0/1421	1.03	6/1921 (0.3%)
5	uL2	0.21	0/1948	0.54	0/2617
6	uL3	0.21	0/3146	0.51	0/4228
7	uL4	0.29	0/2800	0.70	2/3790 (0.1%)
8	uL18	0.33	1/2425 (0.0%)	0.68	2/3271 (0.1%)
9	eL6	0.36	0/1260	0.82	1/1694 (0.1%)
10	uL30	0.26	0/1821	0.74	4/2451 (0.2%)
11	eL8	0.32	0/1836	0.68	0/2481
12	uL6	0.28	0/1539	0.60	0/2073
13	uL16	0.25	0/1767	0.57	1/2368 (0.0%)
14	uL5	0.78	4/1374 (0.3%)	1.13	6/1842 (0.3%)
15	eL13	0.32	0/1568	0.76	1/2106 (0.0%)
16	eL14	0.37	0/1068	0.71	1/1438 (0.1%)
17	eL15	0.24	0/1757	0.57	0/2354
18	uL13	0.39	3/1585 (0.2%)	0.64	2/2128 (0.1%)
19	uL22	0.24	0/1218	0.54	0/1641
20	eL18	0.29	0/1465	0.64	0/1965
21	eL19	0.32	1/1440 (0.1%)	0.61	1/1921 (0.1%)
22	eL20	0.22	0/1481	0.54	0/1990
23	eL21	0.26	0/1300	0.55	0/1743
24	eL22	0.42	0/786	0.87	1/1065 (0.1%)
25	uL14	0.18	0/978	0.44	0/1316
26	eL24	0.16	0/533	0.46	0/707
27	uL23	0.27	0/974	0.70	2/1314 (0.2%)
28	uL24	0.44	0/1004	0.98	0/1341
29	eL27	0.28	0/1118	0.67	0/1497
30	uL15	0.34	0/1204	0.73	2/1612 (0.1%)
31	eL29	0.21	0/473	0.62	0/629
32	eL30	0.30	0/750	0.52	0/1008

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	eL31	0.38	1/897 (0.1%)	0.66	1/1205 (0.1%)
34	eL32	0.26	0/1041	0.67	2/1394 (0.1%)
35	eL33	0.26	0/868	0.59	0/1168
36	eL34	0.19	0/871	0.54	0/1164
37	uL29	0.29	0/978	0.64	0/1301
38	eL36	0.31	0/778	0.74	0/1034
39	eL37	0.22	0/680	0.63	0/901
40	eL38	0.35	0/618	0.84	2/826 (0.2%)
41	eL39	0.30	0/443	0.70	0/588
42	eL40	0.16	0/423	0.47	0/562
43	eL41	0.18	0/234	0.55	0/300
44	eL42	0.22	0/831	0.62	0/1097
45	eL43	0.17	0/701	0.51	0/934
46	18S	0.17	1/41291 (0.0%)	0.41	1/64331 (0.0%)
47	uS2	0.31	0/1617	0.69	0/2215
48	eS1	0.60	0/1714	1.07	8/2308 (0.3%)
49	uS5	0.31	0/1665	0.72	1/2263 (0.0%)
50	uS3	0.50	2/1429 (0.1%)	0.87	5/1913 (0.3%)
51	eS4	0.25	0/2097	0.62	0/2823
52	uS7	0.53	0/1629	1.03	4/2202 (0.2%)
53	eS6	0.39	0/1790	0.92	3/2393 (0.1%)
54	eS7	0.38	0/1506	0.79	1/2028 (0.0%)
55	eS8	0.29	0/1482	0.73	2/1980 (0.1%)
56	uS4	0.31	0/1519	0.78	4/2035 (0.2%)
57	eS10	0.56	0/309	1.01	1/416 (0.2%)
58	uS17	0.23	0/1172	0.54	1/1580 (0.1%)
59	uS15	0.30	1/1215 (0.1%)	0.63	0/1638
60	uS11	0.33	0/901	0.77	2/1217 (0.2%)
61	uS19	0.34	0/747	0.81	0/1002
62	uS9	0.43	0/1088	1.03	2/1459 (0.1%)
63	eS17	0.52	0/971	1.01	2/1303 (0.2%)
64	uS13	0.48	0/1211	1.00	1/1628 (0.1%)
65	eS19	0.49	1/1130 (0.1%)	0.81	0/1517
66	uS10	0.43	0/250	0.68	0/336
67	eS21	0.26	0/693	0.67	0/935
68	uS8	0.19	0/1038	0.58	1/1395 (0.1%)
69	uS12	0.22	0/1139	0.63	2/1518 (0.1%)
70	eS24	0.27	0/1087	0.63	0/1449
71	eS25	0.79	2/571 (0.4%)	1.24	6/768 (0.8%)
72	eS26	0.37	0/761	0.75	1/1016 (0.1%)
73	eS27	0.32	0/600	0.87	2/813 (0.2%)
74	eS28	0.50	0/499	0.99	1/670 (0.1%)
75	uS14	0.30	0/412	0.62	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	eS30	0.29	0/433	0.81	0/575
77	RACK	0.66	1/2489 (0.0%)	1.17	10/3389 (0.3%)
78	eS31	0.45	0/279	1.14	1/369 (0.3%)
79	eEF2	0.25	0/6673	0.66	11/9032 (0.1%)
80	ASIT	0.16	0/1784	0.42	0/2780
81	PSIT	0.18	0/1836	0.42	0/2859
82	mRNA	0.10	0/188	0.26	0/290
83	uL11	0.16	0/670	0.48	0/926
All	All	0.26	18/221614 (0.0%)	0.56	110/325225 (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
4	uL10	0	4
6	uL3	0	1
10	uL30	0	2
11	eL8	0	2
12	uL6	0	1
14	uL5	0	5
15	eL13	0	1
18	uL13	0	1
20	eL18	0	1
21	eL19	0	1
22	eL20	0	1
25	uL14	0	1
28	uL24	0	1
29	eL27	0	3
30	uL15	0	4
31	eL29	0	1
35	eL33	0	1
38	eL36	0	1
40	eL38	0	1
41	eL39	0	2
44	eL42	0	1
47	uS2	0	2
48	eS1	0	8
49	uS5	0	4
51	eS4	0	2
52	uS7	0	5

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

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	uL5	29	ARG	CG-CD	9.72	1.81	1.52
14	uL5	29	ARG	CB-CG	8.04	1.76	1.52
14	uL5	29	ARG	CD-NE	7.79	1.57	1.46
71	eS25	89	ILE	C-N	7.42	1.41	1.33
8	uL18	296	GLN	CD-OE1	-7.26	1.09	1.23

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	eS1	61	LEU	CB-CG-CD1	11.91	146.43	110.70
62	uS9	39	VAL	CA-C-N	11.53	149.92	121.80
62	uS9	39	VAL	C-N-CA	11.53	149.92	121.80
48	eS1	61	LEU	CD1-CG-CD2	-9.85	89.14	110.80
18	uL13	170	LYS	CD-CE-NZ	-9.76	80.67	111.90

There are no chirality outliers.

5 of 120 planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	uL10	174/312 (56%)	127 (73%)	42 (24%)	5 (3%)	3	20
5	uL2	250/254 (98%)	230 (92%)	20 (8%)	0	100	100
6	uL3	384/387 (99%)	336 (88%)	47 (12%)	1 (0%)	36	70
7	uL4	359/362 (99%)	307 (86%)	50 (14%)	2 (1%)	21	56
8	uL18	294/297 (99%)	260 (88%)	33 (11%)	1 (0%)	36	70
9	eL6	152/176 (86%)	127 (84%)	25 (16%)	0	100	100
10	uL30	220/244 (90%)	199 (90%)	19 (9%)	2 (1%)	14	48
11	eL8	231/256 (90%)	200 (87%)	29 (13%)	2 (1%)	14	48
12	uL6	189/191 (99%)	162 (86%)	26 (14%)	1 (0%)	24	60
13	uL16	209/221 (95%)	185 (88%)	24 (12%)	0	100	100
14	uL5	167/174 (96%)	125 (75%)	37 (22%)	5 (3%)	3	19
15	eL13	191/199 (96%)	152 (80%)	34 (18%)	5 (3%)	4	23
16	eL14	134/138 (97%)	118 (88%)	16 (12%)	0	100	100
17	eL15	201/204 (98%)	173 (86%)	27 (13%)	1 (0%)	24	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	uL13	195/199 (98%)	182 (93%)	10 (5%)	3 (2%)	8	35
19	uL22	149/184 (81%)	134 (90%)	15 (10%)	0	100	100
20	eL18	183/186 (98%)	153 (84%)	30 (16%)	0	100	100
21	eL19	174/189 (92%)	157 (90%)	15 (9%)	2 (1%)	11	43
22	eL20	170/172 (99%)	155 (91%)	15 (9%)	0	100	100
23	eL21	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	56
24	eL22	95/121 (78%)	83 (87%)	12 (13%)	0	100	100
25	uL14	127/137 (93%)	122 (96%)	5 (4%)	0	100	100
26	eL24	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
27	uL23	118/142 (83%)	94 (80%)	24 (20%)	0	100	100
28	uL24	124/127 (98%)	107 (86%)	17 (14%)	0	100	100
29	eL27	133/136 (98%)	110 (83%)	21 (16%)	2 (2%)	8	35
30	uL15	146/149 (98%)	127 (87%)	16 (11%)	3 (2%)	5	27
31	eL29	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
32	eL30	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	11	43
33	eL31	107/113 (95%)	93 (87%)	13 (12%)	1 (1%)	14	48
34	eL32	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	7	34
35	eL33	104/107 (97%)	99 (95%)	4 (4%)	1 (1%)	12	45
36	eL34	107/121 (88%)	101 (94%)	6 (6%)	0	100	100
37	uL29	117/120 (98%)	101 (86%)	16 (14%)	0	100	100
38	eL36	97/100 (97%)	75 (77%)	20 (21%)	2 (2%)	5	27
39	eL37	82/88 (93%)	72 (88%)	9 (11%)	1 (1%)	10	40
40	eL38	75/78 (96%)	59 (79%)	15 (20%)	1 (1%)	9	38
41	eL39	48/51 (94%)	40 (83%)	8 (17%)	0	100	100
42	eL40	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
43	eL41	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
44	eL42	100/106 (94%)	77 (77%)	22 (22%)	1 (1%)	12	45
45	eL43	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
47	uS2	204/252 (81%)	165 (81%)	38 (19%)	1 (0%)	24	60
48	eS1	210/255 (82%)	150 (71%)	54 (26%)	6 (3%)	3	20
49	uS5	215/254 (85%)	185 (86%)	28 (13%)	2 (1%)	14	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	uS3	177/240 (74%)	138 (78%)	36 (20%)	3 (2%)	7	32
51	eS4	256/261 (98%)	219 (86%)	34 (13%)	3 (1%)	10	40
52	uS7	204/225 (91%)	149 (73%)	52 (26%)	3 (2%)	8	35
53	eS6	217/236 (92%)	176 (81%)	34 (16%)	7 (3%)	3	18
54	eS7	182/190 (96%)	145 (80%)	34 (19%)	3 (2%)	7	34
55	eS8	180/200 (90%)	149 (83%)	29 (16%)	2 (1%)	11	43
56	uS4	183/197 (93%)	151 (82%)	28 (15%)	4 (2%)	5	26
57	eS10	29/105 (28%)	19 (66%)	9 (31%)	1 (3%)	3	17
58	uS17	140/156 (90%)	116 (83%)	22 (16%)	2 (1%)	9	36
59	uS15	148/151 (98%)	127 (86%)	20 (14%)	1 (1%)	18	53
60	uS11	125/137 (91%)	102 (82%)	22 (18%)	1 (1%)	16	50
61	uS19	85/142 (60%)	60 (71%)	23 (27%)	2 (2%)	4	24
62	uS9	134/143 (94%)	98 (73%)	32 (24%)	4 (3%)	3	19
63	eS17	119/136 (88%)	91 (76%)	26 (22%)	2 (2%)	7	32
64	uS13	143/146 (98%)	110 (77%)	26 (18%)	7 (5%)	1	10
65	eS19	141/144 (98%)	106 (75%)	35 (25%)	0	100	100
66	uS10	28/121 (23%)	25 (89%)	3 (11%)	0	100	100
67	eS21	85/87 (98%)	66 (78%)	19 (22%)	0	100	100
68	uS8	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	50
69	uS12	142/145 (98%)	129 (91%)	9 (6%)	4 (3%)	4	21
70	eS24	132/135 (98%)	117 (89%)	15 (11%)	0	100	100
71	eS25	68/108 (63%)	40 (59%)	25 (37%)	3 (4%)	2	12
72	eS26	92/119 (77%)	72 (78%)	16 (17%)	4 (4%)	2	12
73	eS27	77/82 (94%)	62 (80%)	14 (18%)	1 (1%)	9	38
74	eS28	61/67 (91%)	44 (72%)	17 (28%)	0	100	100
75	uS14	47/56 (84%)	42 (89%)	5 (11%)	0	100	100
76	eS30	51/63 (81%)	31 (61%)	18 (35%)	2 (4%)	2	14
77	RACK	316/319 (99%)	202 (64%)	111 (35%)	3 (1%)	14	48
78	eS31	32/152 (21%)	13 (41%)	17 (53%)	2 (6%)	1	6
79	eEF2	839/842 (100%)	717 (86%)	114 (14%)	8 (1%)	12	45
83	uL11	131/165 (79%)	97 (74%)	33 (25%)	1 (1%)	16	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11582/13056 (89%)	9666 (84%)	1787 (15%)	129 (1%)	11	43

5 of 129 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	uL10	152/254 (60%)	142 (93%)	10 (7%)	15	46
5	uL2	193/196 (98%)	187 (97%)	6 (3%)	35	68
6	uL3	320/323 (99%)	301 (94%)	19 (6%)	18	50
7	uL4	288/289 (100%)	276 (96%)	12 (4%)	26	61
8	uL18	244/245 (100%)	226 (93%)	18 (7%)	13	42
9	eL6	134/153 (88%)	124 (92%)	10 (8%)	12	41
10	uL30	186/205 (91%)	174 (94%)	12 (6%)	15	47
11	eL8	187/208 (90%)	180 (96%)	7 (4%)	30	64
12	uL6	171/171 (100%)	164 (96%)	7 (4%)	27	61
13	uL16	183/187 (98%)	177 (97%)	6 (3%)	33	67
14	uL5	147/150 (98%)	135 (92%)	12 (8%)	10	37
15	eL13	154/159 (97%)	143 (93%)	11 (7%)	13	43
16	eL14	107/109 (98%)	96 (90%)	11 (10%)	7	28
17	eL15	175/176 (99%)	165 (94%)	10 (6%)	18	52
18	uL13	160/162 (99%)	156 (98%)	4 (2%)	42	72
19	uL22	122/146 (84%)	116 (95%)	6 (5%)	22	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	eL18	150/151 (99%)	147 (98%)	3 (2%)	48	76
21	eL19	143/154 (93%)	134 (94%)	9 (6%)	16	48
22	eL20	156/156 (100%)	147 (94%)	9 (6%)	18	51
23	eL21	136/137 (99%)	130 (96%)	6 (4%)	25	60
24	eL22	84/107 (78%)	82 (98%)	2 (2%)	43	73
25	uL14	101/105 (96%)	97 (96%)	4 (4%)	28	62
26	eL24	55/129 (43%)	51 (93%)	4 (7%)	13	42
27	uL23	104/118 (88%)	100 (96%)	4 (4%)	29	63
28	uL24	109/110 (99%)	101 (93%)	8 (7%)	13	42
29	eL27	115/116 (99%)	111 (96%)	4 (4%)	32	65
30	uL15	118/119 (99%)	112 (95%)	6 (5%)	21	55
31	eL29	46/47 (98%)	44 (96%)	2 (4%)	26	60
32	eL30	81/88 (92%)	78 (96%)	3 (4%)	30	64
33	eL31	94/97 (97%)	92 (98%)	2 (2%)	47	75
34	eL32	109/111 (98%)	108 (99%)	1 (1%)	70	85
35	eL33	90/91 (99%)	84 (93%)	6 (7%)	15	46
36	eL34	94/103 (91%)	91 (97%)	3 (3%)	34	67
37	uL29	104/105 (99%)	102 (98%)	2 (2%)	50	76
38	eL36	81/82 (99%)	78 (96%)	3 (4%)	30	64
39	eL37	69/71 (97%)	66 (96%)	3 (4%)	26	60
40	eL38	68/69 (99%)	60 (88%)	8 (12%)	5	22
41	eL39	45/46 (98%)	41 (91%)	4 (9%)	9	34
42	eL40	47/116 (40%)	44 (94%)	3 (6%)	16	48
43	eL41	23/23 (100%)	20 (87%)	3 (13%)	4	19
44	eL42	87/91 (96%)	82 (94%)	5 (6%)	18	52
45	eL43	71/72 (99%)	67 (94%)	4 (6%)	19	52
47	uS2	164/210 (78%)	159 (97%)	5 (3%)	36	69
48	eS1	189/224 (84%)	175 (93%)	14 (7%)	13	42
49	uS5	176/205 (86%)	168 (96%)	8 (4%)	24	59
50	uS3	145/195 (74%)	132 (91%)	13 (9%)	9	34
51	eS4	220/222 (99%)	207 (94%)	13 (6%)	18	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	uS7	173/191 (91%)	163 (94%)	10 (6%)	18	51
53	eS6	188/201 (94%)	175 (93%)	13 (7%)	14	45
54	eS7	165/170 (97%)	154 (93%)	11 (7%)	15	46
55	eS8	146/161 (91%)	136 (93%)	10 (7%)	14	45
56	uS4	158/166 (95%)	151 (96%)	7 (4%)	25	60
57	eS10	32/98 (33%)	30 (94%)	2 (6%)	16	48
58	uS17	127/137 (93%)	123 (97%)	4 (3%)	35	68
59	uS15	127/128 (99%)	122 (96%)	5 (4%)	28	62
60	uS11	81/105 (77%)	77 (95%)	4 (5%)	22	56
61	uS19	77/118 (65%)	67 (87%)	10 (13%)	4	19
62	uS9	113/119 (95%)	104 (92%)	9 (8%)	11	38
63	eS17	105/124 (85%)	97 (92%)	8 (8%)	12	41
64	uS13	128/129 (99%)	121 (94%)	7 (6%)	19	53
65	eS19	115/116 (99%)	107 (93%)	8 (7%)	14	44
66	uS10	28/114 (25%)	28 (100%)	0	100	100
67	eS21	74/74 (100%)	69 (93%)	5 (7%)	14	45
68	uS8	110/111 (99%)	107 (97%)	3 (3%)	39	71
69	uS12	119/120 (99%)	115 (97%)	4 (3%)	32	66
70	eS24	112/113 (99%)	102 (91%)	10 (9%)	9	34
71	eS25	61/89 (68%)	56 (92%)	5 (8%)	10	37
72	eS26	81/101 (80%)	80 (99%)	1 (1%)	63	82
73	eS27	68/71 (96%)	65 (96%)	3 (4%)	25	60
74	eS28	56/60 (93%)	52 (93%)	4 (7%)	13	43
75	uS14	43/49 (88%)	36 (84%)	7 (16%)	2	12
76	eS30	46/54 (85%)	42 (91%)	4 (9%)	9	35
77	RACK	259/262 (99%)	241 (93%)	18 (7%)	14	45
78	eS31	30/135 (22%)	28 (93%)	2 (7%)	15	46
79	eEF2	714/714 (100%)	680 (95%)	34 (5%)	23	57
All	All	9733/10833 (90%)	9200 (94%)	533 (6%)	19	53

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

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

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	25S	3151/3396 (92%)	727 (23%)	22 (0%)
2	AB	120/121 (99%)	21 (17%)	1 (0%)
3	58S	157/158 (99%)	37 (23%)	1 (0%)
46	18S	1726/1798 (95%)	510 (29%)	23 (1%)
80	ASIT	73/76 (96%)	29 (39%)	2 (2%)
81	PSIT	76/77 (98%)	21 (27%)	0
82	mRNA	7/8 (87%)	3 (42%)	0
All	All	5310/5634 (94%)	1348 (25%)	49 (0%)

5 of 1348 RNA backbone outliers are listed below:

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

5 of 49 RNA pucker outliers are listed below:

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

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

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

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
80	YG	ASIT	37	80	38,42,43	1.52	5 (13%)	45,62,65	2.37	13 (28%)
79	DDE	eEF2	699	79	18,20,21	1.10	2 (11%)	17,28,30	1.42	3 (17%)

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
80	YG	ASIT	37	80	-	12/24/42/43	0/4/4/4
79	DDE	eEF2	699	79	-	4/20/21/23	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	ASIT	37	YG	O23-C21	-5.31	1.25	1.34
80	ASIT	37	YG	C6-N1	-3.12	1.35	1.42
80	ASIT	37	YG	O18-C16	-3.11	1.25	1.33
80	ASIT	37	YG	C5-C6	-2.96	1.38	1.45
79	eEF2	699	DDE	CD2-CG	2.37	1.41	1.36

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	ASIT	37	YG	C5-C4-N3	-9.18	116.54	123.99
80	ASIT	37	YG	N9-C4-N3	5.53	138.41	129.45
80	ASIT	37	YG	N1-C2-N2	-4.19	108.03	114.03
80	ASIT	37	YG	C1'-N9-C8	-3.85	115.80	126.73
80	ASIT	37	YG	C24-O23-C21	3.80	120.03	115.63

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	eEF2	699	DDE	O-C-CA-CB
80	ASIT	37	YG	C13-C14-C15-N20
80	ASIT	37	YG	N20-C21-O23-C24
80	ASIT	37	YG	O22-C21-O23-C24
80	ASIT	37	YG	C15-C16-O18-C19

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 515 ligands modelled in this entry, 514 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	907	84	33,34,34	1.12	3 (9%)	50,54,54	1.70	10 (20%)

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	907	84	-	3/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	eEF2	907	GTP	PB-O3B	3.51	1.63	1.59
86	eEF2	907	GTP	PA-O3A	2.42	1.62	1.59
86	eEF2	907	GTP	C2-N3	2.33	1.38	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	eEF2	907	GTP	C5-C4-N3	-5.13	120.23	128.39
86	eEF2	907	GTP	C2-N3-C4	4.62	120.25	112.30
86	eEF2	907	GTP	N9-C4-N3	3.65	133.25	125.95
86	eEF2	907	GTP	C2-N1-C6	-2.87	119.91	125.11
86	eEF2	907	GTP	O6-C6-C5	-2.62	119.61	126.53

There are no chirality outliers.

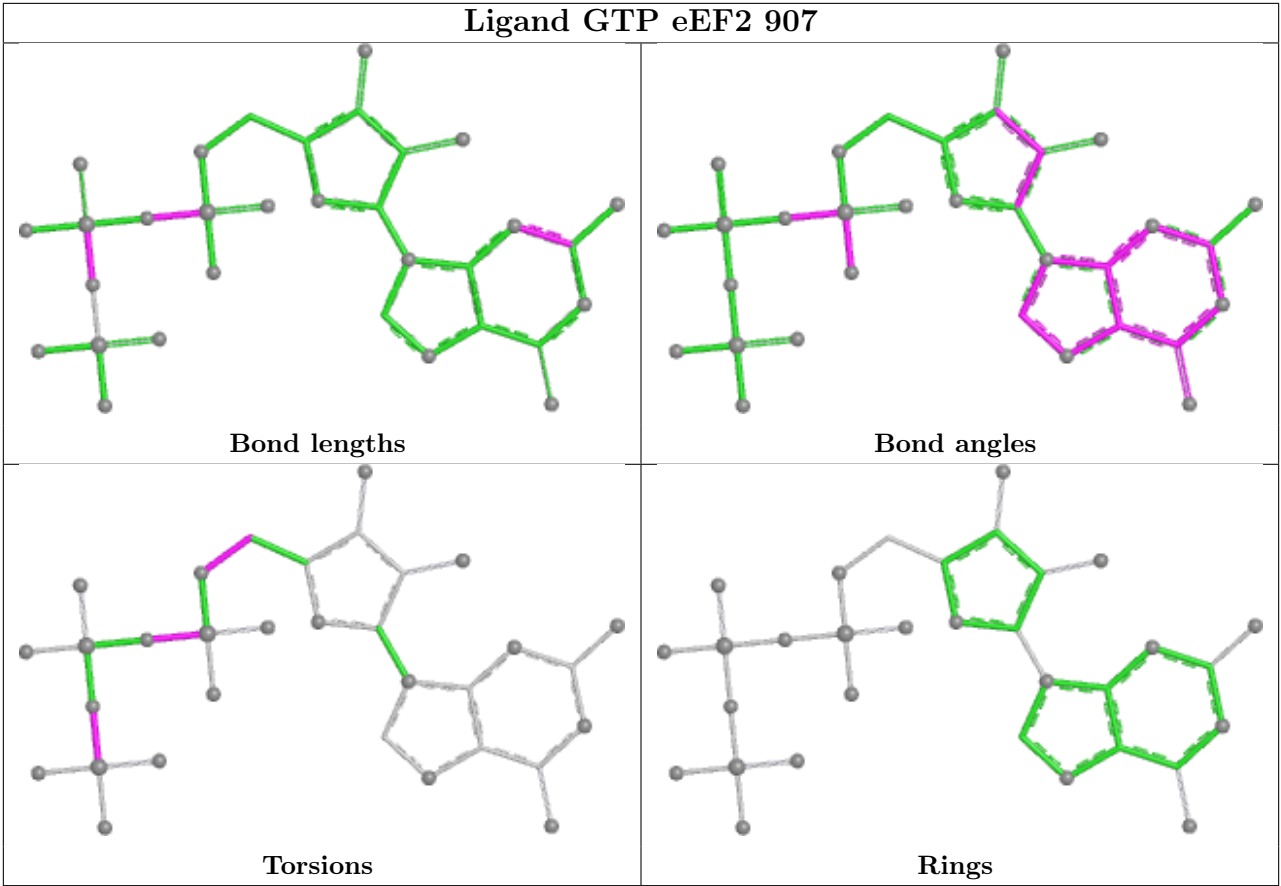
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	eEF2	907	GTP	PB-O3A-PA-O5'
86	eEF2	907	GTP	C4'-C5'-O5'-PA
86	eEF2	907	GTP	PB-O3B-PG-O2G

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	25S	1

All chain breaks are listed below:

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

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	25S	3162/3396 (93%)	-0.78	18 (0%) 85 69	62, 101, 192, 285	0
2	AB	121/121 (100%)	-1.22	1 (0%) 82 64	50, 108, 139, 149	0
3	58S	158/158 (100%)	-0.96	0 100 100	94, 113, 157, 214	0
4	uL10	180/312 (57%)	0.13	9 (5%) 34 18	109, 163, 192, 199	0
5	uL2	252/254 (99%)	0.16	12 (4%) 35 19	65, 81, 107, 190	0
6	uL3	386/387 (99%)	-0.21	4 (1%) 79 59	66, 96, 124, 166	0
7	uL4	361/362 (99%)	0.41	38 (10%) 11 6	79, 123, 153, 163	0
8	uL18	296/297 (99%)	-0.63	0 100 100	88, 126, 161, 176	0
9	eL6	156/176 (88%)	-0.02	14 (8%) 15 8	103, 138, 165, 183	0
10	uL30	222/244 (90%)	-0.03	12 (5%) 31 16	82, 105, 156, 197	0
11	eL8	233/256 (91%)	-0.16	6 (2%) 57 34	95, 127, 186, 210	0
12	uL6	191/191 (100%)	-0.46	0 100 100	73, 103, 127, 167	0
13	uL16	213/221 (96%)	-0.00	6 (2%) 55 32	76, 99, 130, 152	0
14	uL5	169/174 (97%)	-0.16	2 (1%) 76 55	105, 160, 186, 197	0
15	eL13	193/199 (96%)	0.10	9 (4%) 36 19	82, 129, 161, 181	0
16	eL14	136/138 (98%)	-0.34	0 100 100	96, 122, 157, 179	0
17	eL15	203/204 (99%)	0.03	12 (5%) 28 14	74, 101, 118, 131	0
18	uL13	197/199 (98%)	-0.03	13 (6%) 24 12	74, 97, 148, 160	0
19	uL22	151/184 (82%)	-0.34	0 100 100	74, 107, 136, 142	0
20	eL18	185/186 (99%)	0.23	15 (8%) 18 9	88, 117, 136, 156	0
21	eL19	176/189 (93%)	-0.36	1 (0%) 85 69	69, 98, 166, 192	0
22	eL20	172/172 (100%)	-0.34	1 (0%) 85 69	86, 104, 123, 142	0
23	eL21	159/160 (99%)	0.00	10 (6%) 26 13	80, 101, 172, 186	0
24	eL22	97/121 (80%)	-0.07	2 (2%) 63 40	119, 146, 172, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	uL14	129/137 (94%)	-0.10	0 100 100	62, 85, 103, 110	0
26	eL24	63/155 (40%)	-0.11	0 100 100	77, 92, 117, 136	0
27	uL23	120/142 (84%)	0.33	9 (7%) 20 10	96, 117, 142, 157	0
28	uL24	126/127 (99%)	0.08	4 (3%) 50 29	106, 136, 161, 170	0
29	eL27	135/136 (99%)	-0.13	4 (2%) 52 30	93, 114, 142, 158	0
30	uL15	148/149 (99%)	0.19	9 (6%) 27 14	77, 112, 146, 154	0
31	eL29	58/59 (98%)	-0.18	1 (1%) 69 45	82, 116, 156, 186	0
32	eL30	97/105 (92%)	0.06	3 (3%) 51 30	86, 104, 148, 154	0
33	eL31	109/113 (96%)	-0.40	0 100 100	80, 111, 179, 189	0
34	eL32	127/130 (97%)	0.29	6 (4%) 36 19	84, 120, 161, 165	0
35	eL33	106/107 (99%)	-0.12	4 (3%) 44 24	89, 108, 154, 182	0
36	eL34	109/121 (90%)	0.65	17 (15%) 5 3	77, 96, 144, 167	0
37	uL29	119/120 (99%)	-0.29	0 100 100	102, 128, 155, 167	0
38	eL36	99/100 (99%)	-0.39	0 100 100	102, 124, 148, 197	0
39	eL37	84/88 (95%)	-0.02	4 (4%) 35 19	68, 98, 127, 149	0
40	eL38	77/78 (98%)	-0.15	0 100 100	102, 130, 154, 159	0
41	eL39	50/51 (98%)	0.10	3 (6%) 27 14	91, 109, 133, 144	0
42	eL40	52/128 (40%)	-0.34	0 100 100	75, 90, 112, 119	0
43	eL41	25/25 (100%)	0.17	1 (4%) 42 23	88, 102, 112, 117	0
44	eL42	102/106 (96%)	-0.03	0 100 100	75, 106, 134, 165	0
45	eL43	91/92 (98%)	0.09	5 (5%) 30 15	67, 85, 106, 124	0
46	18S	1732/1798 (96%)	-0.91	12 (0%) 84 66	65, 110, 249, 326	0
47	uS2	206/252 (81%)	-0.28	1 (0%) 87 72	92, 123, 160, 173	0
48	eS1	212/255 (83%)	0.41	14 (6%) 24 12	87, 141, 189, 206	0
49	uS5	217/254 (85%)	-0.20	6 (2%) 55 32	80, 105, 146, 187	0
50	uS3	183/240 (76%)	-0.29	1 (0%) 87 72	106, 152, 188, 200	0
51	eS4	258/261 (98%)	-0.19	5 (1%) 66 43	72, 99, 123, 189	0
52	uS7	206/225 (91%)	-0.09	3 (1%) 72 49	137, 179, 204, 219	0
53	eS6	219/236 (92%)	-0.12	6 (2%) 56 33	78, 125, 163, 187	0
54	eS7	184/190 (96%)	-0.32	0 100 100	88, 140, 196, 210	0
55	eS8	184/200 (92%)	-0.62	0 100 100	72, 104, 155, 192	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
56	uS4	185/197 (93%)	-0.27	2 (1%) 78 57	83, 108, 147, 200	0
57	eS10	33/105 (31%)	0.02	1 (3%) 52 30	155, 179, 188, 192	0
58	uS17	142/156 (91%)	-0.71	1 (0%) 84 66	65, 89, 149, 163	0
59	uS15	150/151 (99%)	-0.31	1 (0%) 84 66	74, 98, 127, 144	0
60	uS11	127/137 (92%)	0.34	8 (6%) 26 13	78, 124, 157, 168	0
61	uS19	91/142 (64%)	0.31	6 (6%) 24 12	139, 167, 193, 202	0
62	uS9	136/143 (95%)	-0.26	2 (1%) 72 49	119, 174, 201, 204	0
63	eS17	121/136 (88%)	-0.25	2 (1%) 69 45	122, 161, 189, 198	0
64	uS13	145/146 (99%)	-0.26	2 (1%) 73 51	126, 161, 194, 210	0
65	eS19	143/144 (99%)	-0.45	0 100 100	130, 160, 185, 195	0
66	uS10	30/121 (24%)	-0.29	0 100 100	111, 123, 158, 161	0
67	eS21	87/87 (100%)	-0.42	0 100 100	91, 111, 161, 168	0
68	uS8	129/130 (99%)	-0.68	0 100 100	73, 88, 103, 114	0
69	uS12	144/145 (99%)	-0.41	1 (0%) 84 66	66, 87, 113, 128	0
70	eS24	134/135 (99%)	-0.15	3 (2%) 62 39	86, 115, 175, 191	0
71	eS25	70/108 (64%)	-0.17	0 100 100	171, 203, 214, 218	0
72	eS26	94/119 (78%)	0.10	4 (4%) 40 21	77, 97, 158, 175	0
73	eS27	79/82 (96%)	-0.18	1 (1%) 75 53	85, 107, 173, 178	0
74	eS28	63/67 (94%)	-0.16	0 100 100	141, 182, 207, 214	0
75	uS14	49/56 (87%)	-0.09	4 (8%) 17 9	115, 133, 146, 150	0
76	eS30	53/63 (84%)	-0.30	1 (1%) 66 43	94, 120, 186, 189	0
77	RACK	318/319 (99%)	-0.19	2 (0%) 85 69	186, 211, 224, 230	0
78	eS31	36/152 (23%)	-0.13	0 100 100	151, 195, 204, 213	0
79	eEF2	841/842 (99%)	-0.29	16 (1%) 66 43	77, 112, 148, 178	0
80	ASIT	75/76 (98%)	-0.33	0 100 100	114, 197, 233, 248	0
81	PSIT	77/77 (100%)	-0.47	2 (2%) 57 34	81, 162, 191, 199	0
82	mRNA	8/8 (100%)	-0.32	0 100 100	115, 121, 141, 160	0
83	uL11	137/165 (83%)	0.32	8 (5%) 29 15	115, 144, 157, 168	0
All	All	17093/18690 (91%)	-0.35	370 (2%) 62 39	50, 114, 195, 326	0

The worst 5 of 370 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
36	eL34	30	LEU	9.0
15	eL13	9	ILE	8.9
11	eL8	161	GLU	8.4
7	uL4	182	LEU	7.7
7	uL4	108	LYS	7.7

6.2 Non-standard residues in protein, DNA, RNA chains [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
80	YG	ASIT	37	39/40	0.88	0.11	102,130,141,141	0
79	DDE	eEF2	699	20/21	0.94	0.25	102,119,130,134	0

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	3515	1/1	-0.04	0.32	122,122,122,122	0
84	MG	25S	3547	1/1	-0.02	0.32	109,109,109,109	0
84	MG	25S	3581[A]	1/1	0.03	0.36	86,86,86,86	1
84	MG	25S	3581[B]	1/1	0.03	0.36	87,87,87,87	1
84	MG	25S	3629[A]	1/1	0.06	0.32	69,69,69,69	1
84	MG	25S	3629[B]	1/1	0.06	0.32	74,74,74,74	1
84	MG	25S	3461[A]	1/1	0.19	0.41	68,68,68,68	1
84	MG	25S	3461[B]	1/1	0.19	0.41	68,68,68,68	1
84	MG	18S	1896	1/1	0.34	0.29	109,109,109,109	0
84	MG	25S	3483	1/1	0.38	0.28	105,105,105,105	0
84	MG	25S	3687	1/1	0.39	0.31	109,109,109,109	0
84	MG	18S	1894	1/1	0.42	0.21	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
84	MG	58S	207	1/1	0.44	0.23	104,104,104,104	0
84	MG	25S	3656	1/1	0.45	0.27	128,128,128,128	0
84	MG	25S	3704	1/1	0.46	0.27	106,106,106,106	0
84	MG	25S	3552	1/1	0.46	0.25	97,97,97,97	0
84	MG	25S	3715	1/1	0.47	0.22	97,97,97,97	0
84	MG	25S	3714	1/1	0.48	0.26	112,112,112,112	0
84	MG	25S	3700	1/1	0.49	0.27	105,105,105,105	0
84	MG	eEF2	906	1/1	0.49	0.27	110,110,110,110	0
84	MG	PSIT	103	1/1	0.52	0.19	125,125,125,125	0
84	MG	25S	3628	1/1	0.53	0.33	107,107,107,107	0
84	MG	25S	3618[A]	1/1	0.55	0.30	61,61,61,61	1
84	MG	25S	3618[B]	1/1	0.55	0.30	59,59,59,59	1
84	MG	25S	3645	1/1	0.55	0.21	104,104,104,104	0
84	MG	25S	3649	1/1	0.55	0.23	129,129,129,129	0
84	MG	25S	3538	1/1	0.55	0.30	79,79,79,79	0
84	MG	25S	3446[A]	1/1	0.56	0.28	70,70,70,70	1
84	MG	18S	1842	1/1	0.56	0.17	97,97,97,97	0
84	MG	25S	3446[B]	1/1	0.56	0.28	73,73,73,73	1
84	MG	25S	3681	1/1	0.57	0.21	113,113,113,113	0
84	MG	25S	3578	1/1	0.57	0.31	107,107,107,107	0
84	MG	25S	3679	1/1	0.58	0.25	105,105,105,105	0
84	MG	25S	3580	1/1	0.58	0.15	85,85,85,85	0
84	MG	18S	1922	1/1	0.58	0.14	91,91,91,91	0
84	MG	25S	3674	1/1	0.58	0.17	102,102,102,102	0
84	MG	18S	1886	1/1	0.58	0.35	108,108,108,108	0
84	MG	18S	1832	1/1	0.59	0.14	105,105,105,105	0
84	MG	25S	3664	1/1	0.60	0.24	108,108,108,108	0
84	MG	25S	3526	1/1	0.60	0.27	92,92,92,92	0
84	MG	25S	3703	1/1	0.60	0.26	118,118,118,118	0
84	MG	25S	3504	1/1	0.60	0.17	91,91,91,91	0
84	MG	25S	3624	1/1	0.60	0.30	115,115,115,115	0
84	MG	PSIT	105	1/1	0.60	0.14	100,100,100,100	0
84	MG	eS6	302	1/1	0.61	0.21	119,119,119,119	0
84	MG	25S	3566	1/1	0.61	0.16	77,77,77,77	0
84	MG	18S	1859	1/1	0.62	0.14	124,124,124,124	0
84	MG	ASIT	101	1/1	0.62	0.25	107,107,107,107	0
84	MG	18S	1834	1/1	0.62	0.20	123,123,123,123	0
84	MG	25S	3668	1/1	0.62	0.30	87,87,87,87	0
84	MG	18S	1883	1/1	0.63	0.21	112,112,112,112	0
84	MG	25S	3644	1/1	0.63	0.13	88,88,88,88	0
84	MG	25S	3667	1/1	0.63	0.29	100,100,100,100	0
84	MG	25S	3716	1/1	0.63	0.26	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3677	1/1	0.63	0.20	85,85,85,85	0
84	MG	eL40	201	1/1	0.64	0.42	98,98,98,98	0
84	MG	25S	3506	1/1	0.64	0.19	96,96,96,96	0
84	MG	25S	3654	1/1	0.64	0.18	112,112,112,112	0
84	MG	25S	3474	1/1	0.65	0.25	109,109,109,109	0
84	MG	25S	3632	1/1	0.66	0.29	86,86,86,86	0
84	MG	25S	3519	1/1	0.66	0.26	102,102,102,102	0
84	MG	25S	3623	1/1	0.66	0.09	80,80,80,80	0
84	MG	25S	3402[B]	1/1	0.67	0.31	64,64,64,64	1
84	MG	25S	3402[A]	1/1	0.67	0.31	62,62,62,62	1
84	MG	uS12	203	1/1	0.67	0.23	93,93,93,93	0
84	MG	25S	3617	1/1	0.67	0.20	103,103,103,103	0
84	MG	eL42	201	1/1	0.67	0.34	110,110,110,110	0
84	MG	25S	3694	1/1	0.67	0.24	88,88,88,88	0
84	MG	25S	3695	1/1	0.67	0.22	95,95,95,95	0
84	MG	18S	1914	1/1	0.68	0.20	85,85,85,85	0
84	MG	25S	3607	1/1	0.68	0.20	90,90,90,90	0
84	MG	18S	1864	1/1	0.69	0.12	103,103,103,103	0
84	MG	25S	3702	1/1	0.70	0.15	117,117,117,117	0
84	MG	25S	3459	1/1	0.70	0.32	77,77,77,77	0
84	MG	eEF2	904	1/1	0.70	0.22	82,82,82,82	0
84	MG	25S	3517	1/1	0.70	0.32	96,96,96,96	0
84	MG	25S	3713[A]	1/1	0.70	0.31	55,55,55,55	1
84	MG	eL33	201	1/1	0.70	0.15	109,109,109,109	0
84	MG	25S	3713[B]	1/1	0.70	0.31	72,72,72,72	1
84	MG	18S	1877	1/1	0.71	0.14	99,99,99,99	0
84	MG	eS6	301	1/1	0.71	0.18	137,137,137,137	0
84	MG	25S	3438	1/1	0.71	0.37	85,85,85,85	0
84	MG	25S	3697	1/1	0.71	0.20	86,86,86,86	0
84	MG	25S	3626	1/1	0.71	0.21	95,95,95,95	0
84	MG	25S	3672	1/1	0.71	0.19	89,89,89,89	0
84	MG	18S	1899	1/1	0.71	0.24	97,97,97,97	0
84	MG	18S	1913	1/1	0.71	0.20	104,104,104,104	0
84	MG	18S	1873	1/1	0.71	0.16	85,85,85,85	0
84	MG	25S	3615	1/1	0.72	0.26	110,110,110,110	0
84	MG	25S	3406	1/1	0.72	0.30	74,74,74,74	0
84	MG	25S	3550	1/1	0.72	0.21	82,82,82,82	0
84	MG	18S	1840	1/1	0.72	0.25	85,85,85,85	0
84	MG	25S	3693	1/1	0.72	0.19	84,84,84,84	0
84	MG	25S	3633	1/1	0.72	0.22	95,95,95,95	0
84	MG	18S	1912	1/1	0.72	0.11	92,92,92,92	0
84	MG	25S	3707	1/1	0.72	0.23	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3482	1/1	0.72	0.24	84,84,84,84	0
84	MG	25S	3655	1/1	0.73	0.18	101,101,101,101	0
84	MG	25S	3636	1/1	0.73	0.34	95,95,95,95	0
84	MG	25S	3612	1/1	0.73	0.20	74,74,74,74	0
84	MG	25S	3625	1/1	0.73	0.13	96,96,96,96	0
84	MG	25S	3488	1/1	0.73	0.21	94,94,94,94	0
84	MG	18S	1816	1/1	0.73	0.11	70,70,70,70	0
84	MG	18S	1822	1/1	0.73	0.37	75,75,75,75	0
84	MG	25S	3553	1/1	0.73	0.25	82,82,82,82	0
84	MG	25S	3503	1/1	0.74	0.13	92,92,92,92	0
84	MG	25S	3590	1/1	0.74	0.28	93,93,93,93	0
84	MG	25S	3686	1/1	0.74	0.08	110,110,110,110	0
84	MG	eS1	301	1/1	0.74	0.11	127,127,127,127	0
84	MG	25S	3524	1/1	0.74	0.24	89,89,89,89	0
84	MG	18S	1854	1/1	0.74	0.30	80,80,80,80	0
84	MG	25S	3456	1/1	0.75	0.10	73,73,73,73	0
84	MG	eL41	101	1/1	0.75	0.22	70,70,70,70	0
84	MG	25S	3549	1/1	0.75	0.24	89,89,89,89	0
84	MG	25S	3430	1/1	0.75	0.20	92,92,92,92	0
84	MG	18S	1906	1/1	0.75	0.18	91,91,91,91	0
84	MG	18S	1821	1/1	0.75	0.12	135,135,135,135	0
84	MG	25S	3689	1/1	0.75	0.32	121,121,121,121	0
84	MG	eL31	201	1/1	0.75	0.29	93,93,93,93	0
84	MG	25S	3500	1/1	0.75	0.17	87,87,87,87	0
84	MG	25S	3670	1/1	0.76	0.10	85,85,85,85	0
84	MG	25S	3512	1/1	0.76	0.39	101,101,101,101	0
84	MG	25S	3589	1/1	0.76	0.26	77,77,77,77	0
84	MG	25S	3452	1/1	0.76	0.29	79,79,79,79	0
84	MG	25S	3510	1/1	0.76	0.31	91,91,91,91	0
84	MG	25S	3621	1/1	0.76	0.17	76,76,76,76	0
84	MG	25S	3684	1/1	0.76	0.22	91,91,91,91	0
84	MG	eEF2	905	1/1	0.76	0.21	87,87,87,87	0
84	MG	18S	1901	1/1	0.76	0.18	115,115,115,115	0
84	MG	25S	3565	1/1	0.76	0.25	93,93,93,93	0
84	MG	18S	1867	1/1	0.76	0.32	92,92,92,92	0
84	MG	18S	1872	1/1	0.76	0.31	90,90,90,90	0
84	MG	25S	3477	1/1	0.77	0.20	74,74,74,74	0
84	MG	18S	1805	1/1	0.77	0.24	73,73,73,73	0
84	MG	18S	1902	1/1	0.77	0.07	115,115,115,115	0
84	MG	18S	1892	1/1	0.77	0.28	88,88,88,88	0
84	MG	uL3	401	1/1	0.77	0.30	60,60,60,60	0
84	MG	25S	3560	1/1	0.77	0.21	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	18S	1841	1/1	0.78	0.30	87,87,87,87	0
84	MG	18S	1900	1/1	0.78	0.15	72,72,72,72	0
84	MG	25S	3604	1/1	0.78	0.18	82,82,82,82	0
84	MG	25S	3543	1/1	0.78	0.22	81,81,81,81	0
84	MG	uS14	101	1/1	0.78	0.12	82,82,82,82	0
84	MG	18S	1825	1/1	0.78	0.10	122,122,122,122	0
84	MG	18S	1911	1/1	0.78	0.08	93,93,93,93	0
84	MG	25S	3641	1/1	0.78	0.08	93,93,93,93	0
84	MG	25S	3502	1/1	0.78	0.39	97,97,97,97	0
84	MG	25S	3539	1/1	0.78	0.24	55,55,55,55	0
84	MG	18S	1898	1/1	0.78	0.15	89,89,89,89	0
84	MG	25S	3493	1/1	0.79	0.23	77,77,77,77	0
84	MG	AB	204	1/1	0.79	0.07	107,107,107,107	0
84	MG	25S	3647	1/1	0.79	0.10	98,98,98,98	0
84	MG	25S	3706	1/1	0.79	0.19	76,76,76,76	0
84	MG	uS12	201	1/1	0.79	0.20	101,101,101,101	0
84	MG	25S	3610	1/1	0.79	0.11	78,78,78,78	0
84	MG	25S	3710	1/1	0.79	0.25	100,100,100,100	0
84	MG	25S	3498	1/1	0.79	0.22	97,97,97,97	0
84	MG	25S	3685	1/1	0.79	0.15	99,99,99,99	0
84	MG	18S	1891	1/1	0.79	0.19	133,133,133,133	0
84	MG	25S	3479	1/1	0.79	0.26	94,94,94,94	0
84	MG	25S	3440	1/1	0.79	0.18	82,82,82,82	0
84	MG	18S	1920	1/1	0.79	0.15	82,82,82,82	0
84	MG	18S	1860	1/1	0.80	0.19	79,79,79,79	0
84	MG	25S	3640	1/1	0.80	0.30	107,107,107,107	0
84	MG	25S	3460	1/1	0.80	0.25	69,69,69,69	0
84	MG	25S	3696	1/1	0.80	0.26	87,87,87,87	0
84	MG	25S	3571	1/1	0.80	0.24	118,118,118,118	0
84	MG	18S	1919	1/1	0.80	0.25	92,92,92,92	0
84	MG	18S	1850	1/1	0.80	0.11	77,77,77,77	0
84	MG	25S	3692	1/1	0.80	0.21	88,88,88,88	0
84	MG	18S	1885	1/1	0.80	0.24	79,79,79,79	0
84	MG	25S	3521	1/1	0.80	0.17	66,66,66,66	0
84	MG	25S	3609	1/1	0.81	0.23	108,108,108,108	0
84	MG	25S	3485	1/1	0.81	0.26	61,61,61,61	0
84	MG	25S	3421	1/1	0.81	0.29	81,81,81,81	0
84	MG	25S	3457	1/1	0.81	0.35	86,86,86,86	0
84	MG	18S	1917	1/1	0.81	0.15	71,71,71,71	0
84	MG	25S	3682	1/1	0.81	0.21	98,98,98,98	0
84	MG	25S	3508	1/1	0.81	0.15	87,87,87,87	0
84	MG	18S	1921	1/1	0.81	0.18	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3630	1/1	0.81	0.17	99,99,99,99	0
84	MG	25S	3709	1/1	0.81	0.18	95,95,95,95	0
84	MG	eS4	302	1/1	0.81	0.22	83,83,83,83	0
84	MG	25S	3465	1/1	0.81	0.23	69,69,69,69	0
84	MG	18S	1824	1/1	0.81	0.22	79,79,79,79	0
84	MG	uS19	201	1/1	0.81	0.17	101,101,101,101	0
84	MG	25S	3657	1/1	0.81	0.27	78,78,78,78	0
84	MG	25S	3663	1/1	0.81	0.19	97,97,97,97	0
84	MG	25S	3691	1/1	0.81	0.23	87,87,87,87	0
84	MG	25S	3556	1/1	0.81	0.17	86,86,86,86	0
84	MG	25S	3472	1/1	0.81	0.28	82,82,82,82	0
84	MG	AB	202	1/1	0.81	0.13	73,73,73,73	0
84	MG	25S	3637	1/1	0.81	0.16	86,86,86,86	0
84	MG	25S	3473	1/1	0.81	0.21	79,79,79,79	0
84	MG	25S	3516	1/1	0.81	0.21	68,68,68,68	0
84	MG	18S	1851	1/1	0.82	0.10	82,82,82,82	0
84	MG	18S	1908	1/1	0.82	0.10	81,81,81,81	0
84	MG	25S	3532	1/1	0.82	0.35	73,73,73,73	0
84	MG	25S	3576	1/1	0.82	0.12	136,136,136,136	0
84	MG	25S	3497	1/1	0.82	0.45	84,84,84,84	0
84	MG	25S	3600	1/1	0.82	0.41	100,100,100,100	0
84	MG	18S	1915	1/1	0.82	0.15	96,96,96,96	0
84	MG	25S	3579	1/1	0.82	0.29	61,61,61,61	0
84	MG	18S	1808	1/1	0.82	0.21	65,65,65,65	0
84	MG	25S	3557	1/1	0.82	0.18	83,83,83,83	0
84	MG	18S	1875	1/1	0.82	0.17	75,75,75,75	0
84	MG	PSIT	102	1/1	0.82	0.28	86,86,86,86	0
84	MG	18S	1817	1/1	0.82	0.12	90,90,90,90	0
84	MG	25S	3567	1/1	0.82	0.47	108,108,108,108	0
84	MG	25S	3699	1/1	0.83	0.14	76,76,76,76	0
84	MG	25S	3588	1/1	0.83	0.21	78,78,78,78	0
84	MG	eS4	303	1/1	0.83	0.13	96,96,96,96	0
84	MG	18S	1818	1/1	0.83	0.39	87,87,87,87	0
84	MG	18S	1839	1/1	0.83	0.36	85,85,85,85	0
84	MG	uL18	301	1/1	0.83	0.11	109,109,109,109	0
84	MG	25S	3620	1/1	0.83	0.26	85,85,85,85	0
84	MG	25S	3445	1/1	0.83	0.16	72,72,72,72	0
84	MG	25S	3412	1/1	0.84	0.41	59,59,59,59	0
84	MG	25S	3575	1/1	0.84	0.18	64,64,64,64	0
84	MG	25S	3648	1/1	0.84	0.20	87,87,87,87	0
84	MG	25S	3599	1/1	0.84	0.12	91,91,91,91	0
84	MG	18S	1865	1/1	0.84	0.27	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3541	1/1	0.84	0.19	74,74,74,74	0
84	MG	25S	3443	1/1	0.84	0.17	65,65,65,65	0
84	MG	18S	1905	1/1	0.84	0.20	80,80,80,80	0
84	MG	25S	3401	1/1	0.84	0.33	58,58,58,58	0
84	MG	18S	1874	1/1	0.84	0.10	81,81,81,81	0
84	MG	25S	3561	1/1	0.84	0.10	61,61,61,61	0
84	MG	25S	3462	1/1	0.84	0.26	64,64,64,64	0
84	MG	25S	3534	1/1	0.84	0.08	86,86,86,86	0
84	MG	18S	1804	1/1	0.84	0.22	71,71,71,71	0
84	MG	25S	3463	1/1	0.84	0.24	78,78,78,78	0
84	MG	25S	3701	1/1	0.84	0.06	105,105,105,105	0
84	MG	25S	3717	1/1	0.84	0.17	88,88,88,88	0
84	MG	18S	1893	1/1	0.84	0.23	75,75,75,75	0
84	MG	mRNA	600	1/1	0.84	0.07	82,82,82,82	0
84	MG	58S	202	1/1	0.85	0.11	97,97,97,97	0
84	MG	58S	203	1/1	0.85	0.07	117,117,117,117	0
84	MG	58S	206	1/1	0.85	0.23	87,87,87,87	0
84	MG	18S	1844	1/1	0.85	0.24	77,77,77,77	0
84	MG	25S	3466	1/1	0.85	0.29	75,75,75,75	0
84	MG	25S	3487	1/1	0.85	0.31	72,72,72,72	0
84	MG	25S	3427	1/1	0.85	0.23	67,67,67,67	0
84	MG	18S	1857	1/1	0.85	0.07	97,97,97,97	0
84	MG	25S	3490	1/1	0.85	0.17	80,80,80,80	0
84	MG	25S	3484	1/1	0.85	0.23	87,87,87,87	0
84	MG	25S	3591	1/1	0.85	0.16	99,99,99,99	0
84	MG	18S	1895	1/1	0.85	0.18	92,92,92,92	0
84	MG	PSIT	101	1/1	0.85	0.10	87,87,87,87	0
84	MG	25S	3570	1/1	0.85	0.22	83,83,83,83	0
84	MG	AB	203	1/1	0.85	0.17	71,71,71,71	0
84	MG	18S	1869	1/1	0.85	0.20	75,75,75,75	0
84	MG	PSIT	106	1/1	0.85	0.17	92,92,92,92	0
84	MG	25S	3646	1/1	0.85	0.19	85,85,85,85	0
84	MG	25S	3425	1/1	0.86	0.20	64,64,64,64	0
84	MG	25S	3658	1/1	0.86	0.29	78,78,78,78	0
84	MG	18S	1897	1/1	0.86	0.17	102,102,102,102	0
84	MG	eL15	301	1/1	0.86	0.12	83,83,83,83	0
84	MG	eL18	201	1/1	0.86	0.20	89,89,89,89	0
84	MG	18S	1826	1/1	0.86	0.21	86,86,86,86	0
84	MG	25S	3464	1/1	0.86	0.14	65,65,65,65	0
84	MG	25S	3531	1/1	0.86	0.06	78,78,78,78	0
84	MG	18S	1835	1/1	0.86	0.23	79,79,79,79	0
84	MG	25S	3501	1/1	0.86	0.12	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3594	1/1	0.86	0.10	102,102,102,102	0
84	MG	25S	3669	1/1	0.86	0.12	84,84,84,84	0
84	MG	25S	3688	1/1	0.86	0.27	98,98,98,98	0
84	MG	25S	3598	1/1	0.86	0.15	69,69,69,69	0
84	MG	18S	1848	1/1	0.86	0.16	83,83,83,83	0
84	MG	18S	1888	1/1	0.86	0.08	61,61,61,61	0
84	MG	25S	3671	1/1	0.86	0.29	75,75,75,75	0
84	MG	25S	3480	1/1	0.86	0.23	69,69,69,69	0
84	MG	25S	3627	1/1	0.86	0.11	84,84,84,84	0
84	MG	25S	3470	1/1	0.86	0.10	83,83,83,83	0
84	MG	18S	1809	1/1	0.87	0.21	91,91,91,91	0
84	MG	18S	1814	1/1	0.87	0.21	88,88,88,88	0
84	MG	eL30	201	1/1	0.87	0.33	81,81,81,81	0
84	MG	eL30	202	1/1	0.87	0.32	69,69,69,69	0
84	MG	25S	3404	1/1	0.87	0.18	61,61,61,61	0
84	MG	18S	1879	1/1	0.87	0.14	135,135,135,135	0
84	MG	25S	3505	1/1	0.87	0.20	71,71,71,71	0
84	MG	25S	3468	1/1	0.87	0.18	91,91,91,91	0
84	MG	eEF2	903	1/1	0.87	0.24	78,78,78,78	0
84	MG	18S	1853	1/1	0.87	0.38	70,70,70,70	0
84	MG	25S	3476	1/1	0.87	0.20	64,64,64,64	0
84	MG	25S	3431	1/1	0.87	0.33	61,61,61,61	0
84	MG	eL42	202	1/1	0.87	0.26	90,90,90,90	0
84	MG	25S	3564	1/1	0.87	0.17	105,105,105,105	0
84	MG	25S	3442	1/1	0.87	0.21	67,67,67,67	0
84	MG	18S	1806	1/1	0.87	0.25	60,60,60,60	0
84	MG	18S	1866	1/1	0.87	0.18	66,66,66,66	0
84	MG	18S	1837	1/1	0.87	0.26	61,61,61,61	0
84	MG	25S	3608	1/1	0.87	0.18	71,71,71,71	0
84	MG	25S	3652	1/1	0.88	0.22	67,67,67,67	0
84	MG	25S	3426	1/1	0.88	0.38	50,50,50,50	0
84	MG	25S	3678	1/1	0.88	0.06	94,94,94,94	0
84	MG	25S	3622	1/1	0.88	0.21	78,78,78,78	0
84	MG	25S	3698	1/1	0.88	0.22	82,82,82,82	0
84	MG	25S	3409	1/1	0.88	0.17	62,62,62,62	0
84	MG	25S	3435	1/1	0.88	0.19	71,71,71,71	0
84	MG	25S	3639	1/1	0.88	0.13	90,90,90,90	0
84	MG	58S	201	1/1	0.88	0.16	77,77,77,77	0
84	MG	25S	3475	1/1	0.88	0.20	58,58,58,58	0
84	MG	18S	1876	1/1	0.88	0.19	83,83,83,83	0
84	MG	25S	3582	1/1	0.88	0.21	78,78,78,78	0
84	MG	25S	3616	1/1	0.88	0.12	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	18S	1882	1/1	0.88	0.05	75,75,75,75	0
84	MG	25S	3587	1/1	0.88	0.09	70,70,70,70	0
84	MG	25S	3602	1/1	0.88	0.08	64,64,64,64	0
84	MG	25S	3708	1/1	0.88	0.29	86,86,86,86	0
84	MG	25S	3577	1/1	0.88	0.12	76,76,76,76	0
84	MG	18S	1819	1/1	0.88	0.20	62,62,62,62	0
84	MG	25S	3429	1/1	0.88	0.18	72,72,72,72	0
84	MG	25S	3631	1/1	0.88	0.19	101,101,101,101	0
84	MG	25S	3416	1/1	0.89	0.32	63,63,63,63	0
84	MG	25S	3711	1/1	0.89	0.15	94,94,94,94	0
84	MG	25S	3712	1/1	0.89	0.21	72,72,72,72	0
84	MG	25S	3467	1/1	0.89	0.18	69,69,69,69	0
84	MG	25S	3417	1/1	0.89	0.25	59,59,59,59	0
84	MG	25S	3413	1/1	0.89	0.22	55,55,55,55	0
84	MG	25S	3592	1/1	0.89	0.19	111,111,111,111	0
84	MG	25S	3659	1/1	0.89	0.17	74,74,74,74	0
84	MG	25S	3542	1/1	0.89	0.06	98,98,98,98	0
84	MG	AB	201	1/1	0.89	0.16	102,102,102,102	0
84	MG	25S	3683	1/1	0.89	0.10	75,75,75,75	0
84	MG	25S	3471	1/1	0.89	0.11	64,64,64,64	0
84	MG	25S	3665	1/1	0.89	0.20	87,87,87,87	0
84	MG	25S	3666	1/1	0.89	0.21	85,85,85,85	0
84	MG	25S	3544	1/1	0.89	0.20	71,71,71,71	0
84	MG	18S	1847	1/1	0.89	0.08	61,61,61,61	0
84	MG	25S	3530	1/1	0.89	0.18	61,61,61,61	0
84	MG	18S	1884	1/1	0.89	0.12	83,83,83,83	0
84	MG	25S	3548	1/1	0.89	0.12	79,79,79,79	0
84	MG	25S	3441	1/1	0.89	0.17	58,58,58,58	0
84	MG	uL2	303	1/1	0.89	0.21	91,91,91,91	0
84	MG	25S	3432	1/1	0.89	0.28	67,67,67,67	0
84	MG	25S	3495	1/1	0.90	0.18	84,84,84,84	0
84	MG	25S	3513	1/1	0.90	0.13	67,67,67,67	0
84	MG	18S	1801	1/1	0.90	0.18	66,66,66,66	0
84	MG	eEF2	902	1/1	0.90	0.17	75,75,75,75	0
84	MG	eL20	201	1/1	0.90	0.11	79,79,79,79	0
84	MG	18S	1881	1/1	0.90	0.13	85,85,85,85	0
84	MG	58S	204	1/1	0.90	0.30	76,76,76,76	0
84	MG	25S	3405	1/1	0.90	0.20	59,59,59,59	0
84	MG	25S	3415	1/1	0.90	0.13	78,78,78,78	0
84	MG	25S	3568	1/1	0.90	0.10	69,69,69,69	0
84	MG	18S	1828	1/1	0.90	0.14	83,83,83,83	0
84	MG	18S	1870	1/1	0.90	0.12	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	18S	1831	1/1	0.90	0.16	114,114,114,114	0
84	MG	25S	3439	1/1	0.90	0.15	63,63,63,63	0
84	MG	25S	3518	1/1	0.90	0.08	95,95,95,95	0
84	MG	18S	1918	1/1	0.91	0.08	121,121,121,121	0
84	MG	25S	3535	1/1	0.91	0.08	85,85,85,85	0
84	MG	25S	3436	1/1	0.91	0.30	69,69,69,69	0
84	MG	18S	1856	1/1	0.91	0.29	63,63,63,63	0
84	MG	25S	3458	1/1	0.91	0.19	68,68,68,68	0
84	MG	25S	3424	1/1	0.91	0.23	61,61,61,61	0
84	MG	eS4	301	1/1	0.91	0.15	84,84,84,84	0
84	MG	25S	3563	1/1	0.91	0.14	82,82,82,82	0
84	MG	18S	1861	1/1	0.91	0.16	54,54,54,54	0
84	MG	25S	3410	1/1	0.91	0.21	57,57,57,57	0
84	MG	25S	3523	1/1	0.91	0.06	80,80,80,80	0
84	MG	25S	3585	1/1	0.91	0.16	76,76,76,76	0
84	MG	25S	3586	1/1	0.91	0.27	83,83,83,83	0
84	MG	uS12	202	1/1	0.91	0.13	84,84,84,84	0
84	MG	25S	3680	1/1	0.91	0.09	78,78,78,78	0
84	MG	25S	3509	1/1	0.91	0.13	76,76,76,76	0
84	MG	25S	3453	1/1	0.91	0.21	75,75,75,75	0
84	MG	25S	3527	1/1	0.91	0.11	81,81,81,81	0
84	MG	25S	3634	1/1	0.91	0.06	84,84,84,84	0
84	MG	25S	3660	1/1	0.91	0.16	86,86,86,86	0
84	MG	25S	3455	1/1	0.91	0.23	44,44,44,44	0
84	MG	18S	1813	1/1	0.91	0.11	109,109,109,109	0
84	MG	25S	3486	1/1	0.91	0.21	57,57,57,57	0
84	MG	25S	3574	1/1	0.91	0.14	73,73,73,73	0
84	MG	25S	3414	1/1	0.91	0.17	44,44,44,44	0
84	MG	25S	3478	1/1	0.91	0.32	79,79,79,79	0
84	MG	18S	1916	1/1	0.91	0.08	81,81,81,81	0
84	MG	18S	1852	1/1	0.91	0.18	71,71,71,71	0
84	MG	18S	1909	1/1	0.92	0.08	94,94,94,94	0
84	MG	25S	3540	1/1	0.92	0.11	63,63,63,63	0
84	MG	25S	3514	1/1	0.92	0.05	89,89,89,89	0
84	MG	25S	3496	1/1	0.92	0.28	75,75,75,75	0
84	MG	25S	3433	1/1	0.92	0.19	45,45,45,45	0
84	MG	18S	1820	1/1	0.92	0.15	77,77,77,77	0
84	MG	25S	3481	1/1	0.92	0.17	87,87,87,87	0
84	MG	25S	3536	1/1	0.92	0.06	86,86,86,86	0
84	MG	25S	3676	1/1	0.92	0.12	90,90,90,90	0
84	MG	18S	1802	1/1	0.92	0.13	56,56,56,56	0
84	MG	25S	3662	1/1	0.92	0.18	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3418	1/1	0.92	0.21	50,50,50,50	0
84	MG	uL22	201	1/1	0.92	0.16	78,78,78,78	0
84	MG	25S	3573	1/1	0.92	0.07	74,74,74,74	0
84	MG	25S	3408	1/1	0.92	0.14	68,68,68,68	0
84	MG	PSIT	104	1/1	0.92	0.10	104,104,104,104	0
84	MG	18S	1810	1/1	0.92	0.25	64,64,64,64	0
84	MG	25S	3595	1/1	0.92	0.11	86,86,86,86	0
84	MG	25S	3596	1/1	0.92	0.17	51,51,51,51	0
86	GTP	eEF2	907	32/32	0.92	0.08	74,93,109,114	0
84	MG	25S	3572	1/1	0.93	0.09	111,111,111,111	0
84	MG	18S	1807	1/1	0.93	0.19	60,60,60,60	0
84	MG	25S	3597	1/1	0.93	0.16	62,62,62,62	0
84	MG	25S	3499	1/1	0.93	0.14	78,78,78,78	0
84	MG	18S	1838	1/1	0.93	0.12	60,60,60,60	0
84	MG	25S	3447	1/1	0.93	0.27	66,66,66,66	0
84	MG	25S	3444	1/1	0.93	0.13	77,77,77,77	0
84	MG	uS15	201	1/1	0.93	0.07	63,63,63,63	0
84	MG	25S	3420	1/1	0.93	0.18	58,58,58,58	0
84	MG	18S	1815	1/1	0.93	0.31	63,63,63,63	0
84	MG	25S	3603	1/1	0.93	0.07	84,84,84,84	0
84	MG	18S	1846	1/1	0.93	0.15	63,63,63,63	0
84	MG	18S	1907	1/1	0.93	0.09	82,82,82,82	0
84	MG	25S	3494	1/1	0.93	0.20	78,78,78,78	0
84	MG	AB	205	1/1	0.93	0.09	101,101,101,101	0
84	MG	18S	1910	1/1	0.93	0.10	71,71,71,71	0
84	MG	25S	3635	1/1	0.93	0.11	80,80,80,80	0
84	MG	25S	3554	1/1	0.93	0.21	74,74,74,74	0
84	MG	25S	3545	1/1	0.93	0.08	81,81,81,81	0
84	MG	25S	3638	1/1	0.93	0.05	83,83,83,83	0
84	MG	25S	3569	1/1	0.93	0.23	72,72,72,72	0
84	MG	25S	3546	1/1	0.93	0.21	59,59,59,59	0
84	MG	18S	1803	1/1	0.93	0.08	54,54,54,54	0
84	MG	18S	1890	1/1	0.93	0.07	71,71,71,71	0
84	MG	25S	3661	1/1	0.93	0.18	53,53,53,53	0
84	MG	18S	1829	1/1	0.93	0.17	62,62,62,62	0
84	MG	25S	3522	1/1	0.93	0.10	67,67,67,67	0
84	MG	25S	3653	1/1	0.94	0.08	72,72,72,72	0
84	MG	18S	1843	1/1	0.94	0.09	72,72,72,72	0
84	MG	25S	3555	1/1	0.94	0.09	62,62,62,62	0
84	MG	25S	3583	1/1	0.94	0.07	90,90,90,90	0
84	MG	25S	3469	1/1	0.94	0.15	57,57,57,57	0
84	MG	25S	3492	1/1	0.94	0.06	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	uL2	301	1/1	0.94	0.23	64,64,64,64	0
84	MG	25S	3558	1/1	0.94	0.11	64,64,64,64	0
84	MG	25S	3422	1/1	0.94	0.12	81,81,81,81	0
84	MG	18S	1827	1/1	0.94	0.26	70,70,70,70	0
84	MG	25S	3537	1/1	0.94	0.18	58,58,58,58	0
84	MG	25S	3525	1/1	0.94	0.12	86,86,86,86	0
84	MG	25S	3428	1/1	0.94	0.32	64,64,64,64	0
84	MG	25S	3448	1/1	0.94	0.11	88,88,88,88	0
84	MG	25S	3551	1/1	0.94	0.06	80,80,80,80	0
84	MG	18S	1812	1/1	0.94	0.18	56,56,56,56	0
84	MG	18S	1862	1/1	0.94	0.08	62,62,62,62	0
84	MG	18S	1863	1/1	0.94	0.07	85,85,85,85	0
84	MG	25S	3613	1/1	0.94	0.12	87,87,87,87	0
84	MG	25S	3614	1/1	0.94	0.08	105,105,105,105	0
84	MG	25S	3419	1/1	0.94	0.16	48,48,48,48	0
84	MG	25S	3520	1/1	0.94	0.06	82,82,82,82	0
84	MG	18S	1868	1/1	0.94	0.07	70,70,70,70	0
85	ZN	eS31	201	1/1	0.94	0.04	210,210,210,210	0
84	MG	25S	3489	1/1	0.94	0.06	110,110,110,110	0
84	MG	25S	3411	1/1	0.95	0.13	75,75,75,75	0
84	MG	25S	3407	1/1	0.95	0.36	61,61,61,61	0
84	MG	uL14	201	1/1	0.95	0.20	55,55,55,55	0
84	MG	18S	1889	1/1	0.95	0.11	58,58,58,58	0
84	MG	25S	3507	1/1	0.95	0.18	62,62,62,62	0
84	MG	25S	3437	1/1	0.95	0.18	64,64,64,64	0
84	MG	18S	1849	1/1	0.95	0.08	60,60,60,60	0
84	MG	25S	3449	1/1	0.95	0.04	65,65,65,65	0
84	MG	18S	1830	1/1	0.95	0.15	69,69,69,69	0
84	MG	25S	3690	1/1	0.95	0.11	66,66,66,66	0
84	MG	25S	3642	1/1	0.95	0.04	91,91,91,91	0
84	MG	25S	3643	1/1	0.95	0.06	69,69,69,69	0
84	MG	25S	3705	1/1	0.95	0.11	72,72,72,72	0
84	MG	25S	3605	1/1	0.95	0.06	88,88,88,88	0
84	MG	25S	3491	1/1	0.95	0.34	63,63,63,63	0
84	MG	18S	1880	1/1	0.95	0.03	74,74,74,74	0
84	MG	uL18	302	1/1	0.95	0.14	75,75,75,75	0
84	MG	18S	1903	1/1	0.95	0.06	97,97,97,97	0
84	MG	uL16	301	1/1	0.95	0.10	77,77,77,77	0
84	MG	25S	3511	1/1	0.95	0.06	80,80,80,80	0
84	MG	25S	3450	1/1	0.95	0.13	62,62,62,62	0
84	MG	eS26	201	1/1	0.96	0.34	52,52,52,52	0
84	MG	25S	3675	1/1	0.96	0.04	66,66,66,66	0

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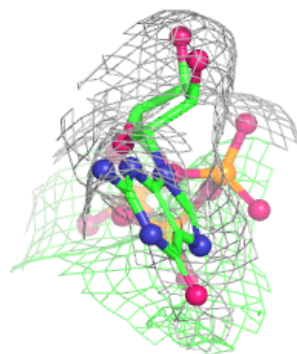
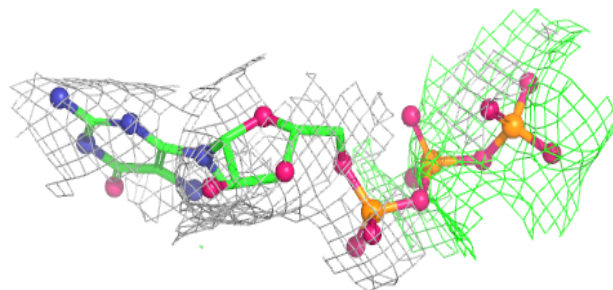
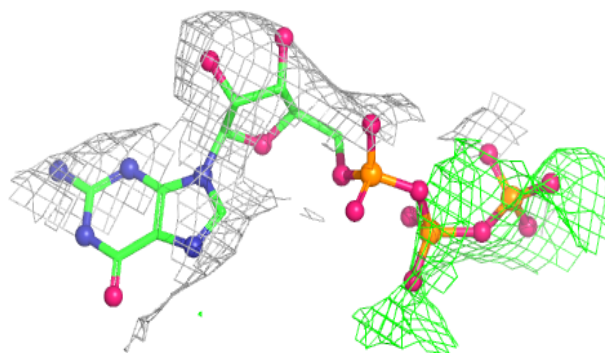
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	eEF2	901	1/1	0.96	0.07	66,66,66,66	0
84	MG	25S	3423	1/1	0.96	0.13	65,65,65,65	0
84	MG	18S	1836	1/1	0.96	0.09	86,86,86,86	0
84	MG	25S	3584	1/1	0.96	0.10	68,68,68,68	0
84	MG	25S	3454	1/1	0.96	0.18	78,78,78,78	0
84	MG	25S	3650	1/1	0.96	0.11	69,69,69,69	0
84	MG	18S	1811	1/1	0.96	0.07	58,58,58,58	0
84	MG	25S	3651	1/1	0.96	0.09	74,74,74,74	0
84	MG	18S	1858	1/1	0.96	0.09	73,73,73,73	0
84	MG	25S	3529	1/1	0.96	0.24	49,49,49,49	0
84	MG	25S	3593	1/1	0.96	0.08	95,95,95,95	0
84	MG	25S	3562	1/1	0.96	0.12	57,57,57,57	0
84	MG	18S	1845	1/1	0.96	0.10	66,66,66,66	0
84	MG	58S	205	1/1	0.96	0.05	93,93,93,93	0
84	MG	25S	3673	1/1	0.96	0.14	63,63,63,63	0
84	MG	25S	3533	1/1	0.96	0.13	55,55,55,55	0
84	MG	25S	3559	1/1	0.97	0.11	77,77,77,77	0
84	MG	25S	3451	1/1	0.97	0.11	51,51,51,51	0
84	MG	18S	1823	1/1	0.97	0.04	128,128,128,128	0
84	MG	18S	1855	1/1	0.97	0.08	65,65,65,65	0
84	MG	18S	1904	1/1	0.97	0.05	87,87,87,87	0
84	MG	25S	3611	1/1	0.97	0.03	64,64,64,64	0
84	MG	25S	3403	1/1	0.97	0.16	54,54,54,54	0
84	MG	25S	3619	1/1	0.97	0.05	83,83,83,83	0
84	MG	25S	3606	1/1	0.97	0.09	70,70,70,70	0
84	MG	uL2	302	1/1	0.97	0.04	61,61,61,61	0
84	MG	25S	3601	1/1	0.97	0.06	72,72,72,72	0
84	MG	25S	3528	1/1	0.97	0.04	75,75,75,75	0
84	MG	18S	1887	1/1	0.97	0.03	49,49,49,49	0
84	MG	18S	1871	1/1	0.98	0.02	73,73,73,73	0
84	MG	25S	3434	1/1	0.98	0.11	56,56,56,56	0
85	ZN	eL34	201	1/1	0.98	0.04	120,120,120,120	0
85	ZN	eL37	101	1/1	0.98	0.12	124,124,124,124	0
85	ZN	eL40	202	1/1	0.98	0.18	170,170,170,170	0
84	MG	18S	1833	1/1	0.98	0.07	105,105,105,105	0
84	MG	eL32	201	1/1	0.98	0.05	83,83,83,83	0
85	ZN	eL43	101	1/1	0.99	0.18	124,124,124,124	0
85	ZN	eS26	202	1/1	0.99	0.02	79,79,79,79	0
85	ZN	uS14	102	1/1	0.99	0.02	139,139,139,139	0
84	MG	18S	1878	1/1	0.99	0.07	76,76,76,76	0
85	ZN	eL42	203	1/1	0.99	0.03	113,113,113,113	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 907:

$2mF_o - DF_c$ (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.