



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:20 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 Full wwPDB X-ray Structure Validation 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

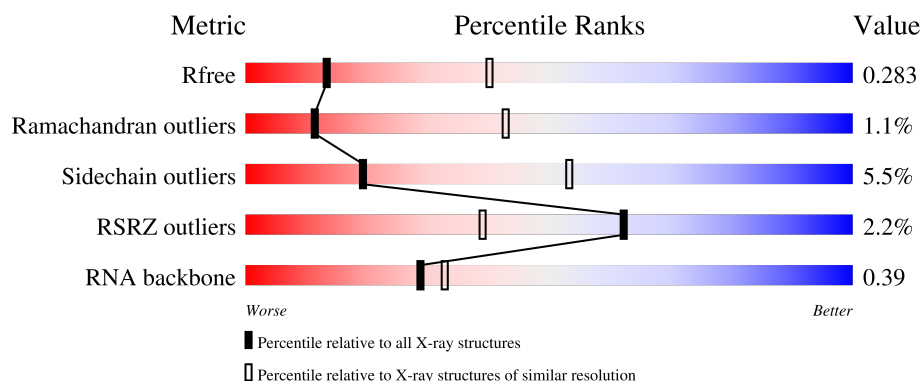
1 Overall quality at a glance

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	

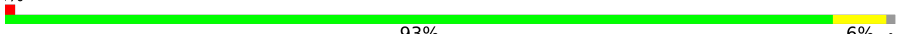
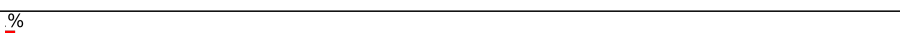
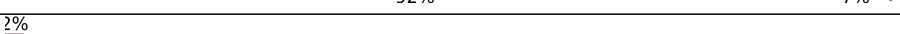
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Mol	Chain	Length	Quality of chain
30	uL15	149	
31	eL29	59	
32	eL30	105	
33	eL31	113	
34	eL32	130	
35	eL33	107	
36	eL34	121	
37	uL29	120	
38	eL36	100	
39	eL37	88	
40	eL38	78	
41	eL39	51	
42	eL40	128	
43	eL41	25	
44	eL42	106	
45	eL43	92	
46	18S	1798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

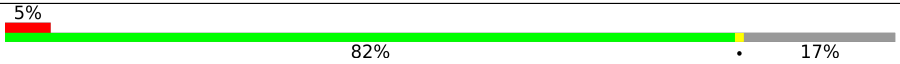
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Mol	Chain	Length	Quality of chain
55	eS8	200	
56	uS4	197	
57	eS10	105	
58	uS17	156	
59	uS15	151	
60	uS11	137	
61	uS19	142	
62	uS9	143	
63	eS17	136	
64	uS13	146	
65	eS19	144	
66	uS10	121	
67	eS21	87	
68	uS8	130	
69	uS12	145	
70	eS24	135	
71	eS25	108	
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	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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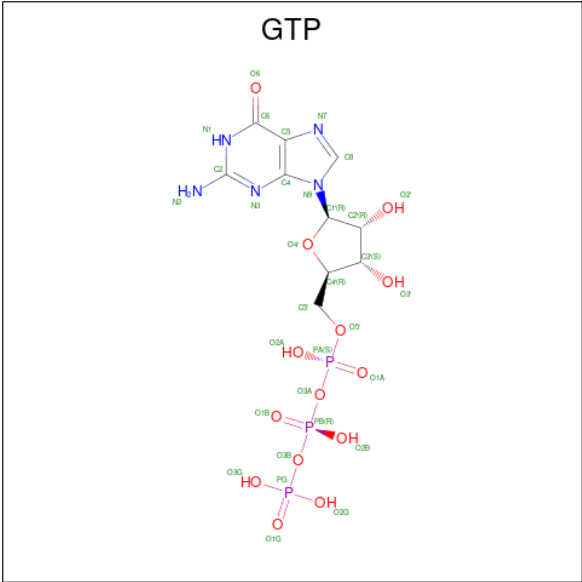
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
84	eS6	2	Total	Mg	0	0
			2	2		
84	uS15	1	Total	Mg	0	0
			1	1		
84	uS19	1	Total	Mg	0	0
			1	1		
84	uS12	3	Total	Mg	0	0
			3	3		
84	eS26	1	Total	Mg	0	0
			1	1		
84	uS14	1	Total	Mg	0	0
			1	1		
84	eEF2	6	Total	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).

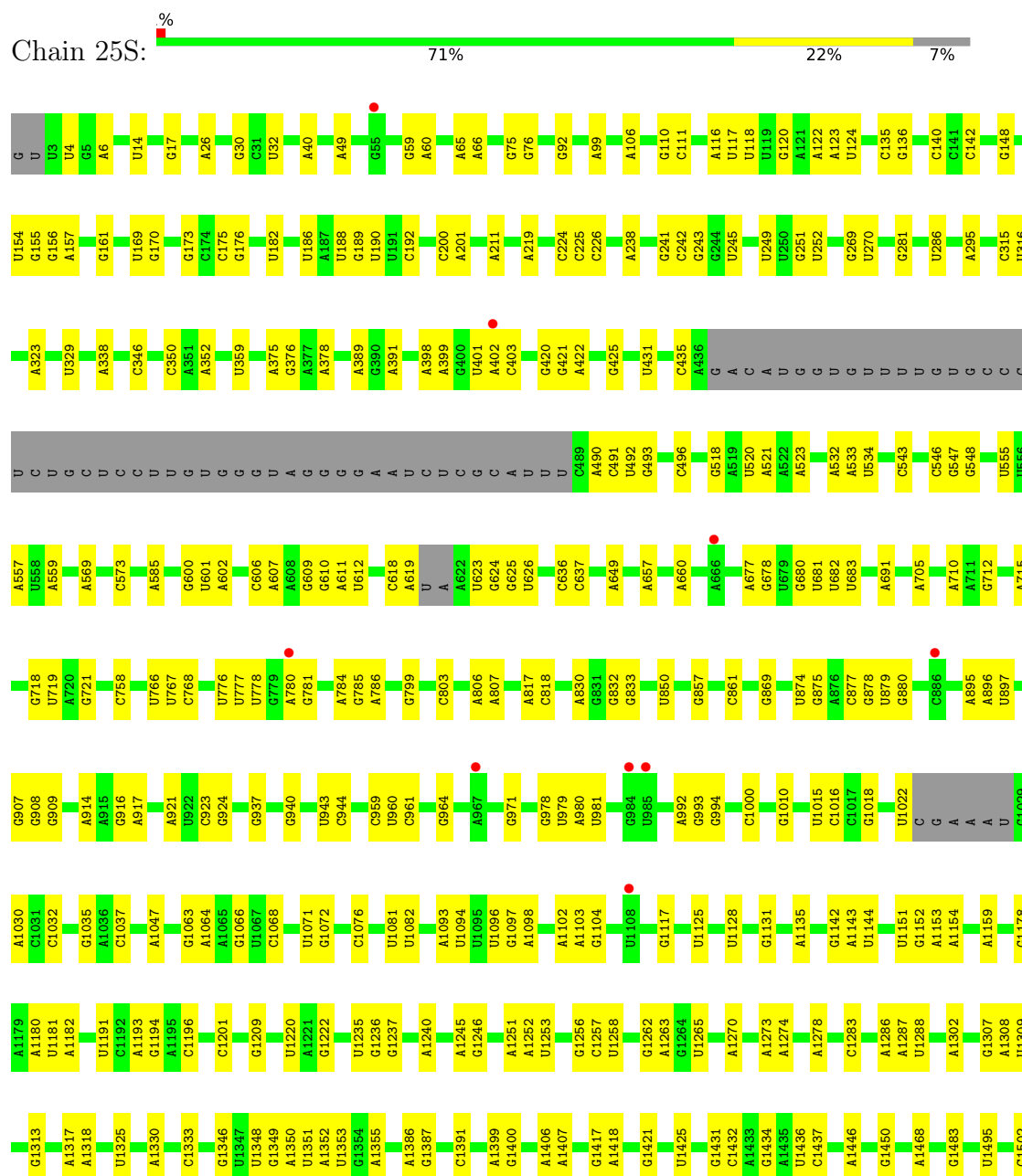


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
86	eEF2	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

3 Residue-property plots [i](#)

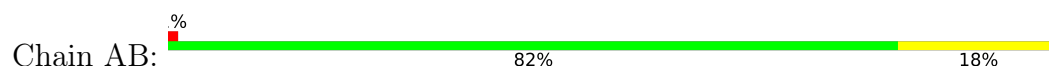
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

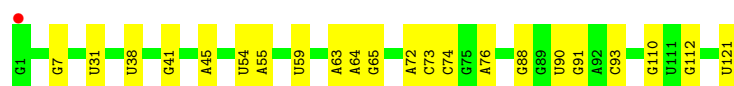
• Molecule 1: 25S rRNA



A3279	U3171	G2972	A2808	A2673	G2522	G2450	G2122	U	A1506
U3280	A3172	U2979	C2809	A2674	A2523	G2451	A2279	A	A1643
U3281	G3173	U2979	C2810	G2677	A2523	G2454	A2280	G	C1644
U3282	G3176	C2983	G2814	A2678	G2534	U2455	A2281	A	U1645
U3283	G3177	C2984	U3178	U2681	G2535	U	A2295	G	G1646
G3288	A3178	G2990	A3179	U2689	A2536	A	U2298	G	A1654
G3289	U3179	G2990	U3180	A2690	U2537	G	U2298	C	G1685
A3294	C3181	U2996	U2827	G2690	A2540	A	C2306	C	A1656
G3303	A3187	G2997	A2838	A2691	U2541	U	G2307	U	C1657
U3304	U3196	U2998	U2842	A2695	U2542	A	U2162	G	U1695
U3313	G3197	C3002	U2843	A2696	U2543	A2458	A2168	U1885	U1695
U3316	U3198	G3003	U2844	A2697	G2549	G2463	G2169	A1886	U1716
A3316	U3206	C3004	C2845	A2704	G2549	U2464	U2170	U1894	U1717
U3319	U3207	A3005	U2846	A2705	C2552	G2465	G2171	U1880	U1549
A3320	U3208	A3012	A2847	G2714	U2553	G	A2172	G1906	U1724
G3333	G3209	A3049	G2871	G2720	G2555	C	U2184	U1920	A1741
A3333	A3210	A2872	A2872	A2721	G2560	U	U2185	G1935	U1557
U3341	A3215	U2875	G2728	G2728	A2561	U	A2188	G1948	A1749
A3342	G3216	C2876	U2729	U2729	G2564	G	U2205	C1951	A1750
G3345	C3217	A2887	C2737	C2737	A2569	C	G2206	A1752	C1562
G3348	A3218	U2888	U2888	U2571	U2570	G	A2207	G1753	C1563
C3349	G3219	C2889	C2889	U2744	C2572	C	A2208	C1759	U1564
C3350	A3227	C3092	C2899	U2750	G2573	A	U2209	C	U1567
U3351	G3228	G3101	A2911	G2753	G2585	U	G2210	A	U1568
U3352	G3232	G3109	G2914	G2754	G2586	G2483	A2213	G	U1763
G3353	A3244	C3115	U2923	C2755	U2587	A2484	G2382	C	A1571
U	G3245	G3116	C2924	U2759	A2593	A2485	A2223	A	G1766
U	U3357	C3247	C2925	A2762	G2606	A2486	A2224	G	C1767
A3359	G3249	U3121	U2935	U2771	G2607	U2487	C2245	C	U1788
U3368	G3254	A3122	A2936	C2772	G2614	C	G2246	C	C1578
G3369	U3255	A3130	G2937	C2773	G2621	U	A2397	U	C1579
C3378	G3256	U3131	G2938	C2776	A2626	A2493	G2249	A	A1580
U3382	G3260	A3142	A2941	C2777	C2627	U2497	G2250	C	C1581
G3386	G3263	C3143	C2942	C2778	A2628	C2498	G2251	A	C1582
U3389	A3268	G3149	A2946	A2790	A2636	U2501	A2397	G	U1797
G3390	U3269	U3153	G2947	U2795	A2637	A	A2398	A	A1589
U3396	G3271	U3155	C2948	C2796	C2638	G2503	A2262	U	G1808
C3272	U3270	U3157	G2951	G2799	G2648	C2507	U2415	A	U1595
A3273	C3272	C3158	U2952	A2799	U2652	U2508	A2116	C	G1812
U3275	U3275	G3158	U2953	A2801	U2652	U2509	U2417	C	A1813
U3276	U3276	A3168	U2954	A2804	A2656	U2510	G2418	C	U1815
U3277	U3277	U3169	U2955	A2805	A2657	A2511	A2419	U	A1816
C3278	U3278	A3170	A2971	C2804	A2657	U2514	U2436	C	G1817
						A2515	A2449	C	U1820
								C	U1821
								C	U1840
								C	U1629
								C	U1630
								C	C1531
								C	A1842
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• Molecule 2: 5S rRNA





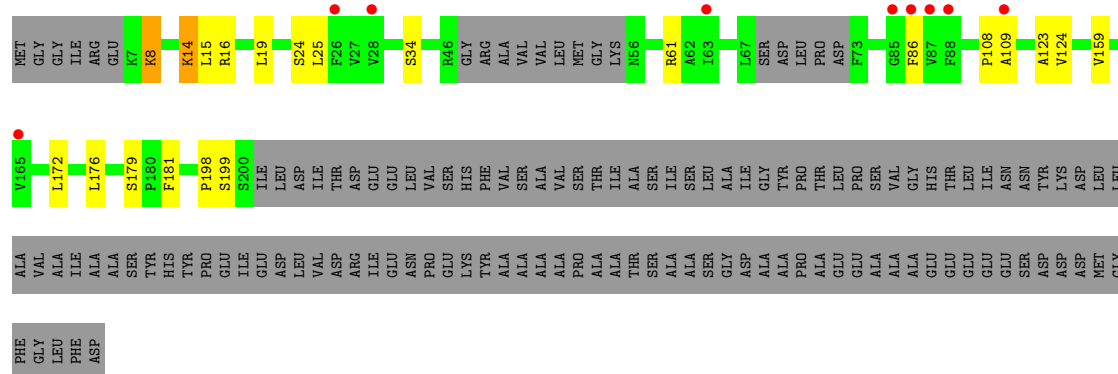
- Molecule 3: 5.8S rRNA

Chain 58S: 77% 23%



- Molecule 4: 60S acidic ribosomal protein P0

Chain uL10: 3% 51% 6% 42%



- Molecule 5: 60S ribosomal protein L2-B

Chain uL2: 5% 97% 2%



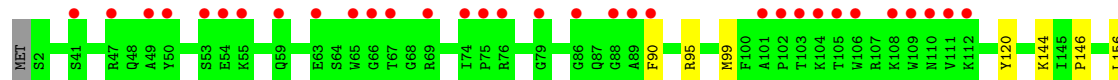
- Molecule 6: 60S ribosomal protein L3

Chain uL3: 94% 5%



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

Chain uL4: 10% 96% 4%





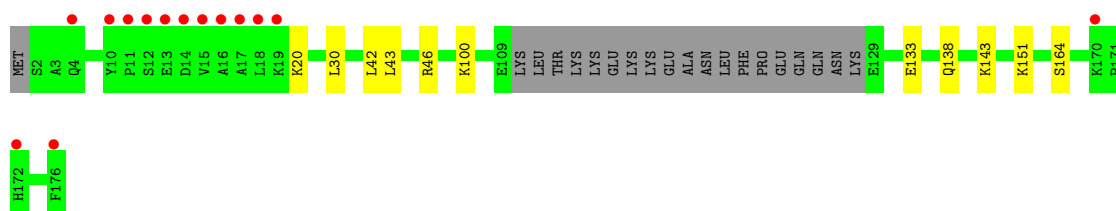
- Molecule 8: 60S ribosomal protein L5

Chain uL18: 93% 6%



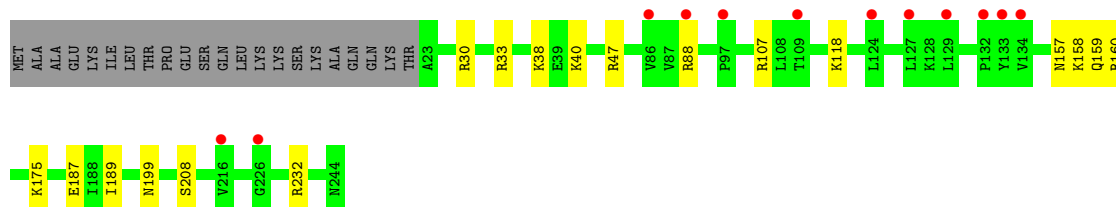
- Molecule 9: 60S ribosomal protein L6

Chain eL6: 8% 82% 6% 11%



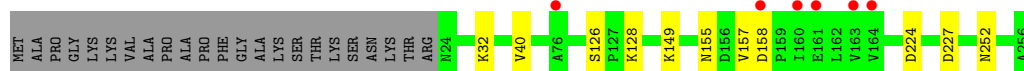
- Molecule 10: 60S ribosomal protein L7-A

Chain uL30: 5% 84% 7% 9%



- Molecule 11: 60S ribosomal protein L8-A

Chain eL8: 2% 87% 9%



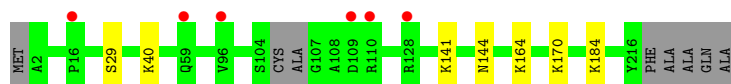
- Molecule 12: 60S ribosomal protein L9-A

Chain uL6: 95% 5%

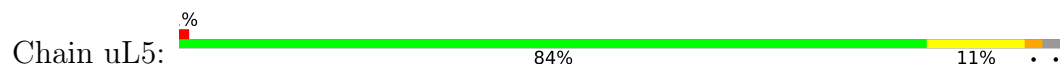


- Molecule 13: 60S ribosomal protein L10

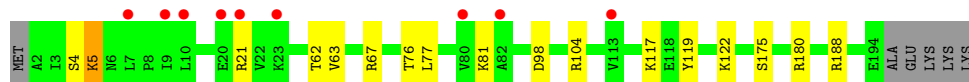
Chain uL16: 3% 93% 2%



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



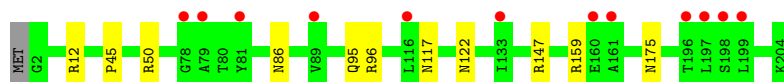
- Molecule 15: 60S ribosomal protein L13



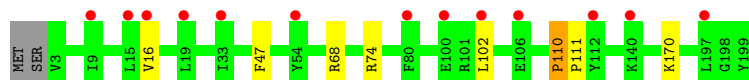
- Molecule 16: 60S ribosomal protein L14-A



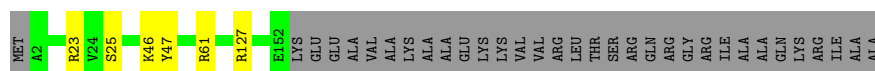
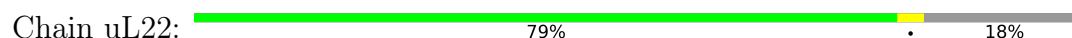
- Molecule 17: 60S ribosomal protein L15-A



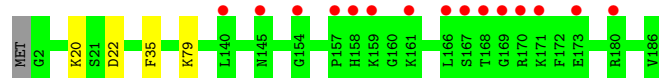
- Molecule 18: 60S ribosomal protein L16-A



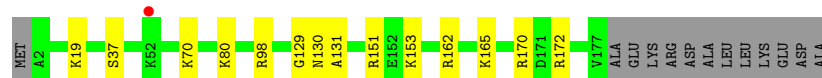
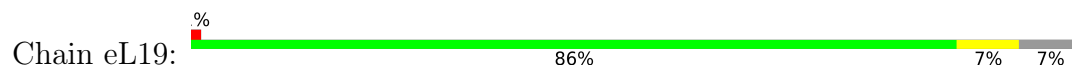
- Molecule 19: BJ4_G0005750.mRNA.1.CDS.1



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



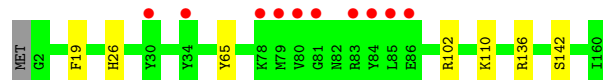
- Molecule 21: 60S ribosomal protein L19-A



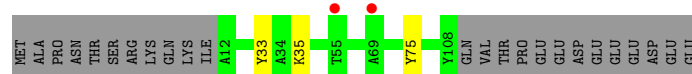
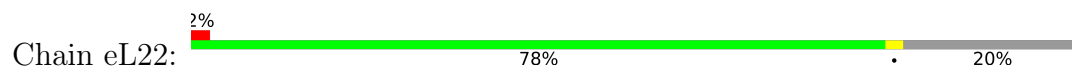
- Molecule 22: 60S ribosomal protein L20



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



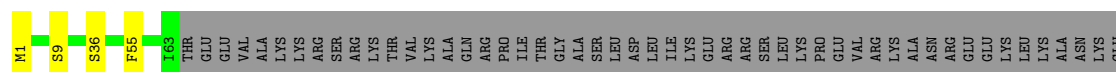
- Molecule 24: 60S ribosomal protein L22-A



- Molecule 25: 60S ribosomal protein L23-B

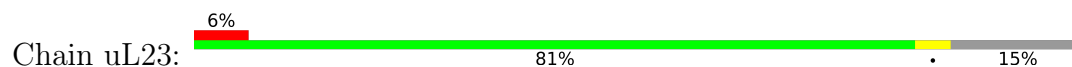


- Molecule 26: 60S ribosomal protein L24-A



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
LYS
VAL
VAL
LYS
GLY
THR
ASN
GLY
LYS
LYS
A23
L24
R27
K74
F81
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
I10
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I16
S63
K64
F85
D97
A105

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

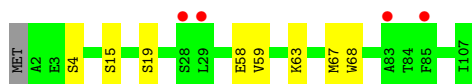




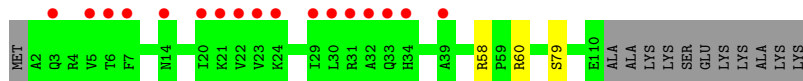
- Molecule 34: HN1_G0013350.mRNA.1.CDS.1



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



- Molecule 36: 60S ribosomal protein L34-A



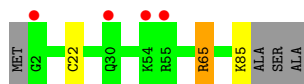
- Molecule 37: BJ4_G0044250.mRNA.1.CDS.1



- Molecule 38: 60S ribosomal protein L36-A



- Molecule 39: Ribosomal protein L37

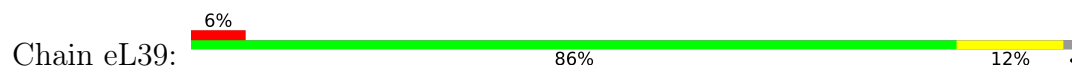


- Molecule 40: BJ4_G0032190.mRNA.1.CDS.1

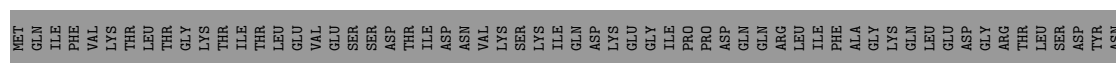




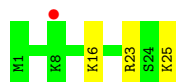
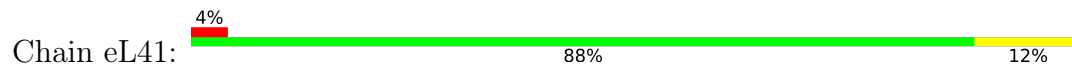
- Molecule 41: 60S ribosomal protein L39



- Molecule 42: Ubiquitin



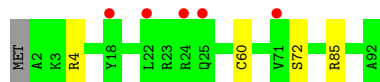
- Molecule 43: eL41



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

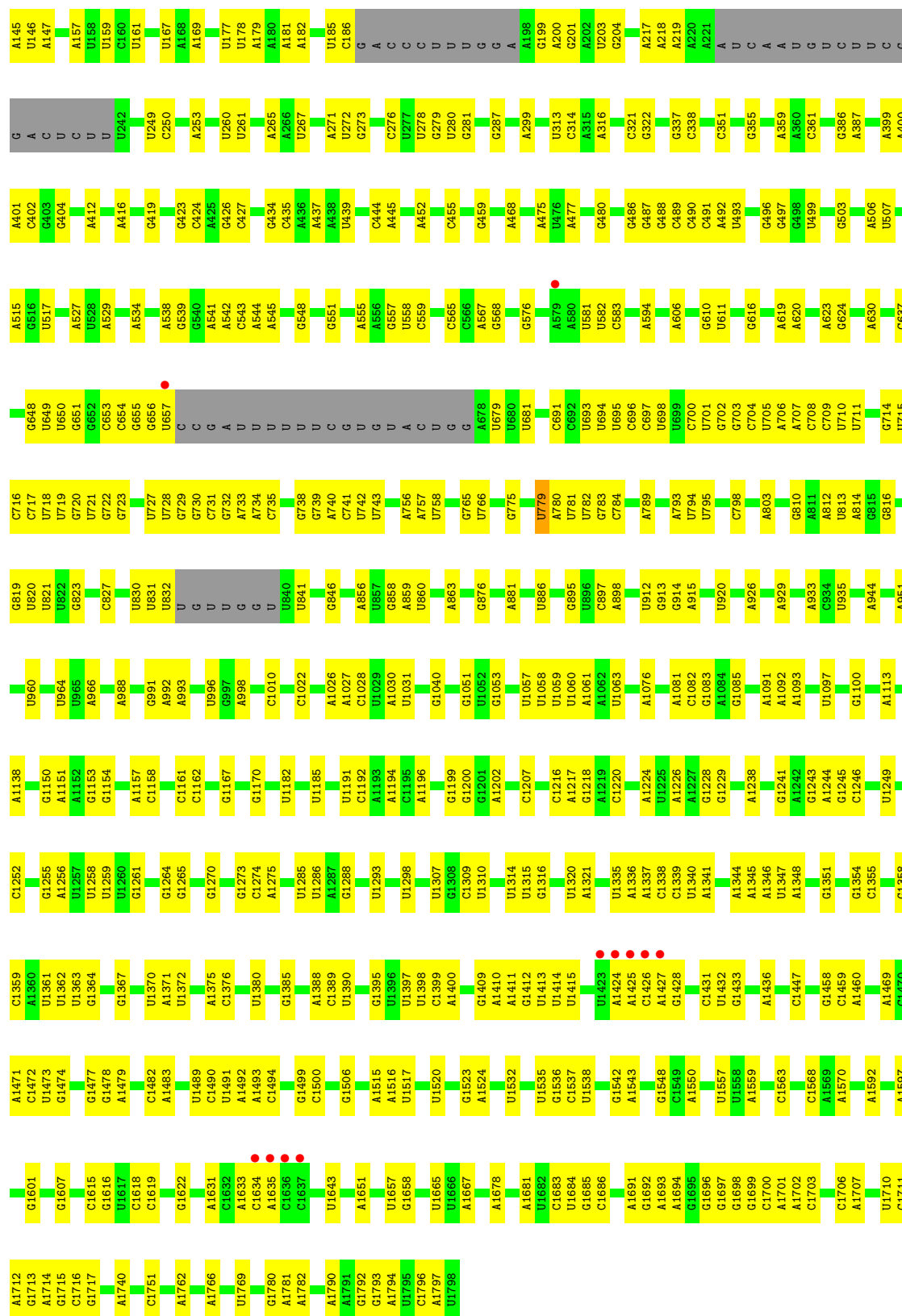


- Molecule 45: 60S ribosomal protein L43-A



- Molecule 46: 18S rRNA

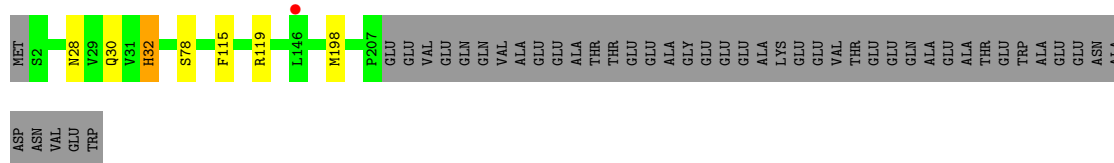




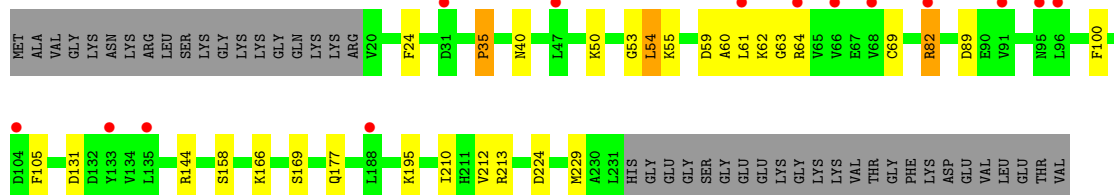
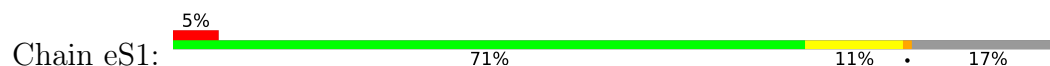
• Molecule 47: 40S ribosomal protein S0

Chain uS2:

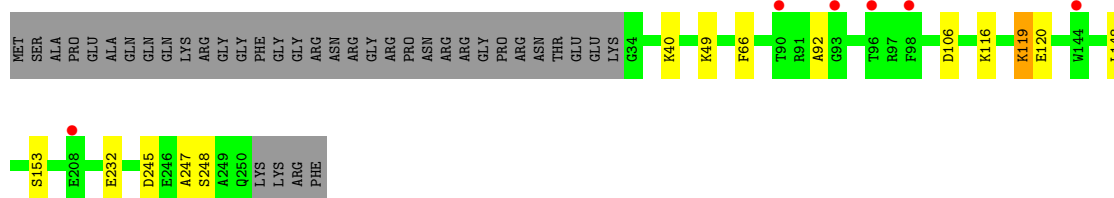
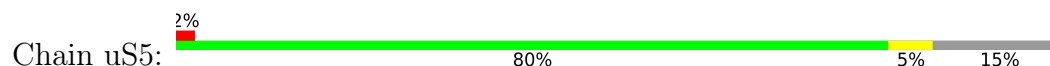




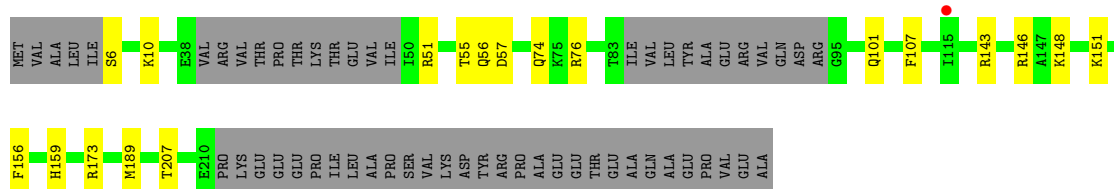
- Molecule 48: 40S ribosomal protein S1



- Molecule 49: 40S ribosomal protein S2



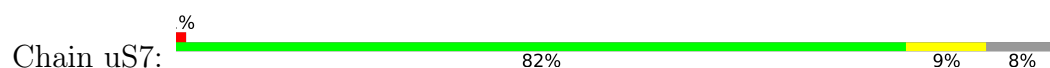
- Molecule 50: BJ4_G0045400.mRNA.1.CDS.1

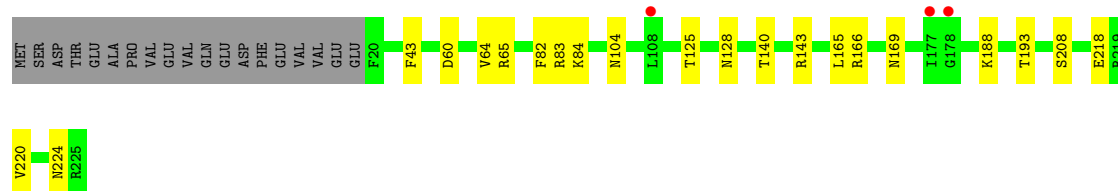


- Molecule 51: 40S ribosomal protein S4

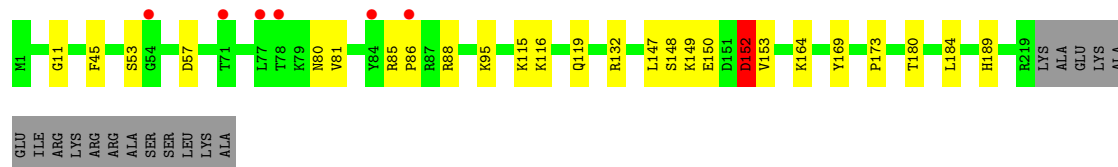
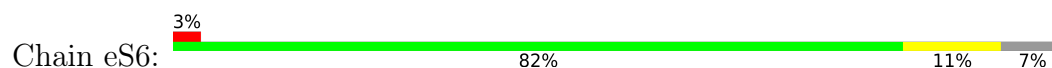


- Molecule 52: Rps5p





- Molecule 53: 40S ribosomal protein S6



- Molecule 54: 40S ribosomal protein S7



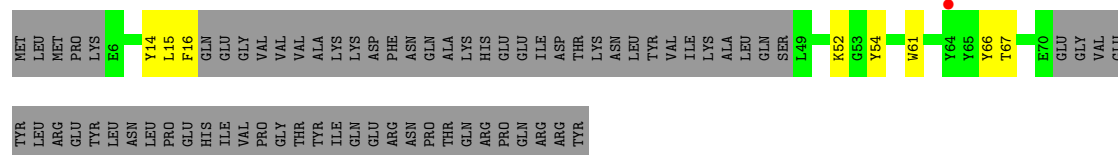
- Molecule 55: 40S ribosomal protein S8



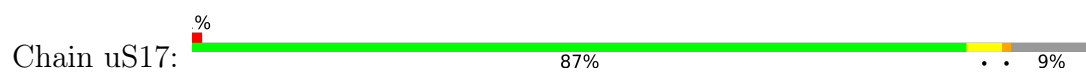
- Molecule 56: BJ4_G0026100.mRNA.1.CDS.1



- Molecule 57: 40S ribosomal protein S10-A



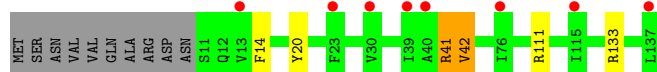
- Molecule 58: 40S ribosomal protein S11-B



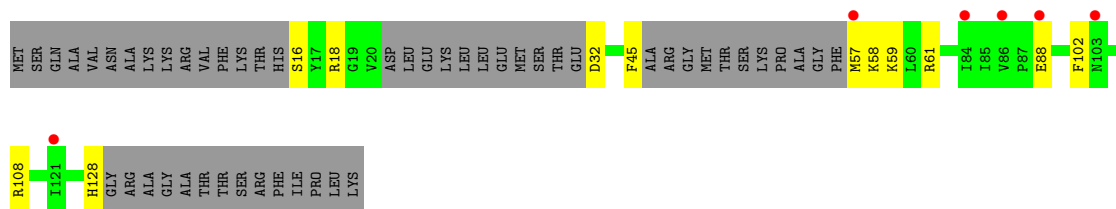
- Molecule 59: 40S ribosomal protein S13



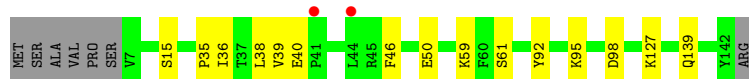
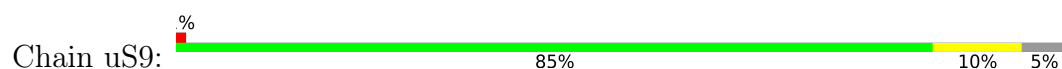
- Molecule 60: 40S ribosomal protein S14-A



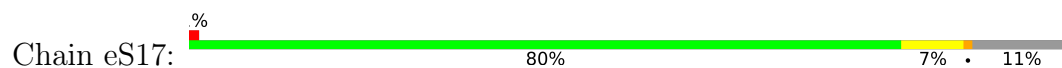
- Molecule 61: 40S ribosomal protein S15



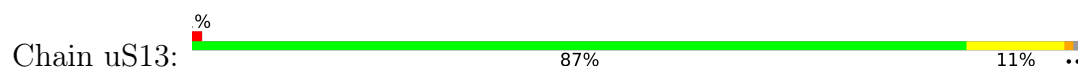
- Molecule 62: BJ4_G0008010.mRNA.1.CDS.1



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



- Molecule 64: 40S ribosomal protein S18-B





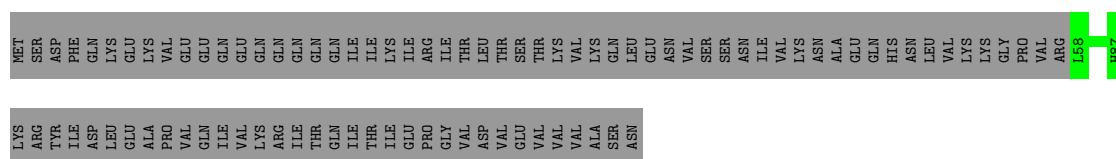
- Molecule 65: 40S ribosomal protein S19-A

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% .



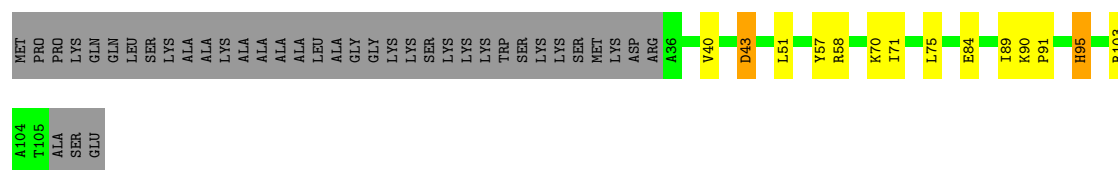
- Molecule 70: 40S ribosomal protein S24

Chain eS24: 90% 9% .



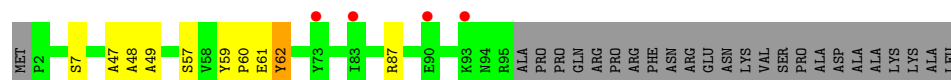
- Molecule 71: 40S ribosomal protein S25

Chain eS25: 

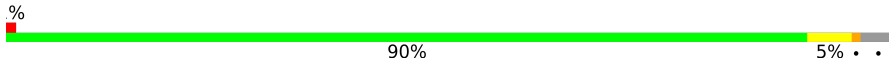


- Molecule 72: 40S ribosomal protein S26

Chain eS26: 



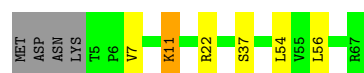
- Molecule 73: 40S ribosomal protein S27-A

Chain eS27: 



- Molecule 74: eS28

Chain eS28: 



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

Chain uS14: 

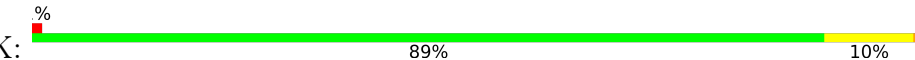


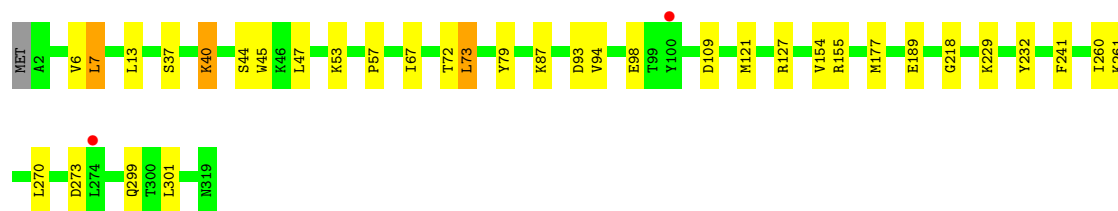
- Molecule 76: 40S ribosomal protein S30

Chain eS30: 



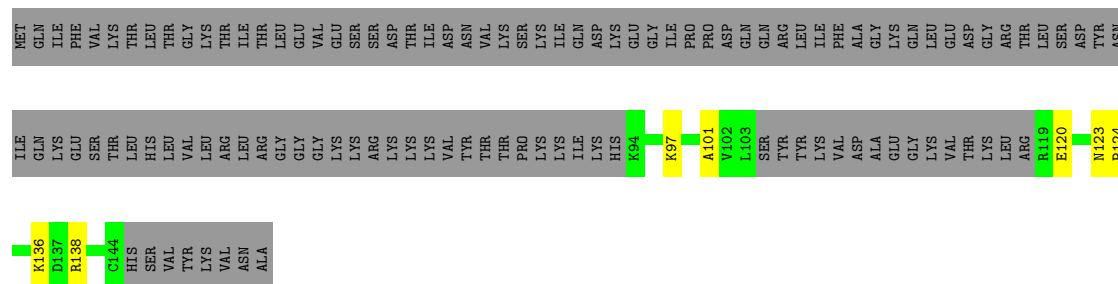
- Molecule 77: BJ4_G0022010.mRNA.1.CDS.1

Chain RACK: 



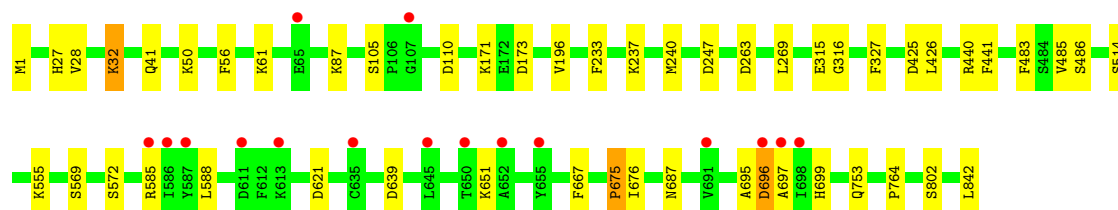
• Molecule 78: Ubiquitin-40S ribosomal protein S31

Chain eS31: 19% 5% 76%



• Molecule 79: Elongation factor 2

Chain eEF2: 2% 94% 6%



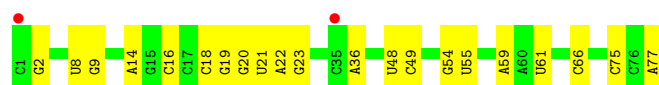
• Molecule 80: PHE tRNA

Chain ASIT: 61% 39%



• Molecule 81: FMET tRNA

Chain PSIT: 3% 73% 27%

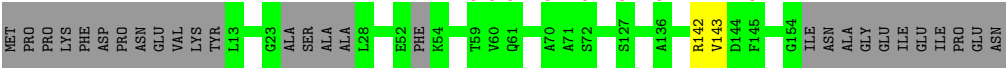
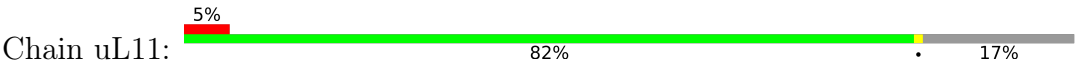


• Molecule 82: MRNA

Chain mRNA: 62% 38%



- 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

All (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
18	uL13	170	LYS	CE-NZ	7.20	1.71	1.49
71	eS25	91	PRO	CB-CG	7.19	1.85	1.49
21	eL19	162	ARG	NE-CZ	7.15	1.41	1.33
46	18S	779	U	C1'-N1	6.01	1.57	1.48
33	eL31	89	LEU	CG-CD1	5.84	1.71	1.52
50	uS3	10	LYS	CD-CE	5.77	1.69	1.52
14	uL5	29	ARG	NE-CZ	5.62	1.39	1.33
59	uS15	136	PRO	CA-C	-5.60	1.47	1.52
18	uL13	170	LYS	CA-C	-5.54	1.44	1.52
18	uL13	170	LYS	CD-CE	-5.48	1.36	1.52
65	eS19	103	LYS	CB-CG	5.14	1.67	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	uS3	10	LYS	CG-CD	-5.06	1.37	1.52
77	RACK	155	ARG	CD-NE	-5.06	1.39	1.46

All (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
10	uL30	157	ASN	CA-C-N	9.45	139.58	121.54
10	uL30	157	ASN	C-N-CA	9.45	139.58	121.54
14	uL5	29	ARG	CB-CG-CD	9.39	132.89	111.30
79	eEF2	32	LYS	CA-C-O	-9.34	111.01	120.82
55	eS8	119	GLN	CA-C-N	8.92	137.75	121.70
55	eS8	119	GLN	C-N-CA	8.92	137.75	121.70
63	eS17	23	LYS	CA-C-N	8.79	138.32	121.54
63	eS17	23	LYS	C-N-CA	8.79	138.32	121.54
79	eEF2	695	ALA	CA-C-N	8.70	138.16	121.54
79	eEF2	695	ALA	C-N-CA	8.70	138.16	121.54
14	uL5	55	ARG	N-CA-C	-7.69	94.43	110.80
73	eS27	42	ASN	N-CA-C	-7.48	94.86	110.80
53	eS6	152	ASP	CA-C-N	7.43	135.35	121.97
53	eS6	152	ASP	C-N-CA	7.43	135.35	121.97
10	uL30	118	LYS	CA-C-N	-7.25	113.89	122.22
10	uL30	118	LYS	C-N-CA	-7.25	113.89	122.22
54	eS7	104	ARG	N-CA-C	-7.20	106.41	114.62
14	uL5	75	LYS	CG-CD-CE	7.20	127.85	111.30
79	eEF2	485	VAL	CA-C-N	-7.04	109.62	123.56
79	eEF2	485	VAL	C-N-CA	-7.04	109.62	123.56
50	uS3	55	THR	CA-C-N	-6.97	111.61	122.42
50	uS3	55	THR	C-N-CA	-6.97	111.61	122.42
77	RACK	7	LEU	CD1-CG-CD2	6.94	126.07	110.80
4	uL10	176	LEU	CA-CB-CG	6.65	139.56	116.30
7	uL4	292	SER	CA-C-N	-6.59	108.76	121.94
7	uL4	292	SER	C-N-CA	-6.59	108.76	121.94
52	uS7	143	ARG	NE-CZ-NH1	-6.58	114.92	121.50
73	eS27	41	LEU	CA-CB-CG	6.48	138.99	116.30
71	eS25	90	LYS	CB-CA-C	-6.46	100.47	110.62
77	RACK	72	THR	CA-CB-CG2	6.40	121.38	110.50
77	RACK	301	LEU	CA-C-N	6.38	130.19	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	RACK	301	LEU	C-N-CA	6.38	130.19	120.82
4	uL10	15	LEU	CA-C-N	-6.34	111.66	122.56
4	uL10	15	LEU	C-N-CA	-6.34	111.66	122.56
18	uL13	170	LYS	CG-CD-CE	-6.30	96.80	111.30
79	eEF2	32	LYS	CA-C-N	-6.26	108.77	121.18
79	eEF2	32	LYS	C-N-CA	-6.26	108.77	121.18
4	uL10	14	LYS	CA-C-N	-6.26	109.38	121.58
4	uL10	14	LYS	C-N-CA	-6.26	109.38	121.58
79	eEF2	196	VAL	N-CA-C	-6.24	107.78	113.71
24	eL22	35	LYS	CB-CG-CD	6.13	125.41	111.30
56	uS4	93	LEU	N-CA-C	6.13	123.86	110.80
27	uL23	24	LEU	CA-C-N	6.09	131.78	120.95
27	uL23	24	LEU	C-N-CA	6.09	131.78	120.95
48	eS1	61	LEU	CA-CB-CG	6.08	137.57	116.30
77	RACK	57	PRO	N-CA-C	6.00	120.92	111.38
48	eS1	60	ALA	CA-C-N	5.98	130.33	120.94
48	eS1	60	ALA	C-N-CA	5.98	130.33	120.94
48	eS1	64	ARG	NE-CZ-NH1	-5.98	115.52	121.50
71	eS25	91	PRO	N-CA-C	5.97	120.87	111.38
50	uS3	10	LYS	CG-CD-CE	-5.87	97.79	111.30
56	uS4	64	GLU	CA-C-N	5.77	133.49	123.91
56	uS4	64	GLU	C-N-CA	5.77	133.49	123.91
71	eS25	90	LYS	N-CA-C	5.77	119.74	107.91
77	RACK	273	ASP	N-CA-C	5.73	117.11	108.46
21	eL19	165	LYS	CD-CE-NZ	-5.72	93.61	111.90
49	uS5	119	LYS	CA-CB-CG	5.71	125.51	114.10
48	eS1	213	ARG	N-CA-C	5.64	122.82	110.80
33	eL31	89	LEU	CD1-CG-CD2	5.62	123.16	110.80
79	eEF2	316	GLY	CA-C-N	5.60	132.24	121.54
79	eEF2	316	GLY	C-N-CA	5.60	132.24	121.54
14	uL5	75	LYS	N-CA-CB	5.57	118.91	110.28
58	uS17	6	THR	N-CA-C	-5.53	104.11	111.02
79	eEF2	696	ASP	N-CA-C	5.53	122.57	110.80
50	uS3	10	LYS	CA-CB-CG	5.50	125.10	114.10
74	eS28	54	LEU	CA-CB-CG	5.45	135.36	116.30
16	eL14	133	LYS	CD-CE-NZ	-5.44	94.49	111.90
77	RACK	47	LEU	CA-CB-CG	5.41	135.22	116.30
71	eS25	95	HIS	CA-CB-CG	-5.38	108.42	113.80
14	uL5	75	LYS	CA-CB-CG	-5.38	103.35	114.10
48	eS1	82	ARG	N-CA-C	5.35	122.20	110.80
52	uS7	220	VAL	CA-C-N	-5.34	116.09	122.44
52	uS7	220	VAL	C-N-CA	-5.34	116.09	122.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	eL6	42	LEU	CA-CB-CG	5.33	134.96	116.30
52	uS7	140	THR	N-CA-C	5.32	120.88	110.56
77	RACK	270	LEU	CB-CG-CD1	-5.31	94.76	110.70
14	uL5	29	ARG	CD-NE-CZ	5.30	131.82	124.40
68	uS8	30	SER	N-CA-C	5.29	117.10	110.91
50	uS3	207	THR	N-CA-C	5.25	116.39	108.46
46	18S	1389	C	O3'-P-O5'	5.24	111.86	104.00
53	eS6	88	ARG	N-CA-C	5.21	116.56	107.49
4	uL10	172	LEU	CA-CB-CG	5.20	134.50	116.30
30	uL15	77	LYS	CA-C-N	5.19	131.45	121.54
30	uL15	77	LYS	C-N-CA	5.19	131.45	121.54
15	eL13	119	TYR	CA-CB-CG	5.19	123.24	113.90
13	uL16	184	LYS	CB-CG-CD	5.19	123.23	111.30
69	uS12	112	LYS	CA-C-N	5.18	131.43	121.54
69	uS12	112	LYS	C-N-CA	5.18	131.43	121.54
71	eS25	91	PRO	CB-CG-CD	-5.17	89.56	106.10
8	uL18	43	LYS	CA-C-N	5.17	131.41	121.54
8	uL18	43	LYS	C-N-CA	5.17	131.41	121.54
77	RACK	218	GLY	N-CA-C	5.15	125.39	113.18
77	RACK	13	LEU	CA-CB-CG	5.14	134.29	116.30
71	eS25	75	LEU	CA-CB-CG	-5.12	98.39	116.30
78	eS31	136	LYS	CA-CB-CG	5.10	124.31	114.10
60	uS11	41	ARG	N-CA-C	5.10	117.74	111.82
60	uS11	42	VAL	N-CA-C	5.10	119.95	109.34
40	eL38	35	GLY	CA-C-N	-5.07	114.57	121.61
40	eL38	35	GLY	C-N-CA	-5.07	114.57	121.61
57	eS10	15	LEU	CA-CB-CG	5.06	134.01	116.30
72	eS26	61	GLU	N-CA-C	5.04	121.53	110.80
56	uS4	134	ILE	N-CA-C	5.04	119.82	109.34
34	eL32	86	THR	CA-C-N	5.02	133.26	121.52
34	eL32	86	THR	C-N-CA	5.02	133.26	121.52
64	uS13	61	LEU	CA-CB-CG	5.01	133.85	116.30

There are no chirality outliers.

All (120) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
77	RACK	154	VAL	Peptide
77	RACK	260	ILE	Peptide
77	RACK	6	VAL	Peptide
77	RACK	7	LEU	Peptide
77	RACK	73	LEU	Peptide

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Mol	Chain	Res	Type	Group
77	RACK	93	ASP	Peptide
77	RACK	98	GLU	Peptide
79	eEF2	27	HIS	Peptide
79	eEF2	315	GLU	Peptide
79	eEF2	440	ARG	Peptide
79	eEF2	675	PRO	Peptide
79	eEF2	696	ASP	Peptide
15	eL13	4	SER	Peptide
20	eL18	20	LYS	Peptide
21	eL19	129	GLY	Peptide
22	eL20	22	PRO	Peptide
29	eL27	100	THR	Peptide
29	eL27	101	PHE	Peptide
29	eL27	34	LYS	Peptide
31	eL29	24	PRO	Peptide
35	eL33	58	GLU	Peptide
38	eL36	19	SER	Peptide
40	eL38	69	LEU	Peptide
41	eL39	27	ILE	Peptide
41	eL39	30	ARG	Peptide
44	eL42	14	GLY	Peptide
11	eL8	155	ASN	Peptide
11	eL8	158	ASP	Peptide
48	eS1	131	ASP	Peptide
48	eS1	177	GLN	Peptide
48	eS1	212	VAL	Peptide
48	eS1	35	PRO	Peptide
48	eS1	50	LYS	Peptide
48	eS1	53	GLY	Peptide
48	eS1	54	LEU	Peptide
48	eS1	62	LYS	Peptide
57	eS10	52	LYS	Peptide
57	eS10	54	TYR	Peptide
57	eS10	61	TRP	Peptide
57	eS10	67	THR	Peptide
63	eS17	103	ASP	Peptide
63	eS17	112	SER	Peptide
63	eS17	70	SER	Peptide
65	eS19	49	ASP	Peptide
65	eS19	7	ARG	Sidechain
65	eS19	9	VAL	Peptide
70	eS24	5	VAL	Peptide

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Mol	Chain	Res	Type	Group
70	eS24	51	GLU	Peptide
71	eS25	43	ASP	Peptide
71	eS25	70	LYS	Peptide
71	eS25	71	ILE	Peptide
72	eS26	47	ALA	Peptide
72	eS26	57	SER	Peptide
72	eS26	60	PRO	Peptide
72	eS26	62	TYR	Peptide
72	eS26	7	SER	Peptide
74	eS28	11	LYS	Peptide
74	eS28	7	VAL	Peptide
78	eS31	101	ALA	Peptide
78	eS31	97	LYS	Peptide
51	eS4	118	GLU	Peptide
51	eS4	154	ILE	Peptide
53	eS6	147	LEU	Peptide
53	eS6	173	PRO	Peptide
53	eS6	180	THR	Peptide
53	eS6	57	ASP	Peptide
53	eS6	80	ASN	Peptide
53	eS6	86	PRO	Peptide
54	eS7	103	SER	Peptide
54	eS7	106	SER	Peptide
54	eS7	11	GLN	Peptide
54	eS7	27	LEU	Peptide
54	eS7	86	GLN	Peptide
4	uL10	108	PRO	Peptide
4	uL10	123	ALA	Peptide
4	uL10	198	PRO	Peptide
4	uL10	8	LYS	Peptide
83	uL11	142	ARG	Peptide
18	uL13	110	PRO	Peptide
25	uL14	66	LYS	Peptide
30	uL15	115	LYS	Peptide
30	uL15	116	GLY	Peptide
30	uL15	23	GLY	Peptide
30	uL15	91	LEU	Peptide
28	uL24	65	GLY	Peptide
6	uL3	349	LYS	Peptide
10	uL30	189	ILE	Peptide
10	uL30	232	ARG	Peptide
14	uL5	101	ASN	Peptide

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Mol	Chain	Res	Type	Group
14	uL5	108	GLU	Peptide
14	uL5	53	THR	Peptide
14	uL5	90	GLN	Peptide
14	uL5	94	ARG	Peptide
12	uL6	21	LYS	Peptide
60	uS11	41	ARG	Peptide
69	uS12	88	PRO	Peptide
64	uS13	101	LEU	Peptide
64	uS13	13	HIS	Peptide
64	uS13	60	GLU	Peptide
64	uS13	90	ASN	Peptide
64	uS13	91	ASP	Peptide
59	uS15	105	ASN	Peptide
59	uS15	140	LYS	Peptide
58	uS17	6	THR	Peptide
47	uS2	115	PHE	Peptide
47	uS2	32	HIS	Peptide
56	uS4	117	GLY	Peptide
56	uS4	133	HIS	Peptide
56	uS4	92	LYS	Peptide
49	uS5	120	GLU	Peptide
49	uS5	247	ALA	Peptide
49	uS5	49	LYS	Peptide
49	uS5	92	ALA	Peptide
52	uS7	104	ASN	Peptide
52	uS7	125	THR	Peptide
52	uS7	193	THR	Peptide
52	uS7	218	GLU	Peptide
52	uS7	65	ARG	Peptide
68	uS8	54	ASP	Peptide
62	uS9	40	GLU	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	eS19	141/144 (98%)	106 (75%)	35 (25%)	0	100	100
66	uS10	28/121 (23%)	25 (89%)	3 (11%)	0	100	100
67	eS21	85/87 (98%)	66 (78%)	19 (22%)	0	100	100
68	uS8	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	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
All	All	11582/13056 (89%)	9666 (84%)	1787 (15%)	129 (1%)	11	43

All (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
18	uL13	111	PRO
29	eL27	102	GLU
30	uL15	24	LYS
30	uL15	78	LEU
30	uL15	117	ARG
48	eS1	54	LEU
49	uS5	40	LYS
53	eS6	148	SER
53	eS6	149	LYS
53	eS6	153	VAL

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Mol	Chain	Res	Type
56	uS4	134	ILE
58	uS17	7	VAL
60	uS11	42	VAL
63	eS17	23	LYS
63	eS17	24	LEU
64	uS13	91	ASP
64	uS13	102	ALA
69	uS12	113	ALA
72	eS26	49	ALA
76	eS30	46	ASN
77	RACK	94	VAL
79	eEF2	676	ILE
83	uL11	143	VAL
12	uL6	22	SER
14	uL5	54	VAL
14	uL5	55	ARG
14	uL5	92	ARG
15	eL13	5	LYS
15	eL13	77	LEU
18	uL13	110	PRO
38	eL36	98	ARG
48	eS1	63	GLY
50	uS3	148	LYS
51	eS4	194	THR
53	eS6	81	VAL
53	eS6	119	GLN
54	eS7	65	PRO
61	uS19	102	PHE
64	uS13	14	ILE
64	uS13	92	ILE
71	eS25	95	HIS
73	eS27	42	ASN
79	eEF2	675	PRO
79	eEF2	697	ALA
8	uL18	261	THR
14	uL5	111	ASP
17	eL15	95	GLN
23	eL21	19	PHE
29	eL27	101	PHE
35	eL33	59	VAL
47	uS2	28	ASN
49	uS5	248	SER

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Mol	Chain	Res	Type
50	uS3	57	ASP
51	eS4	156	VAL
52	uS7	43	PHE
54	eS7	103	SER
54	eS7	107	ARG
55	eS8	11	ARG
56	uS4	162	SER
56	uS4	163	PRO
57	eS10	14	TYR
59	uS15	106	ARG
62	uS9	15	SER
64	uS13	61	LEU
64	uS13	103	ASN
64	uS13	145	ARG
71	eS25	40	VAL
76	eS30	45	VAL
78	eS31	124	PRO
79	eEF2	50	LYS
79	eEF2	572	SER
79	eEF2	764	PRO
10	uL30	160	ARG
21	eL19	130	ASN
39	eL37	65	ARG
50	uS3	146	ARG
52	uS7	128	ASN
69	uS12	89	ASN
72	eS26	48	ALA
72	eS26	59	TYR
72	eS26	62	TYR
78	eS31	123	ASN
79	eEF2	263	ASP
11	eL8	40	VAL
14	uL5	116	TYR
15	eL13	62	THR
32	eL30	11	ASN
34	eL32	86	THR
40	eL38	33	LYS
48	eS1	55	LYS
48	eS1	158	SER
51	eS4	155	LYS
55	eS8	23	LYS
56	uS4	133	HIS

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Mol	Chain	Res	Type
58	uS17	8	GLN
77	RACK	40	LYS
4	uL10	19	LEU
15	eL13	76	THR
21	eL19	131	ALA
38	eL36	35	ASN
48	eS1	35	PRO
53	eS6	152	ASP
61	uS19	18	ARG
62	uS9	50	GLU
69	uS12	41	SER
71	eS25	43	ASP
6	uL3	188	ILE
33	eL31	88	PRO
48	eS1	210	ILE
68	uS8	67	GLY
69	uS12	68	ILE
77	RACK	67	ILE
79	eEF2	28	VAL
7	uL4	146	PRO
34	eL32	68	PRO
11	eL8	157	VAL
44	eL42	14	GLY
4	uL10	124	VAL
52	uS7	64	VAL
62	uS9	35	PRO
62	uS9	36	ILE
4	uL10	159	VAL
18	uL13	16	VAL
53	eS6	11	GLY

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

All (533) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	uL10	8	LYS
4	uL10	14	LYS
4	uL10	16	ARG
4	uL10	24	SER
4	uL10	25	LEU
4	uL10	34	SER
4	uL10	61	ARG
4	uL10	86	PHE
4	uL10	179	SER
4	uL10	181	PHE
5	uL2	42	ARG
5	uL2	46	LYS
5	uL2	64	ARG
5	uL2	160	SER
5	uL2	195	SER
5	uL2	247	ARG
6	uL3	2	SER
6	uL3	10	ARG
6	uL3	30	LYS
6	uL3	36	ASP
6	uL3	67	PHE

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Mol	Chain	Res	Type
6	uL3	124	LYS
6	uL3	128	LYS
6	uL3	139	GLN
6	uL3	167	ARG
6	uL3	196	ARG
6	uL3	197	GLU
6	uL3	206	ASP
6	uL3	222	LYS
6	uL3	226	PHE
6	uL3	272	TYR
6	uL3	320	ASP
6	uL3	332	ARG
6	uL3	367	LYS
6	uL3	383	LEU
7	uL4	90	PHE
7	uL4	95	ARG
7	uL4	99	MET
7	uL4	120	TYR
7	uL4	144	LYS
7	uL4	156	LEU
7	uL4	170	LYS
7	uL4	193	LYS
7	uL4	247	PHE
7	uL4	292	SER
7	uL4	300	ARG
7	uL4	362	ASP
8	uL18	3	PHE
8	uL18	15	ARG
8	uL18	58	LYS
8	uL18	81	HIS
8	uL18	95	TRP
8	uL18	123	GLU
8	uL18	137	ASP
8	uL18	145	PHE
8	uL18	184	ASP
8	uL18	185	PHE
8	uL18	193	GLU
8	uL18	224	LYS
8	uL18	248	ARG
8	uL18	260	PHE
8	uL18	271	LYS
8	uL18	278	SER

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Mol	Chain	Res	Type
8	uL18	285	ARG
8	uL18	296	GLN
9	eL6	20	LYS
9	eL6	30	LEU
9	eL6	43	LEU
9	eL6	46	ARG
9	eL6	100	LYS
9	eL6	133	GLU
9	eL6	138	GLN
9	eL6	143	LYS
9	eL6	151	LYS
9	eL6	164	SER
10	uL30	30	ARG
10	uL30	33	ARG
10	uL30	38	LYS
10	uL30	40	LYS
10	uL30	47	ARG
10	uL30	88	ARG
10	uL30	107	ARG
10	uL30	158	LYS
10	uL30	175	LYS
10	uL30	187	GLU
10	uL30	199	ASN
10	uL30	208	SER
11	eL8	32	LYS
11	eL8	126	SER
11	eL8	128	LYS
11	eL8	149	LYS
11	eL8	224	ASP
11	eL8	227	ASP
11	eL8	252	ASN
12	uL6	36	LYS
12	uL6	92	TYR
12	uL6	106	LYS
12	uL6	130	ASP
12	uL6	170	LYS
12	uL6	177	ASP
12	uL6	190	ASP
13	uL16	29	SER
13	uL16	40	LYS
13	uL16	141	LYS
13	uL16	144	ASN

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Mol	Chain	Res	Type
13	uL16	164	LYS
13	uL16	170	LYS
14	uL5	9	MET
14	uL5	34	SER
14	uL5	41	SER
14	uL5	51	ARG
14	uL5	57	PHE
14	uL5	72	ARG
14	uL5	84	LEU
14	uL5	94	ARG
14	uL5	116	TYR
14	uL5	153	LYS
14	uL5	156	LYS
14	uL5	164	LYS
15	eL13	5	LYS
15	eL13	21	ARG
15	eL13	67	ARG
15	eL13	81	LYS
15	eL13	98	ASP
15	eL13	104	ARG
15	eL13	117	LYS
15	eL13	122	LYS
15	eL13	175	SER
15	eL13	180	ARG
15	eL13	188	ARG
16	eL14	4	ASP
16	eL14	12	TRP
16	eL14	41	GLN
16	eL14	77	ARG
16	eL14	83	LYS
16	eL14	91	CYS
16	eL14	93	LYS
16	eL14	102	LYS
16	eL14	117	ARG
16	eL14	121	MET
16	eL14	129	TYR
17	eL15	12	ARG
17	eL15	45	PRO
17	eL15	50	ARG
17	eL15	86	ASN
17	eL15	96	ARG
17	eL15	117	ASN

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Mol	Chain	Res	Type
17	eL15	122	ASN
17	eL15	147	ARG
17	eL15	159	ARG
17	eL15	175	ASN
18	uL13	47	PHE
18	uL13	68	ARG
18	uL13	74	ARG
18	uL13	102	LEU
19	uL22	23	ARG
19	uL22	25	SER
19	uL22	46	LYS
19	uL22	47	TYR
19	uL22	61	ARG
19	uL22	127	ARG
20	eL18	22	ASP
20	eL18	35	PHE
20	eL18	79	LYS
21	eL19	19	LYS
21	eL19	37	SER
21	eL19	70	LYS
21	eL19	80	LYS
21	eL19	98	ARG
21	eL19	151	ARG
21	eL19	153	LYS
21	eL19	170	ARG
21	eL19	172	ARG
22	eL20	18	SER
22	eL20	55	SER
22	eL20	80	ARG
22	eL20	90	MET
22	eL20	91	TYR
22	eL20	98	SER
22	eL20	118	PHE
22	eL20	122	HIS
22	eL20	167	ARG
23	eL21	26	HIS
23	eL21	65	TYR
23	eL21	102	ARG
23	eL21	110	LYS
23	eL21	136	ARG
23	eL21	142	SER
24	eL22	33	TYR

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Mol	Chain	Res	Type
24	eL22	75	TYR
25	uL14	32	ARG
25	uL14	42	SER
25	uL14	45	ARG
25	uL14	120	LYS
26	eL24	1	MET
26	eL24	9	SER
26	eL24	36	SER
26	eL24	55	PHE
27	uL23	27	ARG
27	uL23	74	LYS
27	uL23	109	LYS
27	uL23	138	ARG
28	uL24	5	SER
28	uL24	6	LEU
28	uL24	51	ARG
28	uL24	55	GLU
28	uL24	60	ARG
28	uL24	74	TYR
28	uL24	112	ASP
28	uL24	114	ASP
29	eL27	3	LYS
29	eL27	30	ASP
29	eL27	56	LYS
29	eL27	92	PHE
30	uL15	4	ARG
30	uL15	27	LYS
30	uL15	60	TYR
30	uL15	78	LEU
30	uL15	95	SER
30	uL15	96	LYS
31	eL29	22	LYS
31	eL29	27	TYR
32	eL30	63	SER
32	eL30	64	LYS
32	eL30	85	PHE
33	eL31	6	ASP
33	eL31	112	ASP
34	eL32	18	LYS
35	eL33	4	SER
35	eL33	15	SER
35	eL33	19	SER

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Mol	Chain	Res	Type
35	eL33	63	LYS
35	eL33	67	MET
35	eL33	68	TRP
36	eL34	58	ARG
36	eL34	60	ARG
36	eL34	79	SER
37	uL29	94	LYS
37	uL29	107	LYS
38	eL36	45	ARG
38	eL36	60	LEU
38	eL36	84	LYS
39	eL37	22	CYS
39	eL37	65	ARG
39	eL37	85	LYS
40	eL38	11	PHE
40	eL38	28	ASN
40	eL38	29	LYS
40	eL38	46	ARG
40	eL38	63	LYS
40	eL38	68	SER
40	eL38	74	LYS
40	eL38	76	ASN
41	eL39	5	LYS
41	eL39	20	ASN
41	eL39	37	TYR
41	eL39	41	ARG
42	eL40	87	SER
42	eL40	97	ARG
42	eL40	127	LEU
43	eL41	16	LYS
43	eL41	23	ARG
43	eL41	25	LYS
44	eL42	13	LYS
44	eL42	29	LYS
44	eL42	34	SER
44	eL42	53	GLN
44	eL42	97	LYS
45	eL43	4	ARG
45	eL43	60	CYS
45	eL43	72	SER
45	eL43	85	ARG
47	uS2	30	GLN

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Mol	Chain	Res	Type
47	uS2	32	HIS
47	uS2	78	SER
47	uS2	119	ARG
47	uS2	198	MET
48	eS1	24	PHE
48	eS1	40	ASN
48	eS1	59	ASP
48	eS1	69	CYS
48	eS1	82	ARG
48	eS1	89	ASP
48	eS1	100	PHE
48	eS1	105	PHE
48	eS1	144	ARG
48	eS1	166	LYS
48	eS1	169	SER
48	eS1	195	LYS
48	eS1	224	ASP
48	eS1	229	MET
49	uS5	66	PHE
49	uS5	106	ASP
49	uS5	116	LYS
49	uS5	119	LYS
49	uS5	148	LEU
49	uS5	153	SER
49	uS5	232	GLU
49	uS5	245	ASP
50	uS3	6	SER
50	uS3	51	ARG
50	uS3	56	GLN
50	uS3	74	GLN
50	uS3	76	ARG
50	uS3	101	GLN
50	uS3	107	PHE
50	uS3	143	ARG
50	uS3	151	LYS
50	uS3	156	PHE
50	uS3	159	HIS
50	uS3	173	ARG
50	uS3	189	MET
51	eS4	17	HIS
51	eS4	41	SER
51	eS4	49	ARG

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Mol	Chain	Res	Type
51	eS4	51	ARG
51	eS4	68	ARG
51	eS4	69	HIS
51	eS4	158	ASP
51	eS4	200	ARG
51	eS4	206	ASP
51	eS4	213	SER
51	eS4	240	LYS
51	eS4	254	ARG
51	eS4	256	ARG
52	uS7	60	ASP
52	uS7	82	PHE
52	uS7	83	ARG
52	uS7	84	LYS
52	uS7	165	LEU
52	uS7	166	ARG
52	uS7	169	ASN
52	uS7	188	LYS
52	uS7	208	SER
52	uS7	224	ASN
53	eS6	45	PHE
53	eS6	53	SER
53	eS6	85	ARG
53	eS6	95	LYS
53	eS6	115	LYS
53	eS6	116	LYS
53	eS6	132	ARG
53	eS6	150	GLU
53	eS6	152	ASP
53	eS6	164	LYS
53	eS6	169	TYR
53	eS6	184	LEU
53	eS6	189	HIS
54	eS7	24	PHE
54	eS7	35	LYS
54	eS7	58	LEU
54	eS7	71	HIS
54	eS7	72	LYS
54	eS7	77	LEU
54	eS7	85	PHE
54	eS7	104	ARG
54	eS7	107	ARG

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Mol	Chain	Res	Type
54	eS7	127	GLU
54	eS7	141	ARG
55	eS8	9	HIS
55	eS8	18	ARG
55	eS8	20	GLN
55	eS8	21	PHE
55	eS8	25	ARG
55	eS8	42	ARG
55	eS8	109	PHE
55	eS8	146	ARG
55	eS8	179	CYS
55	eS8	200	LYS
56	uS4	10	LYS
56	uS4	50	SER
56	uS4	74	ASN
56	uS4	95	TYR
56	uS4	115	LYS
56	uS4	138	LYS
56	uS4	164	PHE
57	eS10	16	PHE
57	eS10	66	TYR
58	uS17	32	LYS
58	uS17	67	ARG
58	uS17	132	SER
58	uS17	138	ASN
59	uS15	27	LYS
59	uS15	40	TYR
59	uS15	58	HIS
59	uS15	73	ARG
59	uS15	103	GLU
60	uS11	14	PHE
60	uS11	20	TYR
60	uS11	111	ARG
60	uS11	133	ARG
61	uS19	16	SER
61	uS19	32	ASP
61	uS19	45	PHE
61	uS19	57	MET
61	uS19	58	LYS
61	uS19	59	LYS
61	uS19	61	ARG
61	uS19	88	GLU

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Mol	Chain	Res	Type
61	uS19	108	ARG
61	uS19	128	HIS
62	uS9	38	LEU
62	uS9	46	PHE
62	uS9	59	LYS
62	uS9	61	SER
62	uS9	92	TYR
62	uS9	95	LYS
62	uS9	98	ASP
62	uS9	127	LYS
62	uS9	139	GLN
63	eS17	5	ARG
63	eS17	28	PHE
63	eS17	60	ARG
63	eS17	67	ARG
63	eS17	71	PHE
63	eS17	84	TYR
63	eS17	103	ASP
63	eS17	108	ASP
64	uS13	6	GLN
64	uS13	7	GLU
64	uS13	63	GLN
64	uS13	68	ARG
64	uS13	84	TRP
64	uS13	96	LYS
64	uS13	112	ASP
65	eS19	7	ARG
65	eS19	18	TYR
65	eS19	20	SER
65	eS19	24	ARG
65	eS19	33	TYR
65	eS19	60	SER
65	eS19	69	LYS
65	eS19	130	ARG
67	eS21	17	CYS
67	eS21	21	ASN
67	eS21	22	ARG
67	eS21	65	SER
67	eS21	71	ARG
68	uS8	31	SER
68	uS8	68	ARG
68	uS8	93	LEU

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Mol	Chain	Res	Type
69	uS12	19	ARG
69	uS12	94	ASN
69	uS12	107	PHE
69	uS12	114	LYS
70	eS24	10	ARG
70	eS24	32	ARG
70	eS24	41	ARG
70	eS24	49	LYS
70	eS24	52	LYS
70	eS24	68	LYS
70	eS24	78	SER
70	eS24	98	GLU
70	eS24	105	ARG
70	eS24	135	ASP
71	eS25	51	LEU
71	eS25	57	TYR
71	eS25	58	ARG
71	eS25	84	GLU
71	eS25	103	ARG
72	eS26	87	ARG
73	eS27	22	LYS
73	eS27	58	SER
73	eS27	64	CYS
74	eS28	11	LYS
74	eS28	22	ARG
74	eS28	37	SER
74	eS28	56	LEU
75	uS14	10	HIS
75	uS14	12	ARG
75	uS14	19	ARG
75	uS14	36	LEU
75	uS14	40	ARG
75	uS14	44	ARG
75	uS14	46	LYS
76	eS30	7	SER
76	eS30	29	LYS
76	eS30	31	LYS
76	eS30	43	ARG
77	RACK	37	SER
77	RACK	40	LYS
77	RACK	44	SER
77	RACK	45	TRP

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Mol	Chain	Res	Type
77	RACK	53	LYS
77	RACK	73	LEU
77	RACK	79	TYR
77	RACK	87	LYS
77	RACK	109	ASP
77	RACK	121	MET
77	RACK	127	ARG
77	RACK	177	MET
77	RACK	189	GLU
77	RACK	229	LYS
77	RACK	232	TYR
77	RACK	241	PHE
77	RACK	261	LYS
77	RACK	299	GLN
78	eS31	120	GLU
78	eS31	138	ARG
79	eEF2	1	MET
79	eEF2	32	LYS
79	eEF2	41	GLN
79	eEF2	56	PHE
79	eEF2	61	LYS
79	eEF2	87	LYS
79	eEF2	105	SER
79	eEF2	110	ASP
79	eEF2	171	LYS
79	eEF2	173	ASP
79	eEF2	233	PHE
79	eEF2	237	LYS
79	eEF2	240	MET
79	eEF2	247	ASP
79	eEF2	269	LEU
79	eEF2	327	PHE
79	eEF2	425	ASP
79	eEF2	426	LEU
79	eEF2	441	PHE
79	eEF2	483	PHE
79	eEF2	486	SER
79	eEF2	514	SER
79	eEF2	555	LYS
79	eEF2	569	SER
79	eEF2	585	ARG
79	eEF2	588	LEU

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Mol	Chain	Res	Type
79	eEF2	621	ASP
79	eEF2	639	ASP
79	eEF2	651	LYS
79	eEF2	667	PHE
79	eEF2	687	ASN
79	eEF2	753	GLN
79	eEF2	802	SER
79	eEF2	842	LEU

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	25S	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%)

All (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
1	25S	30	G
1	25S	32	U
1	25S	40	A
1	25S	49	A
1	25S	59	G
1	25S	60	A
1	25S	65	A
1	25S	66	A
1	25S	75	G

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Mol	Chain	Res	Type
1	25S	76	G
1	25S	92	G
1	25S	99	A
1	25S	106	A
1	25S	110	G
1	25S	111	C
1	25S	116	A
1	25S	117	U
1	25S	118	U
1	25S	120	G
1	25S	122	A
1	25S	123	A
1	25S	124	U
1	25S	135	C
1	25S	136	G
1	25S	140	C
1	25S	142	C
1	25S	148	G
1	25S	154	U
1	25S	155	G
1	25S	156	G
1	25S	157	A
1	25S	161	G
1	25S	169	U
1	25S	170	G
1	25S	173	G
1	25S	175	C
1	25S	176	G
1	25S	182	U
1	25S	186	U
1	25S	188	U
1	25S	189	G
1	25S	190	U
1	25S	192	C
1	25S	200	C
1	25S	201	A
1	25S	211	A
1	25S	219	A
1	25S	224	C
1	25S	225	C
1	25S	226	C
1	25S	238	A

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Mol	Chain	Res	Type
1	25S	241	G
1	25S	242	C
1	25S	243	G
1	25S	245	U
1	25S	249	U
1	25S	251	G
1	25S	252	U
1	25S	269	G
1	25S	270	U
1	25S	281	G
1	25S	286	U
1	25S	295	A
1	25S	315	C
1	25S	316	U
1	25S	323	A
1	25S	329	U
1	25S	338	A
1	25S	346	C
1	25S	350	C
1	25S	352	A
1	25S	359	U
1	25S	375	A
1	25S	376	G
1	25S	378	A
1	25S	389	A
1	25S	391	A
1	25S	398	A
1	25S	399	A
1	25S	401	U
1	25S	402	A
1	25S	403	C
1	25S	420	G
1	25S	421	G
1	25S	422	A
1	25S	425	G
1	25S	431	U
1	25S	435	C
1	25S	490	A
1	25S	492	U
1	25S	493	G
1	25S	496	C
1	25S	518	G

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Mol	Chain	Res	Type
1	25S	520	U
1	25S	521	A
1	25S	523	A
1	25S	532	A
1	25S	533	A
1	25S	534	U
1	25S	543	C
1	25S	546	C
1	25S	547	G
1	25S	548	G
1	25S	555	U
1	25S	557	A
1	25S	559	A
1	25S	569	A
1	25S	573	C
1	25S	585	A
1	25S	600	G
1	25S	601	U
1	25S	602	A
1	25S	606	C
1	25S	607	A
1	25S	609	G
1	25S	610	G
1	25S	611	A
1	25S	612	U
1	25S	618	C
1	25S	619	A
1	25S	623	U
1	25S	624	G
1	25S	625	G
1	25S	626	U
1	25S	636	C
1	25S	637	C
1	25S	649	A
1	25S	657	A
1	25S	660	A
1	25S	677	A
1	25S	678	G
1	25S	680	G
1	25S	681	U
1	25S	682	U
1	25S	683	U

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Mol	Chain	Res	Type
1	25S	691	A
1	25S	705	A
1	25S	710	A
1	25S	712	G
1	25S	715	A
1	25S	718	G
1	25S	719	U
1	25S	721	G
1	25S	758	C
1	25S	766	U
1	25S	767	U
1	25S	768	C
1	25S	776	U
1	25S	777	U
1	25S	778	U
1	25S	780	A
1	25S	781	G
1	25S	784	A
1	25S	785	G
1	25S	786	A
1	25S	799	G
1	25S	803	C
1	25S	806	A
1	25S	807	A
1	25S	817	A
1	25S	818	C
1	25S	830	A
1	25S	832	G
1	25S	833	G
1	25S	850	U
1	25S	857	G
1	25S	861	C
1	25S	869	G
1	25S	874	U
1	25S	875	G
1	25S	877	C
1	25S	878	G
1	25S	879	U
1	25S	880	G
1	25S	895	A
1	25S	896	A
1	25S	897	U

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Mol	Chain	Res	Type
1	25S	907	G
1	25S	908	G
1	25S	909	G
1	25S	914	A
1	25S	916	G
1	25S	917	A
1	25S	921	A
1	25S	923	C
1	25S	924	G
1	25S	937	G
1	25S	940	G
1	25S	943	U
1	25S	944	C
1	25S	959	C
1	25S	960	U
1	25S	961	C
1	25S	964	G
1	25S	971	G
1	25S	978	G
1	25S	979	U
1	25S	980	A
1	25S	981	U
1	25S	992	A
1	25S	994	G
1	25S	1000	C
1	25S	1010	G
1	25S	1015	U
1	25S	1016	C
1	25S	1018	G
1	25S	1022	U
1	25S	1030	A
1	25S	1032	C
1	25S	1035	G
1	25S	1037	C
1	25S	1047	A
1	25S	1063	G
1	25S	1064	A
1	25S	1066	G
1	25S	1068	C
1	25S	1071	U
1	25S	1072	G
1	25S	1076	C

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Mol	Chain	Res	Type
1	25S	1081	U
1	25S	1082	U
1	25S	1093	A
1	25S	1094	U
1	25S	1096	U
1	25S	1097	G
1	25S	1098	A
1	25S	1102	A
1	25S	1103	A
1	25S	1104	G
1	25S	1117	G
1	25S	1125	U
1	25S	1128	U
1	25S	1131	G
1	25S	1135	A
1	25S	1142	G
1	25S	1143	A
1	25S	1144	U
1	25S	1151	U
1	25S	1152	G
1	25S	1153	A
1	25S	1154	A
1	25S	1159	A
1	25S	1178	G
1	25S	1180	A
1	25S	1181	U
1	25S	1182	A
1	25S	1191	U
1	25S	1193	A
1	25S	1194	G
1	25S	1196	C
1	25S	1201	C
1	25S	1209	G
1	25S	1220	U
1	25S	1222	G
1	25S	1235	U
1	25S	1236	G
1	25S	1237	G
1	25S	1240	A
1	25S	1245	A
1	25S	1246	G
1	25S	1251	A

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Mol	Chain	Res	Type
1	25S	1252	A
1	25S	1253	U
1	25S	1256	G
1	25S	1257	C
1	25S	1258	U
1	25S	1262	G
1	25S	1263	A
1	25S	1265	U
1	25S	1270	A
1	25S	1273	A
1	25S	1274	A
1	25S	1278	A
1	25S	1283	C
1	25S	1286	A
1	25S	1287	A
1	25S	1288	U
1	25S	1302	A
1	25S	1307	G
1	25S	1308	A
1	25S	1309	U
1	25S	1313	G
1	25S	1317	A
1	25S	1318	A
1	25S	1325	U
1	25S	1330	A
1	25S	1333	C
1	25S	1346	G
1	25S	1348	U
1	25S	1349	G
1	25S	1350	A
1	25S	1351	U
1	25S	1352	A
1	25S	1353	U
1	25S	1355	A
1	25S	1386	A
1	25S	1387	G
1	25S	1391	C
1	25S	1399	A
1	25S	1400	G
1	25S	1406	A
1	25S	1407	A
1	25S	1417	G

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Mol	Chain	Res	Type
1	25S	1418	A
1	25S	1421	G
1	25S	1425	U
1	25S	1431	G
1	25S	1432	C
1	25S	1434	G
1	25S	1436	U
1	25S	1437	C
1	25S	1446	A
1	25S	1450	G
1	25S	1468	A
1	25S	1483	G
1	25S	1495	U
1	25S	1502	C
1	25S	1506	A
1	25S	1507	G
1	25S	1508	C
1	25S	1510	G
1	25S	1523	U
1	25S	1527	C
1	25S	1536	G
1	25S	1546	A
1	25S	1549	U
1	25S	1553	U
1	25S	1556	C
1	25S	1557	A
1	25S	1560	G
1	25S	1562	C
1	25S	1563	C
1	25S	1564	U
1	25S	1567	U
1	25S	1568	U
1	25S	1569	U
1	25S	1570	U
1	25S	1571	A
1	25S	1572	U
1	25S	1575	A
1	25S	1578	C
1	25S	1580	A
1	25S	1581	C
1	25S	1582	C
1	25S	1589	A

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Mol	Chain	Res	Type
1	25S	1595	U
1	25S	1596	C
1	25S	1605	A
1	25S	1606	U
1	25S	1620	U
1	25S	1622	U
1	25S	1628	C
1	25S	1629	U
1	25S	1630	U
1	25S	1632	A
1	25S	1643	A
1	25S	1644	C
1	25S	1645	U
1	25S	1646	G
1	25S	1654	A
1	25S	1656	A
1	25S	1657	C
1	25S	1695	U
1	25S	1716	U
1	25S	1717	U
1	25S	1724	U
1	25S	1741	A
1	25S	1744	G
1	25S	1749	A
1	25S	1750	A
1	25S	1751	G
1	25S	1753	G
1	25S	1759	C
1	25S	1762	C
1	25S	1763	U
1	25S	1764	U
1	25S	1765	U
1	25S	1767	C
1	25S	1769	G
1	25S	1773	C
1	25S	1796	G
1	25S	1797	A
1	25S	1808	G
1	25S	1812	G
1	25S	1813	A
1	25S	1815	U
1	25S	1816	A

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Mol	Chain	Res	Type
1	25S	1817	G
1	25S	1820	U
1	25S	1821	U
1	25S	1840	U
1	25S	1842	A
1	25S	1848	G
1	25S	1866	C
1	25S	1867	A
1	25S	1878	G
1	25S	1879	A
1	25S	1880	U
1	25S	1885	U
1	25S	1886	A
1	25S	1894	U
1	25S	1906	G
1	25S	1920	U
1	25S	1934	G
1	25S	1935	G
1	25S	1948	G
1	25S	1951	C
1	25S	1952	G
1	25S	2093	A
1	25S	2094	C
1	25S	2095	G
1	25S	2099	A
1	25S	2101	C
1	25S	2102	U
1	25S	2112	U
1	25S	2114	C
1	25S	2122	G
1	25S	2126	A
1	25S	2131	A
1	25S	2140	U
1	25S	2158	A
1	25S	2162	U
1	25S	2168	A
1	25S	2169	G
1	25S	2170	U
1	25S	2171	G
1	25S	2172	A
1	25S	2176	U
1	25S	2184	U

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Mol	Chain	Res	Type
1	25S	2185	G
1	25S	2188	A
1	25S	2205	U
1	25S	2206	G
1	25S	2207	A
1	25S	2208	A
1	25S	2209	U
1	25S	2210	G
1	25S	2213	A
1	25S	2223	A
1	25S	2225	U
1	25S	2244	A
1	25S	2246	G
1	25S	2249	G
1	25S	2251	G
1	25S	2252	A
1	25S	2256	A
1	25S	2257	C
1	25S	2262	A
1	25S	2269	U
1	25S	2270	A
1	25S	2272	G
1	25S	2273	G
1	25S	2274	U
1	25S	2276	G
1	25S	2279	A
1	25S	2281	A
1	25S	2295	A
1	25S	2298	U
1	25S	2306	C
1	25S	2307	G
1	25S	2310	U
1	25S	2313	A
1	25S	2314	U
1	25S	2315	G
1	25S	2335	G
1	25S	2336	U
1	25S	2341	A
1	25S	2349	U
1	25S	2361	A
1	25S	2363	A
1	25S	2373	A

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Mol	Chain	Res	Type
1	25S	2374	C
1	25S	2375	G
1	25S	2382	G
1	25S	2385	G
1	25S	2388	U
1	25S	2393	G
1	25S	2397	A
1	25S	2398	A
1	25S	2402	A
1	25S	2403	G
1	25S	2404	A
1	25S	2411	U
1	25S	2415	C
1	25S	2416	U
1	25S	2418	G
1	25S	2419	A
1	25S	2436	U
1	25S	2449	A
1	25S	2450	G
1	25S	2451	G
1	25S	2454	G
1	25S	2455	U
1	25S	2465	G
1	25S	2485	A
1	25S	2487	U
1	25S	2497	U
1	25S	2498	C
1	25S	2507	C
1	25S	2509	U
1	25S	2510	U
1	25S	2511	A
1	25S	2514	U
1	25S	2515	A
1	25S	2522	G
1	25S	2523	A
1	25S	2534	G
1	25S	2535	A
1	25S	2536	A
1	25S	2537	U
1	25S	2540	A
1	25S	2541	U
1	25S	2542	U

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Mol	Chain	Res	Type
1	25S	2543	U
1	25S	2549	G
1	25S	2552	C
1	25S	2554	A
1	25S	2555	G
1	25S	2560	C
1	25S	2561	A
1	25S	2564	G
1	25S	2569	A
1	25S	2570	U
1	25S	2571	U
1	25S	2573	G
1	25S	2585	G
1	25S	2586	G
1	25S	2587	U
1	25S	2593	A
1	25S	2606	G
1	25S	2607	G
1	25S	2614	G
1	25S	2621	G
1	25S	2626	A
1	25S	2628	A
1	25S	2636	A
1	25S	2638	C
1	25S	2648	G
1	25S	2652	U
1	25S	2656	A
1	25S	2657	A
1	25S	2673	A
1	25S	2674	A
1	25S	2677	G
1	25S	2678	A
1	25S	2681	U
1	25S	2689	A
1	25S	2691	A
1	25S	2695	A
1	25S	2696	A
1	25S	2704	A
1	25S	2705	A
1	25S	2714	G
1	25S	2720	G
1	25S	2721	A

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Mol	Chain	Res	Type
1	25S	2728	G
1	25S	2729	U
1	25S	2737	C
1	25S	2744	U
1	25S	2750	U
1	25S	2753	G
1	25S	2754	G
1	25S	2755	C
1	25S	2759	U
1	25S	2762	A
1	25S	2771	U
1	25S	2772	C
1	25S	2773	C
1	25S	2776	C
1	25S	2777	G
1	25S	2778	G
1	25S	2779	A
1	25S	2795	U
1	25S	2796	G
1	25S	2799	A
1	25S	2800	G
1	25S	2801	A
1	25S	2804	A
1	25S	2805	G
1	25S	2808	A
1	25S	2810	C
1	25S	2814	G
1	25S	2817	A
1	25S	2827	U
1	25S	2838	A
1	25S	2843	U
1	25S	2845	A
1	25S	2846	U
1	25S	2847	A
1	25S	2871	G
1	25S	2872	A
1	25S	2875	U
1	25S	2876	C
1	25S	2887	A
1	25S	2889	C
1	25S	2899	C
1	25S	2911	A

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Mol	Chain	Res	Type
1	25S	2914	G
1	25S	2923	U
1	25S	2925	C
1	25S	2935	U
1	25S	2936	A
1	25S	2938	G
1	25S	2941	A
1	25S	2942	C
1	25S	2943	G
1	25S	2946	A
1	25S	2947	G
1	25S	2948	C
1	25S	2951	G
1	25S	2952	G
1	25S	2954	U
1	25S	2955	U
1	25S	2971	A
1	25S	2972	G
1	25S	2979	U
1	25S	2983	C
1	25S	2984	C
1	25S	2990	G
1	25S	2996	U
1	25S	2997	G
1	25S	2998	U
1	25S	3002	C
1	25S	3005	A
1	25S	3012	A
1	25S	3049	A
1	25S	3056	U
1	25S	3059	G
1	25S	3078	U
1	25S	3079	U
1	25S	3080	G
1	25S	3092	C
1	25S	3101	G
1	25S	3109	G
1	25S	3115	C
1	25S	3116	G
1	25S	3122	A
1	25S	3130	A
1	25S	3131	U

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Mol	Chain	Res	Type
1	25S	3142	A
1	25S	3143	C
1	25S	3149	G
1	25S	3153	U
1	25S	3154	C
1	25S	3156	U
1	25S	3157	U
1	25S	3158	G
1	25S	3168	A
1	25S	3170	A
1	25S	3172	A
1	25S	3173	G
1	25S	3176	G
1	25S	3177	G
1	25S	3179	U
1	25S	3180	A
1	25S	3181	C
1	25S	3187	A
1	25S	3196	U
1	25S	3197	G
1	25S	3198	U
1	25S	3206	C
1	25S	3207	U
1	25S	3209	A
1	25S	3210	A
1	25S	3215	A
1	25S	3217	C
1	25S	3218	A
1	25S	3219	G
1	25S	3227	A
1	25S	3228	C
1	25S	3232	G
1	25S	3244	A
1	25S	3245	A
1	25S	3246	G
1	25S	3247	G
1	25S	3249	C
1	25S	3254	G
1	25S	3256	G
1	25S	3260	G
1	25S	3263	G
1	25S	3268	A

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Mol	Chain	Res	Type
1	25S	3269	U
1	25S	3270	U
1	25S	3271	G
1	25S	3272	C
1	25S	3273	A
1	25S	3274	A
1	25S	3276	G
1	25S	3277	U
1	25S	3278	C
1	25S	3279	A
1	25S	3280	U
1	25S	3281	U
1	25S	3283	U
1	25S	3288	G
1	25S	3289	G
1	25S	3294	A
1	25S	3303	G
1	25S	3304	U
1	25S	3313	U
1	25S	3316	A
1	25S	3319	U
1	25S	3320	A
1	25S	3333	G
1	25S	3341	U
1	25S	3342	A
1	25S	3345	G
1	25S	3348	G
1	25S	3349	C
1	25S	3350	C
1	25S	3352	U
1	25S	3353	G
1	25S	3357	U
1	25S	3358	U
1	25S	3359	A
1	25S	3368	U
1	25S	3369	G
1	25S	3378	C
1	25S	3382	U
1	25S	3386	G
1	25S	3389	U
1	25S	3390	G
2	AB	7	G

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Mol	Chain	Res	Type
2	AB	31	U
2	AB	38	U
2	AB	41	G
2	AB	45	A
2	AB	54	U
2	AB	55	A
2	AB	59	U
2	AB	63	A
2	AB	64	A
2	AB	65	G
2	AB	73	C
2	AB	74	C
2	AB	76	A
2	AB	88	G
2	AB	90	U
2	AB	91	G
2	AB	93	C
2	AB	110	G
2	AB	112	G
2	AB	121	U
3	58S	2	A
3	58S	22	U
3	58S	23	U
3	58S	34	U
3	58S	35	C
3	58S	51	G
3	58S	52	A
3	58S	53	A
3	58S	59	A
3	58S	62	C
3	58S	63	G
3	58S	80	A
3	58S	81	U
3	58S	82	U
3	58S	83	C
3	58S	84	C
3	58S	85	G
3	58S	86	U
3	58S	87	G
3	58S	91	C
3	58S	92	A
3	58S	95	G

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Mol	Chain	Res	Type
3	58S	104	A
3	58S	105	A
3	58S	106	C
3	58S	113	U
3	58S	125	U
3	58S	126	A
3	58S	127	U
3	58S	128	U
3	58S	130	C
3	58S	131	A
3	58S	151	C
3	58S	152	G
3	58S	155	A
3	58S	157	U
3	58S	158	U
46	18S	4	C
46	18S	14	C
46	18S	17	C
46	18S	25	C
46	18S	26	A
46	18S	34	G
46	18S	42	G
46	18S	45	U
46	18S	47	A
46	18S	61	A
46	18S	68	A
46	18S	70	C
46	18S	78	A
46	18S	80	A
46	18S	105	A
46	18S	111	U
46	18S	113	U
46	18S	114	C
46	18S	127	G
46	18S	129	U
46	18S	130	C
46	18S	131	C
46	18S	137	U
46	18S	138	A
46	18S	140	A
46	18S	141	U
46	18S	144	U

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Mol	Chain	Res	Type
46	18S	145	A
46	18S	146	U
46	18S	147	A
46	18S	157	A
46	18S	159	U
46	18S	161	U
46	18S	167	U
46	18S	169	A
46	18S	177	U
46	18S	178	U
46	18S	179	A
46	18S	181	A
46	18S	182	A
46	18S	185	U
46	18S	186	C
46	18S	199	G
46	18S	200	A
46	18S	201	G
46	18S	203	U
46	18S	204	G
46	18S	217	A
46	18S	218	A
46	18S	219	A
46	18S	249	U
46	18S	250	C
46	18S	253	A
46	18S	260	U
46	18S	261	U
46	18S	265	A
46	18S	267	U
46	18S	271	A
46	18S	272	U
46	18S	276	C
46	18S	278	U
46	18S	279	G
46	18S	280	U
46	18S	281	G
46	18S	287	G
46	18S	299	A
46	18S	313	U
46	18S	314	C
46	18S	316	A

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Mol	Chain	Res	Type
46	18S	321	C
46	18S	322	G
46	18S	337	G
46	18S	338	C
46	18S	351	C
46	18S	355	G
46	18S	359	A
46	18S	361	C
46	18S	386	G
46	18S	387	A
46	18S	399	A
46	18S	400	A
46	18S	401	A
46	18S	402	C
46	18S	404	G
46	18S	412	A
46	18S	416	A
46	18S	419	G
46	18S	423	G
46	18S	424	C
46	18S	426	G
46	18S	427	C
46	18S	434	G
46	18S	435	C
46	18S	437	A
46	18S	439	U
46	18S	444	C
46	18S	445	A
46	18S	452	A
46	18S	455	C
46	18S	459	G
46	18S	468	A
46	18S	475	A
46	18S	477	A
46	18S	480	G
46	18S	486	G
46	18S	488	G
46	18S	489	C
46	18S	490	C
46	18S	491	C
46	18S	492	A
46	18S	493	U

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Mol	Chain	Res	Type
46	18S	496	G
46	18S	497	G
46	18S	499	U
46	18S	503	G
46	18S	506	A
46	18S	507	U
46	18S	515	A
46	18S	517	U
46	18S	527	A
46	18S	529	A
46	18S	534	A
46	18S	538	A
46	18S	539	G
46	18S	541	A
46	18S	542	A
46	18S	543	C
46	18S	544	A
46	18S	545	A
46	18S	548	G
46	18S	551	G
46	18S	555	A
46	18S	557	G
46	18S	558	U
46	18S	559	C
46	18S	565	C
46	18S	567	A
46	18S	568	G
46	18S	576	G
46	18S	581	U
46	18S	582	U
46	18S	583	C
46	18S	594	A
46	18S	606	A
46	18S	610	G
46	18S	611	U
46	18S	616	G
46	18S	619	A
46	18S	620	A
46	18S	623	A
46	18S	624	G
46	18S	630	A
46	18S	637	C

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Mol	Chain	Res	Type
46	18S	648	G
46	18S	649	U
46	18S	650	U
46	18S	651	G
46	18S	653	C
46	18S	654	C
46	18S	655	G
46	18S	656	G
46	18S	657	U
46	18S	679	U
46	18S	681	U
46	18S	691	C
46	18S	693	U
46	18S	694	U
46	18S	695	U
46	18S	696	C
46	18S	697	C
46	18S	698	U
46	18S	700	C
46	18S	701	U
46	18S	702	G
46	18S	703	G
46	18S	704	C
46	18S	705	U
46	18S	706	A
46	18S	707	A
46	18S	708	C
46	18S	709	C
46	18S	710	U
46	18S	711	U
46	18S	714	G
46	18S	715	U
46	18S	716	C
46	18S	717	C
46	18S	718	U
46	18S	719	U
46	18S	720	G
46	18S	721	U
46	18S	722	G
46	18S	723	G
46	18S	727	U
46	18S	728	U

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Mol	Chain	Res	Type
46	18S	729	G
46	18S	730	G
46	18S	731	C
46	18S	732	G
46	18S	733	A
46	18S	734	A
46	18S	735	C
46	18S	738	G
46	18S	739	G
46	18S	740	A
46	18S	741	C
46	18S	742	U
46	18S	743	U
46	18S	756	A
46	18S	757	A
46	18S	758	U
46	18S	765	G
46	18S	766	U
46	18S	775	G
46	18S	779	U
46	18S	780	A
46	18S	781	U
46	18S	782	U
46	18S	783	G
46	18S	784	C
46	18S	789	A
46	18S	793	A
46	18S	794	U
46	18S	795	U
46	18S	798	C
46	18S	803	A
46	18S	810	G
46	18S	812	A
46	18S	813	U
46	18S	814	A
46	18S	816	G
46	18S	819	G
46	18S	820	U
46	18S	821	U
46	18S	823	G
46	18S	827	C
46	18S	830	U

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Mol	Chain	Res	Type
46	18S	831	U
46	18S	832	U
46	18S	841	U
46	18S	846	G
46	18S	856	A
46	18S	858	G
46	18S	859	A
46	18S	860	U
46	18S	863	A
46	18S	876	G
46	18S	881	A
46	18S	886	U
46	18S	895	G
46	18S	897	C
46	18S	898	A
46	18S	912	U
46	18S	913	G
46	18S	914	G
46	18S	915	A
46	18S	920	U
46	18S	926	A
46	18S	929	A
46	18S	933	A
46	18S	935	U
46	18S	944	A
46	18S	951	A
46	18S	960	U
46	18S	964	U
46	18S	966	A
46	18S	988	A
46	18S	991	G
46	18S	992	A
46	18S	993	A
46	18S	996	U
46	18S	998	A
46	18S	1010	C
46	18S	1022	C
46	18S	1026	A
46	18S	1027	A
46	18S	1028	C
46	18S	1030	A
46	18S	1031	U

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Mol	Chain	Res	Type
46	18S	1040	G
46	18S	1051	G
46	18S	1053	G
46	18S	1057	U
46	18S	1058	U
46	18S	1059	U
46	18S	1060	U
46	18S	1061	A
46	18S	1063	U
46	18S	1076	A
46	18S	1081	A
46	18S	1082	C
46	18S	1083	G
46	18S	1085	G
46	18S	1091	A
46	18S	1092	A
46	18S	1093	A
46	18S	1097	U
46	18S	1100	G
46	18S	1113	A
46	18S	1138	A
46	18S	1150	G
46	18S	1151	A
46	18S	1153	G
46	18S	1154	G
46	18S	1157	A
46	18S	1158	C
46	18S	1162	C
46	18S	1167	G
46	18S	1170	G
46	18S	1182	U
46	18S	1185	U
46	18S	1191	U
46	18S	1192	C
46	18S	1194	A
46	18S	1196	A
46	18S	1199	G
46	18S	1200	G
46	18S	1202	A
46	18S	1207	C
46	18S	1216	C
46	18S	1217	A

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Mol	Chain	Res	Type
46	18S	1218	G
46	18S	1220	C
46	18S	1224	A
46	18S	1226	A
46	18S	1228	G
46	18S	1229	G
46	18S	1238	A
46	18S	1241	G
46	18S	1243	G
46	18S	1244	A
46	18S	1245	G
46	18S	1246	C
46	18S	1249	U
46	18S	1252	C
46	18S	1255	G
46	18S	1256	A
46	18S	1258	U
46	18S	1259	U
46	18S	1261	G
46	18S	1264	G
46	18S	1265	G
46	18S	1270	G
46	18S	1273	G
46	18S	1274	C
46	18S	1275	A
46	18S	1285	U
46	18S	1286	U
46	18S	1288	G
46	18S	1293	U
46	18S	1298	U
46	18S	1307	U
46	18S	1309	C
46	18S	1310	U
46	18S	1314	U
46	18S	1315	U
46	18S	1316	G
46	18S	1320	U
46	18S	1321	A
46	18S	1336	A
46	18S	1337	A
46	18S	1338	C
46	18S	1339	C

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Mol	Chain	Res	Type
46	18S	1340	U
46	18S	1341	A
46	18S	1344	A
46	18S	1345	A
46	18S	1346	A
46	18S	1347	U
46	18S	1348	A
46	18S	1351	G
46	18S	1354	G
46	18S	1355	C
46	18S	1358	G
46	18S	1359	C
46	18S	1361	U
46	18S	1362	U
46	18S	1363	U
46	18S	1364	G
46	18S	1367	G
46	18S	1370	U
46	18S	1371	A
46	18S	1372	U
46	18S	1375	A
46	18S	1376	C
46	18S	1380	U
46	18S	1385	G
46	18S	1388	A
46	18S	1390	U
46	18S	1395	G
46	18S	1397	U
46	18S	1398	U
46	18S	1399	C
46	18S	1400	A
46	18S	1409	G
46	18S	1411	A
46	18S	1412	G
46	18S	1413	U
46	18S	1414	U
46	18S	1415	U
46	18S	1424	A
46	18S	1425	A
46	18S	1426	C
46	18S	1427	A
46	18S	1428	G

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Mol	Chain	Res	Type
46	18S	1431	C
46	18S	1432	U
46	18S	1433	G
46	18S	1436	A
46	18S	1447	C
46	18S	1459	C
46	18S	1460	A
46	18S	1469	A
46	18S	1471	A
46	18S	1472	C
46	18S	1473	U
46	18S	1474	G
46	18S	1477	G
46	18S	1478	G
46	18S	1479	A
46	18S	1482	C
46	18S	1483	A
46	18S	1489	U
46	18S	1490	C
46	18S	1492	A
46	18S	1493	A
46	18S	1494	C
46	18S	1499	G
46	18S	1500	C
46	18S	1506	G
46	18S	1515	A
46	18S	1516	A
46	18S	1517	U
46	18S	1520	U
46	18S	1523	G
46	18S	1524	A
46	18S	1532	U
46	18S	1535	U
46	18S	1536	G
46	18S	1537	C
46	18S	1538	U
46	18S	1542	G
46	18S	1543	A
46	18S	1548	G
46	18S	1550	A
46	18S	1557	U
46	18S	1559	A

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Mol	Chain	Res	Type
46	18S	1563	C
46	18S	1568	C
46	18S	1570	A
46	18S	1592	A
46	18S	1597	A
46	18S	1601	G
46	18S	1607	G
46	18S	1615	C
46	18S	1616	G
46	18S	1618	C
46	18S	1619	C
46	18S	1622	G
46	18S	1631	A
46	18S	1633	A
46	18S	1634	C
46	18S	1635	A
46	18S	1643	U
46	18S	1651	A
46	18S	1657	U
46	18S	1658	G
46	18S	1665	U
46	18S	1667	A
46	18S	1678	A
46	18S	1681	A
46	18S	1683	C
46	18S	1685	G
46	18S	1686	C
46	18S	1691	A
46	18S	1692	G
46	18S	1693	A
46	18S	1694	A
46	18S	1696	G
46	18S	1697	G
46	18S	1698	G
46	18S	1699	G
46	18S	1700	C
46	18S	1701	A
46	18S	1702	A
46	18S	1703	C
46	18S	1706	C
46	18S	1707	A
46	18S	1710	U

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Mol	Chain	Res	Type
46	18S	1711	C
46	18S	1712	A
46	18S	1713	G
46	18S	1714	A
46	18S	1715	G
46	18S	1716	C
46	18S	1717	G
46	18S	1740	A
46	18S	1751	C
46	18S	1762	A
46	18S	1766	A
46	18S	1769	U
46	18S	1780	G
46	18S	1781	A
46	18S	1782	A
46	18S	1790	A
46	18S	1792	G
46	18S	1793	G
46	18S	1794	A
46	18S	1796	C
46	18S	1797	A
80	ASIT	2	C
80	ASIT	3	C
80	ASIT	4	C
80	ASIT	7	A
80	ASIT	9	A
80	ASIT	10	G
80	ASIT	11	C
80	ASIT	13	C
80	ASIT	15	G
80	ASIT	16	U
80	ASIT	17	C
80	ASIT	18	G
80	ASIT	19	G
80	ASIT	20	U
80	ASIT	21	A
80	ASIT	25	C
80	ASIT	41	C
80	ASIT	47	U
80	ASIT	48	C
80	ASIT	49	C
80	ASIT	58	A

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Mol	Chain	Res	Type
80	ASIT	59	U
80	ASIT	60	U
80	ASIT	64	A
80	ASIT	65	G
80	ASIT	68	C
80	ASIT	69	G
80	ASIT	70	G
80	ASIT	74	C
81	PSIT	2	G
81	PSIT	8	U
81	PSIT	9	G
81	PSIT	14	A
81	PSIT	16	C
81	PSIT	18	C
81	PSIT	19	G
81	PSIT	20	G
81	PSIT	21	U
81	PSIT	22	A
81	PSIT	23	G
81	PSIT	36	A
81	PSIT	48	U
81	PSIT	49	C
81	PSIT	54	G
81	PSIT	55	U
81	PSIT	59	A
81	PSIT	61	U
81	PSIT	66	C
81	PSIT	75	C
81	PSIT	77	A
82	mRNA	4	U
82	mRNA	5	U
82	mRNA	8	A

All (49) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	25S	40	A
1	25S	491	C
1	25S	601	U
1	25S	916	G
1	25S	959	C
1	25S	993	G

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Mol	Chain	Res	Type
1	25S	1154	A
1	25S	1562	C
1	25S	1605	A
1	25S	1814	A
1	25S	1820	U
1	25S	2209	U
1	25S	2306	C
1	25S	2313	A
1	25S	2372	A
1	25S	2418	G
1	25S	2570	U
1	25S	2842	U
1	25S	2971	A
1	25S	3004	C
1	25S	3121	U
1	25S	3206	C
2	AB	72	A
3	58S	126	A
46	18S	45	U
46	18S	77	U
46	18S	143	G
46	18S	145	A
46	18S	199	G
46	18S	487	G
46	18S	695	U
46	18S	717	C
46	18S	781	U
46	18S	812	A
46	18S	858	G
46	18S	1082	C
46	18S	1161	C
46	18S	1244	A
46	18S	1273	G
46	18S	1335	U
46	18S	1399	C
46	18S	1410	A
46	18S	1458	G
46	18S	1489	U
46	18S	1491	U
46	18S	1633	A
46	18S	1684	U
80	ASIT	10	G

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Mol	Chain	Res	Type
80	ASIT	69	G

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

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

All (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
80	ASIT	37	YG	C5-N7	-2.30	1.34	1.39
79	eEF2	699	DDE	CA-N	-2.04	1.42	1.48

All (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
79	eEF2	699	DDE	CA-CB-CG	-3.73	104.58	113.77
80	ASIT	37	YG	O23-C21-O22	-3.25	119.89	124.62
80	ASIT	37	YG	C13-C14-C15	-3.16	107.33	113.16
80	ASIT	37	YG	O23-C21-N20	3.08	115.95	110.77
80	ASIT	37	YG	O18-C16-C15	2.95	119.00	111.49
80	ASIT	37	YG	N3-C2-N2	2.85	130.56	126.62
80	ASIT	37	YG	O6-C6-C5	-2.64	117.79	124.59
79	eEF2	699	DDE	CAU-CBW-CBI	-2.48	106.37	111.22
80	ASIT	37	YG	C19-O18-C16	2.17	120.85	115.92
79	eEF2	699	DDE	CB-CG-CD2	-2.15	124.94	129.33
80	ASIT	37	YG	O18-C16-O17	-2.05	119.87	123.85

There are no chirality outliers.

All (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
80	ASIT	37	YG	O17-C16-O18-C19
80	ASIT	37	YG	C3'-C4'-C5'-O5'
80	ASIT	37	YG	C13-C14-C15-C16
80	ASIT	37	YG	O4'-C4'-C5'-O5'
79	eEF2	699	DDE	OAG-CBI-CBW-NCB
79	eEF2	699	DDE	OAG-CBI-CBW-CAU
80	ASIT	37	YG	N20-C15-C16-O18
80	ASIT	37	YG	N20-C15-C16-O17
79	eEF2	699	DDE	NAD-CBI-CBW-CAU
80	ASIT	37	YG	N1-C12-C13-C14
80	ASIT	37	YG	C4'-C5'-O5'-P

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

All (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
86	eEF2	907	GTP	N9-C8-N7	-2.57	108.63	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	eEF2	907	GTP	C5-C6-N1	2.54	119.72	113.25
86	eEF2	907	GTP	C8-N7-C5	2.34	108.42	104.26
86	eEF2	907	GTP	C3'-C2'-C1'	2.30	105.82	101.46
86	eEF2	907	GTP	O3A-PA-O1A	-2.01	104.66	110.70

There are no chirality outliers.

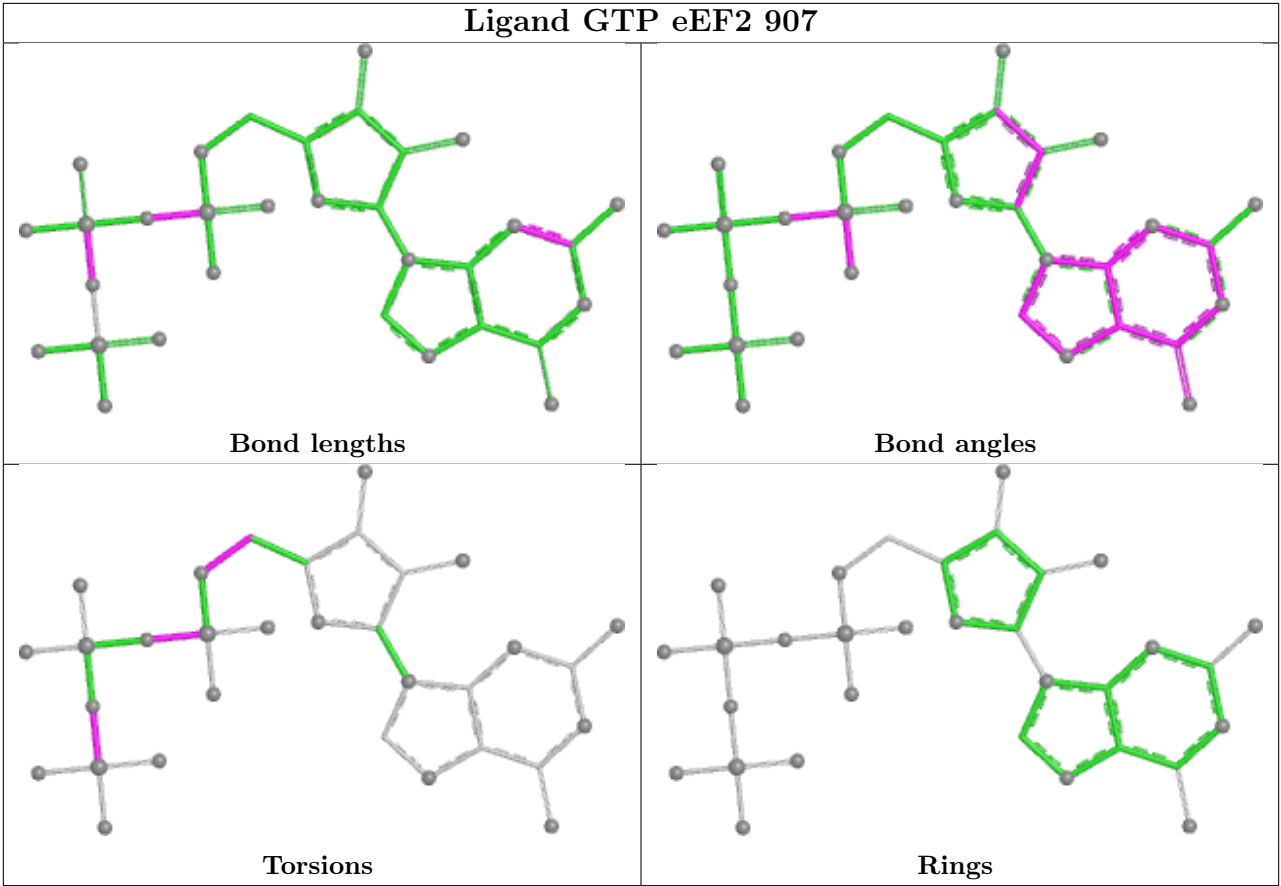
All (3) torsion outliers are listed below:

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

All (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
7	uL4	65	TRP	7.6
36	eL34	22	VAL	6.9
7	uL4	109	TRP	6.9
7	uL4	90	PHE	6.7
9	eL6	13	GLU	6.1
23	eL21	85	LEU	6.1
51	eS4	23	LEU	6.1
10	uL30	133	TYR	5.9
30	uL15	46	ASP	5.7
36	eL34	29	ILE	5.7
7	uL4	55	LYS	5.5
7	uL4	106	TRP	5.5
7	uL4	105	THR	5.4
36	eL34	33	GLN	5.3
23	eL21	86	GLU	5.3
15	eL13	21	ARG	5.2
7	uL4	104	LYS	5.2
36	eL34	7	PHE	5.1
81	PSIT	1	C	5.1
7	uL4	69	ARG	5.0
48	eS1	82	ARG	5.0
20	eL18	166	LEU	5.0
27	uL23	84	PHE	4.9
36	eL34	32	ALA	4.9
72	eS26	73	TYR	4.9
79	eEF2	65	GLU	4.9
15	eL13	10	LEU	4.6
11	eL8	163	VAL	4.6
1	25S	2728	G	4.6
23	eL21	79	MET	4.6
7	uL4	54	GLU	4.5
36	eL34	3	GLN	4.5
46	18S	1635	A	4.5
7	uL4	89	ALA	4.5
9	eL6	11	PRO	4.5
28	uL24	20	PHE	4.5
36	eL34	21	LYS	4.4
36	eL34	31	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
14	uL5	147	THR	4.4
9	eL6	14	ASP	4.4
20	eL18	158	HIS	4.3
7	uL4	111	VAL	4.3
30	uL15	56	VAL	4.3
35	eL33	28	SER	4.3
20	eL18	159	LYS	4.3
5	uL2	25	GLY	4.3
1	25S	985	U	4.2
29	eL27	31	GLU	4.2
6	uL3	246	LEU	4.2
36	eL34	5	VAL	4.2
79	eEF2	586	ILE	4.2
46	18S	1634	C	4.2
27	uL23	118	GLY	4.1
30	uL15	47	LYS	4.1
7	uL4	53	SER	4.1
20	eL18	154	GLY	4.1
7	uL4	168	ALA	4.0
7	uL4	74	ILE	3.9
7	uL4	47	ARG	3.9
6	uL3	245	GLY	3.9
79	eEF2	655	TYR	3.9
7	uL4	79	GLY	3.9
10	uL30	132	PRO	3.9
48	eS1	66	VAL	3.8
1	25S	2772	C	3.8
36	eL34	14	ASN	3.8
9	eL6	15	VAL	3.8
83	uL11	136	ALA	3.8
7	uL4	103	THR	3.8
18	uL13	15	LEU	3.8
14	uL5	146	GLY	3.7
23	eL21	81	GLY	3.7
20	eL18	145	ASN	3.7
79	eEF2	587	TYR	3.7
46	18S	1424	A	3.7
15	eL13	23	LYS	3.7
53	eS6	77	LEU	3.6
23	eL21	83	ARG	3.6
32	eL30	97	ASP	3.6
64	uS13	51	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
5	uL2	252	THR	3.5
11	eL8	160	ILE	3.5
46	18S	1637	C	3.5
70	eS24	85	PHE	3.5
20	eL18	171	LYS	3.5
63	eS17	35	CYS	3.5
18	uL13	80	PHE	3.5
5	uL2	73	GLU	3.4
22	eL20	163	PHE	3.4
36	eL34	23	VAL	3.4
39	eL37	30	GLN	3.4
21	eL19	52	LYS	3.3
4	uL10	28	VAL	3.3
7	uL4	41	SER	3.3
46	18S	1427	A	3.3
7	uL4	49	ALA	3.3
1	25S	886	C	3.3
48	eS1	68	VAL	3.3
7	uL4	59	GLN	3.3
13	uL16	96	VAL	3.3
15	eL13	20	GLU	3.3
45	eL43	18	TYR	3.3
75	uS14	43	PHE	3.3
83	uL11	59	THR	3.2
61	uS19	103	ASN	3.2
1	25S	402	A	3.2
9	eL6	18	LEU	3.2
62	uS9	41	PRO	3.2
4	uL10	86	PHE	3.2
60	uS11	115	ILE	3.2
30	uL15	44	ASN	3.2
18	uL13	54	TYR	3.2
23	eL21	84	TYR	3.2
13	uL16	109	ASP	3.1
5	uL2	245	LEU	3.1
61	uS19	88	GLU	3.1
27	uL23	83	VAL	3.1
79	eEF2	698	ILE	3.1
60	uS11	76	ILE	3.1
46	18S	1426	C	3.1
17	eL15	198	SER	3.1
1	25S	967	A	3.1

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Mol	Chain	Res	Type	RSRZ
36	eL34	6	THR	3.1
56	uS4	58	ASP	3.1
56	uS4	12	TYR	3.1
46	18S	1425	A	3.1
45	eL43	25	GLN	3.0
53	eS6	86	PRO	3.0
5	uL2	180	LEU	3.0
34	eL32	2	ALA	3.0
7	uL4	63	GLU	3.0
72	eS26	90	GLU	3.0
2	AB	1	G	3.0
76	eS30	51	ASN	3.0
62	uS9	44	LEU	3.0
17	eL15	79	ALA	3.0
60	uS11	13	VAL	3.0
10	uL30	124	LEU	2.9
39	eL37	55	ARG	2.9
7	uL4	66	GLY	2.9
10	uL30	109	THR	2.9
27	uL23	82	LEU	2.9
35	eL33	29	LEU	2.9
23	eL21	34	TYR	2.9
41	eL39	36	ARG	2.9
11	eL8	76	ALA	2.9
23	eL21	78	LYS	2.9
10	uL30	129	LEU	2.9
50	uS3	115	ILE	2.9
30	uL15	110	GLY	2.8
34	eL32	18	LYS	2.8
5	uL2	246	LEU	2.8
30	uL15	112	ILE	2.8
79	eEF2	645	LEU	2.8
9	eL6	17	ALA	2.8
1	25S	55	G	2.8
79	eEF2	611	ASP	2.8
43	eL41	8	LYS	2.8
27	uL23	24	LEU	2.8
7	uL4	169	LEU	2.8
7	uL4	50	TYR	2.8
48	eS1	61	LEU	2.8
51	eS4	38	LEU	2.8
53	eS6	78	THR	2.8

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Mol	Chain	Res	Type	RSRZ
5	uL2	253	GLN	2.8
10	uL30	97	PRO	2.8
83	uL11	127	SER	2.8
69	uS12	122	PHE	2.7
24	eL22	69	ALA	2.7
36	eL34	39	ALA	2.7
10	uL30	134	VAL	2.7
10	uL30	127	LEU	2.7
17	eL15	199	LEU	2.7
20	eL18	173	GLU	2.7
28	uL24	21	THR	2.7
10	uL30	216	VAL	2.7
28	uL24	66	GLN	2.7
18	uL13	19	LEU	2.7
9	eL6	176	PHE	2.7
75	uS14	50	ILE	2.7
1	25S	780	A	2.7
17	eL15	196	THR	2.7
20	eL18	169	GLY	2.7
79	eEF2	107	GLY	2.7
36	eL34	24	LYS	2.7
7	uL4	236	LEU	2.7
30	uL15	48	TYR	2.7
27	uL23	124	VAL	2.7
79	eEF2	585	ARG	2.7
7	uL4	86	GLY	2.7
49	uS5	93	GLY	2.7
1	25S	2463	G	2.7
10	uL30	86	VAL	2.7
60	uS11	137	LEU	2.7
9	eL6	10	TYR	2.6
34	eL32	50	ILE	2.6
46	18S	1423	U	2.6
53	eS6	71	THR	2.6
60	uS11	40	ALA	2.6
9	eL6	12	SER	2.6
20	eL18	180	ARG	2.6
36	eL34	34	HIS	2.6
79	eEF2	696	ASP	2.6
83	uL11	70	ALA	2.6
28	uL24	78	PHE	2.6
7	uL4	88	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
64	uS13	109	LEU	2.6
73	eS27	2	VAL	2.6
20	eL18	167	SER	2.6
35	eL33	85	PHE	2.6
17	eL15	197	LEU	2.6
4	uL10	87	VAL	2.6
15	eL13	82	ALA	2.6
72	eS26	93	LYS	2.6
7	uL4	102	PRO	2.5
52	uS7	178	GLY	2.5
45	eL43	22	LEU	2.5
5	uL2	198	LYS	2.5
60	uS11	39	ILE	2.5
30	uL15	68	PHE	2.5
49	uS5	98	PHE	2.5
53	eS6	84	TYR	2.5
52	uS7	108	LEU	2.5
17	eL15	81	TYR	2.5
48	eS1	47	LEU	2.5
48	eS1	96	LEU	2.5
39	eL37	2	GLY	2.5
27	uL23	85	GLN	2.5
6	uL3	252	ILE	2.5
1	25S	2487	U	2.5
20	eL18	168	THR	2.5
9	eL6	16	ALA	2.4
18	uL13	33	ILE	2.4
49	uS5	144	TRP	2.4
70	eS24	74	LEU	2.4
1	25S	1108	U	2.4
1	25S	666	A	2.4
31	eL29	24	PRO	2.4
27	uL23	23	ALA	2.4
77	RACK	274	LEU	2.4
15	eL13	80	VAL	2.4
18	uL13	112	TYR	2.4
4	uL10	88	PHE	2.4
34	eL32	10	VAL	2.4
48	eS1	104	ASP	2.4
27	uL23	81	ILE	2.4
13	uL16	59	GLN	2.4
4	uL10	26	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
17	eL15	116	LEU	2.4
4	uL10	85	GLY	2.3
4	uL10	109	ALA	2.3
7	uL4	112	LYS	2.3
9	eL6	172	HIS	2.3
83	uL11	61	GLN	2.3
1	25S	2484	A	2.3
29	eL27	32	GLY	2.3
34	eL32	86	THR	2.3
77	RACK	100	TYR	2.3
61	uS19	121	ILE	2.3
1	25S	2790	A	2.3
5	uL2	76	PHE	2.3
32	eL30	15	ALA	2.3
1	25S	984	G	2.3
51	eS4	47	PHE	2.3
9	eL6	4	GLN	2.3
10	uL30	88	ARG	2.3
79	eEF2	635	CYS	2.3
18	uL13	16	VAL	2.3
48	eS1	31	ASP	2.3
79	eEF2	691	VAL	2.3
49	uS5	208	GLU	2.2
34	eL32	108	ILE	2.2
18	uL13	197	LEU	2.2
83	uL11	145	PHE	2.2
79	eEF2	613	LYS	2.2
13	uL16	110	ARG	2.2
5	uL2	233	GLN	2.2
15	eL13	113	VAL	2.2
41	eL39	11	GLN	2.2
20	eL18	157	PRO	2.2
41	eL39	39	ALA	2.2
63	eS17	93	LEU	2.2
60	uS11	23	PHE	2.2
75	uS14	52	PHE	2.2
79	eEF2	650	THR	2.2
20	eL18	170	ARG	2.2
7	uL4	276	LEU	2.2
13	uL16	128	ARG	2.2
48	eS1	64	ARG	2.2
7	uL4	67	THR	2.2

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Mol	Chain	Res	Type	RSRZ
29	eL27	35	SER	2.2
51	eS4	64	ILE	2.2
58	uS17	86	ILE	2.2
1	25S	2465	G	2.2
18	uL13	102	LEU	2.2
7	uL4	75	PRO	2.2
7	uL4	101	ALA	2.2
9	eL6	19	LYS	2.2
46	18S	1636	C	2.2
30	uL15	49	HIS	2.2
17	eL15	89	VAL	2.2
57	eS10	64	TYR	2.2
18	uL13	9	ILE	2.2
83	uL11	72	SER	2.2
47	uS2	146	LEU	2.2
48	eS1	135	LEU	2.2
17	eL15	160	GLU	2.2
17	eL15	133	ILE	2.1
18	uL13	140	LYS	2.1
79	eEF2	652	ALA	2.1
17	eL15	78	GLY	2.1
7	uL4	110	ASN	2.1
48	eS1	95	ASN	2.1
11	eL8	164	VAL	2.1
49	uS5	90	THR	2.1
48	eS1	133	TYR	2.1
6	uL3	237	LYS	2.1
20	eL18	161	LYS	2.1
29	eL27	80	LEU	2.1
48	eS1	188	LEU	2.1
61	uS19	57	MET	2.1
45	eL43	24	ARG	2.1
79	eEF2	697	ALA	2.1
46	18S	25	C	2.1
49	uS5	96	THR	2.1
17	eL15	161	ALA	2.1
35	eL33	83	ALA	2.1
1	25S	1850	A	2.1
13	uL16	16	PRO	2.1
72	eS26	83	ILE	2.1
7	uL4	76	ARG	2.1
46	18S	657	U	2.1

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Mol	Chain	Res	Type	RSRZ
5	uL2	60	LYS	2.1
46	18S	579	A	2.1
4	uL10	63	ILE	2.1
20	eL18	140	LEU	2.1
61	uS19	84	ILE	2.1
70	eS24	44	LEU	2.1
24	eL22	55	THR	2.1
1	25S	2454	G	2.1
10	uL30	226	GLY	2.1
59	uS15	2	GLY	2.1
4	uL10	165	VAL	2.0
45	eL43	71	VAL	2.0
15	eL13	7	LEU	2.0
32	eL30	16	LEU	2.0
51	eS4	65	LEU	2.0
11	eL8	158	ASP	2.0
23	eL21	30	TYR	2.0
53	eS6	54	GLY	2.0
9	eL6	170	LYS	2.0
18	uL13	100	GLU	2.0
23	eL21	80	VAL	2.0
48	eS1	91	VAL	2.0
60	uS11	30	VAL	2.0
61	uS19	86	VAL	2.0
81	PSIT	35	C	2.0
36	eL34	20	ILE	2.0
7	uL4	174	ALA	2.0
75	uS14	8	PHE	2.0
5	uL2	24	GLN	2.0
39	eL37	54	LYS	2.0
18	uL13	106	GLU	2.0
83	uL11	60	VAL	2.0
52	uS7	177	ILE	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	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($\text{\AA}^2$)	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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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
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

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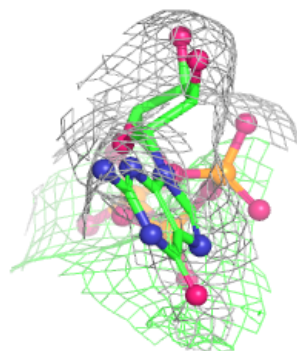
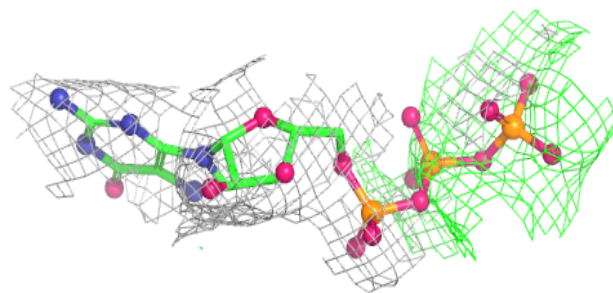
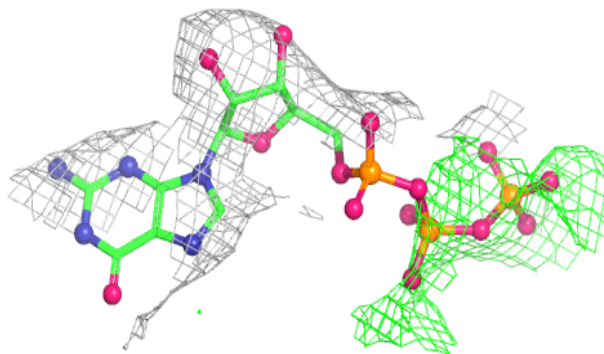
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
84	MG	25S	3533	1/1	0.96	0.13	55,55,55,55	0
84	MG	25S	3559	1/1	0.97	0.11	77,77,77,77	0
84	MG	25S	3451	1/1	0.97	0.11	51,51,51,51	0
84	MG	18S	1823	1/1	0.97	0.04	128,128,128,128	0
84	MG	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.