



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:10 AM UTC

PDB ID : 8P60 / pdb_00008p60
EMDB ID : EMD-17457
Title : Spraguea lophii ribosome dimer
Authors : Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Connors, R.; Williams, B.
Deposited on : 2023-05-24
Resolution : 14.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

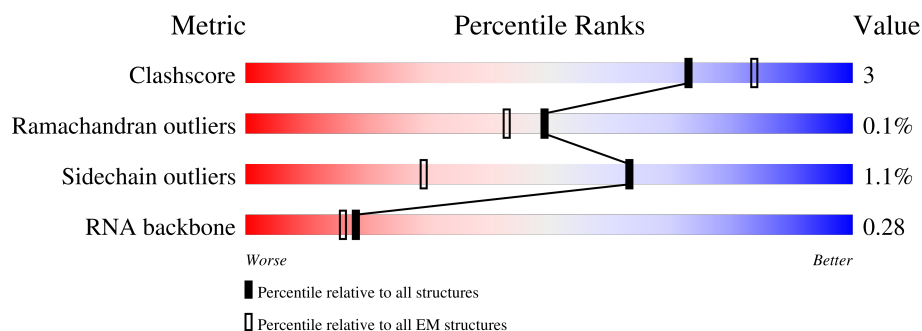
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 14.30 Å.

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



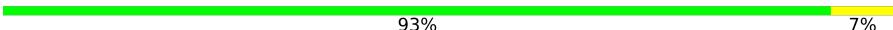
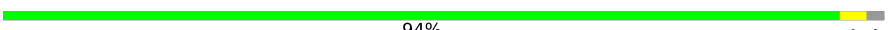
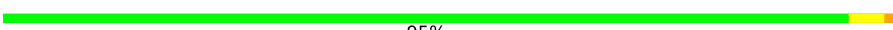
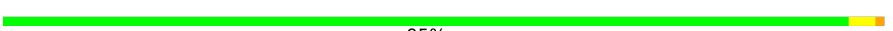
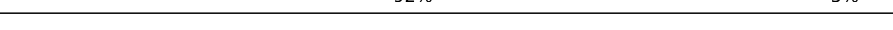
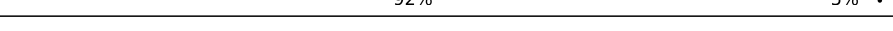
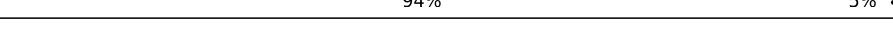
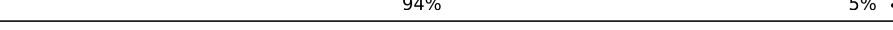
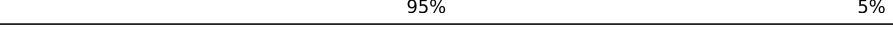
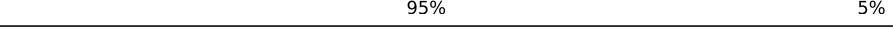
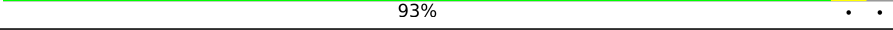
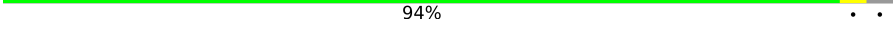
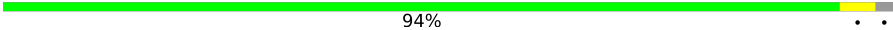
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	K50	2618	60% 30% • 5%
1	L50	2618	60% 30% • 5%
2	K70	119	59% 37% • •
2	L70	119	60% 36% • •
3	KA0	246	96% •
3	LA0	246	96% •
4	KAA	147	93% 7%

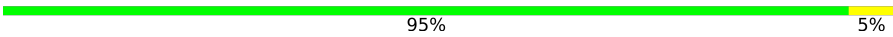
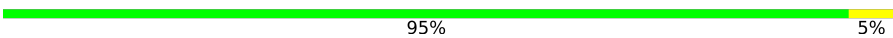
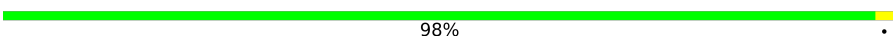
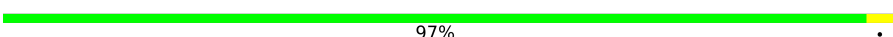
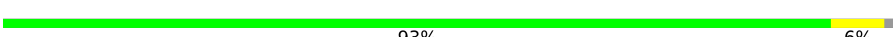
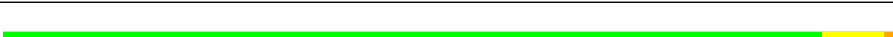
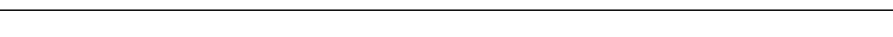
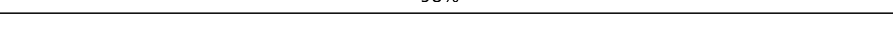
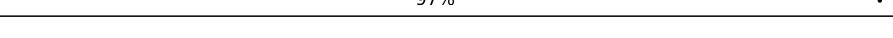
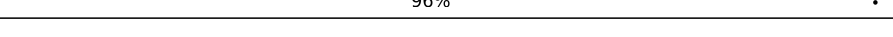
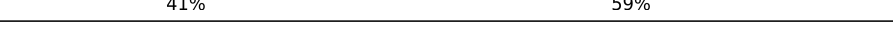
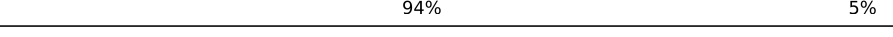
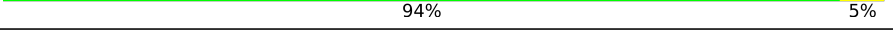
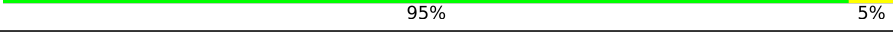
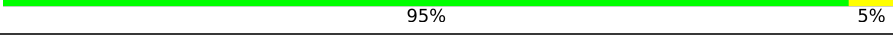
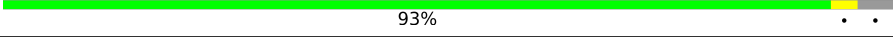
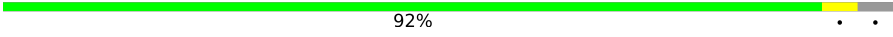
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Mol	Chain	Length	Quality of chain
4	LAA	147	 93% 7%
5	KB0	392	 94% ..
5	LB0	392	 94% ..
6	KC0	328	 95% ..
6	LC0	328	 95% ..
7	KCC	110	 88% .. 10%
7	LCC	110	 88% .. 10%
8	KD0	291	 93% ..
8	LD0	291	 92% ..
9	KDD	110	 98% ..
9	LDD	110	 99% ..
10	KE0	171	 89% 6% ..
10	LE0	171	 89% 6% ..
11	KEE	139	 92% 5% ..
11	LEE	139	 92% 5% ..
12	KF0	235	 94% 5% ..
12	LF0	235	 94% 5% ..
13	KFF	111	 95% 5%
13	LFF	111	 95% 5%
14	KG0	206	 93% ..
14	LG0	206	 94% ..
15	KGG	106	 92% 5% ..
15	LGG	106	 92% 6% ..
16	KH0	187	 94% ..
16	LH0	187	 94% ..

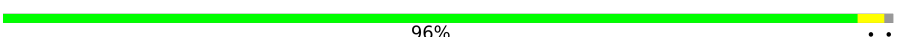
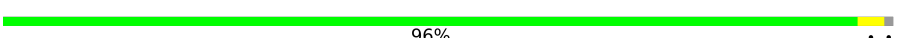
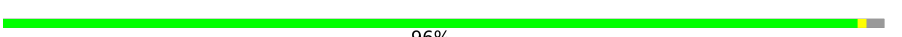
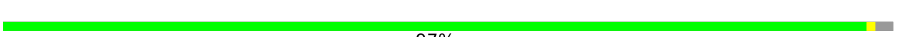
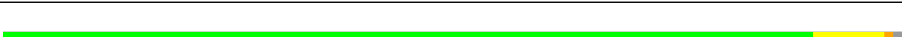
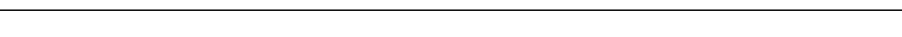
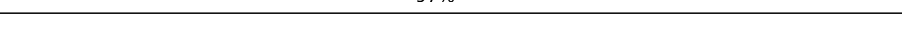
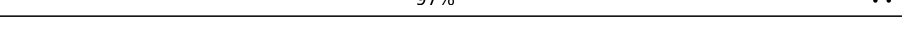
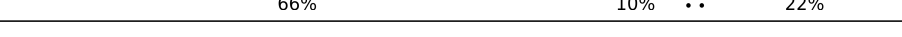
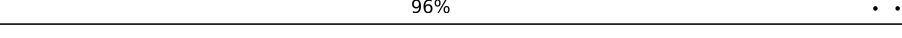
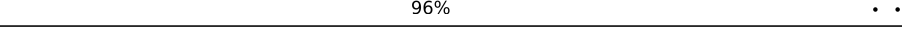
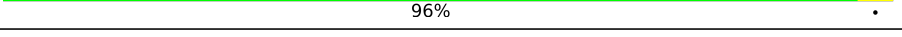
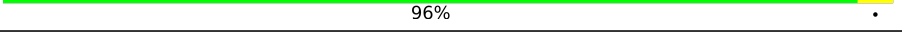
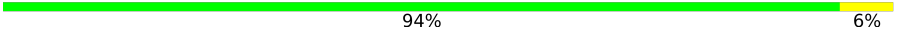
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Mol	Chain	Length	Quality of chain
17	KHH	119	 95% 5%
17	LHH	119	 95% 5%
18	KI0	218	 98% .
18	LI0	218	 97% .
19	KII	98	 92% 7% .
19	LII	98	 93% 6% .
20	KJ0	171	 91% 6% .
20	LJ0	171	 91% 6% .
21	KJJ	92	 90% 7% .
21	LJJ	92	 90% 7% .
22	KL0	165	 92% 7% ..
22	LL0	165	 91% 8% ..
23	KLL	52	 98% .
23	LLL	52	 98% .
24	KM0	115	 97% .
24	LM0	115	 96% .
25	KMM	127	 41% 59%
25	LMM	127	 41% 59%
26	KN0	204	 94% 5%
26	LN0	204	 94% 5%
27	KO0	198	 95% 5%
27	LO0	198	 95% 5%
28	KOO	104	 93% . .
28	LOO	104	 92% . .
29	KP0	167	 87% . . 8%

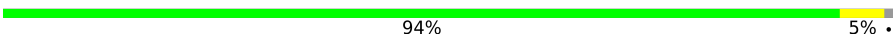
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Mol	Chain	Length	Quality of chain
29	LP0	167	 89% .. 8%
30	KPP	89	 92% ...
30	LPP	89	 92% ...
31	KQ0	183	 96% ..
31	LQ0	183	 96% ..
32	KR0	168	 96% ..
32	LR0	168	 97% ..
33	KS0	171	 96% ..
33	LS0	171	 96% ..
34	KT0	158	 91% 8% ..
34	LT0	158	 91% 8% ..
35	KU0	113	 86% 12%
35	LU0	113	 86% 12%
36	KV0	142	 97% ..
36	LV0	142	 97% ..
37	KW0	131	 66% 10% .. 22%
37	LW0	131	 66% 10% .. 22%
38	KX0	113	 96% ..
38	LX0	113	 96% ..
39	KY0	131	 96% .
39	LY0	131	 96% .
40	KZ0	153	 75% 23%
40	LZ0	153	 75% 23%
41	MD1	151	 94% 6%
41	MD2	151	 94% 6%

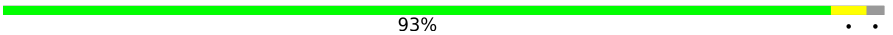
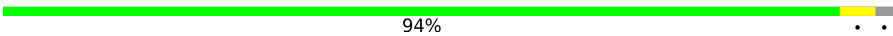
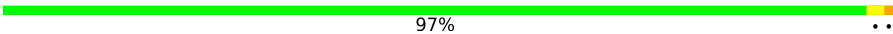
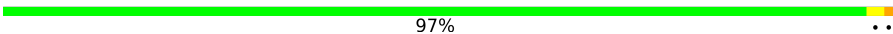
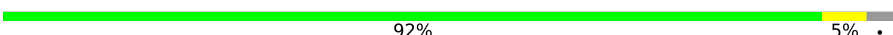
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Mol	Chain	Length	Quality of chain
42	R60	1368	
42	S60	1368	
43	RA0	233	
43	SA0	233	
44	RAA	102	
44	SAA	102	
45	RB0	230	
45	SB0	230	
46	RBB	82	
46	SBB	82	
47	RC0	248	
47	SC0	248	
48	RCC	65	
48	SCC	65	
49	RD0	242	
49	SD0	242	
50	RDD	65	
50	SDD	65	
51	RE0	280	
51	SE0	280	
52	REE	60	
52	SEE	60	
53	RF0	195	
53	SF0	195	
54	RFF	150	

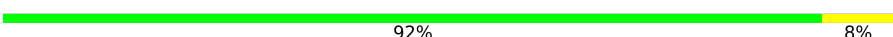
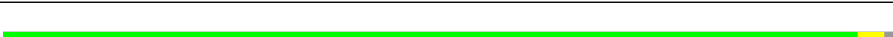
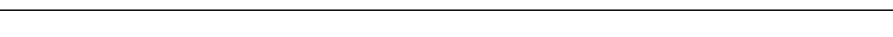
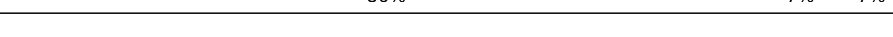
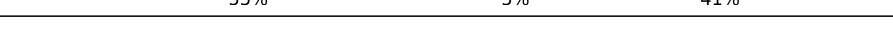
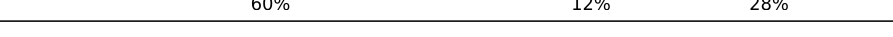
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Mol	Chain	Length	Quality of chain
54	SFF	150	
55	RG0	230	
55	SG0	230	
56	RGG	326	
56	SGG	326	
57	RH0	164	
57	SH0	164	
58	RI0	173	
58	SI0	173	
59	RJ0	184	
59	SJ0	184	
60	RK0	107	
60	SK0	107	
61	RL0	155	
61	SL0	155	
62	RM0	130	
62	SM0	130	
63	RN0	143	
63	SN0	143	
64	RO0	135	
64	SO0	135	
65	RQ0	143	
65	SQ0	143	
66	RR0	120	
66	SR0	120	

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Mol	Chain	Length	Quality of chain
67	RS0	160	
67	SS0	160	
68	RT0	143	
68	ST0	143	
69	RU0	119	
69	SU0	119	
70	RV0	67	
70	SV0	67	
71	RW0	128	
71	SW0	128	
72	RX0	141	
72	SX0	141	
73	RY0	146	
73	SY0	146	
74	RZ0	128	
74	SZ0	128	
75	RP0	163	
75	SP0	163	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 343629 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		
1	K50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		
2	K70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		
3	KA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		

- Molecule 4 is a protein called Ribosomal protein L18e/L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		
4	KAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
5	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
6	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
7	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
8	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
9	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	KE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		
11	KEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		
12	KF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		
13	KFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		
14	KG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		
15	KGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		
16	KH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		
17	KHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		
18	KI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		
19	KII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
20	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
21	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
22	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
23	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
24	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
25	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
27	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
28	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
29	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
30	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
31	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
32	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
33	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		
34	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		
35	KU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		
36	KV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		
37	KW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		
38	KX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		
39	KY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		
40	KZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a protein called DNL-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		
41	MD2	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 42 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	R60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

- Molecule 43 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		
43	RA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		
44	RAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 45 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		
45	RB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 46 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		
46	RBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		
47	RC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		

- Molecule 48 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
48	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		
49	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 50 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
50	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
51	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 52 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SEE	56	Total	C	N	O	0	0
			447	284	89	74		
52	REE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
53	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 54 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SFF	58	Total	C	N	O	S	0	0
			422	261	77	79	5		
54	RFF	58	Total	C	N	O	S	0	0
			417	259	74	79	5		

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		
55	RG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		

- Molecule 56 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		
56	RGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
57	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	RI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		
59	RJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		
60	RK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		
61	RL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		
62	RM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		
63	RN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
64	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
65	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
66	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
67	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 68 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
68	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
69	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 70 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
70	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 71 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
71	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 72 is a protein called Ribosomal protein S12/S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
72	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 73 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
73	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 75 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
75	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 76 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	LGG	1	Total	Zn	0
			1	1	
76	LJJ	1	Total	Zn	0
			1	1	
76	LMM	1	Total	Zn	0
			1	1	
76	LOO	1	Total	Zn	0
			1	1	
76	LPP	1	Total	Zn	0
			1	1	
76	SAA	1	Total	Zn	0
			1	1	
76	SBB	1	Total	Zn	0
			1	1	
76	SDD	1	Total	Zn	0
			1	1	
76	SFF	1	Total	Zn	0
			1	1	
76	KGG	1	Total	Zn	0
			1	1	
76	KJJ	1	Total	Zn	0
			1	1	
76	KMM	1	Total	Zn	0
			1	1	
76	KOO	1	Total	Zn	0
			1	1	
76	KPP	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
76	RAA	1	Total 1	Zn 1	0
76	RBB	1	Total 1	Zn 1	0
76	RDD	1	Total 1	Zn 1	0
76	RFF	1	Total 1	Zn 1	0

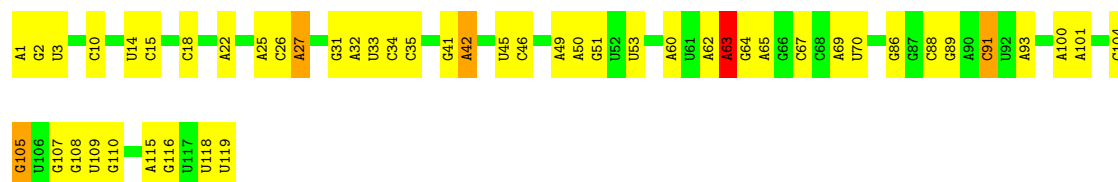
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A2593	A2491	G2377	C2267	U2163	G2061	G1979	A	G1832	U1705	A1610	U1384	U1174	G1175	A1176
G2594	U2492	U2378	G2272	G2167	G2063	G1981	A	G1831	G1708	A1611	U1488	G1385	U1277	G1177
U2595	G2493	G2379	G2275	G2168	A2065	U1983	C	A1833	G1709	G1612	G1386	G1387	U1278	
G2596	C2497	A2394	G2279	A2169	U2066	G1985	A	A1834	U1710	A1613	U1489		C1282	G1151
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U2599	A2501	A2399	G2286	A2171	U2073	G1991	A	A1837	A1717	A1617	U1491	U1395	G1284	G1183
G2600	C2502	C2401	G2291	C2177	A2074	G1995	A	G1838	G1718	G1619	U1492	G1396	A1293	
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			G2261	U2152	U2054	U2054	A1967	A	A1819	U1695	A1601	G1474	U1370	G1267
			C2262	U2152	U2057	U2057	G1968	G	C1820	U1696	A1601	A1475	U1370	A1269
				G2160	G2058	G2058	G1973	G	G1821	G1697				

Chain K50: 60% 30% 5%

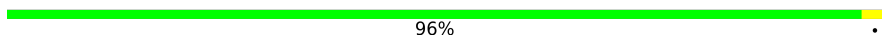


- Molecule 2: RNA 5S

Chain K70: 



- Molecule 3: 60S ribosomal protein L8

Chain LA0: 

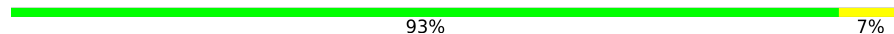


- Molecule 3: 60S ribosomal protein L8

Chain KA0: 

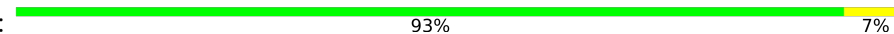


- Molecule 4: Ribosomal protein L18e/L15P

Chain LAA: 

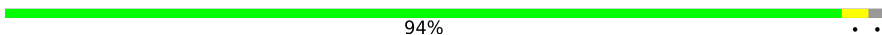


- Molecule 4: Ribosomal protein L18e/L15P

Chain KAA: 

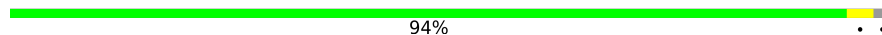


- Molecule 5: 60S ribosomal protein L3

Chain LB0: 



- Molecule 5: 60S ribosomal protein L3

Chain KB0: 



- Molecule 6: 60S ribosomal protein L4

Chain LC0: 95%



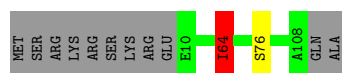
- Molecule 6: 60S ribosomal protein L4

Chain KC0: 95%



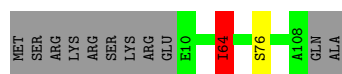
- Molecule 7: 60S ribosomal protein L3

Chain LCC: 88%



- Molecule 7: 60S ribosomal protein L3

Chain KCC: 88%



- Molecule 8: 60S ribosomal protein L5

Chain LD0: 92%



- Molecule 8: 60S ribosomal protein L5

Chain KD0: 93%



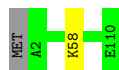
- Molecule 9: 60S ribosomal protein L31

Chain LDD: 99%



- Molecule 9: 60S ribosomal protein L31

Chain KDD: 98% ..



- Molecule 10: 60S ribosomal protein L6

Chain LE0: 89% 6% . .



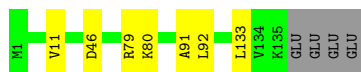
- Molecule 10: 60S ribosomal protein L6

Chain KE0: 89% 6% . .



- Molecule 11: 60S ribosomal protein L32

Chain LEE: 92% 5% .



- Molecule 11: 60S ribosomal protein L32

Chain KEE: 92% 5% .



- Molecule 12: 60S ribosomal protein L7

Chain LF0: 94% 5% .



- Molecule 12: 60S ribosomal protein L7

Chain KF0: 94% 5% .



- Molecule 13: 60S ribosomal protein L35a

Chain LFF: 95% 5%



- Molecule 13: 60S ribosomal protein L35a

Chain KFF: 95% 5%



- Molecule 14: 60S ribosomal protein L8

Chain LG0: 94% . .



- Molecule 14: 60S ribosomal protein L8

Chain KG0: 93% . .



- Molecule 15: Ribosomal protein L34

Chain LGG: 92% 6% ..



- Molecule 15: Ribosomal protein L34

Chain KGG: 92% 5% ..



- Molecule 16: 60S ribosomal protein L9

Chain LH0: 94% . .



- Molecule 16: 60S ribosomal protein L9

Chain KH0: 94%



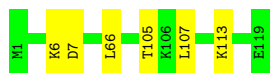
- Molecule 17: Ribosomal L29 protein

Chain LHH: 95%



- Molecule 17: Ribosomal L29 protein

Chain KHH: 95%



- Molecule 18: S60 ribosomal protein L10

Chain LI0: 97%



- Molecule 18: S60 ribosomal protein L10

Chain KI0: 98%



- Molecule 19: 60S ribosomal protein L36

Chain LII: 93%



- Molecule 19: 60S ribosomal protein L36

Chain KII: 92%



- Molecule 20: 60S ribosomal protein L11

Chain LJ0: 91% 6% .



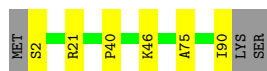
- Molecule 20: 60S ribosomal protein L11

Chain KJ0: 91% 6% .



- Molecule 21: 60S ribosomal protein L37

Chain LJJ: 90% 7% .



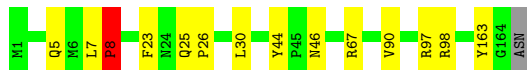
- Molecule 21: 60S ribosomal protein L37

Chain KJJ: 90% 7% .



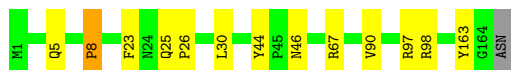
- Molecule 22: 60S ribosomal protein L13

Chain LL0: 91% 8% ..



- Molecule 22: 60S ribosomal protein L13

Chain KL0: 92% 7% ..



- Molecule 23: 60S ribosomal protein L39

Chain LLL: 98% .



- Molecule 23: 60S ribosomal protein L39

Chain KLL: 98%



- Molecule 24: Transposase

Chain LM0: 96%



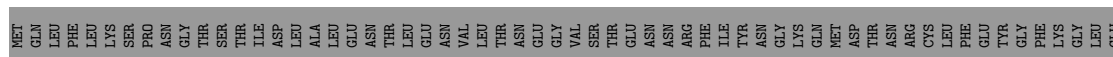
- Molecule 24: Transposase

Chain KM0: 97%



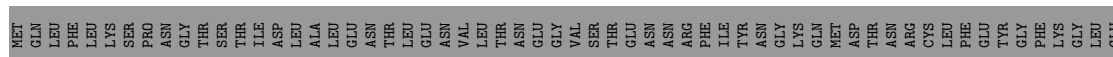
- Molecule 25: Ubiquitin

Chain LMM: 41% 59%



- Molecule 25: Ubiquitin

Chain KMM: 41% 59%

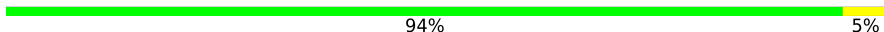


- Molecule 26: Ribosomal protein L15

Chain LN0: 94% 5%

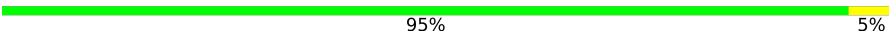


- Molecule 26: Ribosomal protein L15

Chain KN0:  94% 5%

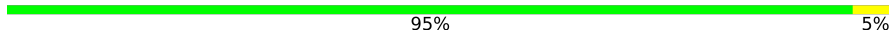


- Molecule 27: Ribosomal protein L13A

Chain LO0:  95% 5%



- Molecule 27: Ribosomal protein L13A

Chain KO0:  95% 5%

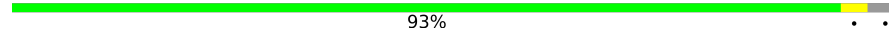


- Molecule 28: 60S ribosomal protein L44

Chain LOO:  92% . .



- Molecule 28: 60S ribosomal protein L44

Chain KOO:  93% . .



- Molecule 29: 60S ribosomal protein L17

Chain LP0:  89% . . 8%



- Molecule 29: 60S ribosomal protein L17

Chain KP0:  87% . . 8%



- Molecule 30: 60S ribosomal protein L37a

Chain LPP:  92% ..

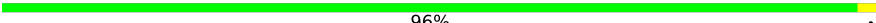


- Molecule 30: 60S ribosomal protein L37a

Chain KPP:  92% ..

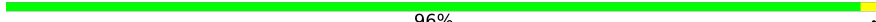


- Molecule 31: 60S ribosomal protein L18

Chain LQ0:  96% ..

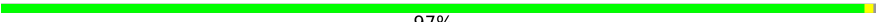


- Molecule 31: 60S ribosomal protein L18

Chain KQ0:  96% ..

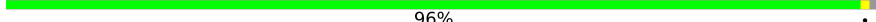


- Molecule 32: 60S ribosomal protein L19

Chain LR0:  97% ..

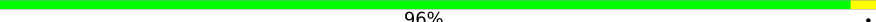


- Molecule 32: 60S ribosomal protein L19

Chain KR0:  96% ..

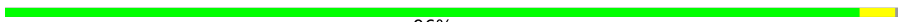


- Molecule 33: 60S ribosomal protein L20

Chain LS0:  96% ..



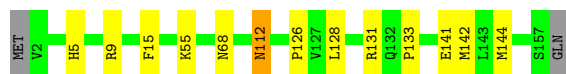
- Molecule 33: 60S ribosomal protein L20

Chain KS0:  96% ..



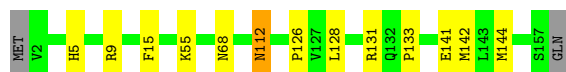
- Molecule 34: 60s ribosomal protein L21

Chain LT0:  91% 8% ..



- Molecule 34: 60s ribosomal protein L21

Chain KT0:  91% 8% ..



- Molecule 35: 60S ribosomal protein L22

Chain LU0:  86% 12%

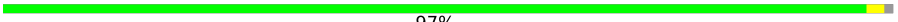


- Molecule 35: 60S ribosomal protein L22

Chain KU0:  86% 12%

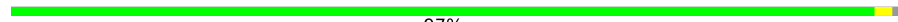


- Molecule 36: Ribosomal protein L23

Chain LV0:  97% ..



- Molecule 36: Ribosomal protein L23

Chain KV0:  97% ..



- Molecule 37: Ribosomal protein L24E

Chain LW0:  66% 10% 22%

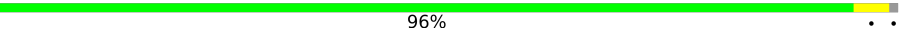


- Molecule 37: Ribosomal protein L24E

Chain KW0:  66% 10% 22%

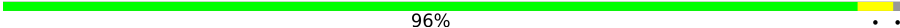


- Molecule 38: 60S ribosomal protein L23a

Chain LX0:  96%

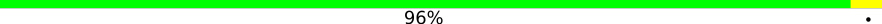


- Molecule 38: 60S ribosomal protein L23a

Chain KX0:  96%

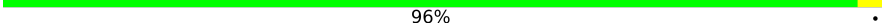


- Molecule 39: 60S ribosomal protein L26

Chain LY0:  96%



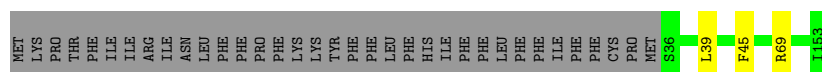
- Molecule 39: 60S ribosomal protein L26

Chain KY0:  96%



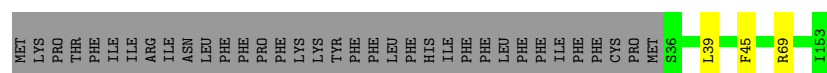
- Molecule 40: 60S ribosomal protein L27

Chain LZ0:  75% 23%

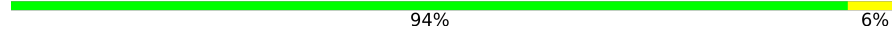


- Molecule 40: 60S ribosomal protein L27

Chain KZ0:  75% 23%

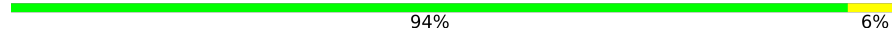


- Molecule 41: DNL-type domain-containing protein

Chain MD1:  94% 6%



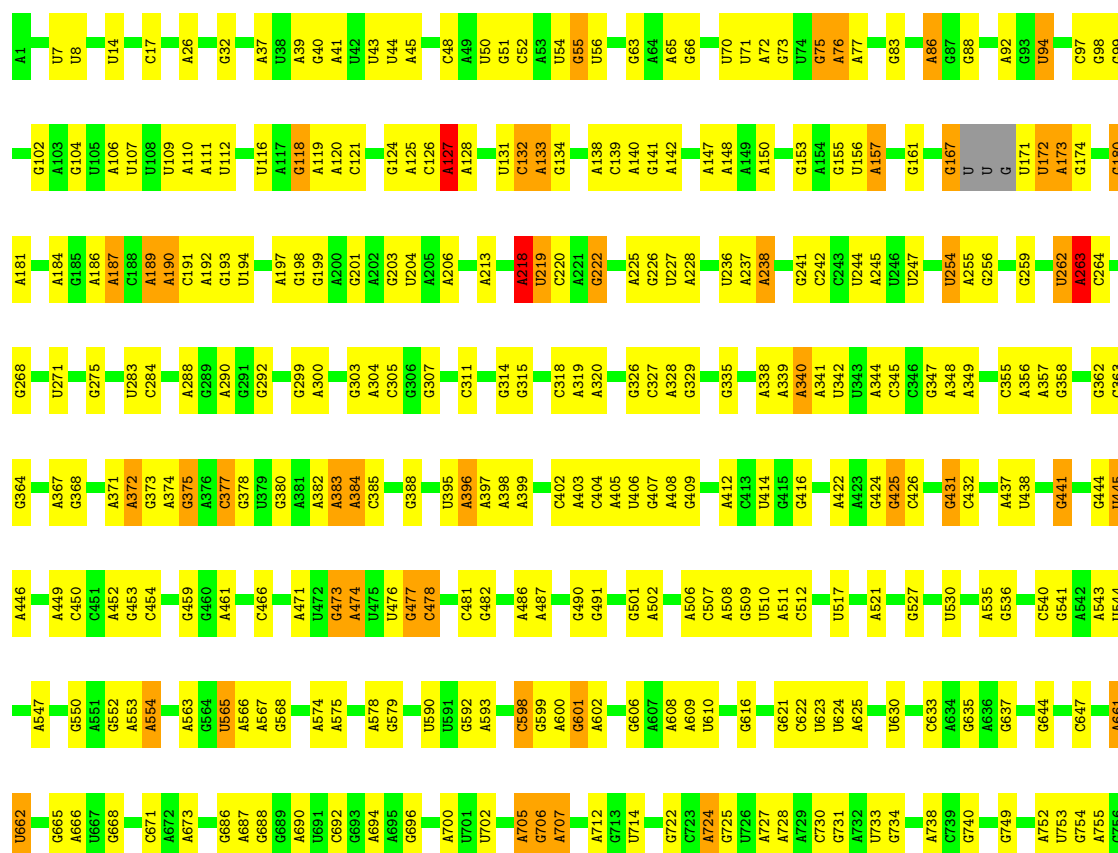
- Molecule 41: DNL-type domain-containing protein

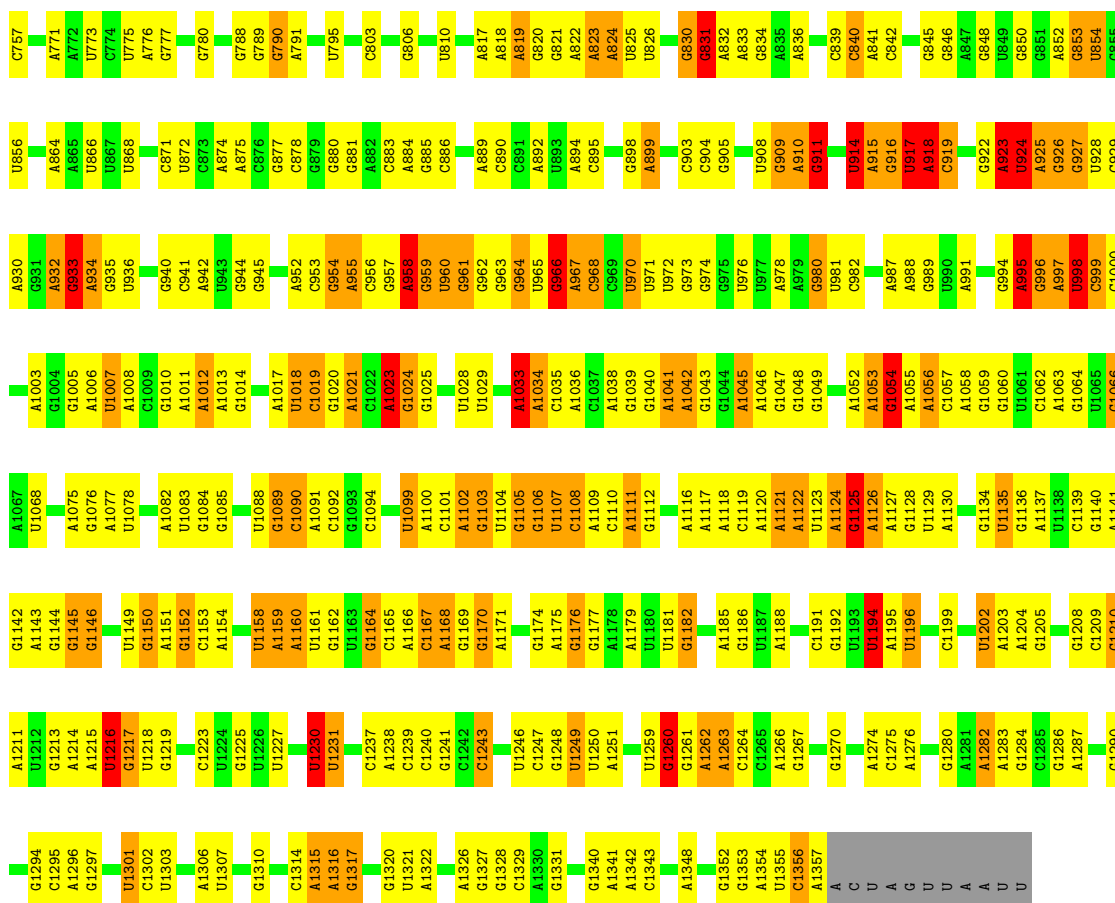
Chain MD2:  94% 6%

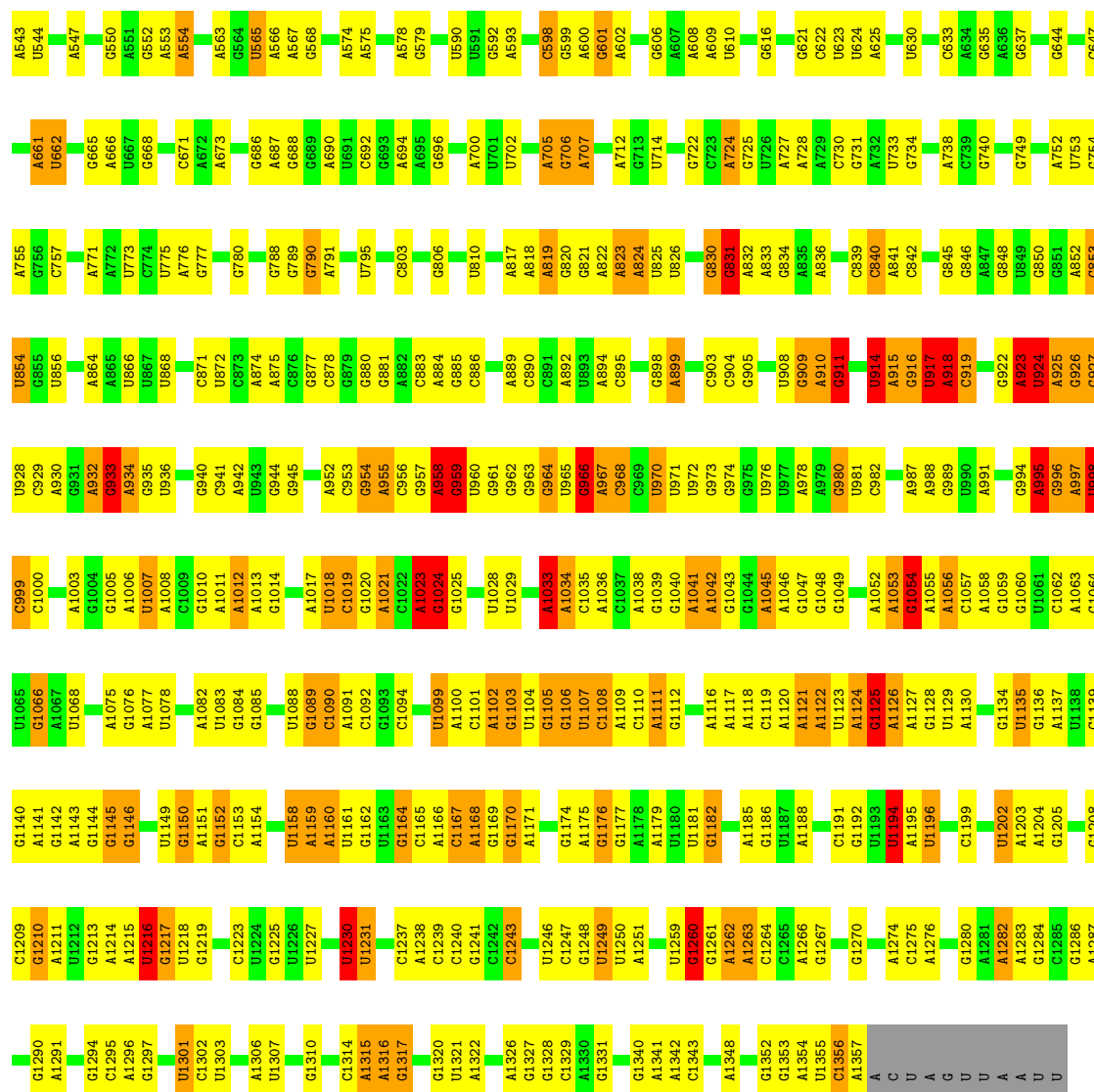


- Molecule 42: RNA 16S

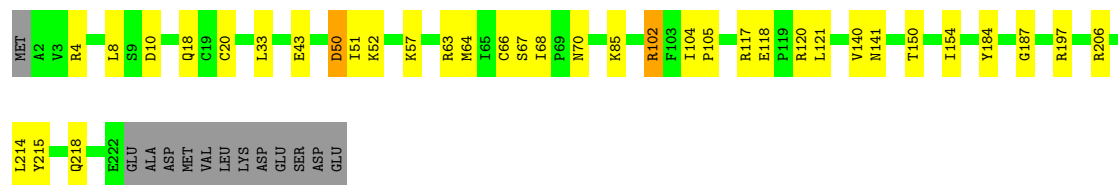
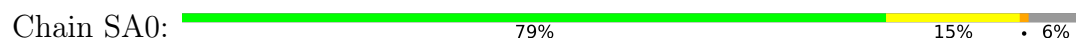
Chain S60:  49% 38% 10%



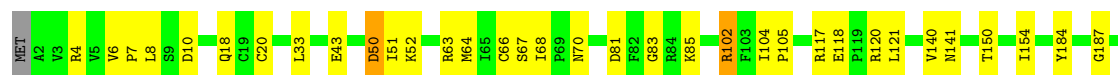
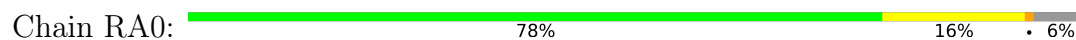


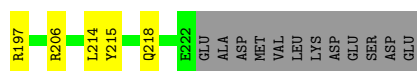


• Molecule 43: 40S ribosomal protein S0



• Molecule 43: 40S ribosomal protein S0





- Molecule 44: 40S ribosomal protein S26

Chain SAA: 92% 7%



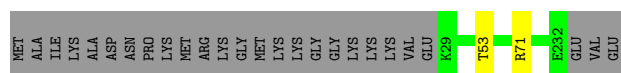
- Molecule 44: 40S ribosomal protein S26

Chain RAA: 92% 7%



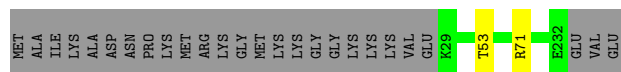
- Molecule 45: 40S ribosomal protein S1

Chain SB0: 88% 11%



- Molecule 45: 40S ribosomal protein S1

Chain RB0: 88% 11%



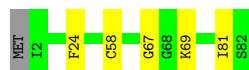
- Molecule 46: 40S ribosomal protein S27

Chain SBB: 94% 5%



- Molecule 46: 40S ribosomal protein S27

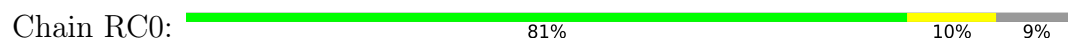
Chain RBB: 93% 6%



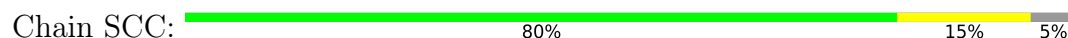
- Molecule 47: 40S ribosomal protein S2

Chain SC0: 81% 10% 9%

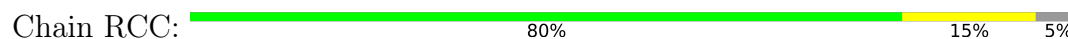
- Molecule 47: 40S ribosomal protein S2



- Molecule 48: 40S ribosomal protein S28



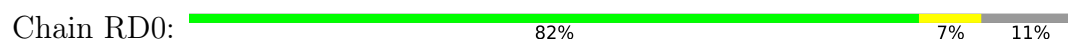
- Molecule 48: 40S ribosomal protein S28



- Molecule 49: 40S ribosomal protein S3



- Molecule 49: 40S ribosomal protein S3



- Molecule 50: 40S ribosomal protein S29





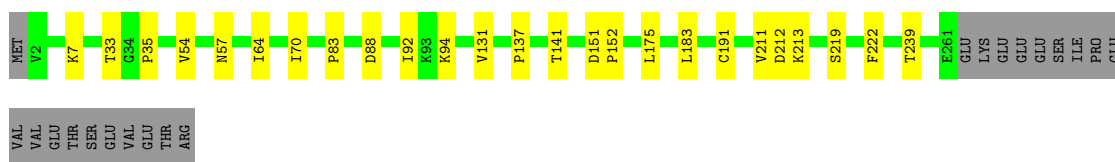
- Molecule 50: 40S ribosomal protein S29

Chain RDD: 86% 14%



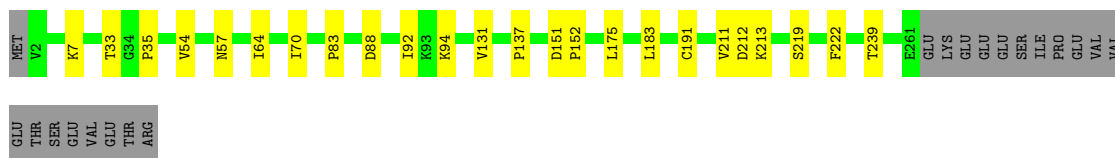
- Molecule 51: 40S ribosomal protein S4

Chain SE0: 84% 9% 7%



- Molecule 51: 40S ribosomal protein S4

Chain RE0: 84% 9% 7%



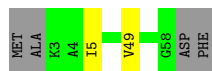
- Molecule 52: 40S ribosomal protein S30

Chain SEE: 90% 7%



- Molecule 52: 40S ribosomal protein S30

Chain REE: 90% 7%



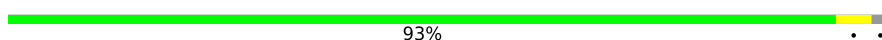
- Molecule 53: 40S ribosomal protein S5

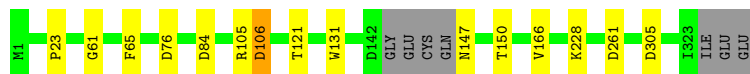
Chain SF0: 86% 12%



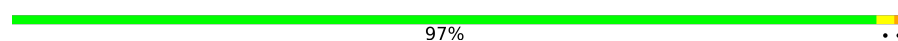
- | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|------|------|------|------|------|------|-----|-----|-----|
| W1 | P23 | G61 | F65 | D76 | D84 | R105 | D106 | T121 | W131 | D142 | GLY | GLU | CYS | GLN | N147 | T150 | V166 | K228 | D305 | T323 | I1E | GLU | GLU |
|----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|------|------|------|------|------|------|-----|-----|-----|

- Molecule 56: Guanine nucleotide binding protein beta subunit

Chain RGG:  93% . .

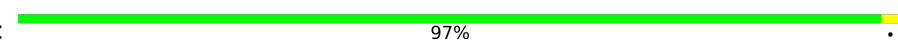


- Molecule 57: 40S ribosomal protein S7

Chain SH0:  97% . . .



- Molecule 57: 40S ribosomal protein S7

Chain RH0:  97% . . .

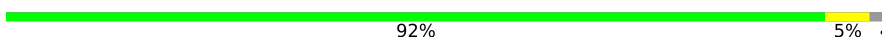


- Molecule 58: 40S ribosomal protein S8

Chain SI0:  91% 5% .



- Molecule 58: 40S ribosomal protein S8

Chain RI0:  92% 5% .



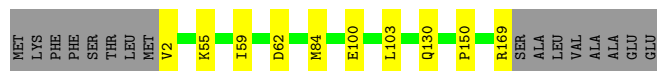
- Molecule 59: 40S ribosomal protein S9

Chain SJ0:  86% 5% 9%



- Molecule 59: 40S ribosomal protein S9

Chain RJ0:  86% 5% 9%



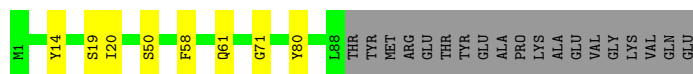
- Molecule 60: 40S ribosomal protein S10

Chain SK0:  75% 7% 18%



- Molecule 60: 40S ribosomal protein S10

Chain RK0:  75% 7% 18%



- Molecule 61: 40S ribosomal protein S11

Chain SL0:  92% 5% .



- Molecule 61: 40S ribosomal protein S11

Chain RL0:  92% 5% .



- Molecule 62: 40S ribosomal protein S12

Chain SM0:  82% 5% 13%



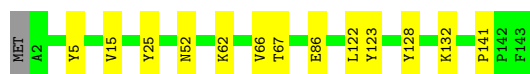
- Molecule 62: 40S ribosomal protein S12

Chain RM0:  82% 5% 13%



- Molecule 63: 40S ribosomal protein S13

Chain SN0:  90% 9% .



- Molecule 63: 40S ribosomal protein S13

Chain RN0:  90% 9% .



- Molecule 64: 40S ribosomal protein S14

Chain SO0:  88% 7% .



- Molecule 64: 40S ribosomal protein S14

Chain RO0:  88% 7% .



- Molecule 65: 40S ribosomal protein S16

Chain SQ0:  92% 8% .



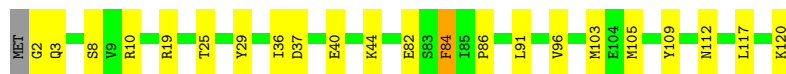
- Molecule 65: 40S ribosomal protein S16

Chain RQ0:  92% 8% .



- Molecule 66: 40S ribosomal protein S17

Chain SR0:  81% 18% ..



- Molecule 66: 40S ribosomal protein S17

Chain RR0:  80% 18% ..



- Molecule 67: 40S ribosomal protein S18



Chain RV0:  81% 16% .



- Molecule 71: 40S ribosomal protein S15A

Chain SW0:  91% 9%

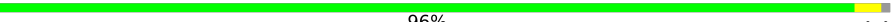


- Molecule 71: 40S ribosomal protein S15A

Chain RW0:  91% 9%

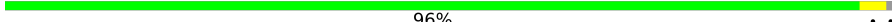


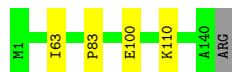
- Molecule 72: Ribosomal protein S12/S23

Chain SX0:  96% . .



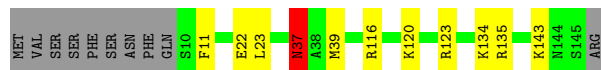
- Molecule 72: Ribosomal protein S12/S23

Chain RX0:  96% . .



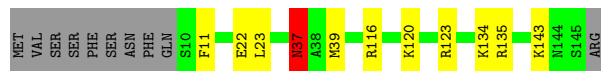
- Molecule 73: 40s ribosomal protein s24

Chain SY0:  86% 7% . 7%



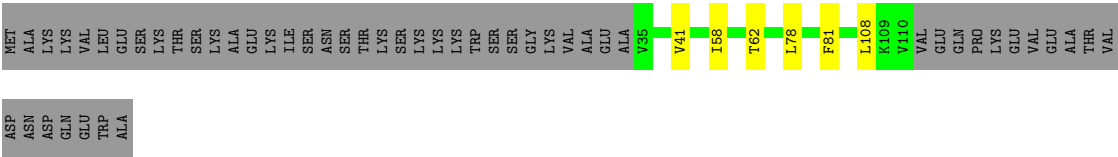
- Molecule 73: 40s ribosomal protein s24

Chain RY0:  86% 7% . 7%



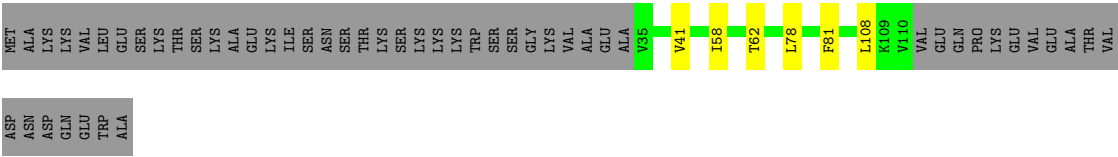
- Molecule 74: 40S ribosomal protein S25

Chain SZ0: 55% 5% 41%



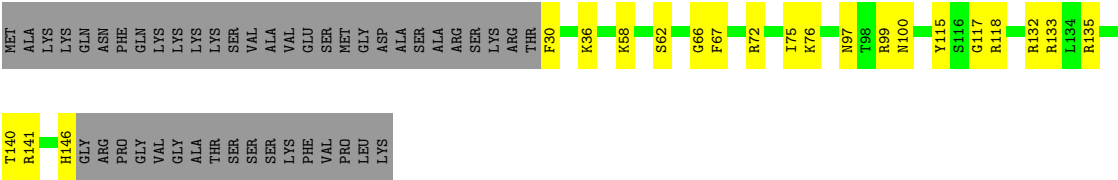
• Molecule 74: 40S ribosomal protein S25

Chain RZ0: 55% 5% 41%



• Molecule 75: Ribosomal protein S19

Chain SP0: 59% 13% 28%



• Molecule 75: Ribosomal protein S19

Chain RP0: 60% 12% 28%



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	1344	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120, 120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	K50	0.70	0/60107	1.07	182/93753 (0.2%)
1	L50	0.70	0/60107	1.07	181/93753 (0.2%)
2	K70	0.71	0/2844	1.02	8/4429 (0.2%)
2	L70	0.71	0/2844	1.02	8/4429 (0.2%)
3	KA0	0.54	0/1926	1.05	0/2590
3	LA0	0.54	0/1926	1.05	0/2590
4	KAA	0.55	0/1191	0.94	0/1586
4	LAA	0.55	0/1191	0.94	0/1586
5	KB0	0.52	0/3092	0.99	2/4144 (0.0%)
5	LB0	0.52	0/3092	0.99	2/4144 (0.0%)
6	KC0	0.51	0/2646	1.07	3/3555 (0.1%)
6	LC0	0.51	0/2646	1.07	3/3555 (0.1%)
7	KCC	0.49	0/794	1.01	0/1067
7	LCC	0.49	0/794	1.01	0/1067
8	KD0	0.44	0/2328	1.05	3/3098 (0.1%)
8	LD0	0.44	0/2328	1.05	3/3098 (0.1%)
9	KDD	0.49	0/913	0.97	0/1223
9	LDD	0.49	0/913	0.97	0/1223
10	KE0	0.46	0/1394	1.02	3/1875 (0.2%)
10	LE0	0.46	0/1394	1.03	3/1875 (0.2%)
11	KEE	0.49	0/1108	1.05	1/1477 (0.1%)
11	LEE	0.49	0/1108	1.05	1/1477 (0.1%)
12	KF0	0.48	0/1963	0.99	2/2618 (0.1%)
12	LF0	0.48	0/1963	1.00	2/2618 (0.1%)
13	KFF	0.54	0/906	1.03	0/1207
13	LFF	0.53	0/906	1.02	0/1207
14	KG0	0.47	0/1612	1.06	0/2163
14	LG0	0.47	0/1612	1.06	0/2163
15	KGG	0.49	0/825	1.12	2/1090 (0.2%)
15	LGG	0.49	0/825	1.13	2/1090 (0.2%)
16	KH0	0.48	0/1503	0.95	0/2018
16	LH0	0.48	0/1503	0.95	0/2018

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	KHH	0.44	0/999	1.03	0/1324
17	LHH	0.44	0/999	1.03	0/1324
18	KI0	0.51	0/1781	0.99	1/2382 (0.0%)
18	LI0	0.51	0/1781	0.99	1/2382 (0.0%)
19	KII	0.47	0/790	1.00	0/1041
19	LII	0.47	0/790	1.00	0/1041
20	KJ0	0.47	0/1350	1.02	1/1797 (0.1%)
20	LJ0	0.47	0/1350	1.02	1/1797 (0.1%)
21	KJJ	0.53	0/710	1.14	1/932 (0.1%)
21	LJJ	0.53	0/710	1.14	1/932 (0.1%)
22	KL0	0.48	0/1374	1.12	2/1827 (0.1%)
22	LL0	0.49	0/1374	1.12	2/1827 (0.1%)
23	KLL	0.51	0/435	1.02	0/576
23	LLL	0.51	0/435	1.02	0/576
24	KM0	0.50	0/935	1.04	0/1251
24	LM0	0.50	0/935	1.03	0/1251
25	KMM	0.52	0/431	1.04	0/568
25	LMM	0.52	0/431	1.04	0/568
26	KN0	0.53	0/1722	1.03	3/2297 (0.1%)
26	LN0	0.53	0/1722	1.03	3/2297 (0.1%)
27	KO0	0.50	0/1626	1.03	2/2168 (0.1%)
27	LO0	0.50	0/1626	1.03	2/2168 (0.1%)
28	KOO	0.54	0/811	1.00	0/1071
28	LOO	0.54	0/811	1.01	0/1071
29	KP0	0.54	0/1262	1.11	0/1689
29	LP0	0.54	0/1262	1.11	0/1689
30	KPP	0.53	0/693	1.12	2/918 (0.2%)
30	LPP	0.53	0/693	1.12	2/918 (0.2%)
31	KQ0	0.47	0/1512	0.99	0/2014
31	LQ0	0.47	0/1512	0.99	0/2014
32	KR0	0.50	0/1352	1.04	0/1790
32	LR0	0.49	0/1352	1.04	0/1790
33	KS0	0.49	0/1422	0.99	1/1898 (0.1%)
33	LS0	0.49	0/1422	0.99	1/1898 (0.1%)
34	KT0	0.50	0/1294	0.98	1/1736 (0.1%)
34	LT0	0.50	0/1294	0.98	1/1736 (0.1%)
35	KU0	0.47	0/826	0.99	0/1104
35	LU0	0.47	0/826	0.99	0/1104
36	KV0	0.55	0/1068	1.03	1/1429 (0.1%)
36	LV0	0.55	0/1068	1.03	1/1429 (0.1%)
37	KW0	0.64	0/849	1.14	2/1129 (0.2%)
37	LW0	0.64	0/849	1.15	2/1129 (0.2%)
38	KX0	0.48	0/883	1.03	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	LX0	0.48	0/883	1.03	0/1175
39	KY0	0.49	0/1058	1.08	1/1399 (0.1%)
39	LY0	0.49	0/1058	1.08	1/1399 (0.1%)
40	KZ0	0.48	0/976	1.09	2/1302 (0.2%)
40	LZ0	0.48	0/976	1.09	2/1302 (0.2%)
41	MD1	0.66	0/1249	1.06	1/1677 (0.1%)
41	MD2	0.66	0/1249	1.06	1/1677 (0.1%)
42	R60	0.99	6/32725 (0.0%)	1.11	127/51066 (0.2%)
42	S60	0.99	6/32725 (0.0%)	1.11	125/51066 (0.2%)
43	RA0	0.59	1/1751 (0.1%)	1.01	1/2358 (0.0%)
43	SA0	0.59	1/1751 (0.1%)	1.01	1/2358 (0.0%)
44	RAA	0.57	0/839	1.06	0/1120
44	SAA	0.57	0/839	1.06	0/1120
45	RB0	0.50	0/1623	1.01	0/2169
45	SB0	0.50	0/1623	1.01	0/2169
46	RBB	0.57	0/634	0.99	0/844
46	SBB	0.57	0/634	0.99	0/844
47	RC0	0.51	0/1751	1.05	2/2359 (0.1%)
47	SC0	0.51	0/1751	1.05	2/2359 (0.1%)
48	RCC	0.54	0/480	0.97	2/644 (0.3%)
48	SCC	0.53	0/480	0.97	2/644 (0.3%)
49	RD0	0.50	0/1721	1.04	0/2304
49	SD0	0.51	0/1721	1.04	0/2304
50	RDD	0.51	0/559	1.00	1/742 (0.1%)
50	SDD	0.51	0/559	1.00	1/742 (0.1%)
51	RE0	0.54	0/2080	1.07	5/2804 (0.2%)
51	SE0	0.54	0/2080	1.07	7/2804 (0.2%)
52	REE	0.56	0/453	1.10	1/596 (0.2%)
52	SEE	0.57	0/453	1.10	1/596 (0.2%)
53	RF0	0.50	0/1527	1.09	2/2045 (0.1%)
53	SF0	0.50	0/1527	1.09	2/2045 (0.1%)
54	RFF	0.62	0/422	1.00	0/568
54	SFF	0.62	0/427	1.00	0/573
55	RG0	0.49	0/1864	1.05	1/2485 (0.0%)
55	SG0	0.48	0/1864	1.05	1/2485 (0.0%)
56	RGG	0.58	0/2517	1.05	4/3397 (0.1%)
56	SGG	0.58	0/2517	1.05	3/3397 (0.1%)
57	RH0	0.45	0/1356	1.02	1/1820 (0.1%)
57	SH0	0.45	0/1356	1.02	1/1820 (0.1%)
58	RI0	0.54	0/1369	1.02	1/1825 (0.1%)
58	SI0	0.54	0/1369	1.02	1/1825 (0.1%)
59	RJ0	0.51	0/1403	1.05	0/1880
59	SJ0	0.51	0/1403	1.05	0/1880

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	RK0	0.49	0/750	1.08	0/1009
60	SK0	0.49	0/750	1.08	0/1009
61	RL0	0.55	0/1252	0.99	1/1672 (0.1%)
61	SL0	0.55	0/1252	0.99	1/1672 (0.1%)
62	RM0	0.56	0/881	1.15	1/1182 (0.1%)
62	SM0	0.56	0/881	1.15	1/1182 (0.1%)
63	RN0	0.58	0/1154	1.15	2/1557 (0.1%)
63	SN0	0.57	0/1154	1.15	2/1557 (0.1%)
64	RO0	0.54	0/993	1.09	1/1326 (0.1%)
64	SO0	0.55	0/993	1.09	1/1326 (0.1%)
65	RQ0	0.57	0/1163	1.05	2/1556 (0.1%)
65	SQ0	0.57	0/1163	1.05	2/1556 (0.1%)
66	RR0	0.73	0/985	1.29	1/1315 (0.1%)
66	SR0	0.73	0/985	1.29	0/1315
67	RS0	0.57	0/1165	1.12	0/1566
67	SS0	0.57	0/1165	1.12	1/1566 (0.1%)
68	RT0	0.55	0/1181	1.14	1/1585 (0.1%)
68	ST0	0.55	0/1181	1.14	1/1585 (0.1%)
69	RU0	0.56	0/824	1.09	4/1110 (0.4%)
69	SU0	0.56	0/824	1.09	4/1110 (0.4%)
70	RV0	0.50	0/525	0.96	0/700
70	SV0	0.49	0/525	0.96	0/700
71	RW0	0.51	0/1037	1.00	0/1389
71	SW0	0.51	0/1037	1.00	0/1389
72	RX0	0.55	0/1113	1.05	1/1486 (0.1%)
72	SX0	0.55	0/1113	1.05	1/1486 (0.1%)
73	RY0	0.49	0/1131	1.10	1/1503 (0.1%)
73	SY0	0.49	0/1131	1.11	1/1503 (0.1%)
74	RZ0	0.57	0/640	1.09	0/855
74	SZ0	0.56	0/640	1.09	0/855
75	RP0	0.53	0/964	1.08	0/1289
75	SP0	0.54	0/964	1.08	0/1289
All	All	0.69	14/366789 (0.0%)	1.07	778/533031 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	KC0	0	1
6	LC0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	KFF	0	1
13	LFF	0	1
15	KGG	0	1
15	LGG	0	1
All	All	0	6

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	RA0	20	CYS	C-N	14.56	1.53	1.34
43	SA0	20	CYS	C-N	14.50	1.53	1.34
42	S60	934	A	P-O5'	6.94	1.70	1.59
42	R60	934	A	P-O5'	6.92	1.70	1.59
42	R60	934	A	O5'-C5'	6.66	1.52	1.42

The worst 5 of 778 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L50	1148	A	C4'-C3'-O3'	14.10	130.55	109.40
1	K50	1148	A	C4'-C3'-O3'	14.08	130.52	109.40
1	K50	330	G	C2'-C3'-O3'	12.46	132.40	113.70
1	L50	523	A	C1'-C2'-O2'	-12.45	93.13	111.80
1	L50	330	G	C2'-C3'-O3'	12.44	132.36	113.70

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	KC0	87	ALA	Peptide
13	KFF	101	ILE	Peptide
6	LC0	87	ALA	Peptide
13	LFF	101	ILE	Peptide
15	LGG	77	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K50	53655	0	26955	123	0
1	L50	53655	0	26955	123	0
2	K70	2542	0	1282	9	0
2	L70	2542	0	1282	8	0
3	KA0	1889	0	1985	12	0
3	LA0	1889	0	1985	12	0
4	KAA	1167	0	1214	7	0
4	LAA	1167	0	1214	6	0
5	KB0	3039	0	3183	5	0
5	LB0	3039	0	3183	6	0
6	KC0	2604	0	2638	12	0
6	LC0	2604	0	2638	11	0
7	KCC	781	0	803	2	0
7	LCC	781	0	803	2	0
8	KD0	2298	0	2384	7	0
8	LD0	2298	0	2384	8	0
9	KDD	895	0	948	1	0
9	LDD	895	0	948	0	0
10	KE0	1371	0	1389	15	0
10	LE0	1371	0	1389	14	0
11	KEE	1090	0	1173	11	0
11	LEE	1090	0	1173	11	0
12	KF0	1933	0	2011	12	0
12	LF0	1933	0	2011	12	0
13	KFF	893	0	945	3	0
13	LFF	893	0	945	3	0
14	KG0	1590	0	1709	6	0
14	LG0	1590	0	1709	5	0
15	KGG	819	0	882	2	0
15	LGG	819	0	882	3	0
16	KH0	1477	0	1528	3	0
16	LH0	1477	0	1528	3	0
17	KHH	992	0	1097	5	0
17	LHH	992	0	1097	5	0
18	KI0	1750	0	1797	2	0
18	LI0	1750	0	1797	3	0
19	KII	784	0	874	5	0
19	LII	784	0	874	4	0
20	KJ0	1332	0	1411	12	0
20	LJ0	1332	0	1411	12	0
21	KJJ	701	0	753	4	0
21	LJJ	701	0	753	4	0
22	KL0	1353	0	1433	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	LL0	1353	0	1433	5	0
23	KLL	427	0	468	0	0
23	LLL	427	0	468	0	0
24	KM0	927	0	961	4	0
24	LM0	927	0	961	5	0
25	KMM	427	0	461	0	0
25	LMM	427	0	461	0	0
26	KN0	1688	0	1752	6	0
26	LN0	1688	0	1752	6	0
27	KO0	1598	0	1681	5	0
27	LO0	1598	0	1681	5	0
28	KOO	801	0	886	3	0
28	LOO	801	0	886	4	0
29	KP0	1238	0	1304	4	0
29	LP0	1238	0	1304	3	0
30	KPP	684	0	720	2	0
30	LPP	684	0	720	2	0
31	KQ0	1491	0	1587	6	0
31	LQ0	1491	0	1587	7	0
32	KR0	1336	0	1430	1	0
32	LR0	1336	0	1430	0	0
33	KS0	1400	0	1450	1	0
33	LS0	1400	0	1450	1	0
34	KT0	1270	0	1321	18	0
34	LT0	1270	0	1321	18	0
35	KU0	810	0	834	1	0
35	LU0	810	0	834	1	0
36	KV0	1057	0	1139	1	0
36	LV0	1057	0	1139	1	0
37	KW0	832	0	873	47	0
37	LW0	832	0	873	47	0
38	KX0	874	0	956	5	0
38	LX0	874	0	956	5	0
39	KY0	1048	0	1135	2	0
39	LY0	1048	0	1135	2	0
40	KZ0	963	0	1022	2	0
40	LZ0	963	0	1022	2	0
41	MD1	1229	0	1216	10	0
41	MD2	1229	0	1216	9	0
42	R60	29181	0	14605	320	0
42	S60	29181	0	14604	323	0
43	RA0	1725	0	1750	144	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SA0	1725	0	1750	140	0
44	RAA	827	0	859	17	0
44	SAA	827	0	859	17	0
45	RB0	1609	0	1728	6	0
45	SB0	1609	0	1728	6	0
46	RBB	627	0	651	4	0
46	SBB	627	0	651	3	0
47	RC0	1727	0	1802	97	0
47	SC0	1727	0	1802	95	0
48	RCC	476	0	488	17	0
48	SCC	476	0	488	17	0
49	RD0	1700	0	1815	32	0
49	SD0	1700	0	1815	32	0
50	RDD	550	0	542	28	0
50	SDD	550	0	542	30	0
51	RE0	2044	0	2116	26	0
51	SE0	2044	0	2116	26	0
52	REE	447	0	483	1	0
52	SEE	447	0	483	1	0
53	RF0	1509	0	1604	39	0
53	SF0	1509	0	1604	40	0
54	RFF	417	0	402	42	0
54	SFF	422	0	412	44	0
55	RG0	1836	0	1972	41	0
55	SG0	1836	0	1972	40	0
56	RGG	2478	0	2458	24	0
56	SGG	2478	0	2458	24	0
57	RH0	1335	0	1356	2	0
57	SH0	1335	0	1356	2	0
58	RI0	1347	0	1379	9	0
58	SI0	1347	0	1379	10	0
59	RJ0	1379	0	1436	17	0
59	SJ0	1379	0	1436	16	0
60	RK0	737	0	746	16	0
60	SK0	737	0	746	16	0
61	RL0	1229	0	1302	5	0
61	SL0	1229	0	1302	5	0
62	RM0	876	0	937	6	0
62	SM0	876	0	937	5	0
63	RN0	1130	0	1189	11	0
63	SN0	1130	0	1189	11	0
64	RO0	983	0	1028	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	SO0	983	0	1028	14	0
65	RQ0	1143	0	1171	20	0
65	SQ0	1143	0	1171	20	0
66	RR0	974	0	1003	101	0
66	SR0	974	0	1003	101	0
67	RS0	1150	0	1207	35	0
67	SS0	1150	0	1207	36	0
68	RT0	1161	0	1219	10	0
68	ST0	1161	0	1219	10	0
69	RU0	809	0	838	14	0
69	SU0	809	0	838	14	0
70	RV0	521	0	525	73	0
70	SV0	521	0	525	73	0
71	RW0	1022	0	1052	20	0
71	SW0	1022	0	1052	19	0
72	RX0	1098	0	1183	3	0
72	SX0	1098	0	1183	3	0
73	RY0	1118	0	1166	14	0
73	SY0	1118	0	1166	11	0
74	RZ0	633	0	678	14	0
74	SZ0	633	0	678	13	0
75	RP0	950	0	984	56	0
75	SP0	950	0	984	59	0
76	KGG	1	0	0	0	0
76	KJJ	1	0	0	0	0
76	KMM	1	0	0	0	0
76	KOO	1	0	0	0	0
76	KPP	1	0	0	0	0
76	LGG	1	0	0	0	0
76	LJJ	1	0	0	0	0
76	LMM	1	0	0	0	0
76	LOO	1	0	0	0	0
76	LPP	1	0	0	0	0
76	RAA	1	0	0	0	0
76	RBB	1	0	0	0	0
76	RDD	1	0	0	0	0
76	RFF	1	0	0	0	0
76	SAA	1	0	0	0	0
76	SBB	1	0	0	0	0
76	SDD	1	0	0	0	0
76	SFF	1	0	0	0	0
All	All	343629	0	266537	2024	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 2024 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CD1	1.35	1.54
43:RA0:70:ASN:HB2	47:RC0:240:ILE:CD1	1.35	1.49
47:SC0:51:SER:HB2	70:SV0:6:ARG:NH2	1.30	1.45
49:SD0:238:PRO:C	66:SR0:19:ARG:HH12	1.27	1.42
47:RC0:51:SER:HB2	70:RV0:6:ARG:NH2	1.30	1.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	KA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
3	LA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
4	KAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
4	LAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
5	KB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
5	LB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
6	KC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	36	72
6	LC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	36	72
7	KCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	12	49
7	LCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	12	49
8	KD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
8	LD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	KDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
9	LDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
10	KE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
10	LE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
11	KEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
11	LEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
12	KF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
12	LF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
13	KFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
13	LFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
14	KG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
14	LG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
15	KGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	12	49
15	LGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	12	49
16	KH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
16	LH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
17	KHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
17	LHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	KI0	215/218 (99%)	213 (99%)	2 (1%)	0	100	100
18	LI0	215/218 (99%)	214 (100%)	1 (0%)	0	100	100
19	KII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
19	LII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
20	KJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
20	LJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
21	KJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
21	LJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
22	KL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	21	59
22	LL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	21	59
23	KLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
23	LLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
24	KM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	LM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	51
25	KMM	50/127 (39%)	50 (100%)	0	0	100	100
25	LMM	50/127 (39%)	50 (100%)	0	0	100	100
26	KN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
26	LN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
27	KO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
27	LO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
28	KOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
28	LOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
29	KP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
29	LP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
30	KPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	10	44
30	LPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	10	44
31	KQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
31	LQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
32	KR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
32	LR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
33	KS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
33	LS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
34	KT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
34	LT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
35	KU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
35	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
36	KV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
36	LV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
37	KW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	12	49
37	LW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	12	49
38	KX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
38	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
39	KY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
39	LY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	KZ0	116/153 (76%)	116 (100%)	0	0	100	100
40	LZ0	116/153 (76%)	116 (100%)	0	0	100	100
41	MD1	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
41	MD2	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
43	RA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
43	SA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
44	RAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
44	SAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
45	RB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
45	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
46	RBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
46	SBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
47	RC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
47	SC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
48	RCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
48	SCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
49	RD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
49	SD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
50	RDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	SDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
51	RE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
51	SE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
52	REE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
52	SEE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
53	RF0	190/195 (97%)	181 (95%)	9 (5%)	0	100	100
53	SF0	190/195 (97%)	180 (95%)	10 (5%)	0	100	100
54	RFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
54	SFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
55	RG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
55	SG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
56	RGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	36	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	SGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	36	72
57	RH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	21	59
57	SH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	21	59
58	RI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
58	SI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
59	RJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
59	SJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
60	RK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	10	44
60	SK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	10	44
61	RL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
61	SL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
62	RM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
62	SM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
63	RN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
63	SN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
64	RO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
64	SO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
65	RQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
65	SQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
66	RR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
66	SR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
67	RS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	18	56
67	SS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	18	56
68	RT0	140/143 (98%)	140 (100%)	0	0	100	100
68	ST0	140/143 (98%)	140 (100%)	0	0	100	100
69	RU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
69	SU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
70	RV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
70	SV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
71	RW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
71	SW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	RX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
72	SX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
73	RY0	134/146 (92%)	121 (90%)	11 (8%)	2 (2%)	8	40
73	SY0	134/146 (92%)	122 (91%)	10 (8%)	2 (2%)	8	40
74	RZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
74	SZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
75	RP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
75	SP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
All	All	21258/22938 (93%)	20523 (96%)	709 (3%)	26 (0%)	49	83

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LGG	78	GLY
73	SY0	134	LYS
15	KGG	78	GLY
73	RY0	134	LYS
30	LPP	18	TYR

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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	KA0	202/203 (100%)	199 (98%)	3 (2%)	57	72
3	LA0	202/203 (100%)	199 (98%)	3 (2%)	57	72
4	KAA	123/123 (100%)	119 (97%)	4 (3%)	33	55
4	LAA	123/123 (100%)	119 (97%)	4 (3%)	33	55
5	KB0	328/336 (98%)	319 (97%)	9 (3%)	39	61
5	LB0	328/336 (98%)	319 (97%)	9 (3%)	39	61
6	KC0	277/278 (100%)	274 (99%)	3 (1%)	65	76
6	LC0	277/278 (100%)	274 (99%)	3 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	KCC	87/97 (90%)	85 (98%)	2 (2%)	44	64
7	LCC	87/97 (90%)	85 (98%)	2 (2%)	44	64
8	KD0	251/261 (96%)	249 (99%)	2 (1%)	73	80
8	LD0	251/261 (96%)	249 (99%)	2 (1%)	73	80
9	KDD	99/100 (99%)	99 (100%)	0	100	100
9	LDD	99/100 (99%)	99 (100%)	0	100	100
10	KE0	153/159 (96%)	150 (98%)	3 (2%)	48	66
10	LE0	153/159 (96%)	150 (98%)	3 (2%)	48	66
11	KEE	118/122 (97%)	118 (100%)	0	100	100
11	LEE	118/122 (97%)	118 (100%)	0	100	100
12	KF0	212/216 (98%)	211 (100%)	1 (0%)	81	83
12	LF0	212/216 (98%)	211 (100%)	1 (0%)	81	83
13	KFF	98/98 (100%)	98 (100%)	0	100	100
13	LFF	98/98 (100%)	98 (100%)	0	100	100
14	KG0	183/190 (96%)	183 (100%)	0	100	100
14	LG0	183/190 (96%)	183 (100%)	0	100	100
15	KGG	88/90 (98%)	86 (98%)	2 (2%)	44	64
15	LGG	88/90 (98%)	86 (98%)	2 (2%)	44	64
16	KH0	165/169 (98%)	161 (98%)	4 (2%)	43	64
16	LH0	165/169 (98%)	161 (98%)	4 (2%)	43	64
17	KHH	110/110 (100%)	109 (99%)	1 (1%)	70	79
17	LHH	110/110 (100%)	109 (99%)	1 (1%)	70	79
18	KI0	188/189 (100%)	188 (100%)	0	100	100
18	LI0	188/189 (100%)	188 (100%)	0	100	100
19	KII	84/84 (100%)	82 (98%)	2 (2%)	43	64
19	LII	84/84 (100%)	82 (98%)	2 (2%)	43	64
20	KJ0	146/149 (98%)	144 (99%)	2 (1%)	59	72
20	LJ0	146/149 (98%)	144 (99%)	2 (1%)	59	72
21	KJJ	78/81 (96%)	77 (99%)	1 (1%)	61	74
21	LJJ	78/81 (96%)	77 (99%)	1 (1%)	61	74
22	KL0	148/149 (99%)	142 (96%)	6 (4%)	27	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	LL0	148/149 (99%)	142 (96%)	6 (4%)	27	49
23	KLL	46/47 (98%)	46 (100%)	0	100	100
23	LLL	46/47 (98%)	46 (100%)	0	100	100
24	KM0	110/110 (100%)	110 (100%)	0	100	100
24	LM0	110/110 (100%)	110 (100%)	0	100	100
25	KMM	46/112 (41%)	46 (100%)	0	100	100
25	LMM	46/112 (41%)	46 (100%)	0	100	100
26	KN0	175/176 (99%)	171 (98%)	4 (2%)	44	64
26	LN0	175/176 (99%)	171 (98%)	4 (2%)	44	64
27	KO0	178/178 (100%)	177 (99%)	1 (1%)	78	83
27	LO0	178/178 (100%)	177 (99%)	1 (1%)	78	83
28	KOO	85/89 (96%)	85 (100%)	0	100	100
28	LOO	85/89 (96%)	85 (100%)	0	100	100
29	KP0	135/147 (92%)	132 (98%)	3 (2%)	45	64
29	LP0	135/147 (92%)	132 (98%)	3 (2%)	45	64
30	KPP	75/77 (97%)	73 (97%)	2 (3%)	39	61
30	LPP	75/77 (97%)	73 (97%)	2 (3%)	39	61
31	KQ0	165/166 (99%)	165 (100%)	0	100	100
31	LQ0	165/166 (99%)	165 (100%)	0	100	100
32	KR0	142/145 (98%)	141 (99%)	1 (1%)	76	81
32	LR0	142/145 (98%)	141 (99%)	1 (1%)	76	81
33	KS0	155/156 (99%)	152 (98%)	3 (2%)	50	67
33	LS0	155/156 (99%)	152 (98%)	3 (2%)	50	67
34	KT0	140/142 (99%)	138 (99%)	2 (1%)	59	72
34	LT0	140/142 (99%)	138 (99%)	2 (1%)	59	72
35	KU0	89/98 (91%)	88 (99%)	1 (1%)	65	76
35	LU0	89/98 (91%)	88 (99%)	1 (1%)	65	76
36	KV0	113/114 (99%)	112 (99%)	1 (1%)	70	79
36	LV0	113/114 (99%)	112 (99%)	1 (1%)	70	79
37	KW0	93/120 (78%)	89 (96%)	4 (4%)	26	47
37	LW0	93/120 (78%)	89 (96%)	4 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	KX0	92/93 (99%)	91 (99%)	1 (1%)	65	76
38	LX0	92/93 (99%)	91 (99%)	1 (1%)	65	76
39	KY0	116/116 (100%)	114 (98%)	2 (2%)	53	69
39	LY0	116/116 (100%)	114 (98%)	2 (2%)	53	69
40	KZ0	106/141 (75%)	106 (100%)	0	100	100
40	LZ0	106/141 (75%)	106 (100%)	0	100	100
41	MD1	139/139 (100%)	139 (100%)	0	100	100
41	MD2	139/139 (100%)	139 (100%)	0	100	100
43	RA0	194/206 (94%)	191 (98%)	3 (2%)	57	72
43	SA0	194/206 (94%)	191 (98%)	3 (2%)	57	72
44	RAA	92/93 (99%)	92 (100%)	0	100	100
44	SAA	92/93 (99%)	92 (100%)	0	100	100
45	RB0	182/203 (90%)	182 (100%)	0	100	100
45	SB0	182/203 (90%)	182 (100%)	0	100	100
46	RBB	72/73 (99%)	71 (99%)	1 (1%)	59	72
46	SBB	72/73 (99%)	71 (99%)	1 (1%)	59	72
47	RC0	187/209 (90%)	185 (99%)	2 (1%)	65	76
47	SC0	187/209 (90%)	185 (99%)	2 (1%)	65	76
48	RCC	51/54 (94%)	51 (100%)	0	100	100
48	SCC	51/54 (94%)	51 (100%)	0	100	100
49	RD0	189/215 (88%)	189 (100%)	0	100	100
49	SD0	189/215 (88%)	189 (100%)	0	100	100
50	RDD	57/57 (100%)	57 (100%)	0	100	100
50	SDD	57/57 (100%)	57 (100%)	0	100	100
51	RE0	231/251 (92%)	229 (99%)	2 (1%)	70	79
51	SE0	231/251 (92%)	229 (99%)	2 (1%)	70	79
52	REE	44/47 (94%)	44 (100%)	0	100	100
52	SEE	44/47 (94%)	44 (100%)	0	100	100
53	RF0	167/170 (98%)	163 (98%)	4 (2%)	43	64
53	SF0	167/170 (98%)	163 (98%)	4 (2%)	43	64
54	RFF	45/136 (33%)	44 (98%)	1 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	SFF	46/136 (34%)	45 (98%)	1 (2%)	45	64
55	RG0	199/199 (100%)	195 (98%)	4 (2%)	48	66
55	SG0	199/199 (100%)	195 (98%)	4 (2%)	48	66
56	RGG	282/288 (98%)	278 (99%)	4 (1%)	59	72
56	SGG	282/288 (98%)	278 (99%)	4 (1%)	59	72
57	RH0	153/154 (99%)	153 (100%)	0	100	100
57	SH0	153/154 (99%)	153 (100%)	0	100	100
58	RI0	147/153 (96%)	147 (100%)	0	100	100
58	SI0	147/153 (96%)	147 (100%)	0	100	100
59	RJ0	152/165 (92%)	150 (99%)	2 (1%)	61	74
59	SJ0	152/165 (92%)	150 (99%)	2 (1%)	61	74
60	RK0	83/99 (84%)	82 (99%)	1 (1%)	63	75
60	SK0	83/99 (84%)	82 (99%)	1 (1%)	63	75
61	RL0	140/145 (97%)	139 (99%)	1 (1%)	76	81
61	SL0	140/145 (97%)	139 (99%)	1 (1%)	76	81
62	RM0	99/114 (87%)	99 (100%)	0	100	100
62	SM0	99/114 (87%)	99 (100%)	0	100	100
63	RN0	126/127 (99%)	126 (100%)	0	100	100
63	SN0	126/127 (99%)	126 (100%)	0	100	100
64	RO0	102/108 (94%)	101 (99%)	1 (1%)	68	78
64	SO0	102/108 (94%)	101 (99%)	1 (1%)	68	78
65	RQ0	120/121 (99%)	119 (99%)	1 (1%)	73	80
65	SQ0	120/121 (99%)	119 (99%)	1 (1%)	73	80
66	RR0	109/111 (98%)	108 (99%)	1 (1%)	70	79
66	SR0	109/111 (98%)	108 (99%)	1 (1%)	70	79
67	RS0	125/138 (91%)	124 (99%)	1 (1%)	73	80
67	SS0	125/138 (91%)	124 (99%)	1 (1%)	73	80
68	RT0	129/130 (99%)	127 (98%)	2 (2%)	55	70
68	ST0	129/130 (99%)	127 (98%)	2 (2%)	55	70
69	RU0	92/110 (84%)	92 (100%)	0	100	100
69	SU0	92/110 (84%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	RV0	61/63 (97%)	61 (100%)	0	100	100
70	SV0	61/63 (97%)	61 (100%)	0	100	100
71	RW0	111/111 (100%)	110 (99%)	1 (1%)	70	79
71	SW0	111/111 (100%)	110 (99%)	1 (1%)	70	79
72	RX0	115/116 (99%)	115 (100%)	0	100	100
72	SX0	115/116 (99%)	115 (100%)	0	100	100
73	RY0	126/136 (93%)	121 (96%)	5 (4%)	28	49
73	SY0	126/136 (93%)	121 (96%)	5 (4%)	28	49
74	RZ0	73/118 (62%)	73 (100%)	0	100	100
74	SZ0	73/118 (62%)	73 (100%)	0	100	100
75	RP0	107/144 (74%)	106 (99%)	1 (1%)	70	79
75	SP0	107/144 (74%)	106 (99%)	1 (1%)	70	79
All	All	19001/20268 (94%)	18785 (99%)	216 (1%)	63	76

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	KB0	23	LYS
20	KJ0	106	HIS
59	RJ0	130	GLN
5	KB0	133	LEU
10	KE0	15	LYS

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	K50	2494/2618 (95%)	748 (29%)	103 (4%)
1	L50	2494/2618 (95%)	748 (29%)	102 (4%)
2	K70	118/119 (99%)	36 (30%)	4 (3%)
2	L70	118/119 (99%)	36 (30%)	4 (3%)
42	R60	1352/1368 (98%)	525 (38%)	70 (5%)
42	S60	1352/1368 (98%)	524 (38%)	70 (5%)
All	All	7928/8210 (96%)	2617 (33%)	353 (4%)

5 of 2617 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	13	A
1	L50	15	G
1	L50	21	U

5 of 353 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	K50	1454	U
42	R60	127	A
1	K50	1614	G
1	K50	2060	A
42	R60	355	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17457. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.