



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2022 – 02:45 AM EDT

PDB ID : 5UYP
EMDB ID : EMD-8619
Title : 70S ribosome bound with near-cognate ternary complex base-paired to A site codon, open 30S (Structure II-nc)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.90 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.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

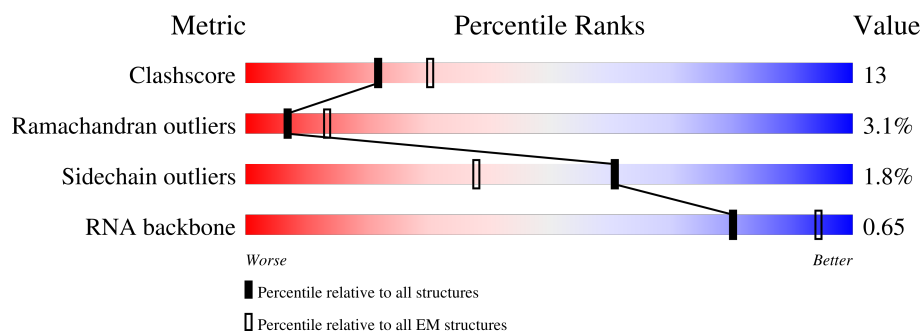
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.




















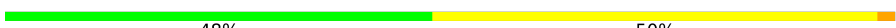







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	04	271	58% 40% .
2	05	209	65% 34% .
3	06	201	68% 31% .
4	07	177	57% 41% ..
5	08	176	60% 40%
6	09	149	56% 42% .
7	10	131	46% 47% 7% .












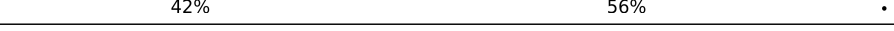







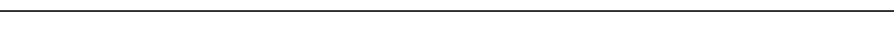

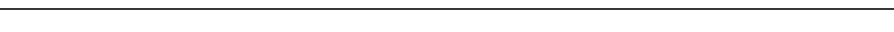
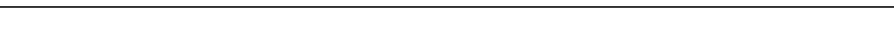


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Mol	Chain	Length	Quality of chain
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	
29	32	46	
30	33	64	
31	34	38	
32	B	218	




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Mol	Chain	Length	Quality of chain
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	
54	01	2903	
55	02	120	
56	W	77	
56	X	77	

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Mol	Chain	Length	Quality of chain
57	V	19	 63% 32% 5%
58	Y	76	 61% 25% 12% .
59	Z	392	 49% 49% ..

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 153780 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 protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	18	114	Total	C	N	O	S	0
			917	574	179	163	1	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O		0
			947	604	192	151		0

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	20	103	Total	C	N	O	S	0
			816	516	153	145	2	0

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	21	110	Total	C	N	O	S	0
			857	532	166	156	3	0

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	22	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	19	Total	C	N	O	P	0	0
			417	188	89	122	18		

- Molecule 58 is a RNA chain called tRNA^{Lys}.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Y	76	Total	C	N	O	P	S	0	0
			1618	723	282	536	76	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	34	U8U	-	insertion	GB 558570689

- Molecule 59 is a protein called Elongation factor Tu 2.

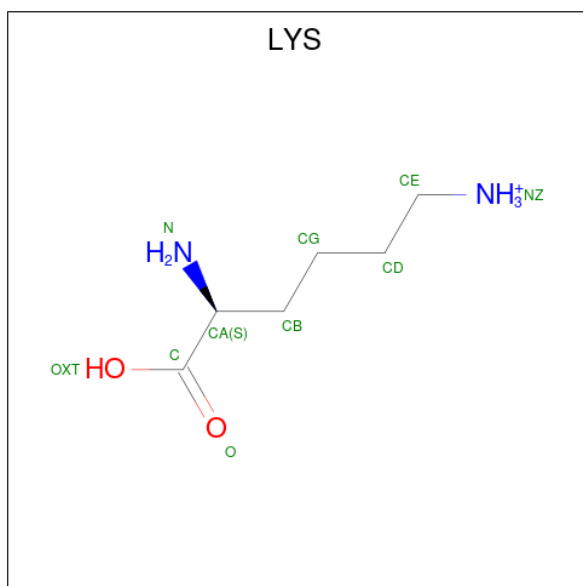
Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: C₆H₁₁NO₃S).



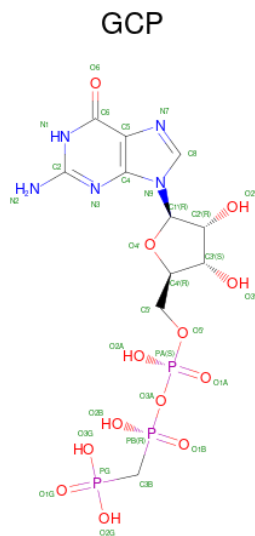
Mol	Chain	Residues	Atoms					AltConf
60	W	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 61 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
61	Y	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

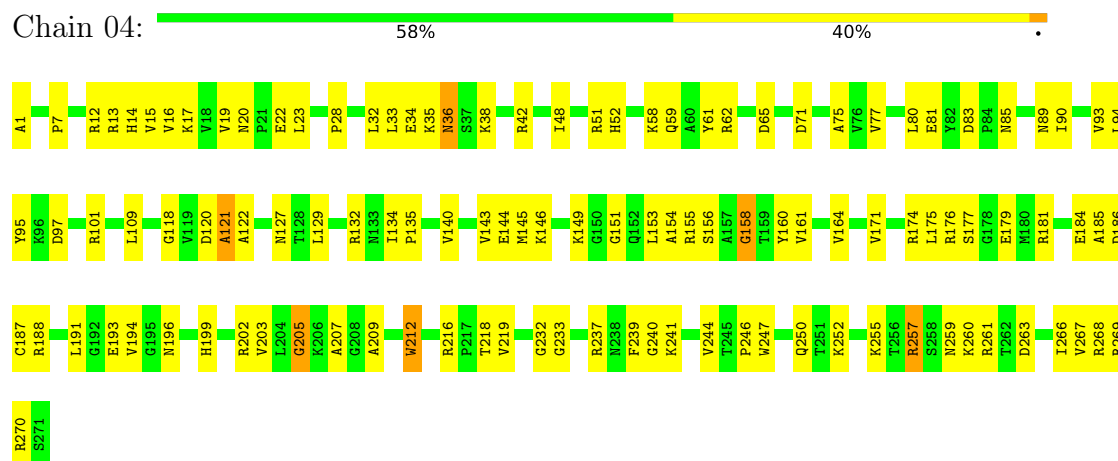


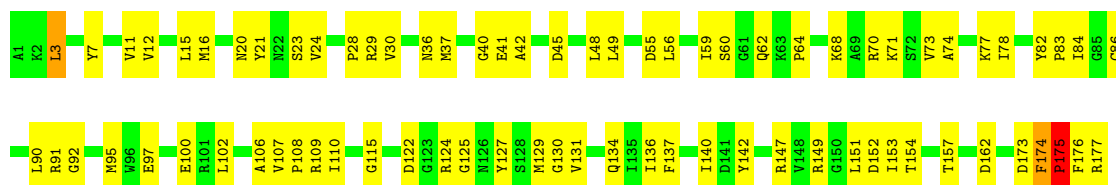
Mol	Chain	Residues	Atoms					AltConf
62	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

3 Residue-property plots

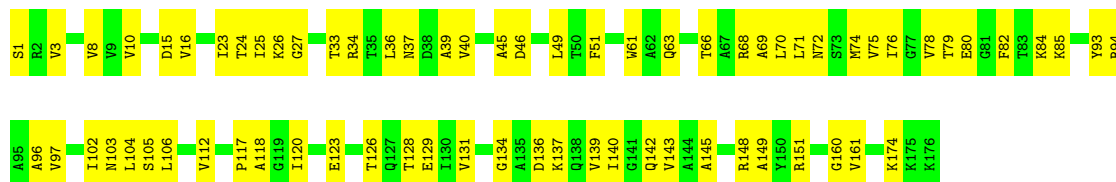
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: 50S ribosomal protein L2

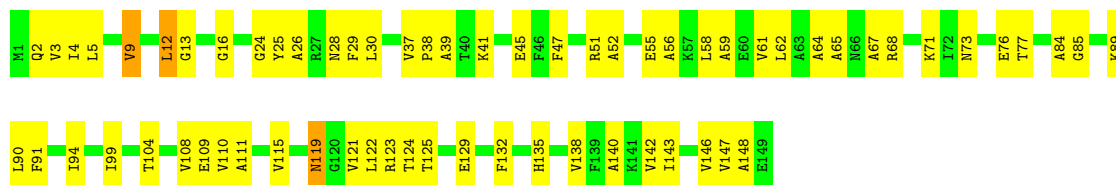




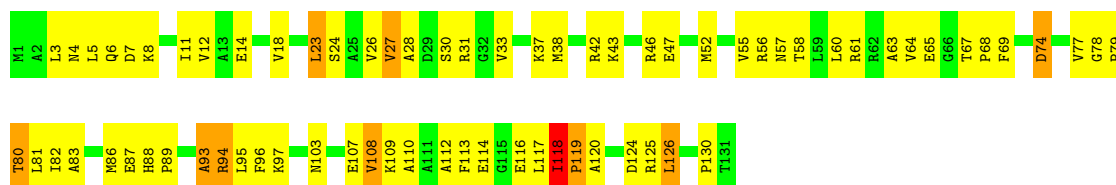
• Molecule 5: 50S ribosomal protein L6



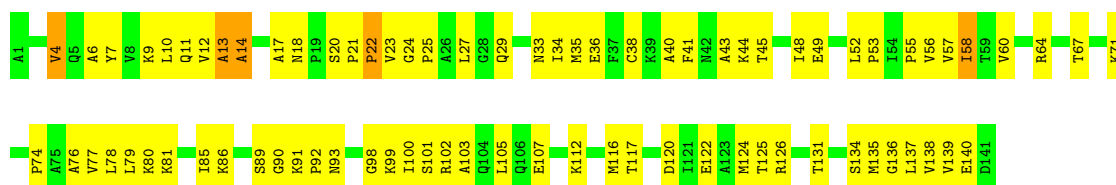
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11



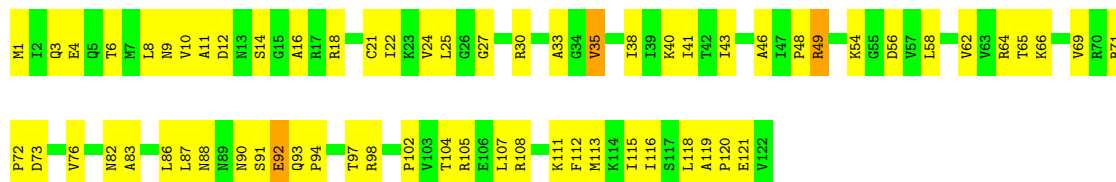
• Molecule 9: 50S ribosomal protein L13





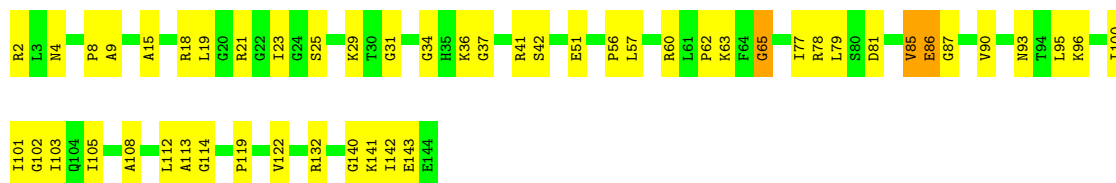
- Molecule 10: 50S ribosomal protein L14

Chain 13: 47% 51% .



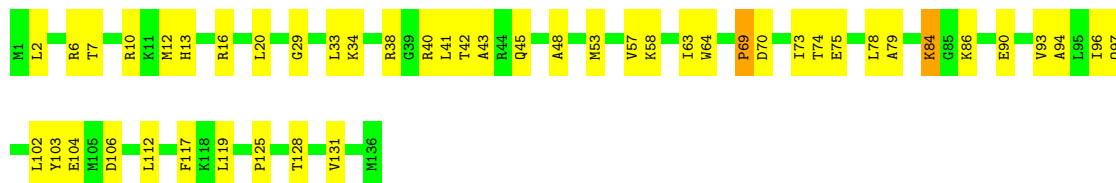
- Molecule 11: 50S ribosomal protein L15

Chain 14: 64% 34% .



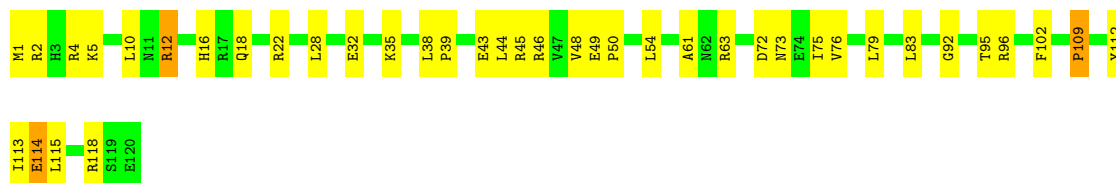
- Molecule 12: 50S ribosomal protein L16

Chain 15: 65% 33% .



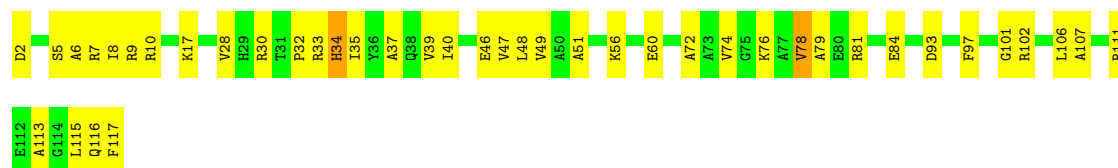
- Molecule 13: 50S ribosomal protein L17

Chain 16: 67% 31% .



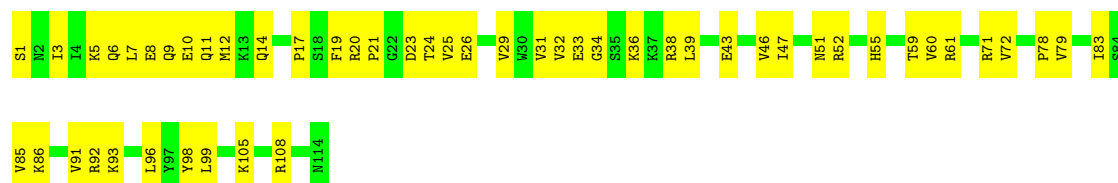
- Molecule 14: 50S ribosomal protein L18

Chain 17: 64% 34% .



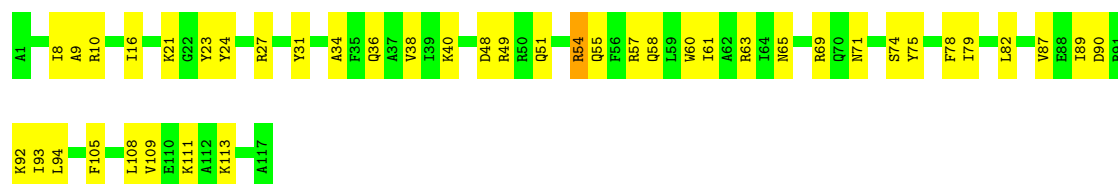
- Molecule 15: 50S ribosomal protein L19

Chain 18: 55% 45%



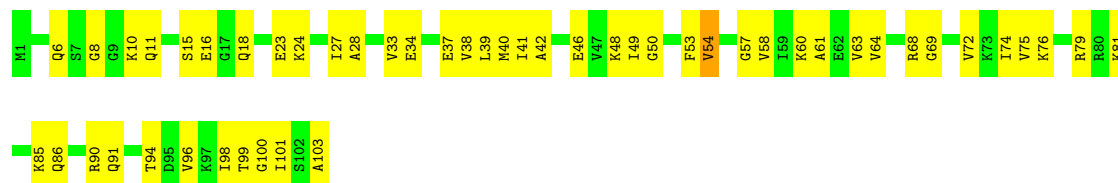
- Molecule 16: 50S ribosomal protein L20

Chain 19: 64% 35%



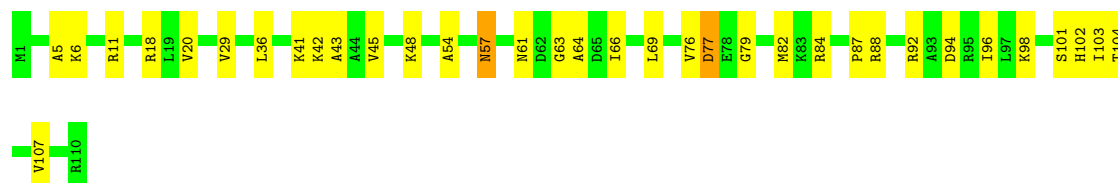
- Molecule 17: 50S ribosomal protein L21

Chain 20: 51% 48%



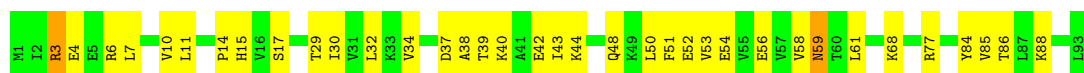
- Molecule 18: 50S ribosomal protein L22

Chain 21: 68% 30%



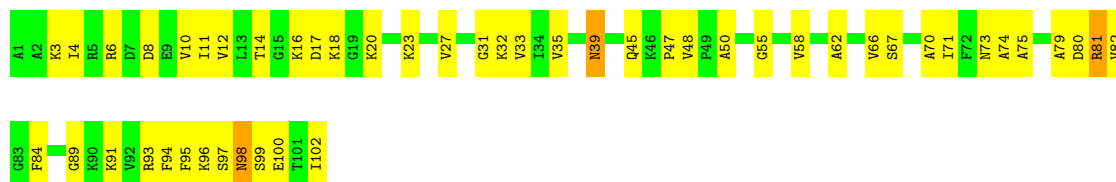
- Molecule 19: 50S ribosomal protein L23

Chain 22: 61% 37%



- Molecule 20: 50S ribosomal protein L24

Chain 23: 52% 45%



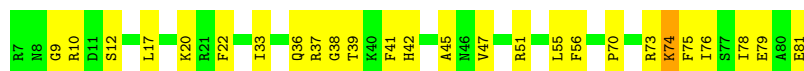
- Molecule 21: 50S ribosomal protein L25

Chain 24: 65% 34%



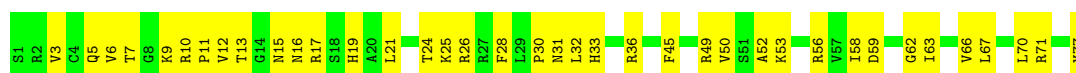
- Molecule 22: 50S ribosomal protein L27

Chain 25: 65% 33%



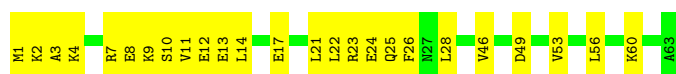
- Molecule 23: 50S ribosomal protein L28

Chain 26: 51% 49%



- Molecule 24: 50S ribosomal protein L29

Chain 27: 60% 40%



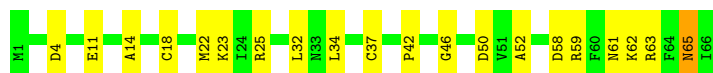
- Molecule 25: 50S ribosomal protein L30

Chain 28: 48% 50%



- Molecule 26: 50S ribosomal protein L31

Chain 29:  70% 29%



- Molecule 27: 50S ribosomal protein L32

Chain 30:  54% 46%



- Molecule 28: 50S ribosomal protein L33

Chain 31:  62% 38%



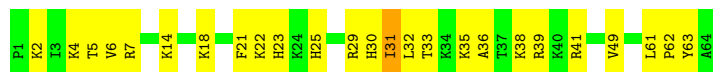
- Molecule 29: 50S ribosomal protein L34

Chain 32:  67% 33%




- Molecule 30: 50S ribosomal protein L35

Chain 33:  61% 38%



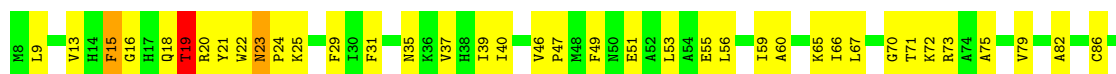
- Molecule 31: 50S ribosomal protein L36

Chain 34:  76% 21%



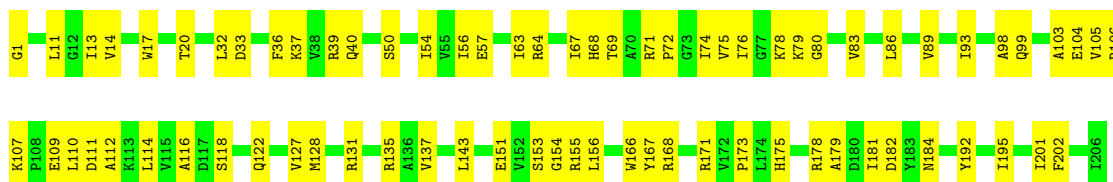
- Molecule 32: 30S ribosomal protein S2

Chain B:  50% 46%

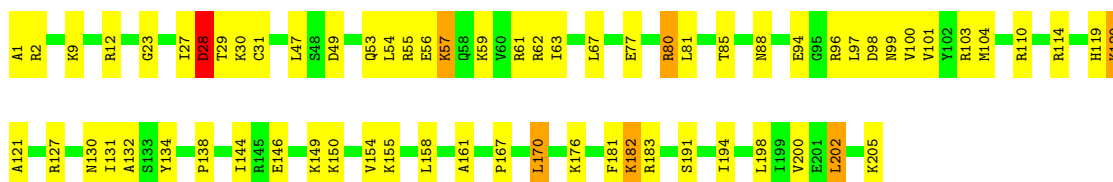




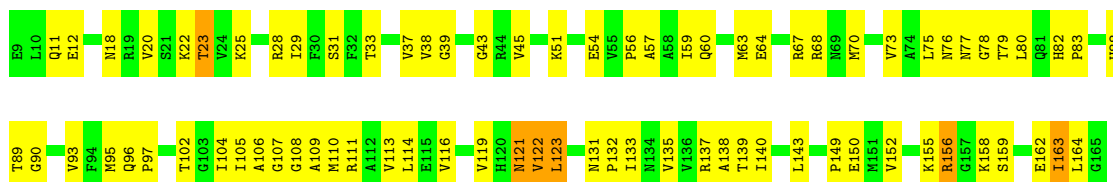
- Molecule 33: 30S ribosomal protein S3



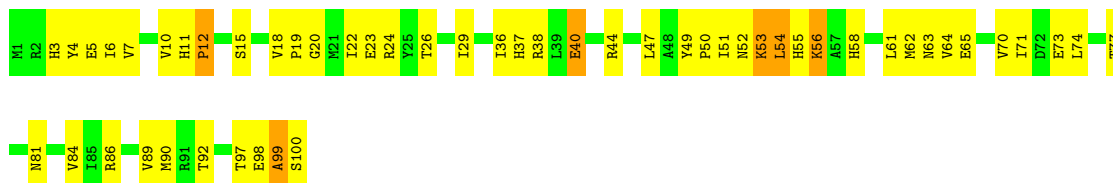
- Molecule 34: 30S ribosomal protein S4



- Molecule 35: 30S ribosomal protein S5



- Molecule 36: 30S ribosomal protein S6



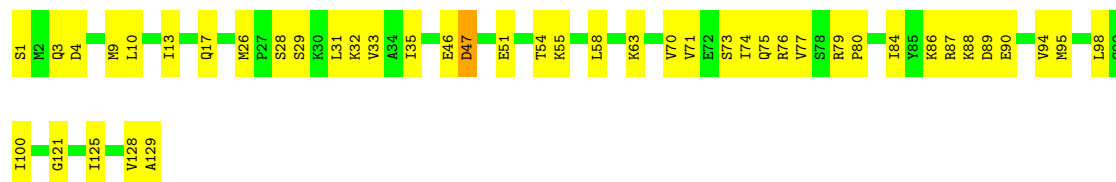
- Molecule 37: 30S ribosomal protein S7





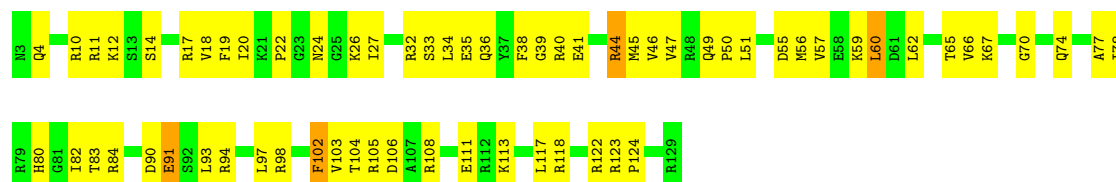
• Molecule 38: 30S ribosomal protein S8

Chain H: 66% 33%



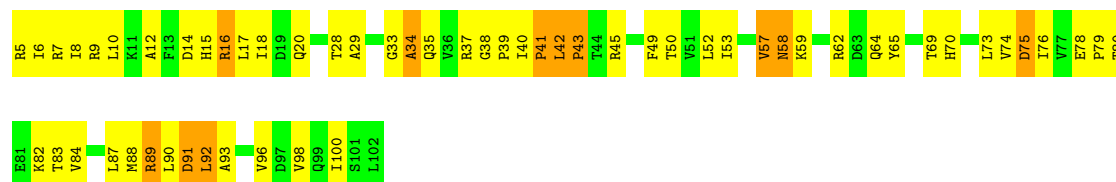
• Molecule 39: 30S ribosomal protein S9

Chain I: 49% 48%



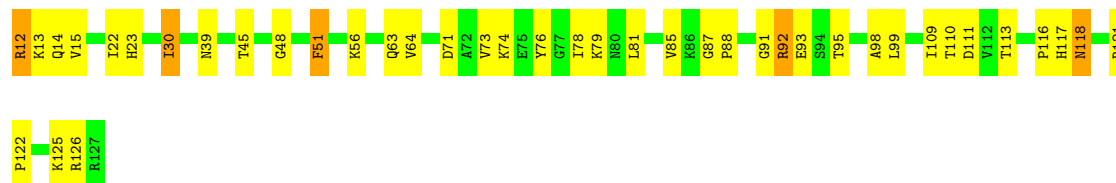
• Molecule 40: 30S ribosomal protein S10

Chain J: 41% 48% 11%



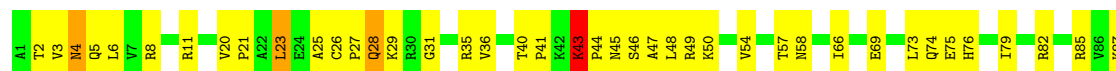
• Molecule 41: 30S ribosomal protein S11

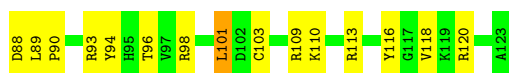
Chain K: 65% 31%



• Molecule 42: 30S ribosomal protein S12

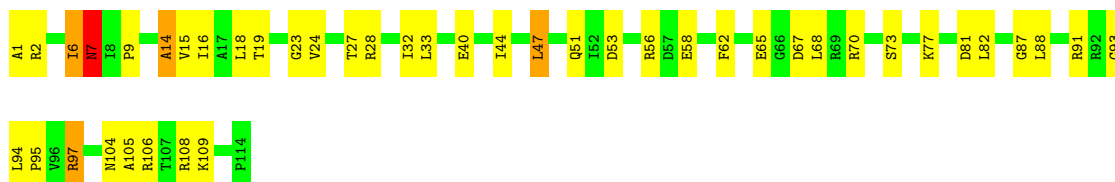
Chain L: 54% 41%





• Molecule 43: 30S ribosomal protein S13

Chain M: 61% 34%



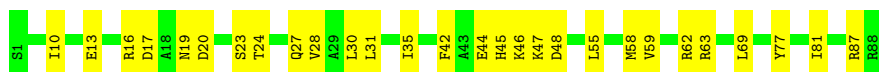
• Molecule 44: 30S ribosomal protein S14

Chain N: 42% 56%



• Molecule 45: 30S ribosomal protein S15

Chain O: 68% 32%



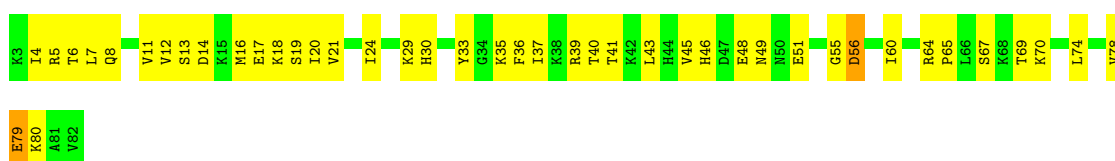
• Molecule 46: 30S ribosomal protein S16

Chain P: 61% 35%



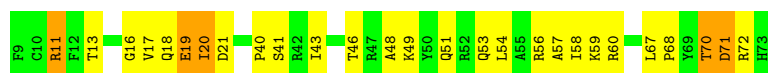
• Molecule 47: 30S ribosomal protein S17

Chain Q: 46% 51%



• Molecule 48: 30S ribosomal protein S18

Chain R: 58% 34% 8%



- Molecule 49: 30S ribosomal protein S19



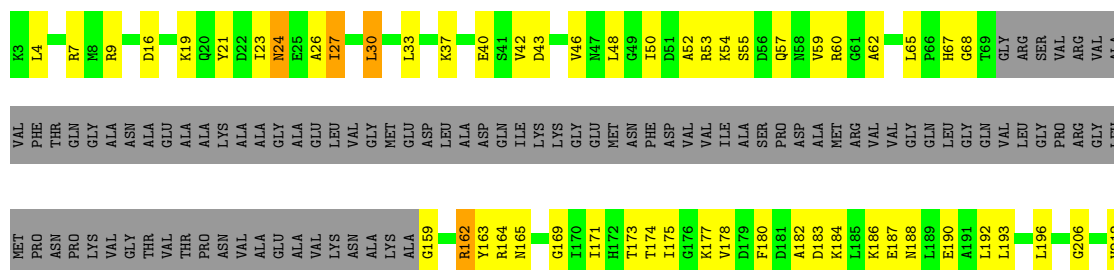
- Molecule 50: 30S ribosomal protein S20



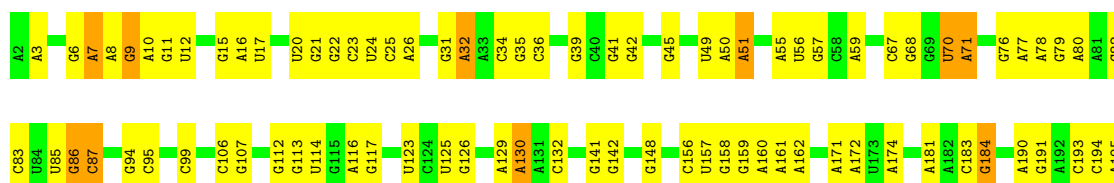
- Molecule 51: 30S ribosomal protein S21

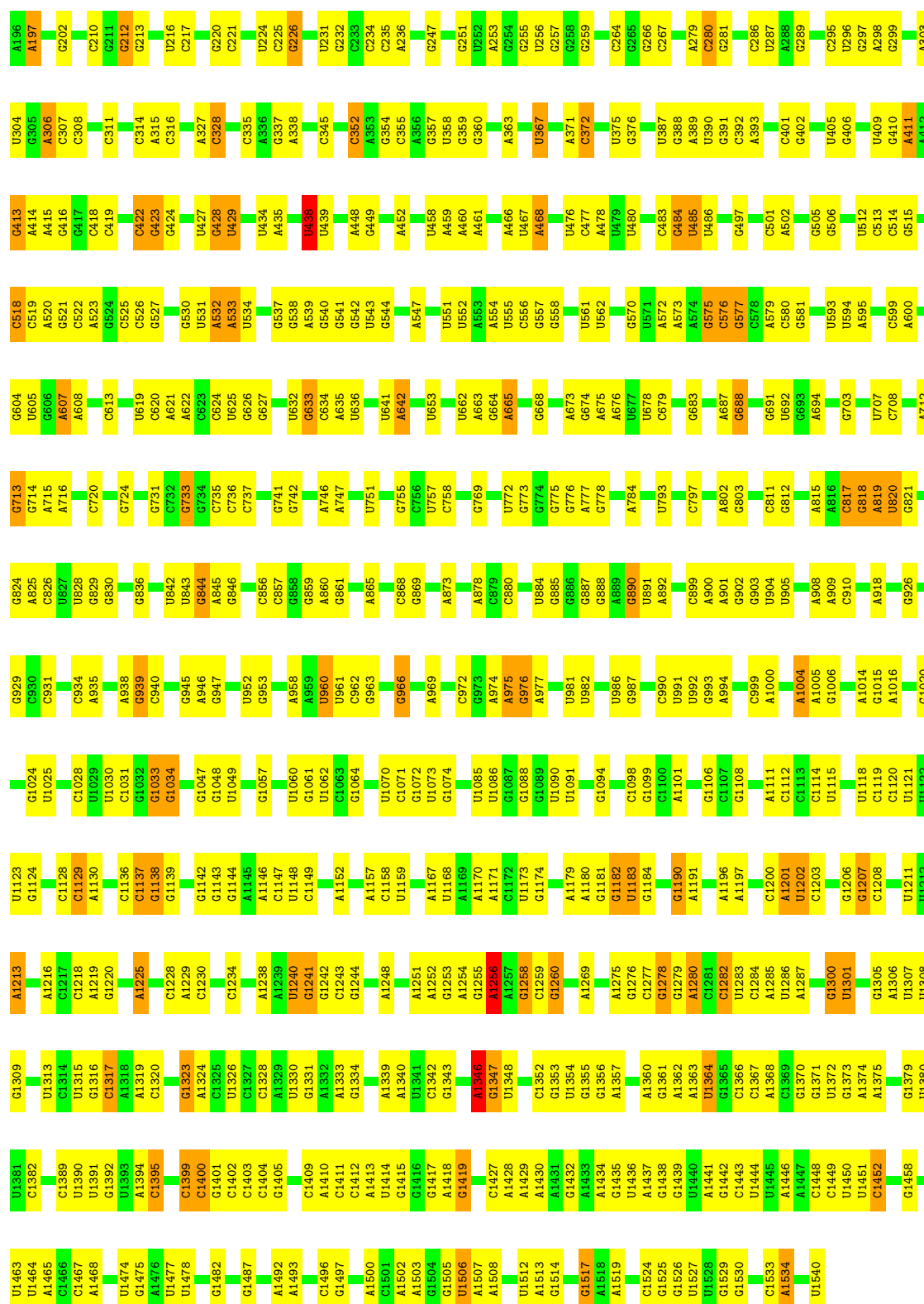


- Molecule 52: 50S ribosomal protein L1



- Molecule 53: 16S ribosomal RNA



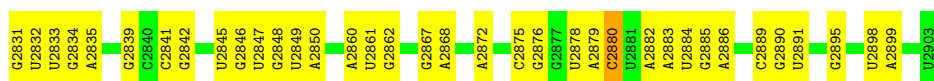


• Molecule 54: 23S ribosomal RNA

Chain 01: 54% 40% 5%

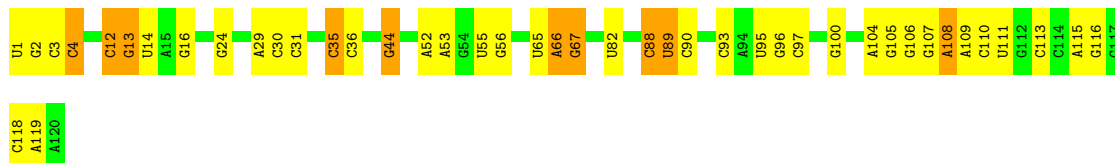
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G1358	A1359	U1273	G1170	A1073	A983	C876	A802	G700	G619	A528	G424	A311	A222	A127	G2
G1360	G1360	A1275	G1171	C1075	C985	A877	U803	U702	G620	A529	G530	G319	C225	C128	G7
C1363	G1364	C1278	U1174	A1077	G989	G881	A804	G703	A621	C531	C433	U321	A226	U138	A10
A1365	A1366	G1279	A1175	C1078	A990	G882	C906	U704	G622	A532	U434	A320	A227	C119	C11
A1367	A1367	G1283	U1176	C1079	C991	C885	U807	G716	G623	A533	C435	A322	C228	C140	U12
G1368	G1368	A1287	C1178	U1083	G992	U886	G808	C717	G624	U534	C436	C323	C229	G141	G17
G1369	G1369	G1288	G1179	A1084	C994	U887	G809	A626	G625	G535	C440	G327	C239	A142	U18
C1370	C1370	U1181	U1180	A1085	C995	C888	U810	C719	A627	A538	U441	G328	C240	A149	A19
G1371	G1371	G1182	U1181	A1085	A996	C889	C812	U720	A627	A538	U442	G329	A241	U150	C20
U1372	U1372	U1183	U1183	A1088	G997	G891	U813	A722	A631	C542	C444	A330	G242	C151	A21
A1373	A1373	G1186	G1186	A1089	A1001	C892	C817	G723	A632	G543	A449	A340	G248	A155	G24
G1374	G1374	G1187	G1187	A1090	G1002	C893	U819	U724	A633	C544	U450	C341	C249	U156	U25
U1375	U1375	U1188	U1188	A1095	C1007	U894	A819	G725	A634	G545	U451	C342	C253	G157	G28
C1376	C1376	U1189	U1189	A1096	C1007	U895	G822	G726	A637	G546	U452	A344	C254	U158	A28
G1377	G1377	G1197	G1197	A1097	C1007	C896	U827	G727	U639	G549	C455	A345	A255	G159	G35
A1378	A1378	U1198	U1198	A1098	G1011	C897	A829	G728	C640	U554	C456	A346	A256	A160	G35
U1379	U1379	U1199	U1199	A1098	U1012	C898	U830	A730	A644	G555	A457	C353	A262	U161	U40
G1380	G1380	C1200	C1200	A1099	C1013	A899	U826	U741	U646	G560	U459	A354	C264	C164	C41
A1383	A1383	G1202	G1202	A1099	C1013	A910	U828	U742	U646	G561	A466	C357	A265	A165	G45
G1384	G1384	A1205	A1205	A1105	C1022	A917	U831	A743	G651	U562	C467	U358	G267	U174	G46
U1385	U1385	G1303	G1303	A1105	G1022	A918	U832	U744	A654	U563	C468	G361	C268	G175	A49
A1386	A1386	C1305	C1305	A1106	G1022	U919	U833	G745	A654	U563	C468	A371	C268	A176	U50
G1387	G1387	G1306	G1306	A1107	G1022	U920	A833	U746	U657	U566	A472	U372	G273	G177	G51
A1400	A1400	A1301	A1301	U1108	C1047	C921	G834	C747	U658	U567	C474	U373	C274	G177	G51
G1401	G1401	A1302	A1302	G1109	G1026	C922	A845	G748	U658	A572	C475	A374	C275	A181	G60
U1416	U1416	G1308	G1308	A1110	A1027	G923	U846	A749	G660	A573	G476	A374	U276	C184	A63
G1417	G1417	U1316	U1316	A1111	A1028	U932	U847	A750	A661	U574	A477	U374	C276	G185	A64
G1418	G1418	U1317	U1317	A1111	A1029	U932	C848	A751	A661	U574	A477	U374	C276	G185	A64
A1419	A1419	U1318	U1318	G1122	U1033	C935	A849	A752	G664	U576	A478	U374	C276	G185	A64
A1420	A1420	C1320	C1320	G1123	U1033	A936	U850	A753	G664	U576	A478	U374	C276	G185	A64
G1423	G1423	A1321	A1321	A1127	G1038	C937	C851	G760	G669	U577	C481	A374	C281	G188	U65
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C1428	C1428	A1327	A1327	G1130	U1046	G940	C854	G763	C672	U581	G489	A374	C281	G188	U65
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A1432	A1432	C1330	C1330	G1138	A1054	C946	C858	G776	A676	U588	G494	A374	C281	G188	U65
A1433	A1433	G1331	G1331	A1139	G1055	C947	U860	G776	A676	U588	G494	A374	C281	G188	U65
A1434	A1434	U1252	U1252	G1139	G1055	C948	A861	U779	C680	U594	G498	A374	C281	G188	U65
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G1436	G1436	G1341	G1341	U1141	C1057	G949	A863	A781	G682	U596	U499	A374	C281	G188	U65
U1437	U1437	G1256	G1256	U1141	C1057	G949	A863	A781	G682	U596	U499	A374	C281	G188	U65
U1438	U1438	C1257	C1257	A1142	U1060	G953	G864	A782	U683	G597	A504	A402	G301	C209	C96
A1439	A1439	U1258	U1258	A1142	U1061	C954	C865	A783	U686	A603	A505	U403	C302	C210	C97
U1440	U1440	G1259	G1259	C1153	G1062	C961	A866	A783	U686	A603	A505	U403	C302	C210	C97
U1441	U1441	A1260	A1260	U1155	G1062	C961	C867	G785	U688	U607	A508	U404	C303	C211	U102
A1442	A1442	U1268	U1268	A1156	U1065	U970	U870	A792	U689	C610	A509	U405	U304	A213	A118
U1443	U1443	A1269	A1269	G1157	U1066	G971	U870	A792	U689	C610	A509	U405	U304	A213	A118
G1444	G1444	G1353	G1353	U1157	U1066	A972	C873	A793	U694	C611	A510	U406	U306	G214	A119
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		G1355	G1355		G1071	G974	C874	C796	U694	C611	A510	U406	U306	G214	A119

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U2798	G2709	U2613	U2514	C2420	A2336	U2257	A2176	G2110	G2027	A1929	C1704	A1705	C1895	A1490
A2799	C2710	A2614	C2515	C2421	A2337	U2258	C2177	U2111	U2028	A1930	C1704	A1705	C1895	A1490
A2800	U2711	U2615	C2516	C2422	C2337	U2259	C2177	U2111	U2028	A1930	C1704	A1705	C1895	A1490
G2801	C2712	G2616	A2517	U2423	C2339	G2260	U2182	G2112	A2030	A1936	C1816	U1713	A1607	G1501
G2802	U2713	U2617	C2518	C2424	A2340	U2261	U2182	G2112	A2030	A1936	C1816	U1713	A1607	G1501
G2803	G2714	G2618	A2518	C2424	A2340	U2261	U2182	G2112	A2030	A1936	C1816	U1713	A1607	G1501
		C2619	G2529	C2427	U2343	C2264	C2186	G2116	G2034	A1939	U1729	G1612	U1506	U1506
U2807	U2720	C2619	A2530	G2428	U2344	U2265	U2187	A2117	G2035	U1940	U1729	G1612	U1506	U1506
G2808	A2721	C2620	A2531	G2429	G2345	U2266	U2188	U2118	C2036	C1941	U1729	G1612	U1506	U1506
A2809	C2722		G2532	U2430	A2346	A2267	U2189	A2119	C2037	C1942	U1729	G1612	U1506	U1506
C2810	C2723	G2623	G2533	U2431	C2347	A2268	G2190	G2120	U2038	C1942	U1729	G1612	U1506	U1506
G2811	U2724	G2624	U2534	A2432	U2348	G2269	A2191	G2121	G2038	C1942	U1729	G1612	U1506	U1506
G2812	G2725	G2625	A2534	A2433	G2349	G2269	U2192	U2122	G2040	C1942	U1729	G1612	U1506	U1506
	A2726	C2626	U2537	U2434	C2350	A2273	G2193	G2123	U2041	A1829	G1625	U1513	C1512	C1512
	A2726	C2626	U2537	U2434	C2350	A2273	G2193	G2123	U2041	A1829	G1625	U1513	C1512	C1512
C2815	A2727	G2627	C2538	A2435	G2351	A2274	U2194	G2124	A2042	C1830	G1626	U1513	C1512	C1512
G2816	U2728	U2628	G2538	U2435	G2351	A2274	U2194	G2124	A2042	C1830	G1626	U1513	C1512	C1512
U2817	C2731	C2630	G2543	C2440	G2355	G2277	U2195	A2126	C2044	U1956	G1628	A1515	A1515	A1515
U2818	G2544	U2636	G2544	U2441	G2356	G2277	U2195	A2126	C2044	U1956	G1628	A1515	A1515	A1515
C2819	G2545	U2637	G2545	C2442	G2357	A2278	A2198	G2128	G2046	C1962	A1744	G1524	G1524	G1524
A2820	U2546	C2633	G2546	C2443	G2357	A2278	A2198	G2128	G2046	C1962	A1744	G1524	G1524	G1524
A2821	G2547	U2638	G2547	C2444	G2357	A2278	A2198	G2128	G2046	C1962	A1744	G1524	G1524	G1524
G2822	C2737	C2636	U2552	U2448	A2358	A2281	C2200	C2129	C2047	C1965	A1745	A1525	A1525	A1525
A2823	U2738	U2637	G2553	U2449	A2359	G2282	C2203	U2130	G2048	A1966	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283	U2203	U2131	G2049	A1967	A1746	C1526	C1526	C1526
		U2638	G2553	U2449	C2360	G2283								



• Molecule 55: 5S ribosomal RNA

Chain 02: 63% 28% 8%



• Molecule 56: tRNA^{fMet}

Chain X: 58% 38% .



• Molecule 56: tRNA^{fMet}

Chain W: 69% 27% .



• Molecule 57: mRNA

Chain V: 63% 32% 5%



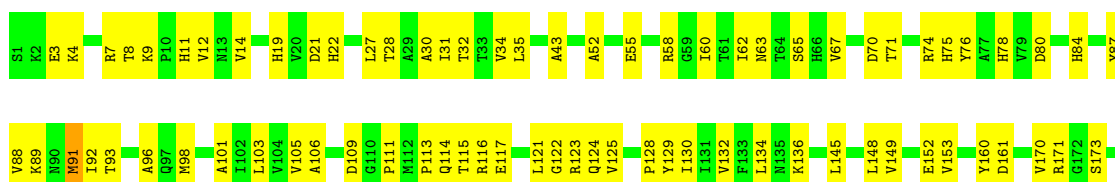
• Molecule 58: tRNA^{Lys}

Chain Y: 61% 25% 12% .



• Molecule 59: Elongation factor Tu 2

Chain Z: 49% 49% ..



A182	A183	E260	F261	E262	K263	L264	L265	D266	E267	G268	R269	A270	G271	E272	N273	V276	R279	E287	R288	G289	Q290	V291	L292	A293	K294	P295	G296	T297	L298	H301	T302	K303	F304	E305	S306	E307	V308	Y309	I310	L311	S312	K313	D314	E315	R318	H319	T320	P321	F322	F323	K324	G325	Q329	F330	Y331
E184	E185	A186	A187	I188	I189	E190	L191	A192	G193	F194	L195	D196	S197	Y198	I199	I206	D207	K208	P209	F210	L211	L212	P213	I214	E215	E216	T217	I220	S221	G222	R223	V226	V227	T228	V231	E232	I235	I236	K237	V242	V245	G246	I247	T250	T256	G257	V258	E259							
F332	R333	T334	T335	D336	V337	T338	G339	T340	I341	E342	L343	F344	E345	G346	V347	E348	M349	V350	M351	P352	I356	K357	M358	V359	V360	T361	L362	I363	H364	P365	I366	A367	M368	D369	D370	G371	L372	R373	F374	A375	I376	R377	T382	V383	G384	A385	G386	V387	V388	A389	K390	V391	L392		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6910	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, FME, U8U

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	04	0.30	0/2122	0.59	0/2852
2	05	0.32	0/1586	0.57	0/2134
3	06	0.32	0/1571	0.59	0/2113
4	07	0.35	0/1435	0.58	0/1926
5	08	0.32	0/1343	0.62	0/1816
6	09	0.35	0/1122	0.62	1/1515 (0.1%)
7	10	0.40	0/1002	0.73	0/1350
8	11	0.37	0/1046	0.66	0/1410
9	12	0.33	0/1152	0.59	0/1551
10	13	0.31	0/948	0.58	0/1268
11	14	0.32	0/1054	0.64	0/1403
12	15	0.33	0/1093	0.59	0/1460
13	16	0.32	0/974	0.55	0/1301
14	17	0.31	0/902	0.56	0/1209
15	18	0.32	0/929	0.60	0/1242
16	19	0.33	0/960	0.52	0/1278
17	20	0.34	0/829	0.65	1/1107 (0.1%)
18	21	0.30	0/864	0.59	0/1156
19	22	0.32	0/745	0.58	0/994
20	23	0.33	0/788	0.62	0/1051
21	24	0.35	0/766	0.59	0/1025
22	25	0.33	0/582	0.54	0/769
23	26	0.31	0/635	0.55	0/848
24	27	0.32	0/510	0.60	0/677
25	28	0.30	0/453	0.58	0/605
26	29	0.35	0/532	0.64	0/709
27	30	0.32	0/450	0.56	0/599
28	31	0.35	0/417	0.57	0/554
29	32	0.33	0/380	0.60	0/498
30	33	0.31	0/513	0.58	0/676
31	34	0.32	0/303	0.60	0/397
32	B	0.36	0/1736	0.63	0/2338

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.34	0/1652	0.54	0/2225
34	D	0.34	0/1665	0.58	0/2227
35	E	0.33	0/1170	0.65	1/1573 (0.1%)
36	F	0.35	0/836	0.64	0/1128
37	G	0.32	0/1196	0.57	0/1602
38	H	0.32	0/989	0.61	0/1326
39	I	0.34	0/1034	0.64	0/1375
40	J	0.34	0/797	0.65	0/1077
41	K	0.33	0/886	0.59	0/1195
42	L	0.32	0/969	0.66	1/1300 (0.1%)
43	M	0.31	0/893	0.59	0/1193
44	N	0.33	0/817	0.56	0/1088
45	O	0.31	0/722	0.53	0/964
46	P	0.33	0/659	0.58	0/884
47	Q	0.34	0/658	0.71	0/881
48	R	0.36	0/545	0.58	0/731
49	S	0.35	0/653	0.63	0/877
50	T	0.31	0/671	0.53	0/888
51	U	0.40	0/551	0.64	0/728
52	03	0.38	0/1034	0.67	0/1387
53	A	0.39	0/36963	0.69	10/57662 (0.0%)
54	01	0.39	0/69796	0.68	3/108888 (0.0%)
55	02	0.41	0/2872	0.68	1/4479 (0.0%)
56	W	0.44	0/1832	0.68	0/2855
56	X	0.48	0/1832	0.68	0/2855
57	V	0.41	0/471	0.63	0/735
58	Y	0.55	1/1780 (0.1%)	0.74	2/2767 (0.1%)
59	Z	0.38	0/3085	0.67	0/4173
All	All	0.38	1/166770 (0.0%)	0.66	20/248894 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	Y	1	G	OP3-P	-7.06	1.52	1.61

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	01	1178	C	N1-C1'-C2'	8.80	125.44	114.00
53	A	1301	U	N1-C1'-C2'	6.29	122.18	114.00
53	A	960	U	N1-C1'-C2'	6.09	121.92	114.00
17	20	50	GLY	N-CA-C	-5.95	98.23	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	A	1256	A	N9-C1'-C2'	5.87	121.63	114.00

There are no chirality outliers.

There are no planarity outliers.

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	04	2083	0	2157	88	0
2	05	1565	0	1616	53	0
3	06	1552	0	1619	48	0
4	07	1411	0	1447	59	0
5	08	1323	0	1374	55	0
6	09	1111	0	1148	52	0
7	10	989	0	1025	60	0
8	11	1032	0	1088	74	0
9	12	1129	0	1162	44	0
10	13	939	0	1012	39	0
11	14	1045	0	1117	46	0
12	15	1074	0	1157	39	0
13	16	961	0	1000	32	0
14	17	892	0	923	34	0
15	18	917	0	965	43	0
16	19	947	0	1022	34	0
17	20	816	0	839	38	0
18	21	857	0	922	36	0
19	22	739	0	807	26	0
20	23	780	0	834	40	0
21	24	753	0	780	25	0
22	25	575	0	592	24	0
23	26	625	0	655	31	0
24	27	509	0	543	23	0
25	28	449	0	491	22	0
26	29	523	0	524	11	0
27	30	444	0	461	24	0
28	31	410	0	440	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	32	377	0	418	15	0
30	33	504	0	574	19	0
31	34	302	0	343	9	0
32	B	1705	0	1732	77	0
33	C	1625	0	1699	58	0
34	D	1643	0	1710	55	0
35	E	1157	0	1199	53	0
36	F	818	0	808	44	0
37	G	1182	0	1240	56	0
38	H	979	0	1034	38	0
39	I	1022	0	1070	57	0
40	J	787	0	828	52	0
41	K	870	0	878	33	0
42	L	955	0	1019	48	0
43	M	884	0	944	42	0
44	N	805	0	847	47	0
45	O	714	0	737	17	0
46	P	649	0	666	33	0
47	Q	649	0	691	32	0
48	R	536	0	552	19	0
49	S	638	0	665	32	0
50	T	665	0	714	30	0
51	U	545	0	579	26	0
52	03	1027	0	1092	58	0
53	A	33012	0	16618	489	0
54	01	62317	0	31346	907	0
55	02	2568	0	1303	42	0
56	W	1640	0	836	14	0
56	X	1640	0	837	20	0
57	V	417	0	209	6	0
58	Y	1618	0	820	23	0
59	Z	3029	0	3043	172	0
60	W	10	0	10	0	0
61	Y	9	0	12	4	0
62	Z	32	0	14	3	0
All	All	153780	0	104807	3324	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 13.

The worst 5 of 3324 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)
54:01:45:G:H5''	54:01:46:G:H5'	1.35	1.07
54:01:1645:G:H5''	54:01:1646:C:H5'	1.42	1.00
7:10:118:ILE:HG23	7:10:119:PRO:HD3	1.43	0.99
4:07:15:LEU:HD13	4:07:28:PRO:HD2	1.41	0.98
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.44	0.96

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
1	04	269/271 (99%)	227 (84%)	35 (13%)	7 (3%)	5	35
2	05	207/209 (99%)	171 (83%)	31 (15%)	5 (2%)	6	37
3	06	199/201 (99%)	172 (86%)	24 (12%)	3 (2%)	10	45
4	07	175/177 (99%)	150 (86%)	22 (13%)	3 (2%)	9	43
5	08	174/176 (99%)	151 (87%)	20 (12%)	3 (2%)	9	43
6	09	147/149 (99%)	119 (81%)	26 (18%)	2 (1%)	11	46
7	10	129/131 (98%)	82 (64%)	37 (29%)	10 (8%)	1	15
8	11	139/141 (99%)	109 (78%)	24 (17%)	6 (4%)	2	26
9	12	140/142 (99%)	123 (88%)	15 (11%)	2 (1%)	11	46
10	13	120/122 (98%)	94 (78%)	18 (15%)	8 (7%)	1	18
11	14	141/143 (99%)	110 (78%)	24 (17%)	7 (5%)	2	23
12	15	134/136 (98%)	112 (84%)	19 (14%)	3 (2%)	6	38
13	16	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	19	57
14	17	114/116 (98%)	98 (86%)	13 (11%)	3 (3%)	5	35
15	18	112/114 (98%)	91 (81%)	21 (19%)	0	100	100
16	19	115/117 (98%)	105 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	20	101/103 (98%)	83 (82%)	17 (17%)	1 (1%)	15	52
18	21	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	8	41
19	22	91/93 (98%)	64 (70%)	24 (26%)	3 (3%)	4	31
20	23	100/102 (98%)	78 (78%)	18 (18%)	4 (4%)	3	27
21	24	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
22	25	73/75 (97%)	62 (85%)	9 (12%)	2 (3%)	5	35
23	26	75/77 (97%)	70 (93%)	4 (5%)	1 (1%)	12	48
24	27	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	28	56/58 (97%)	51 (91%)	4 (7%)	1 (2%)	8	42
26	29	64/66 (97%)	50 (78%)	11 (17%)	3 (5%)	2	24
27	30	54/56 (96%)	47 (87%)	6 (11%)	1 (2%)	8	41
28	31	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	32	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	33	62/64 (97%)	49 (79%)	10 (16%)	3 (5%)	2	24
31	34	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	5	34
32	B	216/218 (99%)	177 (82%)	30 (14%)	9 (4%)	3	26
33	C	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
34	D	203/205 (99%)	169 (83%)	26 (13%)	8 (4%)	3	28
35	E	155/157 (99%)	118 (76%)	27 (17%)	10 (6%)	1	19
36	F	98/100 (98%)	75 (76%)	17 (17%)	6 (6%)	1	20
37	G	149/151 (99%)	124 (83%)	20 (13%)	5 (3%)	3	31
38	H	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	9	44
39	I	125/127 (98%)	92 (74%)	29 (23%)	4 (3%)	4	32
40	J	96/98 (98%)	74 (77%)	11 (12%)	11 (12%)	0	7
41	K	114/116 (98%)	89 (78%)	20 (18%)	5 (4%)	2	25
42	L	121/123 (98%)	94 (78%)	19 (16%)	8 (7%)	1	19
43	M	112/114 (98%)	91 (81%)	17 (15%)	4 (4%)	3	29
44	N	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	7	40
45	O	86/88 (98%)	71 (83%)	13 (15%)	2 (2%)	6	38
46	P	80/82 (98%)	64 (80%)	13 (16%)	3 (4%)	3	28
47	Q	78/80 (98%)	57 (73%)	15 (19%)	6 (8%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	R	63/65 (97%)	50 (79%)	8 (13%)	5 (8%)	1	15
49	S	77/79 (98%)	62 (80%)	12 (16%)	3 (4%)	3	28
50	T	83/85 (98%)	79 (95%)	2 (2%)	2 (2%)	6	37
51	U	63/65 (97%)	39 (62%)	19 (30%)	5 (8%)	1	15
52	03	130/223 (58%)	112 (86%)	15 (12%)	3 (2%)	6	38
59	Z	390/392 (100%)	330 (85%)	53 (14%)	7 (2%)	8	42
All	All	6366/6563 (97%)	5260 (83%)	911 (14%)	195 (3%)	7	32

5 of 195 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	121	ALA
1	04	233	GLY
2	05	170	VAL
3	06	83	VAL
4	07	175	PRO

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	
1	04	216/216 (100%)	211 (98%)	5 (2%)	50	71
2	05	164/164 (100%)	163 (99%)	1 (1%)	86	91
3	06	165/165 (100%)	163 (99%)	2 (1%)	71	83
4	07	148/148 (100%)	145 (98%)	3 (2%)	55	74
5	08	137/137 (100%)	137 (100%)	0	100	100
6	09	114/114 (100%)	113 (99%)	1 (1%)	78	87
7	10	100/100 (100%)	95 (95%)	5 (5%)	24	53
8	11	109/109 (100%)	108 (99%)	1 (1%)	78	87
9	12	116/116 (100%)	116 (100%)	0	100	100
10	13	103/103 (100%)	101 (98%)	2 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	14	102/102 (100%)	102 (100%)	0	100	100
12	15	109/109 (100%)	107 (98%)	2 (2%)	59	77
13	16	100/100 (100%)	98 (98%)	2 (2%)	55	74
14	17	86/86 (100%)	85 (99%)	1 (1%)	71	83
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	87 (98%)	2 (2%)	52	71
17	20	84/84 (100%)	84 (100%)	0	100	100
18	21	93/93 (100%)	91 (98%)	2 (2%)	52	71
19	22	80/80 (100%)	78 (98%)	2 (2%)	47	69
20	23	83/83 (100%)	81 (98%)	2 (2%)	49	69
21	24	78/78 (100%)	77 (99%)	1 (1%)	69	82
22	25	57/57 (100%)	56 (98%)	1 (2%)	59	77
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	55 (100%)	0	100	100
25	28	48/48 (100%)	47 (98%)	1 (2%)	53	73
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	46 (98%)	1 (2%)	53	73
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	50 (98%)	1 (2%)	55	74
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	180/180 (100%)	170 (94%)	10 (6%)	21	51
33	C	170/170 (100%)	170 (100%)	0	100	100
34	D	172/172 (100%)	166 (96%)	6 (4%)	36	62
35	E	119/119 (100%)	115 (97%)	4 (3%)	37	62
36	F	87/87 (100%)	87 (100%)	0	100	100
37	G	124/124 (100%)	123 (99%)	1 (1%)	81	89
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	103 (98%)	2 (2%)	57	75
40	J	86/86 (100%)	84 (98%)	2 (2%)	50	71
41	K	89/89 (100%)	85 (96%)	4 (4%)	27	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	L	103/103 (100%)	100 (97%)	3 (3%)	42	65
43	M	92/92 (100%)	89 (97%)	3 (3%)	38	63
44	N	83/83 (100%)	83 (100%)	0	100	100
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	65 (100%)	0	100	100
47	Q	74/74 (100%)	73 (99%)	1 (1%)	67	81
48	R	56/56 (100%)	52 (93%)	4 (7%)	14	44
49	S	70/70 (100%)	70 (100%)	0	100	100
50	T	65/65 (100%)	64 (98%)	1 (2%)	65	80
51	U	55/55 (100%)	53 (96%)	2 (4%)	35	61
52	03	110/174 (63%)	105 (96%)	5 (4%)	27	56
59	Z	324/325 (100%)	315 (97%)	9 (3%)	43	66
All	All	5285/5350 (99%)	5190 (98%)	95 (2%)	61	77

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	E	163	ILE
43	M	47	LEU
39	I	44	ARG
41	K	117	HIS
48	R	21	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
33	C	122	GLN
37	G	129	ASN
33	C	184	ASN
35	E	60	GLN
39	I	125	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	161 (10%)	7 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
54	01	2902/2903 (99%)	353 (12%)	13 (0%)
55	02	119/120 (99%)	10 (8%)	2 (1%)
56	W	76/77 (98%)	8 (10%)	0
56	X	76/77 (98%)	12 (15%)	1 (1%)
57	V	18/19 (94%)	3 (16%)	0
58	Y	74/76 (97%)	14 (18%)	3 (4%)
All	All	4803/4811 (99%)	561 (11%)	26 (0%)

5 of 561 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	7	A
53	A	9	G
53	A	22	G
53	A	32	A

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	01	1940	U
54	01	2326	C
58	Y	19	G
54	01	2296	U
54	01	2391	G

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

1 non-standard protein/DNA/RNA residue is 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
58	U8U	Y	34	58	19,24,25	1.41	3 (15%)	23,34,37	1.20	2 (8%)

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
58	U8U	Y	34	58	-	3/9/28/29	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	Y	34	U8U	C6-N1	4.17	1.45	1.38
58	Y	34	U8U	C4-C5	2.43	1.50	1.45
58	Y	34	U8U	C2-N3	2.29	1.42	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Y	34	U8U	C5-C6-N1	2.66	126.48	122.91
58	Y	34	U8U	C1'-N1-C6	-2.17	117.52	121.12

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	Y	34	U8U	N-C-C5-C4
58	Y	34	U8U	C2'-C1'-N1-C2
58	Y	34	U8U	N-C-C5-C6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Y	34	U8U	1	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

3 ligands 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$
62	GCP	Z	401	-	27,34,34	1.98	7 (25%)	34,54,54	3.98	17 (50%)
60	FME	W	101	-	8,9,10	0.85	0	7,9,11	1.17	1 (14%)
61	LYS	Y	101	58	7,8,9	0.70	0	3,8,10	0.19	0

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
62	GCP	Z	401	-	-	8/15/38/38	0/3/3/3
60	FME	W	101	-	-	4/7/9/11	-
61	LYS	Y	101	58	-	3/6/7/9	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Z	401	GCP	PB-O3A	-4.91	1.52	1.58
62	Z	401	GCP	O4'-C1'	4.66	1.47	1.41
62	Z	401	GCP	C2'-C1'	3.31	1.58	1.53
62	Z	401	GCP	C5-C6	3.30	1.47	1.41
62	Z	401	GCP	C6-N1	2.85	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Z	401	GCP	C1'-N9-C4	14.24	151.65	126.64
62	Z	401	GCP	C5-C6-N1	-8.82	111.37	123.43
62	Z	401	GCP	O1G-PG-C3B	-7.57	94.92	111.24
62	Z	401	GCP	C2-N1-C6	6.64	126.48	115.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Z	401	GCP	O4'-C1'-C2'	-4.55	100.28	106.93

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

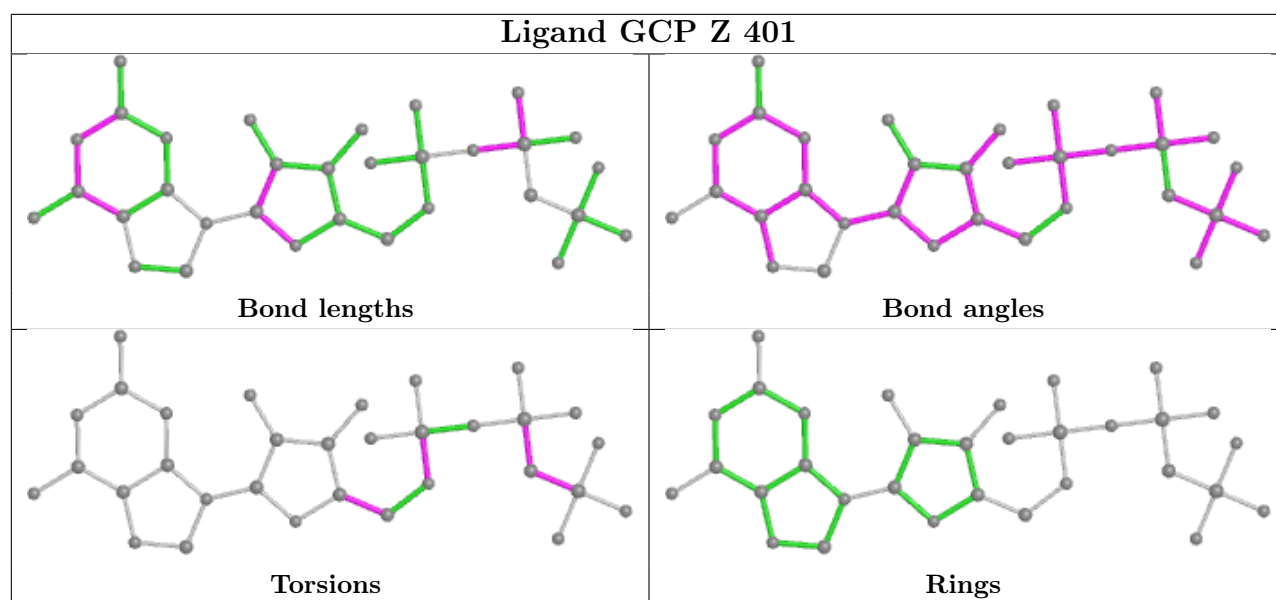
Mol	Chain	Res	Type	Atoms
60	W	101	FME	O1-CN-N-CA
60	W	101	FME	C-CA-CB-CG
60	W	101	FME	O-C-CA-CB
61	Y	101	LYS	N-CA-CB-CG
61	Y	101	LYS	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	Z	401	GCP	3	0
61	Y	101	LYS	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8619. 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 surface views

This section was not generated.

6.5 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.