



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 10:00 am GMT

PDB ID : 4V5N
EMDB ID : EMD-1799
Title : tRNA translocation on the 70S ribosome: the post- translocational translocation intermediate TI(POST)
Authors : Ratje, A.H.; Loerke, J.; Mikolajka, A.; Bruenner, M.; Hildebrand, P.W.; Starosta, A.L.; Doenhoefer, A.; Connell, S.R.; Fucini, P.; Mielke, T.; Whitford, P.C.; Onuchic, J.N.; Yu, Y.; Sanbonmatsu, K.Y.; Hartmann, R.K.; Penczek, P.A.; Wilson, D.N.; Spahn, C.M.T.
Deposited on : 2010-10-21
Resolution : 7.60 Å(reported)
Based on initial models : 2WRI, 2WRJ

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:

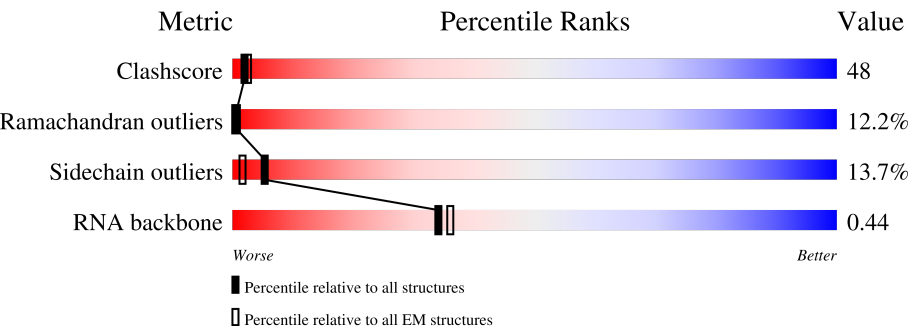
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.60 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.




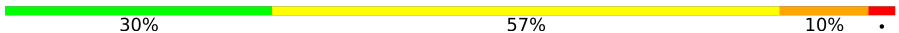
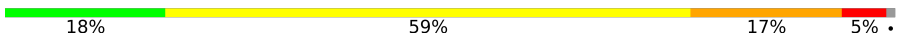


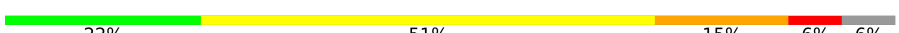
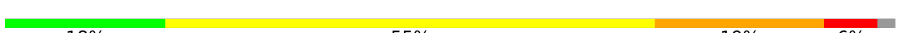




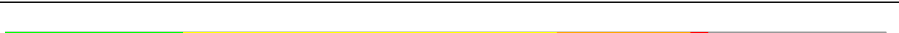



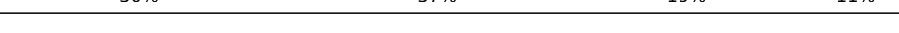


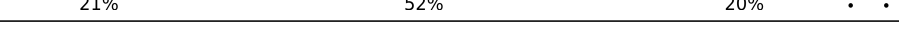






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	AA	1522	<div><div>22%58%18%</div></div>
2	AB	256	<div><div>23%49%14%5%9%</div></div>
3	AC	239	<div><div>24%44%14%5%14%</div></div>
4	AD	209	<div><div>30%49%16%5%</div></div>
5	AE	162	<div><div>31%44%14%7%</div></div>
6	AF	101	<div><div>33%50%15%</div></div>

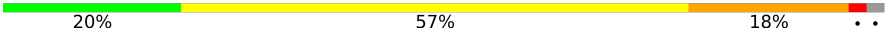
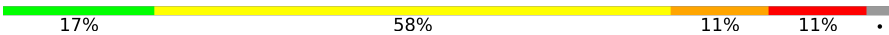
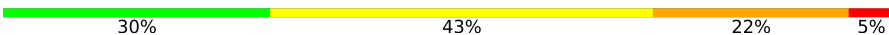



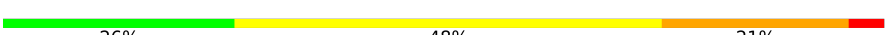
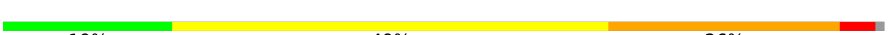



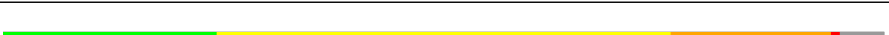

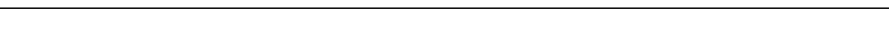
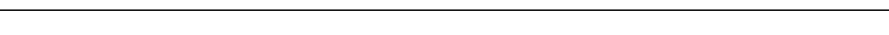
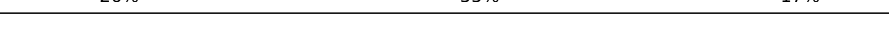

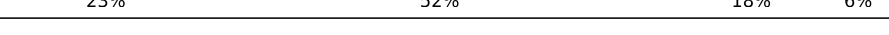
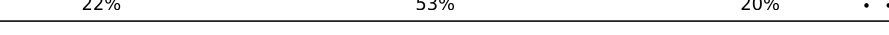


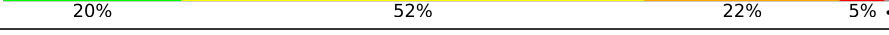
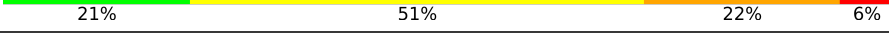
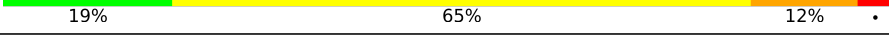
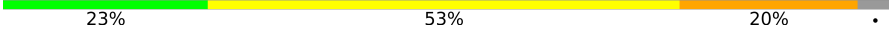
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Mol	Chain	Length	Quality of chain
7	AG	156	
8	AH	138	
9	AI	128	
10	AJ	105	
11	AK	129	
12	AL	132	
13	AM	126	
14	AN	61	
15	AO	89	
16	AP	88	
17	AQ	105	
18	AR	88	
19	AS	93	
20	AT	106	
21	AU	27	
22	AV	77	
23	AX	11	
24	AY	691	
25	B0	85	
26	B1	98	
27	B2	72	
28	B3	60	
29	B4	71	
30	B5	60	
31	B6	54	

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Mol	Chain	Length	Quality of chain
32	B7	49	
33	B8	65	
34	B9	37	
35	BA	2915	
36	BB	122	
37	BC	229	
38	BD	276	
39	BE	206	
40	BF	210	
41	BG	182	
42	BH	180	
43	BK	147	
44	BL	121	
45	BN	140	
46	BO	122	
47	BP	150	
48	BQ	141	
49	BR	118	
50	BS	112	
51	BT	146	
52	BU	118	
53	BV	101	
54	BW	113	
55	BX	96	
56	BY	110	

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Mol	Chain	Length	Quality of chain
57	BZ	206	<div><div></div><div>20%</div><div>43%</div><div>19%</div><div>7%</div><div>11%</div></div>

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 152777 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 16S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1504	Total	C	N	O	P	0	0
			32329	14390	5992	10444	1503		

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			794	499	156	138	1		

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	124	Total	C	N	O	S	0	0
			987	611	205	169	2		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14 TYPE Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	70	Total	C	N	O		0	0
			574	367	112	95			

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	78	Total	C	N	O	S	0	0
			629	403	114	110	2		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a RNA chain called TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	11	Total	C	N	O	P	0	0
			230	105	41	74	10		

- Molecule 24 is a protein called ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	666	Total	C	N	O	S	0	0
			5214	3316	892	988	18		

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B0	84	Total	C	N	O	S	0	0
			662	410	140	111	1		

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B1	93	Total	C	N	O	S	0	0
			731	460	145	125	1		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B2	71	Total	C	N	O	S	0	0
			598	370	121	106	1		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B3	59	Total	C	N	O	S	0	0
			467	298	90	78	1		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B4	57	Total	C	N	O	S	0	0
			450	285	77	83	5		

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B5	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B6	50	Total	C	N	O	S	0	0
			433	270	88	71	4		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B7	48	Total	C	N	O	S	0	0
			418	257	104	55	2		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B8	63	Total	C	N	O	S	0	0
			507	326	101	78	2		

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B9	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	2901	Total	C	N	O	P	0	0
			62474	27806	11681	20087	2900		

- Molecule 36 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	228	Total	C	N	O	S	0	0
			1742	1101	319	319	3		

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	275	Total	C	N	O	S	0	0
			2145	1353	428	361	3		

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	204	Total	C	N	O	S	0	0
			1563	988	299	270	6		

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	207	Total	C	N	O	S	0	0
			1623	1035	303	282	3		

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	166	Total	C	N	O	S	0	0
			1268	803	237	227	1		

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BK	139	Total	C	N	O	S	0	0
			1025	653	181	186	5		

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L7/L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BL	67	Total	C	N	O	0	0
			477	301	81	95		

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BN	138	Total	C	N	O	S	0	0
			1104	712	206	182	4		

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BO	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BP	146	Total	C	N	O	S	0	0
			1114	692	227	193	2		

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BQ	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	BR	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 50 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BS	98	Total	C	N	O	0	0
			770	486	154	130		

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BT	137	Total	C	N	O	S	0	0
			1141	710	234	196	1		

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BU	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BV	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BW	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	BX	92	Total	C	N	O	0	0
			725	471	131	123		

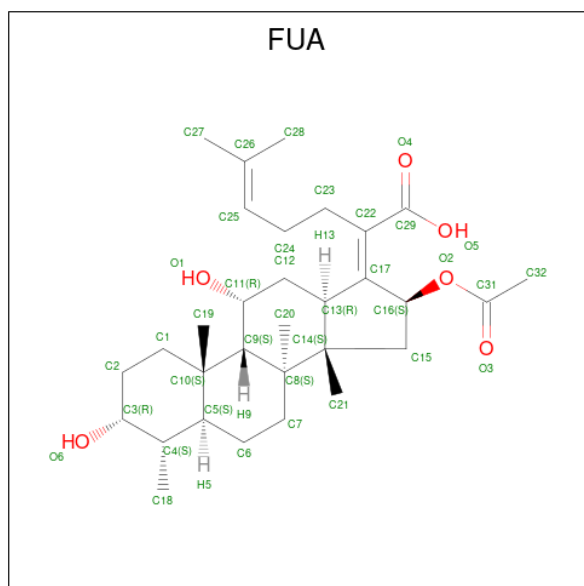
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BY	106	Total	C	N	O	S	0	0
			810	520	154	131	5		

- Molecule 57 is a protein called 50S RIBOSOMAL PROTEIN L25.

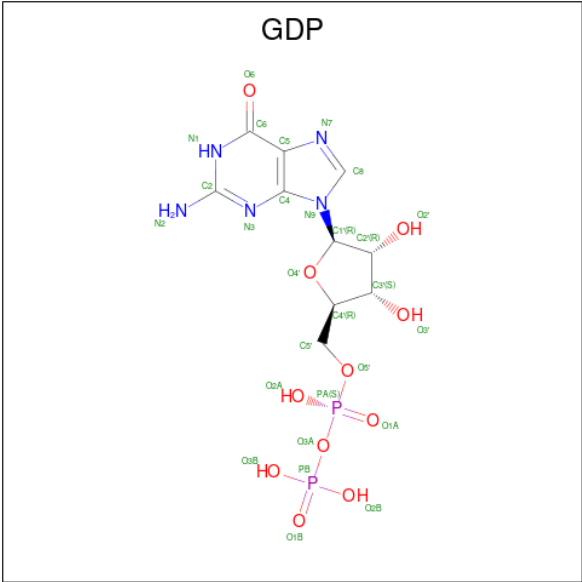
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	184	Total	C	N	O	S	0	0
			1467	936	261	268	2		

- Molecule 58 is FUSIDIC ACID (three-letter code: FUA) (formula: $C_{31}H_{48}O_6$).



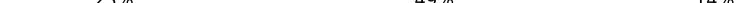
Mol	Chain	Residues	Atoms			AltConf
58	AY	1	Total	C	O	0
			37	31	6	

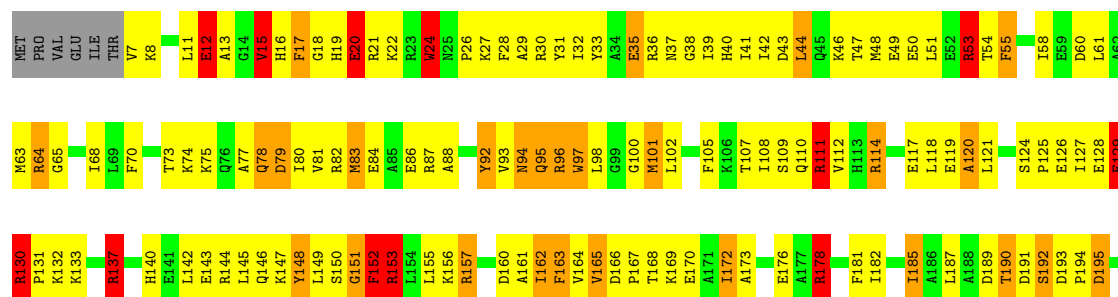
- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
59	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	

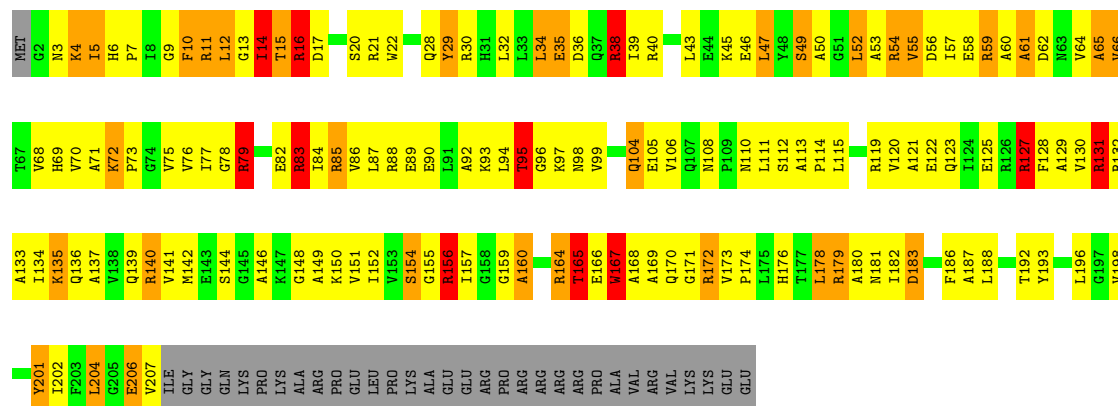
- Molecule 2: 30S RIBOSOMAL PROTEIN S2

Chain AB:  23% 49% 14% 5% 9%

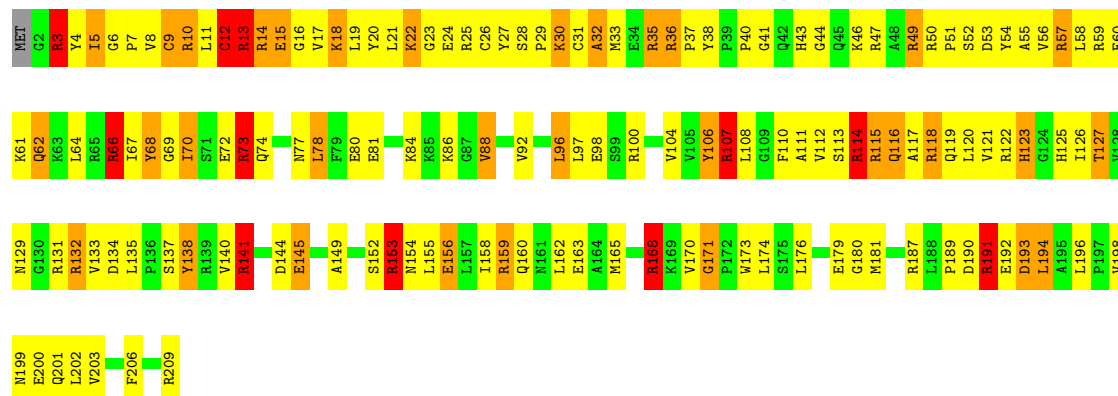




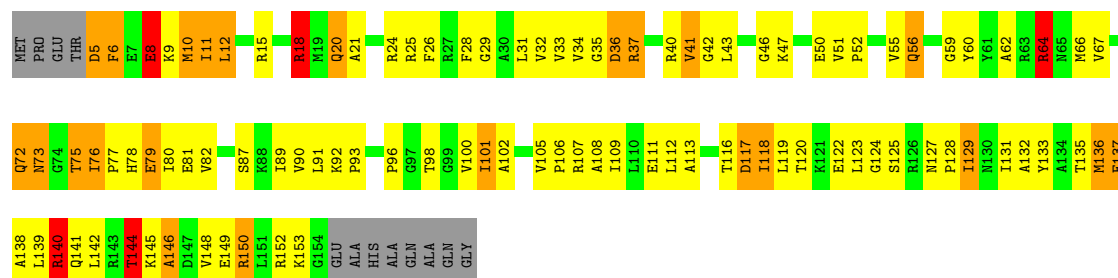
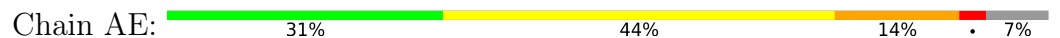
• Molecule 3: 30S RIBOSOMAL PROTEIN S3



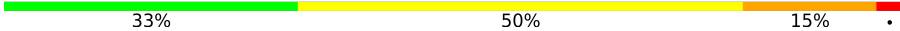
• Molecule 4: 30S RIBOSOMAL PROTEIN S4

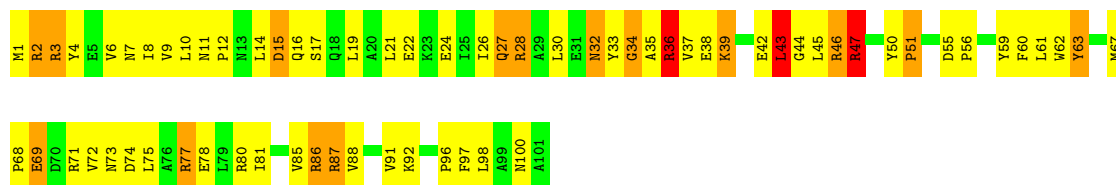


• Molecule 5: 30S RIBOSOMAL PROTEIN S5




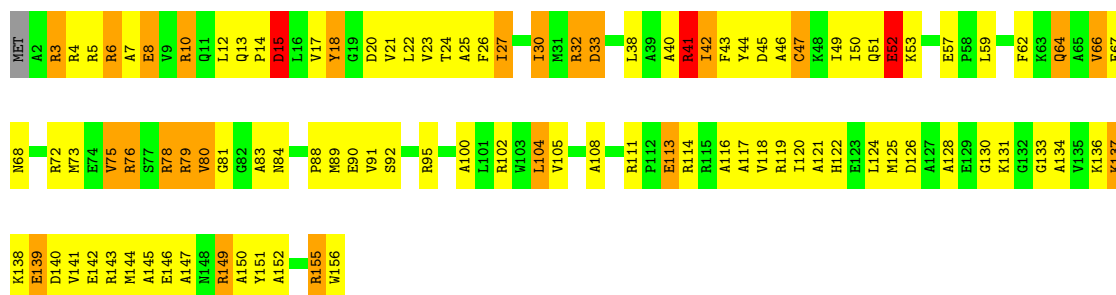
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain AF:  33% 50% 15% .



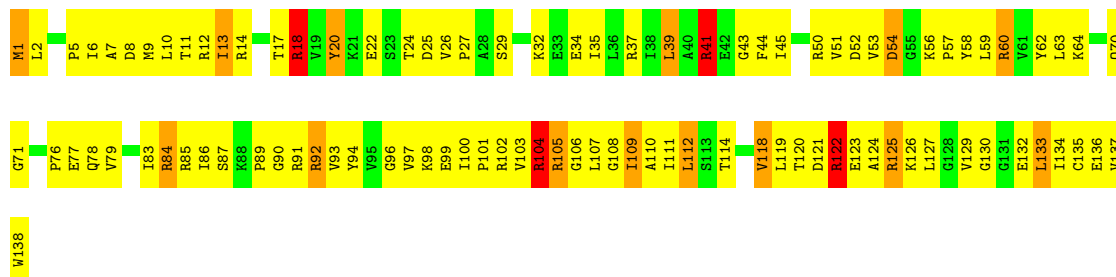
• Molecule 7: 30S RIBOSOMAL PROTEIN S7

Chain AG:  34% 48% 15% ..



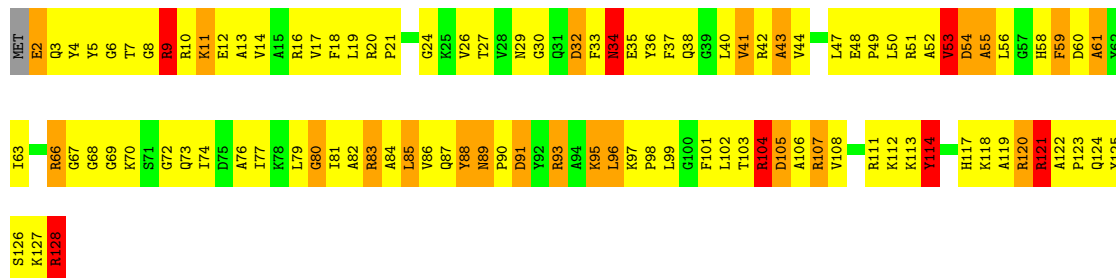
• Molecule 8: 30S RIBOSOMAL PROTEIN S8

Chain AH:  30% 57% 10% .




• Molecule 9: 30S RIBOSOMAL PROTEIN S9

Chain AI:  18% 59% 17% 5% .



• Molecule 10: 30S RIBOSOMAL PROTEIN S10

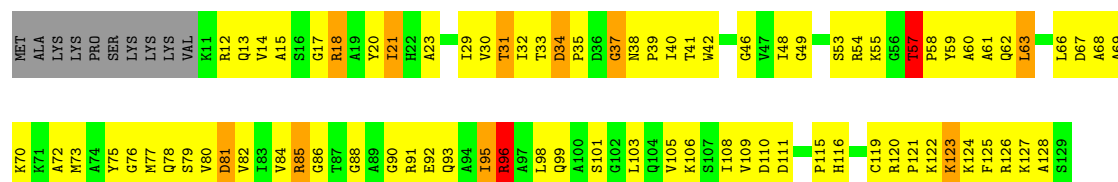
Chain AJ:  11% 54% 22% 6% 7%





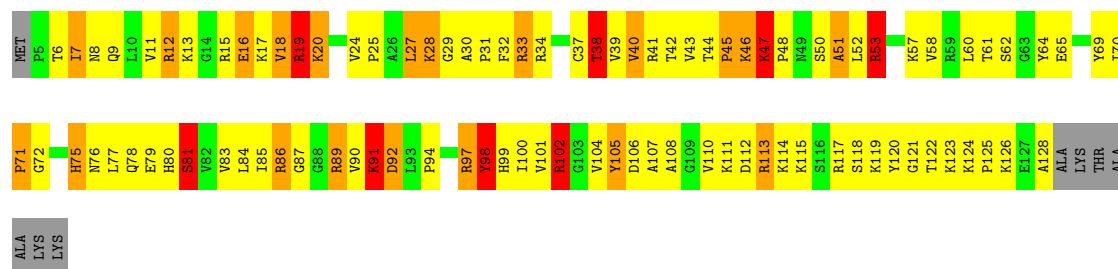
- Molecule 11: 30S RIBOSOMAL PROTEIN S11

Chain AK: 29% 54% 8% • 8%



- Molecule 12: 30S RIBOSOMAL PROTEIN S12

Chain AL: 22% 51% 15% 6% 6%



- Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain AM: 18% 55% 19% 6% •



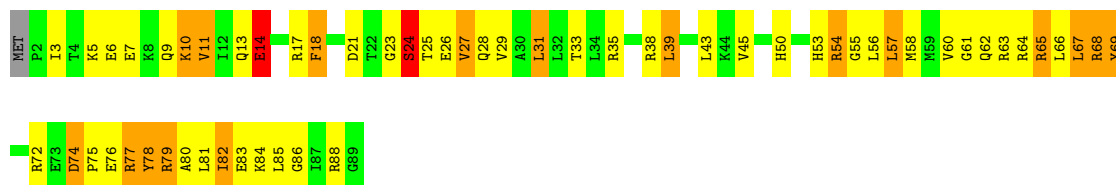
- Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z

Chain AN: 34% 44% 10% 10% •




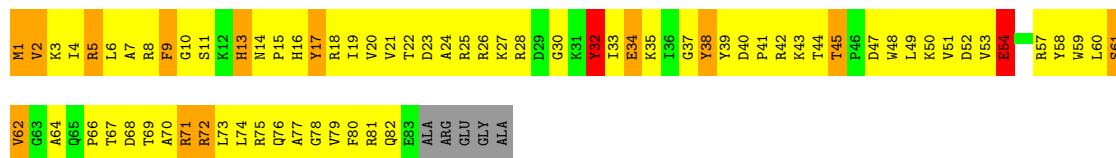
- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain AO:  34% 44% 19% ..



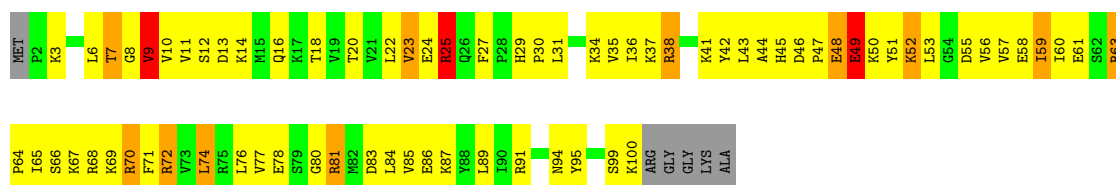
• Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain AP:  11% 66% 15% • 6%




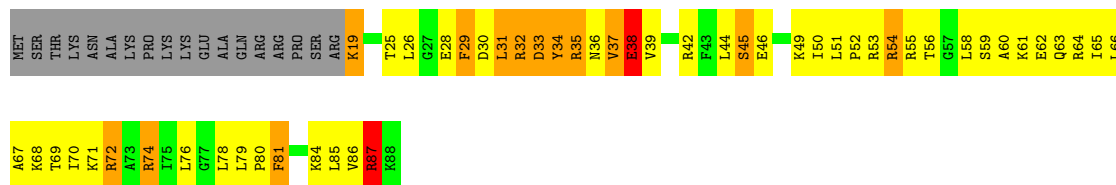
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ:  25% 56% 10% • 6%




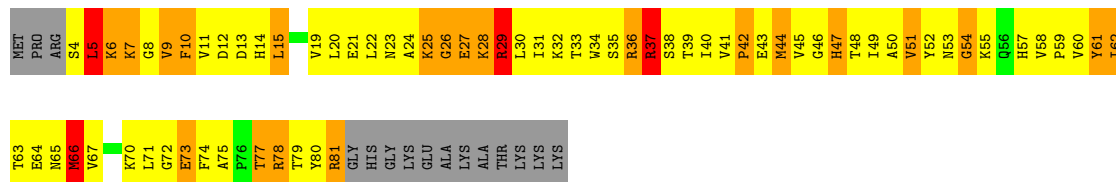
• Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR:  20% 42% 15% • 20%

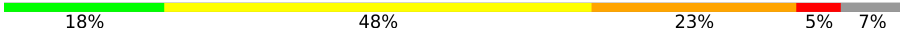


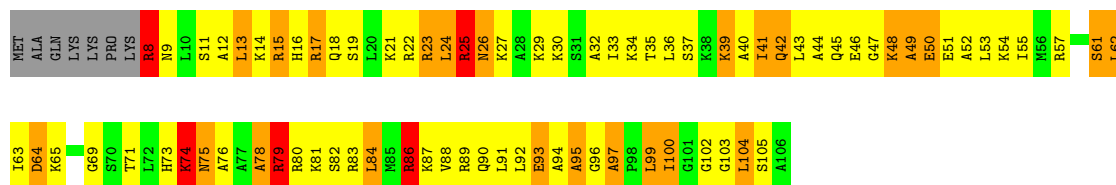
• Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain AS:  8% 49% 23% • 16%




• Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain AT: 



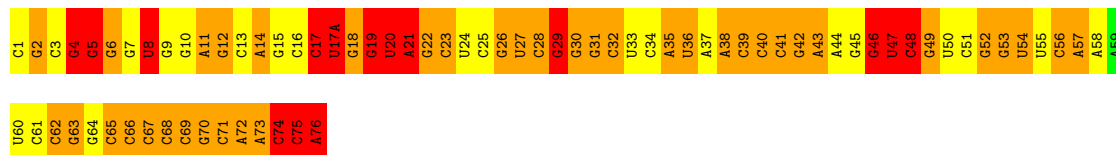
• Molecule 21: 30S RIBOSOMAL PROTEIN THX

Chain AU: 



• Molecule 22: TRNA

Chain AV: 



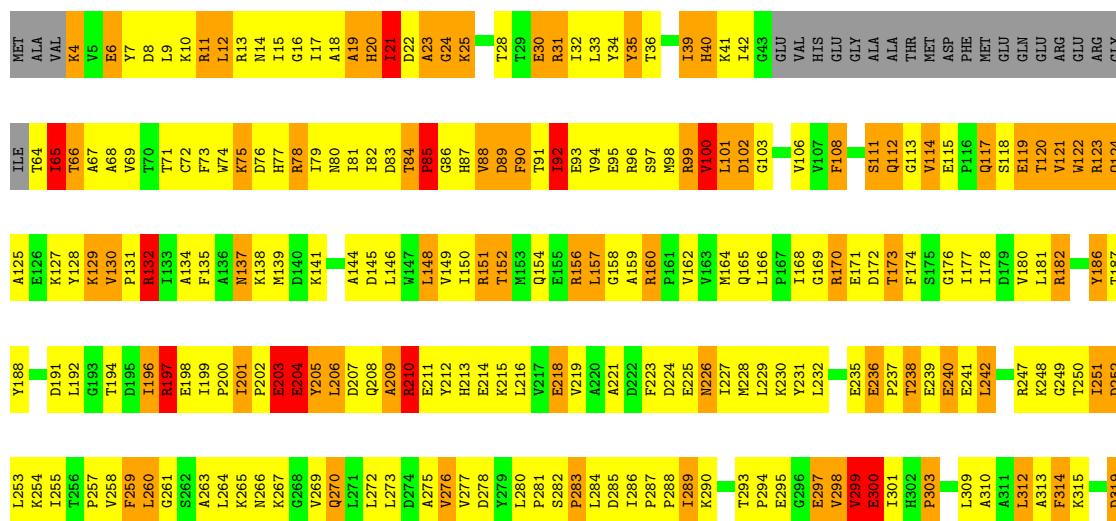
• Molecule 23: MRNA

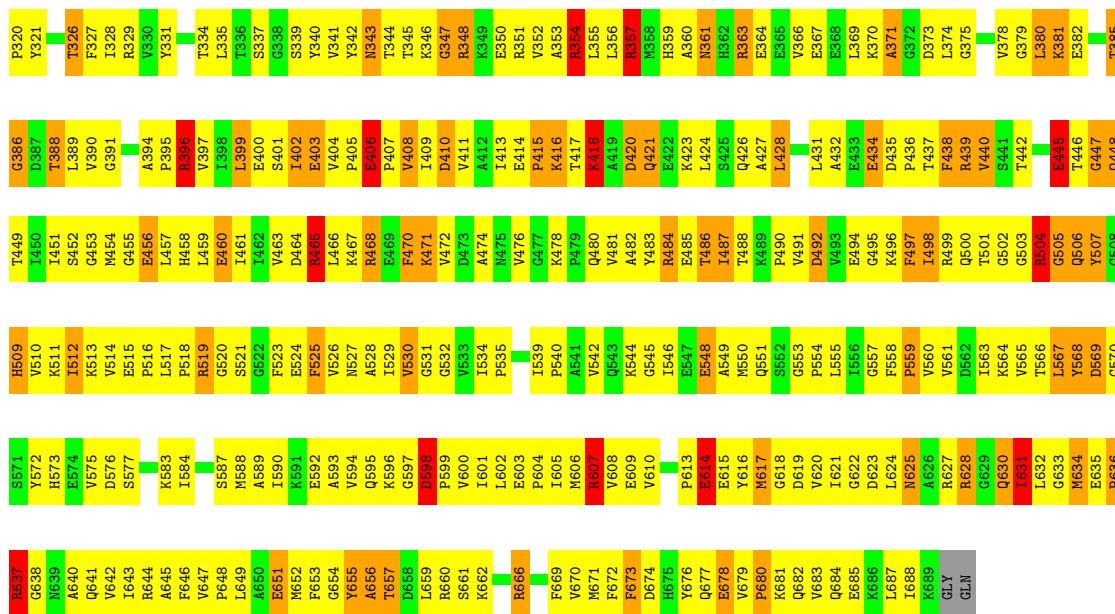
Chain AX: 



• Molecule 24: ELONGATION FACTOR G

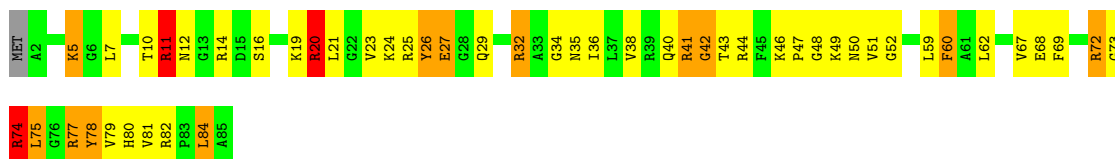
Chain AY: 





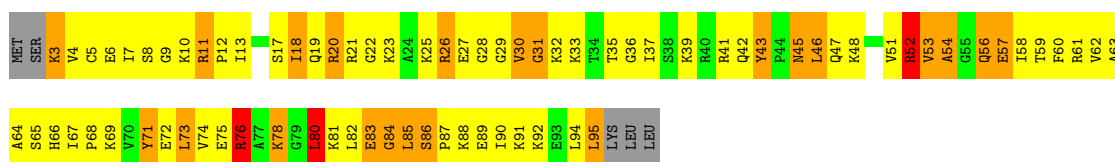
• Molecule 25: 50S RIBOSOMAL PROTEIN L27

Chain B0: 40% 41% 14% 2%



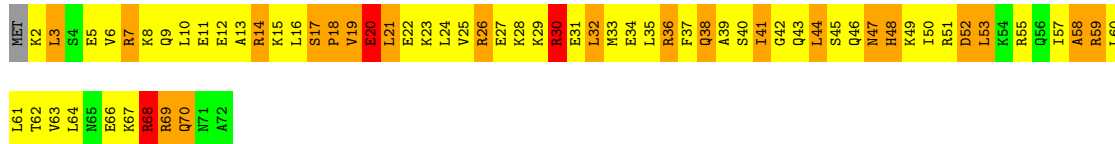
• Molecule 26: 50S RIBOSOMAL PROTEIN L28

Chain B1: 15% 54% 22% 5%



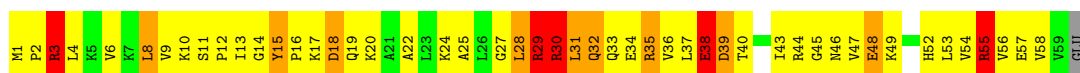
• Molecule 27: 50S RIBOSOMAL PROTEIN L29

Chain B2: 8% 57% 29% 2%

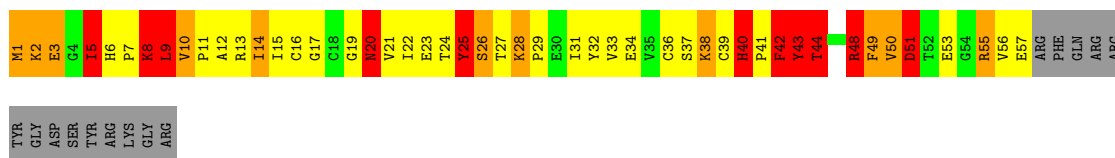


• Molecule 28: 50S RIBOSOMAL PROTEIN L30

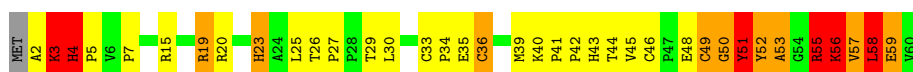
Chain B3: 17% 58% 15% 8%



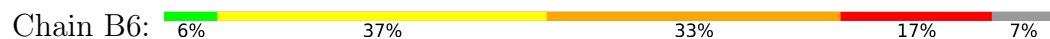
• Molecule 29: 50S RIBOSOMAL PROTEIN L31



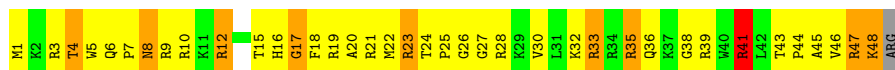
• Molecule 30: 50S RIBOSOMAL PROTEIN L32



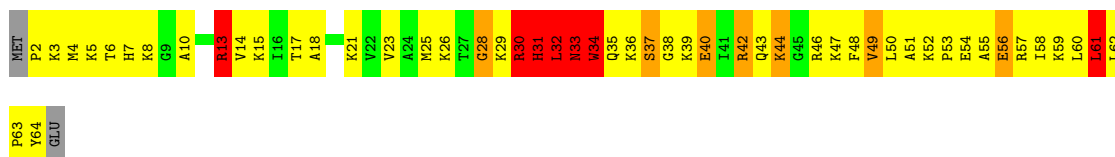
• Molecule 31: 50S RIBOSOMAL PROTEIN L33



• Molecule 32: 50S RIBOSOMAL PROTEIN L34



• Molecule 33: 50S RIBOSOMAL PROTEIN L35



• Molecule 34: 50S RIBOSOMAL PROTEIN L36



• Molecule 35: 23S RIBOSOMAL RNA



G1899	G1830	G1770	G1694	G1634	G1574	G1513	G1453	G1395	G1335	A1275	G1216	A1155	A1095	U1035	G975A
A1900	G1831	G1771	G1695	G1635	C1575	U1514	G1455	A1396	A1336	A1276	C1217	A1156	A1096	U1036	C976
C1901	G1832	G1772	G1696	G1636	C1576	G1515	G1456	U1397	G1337	G1277	C1218	A1157	A1097	G1037	C977
G1903	U1833	A1773	G1697	A1637	A1577	C1516	A1457	C1398	G1338	A1278	G1219	C1158	U1097	G1038	G978
G1904	G1834	G1774	A1698	G1638	U1578	G1517	G1458	C1399	G1339	G1279	A1220	U1159	G1099	G1039	G979
G1905	G1835	U1775	G1699	U1639	U1579	U1518	G1459	G1400	U1340	G1280	C1221	U1160	C1100	G1040	A980
C1906	C1836	G1776	A1700	G1640	A1580	G1519	A1460	G1401	U1341	G1281	C1221A	G1161	U1101	C1041	A981
G1907	C1837	U1777	A1701	A1641	G1581	G1520	G1461	C1402	A1342	U1282	C1222	G1162	C1102	G1042	C982
G1908	G1838	U1778	G1702	G1642	C1582	U1521	C1462	C1403	G1343	U1283	C1223	G1163	A1103	C1043	A983
C1909	G1839	G1779	G1703	G1643	A1583	G1524	C1463	C1404	G1344	A1284	G1224	G1164	G1104	G1044	A984
G1910	G1840	A1780	G1704	G1644	C1584	G1525	C1464	U1405	C1345	G1285	C1225	U1165	U1105	A1045	C985
U1911	U1841	C1781	G1705	G1645	A1586	G1526	G1465	U1406	G1346	A1286	A1226	U1166	G1106	A1046	C986
G1912	G1842	U1782	U1706	G1646	G1587	G1527	G1466	C1407	G1347	U1287	G1227	U1167	G1107	G1047	C987
A1913	C1843	A1783	G1707	G1647	C1588	A1528	G1467	C1408	G1348	U1288	G1228	G1168	U1108	A1048	A988
G1914	G1844	U1784	C1708	G1648	A1589	A1529	C1468	C1409	A1349	U1289	G1229	G1169	C1109	G1049	G989
C1915	G1845	A1785	U1709	G1649	U1590	G1530	A1469	C1410	C1350	C1290	C1230	G1170	A1050	A990	A990
U1916	G1846	A1786	C1710	G1650	C1591	C1531	G1470	C1411	G1351	C1291	G1231	G1171	A1111	G1051	C991
G1917	A1847	U1787	G1711	G1651	C1592	G1532	A1471	U1412	U1352	U1292	G1232	G1172	G1112	G1052	C992
G1918	G1848	C1788	C1712	G1652	G1593	C1533	A1472	G1413	A1353	G1293	C1233	A1174	U1113	G1053	G993
G1919	G1849	A1789	U1713	G1653	G1594	U1534	G1473	G1414	A1354	U1294	U1234	U1175	U1114	A1054	C994
C1920	U1850	C1790	G1714	A1654	G1595	G1535	C1474	U1415	G1355	C1295	G1235	G1176	G1115	G1055	C995
G1921	U1851	A1791	G1717	A1655	A1596	A1536	G1475	G1416	G1356	G1296	G1236	A1177	C1116	G1056	A996
G1922	G1852	G1792	G1718	C1656	A1597	C1536	C1476	C1417	U1357	C1297	A1237	C1178	G1117	A1057	G997
C1923	A1853	C1793	G1719	C1657	C1598	G1537	A1477	G1418	G1358	G1298	G1238	C1179	C1118	G1058	C998
U1924	G1854	U1794	U1720	C1658	C1599	G1538	G1478	A1419	A1359	G1299	G1239	C1180	C1119	G1059	U999
C1925	G1855	C1795	G1721	U1659	C1600	G1539	G1479	U1420	A1360	U1300	U1240	C1181	G1120	U1060	A1000
U1926	A1856	U1796	A1722	G1660	G1601	U1540	G1480	G1421	G1361	A1301	A1241	A1182	C1121	U1061	A1001
G1927	G1857	C1797	G1739	G1661	U1602	G1541	U1481	G1422	C1362	A1302	A1242	G1183	G1122	G1062	A1002
A1928	G1858	U1798	G1740	C1662	A1603	A1542	G1482	G1423	G1363	G1303	C1123	G1184	C1124	G1063	C1003
G1929	A1859	G1799	A1741	C1663	C1604	C1543	G1484	G1424	G1364	C1304	G1244	C1185	C1004	C1064	G1004
C1930	G1860	C1800	G1742	A1664	C1605	A1544	G1485	G1425	A1365	G1305	G1245	G1186	G1125	U1065	G1005
U1931	G1861	G1801	C1743	A1665	G1606	A1545	A1486	A1426	A1366	C1306	A1246	G1187	A1126	U1066	C1006
G1932	G1862	A1802	G1744	G1666	C1607	C1546	G1487	G1427	A1367	A1307	A1247	U1188	A1127	A1067	C1007
C1933	U1863	A1803	C1745	G1667	A1608	C1547	U1488	G1428	G1368	A1308	G1248	A1189	A1128	G1068	C1008
G1934	G1864	C1804	G1746	A1668	A1609	C1548	U1489	C1429	G1369	A1309	U1249	G1190	A1129	A1069	A1009
G1935	G1865	U1805	G1747	A1669	A1610	C1549	A1490	C1430	C1370	G1310	G1250	G1191	U1130	A1070	A1010
A1936	G1866	C1806	G1747	C1670	C1611	C1550	G1491	U1431	G1371	G1311	C1251	G1192	G1131	G1071	G1011
G1937	A1876	G1807	G1747A	U1671	C1612	C1551	G1492	C1432	U1372	U1312	G1252	G1193	A1132	C1072	U1012
A1938	G1877	U1808	G1748	C1672	G1613	G1552	C1493	U1433	A1373	U1313	A1253	A1194	U1133	A1073	G1013
G1939	G1878	A1809	A1749	U1673	A1614	A1553	A1494	A1434	G1374	G1314	A1254	G1195	C1135	G1074	U1014
U1940	C1879	G1810	G1750	G1674	C1615	A1554	A1495	G1435	C1375	G1315	U1255	C1196	G1136	C1075	G1015
G1941	G1881	A1812	C1752	C1675	A1616	G1555	A1496	G1436	C1376	U1316	G1256	G1197	G1137	G1076	G1016
C1942	C1882	G1813	G1753	A1676	C1617	C1556	U1497	C1437	G1377	G1317	C1257	U1198	G1138	A1077	G1017
U1943	G1883	G1814	G1754	A1677	A1618	C1557	C1498	U1438	A1378	C1318	C1258	U1199	G1139	U1078	C1018
G1944	A1884	A1815	C1755	G1678	G1619	A1558	C1499	A1439	A1379	G1319	G1259	C1200	C1140	C1079	U1019
C1945	G1885	G1816	G1756	U1679	G1620	G1559	G1500	G1440	G1380	C1320	G1260	C1201	U1141	G1080	A1020
U1946	C1886	G1817	U1757	G1680	U1621	G1560	C1501	G1441	G1381	A1321	C1261	C1202	U1142	U1081	A1021
G1947	G1887	U1818	G1758	G1682	G1622	G1561	C1502	G1442	G1382	A1322	A1262	G1203	A1142A	U1082	G1022
G1948	G1888	A1819	A1759	C1683	G1623	A1562	U1503	G1443	C1383	U1323	U1263	A1143	U1083	U1083	G1023
C1949	A1889	U1820	U1760	C1684	G1624	G1563	C1504	G1444	A1384	G1324	G1264	U1205	G1144	A1084	G1024
G1950	G1890	A1821	C1761	C1685	G1625	C1564	G1505	A1445	G1385	G1325	A1265	G1206	C1145	A1085	G1025
U1951	G1891	G1822	G1762	C1686	G1626	C1565	C1506	C1445A	C1386	U1326	G1266	C1207	G1146	A1086	U1026
A1952	C1892	G1823	G1763	G1687	G1627	A1566	A1507	C1446	G1387	C1327	U1267	C1208	C1147	G1087	A1027
G1953	G1893	G1824	G1764	U1688	G1628	A1567	A1508	G1447	G1388	G1328	A1268	G1209	A1148	A1088	A1028
C1954	A1894	A1825	C1765	A1689	U1629	G1568	C1509	G1448	G1389	U1329	A1269	U1210	G1149	G1089	A1029
U1955	G1895	G1826	U1766	A1690	C1631	A1569	A1509A	G1449	U1390	G1330	C1270	U1211	C1150	U1090	G1030
C1956	G1896	A1827	G1767	C1691	G1631A	A1570	A1509B	G1450	U1391	A1331	G1271	G1212	G1151	G1091	G1031
G1957	G1897	G1828	U1768	U1692	A1571	C1450A	C1510	C1450A	A1392	G1332	U1272	A1213	C1152	C1092	U1032
C1958	U1898	A1829	G1769	U1693	G1633	G1573	U1512	A1452	U1394	C1333	U1273	A1214	G1154	G1093	U1033
															G1034

G2871	G2811	A2748	U2689	G2569	G2509	U2449	G2389	G2329	A2269	G2139	U2079	A2019	G1959
G2872	G2812	A2749	G2690	G2570	G2510	A2449	G2390	G2330	G2270	G2140	U2080	A2020	A1960
A2873	A2813	G2750	G2691	G2571	U2511	A2451	G2391	U2331	G2271	G2141	G2081	G2021	C1961
G2874	G2814	G2751	G2692	A2572	G2512	C2452	G2392	U2332	U2272	C2142	A2082	U2022	C1962
G2875	G2815	G2752	G2693	C2573	G2513	A2453	A2393	G2333	A2273	U2143	G2083	G2023	U1963
G2876	G2816	A2753	G2694	G2574	U2514	G2454	G2394	G2334	A2274	U2144	G2084	G2024	G1964
G2877	G2817	U2754	G2695	G2575	G2515	G2455	G2395	A2335	C2275	C2145	C2085	C2025	C1965
U2878	G2818	G2755	U2696	G2576	G2516	U2456	G2396	A2336	G2276	U2086	U2086	C2026	A1966
G2879	G2819	U2756	G2697	A2577	C2517	U2457	G2397	G2337	G2277	C2147	U2087	G2027	C1967
G2880	A2820	A2757	G2698	G2578	A2518	A2458	U2398	G2338	A2278	G2148	U2088	U2028	G1968
G2881	A2821	A2758	G2699	G2579	U2519	A2459	G2399	G2339	A2279	G2149	U2089	G2029	A1969
A2882	G2822	G2759	G2700	U2580	G2520	U2460	U2401	G2340	G2280	U2150	G2090	A2030	A1970
A2883	A2823	G2760	G2701	G2581	C2521	U2461	U2402	G2342	G2282	G2151	U2091	A2031	A1971
U2884	G2824	G2761	U2702	G2582	U2522	U2462	G2403	C2344	G2283	G2152	U2092	G2032	A1972
G2885	G2825	G2762	G2703	G2583	G2523	A2463	G2404	U2344	C2284	G2153	G2093	A2033	G1973
G2886	A2826	G2763	G2704	U2584	G2524	C2464	G2405	U2345	C2285	G2154	C2094	U2034	G1974
U2887	G2827	A2764	A2705	U2585	G2525	C2465	A2406	A2346	A2286	G2155	C2095	G2035	G1975
G2888	G2828	G2765	G2706	G2586	G2526	C2466	U2407	G2347	A2287	G2156	U2096	C2036	U1976
G2889	G2829	G2766	G2707	A2587	C2527	G2467	G2408	U2348	A2288	G2157	C2097	G2037	A1977
G2891	G2830	G2767	G2708	G2588	U2528	G2468	U2409	U2349	G2289	A2158	U2098	G2038	A1978
A2892	G2831	G2768	G2709	U2589	G2529	A2469	G2410	G2350	G2290	G2159	U2099	C2039	G1979
G2893	U2832	G2769	G2710	A2590	A2530	G2470	A2411	C2351	U2291	G2160	G2100	C2040	G1980
G2894	G2833	G2770	A2711	C2591	A2531	C2471	A2412	G2352	C2292	G2161	G2101	U2041	A1981
U2895	G2834	U2712	U2713	G2592	G2532	G2472	G2413	A2353	C2293	G2162	U2102	A2042	C1982
G2896	A2835	G2771	A2712A	U2593	A2533	U2473	G2414	G2354	C2294	G2163	C2103	G2043	C1983
U2897	U2836	G2772	A2713	C2594	A2534	C2474	G2415	G2355	G2295	G2164	G2104	C2044	G1984
U	G2837	G2773	G2714	G2595	G2535	C2475	G2416	C2356	U2296	G2165	G2105	C2045	G1985
G	G2838	A2774	G2715	U2596	G2536	A2476	G2417	U2357	C2297	G2166	G2106	G2046	A1986
A	G2839	A2775	U2716	A2597	U2537	C2477	G2418	U2358	A2298	G2167	C2107	U2047	C1987
C	G2840	G2776	G2717	G2598	G2538	A2478	A2419	G2359	G2299	G2168	C2108	G2048	C1988
C	G2841	A2778	G2718	G2599	C2539	G2479	U2420	A2360	G2300	A2169	U2109	G2049	G1989
C	G2842	U2779	G2719	A2600	G2540	C2480	G2421	U2361	C2301	A2170	G2110	G2050	C1990
C	G2843	G2780	U2720	C2601	A2541	G2481	A2422	G2362	G2302	A2171	G2111	A2051	U1991
U	G2844	A2781	A2721	A2602	G2542	C2482	U2423	G2363	G2303	U2172	G2112	G2052	G1992
G	G2845	G2782	G2722	G2603	G2543	C2483	G2424	C2364	G2304	C2173	U2113	G2053	U1993
G	G2846	G2783	G2723	U2604	G2544	G2484	A2425	G2365	G2305	C2174	A2114	A2054	C1994
G	U2847	G2784	C2724	U2605	G2545	G2485	A2426	A2366	U2306	G2175	G2115	G2055	U1995
G	G2848	G2785	A2725	C2606	U2546	G2486	G2427	G2367	C2307	A2176	G2116	G2056	C1996
U2849	A2850	U2786	U2726	G2607	U2547	G2487	G2428	C2368	G2308	C2177	U2117	A2057	G1997
A2851	G2851	G2787	G2727	G2608	G2548	A2488	G2429	A2369	A2309	C2178	U2118	A2058	G1998
G2852	G2852	G2788	U2728	U2609	G2549	G2489	G2430	U2370	A2310	C2179	A2119	A2059	C1999
G2853	G2853	G2789	G2729	C2610	G2550	G2490	A2431	G2371	A2311	U2180	G2120	A2060	G2000
G2854	G2854	C2790	G2730	U2611	U2551	U2491	U2432	G2372	U2312	G2181	G2121	G2061	A2001
G2855	C2855	G2791	G2731	G2612	U2552	U2492	A2433	G2373	C2313	G2182	U2122	A2062	G2002
G2856	G2856	U2792	G2732	U2613	G2553	U2493	A2434	C2374	G2314	C2183	G2123	C2063	G2003
G2857	A2857	G2793	A2733	A2614	U2554	G2494	A2435	G2375	G2315	G2184	G2124	C2064	G2004
G2858	C2858	G2794	G2734	U2615	U2555	G2495	A2436	C2376	G2316	G2185	G2125	C2065	A2005
G2859	G2859	U2795	G2735	C2616	G2556	C2496	A2437	A2377	C2317	G2186	A2126	C2066	C2006
A2860	G2860	G2796	G2736	G2617	G2557	U2497	U2437	A2378	U2317	G2187	G2127	G2067	G2007
G2861	A2861	G2797	G2737	G2618	C2558	C2498	U2438	A2379	G2318	C2188	C2128	U2068	C2008
G2862	G2862	A2801A	A2738	C2619	C2559	C2499	A2439	G2379	U2319	U2189	C2129	G2069	G2009
G2863	G2863	U2801A	U2739	C2620	U2500	U2499	A2440	C2380	A2320	C2190	U2130	G2070	G2010
G2864	C2864	G2802	G2681	A2621	A2561	C2501	C2441	C2381	G2321	G2191	U2131	A2071	U2011
U2865	G2865	G2803	U2741	C2622	U2562	G2502	G2442	C2382	A2322	G2192	U2132	G2072	G2012
G2866	G2866	G2804	G2742	G2623	U2563	A2503	G2443	G2383	G2323	G2193	G2133	G2073	A2013
G2867	G2867	G2805	C2743	G2624	U2564	U2504	G2444	G2384	C2324	G2194	A2134	U2074	A2014
U2868	G2868	G2806	G2744	G2625	A2565	G2505	G2445	C2385	G2325	C2195	A2135	U2075	A2015
G2869	G2869	U2808	G2745	C2626	A2566	U2506	G2446	U2386	G2326	C2196	G2136	U2076	U2016
A2890	G2890	G2746	U2746	G2627	U2567	C2507	G2447	U2387	A2327	U2197	C2137	U2077	U2017
G2891	G2891	A2810	G2747	C2628	G2568	G2508	A2448	A2388	A2328	A2198	G2138	G2078	G2018

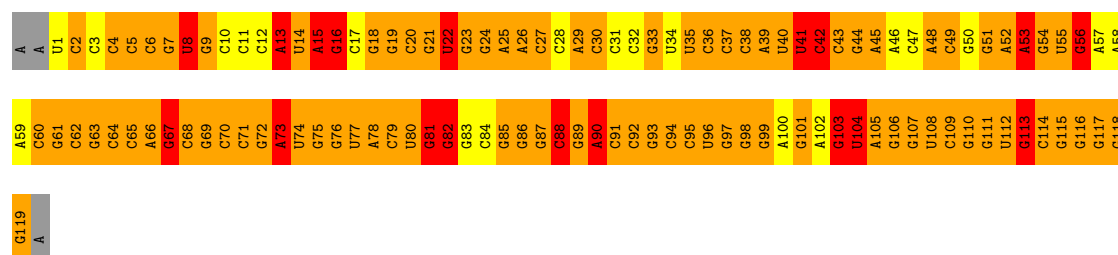
● Molecule 36: 5S RIBOSOMAL RNA

Chain BB:

16%

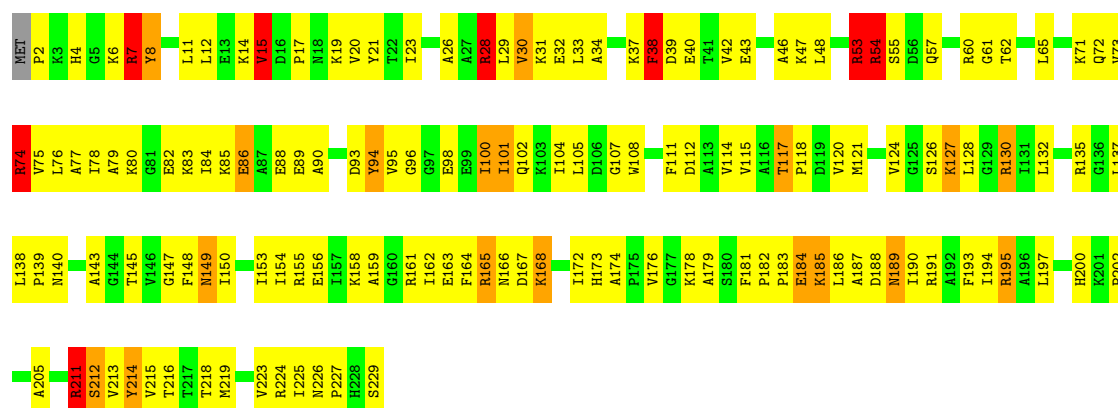
66%

15%



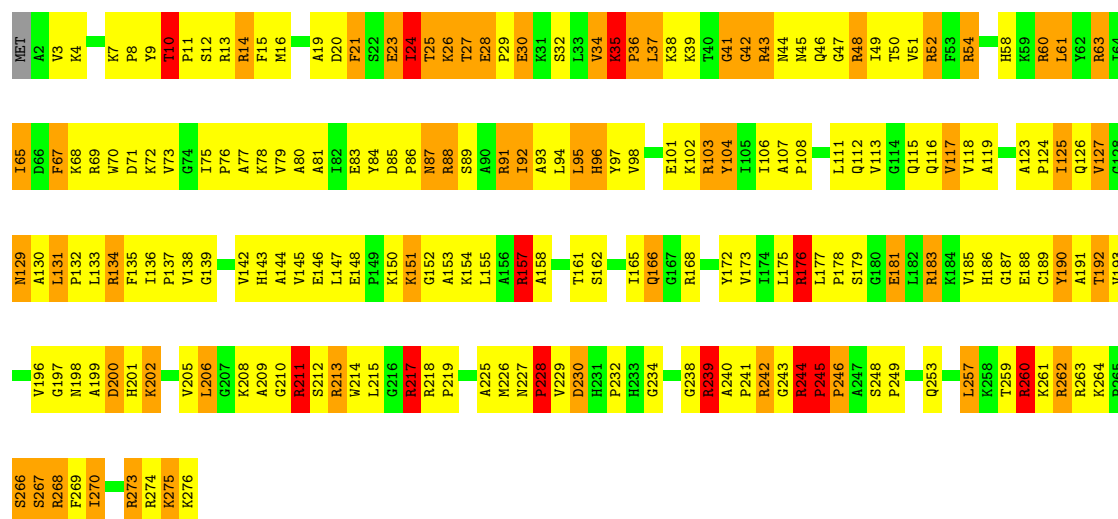
• Molecule 37: 50S RIBOSOMAL PROTEIN L1

Chain BC: 36% 52% 8%



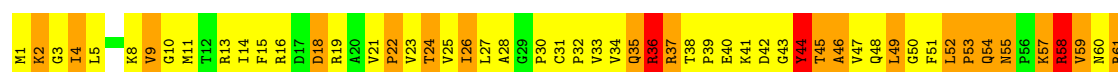
• Molecule 38: 50S RIBOSOMAL PROTEIN L2

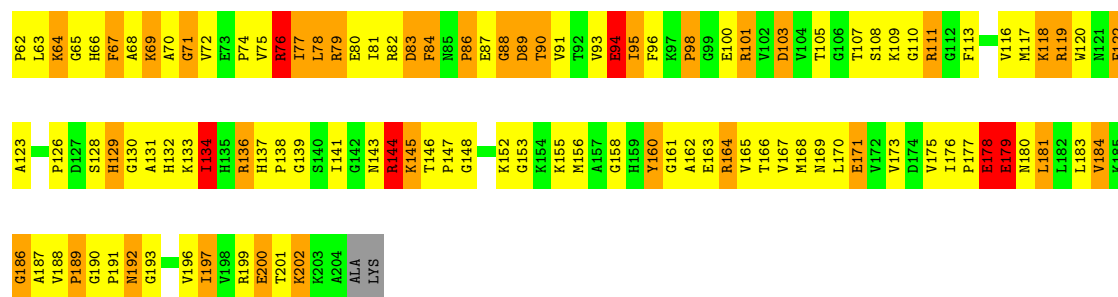
Chain BD: 26% 48% 21%



• Molecule 39: 50S RIBOSOMAL PROTEIN L3

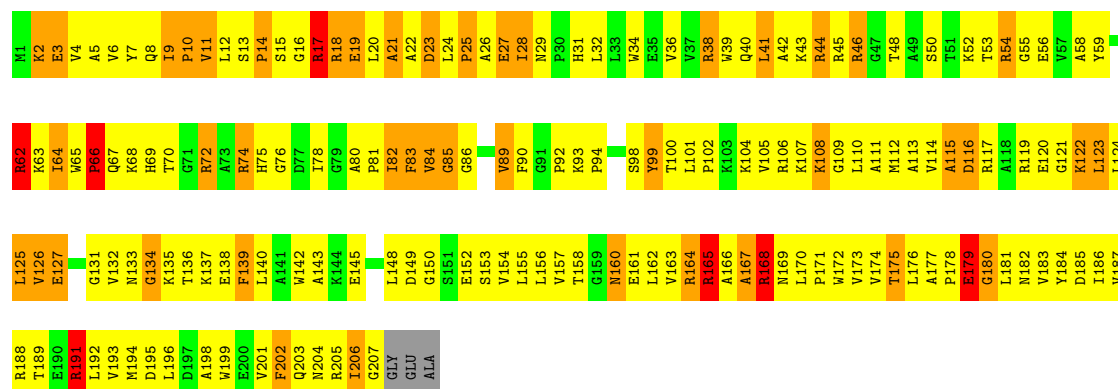
Chain BE: 19% 49% 26%





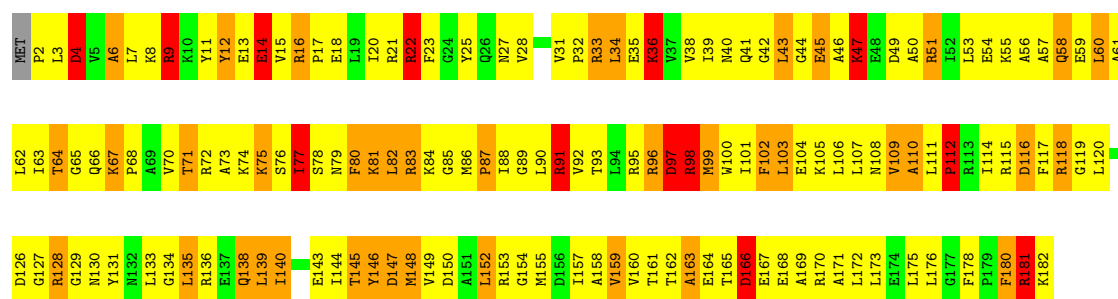
• Molecule 40: 50S RIBOSOMAL PROTEIN L4

Chain BF: 17% 58% 21% . .



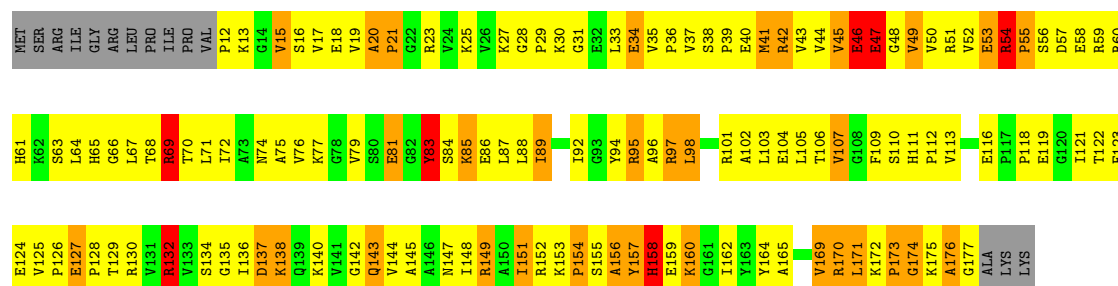
• Molecule 41: 50S RIBOSOMAL PROTEIN L5

Chain BG: 15% 55% 22% 7% .

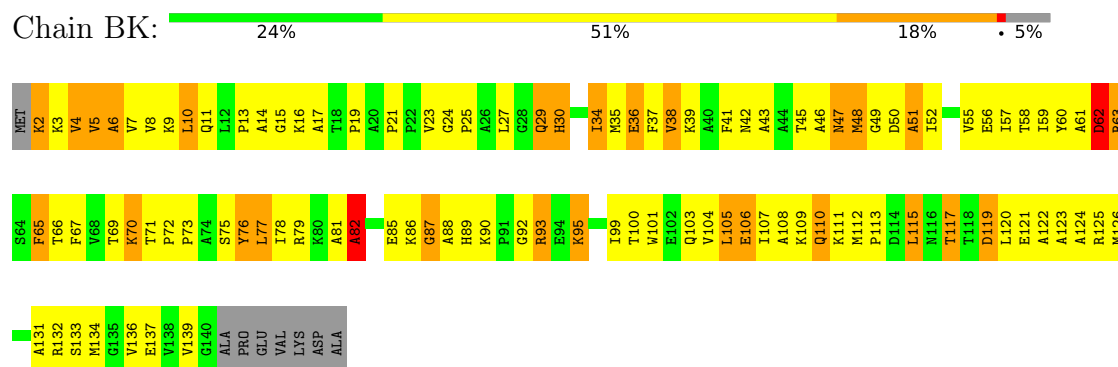


• Molecule 42: 50S RIBOSOMAL PROTEIN L6

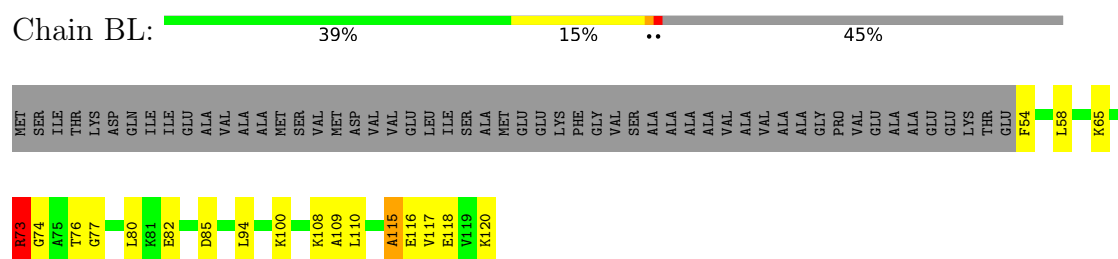
Chain BH: 17% 53% 18% 8%



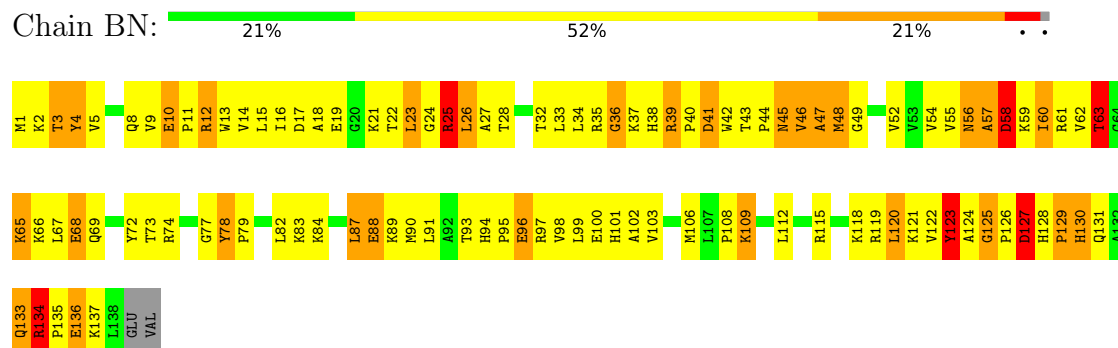
- Molecule 43: 50S RIBOSOMAL PROTEIN L11



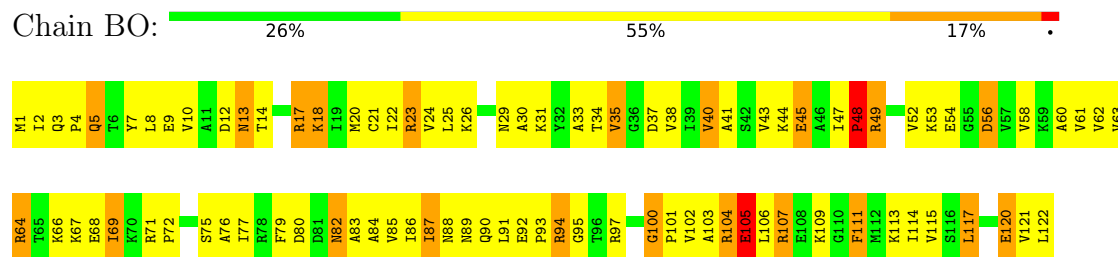
- Molecule 44: 50S RIBOSOMAL PROTEIN L7/L12



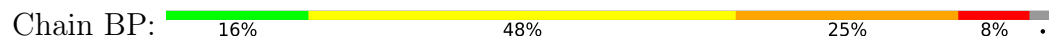
- Molecule 45: 50S RIBOSOMAL PROTEIN L13

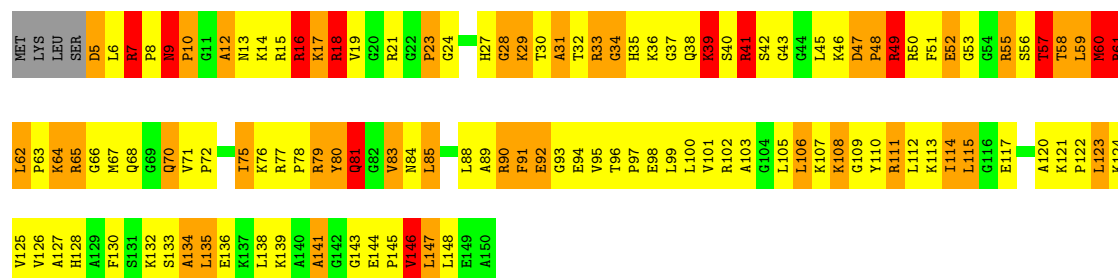


- Molecule 46: 50S RIBOSOMAL PROTEIN L14



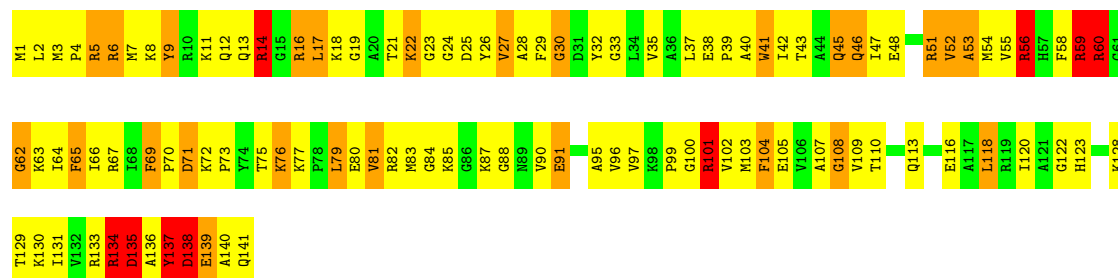
- Molecule 47: 50S RIBOSOMAL PROTEIN L15





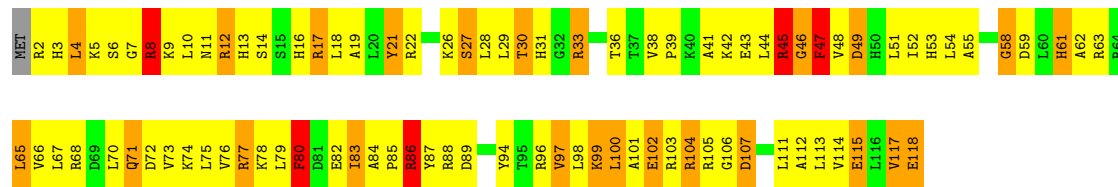
• Molecule 48: 50S RIBOSOMAL PROTEIN L16

Chain BQ: 23% 52% 18% 6%



• Molecule 49: 50S RIBOSOMAL PROTEIN L17

Chain BR: 22% 53% 20%



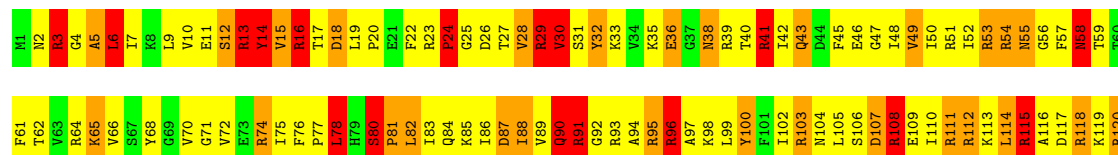
• Molecule 50: 50S RIBOSOMAL PROTEIN L18

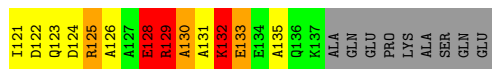
Chain BS: 8% 53% 20% 7% 12%



• Molecule 51: 50S RIBOSOMAL PROTEIN L19

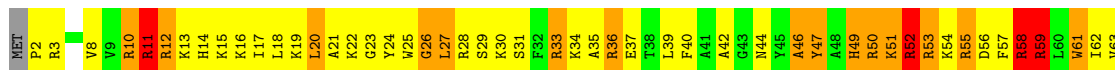
Chain BT: 12% 47% 21% 14% 6%





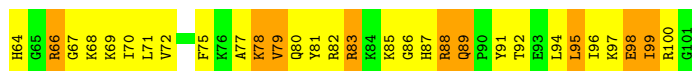
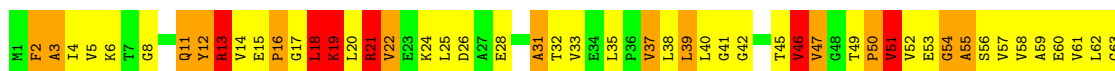
• Molecule 52: 50S RIBOSOMAL PROTEIN L20

Chain BU: 20% 52% 22% 5% .



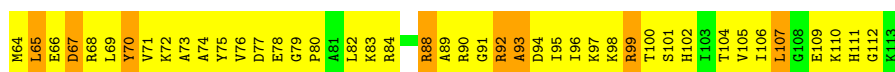
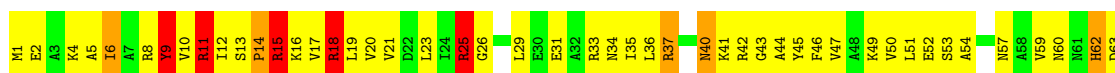
• Molecule 53: 50S RIBOSOMAL PROTEIN L21

Chain BV: 21% 51% 22% 6% .



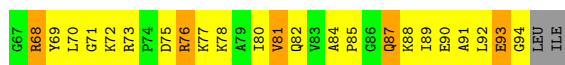
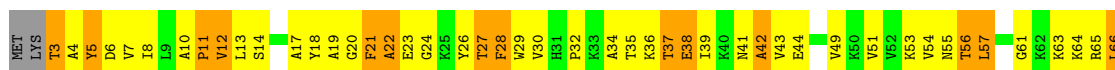
• Molecule 54: 50S RIBOSOMAL PROTEIN L22

Chain BW: 19% 65% 12% .



• Molecule 55: 50S RIBOSOMAL PROTEIN L23

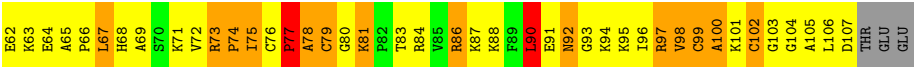
Chain BX: 23% 53% 20% .



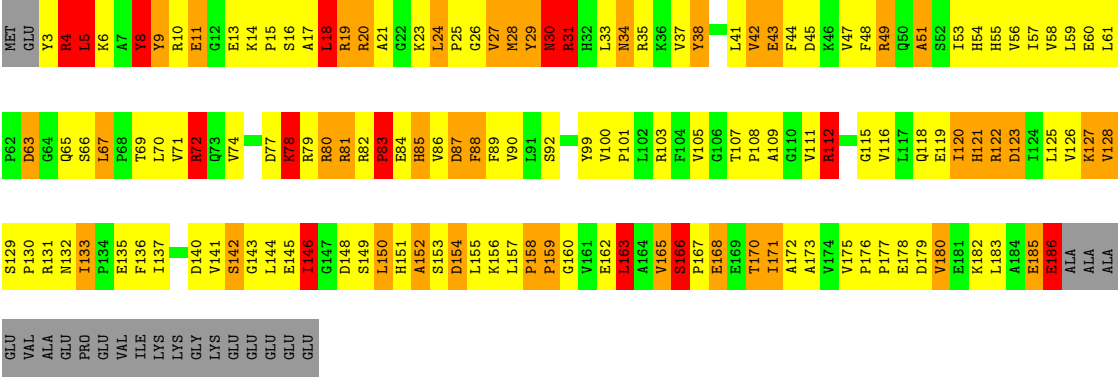
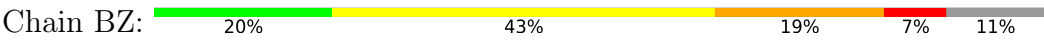
• Molecule 56: 50S RIBOSOMAL PROTEIN L24

Chain BY: 9% 58% 26% . .





● Molecule 57: 50S RIBOSOMAL PROTEIN L25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	AA	2.73	2519/36190 (7.0%)	2.44	3195/56486 (5.7%)
2	AB	1.36	3/1935 (0.2%)	1.50	19/2609 (0.7%)
3	AC	1.44	1/1636 (0.1%)	1.59	20/2205 (0.9%)
4	AD	1.38	0/1733	1.56	26/2318 (1.1%)
5	AE	1.45	1/1162 (0.1%)	1.44	9/1564 (0.6%)
6	AF	1.39	0/856	1.57	12/1154 (1.0%)
7	AG	1.34	1/1276 (0.1%)	1.51	12/1709 (0.7%)
8	AH	1.41	1/1136 (0.1%)	1.60	15/1527 (1.0%)
9	AI	1.48	4/1029 (0.4%)	2.08	17/1379 (1.2%)
10	AJ	1.33	0/807	1.53	8/1085 (0.7%)
11	AK	1.40	1/900 (0.1%)	1.50	6/1213 (0.5%)
12	AL	1.42	1/986 (0.1%)	1.58	13/1320 (1.0%)
13	AM	1.33	0/998	1.68	17/1336 (1.3%)
14	AN	1.52	1/501 (0.2%)	1.72	9/664 (1.4%)
15	AO	1.36	1/745 (0.1%)	1.58	9/992 (0.9%)
16	AP	1.47	1/716 (0.1%)	1.59	11/963 (1.1%)
17	AQ	1.43	1/836 (0.1%)	1.57	11/1117 (1.0%)
18	AR	1.41	1/579 (0.2%)	1.56	12/768 (1.6%)
19	AS	1.30	0/642	1.50	6/865 (0.7%)
20	AT	1.32	0/765	1.53	10/1007 (1.0%)
21	AU	1.50	1/212 (0.5%)	1.82	8/277 (2.9%)
22	AV	2.70	127/1832 (6.9%)	2.42	155/2855 (5.4%)
23	AX	2.50	14/257 (5.4%)	2.35	20/398 (5.0%)
24	AY	1.35	3/5312 (0.1%)	1.53	54/7193 (0.8%)
25	B0	1.32	0/671	1.75	11/892 (1.2%)
26	B1	1.34	1/738 (0.1%)	1.58	9/981 (0.9%)
27	B2	1.32	2/600 (0.3%)	1.60	9/793 (1.1%)
28	B3	1.42	0/472	1.51	5/634 (0.8%)
29	B4	1.28	0/460	1.67	9/621 (1.4%)
30	B5	1.26	0/473	1.57	6/639 (0.9%)
31	B6	1.29	0/440	1.71	9/586 (1.5%)
32	B7	1.37	0/426	1.76	9/561 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B8	1.35	0/515	1.68	7/679 (1.0%)
34	B9	1.36	1/310 (0.3%)	1.54	3/407 (0.7%)
35	BA	2.69	4845/69972 (6.9%)	2.42	5972/109237 (5.5%)
36	BB	2.63	174/2853 (6.1%)	2.36	226/4451 (5.1%)
37	BC	1.32	1/1774 (0.1%)	1.51	18/2391 (0.8%)
38	BD	1.40	5/2195 (0.2%)	1.62	27/2955 (0.9%)
39	BE	1.37	3/1596 (0.2%)	1.52	17/2153 (0.8%)
40	BF	1.36	1/1658 (0.1%)	1.64	27/2244 (1.2%)
41	BG	1.34	1/1499 (0.1%)	1.97	24/2016 (1.2%)
42	BH	1.32	4/1292 (0.3%)	1.50	11/1744 (0.6%)
43	BK	1.27	1/1044 (0.1%)	1.39	8/1416 (0.6%)
44	BL	1.08	0/478	1.54	3/640 (0.5%)
45	BN	1.34	2/1131 (0.2%)	1.52	11/1525 (0.7%)
46	BO	1.40	2/943 (0.2%)	1.55	9/1269 (0.7%)
47	BP	1.38	1/1131 (0.1%)	1.64	20/1504 (1.3%)
48	BQ	1.43	3/1143 (0.3%)	1.59	18/1527 (1.2%)
49	BR	1.35	2/974 (0.2%)	1.57	14/1302 (1.1%)
50	BS	1.36	1/778 (0.1%)	1.71	13/1036 (1.3%)
51	BT	1.32	0/1155	1.77	33/1542 (2.1%)
52	BU	1.35	1/975 (0.1%)	1.59	18/1297 (1.4%)
53	BV	1.27	0/790	1.55	9/1057 (0.9%)
54	BW	1.33	0/907	1.59	11/1216 (0.9%)
55	BX	1.37	0/739	1.39	5/993 (0.5%)
56	BY	1.29	0/823	1.43	4/1098 (0.4%)
57	BZ	1.41	2/1499 (0.1%)	1.54	16/2035 (0.8%)
All	All	2.35	7735/165495 (4.7%)	2.21	10265/246445 (4.2%)

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
1	AA	1	111
2	AB	0	10
3	AC	0	1
4	AD	0	14
5	AE	0	3
6	AF	0	5
7	AG	0	11
8	AH	0	8
9	AI	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	AJ	0	3
11	AK	0	3
12	AL	0	3
13	AM	0	6
14	AN	0	3
15	AO	0	2
16	AP	0	2
18	AR	0	1
20	AT	0	7
21	AU	0	1
22	AV	0	4
23	AX	0	2
24	AY	0	19
25	B0	0	3
26	B1	0	3
27	B2	0	5
28	B3	0	4
29	B4	0	1
30	B5	0	1
31	B6	0	3
32	B7	0	2
33	B8	0	3
35	BA	2	161
36	BB	0	2
37	BC	0	7
38	BD	0	8
39	BE	0	6
40	BF	0	4
41	BG	0	4
42	BH	0	5
43	BK	0	5
44	BL	0	3
45	BN	0	5
46	BO	0	4
47	BP	0	6
48	BQ	0	4
49	BR	0	3
50	BS	0	3
51	BT	0	10
52	BU	0	4
53	BV	0	3
54	BW	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
55	BX	0	1
56	BY	0	2
57	BZ	0	6
All	All	3	514

The worst 5 of 7735 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BA	1696	G	N7-C5	-15.22	1.30	1.39
1	AA	607	A	N7-C5	-14.64	1.30	1.39
35	BA	406	G	N7-C5	-14.28	1.30	1.39
1	AA	1144	G	C8-N7	-14.17	1.22	1.30
1	AA	1129	C	N3-C4	-13.63	1.24	1.33

The worst 5 of 10265 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	BG	112	PRO	O-C-N	-44.90	50.85	122.70
9	AI	53	VAL	O-C-N	-38.46	61.16	122.70
9	AI	104	ARG	O-C-N	-29.23	75.94	122.70
41	BG	112	PRO	CA-C-N	20.32	161.90	117.20
1	AA	1463	C	C6-N1-C2	18.92	127.87	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	575	G	C3'
35	BA	1799	G	C3'
35	BA	1992	G	C3'

5 of 514 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	108	G	Sidechain
1	AA	21	G	Sidechain
1	AA	37	U	Sidechain
1	AA	39	G	Sidechain
1	AA	5	U	Sidechain

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	AA	32329	0	16035	1572	0
2	AB	1900	0	1951	268	0
3	AC	1612	0	1677	202	0
4	AD	1703	0	1767	195	0
5	AE	1146	0	1207	147	0
6	AF	843	0	857	95	0
7	AG	1257	0	1296	109	0
8	AH	1116	0	1177	98	0
9	AI	1010	0	1037	148	0
10	AJ	794	0	840	178	0
11	AK	885	0	904	79	0
12	AL	970	0	1057	149	0
13	AM	987	0	1059	140	0
14	AN	492	0	533	56	0
15	AO	734	0	771	71	0
16	AP	700	0	720	91	0
17	AQ	823	0	891	71	0
18	AR	574	0	644	92	0
19	AS	629	0	652	142	0
20	AT	763	0	861	124	0
21	AU	208	0	221	15	0
22	AV	1640	0	820	93	0
23	AX	230	0	119	17	0
24	AY	5214	0	5288	759	0
25	B0	662	0	688	86	0
26	B1	731	0	808	132	0
27	B2	598	0	653	123	0
28	B3	467	0	523	75	0
29	B4	450	0	449	101	0
30	B5	459	0	480	97	0
31	B6	433	0	461	177	0
32	B7	418	0	467	45	0
33	B8	507	0	576	112	0
34	B9	307	0	338	41	0
35	BA	62474	0	31032	3259	0
36	BB	2551	0	1278	166	0
37	BC	1742	0	1798	183	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BD	2145	0	2234	311	0
39	BE	1563	0	1629	273	0
40	BF	1623	0	1677	288	0
41	BG	1474	0	1535	278	0
42	BH	1268	0	1337	209	0
43	BK	1025	0	1066	184	0
44	BL	477	0	509	17	0
45	BN	1104	0	1180	154	0
46	BO	933	0	996	116	0
47	BP	1114	0	1187	270	0
48	BQ	1122	0	1179	151	0
49	BR	960	0	1021	157	0
50	BS	770	0	832	177	0
51	BT	1141	0	1202	266	0
52	BU	958	0	1015	166	0
53	BV	779	0	852	142	0
54	BW	896	0	953	123	0
55	BX	725	0	778	97	0
56	BY	810	0	901	174	0
57	BZ	1467	0	1492	249	0
58	AY	37	0	46	17	0
59	AY	28	0	12	6	0
All	All	152777	0	105568	12274	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 48.

The worst 5 of 12274 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)
24:AY:252:ASP:CB	24:AY:254:LYS:HE3	1.55	1.36
37:BC:118:PRO:HA	37:BC:121:MET:CG	1.60	1.31
53:BV:18:LEU:HD22	53:BV:19:LYS:N	1.45	1.30
1:AA:1158:C:C5'	2:AB:133:LYS:HE2	1.62	1.28
53:BV:18:LEU:CD2	53:BV:19:LYS:H	1.50	1.25

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	
2	AB	232/256 (91%)	149 (64%)	49 (21%)	34 (15%)	0	3
3	AC	204/239 (85%)	129 (63%)	56 (28%)	19 (9%)	0	8
4	AD	206/209 (99%)	138 (67%)	49 (24%)	19 (9%)	0	8
5	AE	148/162 (91%)	113 (76%)	25 (17%)	10 (7%)	1	12
6	AF	99/101 (98%)	77 (78%)	18 (18%)	4 (4%)	2	18
7	AG	153/156 (98%)	108 (71%)	35 (23%)	10 (6%)	1	12
8	AH	136/138 (99%)	110 (81%)	23 (17%)	3 (2%)	5	29
9	AI	125/128 (98%)	85 (68%)	24 (19%)	16 (13%)	0	4
10	AJ	96/105 (91%)	60 (62%)	23 (24%)	13 (14%)	0	4
11	AK	117/129 (91%)	91 (78%)	21 (18%)	5 (4%)	2	17
12	AL	122/132 (92%)	82 (67%)	23 (19%)	17 (14%)	0	3
13	AM	122/126 (97%)	73 (60%)	26 (21%)	23 (19%)	0	2
14	AN	58/61 (95%)	49 (84%)	5 (9%)	4 (7%)	1	11
15	AO	86/89 (97%)	55 (64%)	24 (28%)	7 (8%)	1	9
16	AP	81/88 (92%)	56 (69%)	19 (24%)	6 (7%)	1	10
17	AQ	97/105 (92%)	78 (80%)	15 (16%)	4 (4%)	2	18
18	AR	68/88 (77%)	49 (72%)	15 (22%)	4 (6%)	1	13
19	AS	76/93 (82%)	37 (49%)	21 (28%)	18 (24%)	0	1
20	AT	97/106 (92%)	49 (50%)	31 (32%)	17 (18%)	0	2
21	AU	22/27 (82%)	13 (59%)	8 (36%)	1 (4%)	2	17
24	AY	662/691 (96%)	440 (66%)	137 (21%)	85 (13%)	0	4
25	B0	82/85 (96%)	66 (80%)	13 (16%)	3 (4%)	2	20
26	B1	91/98 (93%)	65 (71%)	16 (18%)	10 (11%)	0	5
27	B2	69/72 (96%)	32 (46%)	24 (35%)	13 (19%)	0	2
28	B3	57/60 (95%)	41 (72%)	11 (19%)	5 (9%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	B4	55/71 (78%)	28 (51%)	12 (22%)	15 (27%)	0	0
30	B5	57/60 (95%)	36 (63%)	11 (19%)	10 (18%)	0	2
31	B6	48/54 (89%)	23 (48%)	11 (23%)	14 (29%)	0	0
32	B7	46/49 (94%)	38 (83%)	5 (11%)	3 (6%)	1	12
33	B8	61/65 (94%)	34 (56%)	16 (26%)	11 (18%)	0	2
34	B9	35/37 (95%)	21 (60%)	9 (26%)	5 (14%)	0	3
37	BC	226/229 (99%)	161 (71%)	55 (24%)	10 (4%)	2	17
38	BD	273/276 (99%)	192 (70%)	47 (17%)	34 (12%)	0	4
39	BE	202/206 (98%)	120 (59%)	49 (24%)	33 (16%)	0	2
40	BF	205/210 (98%)	141 (69%)	37 (18%)	27 (13%)	0	4
41	BG	179/182 (98%)	113 (63%)	41 (23%)	25 (14%)	0	3
42	BH	164/180 (91%)	85 (52%)	43 (26%)	36 (22%)	0	1
43	BK	137/147 (93%)	87 (64%)	41 (30%)	9 (7%)	1	12
44	BL	65/121 (54%)	57 (88%)	8 (12%)	0	100	100
45	BN	136/140 (97%)	90 (66%)	28 (21%)	18 (13%)	0	4
46	BO	120/122 (98%)	95 (79%)	16 (13%)	9 (8%)	1	10
47	BP	144/150 (96%)	78 (54%)	40 (28%)	26 (18%)	0	2
48	BQ	139/141 (99%)	103 (74%)	23 (16%)	13 (9%)	0	8
49	BR	115/118 (98%)	80 (70%)	20 (17%)	15 (13%)	0	4
50	BS	96/112 (86%)	46 (48%)	30 (31%)	20 (21%)	0	2
51	BT	135/146 (92%)	76 (56%)	32 (24%)	27 (20%)	0	2
52	BU	115/118 (98%)	75 (65%)	27 (24%)	13 (11%)	0	5
53	BV	99/101 (98%)	71 (72%)	11 (11%)	17 (17%)	0	2
54	BW	111/113 (98%)	78 (70%)	22 (20%)	11 (10%)	0	7
55	BX	90/96 (94%)	58 (64%)	24 (27%)	8 (9%)	0	9
56	BY	104/110 (94%)	50 (48%)	30 (29%)	24 (23%)	0	1
57	BZ	182/206 (88%)	113 (62%)	41 (22%)	28 (15%)	0	3
All	All	6645/7104 (94%)	4394 (66%)	1440 (22%)	811 (12%)	1	4

5 of 811 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	20	GLU

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Mol	Chain	Res	Type
2	AB	195	ASP
2	AB	233	SER
2	AB	239	VAL
3	AC	12	LEU

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	
2	AB	202/220 (92%)	177 (88%)	25 (12%)	4	15
3	AC	160/188 (85%)	134 (84%)	26 (16%)	2	10
4	AD	180/181 (99%)	162 (90%)	18 (10%)	6	20
5	AE	115/123 (94%)	100 (87%)	15 (13%)	3	14
6	AF	90/90 (100%)	81 (90%)	9 (10%)	6	20
7	AG	126/127 (99%)	116 (92%)	10 (8%)	10	29
8	AH	119/119 (100%)	105 (88%)	14 (12%)	4	16
9	AI	98/99 (99%)	88 (90%)	10 (10%)	6	20
10	AJ	88/92 (96%)	73 (83%)	15 (17%)	1	9
11	AK	90/99 (91%)	85 (94%)	5 (6%)	17	38
12	AL	104/109 (95%)	90 (86%)	14 (14%)	3	13
13	AM	99/101 (98%)	87 (88%)	12 (12%)	4	15
14	AN	49/50 (98%)	45 (92%)	4 (8%)	9	28
15	AO	79/80 (99%)	69 (87%)	10 (13%)	3	14
16	AP	72/74 (97%)	67 (93%)	5 (7%)	13	33
17	AQ	94/97 (97%)	82 (87%)	12 (13%)	3	14
18	AR	61/77 (79%)	58 (95%)	3 (5%)	21	42
19	AS	69/80 (86%)	57 (83%)	12 (17%)	1	9
20	AT	76/82 (93%)	67 (88%)	9 (12%)	4	16
21	AU	19/22 (86%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AY	563/582 (97%)	478 (85%)	85 (15%)	2	11
25	B0	66/67 (98%)	58 (88%)	8 (12%)	4	15
26	B1	78/83 (94%)	61 (78%)	17 (22%)	1	5
27	B2	66/67 (98%)	58 (88%)	8 (12%)	4	15
28	B3	51/52 (98%)	44 (86%)	7 (14%)	3	13
29	B4	51/63 (81%)	34 (67%)	17 (33%)	0	1
30	B5	51/52 (98%)	45 (88%)	6 (12%)	4	16
31	B6	49/52 (94%)	35 (71%)	14 (29%)	0	2
32	B7	41/42 (98%)	36 (88%)	5 (12%)	4	15
33	B8	53/55 (96%)	45 (85%)	8 (15%)	2	11
34	B9	34/34 (100%)	29 (85%)	5 (15%)	2	12
37	BC	180/181 (99%)	166 (92%)	14 (8%)	10	29
38	BD	217/218 (100%)	179 (82%)	38 (18%)	1	8
39	BE	165/166 (99%)	135 (82%)	30 (18%)	1	8
40	BF	165/166 (99%)	151 (92%)	14 (8%)	8	27
41	BG	155/156 (99%)	121 (78%)	34 (22%)	1	5
42	BH	136/148 (92%)	124 (91%)	12 (9%)	8	25
43	BK	104/111 (94%)	88 (85%)	16 (15%)	2	11
44	BL	46/85 (54%)	43 (94%)	3 (6%)	14	35
45	BN	117/119 (98%)	98 (84%)	19 (16%)	2	10
46	BO	100/100 (100%)	90 (90%)	10 (10%)	6	20
47	BP	112/116 (97%)	89 (80%)	23 (20%)	1	6
48	BQ	111/111 (100%)	94 (85%)	17 (15%)	2	11
49	BR	100/101 (99%)	85 (85%)	15 (15%)	2	11
50	BS	77/88 (88%)	67 (87%)	10 (13%)	3	14
51	BT	120/127 (94%)	97 (81%)	23 (19%)	1	7
52	BU	92/94 (98%)	84 (91%)	8 (9%)	8	25
53	BV	82/82 (100%)	71 (87%)	11 (13%)	3	13
54	BW	91/92 (99%)	82 (90%)	9 (10%)	6	21
55	BX	74/78 (95%)	62 (84%)	12 (16%)	2	10
56	BY	87/91 (96%)	75 (86%)	12 (14%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
57	BZ	162/179 (90%)	133 (82%)	29 (18%)	1 8
All	All	5586/5868 (95%)	4819 (86%)	767 (14%)	5 13

5 of 767 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	BE	22	PRO
45	BN	26	LEU
39	BE	94	GLU
39	BE	18	ASP
41	BG	80	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 173 such sidechains are listed below:

Mol	Chain	Res	Type
40	BF	133	ASN
49	BR	3	HIS
41	BG	27	ASN
45	BN	101	HIS
51	BT	55	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1522 (98%)	277 (18%)	43 (2%)
22	AV	76/77 (98%)	16 (21%)	0
23	AX	10/11 (90%)	4 (40%)	0
35	BA	2900/2915 (99%)	637 (21%)	77 (2%)
36	BB	118/122 (96%)	25 (21%)	0
All	All	4607/4647 (99%)	959 (20%)	120 (2%)

5 of 959 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	33	A

5 of 120 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	603	A
35	BA	2690	C
35	BA	1210	A
35	BA	2689	U
35	BA	2849	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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$
59	GDP	AY	702	-	24,30,30	2.06	6 (25%)	30,47,47	1.83	7 (23%)
58	FUA	AY	701	-	39,40,40	2.24	14 (35%)	49,64,64	1.87	13 (26%)

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
59	GDP	AY	702	-	-	3/12/32/32	0/3/3/3
58	FUA	AY	701	-	-	5/15/92/92	0/4/4/4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AY	702	GDP	C5-C6	-6.09	1.35	1.47
58	AY	701	FUA	C14-C8	-4.93	1.50	1.59
58	AY	701	FUA	C29-C22	4.78	1.54	1.47
58	AY	701	FUA	C23-C22	-4.73	1.39	1.51
58	AY	701	FUA	C23-C24	-4.57	1.38	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AY	702	GDP	C2-N1-C6	-4.23	117.31	125.10
58	AY	701	FUA	C13-C12-C11	-4.16	106.07	111.90
59	AY	702	GDP	PA-O3A-PB	-4.11	118.74	132.83
58	AY	701	FUA	C6-C5-C10	3.84	116.44	111.65
58	AY	701	FUA	C21-C14-C8	-3.75	108.81	112.27

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AY	701	FUA	C13-C17-C22-C29
58	AY	701	FUA	C17-C22-C23-C24
58	AY	701	FUA	C29-C22-C23-C24
59	AY	702	GDP	C5'-O5'-PA-O3A
58	AY	701	FUA	O3-C31-O2-C16

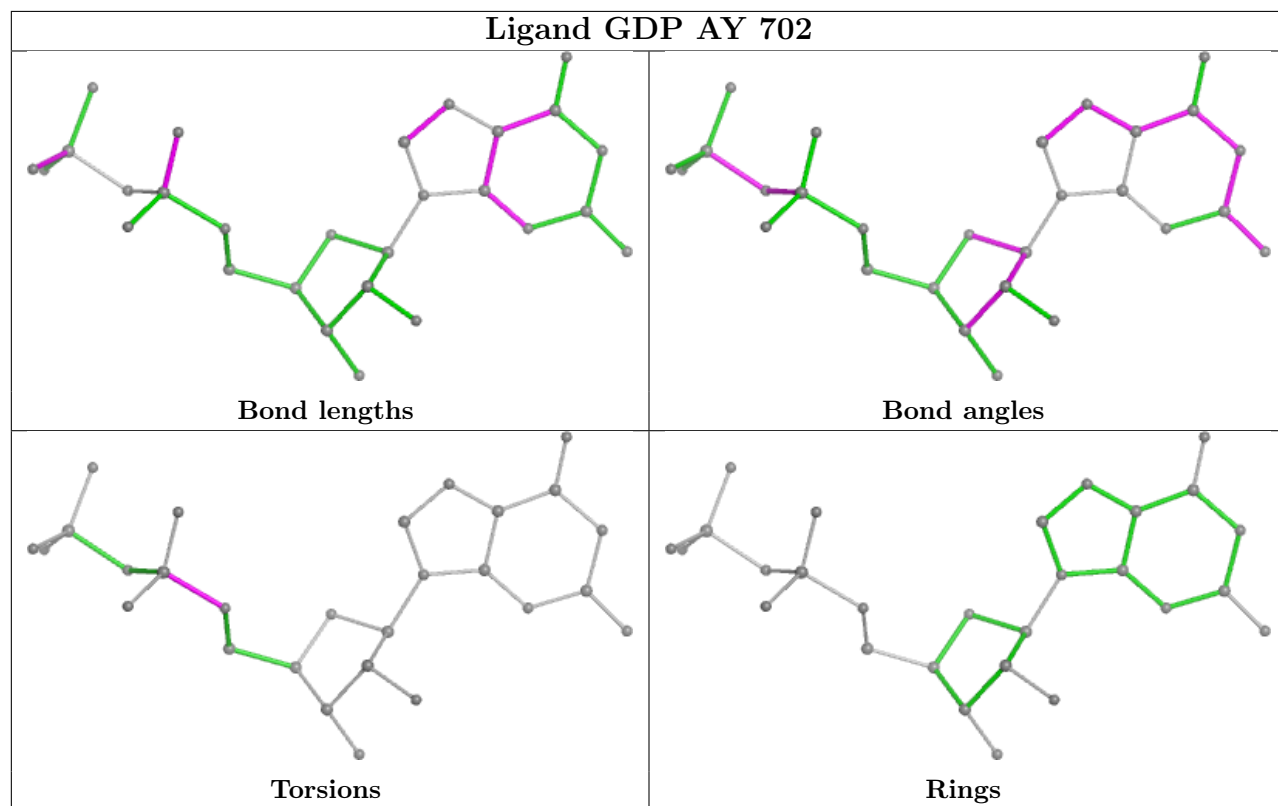
There are no ring outliers.

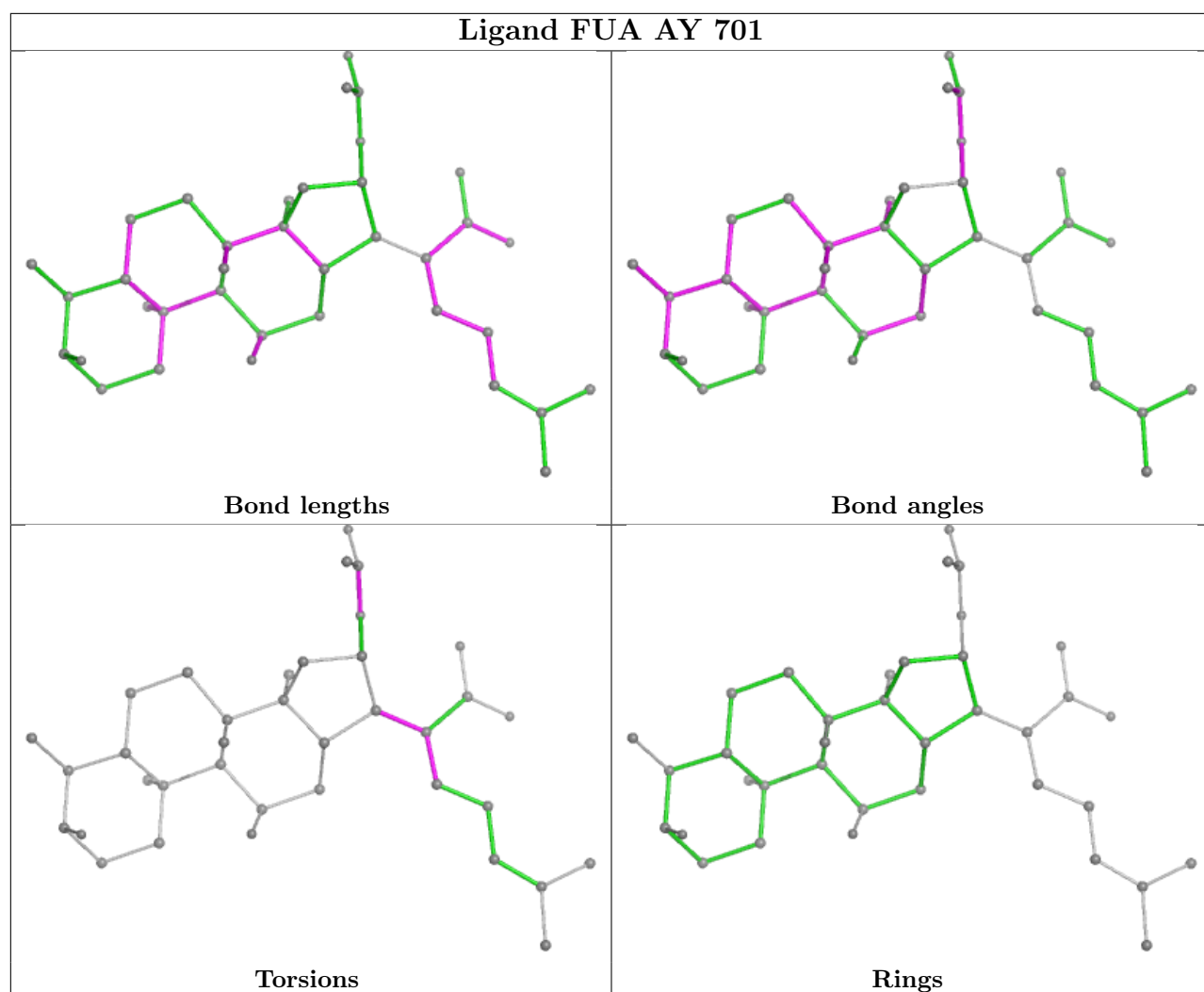
2 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	AY	702	GDP	6	0
58	AY	701	FUA	17	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-1799. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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.