



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:59 PM BST

PDB ID : 4V6T
EMDB ID: : EMD-5386
Title : Structure of the bacterial ribosome complexed by tmRNA-SmpB and EF-G during translocation and MLD-loading
Authors : Ramrath, D.J.F.; Yamamoto, H.; Rother, K.; Wittek, D.; Pech, M.; Mielke, T.; Loerke, J.; Scheerer, P.; Ivanov, P.; Teraoka, Y.; Shpanchenko, O.; Nierhaus, K.H.; Spahn, C.M.T.
Deposited on : 2012-01-27
Resolution : 8.30 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

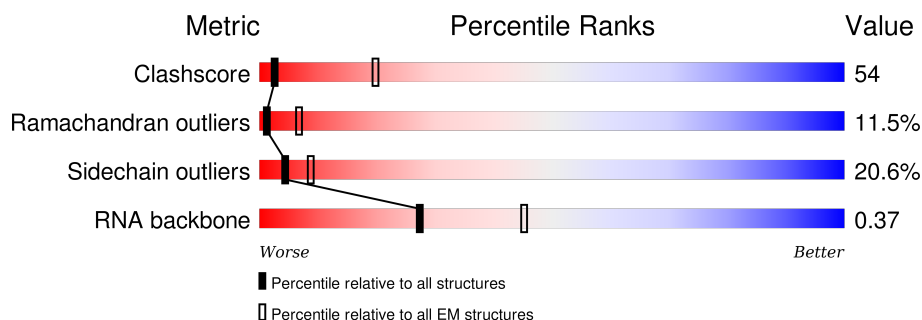
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.30 Å.

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




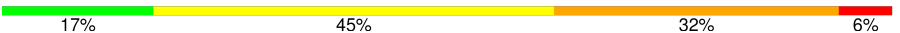
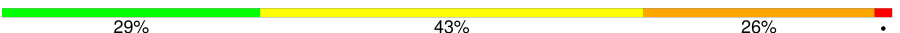

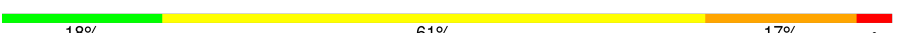
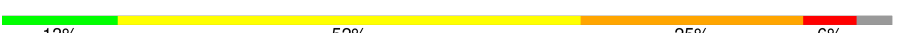
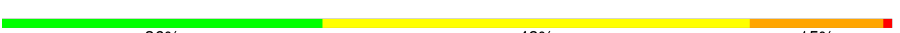




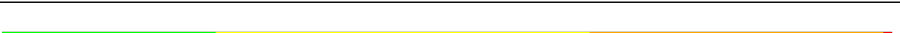





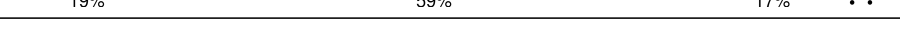




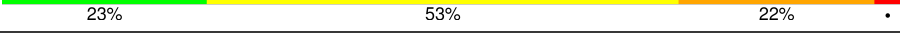

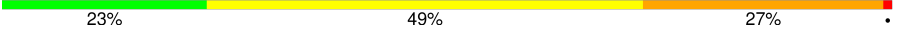
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1539	13% 54% 29% .
2	AB	218	10% 46% 35% 9%
3	AC	206	20% 53% 21% 5%
4	AD	205	21% 45% 31% .
5	AE	150	17% 55% 23% 5%
6	AF	100	20% 50% 25% 5%
7	AG	151	27% 48% 23% .
8	AH	129	21% 58% 19% .





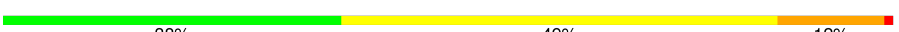
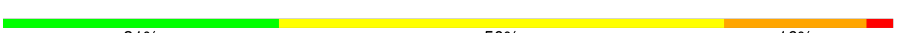
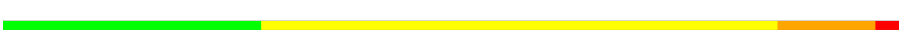





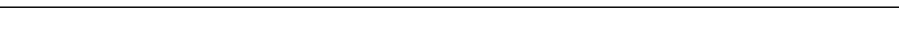



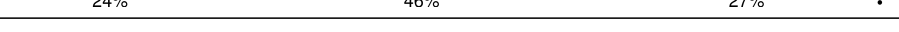






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Mol	Chain	Length	Quality of chain
9	AI	127	
10	AJ	98	
11	AK	117	
12	AL	123	
13	AM	114	
14	AN	100	
15	AO	88	
16	AP	82	
17	AQ	80	
18	AR	55	
19	AS	79	
20	AT	85	
21	AU	51	
22	AV	363	
23	AW	123	
24	AX	77	
25	AY	691	
26	BA	2903	
27	BC	271	
28	BD	209	
29	BE	201	
30	BF	177	
31	BG	176	
32	BH	149	
33	BI	141	

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Mol	Chain	Length	Quality of chain
34	BJ	142	
35	BK	122	
36	BL	143	
37	BM	136	
38	BN	120	
39	BO	116	
40	BP	114	
41	BQ	117	
42	BR	103	
43	BS	110	
44	BT	93	
45	BU	102	
46	BV	94	
47	BW	76	
48	BX	77	
49	BY	63	
50	BZ	58	
51	B0	56	
52	B1	50	
53	B2	46	
54	B3	64	
55	B4	38	
56	BB	119	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	PSU	AV	347	-	-	X	-

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 157519 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1538	Total	C	N	O	P	0	0
			32995	14716	6050	10691	1538		

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- 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
			1625	1028	305	289	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- 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
			1106	687	211	202	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- 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
			1022	634	206	179	3		

- 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
			787	493	150	143	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- 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
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 22 is a RNA chain called full length transfer messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	334	Total	C	N	O	P	0	0
			7135	3185	1286	2330	334		

- Molecule 23 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AW	122	Total	C	N	O	0	0
			993	637	181	175		

- Molecule 24 is a RNA chain called formyl-methionine specific initiator transfer RNA.

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

- Molecule 25 is a protein called elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	667	Total	C	N	O	S	0	1
			5215	3316	893	988	18		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BA	2903	Total	C	N	O	P	0	0
			62319	27801	11467	20149	2902		

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BU	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	B1	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

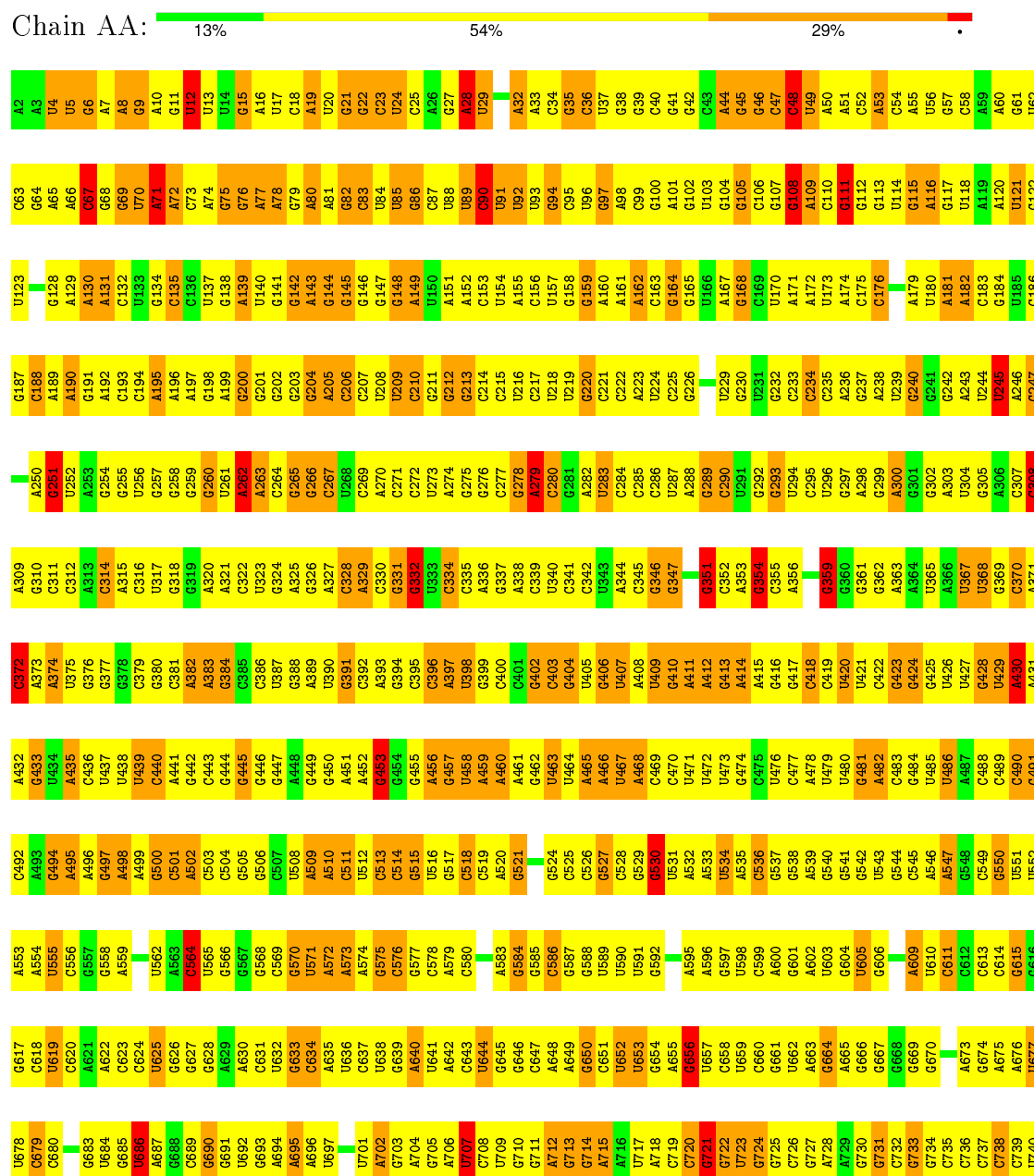
- Molecule 56 is a RNA chain called 5S ribosomal RNA.

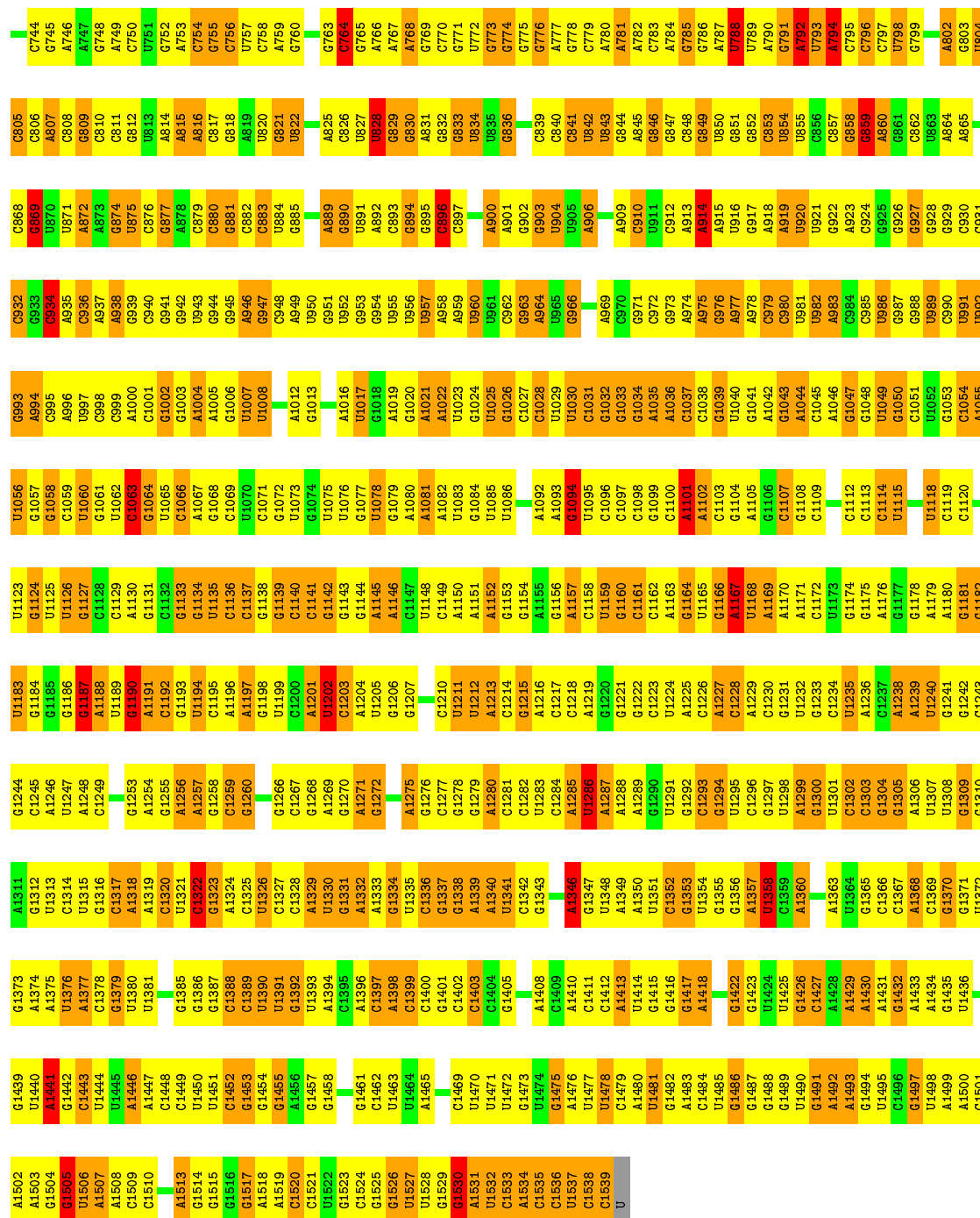
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	BB	119	2548	1135	466	829	118	0	0

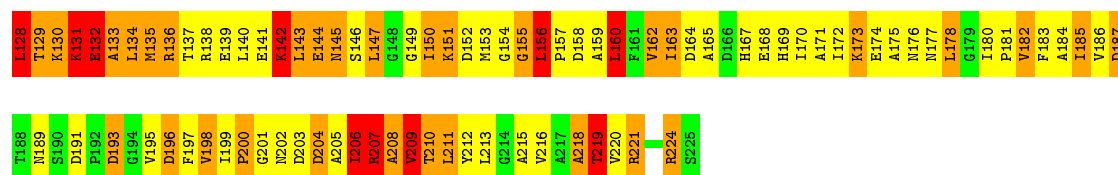
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: 16S ribosomal RNA

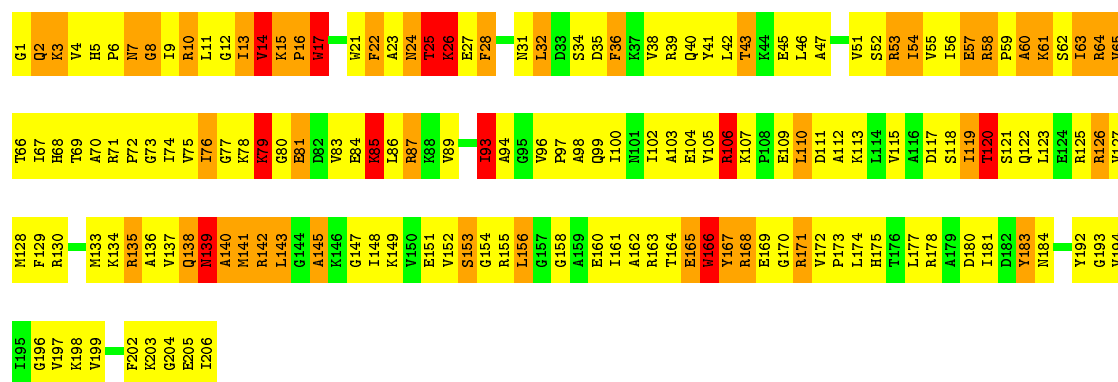


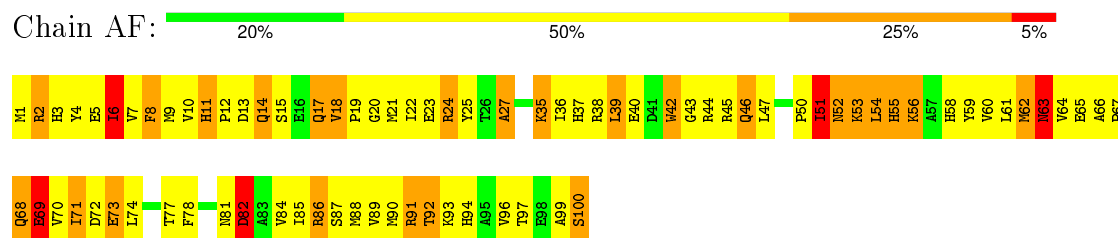




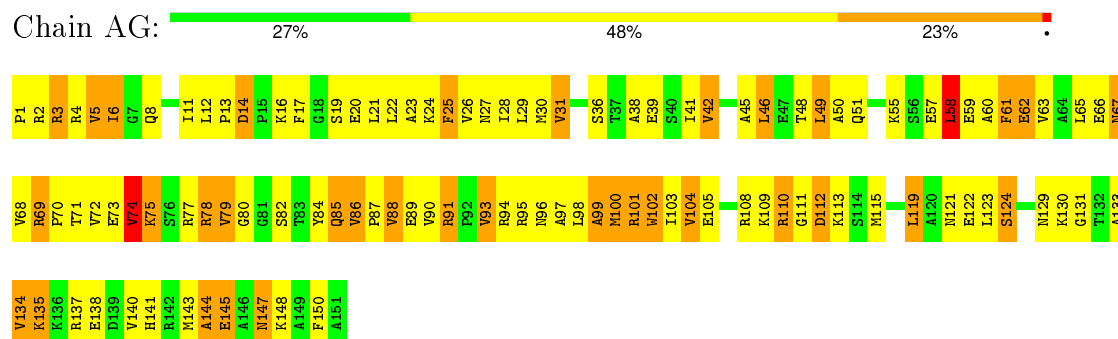
• Molecule 3: 30S ribosomal protein S3

Chain AC: 20% 53% 21% 5%

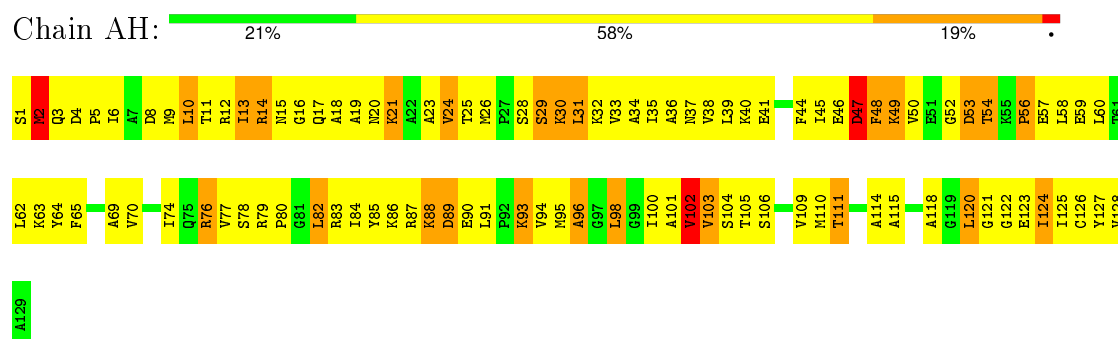




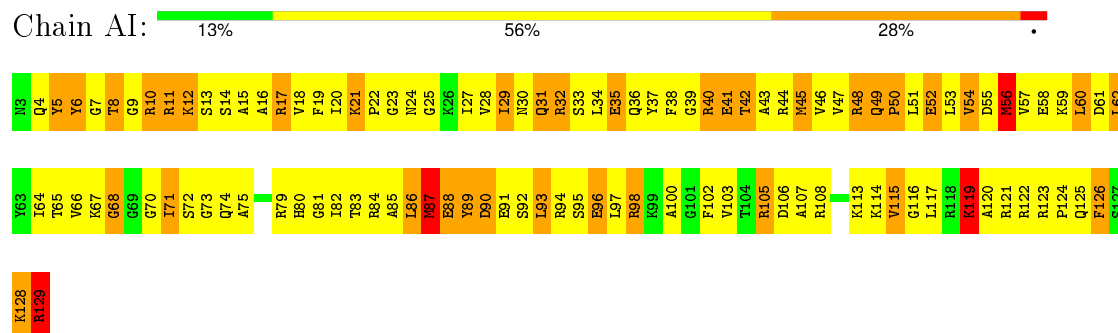
• Molecule 7: 30S ribosomal protein S7



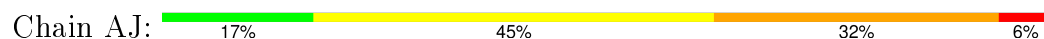
• Molecule 8: 30S ribosomal protein S8

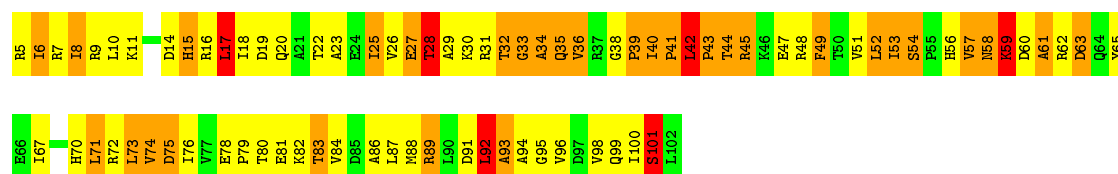


• Molecule 9: 30S ribosomal protein S9



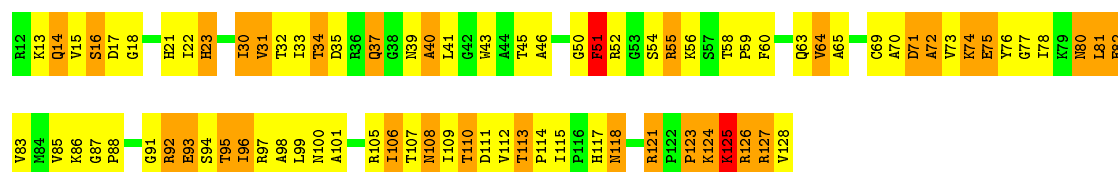
• Molecule 10: 30S ribosomal protein S10





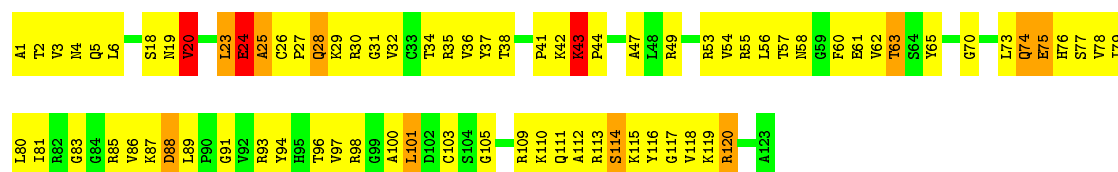
- Molecule 11: 30S ribosomal protein S11

Chain AK: 29% 43% 26% .



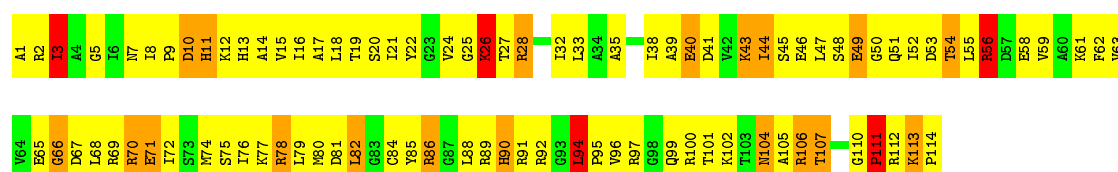
- Molecule 12: 30S ribosomal protein S12

Chain AL: 36% 54% 8% .



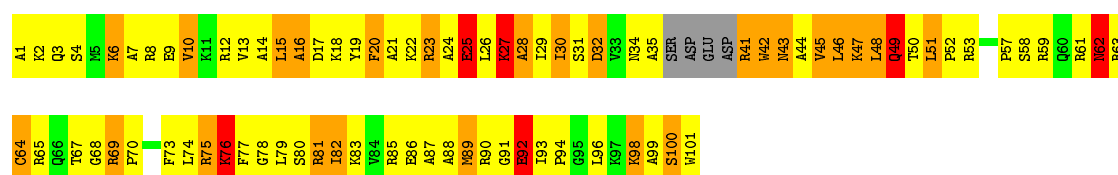
- Molecule 13: 30S ribosomal protein S13

Chain AM: 18% 61% 17% .



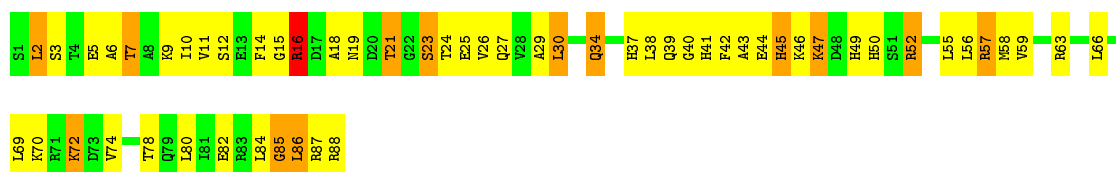
- Molecule 14: 30S ribosomal protein S14

Chain AN: 13% 52% 25% 6% .



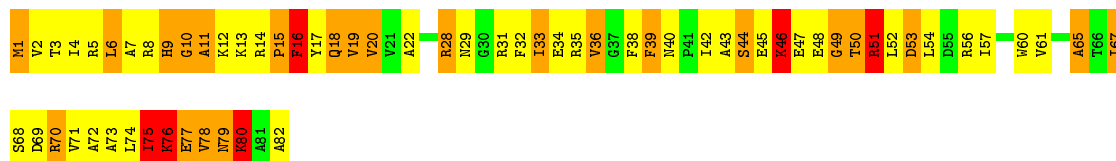
- Molecule 15: 30S ribosomal protein S15

Chain AO: 36% 48% 15% .



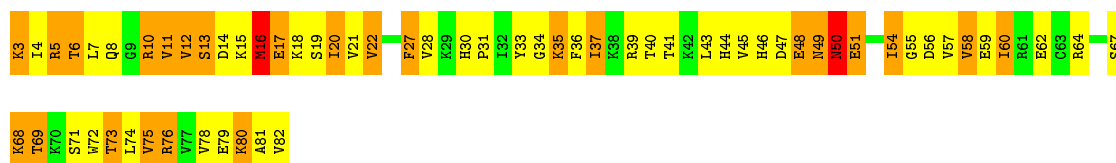
• Molecule 16: 30S ribosomal protein S16

Chain AP: 21% 44% 28% 7%



• Molecule 17: 30S ribosomal protein S17

Chain AQ: 21% 45% 31% .



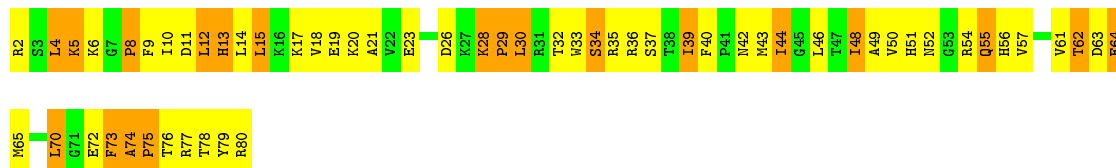
• Molecule 18: 30S ribosomal protein S18

Chain AR: 22% 64% 9% 5%



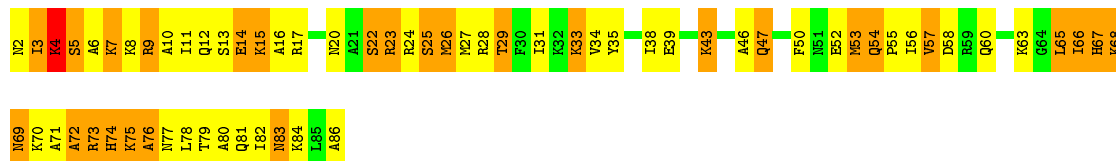
• Molecule 19: 30S ribosomal protein S19

Chain AS: 27% 48% 25%



• Molecule 20: 30S ribosomal protein S20

Chain AT: 24% 42% 33% .



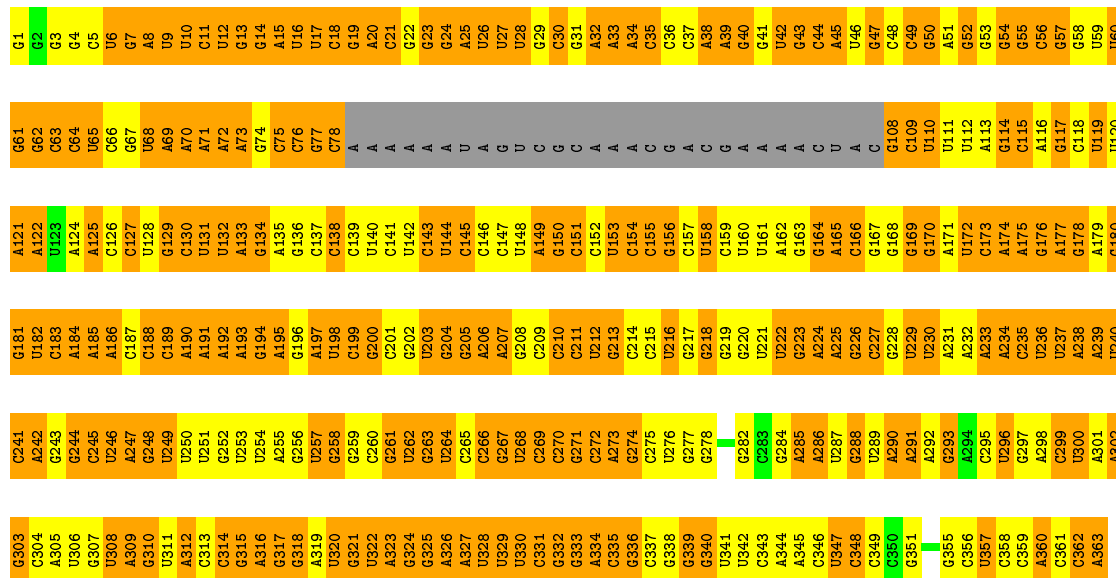
- Molecule 21: 30S ribosomal protein S21

Chain AU: 




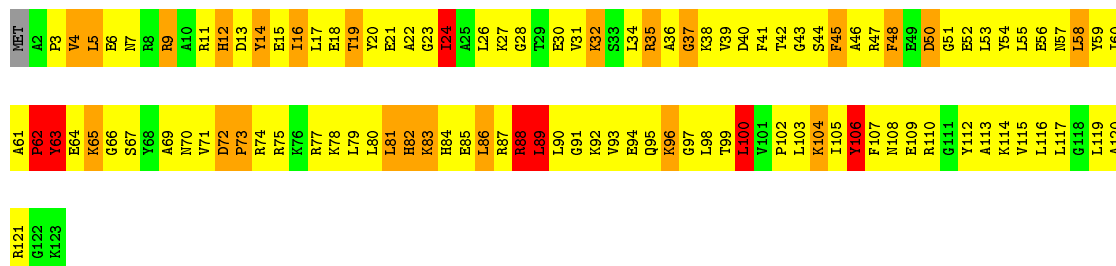
- Molecule 22: full length transfer messenger RNA (tmRNA)

Chain AV: 



- Molecule 23: SsrA-binding protein

Chain AW: 

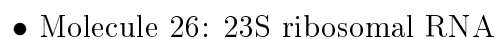


- Molecule 24: formyl-methionine specific initiator transfer RNA

Chain AX: 



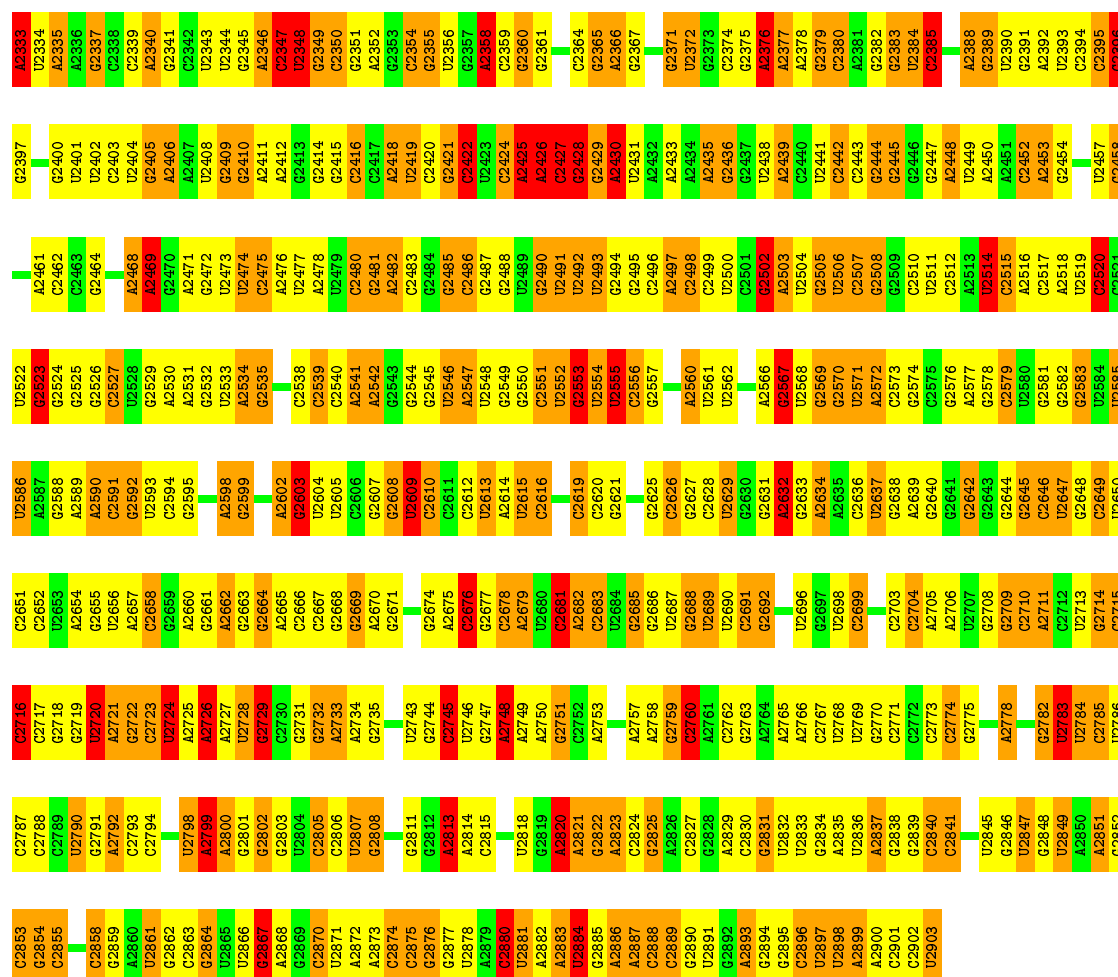
- Molecule 25: elongation factor G

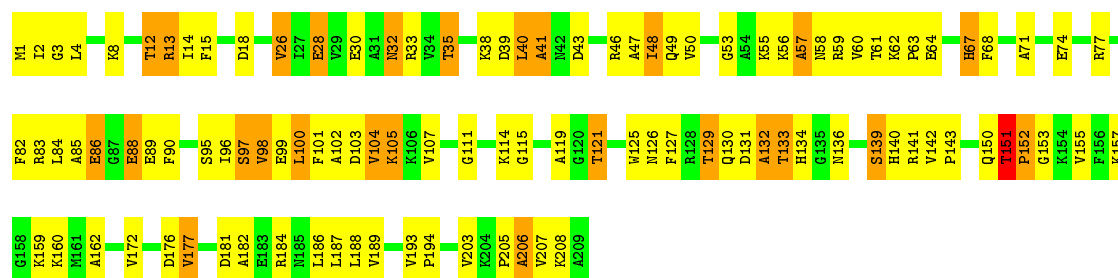


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G1277	G1278	G1279	G1280	G1281	G1282	G1283	A1205	U1141	U1081	A1021	A960	C897	C837	G776	U714	C651	A567	U525	U459	C331	C268
G1284	G1285	G1286	G1287	G1288	G1289	G1290	C1208	A1142	U1082	U1022	C961	C898	U838	G777	A715	U653	U569	A526	A460	C332	C269
U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1209	A1143	U1083	U1023	G962	U839	U839	G778	A716	A654	U569	A527	C461	G333	A270
G1212	G1213	G1214	G1215	G1216	G1217	G1218	U1209	A1144	A1084	G1024	U963	C900	C840	U779	C717	A655	A528	A529	C462	C334	G271
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G1280	G1281	G1282	G1283	G1284	G1285	G1286	U1213	G1154	A1094	G1034	G974	A910	U850	A789	A727	U665	A544	A545	G476	A346	C281
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A1306	A1307	A1308	A1309	A1310	A1311	A1312	U1217	U1158	A1098	G1038	G978	C914	C854	A793	G731	A670	A552	A553	A480	C351	U285
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G1320	G1321	G1322	G1323	G1324	G1325	G1326	U1219	U1160	C1100	A1040	G980	C916	U856	A795	G733	A672	A556	A557	A482	C353	U287
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G1341	G1342	G1343	G1344	G1345	G1346	G1347	U1222	A1163	U1101	G1043	A982	C919	G859	A798	A736	A675	A562	A563	A485	C356	U290
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G1397	G1398	G1399	G1400	G1401	G1402	G1403	U1230	G1171	C1111	G1051	C991	A827	C867	U807	G745	G682	A578	A579	A493	C364	G299
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U1594	U1595	U1596	U1597	U1598	U1599	U1600	U1259	U1200	G1200	U1079	U1019	C956	C896	A836	G775	U713	A598	A599	C523	C393	G328
G1601	G1602	G1603	G1604	G1605	G1606	G1607	U1260	U1201	C1201	U1											

WORLDWIDE
PDB
PROTEIN DATA BANK

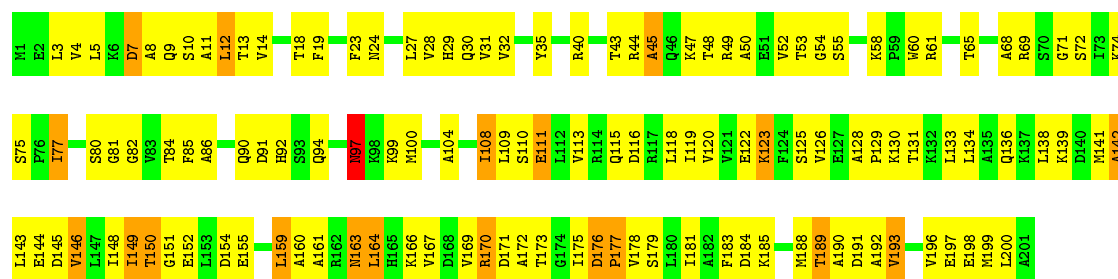
 **EMDataBank**
Unified Data Resource for 3DEM





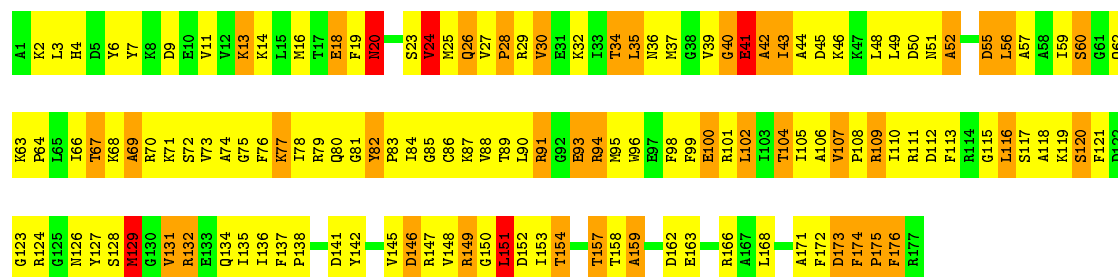
- Molecule 29: 50S ribosomal protein L4

Chain BE:



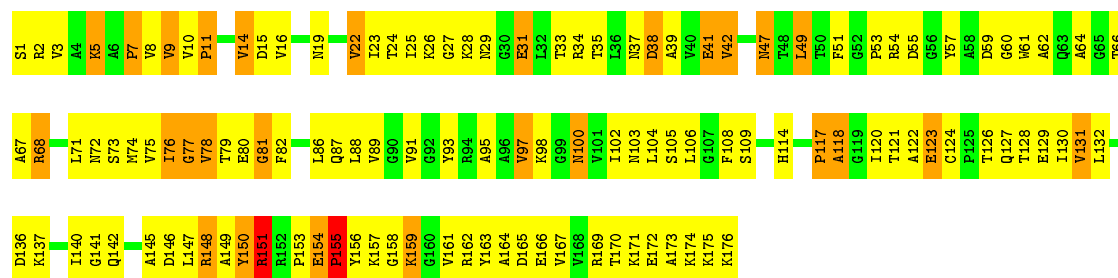
- Molecule 30: 50S ribosomal protein L5

Chain BF:



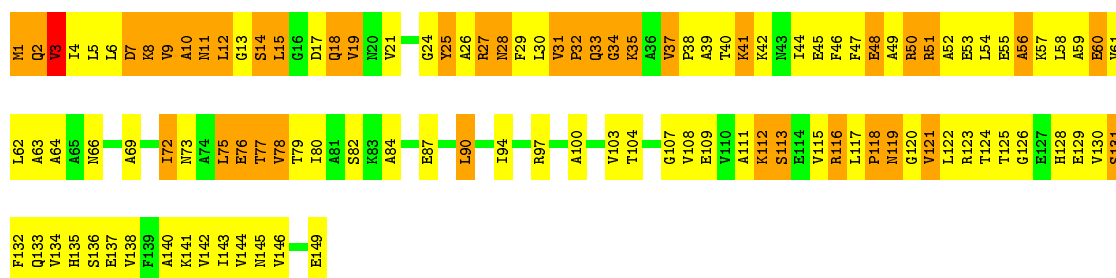
- Molecule 31: 50S ribosomal protein L6

Chain BG:



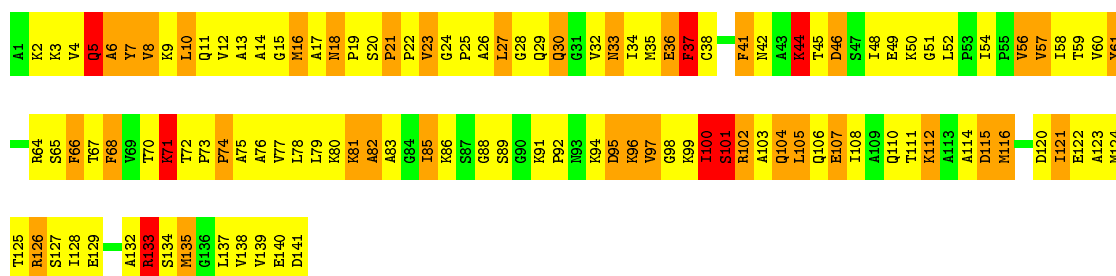
- Molecule 32: 50S ribosomal protein L9

Chain BH:



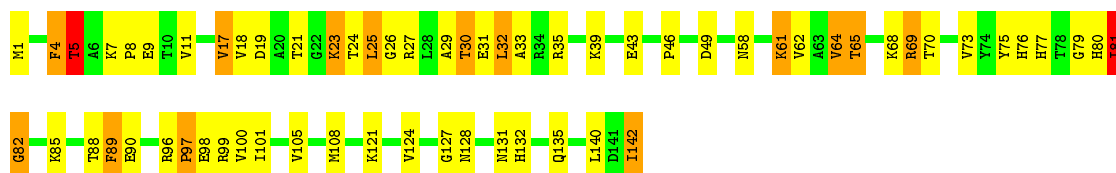
• Molecule 33: 50S ribosomal protein L11

Chain BI: 16% 53% 26% 5%



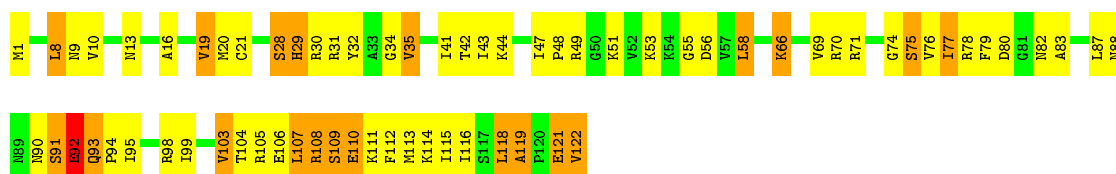
• Molecule 34: 50S ribosomal protein L13

Chain BJ: 56% 33% 10%



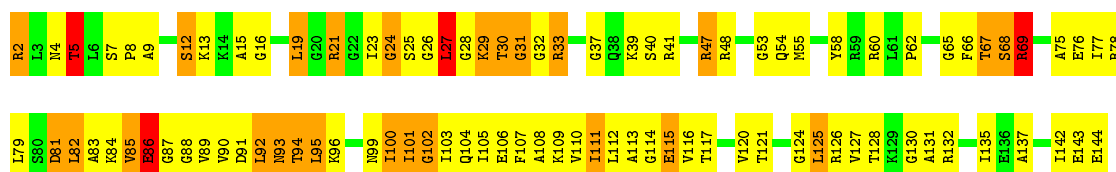
• Molecule 35: 50S ribosomal protein L14

Chain BK: 43% 39% 16%

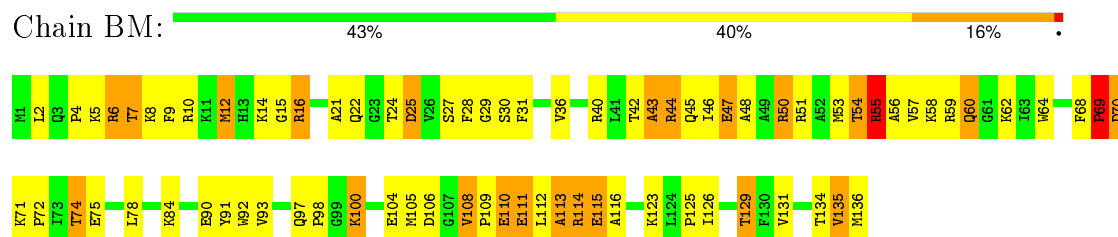


• Molecule 36: 50S ribosomal protein L15

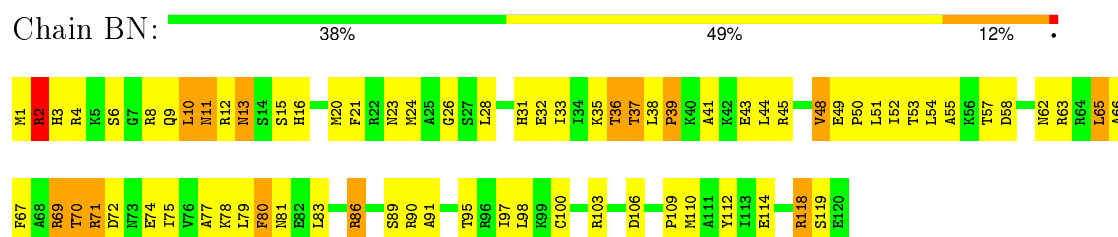
Chain BL: 34% 46% 17%



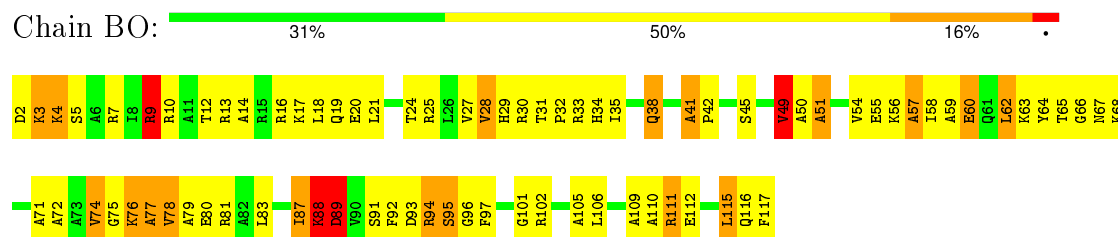
- Molecule 37: 50S ribosomal protein L16



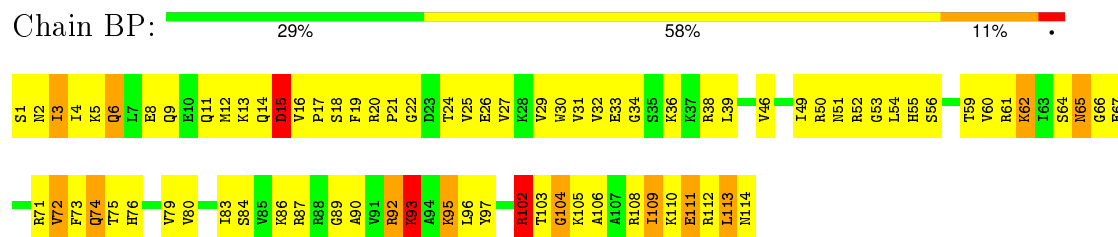
- Molecule 38: 50S ribosomal protein L17



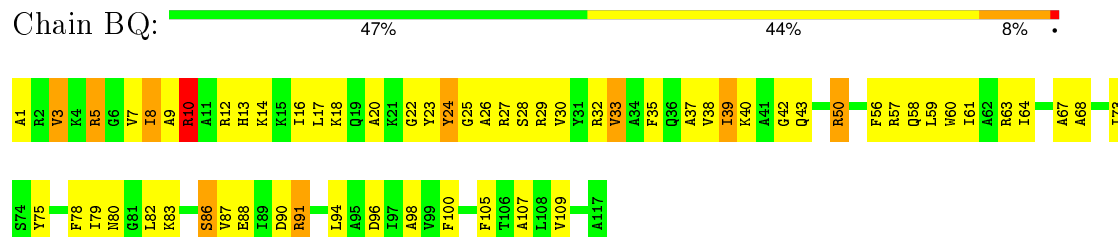
- Molecule 39: 50S ribosomal protein L18



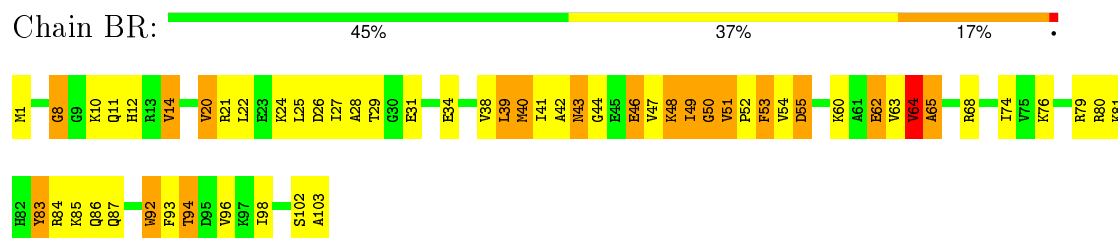
- Molecule 40: 50S ribosomal protein L19



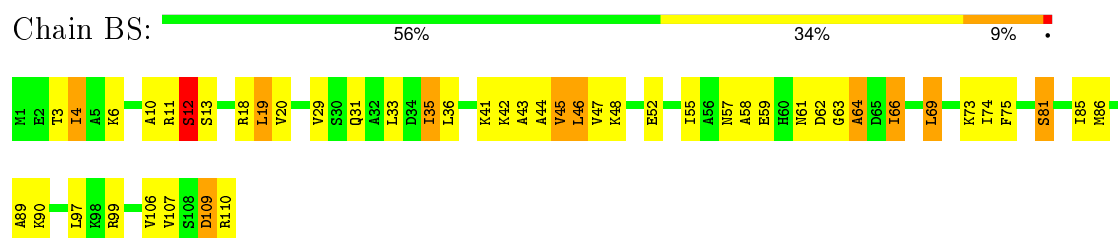
- Molecule 41: 50S ribosomal protein L20



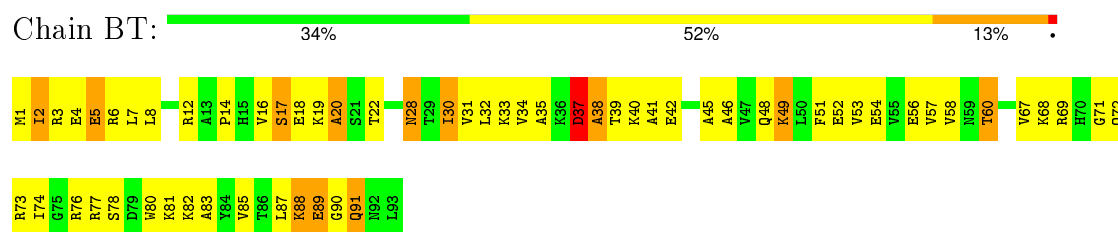
- Molecule 42: 50S ribosomal protein L21



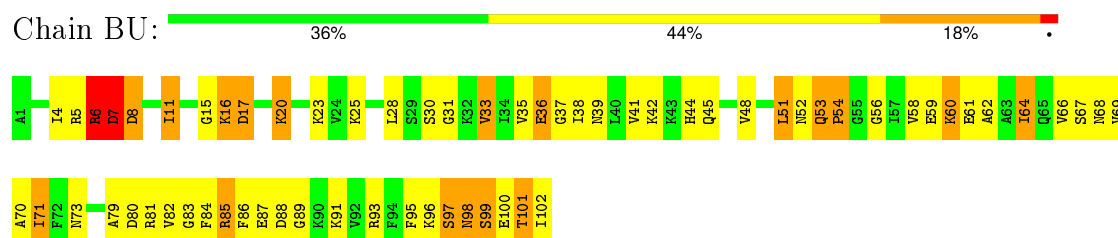
- Molecule 43: 50S ribosomal protein L22



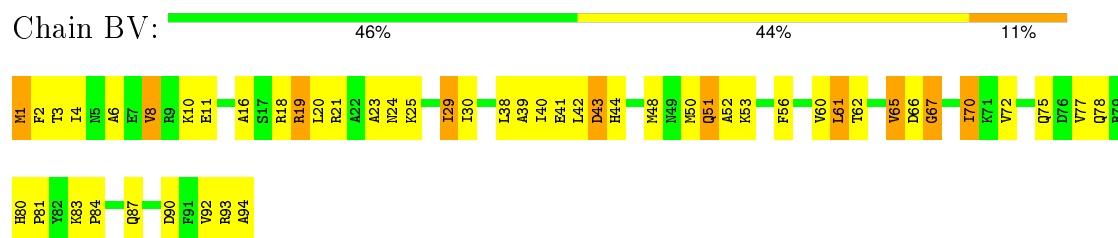
- Molecule 44: 50S ribosomal protein L23



- Molecule 45: 50S ribosomal protein L24

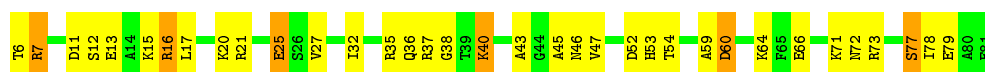


- Molecule 46: 50S ribosomal protein L25



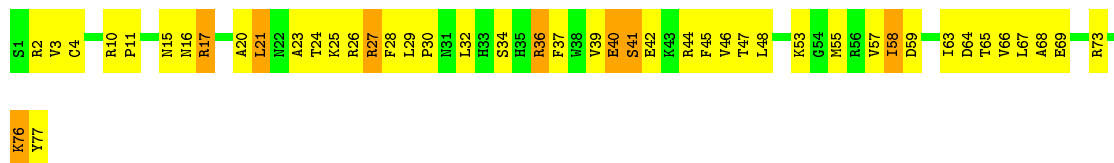
- Molecule 47: 50S ribosomal protein L27





- Molecule 48: 50S ribosomal protein L28

Chain BX: 40% 49% 10%



- Molecule 49: 50S ribosomal protein L29

Chain BY: 24% 46% 27%



- Molecule 50: 50S ribosomal protein L30

Chain BZ: 45% 50% 5%



- Molecule 51: 50S ribosomal protein L32

Chain B0: 48% 38% 14%



- Molecule 52: 50S ribosomal protein L33

Chain B1: 30% 54% 14%



- Molecule 53: 50S ribosomal protein L34

Chain B2: 46% 46% 7%



- Molecule 54: 50S ribosomal protein L35

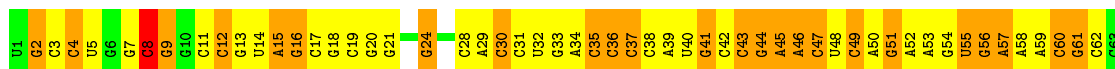
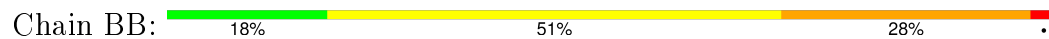
Chain B3: 45% 52% 3%



- Molecule 55: 50S ribosomal protein L36



- Molecule 56: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	68843	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	The volumes were CTF-corrected in defocus groups, with an average of approximately 215 individual images per group	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 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: 5MU, PSU

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	AA	0.85	5/36944 (0.0%)	1.26	314/57632 (0.5%)
10	AJ	0.57	0/797	0.74	0/1077
11	AK	0.67	0/893	0.82	0/1205
12	AL	0.61	0/969	0.81	0/1300
13	AM	0.52	0/893	0.74	0/1193
14	AN	0.55	0/785	0.76	0/1043
15	AO	0.55	0/722	0.73	0/964
16	AP	0.54	0/659	0.82	1/884 (0.1%)
17	AQ	0.57	0/658	0.74	0/881
18	AR	0.61	0/463	0.70	0/621
19	AS	0.48	0/653	0.73	0/877
2	AB	0.60	0/1736	0.79	0/2338
20	AT	0.54	0/671	0.69	0/888
21	AU	0.93	0/431	0.97	0/570
22	AV	0.56	13/7912 (0.2%)	0.91	43/12332 (0.3%)
23	AW	0.79	1/1011 (0.1%)	0.96	1/1354 (0.1%)
24	AX	0.65	0/1832	0.81	0/2855
25	AY	0.40	0/5313	0.69	0/7195
26	BA	1.60	611/69795 (0.9%)	1.67	2068/108884 (1.9%)
27	BC	0.80	0/2122	0.90	1/2852 (0.0%)
28	BD	0.96	0/1586	0.92	1/2134 (0.0%)
29	BE	0.91	0/1571	0.89	1/2113 (0.0%)
3	AC	0.56	0/1652	0.71	0/2225
30	BF	0.65	0/1435	0.74	0/1926
31	BG	0.75	0/1343	0.85	1/1816 (0.1%)
32	BH	0.68	1/1121 (0.1%)	0.77	0/1515
33	BI	0.72	0/1046	0.74	0/1410
34	BJ	1.01	0/1152	0.84	1/1551 (0.1%)
35	BK	0.92	2/948 (0.2%)	0.94	1/1268 (0.1%)
36	BL	0.94	0/1054	1.01	0/1403
37	BM	0.94	0/1093	0.96	0/1460
38	BN	0.91	0/974	0.96	1/1301 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BO	0.76	0/902	0.87	1/1209 (0.1%)
4	AD	0.59	0/1665	0.74	1/2227 (0.0%)
40	BP	0.89	0/929	0.88	1/1242 (0.1%)
41	BQ	1.14	0/960	0.96	1/1278 (0.1%)
42	BR	1.01	1/829 (0.1%)	0.98	0/1107
43	BS	1.08	1/864 (0.1%)	0.97	1/1156 (0.1%)
44	BT	0.82	0/745	0.86	0/994
45	BU	0.91	0/788	0.90	0/1051
46	BV	0.79	0/766	0.81	0/1025
47	BW	1.02	0/582	0.97	0/769
48	BX	0.79	0/635	0.84	0/848
49	BY	0.76	0/510	0.96	1/677 (0.1%)
5	AE	0.62	0/1119	0.85	0/1504
50	BZ	1.04	0/453	0.95	0/605
51	B0	0.96	0/450	0.98	2/599 (0.3%)
52	B1	0.75	0/417	0.76	0/554
53	B2	1.03	0/380	0.99	2/498 (0.4%)
54	B3	0.94	0/513	0.85	0/676
55	B4	0.92	0/303	0.99	0/397
56	BB	1.33	4/2847 (0.1%)	1.58	79/4440 (1.8%)
6	AF	0.65	0/836	0.82	1/1128 (0.1%)
7	AG	0.50	0/1196	0.67	0/1602
8	AH	0.60	0/989	0.78	0/1326
9	AI	0.52	1/1034 (0.1%)	0.71	0/1375
All	All	1.19	640/170946 (0.4%)	1.35	2524/255354 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	AK	0	1
13	AM	0	1
14	AN	0	1
21	AU	0	2
23	AW	0	1
24	AX	0	4
27	BC	0	1
28	BD	0	2
33	BI	0	1
4	AD	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	BR	0	1
45	BU	0	1
5	AE	0	1
50	BZ	0	1
9	AI	0	1
All	All	0	20

The worst 5 of 640 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BA	1142	A	N9-C4	-18.15	1.26	1.37
26	BA	984	A	N9-C4	-13.41	1.29	1.37
26	BA	984	A	C5-C6	-10.40	1.31	1.41
26	BA	528	A	N7-C5	-10.33	1.33	1.39
26	BA	2250	G	N9-C4	-10.21	1.29	1.38

The worst 5 of 2524 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	984	A	C2-N3-C4	-18.77	101.21	110.60
26	BA	2250	G	N3-C4-C5	17.36	137.28	128.60
26	BA	1638	C	N1-C2-O2	-16.58	108.95	118.90
26	BA	1142	A	C2-N3-C4	-16.57	102.31	110.60
26	BA	1142	A	N3-C4-C5	16.05	138.03	126.80

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AD	47	LEU	Peptide
5	AE	100	GLU	Peptide
9	AI	5	TYR	Peptide
11	AK	125	LYS	Peptide
13	AM	111	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32995	0	16600	2523	0
2	AB	1705	0	1731	418	0
3	AC	1625	0	1695	268	0
4	AD	1643	0	1710	290	0
5	AE	1106	0	1147	238	0
6	AF	818	0	808	108	0
7	AG	1182	0	1238	130	0
8	AH	979	0	1034	159	0
9	AI	1022	0	1070	221	0
10	AJ	787	0	828	179	0
11	AK	877	0	887	162	0
12	AL	955	0	1019	110	0
13	AM	884	0	944	162	0
14	AN	774	0	827	134	0
15	AO	714	0	736	63	0
16	AP	649	0	666	105	0
17	AQ	649	0	691	118	0
18	AR	456	0	478	45	0
19	AS	638	0	665	77	0
20	AT	665	0	714	83	0
21	AU	426	0	449	138	0
22	AV	7135	0	3594	2248	0
23	AW	993	0	1030	330	0
24	AX	1640	0	835	261	0
25	AY	5215	0	5279	930	0
26	BA	62319	0	31328	3013	0
27	BC	2083	0	2157	231	0
28	BD	1565	0	1616	117	0
29	BE	1552	0	1619	139	0
30	BF	1411	0	1443	233	0
31	BG	1323	0	1374	154	0
32	BH	1110	0	1148	153	0
33	BI	1032	0	1086	289	0
34	BJ	1129	0	1162	61	0
35	BK	939	0	1012	77	0
36	BL	1045	0	1117	130	0
37	BM	1074	0	1157	125	0
38	BN	961	0	1000	90	0
39	BO	892	0	923	88	0
40	BP	917	0	965	96	0
41	BQ	947	0	1022	63	0
42	BR	816	0	839	84	0
43	BS	857	0	922	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BT	739	0	807	70	0
45	BU	780	0	834	63	0
46	BV	753	0	780	58	0
47	BW	575	0	589	29	0
48	BX	625	0	655	38	0
49	BY	509	0	543	88	0
50	BZ	449	0	491	28	0
51	B0	444	0	461	34	0
52	B1	410	0	440	36	0
53	B2	377	0	418	26	0
54	B3	504	0	574	41	0
55	B4	302	0	343	24	0
56	BB	2548	0	1292	102	0
All	All	157519	0	106792	14112	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 54.

The worst 5 of 14112 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)
23:AW:38:LYS:HE2	26:BA:1910:G:P	1.23	1.71
22:AV:172:U:H2'	22:AV:173:C:C6	1.25	1.65
25:AY:633:GLY:HA2	26:BA:1068:G:C8	1.19	1.62
22:AV:323:A:H2'	22:AV:324:G:C8	1.34	1.62
22:AV:48:C:C2'	22:AV:49:C:H5''	1.25	1.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	216/218 (99%)	109 (50%)	49 (23%)	58 (27%)	0	1
3	AC	204/206 (99%)	126 (62%)	48 (24%)	30 (15%)	0	6
4	AD	203/205 (99%)	123 (61%)	41 (20%)	39 (19%)	0	3
5	AE	148/150 (99%)	87 (59%)	38 (26%)	23 (16%)	0	5
6	AF	98/100 (98%)	62 (63%)	21 (21%)	15 (15%)	0	5
7	AG	149/151 (99%)	85 (57%)	42 (28%)	22 (15%)	0	5
8	AH	127/129 (98%)	79 (62%)	37 (29%)	11 (9%)	1	17
9	AI	125/127 (98%)	76 (61%)	34 (27%)	15 (12%)	0	8
10	AJ	96/98 (98%)	60 (62%)	14 (15%)	22 (23%)	0	2
11	AK	115/117 (98%)	84 (73%)	17 (15%)	14 (12%)	0	8
12	AL	121/123 (98%)	85 (70%)	29 (24%)	7 (6%)	2	27
13	AM	112/114 (98%)	78 (70%)	22 (20%)	12 (11%)	0	11
14	AN	92/100 (92%)	47 (51%)	27 (29%)	18 (20%)	0	3
15	AO	86/88 (98%)	57 (66%)	22 (26%)	7 (8%)	1	19
16	AP	80/82 (98%)	48 (60%)	11 (14%)	21 (26%)	0	1
17	AQ	78/80 (98%)	47 (60%)	18 (23%)	13 (17%)	0	5
18	AR	53/55 (96%)	34 (64%)	13 (24%)	6 (11%)	0	10
19	AS	77/79 (98%)	37 (48%)	28 (36%)	12 (16%)	0	5
20	AT	83/85 (98%)	37 (45%)	31 (37%)	15 (18%)	0	4
21	AU	49/51 (96%)	20 (41%)	15 (31%)	14 (29%)	0	0
23	AW	120/123 (98%)	84 (70%)	24 (20%)	12 (10%)	1	14
25	AY	663/691 (96%)	436 (66%)	136 (20%)	91 (14%)	0	6
27	BC	269/271 (99%)	217 (81%)	31 (12%)	21 (8%)	1	20
28	BD	207/209 (99%)	166 (80%)	30 (14%)	11 (5%)	2	29
29	BE	199/201 (99%)	158 (79%)	32 (16%)	9 (4%)	3	33
30	BF	175/177 (99%)	118 (67%)	38 (22%)	19 (11%)	0	11
31	BG	174/176 (99%)	129 (74%)	30 (17%)	15 (9%)	1	17
32	BH	147/149 (99%)	95 (65%)	29 (20%)	23 (16%)	0	5
33	BI	139/141 (99%)	65 (47%)	47 (34%)	27 (19%)	0	3
34	BJ	140/142 (99%)	123 (88%)	11 (8%)	6 (4%)	3	34
35	BK	120/122 (98%)	88 (73%)	24 (20%)	8 (7%)	1	24
36	BL	141/143 (99%)	99 (70%)	21 (15%)	21 (15%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BM	134/136 (98%)	111 (83%)	14 (10%)	9 (7%)	1	24
38	BN	118/120 (98%)	92 (78%)	20 (17%)	6 (5%)	2	30
39	BO	114/116 (98%)	83 (73%)	17 (15%)	14 (12%)	0	8
40	BP	112/114 (98%)	96 (86%)	12 (11%)	4 (4%)	4	38
41	BQ	115/117 (98%)	100 (87%)	13 (11%)	2 (2%)	11	55
42	BR	101/103 (98%)	84 (83%)	9 (9%)	8 (8%)	1	19
43	BS	108/110 (98%)	90 (83%)	12 (11%)	6 (6%)	2	28
44	BT	91/93 (98%)	67 (74%)	13 (14%)	11 (12%)	0	8
45	BU	100/102 (98%)	75 (75%)	13 (13%)	12 (12%)	0	8
46	BV	92/94 (98%)	79 (86%)	11 (12%)	2 (2%)	8	49
47	BW	74/76 (97%)	68 (92%)	4 (5%)	2 (3%)	6	45
48	BX	75/77 (97%)	64 (85%)	9 (12%)	2 (3%)	6	45
49	BY	61/63 (97%)	34 (56%)	13 (21%)	14 (23%)	0	2
50	BZ	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
51	B0	54/56 (96%)	44 (82%)	8 (15%)	2 (4%)	4	38
52	B1	48/50 (96%)	32 (67%)	12 (25%)	4 (8%)	1	18
53	B2	44/46 (96%)	37 (84%)	6 (14%)	1 (2%)	8	48
54	B3	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
55	B4	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	6	44
All	All	6401/6536 (98%)	4452 (70%)	1212 (19%)	737 (12%)	1	9

5 of 737 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	15	PHE
2	AB	21	TYR
2	AB	33	ALA
2	AB	63	LYS
2	AB	67	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	180/180 (100%)	114 (63%)	66 (37%)	0	1
3	AC	170/170 (100%)	125 (74%)	45 (26%)	0	5
4	AD	172/172 (100%)	132 (77%)	40 (23%)	1	7
5	AE	113/113 (100%)	80 (71%)	33 (29%)	0	3
6	AF	87/87 (100%)	60 (69%)	27 (31%)	0	3
7	AG	124/124 (100%)	90 (73%)	34 (27%)	0	4
8	AH	104/104 (100%)	78 (75%)	26 (25%)	1	6
9	AI	105/105 (100%)	74 (70%)	31 (30%)	0	3
10	AJ	86/86 (100%)	63 (73%)	23 (27%)	0	5
11	AK	90/90 (100%)	66 (73%)	24 (27%)	0	5
12	AL	103/103 (100%)	86 (84%)	17 (16%)	3	19
13	AM	92/92 (100%)	73 (79%)	19 (21%)	1	10
14	AN	79/83 (95%)	56 (71%)	23 (29%)	0	3
15	AO	76/76 (100%)	61 (80%)	15 (20%)	1	12
16	AP	65/65 (100%)	45 (69%)	20 (31%)	0	3
17	AQ	74/74 (100%)	54 (73%)	20 (27%)	0	5
18	AR	48/48 (100%)	40 (83%)	8 (17%)	3	19
19	AS	70/70 (100%)	56 (80%)	14 (20%)	1	11
20	AT	65/65 (100%)	45 (69%)	20 (31%)	0	3
21	AU	44/44 (100%)	23 (52%)	21 (48%)	0	0
23	AW	101/102 (99%)	76 (75%)	25 (25%)	1	6
25	AY	563/582 (97%)	489 (87%)	74 (13%)	5	28
27	BC	216/216 (100%)	182 (84%)	34 (16%)	3	21
28	BD	164/164 (100%)	143 (87%)	21 (13%)	5	29
29	BE	165/165 (100%)	143 (87%)	22 (13%)	5	28
30	BF	148/148 (100%)	112 (76%)	36 (24%)	1	6
31	BG	137/137 (100%)	114 (83%)	23 (17%)	2	19
32	BH	114/114 (100%)	89 (78%)	25 (22%)	1	9
33	BI	109/109 (100%)	78 (72%)	31 (28%)	0	3
34	BJ	116/116 (100%)	97 (84%)	19 (16%)	3	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	BK	103/103 (100%)	85 (82%)	18 (18%)	2	16
36	BL	102/102 (100%)	81 (79%)	21 (21%)	1	10
37	BM	109/109 (100%)	87 (80%)	22 (20%)	1	11
38	BN	100/100 (100%)	83 (83%)	17 (17%)	2	18
39	BO	86/86 (100%)	68 (79%)	18 (21%)	1	10
40	BP	99/99 (100%)	78 (79%)	21 (21%)	1	9
41	BQ	89/89 (100%)	76 (85%)	13 (15%)	4	24
42	BR	84/84 (100%)	70 (83%)	14 (17%)	3	19
43	BS	93/93 (100%)	83 (89%)	10 (11%)	8	35
44	BT	80/80 (100%)	69 (86%)	11 (14%)	4	27
45	BU	83/83 (100%)	64 (77%)	19 (23%)	1	7
46	BV	78/78 (100%)	63 (81%)	15 (19%)	2	13
47	BW	56/58 (97%)	50 (89%)	6 (11%)	8	36
48	BX	67/67 (100%)	56 (84%)	11 (16%)	3	19
49	BY	55/55 (100%)	46 (84%)	9 (16%)	3	19
50	BZ	48/48 (100%)	40 (83%)	8 (17%)	3	19
51	B0	47/47 (100%)	41 (87%)	6 (13%)	5	29
52	B1	45/45 (100%)	38 (84%)	7 (16%)	3	21
53	B2	38/38 (100%)	32 (84%)	6 (16%)	3	21
54	B3	51/51 (100%)	48 (94%)	3 (6%)	24	61
55	B4	34/34 (100%)	28 (82%)	6 (18%)	2	16
All	All	5327/5353 (100%)	4230 (79%)	1097 (21%)	4	10

5 of 1097 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	AT	47	GLN
25	AY	572	TYR
45	BU	60	LYS
21	AU	15	LEU
25	AY	88	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
25	AY	475	ASN
29	BE	90	GLN
49	BY	25	GLN
25	AY	573	HIS
27	BC	85	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	457 (29%)	27 (1%)
22	AV	332/363 (91%)	187 (56%)	32 (9%)
24	AX	76/77 (98%)	37 (48%)	3 (3%)
26	BA	2901/2903 (99%)	770 (26%)	58 (1%)
56	BB	118/119 (99%)	24 (20%)	1 (0%)
All	All	4964/5001 (99%)	1475 (29%)	121 (2%)

5 of 1475 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	6	G
1	AA	7	A
1	AA	9	G
1	AA	12	U

5 of 121 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	AV	308	U
26	BA	271	G
26	BA	2286	G
22	AV	320	U
24	AX	54	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	5MU	AV	341	22	13,22,23	1.44	1 (7%)	16,32,35	2.35	4 (25%)
22	PSU	AV	342	22	15,21,22	1.88	3 (20%)	16,30,33	3.86	5 (31%)
22	PSU	AV	347	22	15,21,22	1.66	3 (20%)	16,30,33	3.76	3 (18%)

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
22	5MU	AV	341	22	-	0/3/25/26	0/2/2/2
22	PSU	AV	342	22	-	0/7/25/26	0/2/2/2
22	PSU	AV	347	22	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AV	342	PSU	C5-C1'	-5.93	1.47	1.52
22	AV	347	PSU	C5-C1'	-5.01	1.47	1.52
22	AV	342	PSU	C6-C5	-2.37	1.35	1.38
22	AV	347	PSU	C2-N1	2.46	1.43	1.38
22	AV	342	PSU	C4-N3	2.48	1.37	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	AV	341	5MU	C5-C4-N3	-5.77	120.50	125.35
22	AV	342	PSU	C5-C1'-C2'	-3.59	109.34	115.44
22	AV	342	PSU	C4-C5-C1'	-2.97	116.22	121.22
22	AV	341	5MU	C2'-C1'-N1	-2.52	106.69	113.46
22	AV	347	PSU	O2'-C2'-C1'	-2.50	106.49	111.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	AV	341	5MU	6	0
22	AV	342	PSU	3	0
22	AV	347	PSU	7	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.