



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:47 PM BST

PDB ID : 4V4B
EMDB ID: : EMD-1067
Title : Structure of the ribosomal 80S-eEF2-sordarin complex from yeast obtained by docking atomic models for RNA and protein components into a 11.7 Å cryo-EM map.
Authors : Spahn, C.M.; Gomez-Lorenzo, M.G.; Grassucci, R.A.; Jorgensen, R.; Andersen, G.R.; Beckmann, R.; Penczek, P.A.; Ballesta, J.P.G.; Frank, J.
Deposited on : 2004-01-06
Resolution : 11.70 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 : unknown
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

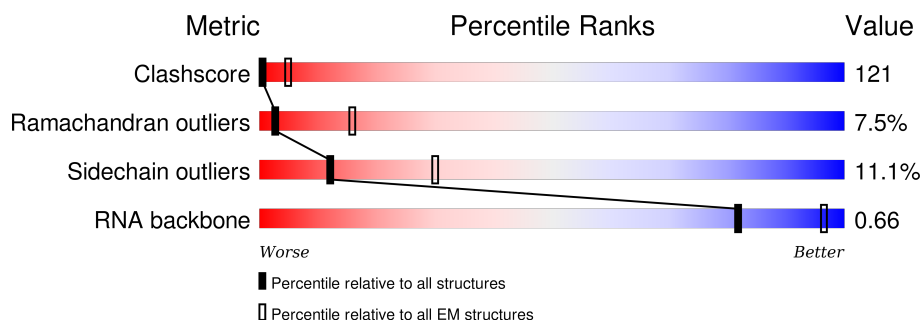
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.70 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.



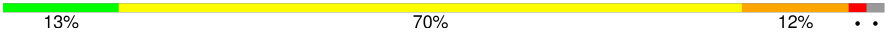
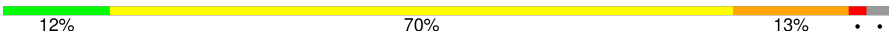
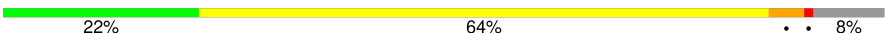


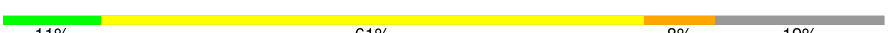
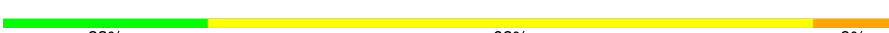




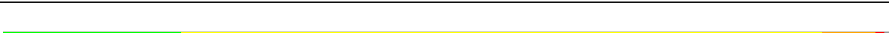













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	1507	25% 57% 12% . .
2	AT	842	62% 33% . .
3	AB	185	23% 69% 7% .
4	AC	192	27% 60% 11% . .
5	AD	179	18% 72% 9% .
6	AE	149	24% 70% 5%
7	AG	150	25% 67% 8%
8	AH	129	19% 71% 8% .

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Mol	Chain	Length	Quality of chain
9	AI	142	
10	AJ	100	
11	AK	136	
12	AL	118	
13	AM	132	
14	AN	36	
15	AO	65	
16	AQ	76	
17	AS	80	
18	B3	2999	
19	B4	125	
20	BA	217	
21	BB	253	
22	BC	386	
23	BD	361	
24	BE	222	
25	BF	162	
26	BG	119	
27	BH	191	
28	BI	168	
29	BJ	173	
30	BK	131	
31	BL	203	
32	BM	146	
33	BN	183	

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Mol	Chain	Length	Quality of chain
34	BO	120	
35	BP	142	
36	BQ	100	
37	BR	137	
38	BS	56	
39	BT	83	
40	BU	126	
41	BV	148	
42	B0	130	
43	BW	112	
44	BX	120	
45	BY	87	
46	BZ	105	
47	B9	91	

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 146792 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1466	Total	C	N	O	P	0	0
			31507	14026	5840	10176	1465		

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AT	819	Total	C	N	O	S	0	0
			6375	4057	1086	1202	30		

- Molecule 3 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	185	Total	C	N	O	S	0	0
			1438	919	261	256	2		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	188	Total	C	N	O	S	0	0
			1469	929	271	263	6		

- Molecule 5 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	178	Total	C	N	O	S	0	0
			1424	893	271	259	1		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	149	Total	C	N	O	S	0	0
			1099	691	206	200	2		

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	150	Total	C	N	O	S	0	0
			1161	714	229	215	3		

- Molecule 8 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	127	Total	C	N	O	S	0	0
			1004	640	183	178	3		

- Molecule 9 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	139	Total	C	N	O	S	0	0
			1094	700	201	193			

- Molecule 10 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	97	Total	C	N	O	S	0	0
			777	492	141	143	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	?	-	VAL	DELETION	UNP P38701

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	125	Total	C	N	O	S	0	0
			925	566	181	175	3		

- Molecule 12 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	118	Total	C	N	O	S	0	0
			906	579	166	159	2		

- Molecule 13 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	131	Total	C	N	O	S	0	0
			1084	675	218	189	2		

- Molecule 14 is a protein called 40S ribosomal protein S29-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	29	Total	C	N	O	S	0	0
			235	141	48	42	4		

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	65	Total	C	N	O	S	0	0
			552	353	107	91	1		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	76	Total	C	N	O	S	0	0
			618	396	120	100	2		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	80	Total	C	N	O	S	0	0
			622	398	110	108	6		

- Molecule 18 is a RNA chain called 5.8S/25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B3	2863	Total	C	N	O	P	0	69
			59964	26726	11030	19346	2862		

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B3	73	C	U	CONFLICT	GB 3377778
B3	74	A	G	CONFLICT	GB 3377778
B3	103	U	C	CONFLICT	GB 3377778
B3	104	G	A	CONFLICT	GB 3377778
B3	?	-	U	DELETION	GB 3377778
B3	?	-	C	DELETION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	130	C	-	INSERTION	GB 3377778
B3	131B	U	-	INSERTION	GB 3377778
B3	200	U	C	CONFLICT	GB 3377778
B3	300	C	U	CONFLICT	GB 3377778
B3	301	G	C	CONFLICT	GB 3377778
B3	318	C	U	CONFLICT	GB 3377778
B3	350	C	G	CONFLICT	GB 3377778
B3	351	G	A	CONFLICT	GB 3377778
B3	363	A	C	CONFLICT	GB 3377778
B3	364	C	U	CONFLICT	GB 3377778
B3	560	C	U	CONFLICT	GB 3377778
B3	574	C	G	CONFLICT	GB 3377778
B3	575	G	A	CONFLICT	GB 3377778
B3	582	C	U	CONFLICT	GB 3377778
B3	583	G	C	CONFLICT	GB 3377778
B3	653	C	U	CONFLICT	GB 3377778
B3	972	C	-	INSERTION	GB 3377778
B3	973	U	-	INSERTION	GB 3377778
B3	974	A	-	INSERTION	GB 3377778
B3	976Z	G	-	INSERTION	GB 3377778
B3	976	G	-	INSERTION	GB 3377778
B3	977	G	-	INSERTION	GB 3377778
B3	978	G	-	INSERTION	GB 3377778
B3	979	G	-	INSERTION	GB 3377778
B3	980	C	-	INSERTION	GB 3377778
B3	981	C	-	INSERTION	GB 3377778
B3	982	C	-	INSERTION	GB 3377778
B3	983	A	-	INSERTION	GB 3377778
B3	984	C	-	INSERTION	GB 3377778
B3	985	C	-	INSERTION	GB 3377778
B3	986	A	-	INSERTION	GB 3377778
B3	987	G	-	INSERTION	GB 3377778
B3	988	C	-	INSERTION	GB 3377778
B3	989	C	-	INSERTION	GB 3377778
B3	990	U	-	INSERTION	GB 3377778
B3	991	A	-	INSERTION	GB 3377778
B3	992	C	-	INSERTION	GB 3377778
B3	993	C	-	INSERTION	GB 3377778
B3	994	A	-	INSERTION	GB 3377778
B3	995	A	-	INSERTION	GB 3377778
B3	1026	C	U	CONFLICT	GB 3377778
B3	1162	U	G	CONFLICT	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	1165	U	G	CONFLICT	GB 3377778
B3	1166	G	A	CONFLICT	GB 3377778
B3	1180	C	U	CONFLICT	GB 3377778
B3	1182	U	C	CONFLICT	GB 3377778
B3	1184	A	C	CONFLICT	GB 3377778
B3	1186	U	C	CONFLICT	GB 3377778
B3	1190	A	G	CONFLICT	GB 3377778
B3	1191	G	A	CONFLICT	GB 3377778
B3	1193	G	A	CONFLICT	GB 3377778
B3	1194	U	A	CONFLICT	GB 3377778
B3	1206	C	U	CONFLICT	GB 3377778
B3	1320	U	C	CONFLICT	GB 3377778
B3	1326	U	C	CONFLICT	GB 3377778
B3	1329	A	G	CONFLICT	GB 3377778
B3	1331	A	G	CONFLICT	GB 3377778
B3	1337	A	G	CONFLICT	GB 3377778
B3	1479	A	G	CONFLICT	GB 3377778
B3	1480	U	A	CONFLICT	GB 3377778
B3	1496	G	A	CONFLICT	GB 3377778
B3	1587	U	A	CONFLICT	GB 3377778
B3	1669	A	G	CONFLICT	GB 3377778
B3	1670	G	A	CONFLICT	GB 3377778
B3	1949	C	G	CONFLICT	GB 3377778
B3	1950	C	G	CONFLICT	GB 3377778
B3	1959	A	G	CONFLICT	GB 3377778
B3	1962	G	C	CONFLICT	GB 3377778
B3	1963	G	C	CONFLICT	GB 3377778
B3	1966	C	U	CONFLICT	GB 3377778
B3	2137	U	A	CONFLICT	GB 3377778
B3	2139	U	G	CONFLICT	GB 3377778
B3	3145	G	-	INSERTION	GB 3377778
B3	2146	G	-	INSERTION	GB 3377778
B3	2147	G	-	INSERTION	GB 3377778
B3	2148	G	-	INSERTION	GB 3377778
B3	2149	A	-	INSERTION	GB 3377778
B3	2150	U	-	INSERTION	GB 3377778
B3	2151	G	-	INSERTION	GB 3377778
B3	2152	C	-	INSERTION	GB 3377778
B3	2153	G	-	INSERTION	GB 3377778
B3	2154	U	-	INSERTION	GB 3377778
B3	2155	A	-	INSERTION	GB 3377778
B3	2156	G	-	INSERTION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	2157	G	-	INSERTION	GB 3377778
B3	2158	A	-	INSERTION	GB 3377778
B3	2159	U	-	INSERTION	GB 3377778
B3	2160	A	-	INSERTION	GB 3377778
B3	2161	G	-	INSERTION	GB 3377778
B3	2162	G	-	INSERTION	GB 3377778
B3	2163	U	-	INSERTION	GB 3377778
B3	2164	G	-	INSERTION	GB 3377778
B3	2165	G	-	INSERTION	GB 3377778
B3	2166	G	-	INSERTION	GB 3377778
B3	2167	A	-	INSERTION	GB 3377778
B3	2168	G	-	INSERTION	GB 3377778
B3	2169	C	-	INSERTION	GB 3377778
B3	2170	G	-	INSERTION	GB 3377778
B3	2171	C	-	INSERTION	GB 3377778
B3	2203	A	-	INSERTION	GB 3377778
B3	2204	A	-	INSERTION	GB 3377778
B3	2205	G	-	INSERTION	GB 3377778
B3	2206	C	-	INSERTION	GB 3377778
B3	2207	G	-	INSERTION	GB 3377778
B3	2208	C	-	INSERTION	GB 3377778
B3	2209	C	-	INSERTION	GB 3377778
B3	2210	G	-	INSERTION	GB 3377778
B3	2211	G	-	INSERTION	GB 3377778
B3	2212	U	-	INSERTION	GB 3377778
B3	2213	G	-	INSERTION	GB 3377778
B3	2214	A	-	INSERTION	GB 3377778
B3	2215	A	-	INSERTION	GB 3377778
B3	2216	A	-	INSERTION	GB 3377778
B3	2217	U	-	INSERTION	GB 3377778
B3	2218	A	-	INSERTION	GB 3377778
B3	2219	C	-	INSERTION	GB 3377778
B3	2220	C	-	INSERTION	GB 3377778
B3	2221	A	-	INSERTION	GB 3377778
B3	2222	C	-	INSERTION	GB 3377778
B3	2223	C	-	INSERTION	GB 3377778
B3	2224	C	-	INSERTION	GB 3377778
B3	2225	U	-	INSERTION	GB 3377778
B3	2226	U	-	INSERTION	GB 3377778
B3	2227	C	-	INSERTION	GB 3377778
B3	2228	C	-	INSERTION	GB 3377778
B3	2229	C	-	INSERTION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	2230	C	-	INSERTION	GB 3377778
B3	2231	G	-	INSERTION	GB 3377778
B3	2232	G	-	INSERTION	GB 3377778
B3	2233	C	-	INSERTION	GB 3377778
B3	2234	U	-	INSERTION	GB 3377778
B3	2235	G	-	INSERTION	GB 3377778
B3	2236	G	-	INSERTION	GB 3377778
B3	2325	C	U	CONFLICT	GB 3377778
B3	2326	U	C	CONFLICT	GB 3377778
B3	2341	G	A	CONFLICT	GB 3377778
B3	2374	A	G	CONFLICT	GB 3377778
B3	2375	G	A	CONFLICT	GB 3377778

- Molecule 19 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B4	122	Total	C	N	O	P	0	0
			2600	1160	472	847	121		

- Molecule 20 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BA	213	Total	C	N	O	S	0	0
			1682	1074	294	305	9		

- Molecule 21 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BB	244	Total	C	N	O	S	0	0
			1855	1156	375	323	1		

- Molecule 22 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BC	359	Total	C	N	O	S	0	0
			2856	1813	541	495	7		

- Molecule 23 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BD	256	Total	C	N	O	S	0	0
			1942	1221	374	344	3		

- Molecule 24 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BE	222	Total	C	N	O	S	0	0
			1799	1140	312	345	2		

- Molecule 25 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BF	161	Total	C	N	O	S	0	0
			1298	854	228	215	1		

- Molecule 26 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BG	119	Total	C	N	O	S	0	0
			886	566	152	166	2		

- Molecule 27 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BH	178	Total	C	N	O	S	0	0
			1410	892	259	256	3		

- Molecule 28 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BI	165	Total	C	N	O	S	0	0
			1326	834	257	228	7		

- Molecule 29 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BJ	165	Total	C	N	O	S	0	0
			1319	826	247	242	4		

- Molecule 30 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BK	131	Total	C	N	O	S	0	0
			978	613	181	182	2		

- Molecule 31 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BL	194	Total	C	N	O	S	0	0
			1637	1022	344	270	1		

- Molecule 32 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BM	146	Total	C	N	O	S	0	0
			1165	754	221	189	1		

- Molecule 33 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BN	147	Total	C	N	O		0	0
			1163	725	226	212			

- Molecule 34 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BO	120	Total	C	N	O	S	0	0
			925	595	169	160	1		

- Molecule 35 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BP	141	Total	C	N	O		0	0
			1145	714	242	189			

- Molecule 36 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BQ	97	Total	C	N	O	S	0	0
			795	505	153	134	3		

- Molecule 37 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BR	131	Total	C	N	O	S	0	0
			977	614	183	173	7		

- Molecule 38 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BS	53	Total	C	N	O	0	0
			439	282	84	73		

- Molecule 39 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BT	77	Total	C	N	O	S	0	0
			614	395	101	116	2		

- Molecule 40 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BU	115	Total	C	N	O	0	0
			911	574	178	159		

- Molecule 41 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BV	143	Total	C	N	O	S	0	0
			1133	723	222	185	3		

- Molecule 42 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B0	109	Total	C	N	O	S	0	0
			880	555	176	148	1		

- Molecule 43 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BW	78	Total	C	N	O	S	0	0
			654	412	132	109	1		

- Molecule 44 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BX	59	Total	C	N	O	S	0	0
			461	294	82	84	1		

- Molecule 45 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BY	52	Total	C	N	O	S	0	0
			402	245	85	68	4		

- Molecule 46 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BZ	91	Total	C	N	O	S	0	0
			740	466	150	119	5		

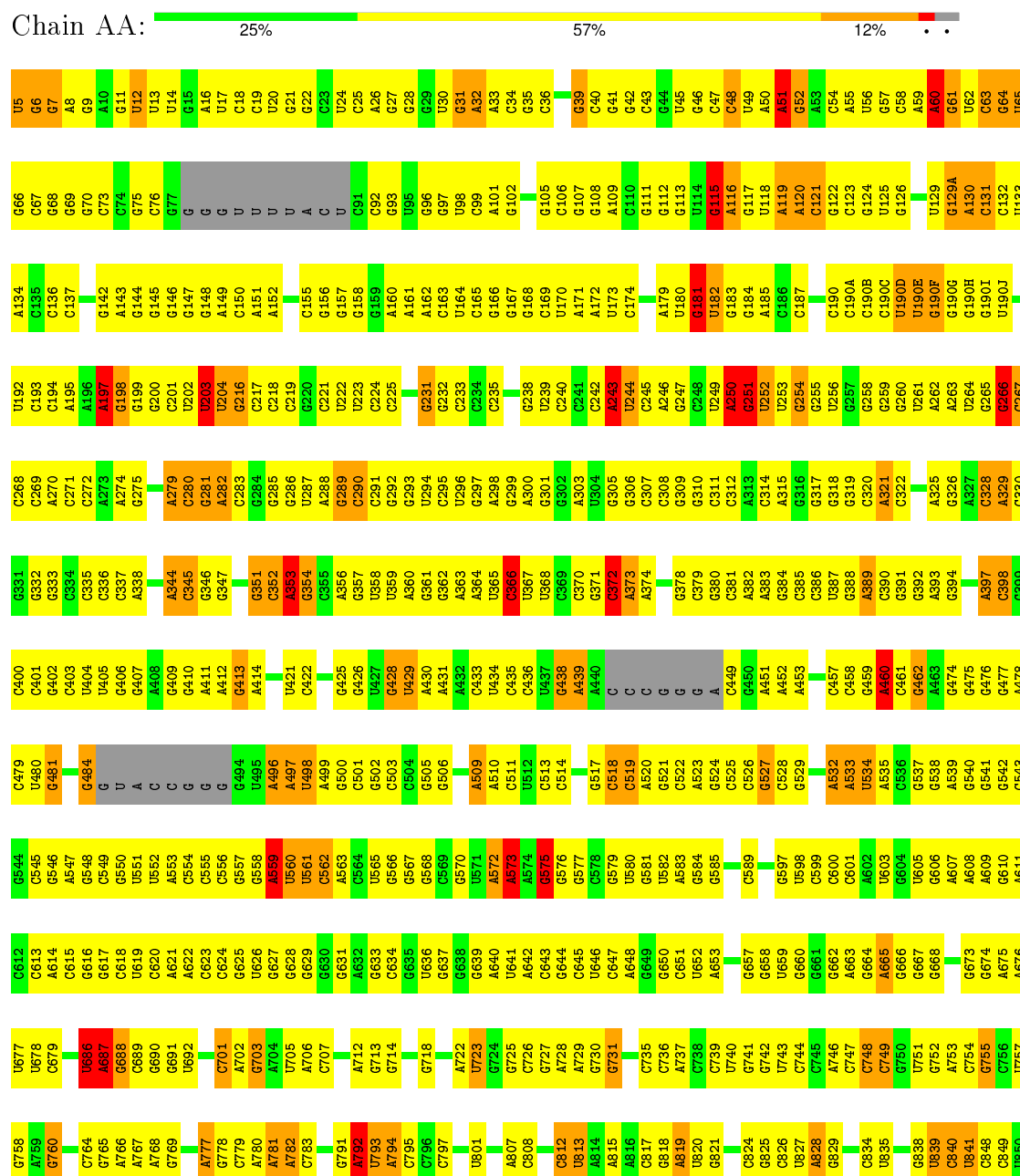
- Molecule 47 is a protein called 60S ribosomal protein L43.

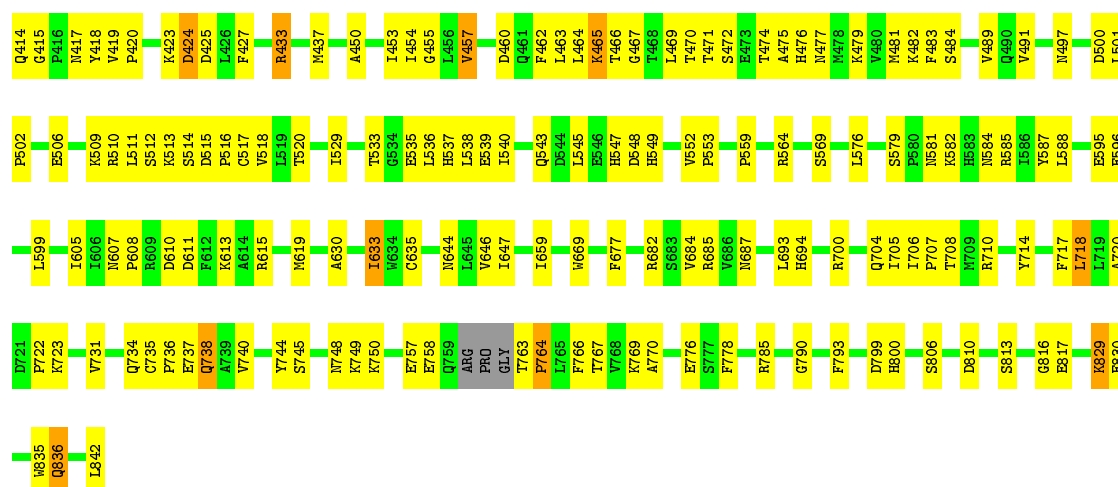
Mol	Chain	Residues	Atoms					AltConf	Trace
47	B9	73	Total	C	N	O	S	0	0
			546	338	105	98	5		

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.

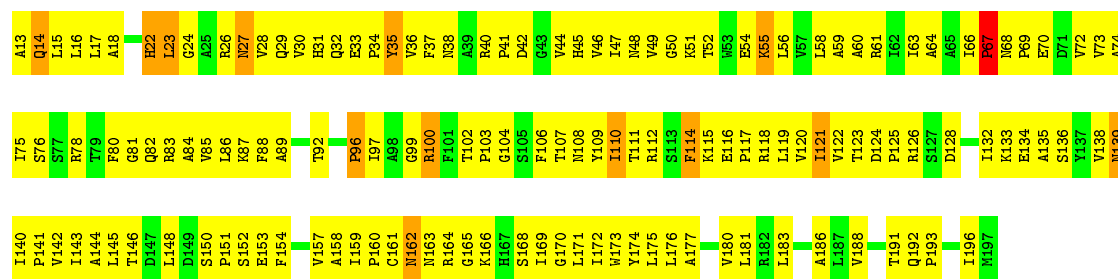
• Molecule 1: 18S ribosomal RNA





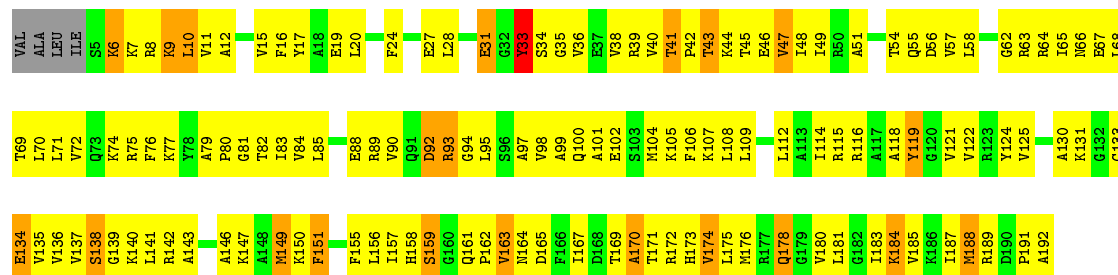
• Molecule 3: 40S ribosomal protein S0-A

Chain AB: 23% 69% 7%



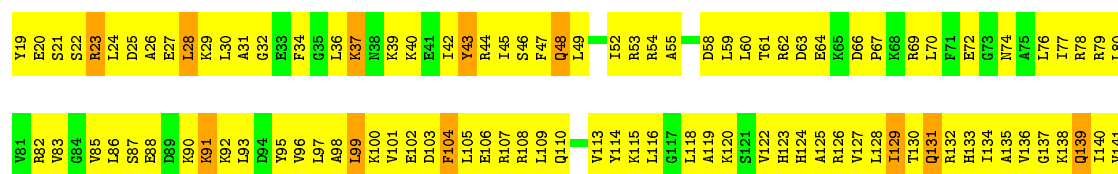
• Molecule 4: 40S ribosomal protein S3

Chain AC: 27% 60% 11%



• Molecule 5: 40S ribosomal protein S9-A

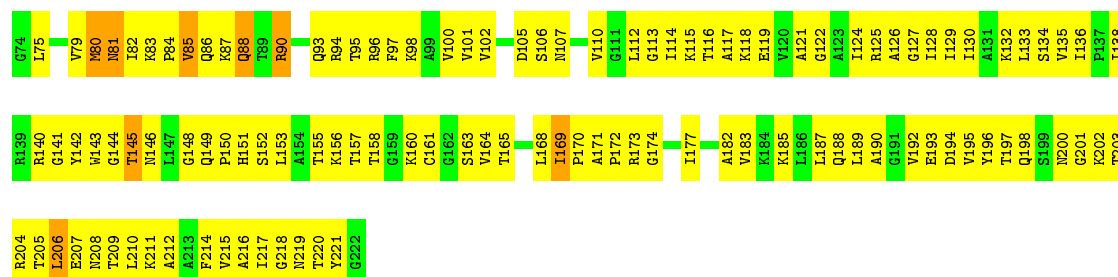
Chain AD: 18% 72% 9%





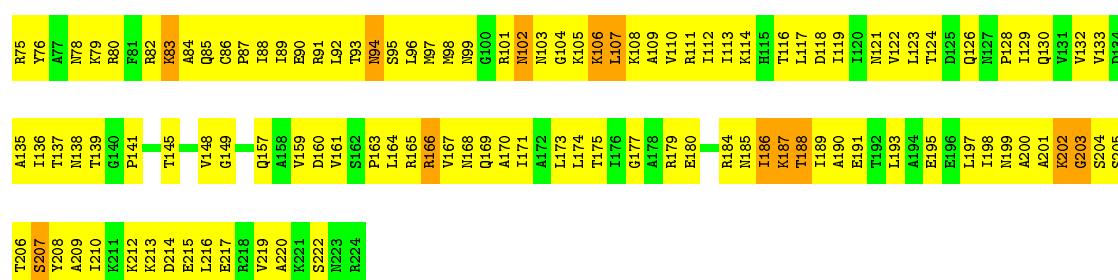
• Molecule 6: 40S ribosomal protein S2

Chain AE: 24% 70% 5%



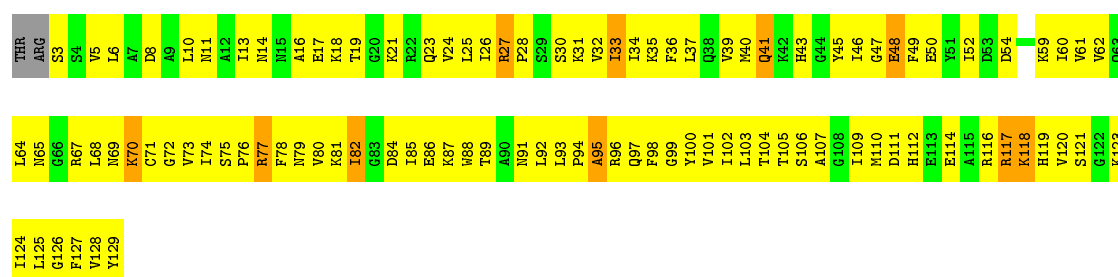
• Molecule 7: 40S ribosomal protein S5

Chain AG: 25% 67% 8%



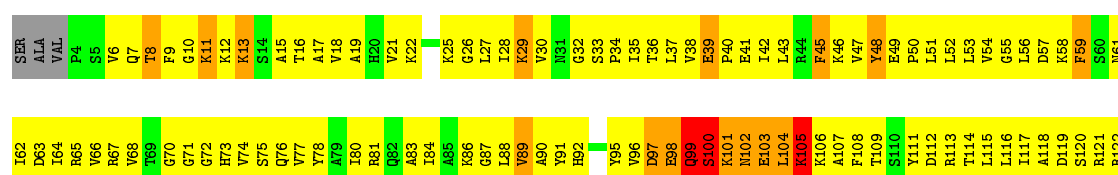
• Molecule 8: 40S ribosomal protein S22

Chain AH: 19% 71% 8%



• Molecule 9: 40S ribosomal protein S16

Chain AI: 13% 70% 12%



P123
E124
P125
K126
K127
F128
G132
A133
R134
S135
R136
F137
Q138
K139
S140
Y141
R142

• Molecule 10: 40S ribosomal protein S20

Chain AJ: 12% 70% 13% . .

K21
I22
R23
I24
VAL
T25
K26
K27
R28
S28
T29
K30
V31
K32
Q33
L34
E35
N36
V37
S38
T41
V42
K43
N44
A45
E46
P49
L50
V51
K52
K53
G54
P55
V56
R57
L58
P59
T60
R61
V62
L63
K64
I65
S66
T67
R68
K69
T70
P71
N72
G73
E74
G75
S76
K77
I78
N79
E80
T81
Y82

E83
M84
R85
I86
VAL
K87
K88
ARG
R89
Y90
I91
D92
L93
E94
A95
P96
V97
Q98
N99
V100
K101
R102
I103
I106
I107
T108
E109
P110
G111
V112
E115
V116
V117
ALA
SER
ASN

• Molecule 11: 40S ribosomal protein S14-A

Chain AK: 22% 64% . . 8%

SER
ASN
VAL
VAL
GLN
ALA
ARG
D8
S9
S10
Q11
V12
G13
G14
V15
A16
R17
I18
Y19
A20
S21
F22
N23
D24
T25
F26
V27
H28
V29
T30
D31
L32
S33
G34
K35
E36
T37
I38
A39
R40
V41
T42
G43
G44
M45
K46
V47
K48
A49
D50
R51
D52
S53
S54
S55
P56
Y57
A58
L61

K62
A63
G64
D65
C92
V66
K69
C70
R71
E72
V73
G74
I75
T76
A77
V78
H79
K81
R82
A84
T85
G86
G87
T88
R89
T90
K91
T92
P93
G94
P95
G96
G97
Q98
L101
R102
A103
L104
L109
R110
I111
G112
R113
I114
E115
D116
V117
T118
P119
V120
P121
S122
D123
S124
T125
R126

K127
R131
R132
GLY
ARG
ARG
LEU

• Molecule 12: 40S ribosomal protein S23

Chain AL: 19% 71% 8% .

N28
Y29
K30
K31
D32
R33
L34
Q35
T36
A37
F38
K39
S40
S41
F42
P43
G44
G45
S46
S47
H48
A49
K50
G51
I52
E55
K56
L57
G58
I59
E60
S61
K62
Q63
P64
N65
S66
A67
I68
R69
K70
C71
V72
R73
V74
Q75
L76
I77
K78
N79
G80
K81
K82
T84
A85
R86
V87
P88

R89
D90
G91
C92
L93
R94
F95
Y96
N99
D100
E101
V102
L103
L104
A105
G106
F107
G108
R109
K110
G111
K112
A113
K114
G115
D116
I117
V120
R121
F122
K123
V124
V125
K126
V127
S128
G129
V130
S131
L132
L133
A134
L135
W136
K139
K140
E141
K142
P143
R144
S145

• Molecule 13: 40S ribosomal protein S18

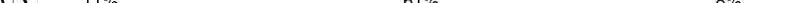
Chain AM: 14% 81% 5% .

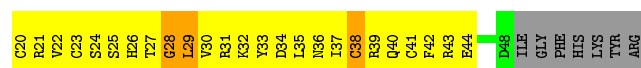
L15
R16
L17
L18
Y19
T20
I21
V22
D23
G24
N25
L26
K27
K28
V29
Y30
A31
L32
T33
D34
G35
K36
G37
Y38
H39
T100
L101
A102
N103
N104
V105
K108
L109
R110
D111
D112
L113
E114
R115
L116
K117
K118
I119
R120
A121
R122
R123
G124
I125
R126
L127
F128
W129
G130
L131
R132
V133
R134
G135
Q136

P76
T77
H78
Y79
K80
I81
P82
A83
W84
F85
L86
N87
R88
Q89
R90
D91
I92
T93
D94
G95
D97
Y98
H99
T100
L101
A102
N103
N104
V105
K108
L109
R110
D111
D112
L113
E114
R115
L116
K117
K118
I119
R120
A121
R122
R123
G124
I125
R126
L127
F128
W129
G130
L131
R132
V133
R134
G135
Q136

H137
T138
K139
T140
T141
G142
R143
R144
R145
ALA

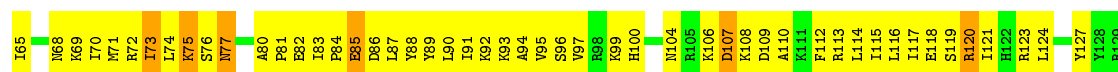
• Molecule 14: 40S ribosomal protein S29-B

Chain AN:  11% 61% 8% 19%



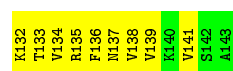
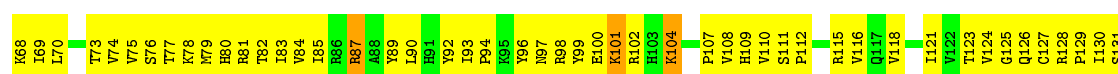
- Molecule 15: 40S ribosomal protein S13

Chain AO: 



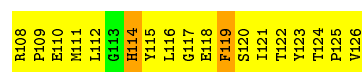
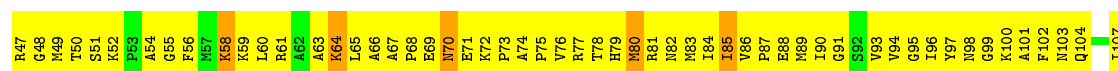
- Molecule 16: 40S ribosomal protein S11

Chain AQ:  24% 72% .



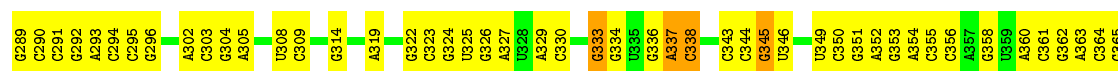
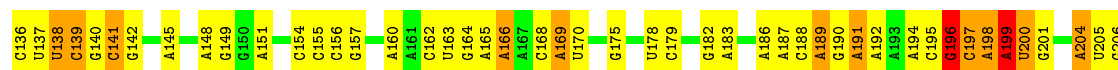
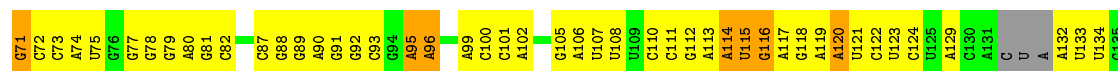
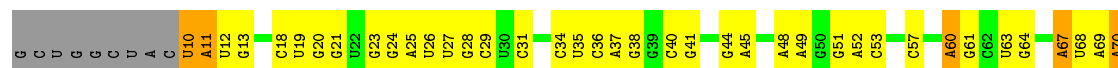
- Molecule 17: 40S ribosomal protein S15

Chain AS:  9% 83% 9%



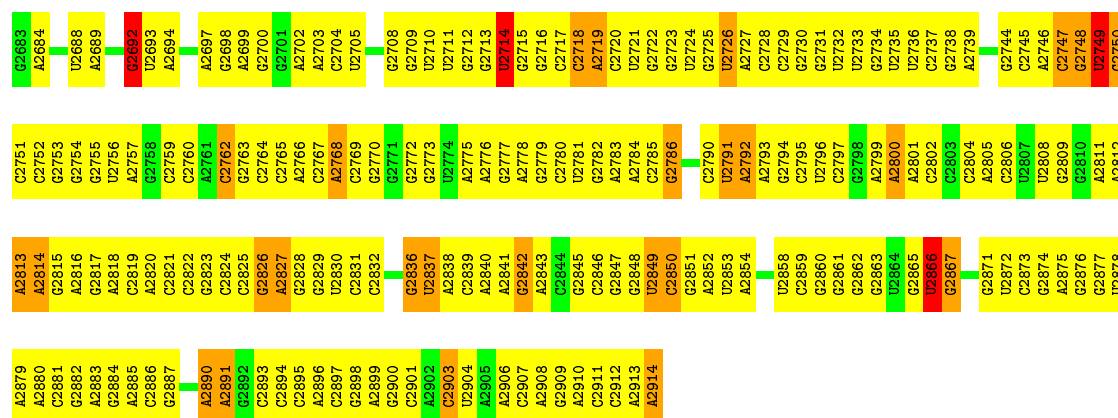
- Molecule 18: 5.8S/25S ribosomal RNA

Chain B3:  33% 52% 9% 5%

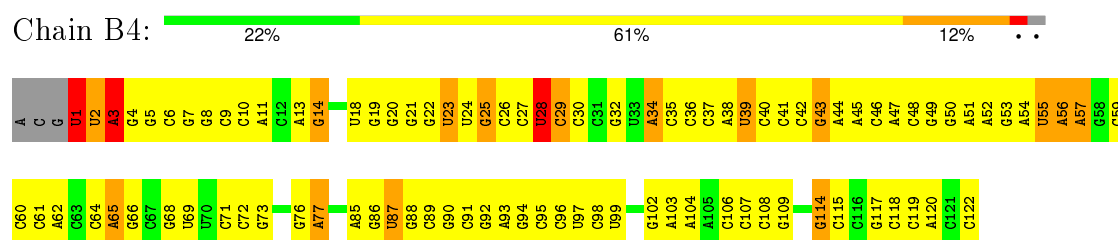


U1473	C1400	U1333	A1259	A1192	A1124	G1052	C	A907	A819	G745	A665	U595	A520	A441	U366
C1474	G1401	C1334	G1260	G1193	U1125	G1053	C	A908	G820	A746	A667	C596	A521	U445	G367
C1477	U1335	U1194	A1261	U1194	C1126	G1054	G	G918	U821	G747	C867	A597	U522	U446	C368
U1478	C1336	C1196	C1263	C1196	U1128	G1055	A	U919	G834	C749	G670	C598	A524	A447	G370
A1485	A1337	U1338	C1267	A1199	U1129	U1056	A	G920	U835	C749	A671	G599	G525	G448	U371
U1408	G1339	C1339	C1268	A1200	U1130	A1058	G	G921	G836	A750	G672	G601	U526	A449	A372
G1409	A1340	C1342	U1269	A1201	G1131	G1059	G	A922	U840	U751	U675	A602	U527	C450	G373
A1414	C1343	C1342	U1270	A1202	A1132	C1060	A	A923	C841	G754	C576	A603	G528	C451	U374
G1415	U1344	C1343	C1273	G1205	G1133	U1061	U	G924	C842	U754	C677	G604	G529	A453	G375
A1494	G1416	A1207	C1273	A1206	U1064	G1063	C	A926	A843	G759	G678	C605	U532	U457	C376
C1495	G1417	C1208	C1277	G1208	U1065	U1066	G	C934	A844	A761	G680	U612	A532	U457	C377
G1496	U1422	U1347	A1278	G1209	G1138	A1067	C	G935	U845	C762	G681	C613	G535	C461	G378
A1497	C1423	U1279	A1280	G1210	U1139	A1067	C	A946	C947	C763	A682	U614	A536	U457	G379
U1501	A1424	G1349	U1280	G1211	U1140	C	A	G938	C947	C764	G683	U616	A537	C461	A380
A1502	G1425	U1350	U1281	C1212	U1141	G1072	C	A939	C848	C765	G684	U617	G538	G471	U382
U1503	C1426	G1351	G1283	C1213	U1142	A1073	C	G940	U850	A766	C685	U618	A540	A472	A383
C1504	A1427	A1352	U1284	G1214	G1143	G1074	G	U941	C851	A767	U688	U619	C541	A473	G384
U1505	C1428	C1353	U1285	A1215	C1147	C	C999	U942	U855	G771	A689	A620	A542	G474	G389
U1506	G1430	A1286	A1287	G1216	U1148	C1080	U1000	A943	U856	G772	A693	C621	U543	C480	G390
C1507	U1431	A1356	U1288	G1217	U1149	A1081	C	G944	G856	G773	A694	G622	G544	U481	U391
U1508	C1432	A1357	U1289	U1218	A1150	C	U1002	U945	A857	A773	C695	U623	G545	G482	U392
C1509	G1433	A1358	G1290	U1219	G1151	C1085	U1003	C946	U858	G774	C696	U624	G545	G483	G393
G1510	A1434	U1359	U1291	G1220	A1152	A1086	C	U947	C859	G775	C697	U625	U548	C483	G394
U1511	G1438	C1360	G1295	G1221	C1153	G1087	A1006	G948	U860	A776	A697	U626	U549	A484	A395
G1512	C1439	C1361	U1298	G1222	A1154	U1096	U1015	U949	G868	G777	A698	C627	C550	A485	U396
A1515	U1440	U1362	U1299	G1223	G1155	G1089	C	G950	G869	C778	C699	A628	A551	A486	A397
C1516	G1441	G1363	G1300	G1225	C1156	A1090	U1009	A951	U701	U779	A700	A629	A552	G487	U398
U1517	A1442	C1364	C1301	G1226	G1157	U1091	C1010	G952	G873	G782	U702	A630	G553	U488	C399
U1518	U1443	U1367	U1304	C1227	G1160	G1093	C	U954	A874	G783	G703	A631	G554	C492	C400
G1520	G1445	C1369	C1305	G1228	U1163	U1094	A1014	G955	A875	A784	C704	A632	U555	C492	C401
C1521	U1446	A1231	U1306	G1229	U1164	U1097	C1015	U956	A876	G785	G705	C633	C556	U493	U402
A1522	A1448	A1307	A1307	A1232	U1165	A1098	U1016	A957	G878	A791	C707	C634	C557	C494	A407
G1523	G1449	U1377	U1309	U1233	G1166	G1099	A1018	C958	C881	G792	A708	C637	U559	G496	A410
C1524	C1450	C1378	U1310	U1234	G1167	G1100	C1019	G960	A882	U793	G709	C638	A561	A498	A411
G1525	U1451	A1379	G1311	G1235	C1168	C1103	A1020	A961	U883	U794	G710	A639	A562	G499	G412
A1526	G1452	U1380	G1312	A1236	U1169	G1104	G1021	G962	C884	G795	A708	G640	G500	G501	G413
U1527	C1453	A1381	A1313	U1237	U1170	G1105	A1022	G963	G885	A796	U713	A566	G502	G501	C414
A1528	U1454	G1382	U1314	C1238	A1171	C1106	C1023	G964	A886	A797	U714	U567	A502	A502	G417
G1529	U1457	U1383	G1315	G1239	G1172	A1105	C1024	A965	G887	G798	U	G643	G503	G503	C418
U1530	A1458	C1384	G1316	G1240	A1173	A1107	U1025	U967	C889	C803	G716	U645	A569	G504	A419
C1534	U1460	G1386	A1318	A1242	A1174	U1109	C1030	G968	C890	C804	C719	G646	C574	C505	U420
U1535	A1461	G1387	G1319	U1244	A1180	G1110	G1031	G969	G891	C804	G720	U647	G575	A507	C421
C1536	C1462	U1388	U1320	U1245	U1181	C	U970	A807	A892	A807	A721	G653	G581	A508	U425
U1538	A1463	G1389	A1321	C1246	U1182	A1114	G1039	G809	A895	G809	G722	U654	C582	U510	G426
U1539	U1464	A1390	G1322	A1247	U1183	U1115	A1040	G810	C896	C728	C728	G656	G582	A511	G431
G1540	G1391	A1391	C	A1248	A1184	U1116	U1041	C811	C897	C729	G729	G657	U584	G512	G432
G1541	C1467	U1392	G1327	U1250	U1186	A1118	U1042	A812	G898	G730	G730	C658	C585	A513	C433
U1544	A1468	C1396	A1328	C1251	U1187	G1119	C1043	C813	A659	U731	U731	C586	G514	G514	U434
C1545	C1469	C1397	A1329	C1251	U1188	U1120	G1044	G814	G902	U814	C	A660	A587	C515	U434
G1546	A1470	A1330	A1330	C1251	A1189	U1121	G1045	U815	U903	U815	C	G661	G588	A516	A438
	A1471	G1398	A1331	C1257	A1190	G1122	C	G816	U904	A736	A737	U662	U589	U517	C439
	C1472	A1399	C1332	G1258	G1191	A1123	C1051	A818	C906	G738	G738	U664	C594	A519	C440

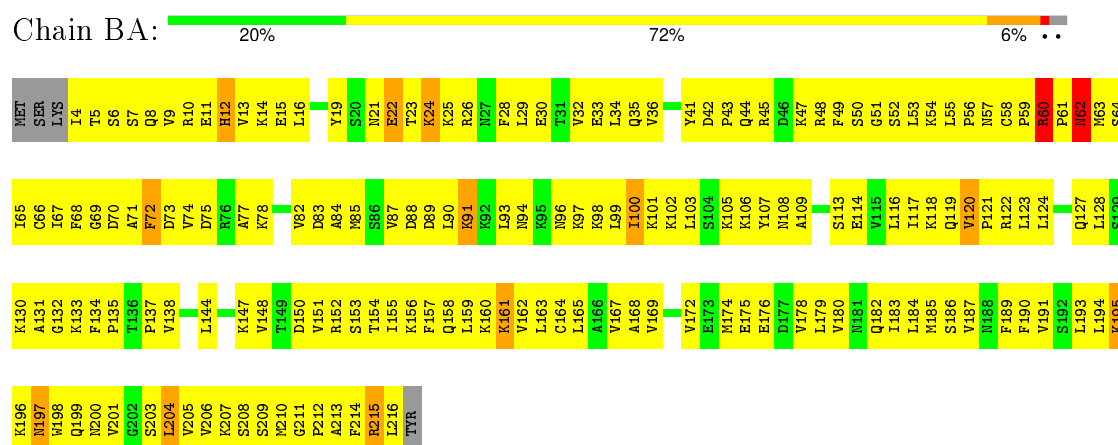


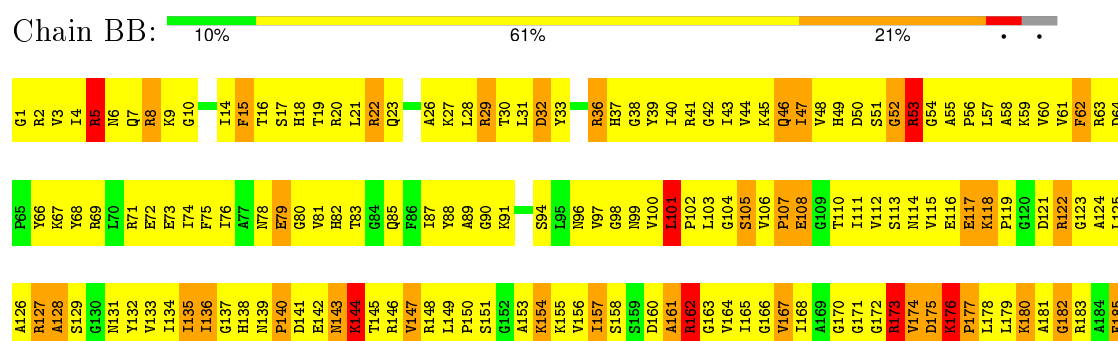
• Molecule 19: 5S RIBOSOMAL RNA




• Molecule 20: 60S ribosomal protein L1

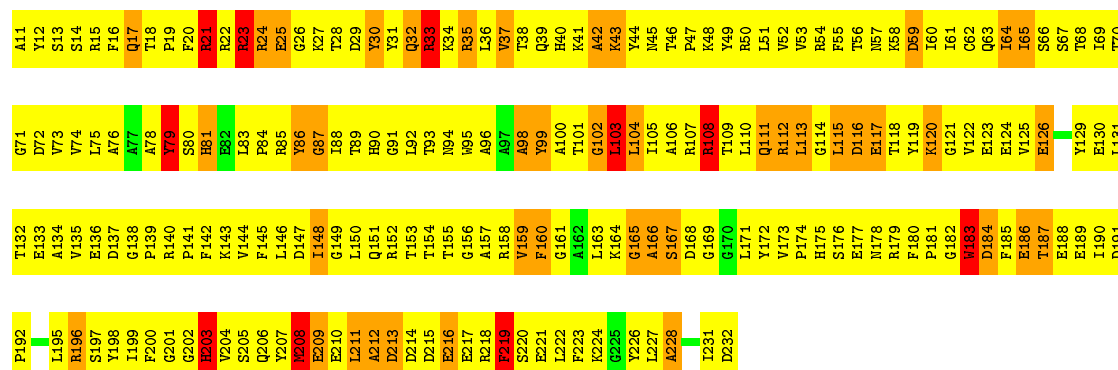


• Molecule 21: 60S ribosomal protein L2




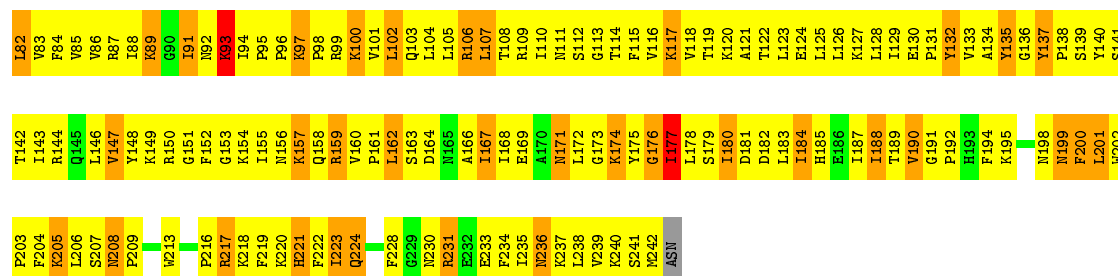
- Molecule 24: 60S ribosomal protein L5

Chain BE:  5% 71% 19% 5%




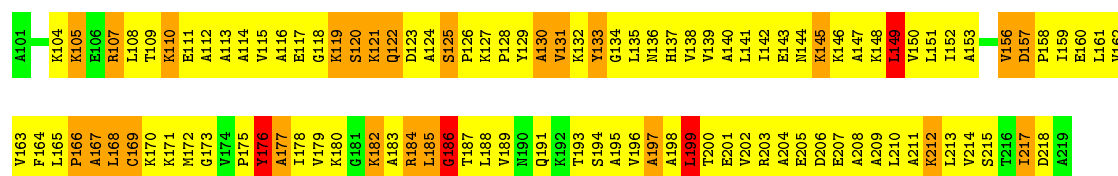
- Molecule 25: 60S ribosomal protein L7-A

Chain BF:  11% 65% 22% ..



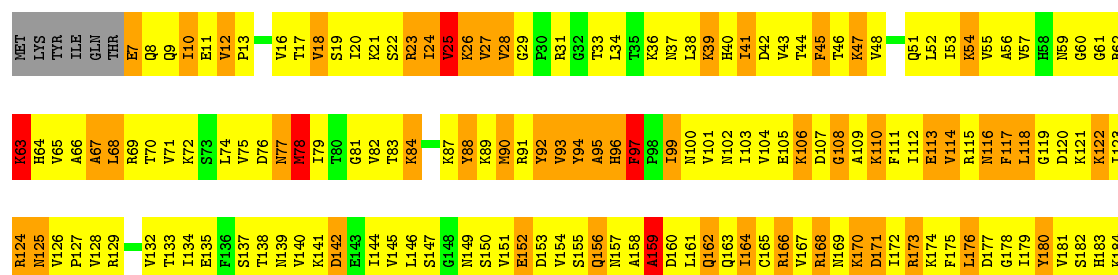
- Molecule 26: 60S ribosomal protein L8-A

Chain BG:  10% 66% 21% .



- Molecule 27: 60S ribosomal protein L9-A

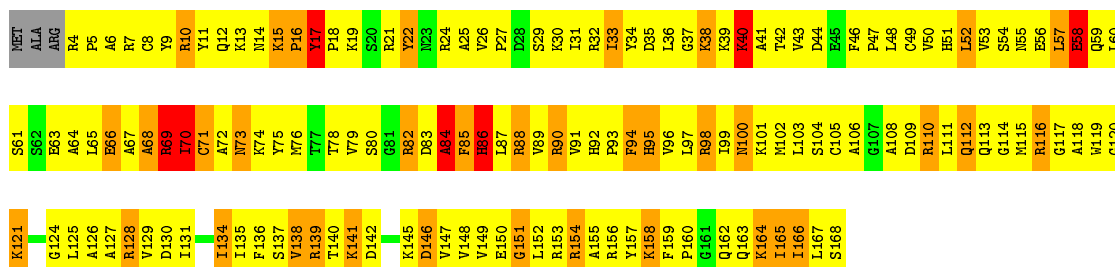
Chain BH:  9% 55% 26% . 7%



GLY
PHE
ILE
THR
GLU
ASP
LEU

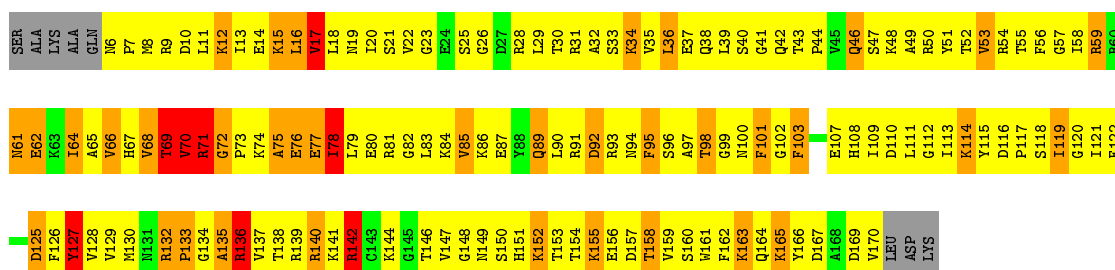
• Molecule 28: 60S ribosomal protein L10

Chain BI: 9% 64% 21% • •



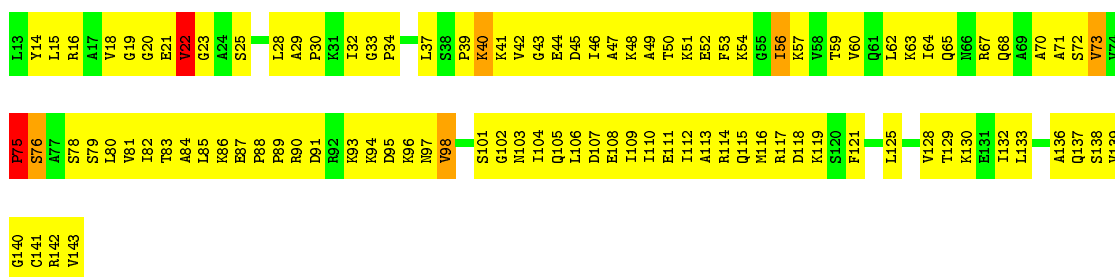
• Molecule 29: 60S ribosomal protein L11

Chain BJ: 9% 61% 21% 5% 5%



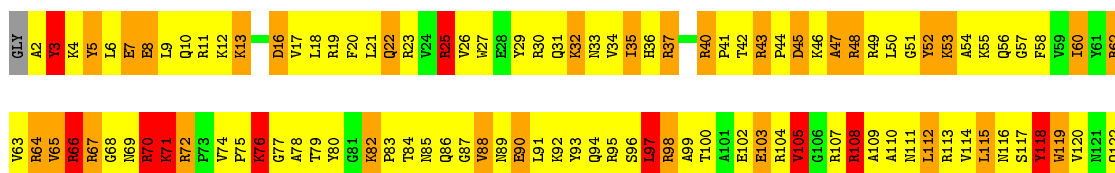
• Molecule 30: 60S ribosomal protein L12

Chain BK: 21% 73% • •

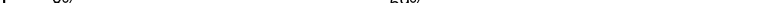


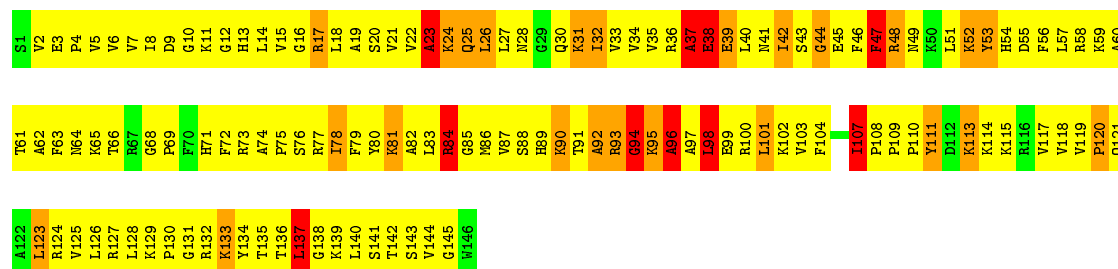
• Molecule 31: 60S ribosomal protein L15-A

Chain BL: 9% 51% 29% 7% •



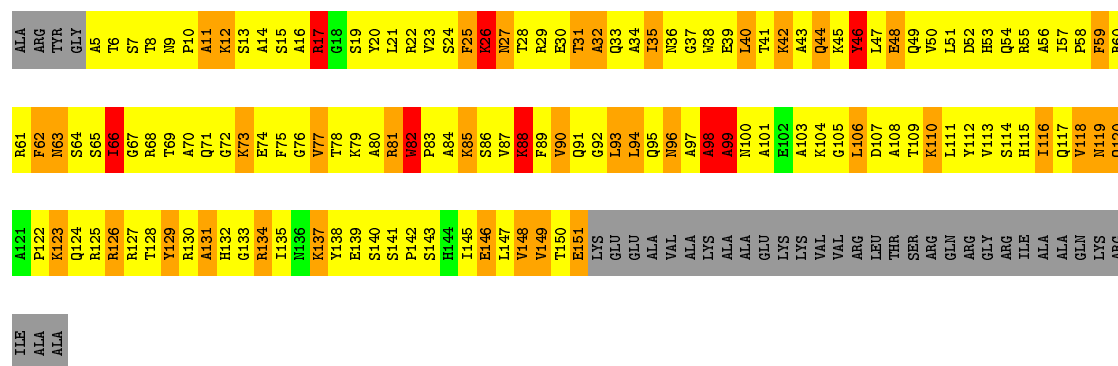
- Molecule 32: 60S ribosomal protein L16-A

Chain BM:  8% 69% 16% 7%




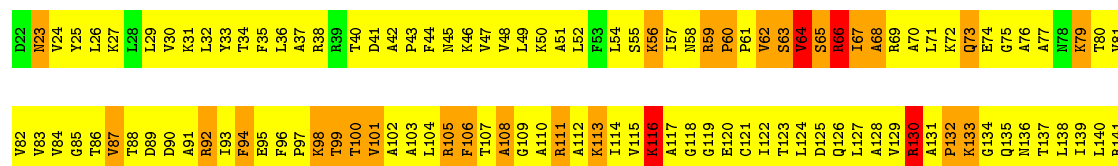
- Molecule 33: 60S ribosomal protein L17-A

Chain BN:  52% 21% 20%




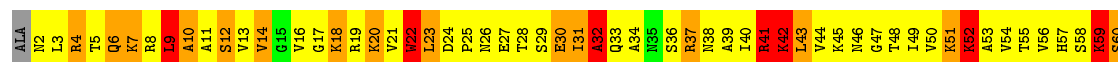
- Molecule 34: 60S ribosomal protein L18

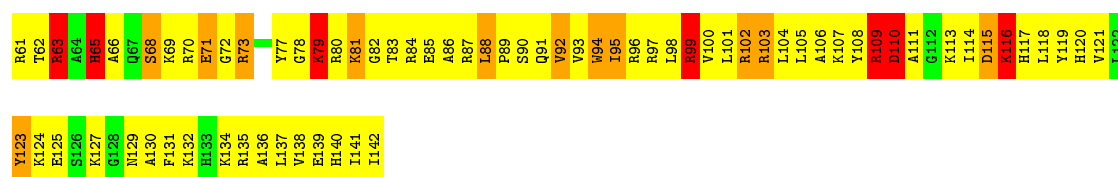
Chain BO:  72% 21%



- Molecule 35: 60S ribosomal protein L19

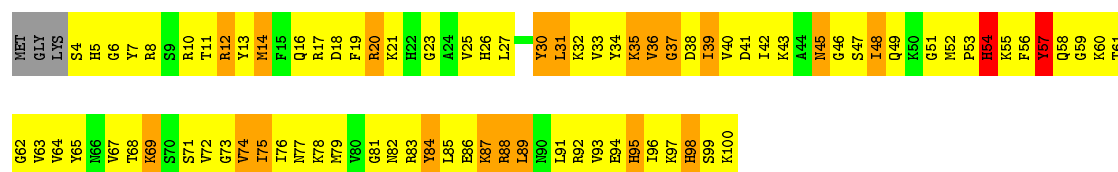
Chain BP: 





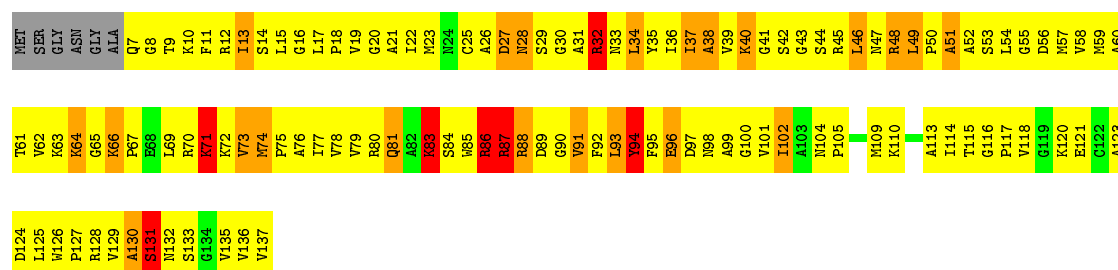
- Molecule 36: 60S ribosomal protein L21-A

Chain BQ: 12% 63% 20% . .



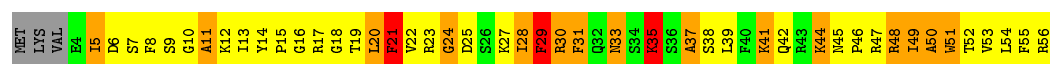
- Molecule 37: 60S ribosomal protein L23

Chain BR: 9% 66% 16% 5% .



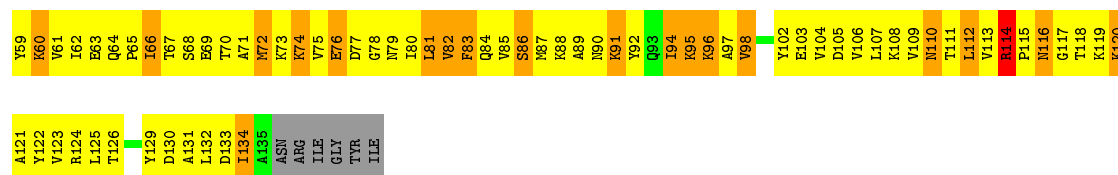
- Molecule 38: 60S ribosomal protein L24-A

Chain BS: 13% 50% 27% 5% 5%



- Molecule 39: 60S ribosomal protein L25

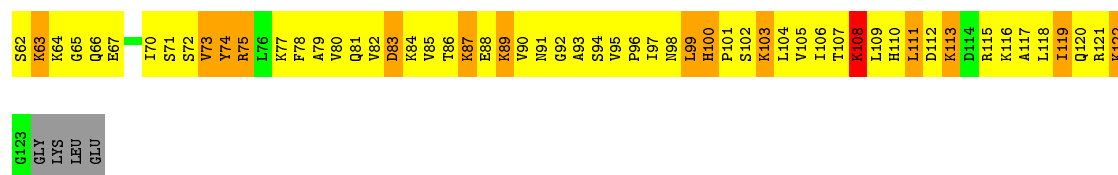
Chain BT: 8% 60% 23% . 7%



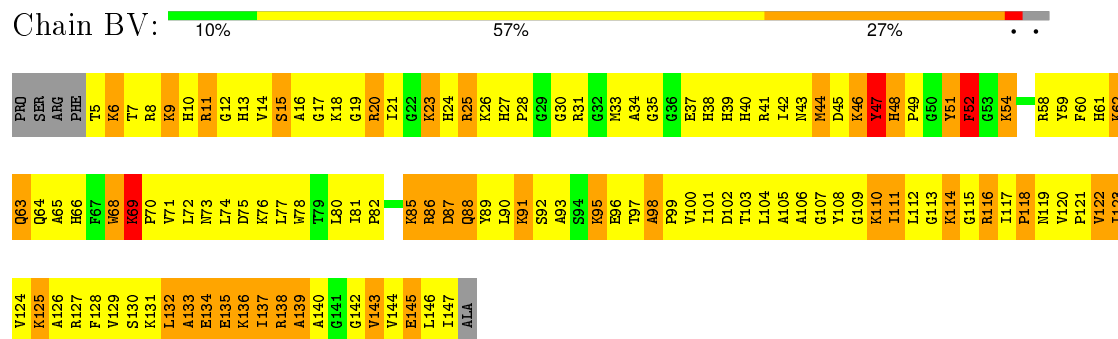
- Molecule 40: 60S ribosomal protein L26-A

Chain BU: 6% 60% 23% . 9%

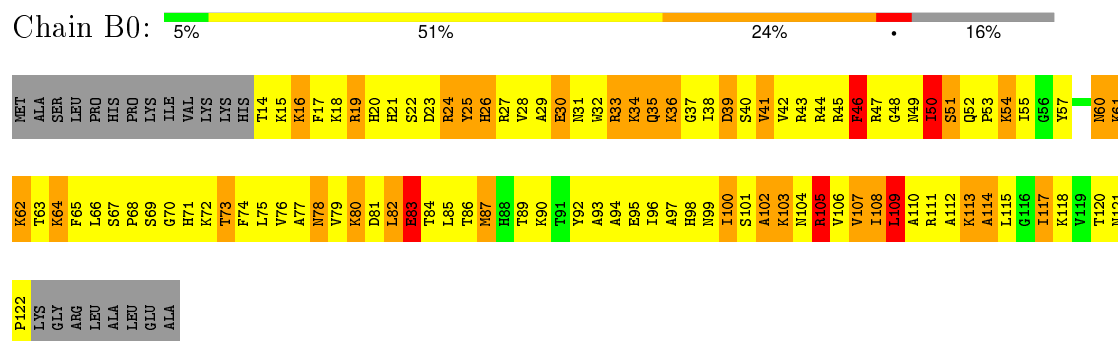




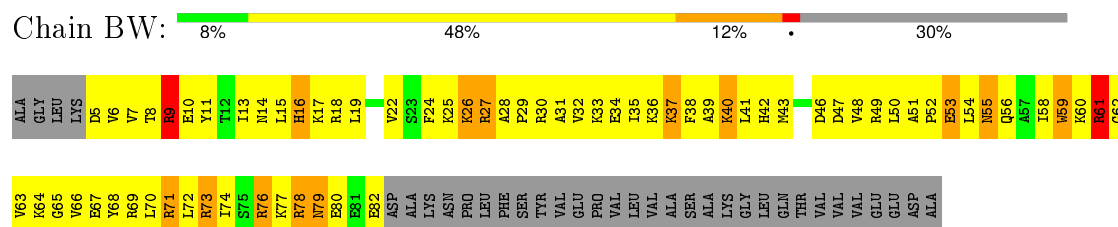
- Molecule 41: 60S ribosomal protein L28



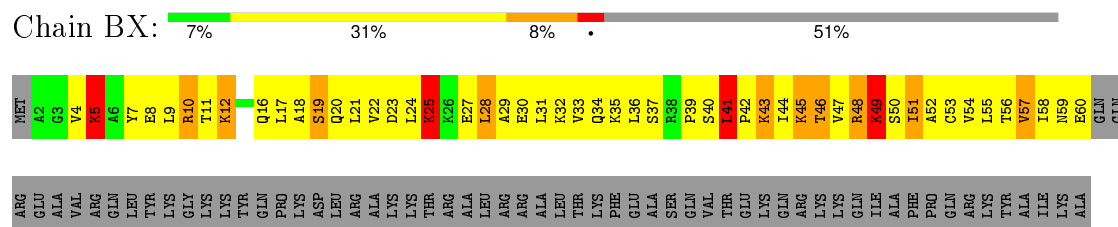
- Molecule 42: 60S ribosomal protein L32



- Molecule 43: 60S ribosomal protein L31

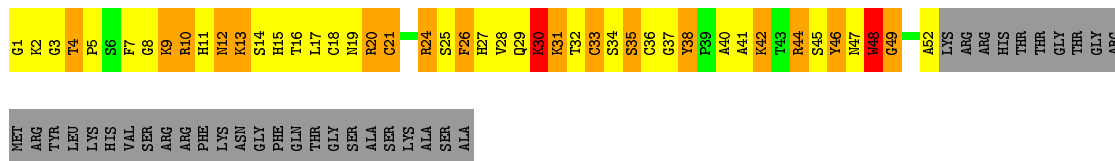


- Molecule 44: 60S ribosomal protein L35




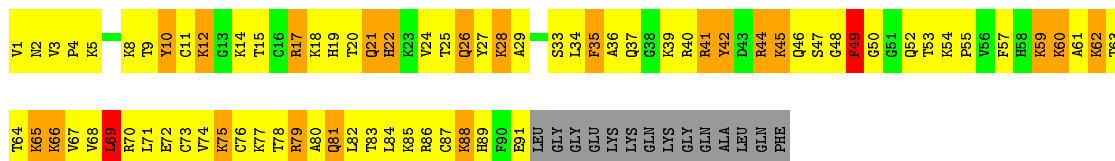
- Molecule 45: 60S ribosomal protein L37-A

Chain BY: 



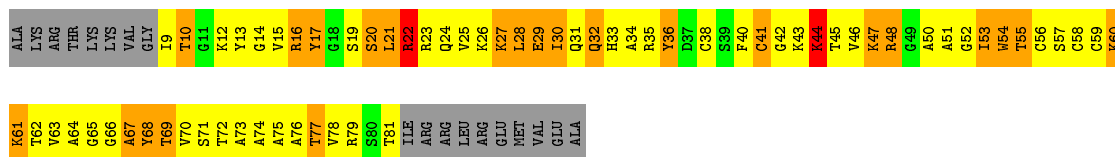
- Molecule 46: 60S ribosomal protein L42

Chain BZ: 



- Molecule 47: 60S ribosomal protein L43

Chain B9: 



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of 3D-maps by Wiener filtration	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	4900	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.49	1/35241 (0.0%)	0.77	43/54932 (0.1%)
10	AJ	0.99	0/787	1.17	0/1063
11	AK	1.10	0/936	1.28	3/1260 (0.2%)
12	AL	0.99	0/920	1.19	1/1226 (0.1%)
13	AM	1.06	0/1100	1.54	4/1476 (0.3%)
14	AN	1.13	0/237	1.37	0/315
15	AO	1.09	0/560	1.06	1/745 (0.1%)
16	AQ	1.08	0/631	1.15	0/852
17	AS	1.03	0/636	1.27	3/855 (0.4%)
18	B3	0.58	5/67026 (0.0%)	0.79	89/104457 (0.1%)
19	B4	0.36	0/2905	0.75	4/4528 (0.1%)
2	AT	0.31	0/6496	0.59	1/8794 (0.0%)
20	BA	0.91	0/1706	1.12	1/2289 (0.0%)
21	BB	1.27	2/1889 (0.1%)	4.30	39/2539 (1.5%)
22	BC	1.19	3/2921 (0.1%)	3.76	53/3933 (1.3%)
23	BD	1.46	5/1979 (0.3%)	3.13	28/2680 (1.0%)
24	BE	1.23	1/1840 (0.1%)	1.67	35/2487 (1.4%)
25	BF	1.05	0/1330	1.33	4/1794 (0.2%)
26	BG	1.05	0/895	1.51	15/1208 (1.2%)
27	BH	1.13	0/1429	1.77	18/1925 (0.9%)
28	BI	1.16	0/1352	2.99	29/1815 (1.6%)
29	BJ	1.20	1/1340 (0.1%)	1.89	20/1797 (1.1%)
3	AB	1.00	0/1471	1.13	2/2007 (0.1%)
30	BK	1.08	1/986 (0.1%)	2.52	7/1320 (0.5%)
31	BL	1.33	1/1671 (0.1%)	3.44	43/2239 (1.9%)
32	BM	1.23	1/1190 (0.1%)	3.77	22/1597 (1.4%)
33	BN	1.19	2/1185 (0.2%)	4.05	30/1597 (1.9%)
34	BO	1.20	2/937 (0.2%)	5.64	22/1266 (1.7%)
35	BP	1.24	1/1162 (0.1%)	2.86	20/1550 (1.3%)
36	BQ	1.10	0/811	1.45	7/1081 (0.6%)
37	BR	1.17	0/992	1.52	10/1333 (0.8%)
38	BS	1.23	0/449	1.66	7/597 (1.2%)
39	BT	1.19	0/621	1.52	5/837 (0.6%)
4	AC	1.04	0/1488	1.19	4/1996 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	BU	1.15	0/922	1.78	6/1232 (0.5%)
41	BV	1.08	0/1162	1.32	6/1556 (0.4%)
42	B0	1.18	1/897 (0.1%)	4.22	12/1201 (1.0%)
43	BW	1.17	0/664	1.46	3/885 (0.3%)
44	BX	1.10	0/463	1.44	3/619 (0.5%)
45	BY	1.35	1/412 (0.2%)	6.06	13/548 (2.4%)
46	BZ	1.15	2/752 (0.3%)	7.19	34/995 (3.4%)
47	B9	1.27	0/553	1.66	6/740 (0.8%)
5	AD	1.06	0/1443	1.21	2/1932 (0.1%)
6	AE	1.03	0/1112	1.17	0/1500
7	AG	1.06	0/1169	1.14	2/1570 (0.1%)
8	AH	0.99	0/1021	1.15	0/1371
9	AI	1.18	5/1114 (0.4%)	1.65	21/1492 (1.4%)
All	All	0.77	35/158803 (0.0%)	1.54	678/236031 (0.3%)

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	4	37
18	B3	19	47
19	B4	2	0
21	BB	0	2
22	BC	0	1
28	BI	0	2
29	BJ	0	1
30	BK	0	1
31	BL	0	1
32	BM	0	2
33	BN	0	1
34	BO	0	2
35	BP	0	1
38	BS	0	1
40	BU	0	1
41	BV	0	1
47	B9	0	1
All	All	25	102

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	B3	1206	C	O3'-P	-58.99	0.90	1.61
18	B3	2133	U	O3'-P	-56.48	0.93	1.61
18	B3	2168	G	O3'-P	-32.11	1.22	1.61
23	BD	64	TRP	CD2-CE2	-26.50	1.09	1.41
23	BD	64	TRP	NE1-CE2	20.96	1.64	1.37

The worst 5 of 678 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BC	297	PHE	CZ-CE2-CD2	-87.49	15.11	120.10
42	B0	46	PHE	CZ-CE2-CD2	-87.16	15.51	120.10
45	BY	26	PHE	CZ-CE2-CD2	-87.13	15.54	120.10
21	BB	15	PHE	CZ-CE2-CD2	-87.10	15.57	120.10
34	BO	94	PHE	CD1-CE1-CZ	-87.08	15.60	120.10

5 of 25 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	181	G	C3'
1	AA	1493	A	C3'
1	AA	1504	G	C3'
1	AA	1528	U	C3'
18	B3	191	A	C3'

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	12	U	Sidechain
1	AA	197	A	Sidechain
1	AA	203	U	Sidechain
1	AA	231	G	Sidechain
1	AA	51	A	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	31507	0	15705	4692	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AT	6375	0	6431	574	0
3	AB	1438	0	1465	366	0
4	AC	1469	0	1534	306	0
5	AD	1424	0	1448	585	0
6	AE	1099	0	1150	351	0
7	AG	1161	0	1217	318	0
8	AH	1004	0	1033	415	0
9	AI	1094	0	1138	718	0
10	AJ	777	0	828	415	0
11	AK	925	0	935	342	0
12	AL	906	0	955	480	0
13	AM	1084	0	1091	719	0
14	AN	235	0	228	263	0
15	AO	552	0	597	174	0
16	AQ	618	0	655	359	0
17	AS	622	0	625	552	0
18	B3	59964	0	29926	9142	0
19	B4	2600	0	1308	630	0
20	BA	1682	0	1750	644	0
21	BB	1855	0	1912	1147	0
22	BC	2856	0	2895	1961	0
23	BD	1942	0	1964	1382	0
24	BE	1799	0	1710	1194	0
25	BF	1298	0	1365	687	0
26	BG	886	0	953	454	0
27	BH	1410	0	1472	794	0
28	BI	1326	0	1355	735	0
29	BJ	1319	0	1334	777	0
30	BK	978	0	1045	469	0
31	BL	1637	0	1668	873	0
32	BM	1165	0	1243	670	0
33	BN	1163	0	1157	768	0
34	BO	925	0	998	447	0
35	BP	1145	0	1215	793	0
36	BQ	795	0	804	454	0
37	BR	977	0	1008	673	0
38	BS	439	0	445	249	0
39	BT	614	0	635	429	0
40	BU	911	0	987	583	0
41	BV	1133	0	1163	782	0
42	B0	880	0	911	664	0
43	BW	654	0	689	315	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BX	461	0	512	338	0
45	BY	402	0	389	346	0
46	BZ	740	0	798	422	0
47	B9	546	0	556	396	0
All	All	146792	0	101202	29887	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 121.

The worst 5 of 29887 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)
1:AA:1329:A:H5'	13:AM:98:TYR:CG	1.25	1.70
18:B3:1694:G:C2	45:BY:5:PRO:HG2	1.20	1.70
18:B3:541:C:C5	42:B0:15:LYS:HG3	1.20	1.69
1:AA:1178:G:P	9:AI:105:LYS:HG2	1.34	1.68
18:B3:2388:C:P	36:BQ:88:ARG:HB3	1.34	1.67

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	AT	811/842 (96%)	779 (96%)	24 (3%)	8 (1%)	19	65
3	AB	183/185 (99%)	159 (87%)	17 (9%)	7 (4%)	4	37
4	AC	186/192 (97%)	169 (91%)	7 (4%)	10 (5%)	2	29
5	AD	176/179 (98%)	157 (89%)	15 (8%)	4 (2%)	8	48
6	AE	145/149 (97%)	134 (92%)	8 (6%)	3 (2%)	9	50
7	AG	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	14	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	125/129 (97%)	113 (90%)	6 (5%)	6 (5%)	3	32
9	AI	137/142 (96%)	118 (86%)	11 (8%)	8 (6%)	2	27
10	AJ	95/100 (95%)	80 (84%)	7 (7%)	8 (8%)	1	18
11	AK	123/136 (90%)	110 (89%)	10 (8%)	3 (2%)	7	47
12	AL	116/118 (98%)	101 (87%)	9 (8%)	6 (5%)	2	30
13	AM	127/132 (96%)	121 (95%)	5 (4%)	1 (1%)	24	69
14	AN	27/36 (75%)	23 (85%)	2 (7%)	2 (7%)	1	21
15	AO	63/65 (97%)	60 (95%)	2 (3%)	1 (2%)	12	56
16	AQ	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
17	AS	78/80 (98%)	70 (90%)	7 (9%)	1 (1%)	15	60
20	BA	207/217 (95%)	193 (93%)	9 (4%)	5 (2%)	7	47
21	BB	242/253 (96%)	163 (67%)	48 (20%)	31 (13%)	0	8
22	BC	357/386 (92%)	268 (75%)	55 (15%)	34 (10%)	1	15
23	BD	254/361 (70%)	182 (72%)	42 (16%)	30 (12%)	0	9
24	BE	220/222 (99%)	166 (76%)	31 (14%)	23 (10%)	1	12
25	BF	159/162 (98%)	118 (74%)	27 (17%)	14 (9%)	1	17
26	BG	117/119 (98%)	80 (68%)	21 (18%)	16 (14%)	0	6
27	BH	176/191 (92%)	113 (64%)	36 (20%)	27 (15%)	0	5
28	BI	163/168 (97%)	106 (65%)	43 (26%)	14 (9%)	1	17
29	BJ	163/173 (94%)	113 (69%)	32 (20%)	18 (11%)	0	11
30	BK	127/131 (97%)	117 (92%)	7 (6%)	3 (2%)	7	47
31	BL	192/203 (95%)	128 (67%)	39 (20%)	25 (13%)	0	7
32	BM	144/146 (99%)	106 (74%)	24 (17%)	14 (10%)	1	14
33	BN	145/183 (79%)	101 (70%)	27 (19%)	17 (12%)	0	9
34	BO	118/120 (98%)	82 (70%)	25 (21%)	11 (9%)	1	16
35	BP	139/142 (98%)	89 (64%)	30 (22%)	20 (14%)	0	6
36	BQ	95/100 (95%)	73 (77%)	13 (14%)	9 (10%)	1	15
37	BR	129/137 (94%)	92 (71%)	23 (18%)	14 (11%)	0	11
38	BS	51/56 (91%)	36 (71%)	8 (16%)	7 (14%)	0	6
39	BT	75/83 (90%)	53 (71%)	13 (17%)	9 (12%)	0	8
40	BU	113/126 (90%)	82 (73%)	15 (13%)	16 (14%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BV	141/148 (95%)	102 (72%)	23 (16%)	16 (11%)	0	10
42	B0	107/130 (82%)	76 (71%)	17 (16%)	14 (13%)	0	7
43	BW	76/112 (68%)	57 (75%)	13 (17%)	6 (8%)	1	19
44	BX	57/120 (48%)	41 (72%)	9 (16%)	7 (12%)	0	8
45	BY	50/87 (58%)	35 (70%)	6 (12%)	9 (18%)	0	4
46	BZ	89/105 (85%)	66 (74%)	17 (19%)	6 (7%)	1	24
47	B9	71/91 (78%)	43 (61%)	17 (24%)	11 (16%)	0	5
All	All	6591/7183 (92%)	5282 (80%)	813 (12%)	496 (8%)	3	21

5 of 496 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AT	106	PRO
2	AT	108	HIS
2	AT	460	ASP
3	AB	23	LEU
3	AB	27	ASN

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	AT	697/715 (98%)	677 (97%)	20 (3%)	50	78
3	AB	153/153 (100%)	146 (95%)	7 (5%)	33	68
4	AC	152/155 (98%)	140 (92%)	12 (8%)	15	51
5	AD	148/149 (99%)	136 (92%)	12 (8%)	15	50
6	AE	115/115 (100%)	109 (95%)	6 (5%)	29	65
7	AG	123/123 (100%)	115 (94%)	8 (6%)	21	58
8	AH	108/110 (98%)	102 (94%)	6 (6%)	26	62
9	AI	116/118 (98%)	111 (96%)	5 (4%)	35	70
10	AJ	91/93 (98%)	82 (90%)	9 (10%)	10	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AK	95/104 (91%)	91 (96%)	4 (4%)	36	70
12	AL	98/98 (100%)	93 (95%)	5 (5%)	29	66
13	AM	116/116 (100%)	113 (97%)	3 (3%)	54	80
14	AN	27/33 (82%)	26 (96%)	1 (4%)	41	73
15	AO	59/59 (100%)	55 (93%)	4 (7%)	20	57
16	AQ	70/70 (100%)	67 (96%)	3 (4%)	35	70
17	AS	66/66 (100%)	63 (96%)	3 (4%)	34	69
20	BA	194/198 (98%)	184 (95%)	10 (5%)	29	65
21	BB	187/195 (96%)	156 (83%)	31 (17%)	3	19
22	BC	299/322 (93%)	252 (84%)	47 (16%)	3	21
23	BD	198/287 (69%)	174 (88%)	24 (12%)	6	31
24	BE	187/187 (100%)	171 (91%)	16 (9%)	13	47
25	BF	142/143 (99%)	121 (85%)	21 (15%)	4	24
26	BG	92/92 (100%)	82 (89%)	10 (11%)	8	35
27	BH	159/171 (93%)	136 (86%)	23 (14%)	4	24
28	BI	141/143 (99%)	118 (84%)	23 (16%)	3	20
29	BJ	143/149 (96%)	119 (83%)	24 (17%)	2	19
30	BK	105/105 (100%)	103 (98%)	2 (2%)	65	86
31	BL	167/175 (95%)	126 (75%)	41 (25%)	1	6
32	BM	123/123 (100%)	106 (86%)	17 (14%)	4	27
33	BN	120/145 (83%)	94 (78%)	26 (22%)	1	9
34	BO	98/98 (100%)	85 (87%)	13 (13%)	5	28
35	BP	119/119 (100%)	90 (76%)	29 (24%)	1	6
36	BQ	86/88 (98%)	76 (88%)	10 (12%)	7	32
37	BR	102/105 (97%)	87 (85%)	15 (15%)	4	24
38	BS	46/49 (94%)	37 (80%)	9 (20%)	1	12
39	BT	68/73 (93%)	59 (87%)	9 (13%)	5	28
40	BU	100/109 (92%)	83 (83%)	17 (17%)	2	18
41	BV	114/118 (97%)	88 (77%)	26 (23%)	1	8
42	B0	94/111 (85%)	70 (74%)	24 (26%)	1	6
43	BW	69/96 (72%)	60 (87%)	9 (13%)	5	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	BX	53/105 (50%)	45 (85%)	8 (15%)	3	23
45	BY	42/70 (60%)	34 (81%)	8 (19%)	2	13
46	BZ	80/90 (89%)	66 (82%)	14 (18%)	2	16
47	B9	56/71 (79%)	44 (79%)	12 (21%)	1	9
All	All	5618/6014 (93%)	4992 (89%)	626 (11%)	12	34

5 of 626 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	BH	125	ASN
31	BL	64	ARG
43	BW	55	ASN
28	BI	33	ILE
29	BJ	34	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 189 such sidechains are listed below:

Mol	Chain	Res	Type
21	BB	99	ASN
23	BD	91	ASN
41	BV	88	GLN
21	BB	186	HIS
22	BC	181	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1440/1507 (95%)	215 (14%)	91 (6%)
18	B3	2758/2999 (91%)	342 (12%)	115 (4%)
19	B4	122/125 (97%)	17 (13%)	5 (4%)
All	All	4320/4631 (93%)	574 (13%)	211 (4%)

5 of 574 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G

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Mol	Chain	Res	Type
1	AA	31	G
1	AA	32	A

5 of 211 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	B3	196	G
18	B3	877	G
18	B3	2714	U
18	B3	282	C
18	B3	496	G

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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
18	B3	35
1	AA	25
20	BA	2
6	AE	1
2	AT	1

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Mol	Chain	Number of breaks
30	BK	1
13	AM	1

The worst 5 of 66 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	142:G	O3'	143:A	P	21.73
1	AT	480:VAL	C	481:MET	N	21.40
1	AA	178:C	O3'	179:A	P	20.38
1	AA	454:C	O3'	455:C	P	14.81
1	B3	1228:C	O3'	1229:C	P	13.08