



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:13 PM BST

PDB ID : 2J28
EMDB ID: : EMD-1261
Title : MODEL OF E. COLI SRP BOUND TO 70S RNCS
Authors : Halic, M.; Blau, M.; Becker, T.; Mielke, T.; Pool, M.R.; Wild, K.; Sinning, I.; Beckmann, R.
Deposited on : 2006-08-16
Resolution : 8.00 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>

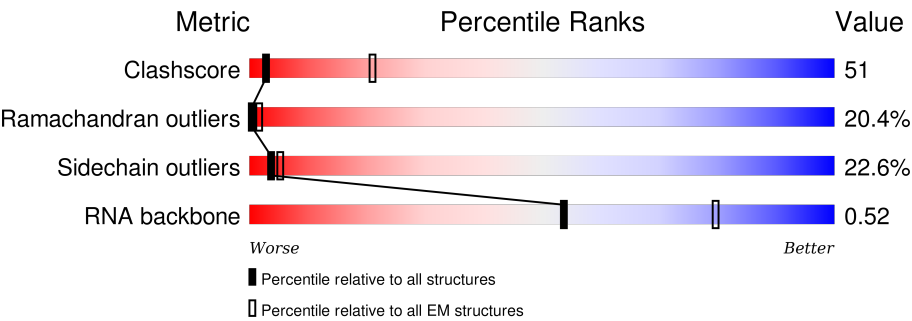
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.00 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.







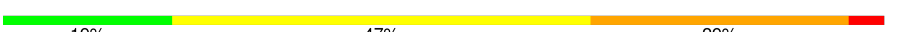
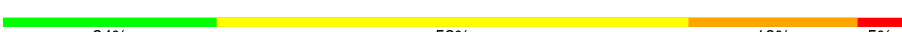
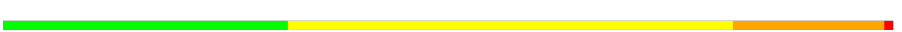





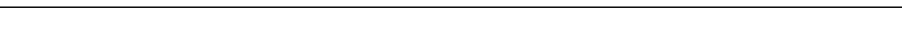

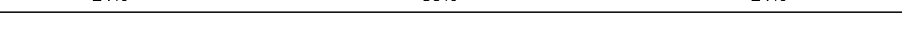
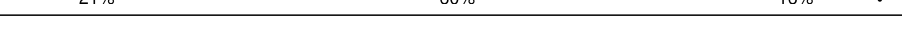
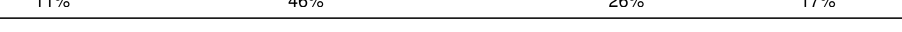
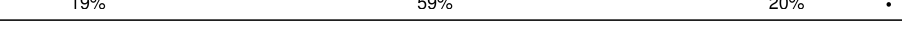

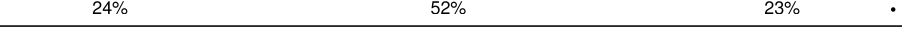




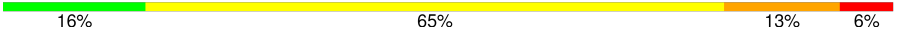
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	0	56	9% 63% 21% 7%
2	1	54	22% 43% 35%
3	2	46	28% 43% 20% 9%
4	3	64	23% 48% 25% .
5	4	38	5% 42% 32% 21%
6	7	18	17% 83%
7	8	74	73% 19% 5% .
8	9	430	5% 48% 39% 8%

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Mol	Chain	Length	Quality of chain
9	A	117	
10	B	2904	
11	C	267	
12	D	209	
13	E	201	
14	F	178	
15	G	176	
16	H	149	
17	I	141	
18	J	140	
19	K	121	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	114	
25	Q	117	
26	R	103	
27	S	110	
28	T	99	
29	U	102	
30	V	94	
31	W	84	
32	X	63	
33	Y	58	

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Mol	Chain	Length	Quality of chain
34	Z	70	<div><div></div><div>19%</div><div>56%</div><div>21%</div><div></div></div>

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95358 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S RIBOSOMAL PROTEIN L32.

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

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called SIGNAL SEQUENCE.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	7	18	Total	C	N	O	0	0
			149	103	23	23		

- Molecule 7 is a RNA chain called 4.5S SIGNAL RECOGNITION PARTICLE RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	74	Total	C	N	O	P	0	0
			1590	709	295	512	74		

- Molecule 8 is a protein called SIGNAL RECOGNITION PARTICLE 54.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	430	Total	C	N	O	S	0	0
			3306	2072	595	617	22		

- Molecule 9 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

- Molecule 10 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	2841	Total	C	N	O	P	0	0
			60995	27210	11229	19715	2841		

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 12 is a protein called 50S RIBOSOMAL PROTEIN L3.

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

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L4.

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

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L6.

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

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L9.

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

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L11.

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

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L16.

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

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L19.

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

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L20.

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

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L21.

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

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L25.

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

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L29.

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

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L30.

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

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 35 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	B	110	Total 110	Mg 110	0
35	N	1	Total 1	Mg 1	0

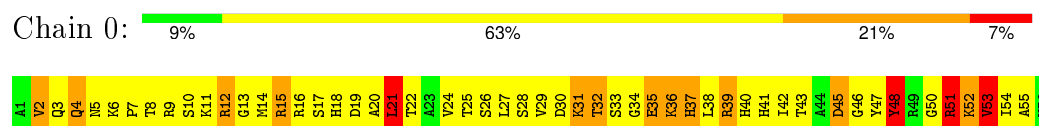
- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	B	506	Total 506	O 506	0
36	N	6	Total 6	O 6	0

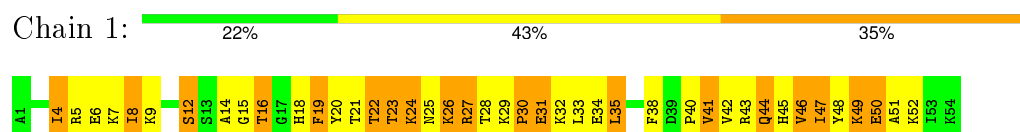
3 Residue-property plots

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.

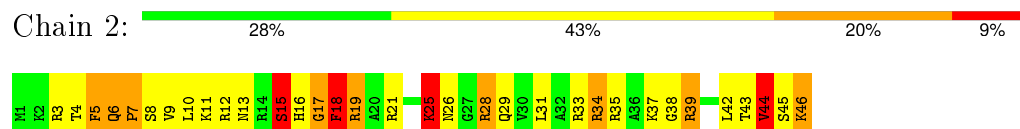
- Molecule 1: 50S RIBOSOMAL PROTEIN L32



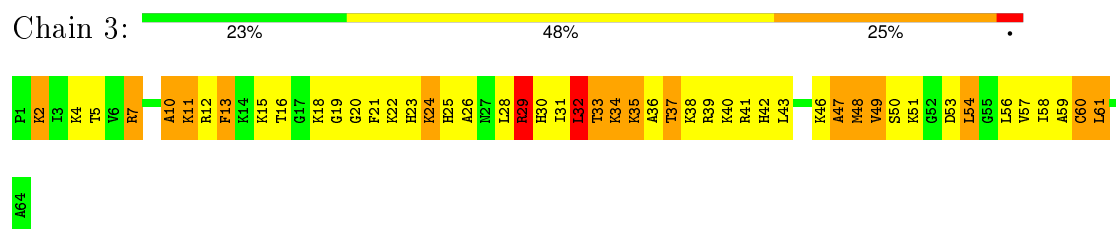
- Molecule 2: 50S RIBOSOMAL PROTEIN L33



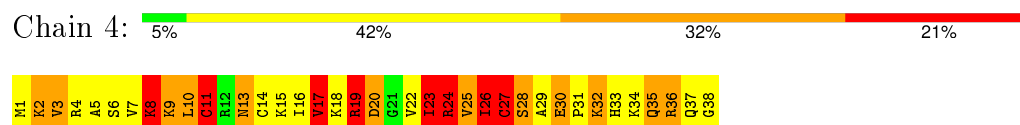
- Molecule 3: 50S RIBOSOMAL PROTEIN L34



- Molecule 4: 50S RIBOSOMAL PROTEIN L35



- Molecule 5: 50S RIBOSOMAL PROTEIN L36



- Molecule 6: SIGNAL SEQUENCE



L50
G51
F52
P53
I54
N55
P56
L57
T58
L59
Y60
V61
T62
V63
Q64
H65
K66
K67

• Molecule 7: 4.5S SIGNAL RECOGNITION PARTICLE RNA

Chain 8: 73% 19% 5%

U13
U22
G23
U29
G30
A39
A47
G48
A55
C62
A63
G75
A76
G78
C84
A85
G86
G87
C88
A89
G90
A91

• Molecule 8: SIGNAL RECOGNITION PARTICLE 54

Chain 9: 5% 48% 39% 8%

F2
D3
N4
L5
T6
D7
R8
L9
S10
R11
T12
L13
R14
N15
I16
S17
G18
R19
G20
R21
L22
T23
R24
N25
G26
Y27
K28
D29
T30
L31
R32
E33
V34
R35
M36
A37
L38
L39
F40
A41
D42
V43
A44
L45
P46
V47
V48
R49
E50
E51
I52
N53
R54
V55
V56
K56
E57
K58
A59
V60
G61

H62
E63
V64
H65
K66
S67
L68
T69
F70
G71
Q72
E73
F74
V75
K76
I77
V78
R79
N80
E81
L82
V83
K84
A85
N86
G87
E88
D89
N90
Q91
E92
T92
L95
Q98
P99
F100
A101
V102
L104
M105
V106
G107
L108
Q109
G110
A111
G112
E113
T114
T115
S116
V117
G118
K119
L120
G121
K122
F123

L124
R125
E126
V127
H128
K129
K130
L131
V132
L133
V134
V135
S136
A137
D138
V139
Y140
R141
P142
A143
I144
V145
K146
Q147
N148
E149
T150
D151
N152
E153
Q154
V155
G156
V157
D158
F159
F160
F161
S162
D163
V164
G165
Q166
K167
P168
V169
D170
I171
V172
M173
A174
A175
L176
K177
E178
A179
K180
L181
K182
F183

Y184
D185
V186
L187
L188
L189
D190
T191
A192
G193
R194
L195
H196
V197
D198
E199
A200
M201
M202
D203
E204
I205
K206
Q207
Y208
E209
A210
S211
I212
N213
P214
V215
L218
F219
V220
V221
D222
A223
M224
G225
G226
Q227
D228
A229
A230
M231
T232
A233
K234
A235
F236
M237
E238
A239
L240
P241
T242
G244

V245
V246
L247
T248
K249
V250
D251
G252
D253
A254
R255
G256
G257
A258
A259
L260
S261
K262
L263
K264
I265
T266
G267
K268
P269
I270
K271
F272
L273
G274
V275
G276
E277
K278
T279
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A281
L282
E283
P284
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P287
D288
R289
I290
M291
S292
R293
L294
L295
G296
M297
G298
Q299
V300
L301
S302
L303
I304

E305
D306
L307
E308
S309
K310
V311
D312
R313
A314
Q315
A316
E317
K318
L319
A320
S321
K322
L323
K324
I325
G326
T327
G328
F329
D330
L331
N332
D333
F334
L335
E336
Q337
L338
R339
Q340
M341
K342
N343
K344
G345
G346
M347
A348
S349
L350
M351
G352
K353
L354
P355
G356
M357
G358
Q359
I360
P361
N362
L363
V364

K365
S366
Q367
M368
D369
D370
K371
F372
L373
V374
R375
K376
E377
A378
I379
L380
N381
K382
K383
T384
K385
K386
E387
R388
A389
K390
F391
E392
L393
I394
K395
G396
S397
R398
R399
R400
A401
T402
A403
A404
G405
C406
G407
M408
Q409
V410
Q411
D412
V413
M414
R415
L416
L417
K418
Q419
P420
D421
D422
M423
Q424

R425
M426
M427
K428
M429
M430
K431

• Molecule 9: 5S RIBOSOMAL RNA

Chain A: 26% 62% 13%

G2
C3
G4
U5
G6
G7
G10
C11
G12
G13
U14
A15
G16
C17
G18
G21
C22
G23
G24
U25
C26
C27
C28
A29
C30
C31
U32
G33
A34
C35
C36
C37
G38
A39
U40
C41
C42
C43
G44
A45
A46
C47
U48
C49
A50
G51
A52
A53
G54
U55
A56
A57
A58
A59
C60
G61
C62
C63

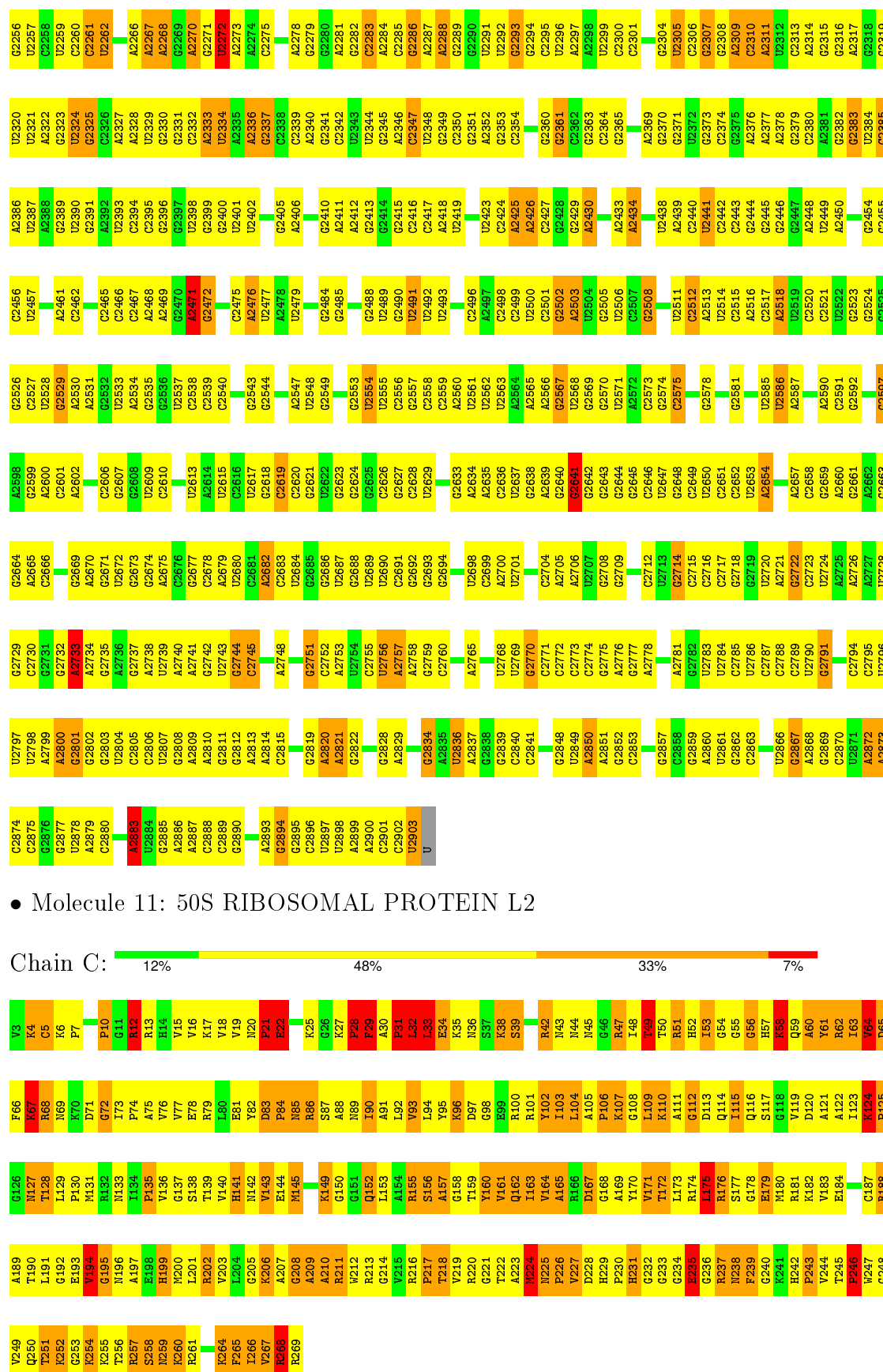
G64
U65
A66
G67
C68
G69
G70
C71
G75
G76
U77
A78
U82
U87
C88
U89
C90
C91
C92
C93
A94
U95
G96
A99
G102
U103
A104
G105
G106
G107
A108
A109
G112
C113
C114
A115
G116
G117
C118

• Molecule 10: 23S RIBOSOMAL RNA

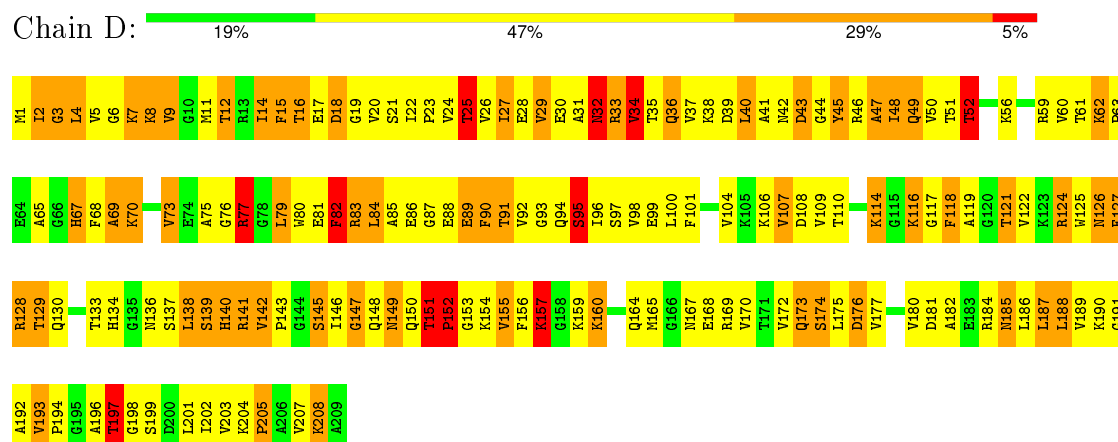
Chain B: 27% 58% 12%

G110	A1028	G962	A900	U839	G763	C678	A608	A547	A483	A412	G350	G283	G215	U139	G70	G1
A1111	A1029	U963	C901	C840	A764	C679	A609	G548	C484	C413	C351	U284	A216	C140	A71	G2
G1112	C1030	G964	C902	G841	G880	G681	C611	G549	C485	A414	A352	G286	A217	G141	U72	U3
U1113	U1033	C965	C903	U842	U766	G682	C612	G550	C486	A415	C353	U287	A218	A142	A73	U4
G1114	G1034	G966	C904	G843	G683	G683	A613	G551	C487	C416	C354	G288	A219	C143	A74	A5
G1115	U1035	U967	A905	A844	G684	G684	A614	G552	C488	C417	U355	U289	A220	G144	G75	A6
G1116	U1036	C968	U906	A845	G685	A885	U615	G553	C489	C418	U356	C289	A221	A145	G7	G8
C1117	G1042	C969	C907	U846	C772	U886	U616	G554	C490	U419	U357	U290	A222	U150	U78	
C1118	C1043	U970	C908	U847	U773	U887	A617	G555	C491	C420	U358	U291	A223	U151	C79	
U1119	U1044	C971	A909	C848	G774	U888	G617	G556	C492	C421	U359	U292	U224	C152	U82	C11
U1120	A1046	A972	A910	A849	G775	U889	G618	C557	C493	G424	C361	A226	C225	A152	A83	U12
C1121	G1047	A973	C912	U850	G776	G690	G620	U558	C494	G425	A362	U296	A227	U153	A84	G15
G1122	G1048	G974	C913	C851	G777	C691	A621	C559	C495	C426	C363	G297	C228	U154	A85	C16
C1123	A1050	A975	U913	U852	G778	C692	A622	C560		U427	C364	C298	C229	A155	G85	G17
G1124	C1051	G976	C914	C853	U779	C693	G623	G561	U499		U365	A230	G230	A156		
G1125	G1052		C915	C854	G780	C694	C624	U562	G500		C366	A300	A231		U18	
A1126	A1053	A981	U916	G855	A781	G700	A625	U563	A504	U431	C367	C301	G232	A160	A19	
A1127	A1054	A982	U917	G856	A782	G701	A626	U564	A505	U432	C368	C302	G233	A161	C20	
G1128	U1055	A983	U918	G857	G783	A702	A627	U565	A506		U369	C303	U234	U162	A21	
A1129	U1056	A984	U919	G858	A784	A703		U566	A507		C370	U304	U235	C163	U92	G22
U1130	U1057		A920	G859	G785	A704		U567	A508	C435	A371	U305	U236	C164	U93	C23
G1131	G1062	C987	C921	U860	U709	U710	A632	U568	A509	C436	C372	U306		C165	A94	G24
U1132	G1063	A988	C922	A861	A794	U711	A633	U569	C509	G438	U373	G307	C240	U166	A95	U25
A1133	C1064	C989	C923	G862	C795	G713	C634	G570	C510	A439	A374	G308	G241	A167	C96	G26
A1134	U1065	A990	A925	A863	C796	U714	C635	U571	U511	C440	C375	A309	G242	G168	C97	G27
G1135		C991	G926	C864	G797	U715	C636	A572	G512	U441	C376	A310	U243	G169	A28	
G1136	G1068	C992	A927	C865			A637	U573	A513	G442	G377	A311	A244	U170	U99	U29
G1137	A1069	G993	A928	A866	C717	C718	G638	A574	A514	A443	C378	G312	G245	U171	U100	G30
U1138	A1070	C994	U929	A867	A719	U719	U639	A575	A515	C444	C379	G313	G246	A172	A101	C31
G1139		C995	U930	C868	C719	U720	C640	U576	C516	C445	G380	C314	G247	A173	U102	C32
C1140	U1076	A996	U931	U870	U721			G577	C517		G381	G315	G248	U174	A103	C33
U1141	A1077	G997	U932	U871	A721		A643	G578	C518	U443	A382		C249	G175	A104	U34
A1142	U1078	C998	A933	U872	A722		A644	G579	U519	A449	C383	G319	G250	A176	A105	U35
A1143	C1079	U999	U934	C873	A723		C645	U580	U520	G450	A384	A320	A251	C106	G36	
A1144	A1080	A1000	C935	G874	U724		U646	C581	C521	U451	C385	U321	G252	G107	C37	
C1145	U1081	A1001	A936	G875	G725			A582	A522	G452	C386	A322	C253	G180	A38	
U1146	U1082	C937	U937	G876	G726			G583	C523	A453	U387	G323	G254	A181	G39	
A1147	U1083	G1002	C938	A877	A727			C584	C524	A454	C388	A324	A255	A182	U40	
U1148	A1084	C1005	G939	A878	G728		A654	G585	U525	C455	G389	G325	G259	C183	C41	
G1149	A1085	C1006	C940	G879	G729		A655	A586	A526	C456	U390	G326	G260	G185	A42	
C1150	A1086	C1007	A941	C818	A730		G656	C587	C527	A457	A391	G327				
A1151	G1087	A1008	C942	A819			U657	U588	A528	G458	U392	U328		G117	G45	
C1152	A1088	C1009	A943	G			U658	U589	C529	U459	C393	G329	G263	G188	A118	
C1153	A1089	U1010	C944	G			C659	A590	C530	A460	C394	A330	C264	G189	C47	
G1154	A1090	G1011	A945	U			C660	U591	C531	C461	U395	A332	A265	U120		
A1155	C1091	U1012	C946	C			A661	A592	A532		C396	A333	G266	A196	A49	
	C1092	C1013	A947	A			G662	U593	G533	A466	U397	G333	C267	A197	G123	
G1156	G1093	A1014	C948	U			G663	U594	U534	G467	C398	C334	C268	C198	G124	
		U1015	C949	C			G664	C595	G535	G468	U399	C335		A199	A52	
G1162	U1097		C950	C			U665	U596	G536	G469	G400	C336	G271			
C1163	A1098	U1018	C951	C			A666	G597	G537	A401	A402	C337		A204	G55	
A1164	G1099	U1019	G952	G			U667	U598	A538	A472	A403	G338	C274	G205	A56	
G1166	C1100	A1020		A			A668	A599	G539		U404	U339	C275	U206		
G1167	U1101	U1021	C953	C			G669	G600	C540	C475	A404	A340	U276	A131	U62	
A1169	U1055	G1023	G956	U			A670	C601	A541	G476	U405	C341	G277	C208	A63	
G1170	G1106	G1024	U958	U			C671	A602	C542		G406		A278	C209	A64	
G1171	G1107	G1025	U959	A			C672	A603	G543	A479	G409		A279	U135	U65	
C1172	U1108	G1026	A960	C			C673	G575	C544	A480	G410		U280	G136	C66	
U1173	C1109	A1027	C961	A899			G674	U606	U546	A482	G411		C281	U137		

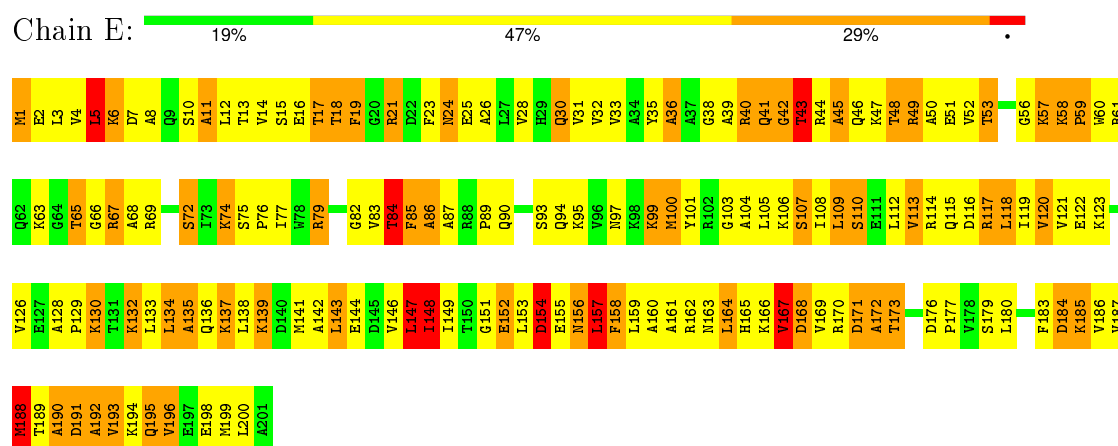


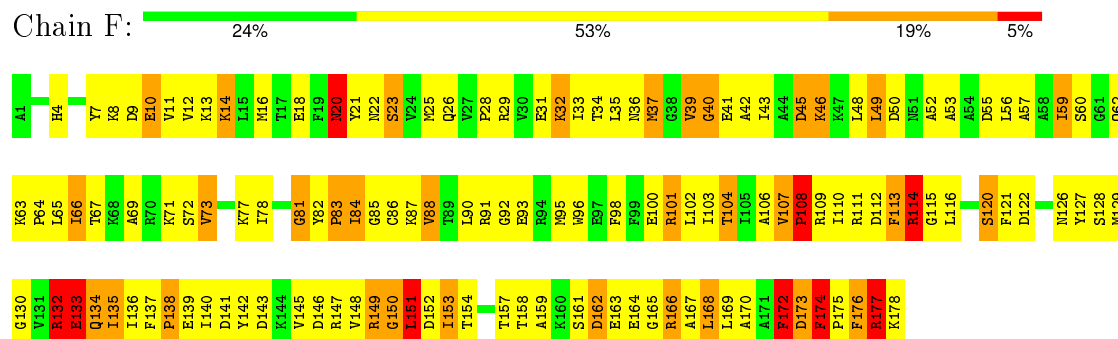
- Molecule 12: 50S RIBOSOMAL PROTEIN L3



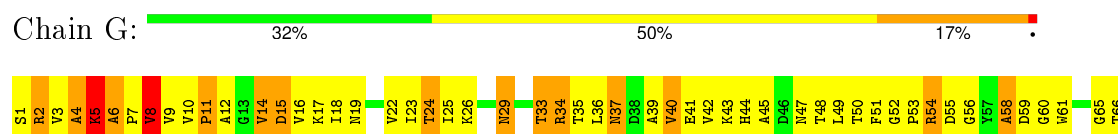
- Molecule 13: 50S RIBOSOMAL PROTEIN L4



- Molecule 14: 50S RIBOSOMAL PROTEIN L5



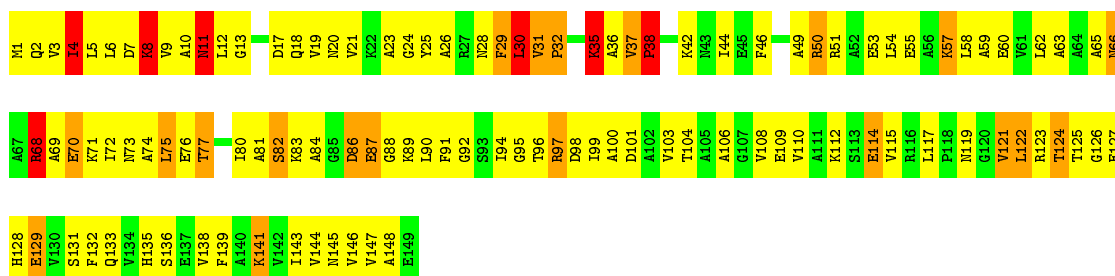
- Molecule 15: 50S RIBOSOMAL PROTEIN L6





• Molecule 16: 50S RIBOSOMAL PROTEIN L9

Chain H: 25% 57% 13% 5%



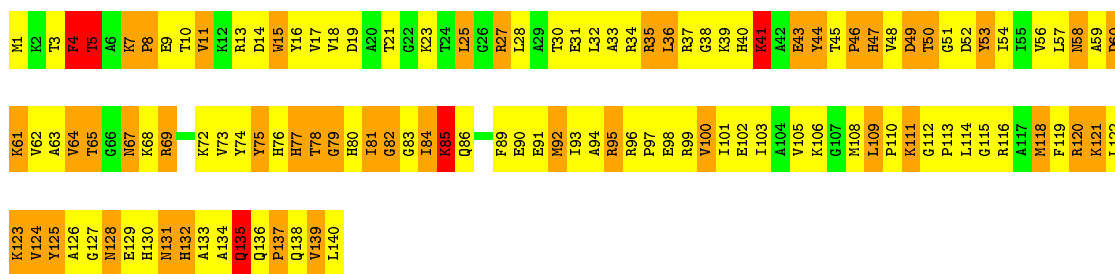
• Molecule 17: 50S RIBOSOMAL PROTEIN L11

Chain I: 34% 59% 7%



• Molecule 18: 50S RIBOSOMAL PROTEIN L13

Chain J: 13% 51% 32%



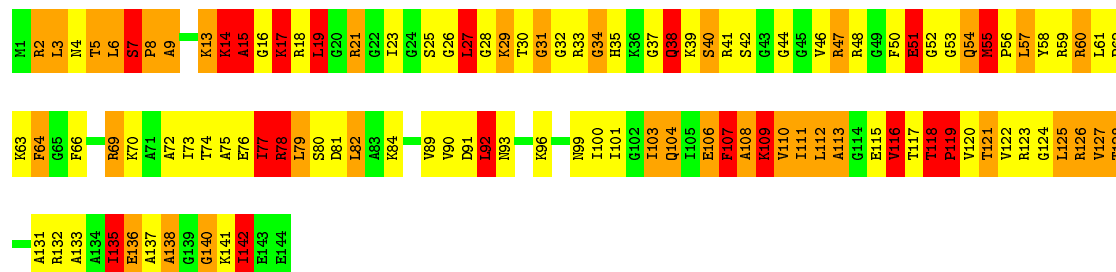
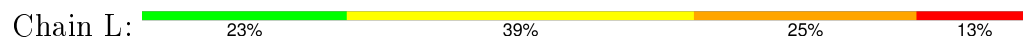
• Molecule 19: 50S RIBOSOMAL PROTEIN L14

Chain K: 17% 57% 24%

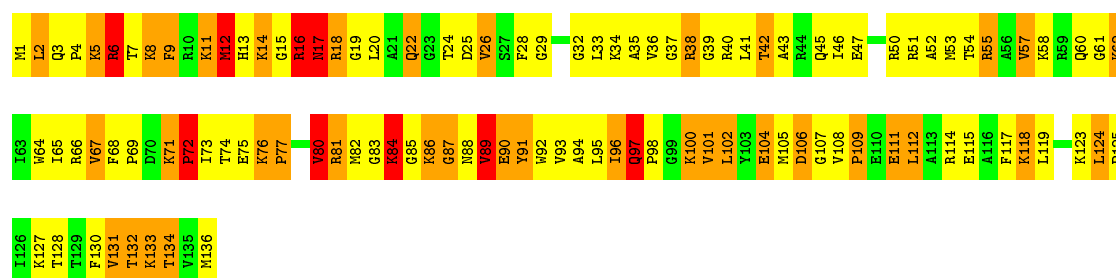
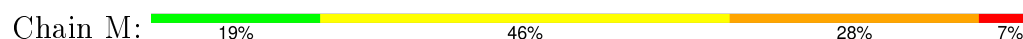




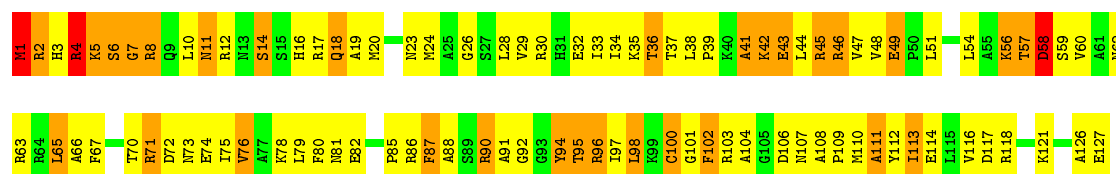
• Molecule 20: 50S RIBOSOMAL PROTEIN L15



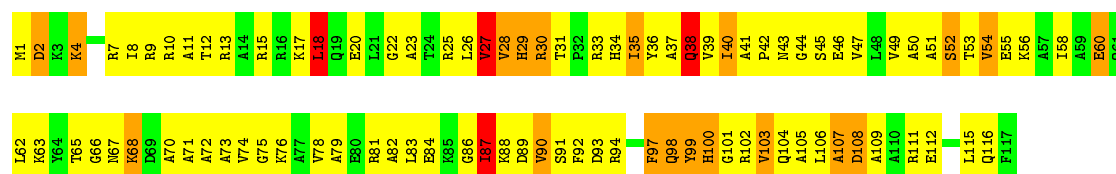
• Molecule 21: 50S RIBOSOMAL PROTEIN L16



• Molecule 22: 50S RIBOSOMAL PROTEIN L17

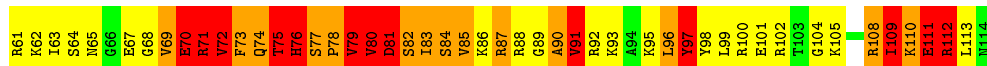


• Molecule 23: 50S RIBOSOMAL PROTEIN L18

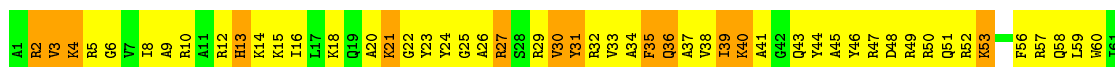


• Molecule 24: 50S RIBOSOMAL PROTEIN L19

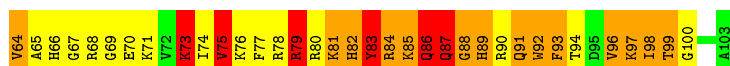
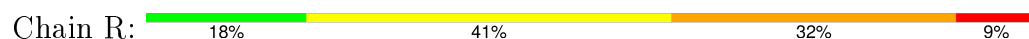




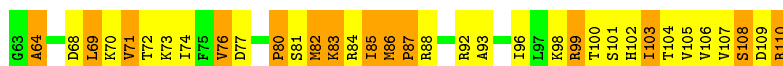
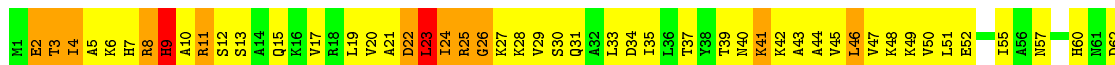
• Molecule 25: 50S RIBOSOMAL PROTEIN L20



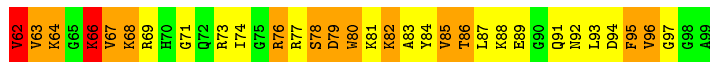
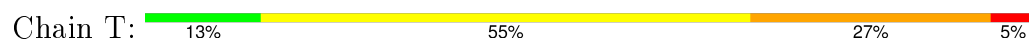
• Molecule 26: 50S RIBOSOMAL PROTEIN L21



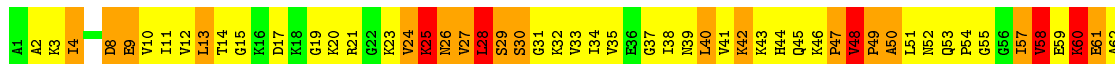
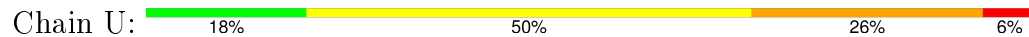
• Molecule 27: 50S RIBOSOMAL PROTEIN L22



• Molecule 28: 50S RIBOSOMAL PROTEIN L23



• Molecule 29: 50S RIBOSOMAL PROTEIN L24





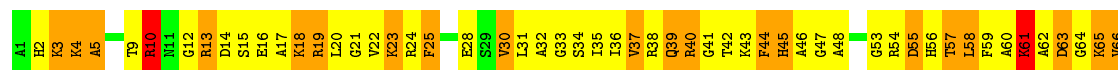
• Molecule 30: 50S RIBOSOMAL PROTEIN L25

Chain V: 34% 55% 10%



• Molecule 31: 50S RIBOSOMAL PROTEIN L27

Chain W: 15% 51% 30%



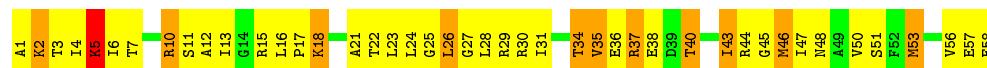
• Molecule 32: 50S RIBOSOMAL PROTEIN L29

Chain X: 16% 65% 13% 6%



• Molecule 33: 50S RIBOSOMAL PROTEIN L30

Chain Y: 24% 55% 19%



• Molecule 34: 50S RIBOSOMAL PROTEIN L31

Chain Z: 19% 56% 21%



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	Not provided	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0	0.41	0/450	0.97	3/599 (0.5%)
10	B	0.34	18/68314 (0.0%)	0.79	78/106569 (0.1%)
11	C	0.40	0/2092	0.90	9/2813 (0.3%)
12	D	0.37	0/1586	0.82	4/2134 (0.2%)
13	E	0.70	4/1571 (0.3%)	0.83	5/2113 (0.2%)
14	F	0.41	1/1444 (0.1%)	1.00	10/1937 (0.5%)
15	G	0.30	0/1343	0.67	1/1816 (0.1%)
16	H	0.34	0/1122	0.71	1/1515 (0.1%)
17	I	0.60	4/1046 (0.4%)	0.76	4/1410 (0.3%)
18	J	0.32	0/1135	0.76	3/1529 (0.2%)
19	K	0.35	0/939	0.99	4/1258 (0.3%)
2	1	0.32	0/448	0.69	0/594
20	L	0.74	1/1062 (0.1%)	1.58	25/1413 (1.8%)
21	M	0.39	0/1093	0.85	5/1460 (0.3%)
22	N	0.37	0/1021	0.80	3/1364 (0.2%)
23	O	0.31	0/910	0.64	0/1219
24	P	0.58	0/929	1.40	16/1242 (1.3%)
25	Q	0.36	0/960	0.75	0/1278
26	R	0.39	0/829	0.82	3/1107 (0.3%)
27	S	0.26	0/864	0.60	0/1156
28	T	0.45	1/784 (0.1%)	0.80	1/1048 (0.1%)
29	U	0.37	0/787	0.94	7/1051 (0.7%)
3	2	0.30	0/380	0.60	0/498
30	V	0.25	0/766	0.46	0/1025
31	W	0.39	0/642	0.81	2/848 (0.2%)
32	X	0.29	0/510	0.66	0/677
33	Y	0.32	0/453	0.69	1/605 (0.2%)
34	Z	0.52	0/559	0.91	1/745 (0.1%)
4	3	0.39	0/513	0.80	1/676 (0.1%)
5	4	0.32	0/303	0.77	0/397
6	7	0.55	0/153	0.72	0/207
7	8	1.57	10/1775 (0.6%)	1.71	18/2755 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	9	4.09	56/3329 (1.7%)	2.78	80/4446 (1.8%)
9	A	0.29	0/2803	0.77	0/4371
All	All	0.84	95/102915 (0.1%)	0.95	285/153875 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	1
10	B	1	65
11	C	0	2
24	P	0	1
26	R	0	1
34	Z	0	1
7	8	0	1
8	9	1	15
9	A	0	1
All	All	2	88

The worst 5 of 95 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	9	300	VAL	CB-CG1	107.27	3.78	1.52
8	9	299	ASP	CB-CG	88.52	3.37	1.51
8	9	333	ASP	CB-CG	82.89	3.25	1.51
8	9	300	VAL	CB-CG2	75.72	3.11	1.52
8	9	370	ASP	CB-CG	68.24	2.95	1.51

The worst 5 of 285 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	9	374	VAL	O-C-N	-71.21	8.76	122.70
8	9	300	VAL	CG1-CB-CG2	-43.96	40.56	110.90
8	9	300	VAL	CA-CB-CG2	-40.13	50.71	110.90
8	9	300	VAL	CA-CB-CG1	-38.94	52.49	110.90
8	9	299	ASP	CA-CB-CG	-37.81	30.22	113.40

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	9	327	ASP	CA
10	B	2076	U	C3'

5 of 88 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	48	TYR	Sidechain
7	8	55	A	Sidechain
8	9	296	GLY	Peptide
8	9	299	ASP	Sidechain
8	9	319	LEU	Mainchain

5.2 Too-close contacts [i](#)

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	0	444	0	461	83	0
2	1	441	0	485	69	0
3	2	377	0	418	65	0
4	3	504	0	574	112	0
5	4	302	0	343	83	0
6	7	149	0	152	103	0
7	8	1590	0	808	81	0
8	9	3306	0	3402	1820	0
9	A	2507	0	1270	95	0
10	B	60995	0	30676	2402	0
11	C	2053	0	2122	416	0
12	D	1565	0	1616	315	0
13	E	1552	0	1619	269	0
14	F	1420	0	1460	172	0
15	G	1323	0	1374	158	0
16	H	1111	0	1148	143	0
17	I	1032	0	1088	218	0
18	J	1112	0	1147	231	0
19	K	930	0	1000	130	0
20	L	1053	0	1129	233	0
21	M	1074	0	1157	191	0
22	N	1008	0	1045	132	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	O	900	0	935	132	0
24	P	917	0	965	206	0
25	Q	947	0	1022	160	0
26	R	816	0	839	178	0
27	S	857	0	922	120	0
28	T	777	0	839	204	0
29	U	779	0	834	138	0
30	V	753	0	780	72	0
31	W	634	0	656	154	0
32	X	509	0	541	138	0
33	Y	449	0	491	64	0
34	Z	549	0	552	104	0
35	B	110	0	0	0	0
35	N	1	0	0	0	0
36	B	506	0	0	7	0
36	N	6	0	0	1	0
All	All	95358	0	63870	8128	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 51.

The worst 5 of 8128 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)
8:9:410:VAL:CG1	10:B:485:C:H5"	1.27	1.65
8:9:145:ILE:CD1	8:9:161:PRO:HG2	1.17	1.64
8:9:334:PHE:CE2	8:9:420:PHE:HE2	1.02	1.63
8:9:2:PHE:CZ	8:9:295:LEU:HD13	1.31	1.62
8:9:334:PHE:CZ	8:9:420:PHE:CE2	1.87	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	
1	0	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0	5
2	1	52/54 (96%)	21 (40%)	22 (42%)	9 (17%)	0	4
3	2	44/46 (96%)	24 (54%)	12 (27%)	8 (18%)	0	4
4	3	62/64 (97%)	35 (56%)	17 (27%)	10 (16%)	0	5
5	4	36/38 (95%)	13 (36%)	11 (31%)	12 (33%)	0	0
6	7	16/18 (89%)	14 (88%)	2 (12%)	0	100	100
8	9	403/430 (94%)	154 (38%)	100 (25%)	149 (37%)	0	0
11	C	265/267 (99%)	97 (37%)	93 (35%)	75 (28%)	0	0
12	D	207/209 (99%)	96 (46%)	67 (32%)	44 (21%)	0	3
13	E	199/201 (99%)	87 (44%)	63 (32%)	49 (25%)	0	2
14	F	176/178 (99%)	92 (52%)	52 (30%)	32 (18%)	0	4
15	G	174/176 (99%)	117 (67%)	39 (22%)	18 (10%)	1	12
16	H	147/149 (99%)	84 (57%)	44 (30%)	19 (13%)	0	7
17	I	139/141 (99%)	123 (88%)	11 (8%)	5 (4%)	4	38
18	J	138/140 (99%)	70 (51%)	36 (26%)	32 (23%)	0	2
19	K	119/121 (98%)	72 (60%)	25 (21%)	22 (18%)	0	3
20	L	142/144 (99%)	66 (46%)	37 (26%)	39 (28%)	0	0
21	M	134/136 (98%)	79 (59%)	31 (23%)	24 (18%)	0	4
22	N	125/127 (98%)	82 (66%)	32 (26%)	11 (9%)	1	17
23	O	115/117 (98%)	64 (56%)	33 (29%)	18 (16%)	0	5
24	P	112/114 (98%)	42 (38%)	38 (34%)	32 (29%)	0	0
25	Q	115/117 (98%)	79 (69%)	22 (19%)	14 (12%)	0	8
26	R	101/103 (98%)	43 (43%)	30 (30%)	28 (28%)	0	0
27	S	108/110 (98%)	67 (62%)	20 (18%)	21 (19%)	0	3
28	T	97/99 (98%)	42 (43%)	33 (34%)	22 (23%)	0	2
29	U	100/102 (98%)	46 (46%)	41 (41%)	13 (13%)	0	7
30	V	92/94 (98%)	59 (64%)	27 (29%)	6 (6%)	1	25
31	W	82/84 (98%)	31 (38%)	29 (35%)	22 (27%)	0	1
32	X	61/63 (97%)	38 (62%)	15 (25%)	8 (13%)	0	7
33	Y	56/58 (97%)	35 (62%)	18 (32%)	3 (5%)	2	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Z	68/70 (97%)	37 (54%)	22 (32%)	9 (13%)	0	7
All	All	3739/3826 (98%)	1939 (52%)	1037 (28%)	763 (20%)	0	3

5 of 763 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	31	LYS
1	0	35	GLU
1	0	45	ASP
2	1	12	SER
2	1	23	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	33 (70%)	14 (30%)	0	3
2	1	48/48 (100%)	33 (69%)	15 (31%)	0	2
3	2	38/38 (100%)	28 (74%)	10 (26%)	0	5
4	3	51/51 (100%)	40 (78%)	11 (22%)	1	9
5	4	34/34 (100%)	17 (50%)	17 (50%)	0	0
6	7	16/17 (94%)	16 (100%)	0	100	100
8	9	357/357 (100%)	329 (92%)	28 (8%)	16	51
11	C	213/213 (100%)	150 (70%)	63 (30%)	0	3
12	D	164/164 (100%)	113 (69%)	51 (31%)	0	2
13	E	165/165 (100%)	127 (77%)	38 (23%)	1	7
14	F	149/149 (100%)	122 (82%)	27 (18%)	2	15
15	G	137/137 (100%)	111 (81%)	26 (19%)	2	13
16	H	114/114 (100%)	90 (79%)	24 (21%)	1	9
17	I	109/109 (100%)	104 (95%)	5 (5%)	33	68
18	J	114/114 (100%)	85 (75%)	29 (25%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	K	102/102 (100%)	81 (79%)	21 (21%)	1	10
20	L	103/103 (100%)	68 (66%)	35 (34%)	0	2
21	M	109/109 (100%)	74 (68%)	35 (32%)	0	2
22	N	103/103 (100%)	76 (74%)	27 (26%)	0	5
23	O	87/87 (100%)	69 (79%)	18 (21%)	1	10
24	P	99/99 (100%)	67 (68%)	32 (32%)	0	2
25	Q	89/89 (100%)	71 (80%)	18 (20%)	1	11
26	R	84/84 (100%)	58 (69%)	26 (31%)	0	3
27	S	93/93 (100%)	77 (83%)	16 (17%)	2	17
28	T	83/83 (100%)	60 (72%)	23 (28%)	0	4
29	U	83/83 (100%)	60 (72%)	23 (28%)	0	4
30	V	78/78 (100%)	69 (88%)	9 (12%)	7	32
31	W	62/62 (100%)	45 (73%)	17 (27%)	0	4
32	X	55/55 (100%)	43 (78%)	12 (22%)	1	9
33	Y	48/48 (100%)	33 (69%)	15 (31%)	0	2
34	Z	62/62 (100%)	46 (74%)	16 (26%)	0	5
All	All	3096/3097 (100%)	2395 (77%)	701 (23%)	4	8

5 of 701 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	H	101	ASP
20	L	51	GLU
31	W	16	GLU
17	I	54	ILE
18	J	132	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
16	H	133	GLN
22	N	9	GLN
30	V	87	GLN
17	I	33	ASN
21	M	17	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2837/2904 (97%)	481 (16%)	22 (0%)
7	8	68/74 (91%)	2 (2%)	1 (1%)
9	A	116/117 (99%)	20 (17%)	1 (0%)
All	All	3021/3095 (97%)	503 (16%)	24 (0%)

5 of 503 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	8	39	A
7	8	85	A
9	A	13	G
9	A	15	A
9	A	16	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	982	C
10	B	1210	G
10	B	2425	A
10	B	1133	A
10	B	1205	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 111 ligands modelled in this entry, 111 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.