



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 05:12 PM UTC

PDB ID : 4V49 / pdb_00004v49
Title : Crystal Structure of a Streptomycin Dependent Ribosome from E. Coli 70S Ribosome.
Authors : Vila-Sanjurjo, A.; Ridgeway, W.K.; Seymaner, V.; Zhang, W.; Santoso, S.; Yu, K.; Cate, J.H.D.
Deposited on : 2003-06-13
Resolution : 8.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

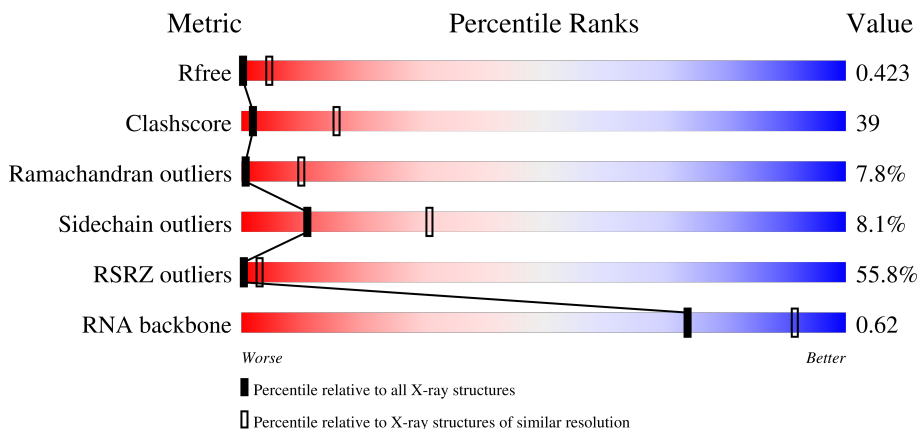
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 8.70 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
Sidechain outliers	187428	1018 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)
RNA backbone	3983	1057 (11.50-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1527	
2	AV	76	
2	AW	76	
3	AU	18	

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Mol	Chain	Length	Quality of chain
4	AB	234	28% 26% 56% 16% .
5	AC	206	51% 27% 52% 18% .
6	AD	208	50% 34% 56% 10%
7	AE	150	55% 31% 53% 14% .
8	AF	101	32% 37% 55% 8%
9	AG	155	40% 39% 53% 8%
10	AH	138	38% 38% 49% 12% .
11	AI	127	34% 26% 63% 10% .
12	AJ	98	51% 14% 59% 27%
13	AK	119	19% 19% 70% 10% .
14	AL	124	42% 32% 53% 15%
15	AM	125	42% 25% 66% 9% .
16	AN	60	57% 20% 60% 18% .
17	AO	88	40% 32% 56% 13%
18	AP	83	61% 31% 61% 6% .
19	AQ	104	44% 38% 52% 9% .
20	AR	73	34% 32% 56% 12%
21	AS	80	32% 21% 61% 18%
22	AT	99	53% 24% 55% 20% .
23	B0	2887	40% 40% 46% 10% ..
24	B9	118	43% 56% 41% .
25	BA	270	98%
26	BB	205	100%
27	BC	197	93% 100%
28	BD	178	99% 98%

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Mol	Chain	Length	Quality of chain
29	BE	177	81% 100%
30	BF	52	94% 100%
31	BG	143	45% 98%
32	BH	143	96% 100%
33	BI	132	97% 99%
34	BJ	141	78% 99%
35	BK	124	98% 100%
36	BL	114	97% 99%
37	BM	111	100% 100%
38	BN	125	91% 99%
39	BO	117	79% 100%
40	BP	100	79% 100%
41	BQ	130	100% 100%
42	BR	93	96% 100%
43	BS	113	99% 100%
44	BT	173	91% 100%
45	BU	86	100% 99%
46	BV	16	100%
47	BW	65	88% 100%
48	BX	55	95% 100%
49	BY	73	95% 100%
50	BZ	58	88% 100%
51	B1	53	96% 100%
52	B2	46	87% 100%
53	B3	63	59% 100%

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Mol	Chain	Length	Quality of chain
54	B4	35	 <p>97% 100%</p>
55	B5	217	 <p>85% 94% 6%</p>

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 122017 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	AA	1527	32819	14610	6085	10597	1527	0	0	0

- Molecule 2 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	AV	76	1625	725	293	531	76	0	0	0
2	AW	76	1625	725	293	531	76	0	0	0

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	AU	9	176	81	24	62	9	0	0	0

- Molecule 4 is a protein called 30S ribosomal protein S2.

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

- Molecule 5 is a protein called 30S ribosomal protein S3.

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

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	AD	208	1702	1066	339	290	7	0	0	0

- Molecule 7 is a protein called 30S ribosomal protein S5.

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

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	AF	101	842	531	155	153	3	0	0	0

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	AG	155	1256	781	252	217	6	0	0	0

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	AH	138	1115	705	215	192	3	0	0	0

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
11	AI	127	1010	639	198	173	0	0	0

- Molecule 12 is a protein called 30S ribosomal protein S10.

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

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AK	119	Total	C	N	O	S	0	0	0
			884	549	168	164	3			

- Molecule 14 is a protein called 30S ribosomal protein S12.

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

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AM	125	Total	C	N	O	S	0	0	0
			996	617	207	170	2			

- Molecule 16 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AN	60	Total	C	N	O	S	0	0	0
			491	312	104	71	4			

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AO	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			

- Molecule 18 is a protein called 30S ribosomal protein S16.

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

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AQ	104	Total	C	N	O	S	0	0	0
			856	547	161	146	2			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
20	AR	73	596	380	118	98	0	0	0

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
21	AS	80	647	414	119	112	2	0	0	0

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
22	AT	99	762	469	162	129	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
23	B0	2825	60636	27047	11191	19573	2825	0	0	0

- Molecule 24 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
24	B9	118	2519	1124	464	813	118	0	0	0

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
25	BA	270	Total C 270 270	0	0	270

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
26	BB	205	Total C 205 205	0	0	205

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
27	BC	197	Total C 197 197	0	0	197

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
28	BD	178	Total C 178 178	0	0	178

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
29	BE	177	Total C 177 177	0	0	177

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
30	BF	52	Total C 52 52	0	0	52

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
31	BG	143	Total C 143 143	0	0	143

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
32	BH	143	Total C 143 143	0	0	143

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
33	BI	132	Total C 132 132	0	0	132

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
34	BJ	141	Total C 141 141	0	0	141

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
35	BK	124	Total C 124 124	0	0	124

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
36	BL	114	Total C 114 114	0	0	114

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
37	BM	111	Total C 111 111	0	0	111

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
38	BN	125	Total C 125 125	0	0	125

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
39	BO	117	Total C 117 117	0	0	117

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
40	BP	100	Total C 100 100	0	0	100

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
41	BQ	130	Total C 130 130	0	0	130

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
42	BR	93	Total C 93 93	0	0	93

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
43	BS	113	Total C 113 113	0	0	113

- Molecule 44 is a protein called general stress protein Ctc.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
44	BT	173	Total C 173 173	0	0	173

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
45	BU	86	Total C 86 86	0	0	86

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
46	BV	16	Total C 16 16	0	0	16

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
47	BW	65	Total C 65 65	0	0	65

- Molecule 48 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
48	BX	55	Total C 55 55	0	0	55

- Molecule 49 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
49	BY	73	Total C 73 73	0	0	73

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
50	BZ	58	Total C 58 58	0	0	58

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
51	B1	53	Total C 53 53	0	0	53

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
52	B2	46	Total C 46 46	0	0	46

- Molecule 53 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
53	B3	63	Total C 63 63	0	0	63

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
54	B4	35	Total C 35 35	0	0	35

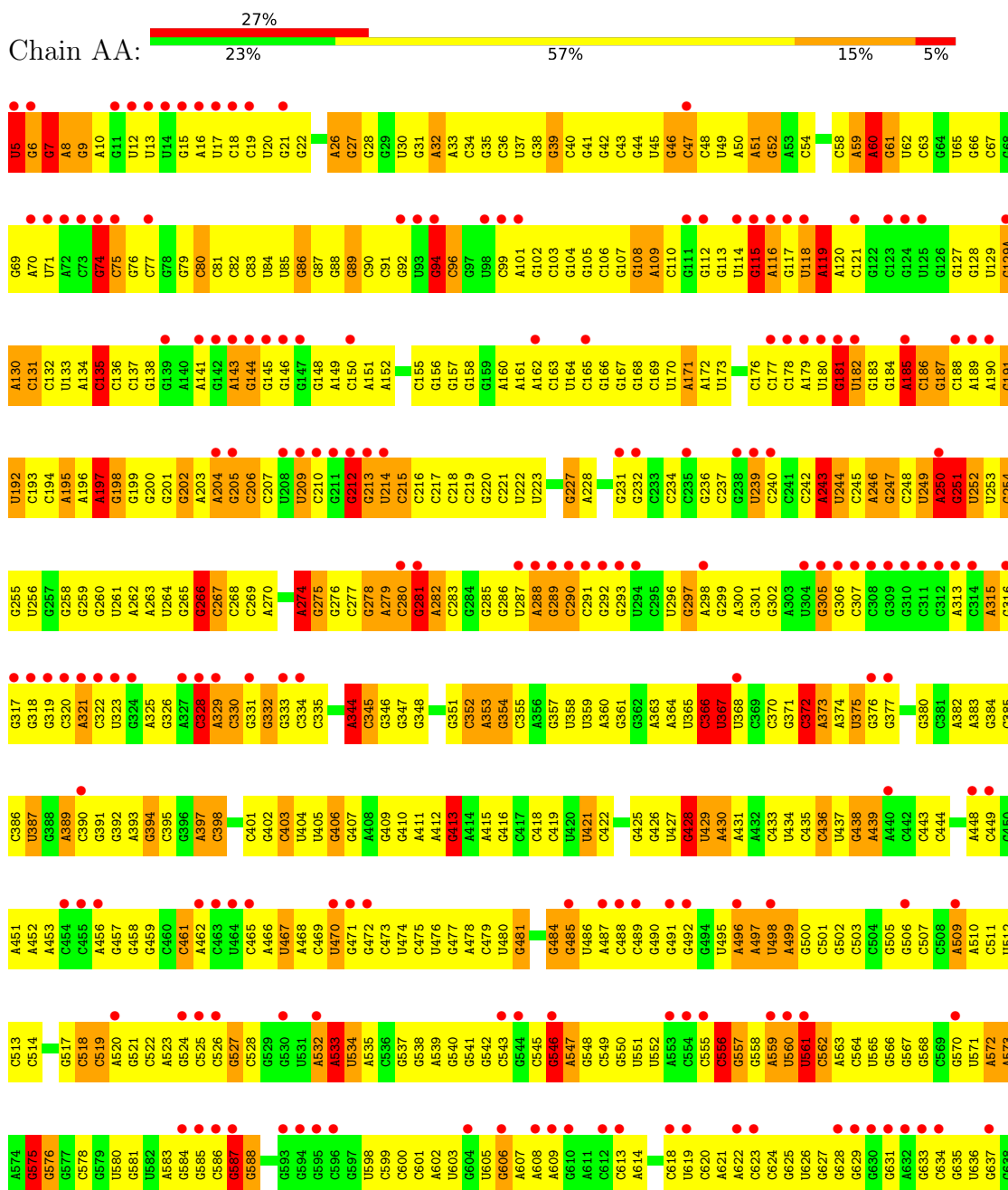
- Molecule 55 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
55	B5	217	Total 217	C 217	0	0	217

3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

● Molecule 1: 16S RIBOSOMAL RNA



G1529
G1530
A1531
U1532
C1533
A1534

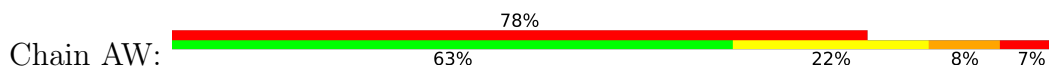
• Molecule 2: tRNA-Phe



G1 C2 G3 C11 U12 U16 U17 G18 G19 G20 A21 G22 A23 G24 C25 G26 C27 C28 A29 G30 G31 A32 C33 G34 A35 A36 G37 U39 C40 U41 G42 G43 A44 G45 G46 U50 G51 U52 U53 U54 U55 C56 C57 A58 A62 G63 A64 G65 U69 C70 G71 A73 C74

C75
A76

• Molecule 2: tRNA-Phe



G1 C2 G3 G4 A5 U6 U7 C11 U12 C13 G14 G15 U16 U17 G18 G19 G20 A21 G22 A23 G24 C25 G26 C27 C28 A29 G30 G31 A32 C33 U34 G35 A36 G37 U39 C40 U41 G42 G43 A44 G45 G46 U47 C48 C49 U50 G51 U52 G53 U54 U55 C56 C57 A58 A61 G62 C63

A64 G65 A66 A67 U68 U69 C70 G71 A73 A76

• Molecule 3: mRNA



A6 U7 G8 U9 U10 C11 A12 A13 A14 C G U A A U

• Molecule 4: 30S ribosomal protein S2



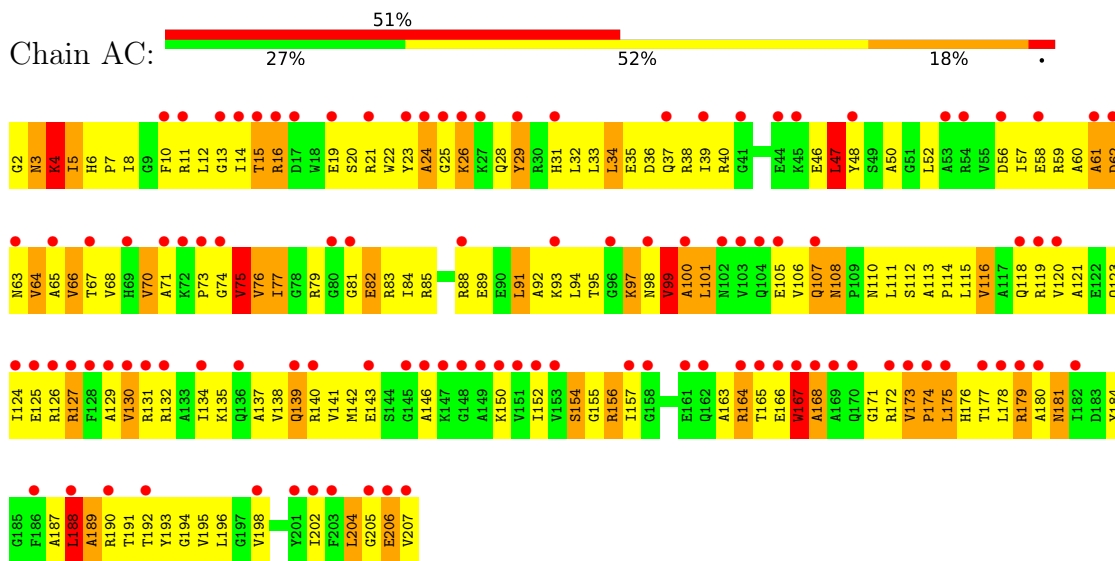
V7 K8 E9 L10 L11 L12 A13 G14 V15 H16 F17 G18 H19 E20 R21 K22 R23 W24 N25 P26 K27 F28 A29 R30 Y31 I32 Y33 A34 E35 R36 N37 G38 L39 H40 I41 D42 D43 L44 Q45 R46 T47 I48 E49 E50 L51 E52 R53 T54 F55 R56 F57 L58 E59 D60 L61 A62 R63 R64 G66

T67 I68 F70 V71 G72 T73 K74 K75 K76 H77 A78 G79 I80 V81 R82 M83 E84 A85 E86 R87 A88 G89 N90 P91 Y92 Y93 N94 Q95 R96 N97 L98 G99 G100 M101 L102 D103 L104 Q105 R106 T107 I108 S109 Q110 R111 R114 L115 T116 E117 L118 E119 A120 D121 F122 L123 S124 P125 I127

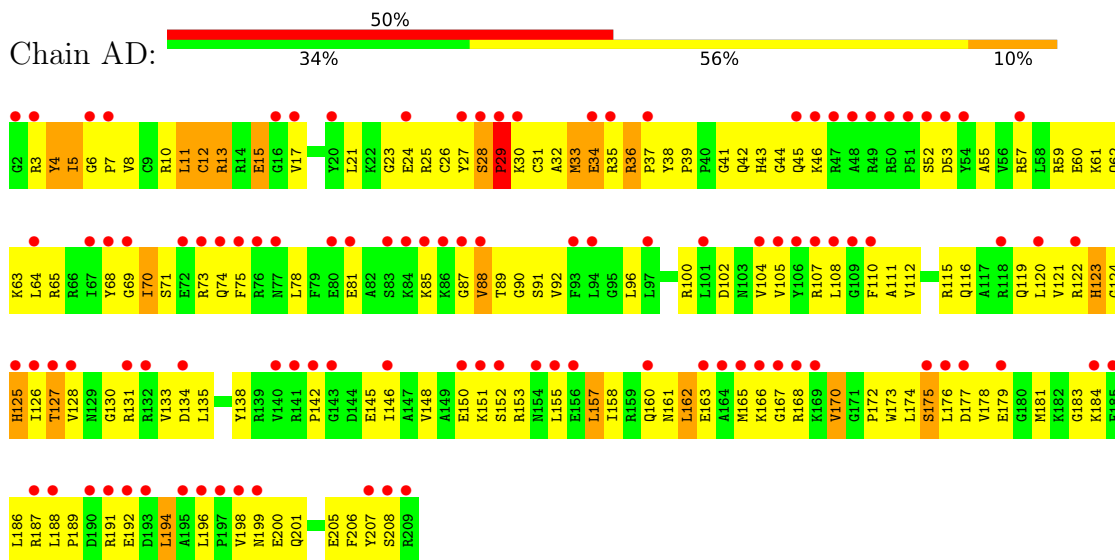
E128 E129 R130 P131 D132 K133 E134 Q135 I136 R137 L138 K139 H140 K141 E142 L143 R144 L145 Q146 K147 Y148 L149 S150 G151 F152 R153 L154 L155 K156 R157 D160 A161 I162 F163 V164 V165 D166 F167 T168 K169 E170 A173 E176 R177 K178 K179 L180 F181 L184 I185 I186 A187 L188 D189 T190 D191

S192 D193 P194 D195 V196 L197 V198 Y199 I200 P201 P202 G203 N204 D205 D206 L207 E208 R209 S210 L211 Q212 L213 I214 L215 S216 V219 D220 L221 I222 I223 Q224 A225 R226 G227 G228 V229 V230 E231 P232 S233 Y236 A237 L238 V239 Q240

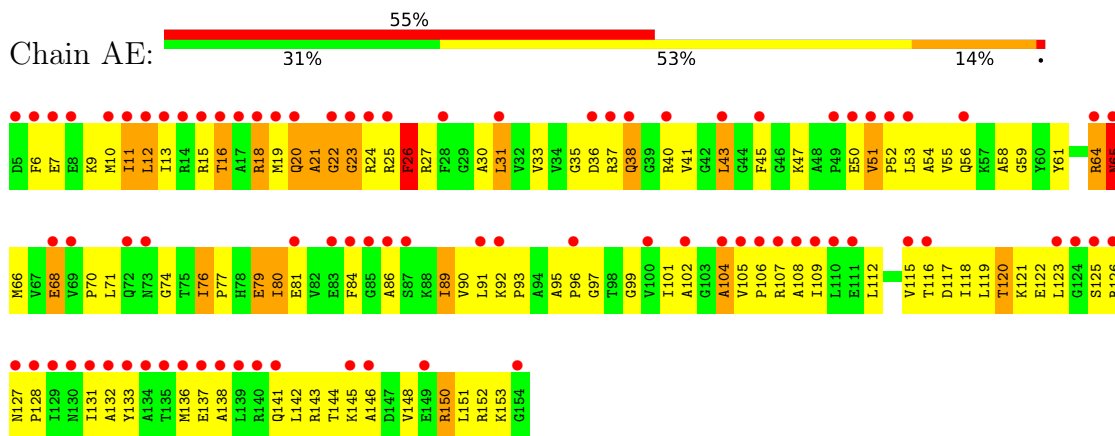
• Molecule 5: 30S ribosomal protein S3



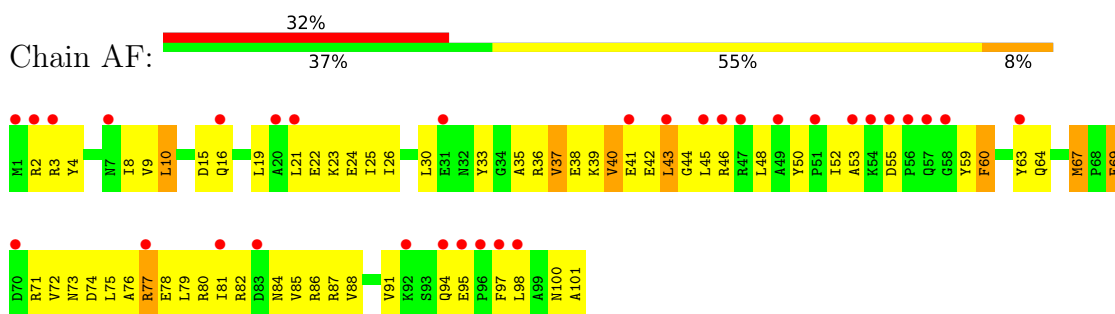
• Molecule 6: 30S ribosomal protein S4



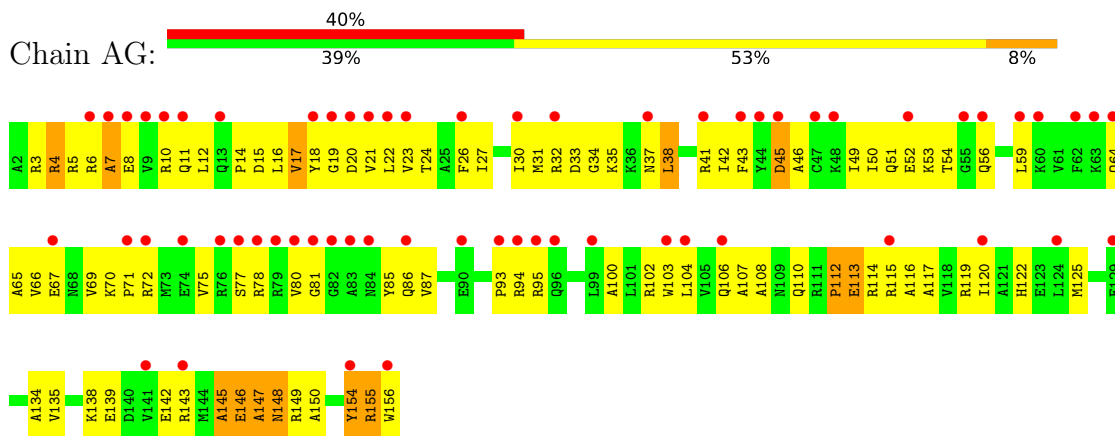
• Molecule 7: 30S ribosomal protein S5



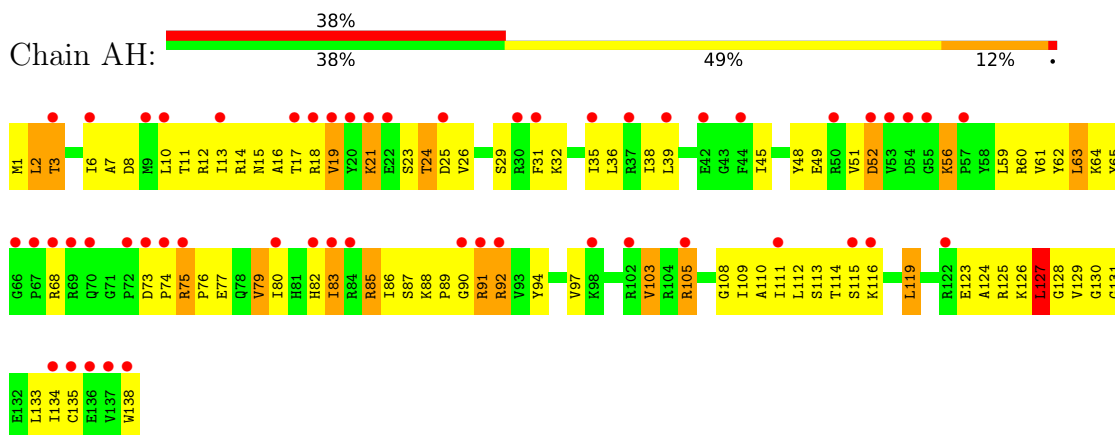
• Molecule 8: 30S ribosomal protein S6



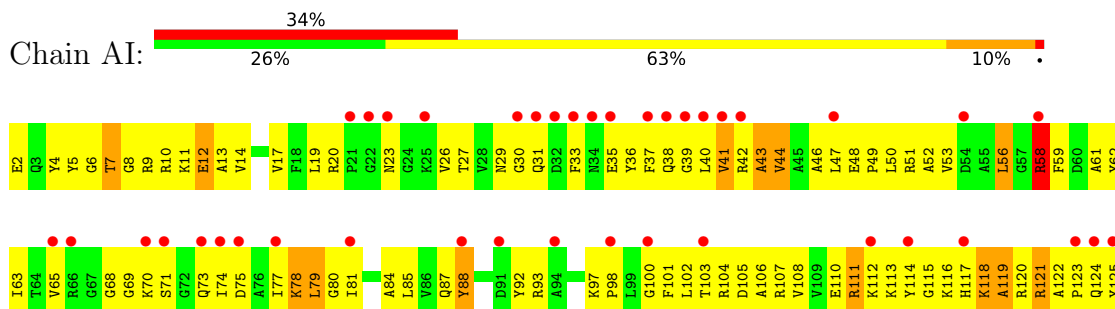
- Molecule 9: 30S ribosomal protein S7



- Molecule 10: 30S ribosomal protein S8

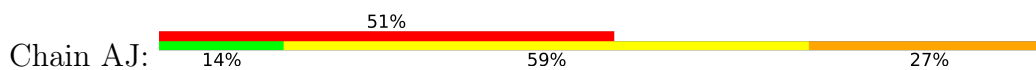


- Molecule 11: 30S ribosomal protein S9



S126
K127
R128

• Molecule 12: 30S ribosomal protein S10



K3 K4 R5 R6 L6 R7 R8 R9 G10 F11 D12 D13 H13 K14 T15 L16 L17 D17 D18 S19 A20 A21 Q21 Q22 K23 L23 V24 E25 E26 A27 A28 R29 S30 G31 G32 A33 G34 V35 S36 G37 P37 I38 P39 L40 P41 T42 R43 V44 R45 R46 F47 T48 V49 R50 R51 G52 P53 P54 K55 H56 H57 D58 S59 R60 R61 E61 H62

F63 E64 L65 R66 T67 R68 R69 R70 L71 V72 D73 H74 T75 N76 P77 N78 R79 R80 A81 Q82 T81 T82 E83 R84 L85 R86 R87 L88 D89 P91 T92 G93 V94 E95 E97 I98 R99 T100

• Molecule 13: 30S ribosomal protein S11



K11 R12 Q13 V14 A15 G17 R18 A19 Y20 Y21 I21 I22 H23 S24 Y25 Y26 N27 N28 T29 I32 T33 D34 R35 R36 G37 N38 P39 L100 Q101 Q102 Q103 Q104 V105 K106 G107 G108 I109 I110 D111 D112 T113 V114 P115 H116 N117 P118 C119 R120 A61 Q62 L63 A64 A65 L66 D67 A68 A69 K70 K71 A72 M73 A74

Y75 G76 M77 Q78 S79 R80 D81 V82 R83 R84 R85 G86 T87 G88 A89 G90 R91 S92 Q93 A94 R95 R96 A97 A98 Q99 A100 S101 G102 L103 Q104 V105 K106 G107 I108 I109 D110 D111 T112 P113 V114 P115 H116 N117 G118 C119 R120 P121 Q122 K123 K124 F125 R126 L127 A128 S129

• Molecule 14: 30S ribosomal protein S12



R5 T6 I7 N8 Q9 L10 V11 R12 K13 G14 R15 E16 K17 V18 V19 K20 K21 S22 K23 V24 P25 A26 L27 L28 K29 R30 R31 R32 R33 R34 G37 T38 V39 V40 R41 T42 T43 V44 P45 K46 K47 P48 M49 S50 A51 L52 L53 R54 K55 V56 V57 V58 R59 L60 T61 S62 G63 Y64 E65 V66 T67

A68 Y69 I70 P71 G72 E73 G74 H75 M76 L77 Q78 E79 H80 S81 V82 V83 V84 L84 I85 R86 G87 G88 R89 V90 R91 D92 L93 G94 G95 V96 R97 Y98 H99 I100 V101 G102 G103 V104 Y105 D106 V110 K111 D112 R113 K114 K115 S116 R117 S118 K119 Y120 G121 T122 K123 K124 P125 K126 E127 A128

• Molecule 15: 30S ribosomal protein S13

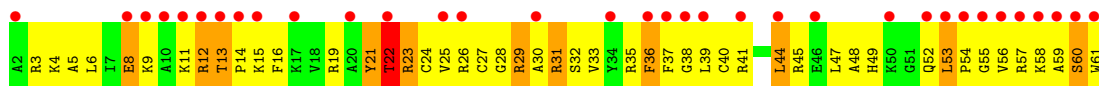


K2 R3 I4 A5 G6 V7 E8 I9 P10 R11 M12 K13 K14 A15 V16 D17 V18 A19 A20 T21 Y22 I23 G24 I25 A28 R29 K30 K31 E32 A33 L34 E35 K36 T37 K38 I39 M40 P41 A42 T43 R44 V45 K46 D47 L48 T49 E50 A51 E52 V53 V54 R55 L56 R57 E58 V59 E60 E61 E62

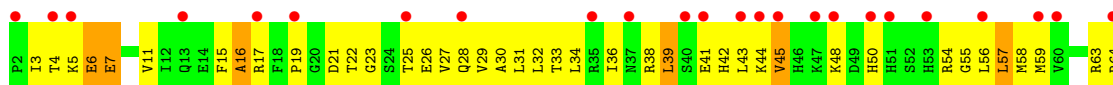
T63 W64 K65 L66 G67 G68 E69 L70 R71 A72 E73 V74 A75 A76 N77 I78 R79 R80 L81 M82 D83 I84 G85 G86 Y87 R88 R89 G90 G91 L92 P93 V94 R95 R96 R97 V98 R99 G100 Q101 R102 T103 R104 T105 M106 A107 R108 T109 R110 P113 R114 K115 T116 V117 A118 G119 K120 K121 K122 A123 P124 R125 E126 K127

• Molecule 16: 30S ribosomal protein S14

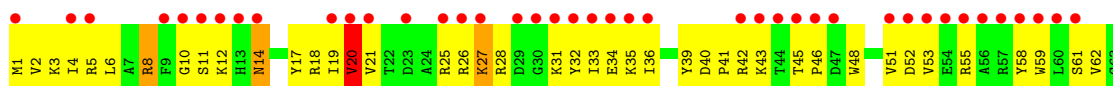




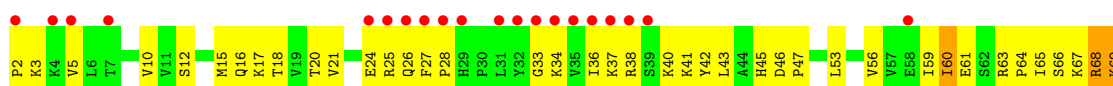
- Molecule 17: 30S ribosomal protein S15



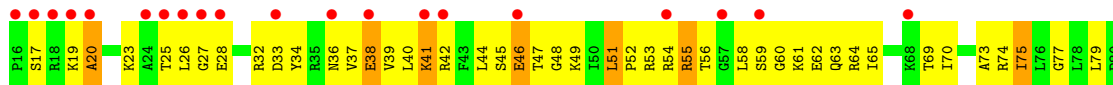
- Molecule 18: 30S ribosomal protein S16



- Molecule 19: 30S ribosomal protein S17

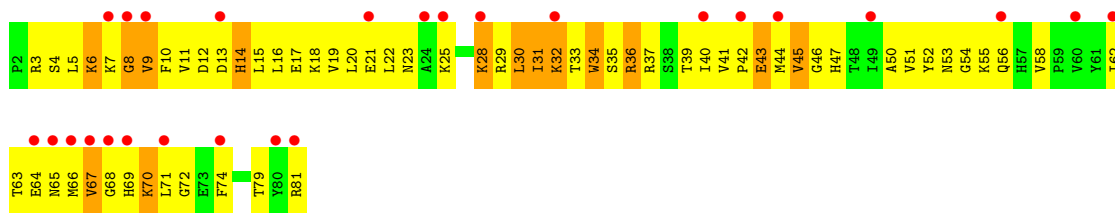


- Molecule 20: 30S ribosomal protein S18

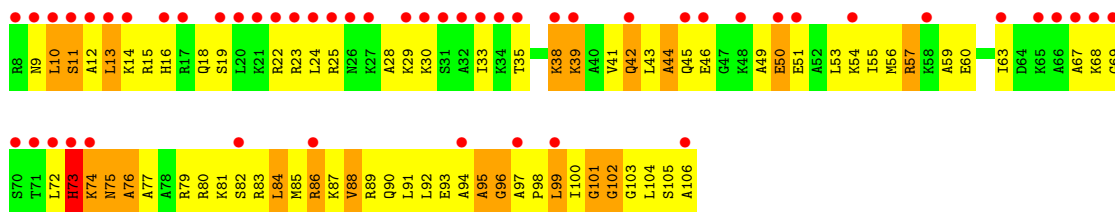


- Molecule 21: 30S ribosomal protein S19

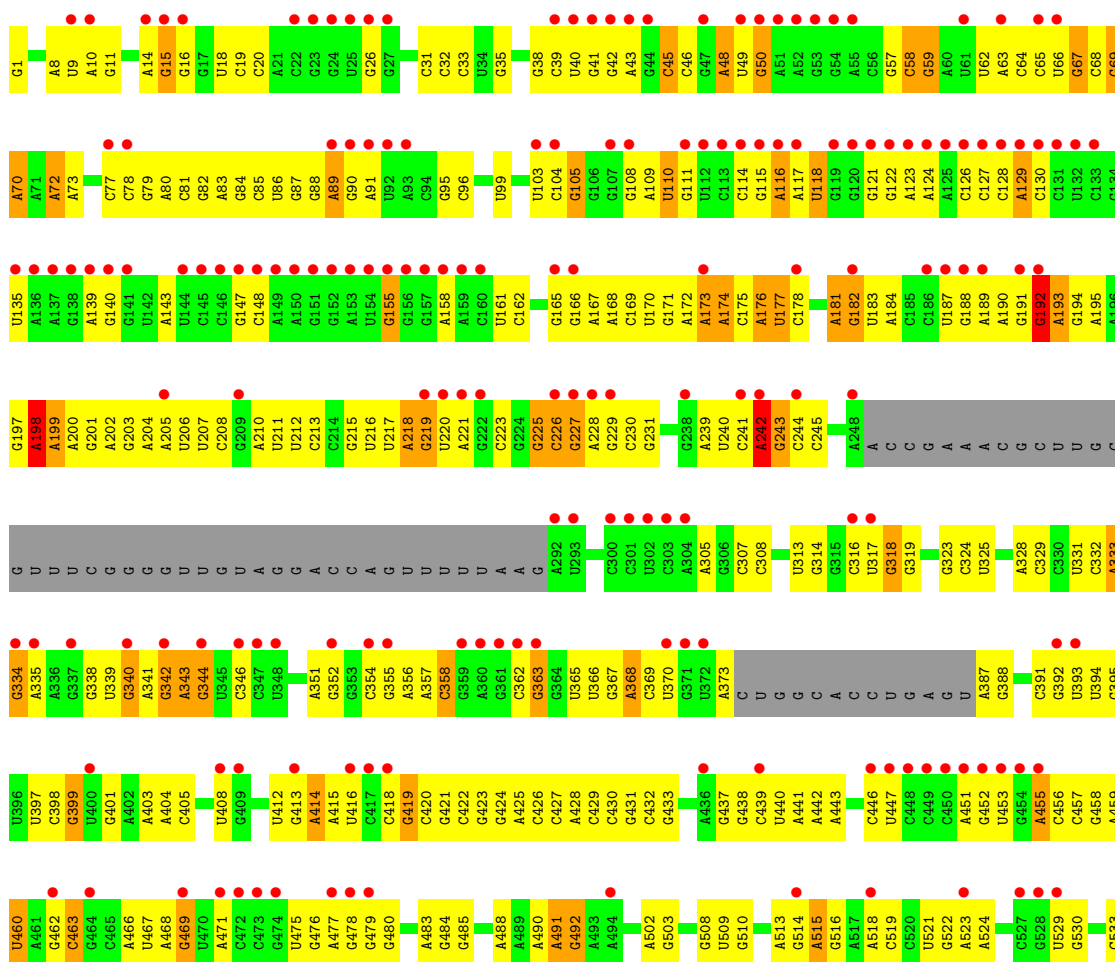




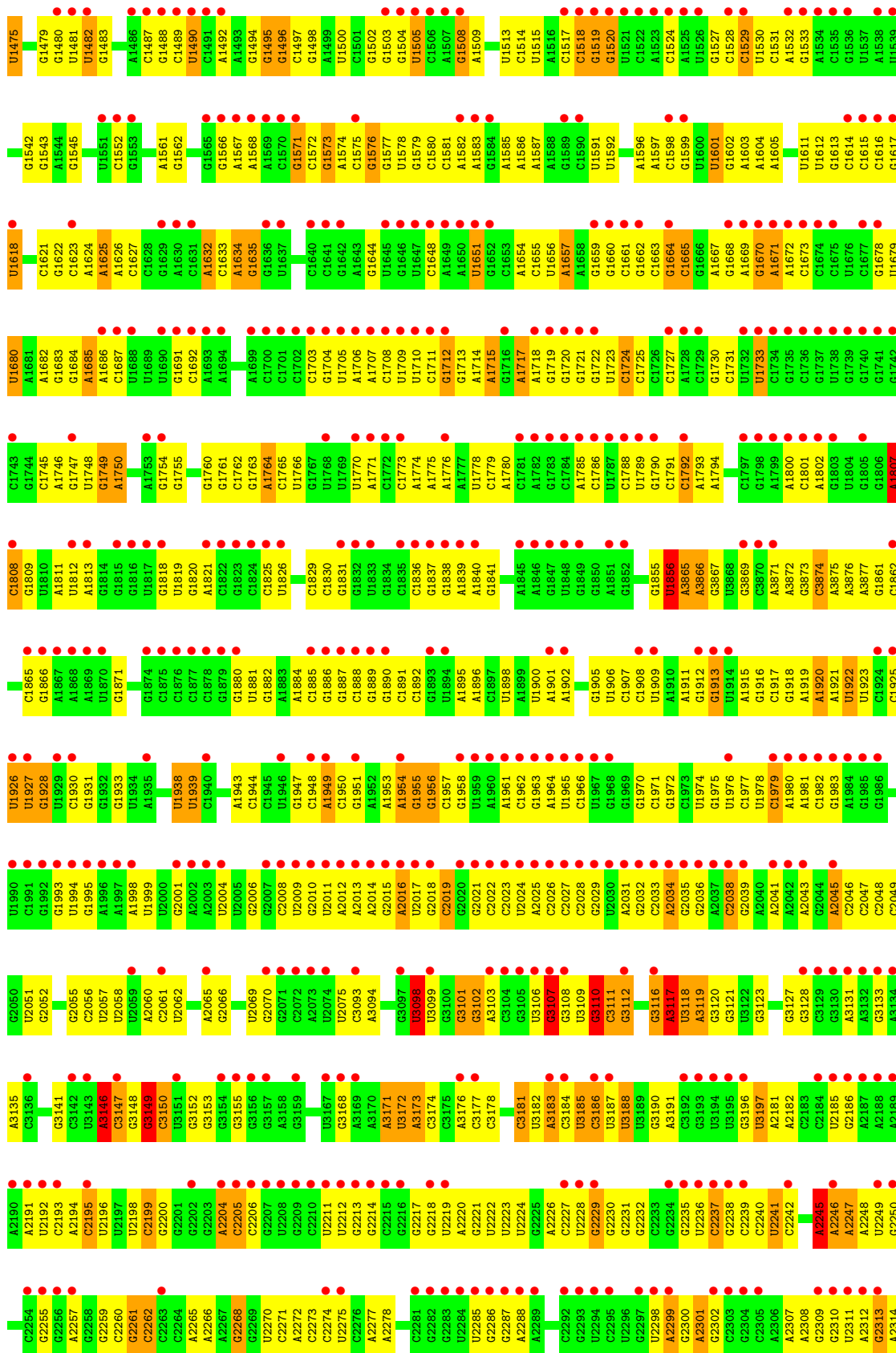
● Molecule 22: 30S ribosomal protein S20

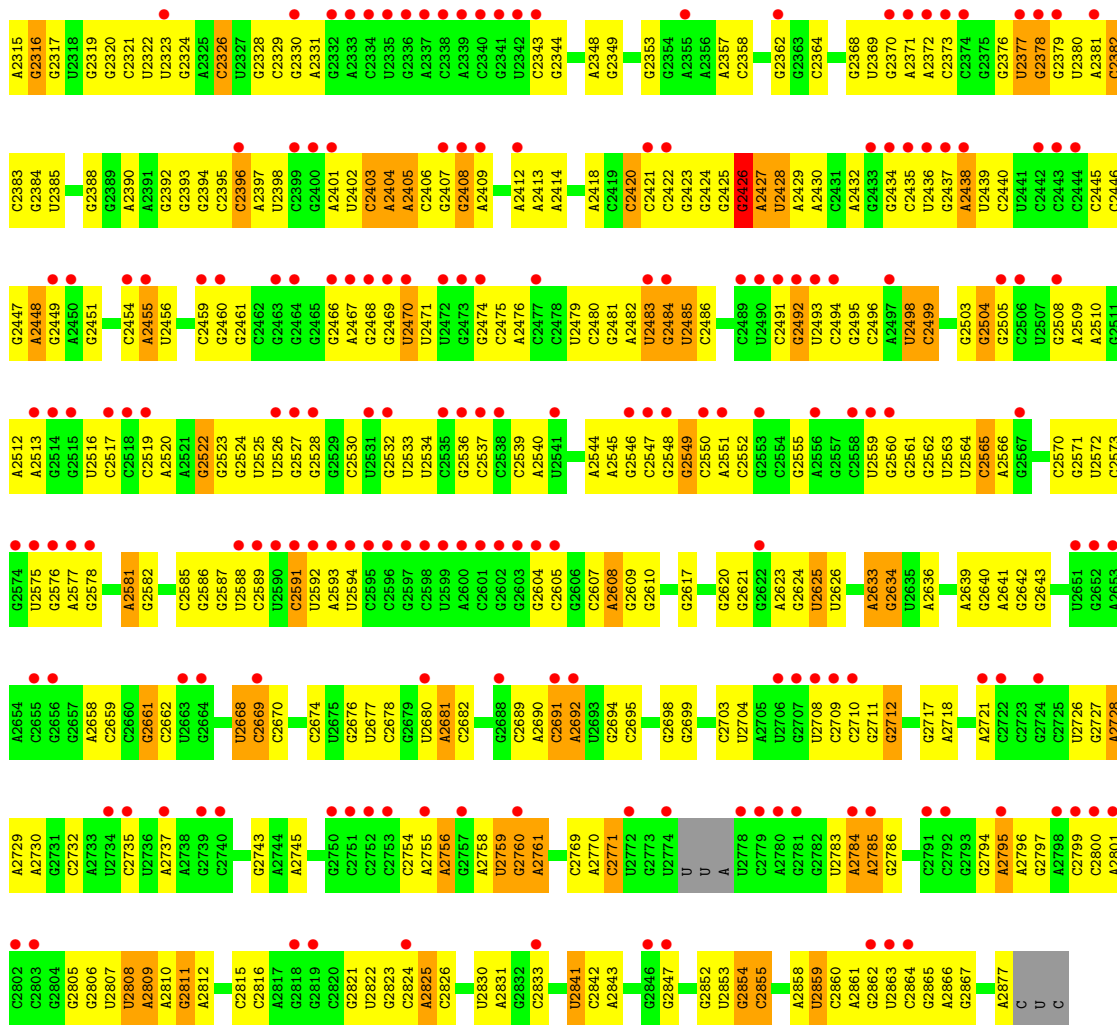


● Molecule 23: 23S RIBOSOMAL RNA

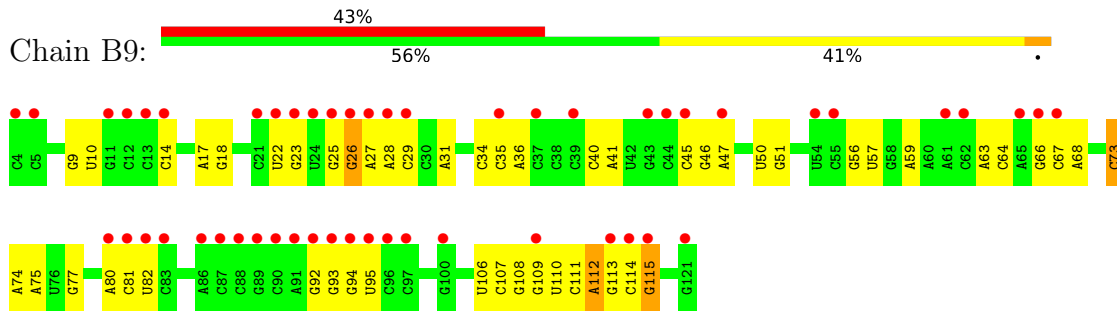


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C602	C603	U604	U605	C611	C612	A613	U616	U617	A618	A619	G620	U621	U622	U623	A624	U625	A626	A627	U628	G629	U630	G631	A632	A633	A634	A635	A636	A637	A638	A639	C640	C641	A642	A643	A644	C645	C646	A647	A648	C651	C652	G653	A654	A655	U656	A657	G658	U659	C659	U660	U661	C663	A665	U666	U667	A668	C602																																																
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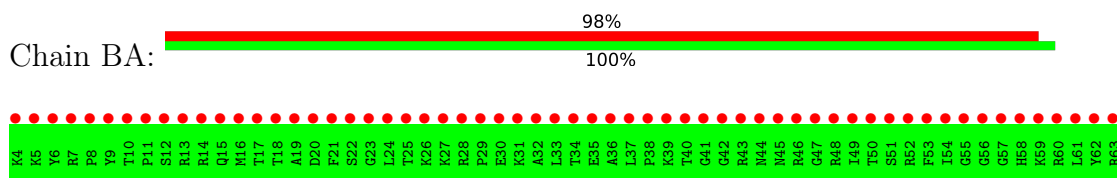


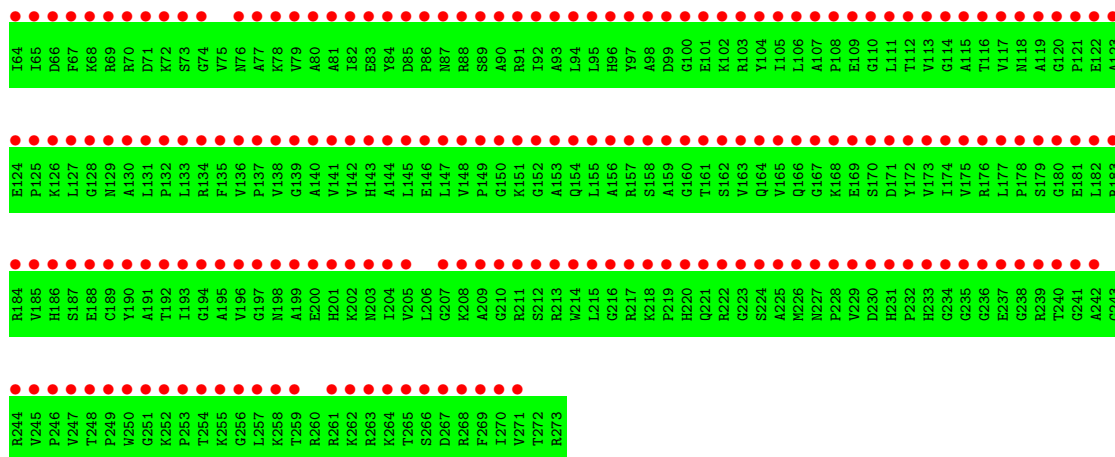


• Molecule 24: 5S RIBOSOMAL RNA

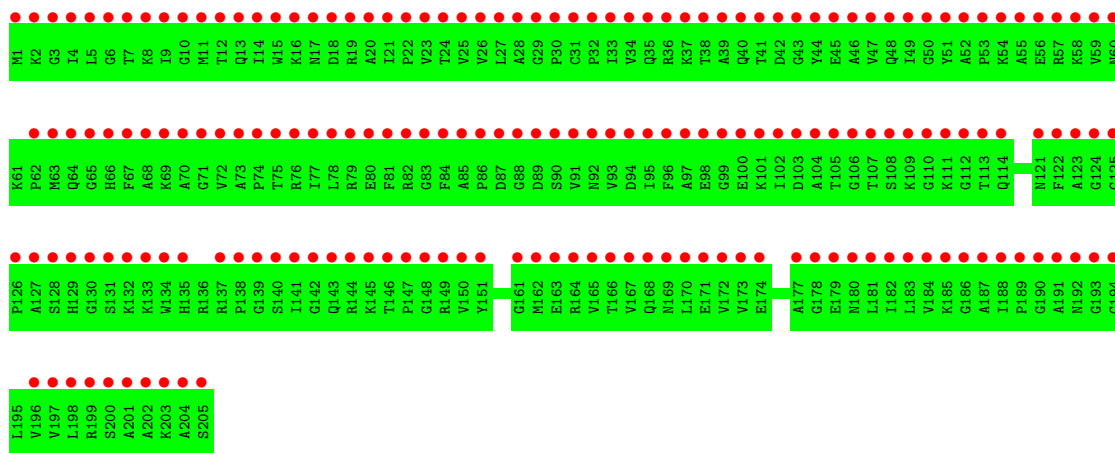


• Molecule 25: 50S ribosomal protein L2

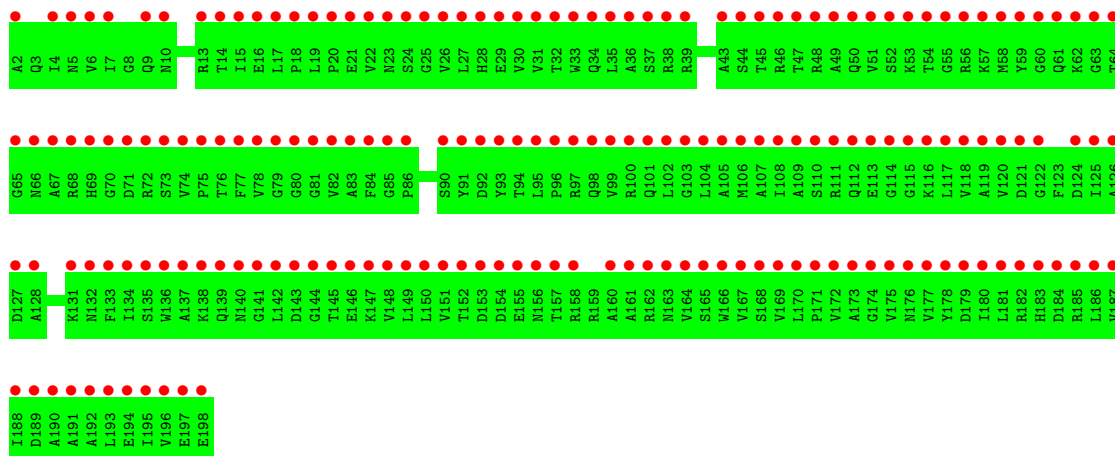




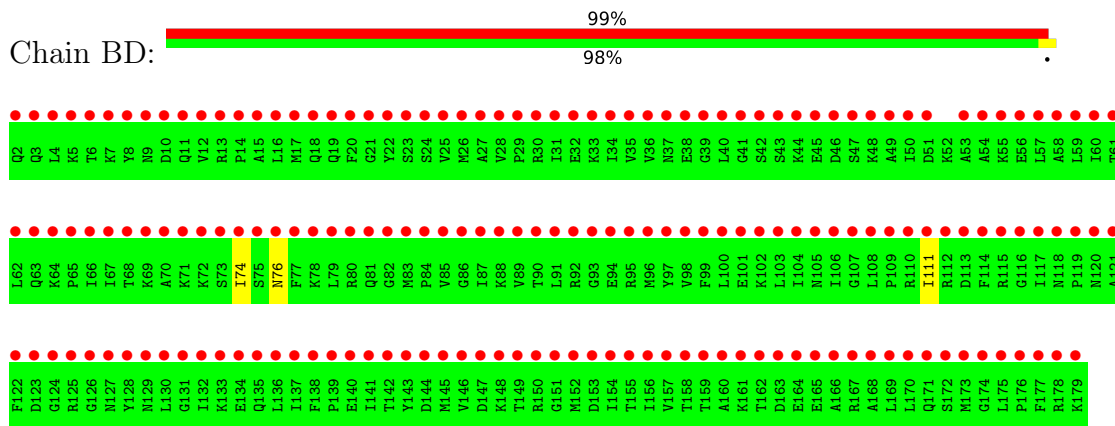
• Molecule 26: 50S ribosomal protein L3



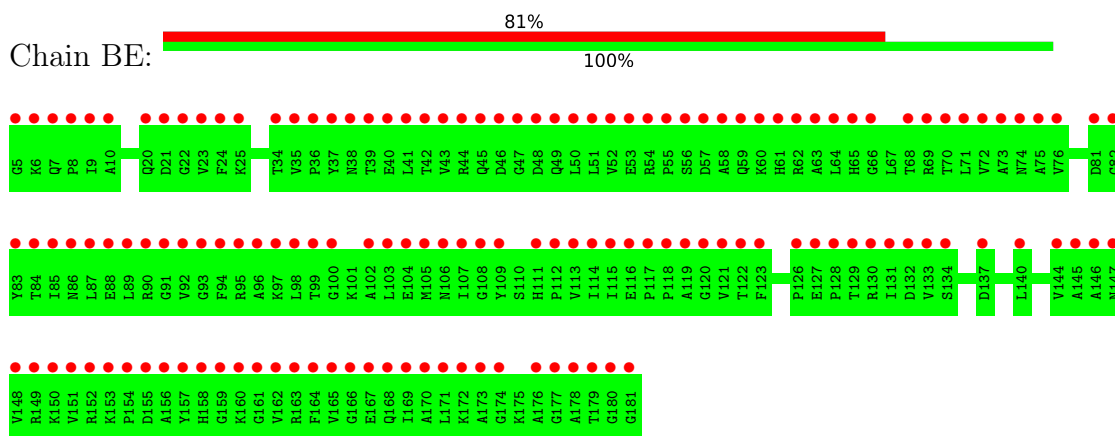
• Molecule 27: 50S ribosomal protein L4



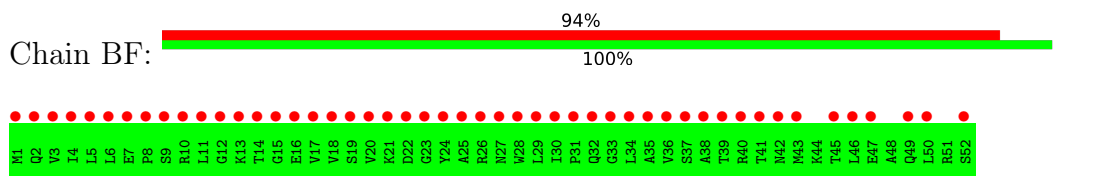
• Molecule 28: 50S ribosomal protein L5



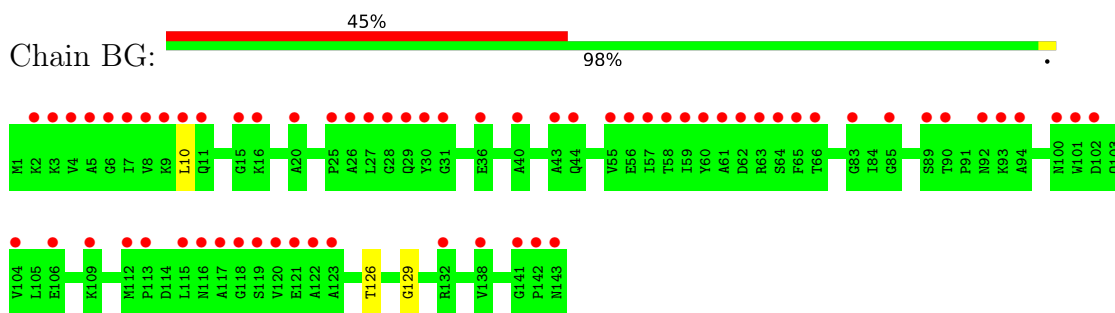
• Molecule 29: 50S ribosomal protein L6



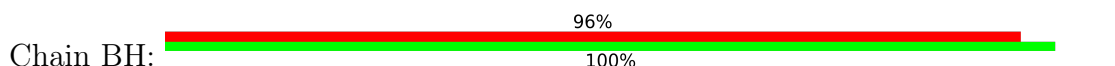
• Molecule 30: 50S ribosomal protein L9



• Molecule 31: 50S ribosomal protein L11



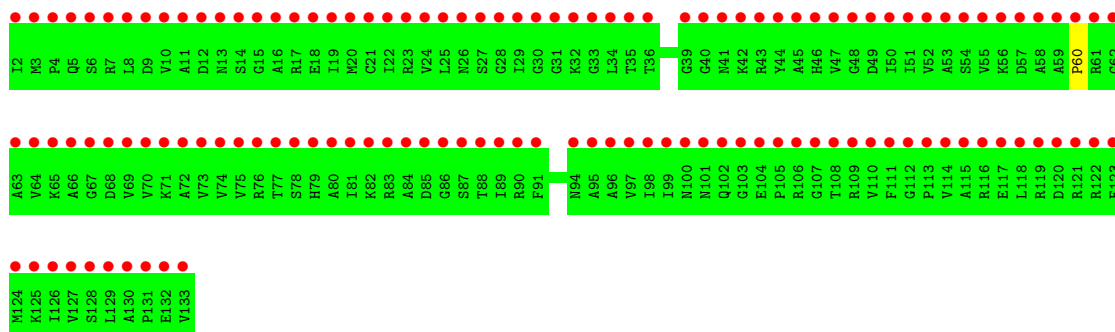
• Molecule 32: 50S ribosomal protein L13





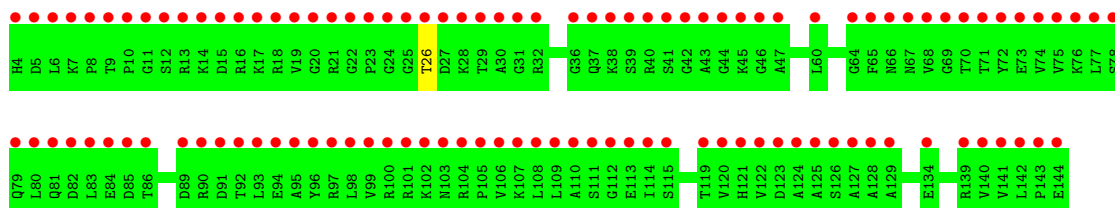
- Molecule 33: 50S ribosomal protein L14

Chain BI: 97%
99%



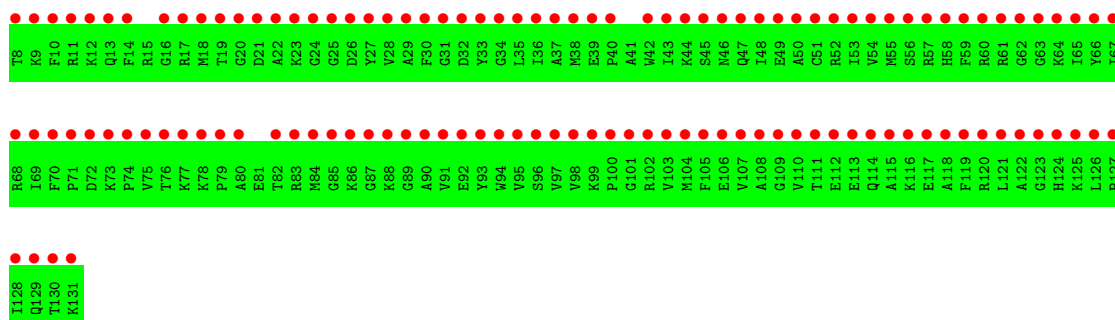
- Molecule 34: 50S ribosomal protein L15

Chain BJ: 78%
99%

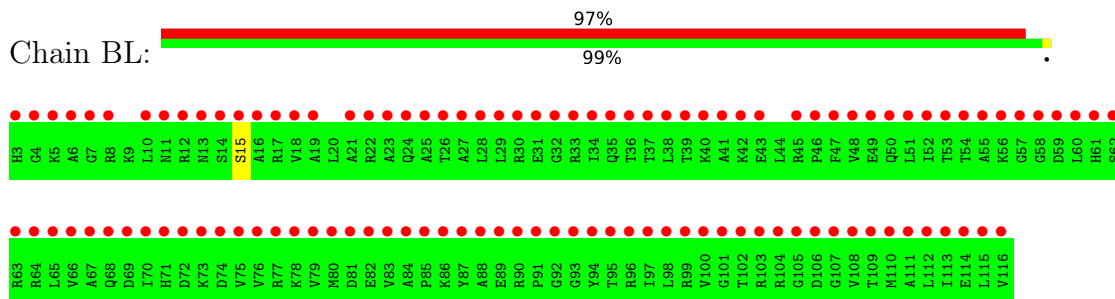


- Molecule 35: 50S ribosomal protein L16

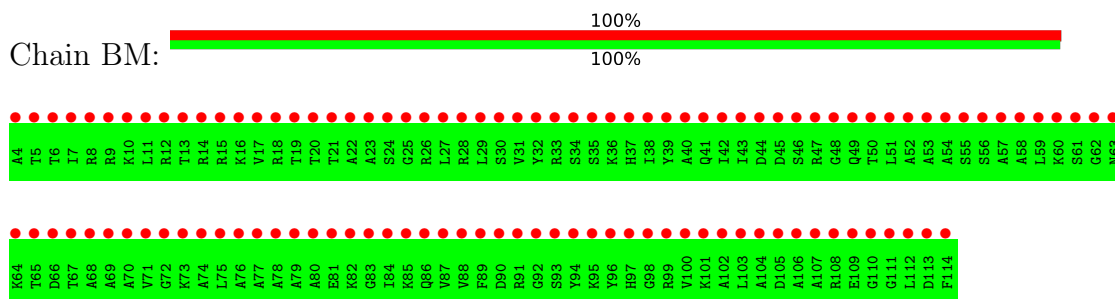
Chain BK: 98%
100%



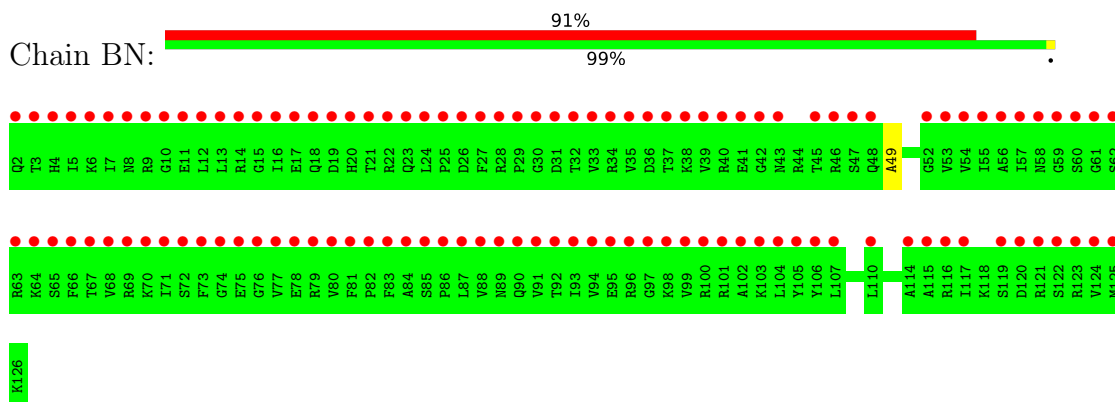
- Molecule 36: 50S ribosomal protein L17



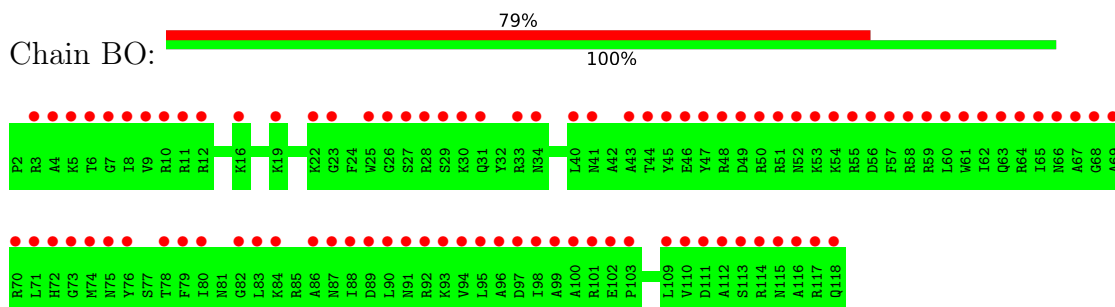
- Molecule 37: 50S ribosomal protein L18



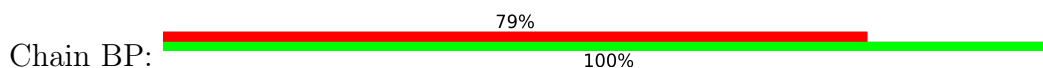
- Molecule 38: 50S ribosomal protein L19

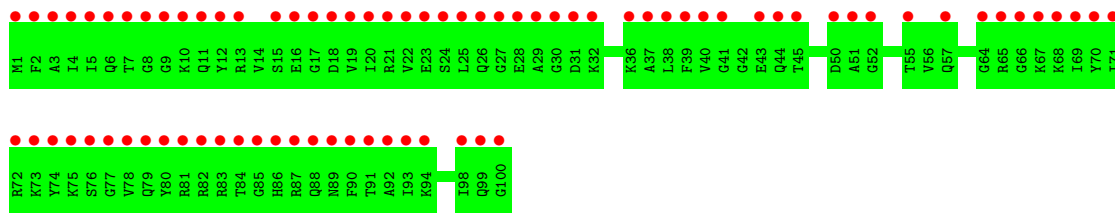


- Molecule 39: 50S ribosomal protein L20

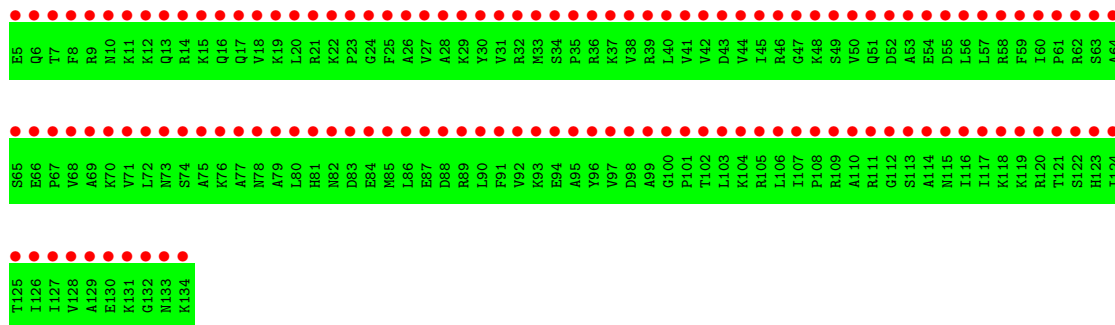


- Molecule 40: 50S ribosomal protein L21

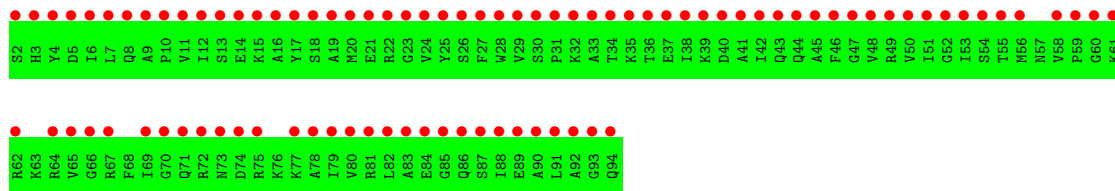




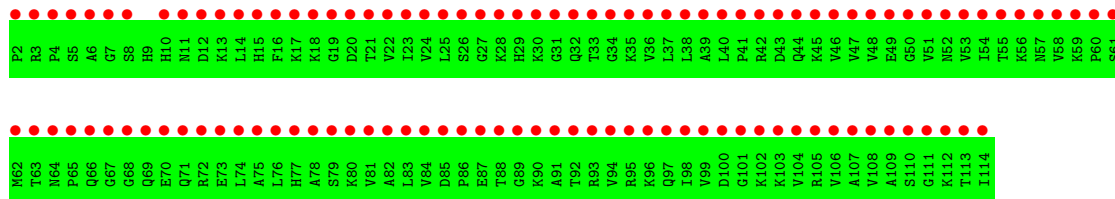
● Molecule 41: 50S ribosomal protein L22



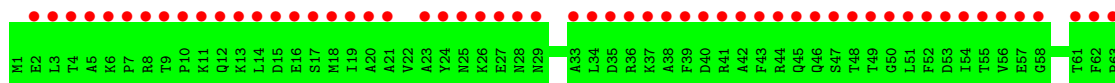
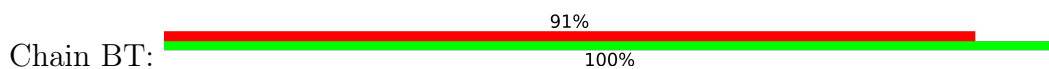
● Molecule 42: 50S ribosomal protein L23

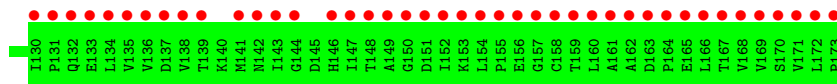
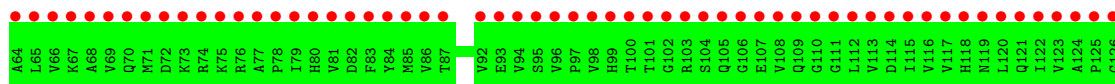


● Molecule 43: 50S ribosomal protein L24

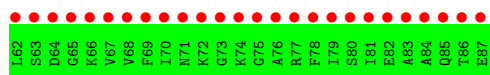
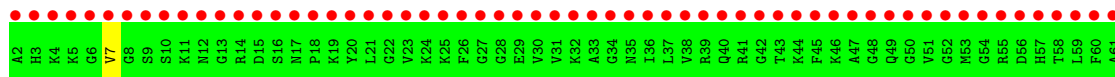


● Molecule 44: general stress protein Ctc





- Molecule 45: 50S ribosomal protein L27

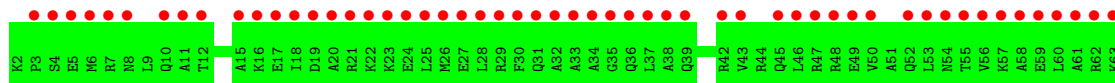


- Molecule 46: 50S RIBOSOMAL PROTEIN L28

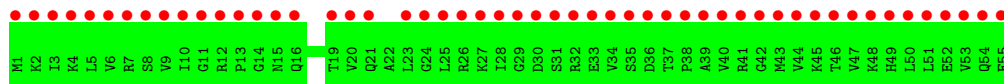


There are no outlier residues recorded for this chain.

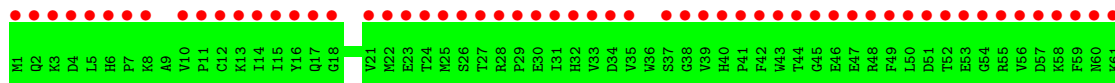
- Molecule 47: 50S ribosomal protein L29

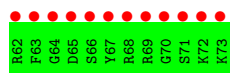


- Molecule 48: 50S ribosomal protein L30

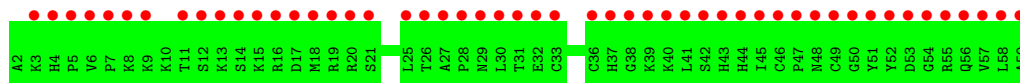
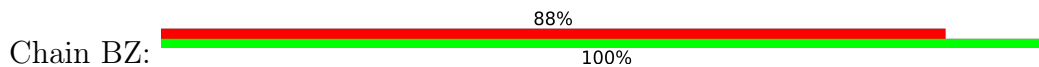


- Molecule 49: 50S ribosomal protein L31

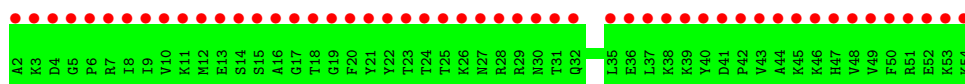




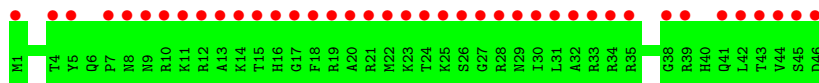
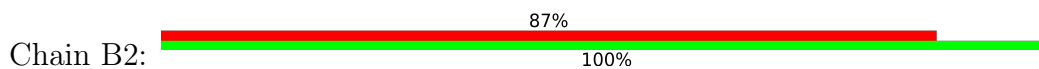
- Molecule 50: 50S ribosomal protein L32



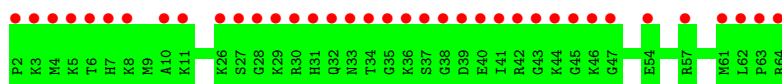
- Molecule 51: 50S ribosomal protein L33



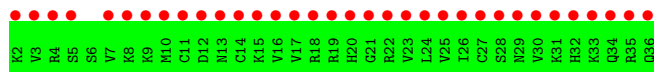
- Molecule 52: 50S ribosomal protein L34



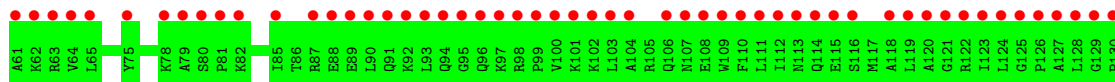
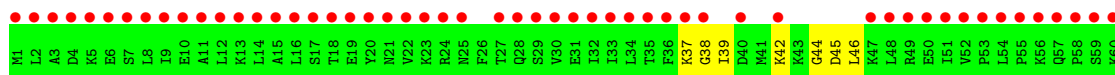
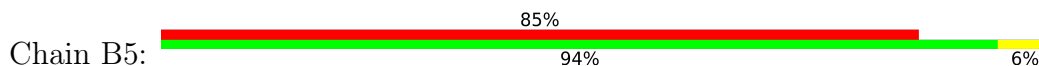
- Molecule 53: 50S ribosomal protein L35

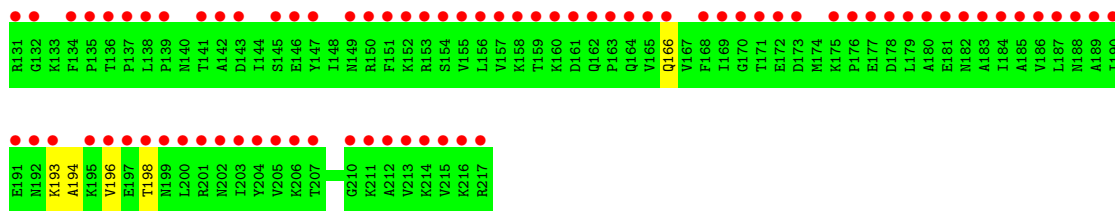


- Molecule 54: 50S ribosomal protein L36



- Molecule 55: 50S ribosomal protein L1P





4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	682.32Å 682.32Å 386.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 8.70 70.00 – 8.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (70.00-8.70) 91.6 (70.00-8.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 8.45Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.394 , 0.415 0.384 , 0.423	Depositor DCC
R_{free} test set	1966 reflections (5.23%)	wwPDB-VP
Wilson B-factor (Å ²)	443.4	Xtrriage
Anisotropy	0.381	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.00 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	122017	wwPDB-VP
Average B, all atoms (Å ²)	641.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	1.23	68/36688 (0.2%)	1.21	295/57135 (0.5%)
2	AV	1.56	14/1817 (0.8%)	1.56	31/2831 (1.1%)
2	AW	1.10	9/1816 (0.5%)	1.56	19/2827 (0.7%)
3	AU	18.66	15/188 (8.0%)	5.19	17/274 (6.2%)
4	AB	0.45	0/1935	1.07	13/2609 (0.5%)
5	AC	0.45	0/1636	1.01	9/2205 (0.4%)
6	AD	0.45	0/1732	0.96	7/2318 (0.3%)
7	AE	0.63	0/1162	1.19	10/1564 (0.6%)
8	AF	0.42	0/855	0.95	4/1154 (0.3%)
9	AG	0.42	0/1275	1.00	7/1709 (0.4%)
10	AH	0.58	0/1135	1.13	9/1527 (0.6%)
11	AI	0.42	0/1028	0.95	5/1378 (0.4%)
12	AJ	0.44	0/807	1.08	6/1085 (0.6%)
13	AK	0.52	0/899	1.07	4/1213 (0.3%)
14	AL	1.05	1/986 (0.1%)	1.12	5/1320 (0.4%)
15	AM	0.67	1/1007 (0.1%)	1.75	5/1347 (0.4%)
16	AN	0.44	0/500	1.21	7/664 (1.1%)
17	AO	0.47	0/744	0.95	3/992 (0.3%)
18	AP	0.52	0/716	1.17	8/963 (0.8%)
19	AQ	0.54	0/869	1.07	1/1159 (0.1%)
20	AR	0.43	0/602	0.96	4/799 (0.5%)
21	AS	0.43	0/661	1.09	5/890 (0.6%)
22	AT	0.51	0/764	1.12	7/1006 (0.7%)
23	B0	0.43	15/67885 (0.0%)	0.63	65/105852 (0.1%)
24	B9	0.57	1/2815 (0.0%)	0.67	3/4384 (0.1%)
All	All	1.06	124/130522 (0.1%)	0.95	549/199205 (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.

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Mol	Chain	#Chirality outliers	#Planarity outliers
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Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	2	40
2	AV	0	7
2	AW	0	7
23	B0	0	5
All	All	2	59

The worst 5 of 124 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AU	8	G	C6-O6	116.77	3.57	1.24
3	AU	14	A	C6-N6	111.89	3.57	1.33
3	AU	13	A	C6-N6	111.88	3.57	1.33
3	AU	6	A	C6-N6	111.82	3.57	1.33
3	AU	12	A	C6-N6	111.72	3.57	1.33

The worst 5 of 549 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	499	A	O3'-P-O5'	-40.97	42.55	104.00
1	AA	884	U	P-O3'-C3'	-38.67	62.19	120.20
1	AA	556	C	O3'-P-O5'	36.58	158.87	104.00
3	AU	8	G	C5-C6-O6	-35.55	21.96	128.60
1	AA	239	U	O3'-P-O5'	-35.13	51.30	104.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	181	G	C3'
1	AA	1528	U	C3'

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	12	U	Sidechain
1	AA	187	G	Sidechain
1	AA	191	G	Sidechain
1	AA	197	A	Sidechain
1	AA	231	G	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	32819	0	16577	3647	5
2	AV	1625	0	821	138	0
2	AW	1625	0	819	98	0
3	AU	176	0	79	11	0
4	AB	1900	0	1951	247	0
5	AC	1612	0	1676	308	0
6	AD	1702	0	1767	239	4
7	AE	1146	0	1207	240	0
8	AF	842	0	857	84	4
9	AG	1256	0	1294	124	0
10	AH	1115	0	1177	127	0
11	AI	1010	0	1043	176	0
12	AJ	794	0	838	220	0
13	AK	884	0	903	194	0
14	AL	970	0	1055	161	0
15	AM	996	0	1071	148	0
16	AN	491	0	531	165	0
17	AO	733	0	771	61	0
18	AP	700	0	720	101	0
19	AQ	856	0	926	363	0
20	AR	596	0	667	84	0
21	AS	647	0	673	131	0
22	AT	762	0	848	268	0
23	B0	60636	0	30552	1928	8
24	B9	2519	0	1287	43	0
25	BA	270	0	0	0	0
26	BB	205	0	0	0	0
27	BC	197	0	0	0	0
28	BD	178	0	0	12	0
29	BE	177	0	0	0	0
30	BF	52	0	0	0	0
31	BG	143	0	0	6	0
32	BH	143	0	0	0	0
33	BI	132	0	0	3	0
34	BJ	141	0	0	1	0
35	BK	124	0	0	0	0
36	BL	114	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	BM	111	0	0	0	0
38	BN	125	0	0	1	0
39	BO	117	0	0	0	0
40	BP	100	0	0	0	0
41	BQ	130	0	0	0	0
42	BR	93	0	0	0	0
43	BS	113	0	0	0	0
44	BT	173	0	0	0	0
45	BU	86	0	0	1	0
46	BV	16	0	0	0	0
47	BW	65	0	0	0	0
48	BX	55	0	0	0	0
49	BY	73	0	0	0	0
50	BZ	58	0	0	0	0
51	B1	53	0	0	0	0
52	B2	46	0	0	0	0
53	B3	63	0	0	0	0
54	B4	35	0	0	0	0
55	B5	217	0	0	35	0
All	All	122017	0	70110	7502	12

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 39.

The worst 5 of 7502 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:293:G:H4'	1:AA:609:A:C2	1.16	1.69
1:AA:675:A:H1'	13:AK:116:HIS:CD2	1.26	1.66
1:AA:21:G:C1'	1:AA:914:A:H62	1.08	1.65
6:AD:88:VAL:CA	7:AE:97:GLY:HA3	1.24	1.64
23:B0:3128:G:H4'	23:B0:3174:C:C4'	1.23	1.64

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AD:172:PRO:O	8:AF:15:ASP:CB[3_555]	1.18	1.02
1:AA:416:G:C4'	23:B0:3153:G:O2'[3_555]	1.79	0.41
1:AA:416:G:O2'	23:B0:3153:G:O2'[3_555]	1.87	0.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AD:172:PRO:O	8:AF:15:ASP:CA[3_555]	1.87	0.33
6:AD:186:LEU:CD1	8:AF:15:ASP:OD2[3_555]	1.91	0.29

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 X-ray entries followed by that with respect to entries of similar resolution.

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	
4	AB	232/234 (99%)	174 (75%)	34 (15%)	24 (10%)	0	6
5	AC	204/206 (99%)	135 (66%)	40 (20%)	29 (14%)	0	3
6	AD	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	2	17
7	AE	148/150 (99%)	130 (88%)	13 (9%)	5 (3%)	3	21
8	AF	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	12	49
9	AG	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	12
10	AH	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	3	23
11	AI	125/127 (98%)	89 (71%)	26 (21%)	10 (8%)	1	9
12	AJ	96/98 (98%)	59 (62%)	20 (21%)	17 (18%)	0	2
13	AK	117/119 (98%)	88 (75%)	20 (17%)	9 (8%)	1	10
14	AL	122/124 (98%)	98 (80%)	15 (12%)	9 (7%)	1	10
15	AM	123/125 (98%)	88 (72%)	27 (22%)	8 (6%)	1	12
16	AN	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	4
17	AO	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	1	14
18	AP	81/83 (98%)	65 (80%)	15 (18%)	1 (1%)	10	44
19	AQ	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	10
20	AR	71/73 (97%)	62 (87%)	7 (10%)	2 (3%)	4	24
21	AS	78/80 (98%)	48 (62%)	19 (24%)	11 (14%)	0	3
22	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2334/2372 (98%)	1792 (77%)	361 (16%)	181 (8%)	1 10

5 of 181 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	9	GLU
4	AB	15	VAL
4	AB	16	HIS
4	AB	17	PHE
4	AB	21	ARG

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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
4	AB	202/202 (100%)	184 (91%)	18 (9%)	9 28
5	AC	160/160 (100%)	141 (88%)	19 (12%)	5 18
6	AD	180/180 (100%)	169 (94%)	11 (6%)	17 38
7	AE	115/115 (100%)	98 (85%)	17 (15%)	3 13
8	AF	90/90 (100%)	86 (96%)	4 (4%)	25 47
9	AG	126/126 (100%)	120 (95%)	6 (5%)	23 44
10	AH	119/119 (100%)	106 (89%)	13 (11%)	6 21
11	AI	98/98 (100%)	90 (92%)	8 (8%)	10 31
12	AJ	88/88 (100%)	79 (90%)	9 (10%)	7 23
13	AK	90/90 (100%)	83 (92%)	7 (8%)	11 32
14	AL	104/104 (100%)	95 (91%)	9 (9%)	9 29
15	AM	100/100 (100%)	93 (93%)	7 (7%)	14 35
16	AN	49/49 (100%)	47 (96%)	2 (4%)	27 49
17	AO	79/79 (100%)	72 (91%)	7 (9%)	9 28
18	AP	72/72 (100%)	67 (93%)	5 (7%)	14 36
19	AQ	96/96 (100%)	90 (94%)	6 (6%)	16 37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	AR	64/64 (100%)	60 (94%)	4 (6%)	16	37
21	AS	71/71 (100%)	70 (99%)	1 (1%)	59	72
22	AT	76/76 (100%)	68 (90%)	8 (10%)	6	21
All	All	1979/1979 (100%)	1818 (92%)	161 (8%)	11	31

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	AL	53	ARG
19	AQ	38	ARG
14	AL	113	ARG
17	AO	6	GLU
20	AR	55	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
15	AM	62	ASN
17	AO	13	GLN
21	AS	14	HIS
7	AE	38	GLN
6	AD	199	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1514/1527 (99%)	234 (15%)	90 (5%)
2	AV	75/76 (98%)	13 (17%)	3 (4%)
2	AW	75/76 (98%)	13 (17%)	3 (4%)
23	B0	2812/2887 (97%)	436 (15%)	56 (1%)
24	B9	117/118 (99%)	10 (8%)	0
3	AU	8/18 (44%)	1 (12%)	0
All	All	4601/4702 (97%)	707 (15%)	152 (3%)

5 of 707 RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
1	AA	9	G
1	AA	27	G
1	AA	31	G

5 of 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	B0	1223	G
23	B0	2204	A
23	B0	1313	U
23	B0	1856	U
23	B0	2759	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
1	AA	108
23	B0	31
2	AW	4
2	AV	4

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Mol	Chain	Number of breaks
24	B9	2
3	AU	1
14	AL	1

The worst 5 of 151 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1443:G	O3'	1445:U	P	10.46
1	AA	1459:C	O3'	1460:A	P	10.16
1	AA	1458:G	O3'	1459:C	P	8.01
1	B0	1888:C	O3'	1889:G	P	6.63
1	B0	3180:U	O3'	3181:C	P	5.39

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1527/1527 (100%)	1.46	409 (26%) 1 8	341, 531, 705, 847	0
2	AV	76/76 (100%)	0.76	10 (13%) 7 15	379, 379, 379, 379	0
2	AW	76/76 (100%)	4.27	59 (77%) 0 1	255, 255, 255, 255	76 (100%)
3	AU	9/18 (50%)	2.50	4 (44%) 0 4	379, 379, 379, 379	0
4	AB	234/234 (100%)	1.33	66 (28%) 1 7	496, 496, 496, 496	0
5	AC	206/206 (100%)	2.71	105 (50%) 0 3	264, 264, 264, 264	0
6	AD	208/208 (100%)	2.76	104 (50%) 0 3	479, 479, 479, 479	0
7	AE	150/150 (100%)	3.19	83 (55%) 0 3	669, 669, 669, 669	0
8	AF	101/101 (100%)	1.48	32 (31%) 1 6	640, 640, 640, 640	0
9	AG	155/155 (100%)	1.89	62 (40%) 1 5	406, 406, 406, 406	0
10	AH	138/138 (100%)	2.18	53 (38%) 1 5	647, 647, 647, 647	0
11	AI	127/127 (100%)	1.61	43 (33%) 1 6	426, 426, 426, 426	0
12	AJ	98/98 (100%)	3.66	50 (51%) 0 3	507, 507, 507, 507	0
13	AK	119/119 (100%)	1.20	23 (19%) 3 11	510, 510, 510, 510	0
14	AL	124/124 (100%)	2.24	52 (41%) 0 4	367, 367, 384, 384	0
15	AM	125/125 (100%)	2.01	53 (42%) 0 4	349, 454, 454, 454	0
16	AN	60/60 (100%)	3.77	34 (56%) 0 3	264, 264, 264, 264	0
17	AO	88/88 (100%)	2.01	35 (39%) 1 5	572, 572, 572, 572	0
18	AP	83/83 (100%)	3.01	51 (61%) 0 2	662, 662, 662, 662	0
19	AQ	104/104 (100%)	2.25	46 (44%) 0 4	670, 670, 670, 670	0
20	AR	73/73 (100%)	1.85	25 (34%) 1 6	640, 640, 640, 640	0
21	AS	80/80 (100%)	1.88	26 (32%) 1 6	545, 545, 545, 545	0
22	AT	99/99 (100%)	2.77	52 (52%) 0 3	744, 744, 744, 744	0
23	B0	2825/2887 (97%)	2.18	1163 (41%) 0 4	517, 737, 737, 936	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
24	B9	118/118 (100%)	2.54	51 (43%) 0 4	772, 938, 938, 938	0
25	BA	270/270 (100%)	10.81	264 (97%) 0 1	737, 737, 737, 737	0
26	BB	205/205 (100%)	6.56	185 (90%) 0 1	737, 737, 737, 737	0
27	BC	197/197 (100%)	9.34	183 (92%) 0 1	737, 737, 737, 737	0
28	BD	178/178 (100%)	9.59	177 (99%) 0 1	938, 938, 938, 938	0
29	BE	177/177 (100%)	6.71	143 (80%) 0 1	737, 737, 737, 737	0
30	BF	52/52 (100%)	9.24	49 (94%) 0 1	737, 737, 737, 737	0
31	BG	143/143 (100%)	3.28	65 (45%) 0 4	907, 907, 907, 907	0
32	BH	143/143 (100%)	7.56	137 (95%) 0 1	737, 737, 737, 737	0
33	BI	132/132 (100%)	10.39	128 (96%) 0 1	737, 737, 737, 737	0
34	BJ	141/141 (100%)	7.21	110 (78%) 0 1	737, 737, 737, 737	0
35	BK	124/124 (100%)	8.23	121 (97%) 0 1	737, 737, 737, 737	0
36	BL	114/114 (100%)	8.64	111 (97%) 0 1	737, 737, 737, 737	0
37	BM	111/111 (100%)	11.31	111 (100%) 0 1	938, 938, 938, 938	0
38	BN	125/125 (100%)	5.96	114 (91%) 0 1	737, 737, 737, 737	0
39	BO	117/117 (100%)	4.65	93 (79%) 0 1	737, 737, 737, 737	0
40	BP	100/100 (100%)	4.55	79 (79%) 0 1	737, 737, 737, 737	0
41	BQ	130/130 (100%)	8.51	130 (100%) 0 1	737, 737, 737, 737	0
42	BR	93/93 (100%)	7.06	89 (95%) 0 1	737, 737, 737, 737	0
43	BS	113/113 (100%)	8.17	112 (99%) 0 1	737, 737, 737, 737	0
44	BT	173/173 (100%)	10.10	157 (90%) 0 1	737, 772, 772, 772	0
45	BU	86/86 (100%)	10.24	86 (100%) 0 1	737, 737, 737, 737	0
46	BV	0/16	-	-	-	-
47	BW	65/65 (100%)	6.27	57 (87%) 0 1	737, 737, 737, 737	0
48	BX	55/55 (100%)	6.59	52 (94%) 0 1	737, 737, 737, 737	0
49	BY	73/73 (100%)	7.31	69 (94%) 0 1	737, 737, 737, 737	0
50	BZ	58/58 (100%)	5.98	51 (87%) 0 1	737, 737, 737, 737	0
51	B1	53/53 (100%)	8.27	51 (96%) 0 1	737, 737, 737, 737	0
52	B2	46/46 (100%)	5.00	40 (86%) 0 1	737, 737, 737, 737	0
53	B3	63/63 (100%)	3.43	37 (58%) 0 3	737, 737, 737, 737	0
54	B4	35/35 (100%)	5.66	34 (97%) 0 1	737, 737, 737, 737	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
55	B5	213/217 (98%)	8.19	185 (86%) 0 1	940, 940, 940, 940	0
All	All	10588/10679 (99%)	4.03	5911 (55%) 0 3	255, 737, 938, 940	76 (0%)

The worst 5 of 5911 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	BT	149	ALA	52.7
44	BT	118	HIS	50.7
45	BU	85	GLN	48.7
37	BM	84	ILE	48.6
37	BM	113	ASP	46.7

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.