



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 14, 2023 – 03:21 AM EDT

PDB ID : 4V4A
Title : Crystal Structure of the Wild Type 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 : 9.50 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

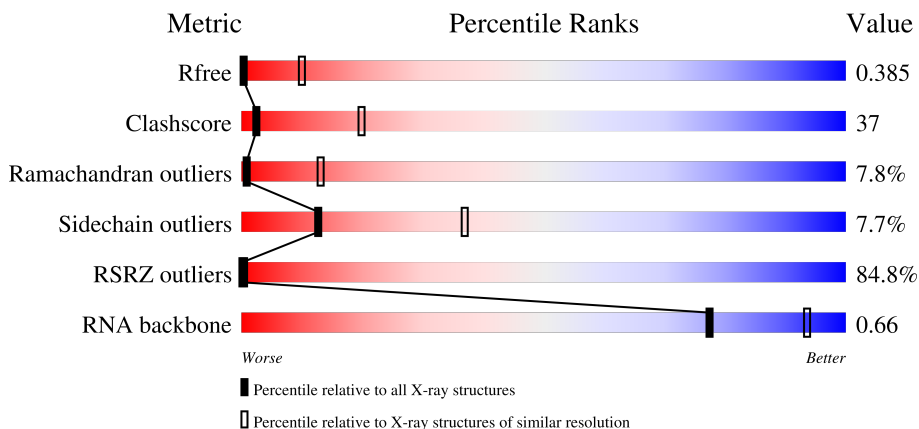
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.50 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}	130704	1005 (11.50-3.90)
Clashscore	141614	1071 (15.00-3.90)
Ramachandran outliers	138981	1003 (11.50-3.90)
Sidechain outliers	138945	1003 (11.50-3.86)
RSRZ outliers	127900	1004 (9.50-3.80)
RNA backbone	3102	1079 (11.50-3.00)

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	1537	Upper bar: 100% Lower bar: 23% (red), 58% (orange), 15% (yellow), 4% (green), 0% (grey)
2	AB	234	Upper bar: 31% Lower bar: 29% (red), 56% (orange), 13% (yellow), 2% (green), 0% (grey)
3	AC	206	Upper bar: 82% Lower bar: 30% (red), 51% (orange), 17% (yellow), 2% (green), 0% (grey)
4	AD	208	Upper bar: 97% Lower bar: 39% (red), 55% (orange), 5% (yellow), 1% (green), 0% (grey)

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Mol	Chain	Length	Quality of chain
5	AE	150	100% 35% 55% 9%
6	AF	101	22% 41% 57%
7	AG	155	68% 41% 55% 5%
8	AH	138	93% 40% 51% 8%
9	AI	127	61% 29% 61% 8%
10	AJ	98	80% 12% 67% 19%
11	AK	119	46% 29% 62% 8%
12	AL	124	100% 31% 57% 11%
13	AM	125	86% 22% 67% 10%
14	AN	60	98% 23% 62% 15%
15	AO	88	99% 38% 52% 10%
16	AP	83	100% 36% 61%
17	AQ	104	100% 43% 47% 9%
18	AR	73	53% 30% 63% 7%
19	AS	80	54% 16% 69% 15%
20	AT	99	100% 24% 61% 14%
21	B0	2887	98% 41% 46% 11%
22	B9	118	100% 56% 41%
23	BA	270	66% 100%
24	BB	205	70% 100%
25	BC	197	94% 100%
26	BD	178	78% 99%
27	BE	177	92% 100%
28	BF	52	23% 100%
29	BG	143	97% 99%

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Mol	Chain	Length	Quality of chain
30	BH	143	71% 100%
31	BI	132	42% 99%
32	BJ	141	82% 99%
33	BK	124	39% 100%
34	BL	114	89% 99%
35	BM	111	33% 100%
36	BN	125	42% 100%
37	BO	117	84% 100%
38	BP	100	83% 100%
39	BQ	130	84% 100%
40	BR	93	77% 100%
41	BS	113	99% 100%
42	BT	173	61% 100%
43	BU	86	69% 100%
44	BV	16	100%
45	BW	65	83% 100%
46	BX	55	82% 100%
47	BY	73	63% 100%
48	BZ	58	78% 100%
49	B1	53	49% 100%
50	B2	46	100%
51	B3	63	98% 100%
52	B4	35	74% 100%
53	B5	217	48% 96%

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 118711 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	1533	32939	14664	6099	10643	1533	0	0	0

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

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

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

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

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

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

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

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

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

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

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

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

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

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

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

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

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

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a RNA chain called 23S RIBOSOMAL RNA.

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

- Molecule 22 is a RNA chain called 5S RIBOSOMAL RNA.

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

- Molecule 23 is a protein called 50S ribosomal protein L2.

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

- Molecule 24 is a protein called 50S ribosomal protein L3.

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

- Molecule 25 is a protein called 50S ribosomal protein L4.

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

- Molecule 26 is a protein called 50S ribosomal protein L5.

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

- Molecule 27 is a protein called 50S ribosomal protein L6.

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

- Molecule 28 is a protein called 50S ribosomal protein L9.

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

- Molecule 29 is a protein called 50S ribosomal protein L11.

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

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

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

- Molecule 32 is a protein called 50S ribosomal protein L15.

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

- Molecule 33 is a protein called 50S ribosomal protein L16.

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

- Molecule 34 is a protein called 50S ribosomal protein L17.

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

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

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

- Molecule 41 is a protein called 50S ribosomal protein L24.

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

- Molecule 42 is a protein called general stress protein Ctc.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

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

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L35.

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

- Molecule 52 is a protein called 50S ribosomal protein L36.

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

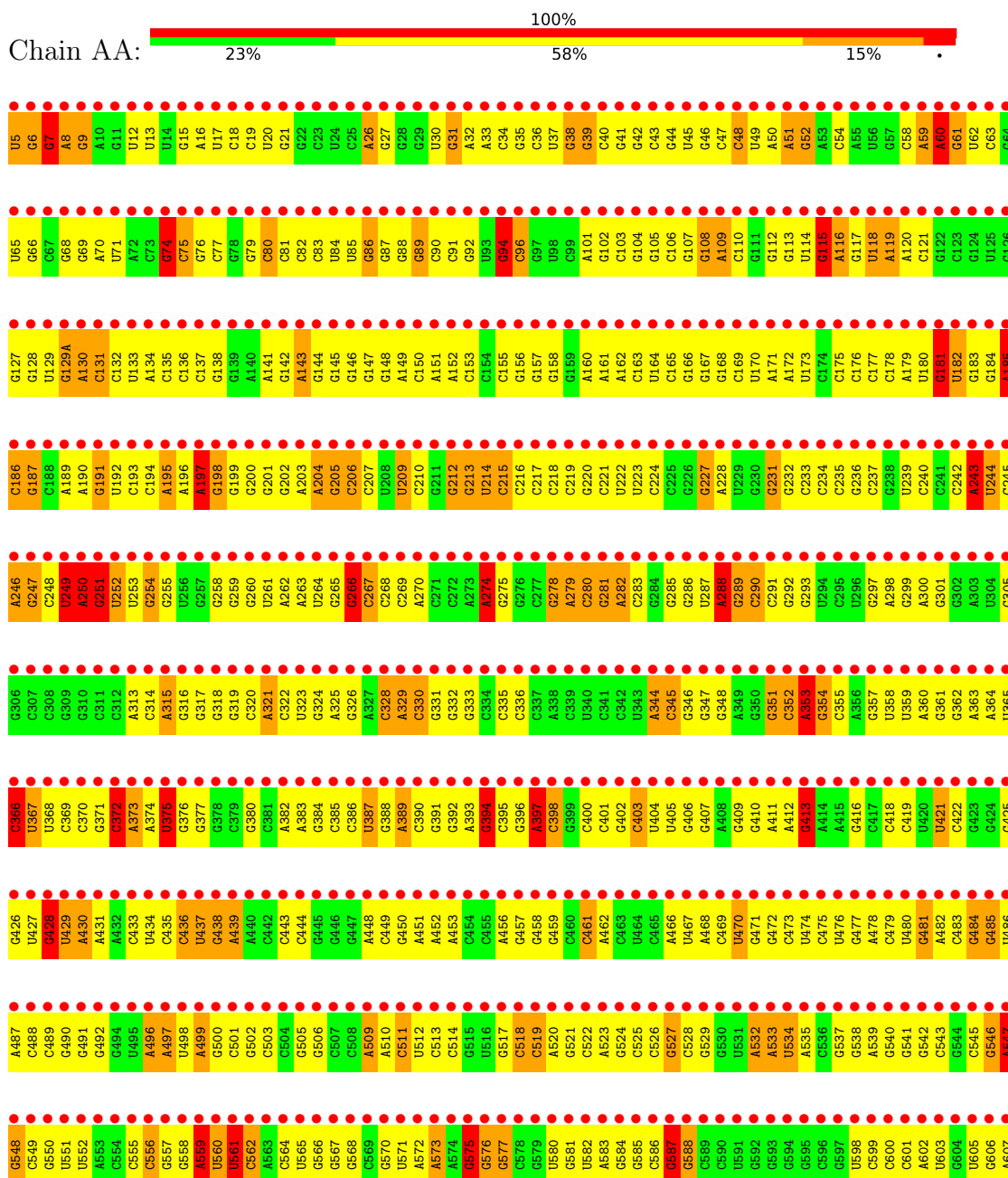
- Molecule 53 is a protein called 50S ribosomal protein L1P.

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

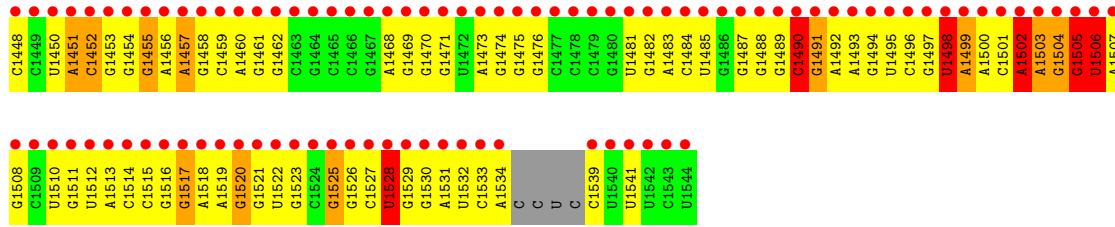
3 Residue-property plots [i](#)

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.

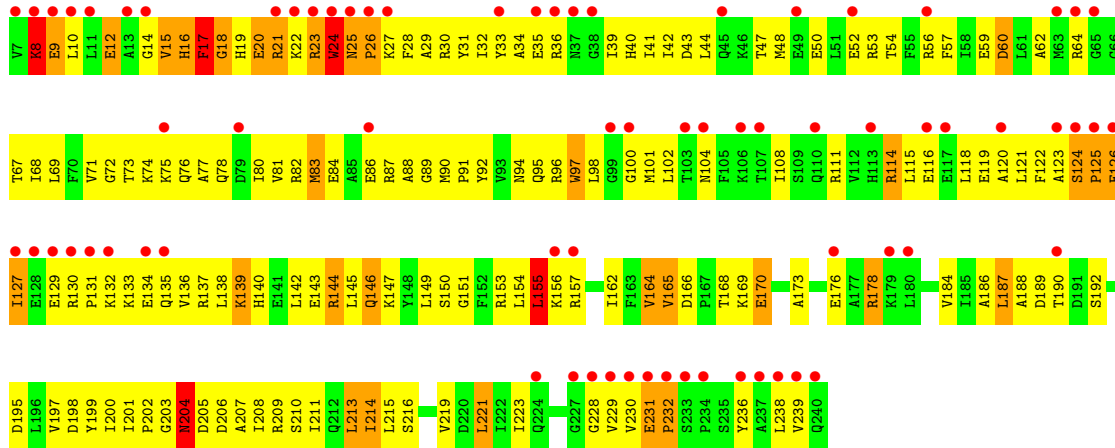
• Molecule 1: 16S RIBOSOMAL RNA



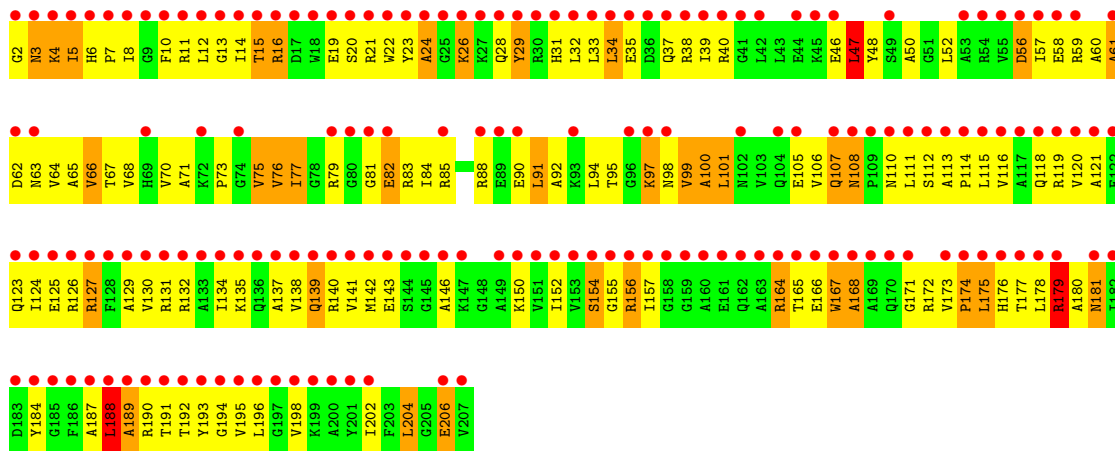
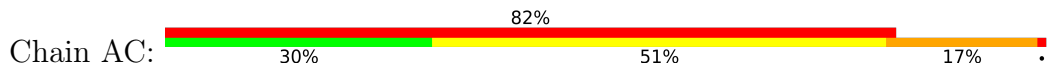
A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667		
U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	U689	U690	U691	U692	U693	U694	U695	U696	U697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727		
A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787		
U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847		
C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907		
A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967		
A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000	A1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	A1011	A1012	A1013	A1014	A1015	A1016	A1017	A1018	A1019	A1020	A1021	A1022	A1023	A1024	A1025	A1026			
C1027	C1028	U1029	U1030	C1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038	U1039	U1040	A1041	A1042	A1043	A1044	A1045	A1046	U1047	U1048	U1049	U1050	U1051	U1052	U1053	U1054	U1055	U1056	U1057	U1058	U1059	U1060	U1061	U1062	U1063	U1064	U1065	U1066	U1067	U1068	U1069	U1070	U1071	U1072	U1073	U1074	U1075	U1076	U1077	U1078	U1079	U1080	U1081	U1082	U1083	U1084	U1085	U1086	U1087	
G1087	G1088	G1089	U1090	U1091	U1092	U1093	U1094	U1095	U1096	U1097	U1098	U1099	U1100	A1101	A1102	A1103	A1104	A1105	A1106	A1107	A1108	A1109	A1110	A1111	A1112	A1113	A1114	A1115	A1116	A1117	A1118	A1119	A1120	A1121	A1122	A1123	A1124	A1125	A1126	A1127	A1128	A1129	A1130	A1131	A1132	A1133	A1134	U1135	U1136	U1137	U1138	U1139	A1140	A1141	A1142	A1143	A1144	A1145	A1146		
C1147	U1148	C1149	U1150	A1151	A1152	C1153	C1154	C1155	C1156	A1157	C1158	U1159	A1160	A1161	C1162	C1163	A1164	C1165	C1166	A1167	A1168	A1169	A1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	A1179	A1180	C1181	C1182	A1183	C1184	C1185	C1186	C1187	A1188	C1189	C1190	A1191	A1192	C1193	U1194	C1195	U1196	C1197	C1198	U1199	C1200	A1201	C1202	C1203	C1204	A1205	C1206	C1207	
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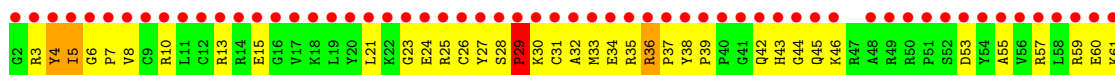
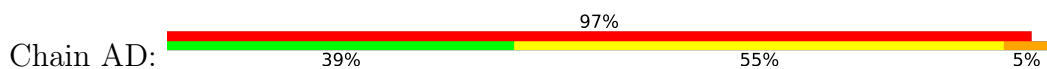
• Molecule 2: 30S ribosomal protein S2

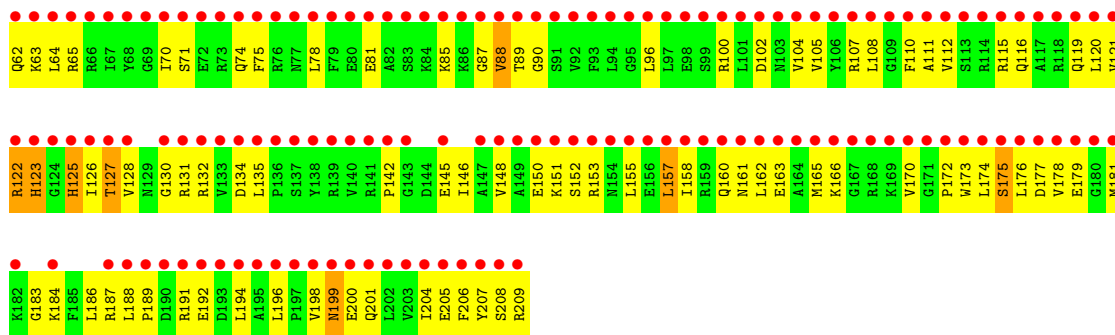


• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

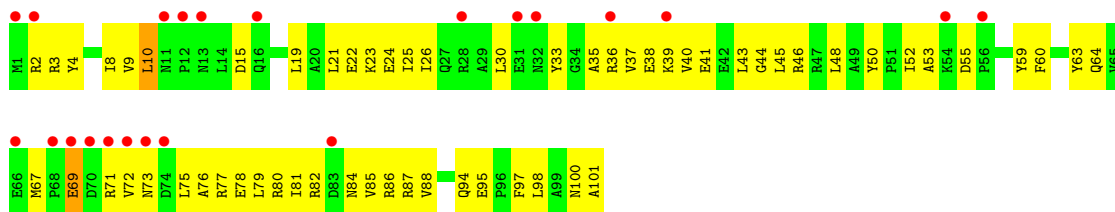




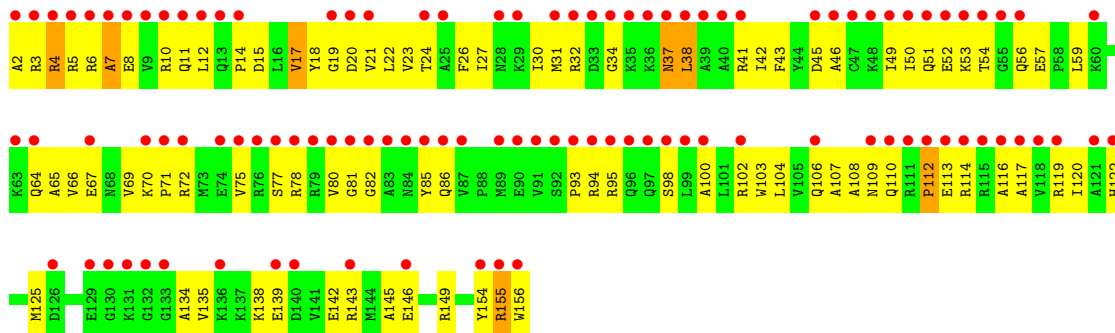
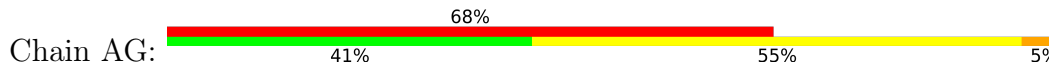
• Molecule 5: 30S ribosomal protein S5



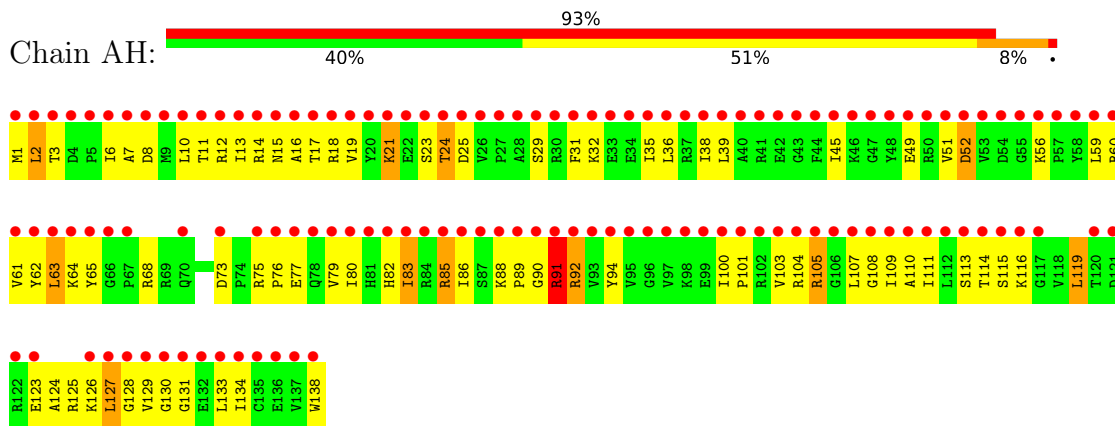
• Molecule 6: 30S ribosomal protein S6



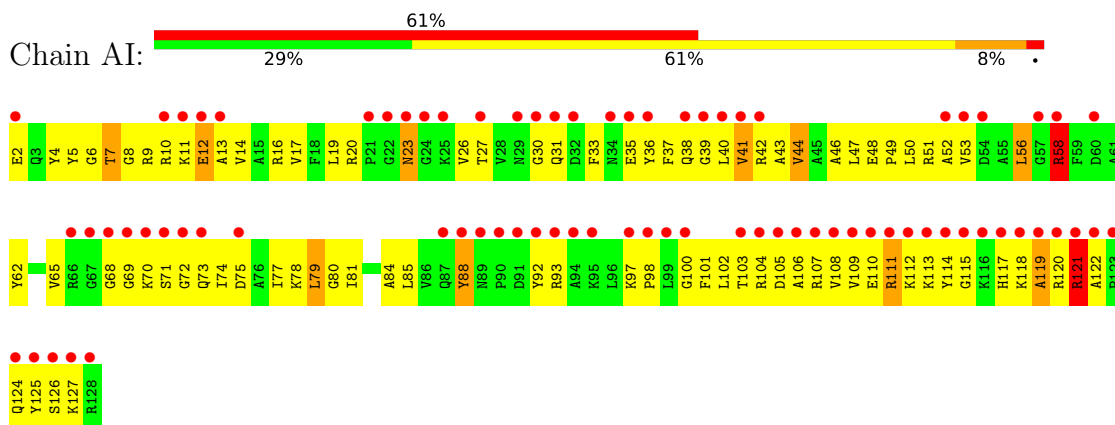
• Molecule 7: 30S ribosomal protein S7



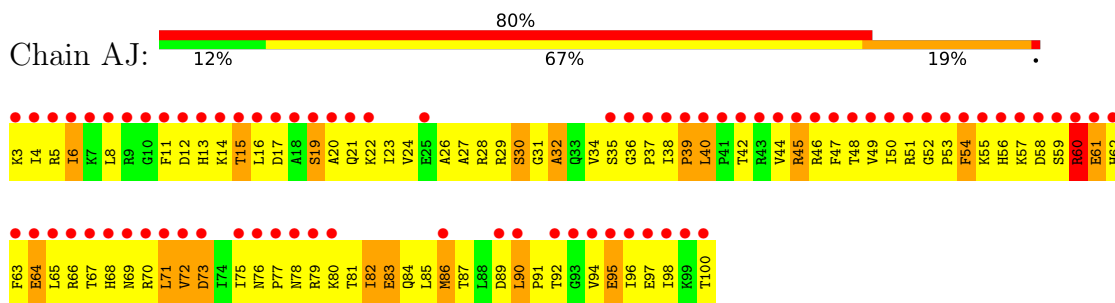
• Molecule 8: 30S ribosomal protein S8



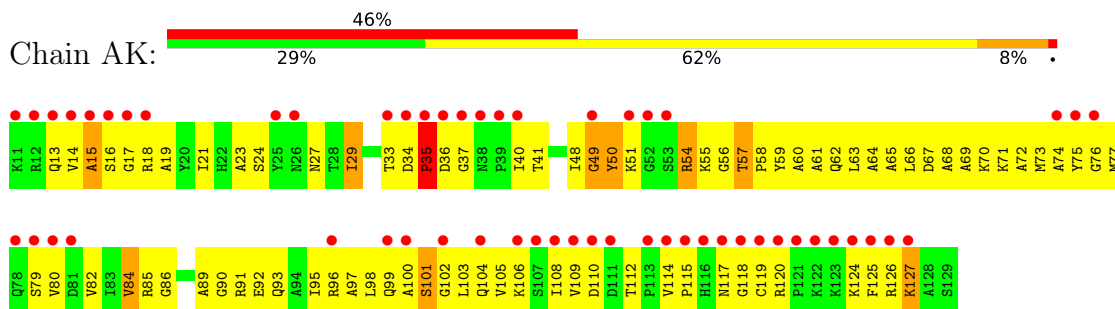
• Molecule 9: 30S ribosomal protein S9



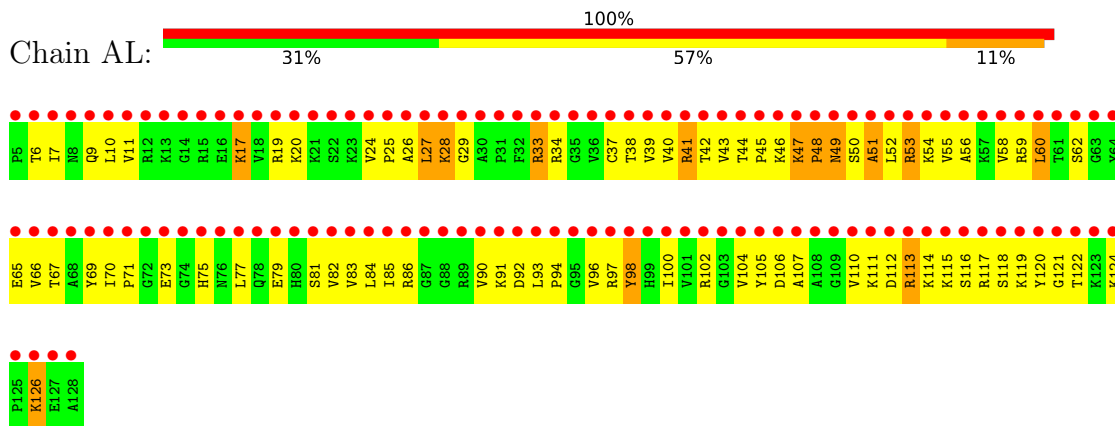
• Molecule 10: 30S ribosomal protein S10



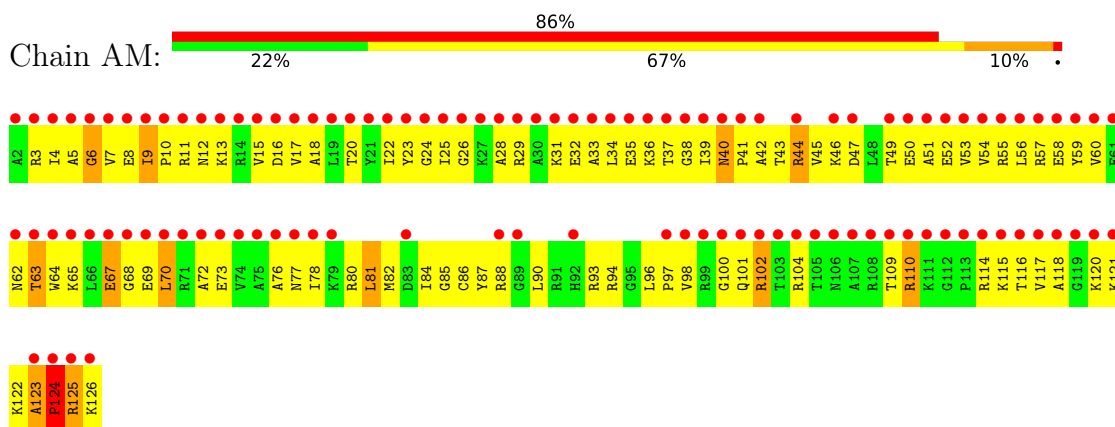
• Molecule 11: 30S ribosomal protein S11



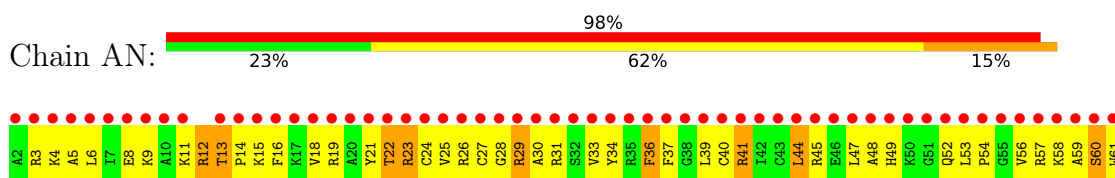
- Molecule 12: 30S ribosomal protein S12



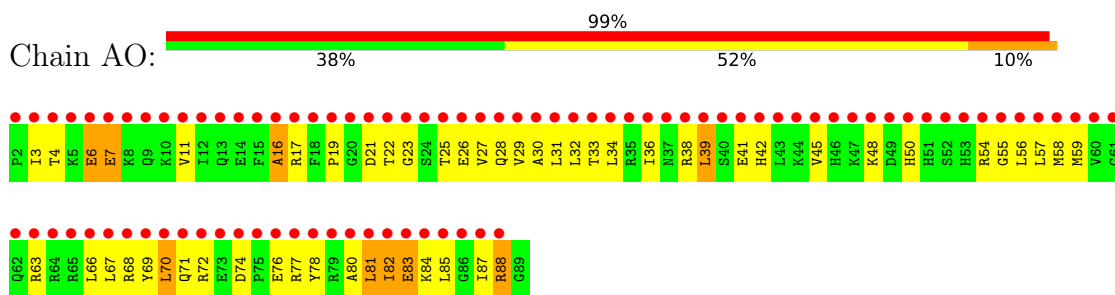
- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14

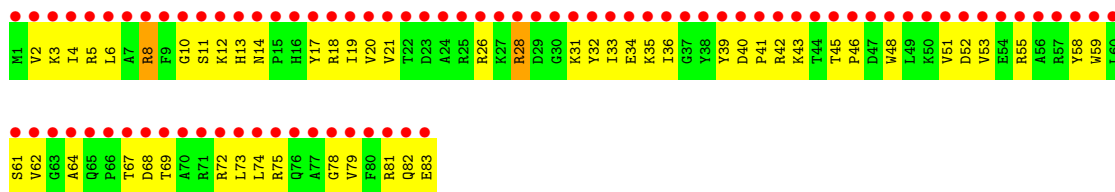


- Molecule 15: 30S ribosomal protein S15

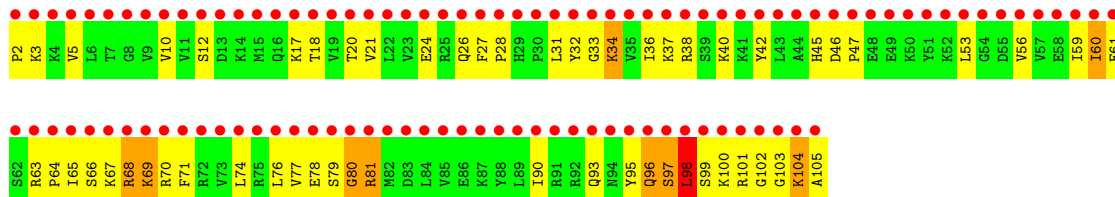
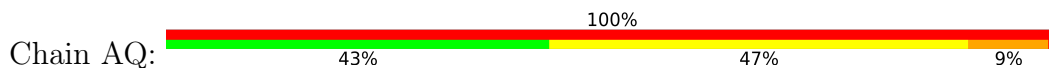


- Molecule 16: 30S ribosomal protein S16

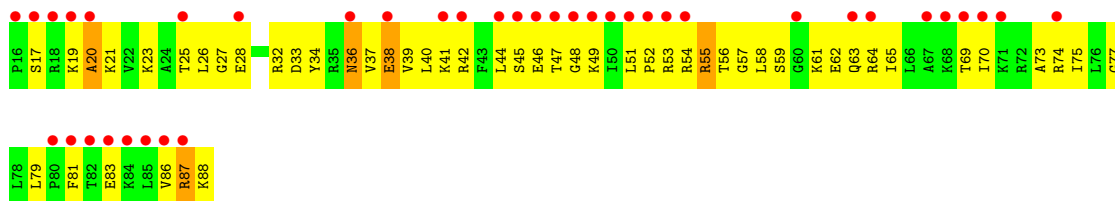




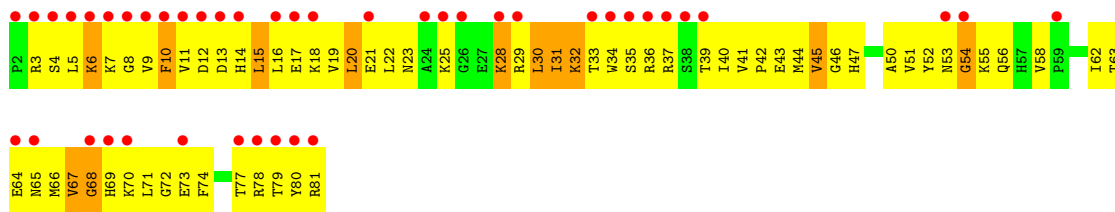
• Molecule 17: 30S ribosomal protein S17



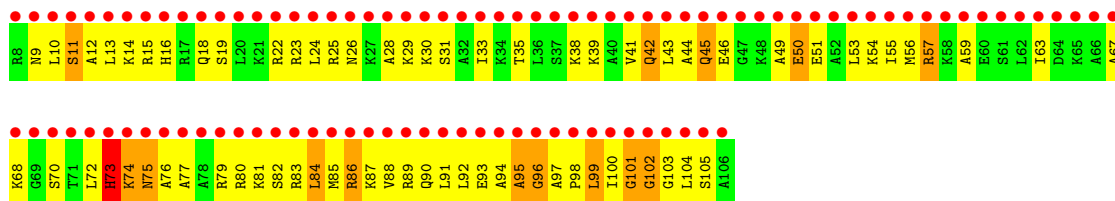
• Molecule 18: 30S ribosomal protein S18



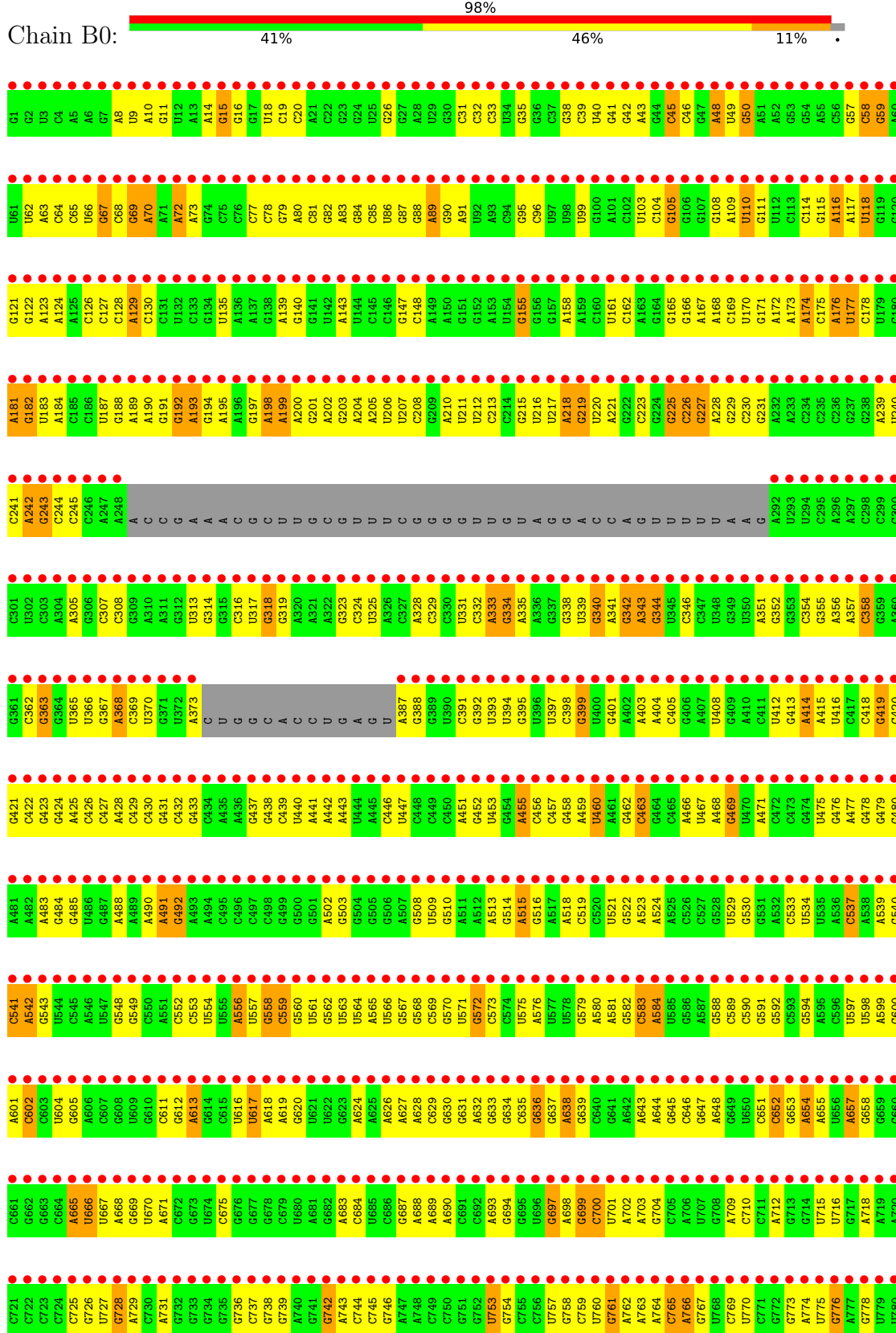
• Molecule 19: 30S ribosomal protein S19



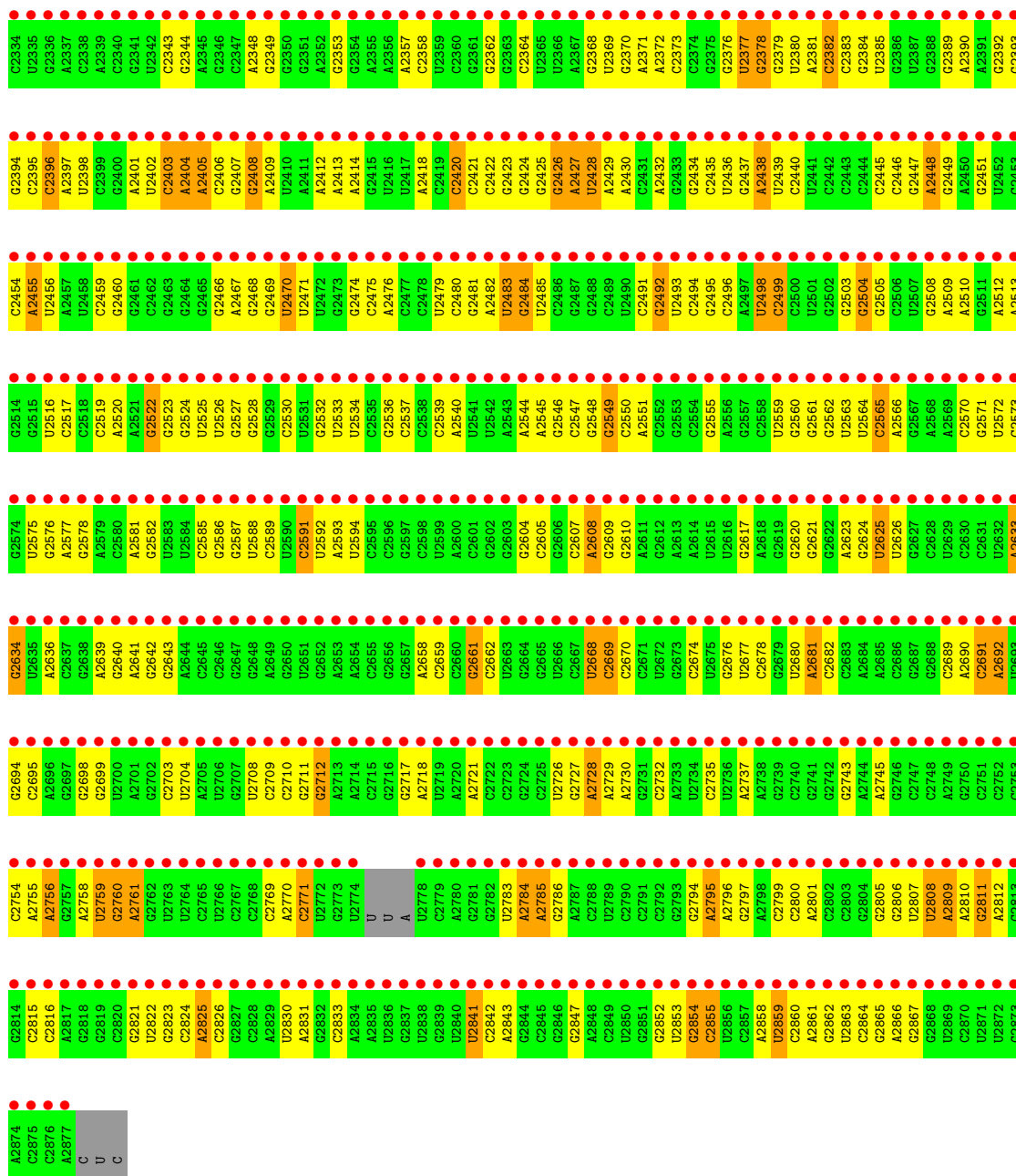
• Molecule 20: 30S ribosomal protein S20



● Molecule 21: 23S RIBOSOMAL RNA



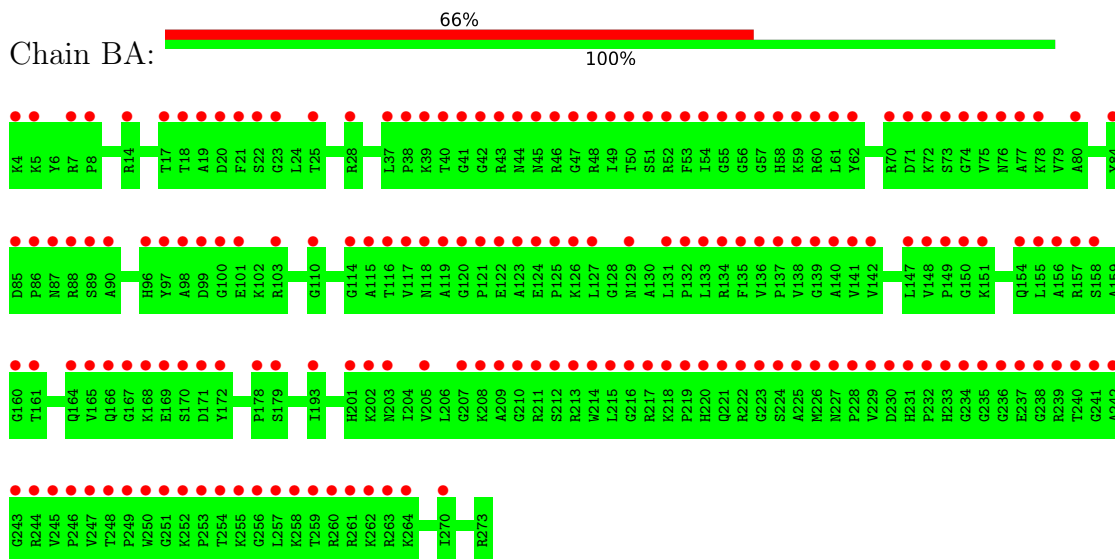
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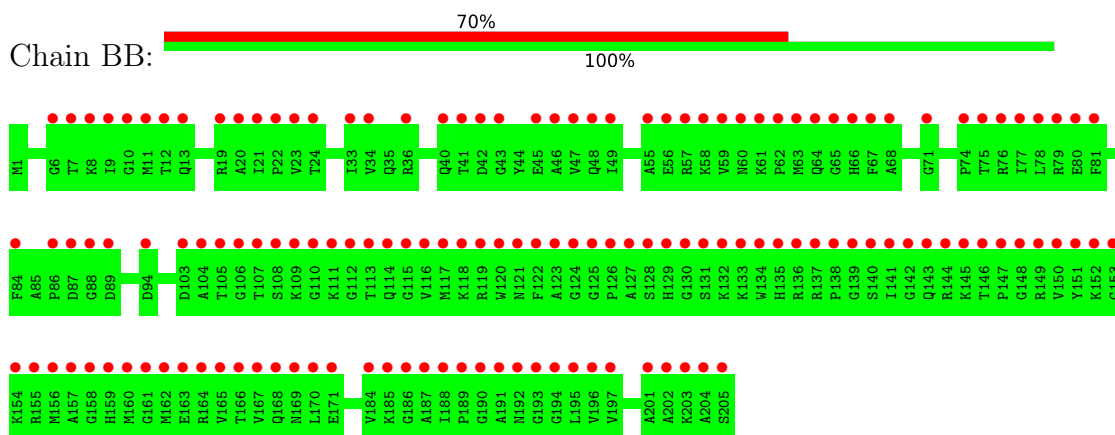
● Molecule 22: 5S RIBOSOMAL RNA



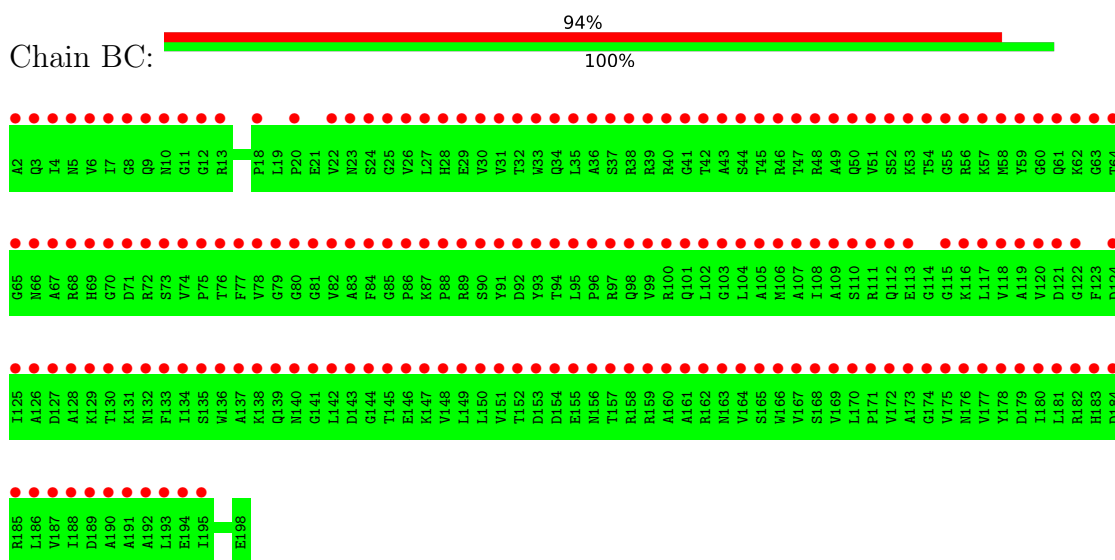
● Molecule 23: 50S ribosomal protein L2



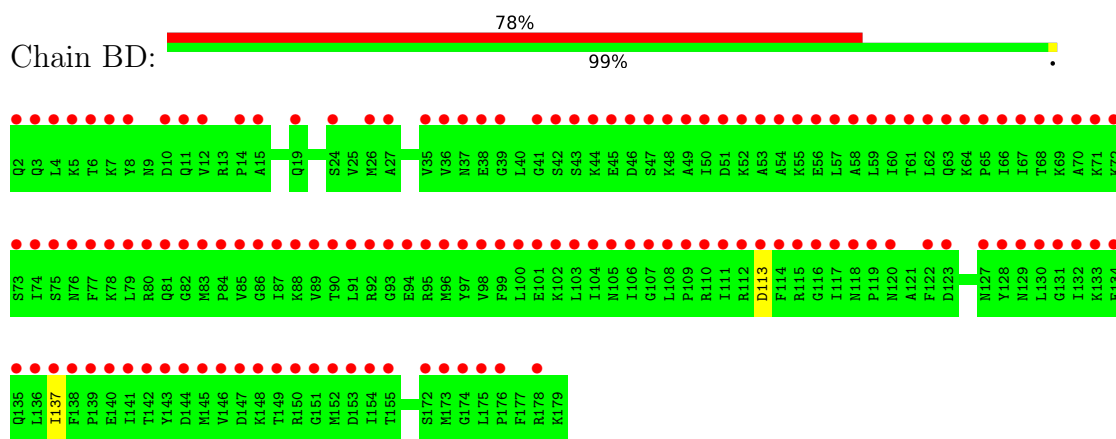
- Molecule 24: 50S ribosomal protein L3



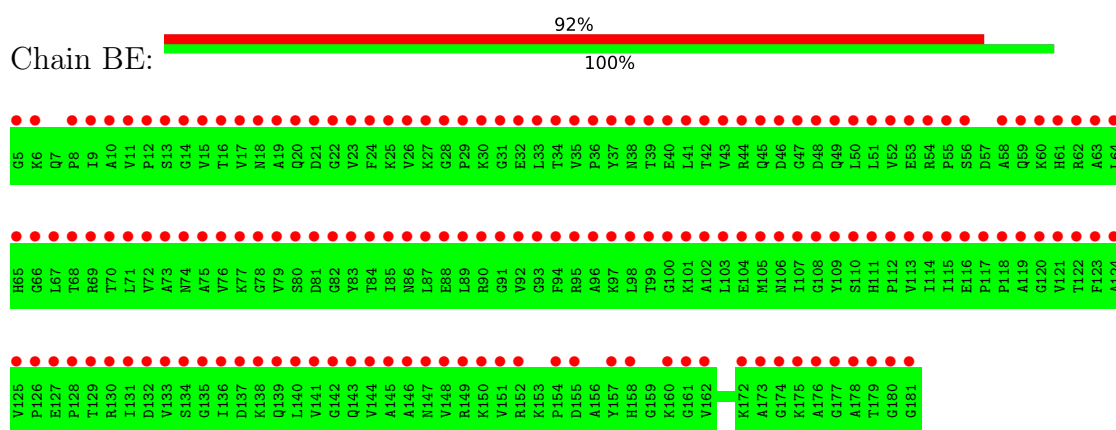
- Molecule 25: 50S ribosomal protein L4



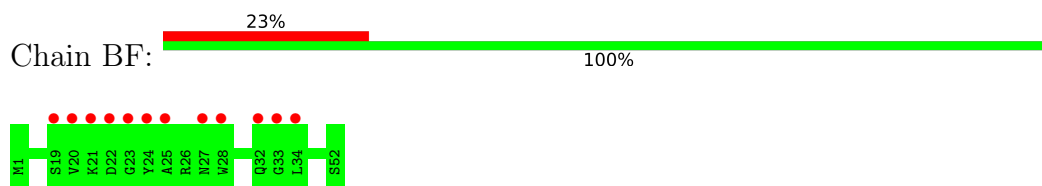
- Molecule 26: 50S ribosomal protein L5



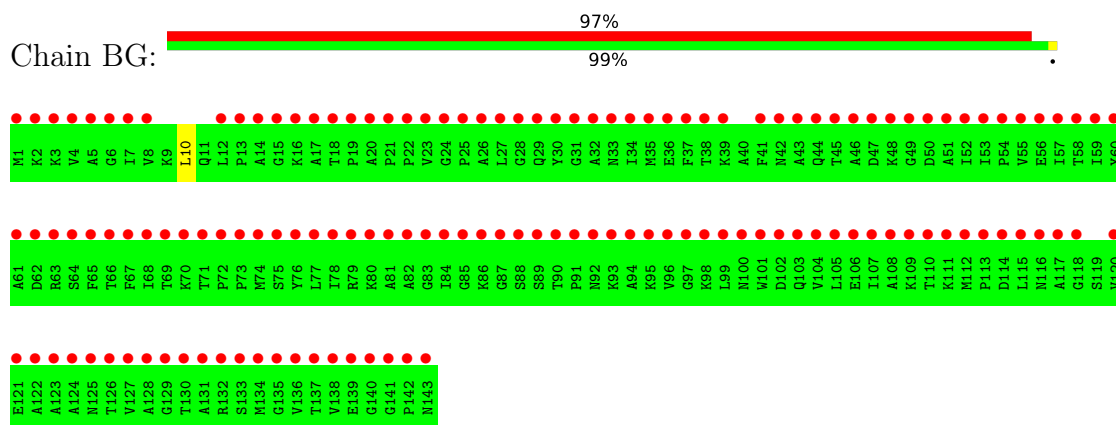
- Molecule 27: 50S ribosomal protein L6



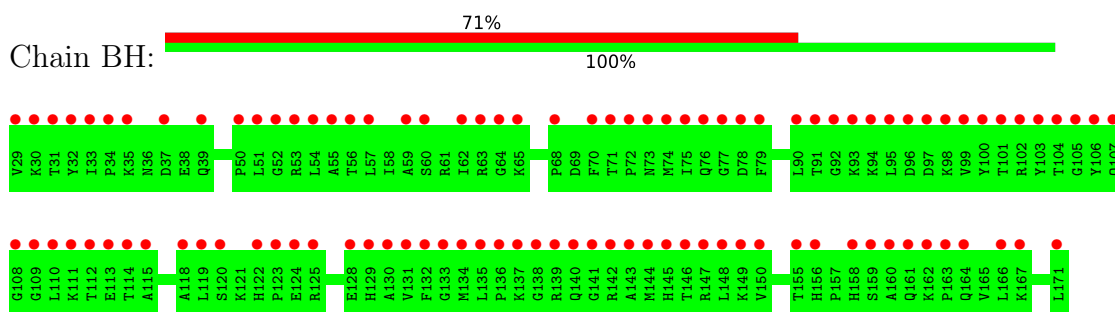
- Molecule 28: 50S ribosomal protein L9



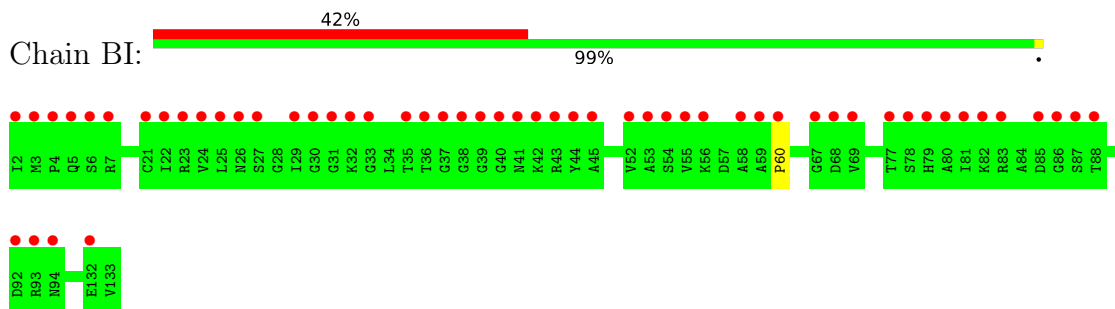
- Molecule 29: 50S ribosomal protein L11



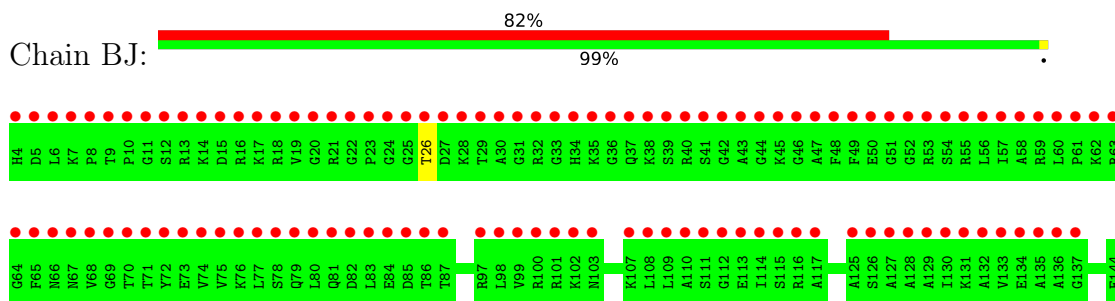
- Molecule 30: 50S ribosomal protein L13



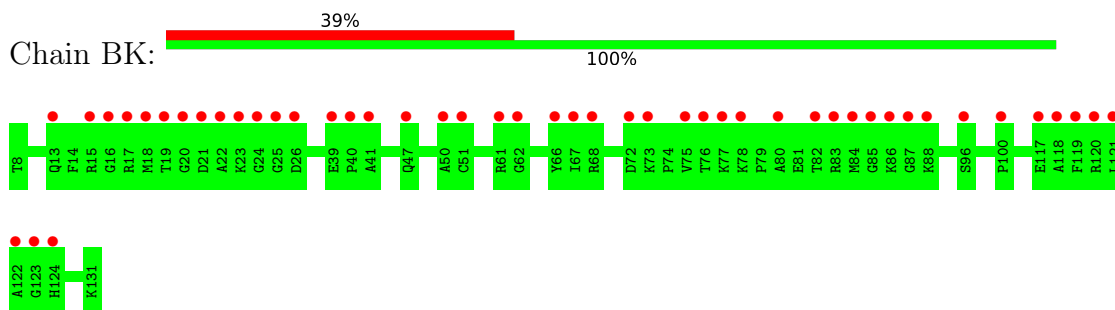
- Molecule 31: 50S ribosomal protein L14



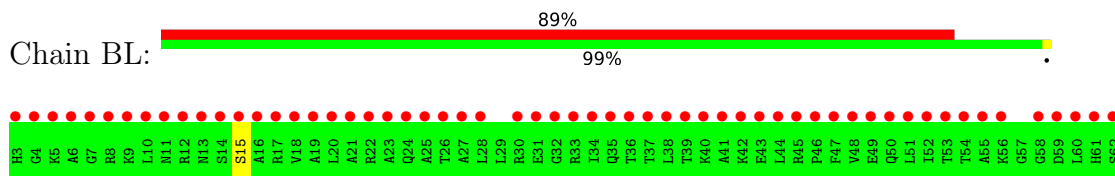
- Molecule 32: 50S ribosomal protein L15

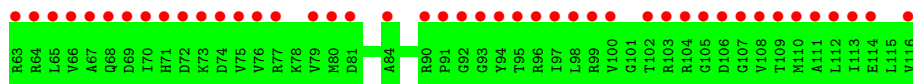


- Molecule 33: 50S ribosomal protein L16

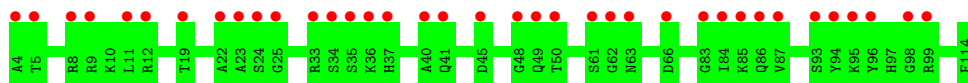


- Molecule 34: 50S ribosomal protein L17

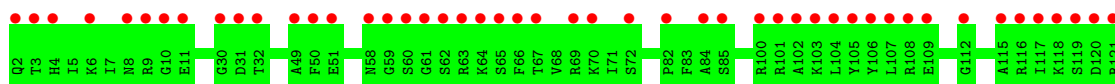




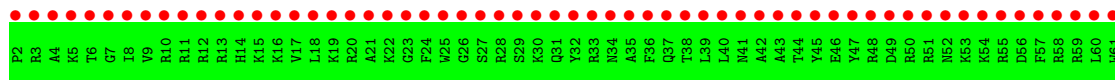
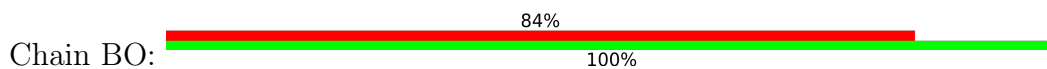
- Molecule 35: 50S ribosomal protein L18



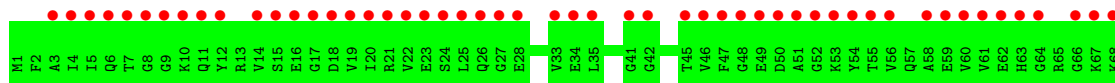
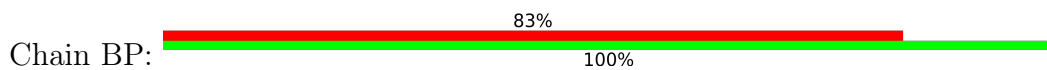
- Molecule 36: 50S ribosomal protein L19



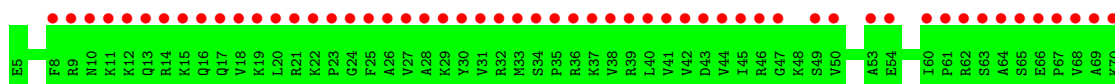
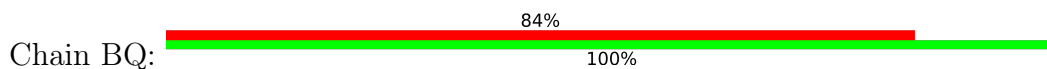
- Molecule 37: 50S ribosomal protein L20

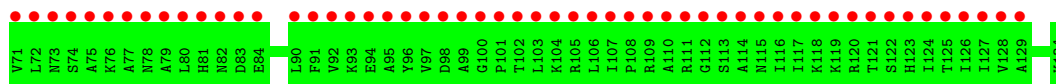


- Molecule 38: 50S ribosomal protein L21

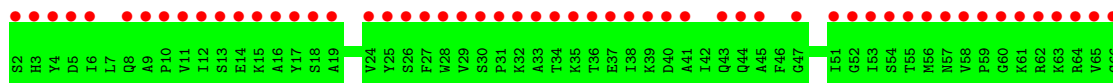
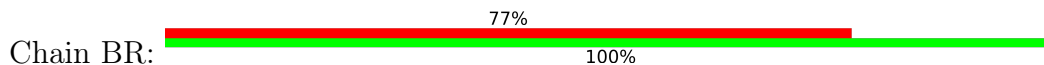


- Molecule 39: 50S ribosomal protein L22

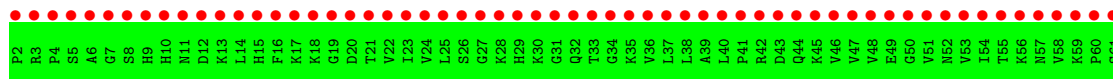




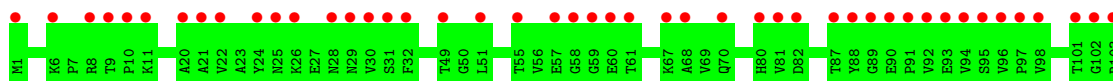
- Molecule 40: 50S ribosomal protein L23



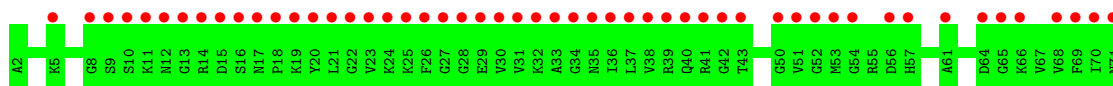
- Molecule 41: 50S ribosomal protein L24



- Molecule 42: general stress protein Ctc



- Molecule 43: 50S ribosomal protein L27




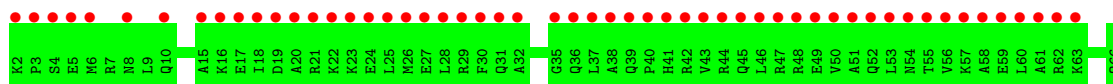
- Molecule 44: 50S RIBOSOMAL PROTEIN L28

Chain BV:  100%


There are no outlier residues recorded for this chain.

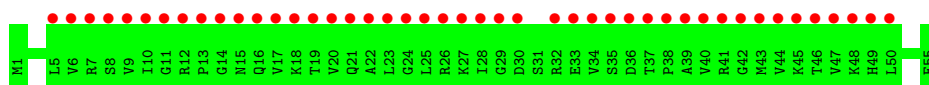
- Molecule 45: 50S ribosomal protein L29

Chain BW:  83%
100%



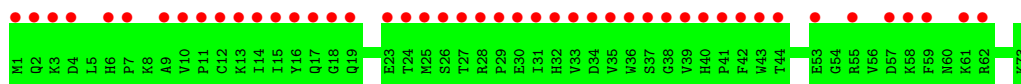
- Molecule 46: 50S ribosomal protein L30

Chain BX:  82%
100%




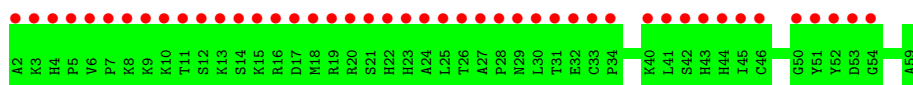
- Molecule 47: 50S ribosomal protein L31

Chain BY:  63%
100%



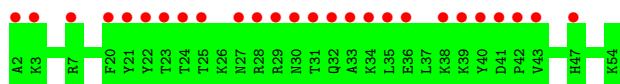
- Molecule 48: 50S ribosomal protein L32

Chain BZ:  78%
100%



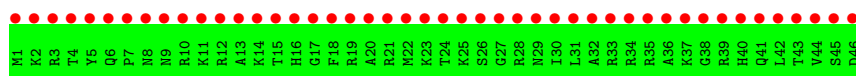
- Molecule 49: 50S ribosomal protein L33

Chain B1:  49%
100%

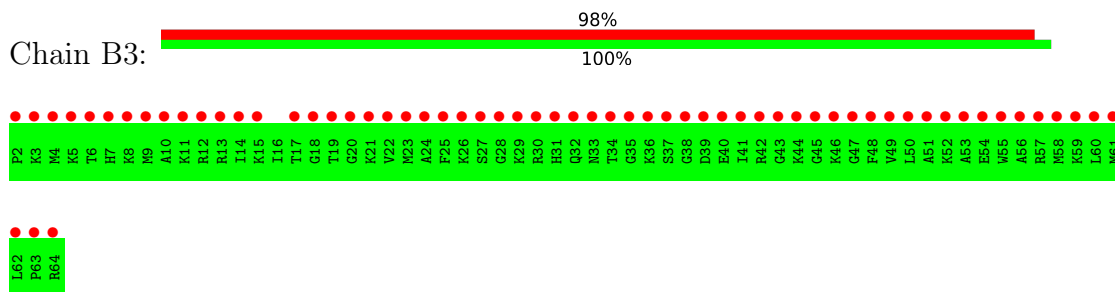


- Molecule 50: 50S ribosomal protein L34

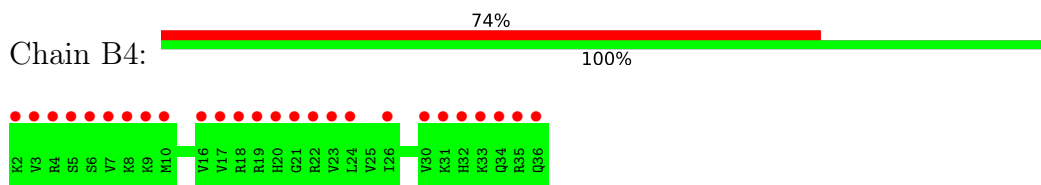
Chain B2:  100%
100%



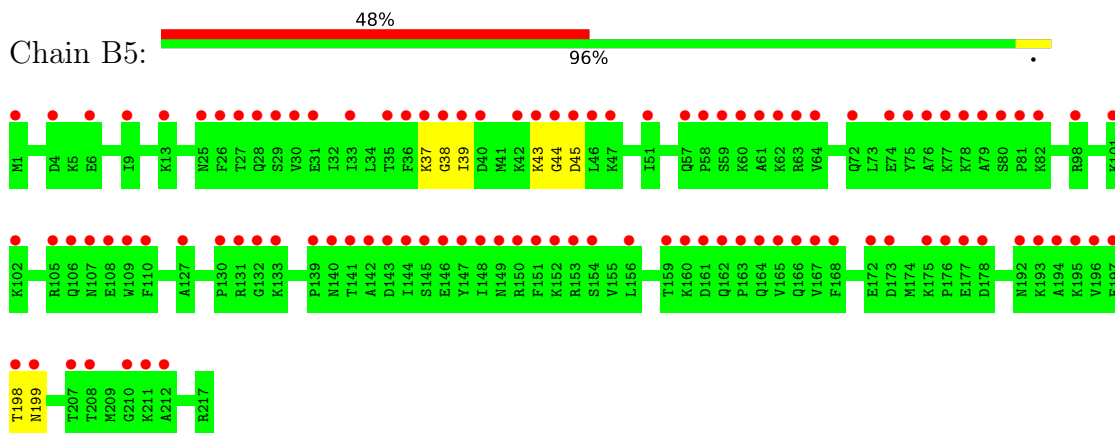
- Molecule 51: 50S ribosomal protein L35



• Molecule 52: 50S ribosomal protein L36



• Molecule 53: 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	683.89Å 683.89Å 386.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 9.50 241.79 – 9.50	Depositor EDS
% Data completeness (in resolution range)	92.1 (70.00-9.50) 87.2 (241.79-9.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.49 (at 9.99Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.389 , 0.407 0.369 , 0.385	Depositor DCC
R_{free} test set	1282 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	437.2	Xtrriage
Anisotropy	0.460	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.31 , -10.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	118711	wwPDB-VP
Average B, all atoms (Å ²)	680.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.90% 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

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 >5	RMSZ	# Z >5
1	AA	1.68	75/36823 (0.2%)	1.26	270/57351 (0.5%)
2	AB	0.37	0/1935	0.68	1/2609 (0.0%)
3	AC	0.38	0/1636	0.66	0/2205
4	AD	0.37	0/1732	0.63	0/2318
5	AE	0.49	0/1162	0.79	0/1564
6	AF	0.33	0/855	0.62	0/1154
7	AG	0.34	0/1275	0.62	0/1709
8	AH	0.44	0/1135	0.74	0/1527
9	AI	0.36	0/1028	0.62	0/1378
10	AJ	0.36	0/807	0.71	0/1085
11	AK	0.39	0/899	0.70	0/1213
12	AL	0.43	0/985	0.73	0/1317
13	AM	0.36	0/1006	0.67	0/1344
14	AN	0.40	0/500	0.78	0/664
15	AO	0.36	0/744	0.63	1/992 (0.1%)
16	AP	0.43	0/716	0.76	0/963
17	AQ	0.44	0/869	0.75	0/1159
18	AR	0.36	0/602	0.63	0/799
19	AS	0.35	0/661	0.72	1/890 (0.1%)
20	AT	0.39	0/764	0.73	0/1006
21	B0	0.50	17/67885 (0.0%)	0.75	48/105852 (0.0%)
22	B9	0.68	1/2815 (0.0%)	0.76	3/4384 (0.1%)
All	All	0.99	93/126834 (0.1%)	0.93	324/193483 (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	AA	2	40
21	B0	0	5
All	All	2	45

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	59	A	O3'-P	-120.85	0.16	1.61
1	AA	1398	A	O3'-P	-86.38	0.57	1.61
1	AA	214	U	O3'-P	-73.42	0.73	1.61
1	AA	394	G	O3'-P	-71.42	0.75	1.61
1	AA	1505	G	O3'-P	-71.04	0.76	1.61

The worst 5 of 324 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	59	A	P-O3'-C3'	-58.31	49.73	119.70
21	B0	1856	U	O3'-P-O5'	-48.57	11.72	104.00
21	B0	3098	U	P-O3'-C3'	42.71	170.95	119.70
1	AA	1490	C	P-O3'-C3'	40.44	168.23	119.70
1	AA	651	C	P-O3'-C3'	-39.22	72.64	119.70

All (2) chirality outliers are listed below:

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

5 of 45 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 [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	AA	32939	0	16652	3455	1
2	AB	1900	0	1951	209	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AC	1612	0	1675	286	0
4	AD	1702	0	1767	217	2
5	AE	1146	0	1207	255	0
6	AF	842	0	855	75	2
7	AG	1256	0	1296	138	2
8	AH	1115	0	1177	126	0
9	AI	1010	0	1043	183	0
10	AJ	794	0	839	206	2
11	AK	884	0	904	81	0
12	AL	970	0	1056	151	0
13	AM	996	0	1068	184	0
14	AN	491	0	529	153	0
15	AO	733	0	770	57	0
16	AP	700	0	720	78	0
17	AQ	856	0	925	239	0
18	AR	596	0	668	77	0
19	AS	647	0	673	156	0
20	AT	762	0	853	286	0
21	B0	60636	0	30557	1717	1
22	B9	2519	0	1287	43	0
23	BA	270	0	0	0	0
24	BB	205	0	0	0	0
25	BC	197	0	0	0	0
26	BD	178	0	0	4	0
27	BE	177	0	0	0	0
28	BF	52	0	0	0	0
29	BG	143	0	0	1	0
30	BH	143	0	0	0	0
31	BI	132	0	0	2	0
32	BJ	141	0	0	1	0
33	BK	124	0	0	0	0
34	BL	114	0	0	1	0
35	BM	111	0	0	0	0
36	BN	125	0	0	0	0
37	BO	117	0	0	0	0
38	BP	100	0	0	0	0
39	BQ	130	0	0	0	0
40	BR	93	0	0	0	0
41	BS	113	0	0	0	0
42	BT	173	0	0	0	0
43	BU	86	0	0	0	0
44	BV	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BW	65	0	0	0	0
46	BX	55	0	0	0	0
47	BY	73	0	0	0	0
48	BZ	58	0	0	0	0
49	B1	53	0	0	0	0
50	B2	46	0	0	0	0
51	B3	63	0	0	0	0
52	B4	35	0	0	0	0
53	B5	217	0	0	22	0
All	All	118711	0	68472	6990	5

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 37.

The worst 5 of 6990 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:1278:U:H5''	1:AA:1279:A:P	1.31	1.68
1:AA:1458:G:C8	1:AA:1459:C:H2'	1.27	1.63
1:AA:191:G:C6	1:AA:192:U:C2	1.90	1.60
1:AA:1475:G:H5''	21:B0:1706:A:C4'	1.13	1.60
1:AA:1475:G:C5'	21:B0:1706:A:H4'	1.32	1.59

All (5) 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)
4:AD:172:PRO:O	6:AF:15:ASP:CB[3_555]	1.83	0.37
1:AA:416:G:OP1	21:B0:3140:G:O2'[3_555]	1.99	0.21
7:AG:51:GLN:NE2	10:AJ:87:THR:OG1[4_555]	2.08	0.12
4:AD:186:LEU:CD1	6:AF:15:ASP:OD2[3_555]	2.14	0.06
7:AG:57:GLU:OE2	10:AJ:89:ASP:OD1[4_555]	2.14	0.06

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	
2	AB	232/234 (99%)	174 (75%)	34 (15%)	24 (10%)	0	8
3	AC	204/206 (99%)	135 (66%)	40 (20%)	29 (14%)	0	4
4	AD	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	2	22
5	AE	148/150 (99%)	130 (88%)	13 (9%)	5 (3%)	3	26
6	AF	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	15	55
7	AG	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	16
8	AH	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	4	29
9	AI	125/127 (98%)	88 (70%)	27 (22%)	10 (8%)	1	12
10	AJ	96/98 (98%)	59 (62%)	20 (21%)	17 (18%)	0	3
11	AK	117/119 (98%)	88 (75%)	20 (17%)	9 (8%)	1	13
12	AL	120/124 (97%)	96 (80%)	15 (12%)	9 (8%)	1	13
13	AM	121/125 (97%)	87 (72%)	26 (22%)	8 (7%)	1	16
14	AN	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	6
15	AO	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	1	18
16	AP	81/83 (98%)	65 (80%)	15 (18%)	1 (1%)	13	50
17	AQ	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	13
18	AR	71/73 (97%)	62 (87%)	7 (10%)	2 (3%)	5	30
19	AS	78/80 (98%)	48 (62%)	19 (24%)	11 (14%)	0	4
20	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	0	5
All	All	2330/2372 (98%)	1788 (77%)	361 (16%)	181 (8%)	1	13

5 of 181 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	9	GLU
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE

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	
2	AB	202/202 (100%)	180 (89%)	22 (11%)	6	23
3	AC	160/160 (100%)	142 (89%)	18 (11%)	6	21
4	AD	180/180 (100%)	172 (96%)	8 (4%)	28	53
5	AE	115/115 (100%)	100 (87%)	15 (13%)	4	18
6	AF	90/90 (100%)	88 (98%)	2 (2%)	52	71
7	AG	126/126 (100%)	122 (97%)	4 (3%)	39	61
8	AH	119/119 (100%)	109 (92%)	10 (8%)	11	33
9	AI	98/98 (100%)	90 (92%)	8 (8%)	11	34
10	AJ	88/88 (100%)	79 (90%)	9 (10%)	7	25
11	AK	90/90 (100%)	84 (93%)	6 (7%)	16	41
12	AL	104/104 (100%)	96 (92%)	8 (8%)	13	37
13	AM	100/100 (100%)	90 (90%)	10 (10%)	7	26
14	AN	49/49 (100%)	47 (96%)	2 (4%)	30	55
15	AO	79/79 (100%)	72 (91%)	7 (9%)	9	30
16	AP	72/72 (100%)	67 (93%)	5 (7%)	15	40
17	AQ	96/96 (100%)	90 (94%)	6 (6%)	18	43
18	AR	64/64 (100%)	61 (95%)	3 (5%)	26	51
19	AS	71/71 (100%)	68 (96%)	3 (4%)	30	54
20	AT	76/76 (100%)	69 (91%)	7 (9%)	9	29
All	All	1979/1979 (100%)	1826 (92%)	153 (8%)	13	37

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	AM	81	LEU
19	AS	10	PHE
13	AM	125	ARG
16	AP	8	ARG

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Mol	Chain	Res	Type
20	AT	75	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
7	AG	37	ASN
19	AS	56	GLN
10	AJ	76	ASN
19	AS	53	ASN
15	AO	37	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1487/1537 (96%)	218 (14%)	89 (5%)
21	B0	2802/2887 (97%)	430 (15%)	55 (1%)
22	B9	116/118 (98%)	10 (8%)	0
All	All	4405/4542 (96%)	658 (14%)	144 (3%)

5 of 658 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G
1	AA	31	G
1	AA	32	A

5 of 144 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	B0	1518	C
21	B0	2824	C
21	B0	1634	A
21	B0	3118	U
1	AA	748	C

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 monosaccharides 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	106
21	B0	31
22	B9	2
13	AM	1
12	AL	1

The worst 5 of 141 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	9.14
1	AA	1458:G	O3'	1459:C	P	8.01
1	B0	1888:C	O3'	1889:G	P	6.96
1	AA	1459:C	O3'	1460:A	P	6.03
1	B0	3180:U	O3'	3181:C	P	5.42

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	1533/1537 (99%)	34.46	1533 (100%) 0 0	207, 548, 819, 940	0
2	AB	234/234 (100%)	1.45	72 (30%) 0 2	754, 754, 754, 754	0
3	AC	206/206 (100%)	5.43	168 (81%) 0 0	378, 378, 378, 378	0
4	AD	208/208 (100%)	14.38	201 (96%) 0 0	709, 709, 709, 709	0
5	AE	150/150 (100%)	14.31	150 (100%) 0 0	756, 756, 756, 756	0
6	AF	101/101 (100%)	1.29	22 (21%) 0 3	748, 748, 748, 748	0
7	AG	155/155 (100%)	4.22	105 (67%) 0 0	374, 374, 374, 374	0
8	AH	138/138 (100%)	7.10	129 (93%) 0 0	856, 856, 856, 856	0
9	AI	127/127 (100%)	7.06	77 (60%) 0 0	439, 439, 439, 439	0
10	AJ	98/98 (100%)	7.10	78 (79%) 0 0	430, 430, 430, 430	0
11	AK	119/119 (100%)	3.04	55 (46%) 0 1	652, 652, 652, 652	0
12	AL	124/124 (100%)	10.88	124 (100%) 0 0	423, 541, 541, 541	0
13	AM	125/125 (100%)	5.97	108 (86%) 0 0	378, 572, 572, 572	0
14	AN	60/60 (100%)	10.29	59 (98%) 0 0	378, 378, 378, 378	0
15	AO	88/88 (100%)	11.20	87 (98%) 0 0	740, 740, 740, 740	0
16	AP	83/83 (100%)	19.81	83 (100%) 0 0	781, 781, 781, 781	0
17	AQ	104/104 (100%)	11.89	104 (100%) 0 0	857, 857, 857, 857	0
18	AR	73/73 (100%)	3.48	39 (53%) 0 1	748, 748, 748, 748	0
19	AS	80/80 (100%)	3.00	43 (53%) 0 1	633, 633, 633, 633	0
20	AT	99/99 (100%)	13.05	99 (100%) 0 0	940, 940, 940, 940	0
21	B0	2825/2887 (97%)	55.87	2825 (100%) 0 0	462, 737, 737, 940	0
22	B9	118/118 (100%)	44.84	118 (100%) 0 0	772, 938, 938, 938	0
23	BA	270/270 (100%)	6.09	179 (66%) 0 0	737, 737, 737, 737	0
24	BB	205/205 (100%)	5.86	143 (69%) 0 0	737, 737, 737, 737	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	BC	197/197 (100%)	8.25	186 (94%) 0 0	737, 737, 737, 737	0
26	BD	178/178 (100%)	17.24	138 (77%) 0 0	938, 938, 938, 938	0
27	BE	177/177 (100%)	13.08	163 (92%) 0 0	737, 737, 737, 737	0
28	BF	52/52 (100%)	1.36	12 (23%) 0 2	737, 737, 737, 737	0
29	BG	143/143 (100%)	17.89	138 (96%) 0 0	907, 907, 907, 907	0
30	BH	143/143 (100%)	5.92	102 (71%) 0 0	737, 737, 737, 737	0
31	BI	132/132 (100%)	3.04	55 (41%) 0 1	737, 737, 737, 737	0
32	BJ	141/141 (100%)	10.40	115 (81%) 0 0	737, 737, 737, 737	0
33	BK	124/124 (100%)	2.41	48 (38%) 0 1	737, 737, 737, 737	0
34	BL	114/114 (100%)	6.99	102 (89%) 0 0	737, 737, 737, 737	0
35	BM	111/111 (100%)	1.78	37 (33%) 0 2	938, 938, 938, 938	0
36	BN	125/125 (100%)	2.62	53 (42%) 0 1	737, 737, 737, 737	0
37	BO	117/117 (100%)	12.38	98 (83%) 0 0	737, 737, 737, 737	0
38	BP	100/100 (100%)	5.91	83 (83%) 0 0	737, 737, 737, 737	0
39	BQ	130/130 (100%)	7.52	109 (83%) 0 0	737, 737, 737, 737	0
40	BR	93/93 (100%)	4.86	72 (77%) 0 0	737, 737, 737, 737	0
41	BS	113/113 (100%)	11.17	112 (99%) 0 0	737, 737, 737, 737	0
42	BT	173/173 (100%)	8.24	105 (60%) 0 0	737, 772, 772, 772	0
43	BU	86/86 (100%)	6.53	59 (68%) 0 0	737, 737, 737, 737	0
44	BV	0/16	-	-	-	-
45	BW	65/65 (100%)	5.83	54 (83%) 0 0	737, 737, 737, 737	0
46	BX	55/55 (100%)	7.60	45 (81%) 0 0	737, 737, 737, 737	0
47	BY	73/73 (100%)	4.25	46 (63%) 0 0	737, 737, 737, 737	0
48	BZ	58/58 (100%)	11.78	45 (77%) 0 0	737, 737, 737, 737	0
49	B1	53/53 (100%)	5.78	26 (49%) 0 1	737, 737, 737, 737	0
50	B2	46/46 (100%)	9.41	46 (100%) 0 0	737, 737, 737, 737	0
51	B3	63/63 (100%)	7.36	62 (98%) 0 0	737, 737, 737, 737	0
52	B4	35/35 (100%)	6.72	26 (74%) 0 0	737, 737, 737, 737	0
53	B5	213/217 (98%)	4.43	104 (48%) 0 1	940, 940, 940, 940	0
All	All	10433/10519 (99%)	25.15	8842 (84%) 0 0	207, 737, 938, 940	0

The worst 5 of 8842 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
21	B0	1989	C	280.5
21	B0	2624	G	227.9
21	B0	1988	A	201.4
21	B0	2480	C	196.7
21	B0	2425	G	192.2

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 monosaccharides 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.