



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:20 PM GMT

PDB ID : 4V49
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

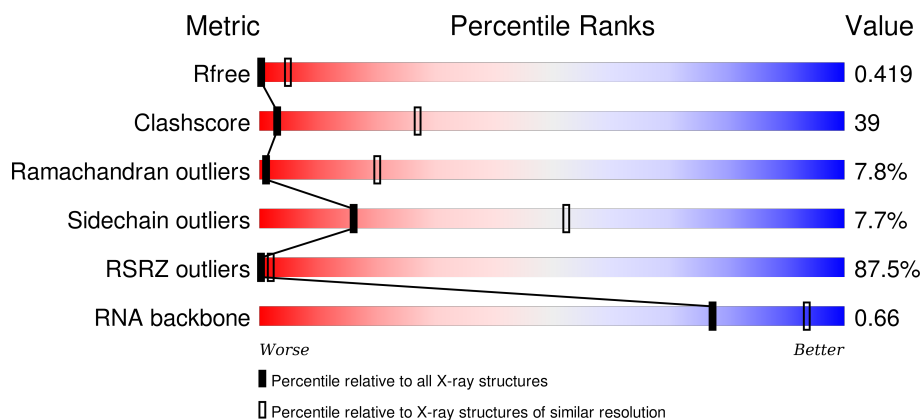
1 Overall quality at a glance

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}	91344	1015 (11.50-3.66)
Clashscore	102246	1064 (11.50-3.70)
Ramachandran outliers	100387	1036 (11.50-3.66)
Sidechain outliers	100360	1006 (11.50-3.66)
RSRZ outliers	91569	1014 (11.50-3.66)
RNA backbone	2183	1106 (11.50-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>100%</div> <div> <div>23%</div> <div>57%</div> <div>16%</div> <div>.</div> </div> </div>
2	AV	76	<div> <div>100%</div> <div> <div>36%</div> <div>39%</div> <div>14%</div> <div>11%</div> </div> </div>
2	AW	76	<div> <div>100%</div> <div> <div>39%</div> <div>39%</div> <div>13%</div> <div>8%</div> </div> </div>
3	AU	18	<div> <div>50%</div> <div> <div>44%</div> <div>6%</div> <div>50%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	AB	234	
5	AC	206	
6	AD	208	
7	AE	150	
8	AF	101	
9	AG	155	
10	AH	138	
11	AI	127	
12	AJ	98	
13	AK	119	
14	AL	124	
15	AM	125	
16	AN	60	
17	AO	88	
18	AP	83	
19	AQ	104	
20	AR	73	
21	AS	80	
22	AT	99	
23	B0	2887	
24	B9	118	
25	BA	270	
26	BB	205	
27	BC	197	
28	BD	178	

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Mol	Chain	Length	Quality of chain
29	BE	177	76% 100%
30	BF	52	33% 100%
31	BG	143	82% 98%
32	BH	143	92% 100%
33	BI	132	42% 99%
34	BJ	141	71% 99%
35	BK	124	38% 100%
36	BL	114	92% 99%
37	BM	111	30% 100%
38	BN	125	54% 99%
39	BO	117	85% 100%
40	BP	100	95% 100%
41	BQ	130	89% 100%
42	BR	93	83% 100%
43	BS	113	98% 100%
44	BT	173	82% 100%
45	BU	86	76% 99%
46	BV	16	100%
47	BW	65	82% 100%
48	BX	55	69% 100%
49	BY	73	63% 100%
50	BZ	58	91% 100%
51	B1	53	43% 100%
52	B2	46	100%
53	B3	63	100%

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

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
1	AA	1527	Total	C	N	O	P	0	0	0
			32819	14610	6085	10597	1527			

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

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

- Molecule 3 is a RNA chain called mRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
20	AR	73	Total	C	N	O	0	0	0
			596	380	118	98			

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

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

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

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

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

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

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

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

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

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

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

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

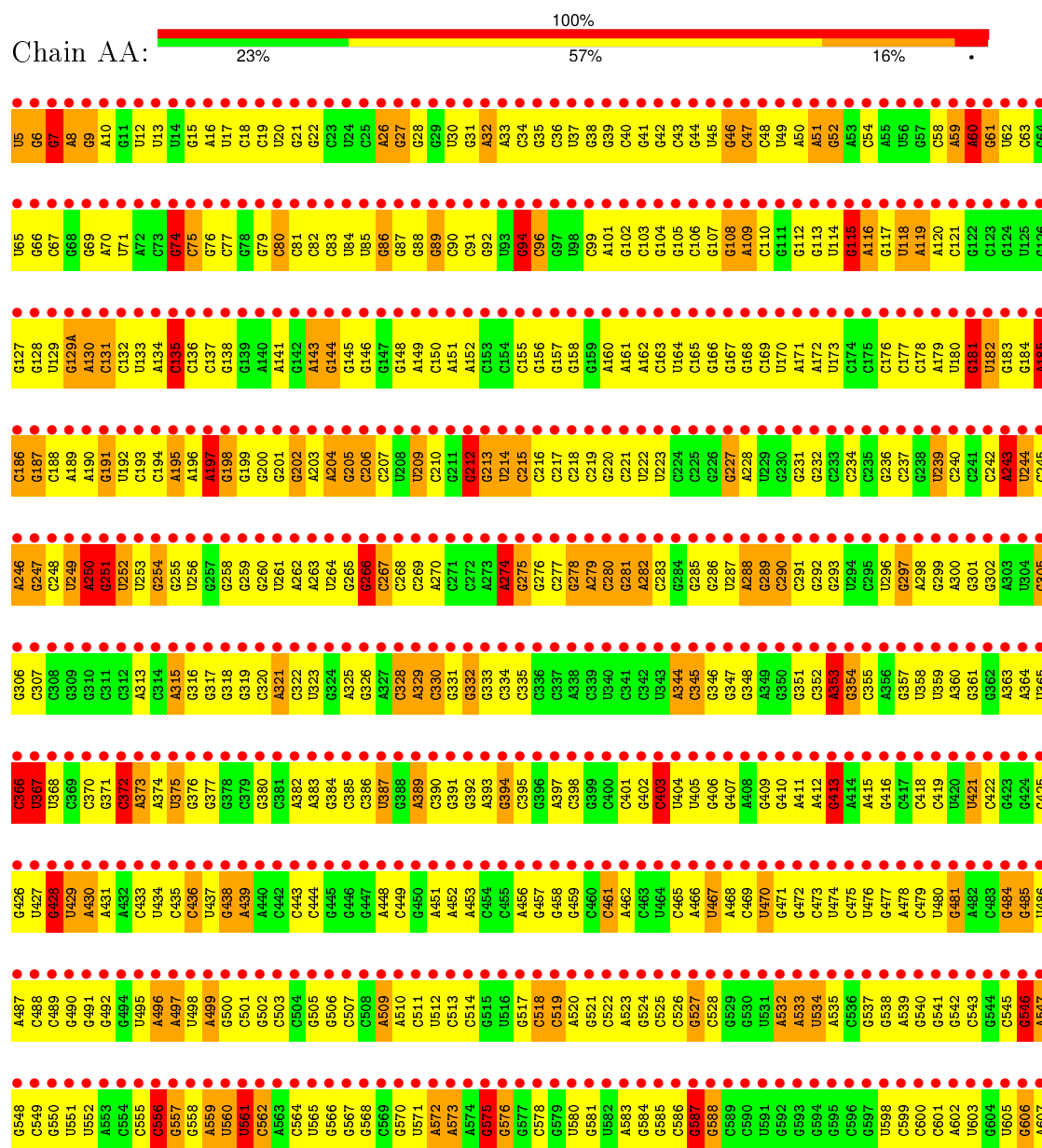
- Molecule 55 is a protein called 50S ribosomal protein L1P.

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

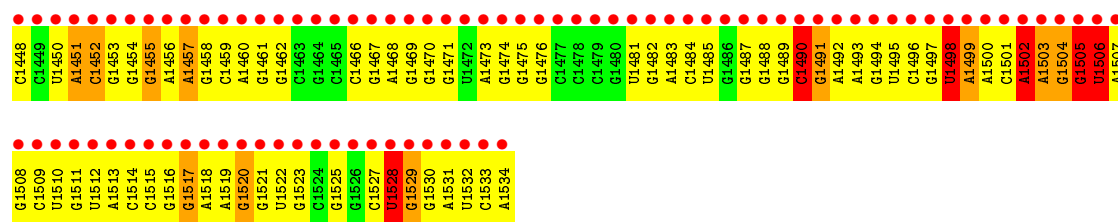
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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 ($\text{RSRZ} > 2$). 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.

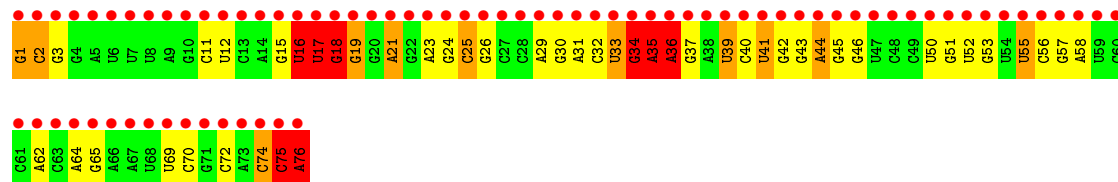
• Molecule 1: 16S RIBOSOMAL RNA



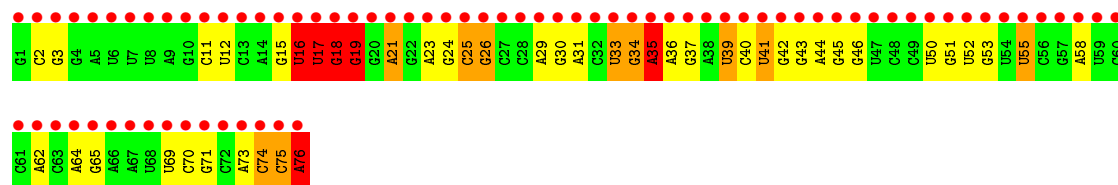
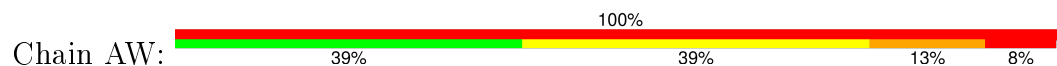
G1387	C1328	A1268	C1208	G1087	C1027	A968	A908	C848	U788	A728	G668	A608
C1388	A1329	A1269	C1209	G1088	C1028	A969	A909	C849	U789	A729	U669	A609
C1389	U1330	G1270	U1210	G1089	U1029	G970	C910	U850	A790	G730	G670	G610
U1390	G1331	G1271	U1211	U1090	U1030	G971	U911	U851	A791	G731	G671	G611
U1391	A1332	G1272	A1212	U1091	C1031	G972	C912	C852	A792	C732	U672	C612
G1392	A1333	A1151	A1213	A1092	G1032	G973	A913	C853	U793	A733	G673	C613
U1393	C1334	C1153	C1214	A1093	G1033	A974	A914	C854	A794	G734	A674	A614
A1394	C1335	C1154	G1215	U1094	G1034	A975	A915	U855	A795	C735	A675	C615
C1395	C1336	G1155	G1216	U1095	A1035	G976	A916	C856	A796	C736	A676	G616
A1396	G1337	A1156	C1217	C1096	A1036	A977	A917	C857	C797	A737	U677	G617
C1397	C1338	A1157	C1218	C1097	G1037	A978	A918	U858	G798	C738	U678	C618
A1398	U1339	C1158	U1219	C1098	C1038	C979	A919	A859	G799	C739	C679	U619
C1399	A1340	U1159	C1220	G1099	C1039	C980	U920	A860	G800	U740	C680	C620
U1400	U1341	G1160	G1221	C1100	U1040	G981	U921	C861	U801	G741	C681	A621
G1401	C1342	C1161	G1222	A1101	A1041	U982	G922	C862	A802	G742	G682	A622
C1402	G1343	C1162	C1223	A1102	G1042	A983	A923	U863	G803	U743	G683	C623
C1403	C1344	C1163	G1224	C1103	C1043	C984	C924	A864	U804	C744	A684	C624
C1404	U1345	G1164	A1225	G1104	A1044	C985	G925	A865	C805	C745	G685	G625
G1405	A1346	C1165	C1226	A1105	C1045	A986	G926	C866	C806	A746	U686	U626
U1406	G1347	G1166	A1227	G1106	A1046	G987	G927	C867	A807	C747	U687	G627
C1407	U1348	A1167	C1228	C1107	U1047	G988	G928	C868	C808	C748	G688	G628
A1408	A1349	A1168	A1229	G1108	G1048	C989	G929	U869	G809	C749	C689	G629
C1409	C1350	A1169	C1230	C1109	U1049	C990	C930	U870	C810	G750	G690	G630
G1410	U1351	G1171	G1231	A1110	G1050	U991	C931	C871	C811	U751	G691	G631
C1411	C1352	C1172	U1232	C1111	C1051	U992	C932	A872	C812	G752	U692	A632
C1412	G1353	G1173	G1233	C1112	U1052	G993	G933	A873	U813	A753	G693	G633
A1413	C1354	G1174	C1234	C1113	A1053	A994	C934	C874	A814	C754	A694	C634
U1414	G1355	C1175	U1235	C1114	G1054	C995	A935	C875	A815	G755	A695	G635
G1415	C1356	A1176	A1236	C1115	A1055	A996	C936	U876	A816	C756	A696	U636
C1416	G1357	G1177	C1237	C1116	U1056	U997	C937	C877	C817	U757	U697	G637
G1417	U1358	C1178	A1238	G1117	C1057	G998	C938	U878	G818	G758	G698	G638
A1418	C1359	A1179	A1239	C1118	G1058	C999	C939	C879	A819	A759	C699	G639
G1419	U1360	A1180	U1240	C1119	C1059	U1000	C940	C890	U820	G760	G700	A640
C1420	G1361	G1181	G1241	C1120	C1060	A1001	G941	C881	G821	G761	C701	U641
U1421	C1362	C1182	C1242	U1121	G1061	G1002	G942	C882	C822	C762	A702	A642
G1422	A1363	A1183	C1243	U1122	U1062	G1003	U943	C883	G823	G763	G703	G643
C1423	G1364	G1184	C1244	A1123	G1063	G2003	G944	U884	C824	C764	A704	G644
U1424	U1365	G1185	A1245	G1124	G1064	A1004	G945	C885	G825	G765	U705	C645
C1425	C1366	G1186	C1246	U1125	U1065	A1005	A946	C886	C826	G766	A706	U646
A1426	G1367	G1187	U1247	U1126	C1066	C1006	G947	U887	U827	A767	C707	C647
U1427	C1368	A1188	A1248	G1127	A1067	C1007	C948	U888	A828	A768	C708	A648
A1428	G1369	C1189	C1249	C1128	G1068	G1008	A949	U889	G829	G769	G709	G649
C1429	U1370	G1190	A1250	C1129	C1069	G1009	U950	C890	G830	C770	G710	G650
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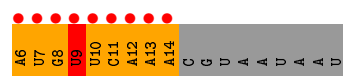
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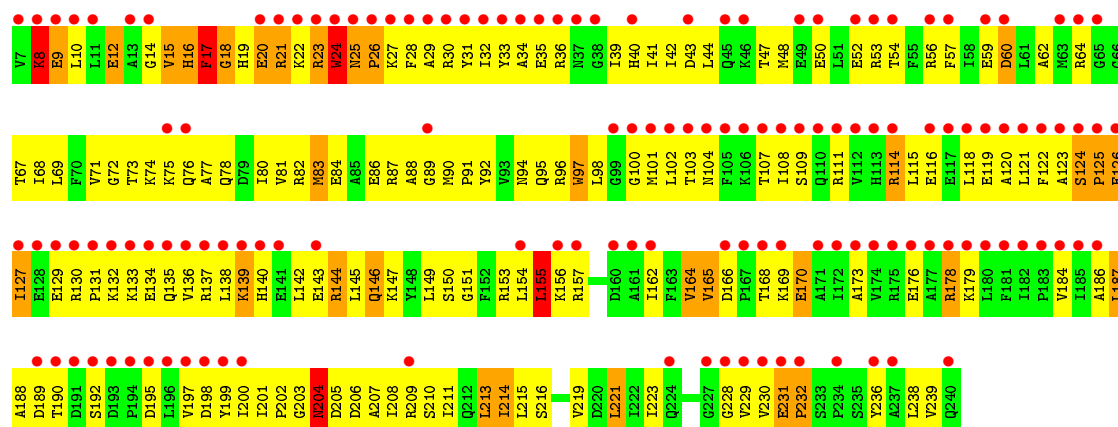
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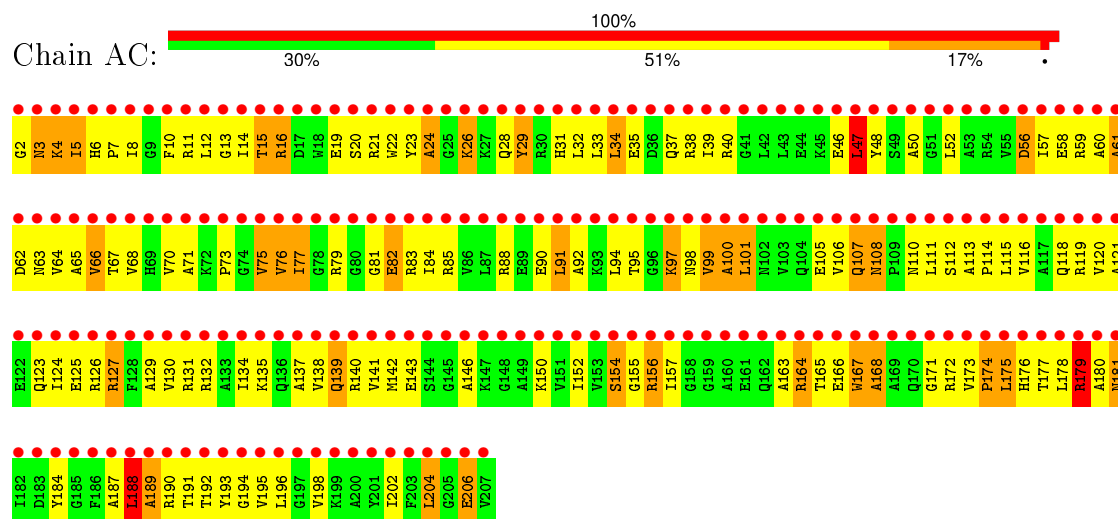
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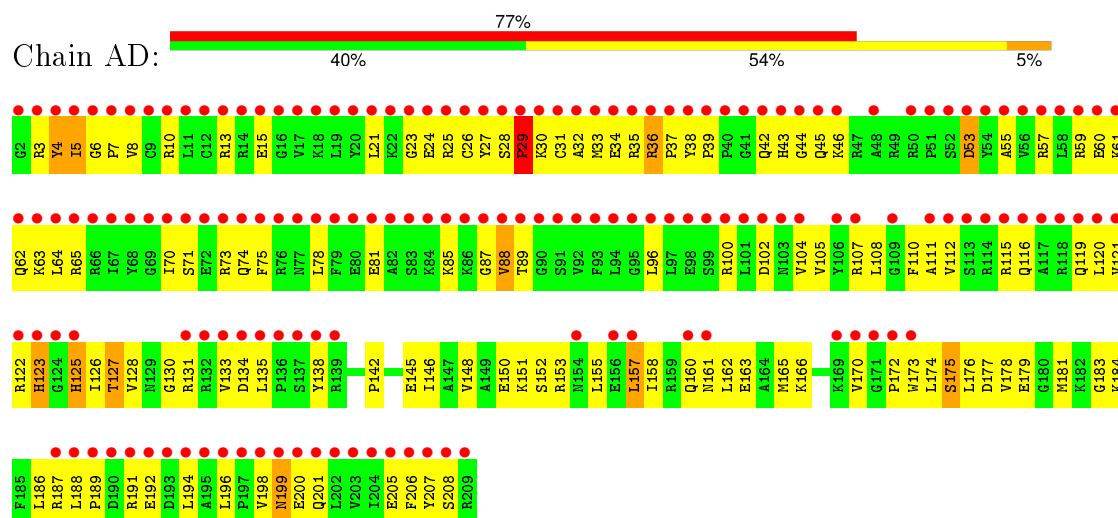
• Molecule 4: 30S ribosomal protein S2



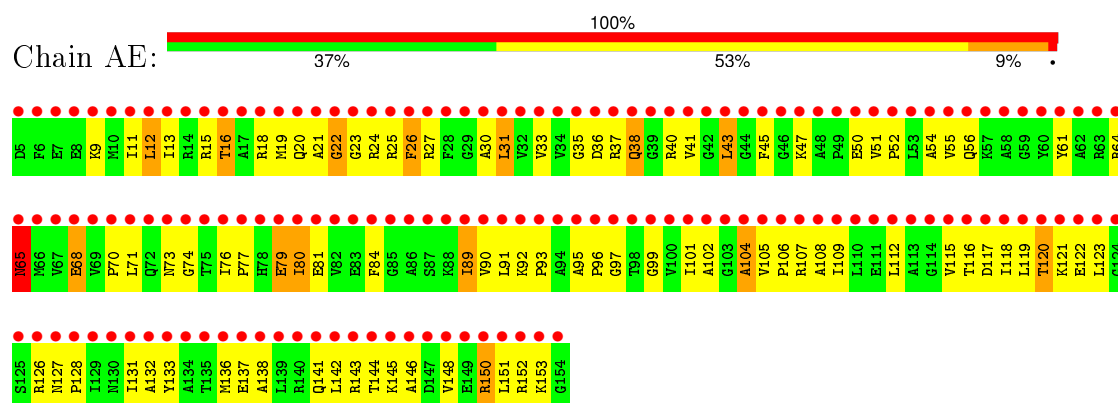
- Molecule 5: 30S ribosomal protein S3



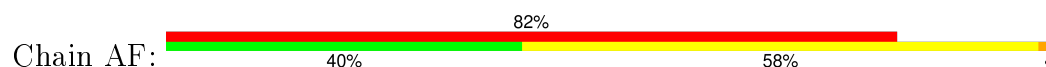
- Molecule 6: 30S ribosomal protein S4

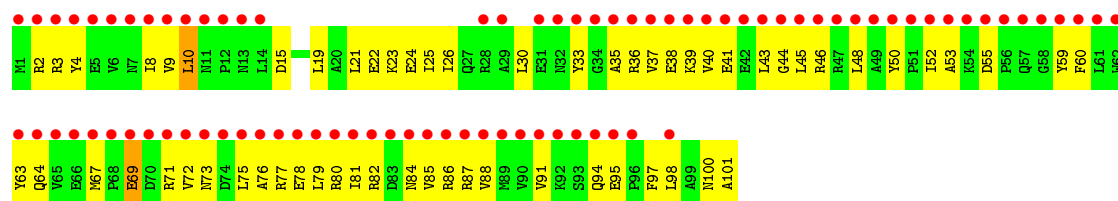


- Molecule 7: 30S ribosomal protein S5

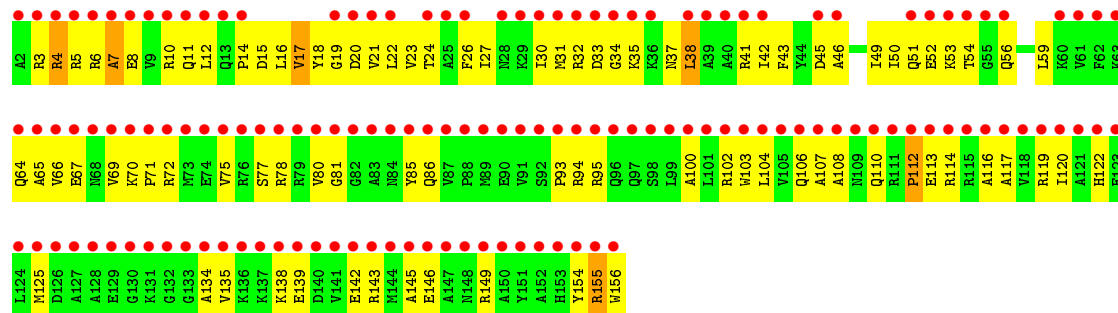
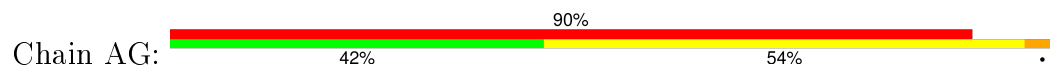


- Molecule 8: 30S ribosomal protein S6

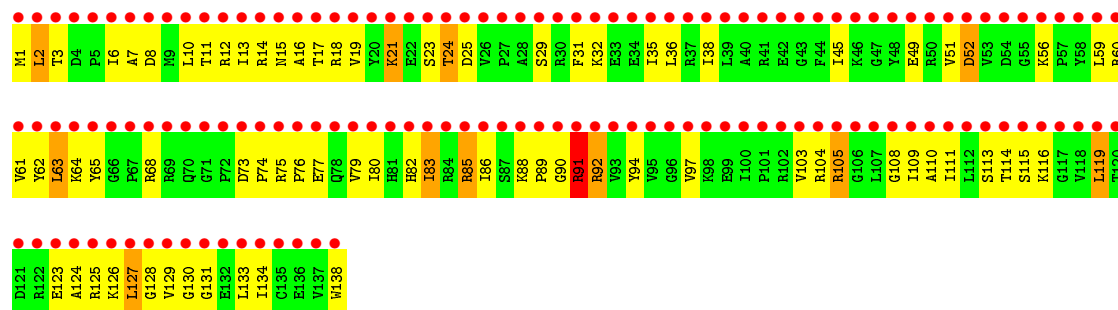
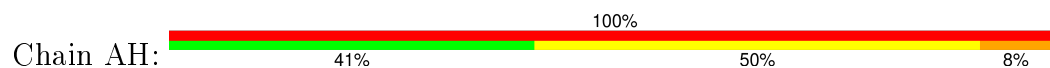




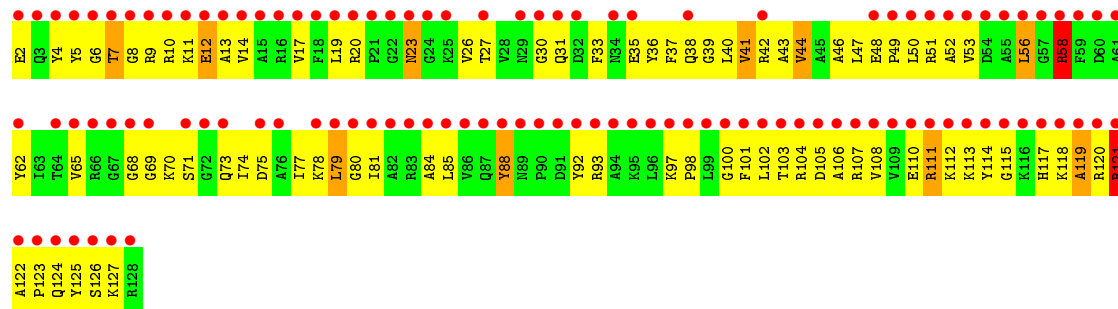
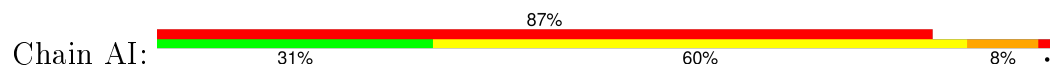
• Molecule 9: 30S ribosomal protein S7



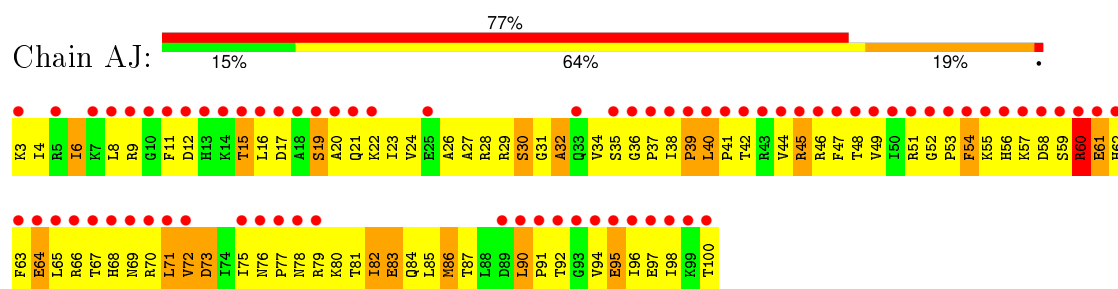
• Molecule 10: 30S ribosomal protein S8



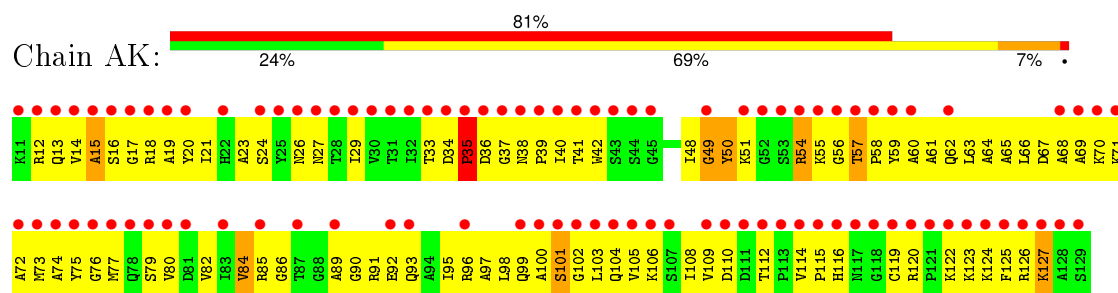
• Molecule 11: 30S ribosomal protein S9



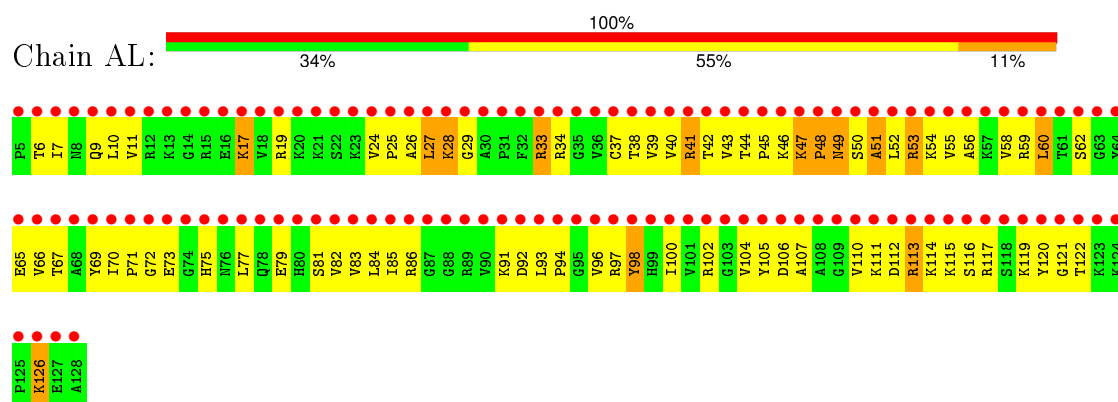
• Molecule 12: 30S ribosomal protein S10



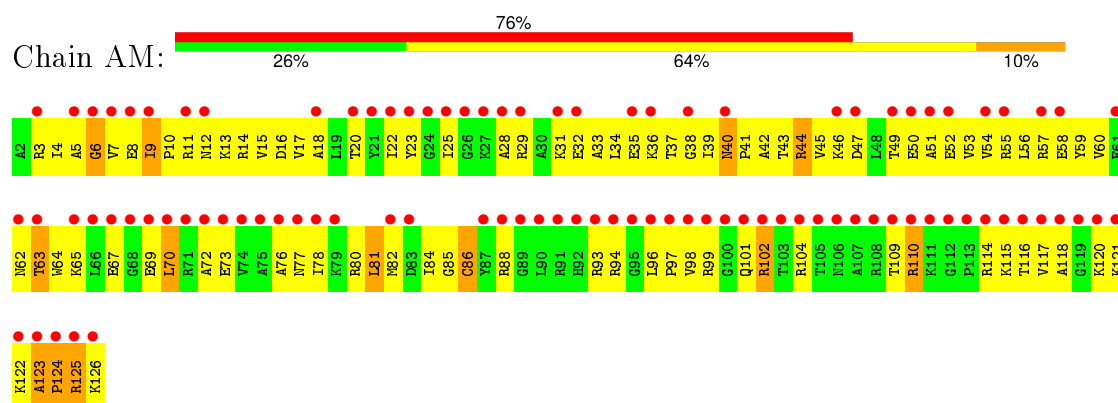
- Molecule 13: 30S ribosomal protein S11



- Molecule 14: 30S ribosomal protein S12



- Molecule 15: 30S ribosomal protein S13

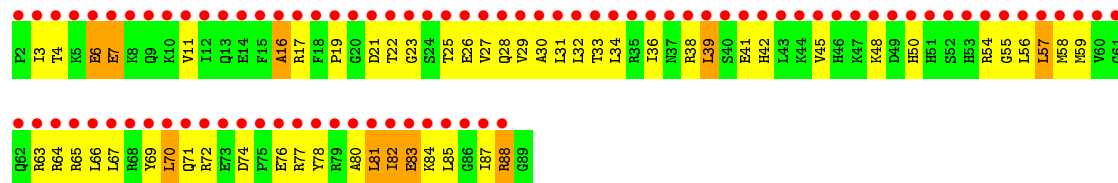


- Molecule 16: 30S ribosomal protein S14

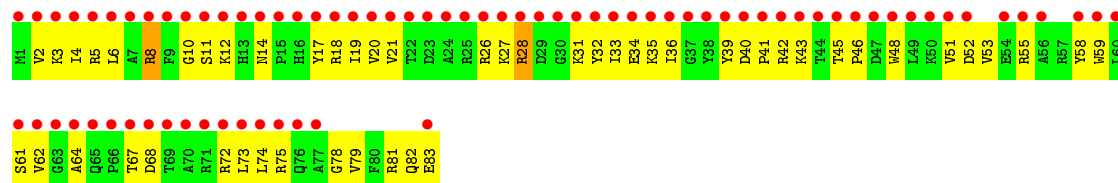




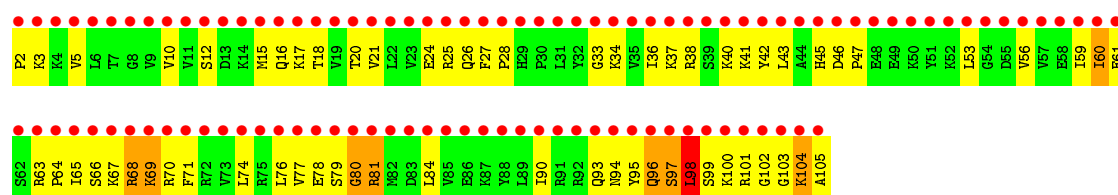
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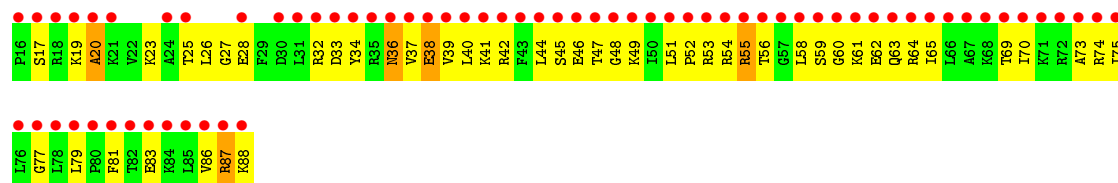
• Molecule 18: 30S ribosomal protein S16



• Molecule 19: 30S ribosomal protein S17

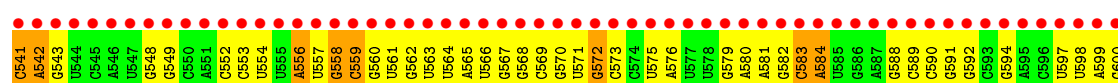


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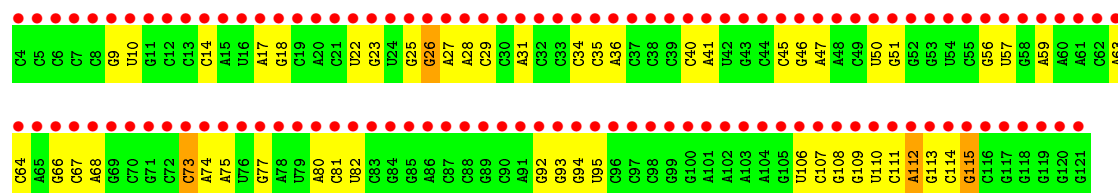
• Molecule 21: 30S ribosomal protein S19



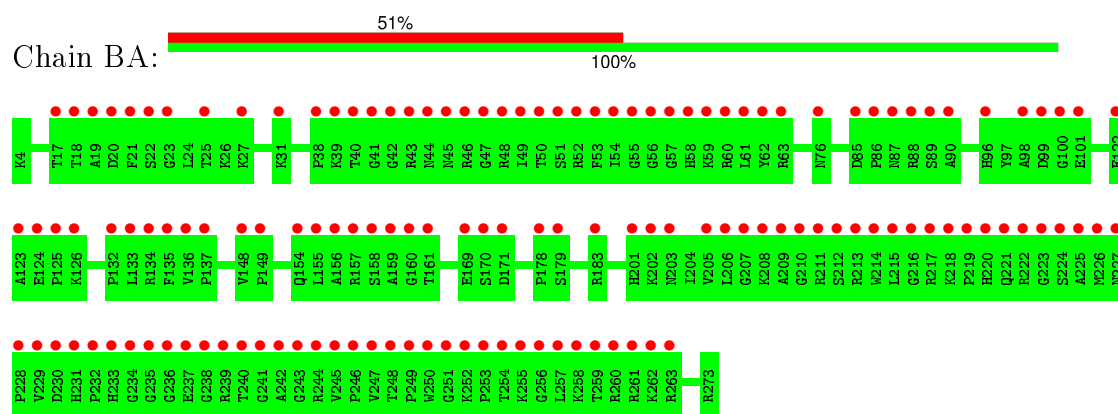


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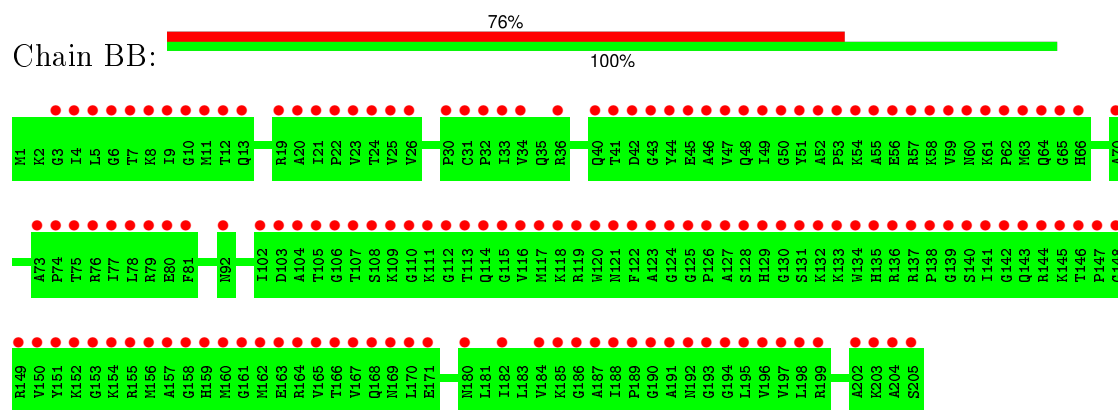
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G2250	C2190	C3147	C2068	C1948	C1888	G1837	A1777	A1657	A1597	U1537	C1477
G2251	A2191	G3148	U2069	A1949	C1889	G1838	U1778	A1658	C1598	U1538	U1478
A2252	U2192	G3149	G2070	C1950	G1890	A1839	G1779	G1659	G1599	U1539	G1479
A2253	C2193	U3150	U2071	G1951	C1891	A1840	A1780	G1660	U1600	C1540	G1480
C2254	A2194	U3151	C2072	A1952	C1892	G1841	G1781	C1661	U1601	G1541	U1481
G2255	C2195	G3152	A2073	A1953	G1893	G1842	A1782	G1662	G1602	G1542	U1482
G2256	U2196	G3153	U2074	A1954	U1894	U1843	G1783	C1663	A1603	G1543	G1483
A2257	U2197	G3154	U2075	G1955	A1895	C1844	C1784	G1664	A1604	A1544	C1484
G2258	U2198	G3155	C3093	G1956	A1896	A1845	A1785	C1665	A1605	G1545	U1485
G2259	C2199	G3156	A3094	C1957	C1897	A1846	C1726	G1666	C1606	C1546	A1486
C2260	G2200	G3157	A3095	G1958	U1898	G1847	U1787	A1667	A1607	U1547	C1487
A3158	A3158	C3157	C3096	U1959	A1899	U1848	C1788	G1668	U1608	U1548	G1488
G2262	G2202	G3159	G3097	A1960	U1900	G1849	U1789	G1669	G1609	C1549	C1489
C2263	G2203	C3160	U3098	A1961	A1901	G1850	G1790	G1670	A1610	U1550	U1490
C2264	A2204	G3161	U3099	C1962	A1902	A1851	C1791	A1671	U1611	C1551	C1491
G2265	C2205	G3162	G3100	G1963	C1903	G1852	C1792	A1672	U1612	C1552	A1492
A2266	C2206	C3163	G3101	A1964	G1904	G1853	U1793	C1673	G1613	G1553	A1493
A2267	G2207	C3164	A2025	U1965	G1905	G1854	A1794	C1674	C1614	G1554	G1494
G2268	U2208	G3165	A3103	C1966	U1906	G1855	G1795	C1675	C1615	A1555	G1495
G2269	G2209	G3166	C2027	U1967	C1907	U1856	A1796	U1676	C1616	A1556	G1496
U2270	C2210	U3167	G3104	G1968	C1908	A3865	C1797	C1677	G1617	G1557	C1497
C2271	U2211	G3168	G3105	G1969	C1909	A3866	G1798	G1678	U1618	G1558	A1498
A2272	C2212	A3169	U3106	G1970	A1910	G3867	A1799	U1679	A1619	G1559	A1499
C2273	G2213	A3170	G3108	C1971	A1911	U3868	A1800	U1680	C1620	A1560	U1500



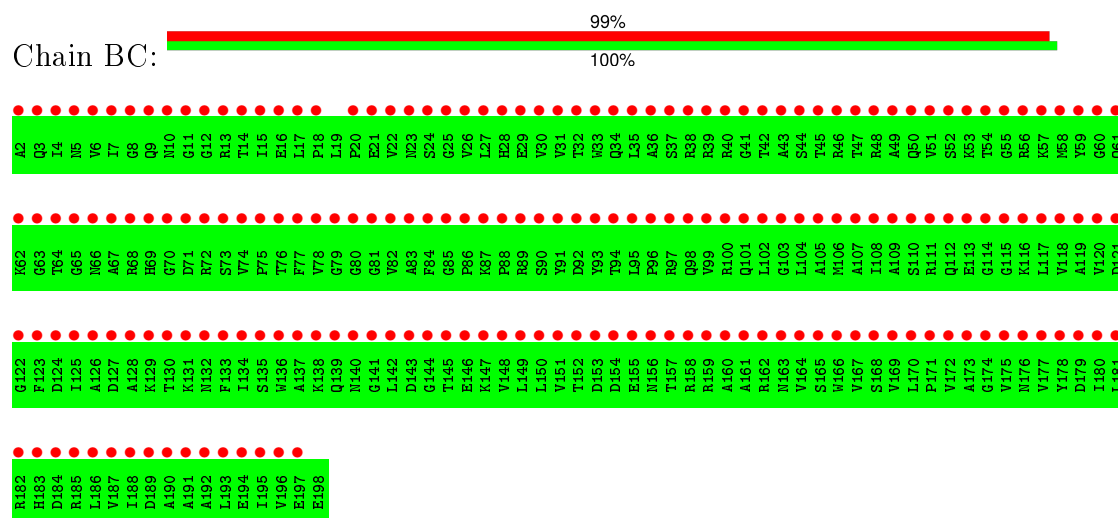
- Molecule 25: 50S ribosomal protein L2



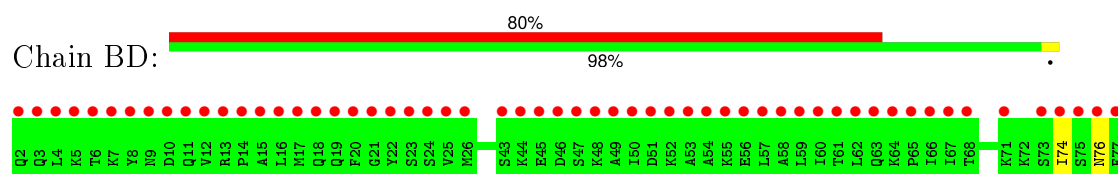
• Molecule 26: 50S ribosomal protein L3

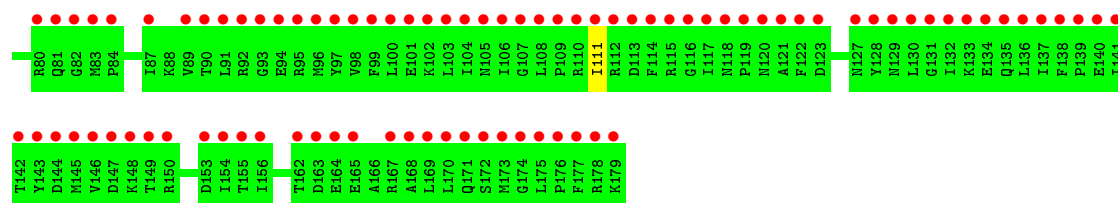


• Molecule 27: 50S ribosomal protein L4

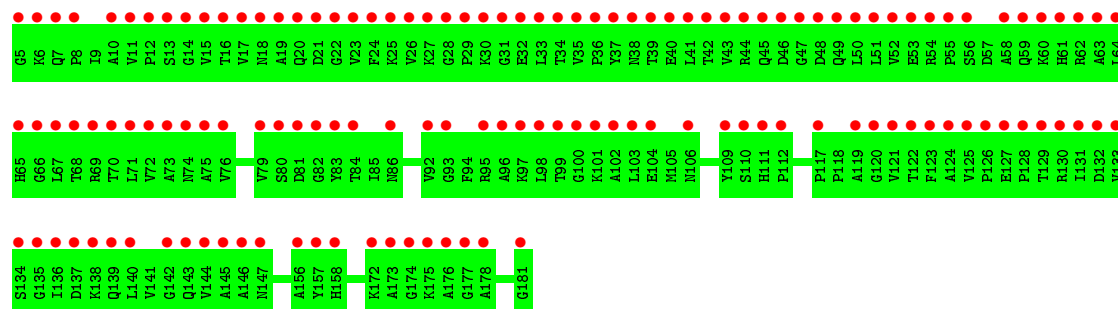
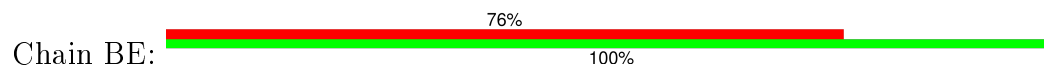


• Molecule 28: 50S ribosomal protein L5





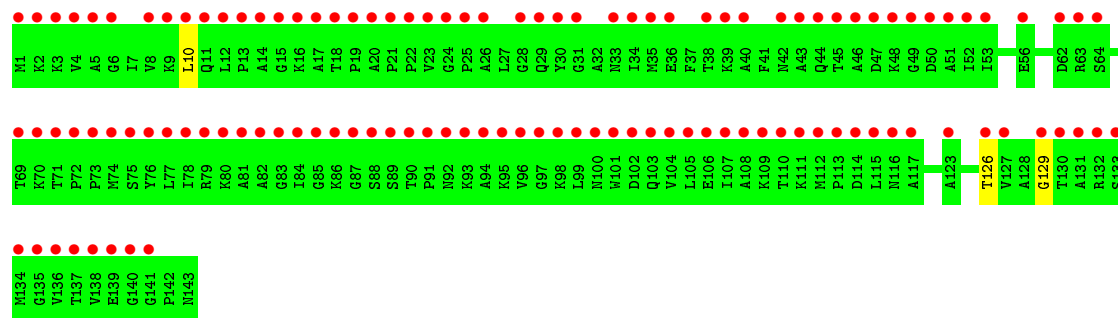
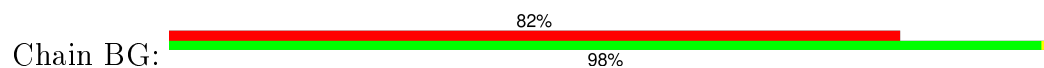
• Molecule 29: 50S ribosomal protein L6



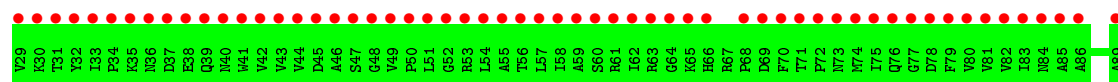
• Molecule 30: 50S ribosomal protein L9

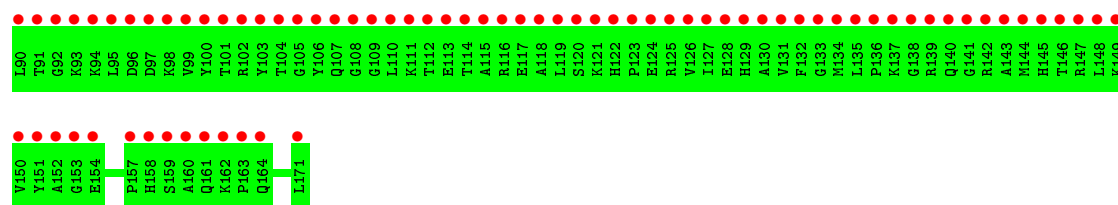


• Molecule 31: 50S ribosomal protein L11



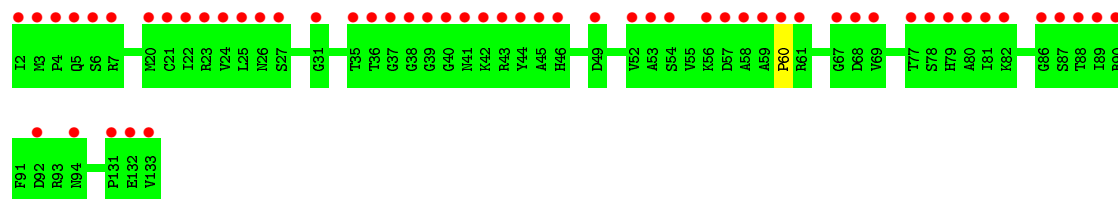
• Molecule 32: 50S ribosomal protein L13





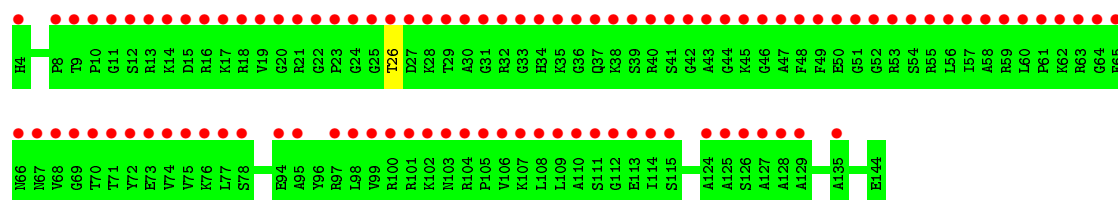
• Molecule 33: 50S ribosomal protein L14

Chain BI: 42% 99%



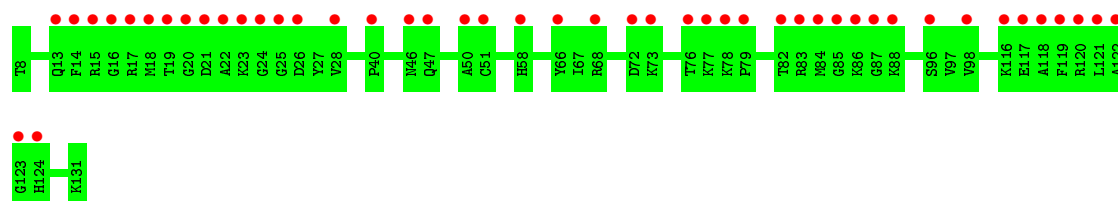
• Molecule 34: 50S ribosomal protein L15

Chain BJ: 71% 99%



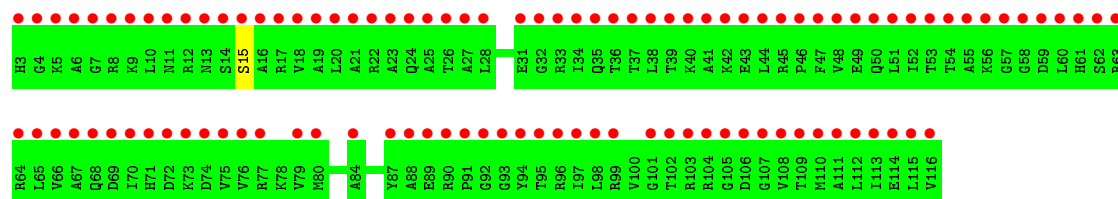
• Molecule 35: 50S ribosomal protein L16

Chain BK: 38% 100%

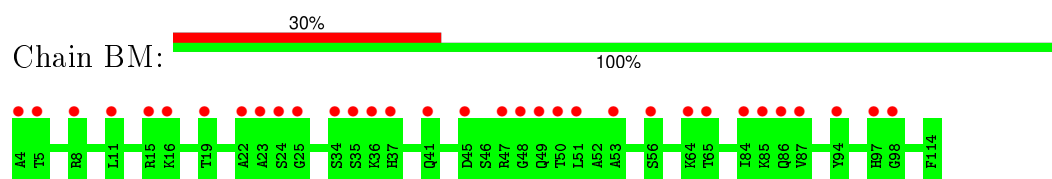


• Molecule 36: 50S ribosomal protein L17

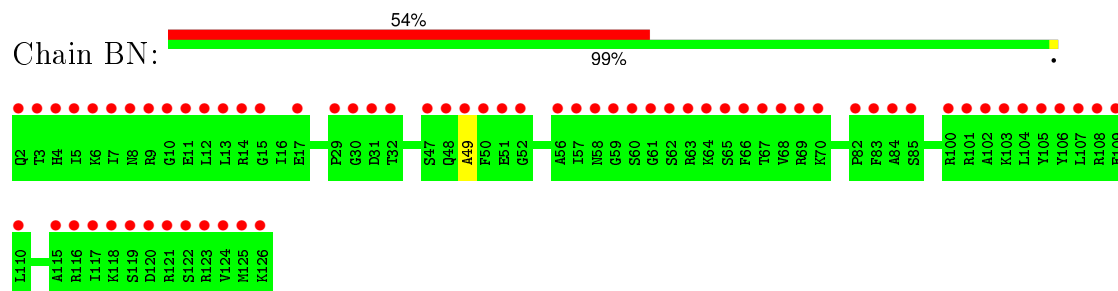
Chain BL: 92% 99%



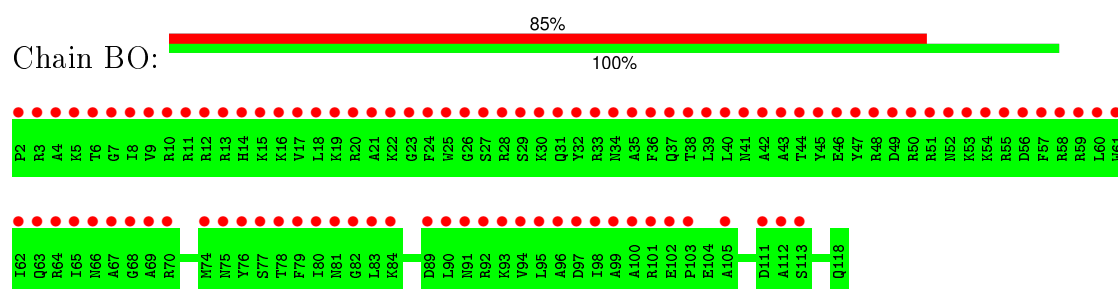
• Molecule 37: 50S ribosomal protein L18



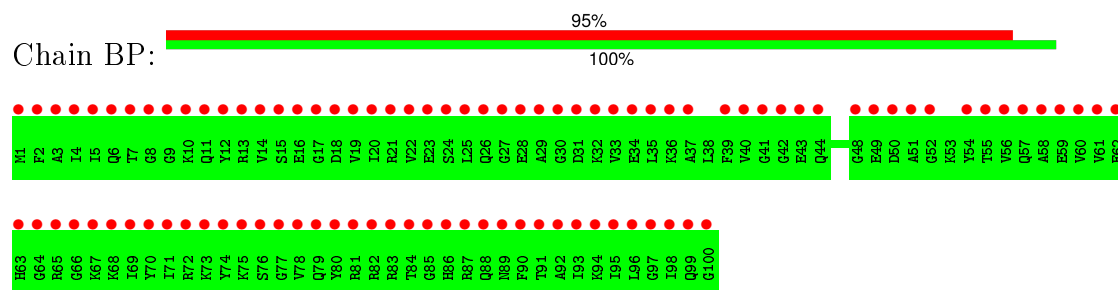
- Molecule 38: 50S ribosomal protein L19



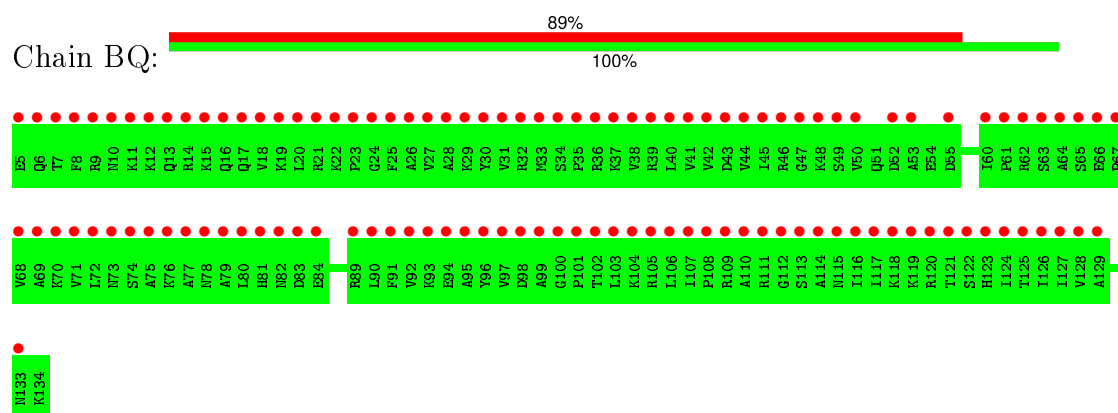
- Molecule 39: 50S ribosomal protein L20



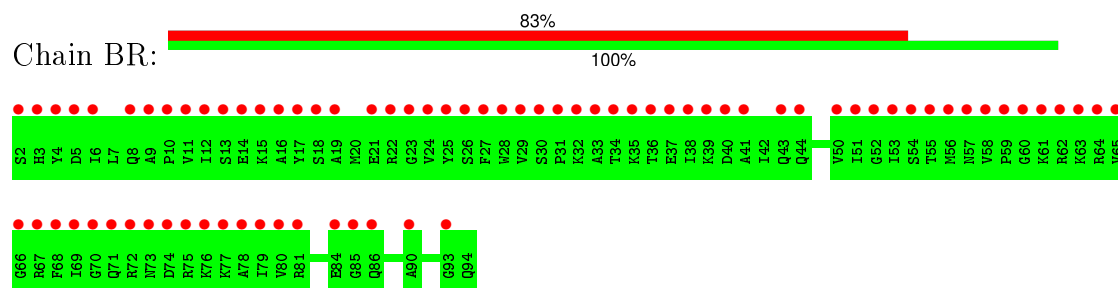
- Molecule 40: 50S ribosomal protein L21



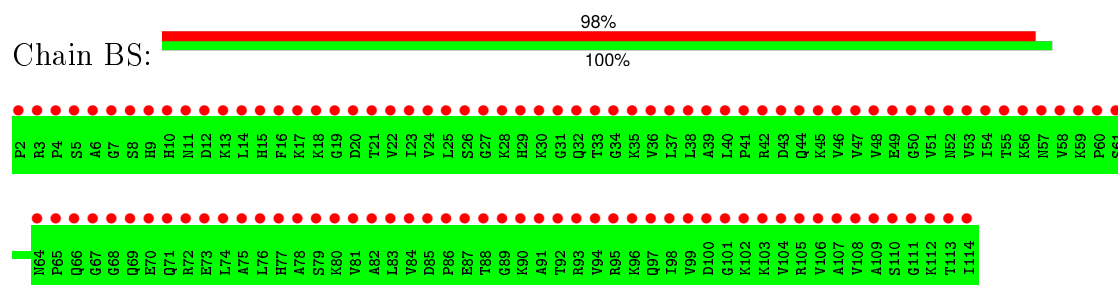
- Molecule 41: 50S ribosomal protein L22



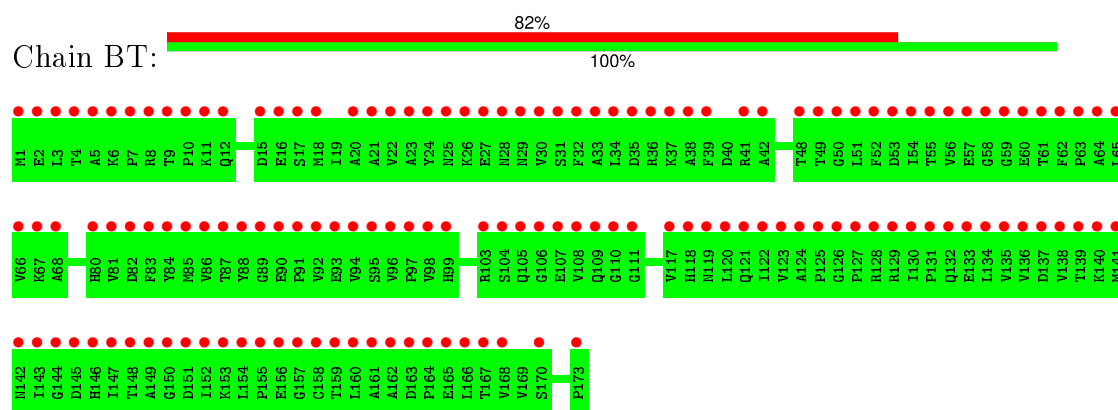
- Molecule 42: 50S ribosomal protein L23



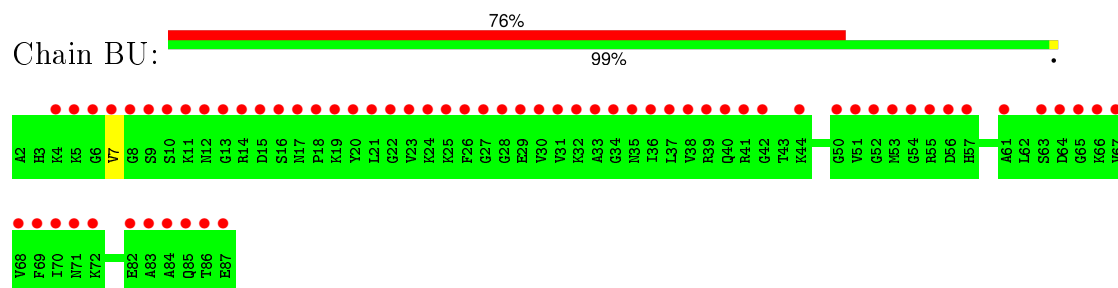
- Molecule 43: 50S ribosomal protein L24



- Molecule 44: general stress protein Ctc



- Molecule 45: 50S ribosomal protein L27

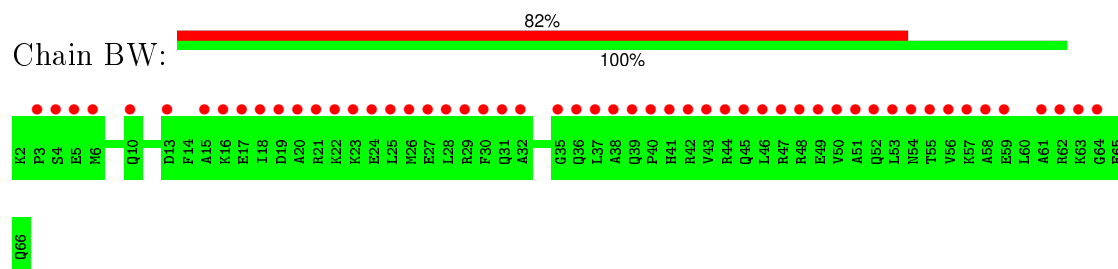


- Molecule 46: 50S RIBOSOMAL PROTEIN L28

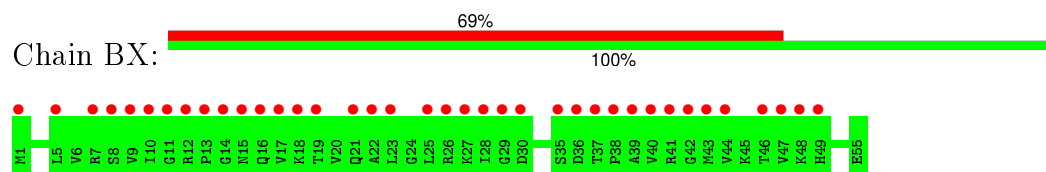


There are no outlier residues recorded for this chain.

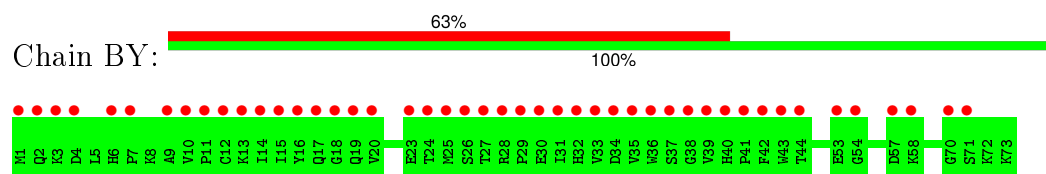
- Molecule 47: 50S ribosomal protein L29



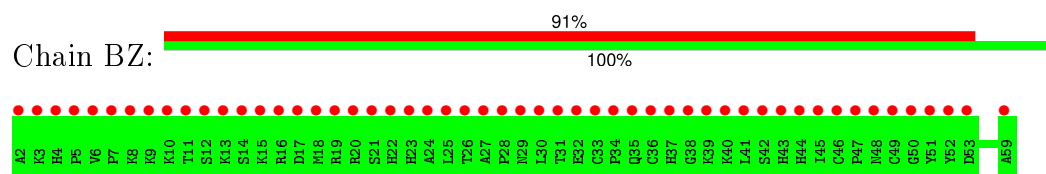
- Molecule 48: 50S ribosomal protein L30



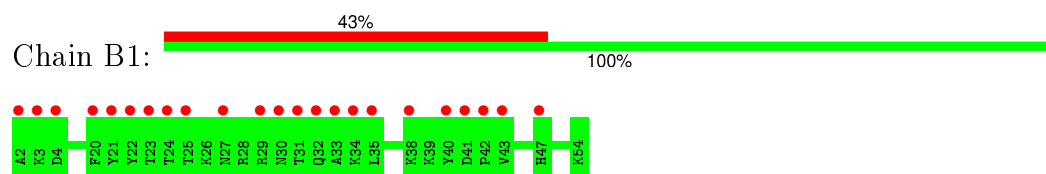
- Molecule 49: 50S ribosomal protein L31



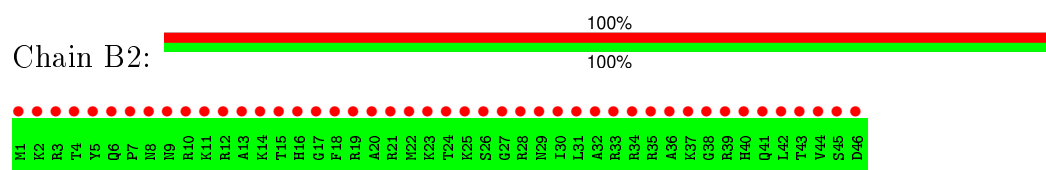
- Molecule 50: 50S ribosomal protein L32



- Molecule 51: 50S ribosomal protein L33

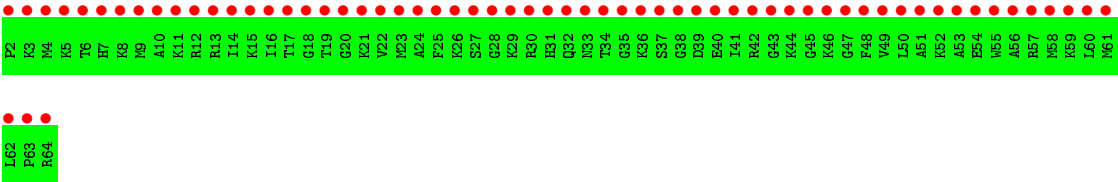


- Molecule 52: 50S ribosomal protein L34

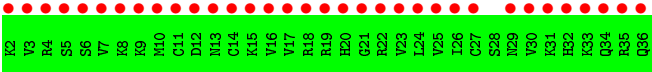


- Molecule 53: 50S ribosomal protein L35

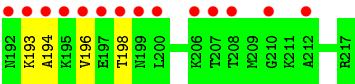
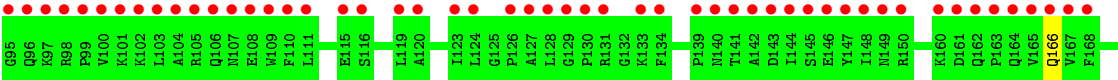
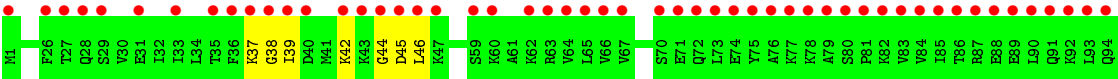




● Molecule 54: 50S ribosomal protein L36



● 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 – 8.70 241.24 – 8.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (70.00-8.70) 93.0 (241.24-8.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 8.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.394 , 0.415 0.382 , 0.419	Depositor DCC
R_{free} test set	1786 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	443.4	Xtriage
Anisotropy	0.381	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.30 , -10.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 37559 reflections	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	122017	wwPDB-VP
Average B, all atoms (Å ²)	641.0	wwPDB-VP

Xtriage'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, 0.375 respectively for untwinned datasets, and 0.333, 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	1.53	69/36688 (0.2%)	1.32	264/57135 (0.5%)
2	AV	2.23	23/1817 (1.3%)	1.84	42/2831 (1.5%)
2	AW	1.75	19/1816 (1.0%)	1.94	32/2827 (1.1%)
3	AU	45.18	35/188 (18.6%)	20.47	49/274 (17.9%)
4	AB	0.37	0/1935	0.68	1/2609 (0.0%)
5	AC	0.38	0/1636	0.66	0/2205
6	AD	0.37	0/1732	0.63	0/2318
7	AE	0.48	0/1162	0.79	0/1564
8	AF	0.34	0/855	0.63	0/1154
9	AG	0.35	0/1275	0.62	0/1709
10	AH	0.44	0/1135	0.74	0/1527
11	AI	0.36	0/1028	0.62	0/1378
12	AJ	0.36	0/807	0.71	0/1085
13	AK	0.39	0/899	0.70	0/1213
14	AL	0.70	1/986 (0.1%)	0.76	1/1320 (0.1%)
15	AM	0.44	1/1007 (0.1%)	1.11	3/1347 (0.2%)
16	AN	0.40	0/500	0.78	0/664
17	AO	0.36	0/744	0.63	1/992 (0.1%)
18	AP	0.43	0/716	0.76	0/963
19	AQ	0.44	0/869	0.75	0/1159
20	AR	0.36	0/602	0.63	0/799
21	AS	0.35	0/661	0.72	1/890 (0.1%)
22	AT	0.39	0/764	0.73	0/1006
23	B0	0.49	17/67885 (0.0%)	0.75	49/105852 (0.0%)
24	B9	0.68	1/2815 (0.0%)	0.76	3/4384 (0.1%)
All	All	1.97	166/130522 (0.1%)	1.25	446/199205 (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.

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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 166 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AU	14	A	C6-N6	279.73	3.57	1.33
3	AU	13	A	C6-N6	279.69	3.57	1.33
3	AU	6	A	C6-N6	279.55	3.57	1.33
3	AU	12	A	C6-N6	279.29	3.57	1.33
3	AU	8	G	C6-O6	259.50	3.57	1.24

The worst 5 of 446 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AU	8	G	C5-C6-O6	-177.72	21.96	128.60
3	AU	6	A	C5-C6-N6	-127.11	22.02	123.70
3	AU	14	A	C5-C6-N6	-127.08	22.03	123.70
3	AU	12	A	C5-C6-N6	-127.07	22.05	123.70
3	AU	13	A	C5-C6-N6	-127.04	22.07	123.70

All (2) chirality outliers are listed below:

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

5 of 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	3629	5
2	AV	1625	0	821	141	0
2	AW	1625	0	819	141	0
3	AU	176	0	79	11	0
4	AB	1900	0	1951	231	0
5	AC	1612	0	1676	292	0
6	AD	1702	0	1767	227	4
7	AE	1146	0	1207	233	0
8	AF	842	0	857	81	4
9	AG	1256	0	1294	119	0
10	AH	1115	0	1177	122	0
11	AI	1010	0	1043	172	0
12	AJ	794	0	838	216	0
13	AK	884	0	903	187	0
14	AL	970	0	1055	157	0
15	AM	996	0	1071	145	0
16	AN	491	0	531	160	0
17	AO	733	0	771	55	0
18	AP	700	0	720	96	0
19	AQ	856	0	926	355	0
20	AR	596	0	667	83	0
21	AS	647	0	673	129	0
22	AT	762	0	848	259	0
23	B0	60636	0	30552	1930	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	7	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	36	0
All	All	122017	0	70110	7429	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 7429 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
6:AD:172:PRO:O	8:AF:15:ASP:CA[3_555]	1.87	0.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:416:G:O2'	23:B0:3153:G:O2'[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%)	1	12
5	AC	204/206 (99%)	135 (66%)	40 (20%)	29 (14%)	0	6
6	AD	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	3	33
7	AE	148/150 (99%)	130 (88%)	13 (9%)	5 (3%)	5	40
8	AF	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	19	65
9	AG	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	25
10	AH	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	6	43
11	AI	125/127 (98%)	89 (71%)	26 (21%)	10 (8%)	1	19
12	AJ	96/98 (98%)	59 (62%)	20 (21%)	17 (18%)	0	4
13	AK	117/119 (98%)	88 (75%)	20 (17%)	9 (8%)	1	20
14	AL	122/124 (98%)	98 (80%)	15 (12%)	9 (7%)	1	21
15	AM	123/125 (98%)	88 (72%)	27 (22%)	8 (6%)	1	25
16	AN	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	8
17	AO	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	2	27
18	AP	81/83 (98%)	65 (80%)	15 (18%)	1 (1%)	16	61
19	AQ	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	20
20	AR	71/73 (97%)	62 (87%)	7 (10%)	2 (3%)	6	44
21	AS	78/80 (98%)	48 (62%)	19 (24%)	11 (14%)	0	6
22	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2334/2372 (98%)	1792 (77%)	361 (16%)	181 (8%)	1	20

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 ⓘ

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%)	180 (89%)	22 (11%)	8	35
5	AC	160/160 (100%)	142 (89%)	18 (11%)	7	33
6	AD	180/180 (100%)	172 (96%)	8 (4%)	35	69
7	AE	115/115 (100%)	100 (87%)	15 (13%)	5	28
8	AF	90/90 (100%)	88 (98%)	2 (2%)	60	83
9	AG	126/126 (100%)	122 (97%)	4 (3%)	46	76
10	AH	119/119 (100%)	109 (92%)	10 (8%)	14	48
11	AI	98/98 (100%)	90 (92%)	8 (8%)	14	49
12	AJ	88/88 (100%)	79 (90%)	9 (10%)	9	37
13	AK	90/90 (100%)	84 (93%)	6 (7%)	20	57
14	AL	104/104 (100%)	96 (92%)	8 (8%)	16	52
15	AM	100/100 (100%)	90 (90%)	10 (10%)	9	38
16	AN	49/49 (100%)	47 (96%)	2 (4%)	37	71
17	AO	79/79 (100%)	72 (91%)	7 (9%)	12	44
18	AP	72/72 (100%)	67 (93%)	5 (7%)	19	56
19	AQ	96/96 (100%)	90 (94%)	6 (6%)	22	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	AR	64/64 (100%)	61 (95%)	3 (5%)	32	68
21	AS	71/71 (100%)	68 (96%)	3 (4%)	36	70
22	AT	76/76 (100%)	69 (91%)	7 (9%)	11	43
All	All	1979/1979 (100%)	1826 (92%)	153 (8%)	16	52

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

Mol	Chain	Res	Type
10	AH	2	LEU
11	AI	111	ARG
20	AR	38	GLU
10	AH	52	ASP
10	AH	105	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
8	AF	73	ASN
11	AI	23	ASN
21	AS	14	HIS
9	AG	37	ASN
12	AJ	62	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1479/1527 (96%)	217 (14%)	92 (6%)
2	AV	75/76 (98%)	13 (17%)	3 (4%)
2	AW	74/76 (97%)	13 (17%)	3 (4%)
23	B0	2802/2887 (97%)	430 (15%)	56 (1%)
24	B9	116/118 (98%)	10 (8%)	0
3	AU	8/18 (44%)	1 (12%)	0
All	All	4554/4702 (96%)	684 (15%)	154 (3%)

5 of 684 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 154 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	1201	A
1	AA	1451	A
23	B0	3149	G
1	AA	1226	C
1	AA	1302	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	84
23	B0	25
24	B9	2
2	AV	2

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Mol	Chain	Number of breaks
2	AW	1
3	AU	1
14	AL	1

The worst 5 of 116 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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%)	34.56	1527 (100%) 0 0	341, 531, 705, 847	0
2	AV	76/76 (100%)	30.99	76 (100%) 0 0	379, 379, 379, 379	0
2	AW	76/76 (100%)	17.01	76 (100%) 0 0	510, 510, 510, 510	76 (100%)
3	AU	9/18 (50%)	30.40	9 (100%) 0 0	379, 379, 379, 379	0
4	AB	234/234 (100%)	3.18	138 (58%) 0 3	496, 496, 496, 496	0
5	AC	206/206 (100%)	11.67	206 (100%) 0 0	264, 264, 264, 264	0
6	AD	208/208 (100%)	11.26	161 (77%) 0 2	479, 479, 479, 479	0
7	AE	150/150 (100%)	21.21	150 (100%) 0 0	669, 669, 669, 669	0
8	AF	101/101 (100%)	5.28	83 (82%) 0 2	640, 640, 640, 640	0
9	AG	155/155 (100%)	6.52	139 (89%) 0 2	406, 406, 406, 406	0
10	AH	138/138 (100%)	30.08	138 (100%) 0 0	647, 647, 647, 647	0
11	AI	127/127 (100%)	9.92	110 (86%) 0 2	426, 426, 426, 426	0
12	AJ	98/98 (100%)	7.85	75 (76%) 0 2	507, 507, 507, 507	0
13	AK	119/119 (100%)	3.89	96 (80%) 0 2	510, 510, 510, 510	0
14	AL	124/124 (100%)	10.79	124 (100%) 0 0	367, 367, 384, 384	0
15	AM	125/125 (100%)	6.50	95 (76%) 0 2	349, 454, 454, 454	0
16	AN	60/60 (100%)	10.65	60 (100%) 0 0	264, 264, 264, 264	0
17	AO	88/88 (100%)	26.33	87 (98%) 0 0	572, 572, 572, 572	0
18	AP	83/83 (100%)	6.70	76 (91%) 0 1	662, 662, 662, 662	0
19	AQ	104/104 (100%)	13.14	104 (100%) 0 0	670, 670, 670, 670	0
20	AR	73/73 (100%)	6.16	68 (93%) 0 1	640, 640, 640, 640	0
21	AS	80/80 (100%)	1.83	24 (30%) 1 5	545, 545, 545, 545	0
22	AT	99/99 (100%)	9.92	91 (91%) 0 1	744, 744, 744, 744	0
23	B0	2825/2887 (97%)	53.21	2821 (99%) 0 0	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%)	44.21	118 (100%) 0 0	772, 938, 938, 938	0
25	BA	270/270 (100%)	4.38	137 (50%) 0 4	737, 737, 737, 737	0
26	BB	205/205 (100%)	7.71	155 (75%) 0 2	737, 737, 737, 737	0
27	BC	197/197 (100%)	7.48	195 (98%) 0 0	737, 737, 737, 737	0
28	BD	178/178 (100%)	11.40	143 (80%) 0 2	938, 938, 938, 938	0
29	BE	177/177 (100%)	9.26	134 (75%) 0 2	737, 737, 737, 737	0
30	BF	52/52 (100%)	2.67	17 (32%) 1 5	737, 737, 737, 737	0
31	BG	143/143 (100%)	16.75	117 (81%) 0 2	907, 907, 907, 907	0
32	BH	143/143 (100%)	4.48	132 (92%) 0 1	737, 737, 737, 737	0
33	BI	132/132 (100%)	2.78	56 (42%) 0 4	737, 737, 737, 737	0
34	BJ	141/141 (100%)	11.00	100 (70%) 0 3	737, 737, 737, 737	0
35	BK	124/124 (100%)	2.46	47 (37%) 0 4	737, 737, 737, 737	0
36	BL	114/114 (100%)	5.91	105 (92%) 0 1	737, 737, 737, 737	0
37	BM	111/111 (100%)	1.65	33 (29%) 1 5	938, 938, 938, 938	0
38	BN	125/125 (100%)	3.10	67 (53%) 0 4	737, 737, 737, 737	0
39	BO	117/117 (100%)	12.91	99 (84%) 0 2	737, 737, 737, 737	0
40	BP	100/100 (100%)	7.18	95 (95%) 0 1	737, 737, 737, 737	0
41	BQ	130/130 (100%)	10.32	116 (89%) 0 2	737, 737, 737, 737	0
42	BR	93/93 (100%)	6.73	77 (82%) 0 2	737, 737, 737, 737	0
43	BS	113/113 (100%)	8.05	111 (98%) 0 0	737, 737, 737, 737	0
44	BT	173/173 (100%)	12.96	142 (82%) 0 2	737, 772, 772, 772	0
45	BU	86/86 (100%)	6.13	65 (75%) 0 2	737, 737, 737, 737	0
46	BV	0/16	-	-	-	-
47	BW	65/65 (100%)	4.98	53 (81%) 0 2	737, 737, 737, 737	0
48	BX	55/55 (100%)	6.92	38 (69%) 0 3	737, 737, 737, 737	0
49	BY	73/73 (100%)	4.79	46 (63%) 0 3	737, 737, 737, 737	0
50	BZ	58/58 (100%)	12.40	53 (91%) 0 1	737, 737, 737, 737	0
51	B1	53/53 (100%)	2.37	23 (43%) 0 4	737, 737, 737, 737	0
52	B2	46/46 (100%)	11.20	46 (100%) 0 0	737, 737, 737, 737	0
53	B3	63/63 (100%)	5.54	63 (100%) 0 0	737, 737, 737, 737	0
54	B4	35/35 (100%)	4.38	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%)	8.63	118 (55%) 0 3	940, 940, 940, 940	0
All	All	10588/10679 (99%)	25.02	9269 (87%) 0 2	264, 737, 938, 940	76 (0%)

The worst 5 of 9269 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
23	B0	398	C	195.8
23	B0	399	G	180.2
23	B0	2031	A	170.5
23	B0	2523	G	167.1
23	B0	755	C	166.7

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 carbohydrates 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.