



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 01:29 PM UTC

PDB ID : 4V9I / pdb_00004v9i
Title : Crystal structure of thermus thermophilus 70S in complex with tRNAs and mRNA containing a pseudouridine in a stop codon
Authors : Fernandez, I.S.; Ng, C.L.; Kelley, A.C.; Guowei, W.; Yu, Y.T.; Ramakrishnan, V.
Deposited on : 2013-04-04
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

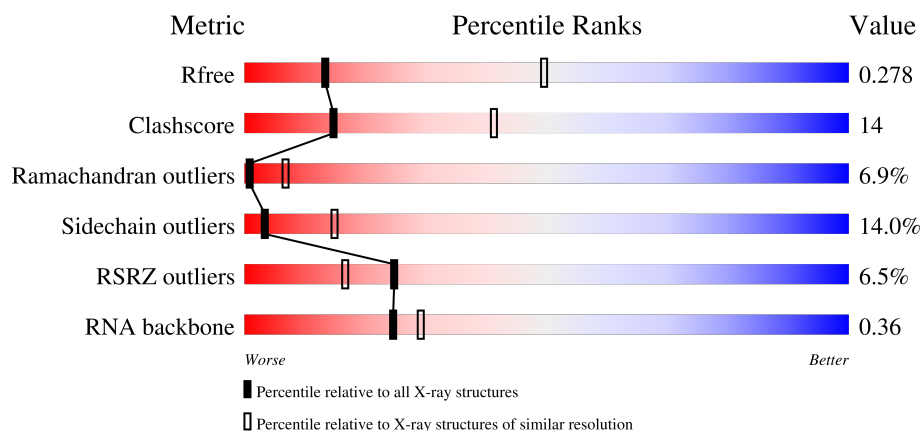
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)
RNA backbone	3983	1048 (3.60-3.00)

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	1504	3% 48% 39% 12% •
1	CA	1504	5% 50% 39% 10% •
2	AB	234	6% 61% 34% 5%
2	CB	234	14% 64% 32% 5%

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Mol	Chain	Length	Quality of chain
3	AC	206	
3	CC	206	
4	AD	208	
4	CD	208	
5	AE	150	
5	CE	150	
6	AF	101	
6	CF	101	
7	AG	155	
7	CG	155	
8	AH	138	
8	CH	138	
9	AI	127	
9	CI	127	
10	AJ	98	
10	CJ	98	
11	AK	119	
11	CK	119	
12	AL	124	
12	CL	124	
13	AM	124	
13	CM	124	
14	AN	60	
14	CN	60	
15	AO	88	

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Mol	Chain	Length	Quality of chain
15	CO	88	
16	AP	83	
16	CP	83	
17	AQ	99	
17	CQ	99	
18	AR	70	
18	CR	70	
19	AS	78	
19	CS	78	
20	AT	99	
20	CT	99	
21	AU	24	
21	CU	24	
22	AV	77	
22	CV	77	
23	AW	76	
23	CW	76	
24	AY	75	
24	CY	75	
25	AX	7	
26	BA	2915	
26	DA	2915	
27	BB	119	
27	DB	119	
28	BC	206	

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Mol	Chain	Length	Quality of chain
29	BD	271	
29	DD	271	
30	BE	204	
30	DE	204	
31	BF	207	
31	DF	207	
32	BG	181	
32	DG	181	
33	BH	159	
33	DH	159	
34	BI	145	
34	DI	145	
35	BJ	130	
35	DJ	130	
36	BN	138	
36	DN	138	
37	BO	122	
37	DO	122	
38	BP	146	
38	DP	146	
39	BQ	141	
39	DQ	141	
40	BR	117	
40	DR	117	
41	BS	98	

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Mol	Chain	Length	Quality of chain
41	DS	98	
42	BT	137	
42	DT	137	
43	BU	117	
43	DU	117	
44	BV	101	
44	DV	101	
45	BW	113	
45	DW	113	
46	BX	92	
46	DX	92	
47	BY	100	
47	DY	100	
48	BZ	176	
48	DZ	176	
49	B0	84	
49	D0	84	
50	B1	93	
50	D1	93	
51	B2	71	
51	D2	71	
52	B3	59	
52	D3	59	
53	B4	30	
53	D4	30	

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Mol	Chain	Length	Quality of chain
54	B5	59	
54	D5	59	
55	B6	44	
55	D6	44	
56	B7	48	
56	D7	48	
57	B8	63	
57	D8	63	
58	B9	36	
58	D9	36	
59	CX	4	
60	DC	196	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	PSU	AX	19	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 295724 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	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			
1	CA	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	CB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	CE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	CF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	CH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			1011	639	198	174			
9	CI	127	Total	C	N	O	0	0	0
			1011	639	198	174			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	58	ARG	HIS	conflict	UNP P80374
CI	58	ARG	HIS	conflict	UNP P80374

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			
10	CJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	CK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			
12	CL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			
13	CM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	CN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	CO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	CP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	70	Total	C	N	O	0	0	0
			574	367	112	95			
18	CR	70	Total	C	N	O	0	0	0
			574	367	112	95			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			
19	CS	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	CT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called 30S Ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	24	Total	C	N	O	0	0	0
			209	128	50	31			
21	CU	24	Total	C	N	O	0	0	0
			209	128	50	31			

- Molecule 22 is a RNA chain called P-SITE tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			
22	CV	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			

- Molecule 23 is a RNA chain called E-SITE tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AW	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
23	CW	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			

- Molecule 24 is a RNA chain called A-SITE tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AY	75	Total	C	N	O	P	0	0	0
			1619	722	309	514	74			
24	CY	75	Total	C	N	O	P	0	0	0
			1619	722	309	514	74			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AY	?	-	C	deletion	GB 443419838
CY	?	-	C	deletion	GB 443419838

- Molecule 25 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	AX	7	Total	C	N	O	P	0	0	0
			151	68	29	47	7			

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BA	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			
26	DA	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	1151	A	G	conflict	GB 55771382
DA	1151	A	G	conflict	GB 55771382

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BB	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			
27	DB	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 28 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BC	190	Total	C	N	O		0	0	0
			1157	706	220	231				

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BD	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			
29	DD	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BE	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			
30	DE	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			

- Molecule 31 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BF	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			
31	DF	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			

- Molecule 32 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
32	DG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BH	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			
33	DH	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			

- Molecule 34 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BI	145	Total	C	N	O	S	0	0	0
			1132	723	200	208	1			
34	DI	145	Total	C	N	O	S	0	0	0
			1132	723	200	208	1			

- Molecule 35 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BJ	130	Total	C	N	O		0	0	0
			651	390	130	131				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
35	DJ	130	Total	C	N	O	0	0	0
			651	390	130	131			

- Molecule 36 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BN	138	Total 1105	C 712	N 206	O 183	S 4	0	0	0
36	DN	138	Total 1105	C 712	N 206	O 183	S 4	0	0	0

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
37	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BP	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			
38	DP	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 39 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BQ	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0
39	DQ	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	BR	117	Total	C	N	O	0	0	0
			960	599	202	159			
40	DR	117	Total	C	N	O	0	0	0
			960	599	202	159			

- Molecule 41 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	BS	98	Total	C	N	O	0	0	0
			771	486	154	131			
41	DS	98	Total	C	N	O	0	0	0
			771	486	154	131			

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BT	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			
42	DT	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			

- Molecule 43 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			
43	DU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	32	ALA	PHE	conflict	UNP P60491
DU	32	ALA	PHE	conflict	UNP P60491

- Molecule 44 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
44	DV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 45 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	DW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	113	ALA	LYS	conflict	UNP Q5SHP3
DW	113	ALA	LYS	conflict	UNP Q5SHP3

- Molecule 46 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BX	92	Total	C	N	O		0	0	0
			726	471	131	124				
46	DX	92	Total	C	N	O		0	0	0
			726	471	131	124				

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BY	100	Total	C	N	O	S	0	0	0
			776	500	148	124	4			
47	DY	100	Total	C	N	O	S	0	0	0
			776	500	148	124	4			

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	BZ	176	Total	C	N	O	S	0	0	0
			1404	897	252	253	2			
48	DZ	176	Total	C	N	O	S	0	0	0
			1404	897	252	253	2			

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	B0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			
49	D0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 50 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B1	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			
50	D1	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B1	81	ARG	LYS	conflict	UNP P60494
D1	81	ARG	LYS	conflict	UNP P60494

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			
51	D2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B3	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			
52	D3	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B4	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			
53	D4	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
54	D5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 55 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B6	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			
55	D6	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	B7	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			
56	D7	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			

- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	B8	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			
57	D8	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	B9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			
58	D9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 59 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	CX	4	Total	C	N	O	P	0	0	0
			85	38	14	29	4			

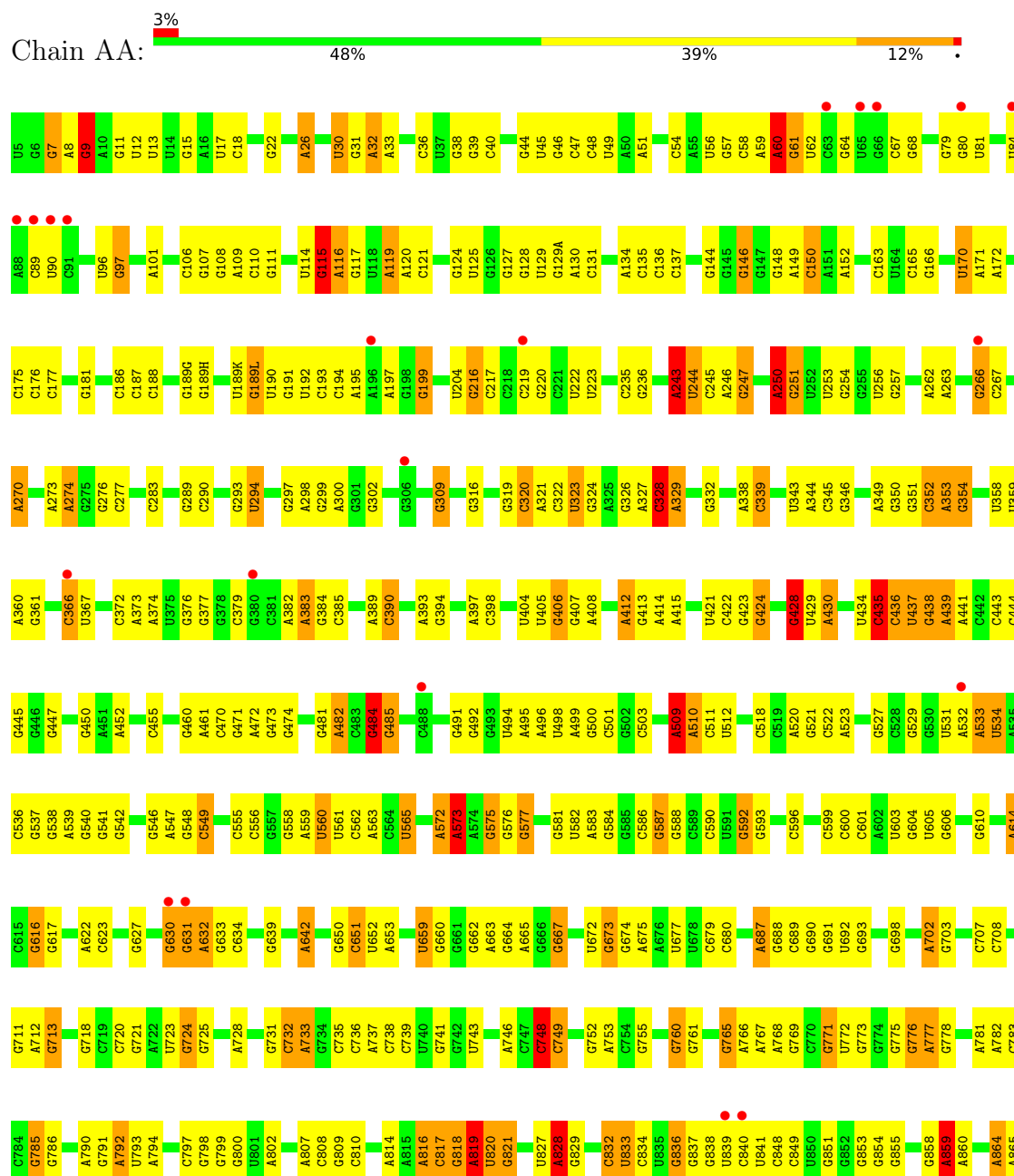
- Molecule 60 is a protein called 50S Ribosomal protein L1.

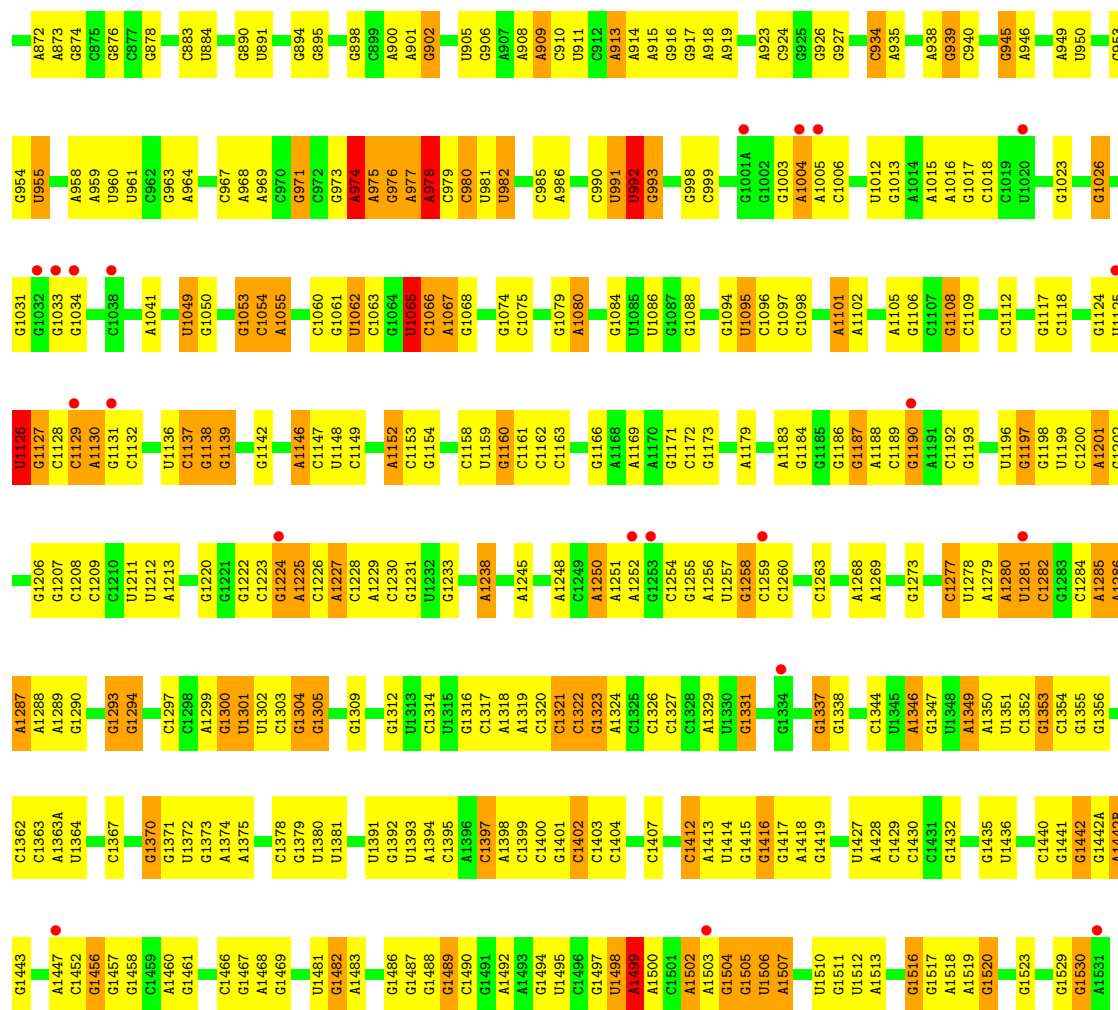
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
60	DC	190	Total	C	N	O	0	0	0
			1157	706	220	231			

3 Residue-property plots

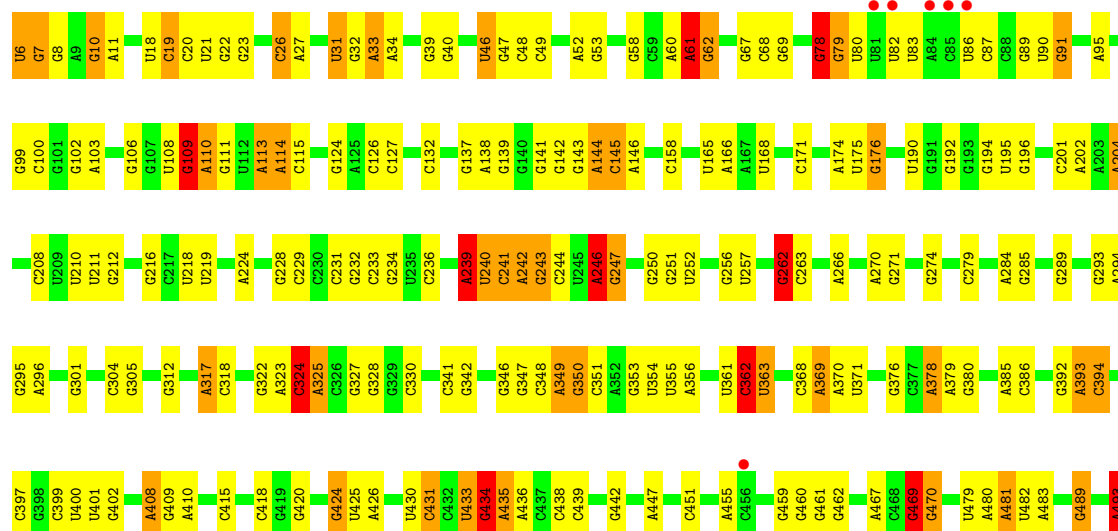
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

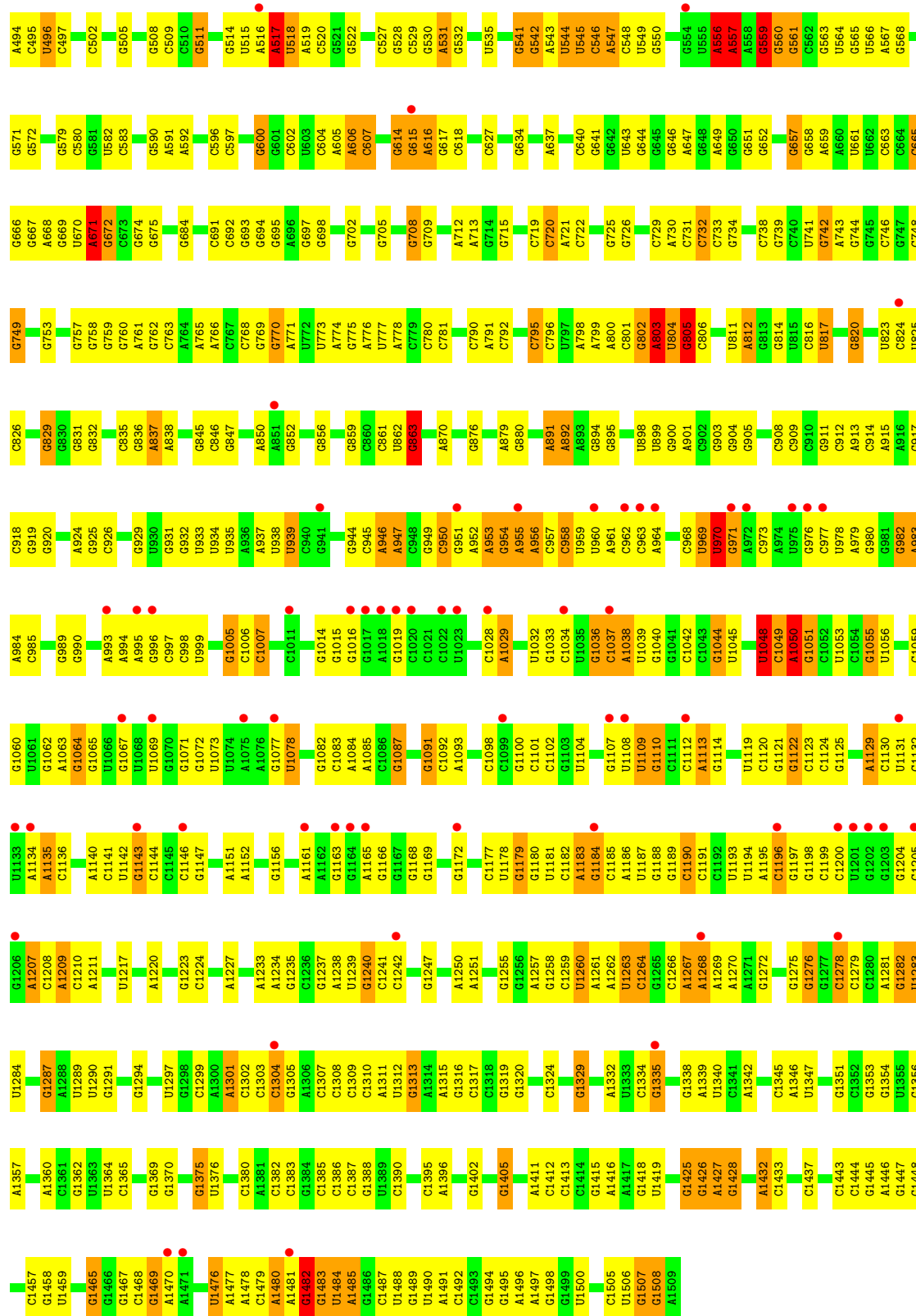
• Molecule 1: 16S ribosomal RNA





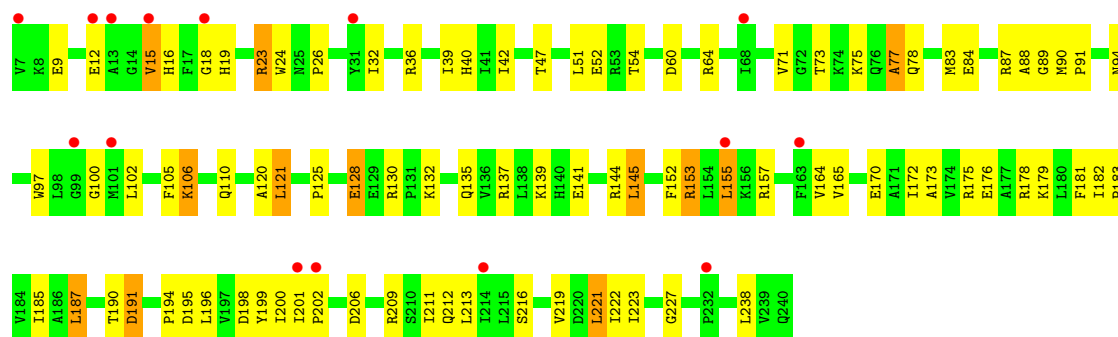
• Molecule 1: 16S ribosomal RNA

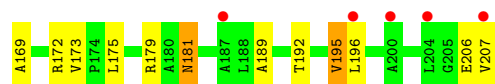




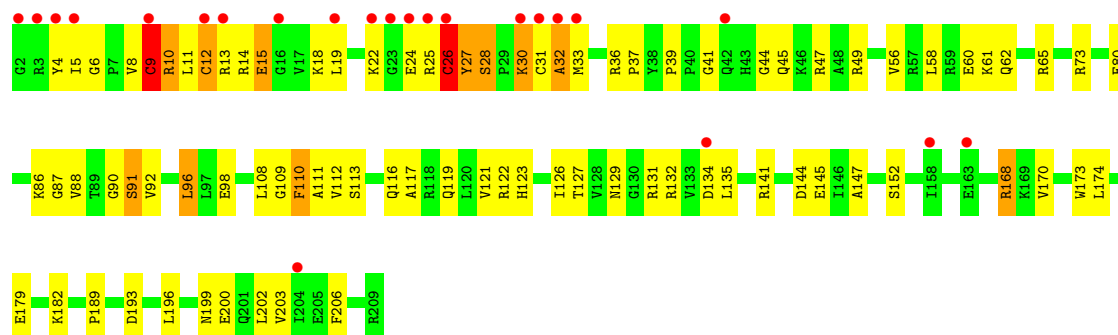
• Molecule 2: 30S Ribosomal protein S2



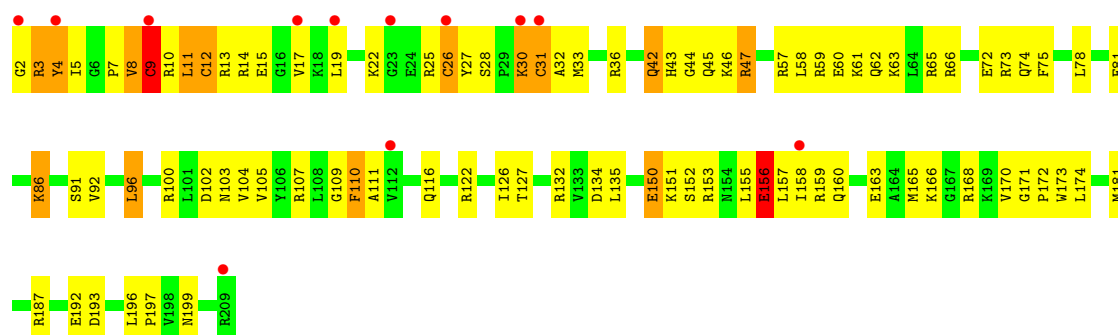




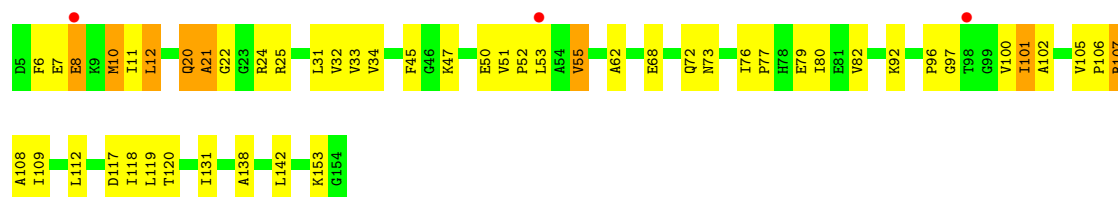
• Molecule 4: 30S Ribosomal protein S4



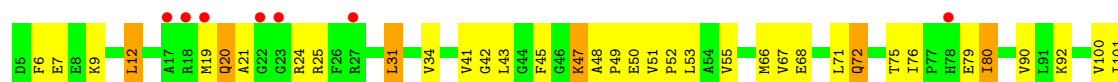
• Molecule 4: 30S Ribosomal protein S4

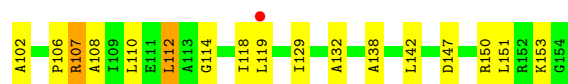


• Molecule 5: 30S Ribosomal protein S5

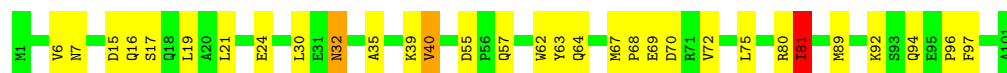


• Molecule 5: 30S Ribosomal protein S5

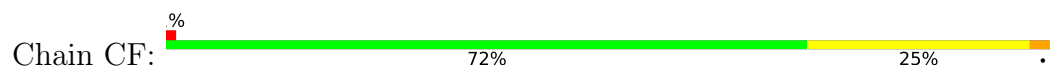




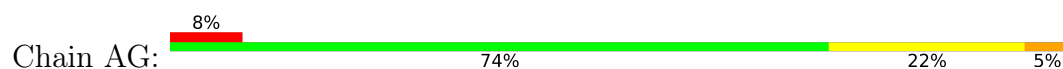
- Molecule 6: 30S Ribosomal protein S6



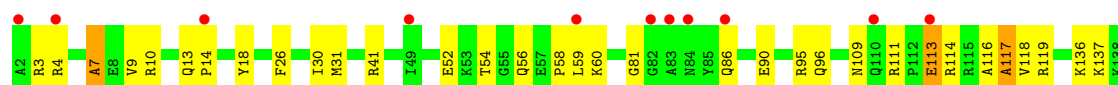
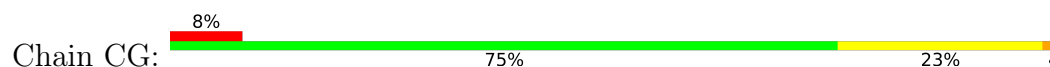
- Molecule 6: 30S Ribosomal protein S6



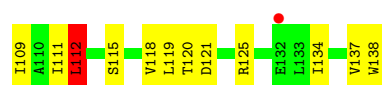
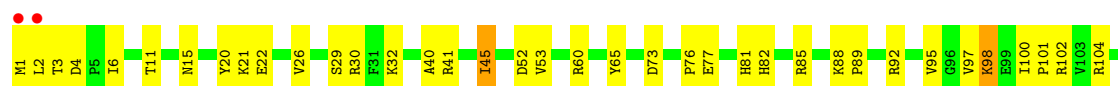
- Molecule 7: 30S Ribosomal protein S7



- Molecule 7: 30S Ribosomal protein S7

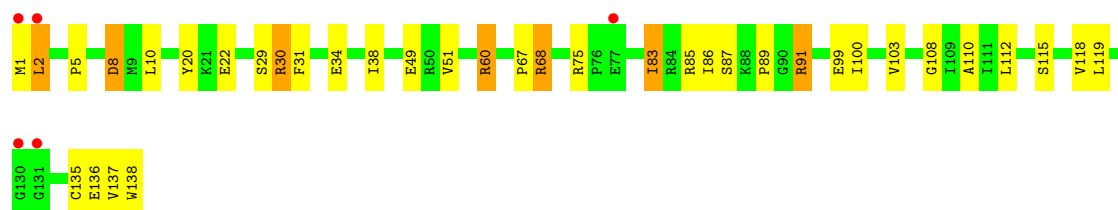


- Molecule 8: 30S Ribosomal protein S8



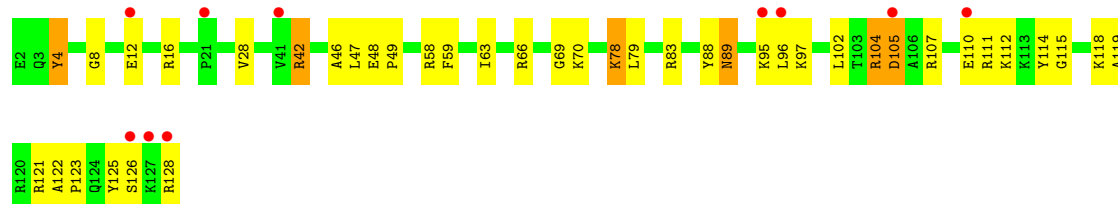
- Molecule 8: 30S Ribosomal protein S8

Chain CH: 



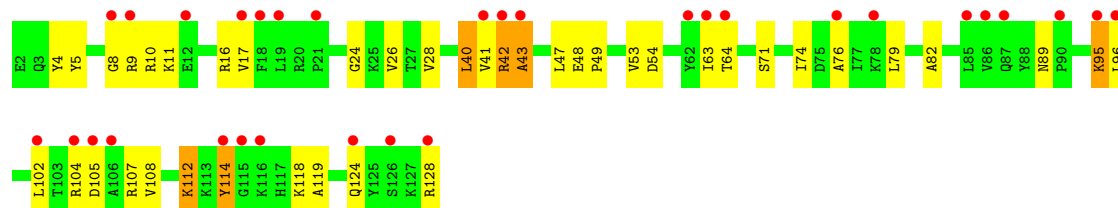
- Molecule 9: 30S Ribosomal protein S9

Chain AI: 



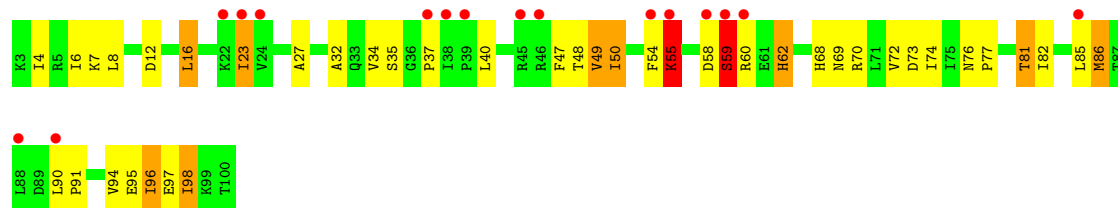
- Molecule 9: 30S Ribosomal protein S9

Chain CI: 



- Molecule 10: 30S Ribosomal protein S10

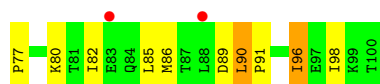
Chain AJ: 



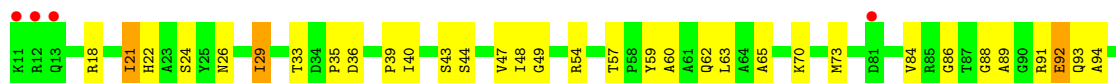
- Molecule 10: 30S Ribosomal protein S10

Chain CJ: 

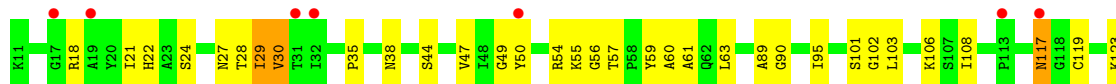




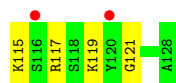
• Molecule 11: 30S Ribosomal protein S11



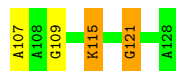
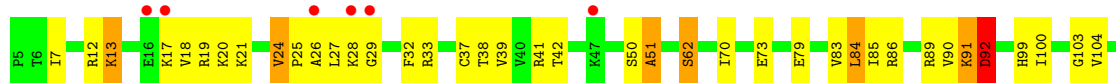
• Molecule 11: 30S Ribosomal protein S11



• Molecule 12: 30S Ribosomal protein S12

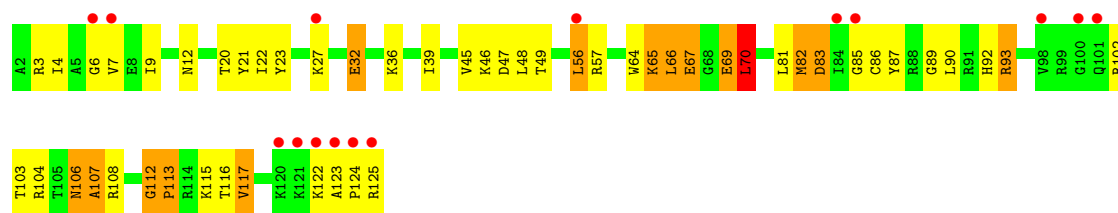


• Molecule 12: 30S Ribosomal protein S12

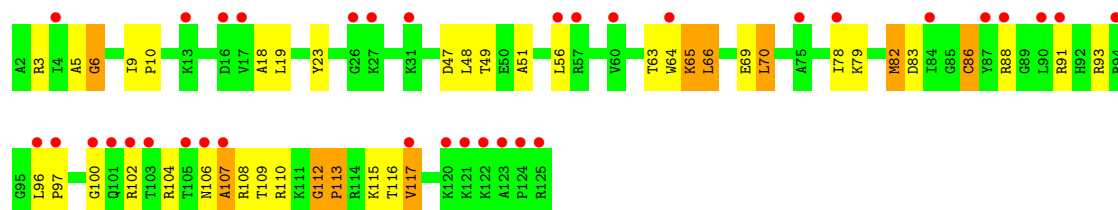


• Molecule 13: 30S Ribosomal protein S13





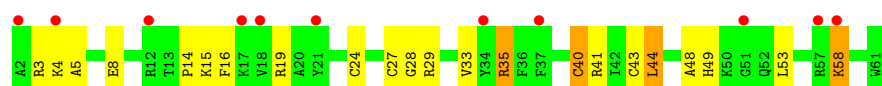
• Molecule 13: 30S Ribosomal protein S13



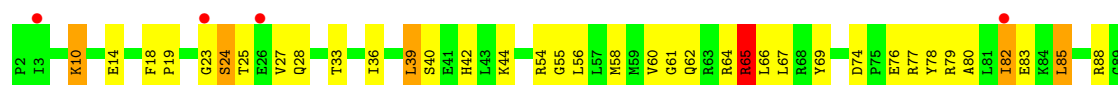
• Molecule 14: 30S Ribosomal protein S14



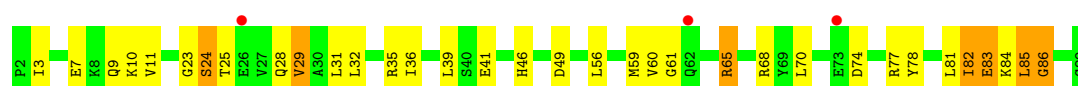
• Molecule 14: 30S Ribosomal protein S14



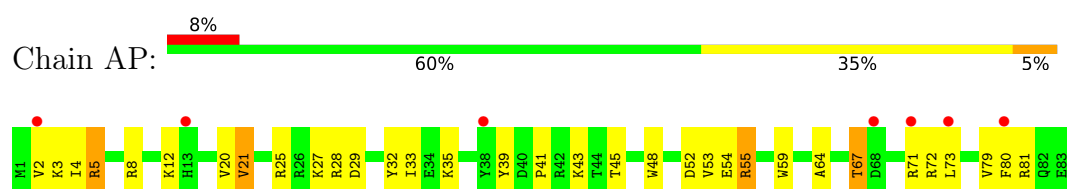
• Molecule 15: 30S Ribosomal protein S15



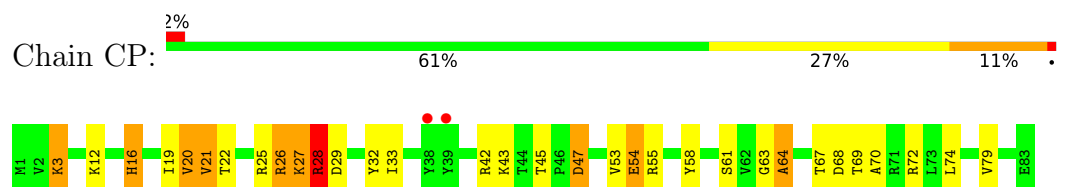
• Molecule 15: 30S Ribosomal protein S15



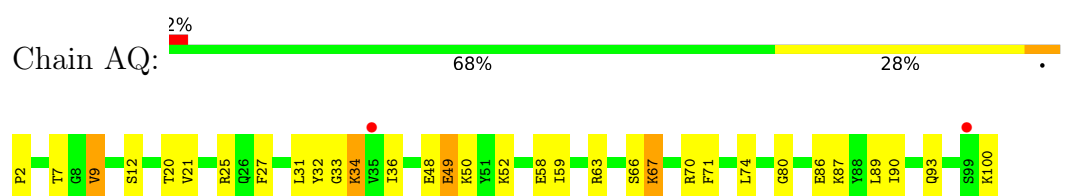
• Molecule 16: 30S Ribosomal protein S16



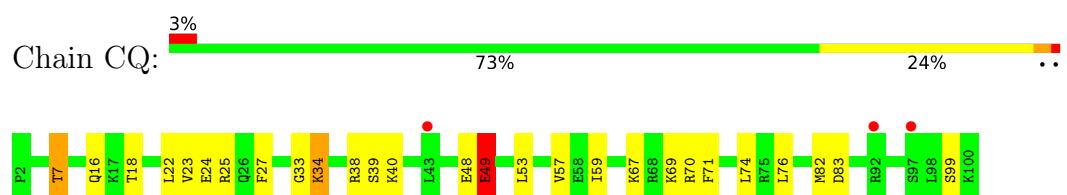
- Molecule 16: 30S Ribosomal protein S16



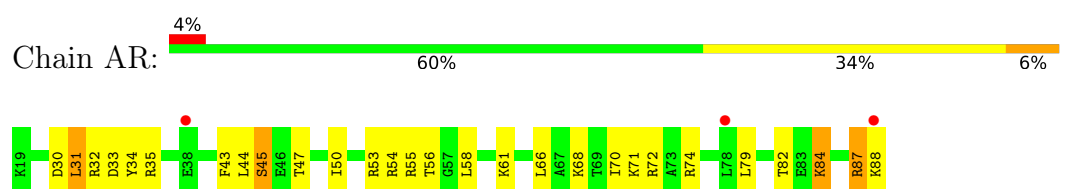
- Molecule 17: 30S Ribosomal protein S17



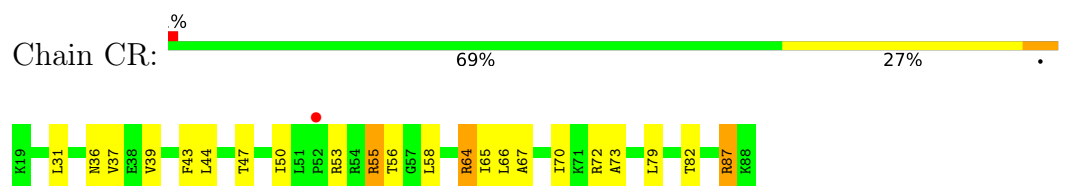
- Molecule 17: 30S Ribosomal protein S17



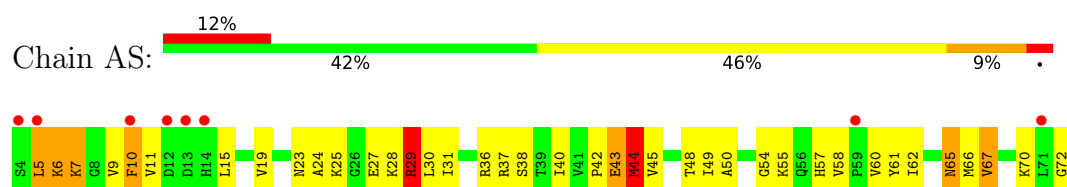
- Molecule 18: 30S Ribosomal protein S18



- Molecule 18: 30S Ribosomal protein S18

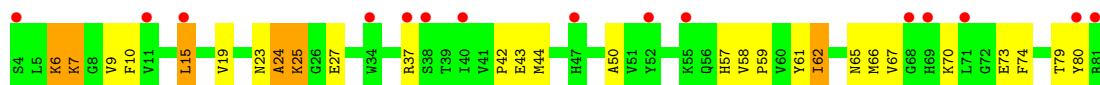


- Molecule 19: 30S Ribosomal protein S19

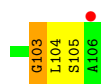




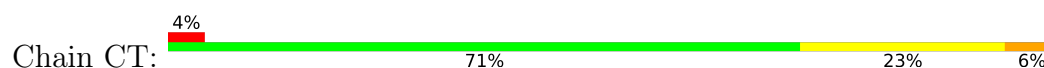
- Molecule 19: 30S Ribosomal protein S19



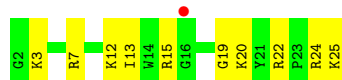
- Molecule 20: 30S Ribosomal protein S20



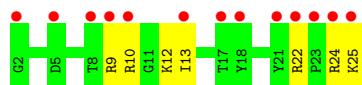
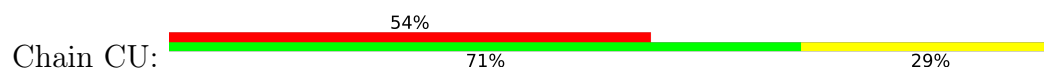
- Molecule 20: 30S Ribosomal protein S20



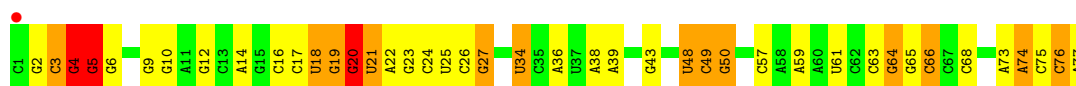
- Molecule 21: 30S Ribosomal protein THX



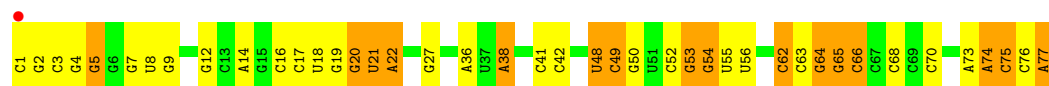
- Molecule 21: 30S Ribosomal protein THX



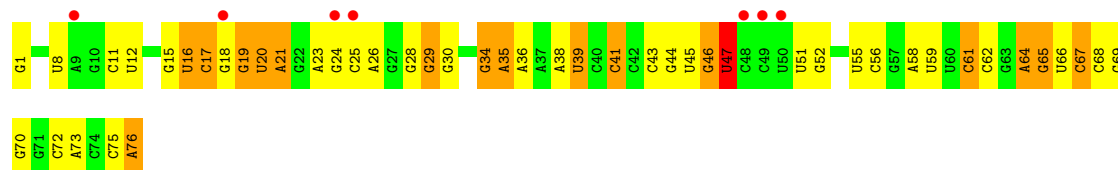
- Molecule 22: P-SITE tRNA



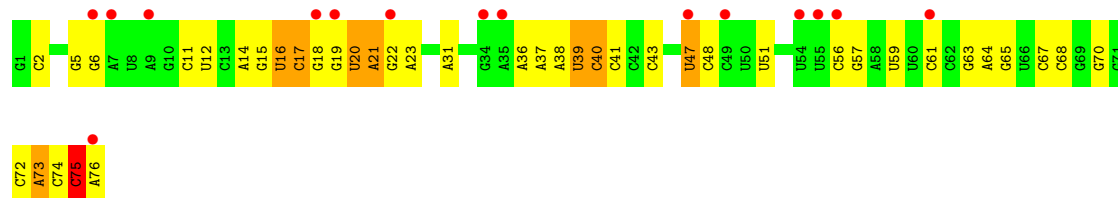
- Molecule 22: P-SITE tRNA



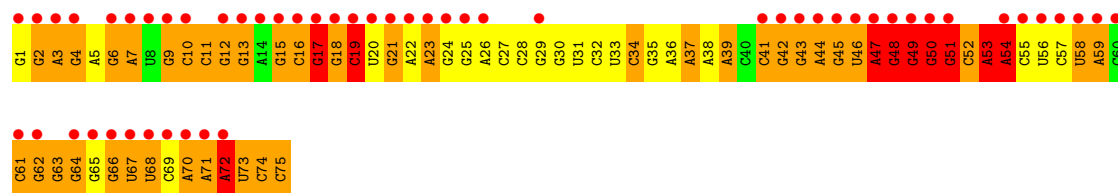
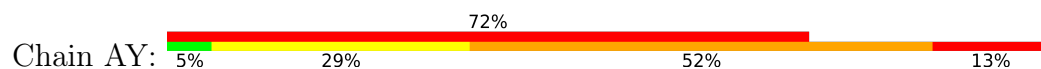
- Molecule 23: E-SITE tRNA



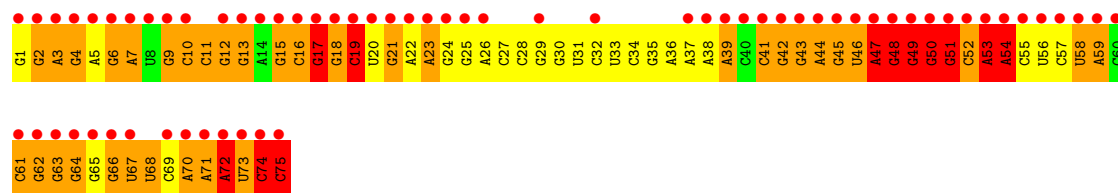
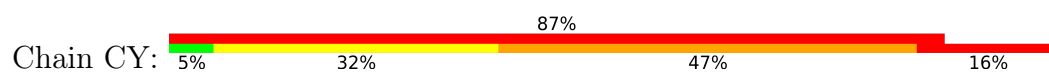
- Molecule 23: E-SITE tRNA



- Molecule 24: A-SITE tRNA



- Molecule 24: A-SITE tRNA



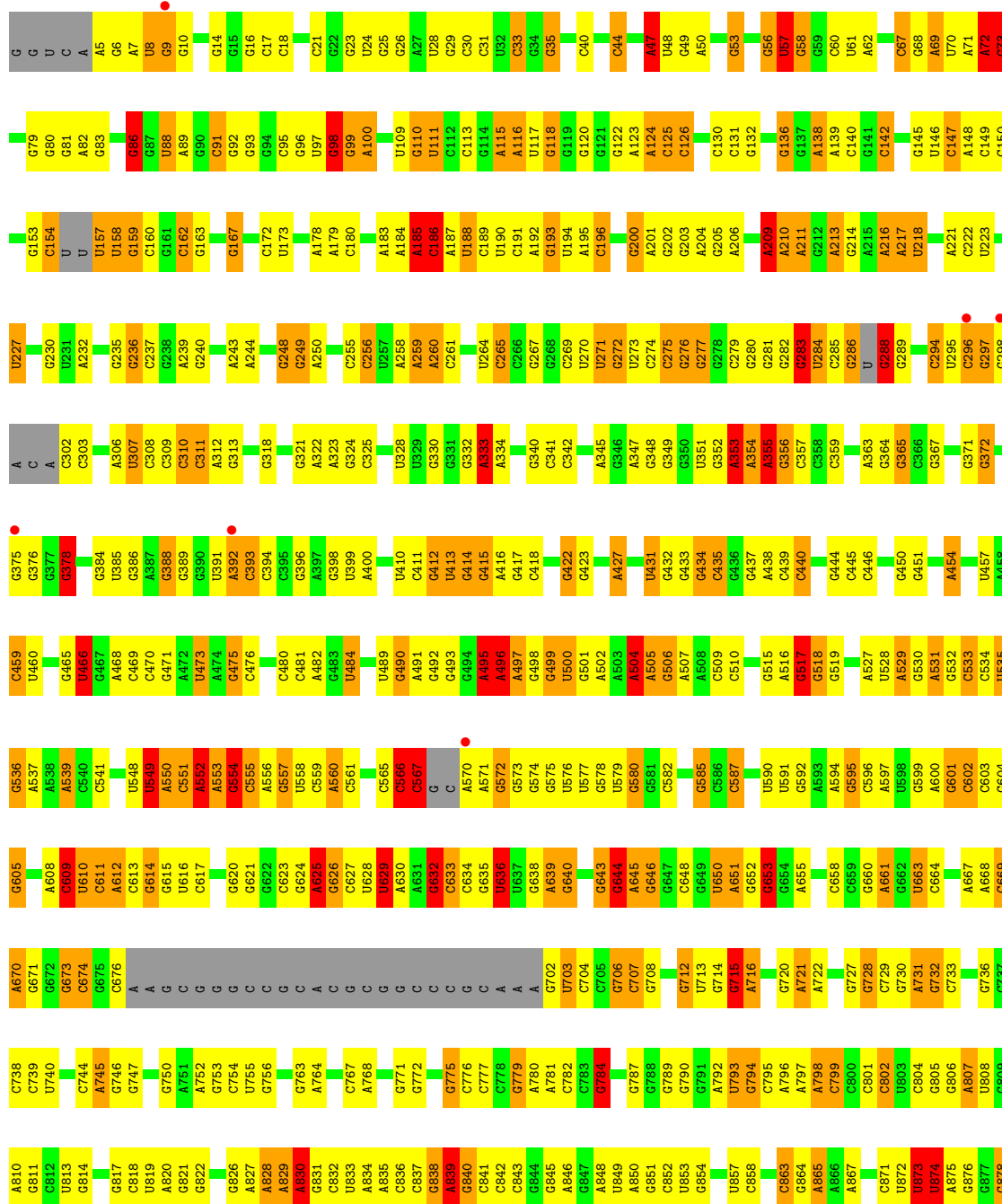
- Molecule 25: mRNA

Chain AX: 29% 14% 43% 14%



• Molecule 26: 23S ribosomal RNA

Chain BA: 36% 37% 19% . .

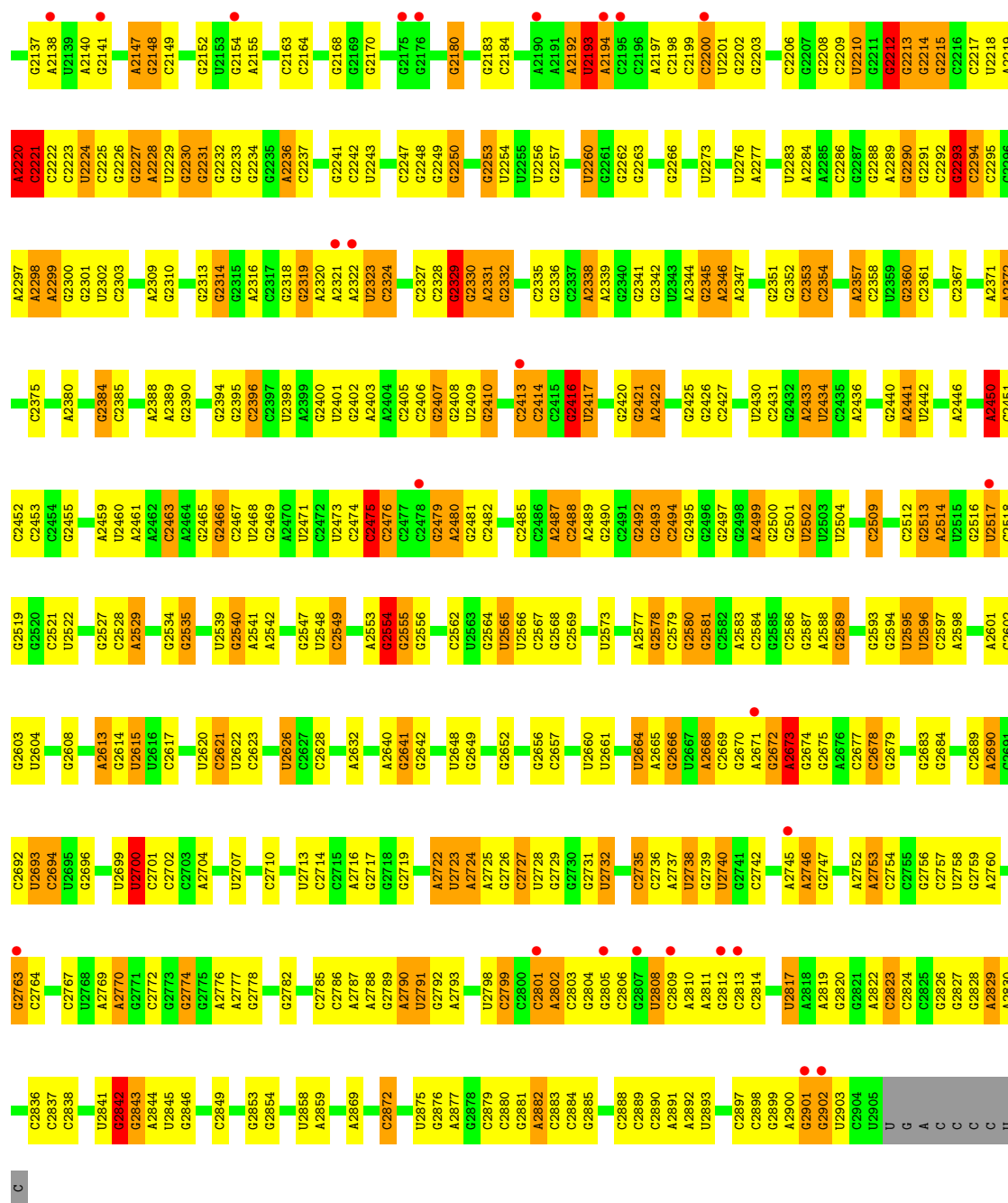


A1832	G1749	A1683	G1605	G1459	C1378	C1306	C1229	C1154	C1094	A1028	U952	U879
A1833	G1763	G1685	A1612	U1460	G1383	A1307	G1230	G1155	A1095	A1029	U955	C880
G1837	U1764	U1685	A1613	G1461	G1384	U1308	G1231	A1156	G1096	A956	U885	U885
U1838	G1765	C1686	G1537	G1462	G1389	U1309	U1232	A1157	C1097	A957	C886	A887
A1839	A1766	A1614	C1538	G1463	A1387	A1310	A1233	U1158	C1098	G1033	G961	C888
A1840	U1767	A1615	A1559	A1464	A1387	U1312	G1234	G1159	A	A1035	A962	C889
G1841	G1768	A1616	A1540	U1465	A1387	U1312	G1235	G1160	A	A1036	A963	C890
A1842	G1769	A1617	A1541	U1466	C1390	A1313	G1236	C1163	G	C1037	G966	C891
G1843	A1769	A1618	U1542	G1471	G1391	A1314	G1237	C1164	A	C1038	U967	C892
G1844	G1770	C1689	C1543	A1472	G1392	C1315	G1238	G1167	G	C1039	C968	U893
C1771	C1692	C1620	C1544	C1473	G1393	C1316	G1239	G1168	G	C1040	C969	C970
C1772	G1693	G1621	G1545	G1474	A1394	A1317	C1245	G1170	U	A1041	C971	A894
A1845	C1694	C1622	G1546	G1475	C1395	A1318	U1255	A1171	U	U1044	A971	A895
G1846	A1694	C1623	C1547	U1476	C1396	A1319	C1261	A1172	G	A1045	G972	G898
G1847	G1695	U1624	U1548	C1477	U1397	A1320	U1249	A1173	C	A1046	G973	G899
U1848	U1696	A1625	C1549	U1478	G1401	A1323	U1250	U1174	U	U1047	G974	G900
U1849	G1697	A1626	C1550	G1479	U1402	G1324	C1262	A1175	U	G1048	G975	G901
U1850	G1698	A1627	C1551	U1480	G1403	G1325	G1263	G1176	U	G1049	G976	G902
A1851	A1699	C1630	A1552	C1482	G1404	A1326	A1254	A1177	A	C1050	A977	C903
G1852	A1700	A1631	A1553	U1483	A1405	U1327	G1255	U1178	G	C1051	G978	U904
G1853	A1701	A1632	C1554	A1484	A1406	G1328	G1256	G1179	A	C1052	C979	U905
G1854	C1702	C1633	A1555	G1485	G1406	A1329	G1257	U1180	G	C1053	C980	G906
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- Molecule 26: 23S ribosomal RNA

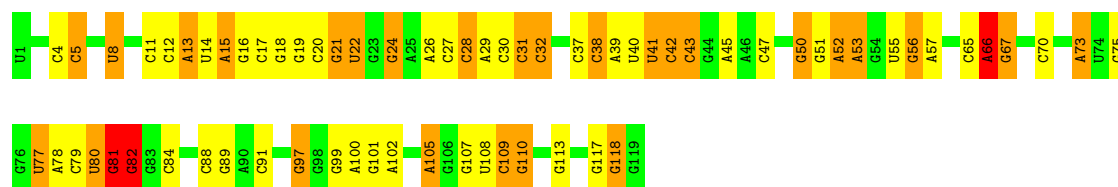


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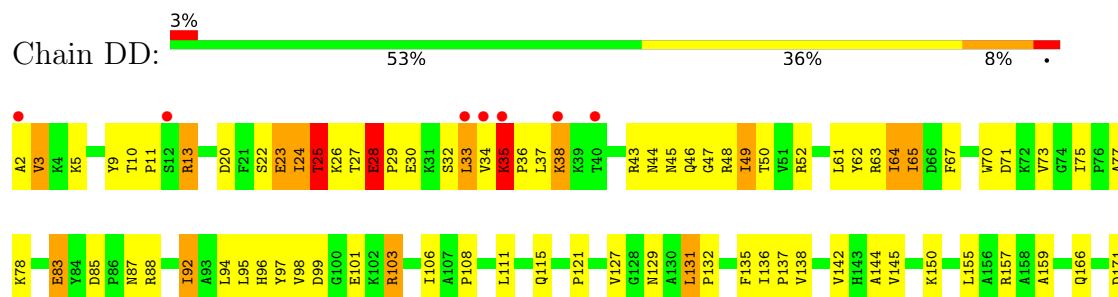


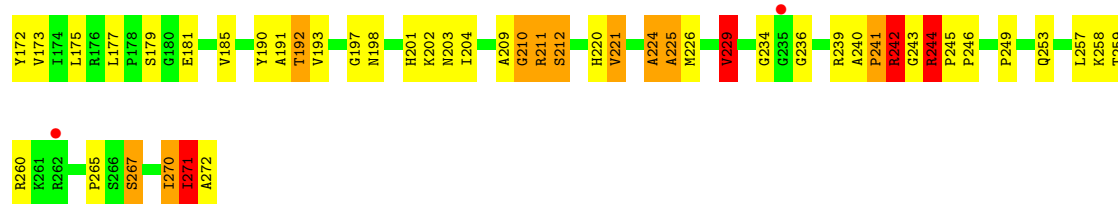
- Molecule 27: 5S ribosomal RNA

Chain BB: 43% 32% 23%

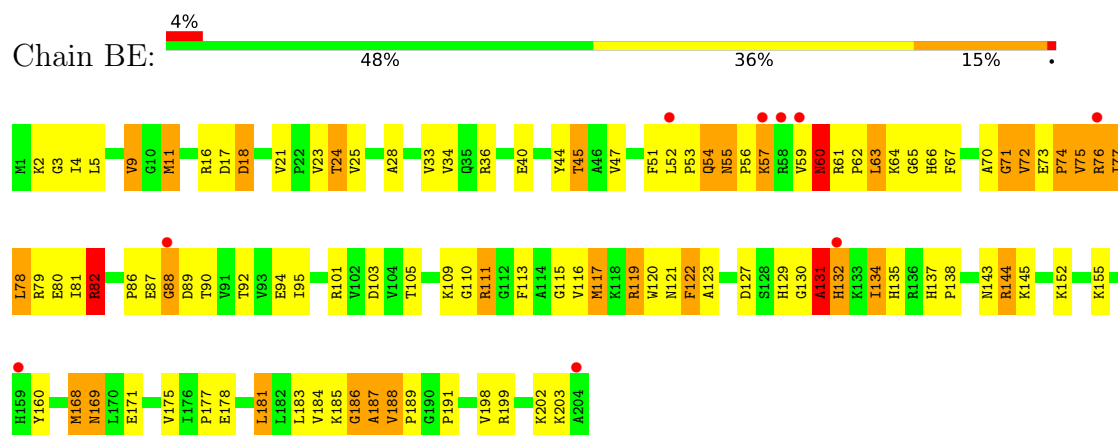


- Molecule 27: 5S ribosomal RNA

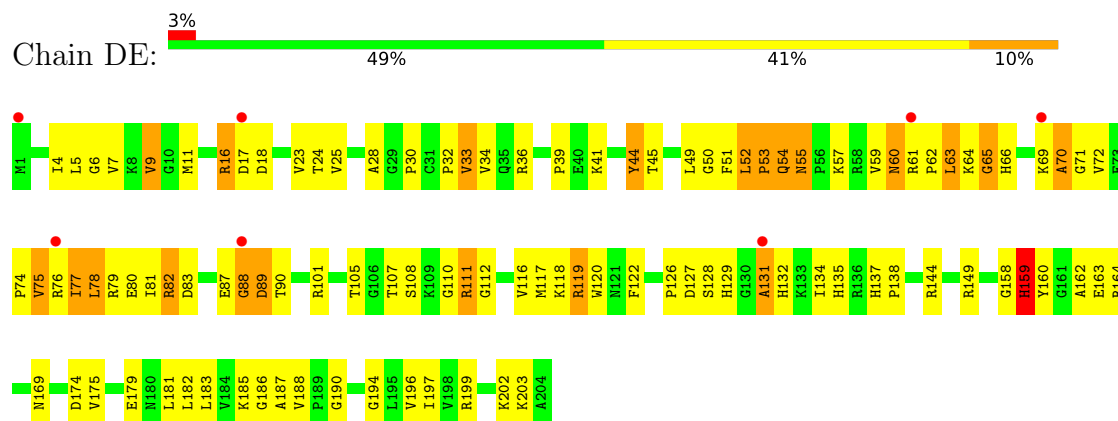




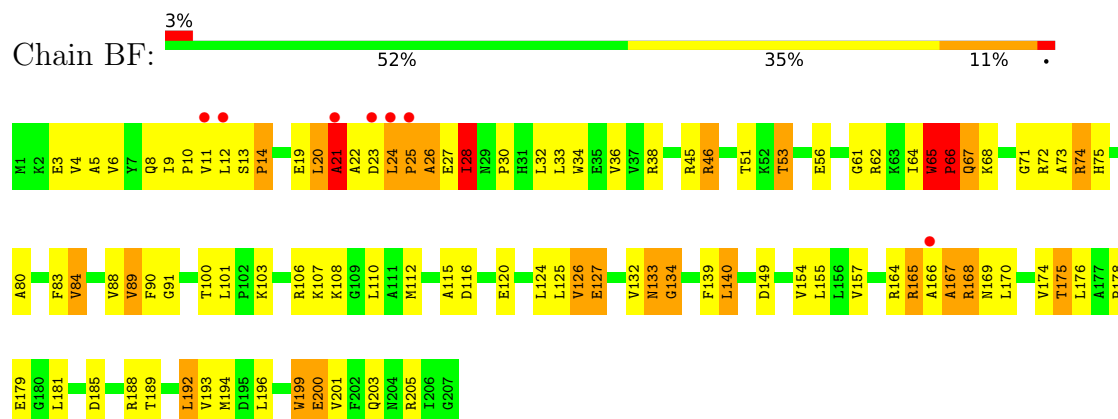
• Molecule 30: 50S ribosomal protein L3



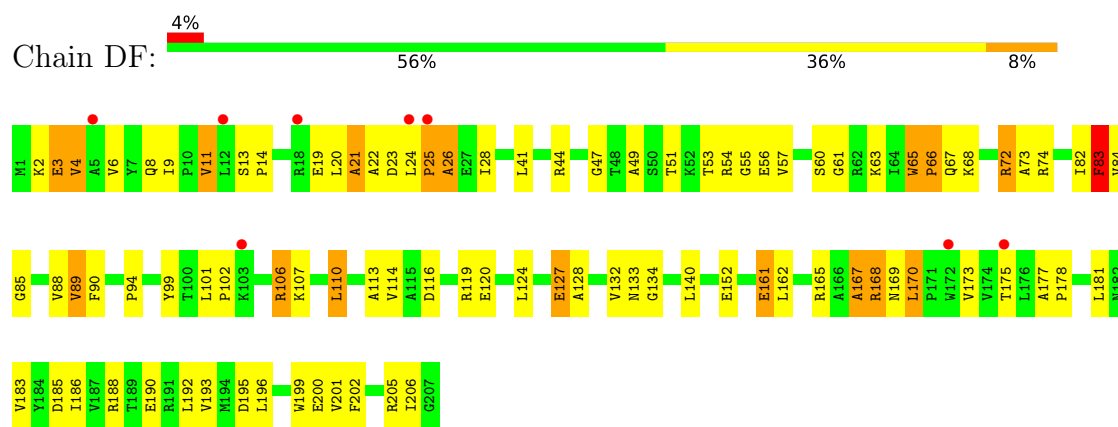
• Molecule 30: 50S ribosomal protein L3



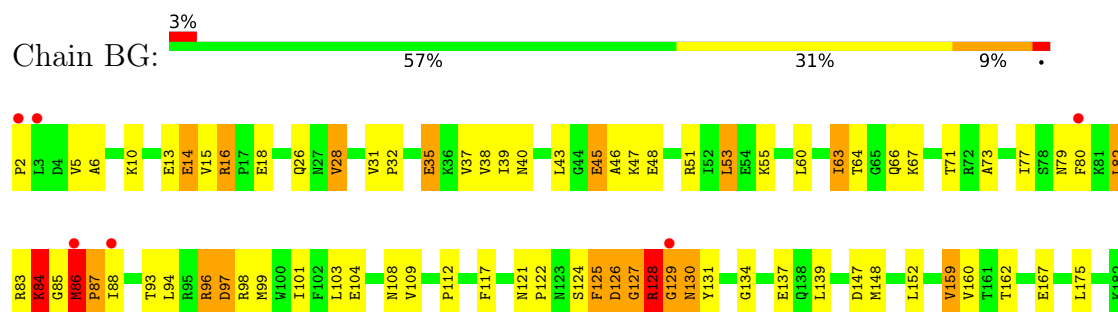
• Molecule 31: 50S ribosomal protein L4



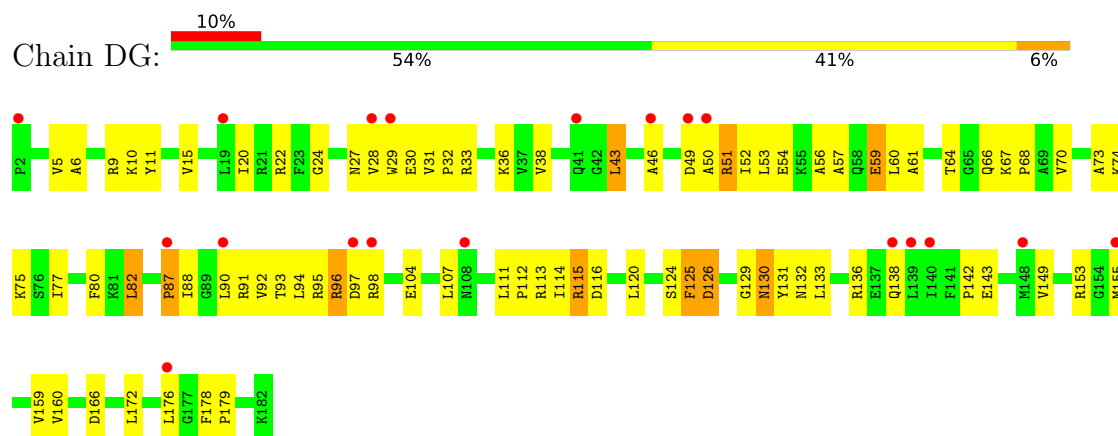
• Molecule 31: 50S ribosomal protein L4



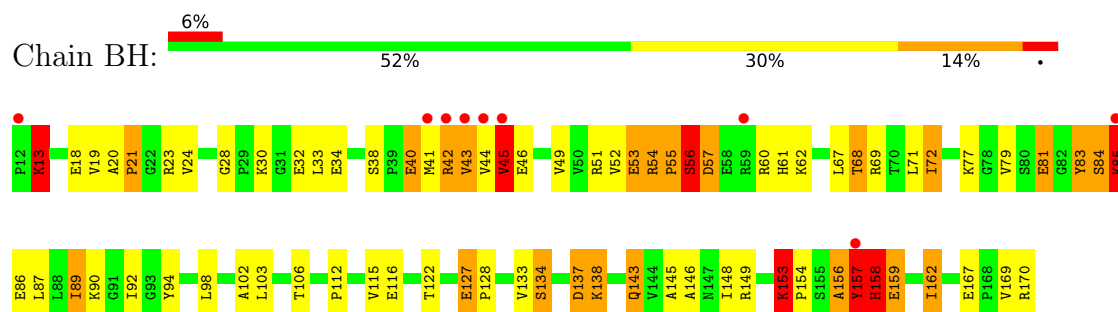
• Molecule 32: 50S ribosomal protein L5



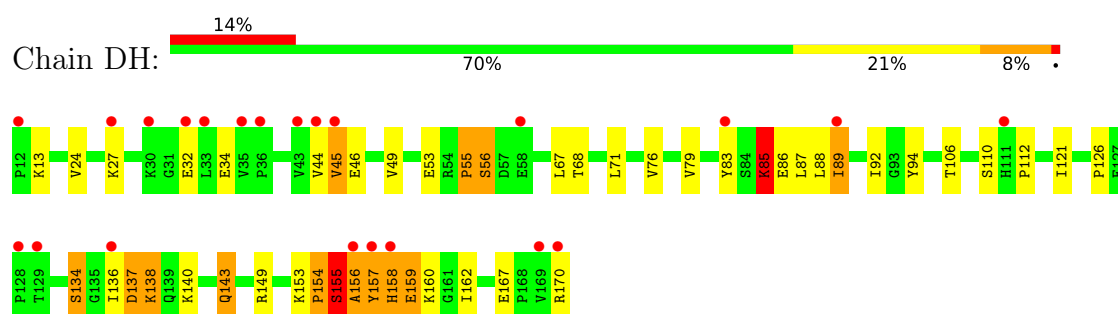
• Molecule 32: 50S ribosomal protein L5



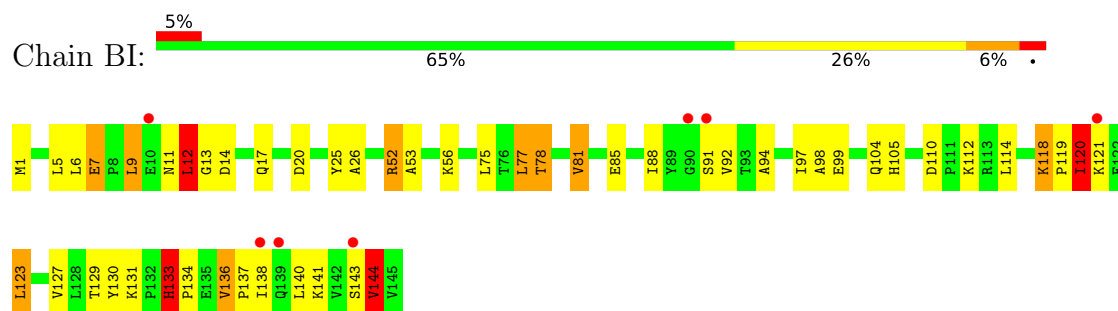
• Molecule 33: 50S ribosomal protein L6



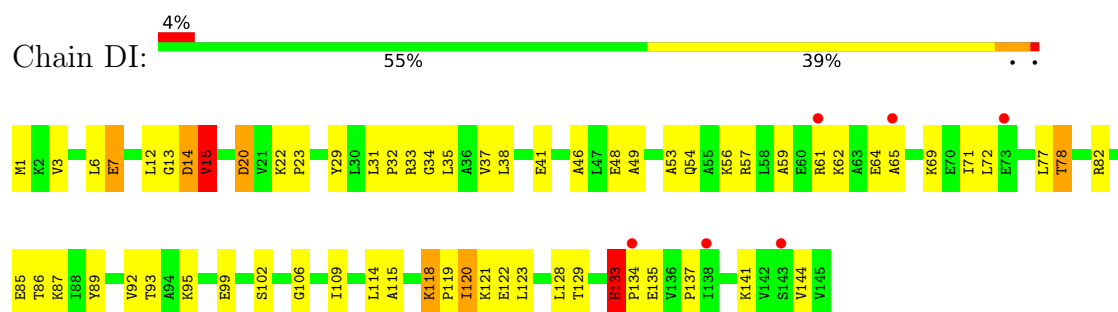
• Molecule 33: 50S ribosomal protein L6



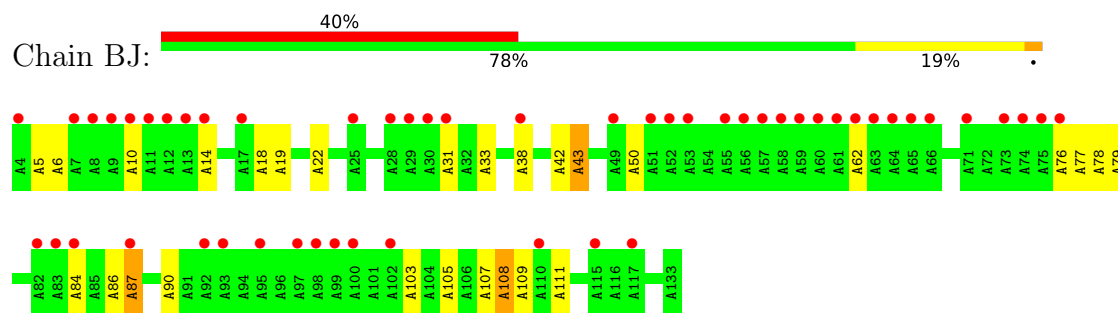
• Molecule 34: 50S ribosomal protein L9



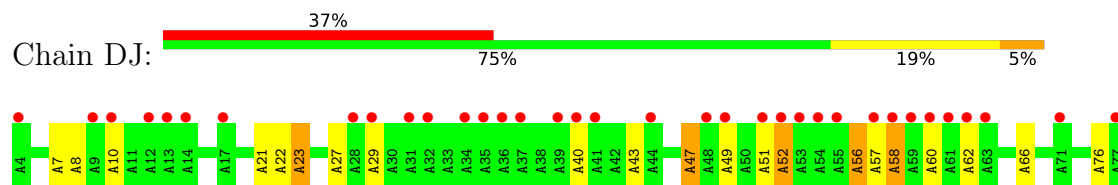
• Molecule 34: 50S ribosomal protein L9



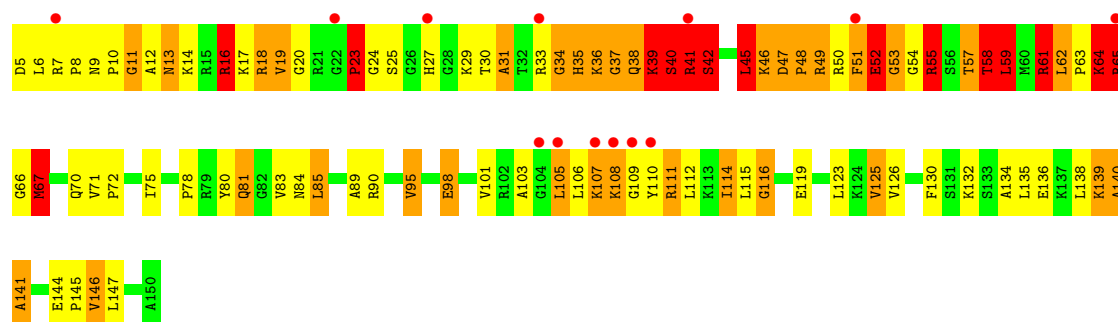
• Molecule 35: 50S ribosomal protein L10



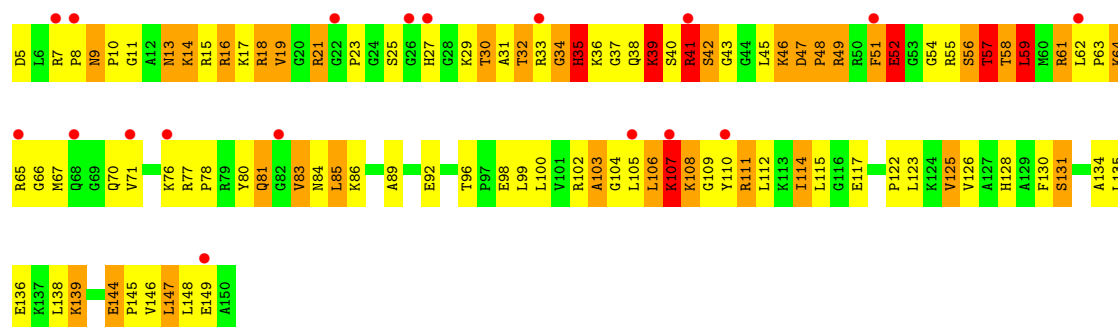
• Molecule 35: 50S ribosomal protein L10



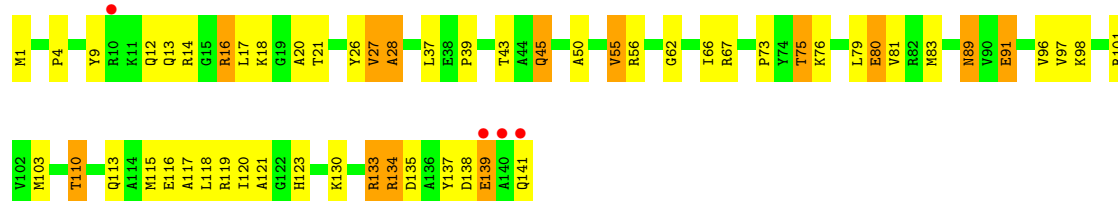




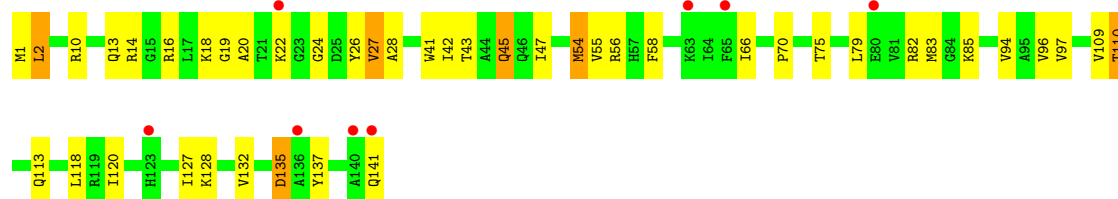
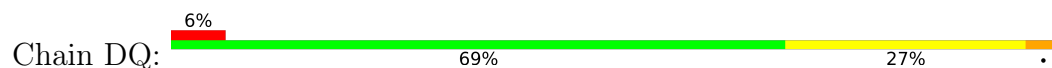
• Molecule 38: 50S ribosomal protein L15



• Molecule 39: 50S ribosomal protein L16

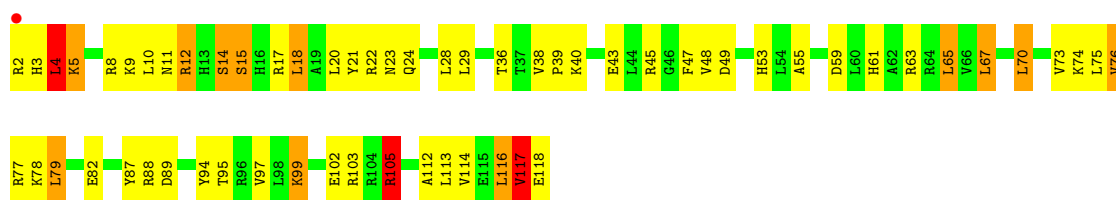


• Molecule 39: 50S ribosomal protein L16

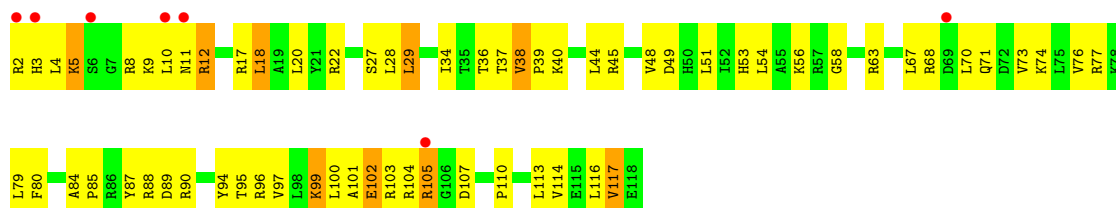


• Molecule 40: 50S ribosomal protein L17

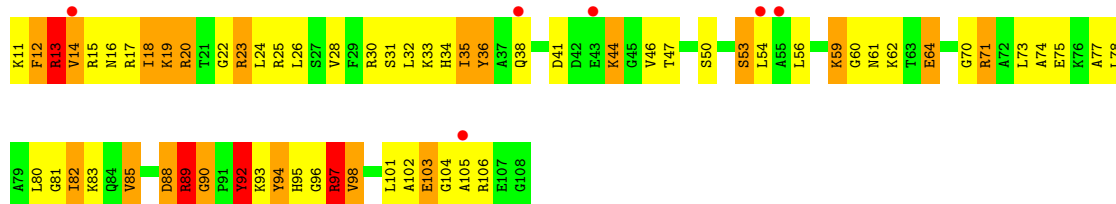




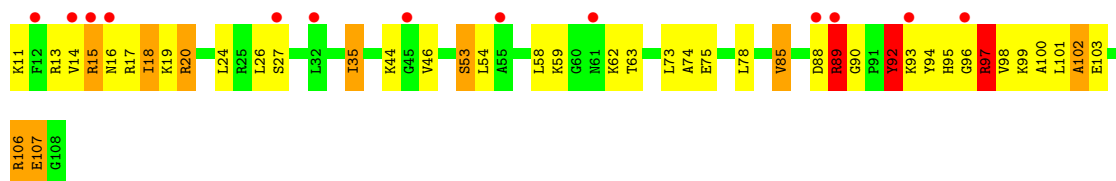
• Molecule 40: 50S ribosomal protein L17



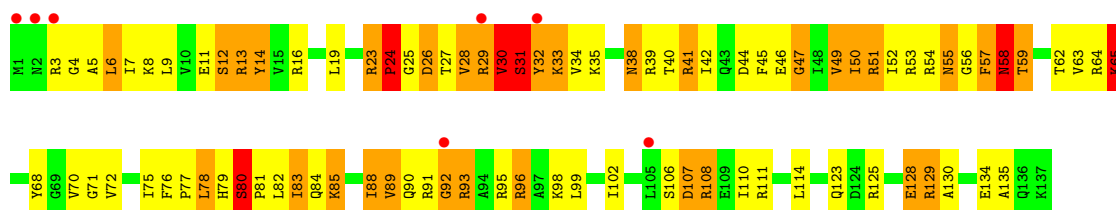
• Molecule 41: 50S ribosomal protein L18



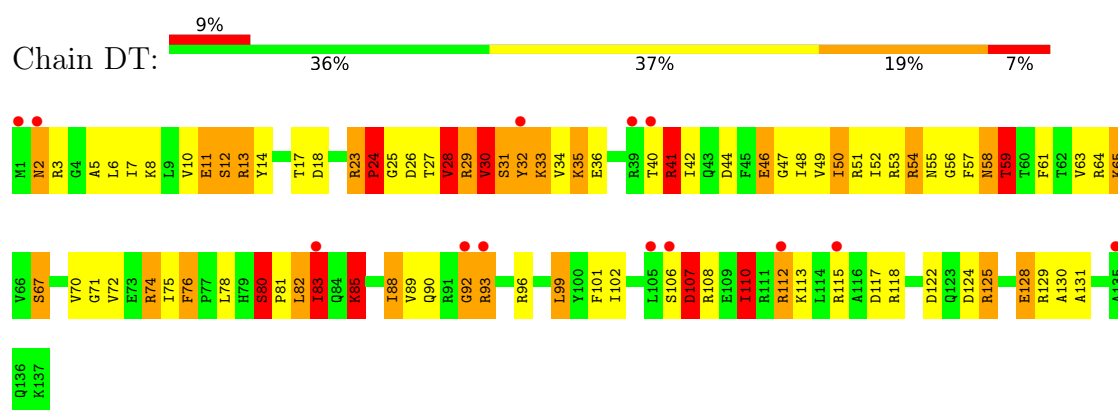
• Molecule 42: 50S ribosomal protein L19



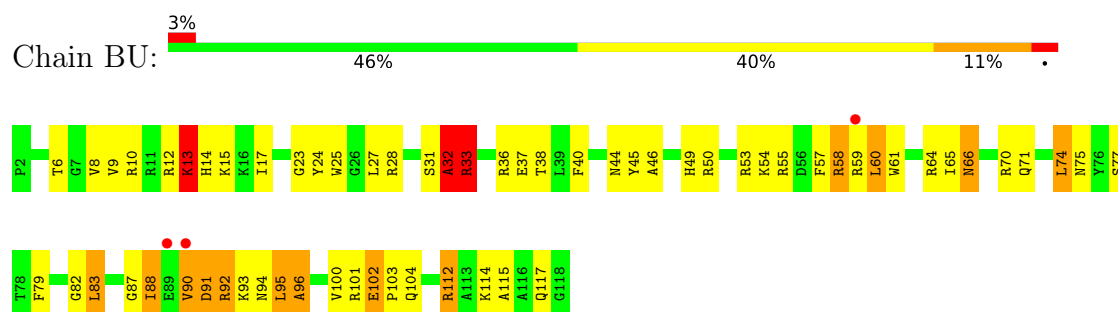
• Molecule 42: 50S ribosomal protein L19



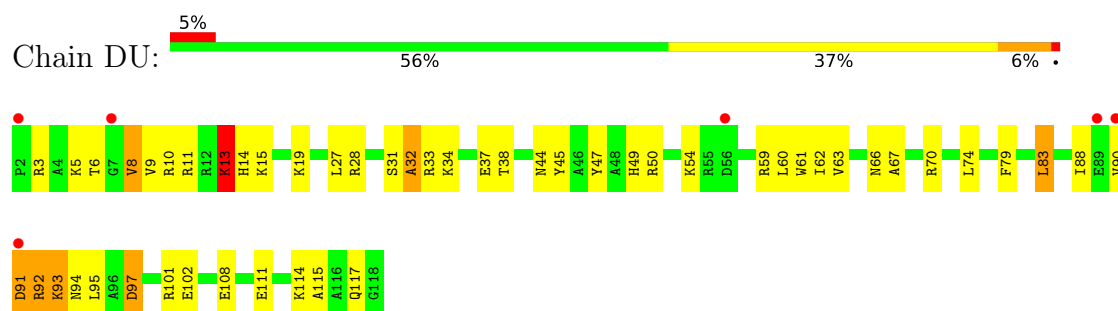
• Molecule 42: 50S ribosomal protein L19



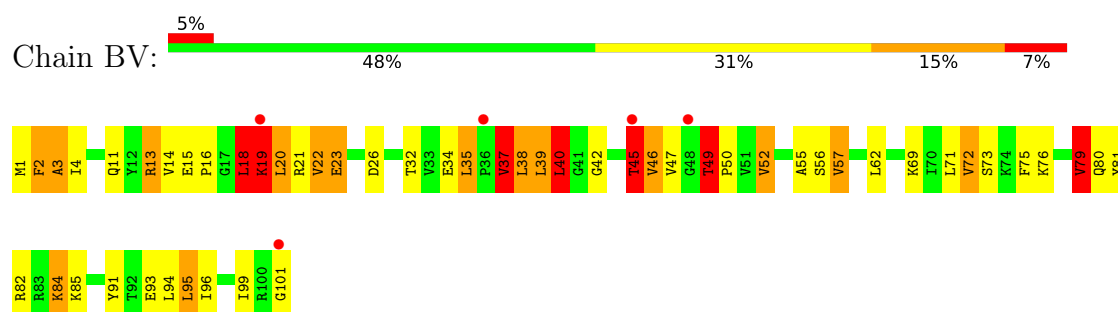
- Molecule 43: 50S ribosomal protein L20



- Molecule 43: 50S ribosomal protein L20



- Molecule 44: 50S ribosomal protein L21

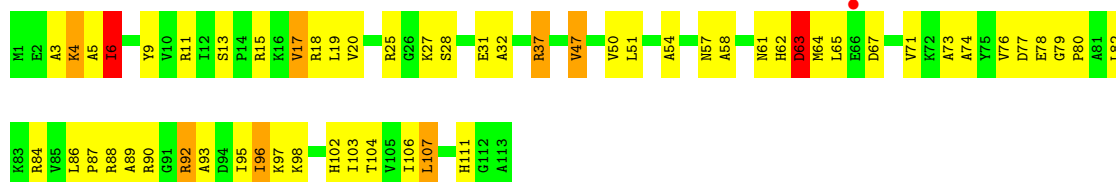


- Molecule 44: 50S ribosomal protein L21

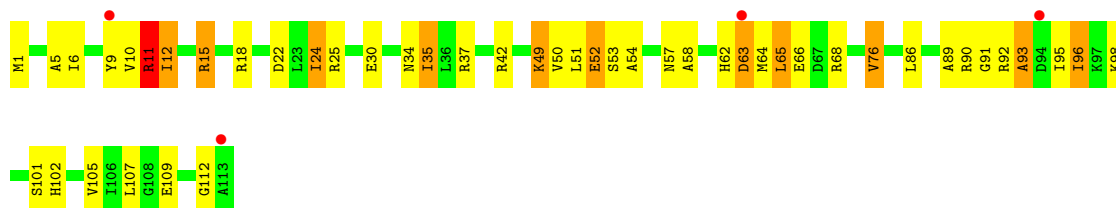




- Molecule 45: 50S ribosomal protein L22



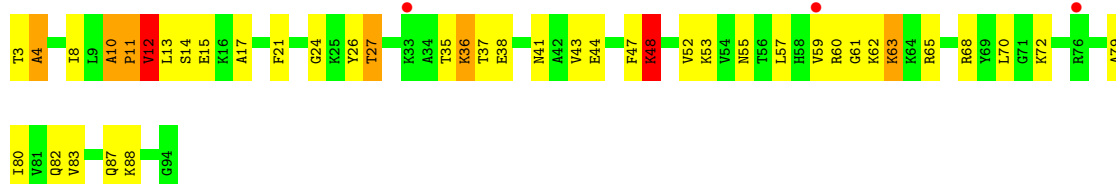
- Molecule 45: 50S ribosomal protein L22



- Molecule 46: 50S ribosomal protein L23

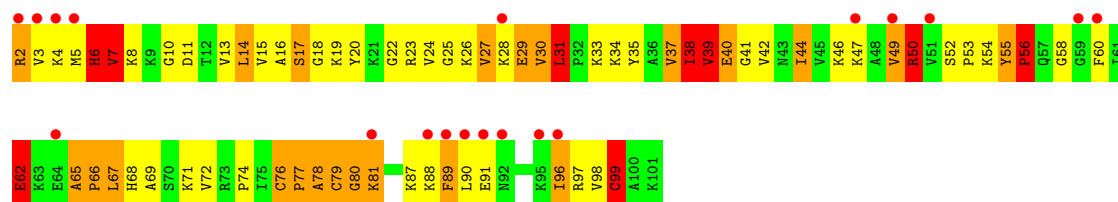


- Molecule 46: 50S ribosomal protein L23

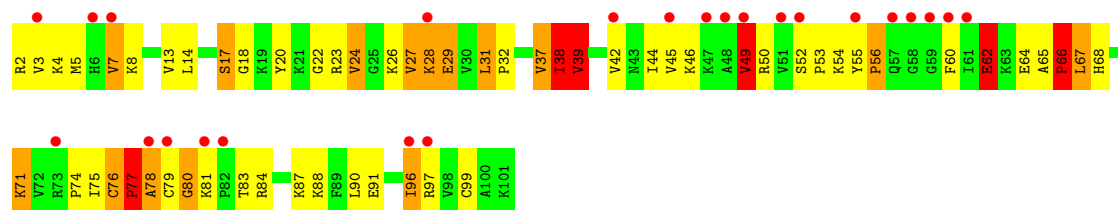
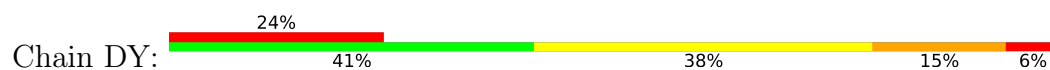


- Molecule 47: 50S ribosomal protein L24

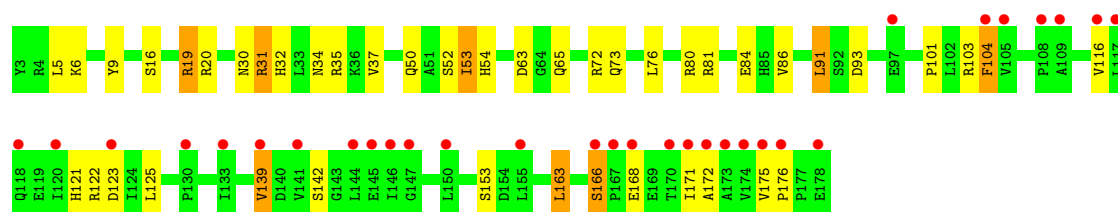
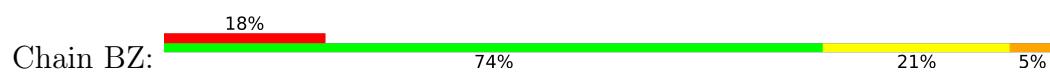




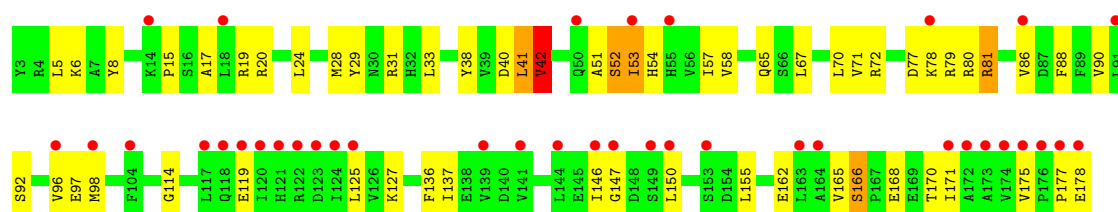
• Molecule 47: 50S ribosomal protein L24



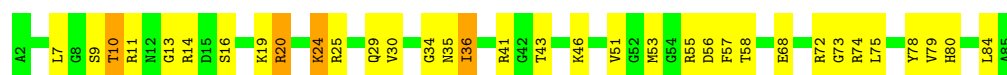
• Molecule 48: 50S ribosomal protein L25



• Molecule 48: 50S ribosomal protein L25



• Molecule 49: 50S ribosomal protein L27

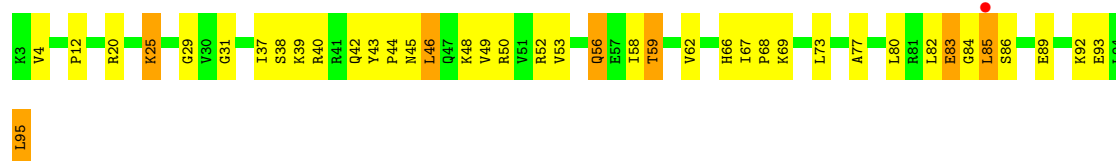


• Molecule 49: 50S ribosomal protein L27

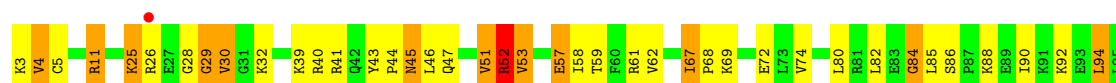




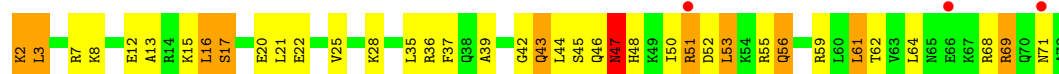
- Molecule 50: 50S ribosomal protein L28



- Molecule 50: 50S ribosomal protein L28



- Molecule 51: 50S ribosomal protein L29



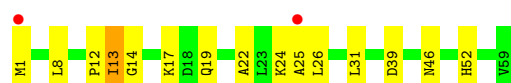
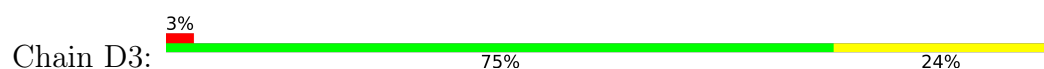
- Molecule 51: 50S ribosomal protein L29



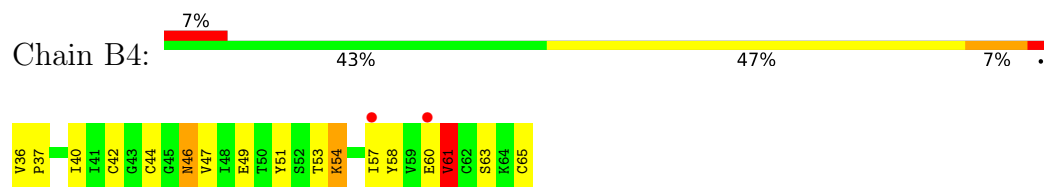
- Molecule 52: 50S ribosomal protein L30



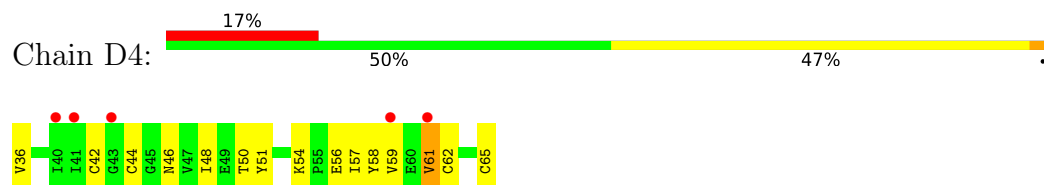
- Molecule 52: 50S ribosomal protein L30



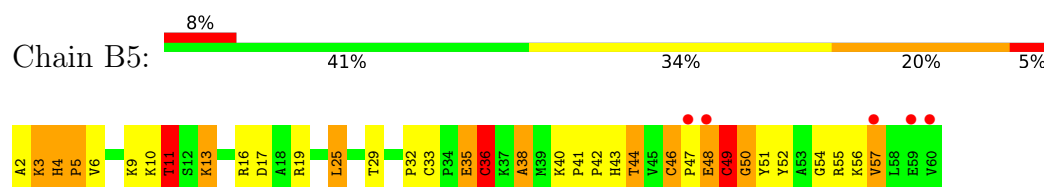
- Molecule 53: 50S ribosomal protein L31



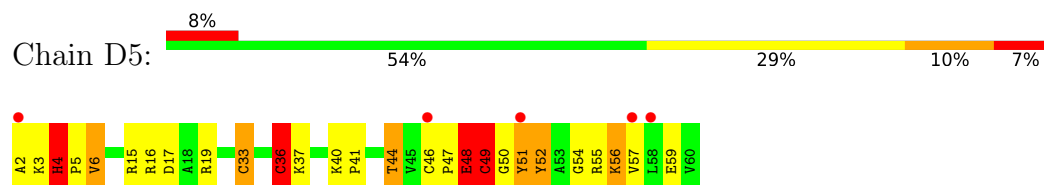
- Molecule 53: 50S ribosomal protein L31



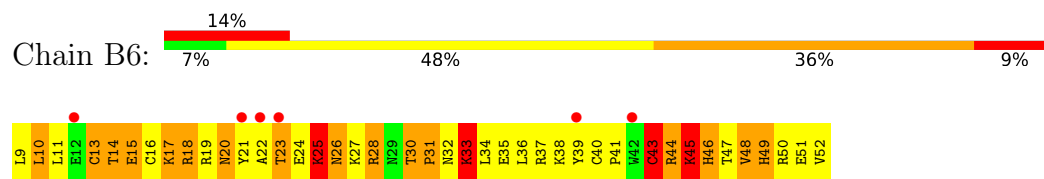
- Molecule 54: 50S ribosomal protein L32



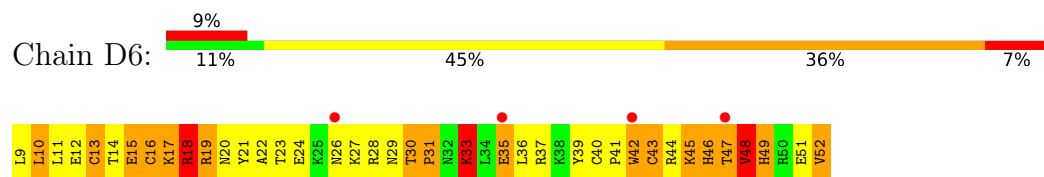
- Molecule 54: 50S ribosomal protein L32



- Molecule 55: 50S ribosomal protein L33



- Molecule 55: 50S ribosomal protein L33



- Molecule 56: 50S ribosomal protein L34

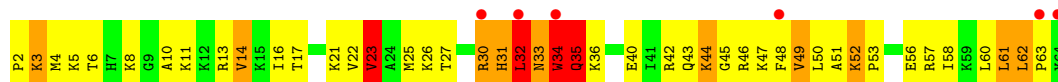




- Molecule 56: 50S ribosomal protein L34



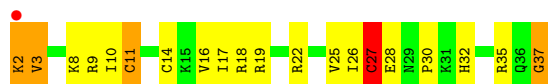
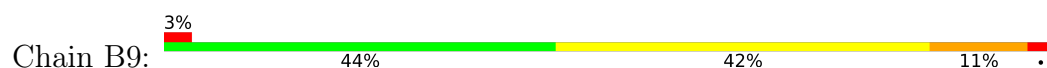
- Molecule 57: 50S ribosomal protein L35



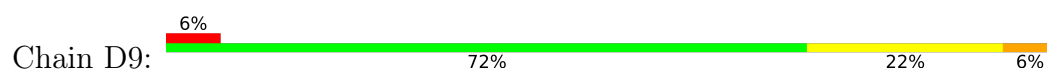
- Molecule 57: 50S ribosomal protein L35



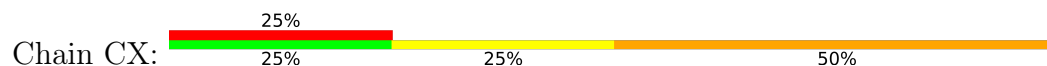
- Molecule 58: 50S ribosomal protein L36



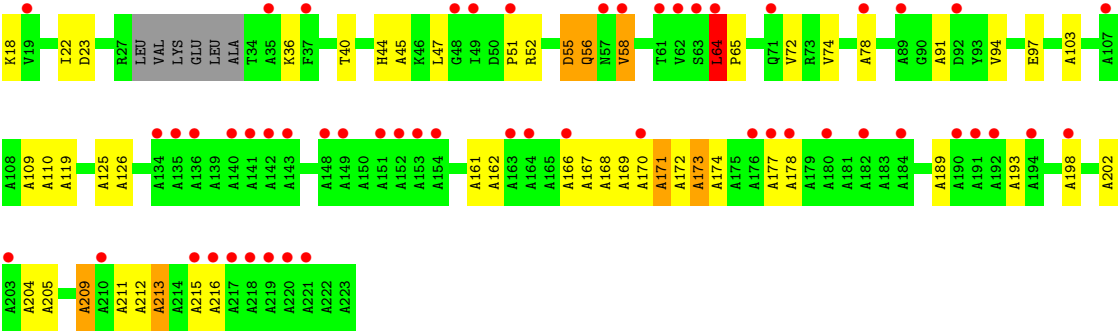
- Molecule 58: 50S ribosomal protein L36



- Molecule 59: mRNA



- Molecule 60: 50S Ribosomal protein L1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.92Å 449.90Å 624.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.57 – 3.30 39.57 – 3.30	Depositor EDS
% Data completeness (in resolution range)	95.6 (39.57-3.30) 95.6 (39.57-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.8.0031	Depositor
R, R_{free}	0.225 , 0.279 0.230 , 0.278	Depositor DCC
R_{free} test set	41956 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	63.7	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	295724	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.64% 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 ⓘ

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

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	0.48	0/36190	0.91	134/56486 (0.2%)
1	CA	0.46	0/36190	0.88	108/56486 (0.2%)
2	AB	0.62	0/1936	0.89	1/2609 (0.0%)
2	CB	0.65	0/1936	0.87	0/2609
3	AC	0.67	0/1637	0.90	0/2205
3	CC	0.64	0/1637	0.85	0/2205
4	AD	0.77	5/1733 (0.3%)	1.01	7/2318 (0.3%)
4	CD	0.74	1/1733 (0.1%)	0.99	5/2318 (0.2%)
5	AE	0.64	0/1163	0.98	0/1564
5	CE	0.64	0/1163	0.97	2/1564 (0.1%)
6	AF	0.66	0/856	0.98	1/1154 (0.1%)
6	CF	0.67	0/856	0.97	2/1154 (0.2%)
7	AG	0.61	0/1276	0.85	0/1709
7	CG	0.56	0/1276	0.89	0/1709
8	AH	0.65	0/1136	0.94	1/1527 (0.1%)
8	CH	0.62	0/1136	0.88	0/1527
9	AI	0.73	1/1029 (0.1%)	0.94	1/1378 (0.1%)
9	CI	0.60	0/1029	0.84	0/1378
10	AJ	0.73	1/808 (0.1%)	0.93	0/1085
10	CJ	0.69	0/808	0.91	1/1085 (0.1%)
11	AK	0.67	0/900	0.90	1/1213 (0.1%)
11	CK	0.64	0/900	1.00	3/1213 (0.2%)
12	AL	0.75	0/987	1.04	2/1320 (0.2%)
12	CL	0.72	0/987	1.00	2/1320 (0.2%)
13	AM	0.65	0/999	1.02	5/1336 (0.4%)
13	CM	0.64	0/999	0.96	5/1336 (0.4%)
14	AN	0.70	0/501	1.04	4/664 (0.6%)
14	CN	0.66	0/501	0.87	0/664
15	AO	0.63	0/745	0.88	0/992
15	CO	0.59	0/745	0.90	0/992
16	AP	0.66	0/717	0.94	1/963 (0.1%)
16	CP	0.69	0/717	0.91	1/963 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.62	0/837	0.88	1/1117 (0.1%)
17	CQ	0.63	0/837	0.96	1/1117 (0.1%)
18	AR	0.65	0/579	1.01	1/768 (0.1%)
18	CR	0.64	0/579	0.96	1/768 (0.1%)
19	AS	0.68	0/643	0.91	0/865
19	CS	0.66	0/643	0.86	1/865 (0.1%)
20	AT	0.64	0/765	0.96	2/1007 (0.2%)
20	CT	0.63	0/765	0.93	0/1007
21	AU	0.67	0/213	0.87	0/277
21	CU	0.77	0/213	0.93	0/277
22	AV	0.46	0/1832	0.95	9/2855 (0.3%)
22	CV	0.45	0/1832	0.85	3/2855 (0.1%)
23	AW	0.42	0/1809	0.79	3/2819 (0.1%)
23	CW	0.41	0/1809	0.79	3/2819 (0.1%)
24	AY	0.83	18/1815 (1.0%)	0.95	12/2833 (0.4%)
24	CY	0.83	18/1815 (1.0%)	0.95	12/2833 (0.4%)
25	AX	0.43	0/147	0.84	0/227
26	BA	0.55	2/67709 (0.0%)	1.11	666/105690 (0.6%)
26	DA	0.49	0/67709	0.98	360/105690 (0.3%)
27	BB	0.49	0/2853	1.03	19/4451 (0.4%)
27	DB	0.43	0/2853	0.88	5/4451 (0.1%)
28	BC	0.81	0/1160	0.86	0/1584
29	BD	0.98	1/2155 (0.0%)	1.31	18/2905 (0.6%)
29	DD	0.83	0/2155	1.12	7/2905 (0.2%)
30	BE	0.99	1/1597 (0.1%)	1.16	7/2153 (0.3%)
30	DE	0.81	3/1597 (0.2%)	1.08	4/2153 (0.2%)
31	BF	0.95	0/1659	1.20	9/2244 (0.4%)
31	DF	0.74	0/1659	1.05	6/2244 (0.3%)
32	BG	0.66	0/1499	0.98	4/2016 (0.2%)
32	DG	0.64	0/1499	0.88	3/2016 (0.1%)
33	BH	0.91	0/1246	1.14	5/1682 (0.3%)
33	DH	0.72	0/1246	0.98	4/1682 (0.2%)
34	BI	0.72	1/1147 (0.1%)	0.97	2/1551 (0.1%)
34	DI	0.70	0/1147	0.94	2/1551 (0.1%)
35	BJ	0.91	0/650	0.89	0/907
35	DJ	0.85	1/650 (0.2%)	0.85	1/907 (0.1%)
36	BN	0.94	0/1132	1.21	4/1525 (0.3%)
36	DN	0.71	0/1132	0.98	4/1525 (0.3%)
37	BO	0.82	0/943	1.05	2/1269 (0.2%)
37	DO	0.73	0/943	1.00	2/1269 (0.2%)
38	BP	1.01	4/1131 (0.4%)	1.37	11/1504 (0.7%)
38	DP	0.85	1/1131 (0.1%)	1.24	7/1504 (0.5%)
39	BQ	0.79	0/1143	1.06	3/1527 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	DQ	0.66	0/1143	0.90	1/1527 (0.1%)
40	BR	0.99	0/974	1.15	0/1302
40	DR	0.79	1/974 (0.1%)	1.03	2/1302 (0.2%)
41	BS	0.83	0/779	1.15	7/1036 (0.7%)
41	DS	0.70	0/779	0.95	0/1036
42	BT	0.83	0/1156	1.25	14/1542 (0.9%)
42	DT	0.79	0/1156	1.19	17/1542 (1.1%)
43	BU	1.02	0/975	1.22	2/1297 (0.2%)
43	DU	0.66	0/975	1.00	2/1297 (0.2%)
44	BV	0.96	0/790	1.15	3/1057 (0.3%)
44	DV	0.72	0/790	0.97	2/1057 (0.2%)
45	BW	0.91	0/907	1.15	2/1216 (0.2%)
45	DW	0.73	0/907	0.93	1/1216 (0.1%)
46	BX	0.91	0/740	1.21	3/993 (0.3%)
46	DX	0.73	0/740	0.96	0/993
47	BY	0.98	1/789 (0.1%)	1.44	11/1051 (1.0%)
47	DY	0.82	0/789	1.18	3/1051 (0.3%)
48	BZ	0.73	0/1436	0.92	3/1949 (0.2%)
48	DZ	0.65	0/1436	0.87	0/1949
49	B0	0.79	0/671	0.99	0/892
49	D0	0.70	0/671	0.88	1/892 (0.1%)
50	B1	0.85	0/741	1.09	2/984 (0.2%)
50	D1	0.76	0/741	1.10	5/984 (0.5%)
51	B2	0.77	0/600	1.05	0/793
51	D2	0.66	0/600	1.02	1/793 (0.1%)
52	B3	0.78	0/473	1.07	0/634
52	D3	0.63	0/473	0.99	0/634
53	B4	0.72	0/229	1.06	0/309
53	D4	0.72	0/229	0.98	0/309
54	B5	1.09	1/473 (0.2%)	1.47	7/639 (1.1%)
54	D5	0.82	0/473	1.25	5/639 (0.8%)
55	B6	1.35	1/388 (0.3%)	2.27	6/518 (1.2%)
55	D6	1.11	0/388	1.40	4/518 (0.8%)
56	B7	0.94	0/427	1.05	0/561
56	D7	0.82	0/427	0.97	0/561
57	B8	1.00	0/516	1.35	3/679 (0.4%)
57	D8	0.75	0/516	1.15	2/679 (0.3%)
58	B9	0.94	0/302	1.23	3/397 (0.8%)
58	D9	0.65	0/302	0.91	0/397
59	CX	0.50	0/94	0.90	0/144
60	DC	0.85	1/1160 (0.1%)	0.85	0/1584
All	All	0.60	63/321233 (0.0%)	1.00	1603/480213 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	1	0
1	CA	1	0
2	AB	0	1
13	AM	0	1
13	CM	0	1
23	AW	1	0
23	CW	1	0
26	BA	22	0
26	DA	20	0
29	BD	0	3
29	DD	0	2
30	BE	0	2
30	DE	0	1
33	BH	0	1
38	BP	0	10
38	DP	0	4
40	BR	0	2
40	DR	0	1
41	BS	0	1
42	BT	0	3
43	BU	0	3
44	BV	0	2
47	BY	0	1
55	B6	0	1
55	D6	0	1
57	B8	0	1
All	All	46	42

The worst 5 of 63 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	B6	47	THR	C-N	15.48	1.53	1.33
9	AI	126	SER	CA-C	9.54	1.56	1.52
24	AY	50	G	C1'-N9	-7.22	1.37	1.48
24	CY	50	G	C1'-N9	-7.21	1.37	1.48
24	CY	66	G	C1'-N9	-7.01	1.37	1.48

The worst 5 of 1603 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	B6	45	LYS	O-C-N	-38.82	73.14	122.82
26	DA	1345	U	C2'-C3'-O3'	17.35	135.53	109.50
26	DA	2013	G	C2'-C3'-O3'	16.43	134.14	109.50
26	BA	2013	G	C2'-C3'-O3'	15.96	133.44	109.50
26	DA	715	G	C2'-C3'-O3'	15.81	133.21	109.50

5 of 46 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	412	A	C1'
23	AW	47	U	C1'
26	BA	98	G	C1'
26	BA	497	A	C3'
26	BA	715	G	C4',C3',C1'

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	23	ARG	Peptide
13	AM	69	GLU	Peptide
29	BD	224	ALA	Peptide
29	BD	244	ARG	Peptide
29	BD	36	PRO	Peptide

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	32329	0	16318	499	1
1	CA	32329	0	16318	468	0
2	AB	1901	0	1951	47	0
2	CB	1901	0	1951	48	0
3	AC	1613	0	1677	45	0
3	CC	1613	0	1677	49	0
4	AD	1703	0	1763	67	0
4	CD	1703	0	1763	59	0
5	AE	1147	0	1207	44	0
5	CE	1147	0	1207	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	AF	843	0	857	18	0
6	CF	843	0	857	19	0
7	AG	1257	0	1296	22	0
7	CG	1257	0	1296	15	0
8	AH	1116	0	1177	30	0
8	CH	1116	0	1177	19	0
9	AI	1011	0	1043	32	0
9	CI	1011	0	1043	28	0
10	AJ	795	0	840	36	0
10	CJ	795	0	840	37	0
11	AK	885	0	904	34	0
11	CK	885	0	904	17	0
12	AL	971	0	1057	18	0
12	CL	971	0	1057	20	0
13	AM	988	0	1059	39	0
13	CM	988	0	1059	27	0
14	AN	492	0	529	16	0
14	CN	492	0	529	21	0
15	AO	734	0	771	22	0
15	CO	734	0	771	24	0
16	AP	701	0	720	22	0
16	CP	701	0	720	20	0
17	AQ	824	0	891	23	0
17	CQ	824	0	891	16	0
18	AR	574	0	644	20	0
18	CR	574	0	644	16	0
19	AS	630	0	652	35	0
19	CS	630	0	652	14	0
20	AT	763	0	861	29	0
20	CT	763	0	861	17	0
21	AU	209	0	221	4	0
21	CU	209	0	221	3	0
22	AV	1640	0	837	29	0
22	CV	1640	0	837	27	0
23	AW	1619	0	822	57	0
23	CW	1619	0	822	21	0
24	AY	1619	0	792	222	0
24	CY	1619	0	792	241	0
25	AX	151	0	76	15	0
26	BA	60459	0	30488	1174	0
26	DA	60459	0	30487	1028	0
27	BB	2551	0	1295	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	DB	2551	0	1295	35	0
28	BC	1157	0	1160	26	0
29	BD	2105	0	2182	140	0
29	DD	2105	0	2182	97	0
30	BE	1564	0	1629	103	0
30	DE	1564	0	1629	73	0
31	BF	1624	0	1677	77	0
31	DF	1624	0	1677	64	0
32	BG	1474	0	1535	57	0
32	DG	1474	0	1535	52	0
33	BH	1223	0	1282	50	0
33	DH	1223	0	1282	26	0
34	BI	1132	0	1218	33	0
34	DI	1132	0	1218	31	1
35	BJ	651	0	649	10	0
35	DJ	651	0	649	15	0
36	BN	1105	0	1180	66	0
36	DN	1105	0	1180	46	0
37	BO	933	0	996	34	0
37	DO	933	0	996	34	0
38	BP	1114	0	1187	143	0
38	DP	1114	0	1187	84	0
39	BQ	1122	0	1179	37	0
39	DQ	1122	0	1179	34	0
40	BR	960	0	1021	50	0
40	DR	960	0	1021	50	0
41	BS	771	0	832	51	0
41	DS	771	0	832	33	0
42	BT	1142	0	1202	95	0
42	DT	1142	0	1202	77	0
43	BU	958	0	1018	67	0
43	DU	958	0	1018	56	0
44	BV	779	0	852	58	0
44	DV	779	0	852	39	0
45	BW	896	0	956	42	0
45	DW	896	0	956	25	0
46	BX	726	0	778	28	0
46	DX	726	0	778	27	0
47	BY	776	0	868	82	0
47	DY	776	0	870	48	0
48	BZ	1404	0	1432	21	0
48	DZ	1404	0	1432	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	B0	662	0	688	20	0
49	D0	662	0	688	21	0
50	B1	734	0	808	24	0
50	D1	734	0	808	23	0
51	B2	598	0	653	27	0
51	D2	598	0	653	15	0
52	B3	468	0	523	20	0
52	D3	468	0	523	12	0
53	B4	226	0	229	8	0
53	D4	226	0	229	5	0
54	B5	459	0	477	48	0
54	D5	459	0	478	23	0
55	B6	381	0	390	55	0
55	D6	381	0	391	34	0
56	B7	419	0	467	16	0
56	D7	419	0	467	17	0
57	B8	508	0	576	58	0
57	D8	508	0	576	37	0
58	B9	299	0	324	19	0
58	D9	299	0	324	7	0
59	CX	85	0	43	7	0
60	DC	1157	0	1160	24	0
All	All	295724	0	201402	6841	1

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 14.

The worst 5 of 6841 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)
24:AY:10:C:H41	24:AY:45:G:N2	1.03	1.51
24:C'Y:7:A:N1	24:C'Y:66:G:N2	1.61	1.48
24:AY:7:A:N1	24:AY:66:G:N2	1.61	1.46
24:C'Y:10:C:H41	24:C'Y:45:G:N2	1.03	1.46
24:C'Y:9:G:H21	24:C'Y:11:C:N4	1.02	1.45

All (1) 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)
1:AA:358:U:OP1	34:DI:87:LYS:NZ[4_455]	2.03	0.17

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%)	170 (73%)	51 (22%)	11 (5%)	2	12
2	CB	232/234 (99%)	181 (78%)	41 (18%)	10 (4%)	2	14
3	AC	204/206 (99%)	150 (74%)	40 (20%)	14 (7%)	1	7
3	CC	204/206 (99%)	159 (78%)	32 (16%)	13 (6%)	1	8
4	AD	206/208 (99%)	155 (75%)	37 (18%)	14 (7%)	1	7
4	CD	206/208 (99%)	160 (78%)	36 (18%)	10 (5%)	1	12
5	AE	148/150 (99%)	129 (87%)	15 (10%)	4 (3%)	4	22
5	CE	148/150 (99%)	130 (88%)	16 (11%)	2 (1%)	9	33
6	AF	99/101 (98%)	89 (90%)	7 (7%)	3 (3%)	3	20
6	CF	99/101 (98%)	88 (89%)	9 (9%)	2 (2%)	6	27
7	AG	153/155 (99%)	133 (87%)	18 (12%)	2 (1%)	9	35
7	CG	153/155 (99%)	130 (85%)	18 (12%)	5 (3%)	3	19
8	AH	136/138 (99%)	119 (88%)	14 (10%)	3 (2%)	5	26
8	CH	136/138 (99%)	115 (85%)	18 (13%)	3 (2%)	5	26
9	AI	125/127 (98%)	96 (77%)	25 (20%)	4 (3%)	3	19
9	CI	125/127 (98%)	101 (81%)	21 (17%)	3 (2%)	4	24
10	AJ	96/98 (98%)	76 (79%)	17 (18%)	3 (3%)	3	20
10	CJ	96/98 (98%)	73 (76%)	18 (19%)	5 (5%)	1	11
11	AK	117/119 (98%)	96 (82%)	19 (16%)	2 (2%)	7	30
11	CK	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	4	23
12	AL	122/124 (98%)	95 (78%)	18 (15%)	9 (7%)	1	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	CL	122/124 (98%)	95 (78%)	20 (16%)	7 (6%)	1	9
13	AM	122/124 (98%)	87 (71%)	23 (19%)	12 (10%)	0	3
13	CM	122/124 (98%)	90 (74%)	23 (19%)	9 (7%)	1	6
14	AN	58/60 (97%)	43 (74%)	11 (19%)	4 (7%)	1	7
14	CN	58/60 (97%)	46 (79%)	8 (14%)	4 (7%)	1	7
15	AO	86/88 (98%)	62 (72%)	19 (22%)	5 (6%)	1	9
15	CO	86/88 (98%)	71 (83%)	10 (12%)	5 (6%)	1	9
16	AP	81/83 (98%)	68 (84%)	13 (16%)	0	100	100
16	CP	81/83 (98%)	64 (79%)	12 (15%)	5 (6%)	1	9
17	AQ	97/99 (98%)	85 (88%)	8 (8%)	4 (4%)	2	15
17	CQ	97/99 (98%)	89 (92%)	5 (5%)	3 (3%)	3	20
18	AR	68/70 (97%)	55 (81%)	8 (12%)	5 (7%)	1	6
18	CR	68/70 (97%)	58 (85%)	6 (9%)	4 (6%)	1	9
19	AS	76/78 (97%)	57 (75%)	11 (14%)	8 (10%)	0	2
19	CS	76/78 (97%)	64 (84%)	8 (10%)	4 (5%)	1	10
20	AT	97/99 (98%)	71 (73%)	22 (23%)	4 (4%)	2	15
20	CT	97/99 (98%)	72 (74%)	21 (22%)	4 (4%)	2	15
21	AU	22/24 (92%)	13 (59%)	7 (32%)	2 (9%)	0	3
21	CU	22/24 (92%)	17 (77%)	4 (18%)	1 (4%)	2	13
28	BC	182/206 (88%)	111 (61%)	50 (28%)	21 (12%)	0	2
29	BD	269/271 (99%)	214 (80%)	34 (13%)	21 (8%)	1	5
29	DD	269/271 (99%)	217 (81%)	31 (12%)	21 (8%)	1	5
30	BE	202/204 (99%)	138 (68%)	47 (23%)	17 (8%)	0	4
30	DE	202/204 (99%)	152 (75%)	35 (17%)	15 (7%)	1	6
31	BF	205/207 (99%)	163 (80%)	28 (14%)	14 (7%)	1	7
31	DF	205/207 (99%)	163 (80%)	28 (14%)	14 (7%)	1	7
32	BG	179/181 (99%)	140 (78%)	27 (15%)	12 (7%)	1	7
32	DG	179/181 (99%)	137 (76%)	31 (17%)	11 (6%)	1	9
33	BH	157/159 (99%)	113 (72%)	24 (15%)	20 (13%)	0	1
33	DH	157/159 (99%)	116 (74%)	25 (16%)	16 (10%)	0	2
34	BI	143/145 (99%)	107 (75%)	29 (20%)	7 (5%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	DI	143/145 (99%)	110 (77%)	25 (18%)	8 (6%)	1	9
35	BJ	128/130 (98%)	70 (55%)	42 (33%)	16 (12%)	0	1
35	DJ	128/130 (98%)	72 (56%)	42 (33%)	14 (11%)	0	2
36	BN	136/138 (99%)	100 (74%)	25 (18%)	11 (8%)	1	5
36	DN	136/138 (99%)	108 (79%)	15 (11%)	13 (10%)	0	3
37	BO	120/122 (98%)	106 (88%)	12 (10%)	2 (2%)	7	30
37	DO	120/122 (98%)	106 (88%)	13 (11%)	1 (1%)	16	45
38	BP	144/146 (99%)	82 (57%)	37 (26%)	25 (17%)	0	0
38	DP	144/146 (99%)	87 (60%)	28 (19%)	29 (20%)	0	0
39	BQ	139/141 (99%)	109 (78%)	25 (18%)	5 (4%)	2	17
39	DQ	139/141 (99%)	116 (84%)	19 (14%)	4 (3%)	3	21
40	BR	115/117 (98%)	93 (81%)	16 (14%)	6 (5%)	1	11
40	DR	115/117 (98%)	92 (80%)	17 (15%)	6 (5%)	1	11
41	BS	96/98 (98%)	58 (60%)	22 (23%)	16 (17%)	0	1
41	DS	96/98 (98%)	63 (66%)	20 (21%)	13 (14%)	0	1
42	BT	135/137 (98%)	95 (70%)	23 (17%)	17 (13%)	0	1
42	DT	135/137 (98%)	89 (66%)	30 (22%)	16 (12%)	0	1
43	BU	115/117 (98%)	90 (78%)	19 (16%)	6 (5%)	1	11
43	DU	115/117 (98%)	92 (80%)	19 (16%)	4 (4%)	3	18
44	BV	99/101 (98%)	74 (75%)	14 (14%)	11 (11%)	0	2
44	DV	99/101 (98%)	72 (73%)	17 (17%)	10 (10%)	0	3
45	BW	111/113 (98%)	92 (83%)	16 (14%)	3 (3%)	4	22
45	DW	111/113 (98%)	96 (86%)	7 (6%)	8 (7%)	1	6
46	BX	90/92 (98%)	80 (89%)	7 (8%)	3 (3%)	3	19
46	DX	90/92 (98%)	75 (83%)	8 (9%)	7 (8%)	1	5
47	BY	98/100 (98%)	53 (54%)	22 (22%)	23 (24%)	0	0
47	DY	98/100 (98%)	60 (61%)	19 (19%)	19 (19%)	0	0
48	BZ	174/176 (99%)	141 (81%)	26 (15%)	7 (4%)	2	15
48	DZ	174/176 (99%)	130 (75%)	33 (19%)	11 (6%)	1	8
49	B0	82/84 (98%)	75 (92%)	6 (7%)	1 (1%)	10	37
49	D0	82/84 (98%)	72 (88%)	9 (11%)	1 (1%)	10	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	B1	91/93 (98%)	76 (84%)	12 (13%)	3 (3%)	3	19
50	D1	91/93 (98%)	74 (81%)	10 (11%)	7 (8%)	1	5
51	B2	69/71 (97%)	53 (77%)	10 (14%)	6 (9%)	0	4
51	D2	69/71 (97%)	54 (78%)	11 (16%)	4 (6%)	1	9
52	B3	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	6	29
52	D3	57/59 (97%)	53 (93%)	3 (5%)	1 (2%)	6	29
53	B4	28/30 (93%)	21 (75%)	4 (14%)	3 (11%)	0	2
53	D4	28/30 (93%)	20 (71%)	5 (18%)	3 (11%)	0	2
54	B5	57/59 (97%)	43 (75%)	9 (16%)	5 (9%)	0	4
54	D5	57/59 (97%)	48 (84%)	4 (7%)	5 (9%)	0	4
55	B6	42/44 (96%)	21 (50%)	8 (19%)	13 (31%)	0	0
55	D6	42/44 (96%)	23 (55%)	7 (17%)	12 (29%)	0	0
56	B7	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
56	D7	46/48 (96%)	45 (98%)	0	1 (2%)	5	26
57	B8	61/63 (97%)	44 (72%)	10 (16%)	7 (12%)	0	2
57	D8	61/63 (97%)	47 (77%)	8 (13%)	6 (10%)	0	3
58	B9	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
58	D9	34/36 (94%)	33 (97%)	1 (3%)	0	100	100
60	DC	182/196 (93%)	115 (63%)	47 (26%)	20 (11%)	0	2
All	All	11898/12136 (98%)	9181 (77%)	1900 (16%)	817 (7%)	1	7

5 of 817 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	106	LYS
2	AB	165	VAL
3	AC	12	LEU
3	AC	20	SER
3	AC	47	LEU

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	
2	AB	202/202 (100%)	186 (92%)	16 (8%)	11	36
2	CB	202/202 (100%)	185 (92%)	17 (8%)	10	34
3	AC	160/160 (100%)	143 (89%)	17 (11%)	6	24
3	CC	160/160 (100%)	149 (93%)	11 (7%)	14	41
4	AD	180/180 (100%)	158 (88%)	22 (12%)	5	19
4	CD	180/180 (100%)	162 (90%)	18 (10%)	7	27
5	AE	115/115 (100%)	104 (90%)	11 (10%)	8	29
5	CE	115/115 (100%)	101 (88%)	14 (12%)	5	19
6	AF	90/90 (100%)	80 (89%)	10 (11%)	6	22
6	CF	90/90 (100%)	85 (94%)	5 (6%)	19	47
7	AG	126/126 (100%)	114 (90%)	12 (10%)	8	29
7	CG	126/126 (100%)	112 (89%)	14 (11%)	6	22
8	AH	119/119 (100%)	105 (88%)	14 (12%)	5	20
8	CH	119/119 (100%)	107 (90%)	12 (10%)	7	26
9	AI	98/98 (100%)	91 (93%)	7 (7%)	13	40
9	CI	98/98 (100%)	87 (89%)	11 (11%)	6	22
10	AJ	88/88 (100%)	76 (86%)	12 (14%)	3	16
10	CJ	88/88 (100%)	80 (91%)	8 (9%)	9	31
11	AK	90/90 (100%)	80 (89%)	10 (11%)	6	22
11	CK	90/90 (100%)	84 (93%)	6 (7%)	15	42
12	AL	104/104 (100%)	89 (86%)	15 (14%)	3	14
12	CL	104/104 (100%)	88 (85%)	16 (15%)	2	12
13	AM	99/99 (100%)	87 (88%)	12 (12%)	5	20
13	CM	99/99 (100%)	88 (89%)	11 (11%)	6	22
14	AN	49/49 (100%)	43 (88%)	6 (12%)	5	19
14	CN	49/49 (100%)	43 (88%)	6 (12%)	5	19
15	AO	79/79 (100%)	73 (92%)	6 (8%)	12	37
15	CO	79/79 (100%)	73 (92%)	6 (8%)	12	37
16	AP	72/72 (100%)	62 (86%)	10 (14%)	3	15
16	CP	72/72 (100%)	61 (85%)	11 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	AQ	94/94 (100%)	90 (96%)	4 (4%)	26	54
17	CQ	94/94 (100%)	89 (95%)	5 (5%)	20	49
18	AR	61/61 (100%)	55 (90%)	6 (10%)	7	28
18	CR	61/61 (100%)	59 (97%)	2 (3%)	33	59
19	AS	69/69 (100%)	54 (78%)	15 (22%)	1	5
19	CS	69/69 (100%)	60 (87%)	9 (13%)	4	17
20	AT	76/76 (100%)	68 (90%)	8 (10%)	6	25
20	CT	76/76 (100%)	66 (87%)	10 (13%)	4	17
21	AU	19/19 (100%)	16 (84%)	3 (16%)	2	12
21	CU	19/19 (100%)	18 (95%)	1 (5%)	20	49
28	BC	61/66 (92%)	54 (88%)	7 (12%)	5	21
29	BD	213/213 (100%)	178 (84%)	35 (16%)	2	11
29	DD	213/213 (100%)	175 (82%)	38 (18%)	2	8
30	BE	165/165 (100%)	134 (81%)	31 (19%)	1	7
30	DE	165/165 (100%)	139 (84%)	26 (16%)	2	12
31	BF	165/165 (100%)	137 (83%)	28 (17%)	2	10
31	DF	165/165 (100%)	147 (89%)	18 (11%)	6	23
32	BG	155/155 (100%)	129 (83%)	26 (17%)	2	11
32	DG	155/155 (100%)	140 (90%)	15 (10%)	8	28
33	BH	132/132 (100%)	103 (78%)	29 (22%)	1	5
33	DH	132/132 (100%)	120 (91%)	12 (9%)	9	31
34	BI	122/122 (100%)	107 (88%)	15 (12%)	4	19
34	DI	122/122 (100%)	103 (84%)	19 (16%)	2	12
36	BN	117/117 (100%)	87 (74%)	30 (26%)	0	2
36	DN	117/117 (100%)	97 (83%)	20 (17%)	2	10
37	BO	100/100 (100%)	91 (91%)	9 (9%)	9	31
37	DO	100/100 (100%)	88 (88%)	12 (12%)	5	20
38	BP	112/112 (100%)	84 (75%)	28 (25%)	0	3
38	DP	112/112 (100%)	82 (73%)	30 (27%)	0	2
39	BQ	111/111 (100%)	96 (86%)	15 (14%)	4	16
39	DQ	111/111 (100%)	98 (88%)	13 (12%)	5	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	BR	100/100 (100%)	82 (82%)	18 (18%)	2	8
40	DR	100/100 (100%)	84 (84%)	16 (16%)	2	11
41	BS	77/77 (100%)	58 (75%)	19 (25%)	1	3
41	DS	77/77 (100%)	66 (86%)	11 (14%)	3	14
42	BT	120/120 (100%)	95 (79%)	25 (21%)	1	6
42	DT	120/120 (100%)	89 (74%)	31 (26%)	0	2
43	BU	92/92 (100%)	77 (84%)	15 (16%)	2	11
43	DU	92/92 (100%)	83 (90%)	9 (10%)	7	28
44	BV	82/82 (100%)	58 (71%)	24 (29%)	0	2
44	DV	82/82 (100%)	64 (78%)	18 (22%)	1	5
45	BW	91/91 (100%)	75 (82%)	16 (18%)	2	9
45	DW	91/91 (100%)	76 (84%)	15 (16%)	2	11
46	BX	74/74 (100%)	65 (88%)	9 (12%)	5	19
46	DX	74/74 (100%)	66 (89%)	8 (11%)	6	23
47	BY	84/84 (100%)	64 (76%)	20 (24%)	1	4
47	DY	84/84 (100%)	68 (81%)	16 (19%)	1	7
48	BZ	155/155 (100%)	139 (90%)	16 (10%)	7	25
48	DZ	155/155 (100%)	146 (94%)	9 (6%)	18	47
49	B0	66/66 (100%)	54 (82%)	12 (18%)	2	8
49	D0	66/66 (100%)	60 (91%)	6 (9%)	9	31
50	B1	78/78 (100%)	67 (86%)	11 (14%)	3	14
50	D1	78/78 (100%)	59 (76%)	19 (24%)	1	3
51	B2	66/66 (100%)	51 (77%)	15 (23%)	1	4
51	D2	66/66 (100%)	59 (89%)	7 (11%)	6	24
52	B3	51/51 (100%)	44 (86%)	7 (14%)	3	16
52	D3	51/51 (100%)	49 (96%)	2 (4%)	28	56
53	B4	27/27 (100%)	22 (82%)	5 (18%)	1	7
53	D4	27/27 (100%)	23 (85%)	4 (15%)	3	13
54	B5	51/51 (100%)	41 (80%)	10 (20%)	1	6
54	D5	51/51 (100%)	42 (82%)	9 (18%)	2	9
55	B6	43/43 (100%)	32 (74%)	11 (26%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	D6	43/43 (100%)	33 (77%)	10 (23%)	1	4
56	B7	41/41 (100%)	32 (78%)	9 (22%)	1	5
56	D7	41/41 (100%)	33 (80%)	8 (20%)	1	6
57	B8	53/53 (100%)	39 (74%)	14 (26%)	0	2
57	D8	53/53 (100%)	43 (81%)	10 (19%)	1	7
58	B9	33/33 (100%)	25 (76%)	8 (24%)	1	3
58	D9	33/33 (100%)	29 (88%)	4 (12%)	5	20
60	DC	61/66 (92%)	55 (90%)	6 (10%)	7	28
All	All	9654/9664 (100%)	8307 (86%)	1347 (14%)	3	15

5 of 1347 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	DC	23	ASP
40	DR	95	THR
29	DD	138	VAL
21	CU	24	ARG
33	DH	155	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 184 such sidechains are listed below:

Mol	Chain	Res	Type
7	CG	97	GLN
33	DH	147	ASN
12	CL	9	GLN
29	DD	198	ASN
37	DO	82	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1504 (99%)	303 (20%)	43 (2%)
1	CA	1504/1504 (100%)	304 (20%)	53 (3%)
22	AV	76/77 (98%)	20 (26%)	4 (5%)
22	CV	76/77 (98%)	24 (31%)	1 (1%)
23	AW	75/76 (98%)	22 (29%)	2 (2%)
23	CW	75/76 (98%)	19 (25%)	2 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	AY	74/75 (98%)	38 (51%)	4 (5%)
24	CY	74/75 (98%)	38 (51%)	4 (5%)
25	AX	5/7 (71%)	4 (80%)	1 (20%)
26	BA	2804/2915 (96%)	804 (28%)	151 (5%)
26	DA	2803/2915 (96%)	774 (27%)	122 (4%)
27	BB	118/119 (99%)	36 (30%)	4 (3%)
27	DB	118/119 (99%)	27 (22%)	4 (3%)
59	CX	3/4 (75%)	2 (66%)	0
All	All	9308/9543 (97%)	2415 (25%)	395 (4%)

5 of 2415 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	8	A
1	AA	9	G
1	AA	13	U
1	AA	22	G

5 of 395 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	495	C
26	DA	355	A
1	CA	671	A
1	CA	1476	U
26	DA	715	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	PSU	AX	19	25,24	18,21,22	1.55	3 (16%)	21,30,33	1.49	3 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	PSU	AX	19	25,24	-	2/7/25/26	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	AX	19	PSU	C2-N1	5.10	1.43	1.36
25	AX	19	PSU	C6-C5	2.58	1.38	1.35
25	AX	19	PSU	C4-C5	-2.05	1.38	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AX	19	PSU	C6-C5-C4	4.23	121.03	118.17
25	AX	19	PSU	C6-N1-C2	-3.19	119.73	122.69
25	AX	19	PSU	O2-C2-N1	2.99	125.87	122.79

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	AX	19	PSU	O4'-C4'-C5'-O5'
25	AX	19	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	AX	19	PSU	7	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
60	DC	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DC	110:ALA	C	119:ALA	N	13.98
1	DC	136:ALA	C	139:ALA	N	11.93

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	1504/1504 (100%)	0.10	42 (2%) 55 36	23, 77, 165, 393	0
1	CA	1504/1504 (100%)	0.26	71 (4%) 36 24	38, 86, 188, 312	0
2	AB	234/234 (100%)	0.65	15 (6%) 25 17	66, 113, 158, 196	0
2	CB	234/234 (100%)	1.04	32 (13%) 6 5	85, 139, 177, 216	0
3	AC	206/206 (100%)	0.55	12 (5%) 29 19	64, 96, 134, 183	0
3	CC	206/206 (100%)	1.08	28 (13%) 7 6	90, 130, 182, 221	0
4	AD	208/208 (100%)	0.60	23 (11%) 10 9	55, 91, 126, 174	0
4	CD	208/208 (100%)	0.31	12 (5%) 29 19	49, 79, 108, 139	0
5	AE	150/150 (100%)	0.20	3 (2%) 65 46	47, 76, 104, 125	0
5	CE	150/150 (100%)	0.45	8 (5%) 32 22	58, 88, 126, 148	0
6	AF	101/101 (100%)	0.12	0 100 100	52, 80, 108, 124	0
6	CF	101/101 (100%)	0.15	1 (0%) 79 63	52, 82, 116, 139	0
7	AG	155/155 (100%)	0.53	12 (7%) 19 14	61, 97, 137, 156	0
7	CG	155/155 (100%)	0.76	13 (8%) 17 13	82, 119, 157, 175	0
8	AH	138/138 (100%)	0.15	3 (2%) 62 43	50, 81, 105, 135	0
8	CH	138/138 (100%)	0.50	5 (3%) 46 31	59, 95, 119, 146	0
9	AI	127/127 (100%)	0.78	10 (7%) 18 14	58, 112, 146, 230	0
9	CI	127/127 (100%)	1.27	31 (24%) 2 1	94, 136, 180, 235	0
10	AJ	98/98 (100%)	1.14	16 (16%) 4 4	67, 119, 160, 187	0
10	CJ	98/98 (100%)	1.59	24 (24%) 2 1	94, 158, 190, 226	0
11	AK	119/119 (100%)	0.36	4 (3%) 48 32	45, 79, 108, 165	0
11	CK	119/119 (100%)	0.61	8 (6%) 24 16	55, 95, 132, 161	0
12	AL	124/124 (100%)	0.40	8 (6%) 25 17	47, 71, 105, 155	0
12	CL	124/124 (100%)	0.49	6 (4%) 35 24	50, 81, 115, 124	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	124/124 (100%)	0.93	15 (12%) 8 7	68, 112, 153, 231	0
13	CM	124/124 (100%)	1.58	35 (28%) 1 1	101, 153, 200, 218	0
14	AN	60/60 (100%)	0.52	3 (5%) 34 23	55, 85, 135, 155	0
14	CN	60/60 (100%)	1.24	11 (18%) 3 3	104, 137, 160, 182	0
15	AO	88/88 (100%)	0.38	4 (4%) 38 25	48, 80, 111, 130	0
15	CO	88/88 (100%)	0.29	3 (3%) 48 32	55, 87, 117, 139	0
16	AP	83/83 (100%)	0.76	7 (8%) 17 13	65, 92, 125, 149	0
16	CP	83/83 (100%)	0.19	2 (2%) 59 40	51, 73, 112, 139	0
17	AQ	99/99 (100%)	0.38	2 (2%) 65 46	51, 90, 112, 117	0
17	CQ	99/99 (100%)	0.38	3 (3%) 52 35	63, 87, 115, 126	0
18	AR	70/70 (100%)	0.35	3 (4%) 40 25	48, 76, 108, 138	0
18	CR	70/70 (100%)	0.32	1 (1%) 73 55	61, 91, 126, 149	0
19	AS	78/78 (100%)	0.91	9 (11%) 9 8	72, 114, 165, 189	0
19	CS	78/78 (100%)	1.35	15 (19%) 3 3	111, 160, 208, 221	0
20	AT	99/99 (100%)	0.73	10 (10%) 12 10	67, 102, 150, 169	0
20	CT	99/99 (100%)	0.52	4 (4%) 42 28	49, 96, 135, 150	0
21	AU	24/24 (100%)	1.02	1 (4%) 40 26	74, 92, 117, 119	0
21	CU	24/24 (100%)	2.54	13 (54%) 0 0	105, 141, 205, 253	0
22	AV	77/77 (100%)	-0.02	1 (1%) 75 56	34, 78, 122, 187	0
22	CV	77/77 (100%)	0.35	1 (1%) 75 56	41, 107, 162, 175	0
23	AW	76/76 (100%)	1.04	7 (9%) 14 11	37, 183, 225, 269	0
23	CW	76/76 (100%)	1.23	15 (19%) 3 3	59, 192, 268, 296	0
24	AY	75/75 (100%)	3.25	54 (72%) 0 0	37, 107, 188, 213	0
24	CY	75/75 (100%)	3.88	65 (86%) 0 0	37, 107, 188, 213	0
25	AX	6/7 (85%)	0.18	0 100 100	50, 53, 106, 116	0
26	BA	2807/2915 (96%)	-0.46	43 (1%) 72 53	9, 38, 151, 312	0
26	DA	2807/2915 (96%)	-0.12	56 (1%) 65 46	24, 64, 168, 297	0
27	BB	119/119 (100%)	-0.25	0 100 100	32, 60, 91, 118	0
27	DB	119/119 (100%)	0.53	5 (4%) 40 26	71, 112, 151, 191	0
28	BC	190/206 (92%)	1.34	36 (18%) 3 3	108, 181, 242, 295	0
29	BD	271/271 (100%)	-0.16	4 (1%) 72 53	18, 36, 76, 122	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
29	DD	271/271 (100%)	0.10	9 (3%) 49 33	23, 56, 91, 127	0
30	BE	204/204 (100%)	0.09	9 (4%) 39 25	18, 48, 92, 134	0
30	DE	204/204 (100%)	0.29	7 (3%) 48 32	28, 65, 120, 165	0
31	BF	207/207 (100%)	0.02	7 (3%) 48 32	17, 48, 133, 191	0
31	DF	207/207 (100%)	0.38	8 (3%) 43 29	31, 87, 149, 214	0
32	BG	181/181 (100%)	0.35	6 (3%) 49 33	56, 82, 129, 172	0
32	DG	181/181 (100%)	0.92	19 (10%) 11 9	82, 128, 167, 210	0
33	BH	159/159 (100%)	0.31	9 (5%) 29 20	32, 68, 118, 181	0
33	DH	159/159 (100%)	0.84	22 (13%) 6 5	70, 128, 180, 235	0
34	BI	145/145 (100%)	0.44	7 (4%) 35 24	44, 95, 123, 159	0
34	DI	145/145 (100%)	0.45	6 (4%) 41 27	48, 101, 137, 159	0
35	BJ	130/130 (100%)	1.86	52 (40%) 1 1	120, 164, 275, 373	0
35	DJ	130/130 (100%)	1.86	48 (36%) 1 1	122, 193, 233, 284	0
36	BN	138/138 (100%)	0.04	6 (4%) 40 25	24, 46, 95, 129	0
36	DN	138/138 (100%)	0.52	7 (5%) 33 22	54, 90, 120, 133	0
37	BO	122/122 (100%)	-0.26	0 100 100	26, 49, 75, 91	0
37	DO	122/122 (100%)	-0.08	1 (0%) 82 68	39, 64, 85, 92	0
38	BP	146/146 (100%)	0.62	13 (8%) 15 12	21, 65, 115, 159	0
38	DP	146/146 (100%)	0.90	18 (12%) 8 7	39, 92, 134, 174	0
39	BQ	141/141 (100%)	0.03	4 (2%) 55 36	27, 51, 85, 188	0
39	DQ	141/141 (100%)	0.55	8 (5%) 29 20	58, 92, 125, 161	0
40	BR	117/117 (100%)	-0.12	1 (0%) 81 65	21, 42, 78, 93	0
40	DR	117/117 (100%)	0.22	7 (5%) 27 19	40, 65, 100, 131	0
41	BS	98/98 (100%)	0.45	6 (6%) 27 18	35, 64, 105, 136	0
41	DS	98/98 (100%)	0.98	13 (13%) 7 6	72, 110, 151, 181	0
42	BT	137/137 (100%)	0.29	7 (5%) 33 22	34, 64, 139, 181	0
42	DT	137/137 (100%)	0.57	13 (9%) 14 11	43, 77, 135, 170	0
43	BU	117/117 (100%)	-0.15	3 (2%) 57 38	15, 37, 73, 98	0
43	DU	117/117 (100%)	0.45	6 (5%) 33 22	40, 80, 135, 155	0
44	BV	101/101 (100%)	0.06	5 (4%) 34 23	24, 51, 85, 119	0
44	DV	101/101 (100%)	0.74	10 (9%) 13 10	60, 110, 143, 183	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
45	BW	113/113 (100%)	-0.22	1 (0%) 81 65	25, 37, 75, 137	0
45	DW	113/113 (100%)	0.27	4 (3%) 47 31	49, 66, 103, 147	0
46	BX	92/92 (100%)	-0.22	0 100 100	25, 44, 73, 82	0
46	DX	92/92 (100%)	0.30	3 (3%) 49 33	43, 77, 98, 114	0
47	BY	100/100 (100%)	0.93	19 (19%) 3 3	34, 66, 163, 201	0
47	DY	100/100 (100%)	1.24	24 (24%) 2 1	56, 100, 175, 209	0
48	BZ	176/176 (100%)	0.97	31 (17%) 4 4	43, 119, 275, 309	0
48	DZ	176/176 (100%)	1.33	38 (21%) 2 2	92, 149, 299, 353	0
49	B0	84/84 (100%)	-0.14	0 100 100	25, 43, 78, 110	0
49	D0	84/84 (100%)	0.57	3 (3%) 46 31	58, 84, 105, 128	0
50	B1	93/93 (100%)	-0.05	1 (1%) 78 60	26, 48, 94, 131	0
50	D1	93/93 (100%)	0.13	1 (1%) 78 60	39, 62, 111, 153	0
51	B2	71/71 (100%)	0.09	3 (4%) 40 26	34, 61, 101, 164	0
51	D2	71/71 (100%)	0.56	6 (8%) 16 13	60, 90, 131, 150	0
52	B3	59/59 (100%)	-0.10	1 (1%) 69 50	29, 48, 92, 149	0
52	D3	59/59 (100%)	0.50	2 (3%) 48 32	65, 101, 135, 253	0
53	B4	30/30 (100%)	0.59	2 (6%) 24 16	69, 116, 141, 154	0
53	D4	30/30 (100%)	0.95	5 (16%) 4 4	121, 142, 163, 173	0
54	B5	59/59 (100%)	0.35	5 (8%) 16 13	21, 42, 139, 213	0
54	D5	59/59 (100%)	0.70	5 (8%) 16 13	42, 67, 130, 179	0
55	B6	44/44 (100%)	0.97	6 (13%) 7 6	30, 60, 93, 118	0
55	D6	44/44 (100%)	0.99	4 (9%) 15 11	51, 90, 113, 121	0
56	B7	48/48 (100%)	-0.11	2 (4%) 40 26	20, 30, 63, 124	0
56	D7	48/48 (100%)	0.09	2 (4%) 40 26	31, 49, 80, 98	0
57	B8	63/63 (100%)	0.30	6 (9%) 14 11	30, 44, 64, 129	0
57	D8	63/63 (100%)	0.85	10 (15%) 5 4	50, 77, 112, 154	0
58	B9	36/36 (100%)	0.25	1 (2%) 55 36	34, 49, 63, 78	0
58	D9	36/36 (100%)	0.82	2 (5%) 30 20	63, 91, 115, 125	0
59	CX	4/4 (100%)	0.37	1 (25%) 2 1	70, 87, 90, 158	0
60	DC	190/196 (96%)	1.59	54 (28%) 1 1	109, 188, 240, 265	0
All	All	21440/21679 (98%)	0.29	1394 (6%) 25 17	9, 77, 180, 393	0

The worst 5 of 1394 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
48	DZ	172	ALA	10.2
9	AI	126	SER	8.4
24	AY	18	G	8.2
24	CY	66	G	7.9
24	CY	17	G	7.7

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	PSU	AX	19	20/21	0.92	0.08	83,95,104,110	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.