



wwPDB X-ray Structure Validation Summary Report ⓘ

May 24, 2020 – 02:34 pm BST

PDB ID : 4WT8
Title : Crystal Structure of bactobolin A bound to 70S ribosome-tRNA complex
Authors : Amunts, A.; Fiedorczuk, K.; Ramakrishnan, V.
Deposited on : 2014-10-29
Resolution : 3.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

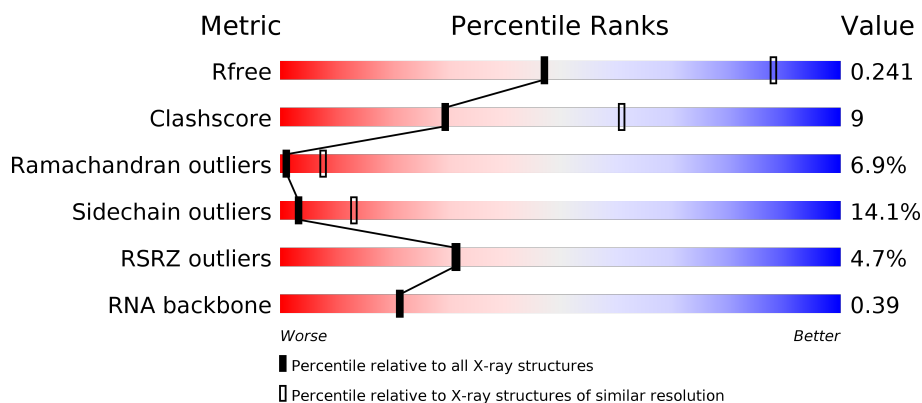
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)
RNA backbone	3102	1006 (3.84-2.96)

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 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	A2	9	
2	AA	234	
2	BA	234	
3	AC	238	

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Mol	Chain	Length	Quality of chain
4	AD	208	
4	BD	208	
5	AE	150	
5	BE	150	
6	AF	101	
6	BF	101	
7	AG	155	
7	BG	155	
8	AH	138	
8	BH	138	
9	AI	127	
9	BI	127	
10	AJ	98	
10	BJ	98	
11	AK	119	
11	BK	119	
12	AL	124	
12	BL	124	
13	AM	124	
13	BM	124	
14	AN	60	
14	BN	60	
15	AO	88	
15	BO	88	
16	AP	83	

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Mol	Chain	Length	Quality of chain
16	BP	83	
17	AR	99	
17	BR	99	
18	AS	70	
18	BS	70	
19	AT	78	
19	BT	78	
20	AU	99	
20	BU	99	
21	AW	24	
21	BW	24	
22	Ab	1504	
22	Bb	1504	
23	B2	10	
24	BC	206	
25	C2	76	
25	C3	76	
25	D3	76	
26	C4	77	
27	CA	206	
28	CB	271	
28	DB	271	
29	CC	204	
29	DC	204	
30	CD	207	

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Mol	Chain	Length	Quality of chain
30	DD	207	
31	CE	181	
31	DE	181	
32	CF	159	
32	DF	159	
33	CI	145	
33	DI	145	
34	CJ	130	
34	DJ	130	
35	CM	138	
35	DM	138	
36	CN	122	
36	DN	122	
37	CO	146	
37	DO	146	
38	CP	141	
38	DP	141	
39	CQ	117	
39	DQ	117	
40	CR	98	
40	DR	98	
41	CS	137	
41	DS	137	
42	CT	117	
42	DT	117	

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Mol	Chain	Length	Quality of chain
43	CU	101	
43	DU	101	
44	CW	113	
45	CX	92	
45	DX	92	
46	CY	100	
46	DY	100	
47	CZ	176	
47	DZ	176	
48	Ca	84	
48	Da	84	
49	CH	93	
49	DH	93	
50	CK	71	
50	DK	71	
51	CL	59	
51	DL	59	
52	C5	30	
52	D5	30	
53	C6	59	
53	D6	59	
54	C7	44	
54	D7	44	
55	C8	48	
55	D8	48	

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Mol	Chain	Length	Quality of chain
56	C9	63	
56	D9	63	
57	C0	36	
57	D0	36	
58	C1	2899	
58	D1	2899	
59	Cs	119	
59	Ds	119	
60	D2	20	
61	D4	76	
62	DA	206	
63	DW	113	
64	DV	55	

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
66	3V6	D1	3001	-	-	X	-
67	MG	D1	3002	-	-	X	-

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 295910 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 mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A2	9	Total	C	N	O	P	0	0	0
			173	76	29	59	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AA	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	BA	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
			1612	1016	314	281	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	BD	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	BE	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	BF	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	BG	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	BH	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	BI	127	Total	C	N	O	0	0	0
			1011	639	198	174			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	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	BJ	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	BK	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	BL	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	BM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	BN	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	BO	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	BP	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	AR	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			
17	BR	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	AS	70	Total	C	N	O	0	0	0
			574	367	112	95			
18	BS	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	AT	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			
19	BT	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	AU	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			
20	BU	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	AW	24	Total	C	N	O	0	0	0
			209	128	50	31			

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

- Molecule 22 is a RNA chain called RNA (1504-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Ab	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			
22	Bb	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	B2	10	Total	C	N	O	P	0	0	0
			194	86	34	64	10			

- Molecule 24 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

- Molecule 25 is a RNA chain called A site tNA, E site tNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	C2	75	Total	C	N	O	P	0	0	0
			1597	713	285	525	74			
25	C3	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
25	D3	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			

- Molecule 26 is a RNA chain called P site trNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	C4	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			

- Molecule 27 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	CA	190	Total	C	N	O	0	0	0
			1156	706	220	230			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	106	ALA	GLY	conflict	UNP Q5SLP7

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	CB	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			
28	DB	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	CC	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			
29	DC	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			

- Molecule 30 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	CD	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			
30	DD	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	CE	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
31	DE	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	CF	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			
32	DF	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called ribosomal L10 protein.

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

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	CM	138	Total	C	N	O	S	0	0	0
			1105	712	206	183	4			
35	DM	138	Total	C	N	O	S	0	0	0
			1105	712	206	183	4			

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	CN	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
36	DN	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	CO	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	DO	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	CP	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
38	DP	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	CQ	117	Total	C	N	O		0	0	0
			960	599	202	159				
39	DQ	117	Total	C	N	O		0	0	0
			960	599	202	159				

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	CR	98	Total	C	N	O		0	0	0
			771	486	154	131				
40	DR	98	Total	C	N	O		0	0	0
			771	486	154	131				

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	CS	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			
41	DS	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	CT	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			
42	DT	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
CT	32	ALA	PHE	conflict	UNP P60491
DT	32	ALA	PHE	conflict	UNP P60491

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	CU	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
43	DU	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called 50S ribosomal protein L23.

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

- Molecule 46 is a protein called 50S ribosomal protein L24.

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

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	Ca	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			
48	Da	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	CH	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			
49	DH	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	CK	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			
50	DK	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	CL	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			
51	DL	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	C5	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			
52	D5	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	C6	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
53	D6	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	C7	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			
54	D7	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	C8	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			
55	D8	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	C9	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			
56	D9	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	C0	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			
57	D0	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 58 is a RNA chain called 23S rRNA (2899-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	C1	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			
58	D1	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			

- Molecule 59 is a RNA chain called 5S rRNA (119-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	Cs	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			
59	Ds	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 60 is a RNA chain called tRNA (5'-D(*AP*UP*CP*CP*CP*CP*GP*UP*GP*UP*CP*CP*UP*UP*GP*GP*UP*UP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	D2	20	Total	C	N	O	P	0	0	0
			416	186	65	146	19			

- Molecule 61 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	D4	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			

- Molecule 62 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
62	DA	190	Total	C	N	O	0	0	0
			1155	705	220	230			

- Molecule 63 is a protein called 50S ribosomal protein L22.

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

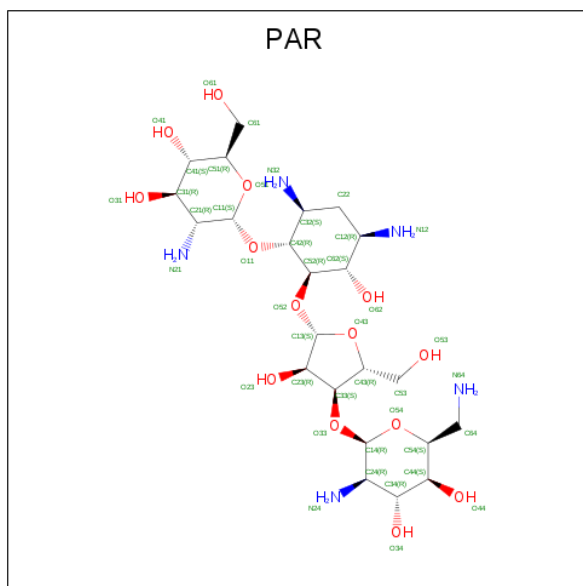
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DW	113	ALA	-	expression tag	UNP Q5SHP3

- Molecule 64 is a RNA chain called DNA (55-MER).

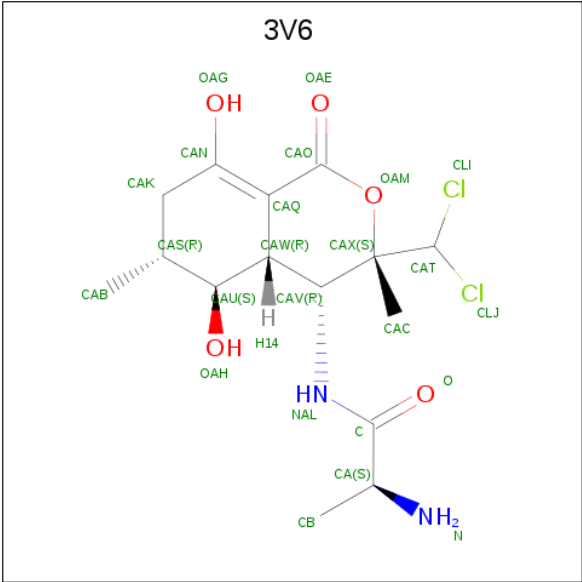
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	DV	55	Total	C	N	O	P	0	0	0
			1167	527	220	379	41			

- Molecule 65 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
65	Ab	1	Total	C	N	O	0	0
			42	23	5	14		
65	Bb	1	Total	C	N	O	0	0
			42	23	5	14		

- Molecule 66 is Bactobolin A (three-letter code: 3V6) (formula: $C_{15}H_{22}Cl_2N_2O_5$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
66	C1	1	Total	C	Cl	N	O	0	0
			24	15	2	2	5		
66	D1	1	Total	C	Cl	N	O	0	0
			24	15	2	2	5		

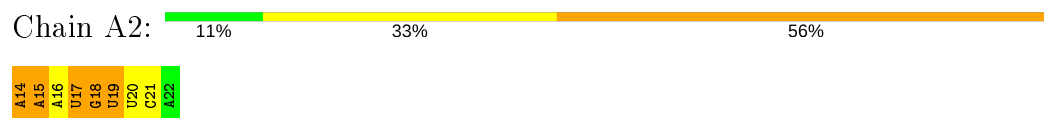
- Molecule 67 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
67	C1	1	Total	Mg	0	0
			1	1		
67	D1	1	Total	Mg	0	0
			1	1		

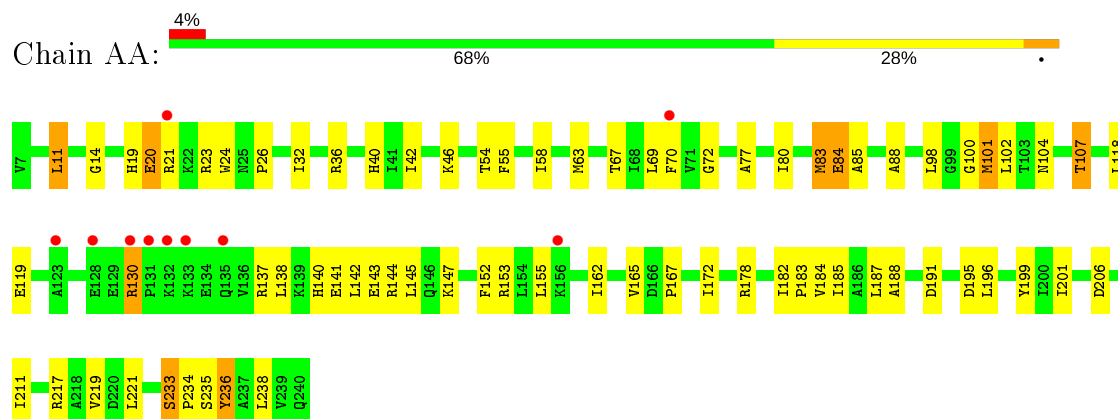
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

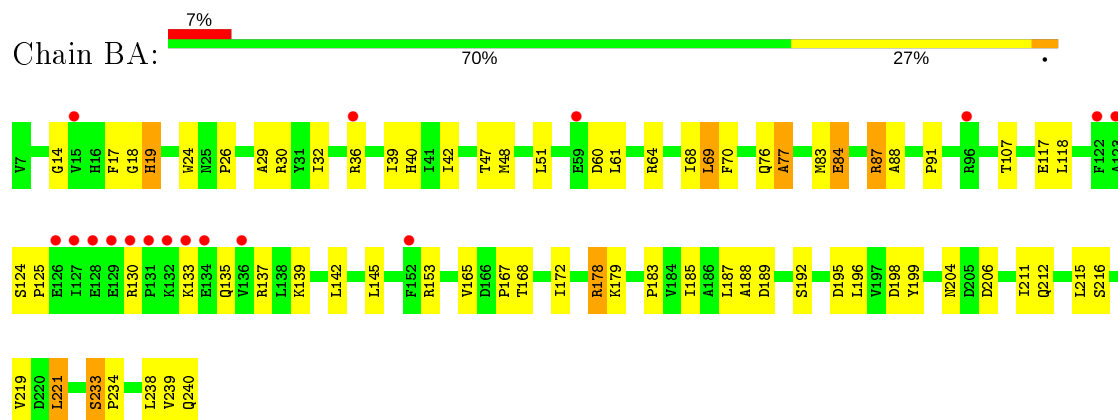
• Molecule 1: mRNA



• Molecule 2: 30S ribosomal protein S2

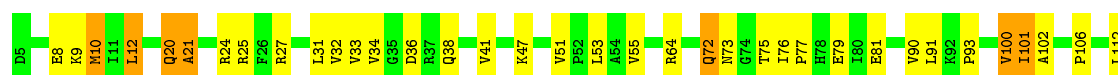


• Molecule 2: 30S ribosomal protein S2



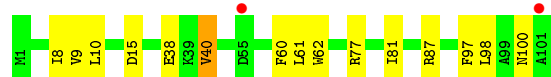
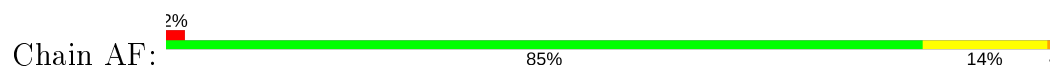
• Molecule 3: 30S ribosomal protein S3



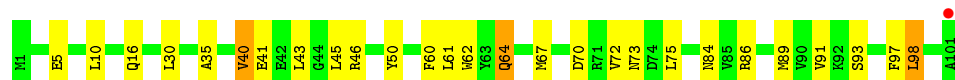
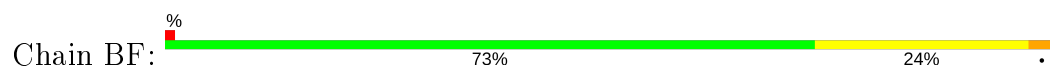




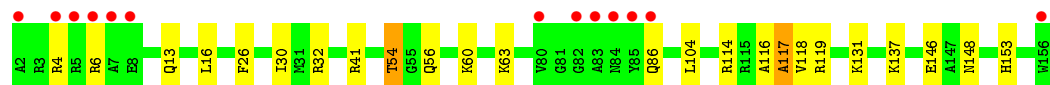
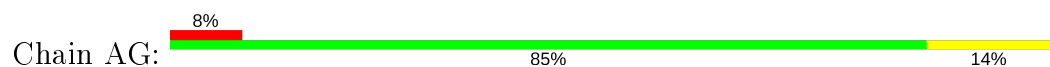
- Molecule 6: 30S ribosomal protein S6



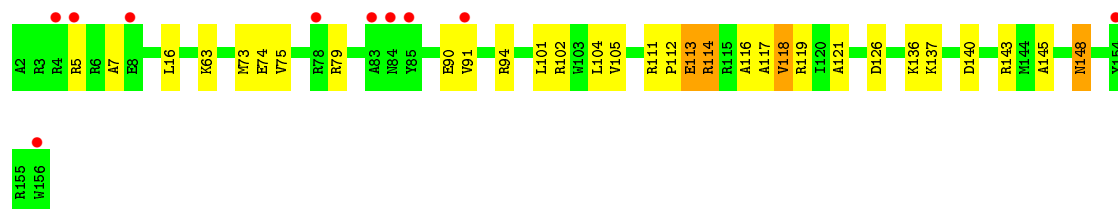
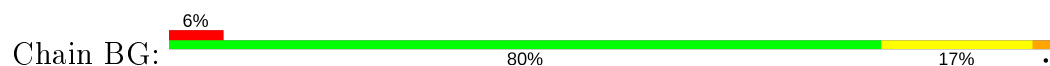
- Molecule 6: 30S ribosomal protein S6



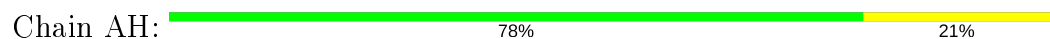
- Molecule 7: 30S ribosomal protein S7



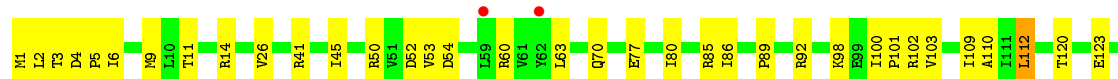
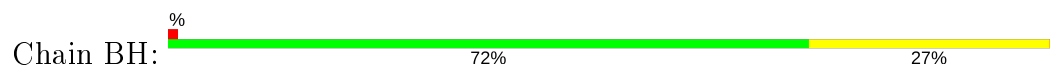
- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8



- Molecule 8: 30S ribosomal protein S8





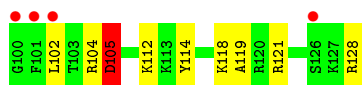
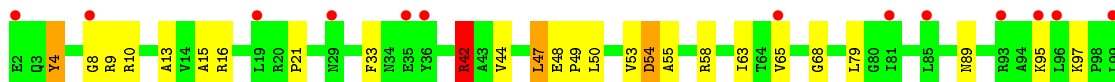
- Molecule 9: 30S ribosomal protein S9

Chain AI: 6% 61% 32% 6%



- Molecule 9: 30S ribosomal protein S9

Chain BI: 13% 72% 24%



- Molecule 10: 30S ribosomal protein S10

Chain AJ: 13% 66% 26% 8%



- Molecule 10: 30S ribosomal protein S10

Chain BJ: 22% 62% 28% 10%

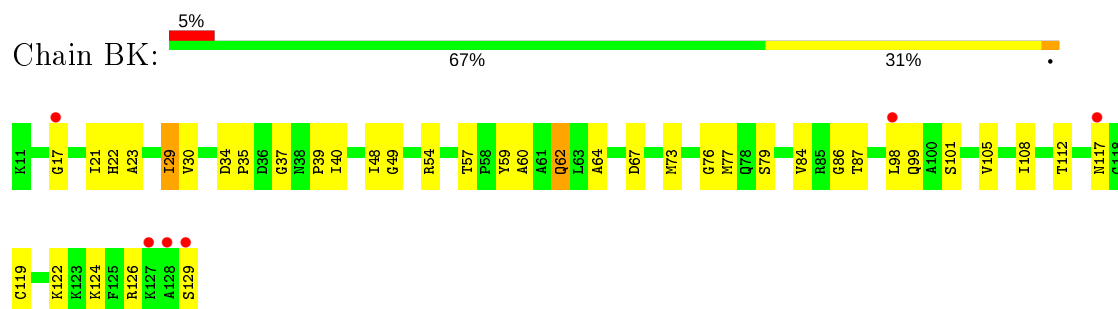


- Molecule 11: 30S ribosomal protein S11

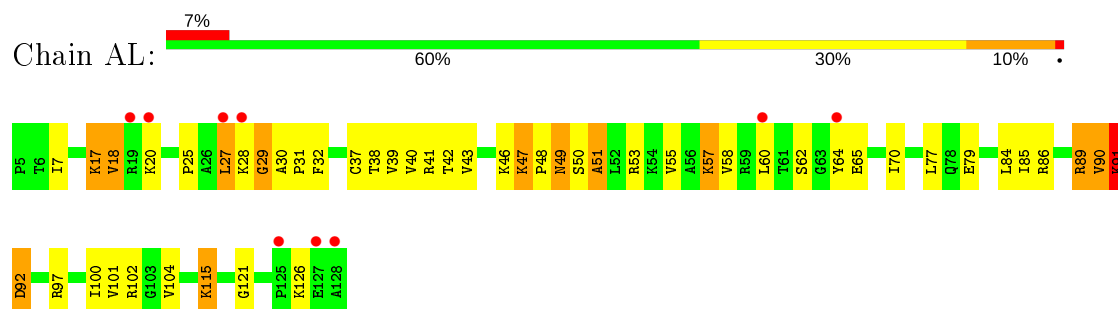
Chain AK: 4% 74% 26%



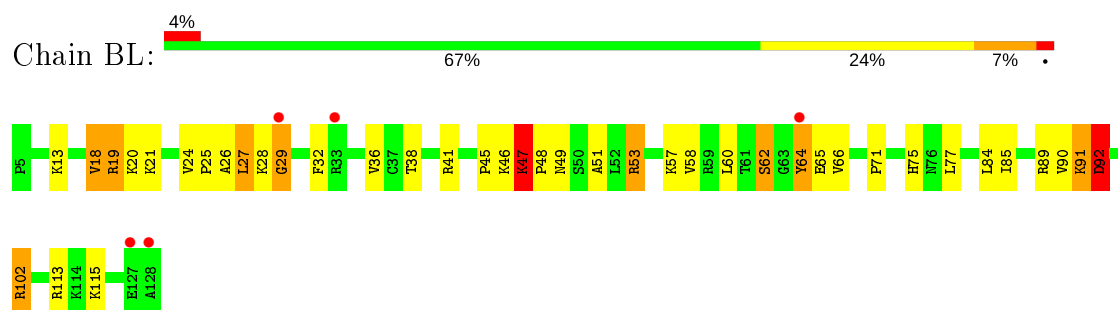
- Molecule 11: 30S ribosomal protein S11



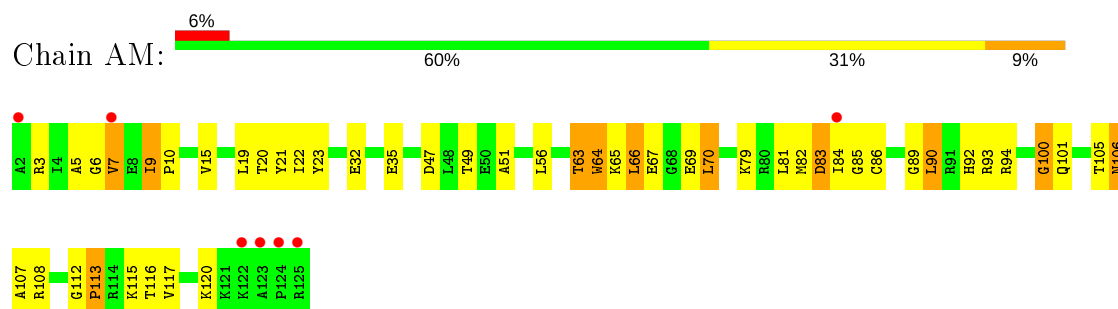
- Molecule 12: 30S ribosomal protein S12



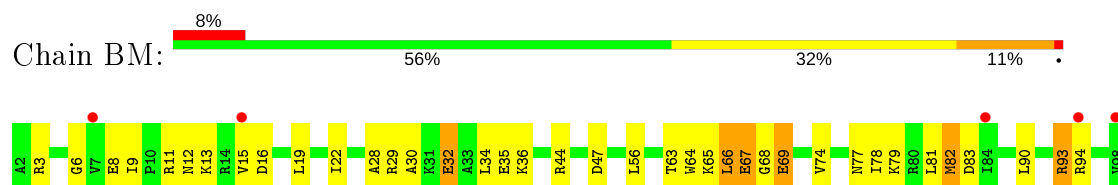
- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

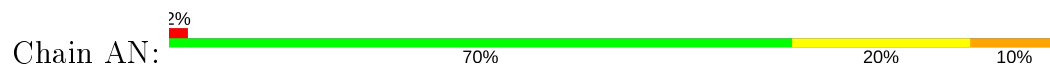


- Molecule 13: 30S ribosomal protein S13





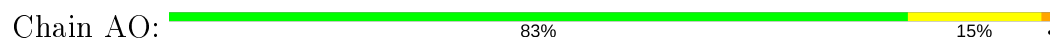
- Molecule 14: 30S ribosomal protein S14 type Z



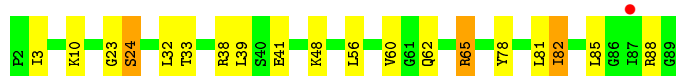
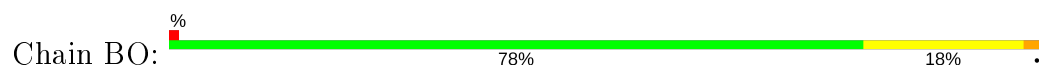
- Molecule 14: 30S ribosomal protein S14 type Z



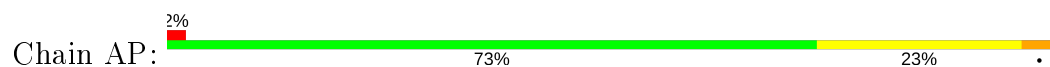
- Molecule 15: 30S ribosomal protein S15



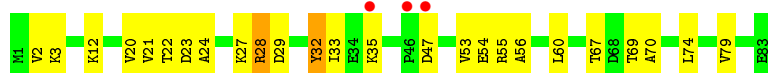
- Molecule 15: 30S ribosomal protein S15



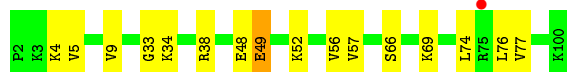
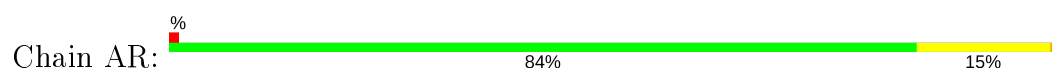
- Molecule 16: 30S ribosomal protein S16



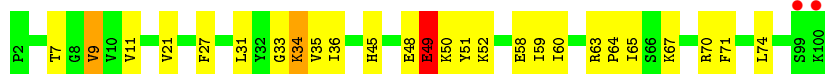
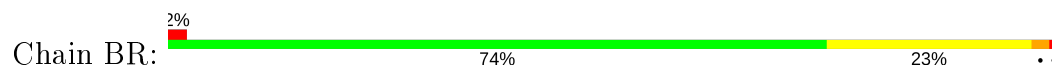
- Molecule 16: 30S ribosomal protein S16



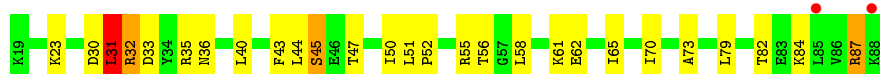
- Molecule 17: 30S ribosomal protein S17



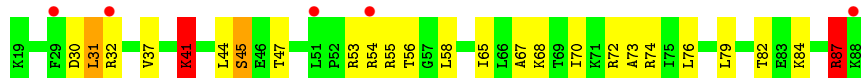
- Molecule 17: 30S ribosomal protein S17



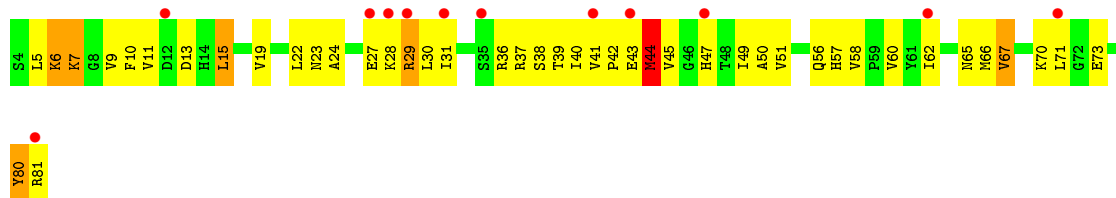
- Molecule 18: 30S ribosomal protein S18



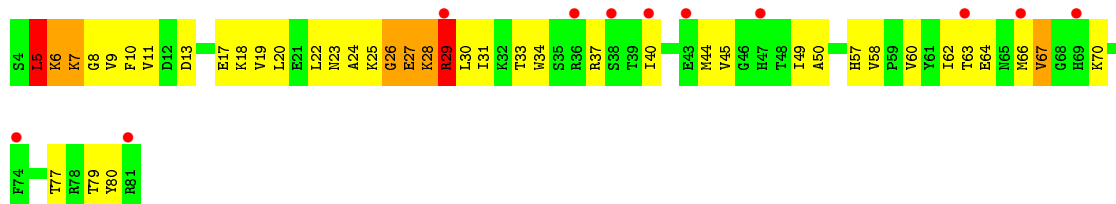
- Molecule 18: 30S ribosomal protein S18



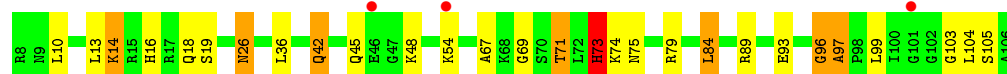
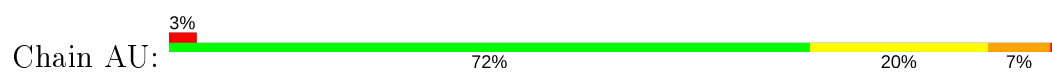
- Molecule 19: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S19



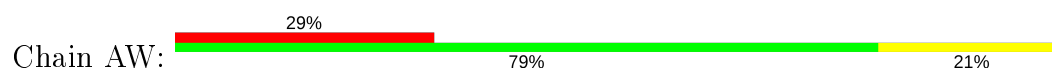
- Molecule 20: 30S ribosomal protein S20



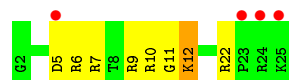
- Molecule 20: 30S ribosomal protein S20



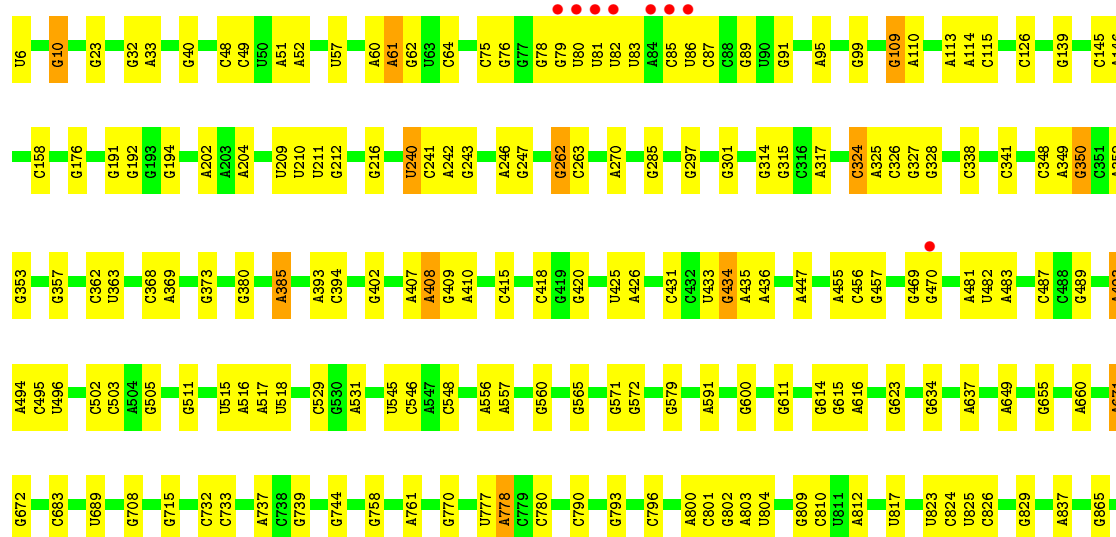
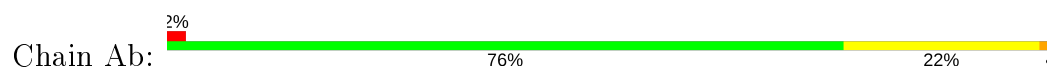
- Molecule 21: 30S ribosomal protein Thx

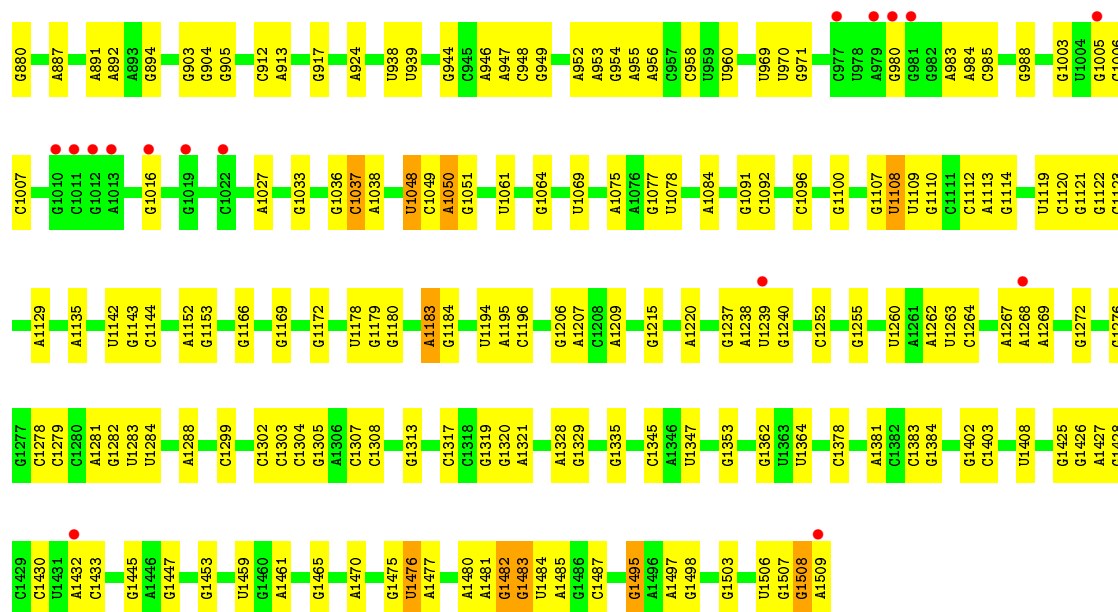


- Molecule 21: 30S ribosomal protein Thx

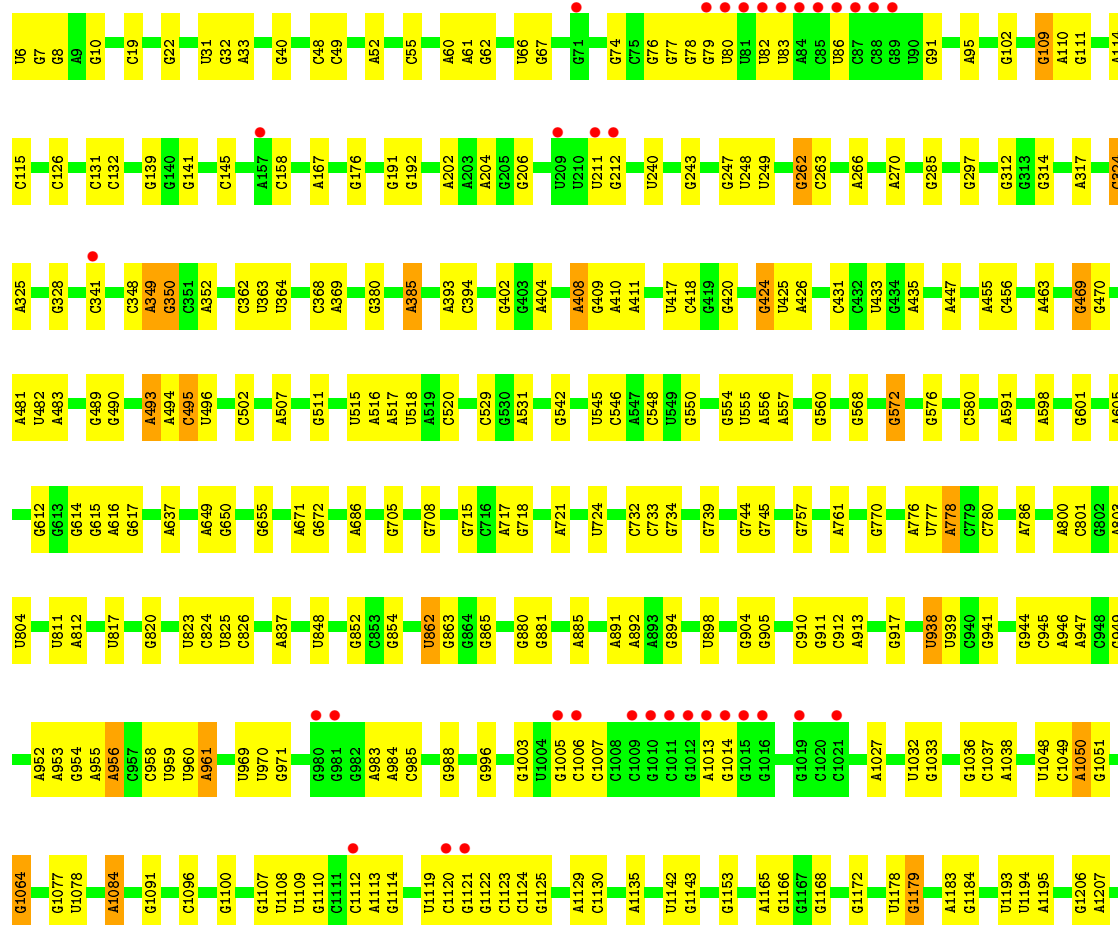
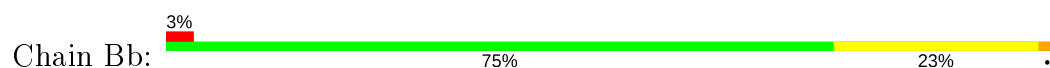


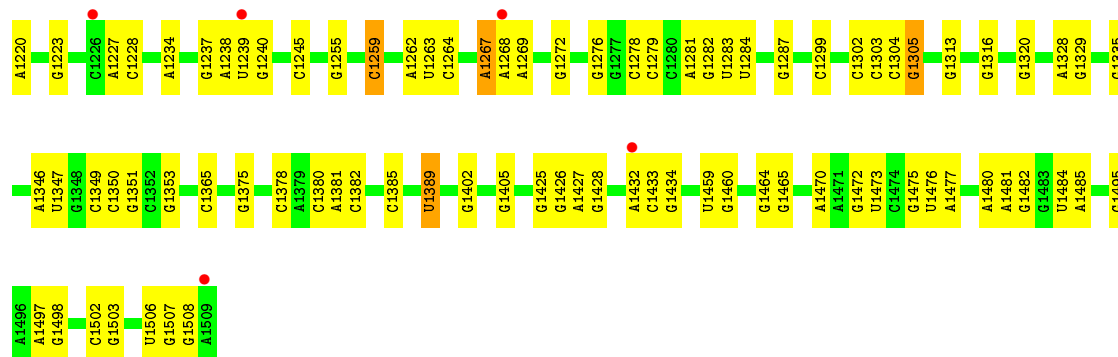
- Molecule 22: RNA (1504-MER)





• Molecule 22: RNA (1504-MER)

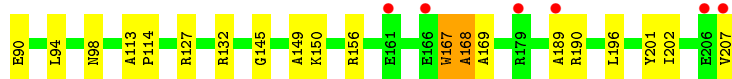
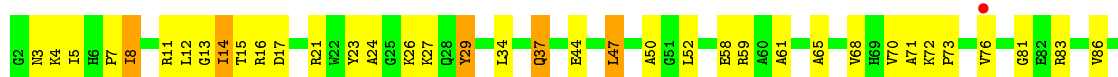
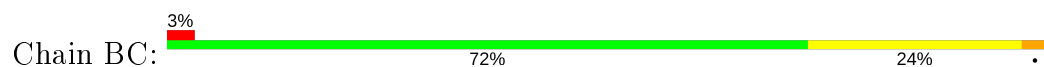




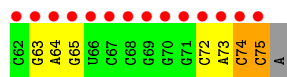
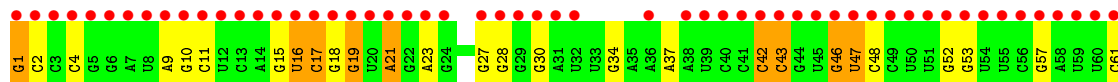
- Molecule 23: mRNA



- Molecule 24: 30S ribosomal protein S3



- Molecule 25: A site tNA, E site tNA

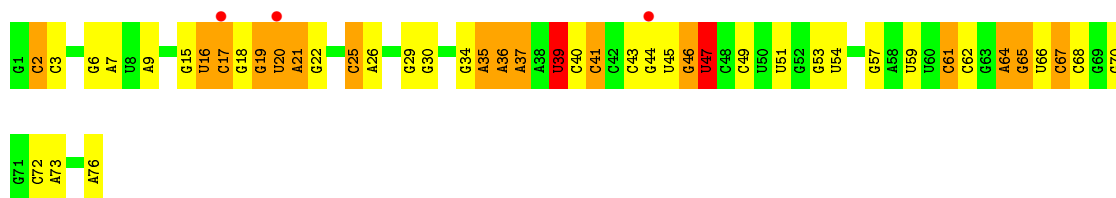


- Molecule 25: A site tNA, E site tNA

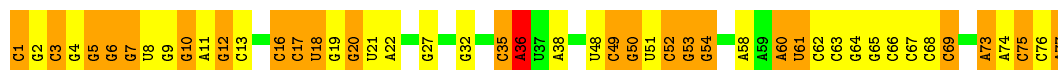


- Molecule 25: A site tNA, E site tNA

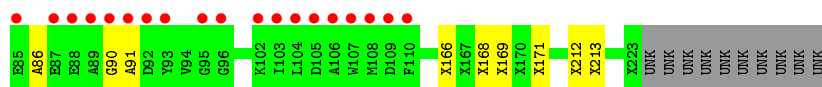
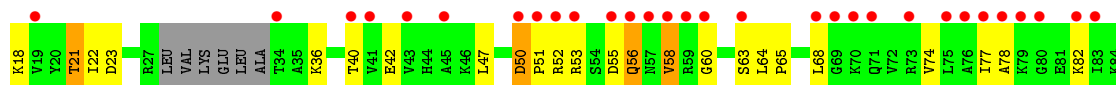
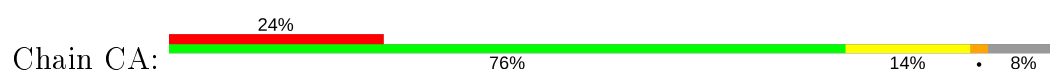




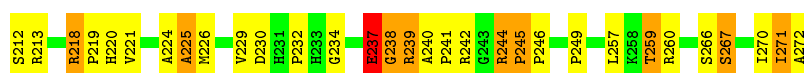
- Molecule 26: P site trNA



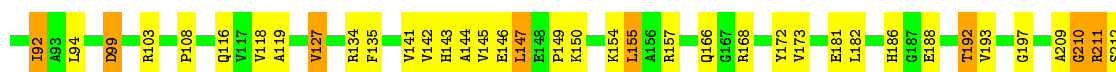
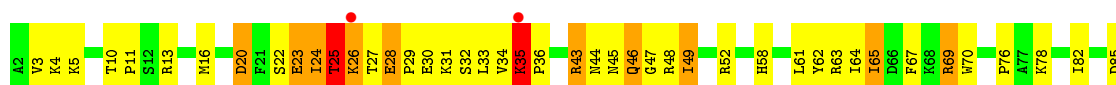
- Molecule 27: 50S ribosomal protein L1



- Molecule 28: 50S ribosomal protein L2

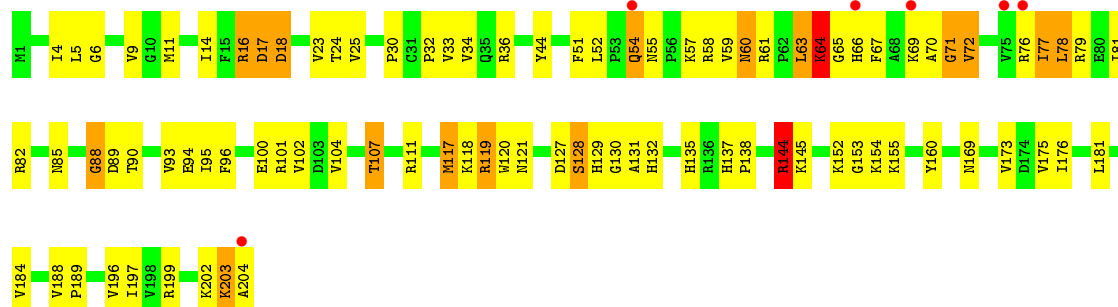


- Molecule 28: 50S ribosomal protein L2

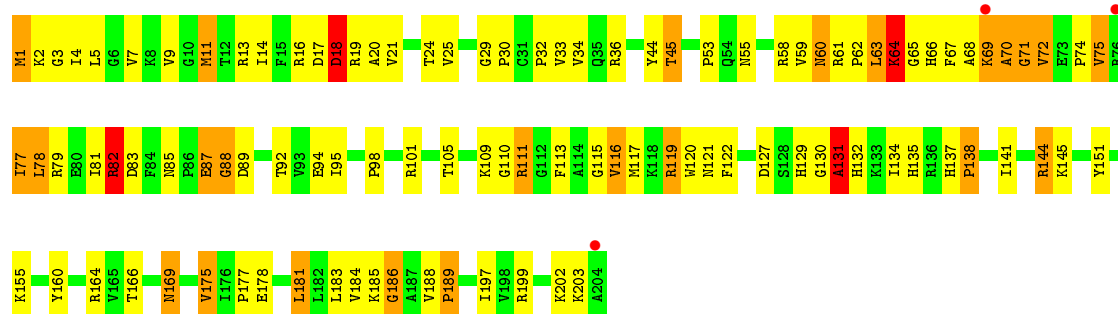




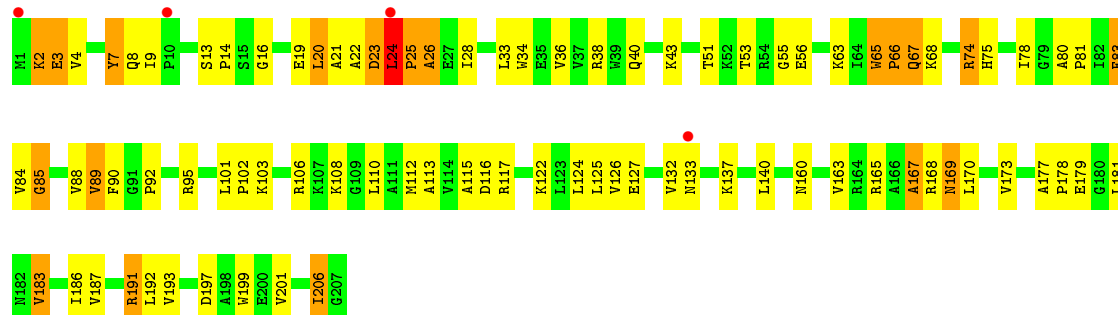
• Molecule 29: 50S ribosomal protein L3



• Molecule 29: 50S ribosomal protein L3

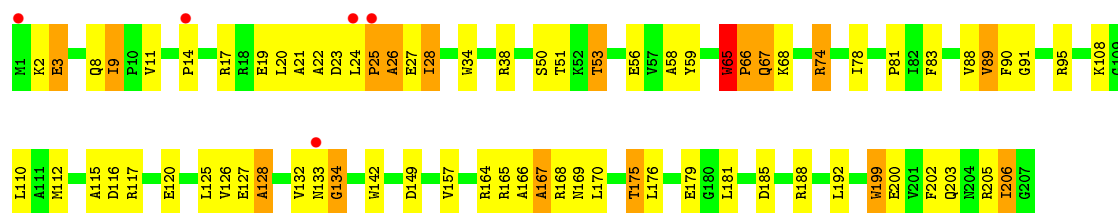


• Molecule 30: 50S ribosomal protein L4

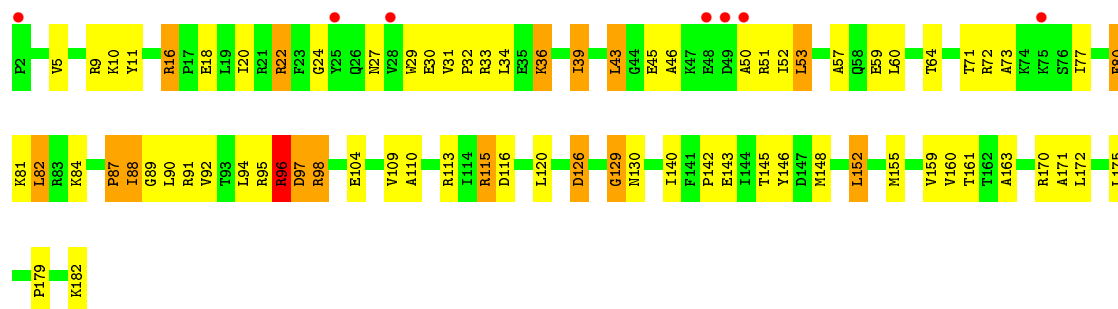


• Molecule 30: 50S ribosomal protein L4

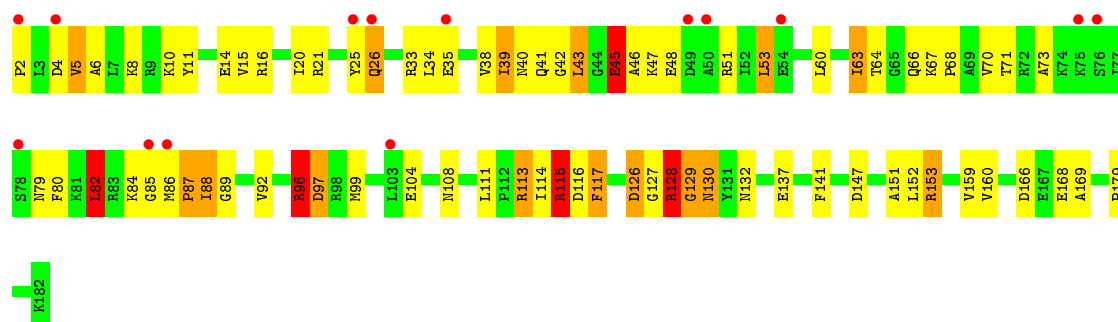




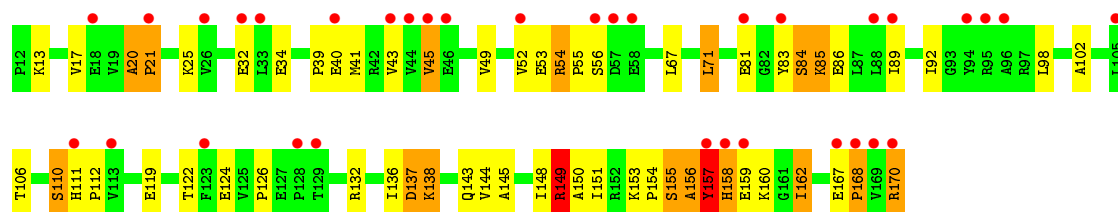
• Molecule 31: 50S ribosomal protein L5



• Molecule 31: 50S ribosomal protein L5

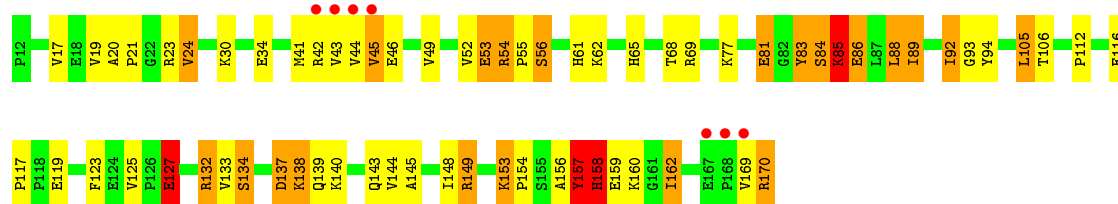


• Molecule 32: 50S ribosomal protein L6

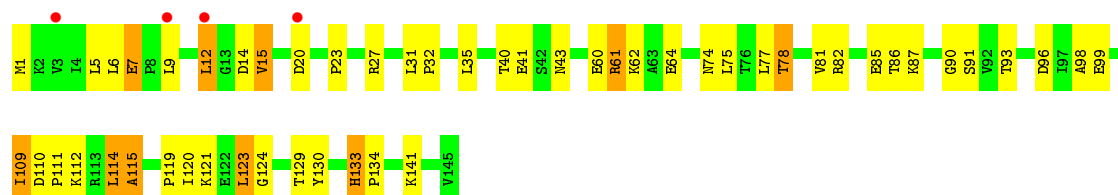


• Molecule 32: 50S ribosomal protein L6

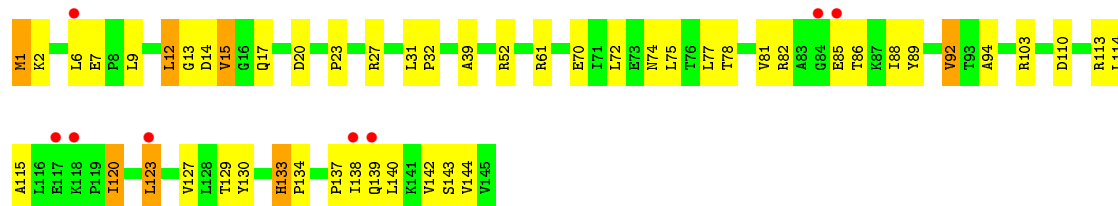




• Molecule 33: 50S ribosomal protein L9



• Molecule 33: 50S ribosomal protein L9



• Molecule 34: ribosomal L10 protein

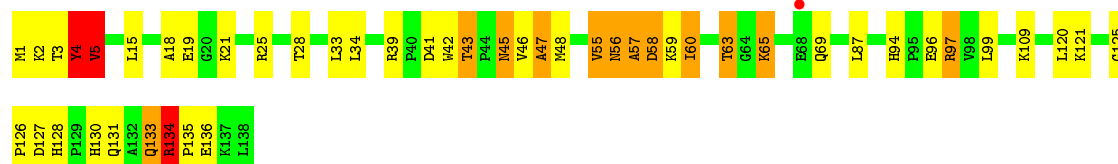


There are no outlier residues recorded for this chain.

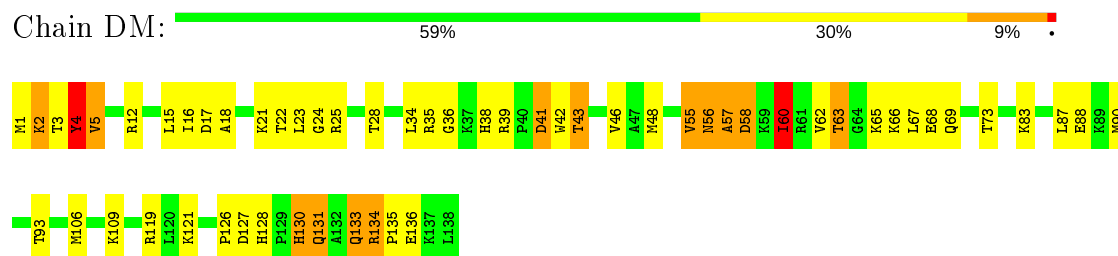
• Molecule 34: ribosomal L10 protein



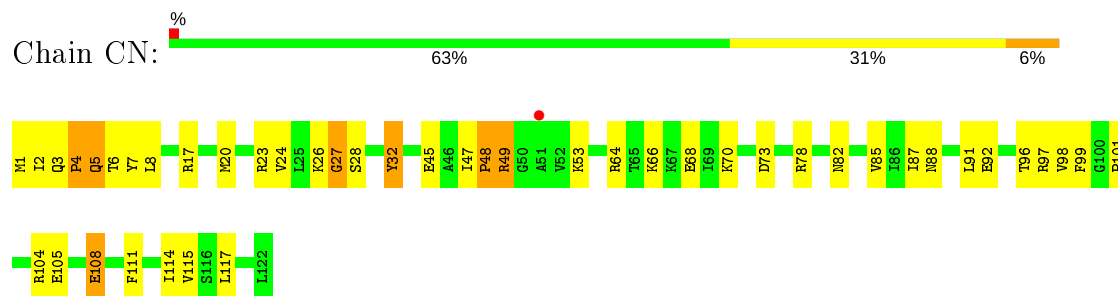
• Molecule 35: 50S ribosomal protein L13



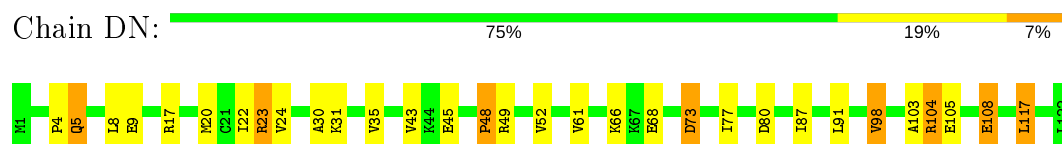
- Molecule 35: 50S ribosomal protein L13



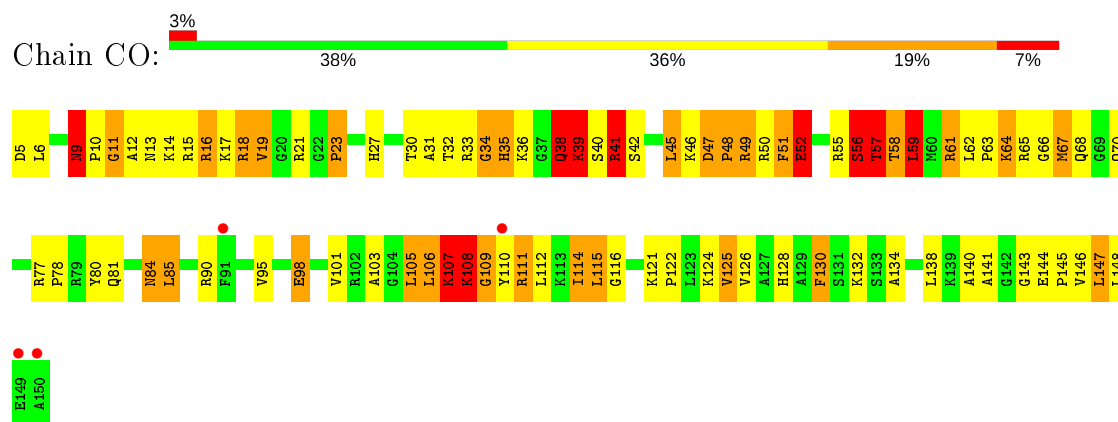
- Molecule 36: 50S ribosomal protein L14



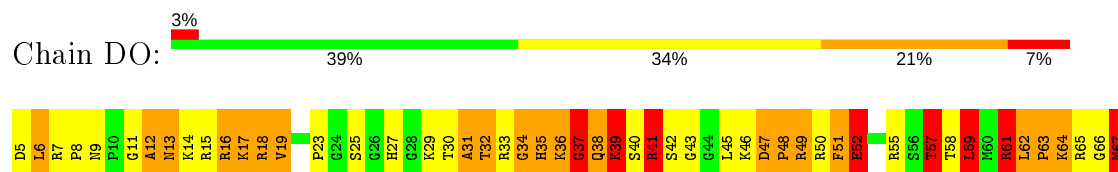
- Molecule 36: 50S ribosomal protein L14

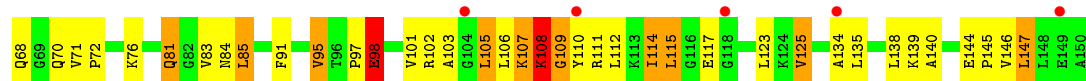


- Molecule 37: 50S ribosomal protein L15

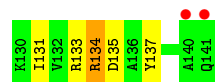
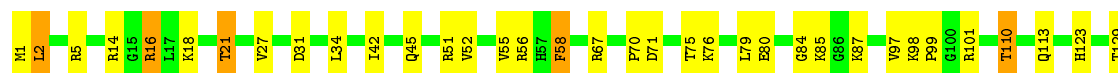
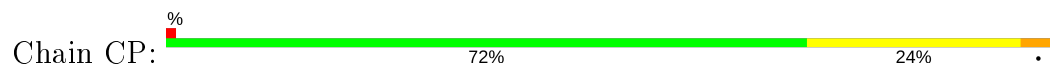


- Molecule 37: 50S ribosomal protein L15

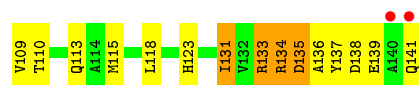
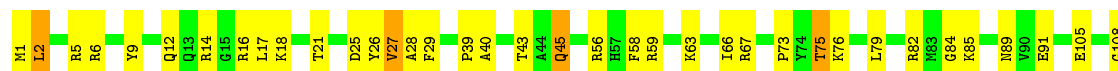




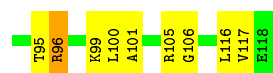
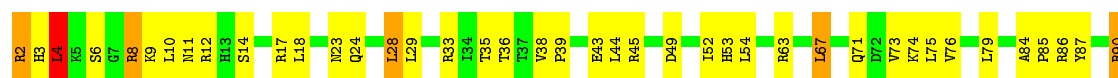
- Molecule 38: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L16



- Molecule 39: 50S ribosomal protein L17

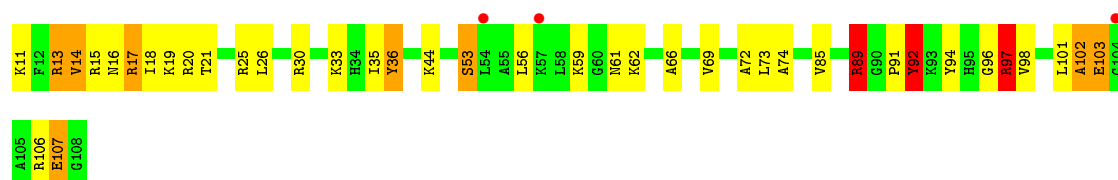


- Molecule 39: 50S ribosomal protein L17

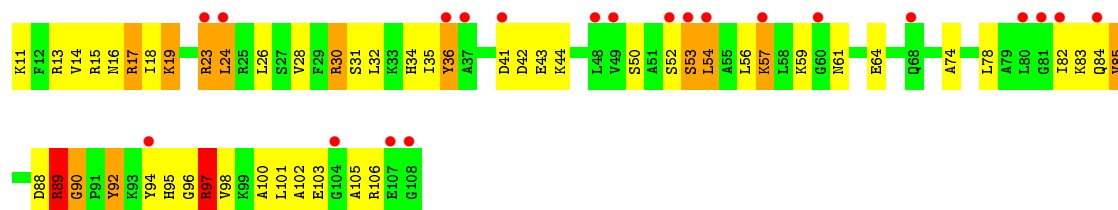


- Molecule 40: 50S ribosomal protein L18

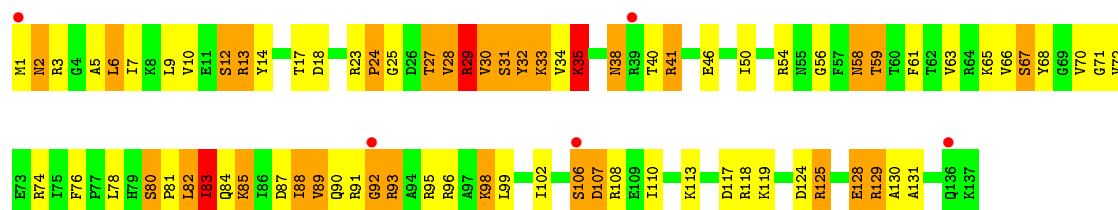




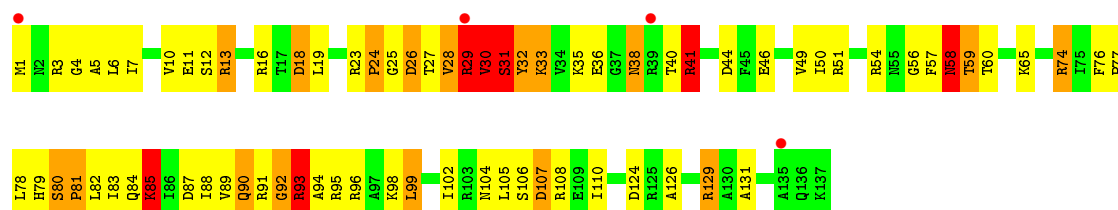
- Molecule 40: 50S ribosomal protein L18



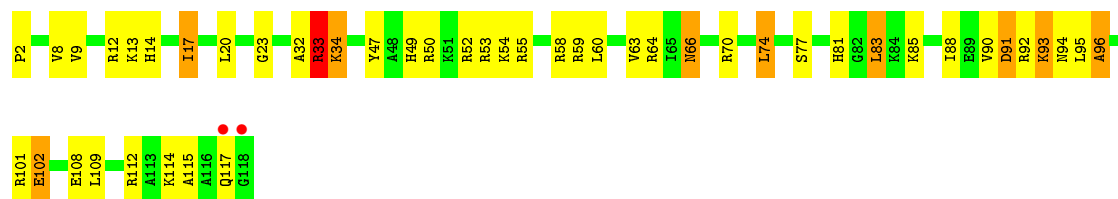
- Molecule 41: 50S ribosomal protein L19



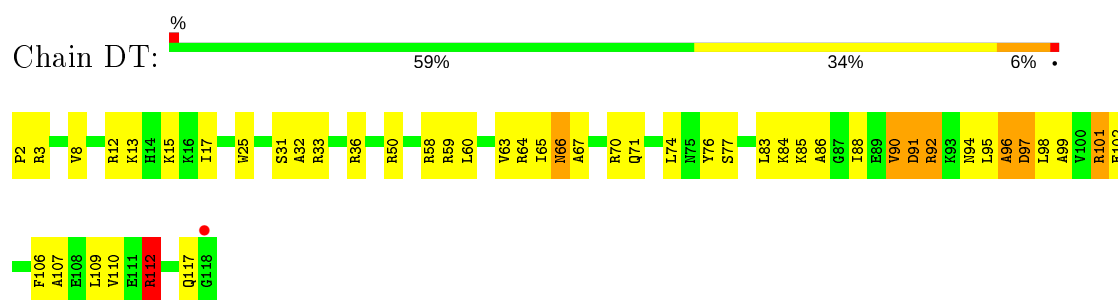
- Molecule 41: 50S ribosomal protein L19



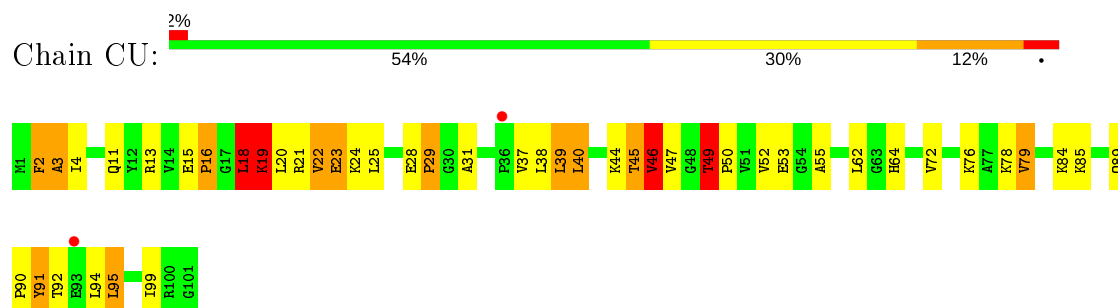
- Molecule 42: 50S ribosomal protein L20



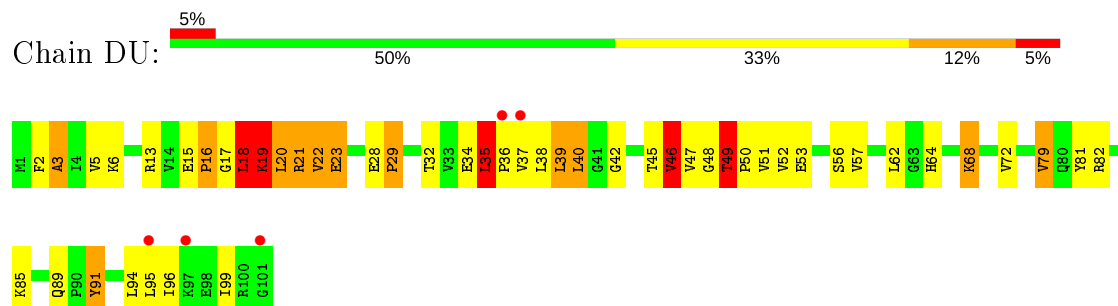
- Molecule 42: 50S ribosomal protein L20



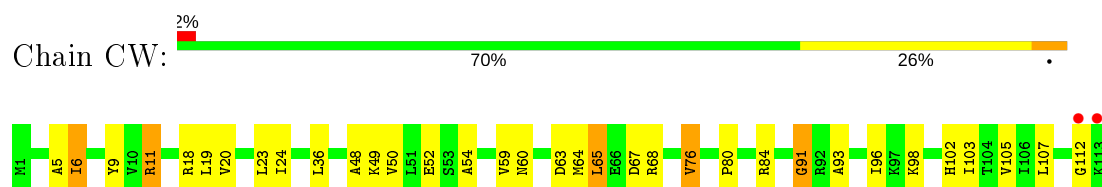
- Molecule 43: 50S ribosomal protein L21



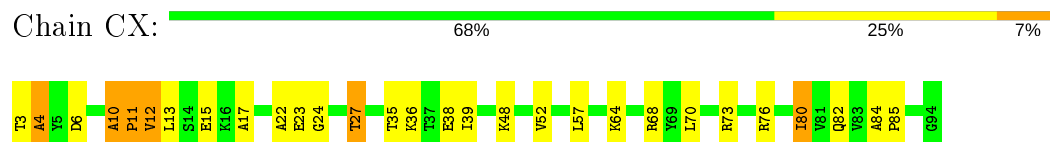
- Molecule 43: 50S ribosomal protein L21



- Molecule 44: 50S ribosomal protein L22

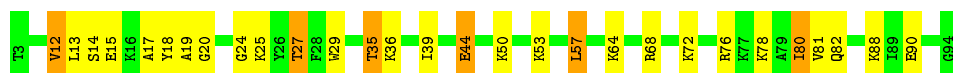


- Molecule 45: 50S ribosomal protein L23

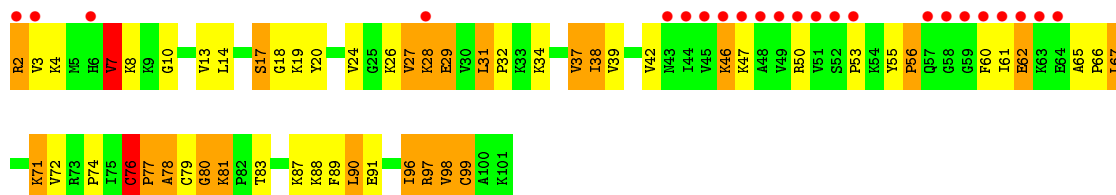


- Molecule 45: 50S ribosomal protein L23

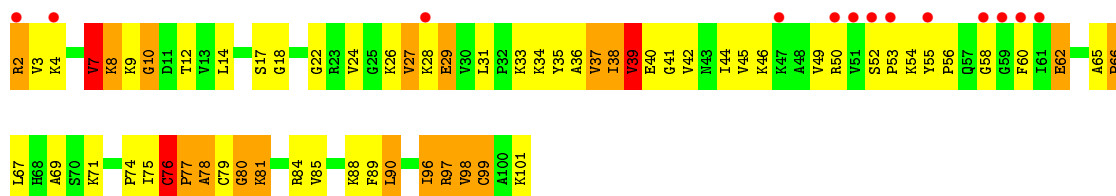




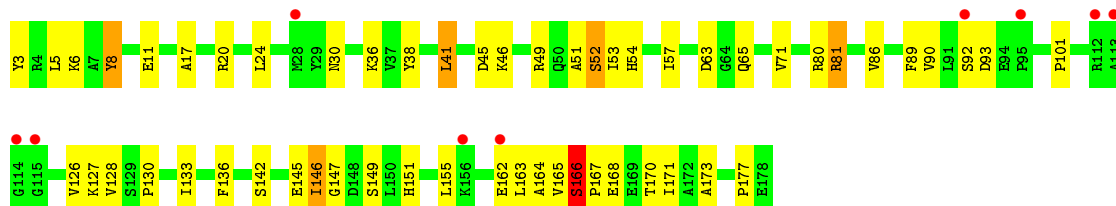
- Molecule 46: 50S ribosomal protein L24



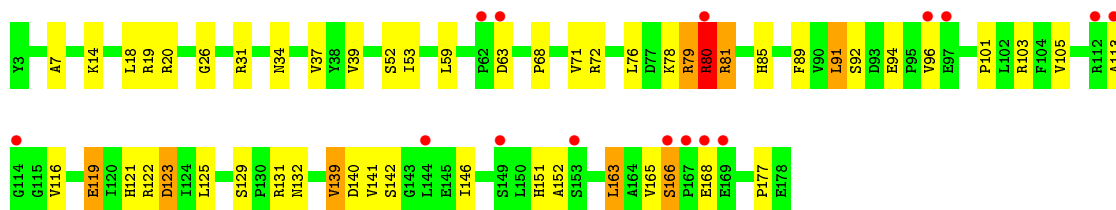
- Molecule 46: 50S ribosomal protein L24



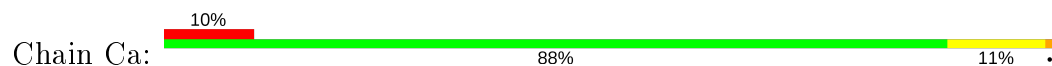
- Molecule 47: 50S ribosomal protein L25



- Molecule 47: 50S ribosomal protein L25

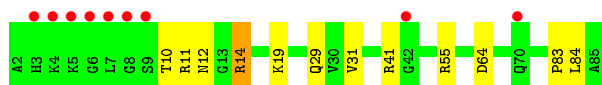
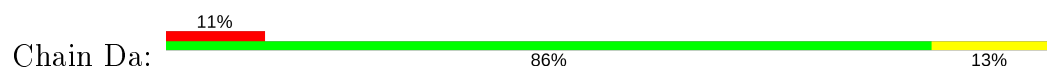


- Molecule 48: 50S ribosomal protein L27

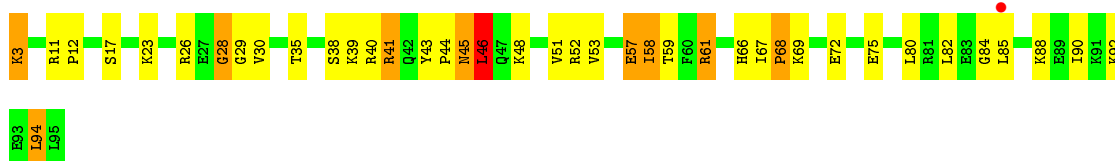




- Molecule 48: 50S ribosomal protein L27



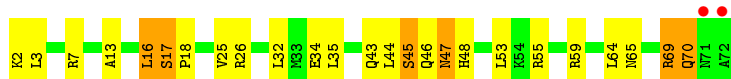
- Molecule 49: 50S ribosomal protein L28



- Molecule 49: 50S ribosomal protein L28



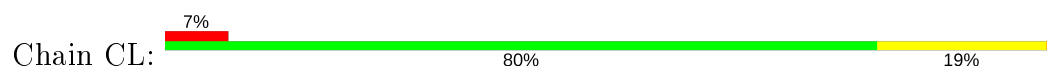
- Molecule 50: 50S ribosomal protein L29



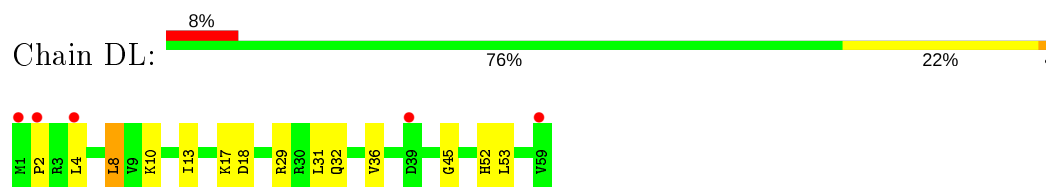
- Molecule 50: 50S ribosomal protein L29



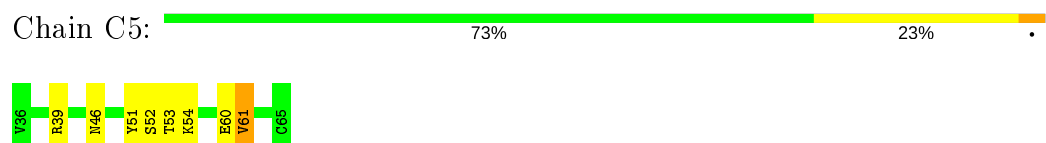
- Molecule 51: 50S ribosomal protein L30



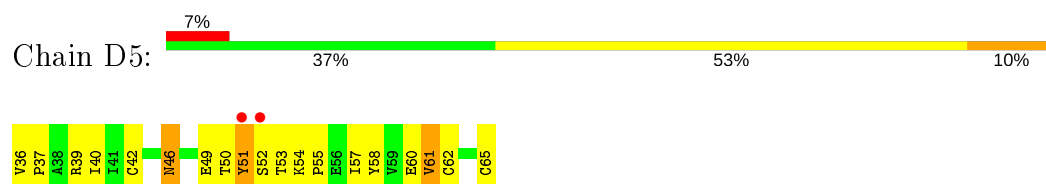
- Molecule 51: 50S ribosomal protein L30



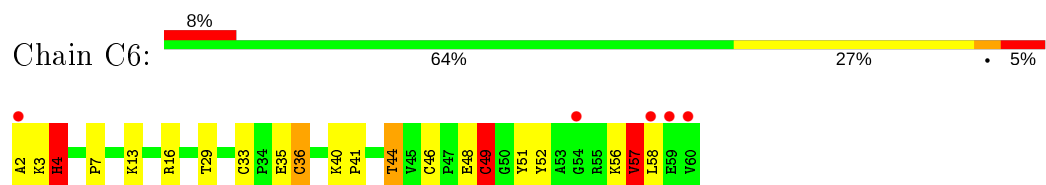
- Molecule 52: 50S ribosomal protein L31



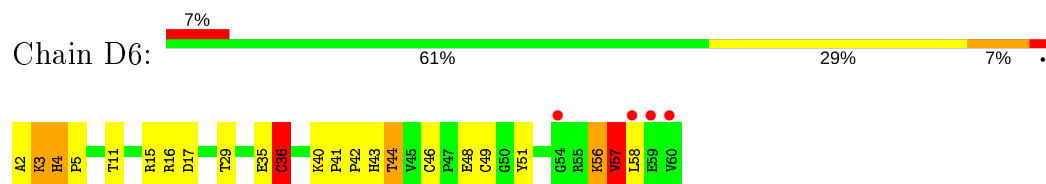
- Molecule 52: 50S ribosomal protein L31



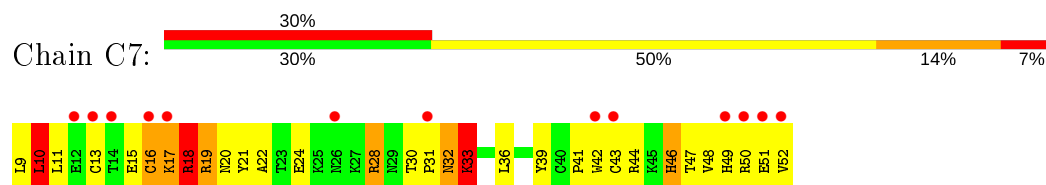
- Molecule 53: 50S ribosomal protein L32



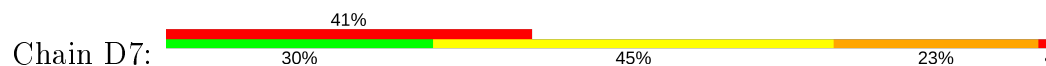
- Molecule 53: 50S ribosomal protein L32

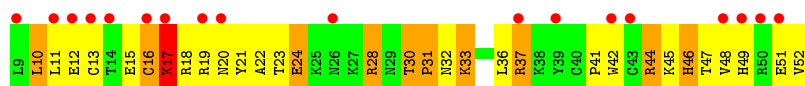


- Molecule 54: 50S ribosomal protein L33

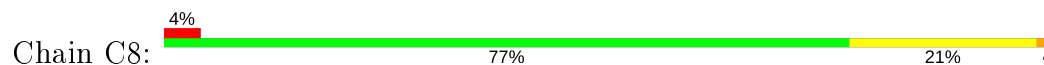


- Molecule 54: 50S ribosomal protein L33





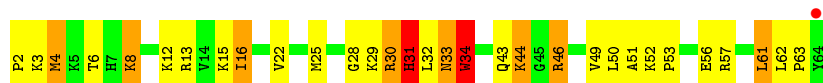
- Molecule 55: 50S ribosomal protein L34



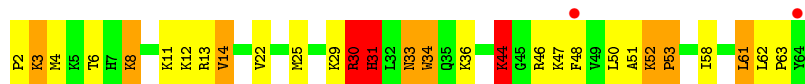
- Molecule 55: 50S ribosomal protein L34



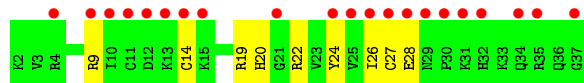
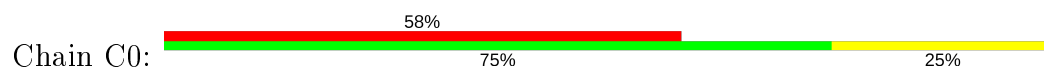
- Molecule 56: 50S ribosomal protein L35



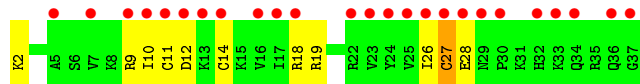
- Molecule 56: 50S ribosomal protein L35



- Molecule 57: 50S ribosomal protein L36



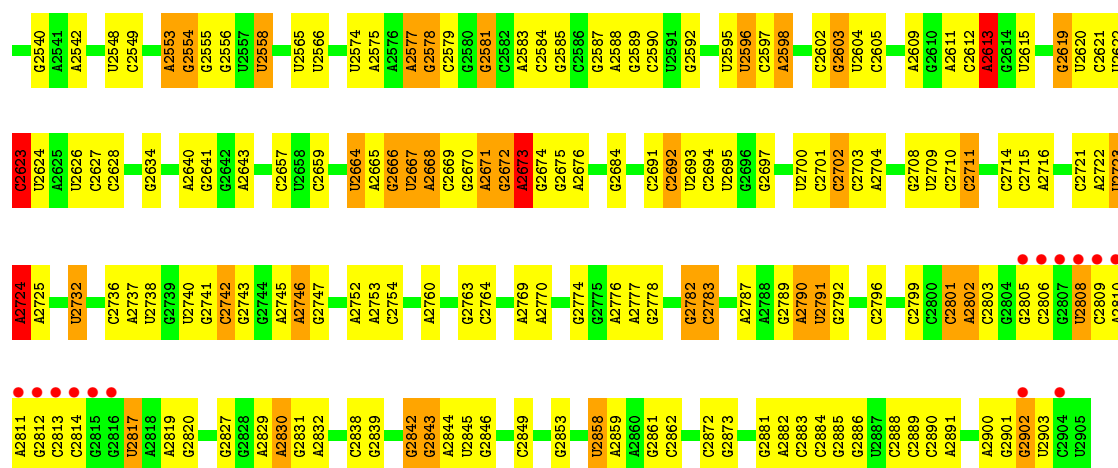
- Molecule 57: 50S ribosomal protein L36



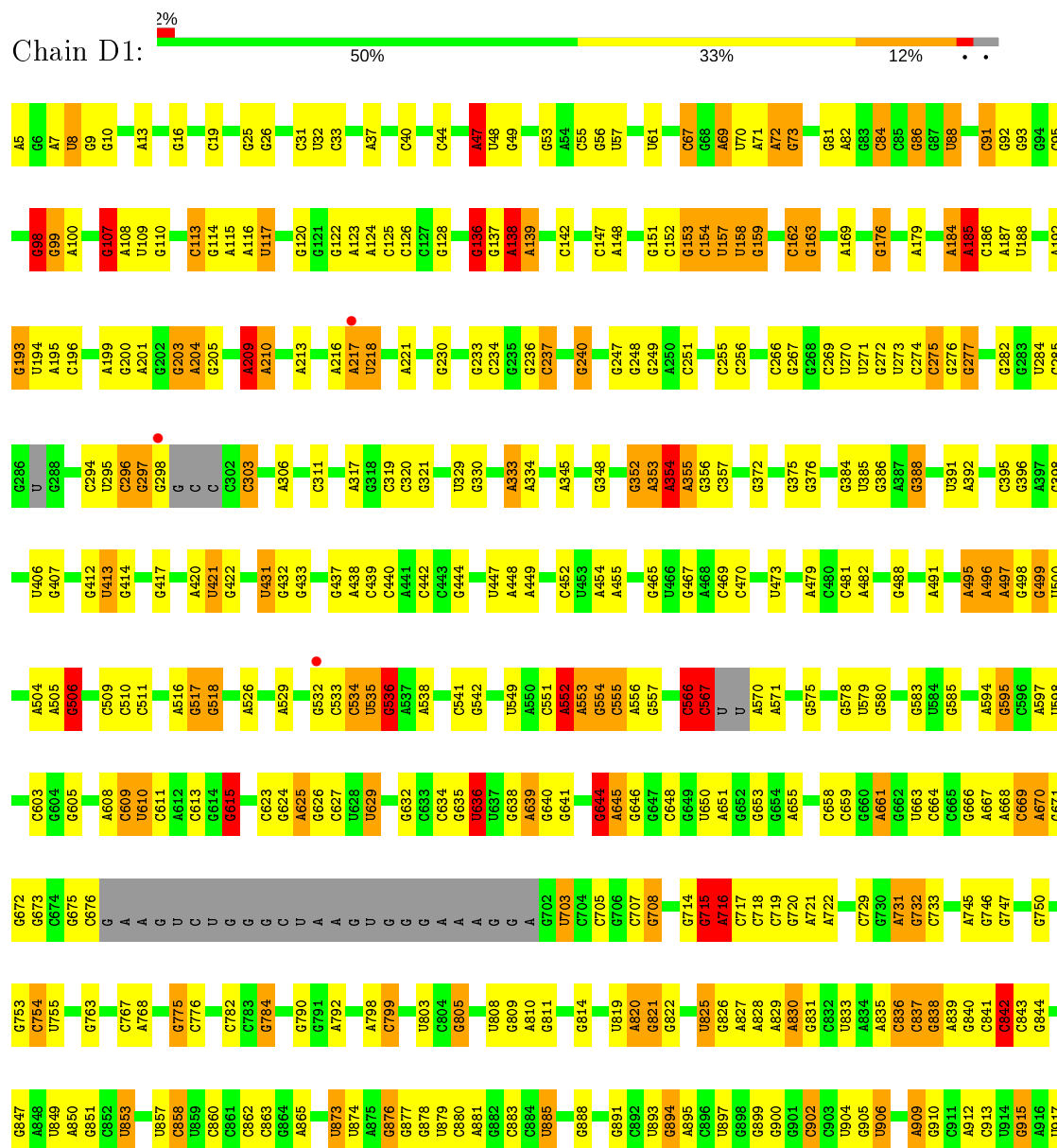
- Molecule 58: 23S rRNA (2899-MER)



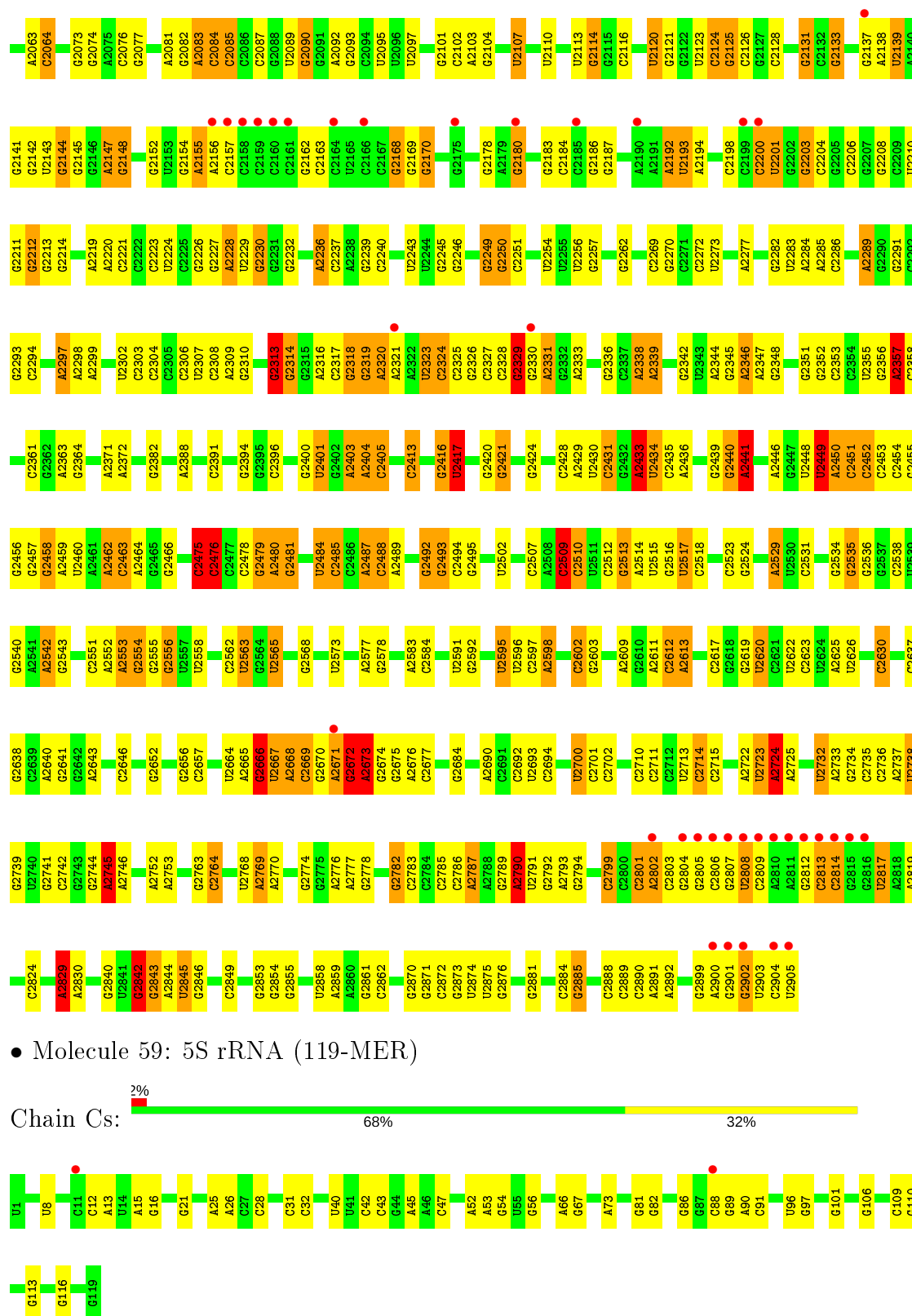


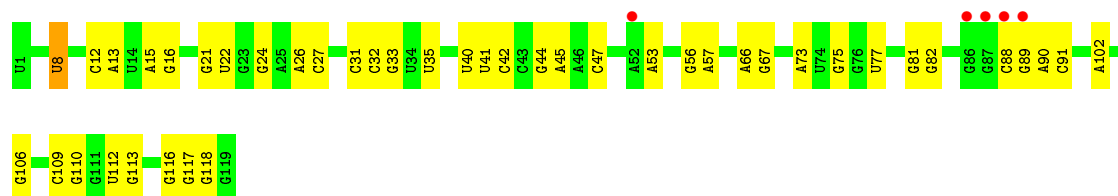


• Molecule 58: 23S rRNA (2899-MER)

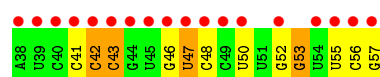


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A1987	C1902	G1829	U1734	C1643	A1556	C1482	A1394	G1309	G1225	G	G1088	C1005	G927
C1988	C1903	G1830	A1735	G1646	G1557	G1486	U1397	A1310	A1226	A	G1089	C1008	G928
G1989	G1904	G1831	C1740	U1647	C1558	G1486	U1397	G1311			A1090	C1009	G929
A1990	A1905	A1832	G1740	C1648	U1559	G1487	G1400	U1312			A1091	G1010	
A1991	C1906	A1833	G1741	A1648	A1573	G1488	G1403	A1313			A1092	C1011	A933
A1992	G1907	A1842	G1742	C1652	A1574	G1489	G1403	A1314			A1093	G1012	C934
A1993	C1908	G1843	G1743	A1653	G1575	A1490	A1405	G1315			A1095	U1013	C935
A1998	A1910	G1844	A1744	A1654	C1576	G1495	G1406	G1316			G1096		A936
A1999	A1911	A1845	G1745	A1655	C1577	A1496		A1317			C1097	A1017	
C2000	G1912	G1846	A1746	A1655	C1578	G1496	G1409	U1318			C1098	G1018	A941
G2001	C1913		A1747	G1658	G1579	C1497	A1410	A1319			A	G1022	C942
A2002	G1917	A1849	G1763	C1660	G	C1498	G1413	A1320			C		C943
C2003	C2003	U1850	U1764	C1661	C	A1499	G1414	G1323			U		A944
C2004	A1851	G1852	G1765	A1660	A	U1500	C1415	G1325			C		A945
G2005	G1852	C1662	A1766	C1662	A	G1501	C1415	G1326			U	A1028	A946
G2006	G1853	G1767	U1767	A1663	G	G1505	C1420	G1326			C		
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C1923	A1855	A1678	G1676	A1677	A	G1507	G1422	A1331			U	A1034	U950
C2008	G1856	G1678	C1676	A1678	C	G1512	A1423	U1249			U	A1035	G951
G1924	G1857	G1679	C1677	A1678	G	C1513	A1424	A1332			A	C1036	U952
G1925	C1857	G1679	C1677	A1679	A1590	G1514	G1425	U1333			A	G1037	C953
C1926	G1858	G1679	C1678	A1679	A1591	G1514	G1425	U1334			A	G1038	A954
A1927	A1859	C1772	C1772	A1679	A1592	G1515	A1429	C1335			A	A1041	A955
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A1937	C1868	C1686	G1780	C1686	C1596	G1521	G1433	C1343			U	A1048	G972
A2022	G1869	G1687	G1780	C1686	C1600	C1522	G1433	C1343			A	C1049	G973
G2023	G1870	A1785	A1785	C1694	A1604	G1524	A1437	U1345			A	C1050	
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C2028	G1950	C1873	A1792	A1698	G1605	G1528	U1439	G1348			C	G1056	A977
C2029	G1951	C1874	G1793	G1699	A1612	G1529	U1441	C1351			U	U1057	G978
A2036	A1953	G1875	G1794	A1700	A1613	C1529	U1441	A1352			A	C1058	
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U2037	G1955	A1878	C1801	C1704	A1615	G1533	C1449	U1357			C	C1060	A985
U2038	G1956	G1879	G1802	U1705	C1621	U1534	U1450	U1357			U	U1064	G986
C2042	A1957	G1880	A1803	C1706	U1622	A1535	U1451	U1358			C	A1065	U987
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G2048	G1986	U1886	U1809	A1711	G1627	A1540	U1460	G1288			C	G996	A997
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		A1897	G1729	C1729	G1637	C1550	G1474	A1219			C	A1077	C999
		U1898	C1730	G1730	G1638	C1551	C1475	U1300			G	U1078	G1000
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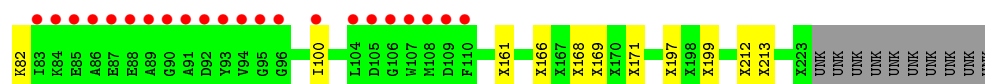
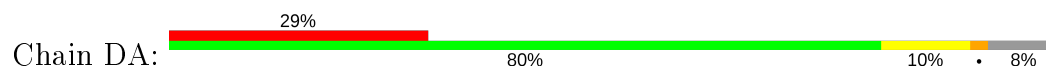
- Molecule 60: tRNA (5'-D(*AP*UP*CP*CP*CP*CP*GP*UP*GP*UP*CP*CP*UP*UP*GP*GP*UP*UP*CP*G)-3')



- Molecule 61: tRNA (76-MER)



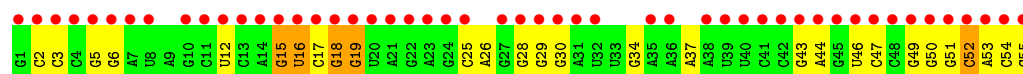
- Molecule 62: 50S ribosomal protein L1



- Molecule 63: 50S ribosomal protein L22



- Molecule 64: DNA (55-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	214.21Å 457.45Å 639.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.91 – 3.40 49.91 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.91-3.40) 98.6 (49.91-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.28	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.204 , 0.241 0.207 , 0.241	Depositor DCC
R_{free} test set	41975 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	74.2	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 78.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	295910	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.91% 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: 3V6, PAR, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A2	0.48	0/192	0.82	0/297
2	AA	0.51	0/1936	0.74	0/2609
2	BA	0.50	0/1936	0.72	0/2609
3	AC	0.62	0/1636	0.82	2/2205 (0.1%)
4	AD	0.64	1/1733 (0.1%)	0.88	2/2318 (0.1%)
4	BD	0.68	2/1733 (0.1%)	0.98	9/2318 (0.4%)
5	AE	0.56	0/1163	0.82	1/1564 (0.1%)
5	BE	0.52	0/1163	0.78	0/1564
6	AF	0.52	0/856	0.78	0/1154
6	BF	0.56	0/856	0.81	0/1154
7	AG	0.51	0/1276	0.75	0/1709
7	BG	0.56	0/1276	0.78	2/1709 (0.1%)
8	AH	0.52	0/1136	0.75	0/1527
8	BH	0.52	0/1136	0.79	0/1527
9	AI	0.57	0/1029	0.82	0/1378
9	BI	0.54	0/1029	0.77	0/1378
10	AJ	0.58	0/808	0.84	0/1085
10	BJ	0.60	0/808	0.81	0/1085
11	AK	0.59	0/900	0.81	0/1213
11	BK	0.54	0/900	0.74	0/1213
12	AL	0.61	0/987	0.86	0/1320
12	BL	0.65	0/987	0.91	1/1320 (0.1%)
13	AM	0.57	0/999	0.86	1/1336 (0.1%)
13	BM	0.59	0/999	0.88	0/1336
14	AN	0.60	0/501	0.91	1/664 (0.2%)
14	BN	0.64	0/501	1.00	2/664 (0.3%)
15	AO	0.51	0/745	0.70	0/992
15	BO	0.53	0/745	0.80	0/992
16	AP	0.59	0/717	0.83	0/963
16	BP	0.56	0/717	0.81	0/963
17	AR	0.55	0/837	0.81	0/1117
17	BR	0.49	0/837	0.75	0/1117

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	AS	0.52	0/579	0.75	0/768
18	BS	0.54	0/579	0.73	0/768
19	AT	0.60	0/643	0.78	1/865 (0.1%)
19	BT	0.55	0/643	0.79	1/865 (0.1%)
20	AU	0.55	0/765	0.85	1/1007 (0.1%)
20	BU	0.50	0/765	0.80	0/1007
21	AW	0.61	0/213	0.90	0/277
21	BW	0.72	0/213	0.88	0/277
22	Ab	0.47	4/36190 (0.0%)	0.82	64/56486 (0.1%)
22	Bb	0.47	3/36190 (0.0%)	0.82	66/56486 (0.1%)
23	B2	0.42	0/216	0.86	0/334
24	BC	0.53	0/1637	0.76	1/2205 (0.0%)
25	C2	0.31	0/1784	0.72	1/2780 (0.0%)
25	C3	0.40	0/1809	0.77	3/2819 (0.1%)
25	D3	0.38	1/1809 (0.1%)	0.74	1/2819 (0.0%)
26	C4	0.49	0/1832	0.95	5/2855 (0.2%)
27	CA	0.55	0/646	0.72	0/869
28	CB	0.73	0/2155	0.99	3/2905 (0.1%)
28	DB	0.80	2/2155 (0.1%)	1.01	6/2905 (0.2%)
29	CC	0.70	1/1597 (0.1%)	0.93	2/2153 (0.1%)
29	DC	0.74	2/1597 (0.1%)	0.96	4/2153 (0.2%)
30	CD	0.65	0/1659	0.89	0/2244
30	DD	0.71	1/1659 (0.1%)	0.93	0/2244
31	CE	0.57	0/1499	0.84	0/2016
31	DE	0.58	0/1499	0.80	0/2016
32	CF	0.59	1/1246 (0.1%)	0.77	1/1682 (0.1%)
32	DF	0.69	1/1246 (0.1%)	0.92	2/1682 (0.1%)
33	CI	0.57	0/1147	0.84	1/1551 (0.1%)
33	DI	0.57	0/1147	0.81	0/1551
35	CM	0.60	0/1132	0.86	1/1525 (0.1%)
35	DM	0.63	0/1132	0.87	0/1525
36	CN	0.64	0/943	0.89	0/1269
36	DN	0.64	0/943	0.87	0/1269
37	CO	0.82	0/1131	1.17	4/1504 (0.3%)
37	DO	0.87	0/1131	1.16	2/1504 (0.1%)
38	CP	0.57	0/1143	0.80	0/1527
38	DP	0.63	0/1143	0.89	0/1527
39	CQ	0.67	0/974	0.99	2/1302 (0.2%)
39	DQ	0.74	0/974	1.08	6/1302 (0.5%)
40	CR	0.64	0/779	0.96	2/1036 (0.2%)
40	DR	0.71	0/779	1.04	2/1036 (0.2%)
41	CS	0.69	0/1156	1.04	0/1542
41	DS	0.73	0/1156	1.12	4/1542 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
42	CT	0.64	0/975	0.92	1/1297 (0.1%)
42	DT	0.75	0/975	1.07	4/1297 (0.3%)
43	CU	0.56	0/790	0.88	0/1057
43	DU	0.63	0/790	0.96	1/1057 (0.1%)
44	CW	0.64	0/907	0.89	0/1216
45	CX	0.63	0/740	0.85	0/993
45	DX	0.69	1/740 (0.1%)	1.01	2/993 (0.2%)
46	CY	0.75	0/789	0.98	0/1051
46	DY	0.80	0/789	1.00	1/1051 (0.1%)
47	CZ	0.51	0/1436	0.77	0/1949
47	DZ	0.53	0/1436	0.77	1/1949 (0.1%)
48	Ca	0.61	0/671	0.87	1/892 (0.1%)
48	Da	0.67	0/671	0.96	1/892 (0.1%)
49	CH	0.65	0/741	0.95	1/984 (0.1%)
49	DH	0.60	0/741	0.89	0/984
50	CK	0.54	0/600	0.83	0/793
50	DK	0.59	0/600	0.84	0/793
51	CL	0.54	0/473	0.80	0/634
51	DL	0.60	0/473	0.83	0/634
52	C5	0.63	0/229	0.86	0/309
52	D5	0.61	0/229	0.80	0/309
53	C6	0.67	0/473	0.91	1/639 (0.2%)
53	D6	0.64	0/473	0.94	1/639 (0.2%)
54	C7	0.89	0/387	1.06	1/515 (0.2%)
54	D7	0.71	0/387	1.01	1/515 (0.2%)
55	C8	0.72	0/427	1.01	1/561 (0.2%)
55	D8	0.78	0/427	0.99	1/561 (0.2%)
56	C9	0.74	0/516	1.08	0/679
56	D9	0.73	0/516	1.04	1/679 (0.1%)
57	C0	0.53	0/302	0.70	0/397
57	D0	0.59	0/302	0.87	0/397
58	C1	0.55	15/67709 (0.0%)	0.91	250/105690 (0.2%)
58	D1	0.58	32/67709 (0.0%)	0.96	353/105690 (0.3%)
59	Cs	0.45	0/2853	0.80	3/4451 (0.1%)
59	Ds	0.49	0/2853	0.85	4/4451 (0.1%)
60	D2	0.34	0/459	0.74	0/712
61	D4	0.48	0/1813	0.86	7/2825 (0.2%)
62	DA	0.55	0/645	0.73	0/867
63	DW	0.66	0/907	0.95	1/1216 (0.1%)
64	DV	0.28	0/1269	0.65	0/1956
All	All	0.56	67/318931 (0.0%)	0.89	845/476973 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AA	0	1
3	AC	0	1
12	AL	0	1
13	AM	0	1
13	BM	0	1
14	BN	0	1
18	BS	0	1
19	AT	0	1
20	AU	0	1
22	Ab	1	0
22	Bb	1	0
25	C3	1	0
25	D3	1	0
28	CB	0	4
28	DB	0	3
29	DC	0	2
30	CD	0	1
31	CE	0	2
32	DF	0	1
33	CI	0	1
34	DJ	0	1
37	CO	0	6
37	DO	0	6
39	DQ	0	1
41	CS	0	1
41	DS	0	3
42	CT	0	1
42	DT	0	1
46	CY	0	1
46	DY	0	2
47	DZ	0	1
48	Da	0	1
53	C6	0	1
54	C7	0	1
54	D7	0	1
56	D9	0	1
58	C1	20	0
58	D1	21	0
All	All	45	52

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	C1	296	C	O3'-P	8.28	1.71	1.61
28	DB	237	GLU	CG-CD	8.11	1.64	1.51
29	DC	127	ASP	CB-CG	8.00	1.68	1.51
58	D1	1346	A	O3'-P	7.44	1.70	1.61
58	D1	1429	A	O3'-P	-7.22	1.52	1.61

The worst 5 of 845 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	C4	36	A	O5'-P-OP2	-17.36	89.87	110.70
58	D1	2028	C	O5'-P-OP2	-16.34	90.99	105.70
58	D1	2603	G	O5'-P-OP2	-16.16	91.15	105.70
58	D1	598	U	O5'-P-OP2	-13.61	93.45	105.70
58	C1	2613	A	O5'-P-OP1	-12.83	94.15	105.70

5 of 45 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
22	Ab	408	A	C1'
22	Bb	408	A	C1'
25	C3	47	U	C1'
58	C1	98	G	C1'
58	C1	715	G	C4',C1',C3'

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AA	23	ARG	Peptide
3	AC	26	LYS	Peptide
12	AL	91	LYS	Peptide
13	AM	69	GLU	Peptide
19	AT	28	LYS	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	A2	173	0	85	16	0
2	AA	1901	0	1951	33	0
2	BA	1901	0	1951	32	0
3	AC	1612	0	1677	30	0
4	AD	1703	0	1763	41	0
4	BD	1703	0	1763	43	0
5	AE	1147	0	1207	27	0
5	BE	1147	0	1207	23	0
6	AF	843	0	857	6	0
6	BF	843	0	857	19	0
7	AG	1257	0	1296	8	0
7	BG	1257	0	1296	15	0
8	AH	1116	0	1177	11	0
8	BH	1116	0	1177	17	0
9	AI	1011	0	1043	29	0
9	BI	1011	0	1043	18	0
10	AJ	795	0	840	22	0
10	BJ	795	0	840	21	0
11	AK	885	0	904	13	0
11	BK	885	0	904	21	0
12	AL	971	0	1057	24	0
12	BL	971	0	1057	17	0
13	AM	988	0	1059	35	0
13	BM	988	0	1059	27	0
14	AN	492	0	529	20	0
14	BN	492	0	529	13	0
15	AO	734	0	771	7	0
15	BO	734	0	771	8	0
16	AP	701	0	720	10	0
16	BP	701	0	720	14	0
17	AR	824	0	891	5	0
17	BR	824	0	891	14	0
18	AS	574	0	644	17	0
18	BS	574	0	644	15	0
19	AT	630	0	652	24	0
19	BT	630	0	652	26	0
20	AU	763	0	861	16	0
20	BU	763	0	861	13	0
21	AW	209	0	221	1	0
21	BW	209	0	221	3	0
22	Ab	32329	0	16318	0	0
22	Bb	32329	0	16318	0	1
23	B2	194	0	95	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	BC	1613	0	1677	26	0
25	C2	1597	0	811	18	0
25	C3	1619	0	822	28	0
25	D3	1619	0	822	46	0
26	C4	1640	0	837	56	0
27	CA	1156	0	755	15	0
28	CB	2105	0	2182	95	0
28	DB	2105	0	2182	88	0
29	CC	1564	0	1629	60	0
29	DC	1564	0	1629	79	0
30	CD	1624	0	1677	61	0
30	DD	1624	0	1677	47	0
31	CE	1474	0	1535	44	0
31	DE	1474	0	1535	57	0
32	CF	1223	0	1282	26	0
32	DF	1223	0	1282	49	0
33	CI	1132	0	1218	25	1
33	DI	1132	0	1218	29	0
34	CJ	651	0	155	0	0
34	DJ	651	0	155	4	0
35	CM	1105	0	1180	34	0
35	DM	1105	0	1180	37	0
36	CN	933	0	996	23	0
36	DN	933	0	996	21	0
37	CO	1114	0	1187	84	0
37	DO	1114	0	1187	103	0
38	CP	1122	0	1179	26	0
38	DP	1122	0	1179	37	0
39	CQ	960	0	1021	30	0
39	DQ	960	0	1021	34	0
40	CR	771	0	832	29	0
40	DR	771	0	832	29	0
41	CS	1142	0	1202	79	0
41	DS	1142	0	1202	80	0
42	CT	958	0	1018	45	0
42	DT	958	0	1018	44	0
43	CU	779	0	852	44	0
43	DU	779	0	852	45	0
44	CW	896	0	953	22	0
45	CX	726	0	778	17	0
45	DX	726	0	778	19	0
46	CY	776	0	870	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	DY	776	0	868	60	0
47	CZ	1404	0	1432	34	0
47	DZ	1404	0	1432	23	0
48	Ca	662	0	688	0	0
48	Da	662	0	688	0	0
49	CH	734	0	808	16	0
49	DH	734	0	808	17	0
50	CK	598	0	653	11	0
50	DK	598	0	653	17	0
51	CL	468	0	523	9	0
51	DL	468	0	523	8	0
52	C5	226	0	229	2	0
52	D5	226	0	229	11	0
53	C6	459	0	478	13	0
53	D6	459	0	477	15	0
54	C7	381	0	390	17	0
54	D7	381	0	390	21	0
55	C8	419	0	467	8	0
55	D8	419	0	467	5	0
56	C9	508	0	576	36	0
56	D9	508	0	576	33	0
57	C0	299	0	326	4	0
57	D0	299	0	324	5	0
58	C1	60459	0	30486	641	0
58	D1	60459	0	30488	729	0
59	Cs	2551	0	1295	0	0
59	Ds	2551	0	1295	0	0
60	D2	416	0	215	8	0
61	D4	1623	0	825	46	0
62	DA	1155	0	757	14	0
63	DW	896	0	956	19	0
64	DV	1167	0	624	15	0
65	Ab	42	0	45	0	0
65	Bb	42	0	45	0	0
66	C1	24	0	20	5	0
66	D1	24	0	21	11	0
67	C1	1	0	0	0	0
67	D1	1	0	0	2	0
All	All	295910	0	199849	3935	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 9.

The worst 5 of 3935 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)
61:D4:2:G:C2	61:D4:73:A:N3	1.85	1.31
58:C1:1331:A:O2'	58:C1:1333:U:OP2	1.54	1.25
58:D1:927:G:O2'	64:DV:19:G:C6	1.93	1.22
58:C1:2492:G:O2'	58:C1:2493:G:OP2	1.60	1.17
29:DC:132:HIS:ND1	58:D1:1704:C:OP1	1.79	1.16

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)
22:Bb:364:U:OP1	33:CI:91:SER:OG[4_455]	2.14	0.06

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	232/234 (99%)	174 (75%)	47 (20%)	11 (5%)	2	15
2	BA	232/234 (99%)	180 (78%)	41 (18%)	11 (5%)	2	15
3	AC	204/238 (86%)	145 (71%)	42 (21%)	17 (8%)	1	5
4	AD	206/208 (99%)	161 (78%)	33 (16%)	12 (6%)	1	11
4	BD	206/208 (99%)	168 (82%)	27 (13%)	11 (5%)	2	13
5	AE	148/150 (99%)	130 (88%)	15 (10%)	3 (2%)	7	30
5	BE	148/150 (99%)	130 (88%)	14 (10%)	4 (3%)	5	26
6	AF	99/101 (98%)	92 (93%)	5 (5%)	2 (2%)	7	30
6	BF	99/101 (98%)	89 (90%)	9 (9%)	1 (1%)	15	46
7	AG	153/155 (99%)	124 (81%)	26 (17%)	3 (2%)	7	30
7	BG	153/155 (99%)	135 (88%)	17 (11%)	1 (1%)	22	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	136/138 (99%)	110 (81%)	24 (18%)	2 (2%)	10	36
8	BH	136/138 (99%)	116 (85%)	19 (14%)	1 (1%)	22	55
9	AI	125/127 (98%)	97 (78%)	23 (18%)	5 (4%)	3	18
9	BI	125/127 (98%)	98 (78%)	22 (18%)	5 (4%)	3	18
10	AJ	96/98 (98%)	79 (82%)	13 (14%)	4 (4%)	3	18
10	BJ	96/98 (98%)	76 (79%)	15 (16%)	5 (5%)	2	13
11	AK	117/119 (98%)	102 (87%)	14 (12%)	1 (1%)	17	49
11	BK	117/119 (98%)	93 (80%)	20 (17%)	4 (3%)	3	21
12	AL	122/124 (98%)	92 (75%)	20 (16%)	10 (8%)	1	5
12	BL	122/124 (98%)	94 (77%)	16 (13%)	12 (10%)	0	4
13	AM	122/124 (98%)	83 (68%)	26 (21%)	13 (11%)	0	3
13	BM	122/124 (98%)	83 (68%)	26 (21%)	13 (11%)	0	3
14	AN	58/60 (97%)	43 (74%)	12 (21%)	3 (5%)	2	13
14	BN	58/60 (97%)	41 (71%)	14 (24%)	3 (5%)	2	13
15	AO	86/88 (98%)	73 (85%)	9 (10%)	4 (5%)	2	15
15	BO	86/88 (98%)	72 (84%)	13 (15%)	1 (1%)	13	41
16	AP	81/83 (98%)	63 (78%)	15 (18%)	3 (4%)	3	20
16	BP	81/83 (98%)	67 (83%)	14 (17%)	0	100	100
17	AR	97/99 (98%)	89 (92%)	5 (5%)	3 (3%)	4	23
17	BR	97/99 (98%)	84 (87%)	10 (10%)	3 (3%)	4	23
18	AS	68/70 (97%)	57 (84%)	5 (7%)	6 (9%)	1	5
18	BS	68/70 (97%)	54 (79%)	10 (15%)	4 (6%)	1	11
19	AT	76/78 (97%)	61 (80%)	7 (9%)	8 (10%)	0	3
19	BT	76/78 (97%)	55 (72%)	13 (17%)	8 (10%)	0	3
20	AU	97/99 (98%)	77 (79%)	14 (14%)	6 (6%)	1	10
20	BU	97/99 (98%)	75 (77%)	19 (20%)	3 (3%)	4	23
21	AW	22/24 (92%)	19 (86%)	2 (9%)	1 (4%)	2	16
21	BW	22/24 (92%)	17 (77%)	3 (14%)	2 (9%)	1	4
24	BC	204/206 (99%)	153 (75%)	41 (20%)	10 (5%)	2	14
27	CA	83/206 (40%)	56 (68%)	22 (26%)	5 (6%)	1	10
28	CB	269/271 (99%)	210 (78%)	39 (14%)	20 (7%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	DB	269/271 (99%)	209 (78%)	38 (14%)	22 (8%)	1	5
29	CC	202/204 (99%)	143 (71%)	43 (21%)	16 (8%)	1	6
29	DC	202/204 (99%)	145 (72%)	32 (16%)	25 (12%)	0	2
30	CD	205/207 (99%)	162 (79%)	30 (15%)	13 (6%)	1	9
30	DD	205/207 (99%)	166 (81%)	24 (12%)	15 (7%)	1	7
31	CE	179/181 (99%)	132 (74%)	32 (18%)	15 (8%)	1	5
31	DE	179/181 (99%)	139 (78%)	28 (16%)	12 (7%)	1	8
32	CF	157/159 (99%)	112 (71%)	25 (16%)	20 (13%)	0	2
32	DF	157/159 (99%)	113 (72%)	26 (17%)	18 (12%)	0	3
33	CI	143/145 (99%)	112 (78%)	22 (15%)	9 (6%)	1	9
33	DI	143/145 (99%)	104 (73%)	29 (20%)	10 (7%)	1	7
35	CM	136/138 (99%)	103 (76%)	24 (18%)	9 (7%)	1	8
35	DM	136/138 (99%)	96 (71%)	30 (22%)	10 (7%)	1	7
36	CN	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	4	22
36	DN	120/122 (98%)	110 (92%)	8 (7%)	2 (2%)	9	34
37	CO	144/146 (99%)	84 (58%)	29 (20%)	31 (22%)	0	0
37	DO	144/146 (99%)	86 (60%)	26 (18%)	32 (22%)	0	0
38	CP	139/141 (99%)	118 (85%)	17 (12%)	4 (3%)	4	24
38	DP	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	3	21
39	CQ	115/117 (98%)	93 (81%)	14 (12%)	8 (7%)	1	7
39	DQ	115/117 (98%)	98 (85%)	11 (10%)	6 (5%)	2	13
40	CR	96/98 (98%)	62 (65%)	23 (24%)	11 (12%)	0	3
40	DR	96/98 (98%)	66 (69%)	15 (16%)	15 (16%)	0	0
41	CS	135/137 (98%)	92 (68%)	24 (18%)	19 (14%)	0	1
41	DS	135/137 (98%)	89 (66%)	28 (21%)	18 (13%)	0	1
42	CT	115/117 (98%)	103 (90%)	10 (9%)	2 (2%)	9	34
42	DT	115/117 (98%)	93 (81%)	15 (13%)	7 (6%)	1	10
43	CU	99/101 (98%)	75 (76%)	11 (11%)	13 (13%)	0	1
43	DU	99/101 (98%)	72 (73%)	13 (13%)	14 (14%)	0	1
44	CW	111/113 (98%)	92 (83%)	12 (11%)	7 (6%)	1	9
45	CX	90/92 (98%)	77 (86%)	7 (8%)	6 (7%)	1	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	DX	90/92 (98%)	79 (88%)	9 (10%)	2 (2%)	6	29
46	CY	98/100 (98%)	60 (61%)	17 (17%)	21 (21%)	0	0
46	DY	98/100 (98%)	60 (61%)	18 (18%)	20 (20%)	0	0
47	CZ	174/176 (99%)	121 (70%)	42 (24%)	11 (6%)	1	9
47	DZ	174/176 (99%)	136 (78%)	28 (16%)	10 (6%)	1	12
48	Ca	82/84 (98%)	72 (88%)	9 (11%)	1 (1%)	13	41
48	Da	82/84 (98%)	74 (90%)	7 (8%)	1 (1%)	13	41
49	CH	91/93 (98%)	73 (80%)	10 (11%)	8 (9%)	1	5
49	DH	91/93 (98%)	73 (80%)	12 (13%)	6 (7%)	1	8
50	CK	69/71 (97%)	50 (72%)	12 (17%)	7 (10%)	0	4
50	DK	69/71 (97%)	54 (78%)	11 (16%)	4 (6%)	1	11
51	CL	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	8	32
51	DL	57/59 (97%)	52 (91%)	3 (5%)	2 (4%)	3	21
52	C5	28/30 (93%)	20 (71%)	5 (18%)	3 (11%)	0	3
52	D5	28/30 (93%)	18 (64%)	7 (25%)	3 (11%)	0	3
53	C6	57/59 (97%)	48 (84%)	5 (9%)	4 (7%)	1	7
53	D6	57/59 (97%)	46 (81%)	7 (12%)	4 (7%)	1	7
54	C7	40/44 (91%)	22 (55%)	9 (22%)	9 (22%)	0	0
54	D7	40/44 (91%)	21 (52%)	8 (20%)	11 (28%)	0	0
55	C8	46/48 (96%)	42 (91%)	4 (9%)	0	100	100
55	D8	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
56	C9	61/63 (97%)	47 (77%)	11 (18%)	3 (5%)	2	14
56	D9	61/63 (97%)	41 (67%)	15 (25%)	5 (8%)	1	5
57	C0	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
57	D0	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
62	DA	83/206 (40%)	52 (63%)	28 (34%)	3 (4%)	3	21
63	DW	111/113 (98%)	94 (85%)	11 (10%)	6 (5%)	2	13
All	All	11440/11918 (96%)	8901 (78%)	1752 (15%)	787 (7%)	1	8

5 of 787 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AA	83	MET

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Mol	Chain	Res	Type
2	AA	165	VAL
3	AC	4	LYS
3	AC	12	LEU
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	AA	202/202 (100%)	180 (89%)	22 (11%)	6	23
2	BA	202/202 (100%)	181 (90%)	21 (10%)	7	25
3	AC	160/187 (86%)	142 (89%)	18 (11%)	6	21
4	AD	180/180 (100%)	162 (90%)	18 (10%)	7	27
4	BD	180/180 (100%)	160 (89%)	20 (11%)	6	22
5	AE	115/115 (100%)	101 (88%)	14 (12%)	5	18
5	BE	115/115 (100%)	102 (89%)	13 (11%)	6	21
6	AF	90/90 (100%)	85 (94%)	5 (6%)	21	51
6	BF	90/90 (100%)	86 (96%)	4 (4%)	28	58
7	AG	126/126 (100%)	113 (90%)	13 (10%)	7	26
7	BG	126/126 (100%)	114 (90%)	12 (10%)	8	29
8	AH	119/119 (100%)	104 (87%)	15 (13%)	4	17
8	BH	119/119 (100%)	104 (87%)	15 (13%)	4	17
9	AI	98/98 (100%)	82 (84%)	16 (16%)	2	9
9	BI	98/98 (100%)	88 (90%)	10 (10%)	7	26
10	AJ	88/88 (100%)	77 (88%)	11 (12%)	4	17
10	BJ	88/88 (100%)	77 (88%)	11 (12%)	4	17
11	AK	90/90 (100%)	82 (91%)	8 (9%)	9	33
11	BK	90/90 (100%)	82 (91%)	8 (9%)	9	33
12	AL	104/104 (100%)	87 (84%)	17 (16%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	BL	104/104 (100%)	88 (85%)	16 (15%)	2	11
13	AM	99/99 (100%)	87 (88%)	12 (12%)	5	18
13	BM	99/99 (100%)	82 (83%)	17 (17%)	2	8
14	AN	49/49 (100%)	45 (92%)	4 (8%)	11	37
14	BN	49/49 (100%)	43 (88%)	6 (12%)	5	18
15	AO	79/79 (100%)	75 (95%)	4 (5%)	24	54
15	BO	79/79 (100%)	72 (91%)	7 (9%)	9	33
16	AP	72/72 (100%)	65 (90%)	7 (10%)	8	28
16	BP	72/72 (100%)	62 (86%)	10 (14%)	3	13
17	AR	94/94 (100%)	90 (96%)	4 (4%)	29	59
17	BR	94/94 (100%)	87 (93%)	7 (7%)	13	42
18	AS	61/61 (100%)	56 (92%)	5 (8%)	11	37
18	BS	61/61 (100%)	53 (87%)	8 (13%)	4	15
19	AT	69/69 (100%)	55 (80%)	14 (20%)	1	3
19	BT	69/69 (100%)	54 (78%)	15 (22%)	1	3
20	AU	76/76 (100%)	68 (90%)	8 (10%)	7	25
20	BU	76/76 (100%)	63 (83%)	13 (17%)	2	8
21	AW	19/19 (100%)	17 (90%)	2 (10%)	7	25
21	BW	19/19 (100%)	17 (90%)	2 (10%)	7	25
24	BC	160/160 (100%)	141 (88%)	19 (12%)	5	19
27	CA	61/74 (82%)	53 (87%)	8 (13%)	4	15
28	CB	213/213 (100%)	179 (84%)	34 (16%)	2	10
28	DB	213/213 (100%)	179 (84%)	34 (16%)	2	10
29	CC	165/165 (100%)	137 (83%)	28 (17%)	2	8
29	DC	165/165 (100%)	142 (86%)	23 (14%)	3	13
30	CD	165/165 (100%)	139 (84%)	26 (16%)	2	10
30	DD	165/165 (100%)	139 (84%)	26 (16%)	2	10
31	CE	155/155 (100%)	140 (90%)	15 (10%)	8	28
31	DE	155/155 (100%)	123 (79%)	32 (21%)	1	3
32	CF	132/132 (100%)	113 (86%)	19 (14%)	3	13
32	DF	132/132 (100%)	110 (83%)	22 (17%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	CI	122/122 (100%)	109 (89%)	13 (11%)	6	24
33	DI	122/122 (100%)	110 (90%)	12 (10%)	8	28
35	CM	117/117 (100%)	96 (82%)	21 (18%)	2	6
35	DM	117/117 (100%)	95 (81%)	22 (19%)	1	4
36	CN	100/100 (100%)	84 (84%)	16 (16%)	2	10
36	DN	100/100 (100%)	88 (88%)	12 (12%)	5	19
37	CO	112/112 (100%)	82 (73%)	30 (27%)	0	1
37	DO	112/112 (100%)	83 (74%)	29 (26%)	0	2
38	CP	111/111 (100%)	99 (89%)	12 (11%)	6	24
38	DP	111/111 (100%)	97 (87%)	14 (13%)	4	17
39	CQ	100/100 (100%)	81 (81%)	19 (19%)	1	4
39	DQ	100/100 (100%)	83 (83%)	17 (17%)	2	8
40	CR	77/77 (100%)	60 (78%)	17 (22%)	1	2
40	DR	77/77 (100%)	58 (75%)	19 (25%)	0	2
41	CS	120/120 (100%)	92 (77%)	28 (23%)	1	2
41	DS	120/120 (100%)	100 (83%)	20 (17%)	2	8
42	CT	92/92 (100%)	79 (86%)	13 (14%)	3	13
42	DT	92/92 (100%)	81 (88%)	11 (12%)	5	19
43	CU	82/82 (100%)	69 (84%)	13 (16%)	2	10
43	DU	82/82 (100%)	61 (74%)	21 (26%)	0	2
44	CW	91/92 (99%)	82 (90%)	9 (10%)	8	27
45	CX	74/74 (100%)	63 (85%)	11 (15%)	3	12
45	DX	74/74 (100%)	60 (81%)	14 (19%)	1	4
46	CY	84/84 (100%)	67 (80%)	17 (20%)	1	3
46	DY	84/84 (100%)	68 (81%)	16 (19%)	1	4
47	CZ	155/155 (100%)	142 (92%)	13 (8%)	11	36
47	DZ	155/155 (100%)	136 (88%)	19 (12%)	4	17
48	Ca	66/66 (100%)	57 (86%)	9 (14%)	3	14
48	Da	66/66 (100%)	56 (85%)	10 (15%)	3	11
49	CH	78/78 (100%)	56 (72%)	22 (28%)	0	1
49	DH	78/78 (100%)	62 (80%)	16 (20%)	1	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	CK	66/66 (100%)	55 (83%)	11 (17%)	2	8
50	DK	66/66 (100%)	53 (80%)	13 (20%)	1	4
51	CL	51/51 (100%)	49 (96%)	2 (4%)	32	61
51	DL	51/51 (100%)	48 (94%)	3 (6%)	19	49
52	C5	27/27 (100%)	24 (89%)	3 (11%)	6	22
52	D5	27/27 (100%)	21 (78%)	6 (22%)	1	2
53	C6	51/51 (100%)	43 (84%)	8 (16%)	2	10
53	D6	51/51 (100%)	42 (82%)	9 (18%)	2	6
54	C7	43/43 (100%)	36 (84%)	7 (16%)	2	9
54	D7	43/43 (100%)	35 (81%)	8 (19%)	1	5
55	C8	41/41 (100%)	37 (90%)	4 (10%)	8	28
55	D8	41/41 (100%)	32 (78%)	9 (22%)	1	3
56	C9	53/53 (100%)	40 (76%)	13 (24%)	0	2
56	D9	53/53 (100%)	43 (81%)	10 (19%)	1	4
57	C0	33/33 (100%)	30 (91%)	3 (9%)	9	32
57	D0	33/33 (100%)	27 (82%)	6 (18%)	1	6
62	DA	61/74 (82%)	53 (87%)	8 (13%)	4	15
63	DW	91/91 (100%)	86 (94%)	5 (6%)	21	51
All	All	9654/9708 (99%)	8293 (86%)	1361 (14%)	3	13

5 of 1361 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	CN	7	TYR
43	CU	95	LEU
47	DZ	39	VAL
37	CO	16	ARG
39	CQ	105	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
35	CM	45	ASN
42	CT	81	HIS
47	DZ	132	ASN

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Mol	Chain	Res	Type
36	CN	5	GLN
39	CQ	24	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	8/9 (88%)	4 (50%)	2 (25%)
22	Ab	1503/1504 (99%)	324 (21%)	0
22	Bb	1503/1504 (99%)	339 (22%)	0
23	B2	8/10 (80%)	4 (50%)	1 (12%)
25	C2	74/76 (97%)	24 (32%)	4 (5%)
25	C3	75/76 (98%)	19 (25%)	1 (1%)
25	D3	75/76 (98%)	31 (41%)	3 (4%)
26	C4	76/77 (98%)	36 (47%)	4 (5%)
58	C1	2800/2899 (96%)	802 (28%)	155 (5%)
58	D1	2800/2899 (96%)	818 (29%)	149 (5%)
59	Cs	118/119 (99%)	35 (29%)	0
59	Ds	118/119 (99%)	40 (33%)	0
60	D2	19/20 (95%)	8 (42%)	1 (5%)
61	D4	75/76 (98%)	23 (30%)	5 (6%)
64	DV	41/55 (74%)	14 (34%)	1 (2%)
All	All	9293/9519 (97%)	2521 (27%)	326 (3%)

5 of 2521 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	15	A
1	A2	17	U
1	A2	18	G
1	A2	19	U
22	Ab	10	G

5 of 326 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	C1	2553	A
58	D1	99	G
58	D1	2475	C
58	C1	2622	U
58	C1	2843	G

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](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
65	PAR	Bb	1601	-	45,45,45	1.52	7 (15%)	64,67,67	2.16	20 (31%)
65	PAR	Ab	1601	-	45,45,45	1.41	5 (11%)	64,67,67	1.82	13 (20%)
66	3V6	D1	3001	67	21,25,25	2.33	9 (42%)	21,39,39	2.98	8 (38%)
66	3V6	C1	3001	67	21,25,25	2.10	8 (38%)	21,39,39	2.07	6 (28%)

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
65	PAR	Bb	1601	-	-	9/18/94/94	0/4/4/4
65	PAR	Ab	1601	-	-	7/18/94/94	2/4/4/4
66	3V6	D1	3001	67	-	4/12/53/53	0/2/2/2
66	3V6	C1	3001	67	-	2/12/53/53	0/2/2/2

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	Bb	1601	PAR	C41-C51	5.97	1.65	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	D1	3001	3V6	CAK-CAN	-5.26	1.42	1.49
65	Ab	1601	PAR	C34-C24	-5.17	1.47	1.53
66	C1	3001	3V6	CAK-CAS	4.31	1.64	1.53
66	D1	3001	3V6	CAS-CAU	3.99	1.59	1.52

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	Ab	1601	PAR	O52-C13-O43	-8.43	102.30	111.43
65	Bb	1601	PAR	O54-C54-C64	-8.17	90.80	106.01
66	D1	3001	3V6	OAM-CAO-OAE	8.11	127.88	117.58
66	D1	3001	3V6	OAG-CAN-CAQ	-5.45	114.56	123.13
65	Bb	1601	PAR	O52-C13-O43	-5.39	105.59	111.43

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
66	D1	3001	3V6	O-C-CA-CB
65	Bb	1601	PAR	C21-C11-O11-C42
65	Ab	1601	PAR	C23-C13-O52-C52
65	Ab	1601	PAR	O43-C13-O52-C52
66	C1	3001	3V6	NAL-C-CA-CB

All (2) ring outliers are listed below:

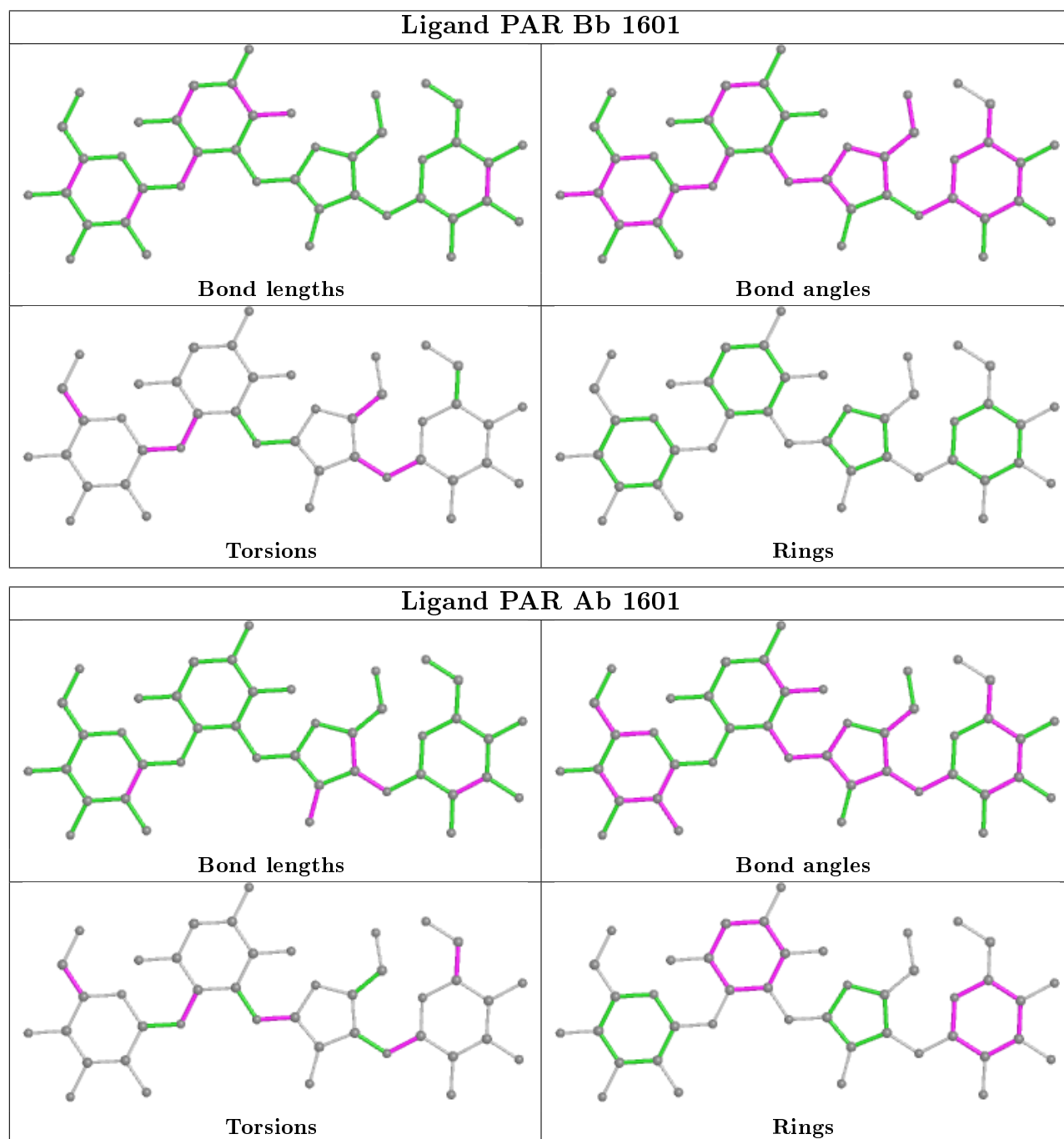
Mol	Chain	Res	Type	Atoms
65	Ab	1601	PAR	C14-C24-C34-C44-C54-O54
65	Ab	1601	PAR	C12-C22-C32-C42-C52-C62

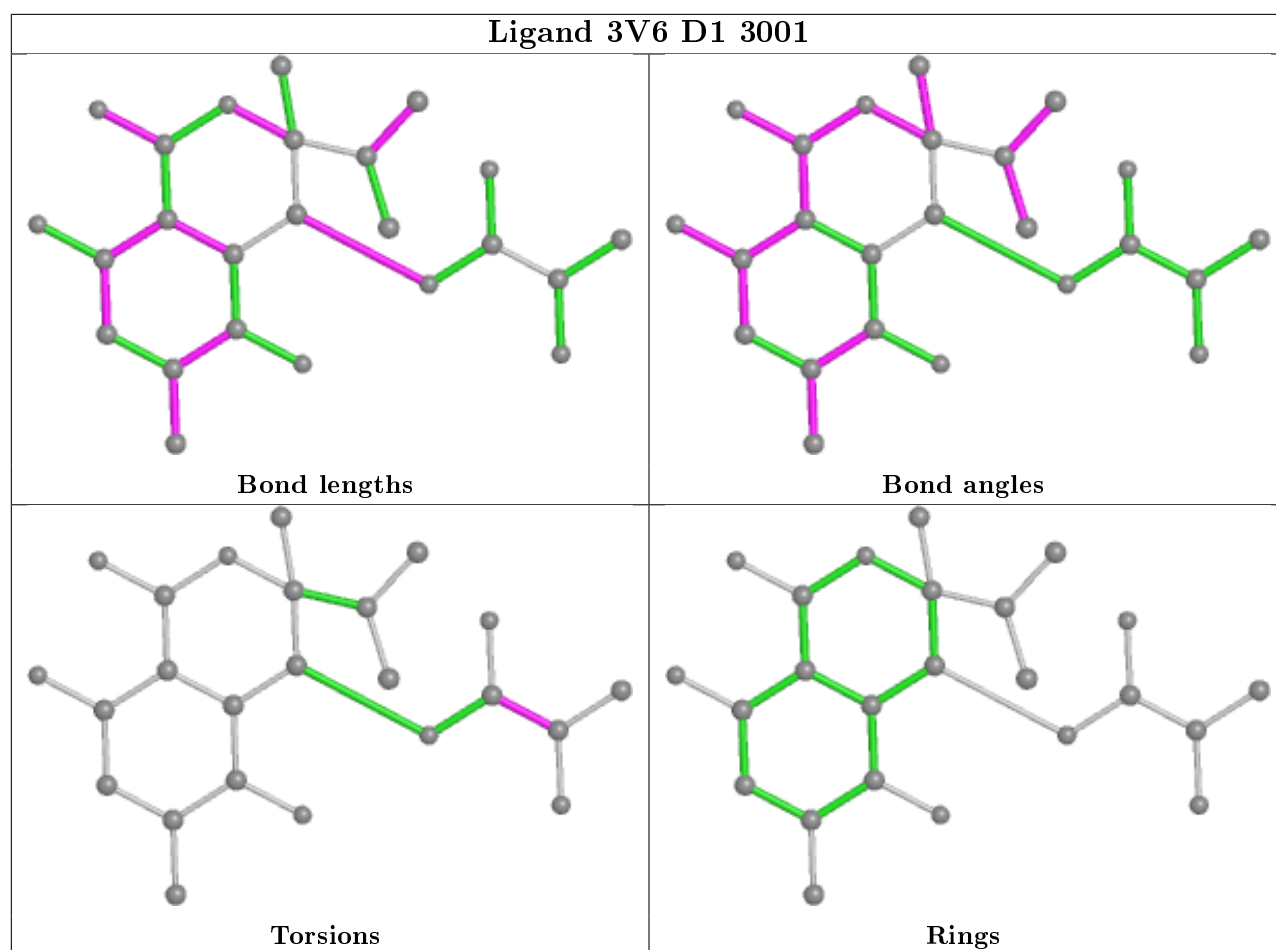
2 monomers are involved in 16 short contacts:

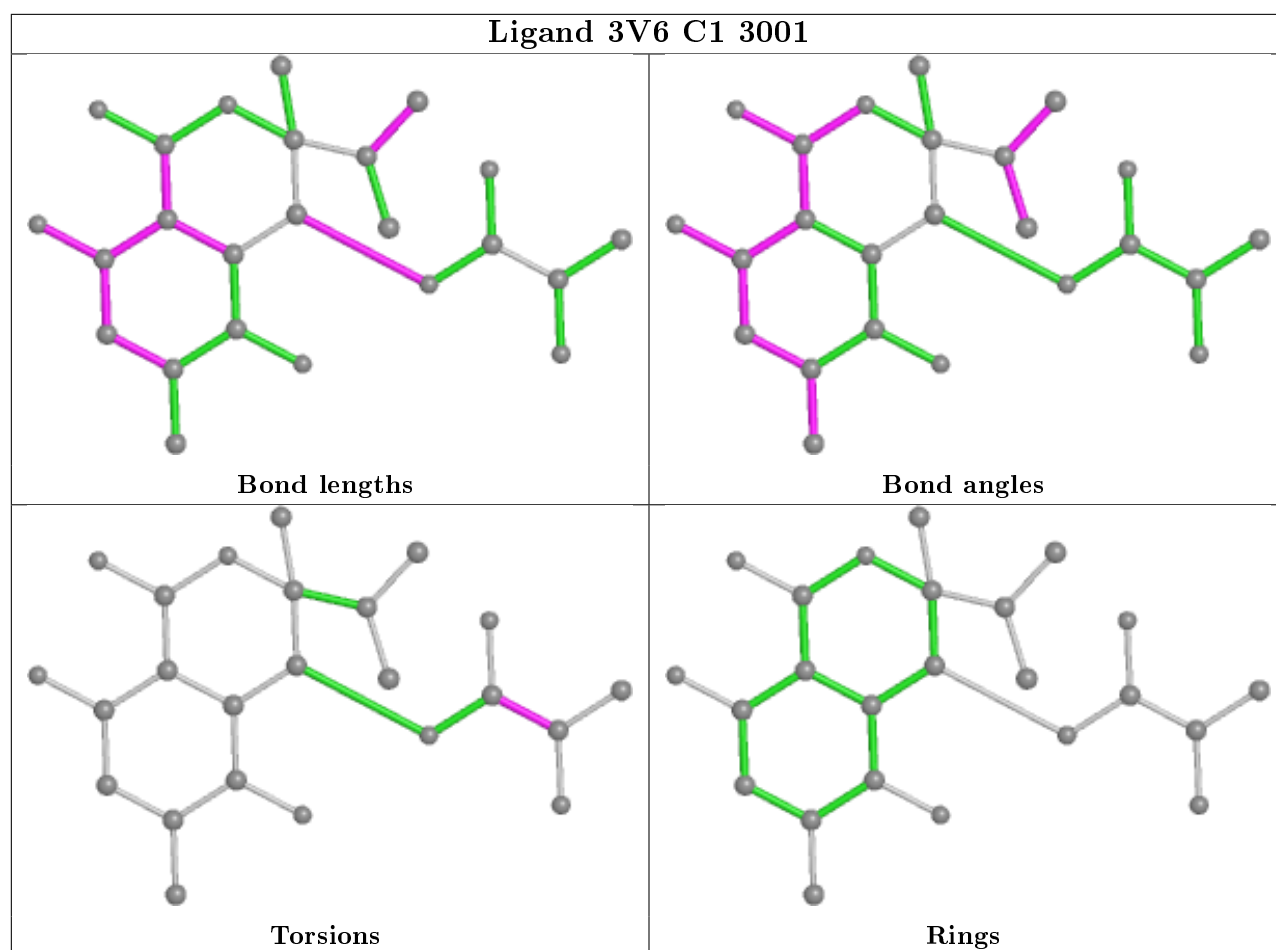
Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	D1	3001	3V6	11	0
66	C1	3001	3V6	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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
27	CA	2
62	DA	2
58	D1	1
54	C7	1
58	C1	1
54	D7	1

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DA	110:PHE	C	119:UNK	N	14.86
1	CA	110:PHE	C	119:UNK	N	12.87
1	CA	136:UNK	C	139:UNK	N	8.88
1	D7	46:HIS	C	47:THR	N	7.64
1	C7	46:HIS	C	47:THR	N	7.62

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	A2	9/9 (100%)	0.01	0 100 100	50, 89, 111, 114	0
2	AA	234/234 (100%)	0.24	10 (4%) 35 35	78, 124, 168, 197	0
2	BA	234/234 (100%)	0.34	17 (7%) 15 17	80, 130, 179, 209	0
3	AC	206/238 (86%)	0.23	14 (6%) 17 19	65, 108, 148, 173	0
4	AD	208/208 (100%)	-0.07	3 (1%) 75 74	51, 86, 123, 147	0
4	BD	208/208 (100%)	-0.15	1 (0%) 91 90	48, 78, 117, 144	0
5	AE	150/150 (100%)	-0.00	3 (2%) 65 64	66, 91, 124, 144	0
5	BE	150/150 (100%)	0.03	0 100 100	57, 83, 122, 141	0
6	AF	101/101 (100%)	-0.29	2 (1%) 65 64	55, 85, 109, 170	0
6	BF	101/101 (100%)	-0.17	1 (0%) 82 81	52, 96, 130, 158	0
7	AG	155/155 (100%)	0.06	13 (8%) 11 13	58, 86, 125, 181	0
7	BG	155/155 (100%)	0.46	10 (6%) 18 20	78, 112, 154, 184	0
8	AH	138/138 (100%)	-0.00	0 100 100	60, 90, 117, 184	0
8	BH	138/138 (100%)	0.27	2 (1%) 75 74	63, 95, 123, 145	0
9	AI	127/127 (100%)	0.46	7 (5%) 25 25	62, 108, 150, 175	0
9	BI	127/127 (100%)	0.88	17 (13%) 3 4	77, 131, 179, 215	0
10	AJ	98/98 (100%)	0.78	13 (13%) 3 4	77, 121, 176, 188	0
10	BJ	98/98 (100%)	1.15	22 (22%) 0 1	65, 134, 173, 202	0
11	AK	119/119 (100%)	-0.02	5 (4%) 36 35	39, 76, 110, 158	0
11	BK	119/119 (100%)	0.49	6 (5%) 28 29	47, 94, 141, 193	0
12	AL	124/124 (100%)	0.34	9 (7%) 15 17	49, 82, 125, 180	0
12	BL	124/124 (100%)	0.07	5 (4%) 38 37	41, 60, 105, 158	0
13	AM	124/124 (100%)	0.30	7 (5%) 24 25	66, 98, 144, 197	0
13	BM	124/124 (100%)	0.73	10 (8%) 12 13	66, 113, 164, 204	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
14	AN	60/60 (100%)	0.25	1 (1%) 70 68	65, 103, 130, 142	0
14	BN	60/60 (100%)	0.30	1 (1%) 70 68	59, 94, 119, 134	0
15	AO	88/88 (100%)	-0.07	0 100 100	46, 76, 112, 123	0
15	BO	88/88 (100%)	0.06	1 (1%) 80 79	55, 94, 120, 132	0
16	AP	83/83 (100%)	0.11	2 (2%) 59 57	52, 73, 101, 136	0
16	BP	83/83 (100%)	0.40	3 (3%) 42 42	59, 89, 135, 152	0
17	AR	99/99 (100%)	0.03	1 (1%) 82 81	59, 80, 108, 115	0
17	BR	99/99 (100%)	0.16	2 (2%) 65 64	65, 94, 126, 135	0
18	AS	70/70 (100%)	0.26	2 (2%) 51 50	56, 88, 119, 156	0
18	BS	70/70 (100%)	0.58	5 (7%) 16 18	66, 94, 142, 180	0
19	AT	78/78 (100%)	0.85	12 (15%) 2 2	67, 110, 164, 180	0
19	BT	78/78 (100%)	1.04	11 (14%) 2 3	79, 118, 161, 184	0
20	AU	99/99 (100%)	0.29	3 (3%) 50 49	62, 86, 125, 146	0
20	BU	99/99 (100%)	0.60	8 (8%) 12 13	64, 107, 146, 154	0
21	AW	24/24 (100%)	1.67	7 (29%) 0 0	63, 80, 112, 138	0
21	BW	24/24 (100%)	1.22	4 (16%) 1 2	64, 91, 132, 163	0
22	Ab	1504/1504 (100%)	-0.17	24 (1%) 72 70	30, 75, 154, 300	0
22	Bb	1504/1504 (100%)	-0.04	39 (2%) 56 54	31, 81, 165, 318	0
23	B2	10/10 (100%)	0.29	0 100 100	60, 107, 138, 172	0
24	BC	206/206 (100%)	0.13	7 (3%) 45 44	64, 105, 149, 169	0
25	C2	75/76 (98%)	7.29	69 (92%) 0 0	99, 250, 345, 377	0
25	C3	76/76 (100%)	0.33	6 (7%) 12 14	60, 130, 198, 227	0
25	D3	76/76 (100%)	0.49	3 (3%) 39 38	59, 147, 212, 228	0
26	C4	77/77 (100%)	-0.31	0 100 100	44, 79, 132, 159	0
27	CA	87/206 (42%)	3.10	49 (56%) 0 0	98, 186, 221, 241	0
28	CB	271/271 (100%)	-0.33	0 100 100	23, 48, 83, 150	0
28	DB	271/271 (100%)	-0.24	4 (1%) 73 72	20, 52, 86, 159	0
29	CC	204/204 (100%)	0.11	6 (2%) 51 50	31, 68, 123, 150	0
29	DC	204/204 (100%)	-0.00	3 (1%) 73 72	24, 61, 124, 169	0
30	CD	207/207 (100%)	-0.27	4 (1%) 66 65	29, 64, 133, 194	0
30	DD	207/207 (100%)	-0.09	5 (2%) 59 57	20, 65, 146, 223	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
31	CE	181/181 (100%)	0.04	7 (3%) 39 38	59, 92, 137, 213	0
31	DE	181/181 (100%)	0.50	14 (7%) 13 15	76, 117, 154, 198	0
32	CF	159/159 (100%)	1.10	34 (21%) 0 1	82, 134, 175, 219	0
32	DF	159/159 (100%)	0.11	7 (4%) 34 34	45, 85, 126, 178	0
33	CI	145/145 (100%)	0.28	4 (2%) 53 51	40, 88, 128, 150	0
33	DI	145/145 (100%)	0.29	8 (5%) 25 25	60, 108, 139, 165	0
34	CJ	0/130	-	-	-	-
34	DJ	0/130	-	-	-	-
35	CM	138/138 (100%)	0.04	1 (0%) 87 87	47, 78, 118, 130	0
35	DM	138/138 (100%)	-0.05	0 100 100	36, 73, 121, 151	0
36	CN	122/122 (100%)	-0.11	1 (0%) 86 85	35, 66, 89, 111	0
36	DN	122/122 (100%)	-0.35	0 100 100	27, 51, 75, 107	0
37	CO	146/146 (100%)	0.25	4 (2%) 54 53	34, 77, 127, 168	0
37	DO	146/146 (100%)	0.28	5 (3%) 45 44	31, 87, 123, 165	0
38	CP	141/141 (100%)	-0.03	2 (1%) 75 74	44, 75, 111, 192	0
38	DP	141/141 (100%)	-0.10	2 (1%) 75 74	42, 71, 106, 219	0
39	CQ	117/117 (100%)	-0.20	0 100 100	38, 63, 94, 127	0
39	DQ	117/117 (100%)	-0.05	0 100 100	27, 61, 99, 130	0
40	CR	98/98 (100%)	0.39	3 (3%) 49 48	47, 89, 130, 176	0
40	DR	98/98 (100%)	1.24	21 (21%) 0 1	68, 113, 143, 163	0
41	CS	137/137 (100%)	0.04	5 (3%) 42 42	45, 79, 142, 200	0
41	DS	137/137 (100%)	0.04	4 (2%) 51 50	43, 71, 148, 192	0
42	CT	117/117 (100%)	-0.10	2 (1%) 70 68	37, 66, 116, 138	0
42	DT	117/117 (100%)	-0.16	1 (0%) 84 83	31, 68, 111, 153	0
43	CU	101/101 (100%)	0.05	2 (1%) 65 64	35, 92, 122, 134	0
43	DU	101/101 (100%)	0.22	5 (4%) 28 29	26, 86, 123, 196	0
44	CW	113/113 (100%)	-0.15	2 (1%) 68 67	38, 54, 90, 182	0
45	CX	92/92 (100%)	-0.28	0 100 100	39, 65, 89, 109	0
45	DX	92/92 (100%)	-0.28	0 100 100	33, 55, 88, 115	0
46	CY	100/100 (100%)	1.16	23 (23%) 0 1	58, 94, 168, 214	0
46	DY	100/100 (100%)	0.83	13 (13%) 3 4	48, 81, 193, 251	0
47	CZ	176/176 (100%)	0.33	9 (5%) 28 28	76, 118, 157, 233	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
47	DZ	176/176 (100%)	0.47	15 (8%) 10 12	69, 119, 173, 203	0
48	Ca	84/84 (100%)	0.62	8 (9%) 8 10	44, 67, 127, 170	0
48	Da	84/84 (100%)	0.60	9 (10%) 6 7	49, 82, 137, 167	0
49	CH	93/93 (100%)	-0.10	1 (1%) 80 79	30, 54, 102, 140	0
49	DH	93/93 (100%)	0.08	1 (1%) 80 79	29, 66, 121, 179	0
50	CK	71/71 (100%)	0.00	2 (2%) 53 51	42, 85, 125, 180	0
50	DK	71/71 (100%)	-0.02	2 (2%) 53 51	37, 68, 124, 179	0
51	CL	59/59 (100%)	0.62	4 (6%) 17 19	45, 72, 111, 223	0
51	DL	59/59 (100%)	0.35	5 (8%) 10 12	48, 79, 120, 213	0
52	C5	30/30 (100%)	-0.31	0 100 100	76, 99, 130, 155	0
52	D5	30/30 (100%)	0.39	2 (6%) 17 19	99, 128, 155, 167	0
53	C6	59/59 (100%)	0.33	5 (8%) 10 12	34, 63, 160, 206	0
53	D6	59/59 (100%)	0.06	4 (6%) 17 19	28, 65, 172, 205	0
54	C7	44/44 (100%)	1.55	13 (29%) 0 0	54, 101, 146, 183	0
54	D7	44/44 (100%)	2.16	18 (40%) 0 0	84, 125, 165, 181	0
55	C8	48/48 (100%)	-0.13	2 (4%) 36 35	26, 40, 79, 139	0
55	D8	48/48 (100%)	-0.17	2 (4%) 36 35	21, 34, 77, 135	0
56	C9	63/63 (100%)	-0.01	1 (1%) 72 70	34, 54, 90, 123	0
56	D9	63/63 (100%)	0.08	2 (3%) 47 46	39, 66, 102, 136	0
57	C0	36/36 (100%)	3.05	21 (58%) 0 0	93, 125, 175, 177	0
57	D0	36/36 (100%)	2.88	25 (69%) 0 0	73, 106, 141, 145	0
58	C1	2807/2899 (96%)	-0.25	30 (1%) 80 79	21, 54, 148, 279	0
58	D1	2807/2899 (96%)	-0.22	44 (1%) 72 70	16, 52, 155, 267	0
59	Cs	119/119 (100%)	-0.25	2 (1%) 70 68	58, 83, 138, 197	0
59	Ds	119/119 (100%)	0.20	5 (4%) 36 35	62, 104, 147, 172	0
60	D2	20/20 (100%)	3.87	18 (90%) 0 0	133, 235, 281, 283	0
61	D4	76/76 (100%)	-0.24	0 100 100	37, 79, 120, 201	0
62	DA	87/206 (42%)	3.23	60 (68%) 0 0	118, 190, 257, 309	0
63	DW	113/113 (100%)	-0.17	2 (1%) 68 67	33, 51, 100, 159	0
64	DV	55/55 (100%)	6.54	50 (90%) 0 0	110, 248, 297, 345	0
All	All	20982/21697 (96%)	0.11	991 (4%) 31 31	16, 77, 159, 377	0

The worst 5 of 991 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	C2	70	G	23.4
64	DV	50	G	21.8
25	C2	71	G	21.6
25	C2	17	C	20.5
25	C2	3	C	20.1

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](#)

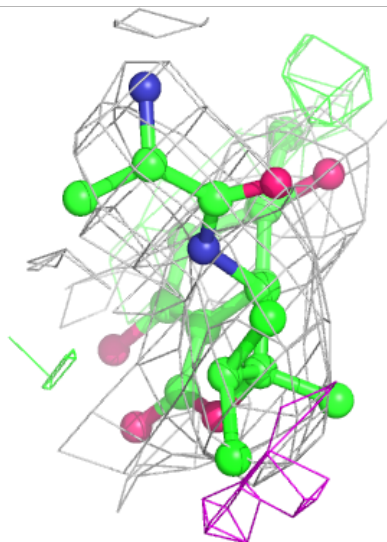
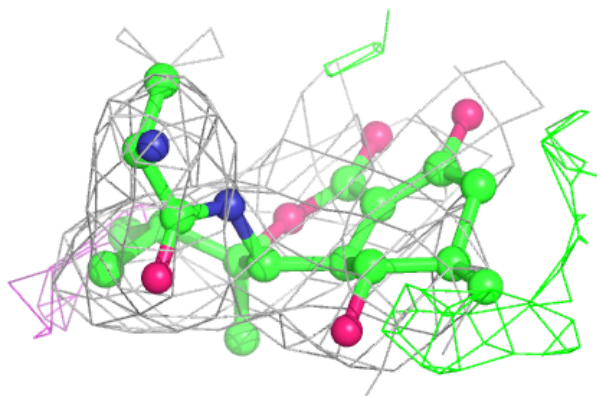
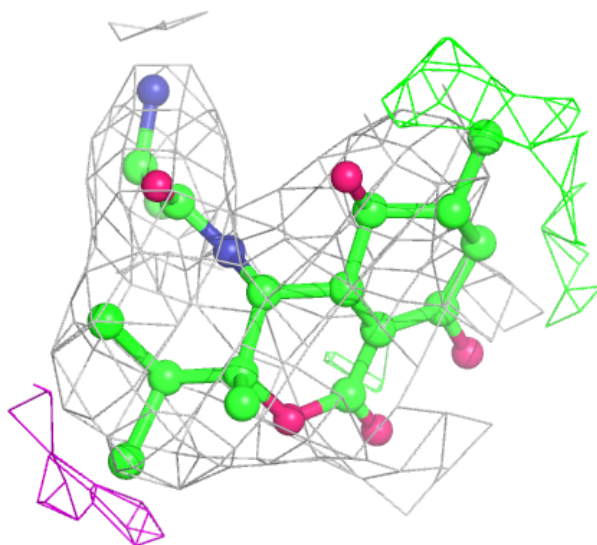
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
66	3V6	C1	3001	24/24	0.92	0.25	46,63,76,91	0
65	PAR	Ab	1601	42/42	0.93	0.20	51,65,75,91	0
67	MG	D1	3002	1/1	0.93	0.24	40,40,40,40	0
66	3V6	D1	3001	24/24	0.94	0.24	32,55,75,86	0
67	MG	C1	3002	1/1	0.95	0.22	41,41,41,41	0
65	PAR	Bb	1601	42/42	0.96	0.20	42,50,56,67	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

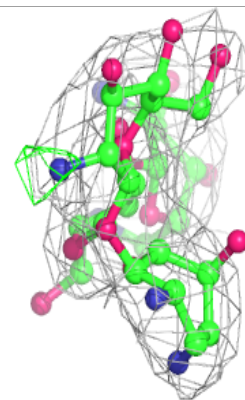
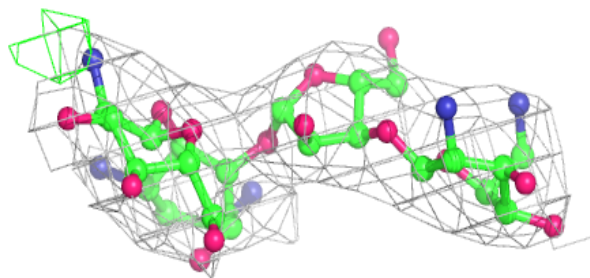
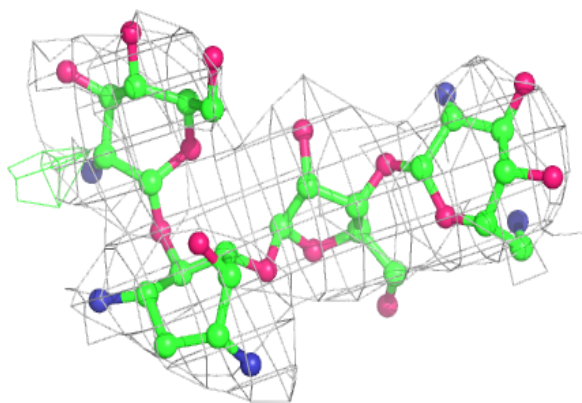
Electron density around 3V6 C1 3001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



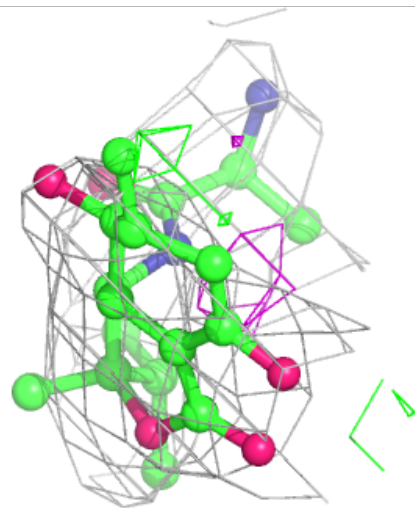
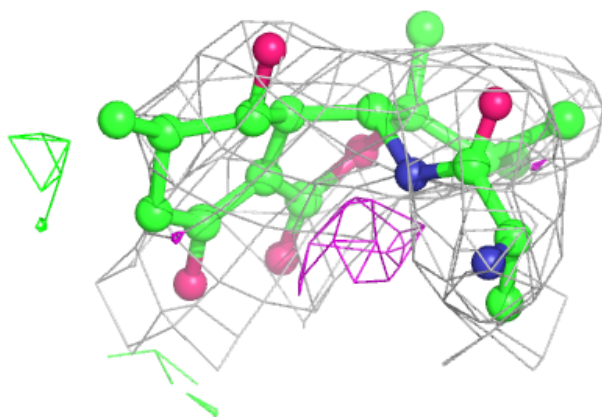
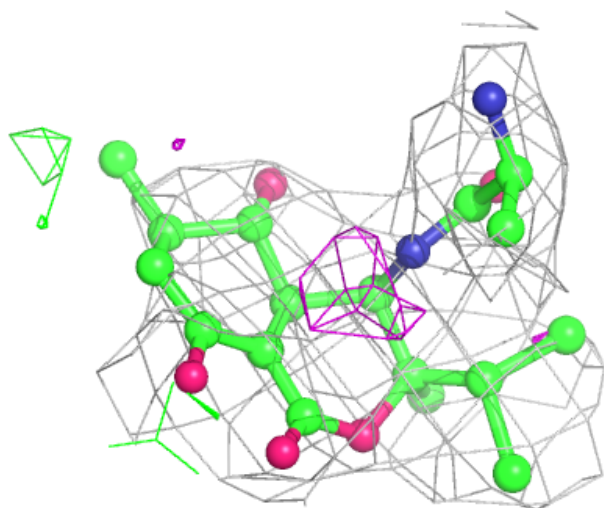
Electron density around PAR Ab 1601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



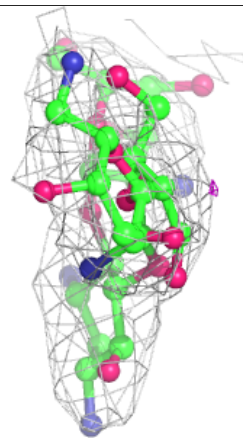
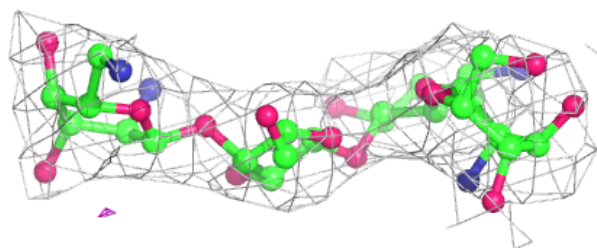
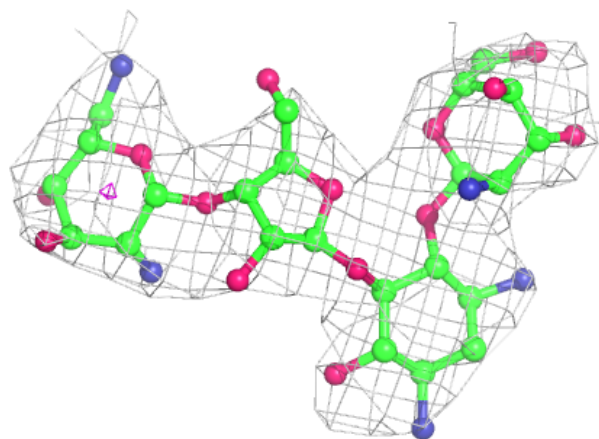
Electron density around 3V6 D1 3001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PAR Bb 1601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.