



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 17, 2023 – 01:31 PM EST

PDB ID : 4U24
Title : Crystal structure of the E. coli ribosome bound to dalfopristin.
Authors : Noeske, J.; Huang, J.; Olivier, N.B.; Giacobbe, R.A.; Zambrowski, M.; Cate, J.H.D.
Deposited on : 2014-07-16
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

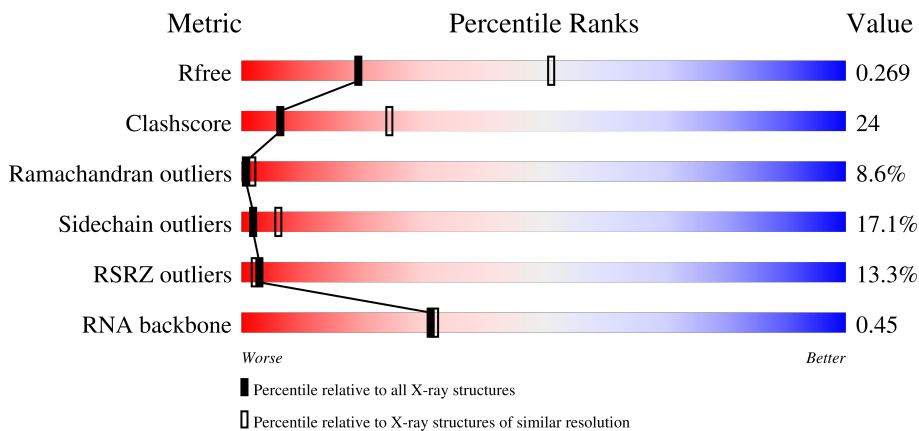
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)
RNA backbone	3102	1007 (3.16-2.64)

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

Mol	Chain	Length	Quality of chain
1	AA	1539	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 30%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 54%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 16%; height: 10px; background-color: orange;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 30% 54% 16% </div>
1	CA	1539	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 30%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 55%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 15%; height: 10px; background-color: orange;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 8% 30% 55% 15% </div>
2	AB	218	<div style="display: flex; align-items: center;"> <div style="width: 17%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 23%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 51%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 21%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: red;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 17% 23% 51% 21% 5% </div>
2	CB	218	<div style="display: flex; align-items: center;"> <div style="width: 22%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 31%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 49%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 18%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 1%; height: 10px; background-color: red;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 22% 31% 49% 18% 1% </div>

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Mol	Chain	Length	Quality of chain
3	AC	206	
3	CC	206	
4	AD	205	
4	CD	205	
5	AE	150	
5	CE	150	
6	AF	100	
6	CF	100	
7	AG	151	
7	CG	151	
8	AH	129	
8	CH	129	
9	AI	127	
9	CI	127	
10	AJ	98	
10	CJ	98	
11	AK	117	
11	CK	117	
12	AL	123	
12	CL	123	
13	AM	114	
13	CM	114	
14	AN	100	
14	CN	100	
15	AO	88	

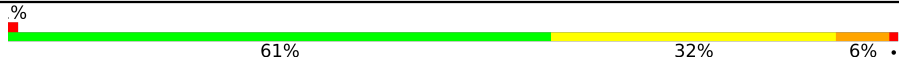

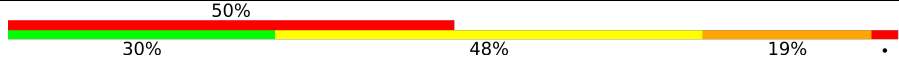


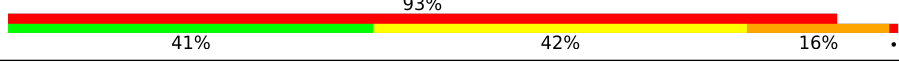
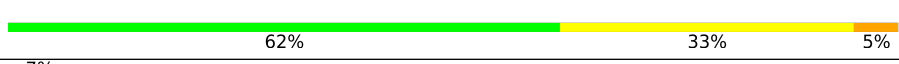
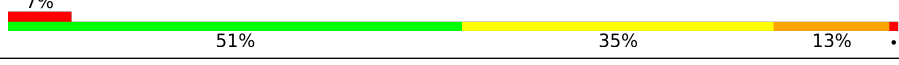
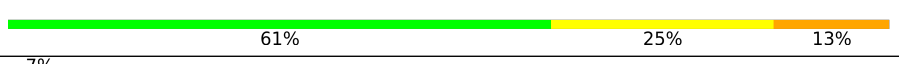


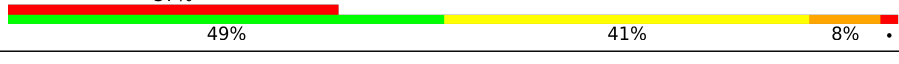

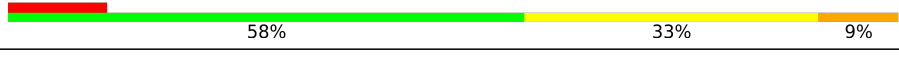
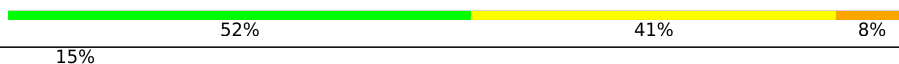
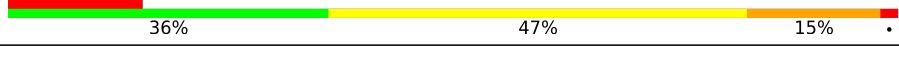









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Mol	Chain	Length	Quality of chain
15	CO	88	
16	AP	82	
16	CP	82	
17	AQ	80	
17	CQ	80	
18	AR	55	
18	CR	55	
19	AS	79	
19	CS	79	
20	AT	85	
20	CT	85	
21	AU	51	
21	CU	51	
22	BA	2903	
22	DA	2903	
23	BB	119	
23	DB	119	
24	BC	271	
24	DC	271	
25	BD	209	
25	DD	209	
26	BE	201	
26	DE	201	
27	BF	177	
27	DF	177	

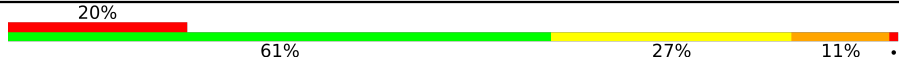


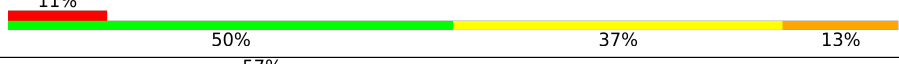

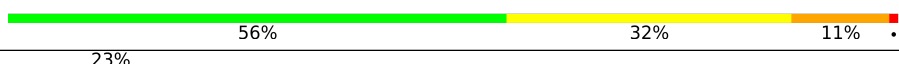
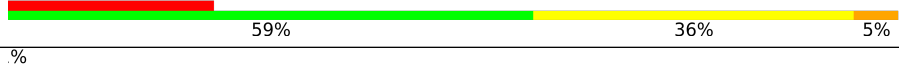

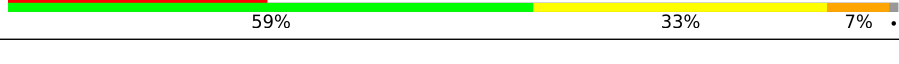



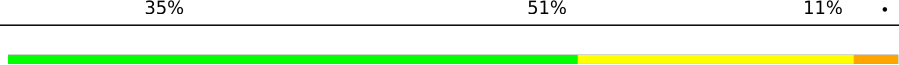
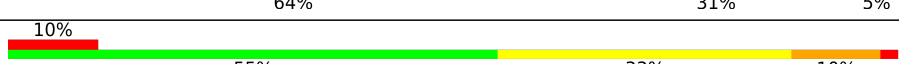


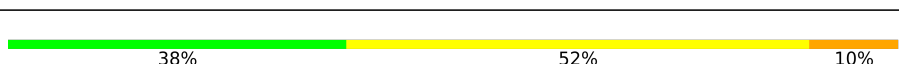
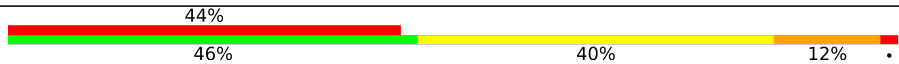
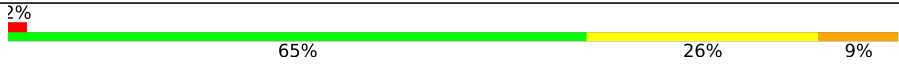


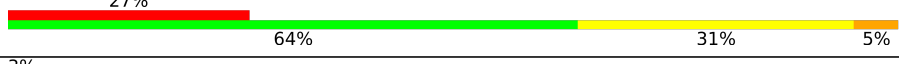
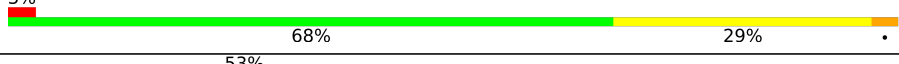


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Mol	Chain	Length	Quality of chain
28	BG	176	
28	DG	176	
29	BH	149	
29	DH	149	
30	BI	141	
30	DI	141	
31	BJ	142	
31	DJ	142	
32	BK	122	
32	DK	122	
33	BL	143	
33	DL	143	
34	BM	136	
34	DM	136	
35	BN	120	
35	DN	120	
36	BO	116	
36	DO	116	
37	BP	114	
37	DP	114	
38	BQ	117	
38	DQ	117	
39	BR	103	
39	DR	103	
40	BS	110	

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Mol	Chain	Length	Quality of chain
40	DS	110	
41	BT	93	
41	DT	93	
42	BU	102	
42	DU	102	
43	BV	94	
43	DV	94	
44	BW	76	
44	DW	76	
45	BX	77	
45	DX	77	
46	BY	63	
46	DY	63	
47	BZ	58	
47	DZ	58	
48	B0	56	
48	D0	56	
49	B1	50	
49	D1	50	
50	B2	46	
50	D2	46	
51	B3	64	
51	D3	64	
52	B4	38	
52	D4	38	

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Mol	Chain	Length	Quality of chain
53	B5	228	<p>82%</p> <p>42% 29% 13% 16%</p>

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
54	MG	AA	1656	-	-	-	X
54	MG	AA	1658	-	-	-	X
54	MG	AA	1662	-	-	-	X
54	MG	AA	1664	-	-	-	X
54	MG	AA	1668	-	-	-	X
54	MG	DA	3003	-	-	-	X
54	MG	DA	3005	-	-	-	X
54	MG	DA	3026	-	-	-	X
54	MG	DA	3028	-	-	-	X
54	MG	DA	3041	-	-	-	X
54	MG	DA	3044	-	-	-	X
54	MG	DA	3061	-	-	-	X
54	MG	DA	3062	-	-	-	X
54	MG	DA	3092	-	-	-	X
54	MG	DA	3100	-	-	-	X
54	MG	DA	3113	-	-	-	X
54	MG	DA	3119	-	-	-	X
54	MG	DA	3133	-	-	-	X
54	MG	DA	3135	-	-	-	X
54	MG	DA	3137	-	-	-	X
54	MG	DA	3151	-	-	-	X
54	MG	DA	3162	-	-	-	X
54	MG	DL	201	-	-	-	X
55	DOL	DA	3001	-	-	X	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 288276 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	AA	1538	Total	C	N	O	P	0	0	0
			32995	14716	6050	10691	1538			
1	CA	1539	Total	C	N	O	P	0	0	0
			33015	14725	6052	10699	1539			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	AB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			
2	CB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	AC	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			
3	CC	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	AD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			
4	CD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- 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
			1106	687	211	202	6			
5	CE	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			
6	CF	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			
7	CG	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			
8	CH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			
9	CI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- 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
			787	493	150	143	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	CJ	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			
11	CK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			
12	CL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			
13	CM	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			
14	CN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- 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
			710	437	143	129	1			
15	CO	88	Total	C	N	O	S	0	0	0
			710	437	143	129	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			
16	CP	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			
17	CQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	55	Total	C	N	O	0	0	0
			456	288	86	82			
18	CR	55	Total	C	N	O	0	0	0
			456	288	86	82			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			
19	CS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			
20	CT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			
21	CU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BA	2897	Total	C	N	O	P	0	0	0
			62195	27745	11446	20107	2897			
22	DA	2897	Total	C	N	O	P	0	0	0
			62195	27745	11446	20107	2897			

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	BB	119	Total	C	N	O	P	0	0	0
			2549	1135	466	829	119			
23	DB	118	Total	C	N	O	P	0	0	0
			2529	1126	464	821	118			

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			
24	DC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			
25	DD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
26	DE	201	1552	974	283	290	5	0	0	0

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
27	BF	177	1411	899	249	257	6	0	0	0
27	DF	177	1411	899	249	257	6	0	0	0

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
28	BG	176	1323	832	243	246	2	0	0	0
28	DG	176	1323	832	243	246	2	0	0	0

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
29	BH	149	1110	699	197	213	1	0	0	0
29	DH	149	1110	699	197	213	1	0	0	0

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
30	BI	141	1032	651	179	196	6	0	0	0
30	DI	141	1032	651	179	196	6	0	0	0

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
31	BJ	142	1129	714	212	199	4	0	0	0
31	DJ	142	1129	714	212	199	4	0	0	0

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			
32	DK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			
33	DL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			
34	DM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			
35	DN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
36	BO	116	Total	C	N	O	0	0	0
			892	552	178	162			
36	DO	116	Total	C	N	O	0	0	0
			892	552	178	162			

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			
37	DP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				
38	DQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			
39	DR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			
40	DS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			
41	DT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
42	BU	102	Total	C	N	O	S	0	0	0
			780	492	146	142				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
42	DU	102	780	492	146	142	0	0	0

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
43	BV	94	753	479	137	134	3	0	0	0
43	DV	94	753	479	137	134	3	0	0	0

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
44	BW	76	580	359	117	103	1	0	0	0
44	DW	75	569	353	113	102	1	0	0	0

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
45	BX	77	625	388	129	106	2	0	0	0
45	DX	77	625	388	129	106	2	0	0	0

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
46	BY	63	509	313	99	95	2	0	0	0
46	DY	63	509	313	99	95	2	0	0	0

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
47	BZ	58	449	281	87	79	2	0	0	0
47	DZ	58	449	281	87	79	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			
48	D0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B1	50	Total	C	N	O	0	0	0
			410	263	75	72			
49	D1	50	Total	C	N	O	0	0	0
			410	263	75	72			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			
50	D2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			
51	D3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			
52	D4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			

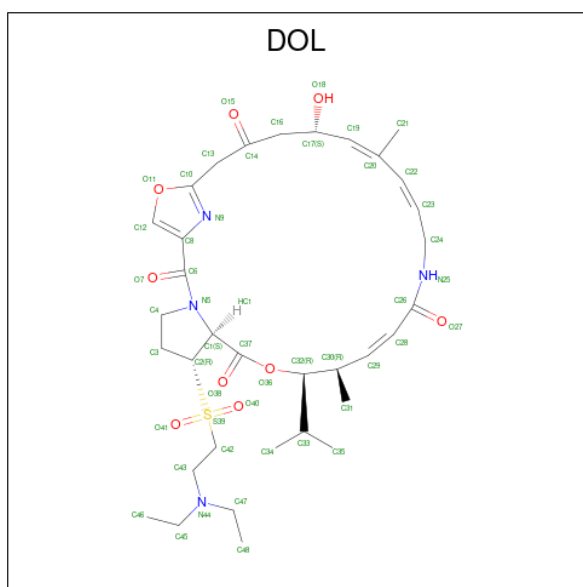
- Molecule 53 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
			Total	C	N				O
53	B5	191	1142	691	221	230	0	0	1

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	AA	70	Total 70	Mg 70	0	0
54	AM	1	Total 1	Mg 1	0	0
54	AN	1	Total 1	Mg 1	0	0
54	BA	194	Total 194	Mg 194	0	0
54	BB	4	Total 4	Mg 4	0	0
54	BQ	1	Total 1	Mg 1	0	0
54	CA	56	Total 56	Mg 56	0	0
54	DA	164	Total 164	Mg 164	0	0
54	DB	3	Total 3	Mg 3	0	0
54	DL	1	Total 1	Mg 1	0	0
54	DQ	1	Total 1	Mg 1	0	0
54	D2	1	Total 1	Mg 1	0	0

- Molecule 55 is 5-(2-DIETHYLAMINO-ETHANESULFONYL)-21-HYDROXY-10-ISOPROPYL-11,19-DIMETHYL-9,26-DIOXA-3,15,28-TRIAZA-TRICYCLO[23.2.1.00,255]OCTACOSA-1(27),12,17,19,25(28)-PENTAENE-2,8,14,23-TETRAONE (three-letter code: DOL) (formula: C₃₄H₅₀N₄O₉S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
55	BA	1	Total	C	N	O	S	0	0
			48	34	4	9	1		
55	DA	1	Total	C	N	O	S	0	0
			48	34	4	9	1		

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B4	1	Total	Zn	0	0
			1	1		
56	D4	1	Total	Zn	0	0
			1	1		

- Molecule 57 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	195	Total	O	0	0
			195	195		
57	AE	1	Total	O	0	0
			1	1		
57	AL	1	Total	O	0	0
			1	1		
57	AN	3	Total	O	0	0
			3	3		
57	AT	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AU	1	Total O 1 1	0	0
57	BA	615	Total O 615 615	0	0
57	BB	13	Total O 13 13	0	0
57	BC	8	Total O 8 8	0	0
57	BD	3	Total O 3 3	0	0
57	BE	2	Total O 2 2	0	0
57	BF	1	Total O 1 1	0	0
57	BL	7	Total O 7 7	0	0
57	BN	5	Total O 5 5	0	0
57	BQ	1	Total O 1 1	0	0
57	BS	1	Total O 1 1	0	0
57	BT	1	Total O 1 1	0	0
57	BU	1	Total O 1 1	0	0
57	BV	1	Total O 1 1	0	0
57	B2	1	Total O 1 1	0	0
57	B3	3	Total O 3 3	0	0
57	B4	2	Total O 2 2	0	0
57	CA	193	Total O 193 193	0	0
57	CL	1	Total O 1 1	0	0
57	CN	1	Total O 1 1	0	0
57	CT	2	Total O 2 2	0	0

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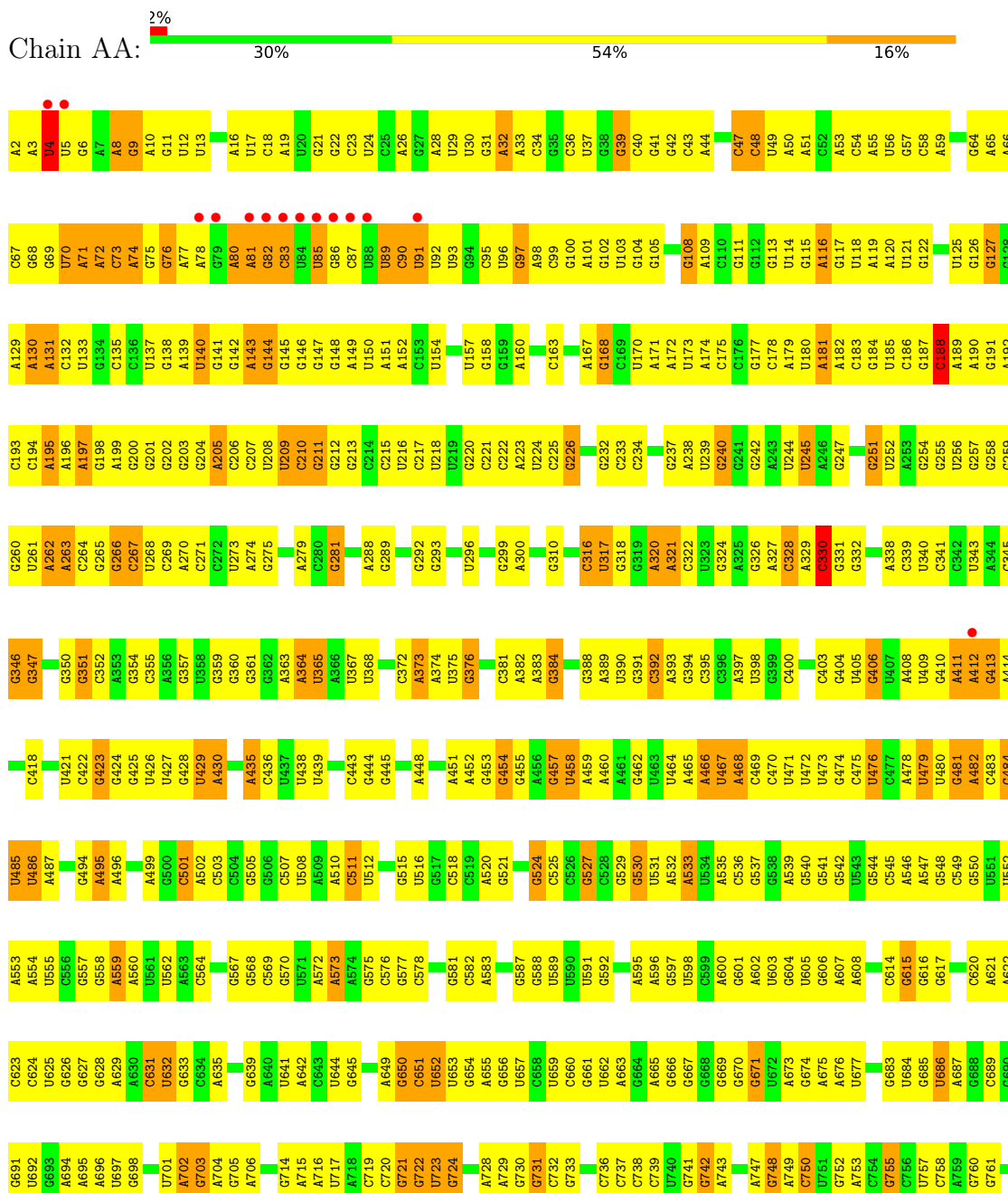
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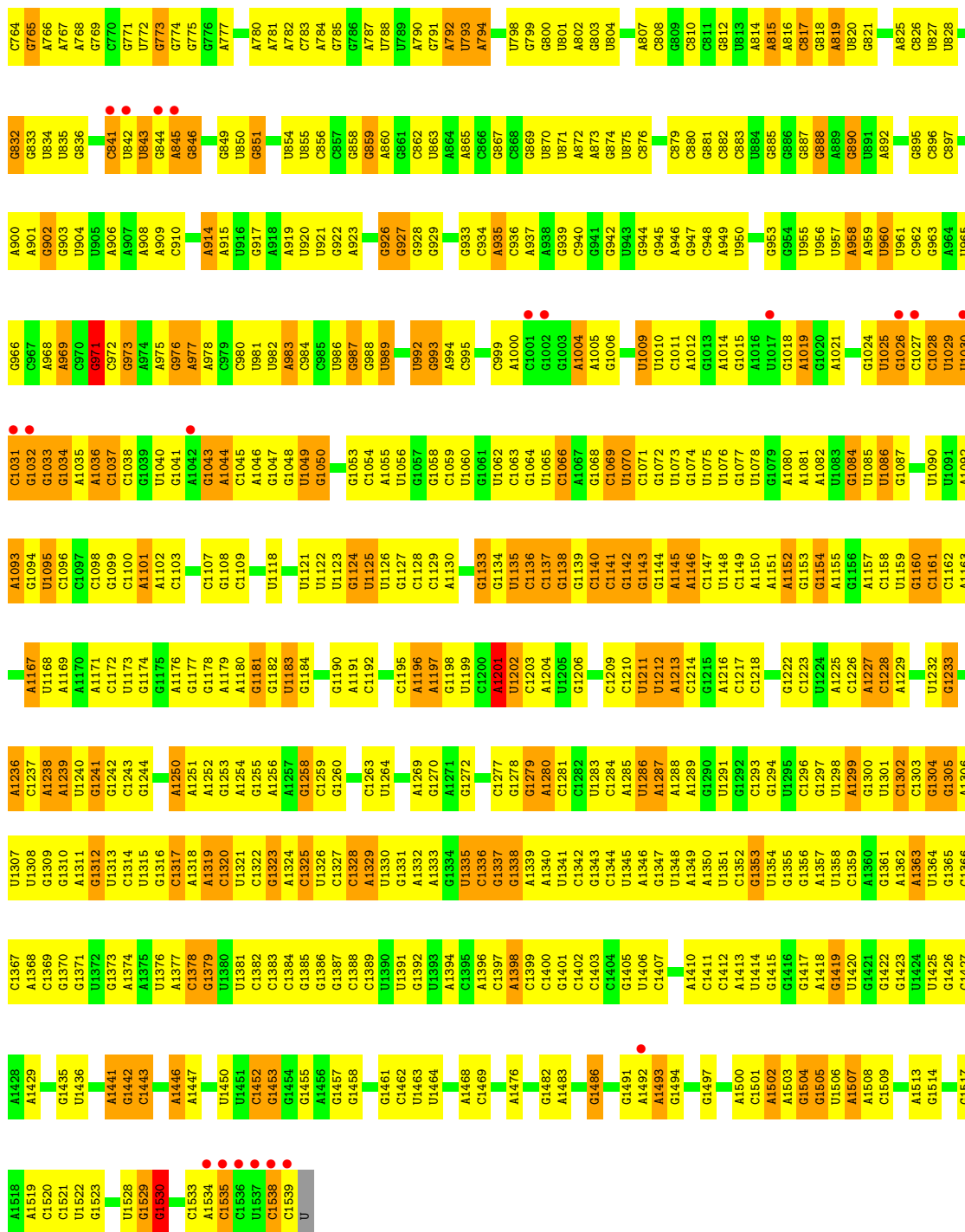
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57	DB	13	Total O 13 13	0	0
57	DC	10	Total O 10 10	0	0
57	DD	4	Total O 4 4	0	0
57	DE	4	Total O 4 4	0	0
57	DJ	1	Total O 1 1	0	0
57	DL	4	Total O 4 4	0	0
57	DN	2	Total O 2 2	0	0
57	DS	2	Total O 2 2	0	0
57	DT	3	Total O 3 3	0	0
57	DU	1	Total O 1 1	0	0
57	DV	1	Total O 1 1	0	0
57	D2	1	Total O 1 1	0	0
57	D3	1	Total O 1 1	0	0
57	D4	1	Total O 1 1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

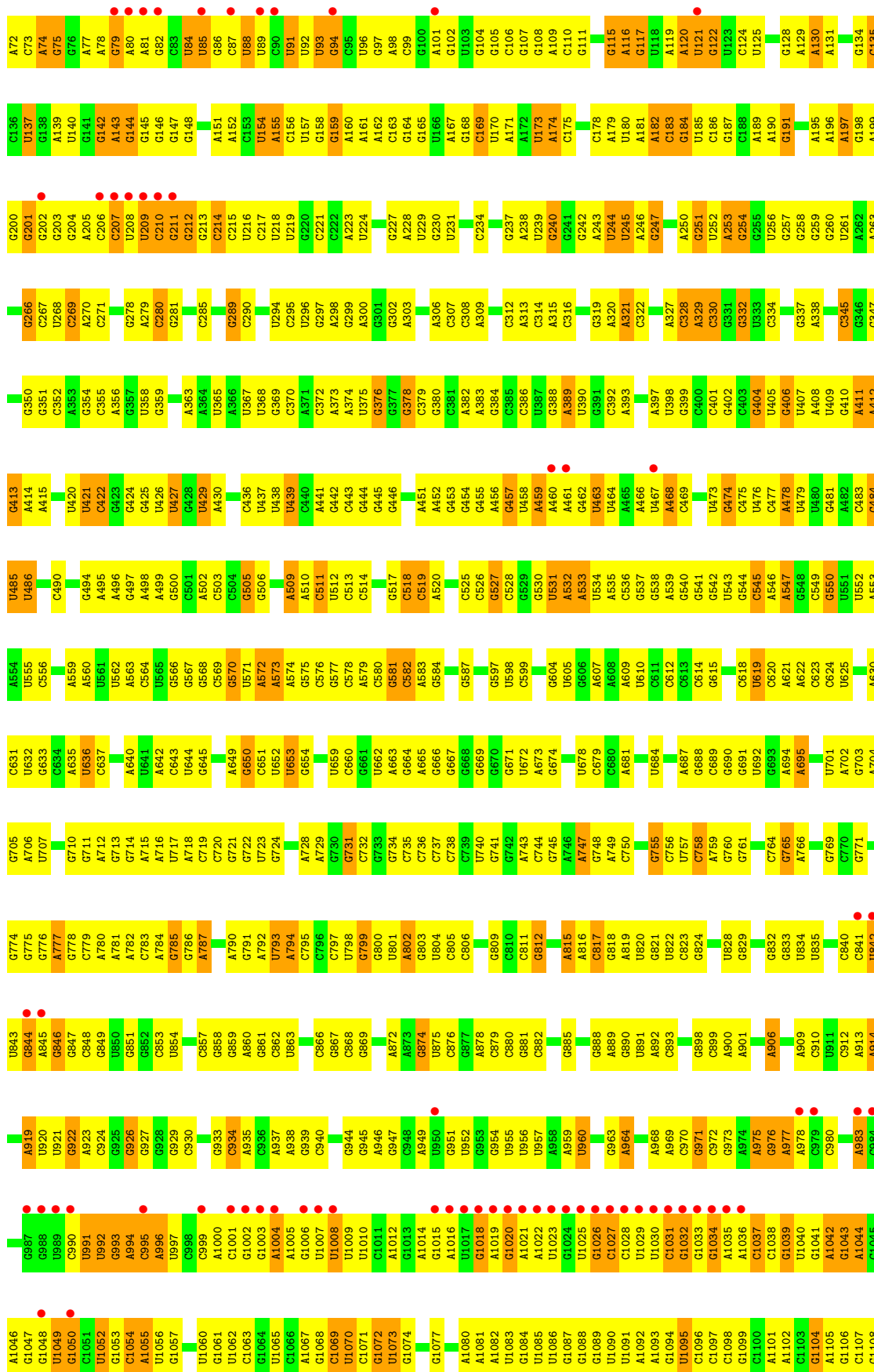
- Molecule 1: 16S rRNA

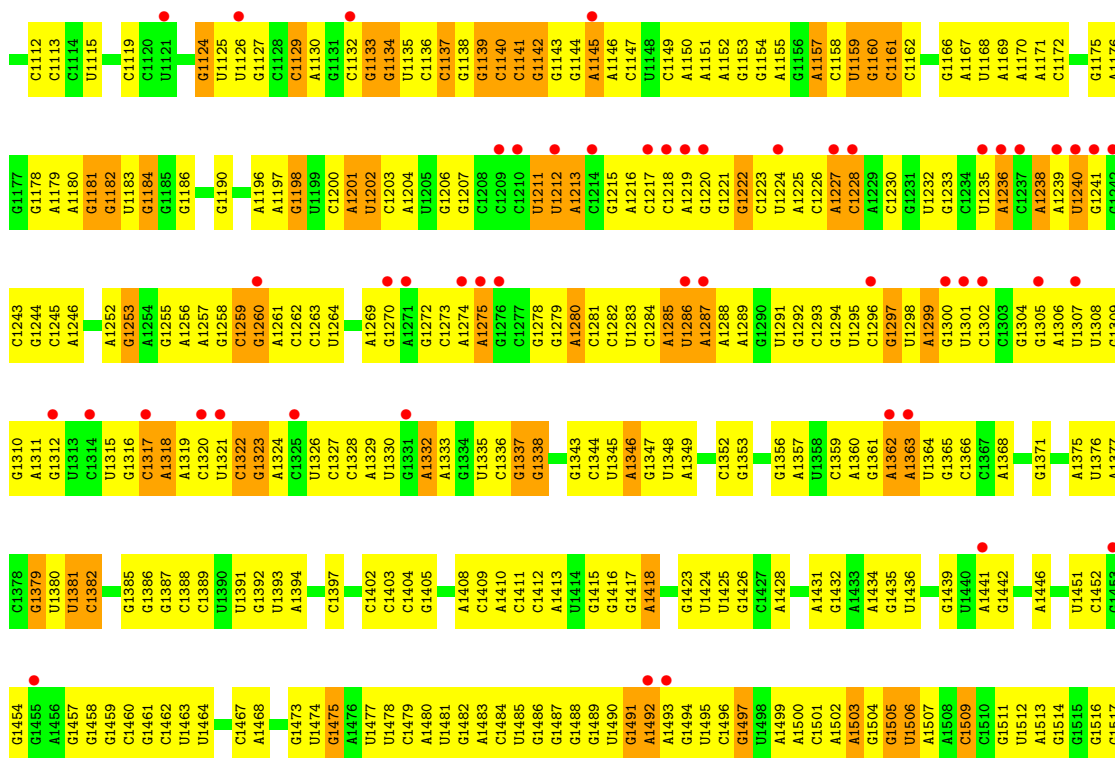




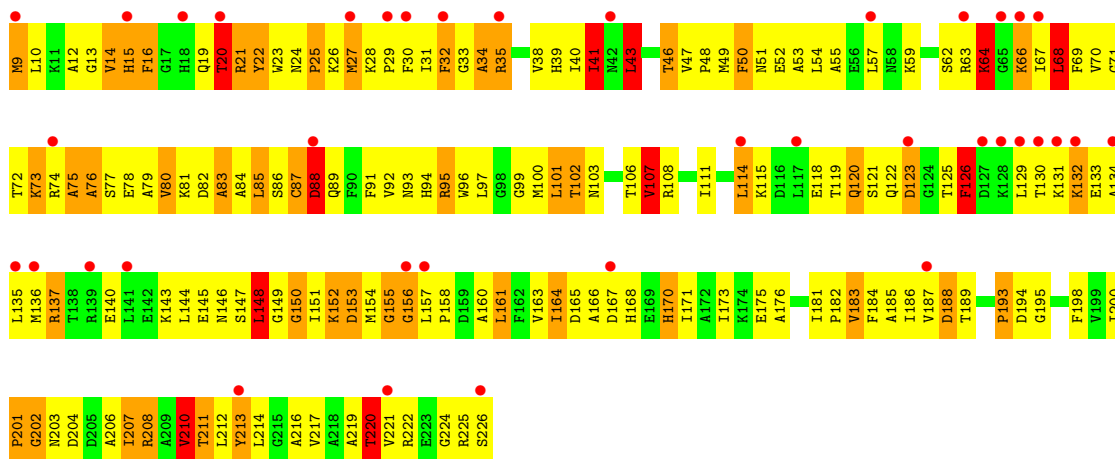
● Molecule 1: 16S rRNA





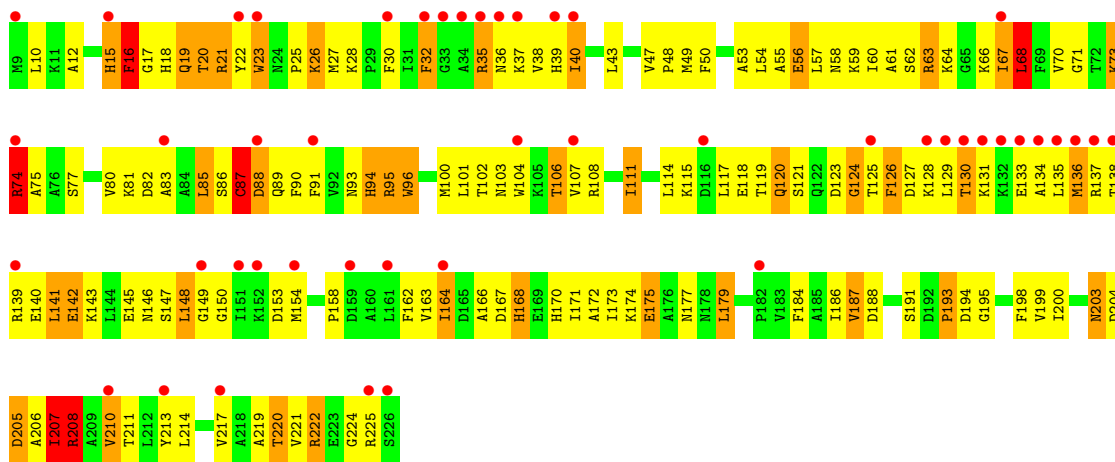


● Molecule 2: 30S ribosomal protein S2

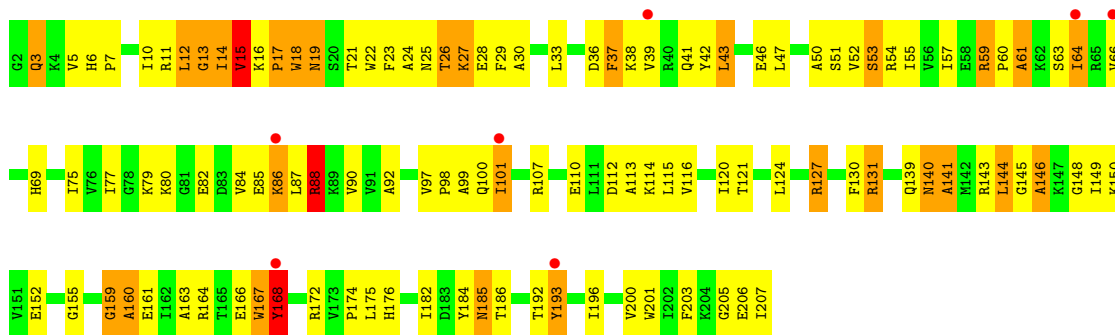
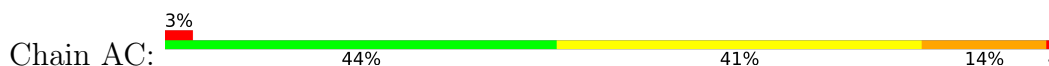


● Molecule 2: 30S ribosomal protein S2

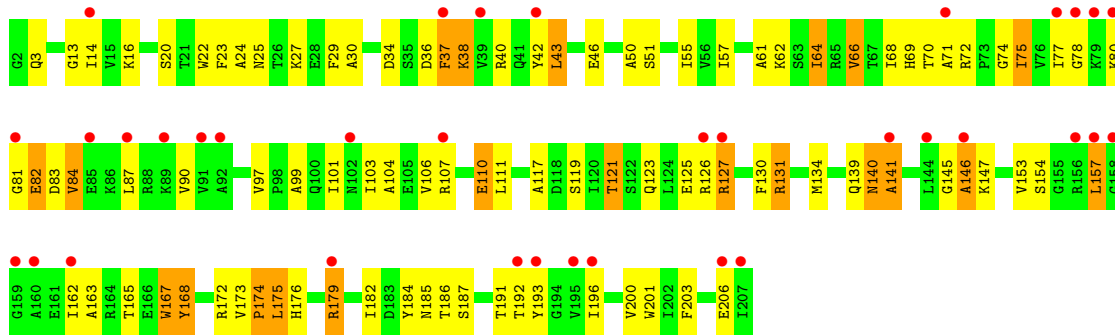




• Molecule 3: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S3

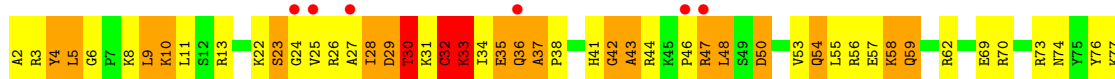


• Molecule 4: 30S ribosomal protein S4

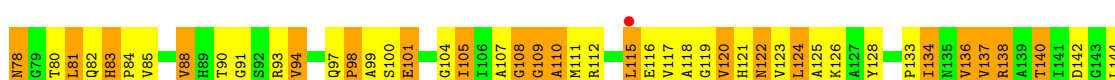




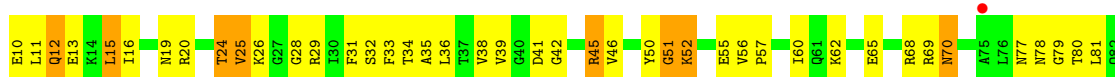
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

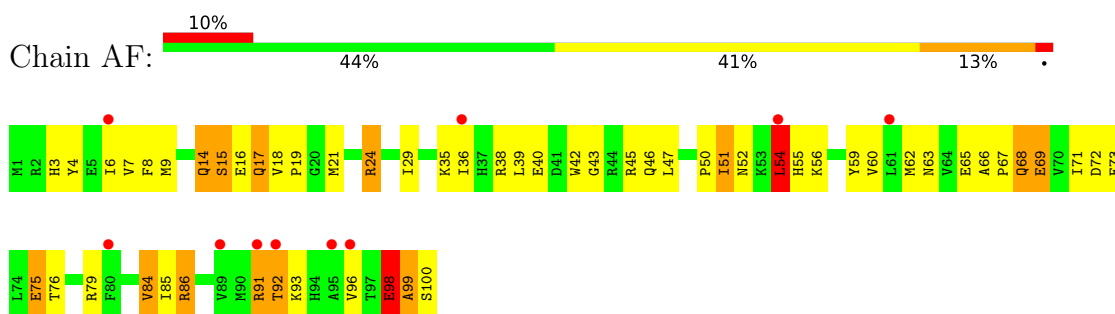


• Molecule 5: 30S ribosomal protein S5

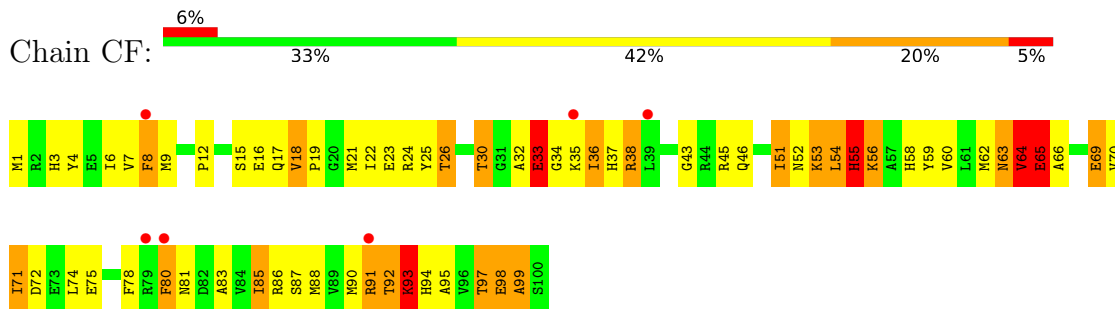


• Molecule 6: 30S ribosomal protein S6

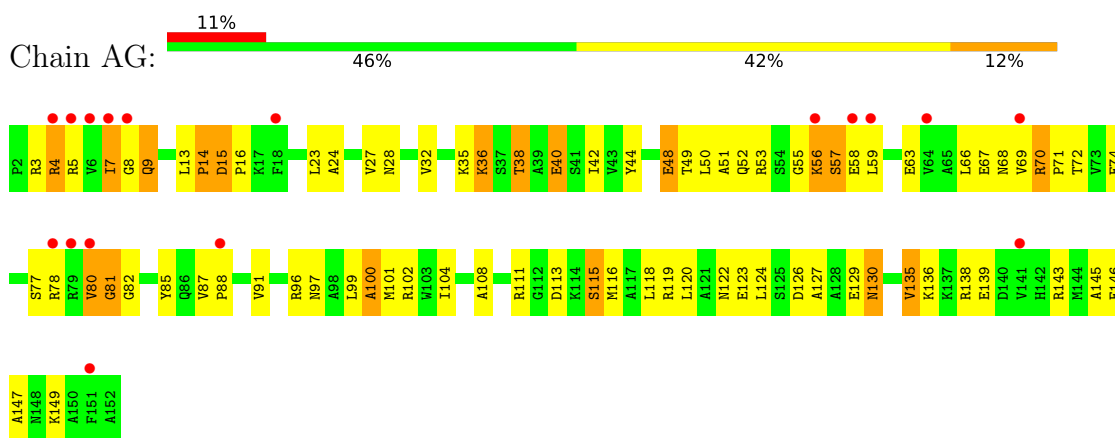




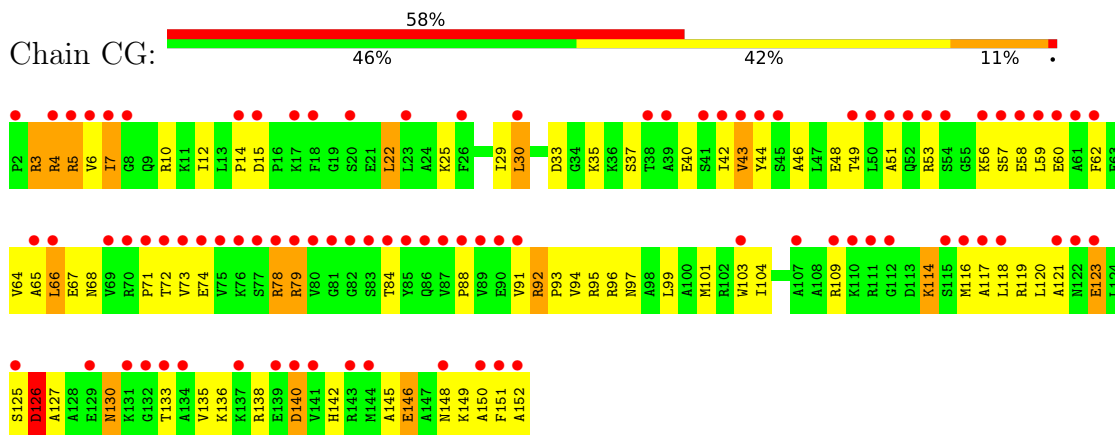
- Molecule 6: 30S ribosomal protein S6



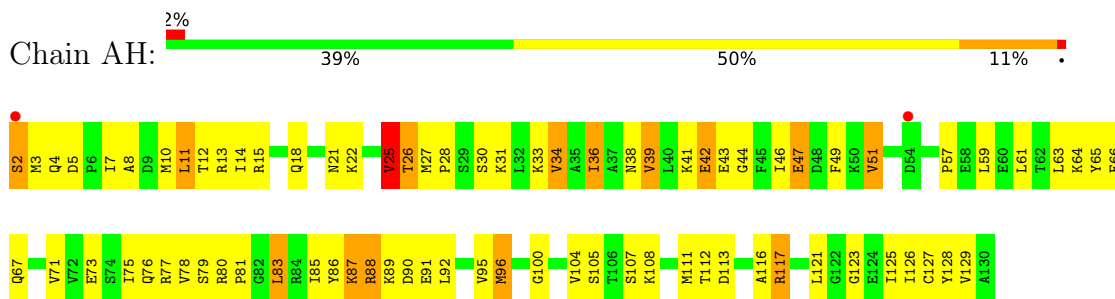
- Molecule 7: 30S ribosomal protein S7



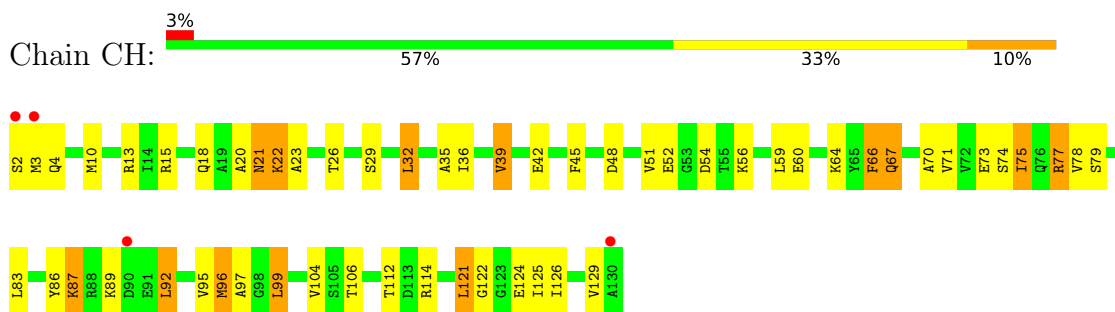
- Molecule 7: 30S ribosomal protein S7



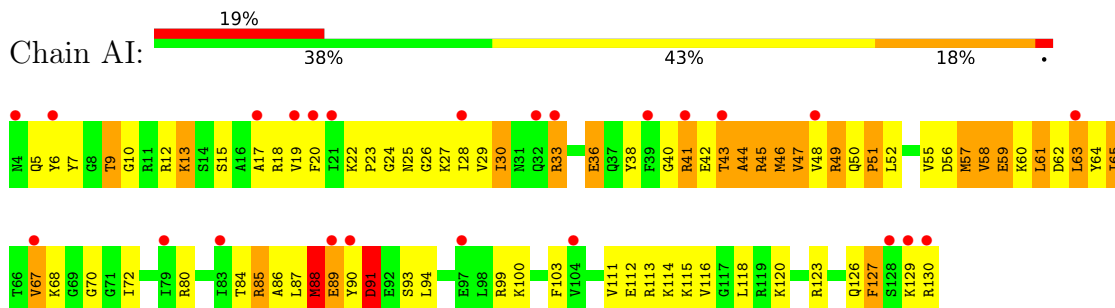
- Molecule 8: 30S ribosomal protein S8



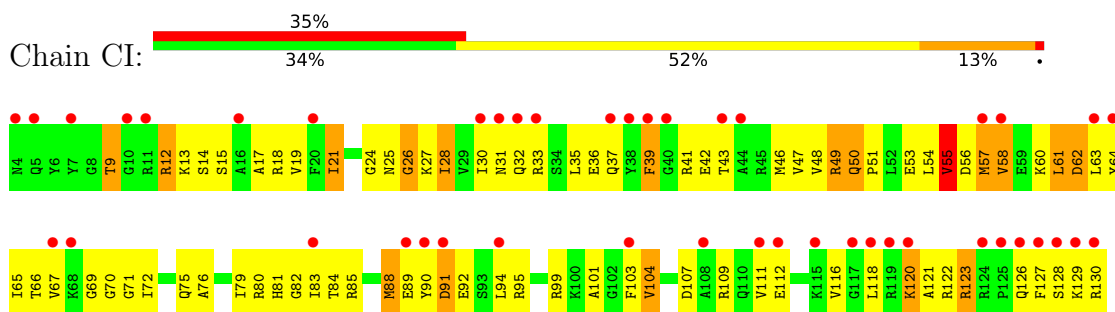
- Molecule 8: 30S ribosomal protein S8



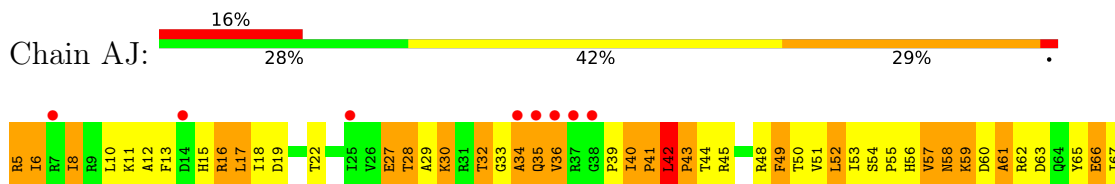
- Molecule 9: 30S ribosomal protein S9

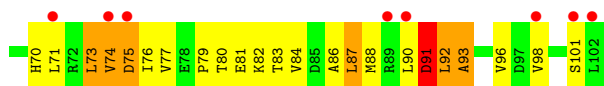


- Molecule 9: 30S ribosomal protein S9

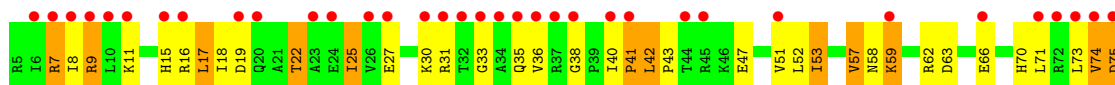
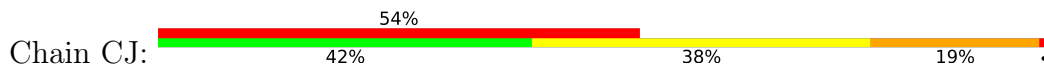


- Molecule 10: 30S ribosomal protein S10

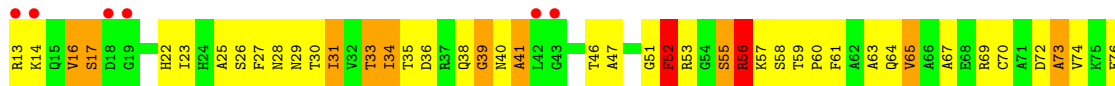




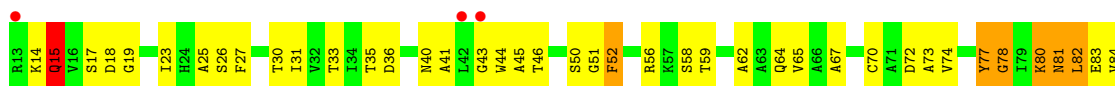
• Molecule 10: 30S ribosomal protein S10



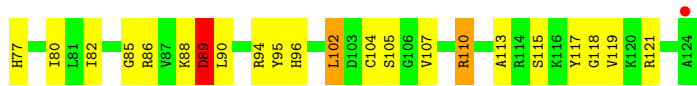
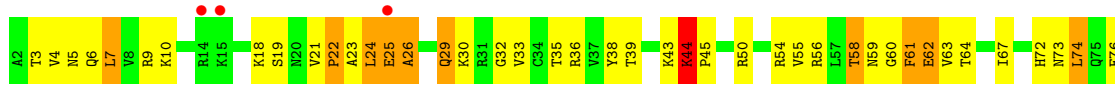
• Molecule 11: 30S ribosomal protein S11



• Molecule 11: 30S ribosomal protein S11

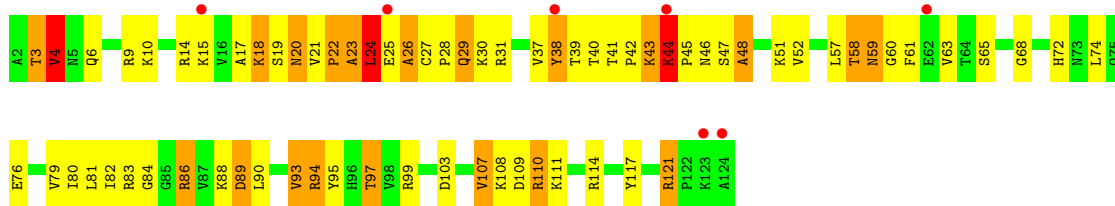


• Molecule 12: 30S ribosomal protein S12

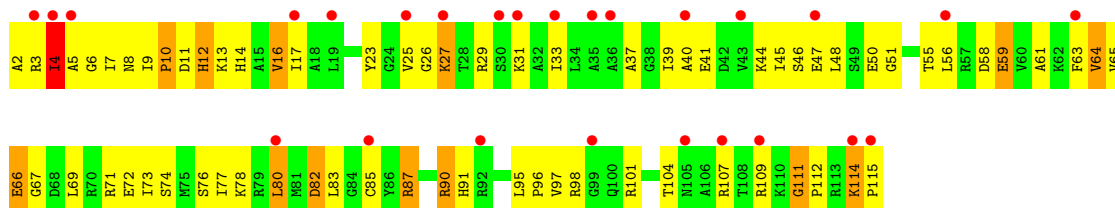


• Molecule 12: 30S ribosomal protein S12

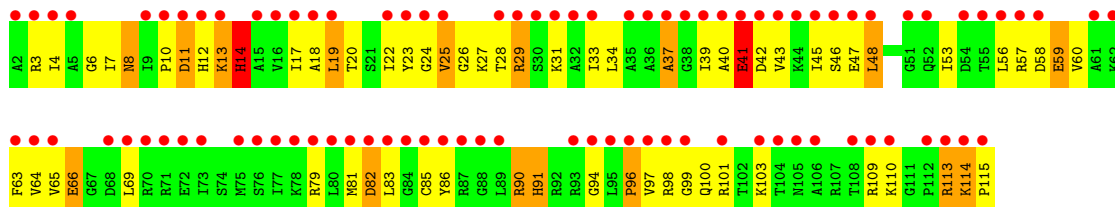
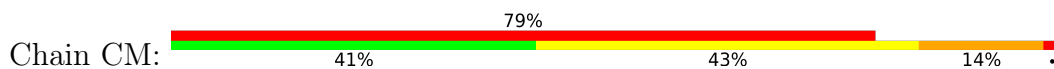




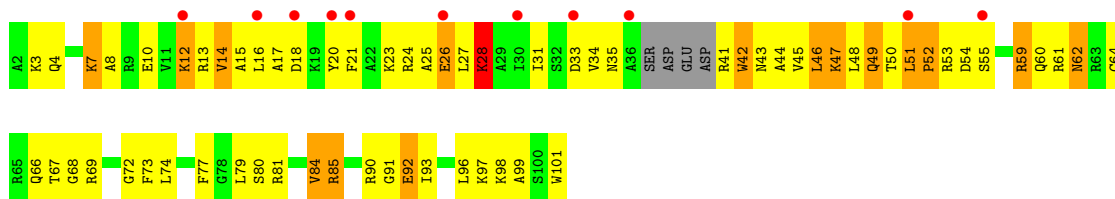
• Molecule 13: 30S ribosomal protein S13



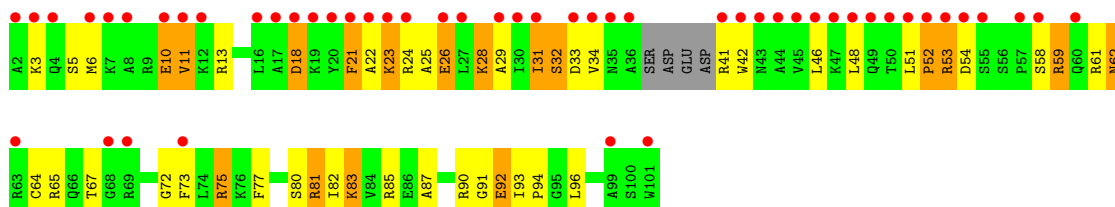
• Molecule 13: 30S ribosomal protein S13



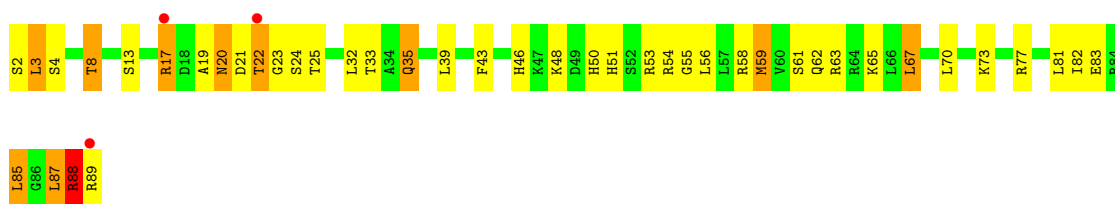
• Molecule 14: 30S ribosomal protein S14



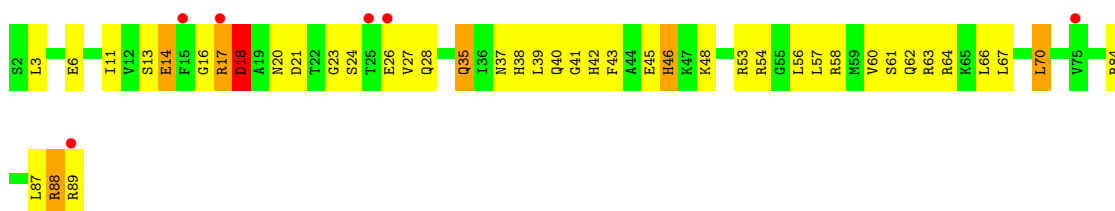
• Molecule 14: 30S ribosomal protein S14



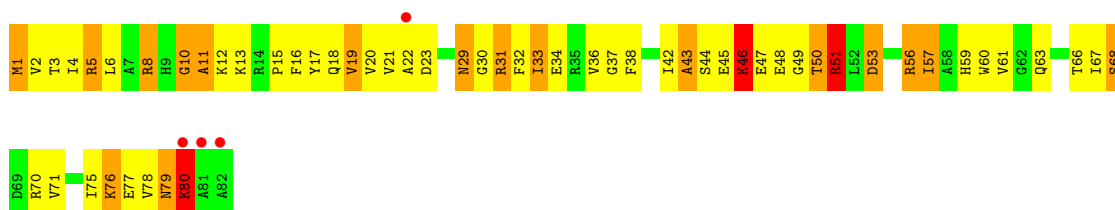
- Molecule 15: 30S ribosomal protein S15



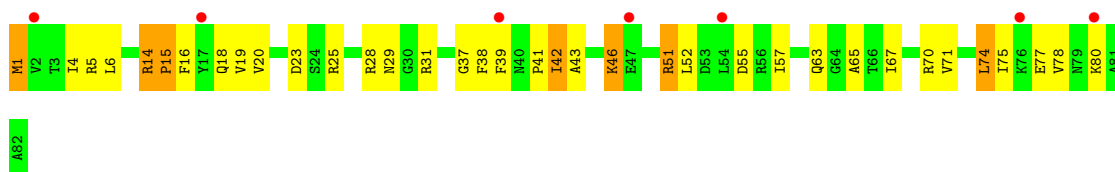
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S16

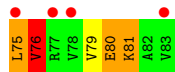
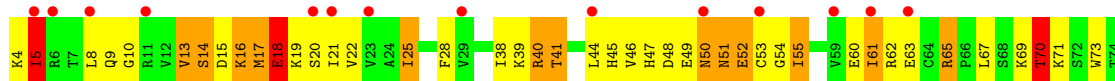


- Molecule 17: 30S ribosomal protein S17

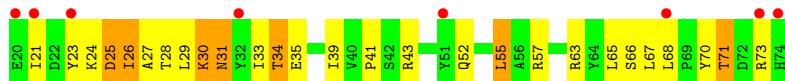




- Molecule 17: 30S ribosomal protein S17



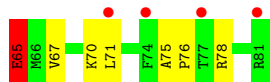
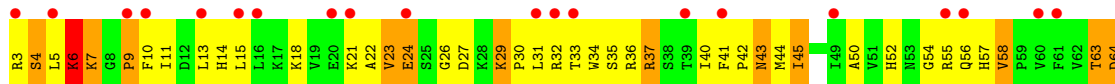
- Molecule 18: 30S ribosomal protein S18



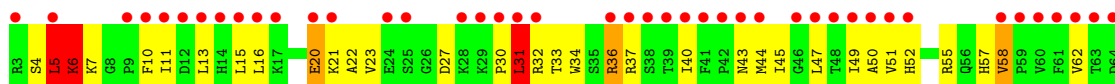
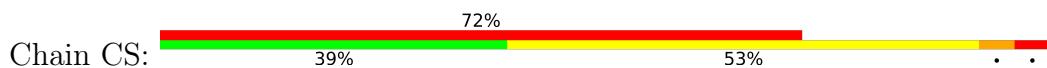
- Molecule 18: 30S ribosomal protein S18



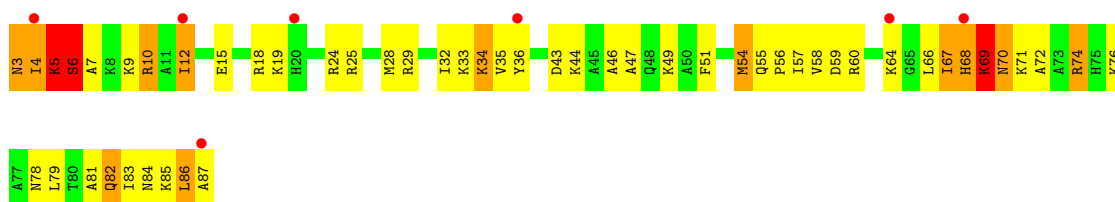
- Molecule 19: 30S ribosomal protein S19



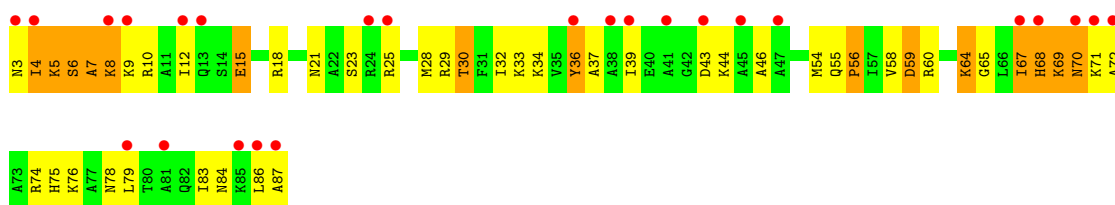
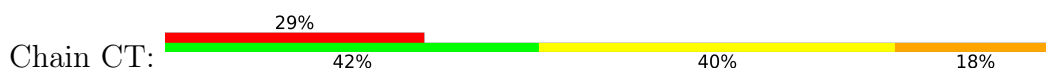
- Molecule 19: 30S ribosomal protein S19



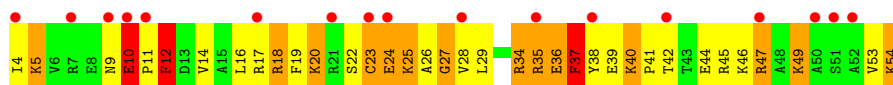
- Molecule 20: 30S ribosomal protein S20



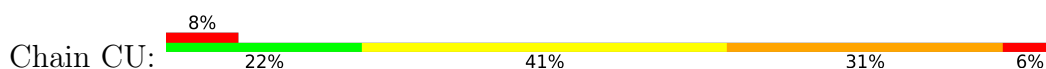
- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein S21

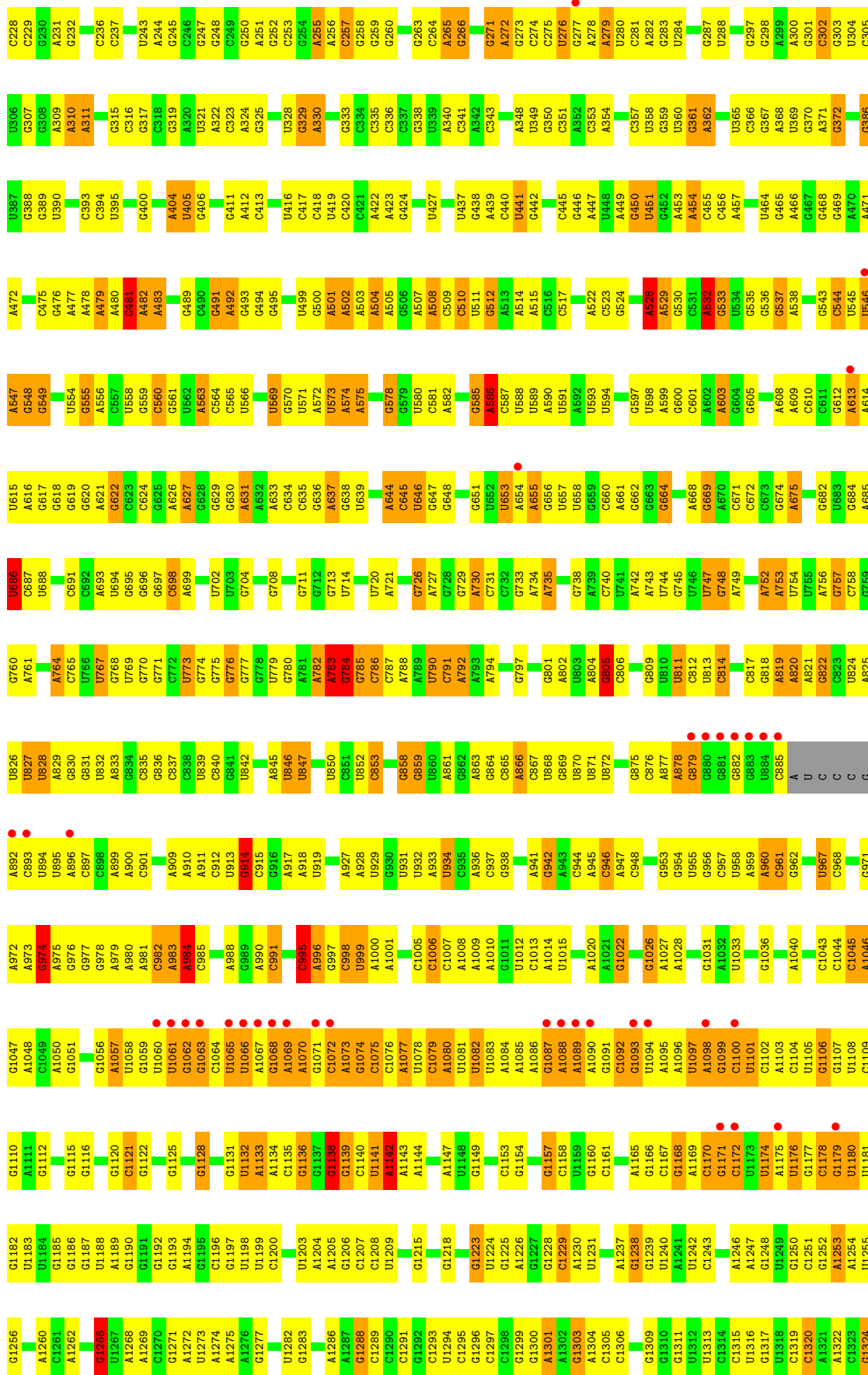


- Molecule 21: 30S ribosomal protein S21

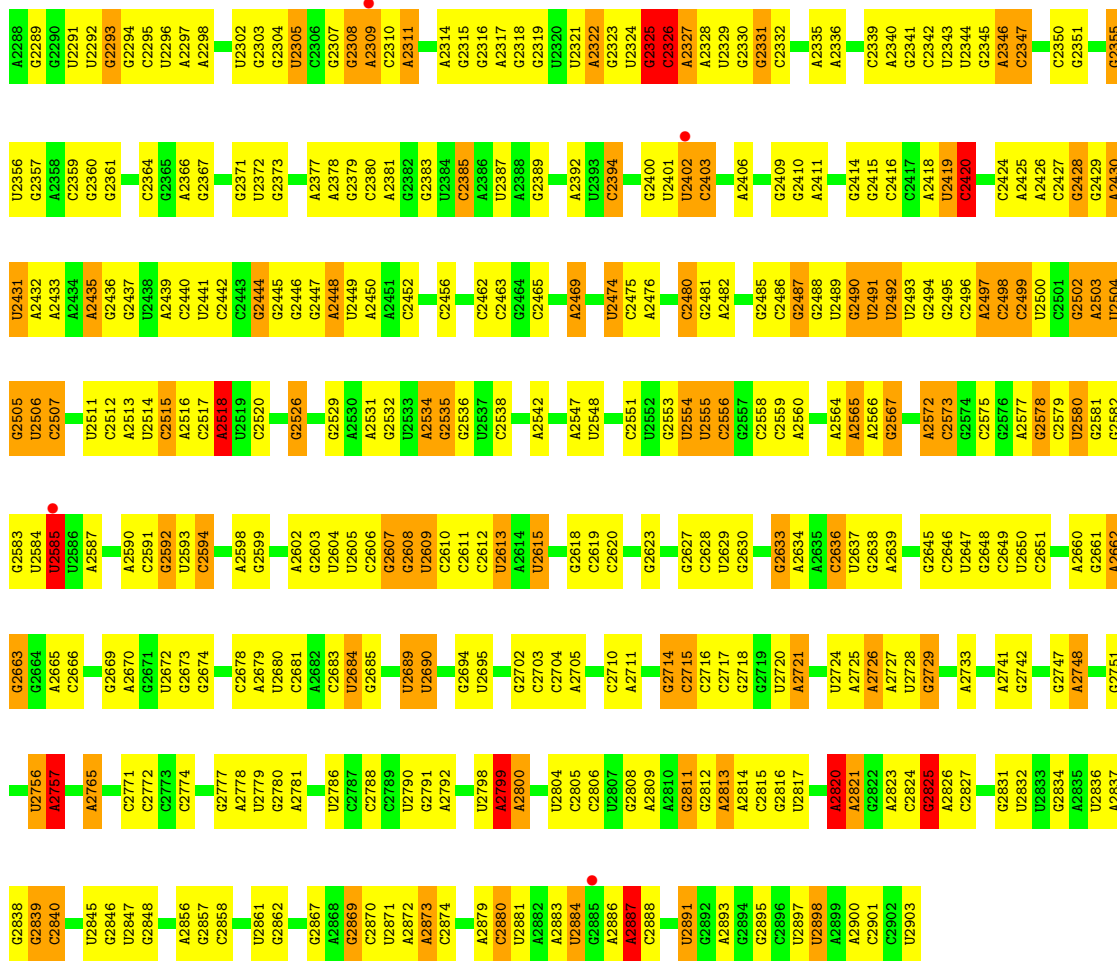


- Molecule 22: 23S rRNA

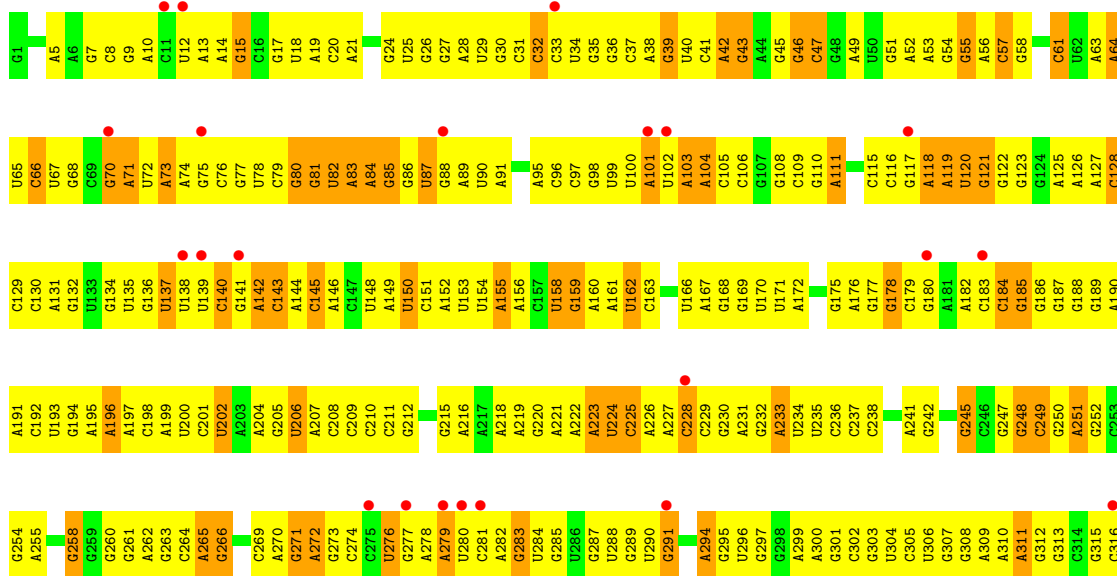
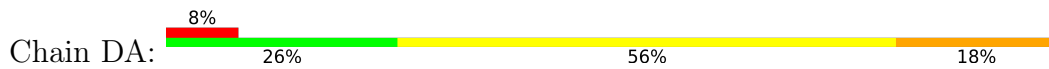


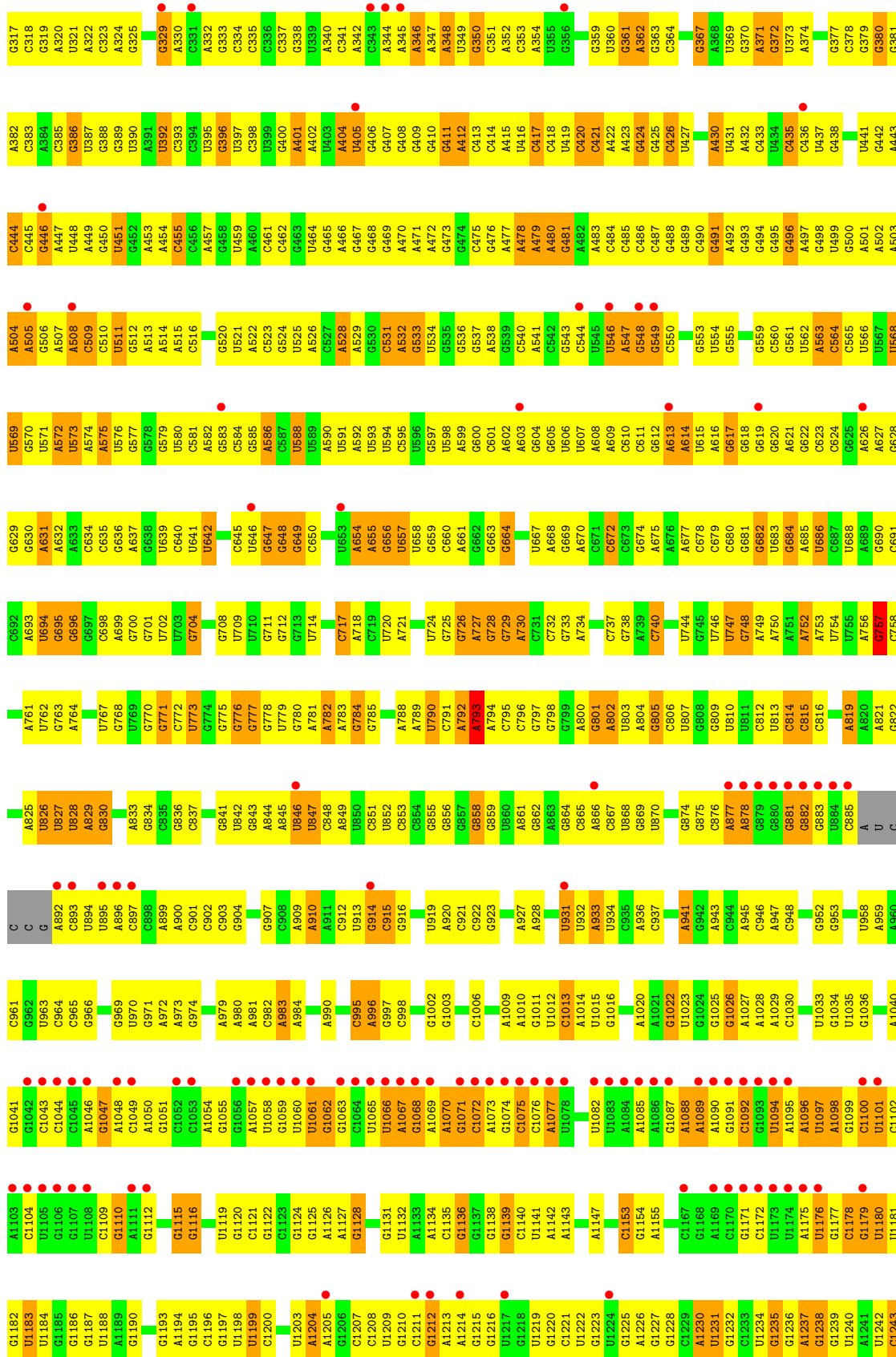


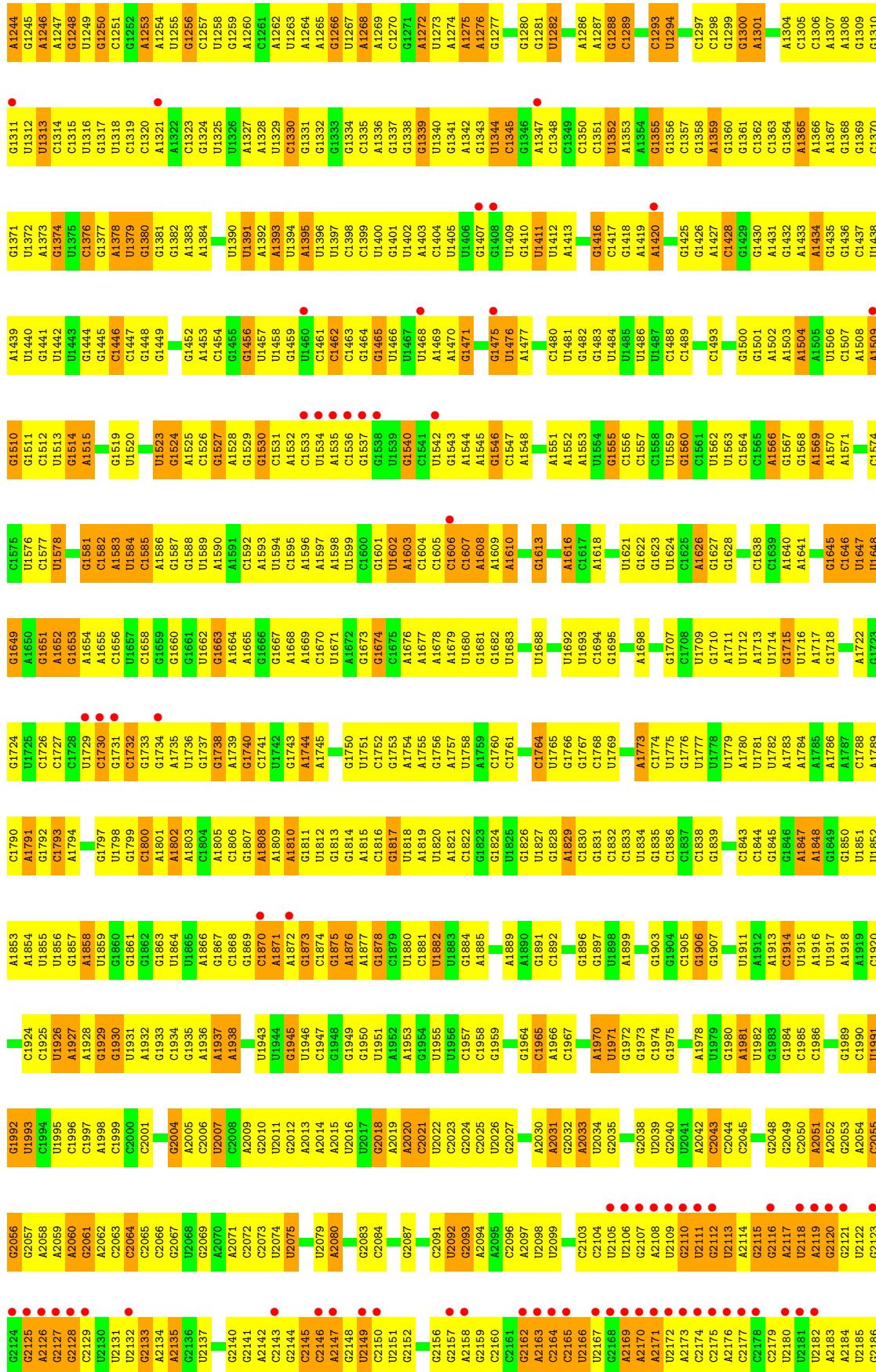
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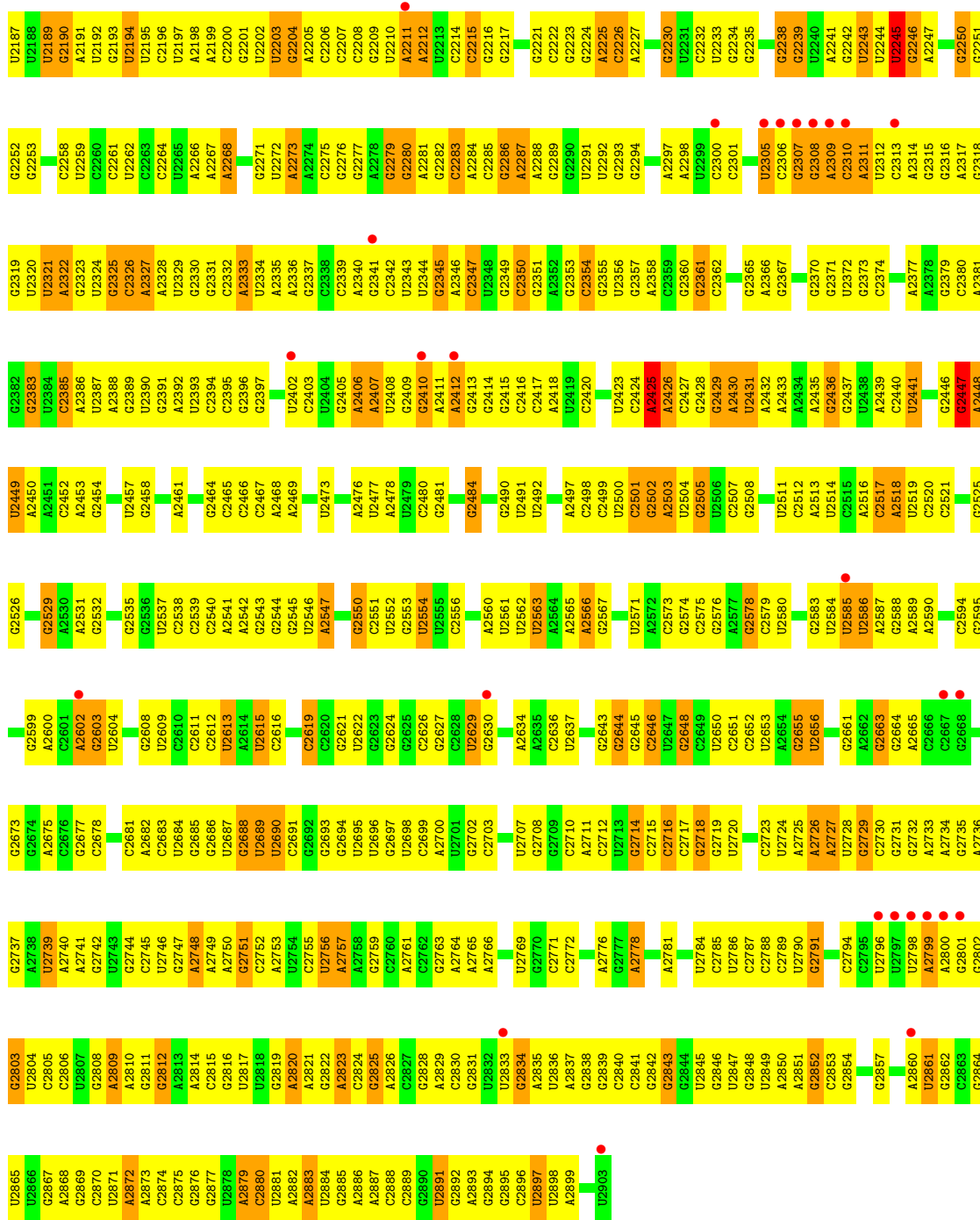


• Molecule 22: 23S rRNA

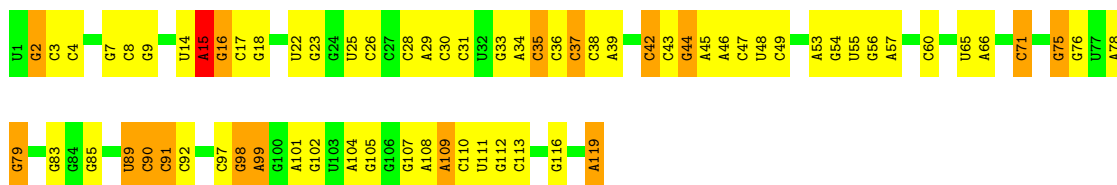




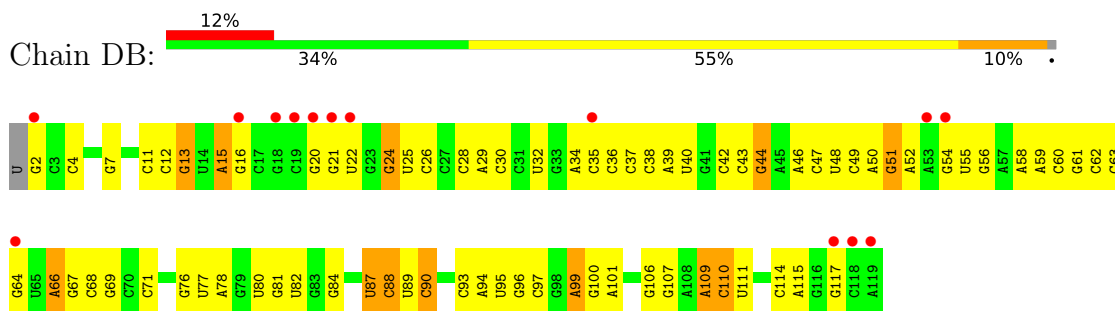




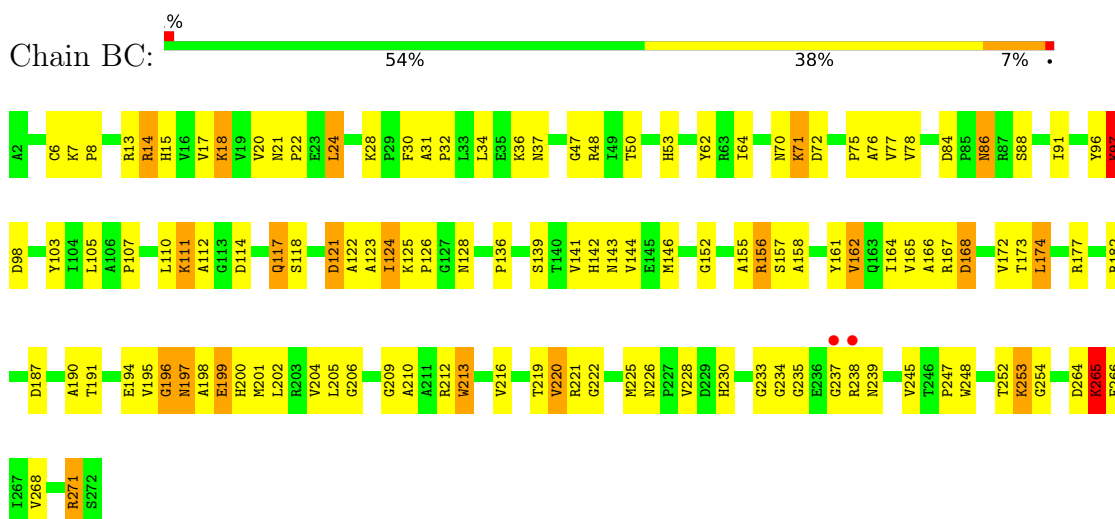
• Molecule 23: 5S rRNA



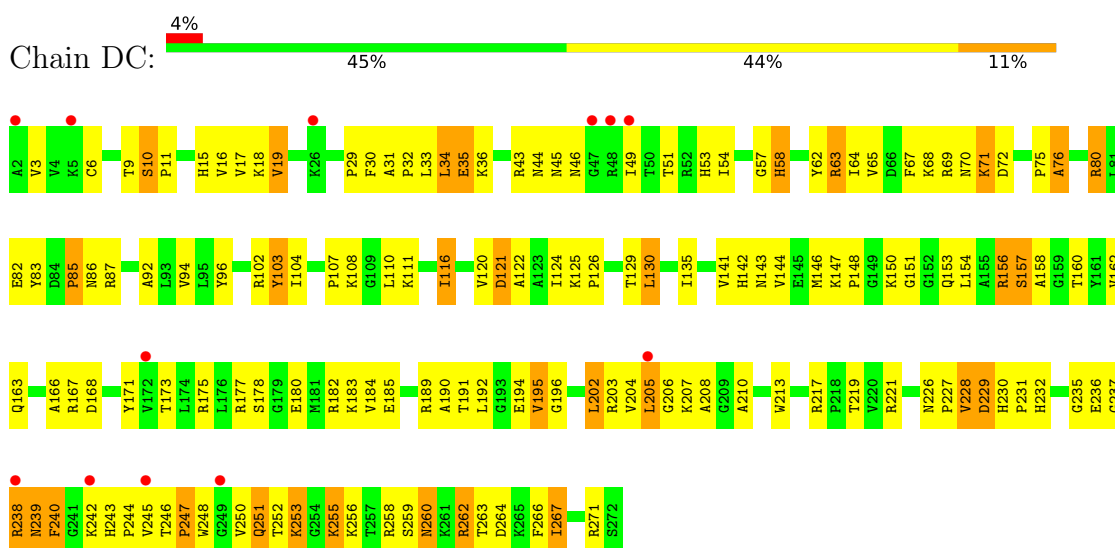
- Molecule 23: 5S rRNA



- Molecule 24: 50S ribosomal protein L2

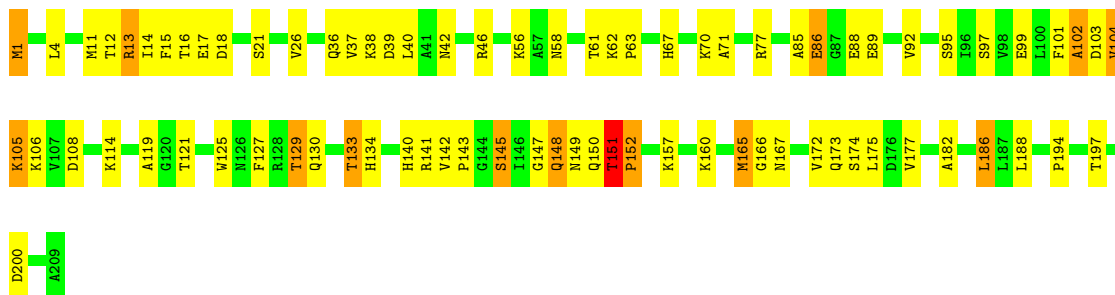


- Molecule 24: 50S ribosomal protein L2

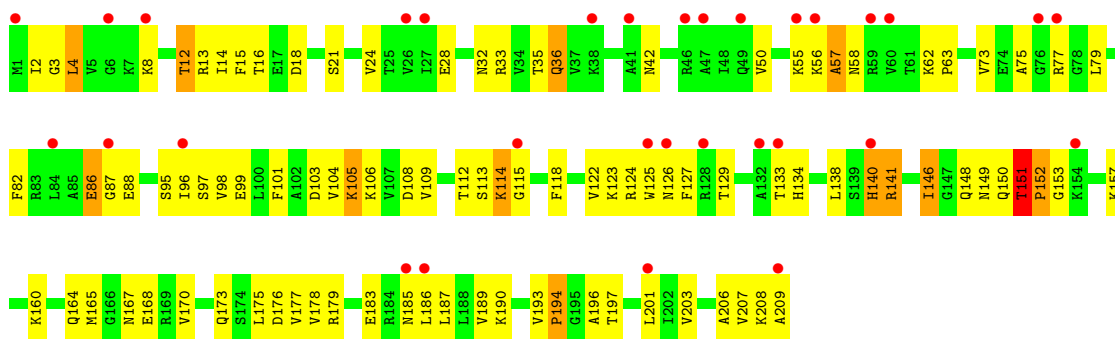


- Molecule 25: 50S ribosomal protein L3

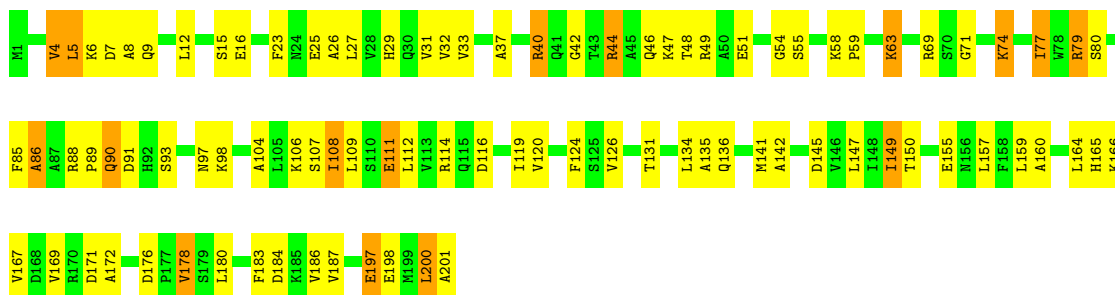




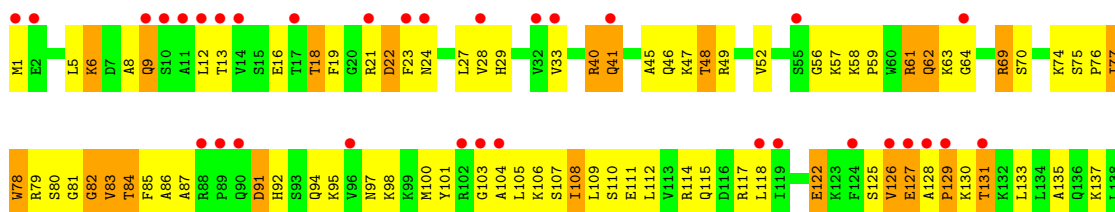
- Molecule 25: 50S ribosomal protein L3



- Molecule 26: 50S ribosomal protein L4

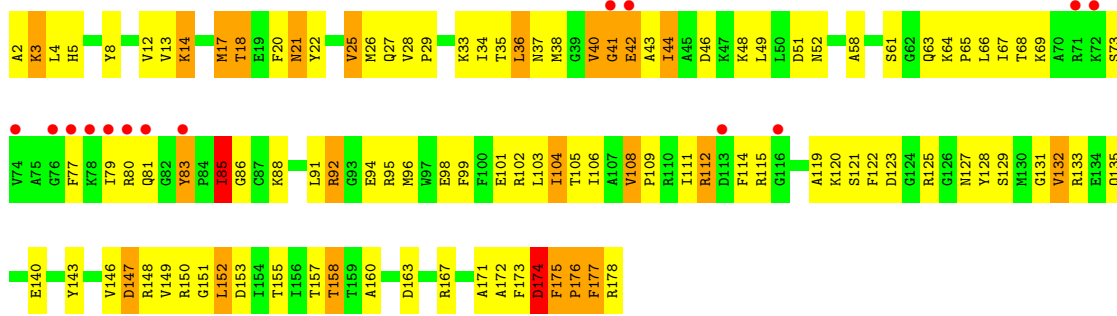


- Molecule 26: 50S ribosomal protein L4

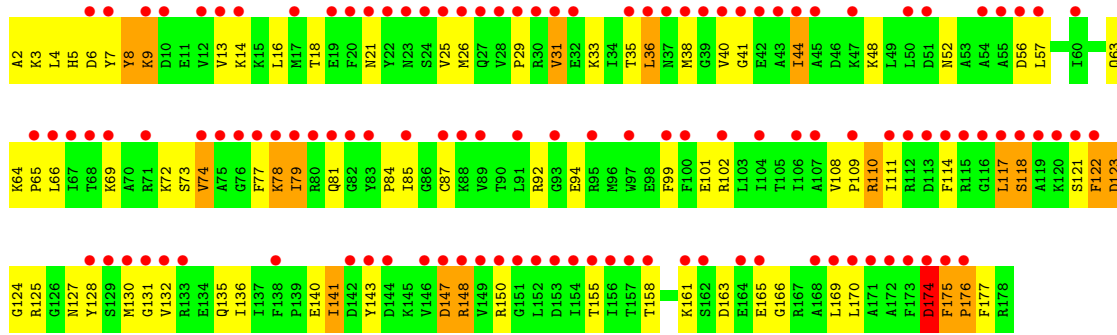




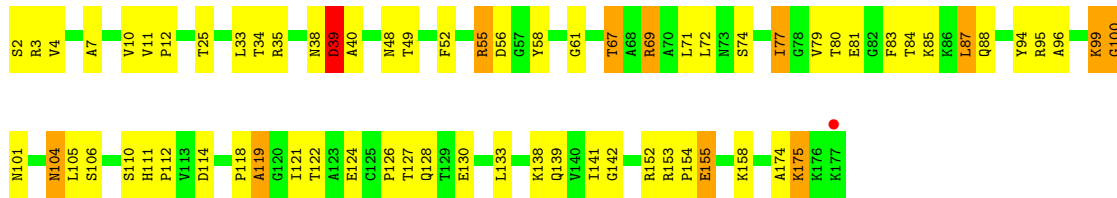
• Molecule 27: 50S ribosomal protein L5



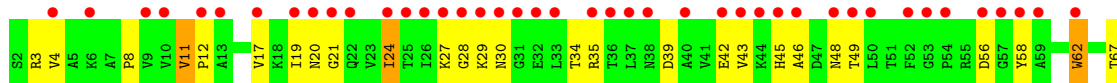
• Molecule 27: 50S ribosomal protein L5

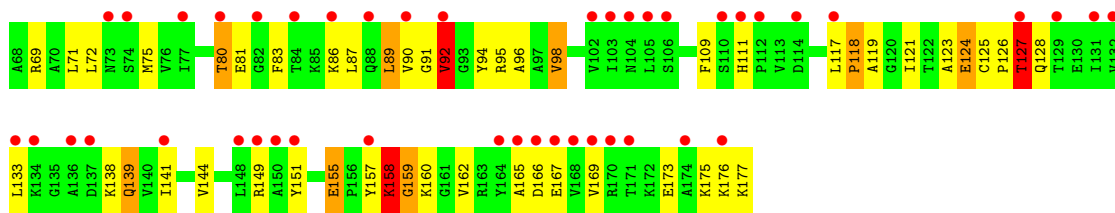


• Molecule 28: 50S ribosomal protein L6

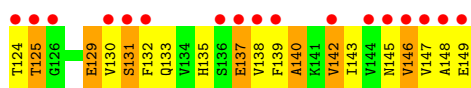
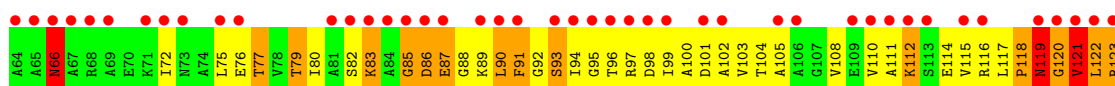
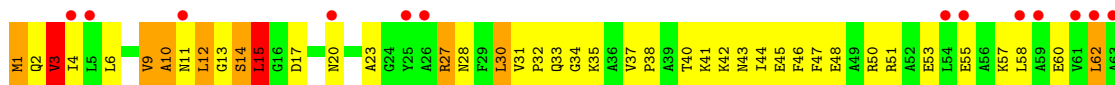


• Molecule 28: 50S ribosomal protein L6

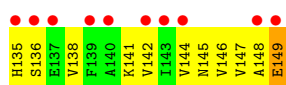
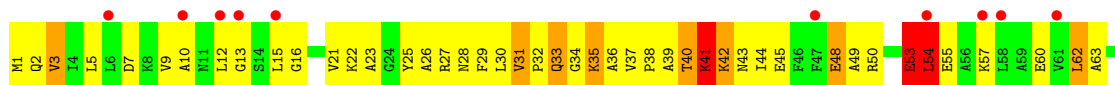




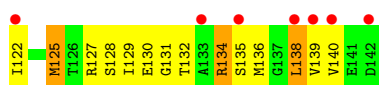
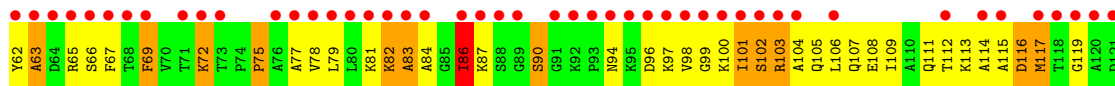
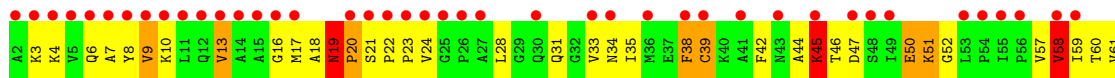
• Molecule 29: 50S ribosomal protein L9



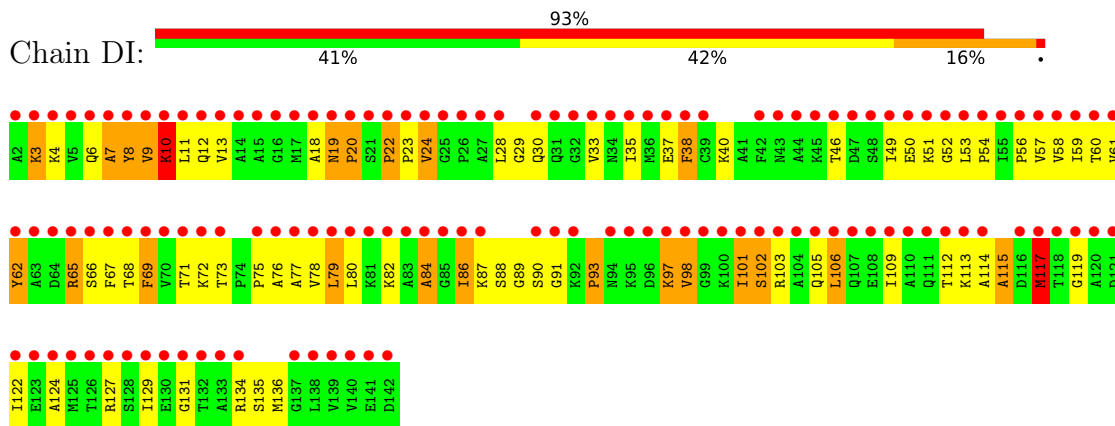
• Molecule 29: 50S ribosomal protein L9



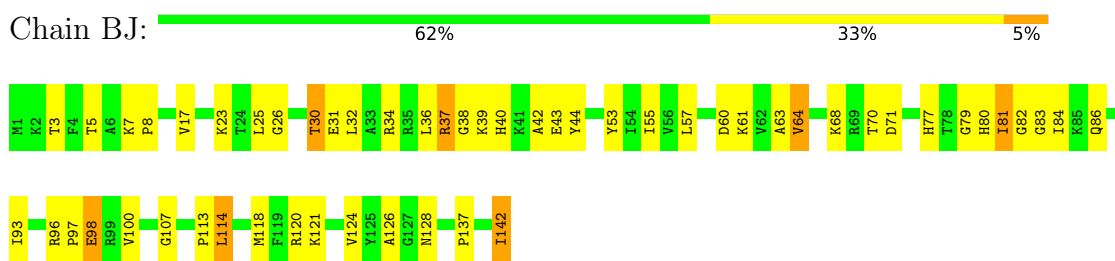
• Molecule 30: 50S ribosomal protein L11



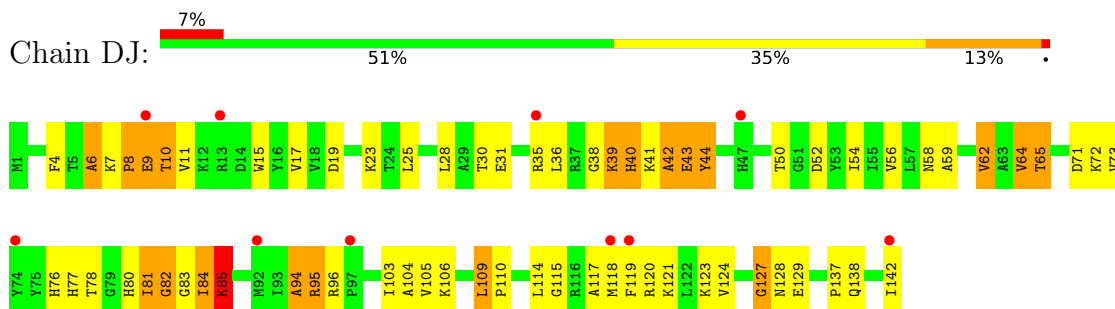
- Molecule 30: 50S ribosomal protein L11



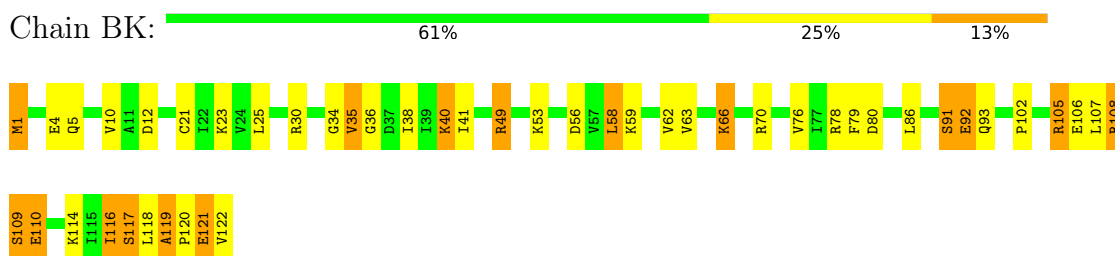
- Molecule 31: 50S ribosomal protein L13



- Molecule 31: 50S ribosomal protein L13

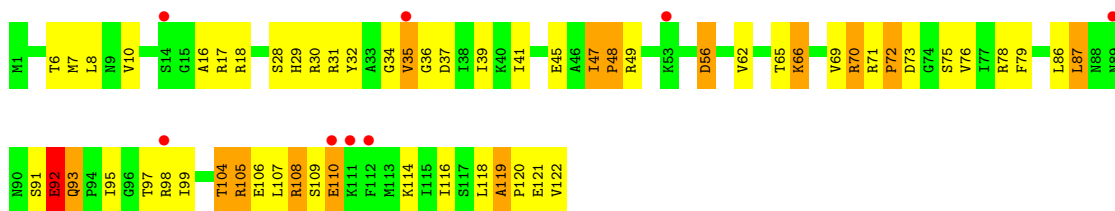


- Molecule 32: 50S ribosomal protein L14



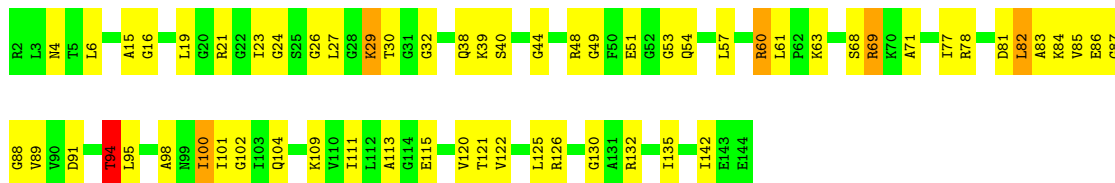
- Molecule 32: 50S ribosomal protein L14





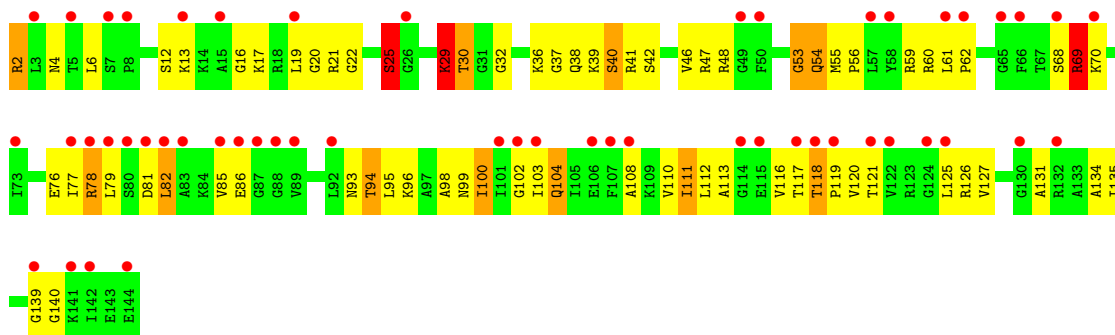
- Molecule 33: 50S ribosomal protein L15

Chain BL: 57% 38% . .



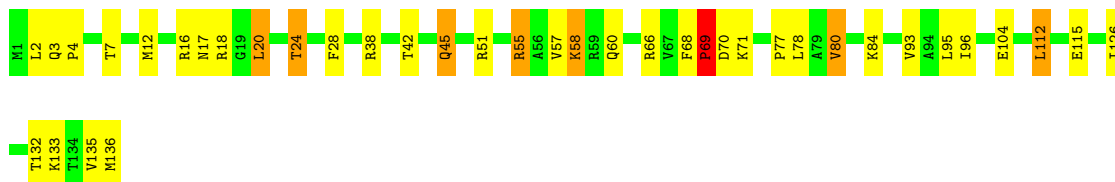
- Molecule 33: 50S ribosomal protein L15

Chain DL: 37% 49% 41% 8% . .



- Molecule 34: 50S ribosomal protein L16

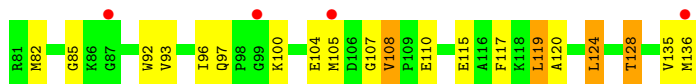
Chain BM: 71% 23% 5% . .



- Molecule 34: 50S ribosomal protein L16

Chain DM: 11% 58% 33% 9%

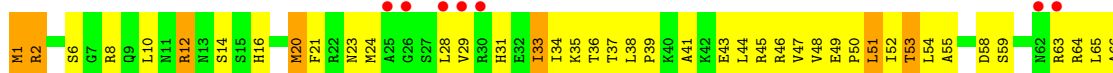




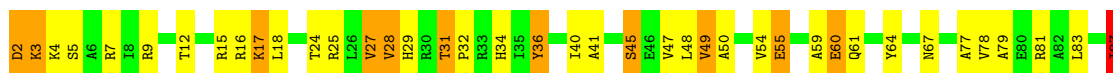
- Molecule 35: 50S ribosomal protein L17



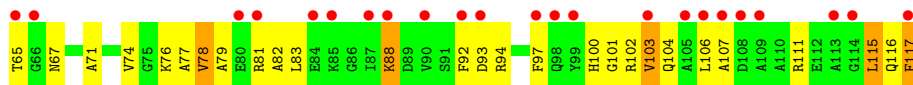
- Molecule 35: 50S ribosomal protein L17



- Molecule 36: 50S ribosomal protein L18

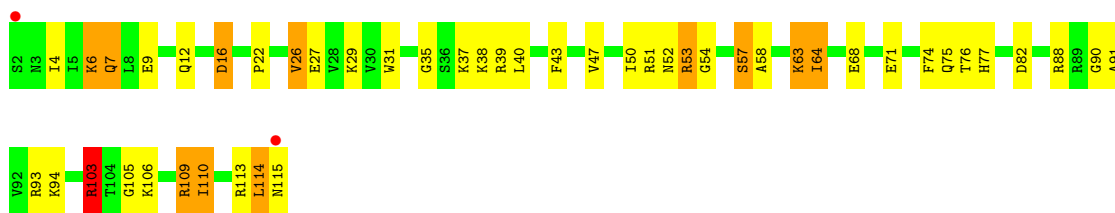


- Molecule 36: 50S ribosomal protein L18

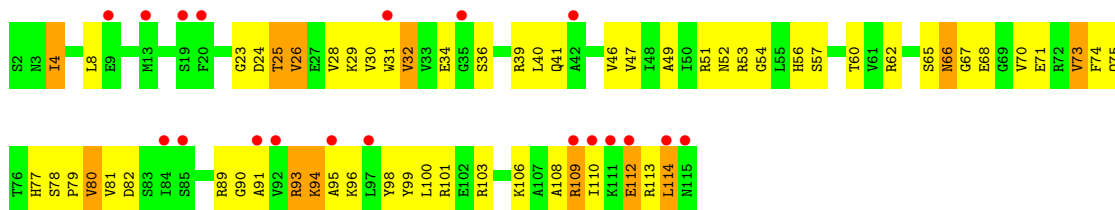


- Molecule 37: 50S ribosomal protein L19

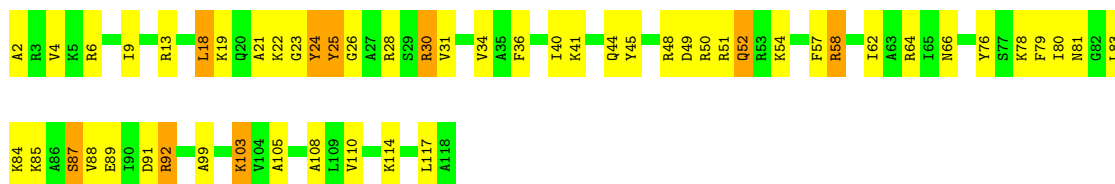




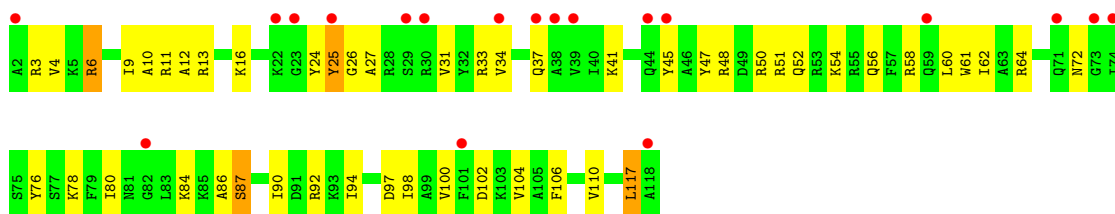
- Molecule 37: 50S ribosomal protein L19



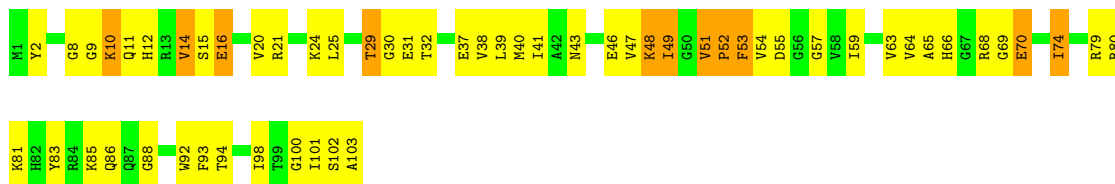
- Molecule 38: 50S ribosomal protein L20



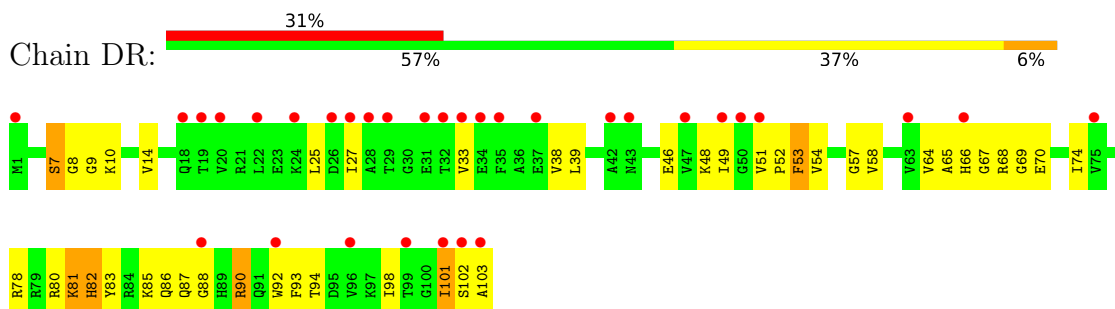
- Molecule 38: 50S ribosomal protein L20



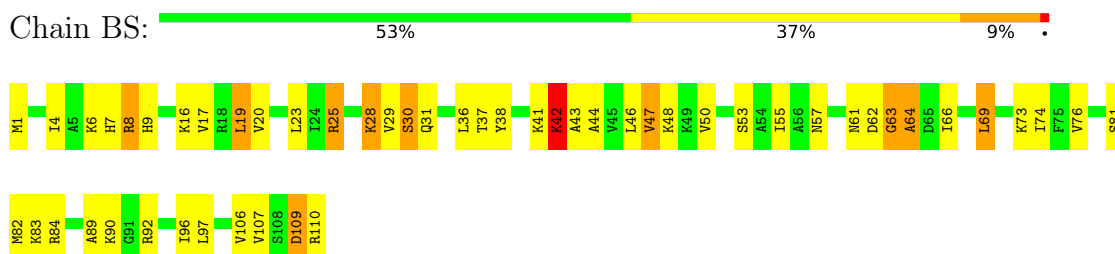
- Molecule 39: 50S ribosomal protein L21



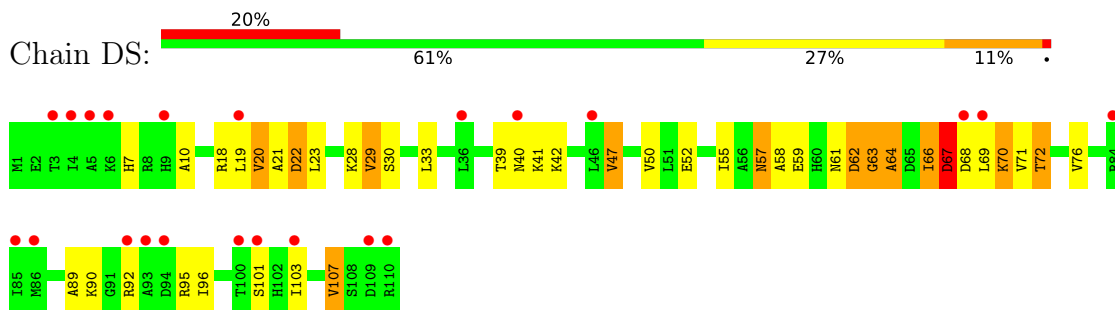
- Molecule 39: 50S ribosomal protein L21



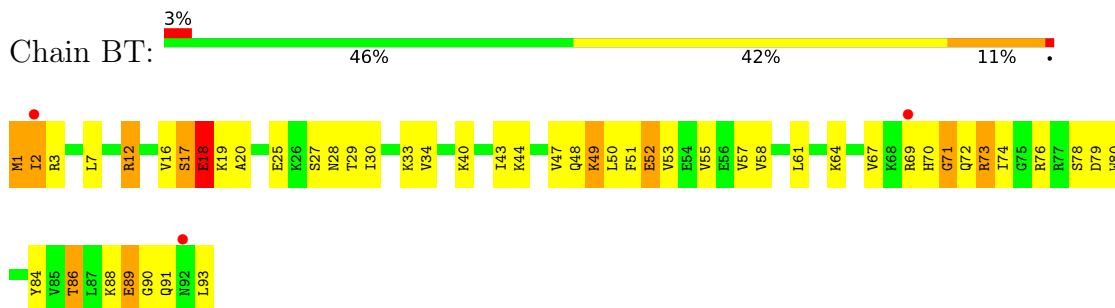
- Molecule 40: 50S ribosomal protein L22



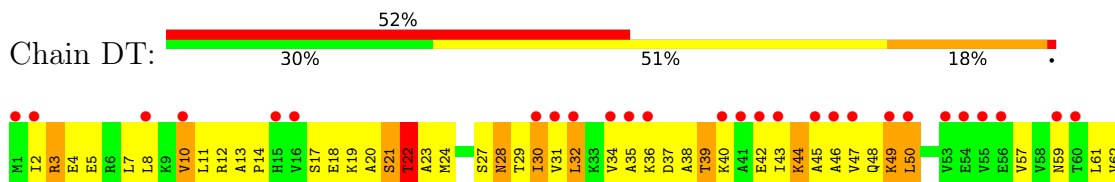
- Molecule 40: 50S ribosomal protein L22

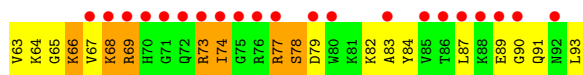


- Molecule 41: 50S ribosomal protein L23

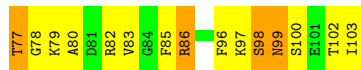


- Molecule 41: 50S ribosomal protein L23

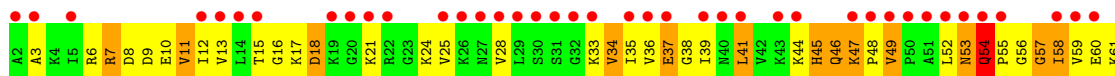




- Molecule 42: 50S ribosomal protein L24



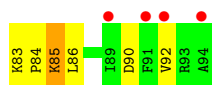
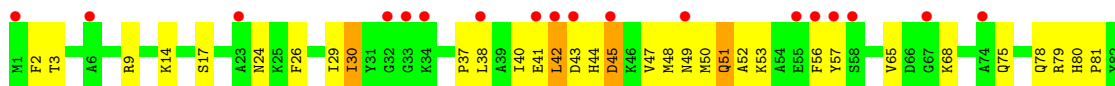
- Molecule 42: 50S ribosomal protein L24



- Molecule 43: 50S ribosomal protein L25

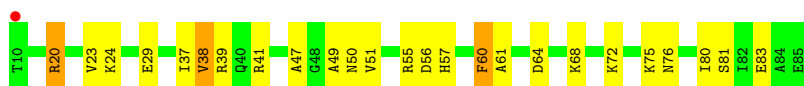


- Molecule 43: 50S ribosomal protein L25

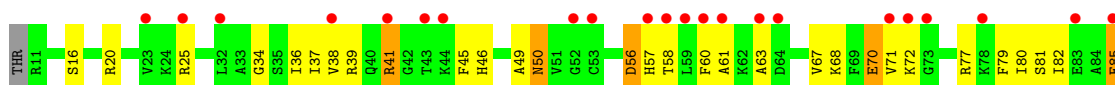


- Molecule 44: 50S ribosomal protein L27

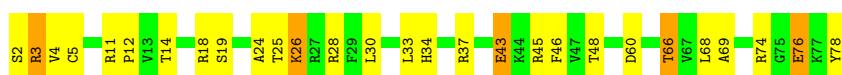




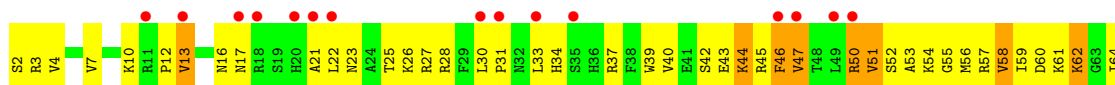
- Molecule 44: 50S ribosomal protein L27



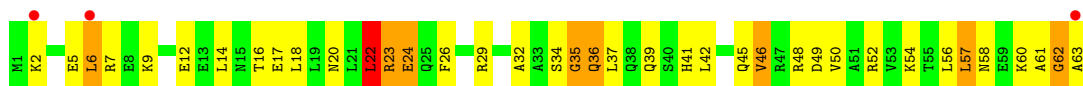
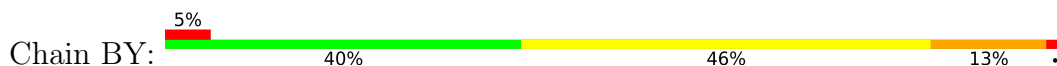
- Molecule 45: 50S ribosomal protein L28



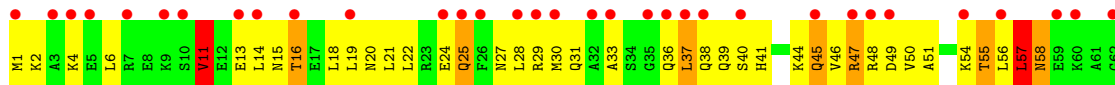
- Molecule 45: 50S ribosomal protein L28



- Molecule 46: 50S ribosomal protein L29



- Molecule 46: 50S ribosomal protein L29

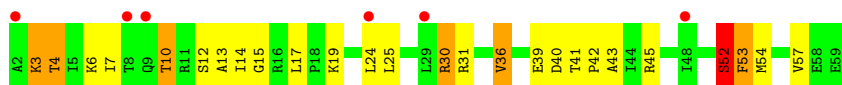


- Molecule 47: 50S ribosomal protein L30

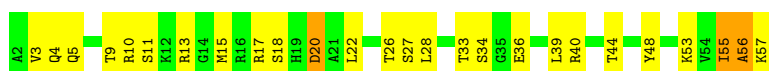




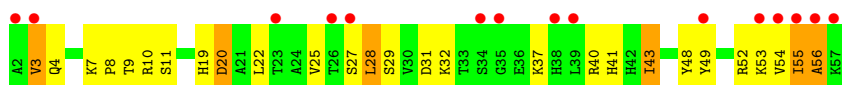
- Molecule 47: 50S ribosomal protein L30



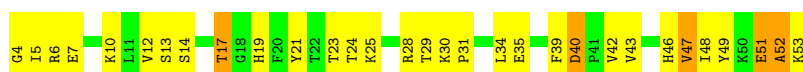
- Molecule 48: 50S ribosomal protein L32



- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33



- Molecule 49: 50S ribosomal protein L33

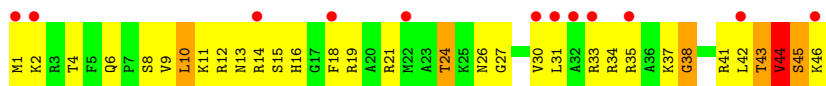


- Molecule 50: 50S ribosomal protein L34



- Molecule 50: 50S ribosomal protein L34





• Molecule 51: 50S ribosomal protein L35



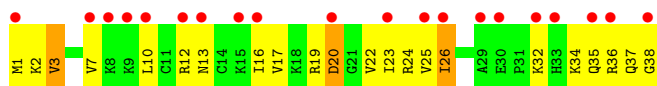
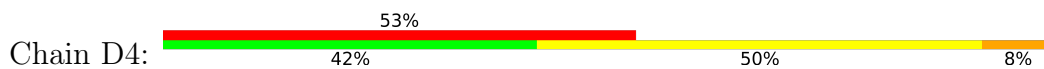
• Molecule 51: 50S ribosomal protein L35



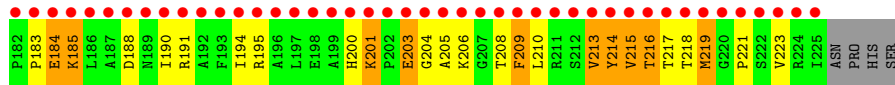
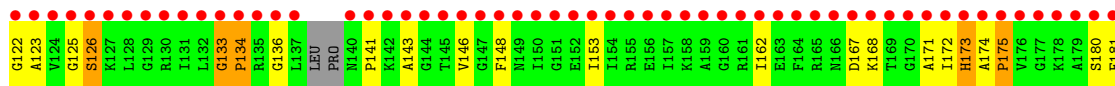
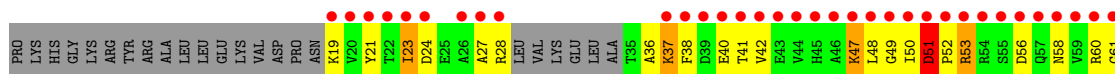
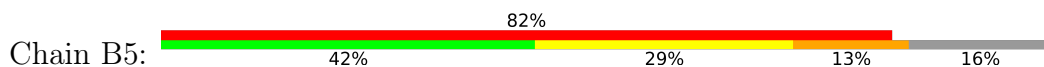
• Molecule 52: 50S ribosomal protein L36



• Molecule 52: 50S ribosomal protein L36



• Molecule 53: 50S ribosomal protein L1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.21Å 433.03Å 619.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.97 – 2.90 39.97 – 2.90	Depositor EDS
% Data completeness (in resolution range)	94.9 (39.97-2.90) 94.9 (39.97-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.90Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.220 , 0.264 0.225 , 0.269	Depositor DCC
R_{free} test set	4701 reflections (0.40%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtrriage
Anisotropy	0.529	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	288276	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: DOL, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.46	0/36944	0.92	22/57632 (0.0%)
1	CA	0.39	0/36966	0.86	4/57666 (0.0%)
2	AB	0.36	0/1736	0.58	0/2338
2	CB	0.32	0/1736	0.53	0/2338
3	AC	0.35	0/1652	0.57	0/2225
3	CC	0.31	0/1652	0.51	0/2225
4	AD	0.36	0/1665	0.61	0/2227
4	CD	0.39	0/1665	0.61	0/2227
5	AE	0.38	0/1119	0.66	0/1504
5	CE	0.37	0/1119	0.65	0/1504
6	AF	0.39	0/836	0.60	0/1128
6	CF	0.33	0/836	0.58	0/1128
7	AG	0.34	0/1196	0.52	0/1602
7	CG	0.31	0/1196	0.51	0/1602
8	AH	0.38	0/989	0.57	0/1326
8	CH	0.31	0/989	0.52	0/1326
9	AI	0.33	0/1034	0.58	0/1375
9	CI	0.31	0/1034	0.55	0/1375
10	AJ	0.36	0/797	0.59	0/1077
10	CJ	0.31	0/797	0.52	0/1077
11	AK	0.36	0/893	0.67	1/1205 (0.1%)
11	CK	0.32	0/893	0.55	0/1205
12	AL	0.41	0/969	0.65	0/1300
12	CL	0.37	0/969	0.63	0/1300
13	AM	0.36	0/893	0.59	0/1193
13	CM	0.32	0/893	0.52	0/1193
14	AN	0.36	0/785	0.58	0/1043
14	CN	0.30	0/785	0.50	0/1043
15	AO	0.36	0/718	0.58	0/959
15	CO	0.32	0/718	0.50	0/959
16	AP	0.38	0/659	0.69	1/884 (0.1%)
16	CP	0.32	0/659	0.55	0/884

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.41	0/658	0.63	0/881
17	CQ	0.33	0/658	0.54	0/881
18	AR	0.35	0/463	0.57	0/621
18	CR	0.33	0/463	0.52	0/621
19	AS	0.36	0/653	0.53	0/877
19	CS	0.32	0/653	0.56	0/877
20	AT	0.36	0/671	0.58	0/888
20	CT	0.30	0/671	0.54	0/888
21	AU	0.45	0/431	0.63	0/570
21	CU	0.42	0/431	0.62	0/570
22	BA	0.84	18/69659 (0.0%)	1.25	413/108672 (0.4%)
22	DA	0.37	0/69659	0.85	11/108672 (0.0%)
23	BB	0.73	0/2850	1.17	11/4444 (0.2%)
23	DB	0.32	0/2828	0.80	0/4410
24	BC	0.50	0/2122	0.70	0/2852
24	DC	0.33	0/2122	0.56	0/2852
25	BD	0.58	0/1586	0.75	1/2134 (0.0%)
25	DD	0.31	0/1586	0.55	0/2134
26	BE	0.50	0/1571	0.67	0/2113
26	DE	0.31	0/1571	0.53	0/2113
27	BF	0.40	0/1435	0.61	0/1926
27	DF	0.29	0/1435	0.48	0/1926
28	BG	0.40	0/1343	0.60	0/1816
28	DG	0.30	0/1343	0.48	0/1816
29	BH	0.36	0/1121	0.66	1/1515 (0.1%)
29	DH	0.35	0/1121	0.56	0/1515
30	BI	0.35	0/1046	0.55	0/1410
30	DI	0.35	0/1046	0.53	0/1410
31	BJ	0.61	0/1152	0.73	0/1551
31	DJ	0.31	0/1152	0.54	0/1551
32	BK	0.61	0/948	0.75	0/1268
32	DK	0.34	0/948	0.55	0/1268
33	BL	0.55	0/1054	0.74	0/1403
33	DL	0.31	0/1054	0.53	0/1403
34	BM	0.58	0/1093	0.73	0/1460
34	DM	0.30	0/1093	0.50	0/1460
35	BN	0.62	0/974	0.79	0/1301
35	DN	0.33	0/974	0.58	1/1301 (0.1%)
36	BO	0.48	0/902	0.64	0/1209
36	DO	0.29	0/902	0.47	0/1209
37	BP	0.55	0/929	0.75	3/1242 (0.2%)
37	DP	0.32	0/929	0.51	0/1242
38	BQ	0.67	0/960	0.78	0/1278

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DQ	0.33	0/960	0.50	0/1278
39	BR	0.64	0/829	0.84	0/1107
39	DR	0.30	0/829	0.53	0/1107
40	BS	0.69	0/864	0.81	0/1156
40	DS	0.32	0/864	0.54	0/1156
41	BT	0.46	0/745	0.69	0/994
41	DT	0.31	0/745	0.51	0/994
42	BU	0.47	0/788	0.66	0/1051
42	DU	0.34	0/788	0.56	0/1051
43	BV	0.51	0/766	0.68	0/1025
43	DV	0.28	0/766	0.44	0/1025
44	BW	0.60	0/587	0.74	0/776
44	DW	0.30	0/576	0.50	0/762
45	BX	0.44	0/635	0.66	0/848
45	DX	0.33	0/635	0.55	0/848
46	BY	0.44	0/510	0.71	0/677
46	DY	0.29	0/510	0.53	0/677
47	BZ	0.55	0/453	0.69	0/605
47	DZ	0.31	0/453	0.51	0/605
48	B0	0.61	0/450	0.77	0/599
48	D0	0.33	0/450	0.54	0/599
49	B1	0.48	0/417	0.62	0/554
49	D1	0.31	0/417	0.50	0/554
50	B2	0.62	0/380	0.81	0/498
50	D2	0.34	0/380	0.55	0/498
51	B3	0.57	0/513	0.69	0/676
51	D3	0.29	0/513	0.49	0/676
52	B4	0.57	0/303	0.70	0/397
52	D4	0.30	0/303	0.54	0/397
53	B5	0.32	0/1145	0.50	0/1556
All	All	0.54	18/310626 (0.0%)	0.92	469/464366 (0.1%)

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
4	CD	0	1
5	AE	0	1
5	CE	0	1
6	CF	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	AK	0	1
12	CL	0	1
25	BD	0	1
25	DD	0	1
All	All	0	8

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	BA	1142	A	N9-C4	-11.42	1.31	1.37
22	BA	984	A	N9-C4	-10.72	1.31	1.37
22	BA	1936	A	N9-C4	-9.94	1.31	1.37
22	BA	528	A	N9-C4	-8.18	1.32	1.37
22	BA	783	A	N9-C4	-6.66	1.33	1.37

The worst 5 of 469 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	984	A	C2-N3-C4	-12.81	104.20	110.60
22	BA	974	G	C4-C5-N7	12.41	115.76	110.80
22	BA	1142	A	C2-N3-C4	-11.77	104.72	110.60
22	BA	1936	A	C2-N3-C4	-11.57	104.81	110.60
22	BA	974	G	C5-C6-O6	-11.27	121.84	128.60

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AE	152	MET	Peptide
11	AK	126	LYS	Peptide
25	BD	151	THR	Peptide
4	CD	152	GLN	Peptide
5	CE	102	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32995	0	16607	1101	3
1	CA	33015	0	16617	1197	0
2	AB	1705	0	1732	163	0
2	CB	1705	0	1732	125	0
3	AC	1625	0	1696	81	0
3	CC	1625	0	1696	76	0
4	AD	1643	0	1707	138	0
4	CD	1643	0	1707	144	0
5	AE	1106	0	1148	98	0
5	CE	1106	0	1148	111	0
6	AF	818	0	808	52	0
6	CF	818	0	808	62	0
7	AG	1182	0	1238	56	0
7	CG	1182	0	1238	70	0
8	AH	979	0	1031	74	0
8	CH	979	0	1031	49	0
9	AI	1022	0	1070	96	0
9	CI	1022	0	1070	76	0
10	AJ	787	0	828	97	0
10	CJ	787	0	828	49	0
11	AK	877	0	887	70	0
11	CK	877	0	887	62	0
12	AL	955	0	1016	57	0
12	CL	955	0	1016	70	0
13	AM	884	0	941	63	0
13	CM	884	0	941	56	0
14	AN	774	0	824	72	0
14	CN	774	0	824	53	0
15	AO	710	0	728	38	0
15	CO	710	0	728	31	0
16	AP	649	0	666	61	0
16	CP	649	0	666	33	0
17	AQ	649	0	691	71	0
17	CQ	649	0	691	50	0
18	AR	456	0	478	19	0
18	CR	456	0	478	23	0
19	AS	638	0	665	50	0
19	CS	638	0	665	37	0
20	AT	665	0	714	60	0
20	CT	665	0	714	49	0
21	AU	426	0	449	51	0
21	CU	426	0	449	50	0
22	BA	62195	0	31280	1688	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	DA	62195	0	31280	2474	0
23	BB	2549	0	1291	64	0
23	DB	2529	0	1281	68	0
24	BC	2083	0	2154	110	0
24	DC	2083	0	2154	136	0
25	BD	1565	0	1616	73	0
25	DD	1565	0	1616	95	0
26	BE	1552	0	1619	73	0
26	DE	1552	0	1619	105	0
27	BF	1411	0	1444	106	0
27	DF	1411	0	1444	58	0
28	BG	1323	0	1371	43	0
28	DG	1323	0	1371	55	0
29	BH	1110	0	1147	145	0
29	DH	1110	0	1148	89	3
30	BI	1032	0	1085	75	0
30	DI	1032	0	1085	85	0
31	BJ	1129	0	1162	44	0
31	DJ	1129	0	1162	54	0
32	BK	939	0	1012	43	0
32	DK	939	0	1012	45	0
33	BL	1045	0	1117	65	0
33	DL	1045	0	1117	79	0
34	BM	1074	0	1157	38	0
34	DM	1074	0	1157	39	0
35	BN	961	0	1000	55	0
35	DN	961	0	1000	77	0
36	BO	892	0	923	51	0
36	DO	892	0	923	44	0
37	BP	917	0	962	42	0
37	DP	917	0	962	60	0
38	BQ	947	0	1019	50	0
38	DQ	947	0	1019	50	0
39	BR	816	0	839	68	0
39	DR	816	0	839	42	0
40	BS	857	0	922	43	0
40	DS	857	0	922	42	0
41	BT	739	0	807	52	0
41	DT	739	0	807	60	0
42	BU	780	0	831	40	0
42	DU	780	0	831	69	0
43	BV	753	0	780	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	DV	753	0	780	24	0
44	BW	580	0	594	15	0
44	DW	569	0	581	24	0
45	BX	625	0	652	19	0
45	DX	625	0	652	44	0
46	BY	509	0	543	34	0
46	DY	509	0	543	29	0
47	BZ	449	0	488	13	0
47	DZ	449	0	488	22	0
48	B0	444	0	458	24	0
48	D0	444	0	458	26	0
49	B1	410	0	440	30	0
49	D1	410	0	440	21	0
50	B2	377	0	418	13	0
50	D2	377	0	418	33	0
51	B3	504	0	572	25	0
51	D3	504	0	572	24	0
52	B4	302	0	340	12	0
52	D4	302	0	340	15	0
53	B5	1142	0	865	66	0
54	AA	70	0	0	0	0
54	AM	1	0	0	0	0
54	AN	1	0	0	0	0
54	BA	194	0	0	0	0
54	BB	4	0	0	0	0
54	BQ	1	0	0	0	0
54	CA	56	0	0	0	0
54	D2	1	0	0	0	0
54	DA	164	0	0	0	0
54	DB	3	0	0	0	0
54	DL	1	0	0	0	0
54	DQ	1	0	0	0	0
55	BA	48	0	50	11	0
55	DA	48	0	50	27	0
56	B4	1	0	0	0	0
56	D4	1	0	0	0	0
57	AA	195	0	0	19	0
57	AE	1	0	0	0	0
57	AL	1	0	0	0	0
57	AN	3	0	0	0	0
57	AT	2	0	0	0	0
57	AU	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	B2	1	0	0	0	0
57	B3	3	0	0	0	0
57	B4	2	0	0	0	0
57	BA	615	0	0	86	0
57	BB	13	0	0	1	0
57	BC	8	0	0	4	0
57	BD	3	0	0	2	0
57	BE	2	0	0	0	0
57	BF	1	0	0	1	0
57	BL	7	0	0	0	0
57	BN	5	0	0	0	0
57	BQ	1	0	0	0	0
57	BS	1	0	0	0	0
57	BT	1	0	0	0	0
57	BU	1	0	0	0	0
57	BV	1	0	0	0	0
57	CA	193	0	0	17	0
57	CL	1	0	0	0	0
57	CN	1	0	0	0	0
57	CT	2	0	0	0	0
57	CU	1	0	0	1	0
57	D2	1	0	0	1	0
57	D3	1	0	0	0	0
57	D4	1	0	0	1	0
57	DA	608	0	0	96	0
57	DB	13	0	0	4	0
57	DC	10	0	0	1	0
57	DD	4	0	0	2	0
57	DE	4	0	0	0	0
57	DJ	1	0	0	0	0
57	DL	4	0	0	1	0
57	DN	2	0	0	0	0
57	DS	2	0	0	0	0
57	DT	3	0	0	1	0
57	DU	1	0	0	0	0
57	DV	1	0	0	0	0
All	All	288276	0	192887	11371	3

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 24.

The worst 5 of 11371 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)
29:BH:117:LEU:O	29:BH:121:VAL:HG23	1.34	1.22
22:DA:2711:A:OP2	57:DA:3546:HOH:O	1.61	1.18
1:AA:111:G:O6	1:AA:330:C:N4	1.78	1.16
22:BA:627:A:OP1	33:BL:78:ARG:NH1	1.79	1.16
22:BA:730:A:OP2	57:BA:3695:HOH:O	1.61	1.16

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:357:G:O2'	29:DH:91:PHE:O[4_455]	2.12	0.08
1:AA:368:U:OP1	29:DH:93:SER:OG[4_455]	2.16	0.04
1:AA:359:G:OP1	29:DH:89:LYS:NZ[4_455]	2.17	0.03

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	216/218 (99%)	132 (61%)	40 (18%)	44 (20%)	0	0
2	CB	216/218 (99%)	142 (66%)	48 (22%)	26 (12%)	0	1
3	AC	204/206 (99%)	149 (73%)	31 (15%)	24 (12%)	0	1
3	CC	204/206 (99%)	154 (76%)	39 (19%)	11 (5%)	2	6
4	AD	203/205 (99%)	133 (66%)	45 (22%)	25 (12%)	0	1
4	CD	203/205 (99%)	147 (72%)	33 (16%)	23 (11%)	0	1
5	AE	148/150 (99%)	102 (69%)	23 (16%)	23 (16%)	0	0
5	CE	148/150 (99%)	98 (66%)	34 (23%)	16 (11%)	0	1
6	AF	98/100 (98%)	67 (68%)	22 (22%)	9 (9%)	1	1
6	CF	98/100 (98%)	66 (67%)	18 (18%)	14 (14%)	0	0
7	AG	149/151 (99%)	110 (74%)	26 (17%)	13 (9%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	CG	149/151 (99%)	120 (80%)	20 (13%)	9 (6%)	1	4
8	AH	127/129 (98%)	87 (68%)	31 (24%)	9 (7%)	1	3
8	CH	127/129 (98%)	102 (80%)	17 (13%)	8 (6%)	1	4
9	AI	125/127 (98%)	88 (70%)	23 (18%)	14 (11%)	0	1
9	CI	125/127 (98%)	89 (71%)	21 (17%)	15 (12%)	0	1
10	AJ	96/98 (98%)	62 (65%)	14 (15%)	20 (21%)	0	0
10	CJ	96/98 (98%)	74 (77%)	10 (10%)	12 (12%)	0	0
11	AK	115/117 (98%)	81 (70%)	15 (13%)	19 (16%)	0	0
11	CK	115/117 (98%)	80 (70%)	26 (23%)	9 (8%)	1	2
12	AL	121/123 (98%)	91 (75%)	20 (16%)	10 (8%)	1	2
12	CL	121/123 (98%)	89 (74%)	20 (16%)	12 (10%)	0	1
13	AM	112/114 (98%)	80 (71%)	21 (19%)	11 (10%)	0	1
13	CM	112/114 (98%)	82 (73%)	17 (15%)	13 (12%)	0	1
14	AN	92/100 (92%)	54 (59%)	29 (32%)	9 (10%)	0	1
14	CN	92/100 (92%)	56 (61%)	22 (24%)	14 (15%)	0	0
15	AO	86/88 (98%)	61 (71%)	19 (22%)	6 (7%)	1	3
15	CO	86/88 (98%)	66 (77%)	16 (19%)	4 (5%)	2	8
16	AP	80/82 (98%)	57 (71%)	11 (14%)	12 (15%)	0	0
16	CP	80/82 (98%)	59 (74%)	16 (20%)	5 (6%)	1	4
17	AQ	78/80 (98%)	55 (70%)	15 (19%)	8 (10%)	0	1
17	CQ	78/80 (98%)	58 (74%)	11 (14%)	9 (12%)	0	1
18	AR	53/55 (96%)	41 (77%)	10 (19%)	2 (4%)	3	13
18	CR	53/55 (96%)	34 (64%)	16 (30%)	3 (6%)	1	5
19	AS	77/79 (98%)	55 (71%)	13 (17%)	9 (12%)	0	1
19	CS	77/79 (98%)	56 (73%)	12 (16%)	9 (12%)	0	1
20	AT	83/85 (98%)	57 (69%)	20 (24%)	6 (7%)	1	3
20	CT	83/85 (98%)	64 (77%)	10 (12%)	9 (11%)	0	1
21	AU	49/51 (96%)	28 (57%)	8 (16%)	13 (26%)	0	0
21	CU	49/51 (96%)	26 (53%)	10 (20%)	13 (26%)	0	0
24	BC	269/271 (99%)	219 (81%)	38 (14%)	12 (4%)	2	9
24	DC	269/271 (99%)	195 (72%)	50 (19%)	24 (9%)	1	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	BD	207/209 (99%)	178 (86%)	22 (11%)	7 (3%)	3	15
25	DD	207/209 (99%)	153 (74%)	45 (22%)	9 (4%)	2	10
26	BE	199/201 (99%)	162 (81%)	34 (17%)	3 (2%)	10	34
26	DE	199/201 (99%)	153 (77%)	29 (15%)	17 (8%)	1	2
27	BF	175/177 (99%)	139 (79%)	28 (16%)	8 (5%)	2	9
27	DF	175/177 (99%)	140 (80%)	23 (13%)	12 (7%)	1	3
28	BG	174/176 (99%)	147 (84%)	18 (10%)	9 (5%)	2	6
28	DG	174/176 (99%)	130 (75%)	29 (17%)	15 (9%)	1	2
29	BH	147/149 (99%)	89 (60%)	37 (25%)	21 (14%)	0	0
29	DH	147/149 (99%)	100 (68%)	32 (22%)	15 (10%)	0	1
30	BI	139/141 (99%)	81 (58%)	34 (24%)	24 (17%)	0	0
30	DI	139/141 (99%)	81 (58%)	38 (27%)	20 (14%)	0	0
31	BJ	140/142 (99%)	130 (93%)	7 (5%)	3 (2%)	7	26
31	DJ	140/142 (99%)	112 (80%)	14 (10%)	14 (10%)	0	1
32	BK	120/122 (98%)	97 (81%)	16 (13%)	7 (6%)	1	5
32	DK	120/122 (98%)	97 (81%)	13 (11%)	10 (8%)	1	2
33	BL	141/143 (99%)	118 (84%)	18 (13%)	5 (4%)	3	14
33	DL	141/143 (99%)	101 (72%)	25 (18%)	15 (11%)	0	1
34	BM	134/136 (98%)	118 (88%)	14 (10%)	2 (2%)	10	34
34	DM	134/136 (98%)	108 (81%)	19 (14%)	7 (5%)	2	6
35	BN	118/120 (98%)	99 (84%)	16 (14%)	3 (2%)	5	21
35	DN	118/120 (98%)	92 (78%)	16 (14%)	10 (8%)	1	2
36	BO	114/116 (98%)	94 (82%)	17 (15%)	3 (3%)	5	20
36	DO	114/116 (98%)	84 (74%)	23 (20%)	7 (6%)	1	4
37	BP	112/114 (98%)	96 (86%)	10 (9%)	6 (5%)	2	6
37	DP	112/114 (98%)	86 (77%)	19 (17%)	7 (6%)	1	4
38	BQ	115/117 (98%)	109 (95%)	4 (4%)	2 (2%)	9	31
38	DQ	115/117 (98%)	93 (81%)	20 (17%)	2 (2%)	9	31
39	BR	101/103 (98%)	81 (80%)	10 (10%)	10 (10%)	0	1
39	DR	101/103 (98%)	73 (72%)	22 (22%)	6 (6%)	1	5
40	BS	108/110 (98%)	92 (85%)	13 (12%)	3 (3%)	5	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	DS	108/110 (98%)	83 (77%)	17 (16%)	8 (7%)	1	2
41	BT	91/93 (98%)	74 (81%)	8 (9%)	9 (10%)	0	1
41	DT	91/93 (98%)	53 (58%)	26 (29%)	12 (13%)	0	0
42	BU	100/102 (98%)	77 (77%)	17 (17%)	6 (6%)	1	4
42	DU	100/102 (98%)	69 (69%)	17 (17%)	14 (14%)	0	0
43	BV	92/94 (98%)	84 (91%)	6 (6%)	2 (2%)	6	24
43	DV	92/94 (98%)	77 (84%)	12 (13%)	3 (3%)	4	15
44	BW	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
44	DW	73/76 (96%)	60 (82%)	13 (18%)	0	100	100
45	BX	75/77 (97%)	66 (88%)	8 (11%)	1 (1%)	12	37
45	DX	75/77 (97%)	57 (76%)	11 (15%)	7 (9%)	0	1
46	BY	61/63 (97%)	42 (69%)	11 (18%)	8 (13%)	0	0
46	DY	61/63 (97%)	46 (75%)	12 (20%)	3 (5%)	2	8
47	BZ	56/58 (97%)	51 (91%)	3 (5%)	2 (4%)	3	14
47	DZ	56/58 (97%)	45 (80%)	7 (12%)	4 (7%)	1	3
48	B0	54/56 (96%)	47 (87%)	4 (7%)	3 (6%)	2	5
48	D0	54/56 (96%)	38 (70%)	12 (22%)	4 (7%)	1	2
49	B1	48/50 (96%)	38 (79%)	7 (15%)	3 (6%)	1	4
49	D1	48/50 (96%)	39 (81%)	4 (8%)	5 (10%)	0	1
50	B2	44/46 (96%)	38 (86%)	4 (9%)	2 (4%)	2	9
50	D2	44/46 (96%)	32 (73%)	8 (18%)	4 (9%)	1	1
51	B3	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	9	32
51	D3	62/64 (97%)	49 (79%)	11 (18%)	2 (3%)	4	16
52	B4	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	5	19
52	D4	36/38 (95%)	31 (86%)	3 (8%)	2 (6%)	2	5
53	B5	183/228 (80%)	85 (46%)	59 (32%)	39 (21%)	0	0
All	All	11418/11672 (98%)	8535 (75%)	1900 (17%)	983 (9%)	1	2

5 of 983 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	16	PHE
2	AB	22	TYR

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Mol	Chain	Res	Type
2	AB	25	PRO
2	AB	34	ALA
2	AB	64	LYS

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	180/180 (100%)	132 (73%)	48 (27%)	0	1
2	CB	180/180 (100%)	132 (73%)	48 (27%)	0	1
3	AC	170/170 (100%)	136 (80%)	34 (20%)	1	4
3	CC	170/170 (100%)	146 (86%)	24 (14%)	3	10
4	AD	172/172 (100%)	138 (80%)	34 (20%)	1	4
4	CD	172/172 (100%)	145 (84%)	27 (16%)	2	8
5	AE	113/113 (100%)	86 (76%)	27 (24%)	0	2
5	CE	113/113 (100%)	84 (74%)	29 (26%)	0	1
6	AF	87/87 (100%)	71 (82%)	16 (18%)	1	5
6	CF	87/87 (100%)	60 (69%)	27 (31%)	0	1
7	AG	124/124 (100%)	105 (85%)	19 (15%)	2	8
7	CG	124/124 (100%)	100 (81%)	24 (19%)	1	4
8	AH	104/104 (100%)	84 (81%)	20 (19%)	1	4
8	CH	104/104 (100%)	84 (81%)	20 (19%)	1	4
9	AI	105/105 (100%)	76 (72%)	29 (28%)	0	1
9	CI	105/105 (100%)	90 (86%)	15 (14%)	3	10
10	AJ	86/86 (100%)	69 (80%)	17 (20%)	1	4
10	CJ	86/86 (100%)	65 (76%)	21 (24%)	0	2
11	AK	90/90 (100%)	75 (83%)	15 (17%)	2	6
11	CK	90/90 (100%)	73 (81%)	17 (19%)	1	4
12	AL	103/103 (100%)	86 (84%)	17 (16%)	2	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	CL	103/103 (100%)	83 (81%)	20 (19%)	1	4
13	AM	92/92 (100%)	76 (83%)	16 (17%)	2	6
13	CM	92/92 (100%)	75 (82%)	17 (18%)	1	5
14	AN	79/83 (95%)	65 (82%)	14 (18%)	2	5
14	CN	79/83 (95%)	71 (90%)	8 (10%)	7	23
15	AO	75/76 (99%)	63 (84%)	12 (16%)	2	7
15	CO	75/76 (99%)	64 (85%)	11 (15%)	3	9
16	AP	65/65 (100%)	49 (75%)	16 (25%)	0	2
16	CP	65/65 (100%)	55 (85%)	10 (15%)	2	8
17	AQ	74/74 (100%)	50 (68%)	24 (32%)	0	0
17	CQ	74/74 (100%)	52 (70%)	22 (30%)	0	1
18	AR	48/48 (100%)	37 (77%)	11 (23%)	1	2
18	CR	48/48 (100%)	39 (81%)	9 (19%)	1	4
19	AS	70/70 (100%)	54 (77%)	16 (23%)	1	2
19	CS	70/70 (100%)	57 (81%)	13 (19%)	1	5
20	AT	65/65 (100%)	51 (78%)	14 (22%)	1	3
20	CT	65/65 (100%)	57 (88%)	8 (12%)	4	14
21	AU	44/44 (100%)	29 (66%)	15 (34%)	0	0
21	CU	44/44 (100%)	27 (61%)	17 (39%)	0	0
24	BC	216/216 (100%)	189 (88%)	27 (12%)	4	14
24	DC	216/216 (100%)	194 (90%)	22 (10%)	7	22
25	BD	164/164 (100%)	147 (90%)	17 (10%)	7	21
25	DD	164/164 (100%)	147 (90%)	17 (10%)	7	21
26	BE	165/165 (100%)	138 (84%)	27 (16%)	2	7
26	DE	165/165 (100%)	139 (84%)	26 (16%)	2	8
27	BF	148/148 (100%)	115 (78%)	33 (22%)	1	3
27	DF	148/148 (100%)	121 (82%)	27 (18%)	1	5
28	BG	137/137 (100%)	120 (88%)	17 (12%)	4	14
28	DG	137/137 (100%)	114 (83%)	23 (17%)	2	6
29	BH	114/114 (100%)	88 (77%)	26 (23%)	1	2
29	DH	114/114 (100%)	88 (77%)	26 (23%)	1	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	BI	109/109 (100%)	83 (76%)	26 (24%)	0	2
30	DI	109/109 (100%)	83 (76%)	26 (24%)	0	2
31	BJ	116/116 (100%)	104 (90%)	12 (10%)	7	22
31	DJ	116/116 (100%)	97 (84%)	19 (16%)	2	7
32	BK	103/103 (100%)	90 (87%)	13 (13%)	4	13
32	DK	103/103 (100%)	92 (89%)	11 (11%)	6	20
33	BL	102/102 (100%)	92 (90%)	10 (10%)	8	24
33	DL	102/102 (100%)	89 (87%)	13 (13%)	4	13
34	BM	109/109 (100%)	100 (92%)	9 (8%)	11	32
34	DM	109/109 (100%)	97 (89%)	12 (11%)	6	19
35	BN	100/100 (100%)	93 (93%)	7 (7%)	15	41
35	DN	100/100 (100%)	77 (77%)	23 (23%)	1	2
36	BO	86/86 (100%)	66 (77%)	20 (23%)	1	2
36	DO	86/86 (100%)	69 (80%)	17 (20%)	1	4
37	BP	99/99 (100%)	84 (85%)	15 (15%)	3	8
37	DP	99/99 (100%)	90 (91%)	9 (9%)	9	28
38	BQ	89/89 (100%)	78 (88%)	11 (12%)	4	14
38	DQ	89/89 (100%)	78 (88%)	11 (12%)	4	14
39	BR	84/84 (100%)	74 (88%)	10 (12%)	5	15
39	DR	84/84 (100%)	79 (94%)	5 (6%)	19	49
40	BS	93/93 (100%)	77 (83%)	16 (17%)	2	6
40	DS	93/93 (100%)	82 (88%)	11 (12%)	5	16
41	BT	80/80 (100%)	70 (88%)	10 (12%)	4	14
41	DT	80/80 (100%)	69 (86%)	11 (14%)	3	10
42	BU	83/83 (100%)	71 (86%)	12 (14%)	3	9
42	DU	83/83 (100%)	68 (82%)	15 (18%)	1	5
43	BV	78/78 (100%)	61 (78%)	17 (22%)	1	3
43	DV	78/78 (100%)	65 (83%)	13 (17%)	2	6
44	BW	57/58 (98%)	48 (84%)	9 (16%)	2	8
44	DW	56/58 (97%)	48 (86%)	8 (14%)	3	10
45	BX	67/67 (100%)	59 (88%)	8 (12%)	5	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	DX	67/67 (100%)	57 (85%)	10 (15%)	3	9
46	BY	55/55 (100%)	49 (89%)	6 (11%)	6	19
46	DY	55/55 (100%)	42 (76%)	13 (24%)	1	2
47	BZ	48/48 (100%)	43 (90%)	5 (10%)	7	21
47	DZ	48/48 (100%)	38 (79%)	10 (21%)	1	3
48	B0	47/47 (100%)	43 (92%)	4 (8%)	10	31
48	D0	47/47 (100%)	42 (89%)	5 (11%)	6	20
49	B1	45/45 (100%)	42 (93%)	3 (7%)	16	43
49	D1	45/45 (100%)	38 (84%)	7 (16%)	2	8
50	B2	38/38 (100%)	34 (90%)	4 (10%)	7	21
50	D2	38/38 (100%)	32 (84%)	6 (16%)	2	8
51	B3	51/51 (100%)	45 (88%)	6 (12%)	5	16
51	D3	51/51 (100%)	46 (90%)	5 (10%)	8	24
52	B4	34/34 (100%)	32 (94%)	2 (6%)	19	49
52	D4	34/34 (100%)	28 (82%)	6 (18%)	2	5
53	B5	61/180 (34%)	47 (77%)	14 (23%)	1	2
All	All	9386/9518 (99%)	7782 (83%)	1604 (17%)	2	6

5 of 1604 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	CE	114	VAL
17	CQ	76	VAL
52	D4	3	VAL
6	CF	63	ASN
5	CE	105	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
14	CN	66	GLN
25	DD	140	HIS
49	D1	26	ASN
15	CO	42	HIS
20	CT	61	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	327 (21%)	10 (0%)
1	CA	1538/1539 (99%)	330 (21%)	8 (0%)
22	BA	2896/2903 (99%)	569 (19%)	27 (0%)
22	DA	2895/2903 (99%)	685 (23%)	30 (1%)
23	BB	118/119 (99%)	17 (14%)	0
23	DB	117/119 (98%)	20 (17%)	0
All	All	9101/9122 (99%)	1948 (21%)	75 (0%)

5 of 1948 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	8	A
1	AA	9	G
1	AA	13	U

5 of 75 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	DA	1514	G
22	DA	2326	C
22	DA	1847	A
22	DA	2162	G
22	BA	1583	A

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 501 ligands modelled in this entry, 499 are monoatomic - leaving 2 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
55	DOL	BA	3001	-	43,50,50	2.84	15 (34%)	51,70,70	2.93	17 (33%)
55	DOL	DA	3001	-	43,50,50	2.94	13 (30%)	51,70,70	2.84	11 (21%)

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
55	DOL	BA	3001	-	-	15/58/77/77	0/2/3/3
55	DOL	DA	3001	-	-	11/58/77/77	0/2/3/3

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	DA	3001	DOL	O15-C14	9.24	1.37	1.21
55	BA	3001	DOL	O15-C14	9.11	1.37	1.21
55	DA	3001	DOL	C22-C23	7.99	1.52	1.32
55	BA	3001	DOL	C22-C23	7.21	1.50	1.32
55	BA	3001	DOL	O38-C37	6.58	1.37	1.21

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	DA	3001	DOL	O40-S39-O41	-15.59	100.41	118.19
55	BA	3001	DOL	O40-S39-O41	-11.60	104.96	118.19
55	BA	3001	DOL	C29-C28-C26	-7.33	104.35	122.69
55	BA	3001	DOL	C43-C42-S39	7.02	126.83	112.14
55	BA	3001	DOL	C8-C6-N5	7.00	127.83	119.76

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

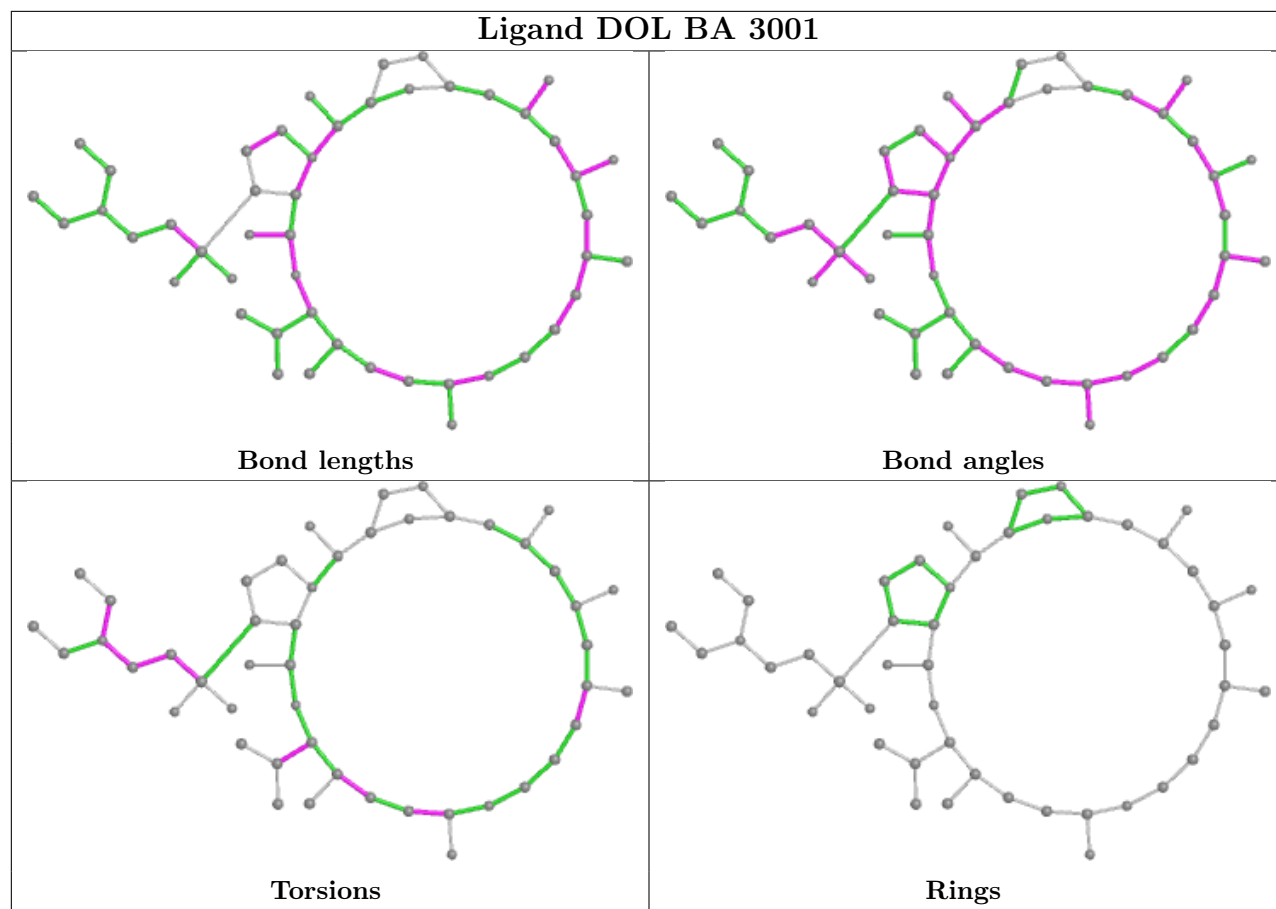
Mol	Chain	Res	Type	Atoms
55	BA	3001	DOL	C43-C42-S39-C2
55	BA	3001	DOL	C43-C42-S39-O41
55	BA	3001	DOL	C43-C42-S39-O40
55	BA	3001	DOL	S39-C42-C43-N44
55	BA	3001	DOL	N25-C26-C28-C29

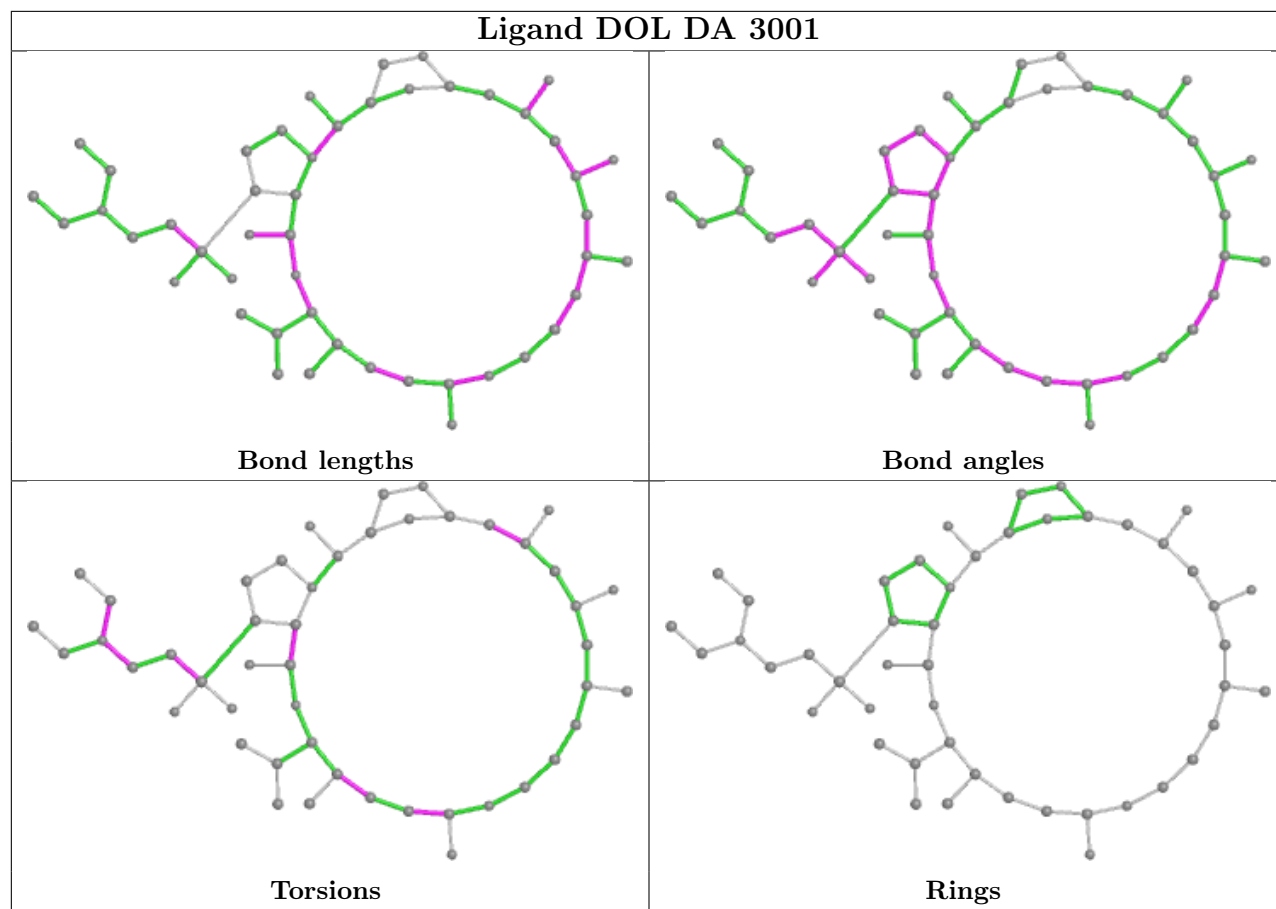
There are no ring outliers.

2 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	BA	3001	DOL	11	0
55	DA	3001	DOL	27	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](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1538/1539 (99%)	-0.11	34 (2%) 62 59	11, 51, 132, 183	0
1	CA	1539/1539 (100%)	0.35	125 (8%) 12 9	24, 70, 147, 178	0
2	AB	218/218 (100%)	1.02	38 (17%) 1 1	40, 75, 101, 117	0
2	CB	218/218 (100%)	1.08	47 (21%) 0 0	60, 88, 108, 123	0
3	AC	206/206 (100%)	0.17	7 (3%) 45 40	37, 58, 80, 95	0
3	CC	206/206 (100%)	0.98	35 (16%) 1 1	55, 80, 98, 108	0
4	AD	205/205 (100%)	0.29	9 (4%) 34 30	33, 57, 80, 100	0
4	CD	205/205 (100%)	-0.08	6 (2%) 51 47	15, 36, 60, 84	0
5	AE	150/150 (100%)	0.15	3 (2%) 65 63	29, 48, 78, 94	0
5	CE	150/150 (100%)	0.27	7 (4%) 31 28	27, 53, 83, 104	0
6	AF	100/100 (100%)	0.48	10 (10%) 7 5	35, 56, 75, 79	0
6	CF	100/100 (100%)	0.54	6 (6%) 21 18	43, 73, 92, 104	0
7	AG	151/151 (100%)	0.79	17 (11%) 5 4	54, 76, 92, 100	0
7	CG	151/151 (100%)	2.73	88 (58%) 0 0	82, 106, 115, 119	0
8	AH	129/129 (100%)	0.02	2 (1%) 72 71	29, 48, 68, 79	0
8	CH	129/129 (100%)	0.26	4 (3%) 49 44	48, 64, 81, 96	0
9	AI	127/127 (100%)	1.09	24 (18%) 1 0	45, 75, 98, 107	0
9	CI	127/127 (100%)	1.74	44 (34%) 0 0	81, 97, 114, 121	0
10	AJ	98/98 (100%)	0.82	16 (16%) 1 1	41, 68, 88, 116	0
10	CJ	98/98 (100%)	2.56	53 (54%) 0 0	73, 98, 115, 124	0
11	AK	117/117 (100%)	0.44	12 (10%) 6 5	28, 62, 92, 120	0
11	CK	117/117 (100%)	0.33	4 (3%) 45 40	36, 68, 82, 90	0
12	AL	123/123 (100%)	0.05	4 (3%) 46 41	20, 35, 65, 97	0
12	CL	123/123 (100%)	0.33	7 (5%) 23 19	33, 50, 75, 96	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	114/114 (100%)	1.16	26 (22%) 0 0	49, 72, 93, 104	0
13	CM	114/114 (100%)	3.75	90 (78%) 0 0	94, 115, 124, 126	0
14	AN	96/100 (96%)	0.71	11 (11%) 4 3	41, 62, 96, 105	0
14	CN	96/100 (96%)	2.36	51 (53%) 0 0	71, 97, 116, 123	0
15	AO	88/88 (100%)	0.20	3 (3%) 45 40	31, 48, 65, 90	0
15	CO	88/88 (100%)	0.38	6 (6%) 17 13	38, 65, 80, 103	0
16	AP	82/82 (100%)	0.33	4 (4%) 29 26	35, 48, 84, 109	0
16	CP	82/82 (100%)	0.63	7 (8%) 10 8	45, 62, 92, 113	0
17	AQ	80/80 (100%)	0.45	4 (5%) 28 25	28, 49, 75, 110	0
17	CQ	80/80 (100%)	1.22	18 (22%) 0 0	43, 79, 98, 100	0
18	AR	55/55 (100%)	0.67	8 (14%) 2 1	42, 55, 78, 101	0
18	CR	55/55 (100%)	0.48	7 (12%) 3 2	36, 55, 78, 109	0
19	AS	79/79 (100%)	1.31	24 (30%) 0 0	56, 72, 89, 97	0
19	CS	79/79 (100%)	3.39	57 (72%) 0 0	98, 115, 124, 129	0
20	AT	85/85 (100%)	0.46	7 (8%) 11 9	36, 48, 70, 95	0
20	CT	85/85 (100%)	1.54	25 (29%) 0 0	54, 78, 96, 101	0
21	AU	51/51 (100%)	1.44	17 (33%) 0 0	44, 76, 97, 105	0
21	CU	51/51 (100%)	0.65	4 (7%) 13 10	45, 71, 100, 103	0
22	BA	2897/2903 (99%)	0.06	140 (4%) 30 27	1, 14, 129, 195	0
22	DA	2897/2903 (99%)	0.60	229 (7%) 12 10	41, 85, 148, 181	0
23	BB	119/119 (100%)	-0.41	0 100 100	2, 23, 50, 80	0
23	DB	118/119 (99%)	0.77	14 (11%) 4 3	69, 115, 134, 143	0
24	BC	271/271 (100%)	-0.33	2 (0%) 87 87	2, 20, 37, 55	0
24	DC	271/271 (100%)	0.46	12 (4%) 34 30	47, 64, 77, 96	0
25	BD	209/209 (100%)	-0.44	0 100 100	0, 10, 36, 65	0
25	DD	209/209 (100%)	0.75	31 (14%) 2 1	53, 72, 88, 96	0
26	BE	201/201 (100%)	-0.37	0 100 100	2, 24, 55, 88	0
26	DE	201/201 (100%)	1.40	50 (24%) 0 0	53, 90, 107, 114	0
27	BF	177/177 (100%)	0.22	14 (7%) 12 10	22, 44, 76, 90	0
27	DF	177/177 (100%)	3.11	120 (67%) 0 0	97, 114, 126, 131	0
28	BG	176/176 (100%)	-0.29	1 (0%) 89 89	16, 36, 57, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DG	176/176 (100%)	2.16	86 (48%) 0 0	77, 96, 111, 121	0
29	BH	149/149 (100%)	2.72	74 (49%) 0 0	25, 102, 121, 129	0
29	DH	149/149 (100%)	1.28	36 (24%) 0 0	25, 92, 107, 115	0
30	BI	141/141 (100%)	3.80	96 (68%) 0 0	90, 117, 127, 134	0
30	DI	141/141 (100%)	5.64	131 (92%) 0 0	105, 126, 137, 143	0
31	BJ	142/142 (100%)	-0.37	0 100 100	1, 6, 23, 36	0
31	DJ	142/142 (100%)	0.55	10 (7%) 16 12	52, 69, 83, 91	0
32	BK	122/122 (100%)	-0.36	0 100 100	3, 12, 31, 62	0
32	DK	122/122 (100%)	0.53	8 (6%) 18 14	48, 66, 84, 96	0
33	BL	143/143 (100%)	-0.32	0 100 100	1, 19, 43, 65	0
33	DL	143/143 (100%)	1.70	53 (37%) 0 0	46, 87, 99, 115	0
34	BM	136/136 (100%)	-0.45	0 100 100	1, 10, 30, 83	0
34	DM	136/136 (100%)	0.62	15 (11%) 5 4	42, 71, 86, 100	0
35	BN	120/120 (100%)	-0.42	0 100 100	3, 8, 18, 63	0
35	DN	120/120 (100%)	0.99	18 (15%) 2 1	59, 79, 94, 112	0
36	BO	116/116 (100%)	-0.32	0 100 100	14, 26, 45, 55	0
36	DO	116/116 (100%)	2.11	59 (50%) 0 0	86, 100, 111, 118	0
37	BP	114/114 (100%)	-0.36	2 (1%) 68 67	8, 17, 41, 72	0
37	DP	114/114 (100%)	0.98	19 (16%) 1 1	61, 75, 86, 95	0
38	BQ	117/117 (100%)	-0.31	0 100 100	0, 3, 13, 34	0
38	DQ	117/117 (100%)	1.02	19 (16%) 1 1	57, 71, 80, 89	0
39	BR	103/103 (100%)	-0.38	0 100 100	1, 13, 30, 58	0
39	DR	103/103 (100%)	1.52	32 (31%) 0 0	58, 81, 94, 104	0
40	BS	110/110 (100%)	-0.42	0 100 100	2, 5, 24, 66	0
40	DS	110/110 (100%)	1.19	22 (20%) 1 0	62, 80, 95, 106	0
41	BT	93/93 (100%)	0.07	3 (3%) 47 43	9, 26, 68, 100	0
41	DT	93/93 (100%)	2.09	48 (51%) 0 0	73, 92, 106, 115	0
42	BU	102/102 (100%)	0.22	11 (10%) 5 4	12, 29, 63, 79	0
42	DU	102/102 (100%)	2.75	58 (56%) 0 0	78, 96, 110, 122	0
43	BV	94/94 (100%)	-0.38	0 100 100	5, 21, 43, 55	0
43	DV	94/94 (100%)	1.16	22 (23%) 0 0	74, 88, 99, 106	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BW	76/76 (100%)	-0.35	1 (1%) 77 77	5, 12, 30, 57	0
44	DW	75/76 (98%)	1.42	22 (29%) 0 0	58, 83, 92, 105	0
45	BX	77/77 (100%)	-0.32	0 100 100	8, 22, 51, 68	0
45	DX	77/77 (100%)	1.02	16 (20%) 1 0	50, 72, 87, 92	0
46	BY	63/63 (100%)	0.21	3 (4%) 30 27	24, 41, 73, 95	0
46	DY	63/63 (100%)	2.05	34 (53%) 0 0	82, 99, 107, 110	0
47	BZ	58/58 (100%)	-0.32	0 100 100	2, 9, 29, 35	0
47	DZ	58/58 (100%)	0.80	6 (10%) 6 5	60, 74, 85, 103	0
48	B0	56/56 (100%)	-0.49	0 100 100	1, 10, 35, 60	0
48	D0	56/56 (100%)	1.41	15 (26%) 0 0	52, 83, 98, 105	0
49	B1	50/50 (100%)	-0.20	0 100 100	15, 27, 51, 58	0
49	D1	50/50 (100%)	2.05	22 (44%) 0 0	74, 90, 95, 105	0
50	B2	46/46 (100%)	-0.34	1 (2%) 62 59	5, 9, 16, 79	0
50	D2	46/46 (100%)	1.23	12 (26%) 0 0	58, 72, 87, 102	0
51	B3	64/64 (100%)	-0.40	0 100 100	4, 10, 20, 29	0
51	D3	64/64 (100%)	1.42	17 (26%) 0 0	62, 75, 84, 95	0
52	B4	38/38 (100%)	-0.08	1 (2%) 56 52	8, 19, 34, 54	0
52	D4	38/38 (100%)	2.51	20 (52%) 0 0	64, 79, 90, 100	0
53	B5	191/228 (83%)	6.30	188 (98%) 0 0	100, 122, 133, 142	0
All	All	20734/20794 (99%)	0.62	2764 (13%) 3 2	0, 64, 125, 195	0

The worst 5 of 2764 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
53	B5	218	THR	28.0
53	B5	140	ASN	21.5
29	BH	130	VAL	18.3
30	BI	53	LEU	17.3
10	AJ	102	LEU	17.2

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	MG	DA	3133	1/1	-0.13	1.03	105,105,105,105	0
54	MG	DA	3077	1/1	0.14	0.37	115,115,115,115	0
54	MG	CA	1636	1/1	0.14	0.24	127,127,127,127	0
54	MG	AA	1666	1/1	0.22	0.37	61,61,61,61	0
54	MG	DA	3100	1/1	0.30	0.42	86,86,86,86	0
54	MG	DA	3135	1/1	0.33	0.66	101,101,101,101	0
54	MG	DA	3026	1/1	0.34	0.49	100,100,100,100	0
54	MG	CA	1604	1/1	0.43	0.16	95,95,95,95	0
54	MG	DA	3019	1/1	0.44	0.32	109,109,109,109	0
54	MG	DA	3029	1/1	0.46	0.25	77,77,77,77	0
54	MG	DA	3062	1/1	0.46	0.61	89,89,89,89	0
54	MG	DA	3003	1/1	0.48	0.63	101,101,101,101	0
54	MG	CA	1629	1/1	0.49	0.10	89,89,89,89	0
54	MG	DA	3119	1/1	0.49	0.81	112,112,112,112	0
54	MG	DA	3099	1/1	0.52	0.39	91,91,91,91	0
54	MG	AA	1664	1/1	0.54	0.71	49,49,49,49	0
54	MG	CA	1615	1/1	0.56	0.18	52,52,52,52	0
54	MG	CA	1631	1/1	0.59	0.23	101,101,101,101	0
54	MG	DA	3005	1/1	0.60	0.53	103,103,103,103	0
54	MG	DA	3046	1/1	0.60	0.13	68,68,68,68	0
54	MG	DA	3028	1/1	0.60	1.15	104,104,104,104	0
54	MG	DL	201	1/1	0.60	0.52	68,68,68,68	0
54	MG	DA	3070	1/1	0.61	0.18	108,108,108,108	0
54	MG	DA	3041	1/1	0.61	0.45	72,72,72,72	0
54	MG	DA	3002	1/1	0.62	0.14	78,78,78,78	0
54	MG	DA	3137	1/1	0.62	0.48	52,52,52,52	0
54	MG	CA	1602	1/1	0.62	0.12	87,87,87,87	0
54	MG	DA	3111	1/1	0.63	0.19	103,103,103,103	0
54	MG	DA	3078	1/1	0.65	0.21	110,110,110,110	0
54	MG	DA	3061	1/1	0.65	2.99	102,102,102,102	0
54	MG	AA	1650	1/1	0.65	0.34	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	MG	CA	1630	1/1	0.66	0.34	120,120,120,120	0
54	MG	DA	3012	1/1	0.67	0.22	78,78,78,78	0
54	MG	DA	3071	1/1	0.67	0.22	87,87,87,87	0
54	MG	DB	203	1/1	0.67	0.09	85,85,85,85	0
54	MG	DA	3103	1/1	0.67	0.15	67,67,67,67	0
54	MG	DA	3113	1/1	0.68	0.58	72,72,72,72	0
54	MG	AA	1658	1/1	0.68	0.67	52,52,52,52	0
54	MG	DA	3093	1/1	0.68	0.36	94,94,94,94	0
54	MG	AA	1637	1/1	0.68	0.14	81,81,81,81	0
54	MG	DA	3136	1/1	0.68	0.18	94,94,94,94	0
54	MG	DA	3009	1/1	0.68	0.20	91,91,91,91	0
54	MG	DA	3147	1/1	0.68	0.26	67,67,67,67	0
54	MG	AA	1618	1/1	0.68	0.29	75,75,75,75	0
54	MG	BA	3189	1/1	0.68	0.21	48,48,48,48	0
54	MG	CA	1628	1/1	0.69	0.31	99,99,99,99	0
54	MG	AA	1662	1/1	0.69	0.46	58,58,58,58	0
54	MG	DA	3048	1/1	0.70	0.32	123,123,123,123	0
54	MG	AA	1656	1/1	0.71	0.94	66,66,66,66	0
54	MG	DA	3044	1/1	0.71	0.46	113,113,113,113	0
54	MG	DA	3091	1/1	0.71	0.17	82,82,82,82	0
54	MG	DA	3092	1/1	0.71	0.78	117,117,117,117	0
54	MG	AA	1669	1/1	0.71	0.28	45,45,45,45	0
54	MG	BA	3027	1/1	0.71	0.30	44,44,44,44	0
54	MG	AA	1668	1/1	0.72	0.91	54,54,54,54	0
54	MG	BA	3049	1/1	0.72	0.17	50,50,50,50	0
54	MG	CA	1635	1/1	0.73	0.35	122,122,122,122	0
54	MG	DA	3162	1/1	0.73	0.69	63,63,63,63	0
54	MG	DB	201	1/1	0.73	0.13	113,113,113,113	0
54	MG	DA	3127	1/1	0.73	0.20	74,74,74,74	0
54	MG	DA	3106	1/1	0.73	0.19	49,49,49,49	0
54	MG	DA	3010	1/1	0.74	0.06	80,80,80,80	0
54	MG	DA	3104	1/1	0.74	0.08	80,80,80,80	0
54	MG	DA	3145	1/1	0.74	0.19	56,56,56,56	0
54	MG	DA	3095	1/1	0.74	0.28	91,91,91,91	0
54	MG	AA	1661	1/1	0.75	0.37	55,55,55,55	0
54	MG	CA	1632	1/1	0.75	0.17	79,79,79,79	0
54	MG	DA	3034	1/1	0.75	0.17	69,69,69,69	0
54	MG	BA	3120	1/1	0.76	0.18	47,47,47,47	0
54	MG	DA	3084	1/1	0.76	0.25	104,104,104,104	0
54	MG	DA	3023	1/1	0.76	0.13	76,76,76,76	0
54	MG	BA	3082	1/1	0.76	0.12	16,16,16,16	0
54	MG	DA	3027	1/1	0.76	0.33	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	MG	DA	3159	1/1	0.77	0.34	47,47,47,47	0
54	MG	DA	3049	1/1	0.77	0.18	87,87,87,87	0
54	MG	DA	3056	1/1	0.77	0.29	91,91,91,91	0
54	MG	CA	1614	1/1	0.77	0.12	49,49,49,49	0
54	MG	BA	3058	1/1	0.77	0.16	9,9,9,9	0
54	MG	CA	1603	1/1	0.78	0.08	37,37,37,37	0
54	MG	BA	3168	1/1	0.78	0.26	41,41,41,41	0
54	MG	AA	1626	1/1	0.78	0.27	53,53,53,53	0
54	MG	AA	1624	1/1	0.78	0.12	46,46,46,46	0
54	MG	DA	3151	1/1	0.78	0.58	56,56,56,56	0
54	MG	DA	3016	1/1	0.79	0.37	73,73,73,73	0
54	MG	DA	3072	1/1	0.79	0.28	86,86,86,86	0
54	MG	DA	3042	1/1	0.79	0.13	87,87,87,87	0
54	MG	CA	1617	1/1	0.79	0.19	57,57,57,57	0
54	MG	CA	1621	1/1	0.79	0.14	72,72,72,72	0
54	MG	AA	1645	1/1	0.79	0.26	54,54,54,54	0
54	MG	DA	3132	1/1	0.80	0.25	64,64,64,64	0
54	MG	DA	3045	1/1	0.80	0.14	87,87,87,87	0
54	MG	DA	3088	1/1	0.80	0.12	75,75,75,75	0
54	MG	DA	3014	1/1	0.80	0.20	78,78,78,78	0
54	MG	DA	3165	1/1	0.80	0.15	100,100,100,100	0
54	MG	CA	1606	1/1	0.80	0.22	90,90,90,90	0
54	MG	DA	3144	1/1	0.80	0.29	72,72,72,72	0
54	MG	CA	1649	1/1	0.80	0.29	61,61,61,61	0
54	MG	BA	3134	1/1	0.81	0.42	54,54,54,54	0
54	MG	DA	3125	1/1	0.81	0.17	59,59,59,59	0
54	MG	AA	1659	1/1	0.81	0.18	62,62,62,62	0
54	MG	BA	3085	1/1	0.81	0.22	29,29,29,29	0
54	MG	CA	1608	1/1	0.81	0.18	80,80,80,80	0
54	MG	DA	3057	1/1	0.81	0.21	92,92,92,92	0
54	MG	AA	1638	1/1	0.81	0.09	64,64,64,64	0
54	MG	DA	3098	1/1	0.81	0.19	60,60,60,60	0
54	MG	DA	3140	1/1	0.81	0.36	42,42,42,42	0
54	MG	DA	3143	1/1	0.81	0.10	73,73,73,73	0
54	MG	DA	3126	1/1	0.82	0.20	77,77,77,77	0
54	MG	BA	3194	1/1	0.82	0.85	41,41,41,41	0
54	MG	BA	3005	1/1	0.82	0.14	45,45,45,45	0
54	MG	DA	3038	1/1	0.82	0.12	64,64,64,64	0
54	MG	DA	3134	1/1	0.82	0.14	54,54,54,54	0
54	MG	CA	1637	1/1	0.82	0.23	64,64,64,64	0
54	MG	AA	1639	1/1	0.82	0.14	45,45,45,45	0
54	MG	DA	3017	1/1	0.82	0.54	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	DA	3060	1/1	0.82	0.36	81,81,81,81	0
54	MG	DA	3080	1/1	0.82	0.20	96,96,96,96	0
54	MG	CA	1610	1/1	0.83	0.08	65,65,65,65	0
54	MG	BA	3090	1/1	0.83	0.17	34,34,34,34	0
54	MG	DA	3058	1/1	0.83	0.92	107,107,107,107	0
54	MG	DA	3085	1/1	0.83	0.17	76,76,76,76	0
54	MG	DA	3008	1/1	0.83	0.30	102,102,102,102	0
54	MG	CA	1605	1/1	0.83	0.17	86,86,86,86	0
54	MG	DA	3124	1/1	0.83	0.17	87,87,87,87	0
54	MG	DA	3011	1/1	0.84	0.15	73,73,73,73	0
54	MG	CA	1653	1/1	0.84	0.17	47,47,47,47	0
54	MG	DA	3032	1/1	0.84	0.23	71,71,71,71	0
54	MG	CA	1626	1/1	0.84	0.20	54,54,54,54	0
54	MG	AA	1657	1/1	0.84	0.29	60,60,60,60	0
54	MG	AA	1651	1/1	0.84	0.20	51,51,51,51	0
54	MG	DA	3006	1/1	0.84	0.06	95,95,95,95	0
54	MG	AA	1619	1/1	0.84	0.08	71,71,71,71	0
54	MG	CA	1638	1/1	0.84	0.06	65,65,65,65	0
54	MG	DA	3116	1/1	0.84	0.33	72,72,72,72	0
54	MG	BA	3057	1/1	0.84	0.20	68,68,68,68	0
54	MG	DA	3107	1/1	0.85	0.12	70,70,70,70	0
54	MG	BA	3076	1/1	0.85	0.17	33,33,33,33	0
54	MG	DA	3161	1/1	0.85	0.30	46,46,46,46	0
54	MG	CA	1611	1/1	0.85	0.25	87,87,87,87	0
54	MG	DA	3047	1/1	0.85	0.11	74,74,74,74	0
54	MG	DA	3031	1/1	0.85	0.14	65,65,65,65	0
54	MG	DA	3120	1/1	0.85	0.18	81,81,81,81	0
54	MG	DA	3089	1/1	0.85	0.32	87,87,87,87	0
54	MG	D2	101	1/1	0.85	0.17	76,76,76,76	0
54	MG	DA	3022	1/1	0.86	0.07	55,55,55,55	0
54	MG	BA	3100	1/1	0.86	0.29	51,51,51,51	0
54	MG	DA	3157	1/1	0.86	0.67	76,76,76,76	0
54	MG	DA	3158	1/1	0.86	0.23	52,52,52,52	0
54	MG	DA	3040	1/1	0.86	0.12	80,80,80,80	0
54	MG	AA	1622	1/1	0.86	0.18	50,50,50,50	0
54	MG	BA	3125	1/1	0.86	0.29	39,39,39,39	0
54	MG	DA	3163	1/1	0.86	0.26	64,64,64,64	0
54	MG	DA	3083	1/1	0.86	0.23	74,74,74,74	0
54	MG	AA	1612	1/1	0.86	0.11	48,48,48,48	0
54	MG	AA	1614	1/1	0.86	0.23	74,74,74,74	0
54	MG	CA	1643	1/1	0.86	0.30	44,44,44,44	0
54	MG	BA	3059	1/1	0.86	0.35	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	CA	1646	1/1	0.87	0.40	97,97,97,97	0
54	MG	DA	3087	1/1	0.87	0.15	64,64,64,64	0
54	MG	DA	3004	1/1	0.87	0.08	78,78,78,78	0
54	MG	DA	3021	1/1	0.87	0.16	53,53,53,53	0
54	MG	BA	3165	1/1	0.87	0.22	38,38,38,38	0
54	MG	AA	1642	1/1	0.87	0.19	32,32,32,32	0
54	MG	DA	3130	1/1	0.87	0.24	80,80,80,80	0
54	MG	DA	3007	1/1	0.87	0.34	119,119,119,119	0
54	MG	AA	1627	1/1	0.87	0.06	48,48,48,48	0
54	MG	DA	3067	1/1	0.87	0.12	53,53,53,53	0
54	MG	DA	3025	1/1	0.88	0.23	68,68,68,68	0
54	MG	AA	1665	1/1	0.88	0.27	47,47,47,47	0
54	MG	DA	3101	1/1	0.88	0.13	63,63,63,63	0
54	MG	BA	3167	1/1	0.88	0.26	32,32,32,32	0
54	MG	CA	1609	1/1	0.88	0.07	87,87,87,87	0
54	MG	CA	1655	1/1	0.88	0.11	45,45,45,45	0
54	MG	BA	3078	1/1	0.88	0.49	87,87,87,87	0
54	MG	DA	3081	1/1	0.88	0.22	66,66,66,66	0
54	MG	DA	3150	1/1	0.88	0.27	50,50,50,50	0
54	MG	DA	3053	1/1	0.88	0.12	44,44,44,44	0
54	MG	DA	3055	1/1	0.88	0.12	59,59,59,59	0
54	MG	BA	3104	1/1	0.88	0.11	8,8,8,8	0
54	MG	AA	1633	1/1	0.88	0.12	51,51,51,51	0
54	MG	DA	3037	1/1	0.88	0.12	92,92,92,92	0
54	MG	AM	201	1/1	0.88	0.85	59,59,59,59	0
54	MG	BA	3089	1/1	0.88	0.13	24,24,24,24	0
54	MG	DA	3164	1/1	0.88	0.26	40,40,40,40	0
54	MG	BA	3137	1/1	0.88	0.36	46,46,46,46	0
54	MG	DA	3066	1/1	0.88	0.14	58,58,58,58	0
54	MG	BA	3146	1/1	0.88	0.18	32,32,32,32	0
54	MG	DA	3096	1/1	0.88	0.11	61,61,61,61	0
54	MG	DA	3068	1/1	0.88	0.14	64,64,64,64	0
55	DOL	DA	3001	48/48	0.88	0.32	28,49,62,81	0
54	MG	AA	1608	1/1	0.89	0.13	27,27,27,27	0
54	MG	CA	1613	1/1	0.89	0.11	20,20,20,20	0
54	MG	DA	3030	1/1	0.89	0.22	70,70,70,70	0
54	MG	CA	1644	1/1	0.89	0.23	43,43,43,43	0
54	MG	CA	1633	1/1	0.89	0.53	76,76,76,76	0
54	MG	BA	3075	1/1	0.89	0.22	35,35,35,35	0
54	MG	DA	3035	1/1	0.89	0.10	79,79,79,79	0
54	MG	DA	3079	1/1	0.89	0.12	98,98,98,98	0
54	MG	DA	3149	1/1	0.89	0.41	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	AA	1631	1/1	0.89	0.14	52,52,52,52	0
54	MG	DA	3094	1/1	0.89	0.30	87,87,87,87	0
54	MG	BA	3042	1/1	0.89	0.34	2,2,2,2	0
54	MG	DA	3015	1/1	0.90	0.13	63,63,63,63	0
54	MG	BA	3147	1/1	0.90	0.47	23,23,23,23	0
54	MG	CA	1656	1/1	0.90	0.27	50,50,50,50	0
54	MG	DA	3109	1/1	0.90	0.14	47,47,47,47	0
54	MG	AA	1644	1/1	0.90	0.38	45,45,45,45	0
54	MG	DA	3112	1/1	0.90	0.42	92,92,92,92	0
54	MG	DA	3146	1/1	0.90	0.40	48,48,48,48	0
54	MG	BA	3101	1/1	0.90	0.10	1,1,1,1	0
54	MG	BA	3079	1/1	0.90	0.08	22,22,22,22	0
54	MG	DA	3118	1/1	0.90	0.09	55,55,55,55	0
54	MG	BA	3116	1/1	0.90	0.20	32,32,32,32	0
54	MG	DA	3156	1/1	0.90	0.19	57,57,57,57	0
54	MG	DA	3024	1/1	0.90	0.19	46,46,46,46	0
54	MG	DA	3121	1/1	0.90	0.06	48,48,48,48	0
54	MG	BA	3119	1/1	0.90	0.09	21,21,21,21	0
54	MG	AA	1607	1/1	0.90	0.05	54,54,54,54	0
54	MG	AA	1667	1/1	0.90	0.16	30,30,30,30	0
54	MG	DA	3075	1/1	0.90	0.19	83,83,83,83	0
54	MG	DA	3129	1/1	0.90	0.15	50,50,50,50	0
54	MG	AA	1647	1/1	0.90	0.17	48,48,48,48	0
54	MG	DA	3131	1/1	0.90	0.61	94,94,94,94	0
54	MG	AA	1606	1/1	0.90	0.08	44,44,44,44	0
54	MG	CA	1627	1/1	0.90	0.28	87,87,87,87	0
54	MG	BA	3094	1/1	0.90	0.10	42,42,42,42	0
54	MG	CA	1607	1/1	0.90	0.09	53,53,53,53	0
54	MG	DA	3122	1/1	0.91	0.10	36,36,36,36	0
54	MG	DA	3123	1/1	0.91	0.14	62,62,62,62	0
54	MG	DA	3148	1/1	0.91	0.19	41,41,41,41	0
54	MG	AA	1643	1/1	0.91	0.16	42,42,42,42	0
54	MG	AA	1609	1/1	0.91	0.12	35,35,35,35	0
54	MG	DA	3043	1/1	0.91	0.10	68,68,68,68	0
54	MG	DA	3153	1/1	0.91	0.12	45,45,45,45	0
54	MG	BA	3195	1/1	0.91	0.57	31,31,31,31	0
54	MG	AA	1625	1/1	0.91	0.13	14,14,14,14	0
54	MG	CA	1634	1/1	0.91	0.12	51,51,51,51	0
54	MG	AA	1663	1/1	0.91	0.11	45,45,45,45	0
54	MG	BA	3015	1/1	0.91	0.09	4,4,4,4	0
54	MG	DA	3018	1/1	0.91	0.17	55,55,55,55	0
54	MG	DA	3074	1/1	0.91	0.09	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	MG	DA	3115	1/1	0.91	0.33	113,113,113,113	0
54	MG	BA	3159	1/1	0.91	0.20	8,8,8,8	0
54	MG	DA	3117	1/1	0.91	0.07	72,72,72,72	0
54	MG	BA	3017	1/1	0.91	0.14	13,13,13,13	0
54	MG	BA	3087	1/1	0.91	0.12	2,2,2,2	0
54	MG	BA	3073	1/1	0.91	0.08	12,12,12,12	0
54	MG	BA	3178	1/1	0.91	0.47	27,27,27,27	0
54	MG	AA	1601	1/1	0.92	0.10	53,53,53,53	0
54	MG	AA	1613	1/1	0.92	0.12	33,33,33,33	0
54	MG	BA	3081	1/1	0.92	0.11	18,18,18,18	0
54	MG	BA	3096	1/1	0.92	0.09	19,19,19,19	0
54	MG	DA	3105	1/1	0.92	0.21	81,81,81,81	0
54	MG	DA	3152	1/1	0.92	0.10	45,45,45,45	0
54	MG	BA	3170	1/1	0.92	0.15	36,36,36,36	0
54	MG	BA	3172	1/1	0.92	0.09	27,27,27,27	0
54	MG	DA	3108	1/1	0.92	0.19	61,61,61,61	0
54	MG	DA	3020	1/1	0.92	0.22	49,49,49,49	0
54	MG	AA	1628	1/1	0.92	0.24	59,59,59,59	0
54	MG	BA	3135	1/1	0.92	0.12	3,3,3,3	0
54	MG	BA	3190	1/1	0.92	0.14	39,39,39,39	0
54	MG	DA	3114	1/1	0.92	0.14	66,66,66,66	0
54	MG	BA	3191	1/1	0.92	0.29	12,12,12,12	0
54	MG	AA	1630	1/1	0.92	0.07	35,35,35,35	0
54	MG	BA	3016	1/1	0.92	0.34	51,51,51,51	0
54	MG	CA	1639	1/1	0.92	0.08	49,49,49,49	0
54	MG	CA	1642	1/1	0.92	0.22	25,25,25,25	0
54	MG	BA	3114	1/1	0.92	0.12	0,0,0,0	0
54	MG	BA	3151	1/1	0.92	0.20	12,12,12,12	0
54	MG	BA	3136	1/1	0.93	0.17	24,24,24,24	0
54	MG	AA	1610	1/1	0.93	0.29	65,65,65,65	0
54	MG	BA	3140	1/1	0.93	0.33	0,0,0,0	0
54	MG	AA	1603	1/1	0.93	0.14	44,44,44,44	0
54	MG	BA	3095	1/1	0.93	0.07	17,17,17,17	0
54	MG	BA	3149	1/1	0.93	0.23	44,44,44,44	0
54	MG	DA	3065	1/1	0.93	0.10	34,34,34,34	0
54	MG	DA	3139	1/1	0.93	0.26	31,31,31,31	0
54	MG	CA	1652	1/1	0.93	0.15	86,86,86,86	0
54	MG	DA	3142	1/1	0.93	0.13	34,34,34,34	0
54	MG	BA	3069	1/1	0.93	0.16	1,1,1,1	0
54	MG	BA	3156	1/1	0.93	0.35	26,26,26,26	0
54	MG	DA	3069	1/1	0.93	0.17	80,80,80,80	0
54	MG	AA	1660	1/1	0.93	0.34	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	BA	3164	1/1	0.93	0.12	4,4,4,4	0
54	MG	DA	3110	1/1	0.93	0.23	39,39,39,39	0
54	MG	BA	3031	1/1	0.93	0.10	20,20,20,20	0
54	MG	DA	3073	1/1	0.93	0.31	61,61,61,61	0
54	MG	BA	3103	1/1	0.93	0.16	0,0,0,0	0
54	MG	BA	3036	1/1	0.93	0.14	10,10,10,10	0
54	MG	DA	3036	1/1	0.93	0.17	62,62,62,62	0
54	MG	CA	1624	1/1	0.93	0.07	39,39,39,39	0
54	MG	BA	3169	1/1	0.93	0.16	29,29,29,29	0
54	MG	BA	3105	1/1	0.93	0.10	10,10,10,10	0
54	MG	BA	3040	1/1	0.93	0.14	2,2,2,2	0
54	MG	AA	1632	1/1	0.93	0.06	37,37,37,37	0
54	MG	BA	3180	1/1	0.93	0.14	29,29,29,29	0
54	MG	BA	3047	1/1	0.93	0.17	4,4,4,4	0
54	MG	BA	3012	1/1	0.93	0.08	19,19,19,19	0
54	MG	BA	3121	1/1	0.93	0.09	2,2,2,2	0
54	MG	BA	3122	1/1	0.93	0.11	25,25,25,25	0
54	MG	DB	202	1/1	0.93	0.10	64,64,64,64	0
54	MG	BA	3052	1/1	0.93	0.08	7,7,7,7	0
54	MG	CA	1601	1/1	0.93	0.11	38,38,38,38	0
54	MG	BA	3054	1/1	0.93	0.09	6,6,6,6	0
54	MG	AA	1604	1/1	0.93	0.11	56,56,56,56	0
54	MG	BA	3086	1/1	0.94	0.15	24,24,24,24	0
54	MG	BA	3161	1/1	0.94	0.16	33,33,33,33	0
54	MG	DA	3033	1/1	0.94	0.16	63,63,63,63	0
54	MG	BA	3162	1/1	0.94	0.11	21,21,21,21	0
54	MG	DA	3138	1/1	0.94	0.22	38,38,38,38	0
54	MG	AN	201	1/1	0.94	0.19	62,62,62,62	0
54	MG	BA	3032	1/1	0.94	0.18	5,5,5,5	0
54	MG	BA	3062	1/1	0.94	0.32	46,46,46,46	0
54	MG	BA	3063	1/1	0.94	0.53	52,52,52,52	0
54	MG	DA	3013	1/1	0.94	0.18	45,45,45,45	0
54	MG	BA	3002	1/1	0.94	0.06	19,19,19,19	0
54	MG	CA	1641	1/1	0.94	0.26	66,66,66,66	0
54	MG	AA	1629	1/1	0.94	0.28	79,79,79,79	0
54	MG	AA	1653	1/1	0.94	0.25	47,47,47,47	0
54	MG	BA	3014	1/1	0.94	0.14	0,0,0,0	0
54	MG	AA	1654	1/1	0.94	0.14	34,34,34,34	0
54	MG	CA	1648	1/1	0.94	0.25	19,19,19,19	0
54	MG	DA	3082	1/1	0.94	0.10	59,59,59,59	0
54	MG	BA	3141	1/1	0.94	0.14	17,17,17,17	0
54	MG	CA	1651	1/1	0.94	0.16	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	CA	1622	1/1	0.94	0.16	46,46,46,46	0
54	MG	DA	3054	1/1	0.94	0.11	48,48,48,48	0
54	MG	BA	3050	1/1	0.94	0.07	18,18,18,18	0
54	MG	DA	3160	1/1	0.94	0.26	64,64,64,64	0
54	MG	AA	1602	1/1	0.94	0.42	55,55,55,55	0
54	MG	DA	3090	1/1	0.94	0.07	84,84,84,84	0
54	MG	BA	3113	1/1	0.94	0.15	39,39,39,39	0
54	MG	BA	3150	1/1	0.94	0.14	29,29,29,29	0
54	MG	DA	3059	1/1	0.94	0.11	39,39,39,39	0
54	MG	DA	3128	1/1	0.94	0.12	79,79,79,79	0
54	MG	AA	1634	1/1	0.94	0.43	73,73,73,73	0
54	MG	BA	3152	1/1	0.94	0.18	12,12,12,12	0
54	MG	AA	1616	1/1	0.94	0.08	57,57,57,57	0
54	MG	DA	3063	1/1	0.94	0.17	50,50,50,50	0
54	MG	DA	3064	1/1	0.94	0.17	53,53,53,53	0
54	MG	AA	1670	1/1	0.95	0.39	58,58,58,58	0
54	MG	AA	1623	1/1	0.95	0.10	41,41,41,41	0
54	MG	CA	1612	1/1	0.95	0.20	46,46,46,46	0
54	MG	DA	3102	1/1	0.95	0.14	61,61,61,61	0
54	MG	BA	3171	1/1	0.95	0.15	28,28,28,28	0
54	MG	BA	3033	1/1	0.95	0.10	9,9,9,9	0
54	MG	BA	3174	1/1	0.95	0.12	14,14,14,14	0
54	MG	CA	1616	1/1	0.95	0.09	38,38,38,38	0
54	MG	BA	3035	1/1	0.95	0.15	3,3,3,3	0
54	MG	BA	3179	1/1	0.95	0.33	30,30,30,30	0
54	MG	BA	3143	1/1	0.95	0.31	22,22,22,22	0
54	MG	CA	1623	1/1	0.95	0.19	50,50,50,50	0
54	MG	BA	3181	1/1	0.95	0.14	16,16,16,16	0
54	MG	BA	3183	1/1	0.95	0.16	19,19,19,19	0
54	MG	BA	3056	1/1	0.95	0.10	2,2,2,2	0
54	MG	BA	3080	1/1	0.95	0.07	42,42,42,42	0
54	MG	BA	3112	1/1	0.95	0.06	29,29,29,29	0
54	MG	BA	3007	1/1	0.95	0.10	24,24,24,24	0
54	MG	BA	3038	1/1	0.95	0.16	31,31,31,31	0
54	MG	BB	201	1/1	0.95	0.07	31,31,31,31	0
54	MG	BB	202	1/1	0.95	0.08	6,6,6,6	0
54	MG	BB	203	1/1	0.95	0.04	8,8,8,8	0
54	MG	BB	204	1/1	0.95	0.41	12,12,12,12	0
54	MG	DA	3052	1/1	0.95	0.10	60,60,60,60	0
54	MG	BA	3115	1/1	0.95	0.14	17,17,17,17	0
54	MG	BA	3009	1/1	0.95	0.13	4,4,4,4	0
54	MG	BA	3060	1/1	0.95	0.07	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	BA	3061	1/1	0.95	0.27	40,40,40,40	0
54	MG	CA	1640	1/1	0.95	0.13	27,27,27,27	0
54	MG	BA	3020	1/1	0.95	0.07	24,24,24,24	0
54	MG	BA	3044	1/1	0.95	0.11	3,3,3,3	0
54	MG	BA	3093	1/1	0.95	0.15	57,57,57,57	0
54	MG	AA	1617	1/1	0.95	0.06	42,42,42,42	0
54	MG	DQ	201	1/1	0.95	0.27	37,37,37,37	0
54	MG	DA	3097	1/1	0.95	0.21	87,87,87,87	0
54	MG	BA	3071	1/1	0.95	0.19	66,66,66,66	0
54	MG	BA	3133	1/1	0.96	0.20	39,39,39,39	0
54	MG	BA	3097	1/1	0.96	0.06	8,8,8,8	0
54	MG	BA	3098	1/1	0.96	0.08	3,3,3,3	0
54	MG	BA	3022	1/1	0.96	0.07	16,16,16,16	0
54	MG	CA	1645	1/1	0.96	0.14	28,28,28,28	0
54	MG	BA	3043	1/1	0.96	0.12	5,5,5,5	0
54	MG	CA	1647	1/1	0.96	0.09	36,36,36,36	0
54	MG	DA	3141	1/1	0.96	0.21	39,39,39,39	0
54	MG	BA	3173	1/1	0.96	0.15	38,38,38,38	0
54	MG	BA	3138	1/1	0.96	0.37	1,1,1,1	0
54	MG	BA	3175	1/1	0.96	0.13	34,34,34,34	0
54	MG	BA	3176	1/1	0.96	0.08	28,28,28,28	0
54	MG	AA	1635	1/1	0.96	0.05	23,23,23,23	0
54	MG	CA	1654	1/1	0.96	0.19	55,55,55,55	0
54	MG	BA	3030	1/1	0.96	0.14	6,6,6,6	0
54	MG	CA	1619	1/1	0.96	0.09	34,34,34,34	0
54	MG	BA	3013	1/1	0.96	0.22	0,0,0,0	0
54	MG	BA	3145	1/1	0.96	0.27	17,17,17,17	0
54	MG	DA	3039	1/1	0.96	0.07	57,57,57,57	0
54	MG	BA	3064	1/1	0.96	0.14	1,1,1,1	0
54	MG	DA	3155	1/1	0.96	0.32	42,42,42,42	0
54	MG	BA	3066	1/1	0.96	0.14	0,0,0,0	0
54	MG	CA	1625	1/1	0.96	0.13	17,17,17,17	0
54	MG	BA	3004	1/1	0.96	0.07	22,22,22,22	0
54	MG	AA	1640	1/1	0.96	0.10	21,21,21,21	0
54	MG	BA	3192	1/1	0.96	0.18	23,23,23,23	0
54	MG	BA	3091	1/1	0.96	0.09	4,4,4,4	0
54	MG	BA	3092	1/1	0.96	0.09	21,21,21,21	0
54	MG	AA	1605	1/1	0.96	0.17	26,26,26,26	0
54	MG	BA	3157	1/1	0.96	0.07	18,18,18,18	0
54	MG	BA	3008	1/1	0.96	0.15	33,33,33,33	0
54	MG	AA	1611	1/1	0.96	0.07	20,20,20,20	0
54	MG	BA	3124	1/1	0.96	0.10	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	BA	3163	1/1	0.96	0.39	12,12,12,12	0
54	MG	BA	3021	1/1	0.96	0.27	0,0,0,0	0
54	MG	BA	3127	1/1	0.96	0.12	5,5,5,5	0
54	MG	BA	3166	1/1	0.96	0.13	23,23,23,23	0
55	DOL	BA	3001	48/48	0.96	0.20	1,7,30,58	0
54	MG	BA	3129	1/1	0.96	0.15	3,3,3,3	0
54	MG	BA	3018	1/1	0.97	0.19	0,0,0,0	0
54	MG	BA	3148	1/1	0.97	0.17	28,28,28,28	0
54	MG	BA	3070	1/1	0.97	0.14	0,0,0,0	0
54	MG	CA	1650	1/1	0.97	0.09	42,42,42,42	0
54	MG	BA	3034	1/1	0.97	0.13	2,2,2,2	0
54	MG	BA	3011	1/1	0.97	0.08	0,0,0,0	0
54	MG	BA	3074	1/1	0.97	0.12	1,1,1,1	0
54	MG	BA	3182	1/1	0.97	0.16	16,16,16,16	0
54	MG	CA	1620	1/1	0.97	0.04	61,61,61,61	0
54	MG	BA	3153	1/1	0.97	0.10	26,26,26,26	0
54	MG	BA	3186	1/1	0.97	0.20	14,14,14,14	0
54	MG	BA	3187	1/1	0.97	0.15	30,30,30,30	0
54	MG	DA	3076	1/1	0.97	0.07	66,66,66,66	0
54	MG	BA	3188	1/1	0.97	0.14	6,6,6,6	0
54	MG	BA	3154	1/1	0.97	0.14	12,12,12,12	0
54	MG	BA	3155	1/1	0.97	0.10	18,18,18,18	0
54	MG	BA	3055	1/1	0.97	0.18	0,0,0,0	0
54	MG	DA	3154	1/1	0.97	0.45	57,57,57,57	0
54	MG	BA	3003	1/1	0.97	0.08	18,18,18,18	0
54	MG	BA	3193	1/1	0.97	0.21	32,32,32,32	0
54	MG	BA	3158	1/1	0.97	0.25	22,22,22,22	0
54	MG	BA	3077	1/1	0.97	0.13	12,12,12,12	0
54	MG	BA	3160	1/1	0.97	0.10	3,3,3,3	0
54	MG	AA	1648	1/1	0.97	0.16	33,33,33,33	0
54	MG	BA	3023	1/1	0.97	0.08	1,1,1,1	0
54	MG	BA	3132	1/1	0.97	0.16	27,27,27,27	0
54	MG	BA	3026	1/1	0.97	0.11	3,3,3,3	0
54	MG	BA	3102	1/1	0.97	0.08	9,9,9,9	0
54	MG	AA	1649	1/1	0.97	0.14	32,32,32,32	0
54	MG	AA	1620	1/1	0.97	0.06	30,30,30,30	0
54	MG	BA	3045	1/1	0.97	0.06	27,27,27,27	0
54	MG	BA	3106	1/1	0.97	0.18	5,5,5,5	0
54	MG	BA	3107	1/1	0.97	0.19	0,0,0,0	0
54	MG	BA	3110	1/1	0.97	0.20	4,4,4,4	0
54	MG	BA	3046	1/1	0.97	0.15	6,6,6,6	0
54	MG	AA	1615	1/1	0.97	0.11	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	AA	1652	1/1	0.97	0.18	18,18,18,18	0
54	MG	AA	1636	1/1	0.98	0.09	17,17,17,17	0
54	MG	BQ	201	1/1	0.98	0.14	7,7,7,7	0
54	MG	BA	3177	1/1	0.98	0.19	12,12,12,12	0
54	MG	BA	3118	1/1	0.98	0.12	4,4,4,4	0
54	MG	AA	1655	1/1	0.98	0.11	44,44,44,44	0
54	MG	BA	3025	1/1	0.98	0.17	2,2,2,2	0
54	MG	BA	3139	1/1	0.98	0.36	0,0,0,0	0
54	MG	BA	3048	1/1	0.98	0.16	9,9,9,9	0
54	MG	AA	1646	1/1	0.98	0.07	54,54,54,54	0
54	MG	BA	3185	1/1	0.98	0.11	13,13,13,13	0
54	MG	DA	3050	1/1	0.98	0.10	48,48,48,48	0
54	MG	DA	3051	1/1	0.98	0.10	32,32,32,32	0
54	MG	BA	3142	1/1	0.98	0.37	0,0,0,0	0
54	MG	BA	3123	1/1	0.98	0.18	0,0,0,0	0
54	MG	AA	1621	1/1	0.98	0.17	19,19,19,19	0
54	MG	BA	3072	1/1	0.98	0.08	7,7,7,7	0
54	MG	BA	3126	1/1	0.98	0.17	4,4,4,4	0
54	MG	BA	3084	1/1	0.98	0.08	16,16,16,16	0
54	MG	BA	3128	1/1	0.98	0.07	0,0,0,0	0
54	MG	BA	3051	1/1	0.98	0.12	1,1,1,1	0
54	MG	DA	3086	1/1	0.98	0.10	74,74,74,74	0
54	MG	BA	3130	1/1	0.98	0.14	0,0,0,0	0
54	MG	CA	1618	1/1	0.98	0.16	35,35,35,35	0
54	MG	BA	3131	1/1	0.98	0.24	1,1,1,1	0
54	MG	BA	3029	1/1	0.98	0.13	23,23,23,23	0
54	MG	BA	3099	1/1	0.98	0.04	5,5,5,5	0
54	MG	BA	3053	1/1	0.98	0.10	6,6,6,6	0
56	ZN	D4	101	1/1	0.98	0.06	91,91,91,91	0
54	MG	BA	3065	1/1	0.99	0.17	1,1,1,1	0
54	MG	BA	3144	1/1	0.99	0.28	6,6,6,6	0
54	MG	BA	3019	1/1	0.99	0.07	14,14,14,14	0
54	MG	BA	3088	1/1	0.99	0.21	2,2,2,2	0
54	MG	BA	3067	1/1	0.99	0.11	1,1,1,1	0
54	MG	BA	3117	1/1	0.99	0.16	2,2,2,2	0
54	MG	BA	3068	1/1	0.99	0.14	1,1,1,1	0
54	MG	BA	3024	1/1	0.99	0.12	0,0,0,0	0
54	MG	BA	3010	1/1	0.99	0.09	0,0,0,0	0
54	MG	BA	3184	1/1	0.99	0.16	3,3,3,3	0
54	MG	BA	3006	1/1	0.99	0.10	43,43,43,43	0
54	MG	BA	3041	1/1	0.99	0.14	2,2,2,2	0
54	MG	BA	3083	1/1	0.99	0.14	2,2,2,2	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
54	MG	BA	3109	1/1	0.99	0.16	6,6,6,6	0
54	MG	AA	1641	1/1	0.99	0.07	24,24,24,24	0
54	MG	BA	3111	1/1	0.99	0.15	4,4,4,4	0
54	MG	BA	3028	1/1	0.99	0.04	6,6,6,6	0
54	MG	BA	3037	1/1	1.00	0.16	0,0,0,0	0
54	MG	BA	3039	1/1	1.00	0.23	0,0,0,0	0
56	ZN	B4	101	1/1	1.00	0.06	36,36,36,36	0
54	MG	BA	3108	1/1	1.00	0.20	1,1,1,1	0

6.5 Other polymers [i](#)

There are no such residues in this entry.