



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2026 – 12:06 PM EDT

PDB ID : 5J8A / pdb_00005j8a
Title : Structure of the E coli 70S ribosome with the U1052G mutation in 16S rRNA bound to tigecycline
Authors : Cocozaki, A.; Ferguson, A.
Deposited on : 2016-04-07
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

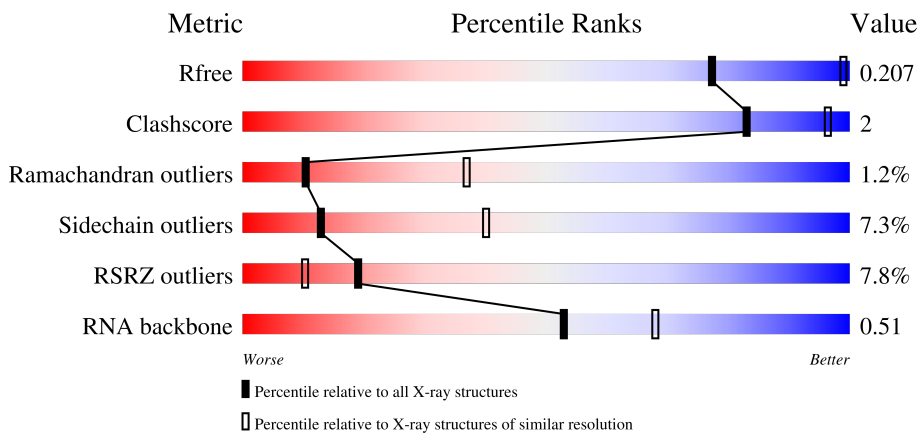
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

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	1534	 5% 76% 21%
1	BA	1534	 6% 75% 23%
2	AB	224	 4% 85% 12%
2	BB	224	 7% 86% 12%

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Mol	Chain	Length	Quality of chain
3	AC	206	3% 84% 15%
3	BC	206	8% 82% 17%
4	AD	205	88% 10%
4	BD	205	85% 13%
5	AE	155	77% 21%
5	BE	155	3% 68% 23% 6%
6	AF	106	% 80% 20%
6	BF	106	3% 70% 23% 6%
7	AG	151	13% 85% 13%
7	BG	151	23% 85% 15%
8	AH	129	3% 76% 22%
8	BH	129	5% 77% 22%
9	AI	127	16% 84% 14%
9	BI	127	21% 83% 16%
10	AJ	99	21% 80% 17%
10	BJ	99	30% 73% 20% 6%
11	AK	117	3% 85% 15%
11	BK	117	8% 78% 20%
12	AL	123	2% 85% 15%
12	BL	123	8% 80% 16%
13	AM	114	20% 76% 20%
13	BM	114	12% 73% 21% 5%
14	AN	100	27% 87% 12%
14	BN	100	17% 89% 11%
15	AO	88	2% 94% 6%

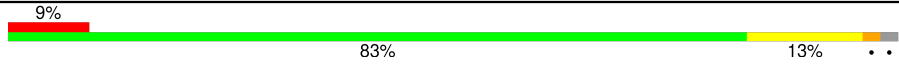














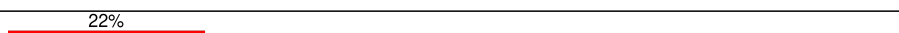
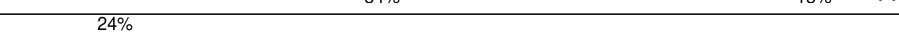








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Mol	Chain	Length	Quality of chain
15	BO	88	95% ..
16	AP	82	80% 20% ..
16	BP	82	74% 23% .
17	AQ	80	79% 19% .
17	BQ	80	64% 31% ..
18	AR	55	84% 15% .
18	BR	55	87% 13% ..
19	AS	79	81% 18% .
19	BS	79	84% 13% ..
20	AT	86	92% 7% .
20	BT	86	74% 15% 8% ..
21	AU	56	80% 20% ..
21	BU	56	82% 18% ..
22	C1	56	84% 12% .
22	D1	56	82% 16% .
23	C2	51	63% 33% ..
23	D2	51	71% 25% .
24	C3	46	85% 13% .
24	D3	46	91% 9% ..
25	C4	64	94% 6% ..
25	D4	64	95% 5% ..
26	C5	38	71% 29% ..
26	D5	38	87% 13% ..
27	C0	58	74% 22% .
27	D0	58	93% 5% .

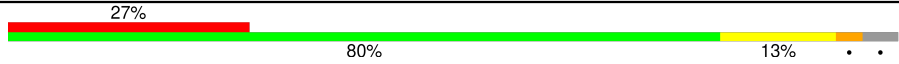
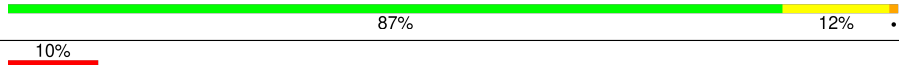
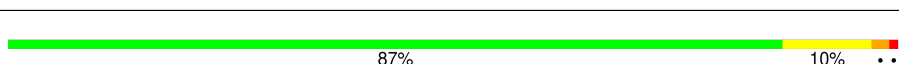
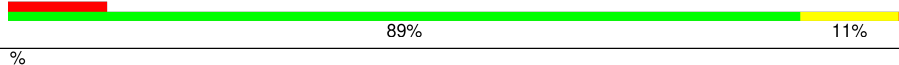
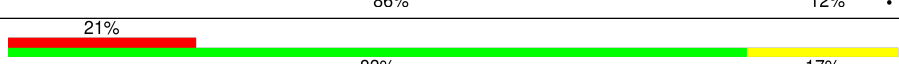




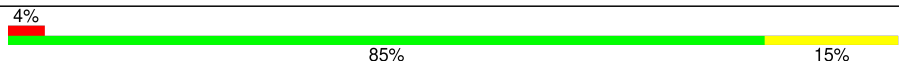

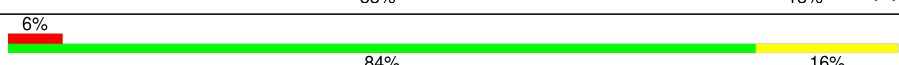




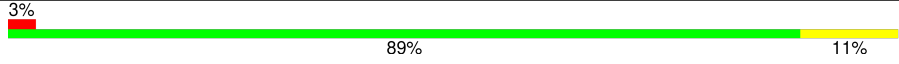



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Mol	Chain	Length	Quality of chain
28	CB	120	
28	DB	120	
29	CC	272	
29	DC	272	
30	CD	209	
31	CA	2904	
32	DD	209	
33	CE	201	
33	DE	201	
34	CF	178	
34	DF	178	
35	CG	176	
35	DG	176	
36	CH	149	
36	DH	149	
37	CJ	135	
37	DJ	135	
38	CK	142	
38	DK	142	
39	CL	123	
39	DL	123	
40	CM	144	
40	DM	144	
41	CN	136	
41	DN	136	

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Mol	Chain	Length	Quality of chain
42	CO	125	
42	DO	125	
43	CP	117	
43	DP	117	
44	CQ	114	
44	DQ	114	
45	CR	117	
45	DR	117	
46	CS	103	
46	DS	103	
47	CT	110	
47	DT	110	
48	CU	93	
48	DU	93	
49	CV	103	
49	DV	103	
50	CW	94	
50	DW	94	
51	CX	83	
51	DX	83	
52	CY	77	
52	DY	77	
53	CZ	62	
53	DZ	62	
54	DI	135	

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Mol	Chain	Length	Quality of chain
55	DA	2904	

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
56	MG	BA	1640	-	-	-	X
56	MG	CA	3021	-	-	-	X
56	MG	CA	3122	-	-	-	X
56	MG	CA	3147	-	-	-	X
56	MG	CA	3148	-	-	-	X
59	PUT	AA	1672	-	-	-	X
67	ACY	DA	3196	-	X	-	-

2 Entry composition [i](#)

There are 70 unique types of molecules in this entry. The entry contains 295207 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	1534	Total	C	N	O	P	0	0	0
			32933	14695	6044	10660	1534			
1	BA	1533	Total	C	N	O	P	0	0	0
			32911	14685	6039	10654	1533			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	1052	G	U	engineered mutation	GB 675819282
BA	1052	G	U	engineered mutation	GB 675819282

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	AB	224	Total	C	N	O	S	0	0	0
			1753	1109	315	321	8			
2	BB	224	Total	C	N	O	S	0	0	0
			1753	1109	315	321	8			

- 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	BC	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			

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	AE	155	1144	711	216	211	6	0	0	0
5	BE	150	1105	687	211	201	6	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	AF	106	862	545	156	154	7	0	0	0
6	BF	100	817	515	148	148	6	0	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	AJ	99	Total 796	C 498	N 152	O 145	S 1	0	0	0
10	BJ	98	Total 787	C 493	N 150	O 143	S 1	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	AL	123	Total 957	C 591	N 196	O 165	S 5	0	0	0
12	BL	123	Total 957	C 591	N 196	O 165	S 5	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	AN	100	Total 805	C 499	N 164	O 139	S 3	0	0	0
14	BN	100	Total 805	C 499	N 164	O 139	S 3	0	0	0

- 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
			714	439	144	130	1			
15	BO	88	Total	C	N	O	S	0	0	0
			714	439	144	130	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	BP	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	BQ	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	BR	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	BS	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	86	Total	C	N	O	S	0	0	0
			670	414	138	115	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BT	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	56	Total	C	N	O	S	0	0	0
			465	290	96	78	1			
21	BU	56	Total	C	N	O	S	0	0	0
			465	290	96	78	1			

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	C1	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			
22	D1	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			

- Molecule 23 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	C2	50	Total	C	N	O	0	0	0
			409	263	75	71			
23	D2	51	Total	C	N	O	0	0	0
			414	266	76	72			

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	C3	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			
24	D3	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	C4	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			
25	D4	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			

- Molecule 26 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
26	C5	38	Total 302	C 185	N 65	O 48	S 4	0	0	0
26	D5	38	Total 302	C 185	N 65	O 48	S 4	0	0	0

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
27	C0	58	Total 449	C 281	N 87	O 79	S 2	0	0	0
27	D0	58	Total 463	C 290	N 90	O 81	S 2	0	2	0

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
28	CB	118	Total 2529	C 1126	N 464	O 821	P 118	0	0	0
28	DB	120	Total 2569	C 1144	N 468	O 837	P 120	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
29	CC	271	Total 2082	C 1288	N 423	O 364	S 7	0	0	0
29	DC	271	Total 2082	C 1288	N 423	O 364	S 7	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
30	CD	209	Total 1565	C 979	N 288	O 294	S 4	0	0	0

- Molecule 31 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
31	CA	2898	Total 62229	C 27768	N 11448	O 20115	P 2898	0	0	0

- Molecule 32 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
32	DD	209	1576	986	290	296	4	0	1	0

- Molecule 33 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
33	CE	201	1552	974	283	290	5	0	0	0
33	DE	201	1551	974	283	289	5	0	0	0

- Molecule 34 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
34	CF	177	1410	899	249	256	6	0	0	0
34	DF	177	1410	899	249	256	6	0	0	0

- Molecule 35 is a protein called 50S ribosomal protein L6.

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

- Molecule 36 is a protein called 50S ribosomal protein L9.

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
37	CJ	134	979	619	169	185	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
37	DJ	134	979	619	169	185	6	0	0	0

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
38	CK	142	1129	714	212	199	4	0	0	0
38	DK	142	1129	714	212	199	4	0	0	0

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
39	CL	122	938	587	180	165	6	0	0	0
39	DL	123	946	593	181	166	6	0	0	0

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
40	CM	144	1053	654	207	190	2	0	0	0
40	DM	144	1053	654	207	190	2	0	0	0

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
41	CN	136	1075	686	205	178	6	0	0	0
41	DN	136	1092	696	211	179	6	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CN	81	4D4	ARG	conflict	UNP P0ADY7
DN	81	4D4	ARG	conflict	UNP P0ADY7

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	CO	120	Total	C	N	O	S	0	0	0
			960	593	196	166	5			
42	DO	125	Total	C	N	O	S	0	0	0
			993	613	202	173	5			

- Molecule 43 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	CP	116	Total	C	N	O		0	0	0
			892	552	178	162				
43	DP	117	Total	C	N	O	S	0	0	0
			900	557	179	163	1			

- Molecule 44 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	CQ	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			
44	DQ	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
45	CR	117	Total	C	N	O		0	0	0
			947	604	192	151				
45	DR	117	Total	C	N	O		0	0	0
			947	604	192	151				

- Molecule 46 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	CS	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			
46	DS	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	CT	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
47	DT	110	857	532	166	156	3	0	0	0

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
48	CU	93	739	466	139	132	2	0	0	0
48	DU	93	738	466	139	131	2	0	0	0

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				
49	CV	102	779	492	146	141		0	0	0
49	DV	102	779	492	146	141		0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
50	CW	94	753	479	137	134	3	0	0	0
50	DW	94	753	479	137	134	3	0	0	0

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
51	CX	75	569	353	113	102	1	0	0	0
51	DX	76	591	365	121	104	1	0	1	0

- Molecule 52 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
52	CY	77	625	388	129	106	2	0	0	0
52	DY	77	625	388	129	106	2	0	0	0

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
53	CZ	62	501	308	98	94	1	0	0	0
53	DZ	62	501	308	98	94	1	0	0	0

- Molecule 54 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
54	DI	135	1023	649	179	192	3	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DI	85	VAL	SER	conflict	UNP P0A7J3
DI	86	THR	MET	conflict	UNP P0A7J3

- Molecule 55 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
55	DA	2897	62423	27855	11485	20176	2907	0	11	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

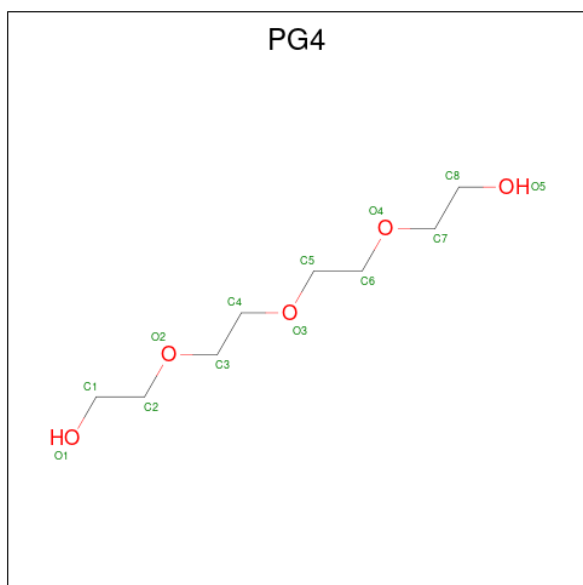
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	72	Total 72	Mg 72	0	0
56	BA	45	Total 45	Mg 45	0	0
56	CB	3	Total 3	Mg 3	0	0
56	CA	156	Total 156	Mg 156	0	0
56	DD	1	Total 1	Mg 1	0	0
56	DM	1	Total 1	Mg 1	0	0
56	DR	1	Total 1	Mg 1	0	0

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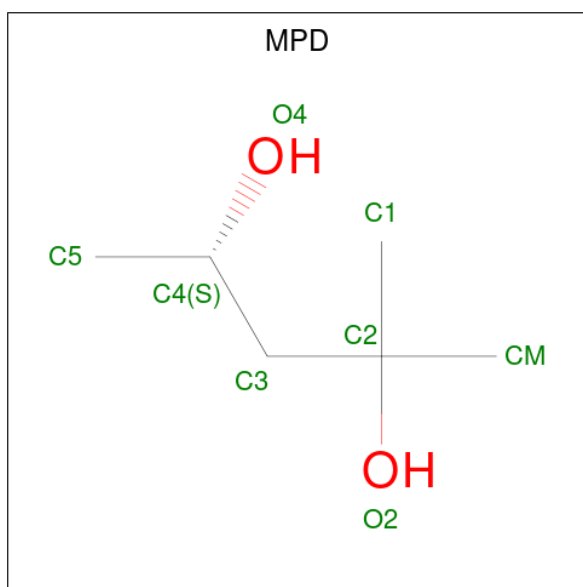
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	DB	9	Total Mg 9 9	0	0
56	DA	184	Total Mg 184 184	0	0

- Molecule 57 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



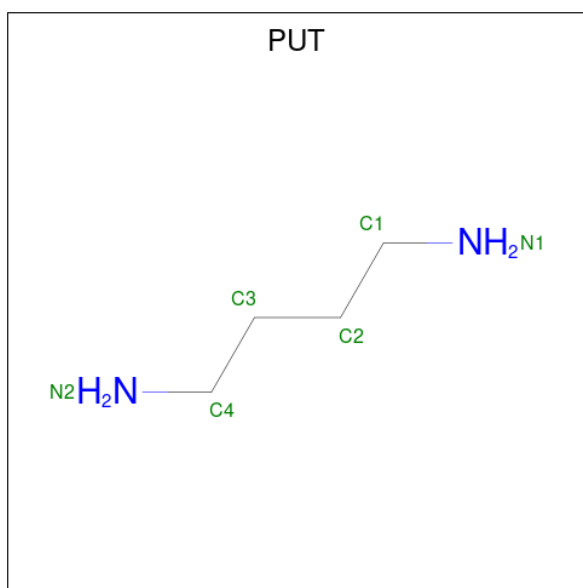
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AA	1	Total C O 13 8 5	0	0
57	BA	1	Total C O 13 8 5	0	0
57	DQ	1	Total C O 13 8 5	0	0
57	DR	1	Total C O 13 8 5	0	0
57	DS	1	Total C O 13 8 5	0	0
57	DA	1	Total C O 13 8 5	0	0
57	DA	1	Total C O 13 8 5	0	0

- Molecule 58 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	AA	1	Total C O 8 6 2	0	0
58	AA	1	Total C O 8 6 2	0	0
58	DE	1	Total C O 8 6 2	0	0
58	DE	1	Total C O 8 6 2	0	0
58	DK	1	Total C O 8 6 2	0	0
58	DN	1	Total C O 8 6 2	0	0
58	DS	1	Total C O 8 6 2	0	0
58	DT	1	Total C O 8 6 2	0	0
58	DT	1	Total C O 8 6 2	0	0
58	DA	1	Total C O 8 6 2	0	0
58	DA	1	Total C O 8 6 2	0	0
58	DA	1	Total C O 8 6 2	0	0
58	DA	1	Total C O 8 6 2	0	0
58	DA	1	Total C O 8 6 2	0	0

- Molecule 59 is 1,4-DIAMINOBTUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



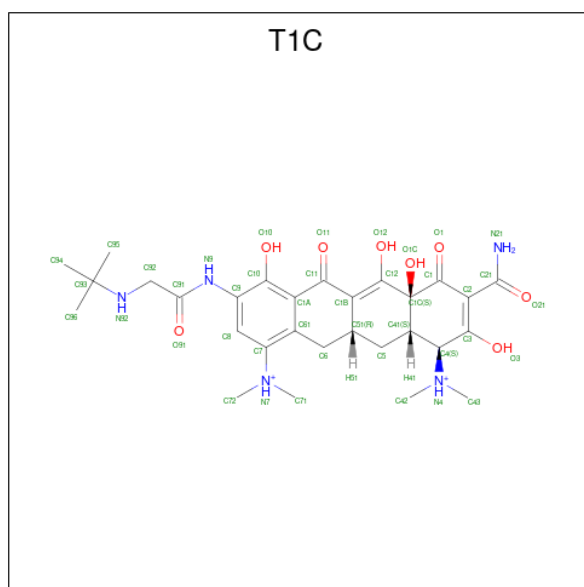
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
59	DA	1	Total	C	N	0	0
			6	4	2		
59	DA	1	Total	C	N	0	0
			6	4	2		
59	DA	1	Total	C	N	0	0
			6	4	2		

- Molecule 60 is TIGECYCLINE (CCD ID: T1C) (formula: C₂₉H₄₁N₅O₈).

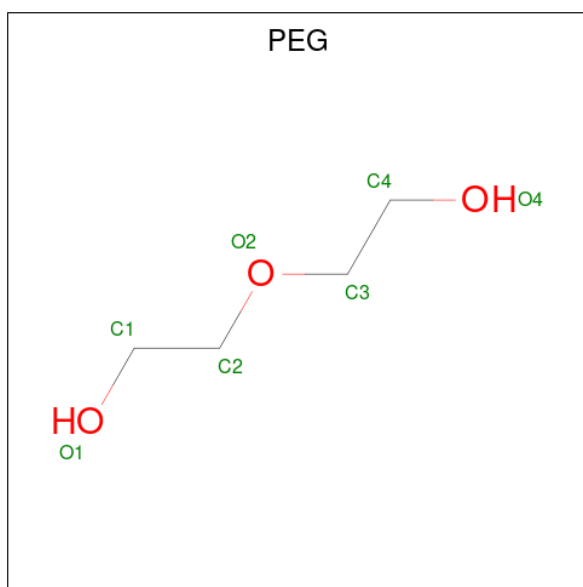


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
60	AA	1	Total	C	N	O	0	0
			42	29	5	8		
60	BA	1	Total	C	N	O	0	0
			42	29	5	8		

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

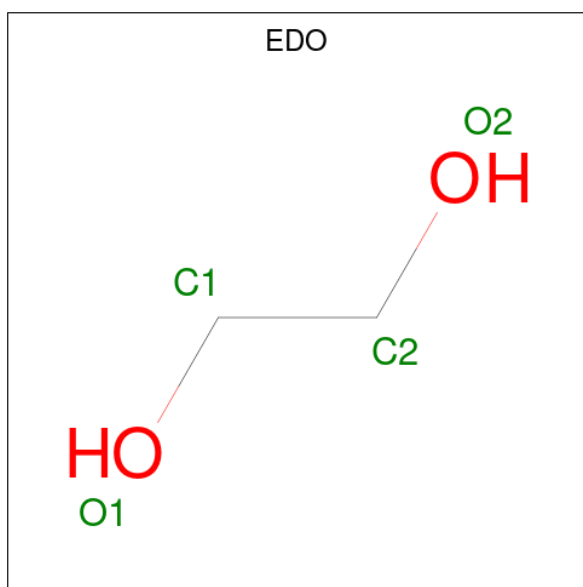
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AB	1	Total	Zn	0	0
			1	1		
61	C5	1	Total	Zn	0	0
			1	1		
61	D5	1	Total	Zn	0	0
			1	1		

- Molecule 62 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



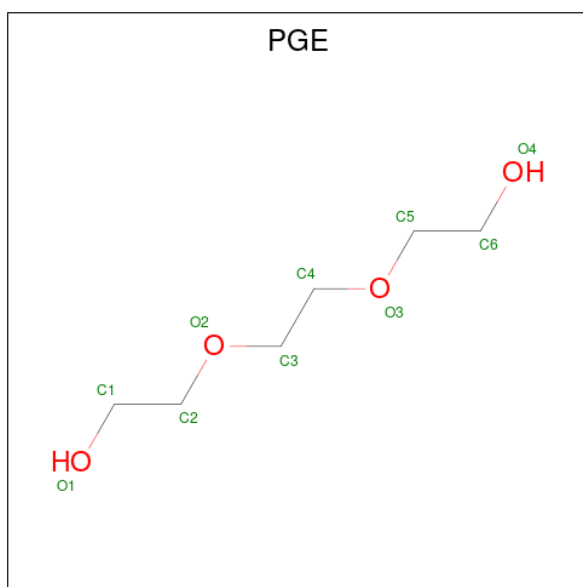
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	AL	1	Total C O 7 4 3	0	0
62	D1	1	Total C O 7 4 3	0	0
62	D3	1	Total C O 7 4 3	0	0
62	DL	1	Total C O 7 4 3	0	0
62	DP	1	Total C O 7 4 3	0	0
62	DQ	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0

- Molecule 63 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



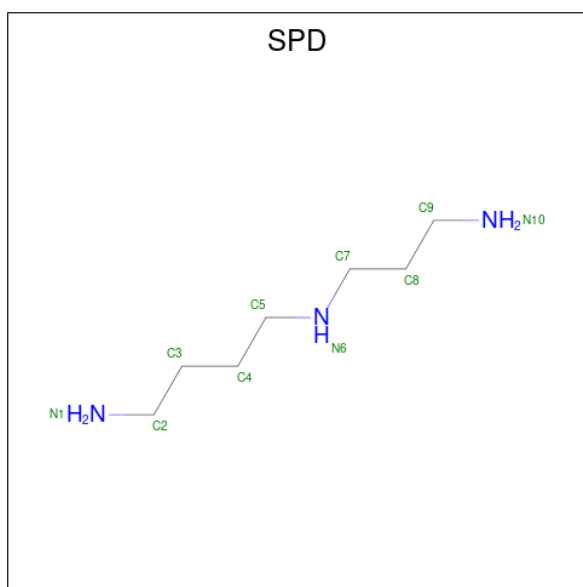
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	D1	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0

- Molecule 64 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



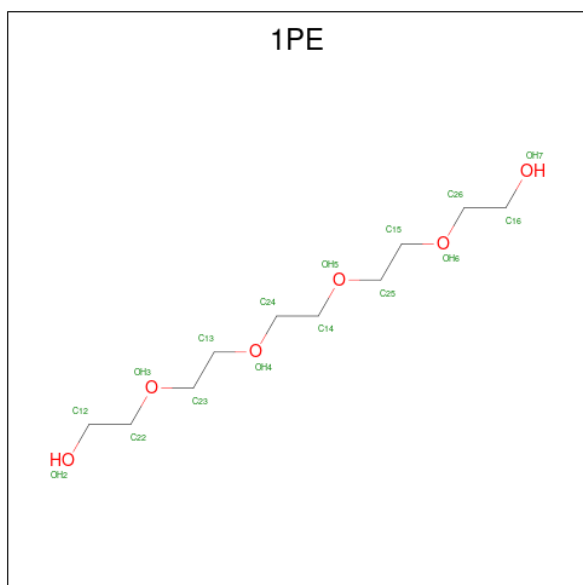
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	D1	1	Total C O 10 6 4	0	0
64	D3	1	Total C O 10 6 4	0	0
64	DS	1	Total C O 10 6 4	0	0
64	DU	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0

- Molecule 65 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



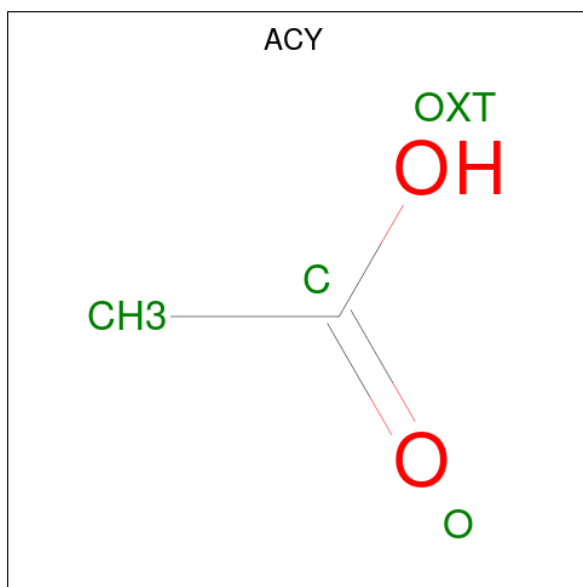
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
65	DA	1	Total	C	N	0	0
			10	7	3		
65	DA	1	Total	C	N	0	0
			10	7	3		
65	DA	1	Total	C	N	0	0
			10	7	3		
65	DA	1	Total	C	N	0	0
			10	7	3		

- Molecule 66 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆).



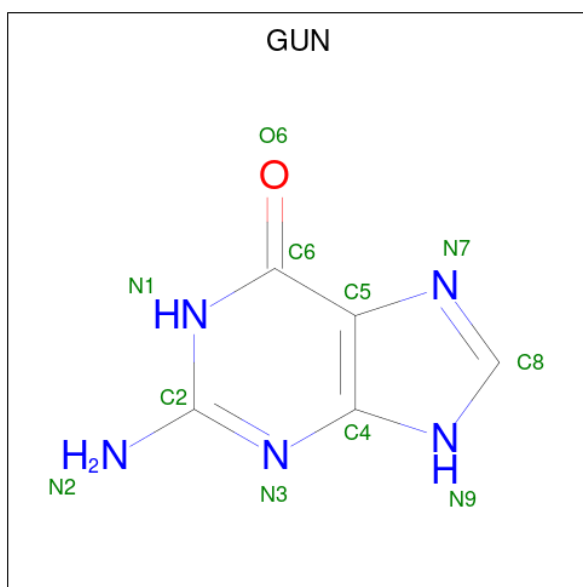
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
66	DA	1	Total	C	O	0	0
			16	10	6		
66	DA	1	Total	C	O	0	0
			16	10	6		

- Molecule 67 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



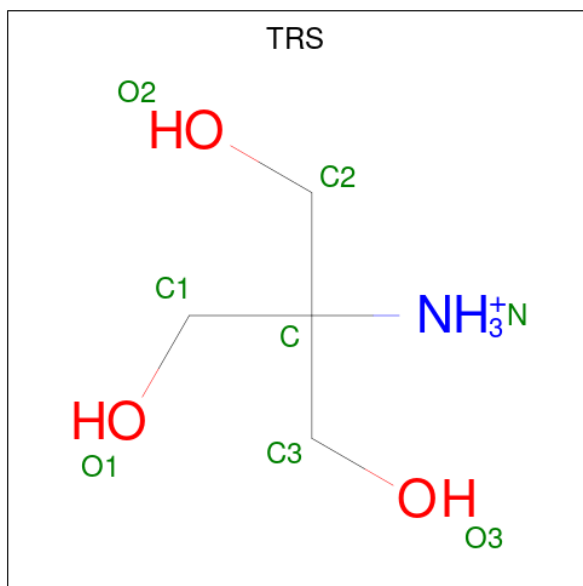
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
67	DA	1	Total	C	O	0	0
			4	2	2		
67	DA	1	Total	C	O	0	0
			4	2	2		
67	DA	1	Total	C	O	0	0
			4	2	2		

- Molecule 68 is GUANINE (CCD ID: GUN) (formula: C₅H₅N₅O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
68	DA	1	11	5	5	1	0	0

- Molecule 69 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
69	DA	1	8	4	1	3	0	0

- Molecule 70 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
70	AA	500	Total 500	O 500	0	0
70	AC	5	Total 5	O 5	0	0
70	AD	2	Total 2	O 2	0	0
70	AE	4	Total 4	O 4	0	0
70	AF	1	Total 1	O 1	0	0
70	AG	1	Total 1	O 1	0	0
70	AH	1	Total 1	O 1	0	0
70	AJ	2	Total 2	O 2	0	0
70	AK	6	Total 6	O 6	0	0
70	AL	10	Total 10	O 10	0	0
70	AM	4	Total 4	O 4	0	0
70	AN	7	Total 7	O 7	0	0
70	AO	2	Total 2	O 2	0	0
70	AP	2	Total 2	O 2	0	0
70	AR	1	Total 1	O 1	0	0
70	AT	3	Total 3	O 3	0	0
70	AU	2	Total 2	O 2	0	0
70	C3	3	Total 3	O 3	0	0
70	C4	1	Total 1	O 1	0	0
70	BA	288	Total 288	O 288	0	0
70	BD	12	Total 12	O 12	0	0
70	BE	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
70	BF	2	Total 2	O 2	0	0
70	BK	2	Total 2	O 2	0	0
70	BL	2	Total 2	O 2	0	0
70	BN	2	Total 2	O 2	0	0
70	BO	1	Total 1	O 1	0	0
70	BP	3	Total 3	O 3	0	0
70	BT	4	Total 4	O 4	0	0
70	BU	1	Total 1	O 1	0	0
70	D1	45	Total 45	O 45	0	0
70	D2	7	Total 7	O 7	0	0
70	D3	23	Total 23	O 23	0	0
70	D4	39	Total 39	O 39	0	0
70	D5	12	Total 12	O 12	0	0
70	D0	21	Total 21	O 21	0	0
70	CB	13	Total 13	O 13	0	0
70	CC	12	Total 12	O 12	0	0
70	CD	6	Total 6	O 6	0	0
70	CA	692	Total 692	O 692	0	0
70	DC	104	Total 104	O 104	0	0
70	DD	92	Total 92	O 92	0	0
70	CE	4	Total 4	O 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
70	CL	1	Total 1	O 1	0	0
70	CM	4	Total 4	O 4	0	0
70	CO	1	Total 1	O 1	0	0
70	CU	3	Total 3	O 3	0	0
70	CV	1	Total 1	O 1	0	0
70	CW	1	Total 1	O 1	0	0
70	CY	1	Total 1	O 1	0	0
70	DE	60	Total 60	O 60	0	0
70	DF	15	Total 15	O 15	0	0
70	DG	6	Total 6	O 6	0	0
70	DH	2	Total 2	O 2	0	0
70	DK	64	Total 64	O 64	0	0
70	DL	51	Total 51	O 51	0	0
70	DM	64	Total 64	O 64	0	0
70	DN	73	Total 73	O 73	0	0
70	DO	46	Total 46	O 46	0	0
70	DP	40	Total 40	O 40	0	0
70	DQ	32	Total 32	O 32	0	0
70	DR	63	Total 63	O 63	0	0
70	DS	44	Total 44	O 44	0	0
70	DT	69	Total 69	O 69	0	0

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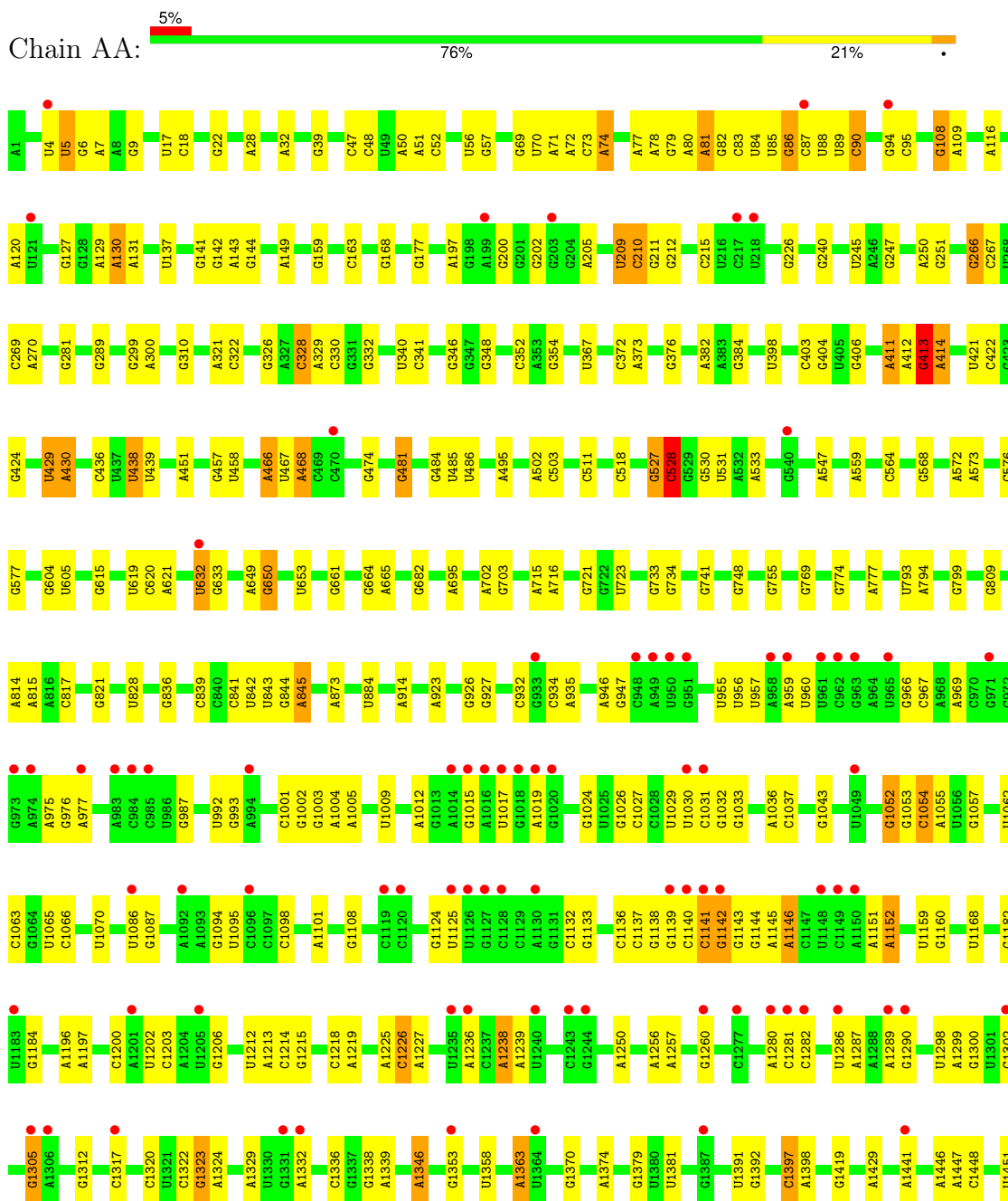
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
70	DU	21	Total O 21 21	0	0
70	DV	20	Total O 20 20	0	0
70	DW	31	Total O 31 31	0	0
70	DX	26	Total O 26 26	0	0
70	DY	11	Total O 11 11	0	0
70	DZ	7	Total O 7 7	0	0
70	DB	213	Total O 213 213	0	0
70	DA	4829	Total O 4829 4829	0	0

3 Residue-property plots [i](#)

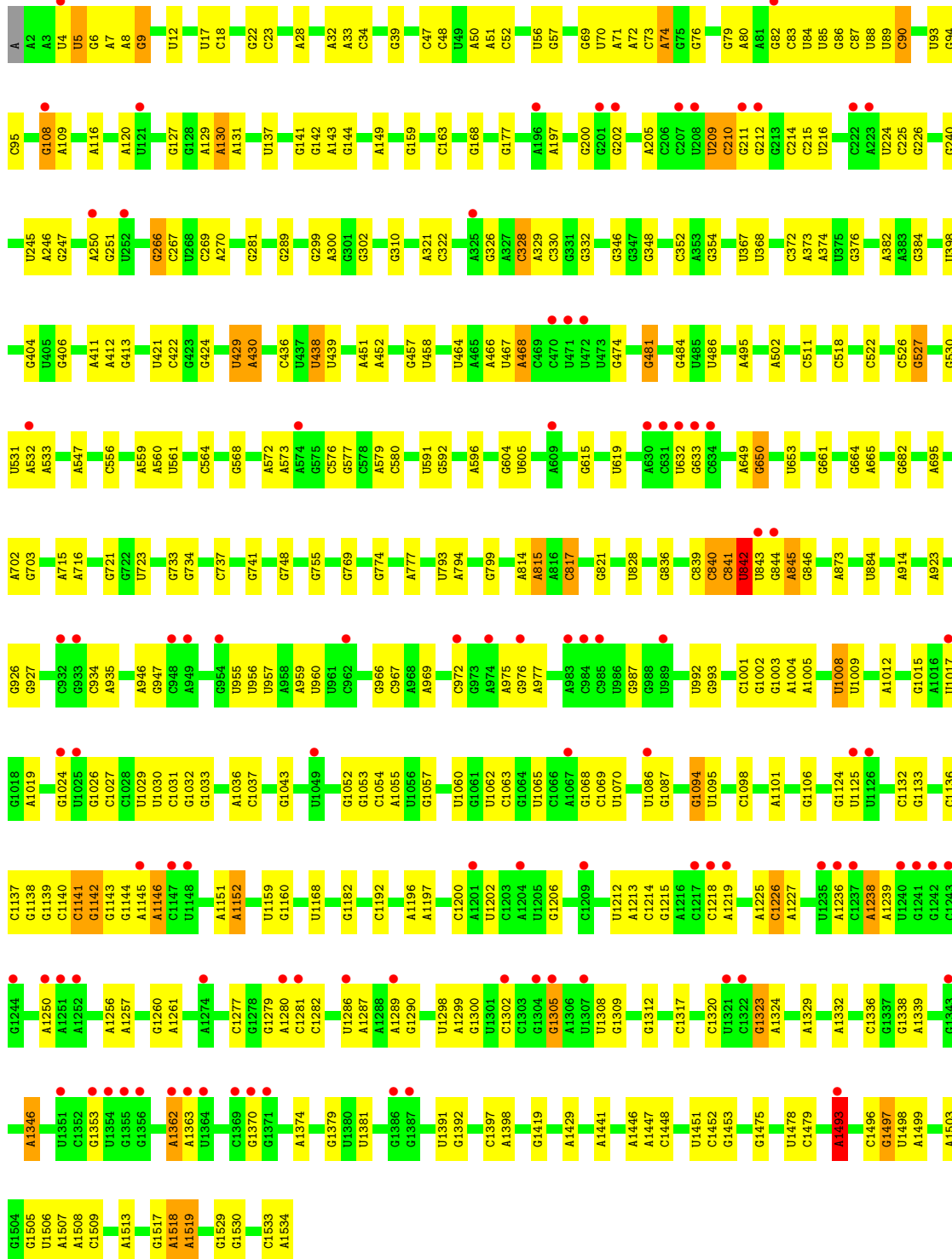
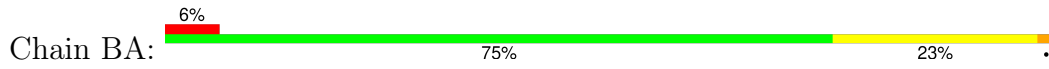
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 16S rRNA

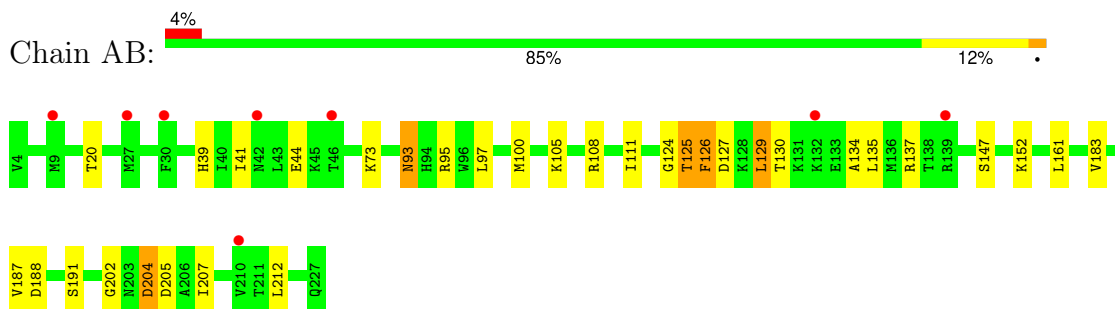




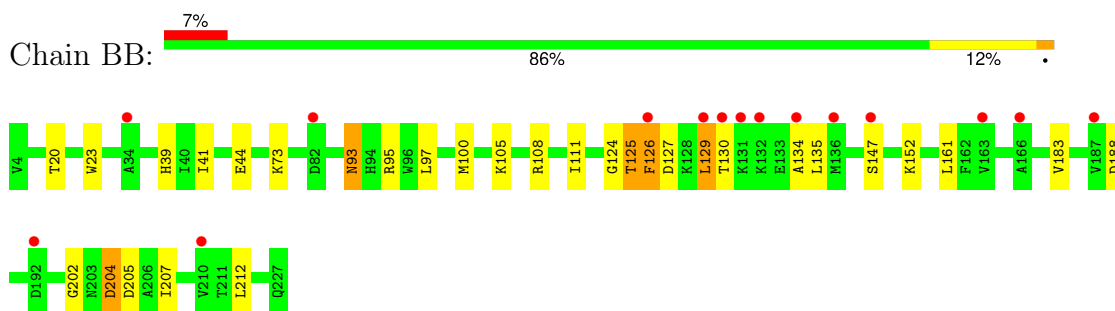
• Molecule 1: 16S rRNA



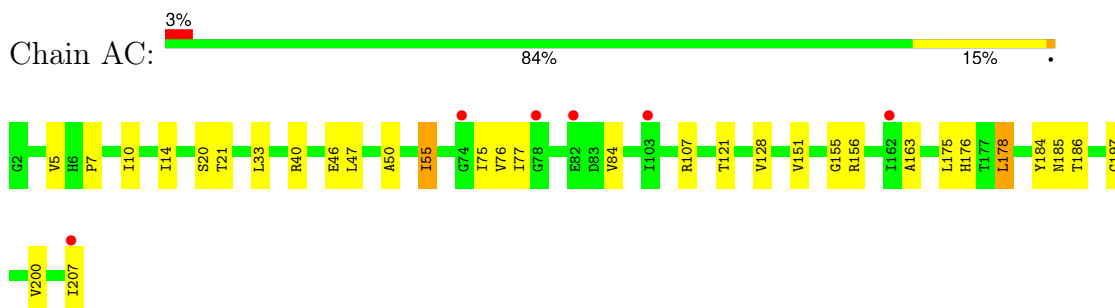
- Molecule 2: 30S ribosomal protein S2



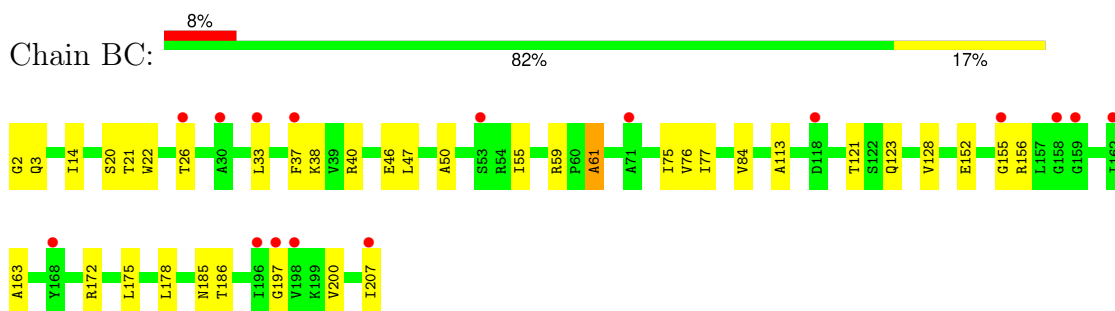
- Molecule 2: 30S ribosomal protein S2



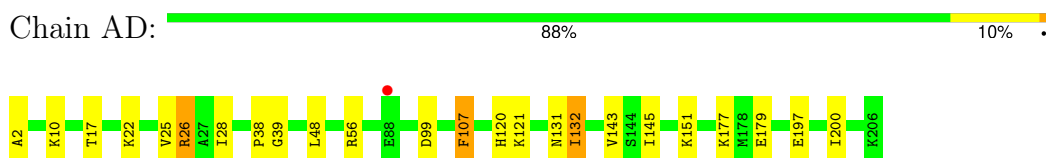
- Molecule 3: 30S ribosomal protein S3




- Molecule 3: 30S ribosomal protein S3



- Molecule 4: 30S ribosomal protein S4




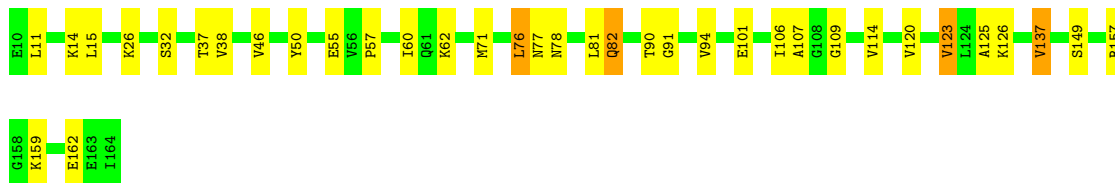
- Molecule 4: 30S ribosomal protein S4

Chain BD:  85% 13%



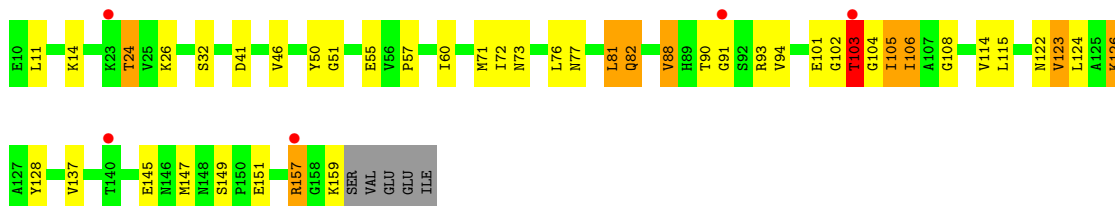
- Molecule 5: 30S ribosomal protein S5

Chain AE:  77% 21%




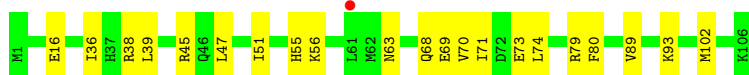
- Molecule 5: 30S ribosomal protein S5

Chain BE:  3% 68% 23% 6%



- Molecule 6: 30S ribosomal protein S6

Chain AF:  3% 80% 20%




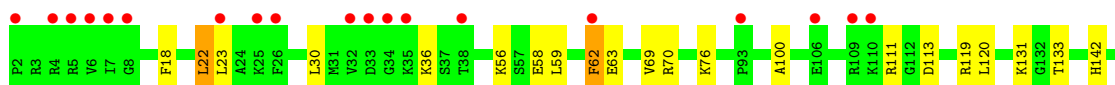
- Molecule 6: 30S ribosomal protein S6

Chain BF:  3% 70% 23% 6%



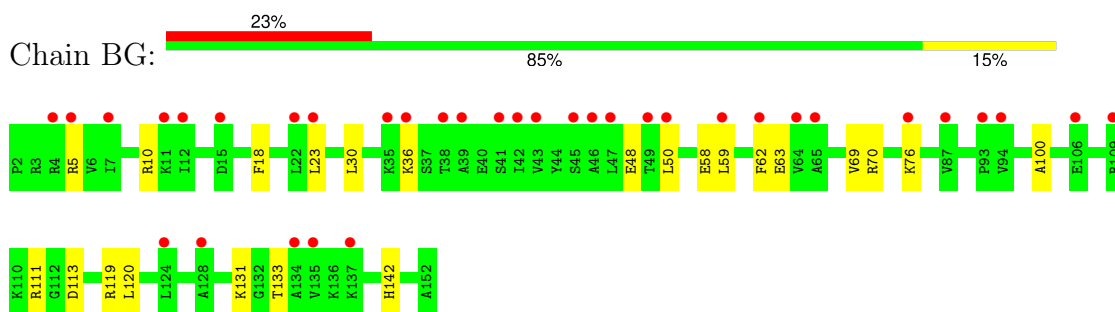
- Molecule 7: 30S ribosomal protein S7

Chain AG:  13% 85% 13%

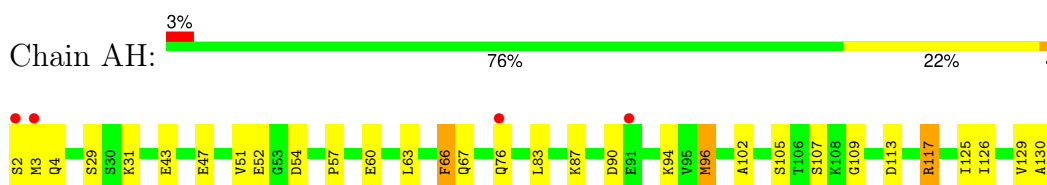


F161
A162

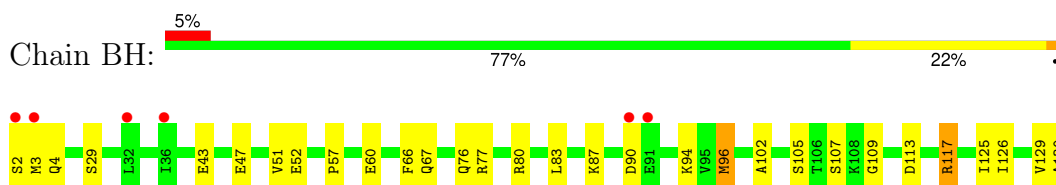
- Molecule 7: 30S ribosomal protein S7



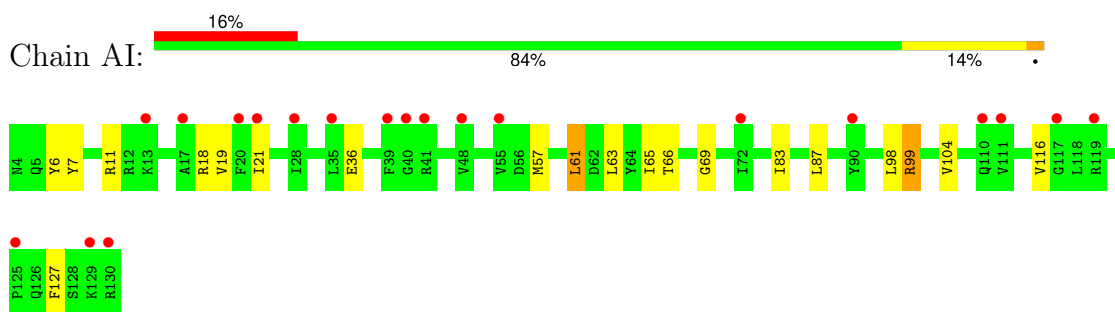
- Molecule 8: 30S ribosomal protein S8



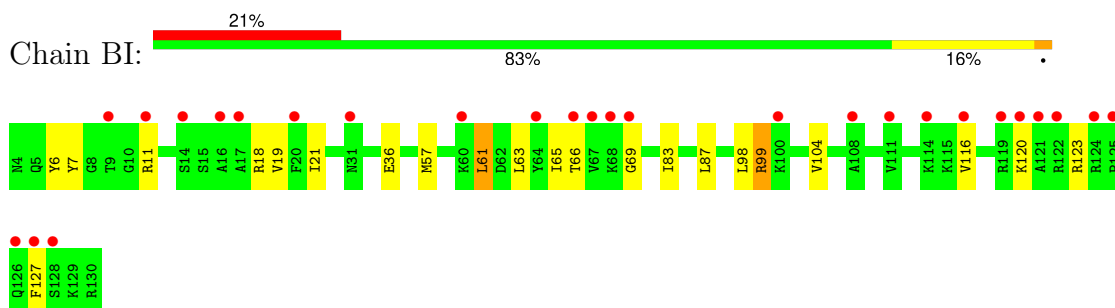
- Molecule 8: 30S ribosomal protein S8



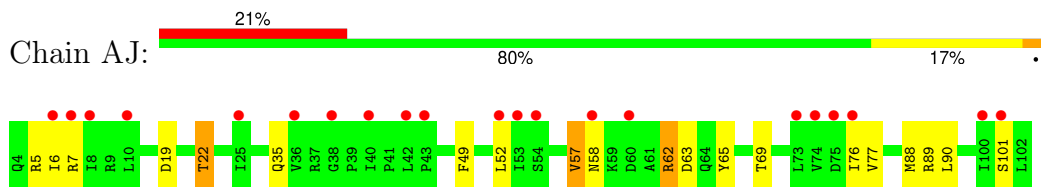
- Molecule 9: 30S ribosomal protein S9



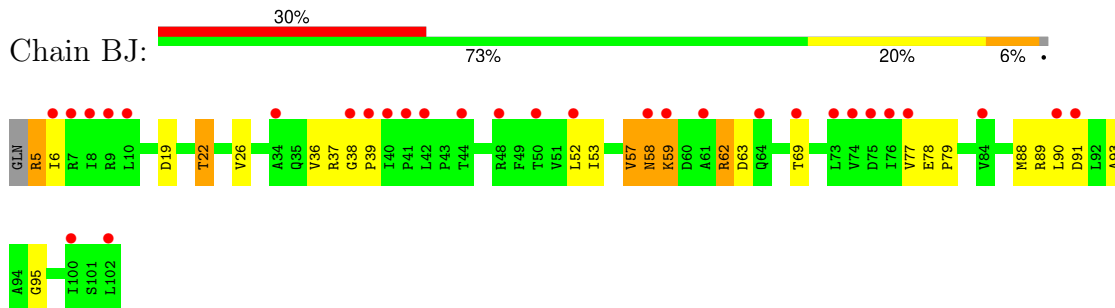
- Molecule 9: 30S ribosomal protein S9



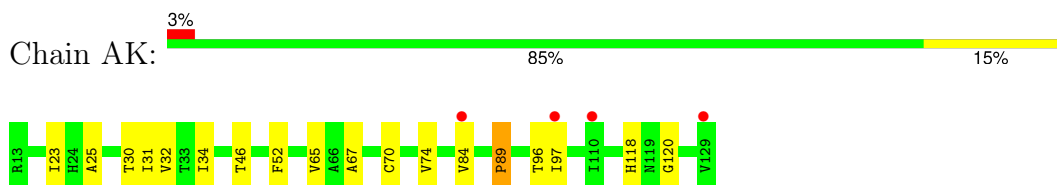
- Molecule 10: 30S ribosomal protein S10



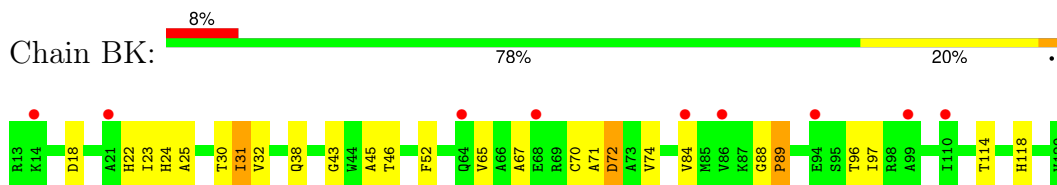
- Molecule 10: 30S ribosomal protein S10



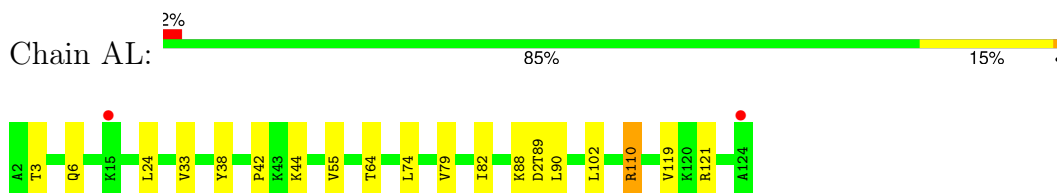
- Molecule 11: 30S ribosomal protein S11



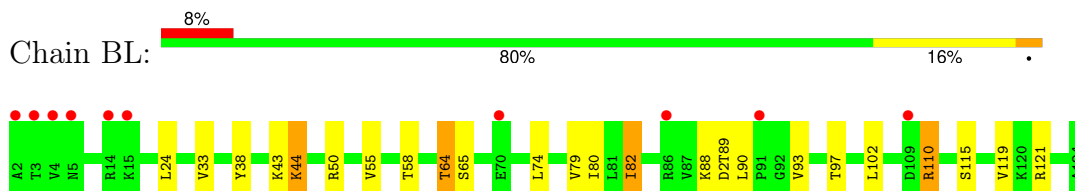
- Molecule 11: 30S ribosomal protein S11



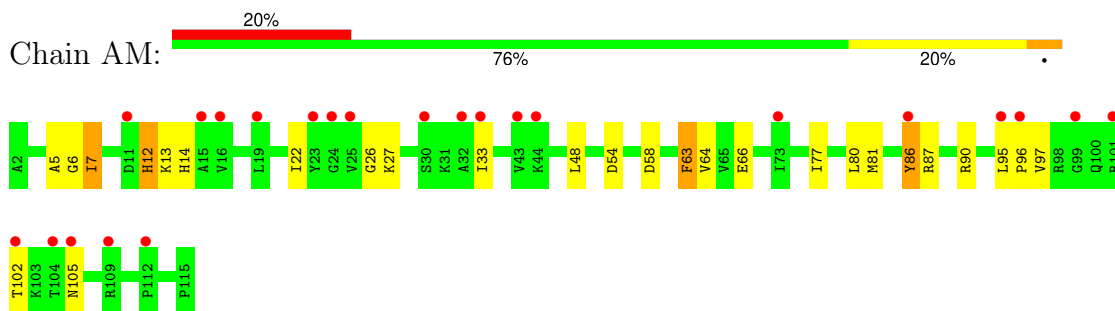
- Molecule 12: 30S ribosomal protein S12



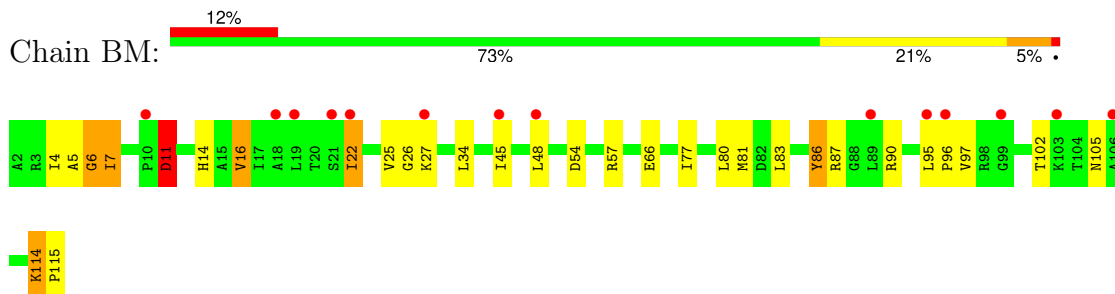
- Molecule 12: 30S ribosomal protein S12



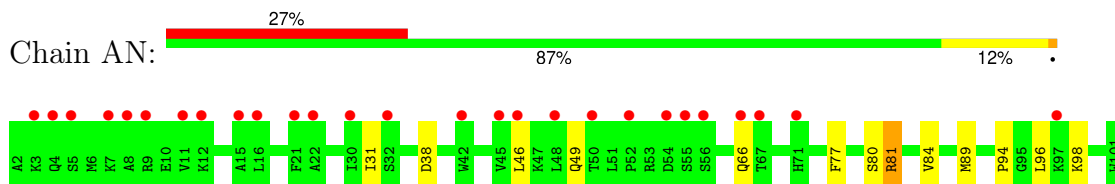
- Molecule 13: 30S ribosomal protein S13



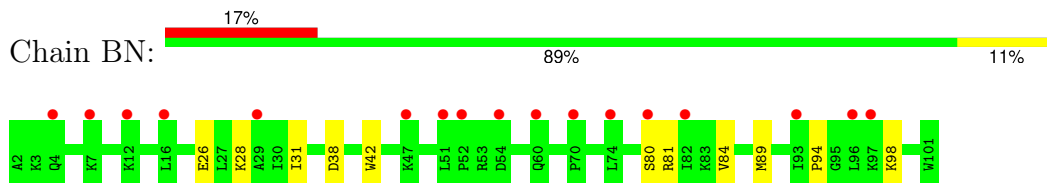
- Molecule 13: 30S ribosomal protein S13



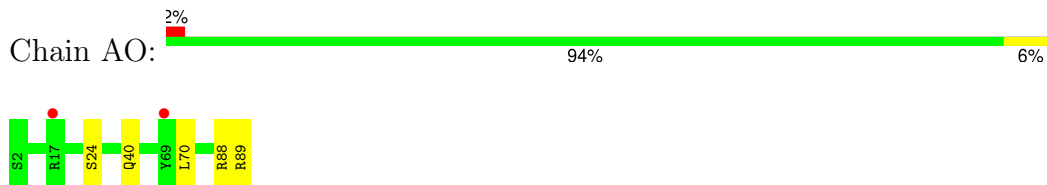
- Molecule 14: 30S ribosomal protein S14



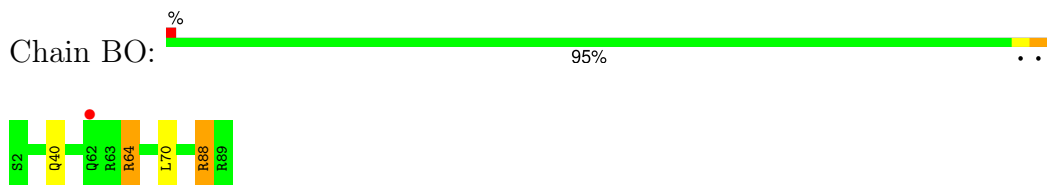
- Molecule 14: 30S ribosomal protein S14



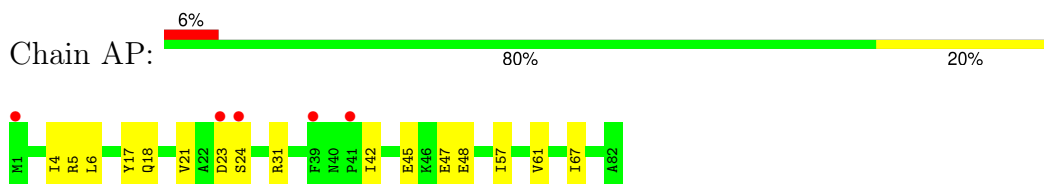
- Molecule 15: 30S ribosomal protein S15



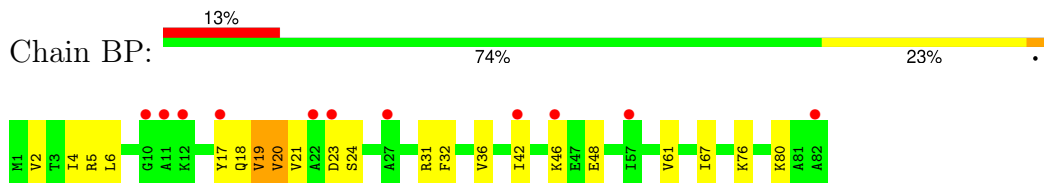
- Molecule 15: 30S ribosomal protein S15



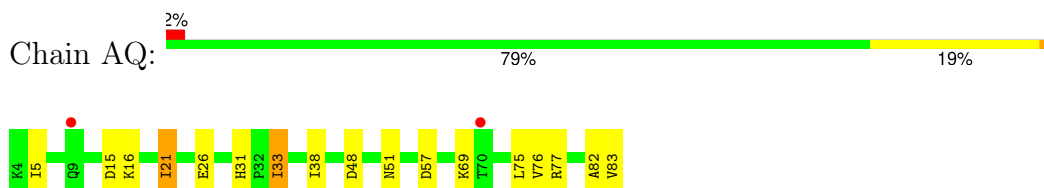
- Molecule 16: 30S ribosomal protein S16



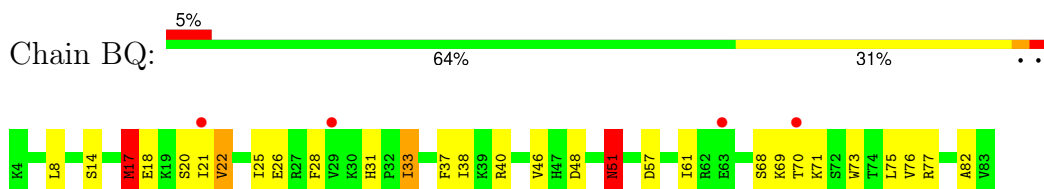
- Molecule 16: 30S ribosomal protein S16



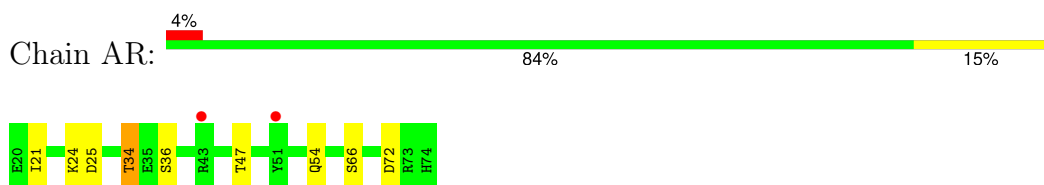
- Molecule 17: 30S ribosomal protein S17



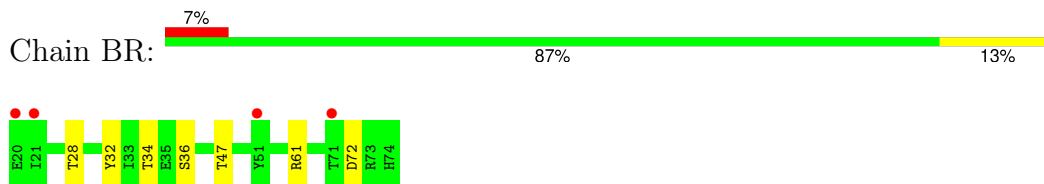
- Molecule 17: 30S ribosomal protein S17



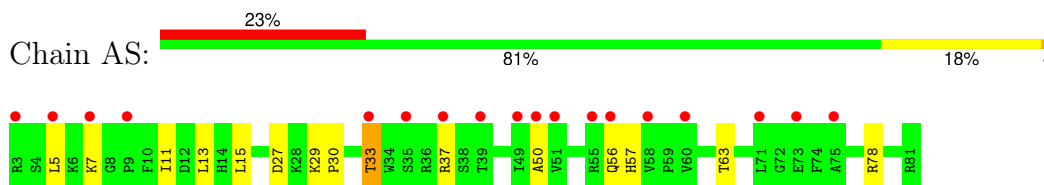
- Molecule 18: 30S ribosomal protein S18



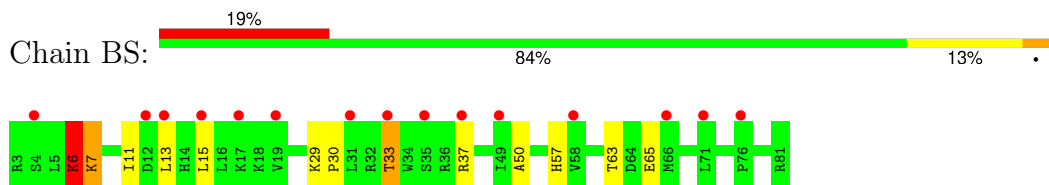
- Molecule 18: 30S ribosomal protein S18



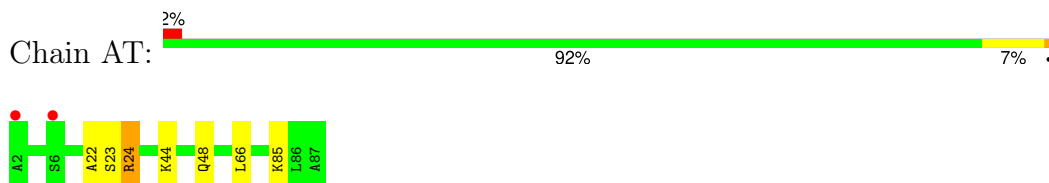
- Molecule 19: 30S ribosomal protein S19



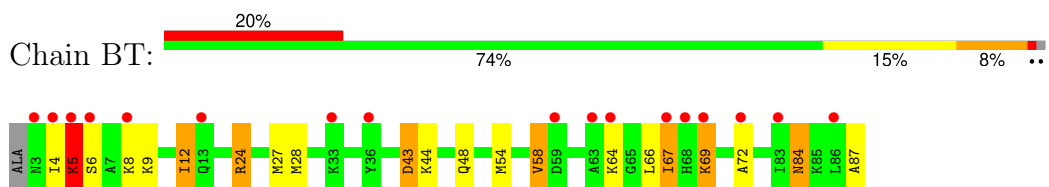
- Molecule 19: 30S ribosomal protein S19



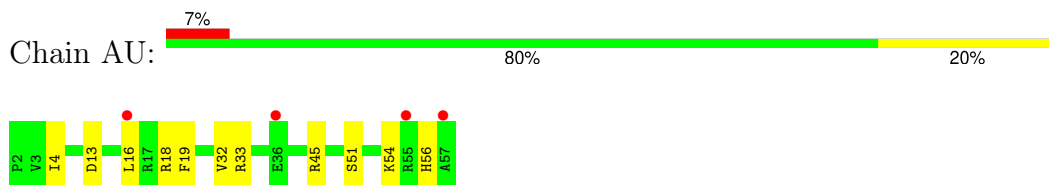
- Molecule 20: 30S ribosomal protein S20



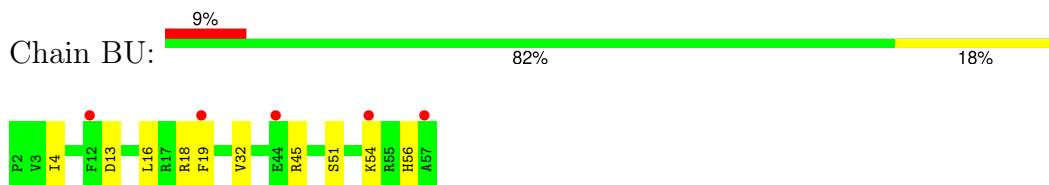
- Molecule 20: 30S ribosomal protein S20



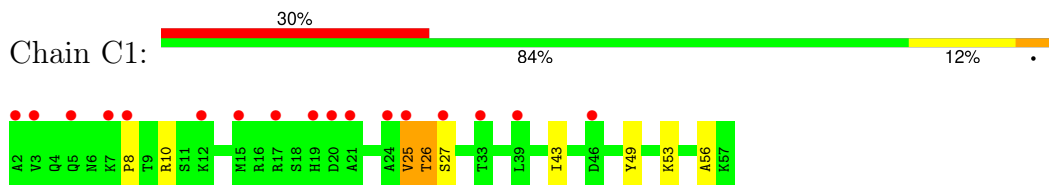
- Molecule 21: 30S ribosomal protein S21



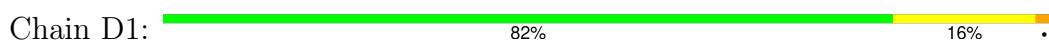
- Molecule 21: 30S ribosomal protein S21



- Molecule 22: 50S ribosomal protein L32

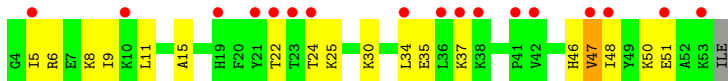


- Molecule 22: 50S ribosomal protein L32

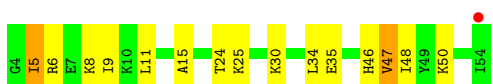
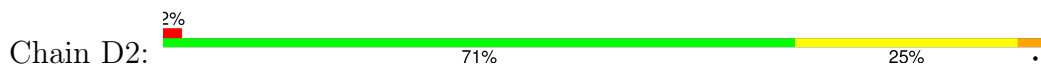




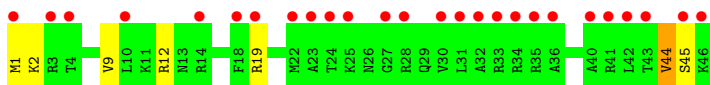
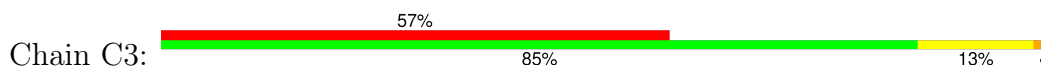
- Molecule 23: 50S ribosomal protein L33



- Molecule 23: 50S ribosomal protein L33



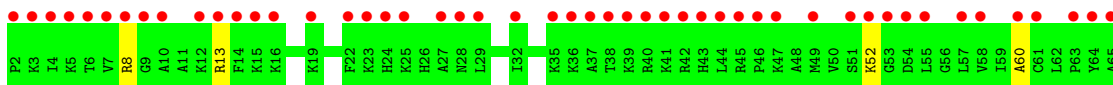
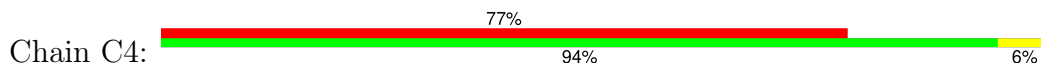
- Molecule 24: 50S ribosomal protein L34



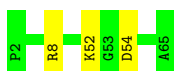
- Molecule 24: 50S ribosomal protein L34



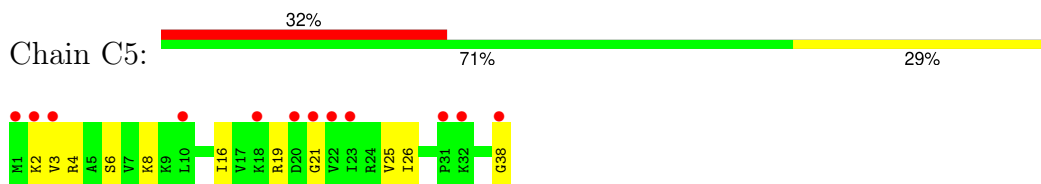
- Molecule 25: 50S ribosomal protein L35



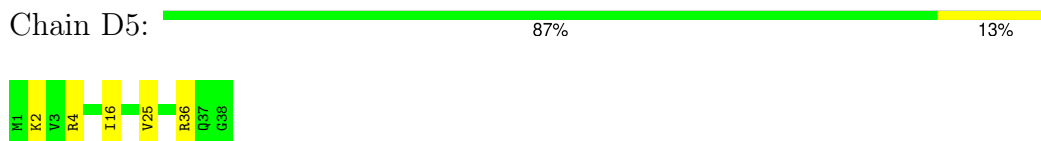
- Molecule 25: 50S ribosomal protein L35



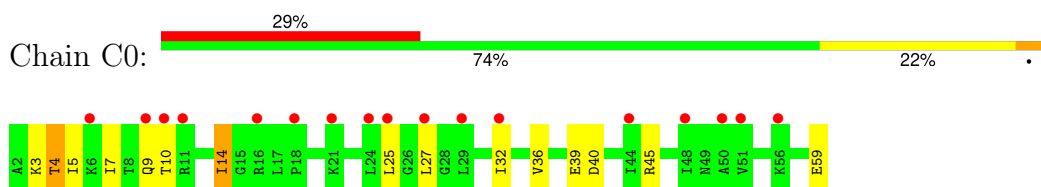
- Molecule 26: 50S ribosomal protein L36



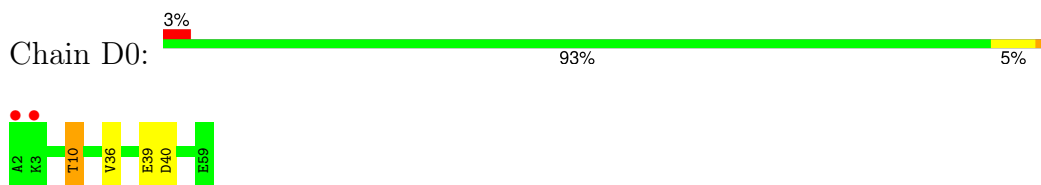
- Molecule 26: 50S ribosomal protein L36



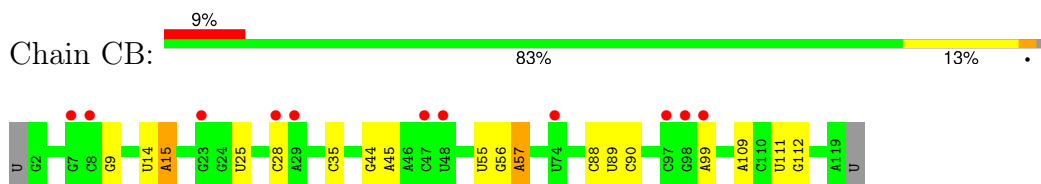
- Molecule 27: 50S ribosomal protein L30



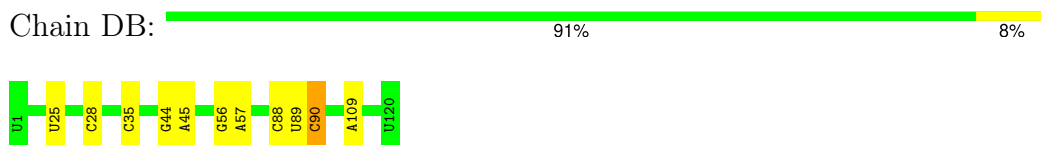
- Molecule 27: 50S ribosomal protein L30



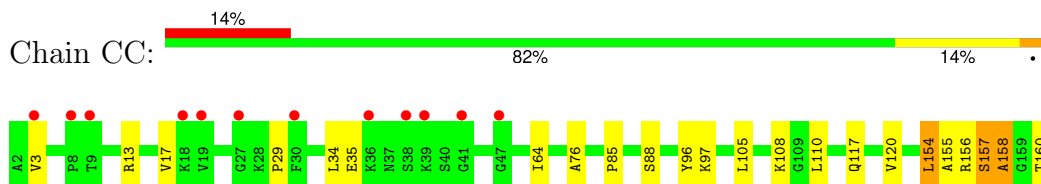
- Molecule 28: 5S rRNA

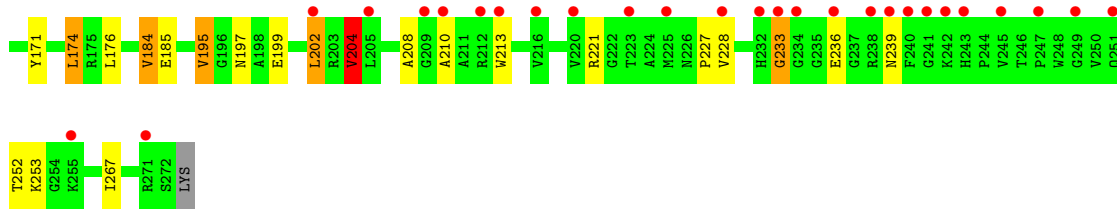


- Molecule 28: 5S rRNA

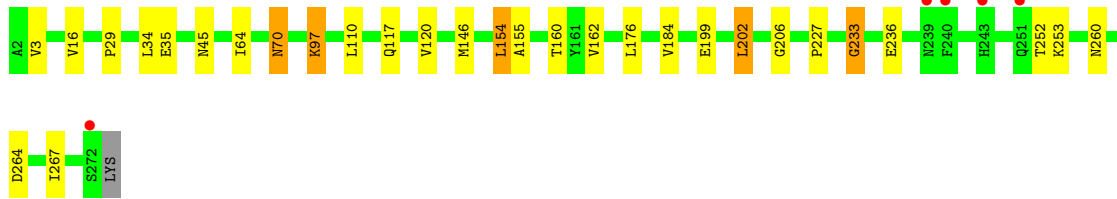
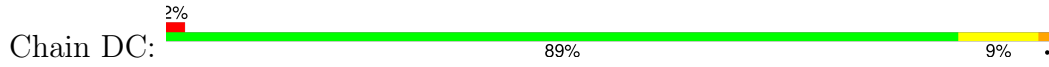


- Molecule 29: 50S ribosomal protein L2

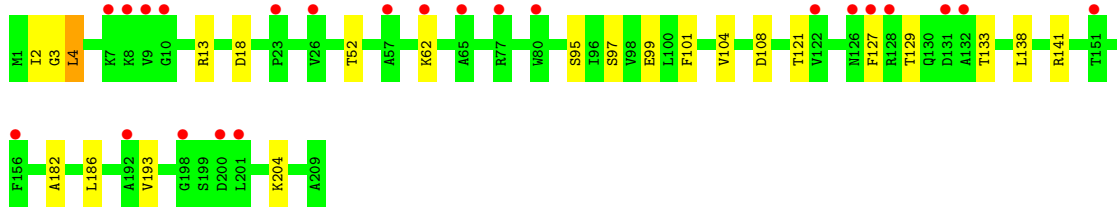
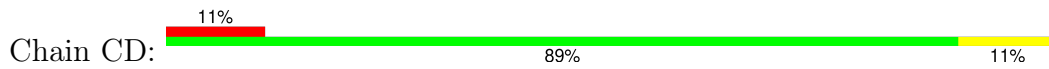




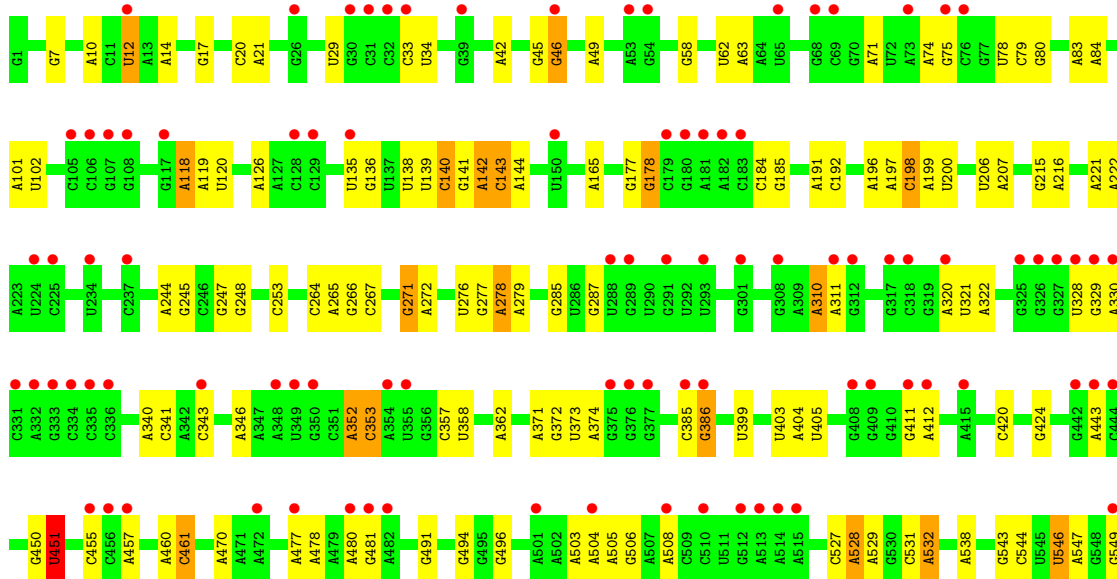
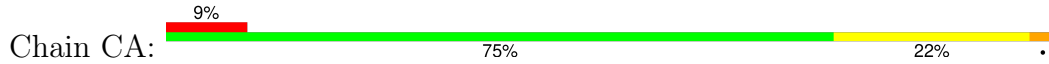
• Molecule 29: 50S ribosomal protein L2

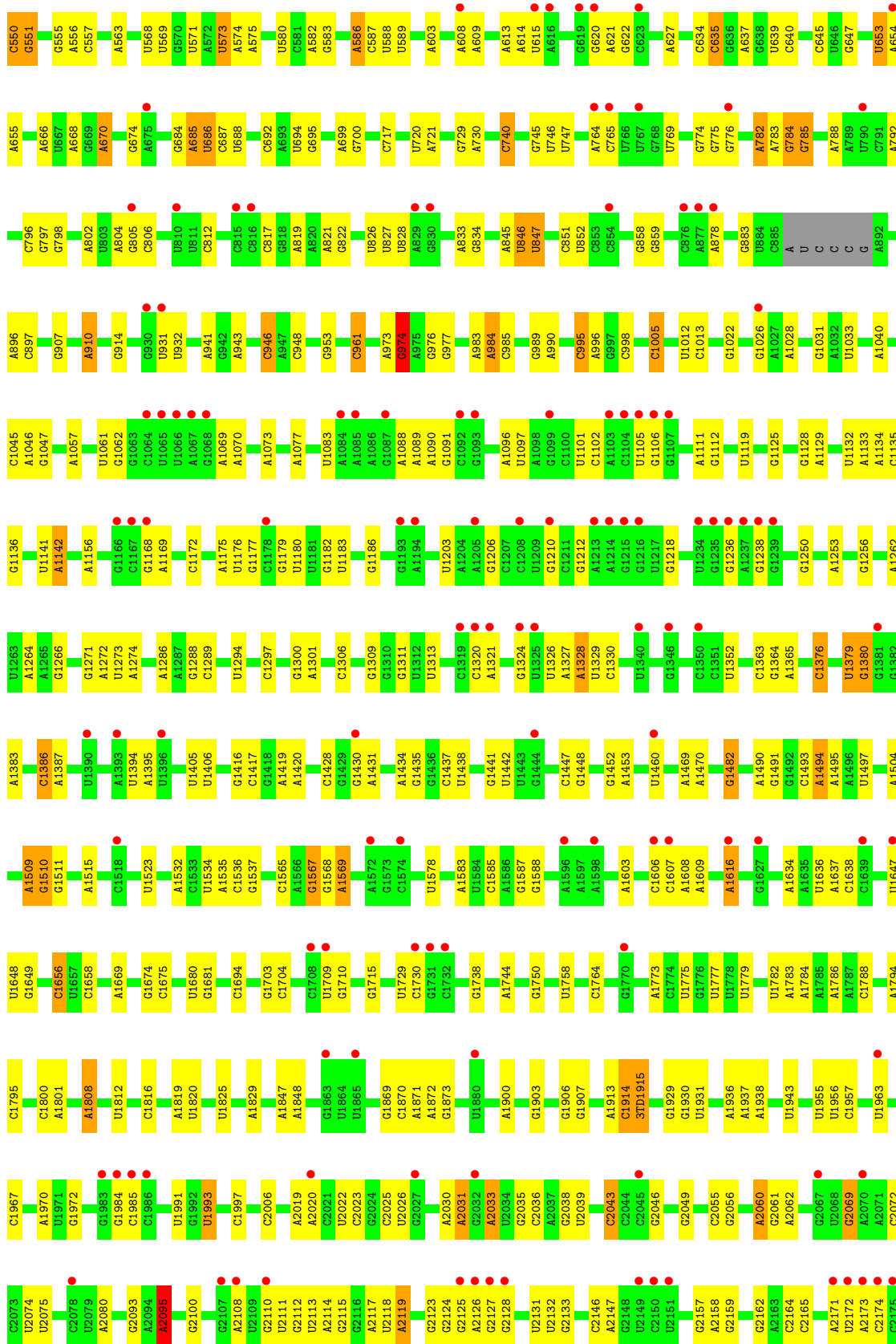


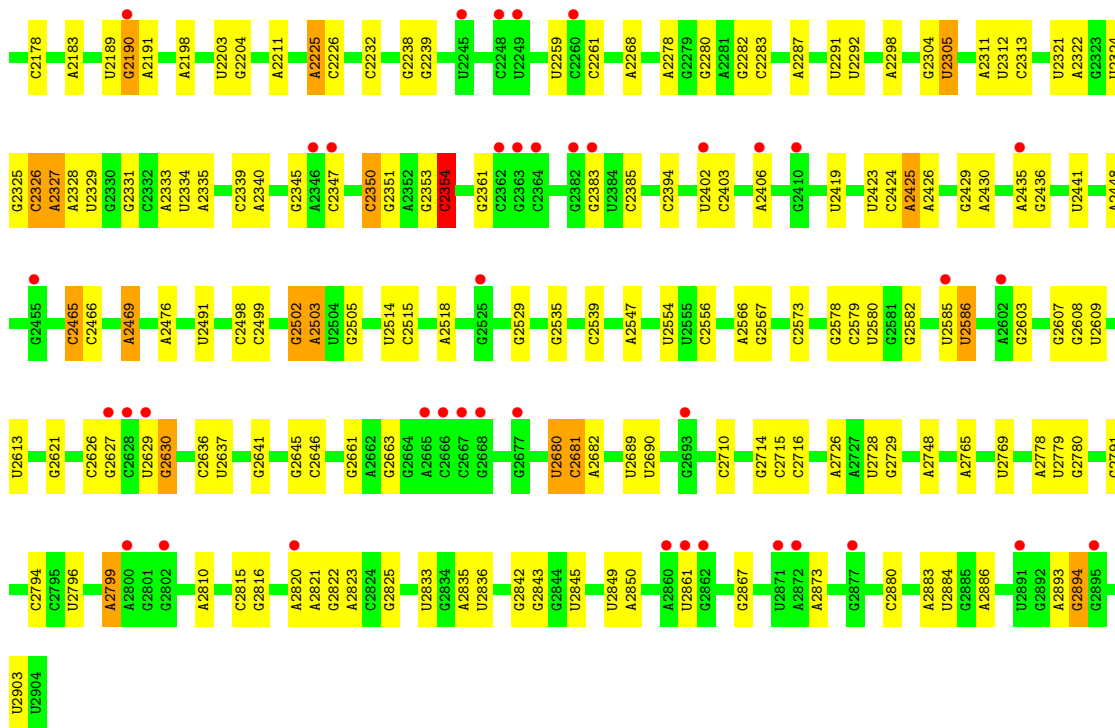
• Molecule 30: 50S ribosomal protein L3



• Molecule 31: 23S rRNA



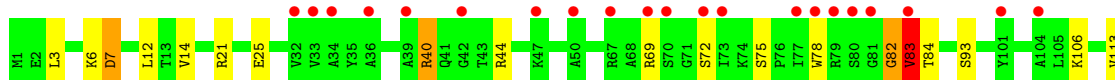
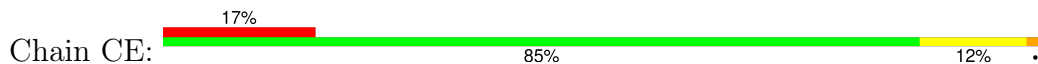




• Molecule 32: 50S ribosomal protein L3



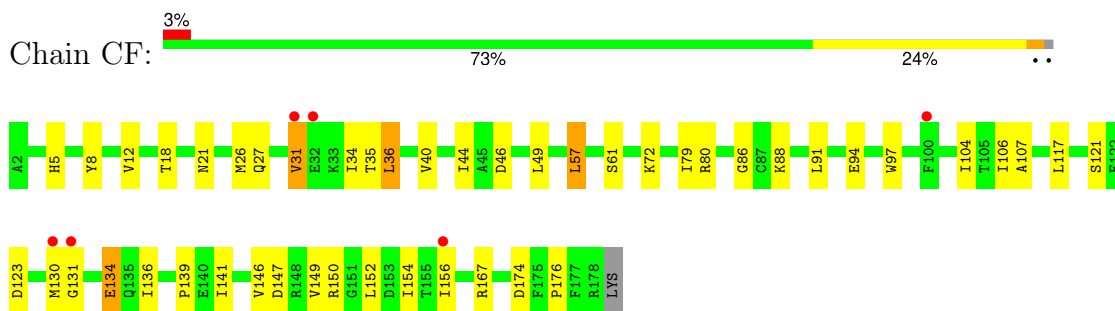
• Molecule 33: 50S ribosomal protein L4



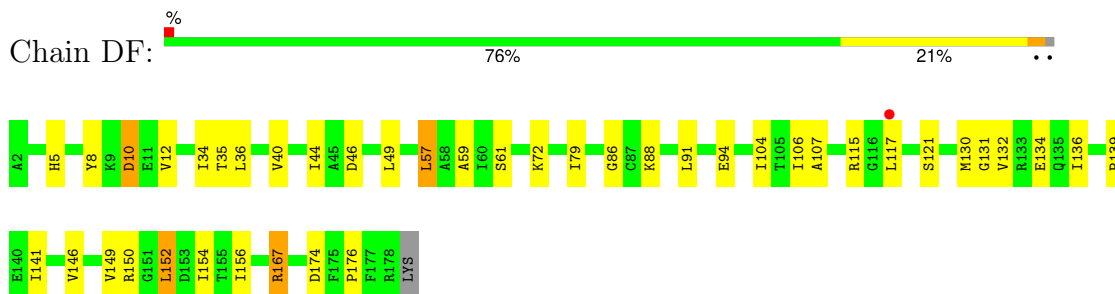
• Molecule 33: 50S ribosomal protein L4



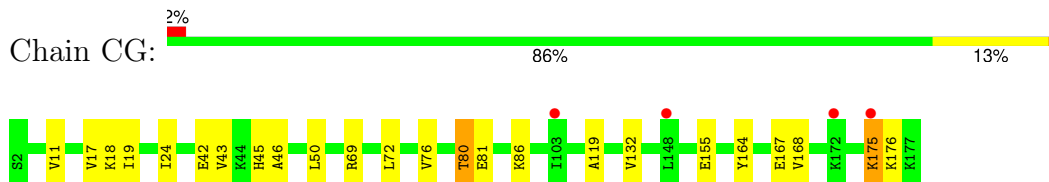
• Molecule 34: 50S ribosomal protein L5



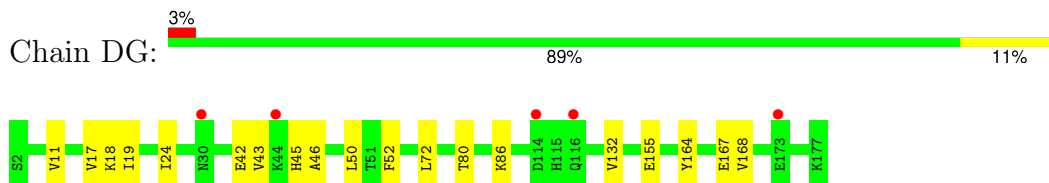
- Molecule 34: 50S ribosomal protein L5



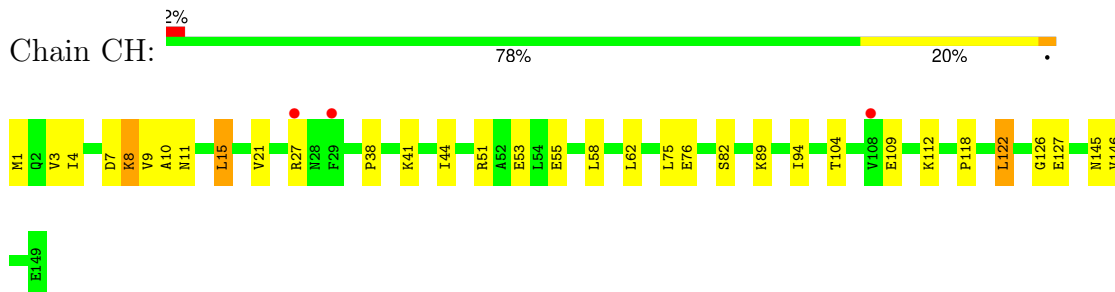
- Molecule 35: 50S ribosomal protein L6



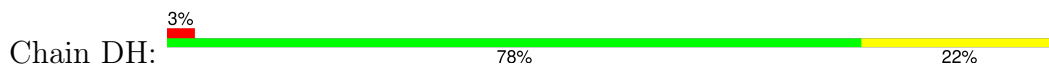
- Molecule 35: 50S ribosomal protein L6

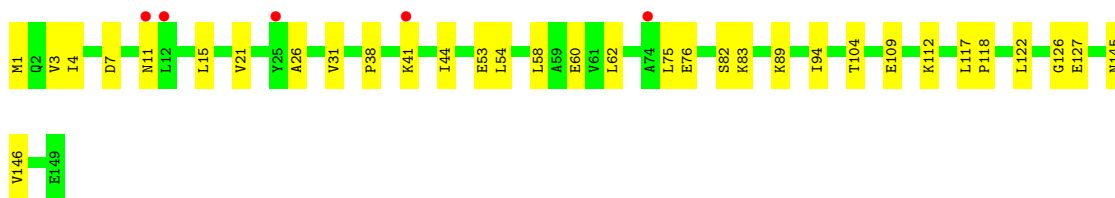


- Molecule 36: 50S ribosomal protein L9

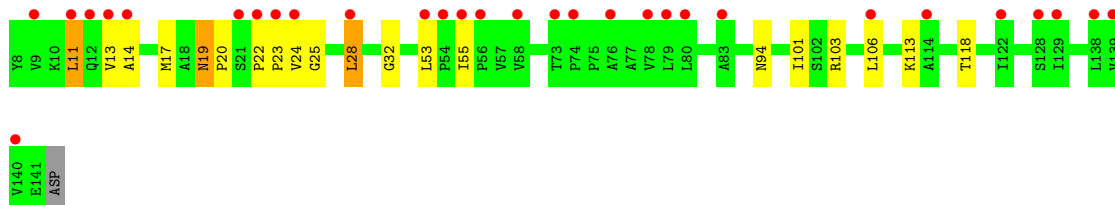
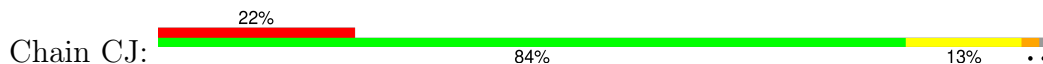


- Molecule 36: 50S ribosomal protein L9

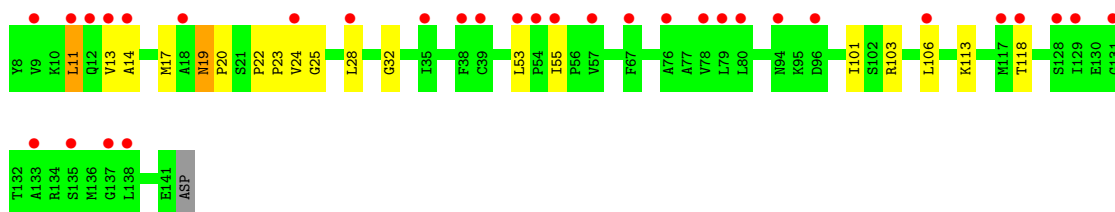
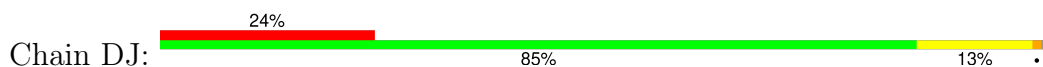




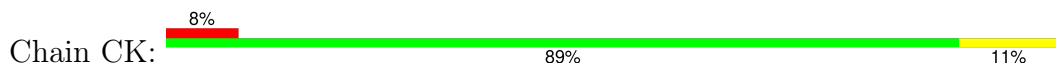
- Molecule 37: 50S ribosomal protein L11



- Molecule 37: 50S ribosomal protein L11



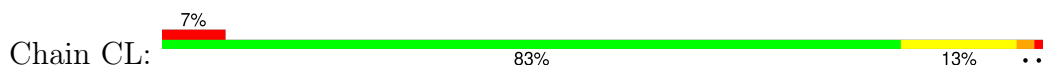
- Molecule 38: 50S ribosomal protein L13




- Molecule 38: 50S ribosomal protein L13

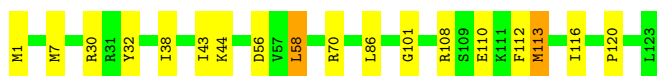


- Molecule 39: 50S ribosomal protein L14




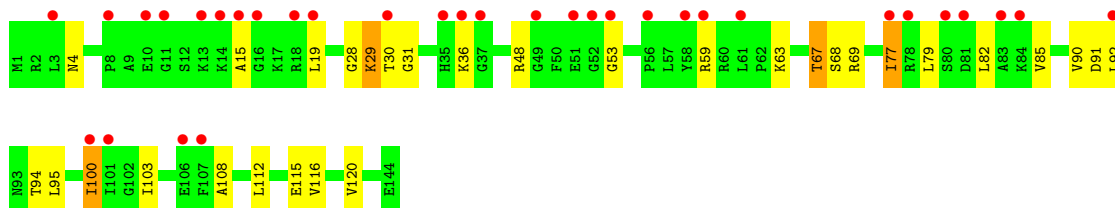
- Molecule 39: 50S ribosomal protein L14

Chain DL:  85% 13%



- Molecule 40: 50S ribosomal protein L15

Chain CM:  23% 78% 19%




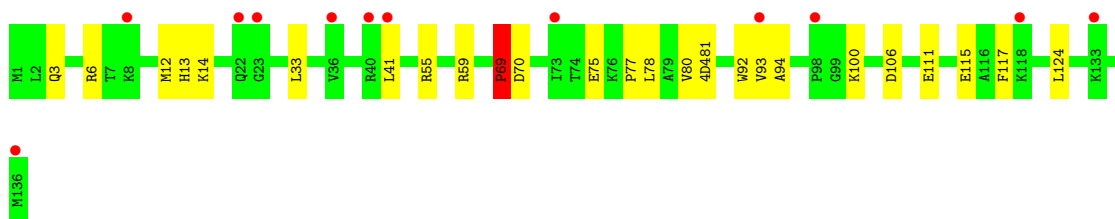
- Molecule 40: 50S ribosomal protein L15

Chain DM:  90% 9%



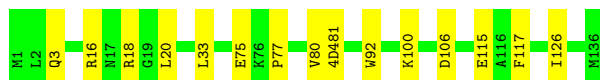
- Molecule 41: 50S ribosomal protein L16

Chain CN:  9% 82% 18%




- Molecule 41: 50S ribosomal protein L16

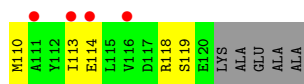
Chain DN:  89% 11%



- Molecule 42: 50S ribosomal protein L17

Chain CO:  27% 80% 13%





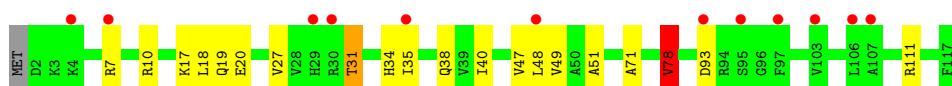
- Molecule 42: 50S ribosomal protein L17

Chain DO: 87% 12%



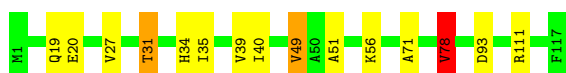
- Molecule 43: 50S ribosomal protein L18

Chain CP: 10% 82% 15%



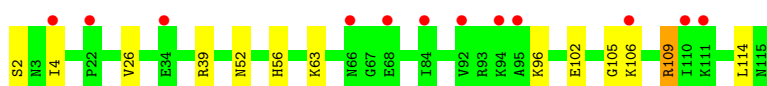
- Molecule 43: 50S ribosomal protein L18

Chain DP: 87% 10%



- Molecule 44: 50S ribosomal protein L19

Chain CQ: 11% 89% 11%



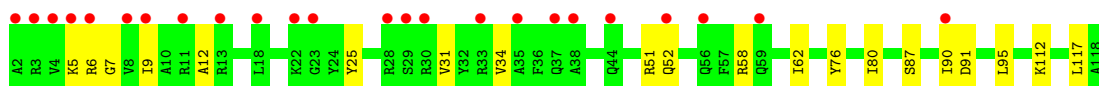
- Molecule 44: 50S ribosomal protein L19

Chain DQ: 86% 12%




- Molecule 45: 50S ribosomal protein L20

Chain CR: 21% 83% 17%




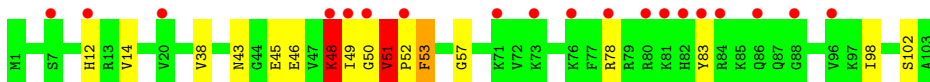
- Molecule 45: 50S ribosomal protein L20

Chain DR:  85% 14%



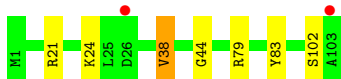
- Molecule 46: 50S ribosomal protein L21

Chain CS:  18% 83% 14%




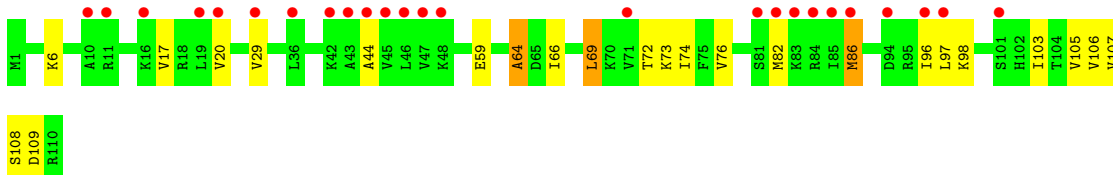
- Molecule 46: 50S ribosomal protein L21

Chain DS:  2% 93% 6%




- Molecule 47: 50S ribosomal protein L22

Chain CT:  23% 78% 19%




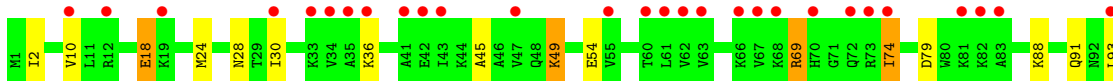
- Molecule 47: 50S ribosomal protein L22

Chain DT:  84% 16%




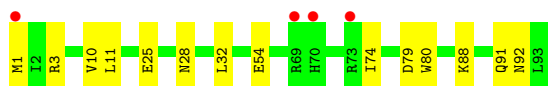
- Molecule 48: 50S ribosomal protein L23

Chain CU:  30% 83% 13%

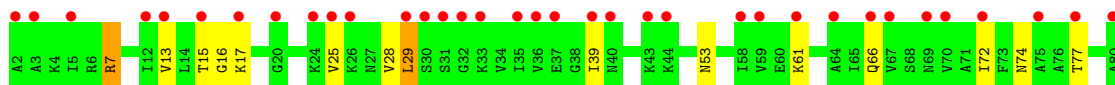
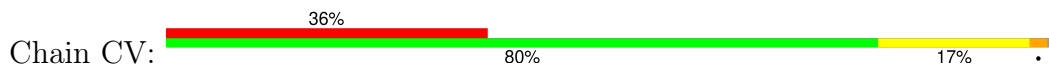


- Molecule 48: 50S ribosomal protein L23

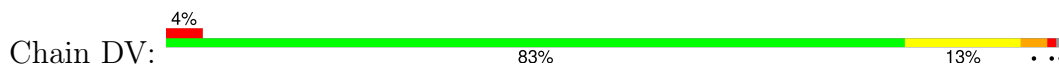
Chain DU:  4% 85% 15%



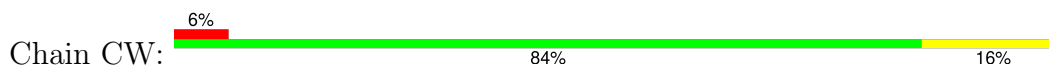
- Molecule 49: 50S ribosomal protein L24



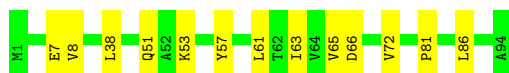
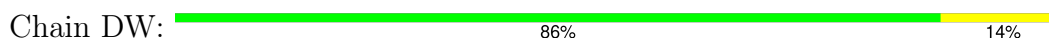
- Molecule 49: 50S ribosomal protein L24



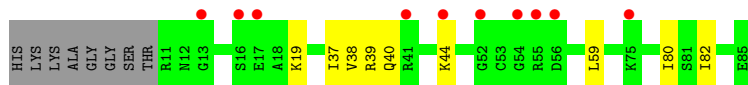
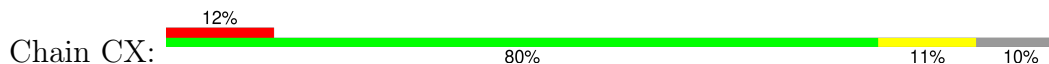
- Molecule 50: 50S ribosomal protein L25



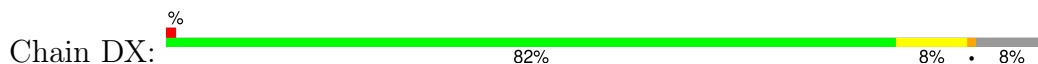
- Molecule 50: 50S ribosomal protein L25



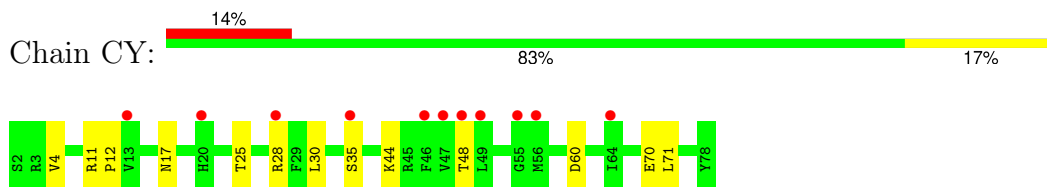
- Molecule 51: 50S ribosomal protein L27



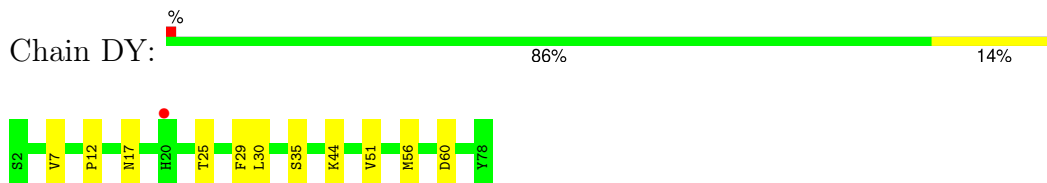
- Molecule 51: 50S ribosomal protein L27



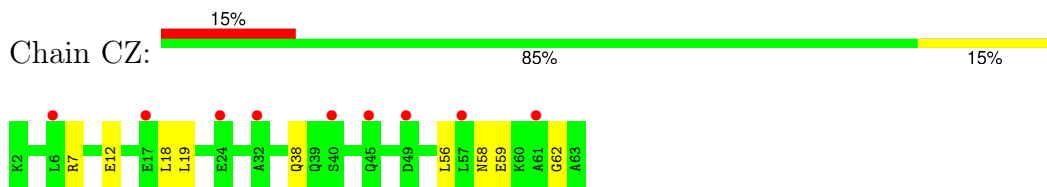
- Molecule 52: 50S ribosomal protein L28



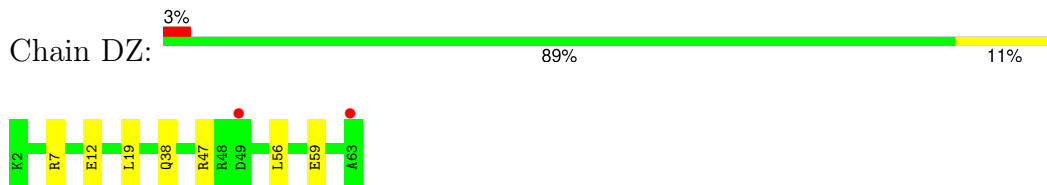
- Molecule 52: 50S ribosomal protein L28



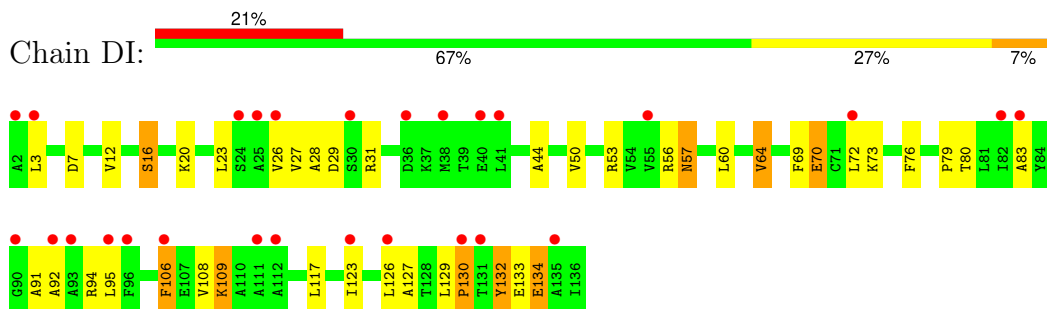
- Molecule 53: 50S ribosomal protein L29



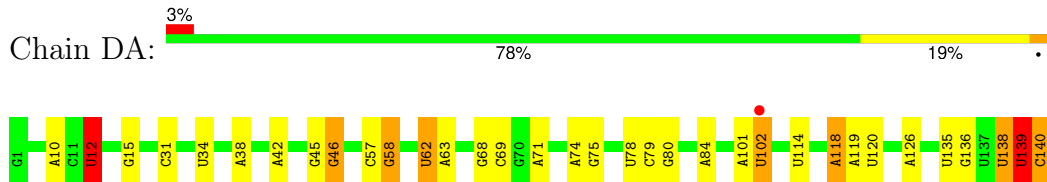
- Molecule 53: 50S ribosomal protein L29

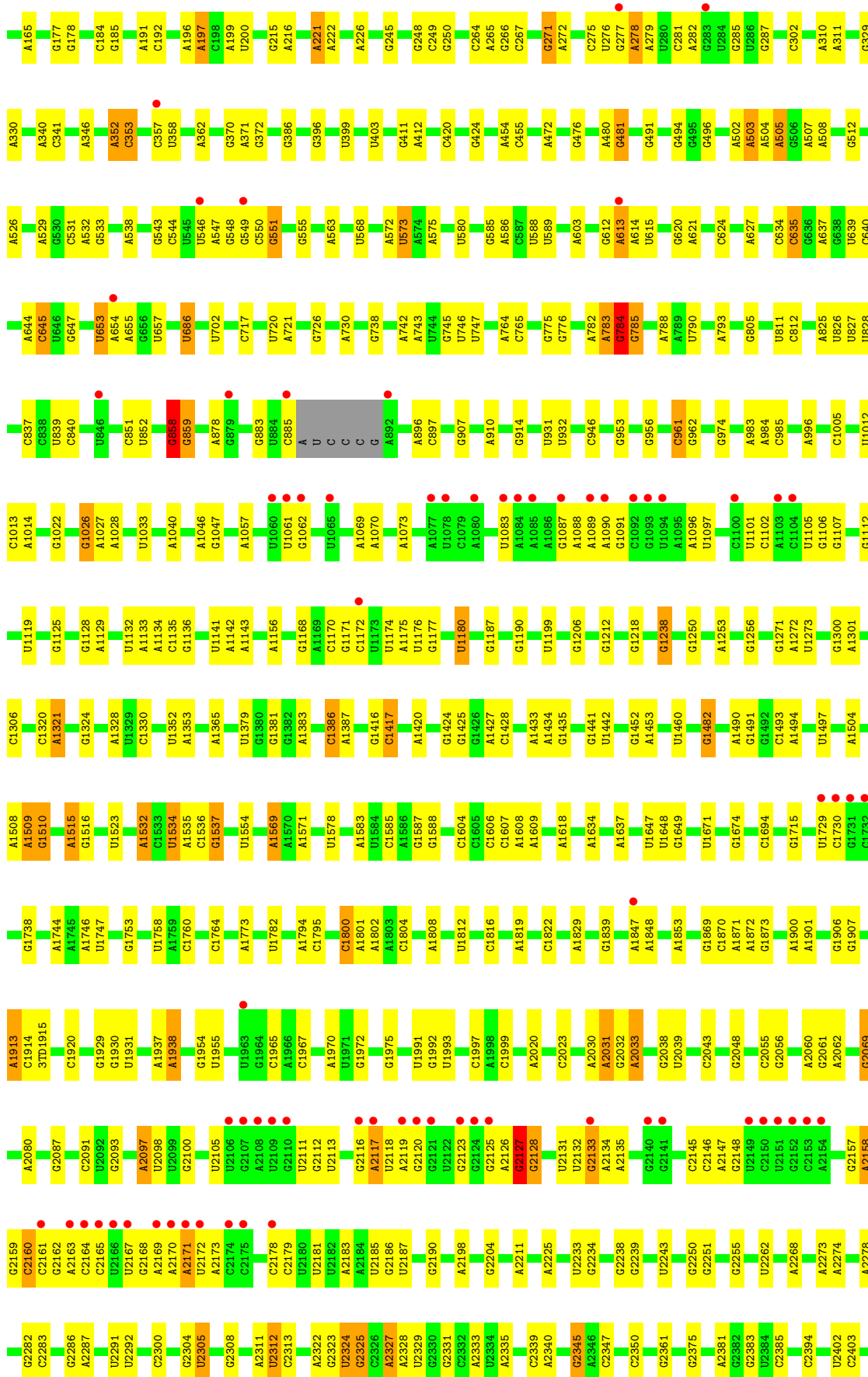


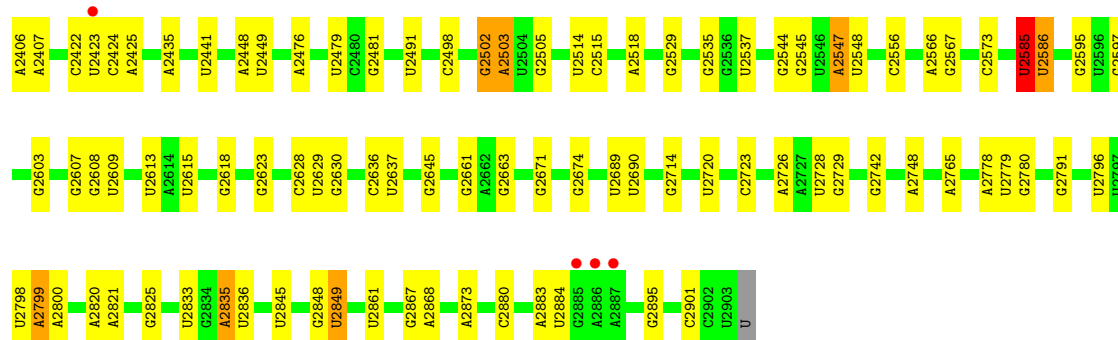
- Molecule 54: 50S ribosomal protein L10



- Molecule 55: 23S rRNA







4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.72Å 435.19Å 622.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.53 – 3.10 48.53 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.53-3.10) 99.7 (48.53-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 3.12Å)	Xtrriage
Refinement program	BUSTER-TNT 2.11.6	Depositor
R, R_{free}	0.171 , 0.192 0.185 , 0.207	Depositor DCC
R_{free} test set	4087 reflections (0.40%)	wwPDB-VP
Wilson B-factor (Å ²)	65.0	Xtrriage
Anisotropy	0.428	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 106.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	295207	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 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: D2T, H2U, 3TD, TRS, PSU, T1C, 1PE, MA6, MEQ, 1MG, 6MZ, 2MA, ACY, MPD, ZN, 5MU, SPD, EDO, PEG, MG, 7MG, UR3, GUN, PGE, 4D4, OMC, OMU, OMG, PUT, 2MG, PG4, 5MC, 4OC

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	0.67	11/36597 (0.0%)	0.67	1/57088 (0.0%)
1	BA	0.68	7/36572 (0.0%)	0.67	2/57049 (0.0%)
2	AB	0.79	0/1784	1.36	5/2403 (0.2%)
2	BB	0.78	0/1784	1.37	5/2403 (0.2%)
3	AC	0.81	0/1652	1.29	2/2225 (0.1%)
3	BC	0.82	0/1652	1.31	6/2225 (0.3%)
4	AD	0.73	0/1665	1.38	7/2227 (0.3%)
4	BD	0.73	0/1665	1.38	7/2227 (0.3%)
5	AE	0.79	0/1157	1.40	8/1557 (0.5%)
5	BE	0.83	0/1118	1.41	6/1504 (0.4%)
6	AF	0.78	0/881	1.31	4/1189 (0.3%)
6	BF	0.80	0/835	1.41	10/1128 (0.9%)
7	AG	0.80	0/1196	1.38	4/1602 (0.2%)
7	BG	0.81	0/1196	1.38	3/1602 (0.2%)
8	AH	0.73	0/989	1.32	1/1326 (0.1%)
8	BH	0.74	0/989	1.32	1/1326 (0.1%)
9	AI	0.78	0/1034	1.32	2/1375 (0.1%)
9	BI	0.78	0/1034	1.31	2/1375 (0.1%)
10	AJ	0.76	0/806	1.26	2/1089 (0.2%)
10	BJ	0.87	0/797	1.31	4/1077 (0.4%)
11	AK	0.78	0/893	1.20	3/1205 (0.2%)
11	BK	0.76	0/893	1.24	3/1205 (0.2%)
12	AL	0.74	0/960	1.24	4/1286 (0.3%)
12	BL	0.76	0/960	1.24	2/1286 (0.2%)
13	AM	0.90	0/893	1.51	9/1193 (0.8%)
13	BM	0.91	0/893	1.50	10/1193 (0.8%)
14	AN	0.81	0/817	1.36	1/1088 (0.1%)
14	BN	0.78	0/817	1.35	1/1088 (0.1%)
15	AO	0.73	0/722	1.46	1/964 (0.1%)
15	BO	0.73	0/722	1.50	0/964

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	AP	0.79	0/659	1.31	4/884 (0.5%)
16	BP	0.83	0/659	1.38	5/884 (0.6%)
17	AQ	0.81	0/658	1.22	2/881 (0.2%)
17	BQ	0.86	0/658	1.32	4/881 (0.5%)
18	AR	0.83	0/463	1.40	3/621 (0.5%)
18	BR	0.81	0/463	1.35	2/621 (0.3%)
19	AS	0.87	0/653	1.23	0/877
19	BS	0.86	0/653	1.23	0/877
20	AT	0.79	0/676	1.54	4/895 (0.4%)
20	BT	0.89	1/671 (0.1%)	1.63	5/888 (0.6%)
21	AU	0.71	0/472	1.35	4/627 (0.6%)
21	BU	0.69	0/472	1.37	2/627 (0.3%)
22	C1	0.87	0/450	1.29	0/599
22	D1	0.86	0/450	1.28	1/599 (0.2%)
23	C2	0.81	0/416	1.24	0/554
23	D2	0.80	0/421	1.24	1/561 (0.2%)
24	C3	0.71	0/380	1.46	0/498
24	D3	0.82	0/380	1.49	1/498 (0.2%)
25	C4	0.74	0/513	1.20	0/676
25	D4	0.80	0/513	1.23	0/676
26	C5	0.76	0/303	1.22	2/397 (0.5%)
26	D5	0.82	0/303	1.13	0/397
27	C0	0.84	0/453	1.38	1/605 (0.2%)
27	D0	0.87	0/467	1.33	2/623 (0.3%)
28	CB	0.64	0/2828	0.67	1/4410 (0.0%)
28	DB	0.67	0/2872	0.69	0/4478
29	CC	0.73	0/2121	1.25	9/2852 (0.3%)
29	DC	0.74	0/2121	1.22	6/2852 (0.2%)
30	CD	0.75	1/1586 (0.1%)	1.15	1/2134 (0.0%)
31	CA	0.69	33/69165 (0.0%)	0.68	5/107896 (0.0%)
32	DD	0.76	0/1576	1.14	3/2119 (0.1%)
33	CE	0.76	0/1571	1.36	10/2113 (0.5%)
33	DE	0.77	0/1570	1.32	6/2113 (0.3%)
34	CF	0.75	0/1434	1.36	8/1926 (0.4%)
34	DF	0.78	0/1434	1.36	12/1926 (0.6%)
35	CG	0.74	0/1343	1.27	6/1816 (0.3%)
35	DG	0.73	0/1343	1.23	2/1816 (0.1%)
36	CH	0.84	0/1121	1.35	2/1515 (0.1%)
36	DH	0.85	1/1121 (0.1%)	1.35	2/1515 (0.1%)
37	CJ	0.93	0/993	1.35	3/1341 (0.2%)
37	DJ	0.93	0/993	1.34	3/1341 (0.2%)
38	CK	0.69	0/1152	1.28	4/1551 (0.3%)
38	DK	0.80	0/1152	1.26	6/1551 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	CL	0.78	0/947	1.20	2/1268 (0.2%)
39	DL	0.80	1/955 (0.1%)	1.17	0/1279
40	CM	0.77	1/1062 (0.1%)	1.36	8/1413 (0.6%)
40	DM	0.73	0/1062	1.25	1/1413 (0.1%)
41	CN	0.74	0/1081	1.27	6/1443 (0.4%)
41	DN	0.76	0/1092	1.25	1/1457 (0.1%)
42	CO	0.74	0/973	1.29	1/1301 (0.1%)
42	DO	0.82	0/1006	1.35	3/1345 (0.2%)
43	CP	0.74	0/902	1.41	6/1209 (0.5%)
43	DP	0.78	0/910	1.38	4/1219 (0.3%)
44	CQ	0.69	0/929	1.15	0/1242
44	DQ	0.73	0/929	1.15	1/1242 (0.1%)
45	CR	0.75	0/960	1.39	3/1278 (0.2%)
45	DR	0.81	0/960	1.36	3/1278 (0.2%)
46	CS	0.72	0/829	1.22	5/1107 (0.5%)
46	DS	0.76	0/829	1.23	1/1107 (0.1%)
47	CT	0.71	0/864	1.34	2/1156 (0.2%)
47	DT	0.78	0/864	1.33	1/1156 (0.1%)
48	CU	0.76	0/745	1.27	3/994 (0.3%)
48	DU	0.76	0/744	1.30	5/994 (0.5%)
49	CV	0.78	0/787	1.30	4/1051 (0.4%)
49	DV	0.76	0/787	1.30	10/1051 (1.0%)
50	CW	0.71	0/766	1.24	0/1025
50	DW	0.76	0/766	1.26	1/1025 (0.1%)
51	CX	0.65	0/576	1.08	1/762 (0.1%)
51	DX	0.72	1/598 (0.2%)	1.09	0/790
52	CY	0.67	0/635	1.33	3/848 (0.4%)
52	DY	0.73	0/635	1.30	2/848 (0.2%)
53	CZ	0.71	0/502	1.51	0/667
53	DZ	0.73	0/502	1.51	0/667
54	DI	0.89	0/1037	1.47	7/1402 (0.5%)
55	DA	0.72	19/69364 (0.0%)	0.71	2/108207 (0.0%)
All	All	0.72	76/309273 (0.0%)	0.90	334/462224 (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
41	CN	0	1
55	DA	0	25
All	All	0	26

The worst 5 of 76 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	CA	2095	A	O5'-C5'	-9.45	1.28	1.42
55	DA	12	U	C1'-N1	8.21	1.60	1.48
55	DA	2585	U	C1'-N1	8.10	1.59	1.47
55	DA	2097	A	O5'-C5'	-7.60	1.31	1.42
31	CA	2425	A	C3'-O3'	7.52	1.54	1.43

The worst 5 of 334 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	BE	50	TYR	CA-C-O	-10.54	113.12	119.55
54	DI	132	TYR	CA-C-N	9.87	139.46	121.70
54	DI	132	TYR	C-N-CA	9.87	139.46	121.70
34	DF	10	ASP	CA-CB-CG	9.17	121.77	112.60
54	DI	106	PHE	CA-CB-CG	8.37	122.17	113.80

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	CN	69	PRO	Mainchain
55	DA	15	G	Sidechain
55	DA	177	G	Sidechain
55	DA	221	A	Sidechain
55	DA	249	C	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32933	0	16593	79	0
1	BA	32911	0	16582	95	0
2	AB	1753	0	1780	8	0
2	BB	1753	0	1780	9	0
3	AC	1625	0	1696	12	0
3	BC	1625	0	1696	13	0
4	AD	1643	0	1707	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	BD	1643	0	1707	16	0
5	AE	1144	0	1185	10	0
5	BE	1105	0	1148	19	0
6	AF	862	0	864	7	0
6	BF	817	0	808	7	0
7	AG	1182	0	1238	5	0
7	BG	1182	0	1238	3	0
8	AH	979	0	1031	11	0
8	BH	979	0	1031	9	0
9	AI	1022	0	1070	10	0
9	BI	1022	0	1070	11	0
10	AJ	796	0	836	10	0
10	BJ	787	0	828	8	0
11	AK	877	0	887	11	0
11	BK	877	0	887	14	0
12	AL	957	0	1017	6	0
12	BL	957	0	1017	8	0
13	AM	884	0	941	11	0
13	BM	884	0	941	16	0
14	AN	805	0	844	7	0
14	BN	805	0	844	6	0
15	AO	714	0	734	0	0
15	BO	714	0	734	1	0
16	AP	649	0	666	6	0
16	BP	649	0	666	6	0
17	AQ	649	0	691	4	0
17	BQ	649	0	691	11	0
18	AR	456	0	478	3	0
18	BR	456	0	478	3	0
19	AS	638	0	665	4	0
19	BS	638	0	665	6	0
20	AT	670	0	719	1	0
20	BT	665	0	714	7	0
21	AU	465	0	491	3	0
21	BU	465	0	491	3	0
22	C1	444	0	458	4	0
22	D1	444	0	458	10	0
23	C2	409	0	440	7	0
23	D2	414	0	442	5	0
24	C3	377	0	418	4	0
24	D3	377	0	418	2	0
25	C4	504	0	572	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	D4	504	0	572	2	0
26	C5	302	0	340	9	0
26	D5	302	0	340	3	0
27	C0	449	0	488	3	0
27	D0	463	0	504	0	0
28	CB	2529	0	1281	7	0
28	DB	2569	0	1301	2	0
29	CC	2082	0	2154	20	0
29	DC	2082	0	2154	11	0
30	CD	1565	0	1616	12	0
31	CA	62229	0	31319	203	0
32	DD	1576	0	1627	11	0
33	CE	1552	0	1619	15	0
33	DE	1551	0	1619	10	0
34	CF	1410	0	1444	19	0
34	DF	1410	0	1444	14	0
35	CG	1323	0	1371	7	0
35	DG	1323	0	1371	6	0
36	CH	1110	0	1148	10	0
36	DH	1110	0	1148	7	0
37	CJ	979	0	1028	7	0
37	DJ	979	0	1028	5	0
38	CK	1129	0	1162	6	0
38	DK	1129	0	1162	5	0
39	CL	938	0	1012	9	0
39	DL	946	0	1023	10	0
40	CM	1053	0	1129	16	0
40	DM	1053	0	1129	7	0
41	CN	1075	0	1154	8	0
41	DN	1092	0	1177	8	0
42	CO	960	0	1000	7	0
42	DO	993	0	1034	6	0
43	CP	892	0	923	6	0
43	DP	900	0	935	6	0
44	CQ	917	0	962	4	0
44	DQ	917	0	962	7	0
45	CR	947	0	1019	11	0
45	DR	947	0	1019	13	0
46	CS	816	0	839	8	0
46	DS	816	0	839	4	0
47	CT	857	0	922	12	0
47	DT	857	0	922	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	CU	739	0	807	6	0
48	DU	738	0	807	4	0
49	CV	779	0	831	6	0
49	DV	779	0	831	6	0
50	CW	753	0	780	7	0
50	DW	753	0	780	7	0
51	CX	569	0	581	4	0
51	DX	591	0	606	4	0
52	CY	625	0	652	4	0
52	DY	625	0	652	4	0
53	CZ	501	0	531	1	0
53	DZ	501	0	531	2	0
54	DI	1023	0	1052	20	0
55	DA	62423	0	31412	163	0
56	AA	72	0	0	0	0
56	BA	45	0	0	0	0
56	CA	156	0	0	0	0
56	CB	3	0	0	0	0
56	DA	184	0	0	0	0
56	DB	9	0	0	0	0
56	DD	1	0	0	0	0
56	DM	1	0	0	0	0
56	DR	1	0	0	0	0
57	AA	13	0	18	1	0
57	BA	13	0	18	1	0
57	DA	26	0	36	0	0
57	DQ	13	0	18	0	0
57	DR	13	0	18	4	0
57	DS	13	0	18	1	0
58	AA	16	0	28	0	0
58	DA	40	0	70	2	0
58	DE	16	0	28	0	0
58	DK	8	0	14	0	0
58	DN	8	0	14	1	0
58	DS	8	0	14	0	0
58	DT	16	0	28	0	0
59	AA	24	0	48	0	0
59	DA	72	0	144	3	0
60	AA	42	0	39	2	0
60	BA	42	0	38	0	0
61	AB	1	0	0	0	0
61	C5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	D5	1	0	0	0	0
62	AL	7	0	10	0	0
62	D1	7	0	10	1	0
62	D3	7	0	10	0	0
62	DA	35	0	50	0	0
62	DL	7	0	10	0	0
62	DP	7	0	10	0	0
62	DQ	7	0	10	0	0
63	D1	4	0	6	0	0
63	DA	28	0	42	1	0
63	DB	16	0	24	0	0
64	D1	10	0	14	2	0
64	D3	10	0	14	0	0
64	DA	50	0	70	5	0
64	DS	10	0	14	1	0
64	DU	10	0	14	1	0
65	DA	40	0	76	2	0
66	DA	32	0	44	3	0
67	DA	12	0	9	0	0
68	DA	11	0	5	0	0
69	DA	8	0	12	1	0
70	AA	500	0	0	0	0
70	AC	5	0	0	0	0
70	AD	2	0	0	0	0
70	AE	4	0	0	0	0
70	AF	1	0	0	0	0
70	AG	1	0	0	0	0
70	AH	1	0	0	0	0
70	AJ	2	0	0	0	0
70	AK	6	0	0	0	0
70	AL	10	0	0	0	0
70	AM	4	0	0	1	0
70	AN	7	0	0	1	0
70	AO	2	0	0	0	0
70	AP	2	0	0	0	0
70	AR	1	0	0	0	0
70	AT	3	0	0	0	0
70	AU	2	0	0	0	0
70	BA	288	0	0	1	0
70	BD	12	0	0	0	0
70	BE	1	0	0	0	0
70	BF	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	BK	2	0	0	0	0
70	BL	2	0	0	0	0
70	BN	2	0	0	0	0
70	BO	1	0	0	0	0
70	BP	3	0	0	0	0
70	BT	4	0	0	0	0
70	BU	1	0	0	0	0
70	C3	3	0	0	0	0
70	C4	1	0	0	0	0
70	CA	692	0	0	2	0
70	CB	13	0	0	0	0
70	CC	12	0	0	0	0
70	CD	6	0	0	0	0
70	CE	4	0	0	0	0
70	CL	1	0	0	0	0
70	CM	4	0	0	0	0
70	CO	1	0	0	0	0
70	CU	3	0	0	0	0
70	CV	1	0	0	0	0
70	CW	1	0	0	0	0
70	CY	1	0	0	0	0
70	D0	21	0	0	0	0
70	D1	45	0	0	0	0
70	D2	7	0	0	0	0
70	D3	23	0	0	0	0
70	D4	39	0	0	0	0
70	D5	12	0	0	0	0
70	DA	4829	0	0	13	0
70	DB	213	0	0	0	0
70	DC	104	0	0	0	0
70	DD	92	0	0	2	0
70	DE	60	0	0	2	0
70	DF	15	0	0	0	0
70	DG	6	0	0	0	0
70	DH	2	0	0	0	0
70	DK	64	0	0	2	0
70	DL	51	0	0	0	0
70	DM	64	0	0	0	0
70	DN	73	0	0	0	0
70	DO	46	0	0	0	0
70	DP	40	0	0	0	0
70	DQ	32	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	DR	63	0	0	1	0
70	DS	44	0	0	0	0
70	DT	69	0	0	1	0
70	DU	21	0	0	0	0
70	DV	20	0	0	0	0
70	DW	31	0	0	0	0
70	DX	26	0	0	0	0
70	DY	11	0	0	0	0
70	DZ	7	0	0	1	0
All	All	295207	0	194493	1142	0

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 2.

The worst 5 of 1142 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)
46:CS:14:VAL:HG21	46:CS:98:ILE:HG13	1.26	1.10
31:CA:1936:A:H2	31:CA:1943:U:H3	1.01	0.98
2:BB:20:THR:HA	2:BB:39:HIS:CE1	1.98	0.97
1:BA:1052:G:H22	1:BA:1206:G:H1	0.98	0.94
55:DA:2796:U:H3	55:DA:2799:A:H61	1.20	0.88

There are no symmetry-related clashes.

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	222/224 (99%)	207 (93%)	11 (5%)	4 (2%)	6 28
2	BB	222/224 (99%)	207 (93%)	11 (5%)	4 (2%)	6 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	204/206 (99%)	194 (95%)	9 (4%)	1 (0%)	24	57
3	BC	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	12	41
4	AD	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
4	BD	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
5	AE	153/155 (99%)	144 (94%)	7 (5%)	2 (1%)	9	35
5	BE	148/155 (96%)	131 (88%)	14 (10%)	3 (2%)	6	25
6	AF	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
6	BF	98/106 (92%)	91 (93%)	5 (5%)	2 (2%)	6	25
7	AG	149/151 (99%)	135 (91%)	13 (9%)	1 (1%)	18	49
7	BG	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
8	AH	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	47
8	BH	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	7	30
9	AI	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
9	BI	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
10	AJ	97/99 (98%)	89 (92%)	7 (7%)	1 (1%)	12	41
10	BJ	96/99 (97%)	77 (80%)	13 (14%)	6 (6%)	1	6
11	AK	115/117 (98%)	105 (91%)	9 (8%)	1 (1%)	14	44
11	BK	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	14	44
12	AL	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
12	BL	120/123 (98%)	111 (92%)	8 (7%)	1 (1%)	16	47
13	AM	112/114 (98%)	102 (91%)	7 (6%)	3 (3%)	4	20
13	BM	112/114 (98%)	101 (90%)	6 (5%)	5 (4%)	2	12
14	AN	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	6	25
14	BN	98/100 (98%)	87 (89%)	10 (10%)	1 (1%)	12	41
15	AO	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
15	BO	86/88 (98%)	83 (96%)	2 (2%)	1 (1%)	10	37
16	AP	80/82 (98%)	73 (91%)	5 (6%)	2 (2%)	4	21
16	BP	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	21
17	AQ	78/80 (98%)	71 (91%)	6 (8%)	1 (1%)	9	35
17	BQ	78/80 (98%)	67 (86%)	7 (9%)	4 (5%)	1	10
18	AR	53/55 (96%)	50 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	BR	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
19	AS	77/79 (98%)	67 (87%)	10 (13%)	0	100	100
19	BS	77/79 (98%)	66 (86%)	10 (13%)	1 (1%)	9	35
20	AT	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
20	BT	83/86 (96%)	79 (95%)	3 (4%)	1 (1%)	10	37
21	AU	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
21	BU	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
22	C1	54/56 (96%)	47 (87%)	4 (7%)	3 (6%)	1	8
22	D1	54/56 (96%)	54 (100%)	0	0	100	100
23	C2	48/51 (94%)	43 (90%)	3 (6%)	2 (4%)	2	13
23	D2	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
24	C3	44/46 (96%)	42 (96%)	1 (2%)	1 (2%)	5	23
24	D3	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
25	C4	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
25	D4	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
26	C5	36/38 (95%)	34 (94%)	1 (3%)	1 (3%)	4	20
26	D5	36/38 (95%)	36 (100%)	0	0	100	100
27	C0	56/58 (97%)	51 (91%)	3 (5%)	2 (4%)	2	16
27	D0	57/58 (98%)	53 (93%)	4 (7%)	0	100	100
29	CC	269/272 (99%)	249 (93%)	15 (6%)	5 (2%)	6	27
29	DC	269/272 (99%)	251 (93%)	16 (6%)	2 (1%)	18	49
30	CD	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
32	DD	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
33	CE	199/201 (99%)	189 (95%)	7 (4%)	3 (2%)	8	32
33	DE	199/201 (99%)	191 (96%)	7 (4%)	1 (0%)	24	57
34	CF	175/178 (98%)	166 (95%)	9 (5%)	0	100	100
34	DF	175/178 (98%)	166 (95%)	9 (5%)	0	100	100
35	CG	174/176 (99%)	162 (93%)	7 (4%)	5 (3%)	3	19
35	DG	174/176 (99%)	165 (95%)	7 (4%)	2 (1%)	11	39
36	CH	147/149 (99%)	130 (88%)	11 (8%)	6 (4%)	2	13
36	DH	147/149 (99%)	133 (90%)	11 (8%)	3 (2%)	6	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	CJ	132/135 (98%)	125 (95%)	3 (2%)	4 (3%)	3	19
37	DJ	132/135 (98%)	125 (95%)	3 (2%)	4 (3%)	3	19
38	CK	140/142 (99%)	135 (96%)	2 (1%)	3 (2%)	5	25
38	DK	140/142 (99%)	136 (97%)	2 (1%)	2 (1%)	9	34
39	CL	120/123 (98%)	114 (95%)	4 (3%)	2 (2%)	7	30
39	DL	121/123 (98%)	116 (96%)	4 (3%)	1 (1%)	16	47
40	CM	142/144 (99%)	132 (93%)	7 (5%)	3 (2%)	5	25
40	DM	142/144 (99%)	136 (96%)	5 (4%)	1 (1%)	18	49
41	CN	133/136 (98%)	125 (94%)	7 (5%)	1 (1%)	16	47
41	DN	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
42	CO	118/125 (94%)	110 (93%)	6 (5%)	2 (2%)	7	30
42	DO	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
43	CP	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
43	DP	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
44	CQ	112/114 (98%)	107 (96%)	4 (4%)	1 (1%)	14	44
44	DQ	112/114 (98%)	107 (96%)	4 (4%)	1 (1%)	14	44
45	CR	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	44
45	DR	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	44
46	CS	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	3	19
46	DS	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	12	41
47	CT	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
47	DT	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
48	CU	91/93 (98%)	87 (96%)	4 (4%)	0	100	100
48	DU	91/93 (98%)	87 (96%)	4 (4%)	0	100	100
49	CV	100/103 (97%)	90 (90%)	6 (6%)	4 (4%)	2	13
49	DV	100/103 (97%)	96 (96%)	2 (2%)	2 (2%)	6	25
50	CW	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
50	DW	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
51	CX	73/83 (88%)	72 (99%)	1 (1%)	0	100	100
51	DX	75/83 (90%)	74 (99%)	1 (1%)	0	100	100
52	CY	75/77 (97%)	72 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	DY	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
53	CZ	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	7	30
53	DZ	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
54	DI	133/135 (98%)	112 (84%)	15 (11%)	6 (4%)	2	12
All	All	11407/11651 (98%)	10682 (94%)	590 (5%)	135 (1%)	10	37

5 of 135 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	126	PHE
3	AC	156	ARG
13	AM	5	ALA
17	AQ	82	ALA
22	C1	25	VAL

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	186/186 (100%)	170 (91%)	16 (9%)	10	34
2	BB	186/186 (100%)	171 (92%)	15 (8%)	11	36
3	AC	170/170 (100%)	156 (92%)	14 (8%)	10	36
3	BC	170/170 (100%)	156 (92%)	14 (8%)	10	36
4	AD	172/172 (100%)	165 (96%)	7 (4%)	27	59
4	BD	172/172 (100%)	165 (96%)	7 (4%)	27	59
5	AE	118/118 (100%)	101 (86%)	17 (14%)	3	14
5	BE	113/118 (96%)	90 (80%)	23 (20%)	1	5
6	AF	92/92 (100%)	84 (91%)	8 (9%)	9	34
6	BF	87/92 (95%)	75 (86%)	12 (14%)	3	15
7	AG	124/124 (100%)	111 (90%)	13 (10%)	6	26
7	BG	124/124 (100%)	108 (87%)	16 (13%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AH	104/104 (100%)	89 (86%)	15 (14%)	3	14
8	BH	104/104 (100%)	90 (86%)	14 (14%)	4	16
9	AI	105/105 (100%)	99 (94%)	6 (6%)	18	49
9	BI	105/105 (100%)	99 (94%)	6 (6%)	18	49
10	AJ	87/87 (100%)	79 (91%)	8 (9%)	8	31
10	BJ	86/87 (99%)	74 (86%)	12 (14%)	3	15
11	AK	90/90 (100%)	90 (100%)	0	100	100
11	BK	90/90 (100%)	85 (94%)	5 (6%)	19	49
12	AL	102/102 (100%)	94 (92%)	8 (8%)	11	38
12	BL	102/102 (100%)	91 (89%)	11 (11%)	6	25
13	AM	92/92 (100%)	84 (91%)	8 (9%)	9	34
13	BM	92/92 (100%)	87 (95%)	5 (5%)	20	50
14	AN	83/83 (100%)	81 (98%)	2 (2%)	43	69
14	BN	83/83 (100%)	81 (98%)	2 (2%)	43	69
15	AO	76/76 (100%)	72 (95%)	4 (5%)	20	51
15	BO	76/76 (100%)	73 (96%)	3 (4%)	28	60
16	AP	65/65 (100%)	63 (97%)	2 (3%)	35	64
16	BP	65/65 (100%)	57 (88%)	8 (12%)	4	20
17	AQ	74/74 (100%)	65 (88%)	9 (12%)	5	20
17	BQ	74/74 (100%)	66 (89%)	8 (11%)	6	25
18	AR	48/48 (100%)	45 (94%)	3 (6%)	16	45
18	BR	48/48 (100%)	47 (98%)	1 (2%)	47	71
19	AS	70/70 (100%)	61 (87%)	9 (13%)	4	18
19	BS	70/70 (100%)	63 (90%)	7 (10%)	7	29
20	AT	65/65 (100%)	60 (92%)	5 (8%)	12	38
20	BT	65/65 (100%)	53 (82%)	12 (18%)	1	8
21	AU	48/48 (100%)	44 (92%)	4 (8%)	10	35
21	BU	48/48 (100%)	44 (92%)	4 (8%)	10	35
22	C1	47/47 (100%)	46 (98%)	1 (2%)	47	71
22	D1	47/47 (100%)	46 (98%)	1 (2%)	47	71
23	C2	45/46 (98%)	41 (91%)	4 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	D2	45/46 (98%)	39 (87%)	6 (13%)	4	17
24	C3	38/38 (100%)	36 (95%)	2 (5%)	20	51
24	D3	38/38 (100%)	37 (97%)	1 (3%)	40	68
25	C4	51/51 (100%)	49 (96%)	2 (4%)	28	60
25	D4	51/51 (100%)	50 (98%)	1 (2%)	48	72
26	C5	34/34 (100%)	33 (97%)	1 (3%)	37	66
26	D5	34/34 (100%)	34 (100%)	0	100	100
27	C0	48/48 (100%)	39 (81%)	9 (19%)	1	7
27	D0	49/48 (102%)	46 (94%)	3 (6%)	17	46
29	CC	216/217 (100%)	200 (93%)	16 (7%)	13	40
29	DC	216/217 (100%)	206 (95%)	10 (5%)	24	55
30	CD	164/164 (100%)	156 (95%)	8 (5%)	22	53
32	DD	163/163 (100%)	157 (96%)	6 (4%)	30	61
33	CE	165/165 (100%)	151 (92%)	14 (8%)	10	35
33	DE	165/165 (100%)	160 (97%)	5 (3%)	36	65
34	CF	148/149 (99%)	129 (87%)	19 (13%)	4	18
34	DF	148/149 (99%)	132 (89%)	16 (11%)	6	25
35	CG	137/137 (100%)	131 (96%)	6 (4%)	25	56
35	DG	137/137 (100%)	131 (96%)	6 (4%)	25	56
36	CH	114/114 (100%)	99 (87%)	15 (13%)	4	17
36	DH	114/114 (100%)	98 (86%)	16 (14%)	3	15
37	CJ	104/105 (99%)	97 (93%)	7 (7%)	15	43
37	DJ	104/105 (99%)	97 (93%)	7 (7%)	15	43
38	CK	116/116 (100%)	112 (97%)	4 (3%)	32	63
38	DK	116/116 (100%)	113 (97%)	3 (3%)	40	68
39	CL	103/104 (99%)	98 (95%)	5 (5%)	22	53
39	DL	104/104 (100%)	101 (97%)	3 (3%)	37	66
40	CM	103/103 (100%)	96 (93%)	7 (7%)	14	42
40	DM	103/103 (100%)	98 (95%)	5 (5%)	22	53
41	CN	108/108 (100%)	101 (94%)	7 (6%)	15	44
41	DN	109/108 (101%)	105 (96%)	4 (4%)	30	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	CO	100/102 (98%)	92 (92%)	8 (8%)	11	37
42	DO	102/102 (100%)	98 (96%)	4 (4%)	28	60
43	CP	86/87 (99%)	77 (90%)	9 (10%)	6	26
43	DP	87/87 (100%)	81 (93%)	6 (7%)	14	41
44	CQ	99/99 (100%)	91 (92%)	8 (8%)	11	36
44	DQ	99/99 (100%)	93 (94%)	6 (6%)	17	46
45	CR	89/89 (100%)	84 (94%)	5 (6%)	19	49
45	DR	89/89 (100%)	86 (97%)	3 (3%)	32	63
46	CS	84/84 (100%)	78 (93%)	6 (7%)	13	41
46	DS	84/84 (100%)	82 (98%)	2 (2%)	43	69
47	CT	93/93 (100%)	87 (94%)	6 (6%)	15	44
47	DT	93/93 (100%)	90 (97%)	3 (3%)	34	64
48	CU	80/80 (100%)	71 (89%)	9 (11%)	5	23
48	DU	80/80 (100%)	76 (95%)	4 (5%)	22	53
49	CV	83/84 (99%)	77 (93%)	6 (7%)	13	40
49	DV	83/84 (99%)	79 (95%)	4 (5%)	23	54
50	CW	78/78 (100%)	72 (92%)	6 (8%)	12	38
50	DW	78/78 (100%)	74 (95%)	4 (5%)	21	52
51	CX	56/62 (90%)	53 (95%)	3 (5%)	20	50
51	DX	58/62 (94%)	55 (95%)	3 (5%)	21	51
52	CY	67/67 (100%)	62 (92%)	5 (8%)	12	39
52	DY	67/67 (100%)	64 (96%)	3 (4%)	24	56
53	CZ	54/54 (100%)	48 (89%)	6 (11%)	6	24
53	DZ	54/54 (100%)	50 (93%)	4 (7%)	13	40
54	DI	103/103 (100%)	95 (92%)	8 (8%)	11	38
All	All	9461/9494 (100%)	8767 (93%)	694 (7%)	13	40

5 of 694 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	CH	76	GLU
53	CZ	38	GLN
38	CK	81	ILE

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Mol	Chain	Res	Type
36	CH	75	LEU
44	CQ	102	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
35	DG	104	ASN
36	DH	20	ASN
47	DT	60	HIS
5	BE	89	HIS
5	BE	77	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1533/1534 (99%)	265 (17%)	31 (2%)
1	BA	1532/1534 (99%)	266 (17%)	36 (2%)
28	CB	117/120 (97%)	12 (10%)	0
28	DB	119/120 (99%)	10 (8%)	0
31	CA	2896/2904 (99%)	477 (16%)	78 (2%)
55	DA	2884/2904 (99%)	418 (14%)	62 (2%)
All	All	9081/9116 (99%)	1448 (15%)	207 (2%)

5 of 1448 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	6	G
1	AA	9	G
1	AA	22	G

5 of 207 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	CA	1536	C
31	CA	2873	A
55	DA	2406	A
31	CA	1647	U
31	CA	2157	G

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

75 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	5MU	DA	1939	55	19,22,23	0.48	0	27,32,35	0.43	0
55	2MG	DA	2445	55	23,26,27	0.51	0	33,38,41	0.39	0
31	1MG	CA	745	31	23,26,27	0.87	1 (4%)	33,39,42	0.69	2 (6%)
1	4OC	AA	1402	1	20,23,24	0.34	0	25,32,35	0.44	0
31	5MU	CA	747	31	19,22,23	0.39	0	27,32,35	0.30	0
55	PSU	DA	955	55	18,21,22	0.67	0	21,30,33	0.53	0
31	2MG	CA	1835	31	23,26,27	0.37	0	33,38,41	0.37	0
55	H2U	DA	2449	55	18,21,22	0.47	0	19,30,33	0.67	1 (5%)
41	4D4	CN	81	41	9,11,12	2.30	2 (22%)	7,13,15	2.55	2 (28%)
1	2MG	BA	1516	1	23,26,27	0.36	0	33,38,41	0.58	0
55	PSU	DA	2457	55	18,21,22	0.54	0	21,30,33	0.46	0
12	D2T	BL	89	12	8,9,10	1.24	1 (12%)	6,11,13	1.33	1 (16%)
55	6MZ	DA	2030	55	22,25,26	0.63	0	29,36,39	0.50	0
55	PSU	DA	2604	55	18,21,22	0.79	0	21,30,33	0.52	0
31	6MZ	CA	1618	31	22,25,26	0.46	0	29,36,39	0.55	0
31	5MU	CA	1939	31	19,22,23	0.43	0	27,32,35	0.36	0
1	2MG	AA	1516	1	23,26,27	0.27	0	33,38,41	0.58	0
31	6MZ	CA	2030	31	22,25,26	0.35	0	29,36,39	0.46	0
12	D2T	AL	89	12	8,9,10	1.37	2 (25%)	6,11,13	1.15	0
1	5MC	BA	967	1	19,22,23	0.30	0	26,32,35	0.40	0
32	MEQ	DD	150[A]	32	8,9,10	0.39	0	5,10,12	0.53	0
1	2MG	BA	966	1	23,26,27	0.32	0	33,38,41	0.41	0
1	UR3	AA	1498	1	19,22,23	0.48	0	26,32,35	0.33	0
1	5MC	AA	967	1	19,22,23	0.32	0	26,32,35	0.42	0
1	PSU	AA	516	56,1	18,21,22	0.33	0	21,30,33	0.48	0
31	PSU	CA	1917	31	18,21,22	0.31	0	21,30,33	0.40	0
1	4OC	BA	1402	1	20,23,24	0.34	0	25,32,35	0.45	0
1	MA6	BA	1519	1	23,26,27	0.53	0	33,38,41	1.13	5 (15%)
32	MEQ	DD	150[B]	32	8,9,10	0.98	1 (12%)	5,10,12	0.73	0
55	PSU	DA	1917	55	18,21,22	0.35	0	21,30,33	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	AA	1519	1	23,26,27	0.54	0	33,38,41	1.10	4 (12%)
31	PSU	CA	955	31	18,21,22	0.31	0	21,30,33	0.50	0
55	OMU	DA	2552	55	19,22,23	0.47	0	25,31,34	0.31	0
31	PSU	CA	2504	31	18,21,22	0.36	0	21,30,33	0.43	0
55	PSU	DA	746	56,55	18,21,22	0.94	1 (5%)	21,30,33	0.32	0
1	5MC	BA	1407	1	19,22,23	0.41	0	26,32,35	0.51	0
55	PSU	DA	2605	55	18,21,22	0.45	0	21,30,33	0.53	0
55	5MC	DA	1962	55	19,22,23	0.54	0	26,32,35	0.44	0
1	2MG	AA	966	1	23,26,27	0.43	0	33,38,41	0.53	0
1	PSU	BA	516	1	18,21,22	0.37	0	21,30,33	0.46	0
31	PSU	CA	1911	31	18,21,22	0.27	0	21,30,33	0.40	0
31	5MC	CA	1962	31	19,22,23	0.28	0	26,32,35	0.37	0
31	2MG	CA	2445	31	23,26,27	0.42	0	33,38,41	0.44	0
31	2MA	CA	2503	31	22,25,26	0.72	0	32,37,40	1.98	6 (18%)
31	OMU	CA	2552	31	19,22,23	0.30	0	25,31,34	0.28	0
55	PSU	DA	1911	55	18,21,22	0.28	0	21,30,33	0.39	0
55	OMG	DA	2251	55	23,26,27	0.39	0	32,38,41	0.35	0
31	OMG	CA	2251	31	23,26,27	0.36	0	32,38,41	0.42	0
31	PSU	CA	746	56,31	18,21,22	0.54	1 (5%)	21,30,33	0.43	0
31	PSU	CA	2457	31	18,21,22	0.66	0	21,30,33	0.48	0
55	6MZ	DA	1618	55	22,25,26	0.44	0	29,36,39	1.40	1 (3%)
1	5MC	AA	1407	1	19,22,23	0.40	0	26,32,35	0.53	0
55	OMC	DA	2498	56,55	19,22,23	0.34	0	25,31,34	0.52	0
1	MA6	BA	1518	1	23,26,27	0.40	0	33,38,41	1.23	4 (12%)
1	2MG	BA	1207	1	23,26,27	0.29	0	33,38,41	0.42	0
1	UR3	BA	1498	1	19,22,23	0.85	0	26,32,35	0.72	1 (3%)
1	MA6	AA	1518	1	23,26,27	0.45	0	33,38,41	1.20	4 (12%)
41	4D4	DN	81[A]	-	9,11,12	1.77	2 (22%)	7,13,15	2.46	2 (28%)
55	7MG	DA	2069	55	23,26,27	4.17	3 (13%)	27,39,42	2.19	6 (22%)
55	5MU	DA	747	55	19,22,23	0.41	0	27,32,35	0.32	0
55	PSU	DA	2580	55	18,21,22	0.74	0	21,30,33	0.63	0
1	7MG	BA	527	1	23,26,27	4.15	2 (8%)	27,39,42	2.58	6 (22%)
55	1MG	DA	745	55	23,26,27	0.85	1 (4%)	33,39,42	0.58	1 (3%)
55	2MG	DA	1835	55	23,26,27	0.30	0	33,38,41	0.33	0
31	PSU	CA	2605	31	18,21,22	0.45	0	21,30,33	0.58	0
55	PSU	DA	2504	55	18,21,22	0.46	0	21,30,33	0.41	0
31	OMC	CA	2498	56,31	19,22,23	0.46	0	25,31,34	0.52	0
55	2MA	DA	2503	56,55	22,25,26	0.76	0	32,37,40	1.79	6 (18%)
41	4D4	DN	81[B]	-	9,11,12	1.85	2 (22%)	7,13,15	2.69	2 (28%)
1	2MG	AA	1207	1	23,26,27	0.23	0	33,38,41	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	3TD	DA	1915	55	19,22,23	0.51	0	23,32,35	0.90	1 (4%)
31	PSU	CA	2580	31	18,21,22	0.50	0	21,30,33	0.60	0
31	7MG	CA	2069	31	23,26,27	4.11	3 (13%)	27,39,42	2.35	6 (22%)
1	7MG	AA	527	1	23,26,27	4.19	2 (8%)	27,39,42	2.57	6 (22%)
31	3TD	CA	1915	31	19,22,23	0.51	0	23,32,35	0.85	1 (4%)

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	5MU	DA	1939	55	-	0/7/25/26	0/2/2/2
55	2MG	DA	2445	55	-	2/9/27/28	0/3/3/3
31	1MG	CA	745	31	-	0/7/25/26	0/3/3/3
1	4OC	AA	1402	1	-	1/9/29/30	0/2/2/2
31	5MU	CA	747	31	-	0/7/25/26	0/2/2/2
55	PSU	DA	955	55	-	0/7/25/26	0/2/2/2
31	2MG	CA	1835	31	-	1/9/27/28	0/3/3/3
55	H2U	DA	2449	55	-	0/7/38/39	0/2/2/2
41	4D4	CN	81	41	-	1/11/12/14	-
1	2MG	BA	1516	1	-	0/9/27/28	0/3/3/3
55	PSU	DA	2457	55	-	0/7/25/26	0/2/2/2
12	D2T	BL	89	12	-	4/7/12/14	-
55	6MZ	DA	2030	55	-	2/9/27/28	0/3/3/3
55	PSU	DA	2604	55	-	0/7/25/26	0/2/2/2
31	6MZ	CA	1618	31	-	1/9/27/28	0/3/3/3
31	5MU	CA	1939	31	-	0/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3
31	6MZ	CA	2030	31	-	2/9/27/28	0/3/3/3
12	D2T	AL	89	12	-	1/7/12/14	-
1	5MC	BA	967	1	-	0/7/25/26	0/2/2/2
32	MEQ	DD	150[A]	32	-	4/8/9/11	-
1	2MG	BA	966	1	-	0/9/27/28	0/3/3/3
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
1	PSU	AA	516	56,1	-	0/7/25/26	0/2/2/2
31	PSU	CA	1917	31	-	0/7/25/26	0/2/2/2
1	4OC	BA	1402	1	-	1/9/29/30	0/2/2/2
1	MA6	BA	1519	1	-	2/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	MEQ	DD	150[B]	32	-	4/8/9/11	-
55	PSU	DA	1917	55	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	2/11/29/30	0/3/3/3
31	PSU	CA	955	31	-	0/7/25/26	0/2/2/2
55	OMU	DA	2552	55	-	1/9/27/28	0/2/2/2
31	PSU	CA	2504	31	-	1/7/25/26	0/2/2/2
55	PSU	DA	746	56,55	-	2/7/25/26	0/2/2/2
1	5MC	BA	1407	1	-	0/7/25/26	0/2/2/2
55	PSU	DA	2605	55	-	0/7/25/26	0/2/2/2
55	5MC	DA	1962	55	-	2/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	0/9/27/28	0/3/3/3
1	PSU	BA	516	1	-	0/7/25/26	0/2/2/2
31	PSU	CA	1911	31	-	0/7/25/26	0/2/2/2
31	5MC	CA	1962	31	-	0/7/25/26	0/2/2/2
31	2MG	CA	2445	31	-	0/9/27/28	0/3/3/3
31	2MA	CA	2503	31	-	1/7/25/26	0/3/3/3
31	OMU	CA	2552	31	-	1/9/27/28	0/2/2/2
55	PSU	DA	1911	55	-	0/7/25/26	0/2/2/2
55	OMG	DA	2251	55	-	1/9/27/28	0/3/3/3
31	OMG	CA	2251	31	-	0/9/27/28	0/3/3/3
31	PSU	CA	746	56,31	-	2/7/25/26	0/2/2/2
31	PSU	CA	2457	31	-	0/7/25/26	0/2/2/2
55	6MZ	DA	1618	55	-	0/9/27/28	0/3/3/3
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
55	OMC	DA	2498	56,55	-	0/9/27/28	0/2/2/2
1	MA6	BA	1518	1	-	0/11/29/30	0/3/3/3
1	2MG	BA	1207	1	-	0/9/27/28	0/3/3/3
1	UR3	BA	1498	1	-	0/7/25/26	0/2/2/2
1	MA6	AA	1518	1	-	0/11/29/30	0/3/3/3
41	4D4	DN	81[A]	-	-	1/11/12/14	-
55	7MG	DA	2069	55	-	1/7/37/38	0/3/3/3
55	5MU	DA	747	55	-	1/7/25/26	0/2/2/2
55	PSU	DA	2580	55	-	0/7/25/26	0/2/2/2
1	7MG	BA	527	1	-	2/7/37/38	0/3/3/3
55	1MG	DA	745	55	-	0/7/25/26	0/3/3/3
55	2MG	DA	1835	55	-	2/9/27/28	0/3/3/3
31	PSU	CA	2605	31	-	0/7/25/26	0/2/2/2
55	PSU	DA	2504	55	-	1/7/25/26	0/2/2/2
31	OMC	CA	2498	56,31	-	0/9/27/28	0/2/2/2
55	2MA	DA	2503	56,55	-	1/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	4D4	DN	81[B]	-	-	3/11/12/14	-
1	2MG	AA	1207	1	-	0/9/27/28	0/3/3/3
55	3TD	DA	1915	55	-	0/7/25/26	0/2/2/2
31	PSU	CA	2580	31	-	0/7/25/26	0/2/2/2
31	7MG	CA	2069	31	-	0/7/37/38	0/3/3/3
1	7MG	AA	527	1	-	2/7/37/38	0/3/3/3
31	3TD	CA	1915	31	-	0/7/25/26	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	527	7MG	C8-N9	-19.65	1.33	1.45
55	DA	2069	7MG	C8-N9	-19.53	1.33	1.45
1	BA	527	7MG	C8-N9	-19.48	1.33	1.45
31	CA	2069	7MG	C8-N9	-19.17	1.33	1.45
41	CN	81	4D4	CZ-NE	6.24	1.45	1.33

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	CA	2503	2MA	N6-C6-N1	8.41	128.38	117.03
55	DA	2503	2MA	N6-C6-N1	7.51	127.16	117.03
55	DA	1618	6MZ	C9-N6-C6	-7.33	116.06	122.85
1	BA	527	7MG	C6-C5-N7	-6.55	121.78	131.93
1	AA	527	7MG	O4'-C1'-N9	6.49	118.14	109.30

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	527	7MG	O4'-C4'-C5'-O5'
1	BA	527	7MG	O4'-C4'-C5'-O5'
1	BA	527	7MG	C3'-C4'-C5'-O5'
32	DD	150[A]	MEQ	N-CA-CB-CG
32	DD	150[A]	MEQ	C-CA-CB-CG

There are no ring outliers.

17 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	DA	2030	6MZ	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	CA	2030	6MZ	1	0
1	BA	967	5MC	1	0
32	DD	150[A]	MEQ	3	0
1	AA	967	5MC	1	0
1	BA	1519	MA6	1	0
32	DD	150[B]	MEQ	1	0
1	AA	1519	MA6	1	0
31	CA	2503	2MA	1	0
55	DA	2251	OMG	1	0
55	DA	2498	OMC	1	0
1	BA	1518	MA6	1	0
1	AA	1518	MA6	1	0
31	CA	2498	OMC	2	0
55	DA	2503	2MA	1	0
31	CA	2580	PSU	1	0
31	CA	1915	3TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 557 ligands modelled in this entry, 475 are monoatomic - leaving 82 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	$\# Z > 2$
59	PUT	AA	1674	-	5,5,5	0.14	0	4,4,4	0.10	0
58	MPD	DT	201	-	7,7,7	0.46	0	9,10,10	0.35	0
59	PUT	DA	3223	-	5,5,5	0.16	0	4,4,4	0.12	0
59	PUT	DA	3189	-	5,5,5	0.29	0	4,4,4	0.20	0
59	PUT	DA	3195	-	5,5,5	0.31	0	4,4,4	0.36	0
64	PGE	DA	3214	-	9,9,9	0.19	0	8,8,8	0.27	0
63	EDO	DA	3197	-	3,3,3	0.60	0	2,2,2	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
59	PUT	AA	1675	-	5,5,5	0.20	0	4,4,4	0.13	0
59	PUT	DA	3184	-	5,5,5	0.15	0	4,4,4	0.11	0
57	PG4	DR	202	-	12,12,12	0.26	0	11,11,11	0.36	0
63	EDO	DB	201	-	3,3,3	0.61	0	2,2,2	0.19	0
67	ACY	DA	3201	-	3,3,3	0.76	0	3,3,3	1.05	0
64	PGE	DA	3217	-	9,9,9	0.16	0	8,8,8	0.13	0
64	PGE	DS	201	-	9,9,9	0.25	0	8,8,8	0.20	0
59	PUT	AA	1673	-	5,5,5	0.10	0	4,4,4	0.07	0
58	MPD	DN	201	-	7,7,7	0.79	0	9,10,10	0.54	0
63	EDO	DA	3208	-	3,3,3	0.60	0	2,2,2	0.22	0
63	EDO	DA	3215	-	3,3,3	0.62	0	2,2,2	0.23	0
59	PUT	DA	3188	-	5,5,5	0.20	0	4,4,4	0.13	0
65	SPD	DA	3224	-	9,9,9	0.19	0	8,8,8	0.40	0
59	PUT	DA	3222	-	5,5,5	0.44	0	4,4,4	0.58	0
59	PUT	DA	3213	-	5,5,5	0.16	0	4,4,4	0.17	0
63	EDO	DA	3002	-	3,3,3	0.62	0	2,2,2	0.24	0
64	PGE	D3	101	-	9,9,9	0.23	0	8,8,8	0.22	0
63	EDO	DA	3194	-	3,3,3	0.72	0	2,2,2	0.15	0
62	PEG	D3	102	-	6,6,6	0.21	0	5,5,5	0.19	0
58	MPD	DA	3204	-	7,7,7	0.69	0	9,10,10	0.69	0
57	PG4	DQ	202	-	12,12,12	0.20	0	11,11,11	0.14	0
58	MPD	DA	3190	-	7,7,7	0.32	0	9,10,10	0.52	0
59	PUT	DA	3221	-	5,5,5	0.16	0	4,4,4	0.11	0
58	MPD	AA	1671	-	7,7,7	0.58	0	9,10,10	0.55	0
58	MPD	DA	3210	-	7,7,7	0.56	0	9,10,10	0.30	0
59	PUT	AA	1672	-	5,5,5	0.19	0	4,4,4	0.21	0
58	MPD	DE	301	-	7,7,7	0.72	0	9,10,10	0.60	0
60	T1C	BA	1643	56	45,45,45	1.05	3 (6%)	56,72,72	1.64	7 (12%)
62	PEG	DA	3218	-	6,6,6	0.17	0	5,5,5	0.08	0
58	MPD	DK	201	-	7,7,7	0.58	0	9,10,10	0.28	0
62	PEG	DQ	201	-	6,6,6	0.13	0	5,5,5	0.09	0
63	EDO	D1	101	-	3,3,3	0.56	0	2,2,2	0.15	0
60	T1C	AA	1680	56	45,45,45	1.06	3 (6%)	56,72,72	1.56	4 (7%)
59	PUT	DA	3219	-	5,5,5	0.16	0	4,4,4	0.20	0
64	PGE	DA	3203	-	9,9,9	0.21	0	8,8,8	0.20	0
67	ACY	DA	3191	-	3,3,3	0.59	0	3,3,3	0.95	0
67	ACY	DA	3196	-	3,3,3	2.27	1 (33%)	3,3,3	2.32	2 (66%)
69	TRS	DA	3220	-	7,7,7	0.31	0	9,9,9	0.34	0
63	EDO	DA	3209	-	3,3,3	0.54	0	2,2,2	0.32	0
57	PG4	BA	1642	-	12,12,12	0.15	0	11,11,11	0.19	0
62	PEG	DA	3227	-	6,6,6	0.22	0	5,5,5	0.14	0
65	SPD	DA	3183	-	9,9,9	0.10	0	8,8,8	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	EDO	DA	3198	-	3,3,3	0.59	0	2,2,2	0.24	0
64	PGE	DA	3225	-	9,9,9	0.12	0	8,8,8	0.17	0
59	PUT	DA	3001	-	5,5,5	0.24	0	4,4,4	0.13	0
63	EDO	DB	211	-	3,3,3	0.64	0	2,2,2	0.14	0
62	PEG	DA	3226	-	6,6,6	0.24	0	5,5,5	0.12	0
62	PEG	DP	201	-	6,6,6	0.16	0	5,5,5	0.08	0
59	PUT	DA	3205	-	5,5,5	0.11	0	4,4,4	0.10	0
62	PEG	DA	3199	-	6,6,6	0.24	0	5,5,5	0.15	0
58	MPD	DT	202	-	7,7,7	0.62	0	9,10,10	0.38	0
63	EDO	DB	213	-	3,3,3	0.66	0	2,2,2	0.08	0
57	PG4	DA	3216	-	12,12,12	0.10	0	11,11,11	0.17	0
57	PG4	DA	3193	-	12,12,12	0.29	0	11,11,11	0.25	0
65	SPD	DA	3187	-	9,9,9	0.21	0	8,8,8	0.19	0
58	MPD	DS	203	-	7,7,7	0.31	0	9,10,10	0.52	0
62	PEG	DA	3200	-	6,6,6	0.35	0	5,5,5	0.21	0
66	1PE	DA	3185	-	15,15,15	0.19	0	14,14,14	0.21	0
57	PG4	DS	202	-	12,12,12	0.46	0	11,11,11	0.29	0
64	PGE	DA	3186	-	9,9,9	0.24	0	8,8,8	0.29	0
57	PG4	AA	1670	-	12,12,12	0.31	0	11,11,11	0.28	0
64	PGE	D1	102	-	9,9,9	0.20	0	8,8,8	0.14	0
58	MPD	DE	302	-	7,7,7	0.79	0	9,10,10	0.61	0
58	MPD	AA	1676	-	7,7,7	0.53	0	9,10,10	0.59	0
58	MPD	DA	3207	-	7,7,7	0.68	0	9,10,10	0.53	0
68	GUN	DA	3211	-	12,12,12	0.37	0	15,17,17	0.31	0
66	1PE	DA	3202	-	15,15,15	0.32	0	14,14,14	0.34	0
59	PUT	DA	3212	-	5,5,5	0.17	0	4,4,4	0.04	0
62	PEG	DL	201	-	6,6,6	0.07	0	5,5,5	0.10	0
58	MPD	DA	3192	-	7,7,7	0.45	0	9,10,10	0.58	0
63	EDO	DB	212	-	3,3,3	0.52	0	2,2,2	0.34	0
62	PEG	D1	103	-	6,6,6	0.31	0	5,5,5	0.15	0
65	SPD	DA	3206	-	9,9,9	0.20	0	8,8,8	0.17	0
64	PGE	DU	101	-	9,9,9	0.23	0	8,8,8	0.12	0
62	PEG	AL	201	-	6,6,6	0.23	0	5,5,5	0.12	0

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
59	PUT	AA	1674	-	-	0/3/3/3	-
58	MPD	DT	201	-	-	3/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	PUT	DA	3223	-	-	1/3/3/3	-
59	PUT	DA	3189	-	-	0/3/3/3	-
59	PUT	DA	3195	-	-	1/3/3/3	-
64	PGE	DA	3214	-	-	2/7/7/7	-
63	EDO	DA	3197	-	-	0/1/1/1	-
59	PUT	AA	1675	-	-	1/3/3/3	-
59	PUT	DA	3184	-	-	0/3/3/3	-
57	PG4	DR	202	-	-	5/10/10/10	-
63	EDO	DB	201	-	-	1/1/1/1	-
64	PGE	DA	3217	-	-	4/7/7/7	-
64	PGE	DS	201	-	-	3/7/7/7	-
59	PUT	AA	1673	-	-	0/3/3/3	-
58	MPD	DN	201	-	-	2/5/5/5	-
63	EDO	DA	3208	-	-	0/1/1/1	-
63	EDO	DA	3215	-	-	1/1/1/1	-
59	PUT	DA	3188	-	-	0/3/3/3	-
65	SPD	DA	3224	-	-	3/7/7/7	-
59	PUT	DA	3222	-	-	0/3/3/3	-
59	PUT	DA	3213	-	-	0/3/3/3	-
63	EDO	DA	3002	-	-	0/1/1/1	-
64	PGE	D3	101	-	-	2/7/7/7	-
63	EDO	DA	3194	-	-	0/1/1/1	-
62	PEG	D3	102	-	-	1/4/4/4	-
58	MPD	DA	3204	-	-	4/5/5/5	-
57	PG4	DQ	202	-	-	1/10/10/10	-
58	MPD	DA	3190	-	-	2/5/5/5	-
59	PUT	DA	3221	-	-	0/3/3/3	-
58	MPD	AA	1671	-	-	0/5/5/5	-
58	MPD	DA	3210	-	-	0/5/5/5	-
59	PUT	AA	1672	-	-	0/3/3/3	-
58	MPD	DE	301	-	-	2/5/5/5	-
60	T1C	BA	1643	56	-	11/22/80/80	0/4/4/4
62	PEG	DA	3218	-	-	1/4/4/4	-
58	MPD	DK	201	-	-	2/5/5/5	-
62	PEG	DQ	201	-	-	1/4/4/4	-
63	EDO	D1	101	-	-	0/1/1/1	-
60	T1C	AA	1680	56	-	6/22/80/80	0/4/4/4
59	PUT	DA	3219	-	-	0/3/3/3	-
64	PGE	DA	3203	-	-	5/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	TRS	DA	3220	-	-	0/9/9/9	-
63	EDO	DA	3209	-	-	0/1/1/1	-
57	PG4	BA	1642	-	-	0/10/10/10	-
62	PEG	DA	3227	-	-	0/4/4/4	-
65	SPD	DA	3183	-	-	1/7/7/7	-
63	EDO	DA	3198	-	-	1/1/1/1	-
64	PGE	DA	3225	-	-	4/7/7/7	-
59	PUT	DA	3001	-	-	0/3/3/3	-
63	EDO	DB	211	-	-	0/1/1/1	-
62	PEG	DA	3226	-	-	2/4/4/4	-
62	PEG	DP	201	-	-	2/4/4/4	-
59	PUT	DA	3205	-	-	0/3/3/3	-
62	PEG	DA	3199	-	-	2/4/4/4	-
58	MPD	DT	202	-	-	2/5/5/5	-
63	EDO	DB	213	-	-	0/1/1/1	-
57	PG4	DA	3216	-	-	3/10/10/10	-
57	PG4	DA	3193	-	-	5/10/10/10	-
65	SPD	DA	3187	-	-	2/7/7/7	-
58	MPD	DS	203	-	-	1/5/5/5	-
62	PEG	DA	3200	-	-	2/4/4/4	-
66	1PE	DA	3185	-	-	5/13/13/13	-
57	PG4	DS	202	-	-	5/10/10/10	-
64	PGE	DA	3186	-	-	3/7/7/7	-
57	PG4	AA	1670	-	-	4/10/10/10	-
64	PGE	D1	102	-	-	3/7/7/7	-
58	MPD	DE	302	-	-	2/5/5/5	-
58	MPD	AA	1676	-	-	4/5/5/5	-
58	MPD	DA	3207	-	-	2/5/5/5	-
68	GUN	DA	3211	-	-	-	0/2/2/2
66	1PE	DA	3202	-	-	4/13/13/13	-
59	PUT	DA	3212	-	-	0/3/3/3	-
62	PEG	DL	201	-	-	2/4/4/4	-
58	MPD	DA	3192	-	-	1/5/5/5	-
63	EDO	DB	212	-	-	1/1/1/1	-
62	PEG	D1	103	-	-	0/4/4/4	-
65	SPD	DA	3206	-	-	3/7/7/7	-
64	PGE	DU	101	-	-	3/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	PEG	AL	201	-	-	2/4/4/4	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	DA	3196	ACY	O-C	3.74	1.38	1.22
60	BA	1643	T1C	C4-C3	3.30	1.58	1.51
60	AA	1680	T1C	C4-C3	2.99	1.57	1.51
60	AA	1680	T1C	C7-C61	2.96	1.43	1.40
60	BA	1643	T1C	C7-C61	2.91	1.43	1.40

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BA	1643	T1C	C92-N92-C93	7.92	125.80	115.77
60	AA	1680	T1C	C92-N92-C93	7.68	125.49	115.77
60	AA	1680	T1C	C8-C9-C10	-5.29	115.41	120.53
60	BA	1643	T1C	C8-C9-C10	-4.69	115.98	120.53
60	BA	1643	T1C	C61-C6-C51	-3.60	108.36	113.12

There are no chirality outliers.

5 of 136 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AA	1676	MPD	C2-C3-C4-C5
58	DA	3192	MPD	C2-C3-C4-O4
60	AA	1680	T1C	C95-C93-N92-C92
60	AA	1680	T1C	C96-C93-N92-C92
60	AA	1680	T1C	C91-C92-N92-C93

There are no ring outliers.

24 monomers are involved in 32 short contacts:

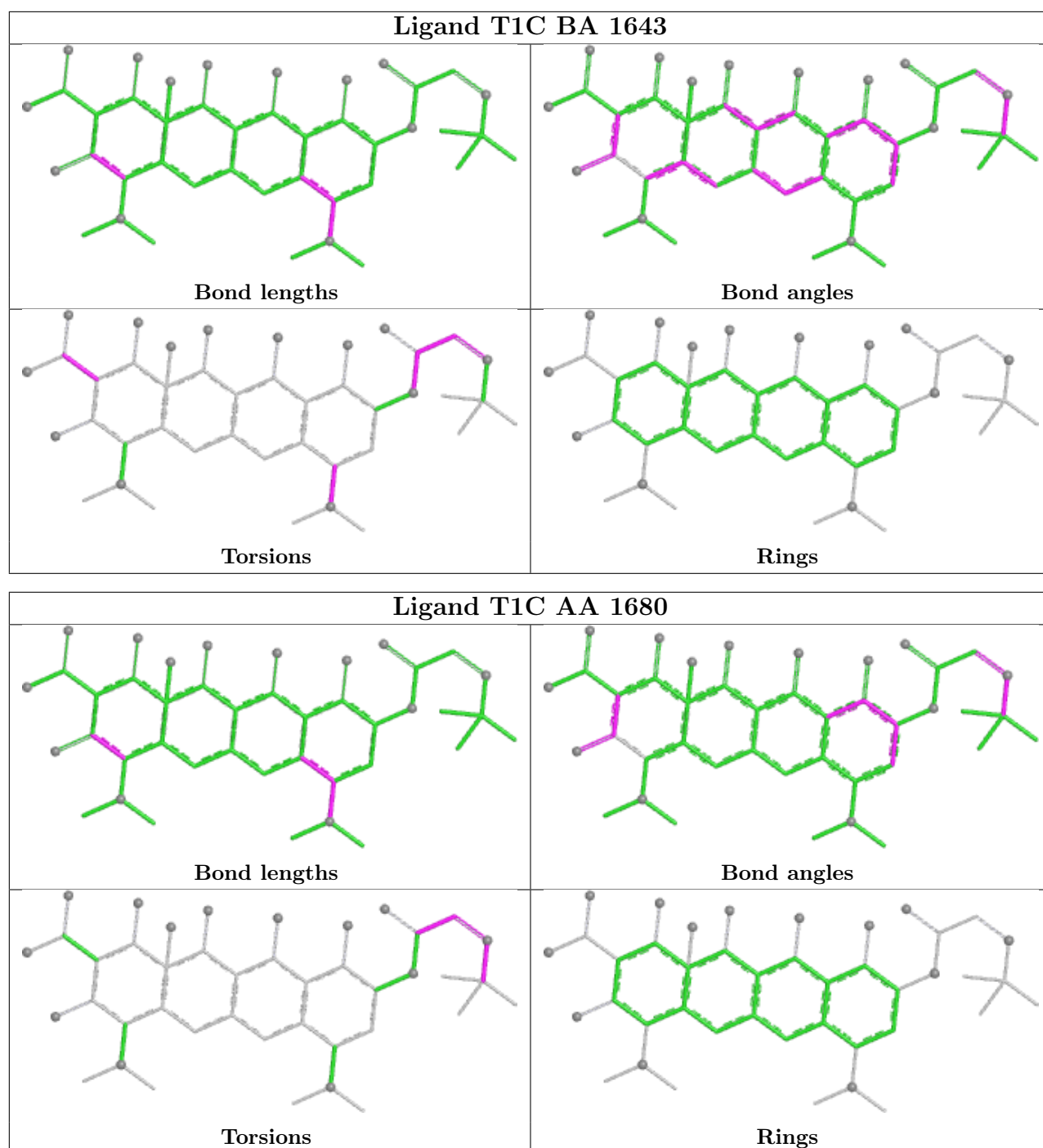
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	DA	3223	PUT	1	0
59	DA	3195	PUT	1	0
64	DA	3214	PGE	1	0
57	DR	202	PG4	4	0
64	DA	3217	PGE	1	0
64	DS	201	PGE	1	0
58	DN	201	MPD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
65	DA	3224	SPD	2	0
58	DA	3204	MPD	1	0
60	AA	1680	T1C	2	0
59	DA	3219	PUT	1	0
64	DA	3203	PGE	1	0
69	DA	3220	TRS	1	0
63	DA	3209	EDO	1	0
57	BA	1642	PG4	1	0
64	DA	3225	PGE	2	0
66	DA	3185	1PE	1	0
57	DS	202	PG4	1	0
57	AA	1670	PG4	1	0
64	D1	102	PGE	2	0
66	DA	3202	1PE	2	0
58	DA	3192	MPD	1	0
62	D1	103	PEG	1	0
64	DU	101	PGE	1	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	1523/1534 (99%)	0.12	84 (5%) 30 16	43, 96, 240, 296	0
1	BA	1522/1534 (99%)	0.37	96 (6%) 26 14	59, 109, 268, 280	0
2	AB	224/224 (100%)	0.50	8 (3%) 46 26	72, 125, 197, 249	0
2	BB	224/224 (100%)	0.71	15 (6%) 24 13	101, 143, 205, 240	0
3	AC	206/206 (100%)	0.29	6 (2%) 53 32	78, 108, 137, 154	0
3	BC	206/206 (100%)	0.60	16 (7%) 19 10	103, 151, 181, 204	0
4	AD	205/205 (100%)	0.15	1 (0%) 87 73	71, 104, 137, 164	0
4	BD	205/205 (100%)	-0.07	0 100 100	51, 77, 108, 132	0
5	AE	155/155 (100%)	0.01	0 100 100	59, 84, 116, 155	0
5	BE	150/155 (96%)	0.41	5 (3%) 49 29	68, 94, 135, 207	0
6	AF	106/106 (100%)	0.29	1 (0%) 81 63	78, 107, 128, 148	0
6	BF	100/106 (94%)	0.34	3 (3%) 52 31	88, 124, 147, 160	0
7	AG	151/151 (100%)	0.96	19 (12%) 8 4	108, 141, 166, 178	0
7	BG	151/151 (100%)	1.34	35 (23%) 2 1	145, 205, 222, 231	0
8	AH	129/129 (100%)	0.19	4 (3%) 51 30	67, 89, 116, 132	0
8	BH	129/129 (100%)	0.34	6 (4%) 36 19	90, 113, 141, 157	0
9	AI	127/127 (100%)	1.05	20 (15%) 5 2	86, 142, 167, 175	0
9	BI	127/127 (100%)	1.47	27 (21%) 2 1	141, 172, 209, 221	0
10	AJ	99/99 (100%)	1.19	21 (21%) 2 1	91, 129, 150, 161	0
10	BJ	98/99 (98%)	1.53	30 (30%) 1 1	144, 175, 196, 202	0
11	AK	117/117 (100%)	0.48	4 (3%) 48 28	59, 117, 141, 150	0
11	BK	117/117 (100%)	0.64	9 (7%) 19 10	69, 115, 149, 175	0
12	AL	122/123 (99%)	-0.02	2 (1%) 70 49	50, 70, 99, 133	0
12	BL	122/123 (99%)	0.54	10 (8%) 17 10	71, 86, 117, 143	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	114/114 (100%)	1.14	23 (20%) 3 1	116, 139, 175, 182	0
13	BM	114/114 (100%)	1.17	14 (12%) 8 5	202, 239, 248, 254	0
14	AN	100/100 (100%)	1.46	27 (27%) 1 1	84, 124, 192, 203	0
14	BN	100/100 (100%)	1.38	17 (17%) 4 2	134, 185, 229, 236	0
15	AO	88/88 (100%)	0.22	2 (2%) 61 39	68, 92, 115, 136	0
15	BO	88/88 (100%)	0.32	1 (1%) 78 59	79, 113, 132, 152	0
16	AP	82/82 (100%)	0.42	5 (6%) 27 15	62, 86, 128, 142	0
16	BP	82/82 (100%)	0.95	11 (13%) 7 4	77, 94, 149, 159	0
17	AQ	80/80 (100%)	0.16	2 (2%) 58 37	64, 88, 118, 134	0
17	BQ	80/80 (100%)	0.72	4 (5%) 34 18	83, 120, 149, 157	0
18	AR	55/55 (100%)	0.46	2 (3%) 46 26	74, 101, 142, 166	0
18	BR	55/55 (100%)	0.55	4 (7%) 21 11	75, 97, 134, 166	0
19	AS	79/79 (100%)	1.43	18 (22%) 2 1	123, 139, 159, 165	0
19	BS	79/79 (100%)	1.17	15 (18%) 3 1	217, 233, 247, 254	0
20	AT	86/86 (100%)	0.44	2 (2%) 61 39	68, 86, 116, 133	0
20	BT	85/86 (98%)	1.24	17 (20%) 3 1	90, 119, 151, 161	0
21	AU	56/56 (100%)	0.63	4 (7%) 22 12	81, 118, 163, 176	0
21	BU	56/56 (100%)	0.64	5 (8%) 15 8	75, 110, 147, 155	0
22	C1	56/56 (100%)	1.74	17 (30%) 1 1	93, 147, 170, 185	0
22	D1	56/56 (100%)	-0.46	0 100 100	21, 47, 72, 112	0
23	C2	50/51 (98%)	1.63	17 (34%) 1 0	145, 160, 172, 198	0
23	D2	51/51 (100%)	0.10	1 (1%) 65 44	56, 69, 100, 116	0
24	C3	46/46 (100%)	2.37	26 (56%) 0 0	102, 130, 139, 152	0
24	D3	46/46 (100%)	-0.36	1 (2%) 62 41	30, 40, 58, 116	0
25	C4	64/64 (100%)	3.00	49 (76%) 0 0	108, 134, 150, 160	0
25	D4	64/64 (100%)	-0.28	0 100 100	32, 41, 57, 75	0
26	C5	38/38 (100%)	1.87	12 (31%) 1 1	115, 134, 145, 151	0
26	D5	38/38 (100%)	-0.35	0 100 100	43, 55, 72, 99	0
27	C0	58/58 (100%)	1.77	17 (29%) 1 1	109, 132, 151, 162	0
27	D0	58/58 (100%)	-0.33	2 (3%) 48 28	27, 37, 61, 83	2 (3%)
28	CB	118/120 (98%)	0.72	11 (9%) 14 8	110, 181, 234, 243	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DB	120/120 (100%)	-0.58	0 100 100	34, 63, 99, 131	0
29	CC	271/272 (99%)	0.75	39 (14%) 6 3	73, 100, 126, 136	0
29	DC	271/272 (99%)	-0.34	5 (1%) 67 47	26, 57, 84, 99	0
30	CD	209/209 (100%)	0.99	23 (11%) 10 5	79, 116, 143, 158	0
31	CA	2876/2904 (99%)	0.79	256 (8%) 15 8	64, 133, 248, 291	0
32	DD	208/209 (99%)	-0.55	1 (0%) 87 73	20, 41, 71, 100	0
33	CE	201/201 (100%)	1.19	35 (17%) 4 2	90, 160, 190, 200	0
33	DE	201/201 (100%)	-0.37	1 (0%) 87 73	25, 62, 104, 136	0
34	CF	177/178 (99%)	0.70	6 (3%) 48 28	201, 219, 227, 235	0
34	DF	177/178 (99%)	0.15	1 (0%) 85 70	54, 89, 132, 150	0
35	CG	176/176 (100%)	0.63	4 (2%) 61 39	140, 167, 194, 206	0
35	DG	176/176 (100%)	-0.05	5 (2%) 55 34	44, 75, 103, 136	0
36	CH	149/149 (100%)	0.46	3 (2%) 65 44	89, 149, 175, 187	0
36	DH	149/149 (100%)	0.62	5 (3%) 48 28	71, 150, 190, 207	0
37	CJ	134/135 (99%)	1.36	30 (22%) 2 1	241, 258, 269, 276	0
37	DJ	134/135 (99%)	1.43	32 (23%) 2 1	210, 234, 245, 252	0
38	CK	142/142 (100%)	0.85	11 (7%) 19 10	84, 109, 134, 142	0
38	DK	142/142 (100%)	-0.61	0 100 100	23, 37, 67, 88	0
39	CL	122/123 (99%)	0.64	8 (6%) 24 13	76, 99, 141, 159	0
39	DL	123/123 (100%)	-0.57	0 100 100	28, 44, 71, 110	0
40	CM	144/144 (100%)	1.33	33 (22%) 2 1	94, 152, 193, 222	0
40	DM	144/144 (100%)	-0.21	2 (1%) 73 53	18, 56, 88, 121	0
41	CN	135/136 (99%)	0.72	12 (8%) 15 8	76, 111, 139, 174	0
41	DN	135/136 (99%)	-0.49	0 100 100	18, 43, 73, 95	1 (0%)
42	CO	120/125 (96%)	1.34	34 (28%) 1 1	93, 124, 143, 189	0
42	DO	125/125 (100%)	-0.52	0 100 100	27, 40, 76, 125	0
43	CP	116/117 (99%)	0.84	12 (10%) 12 6	142, 164, 181, 187	0
43	DP	117/117 (100%)	-0.21	0 100 100	42, 61, 90, 99	0
44	CQ	114/114 (100%)	0.76	12 (10%) 11 6	96, 113, 138, 154	0
44	DQ	114/114 (100%)	-0.30	1 (0%) 81 63	28, 52, 86, 125	0
45	CR	117/117 (100%)	1.16	24 (20%) 2 1	82, 109, 134, 148	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
45	DR	117/117 (100%)	-0.66	0 100 100	19, 34, 52, 82	0
46	CS	103/103 (100%)	1.03	19 (18%) 3 1	101, 124, 166, 174	0
46	DS	103/103 (100%)	-0.55	2 (1%) 66 45	22, 45, 74, 101	0
47	CT	110/110 (100%)	1.50	25 (22%) 2 1	99, 126, 157, 172	0
47	DT	110/110 (100%)	-0.34	0 100 100	26, 37, 67, 120	0
48	CU	93/93 (100%)	1.60	28 (30%) 1 1	124, 154, 178, 190	0
48	DU	93/93 (100%)	0.19	4 (4%) 40 22	41, 63, 120, 139	0
49	CV	102/103 (99%)	1.71	37 (36%) 1 0	132, 164, 197, 206	0
49	DV	102/103 (99%)	-0.04	4 (3%) 43 24	49, 67, 116, 143	0
50	CW	94/94 (100%)	0.49	6 (6%) 25 14	122, 144, 158, 167	0
50	DW	94/94 (100%)	-0.34	0 100 100	38, 58, 88, 96	0
51	CX	75/83 (90%)	1.05	10 (13%) 7 4	95, 126, 138, 176	0
51	DX	76/83 (91%)	-0.30	1 (1%) 75 56	20, 43, 72, 108	1 (1%)
52	CY	77/77 (100%)	1.14	11 (14%) 6 3	87, 116, 146, 163	0
52	DY	77/77 (100%)	-0.19	1 (1%) 75 56	34, 58, 96, 112	0
53	CZ	62/62 (100%)	1.20	9 (14%) 6 3	139, 171, 185, 191	0
53	DZ	62/62 (100%)	0.44	2 (3%) 50 30	51, 81, 123, 140	0
54	DI	135/135 (100%)	1.29	28 (20%) 2 1	82, 161, 211, 226	1 (0%)
55	DA	2873/2904 (98%)	-0.67	79 (2%) 56 35	18, 47, 217, 299	11 (0%)
All	All	20634/20767 (99%)	0.36	1609 (7%) 19 10	18, 106, 237, 299	16 (0%)

The worst 5 of 1609 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
31	CA	2172	U	11.1
7	AG	5	ARG	10.5
1	AA	121	U	9.9
25	C4	36	LYS	9.1
31	CA	331	C	8.7

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column

labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	2MG	BA	966	24/25	0.62	0.14	161,163,169,169	0
1	2MG	BA	1207	24/25	0.64	0.13	169,172,175,177	0
1	5MC	BA	967	21/22	0.72	0.14	156,162,165,165	0
31	PSU	CA	1917	20/21	0.79	0.12	106,115,121,121	0
1	2MG	AA	1207	24/25	0.82	0.12	124,129,130,132	0
31	3TD	CA	1915	21/22	0.85	0.08	132,137,140,141	0
31	PSU	CA	2457	20/21	0.87	0.14	83,88,93,96	0
31	PSU	CA	2504	20/21	0.87	0.15	87,89,95,96	0
1	PSU	BA	516	20/21	0.88	0.10	93,98,101,102	0
31	2MA	CA	2503	23/24	0.88	0.15	90,95,99,100	0
31	PSU	CA	1911	20/21	0.88	0.07	112,123,126,126	0
1	2MG	AA	966	24/25	0.89	0.13	84,94,103,105	0
31	PSU	CA	955	20/21	0.89	0.12	92,93,95,95	0
31	6MZ	CA	1618	23/24	0.90	0.14	112,116,119,120	0
55	PSU	DA	1917	20/21	0.90	0.09	79,84,93,93	0
1	PSU	AA	516	20/21	0.91	0.09	81,85,86,87	0
31	PSU	CA	2580	20/21	0.91	0.09	86,88,93,94	0
55	3TD	DA	1915	21/22	0.91	0.09	105,109,117,117	0
31	6MZ	CA	2030	23/24	0.91	0.12	82,91,100,102	0
12	D2T	AL	89	10/11	0.92	0.12	61,65,85,86	0
1	5MC	BA	1407	21/22	0.92	0.11	81,92,94,95	0
55	PSU	DA	1911	20/21	0.92	0.08	82,85,87,88	0
12	D2T	BL	89	10/11	0.92	0.13	77,82,93,93	0
31	PSU	CA	746	20/21	0.92	0.08	98,101,104,104	0
31	2MG	CA	2445	24/25	0.93	0.15	74,83,85,89	0
31	1MG	CA	745	24/25	0.93	0.10	92,96,97,98	0
1	5MC	AA	967	21/22	0.93	0.12	90,100,103,105	0
31	7MG	CA	2069	24/25	0.93	0.15	84,89,94,94	0
41	4D4	CN	81	12/13	0.93	0.12	85,88,108,110	0
31	OMC	CA	2498	21/22	0.94	0.13	82,84,89,92	0
1	UR3	BA	1498	21/22	0.94	0.09	81,84,87,88	0
31	5MC	CA	1962	21/22	0.94	0.12	67,69,73,76	0
31	5MU	CA	747	21/22	0.94	0.10	95,101,103,106	0
1	7MG	AA	527	24/25	0.95	0.08	60,65,72,74	0
31	OMU	CA	2552	21/22	0.95	0.14	80,82,86,88	0
31	OMG	CA	2251	24/25	0.95	0.10	69,79,82,84	0
1	2MG	BA	1516	24/25	0.95	0.08	67,75,78,81	0
31	5MU	CA	1939	21/22	0.95	0.09	70,73,82,85	0
31	2MG	CA	1835	24/25	0.95	0.09	61,72,77,78	0
1	7MG	BA	527	24/25	0.95	0.08	76,81,88,89	0
31	PSU	CA	2605	20/21	0.96	0.07	73,75,78,80	0
1	MA6	BA	1518	24/25	0.96	0.08	67,73,76,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	MA6	BA	1519	24/25	0.96	0.09	74,77,81,83	0
1	MA6	AA	1518	24/25	0.96	0.08	51,55,58,61	0
1	UR3	AA	1498	21/22	0.96	0.09	58,63,67,70	0
41	4D4	DN	81[A]	12/13	0.96	0.10	32,40,49,51	9
41	4D4	DN	81[B]	12/13	0.96	0.10	12,25,36,36	9
1	5MC	AA	1407	21/22	0.97	0.07	55,57,60,62	0
55	PSU	DA	2604	20/21	0.97	0.07	41,46,56,56	0
1	4OC	BA	1402	22/23	0.97	0.07	79,83,83,84	0
1	4OC	AA	1402	22/23	0.97	0.07	53,61,66,66	0
1	2MG	AA	1516	24/25	0.97	0.07	58,62,63,63	0
32	MEQ	DD	150[B]	10/11	0.98	0.08	23,32,41,41	10
55	5MU	DA	1939	21/22	0.98	0.07	35,37,41,47	0
55	5MC	DA	1962	21/22	0.98	0.08	36,44,48,49	0
55	7MG	DA	2069	24/25	0.98	0.08	32,37,41,43	0
55	2MG	DA	2445	24/25	0.98	0.07	26,29,35,37	0
55	2MA	DA	2503	23/24	0.98	0.06	21,35,41,42	0
55	PSU	DA	2504	20/21	0.98	0.09	37,40,44,44	0
55	OMU	DA	2552	21/22	0.98	0.07	31,34,39,46	0
55	5MU	DA	747	21/22	0.98	0.06	28,33,36,41	0
55	PSU	DA	2605	20/21	0.98	0.06	31,41,43,43	0
55	2MG	DA	1835	24/25	0.98	0.06	41,47,52,52	0
1	MA6	AA	1519	24/25	0.98	0.07	53,56,61,64	0
32	MEQ	DD	150[A]	10/11	0.98	0.08	7,15,29,31	10
55	OMC	DA	2498	21/22	0.99	0.05	21,26,29,30	0
55	PSU	DA	746	20/21	0.99	0.04	21,28,31,35	0
55	1MG	DA	745	24/25	0.99	0.05	25,29,37,41	0
55	6MZ	DA	2030	23/24	0.99	0.05	22,25,29,34	0
55	PSU	DA	2580	20/21	0.99	0.06	20,25,32,34	0
55	PSU	DA	955	20/21	0.99	0.06	25,27,30,30	0
55	OMG	DA	2251	24/25	0.99	0.05	27,32,37,42	0
55	6MZ	DA	1618	23/24	0.99	0.05	26,33,36,36	0
55	H2U	DA	2449	20/21	0.99	0.06	25,29,31,32	0
55	PSU	DA	2457	20/21	0.99	0.04	27,31,37,37	0

6.3 Carbohydrates i

There are no oligosaccharides 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
56	MG	DA	3168	1/1	0.26	0.31	141,141,141,141	0
56	MG	CA	3154	1/1	0.32	0.36	147,147,147,147	0
56	MG	BA	1624	1/1	0.34	0.14	262,262,262,262	0
56	MG	AA	1628	1/1	0.38	0.18	159,159,159,159	0
56	MG	BA	1639	1/1	0.40	0.32	94,94,94,94	0
56	MG	AA	1677	1/1	0.41	0.18	194,194,194,194	0
56	MG	CA	3122	1/1	0.43	0.58	126,126,126,126	0
56	MG	CA	3038	1/1	0.46	0.11	263,263,263,263	0
56	MG	BA	1641	1/1	0.48	0.23	120,120,120,120	0
56	MG	CA	3132	1/1	0.49	0.27	105,105,105,105	0
56	MG	BA	1640	1/1	0.50	0.54	124,124,124,124	0
56	MG	CA	3060	1/1	0.52	0.15	234,234,234,234	0
56	MG	CA	3075	1/1	0.53	0.26	230,230,230,230	0
56	MG	CA	3077	1/1	0.54	0.15	249,249,249,249	0
56	MG	BA	1603	1/1	0.57	0.13	263,263,263,263	0
56	MG	CA	3124	1/1	0.58	0.20	118,118,118,118	0
56	MG	BA	1625	1/1	0.65	0.18	256,256,256,256	0
56	MG	CA	3005	1/1	0.66	0.21	237,237,237,237	0
56	MG	CA	3061	1/1	0.67	0.12	247,247,247,247	0
56	MG	CA	3028	1/1	0.67	0.17	278,278,278,278	0
56	MG	CA	3115	1/1	0.68	0.20	84,84,84,84	0
56	MG	CA	3155	1/1	0.69	0.16	156,156,156,156	0
56	MG	CA	3021	1/1	0.69	0.51	264,264,264,264	0
56	MG	CA	3139	1/1	0.70	0.28	87,87,87,87	0
58	MPD	DE	301	8/8	0.70	0.25	139,140,142,142	0
63	EDO	DB	212	4/4	0.71	0.31	115,115,116,116	0
56	MG	CA	3067	1/1	0.72	0.14	277,277,277,277	0
56	MG	AA	1678	1/1	0.72	0.22	78,78,78,78	0
56	MG	CA	3156	1/1	0.72	0.17	232,232,232,232	0
56	MG	DA	3146	1/1	0.73	0.28	122,122,122,122	0
56	MG	CA	3009	1/1	0.73	0.25	243,243,243,243	0
56	MG	BA	1606	1/1	0.74	0.21	227,227,227,227	0
56	MG	CA	3002	1/1	0.75	0.16	265,265,265,265	0
56	MG	DA	3143	1/1	0.75	0.31	114,114,114,114	0
56	MG	AA	1622	1/1	0.75	0.36	100,100,100,100	0
56	MG	DA	3129	1/1	0.76	0.38	102,102,102,102	0
62	PEG	DP	201	7/7	0.76	0.16	126,127,131,132	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3145	1/1	0.76	0.20	73,73,73,73	0
67	ACY	DA	3196	4/4	0.76	0.25	84,85,87,87	0
59	PUT	AA	1672	6/6	0.77	0.41	99,100,102,103	0
56	MG	CA	3034	1/1	0.77	0.25	246,246,246,246	0
56	MG	CA	3129	1/1	0.78	0.24	104,104,104,104	0
56	MG	CA	3147	1/1	0.78	0.52	58,58,58,58	1
56	MG	CA	3148	1/1	0.78	0.53	51,51,51,51	1
56	MG	CA	3112	1/1	0.79	0.10	75,75,75,75	0
56	MG	BA	1623	1/1	0.79	0.26	248,248,248,248	0
56	MG	CA	3146	1/1	0.79	0.19	144,144,144,144	0
56	MG	BA	1612	1/1	0.79	0.36	182,182,182,182	0
56	MG	DA	3180	1/1	0.79	0.28	106,106,106,106	0
56	MG	CA	3130	1/1	0.80	0.31	89,89,89,89	0
56	MG	BA	1646	1/1	0.80	0.15	108,108,108,108	0
56	MG	CA	3135	1/1	0.80	0.36	101,101,101,101	0
56	MG	AA	1660	1/1	0.80	0.17	284,284,284,284	0
56	MG	CA	3014	1/1	0.80	0.14	216,216,216,216	0
56	MG	CA	3003	1/1	0.80	0.33	278,278,278,278	0
56	MG	CA	3104	1/1	0.80	0.16	258,258,258,258	0
56	MG	CA	3142	1/1	0.81	0.10	78,78,78,78	0
56	MG	AA	1614	1/1	0.81	0.21	85,85,85,85	0
56	MG	CA	3068	1/1	0.81	0.17	216,216,216,216	0
56	MG	CA	3123	1/1	0.81	0.11	113,113,113,113	0
56	MG	AA	1654	1/1	0.81	0.34	262,262,262,262	0
56	MG	CA	3126	1/1	0.81	0.24	86,86,86,86	0
56	MG	CA	3032	1/1	0.82	0.12	241,241,241,241	0
56	MG	CA	3106	1/1	0.82	0.12	83,83,83,83	0
56	MG	CA	3108	1/1	0.82	0.19	83,83,83,83	0
56	MG	AA	1661	1/1	0.82	0.16	173,173,173,173	0
56	MG	CA	3152	1/1	0.82	0.10	151,151,151,151	0
56	MG	CA	3007	1/1	0.82	0.10	214,214,214,214	0
58	MPD	DK	201	8/8	0.83	0.17	120,121,123,124	0
56	MG	CA	3125	1/1	0.83	0.19	89,89,89,89	0
59	PUT	AA	1675	6/6	0.83	0.24	106,109,109,109	0
56	MG	DA	3061	1/1	0.83	0.13	233,233,233,233	0
56	MG	AA	1608	1/1	0.83	0.39	96,96,96,96	0
56	MG	CA	3090	1/1	0.83	0.13	185,185,185,185	0
60	T1C	BA	1643	42/42	0.84	0.18	170,174,179,179	0
56	MG	CA	3072	1/1	0.84	0.12	249,249,249,249	0
63	EDO	DB	211	4/4	0.84	0.36	88,90,92,92	0
56	MG	CA	3140	1/1	0.84	0.10	84,84,84,84	0
64	PGE	D1	102	10/10	0.84	0.28	122,127,128,128	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3047	1/1	0.84	0.32	229,229,229,229	0
59	PUT	DA	3222	6/6	0.85	0.20	48,52,57,58	0
56	MG	AA	1603	1/1	0.85	0.12	83,83,83,83	0
62	PEG	D3	102	7/7	0.85	0.28	114,119,124,125	0
56	MG	BA	1629	1/1	0.85	0.18	168,168,168,168	0
56	MG	CA	3107	1/1	0.85	0.26	83,83,83,83	0
56	MG	CA	3026	1/1	0.85	0.20	173,173,173,173	0
56	MG	CA	3080	1/1	0.85	0.18	151,151,151,151	0
56	MG	BA	1636	1/1	0.85	0.23	72,72,72,72	0
56	MG	DA	3178	1/1	0.86	0.38	88,88,88,88	0
56	MG	CA	3056	1/1	0.86	0.39	71,71,71,71	0
56	MG	AA	1609	1/1	0.86	0.31	89,89,89,89	0
58	MPD	DE	302	8/8	0.86	0.26	93,97,102,102	0
56	MG	AA	1611	1/1	0.86	0.22	108,108,108,108	0
58	MPD	DA	3190	8/8	0.86	0.19	95,97,99,102	0
56	MG	CA	3151	1/1	0.86	0.18	71,71,71,71	0
56	MG	AA	1624	1/1	0.86	0.19	95,95,95,95	0
56	MG	CA	3036	1/1	0.86	0.15	193,193,193,193	0
56	MG	CA	3037	1/1	0.86	0.25	189,189,189,189	0
56	MG	CA	3111	1/1	0.86	0.12	83,83,83,83	0
56	MG	CA	3022	1/1	0.86	0.21	195,195,195,195	0
56	MG	CA	3076	1/1	0.86	0.13	182,182,182,182	0
56	MG	CA	3116	1/1	0.86	0.25	95,95,95,95	0
56	MG	CA	3117	1/1	0.86	0.30	67,67,67,67	0
56	MG	BA	1647	1/1	0.86	0.38	91,91,91,91	0
67	ACY	DA	3201	4/4	0.86	0.25	78,79,79,79	0
69	TRS	DA	3220	8/8	0.86	0.17	125,128,134,134	0
56	MG	CA	3099	1/1	0.87	0.13	160,160,160,160	0
59	PUT	AA	1673	6/6	0.87	0.11	100,102,103,104	0
59	PUT	AA	1674	6/6	0.87	0.33	133,134,135,135	0
56	MG	CA	3136	1/1	0.87	0.37	84,84,84,84	0
56	MG	CA	3149	1/1	0.87	0.13	67,67,67,67	0
56	MG	CA	3137	1/1	0.87	0.17	106,106,106,106	0
56	MG	DA	3176	1/1	0.87	0.28	98,98,98,98	0
56	MG	AA	1618	1/1	0.87	0.32	92,92,92,92	0
56	MG	AA	1664	1/1	0.87	0.15	212,212,212,212	0
57	PG4	AA	1670	13/13	0.87	0.12	78,87,97,97	0
63	EDO	DA	3002	4/4	0.87	0.43	93,94,95,95	0
56	MG	AA	1605	1/1	0.87	0.51	89,89,89,89	0
56	MG	CA	3055	1/1	0.87	0.07	169,169,169,169	0
56	MG	BA	1607	1/1	0.87	0.17	207,207,207,207	0
56	MG	DA	3125	1/1	0.87	0.31	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3084	1/1	0.88	0.20	174,174,174,174	0
56	MG	BA	1604	1/1	0.88	0.09	153,153,153,153	0
56	MG	CA	3110	1/1	0.88	0.09	93,93,93,93	0
56	MG	CA	3094	1/1	0.88	0.13	105,105,105,105	0
57	PG4	DA	3193	13/13	0.88	0.24	85,95,100,101	0
56	MG	DA	3126	1/1	0.88	0.31	61,61,61,61	0
62	PEG	DQ	201	7/7	0.88	0.18	124,127,128,129	0
62	PEG	DA	3199	7/7	0.88	0.21	80,89,93,95	0
56	MG	AA	1615	1/1	0.88	0.33	83,83,83,83	0
56	MG	BA	1644	1/1	0.88	0.18	133,133,133,133	0
58	MPD	DN	201	8/8	0.88	0.18	106,111,116,117	0
56	MG	CA	3127	1/1	0.88	0.24	73,73,73,73	0
58	MPD	DA	3204	8/8	0.88	0.25	112,114,117,117	0
56	MG	DA	3152	1/1	0.88	0.54	66,66,66,66	0
56	MG	BA	1614	1/1	0.88	0.15	171,171,171,171	0
56	MG	CA	3039	1/1	0.89	0.13	175,175,175,175	0
56	MG	DA	3132	1/1	0.89	0.12	70,70,70,70	0
60	T1C	AA	1680	42/42	0.89	0.15	96,107,123,124	0
57	PG4	DQ	202	13/13	0.89	0.11	60,63,76,76	0
61	ZN	C5	101	1/1	0.89	0.10	149,149,149,149	0
62	PEG	AL	201	7/7	0.89	0.13	83,85,94,95	0
56	MG	DA	3136	1/1	0.89	0.27	77,77,77,77	0
56	MG	CA	3073	1/1	0.89	0.17	222,222,222,222	0
56	MG	AA	1616	1/1	0.89	0.54	85,85,85,85	0
56	MG	CA	3092	1/1	0.89	0.07	152,152,152,152	0
56	MG	DA	3164	1/1	0.89	0.32	71,71,71,71	0
58	MPD	DT	201	8/8	0.89	0.27	102,108,109,109	0
56	MG	DA	3167	1/1	0.89	0.29	102,102,102,102	0
56	MG	CA	3138	1/1	0.89	0.20	66,66,66,66	0
64	PGE	DS	201	10/10	0.89	0.12	77,89,91,92	0
56	MG	DA	3170	1/1	0.89	0.25	77,77,77,77	0
56	MG	CB	201	1/1	0.89	0.08	168,168,168,168	0
68	GUN	DA	3211	11/11	0.89	0.18	98,100,101,102	0
56	MG	CA	3001	1/1	0.89	0.17	296,296,296,296	0
57	PG4	DA	3216	13/13	0.90	0.16	99,104,109,110	0
56	MG	AA	1627	1/1	0.90	0.34	91,91,91,91	0
56	MG	CA	3141	1/1	0.90	0.38	80,80,80,80	0
56	MG	DA	3163	1/1	0.90	0.36	91,91,91,91	0
56	MG	BA	1638	1/1	0.90	0.40	78,78,78,78	0
56	MG	CA	3131	1/1	0.90	0.26	78,78,78,78	0
56	MG	AA	1612	1/1	0.90	0.32	77,77,77,77	0
56	MG	CA	3006	1/1	0.90	0.10	155,155,155,155	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	BA	1645	1/1	0.90	0.21	102,102,102,102	0
56	MG	CA	3083	1/1	0.90	0.17	204,204,204,204	0
64	PGE	D3	101	10/10	0.90	0.18	97,99,102,103	0
56	MG	CA	3113	1/1	0.90	0.32	71,71,71,71	0
64	PGE	DA	3203	10/10	0.90	0.19	83,85,88,90	0
56	MG	DA	3141	1/1	0.90	0.33	86,86,86,86	0
57	PG4	BA	1642	13/13	0.90	0.11	88,89,99,100	0
56	MG	CA	3105	1/1	0.90	0.21	262,262,262,262	0
56	MG	DA	3145	1/1	0.90	0.18	79,79,79,79	0
56	MG	CA	3029	1/1	0.91	0.15	143,143,143,143	0
59	PUT	DA	3223	6/6	0.91	0.22	61,62,65,67	0
56	MG	CA	3010	1/1	0.91	0.10	234,234,234,234	0
57	PG4	DS	202	13/13	0.91	0.12	43,51,72,73	0
56	MG	CA	3114	1/1	0.91	0.14	66,66,66,66	0
56	MG	DA	3110	1/1	0.91	0.27	295,295,295,295	0
56	MG	DA	3120	1/1	0.91	0.20	70,70,70,70	0
62	PEG	DL	201	7/7	0.91	0.15	82,85,87,87	0
56	MG	DA	3124	1/1	0.91	0.24	65,65,65,65	0
56	MG	AA	1647	1/1	0.91	0.11	179,179,179,179	0
56	MG	AA	1642	1/1	0.91	0.13	158,158,158,158	0
62	PEG	DA	3226	7/7	0.91	0.23	89,91,98,98	0
56	MG	CA	3150	1/1	0.91	0.19	75,75,75,75	0
56	MG	DA	3172	1/1	0.91	0.49	103,103,103,103	0
58	MPD	DA	3192	8/8	0.91	0.27	95,100,104,105	0
63	EDO	DA	3198	4/4	0.91	0.24	78,81,83,83	0
56	MG	CA	3064	1/1	0.91	0.17	249,249,249,249	0
56	MG	DA	3177	1/1	0.91	0.41	77,77,77,77	0
56	MG	CA	3054	1/1	0.91	0.12	156,156,156,156	0
56	MG	DA	3137	1/1	0.91	0.50	37,37,37,37	1
65	SPD	DA	3183	10/10	0.91	0.15	79,83,87,87	0
56	MG	CA	3078	1/1	0.91	0.09	149,149,149,149	0
59	PUT	DA	3189	6/6	0.91	0.16	45,54,56,56	0
59	PUT	DA	3212	6/6	0.91	0.24	81,84,85,85	0
59	PUT	DA	3221	6/6	0.91	0.25	138,140,141,141	0
59	PUT	DA	3213	6/6	0.92	0.27	105,107,110,110	0
59	PUT	DA	3219	6/6	0.92	0.18	70,75,78,79	0
56	MG	CA	3109	1/1	0.92	0.13	62,62,62,62	0
56	MG	AA	1679	1/1	0.92	0.20	77,77,77,77	0
56	MG	DA	3142	1/1	0.92	0.16	62,62,62,62	0
56	MG	AA	1656	1/1	0.92	0.10	196,196,196,196	0
57	PG4	DR	202	13/13	0.92	0.24	109,117,120,121	0
56	MG	AA	1602	1/1	0.92	0.24	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	1627	1/1	0.92	0.14	124,124,124,124	0
62	PEG	D1	103	7/7	0.92	0.26	85,90,91,91	0
56	MG	AA	1623	1/1	0.92	0.14	69,69,69,69	0
56	MG	DA	3158	1/1	0.92	0.18	191,191,191,191	0
56	MG	DA	3160	1/1	0.92	0.36	74,74,74,74	0
56	MG	DA	3162	1/1	0.92	0.11	85,85,85,85	0
56	MG	DA	3122	1/1	0.92	0.32	100,100,100,100	0
62	PEG	DA	3200	7/7	0.92	0.30	83,85,95,96	0
62	PEG	DA	3218	7/7	0.92	0.33	123,129,133,134	0
56	MG	DA	3123	1/1	0.92	0.30	62,62,62,62	0
58	MPD	DT	202	8/8	0.92	0.25	128,128,130,130	0
56	MG	CA	3008	1/1	0.92	0.17	136,136,136,136	0
56	MG	CA	3057	1/1	0.92	0.09	133,133,133,133	0
56	MG	AA	1621	1/1	0.92	0.46	77,77,77,77	0
58	MPD	DA	3207	8/8	0.92	0.21	77,78,80,80	0
56	MG	DA	3171	1/1	0.92	0.10	73,73,73,73	0
56	MG	CA	3118	1/1	0.92	0.26	59,59,59,59	0
56	MG	DA	3131	1/1	0.92	0.21	62,62,62,62	0
56	MG	AA	1625	1/1	0.92	0.17	86,86,86,86	0
56	MG	AA	1626	1/1	0.92	0.11	99,99,99,99	0
59	PUT	DA	3195	6/6	0.92	0.28	87,91,91,92	0
59	PUT	DA	3205	6/6	0.92	0.35	108,109,111,111	0
56	MG	DA	3179	1/1	0.92	0.22	104,104,104,104	0
62	PEG	DA	3227	7/7	0.93	0.20	97,99,103,104	0
56	MG	CA	3119	1/1	0.93	0.25	89,89,89,89	0
56	MG	CA	3012	1/1	0.93	0.08	95,95,95,95	0
56	MG	DB	208	1/1	0.93	0.10	76,76,76,76	0
56	MG	DA	3173	1/1	0.93	0.20	98,98,98,98	0
63	EDO	DA	3209	4/4	0.93	0.26	135,136,137,138	0
56	MG	DA	3147	1/1	0.93	0.34	65,65,65,65	0
56	MG	DB	209	1/1	0.93	0.12	66,66,66,66	0
56	MG	CA	3065	1/1	0.93	0.09	109,109,109,109	0
64	PGE	DU	101	10/10	0.93	0.15	89,97,104,105	0
56	MG	CA	3101	1/1	0.93	0.08	151,151,151,151	0
56	MG	DA	3133	1/1	0.93	0.13	91,91,91,91	0
65	SPD	DA	3224	10/10	0.93	0.15	50,54,66,68	0
66	1PE	DA	3185	16/16	0.93	0.12	50,55,84,87	0
56	MG	DA	3119	1/1	0.93	0.26	57,57,57,57	0
56	MG	BA	1637	1/1	0.93	0.12	85,85,85,85	0
56	MG	AA	1606	1/1	0.93	0.31	91,91,91,91	0
56	MG	CB	203	1/1	0.93	0.06	145,145,145,145	0
56	MG	DA	3155	1/1	0.94	0.15	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3134	1/1	0.94	0.16	108,108,108,108	0
56	MG	DA	3130	1/1	0.94	0.29	54,54,54,54	0
56	MG	AA	1601	1/1	0.94	0.35	67,67,67,67	0
63	EDO	DB	201	4/4	0.94	0.23	94,97,98,99	0
56	MG	AA	1636	1/1	0.94	0.09	97,97,97,97	0
56	MG	CA	3071	1/1	0.94	0.06	166,166,166,166	0
63	EDO	DB	213	4/4	0.94	0.20	82,82,84,84	0
56	MG	DA	3118	1/1	0.94	0.14	68,68,68,68	0
58	MPD	AA	1671	8/8	0.94	0.24	88,88,90,92	0
58	MPD	AA	1676	8/8	0.94	0.22	95,99,100,101	0
56	MG	AA	1659	1/1	0.94	0.08	115,115,115,115	0
56	MG	DA	3169	1/1	0.94	0.20	69,69,69,69	0
56	MG	AA	1619	1/1	0.94	0.22	92,92,92,92	0
56	MG	AA	1617	1/1	0.94	0.33	96,96,96,96	0
56	MG	CA	3153	1/1	0.94	0.10	64,64,64,64	0
64	PGE	DA	3214	10/10	0.94	0.13	72,73,77,78	0
64	PGE	DA	3225	10/10	0.94	0.16	73,83,94,96	0
56	MG	CA	3093	1/1	0.94	0.07	88,88,88,88	0
65	SPD	DA	3206	10/10	0.94	0.25	87,102,109,110	0
56	MG	BA	1633	1/1	0.94	0.15	229,229,229,229	0
56	MG	BA	1616	1/1	0.94	0.10	122,122,122,122	0
66	1PE	DA	3202	16/16	0.94	0.15	61,64,72,73	0
56	MG	DA	3150	1/1	0.94	0.18	51,51,51,51	0
56	MG	DA	3151	1/1	0.94	0.28	82,82,82,82	0
56	MG	DA	3128	1/1	0.94	0.26	72,72,72,72	0
56	MG	DA	3182	1/1	0.94	0.20	61,61,61,61	0
56	MG	CA	3066	1/1	0.95	0.10	89,89,89,89	0
56	MG	CA	3019	1/1	0.95	0.08	58,58,58,58	0
56	MG	CA	3133	1/1	0.95	0.17	72,72,72,72	0
56	MG	BA	1619	1/1	0.95	0.09	96,96,96,96	0
63	EDO	D1	101	4/4	0.95	0.07	59,60,60,60	0
56	MG	CA	3070	1/1	0.95	0.07	91,91,91,91	0
56	MG	DA	3138	1/1	0.95	0.13	59,59,59,59	0
56	MG	DR	201	1/1	0.95	0.11	42,42,42,42	0
59	PUT	DA	3188	6/6	0.95	0.15	50,53,55,56	0
56	MG	DB	206	1/1	0.95	0.32	80,80,80,80	0
56	MG	DB	207	1/1	0.95	0.13	92,92,92,92	0
56	MG	BA	1635	1/1	0.95	0.07	102,102,102,102	0
63	EDO	DA	3215	4/4	0.95	0.12	65,66,68,70	0
56	MG	CA	3051	1/1	0.95	0.07	80,80,80,80	0
56	MG	CA	3023	1/1	0.95	0.09	158,158,158,158	0
56	MG	CA	3120	1/1	0.95	0.14	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3121	1/1	0.95	0.10	64,64,64,64	0
56	MG	CA	3074	1/1	0.95	0.07	131,131,131,131	0
56	MG	AA	1655	1/1	0.95	0.07	163,163,163,163	0
56	MG	DA	3157	1/1	0.95	0.23	73,73,73,73	0
56	MG	CA	3143	1/1	0.95	0.08	70,70,70,70	0
56	MG	BA	1609	1/1	0.95	0.07	166,166,166,166	0
56	MG	AA	1665	1/1	0.95	0.13	161,161,161,161	0
56	MG	CB	202	1/1	0.95	0.12	116,116,116,116	0
56	MG	AA	1604	1/1	0.95	0.42	70,70,70,70	0
56	MG	DA	3165	1/1	0.95	0.26	62,62,62,62	0
56	MG	CA	3128	1/1	0.95	0.13	75,75,75,75	0
56	MG	AA	1657	1/1	0.95	0.14	136,136,136,136	0
56	MG	BA	1630	1/1	0.95	0.12	153,153,153,153	0
56	MG	CA	3016	1/1	0.96	0.14	107,107,107,107	0
56	MG	DA	3181	1/1	0.96	0.33	83,83,83,83	0
59	PUT	DA	3184	6/6	0.96	0.16	78,80,81,82	0
56	MG	AA	1644	1/1	0.96	0.17	106,106,106,106	0
56	MG	DA	3156	1/1	0.96	0.27	62,62,62,62	0
56	MG	CA	3062	1/1	0.96	0.06	175,175,175,175	0
56	MG	CA	3063	1/1	0.96	0.15	125,125,125,125	0
63	EDO	DA	3194	4/4	0.96	0.13	76,77,78,78	0
63	EDO	DA	3197	4/4	0.96	0.12	65,67,68,69	0
56	MG	CA	3031	1/1	0.96	0.05	64,64,64,64	0
63	EDO	DA	3208	4/4	0.96	0.18	89,90,90,91	0
56	MG	DA	3161	1/1	0.96	0.17	61,61,61,61	0
56	MG	DA	3011	1/1	0.96	0.07	115,115,115,115	0
56	MG	DA	3036	1/1	0.96	0.10	24,24,24,24	0
56	MG	CA	3048	1/1	0.96	0.06	76,76,76,76	0
56	MG	DA	3097	1/1	0.96	0.12	128,128,128,128	0
56	MG	DA	3166	1/1	0.96	0.22	81,81,81,81	0
64	PGE	DA	3186	10/10	0.96	0.09	39,48,55,57	0
56	MG	BA	1618	1/1	0.96	0.07	129,129,129,129	0
56	MG	DA	3140	1/1	0.96	0.10	54,54,54,54	0
64	PGE	DA	3217	10/10	0.96	0.13	85,88,91,92	0
56	MG	AA	1669	1/1	0.96	0.08	134,134,134,134	0
56	MG	CA	3082	1/1	0.96	0.14	114,114,114,114	0
56	MG	CA	3035	1/1	0.96	0.18	91,91,91,91	0
56	MG	DA	3144	1/1	0.96	0.09	72,72,72,72	0
56	MG	DA	3121	1/1	0.96	0.45	68,68,68,68	0
56	MG	CA	3069	1/1	0.96	0.08	88,88,88,88	0
67	ACY	DA	3191	4/4	0.96	0.10	68,70,70,71	0
56	MG	CA	3088	1/1	0.96	0.09	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
58	MPD	DA	3210	8/8	0.96	0.15	87,89,90,91	0
56	MG	AA	1663	1/1	0.96	0.04	90,90,90,90	0
56	MG	AA	1607	1/1	0.96	0.20	65,65,65,65	0
56	MG	CA	3018	1/1	0.97	0.05	85,85,85,85	0
56	MG	DA	3116	1/1	0.97	0.24	72,72,72,72	0
56	MG	CA	3058	1/1	0.97	0.12	98,98,98,98	0
56	MG	CA	3004	1/1	0.97	0.08	159,159,159,159	0
56	MG	AA	1630	1/1	0.97	0.10	134,134,134,134	0
56	MG	BA	1622	1/1	0.97	0.05	85,85,85,85	0
61	ZN	AB	301	1/1	0.97	0.09	171,171,171,171	0
56	MG	BA	1610	1/1	0.97	0.05	93,93,93,93	0
56	MG	CA	3102	1/1	0.97	0.06	113,113,113,113	0
56	MG	CA	3046	1/1	0.97	0.10	111,111,111,111	0
56	MG	DA	3174	1/1	0.97	0.11	74,74,74,74	0
56	MG	AA	1658	1/1	0.97	0.12	98,98,98,98	0
56	MG	CA	3079	1/1	0.97	0.06	115,115,115,115	0
56	MG	DA	3127	1/1	0.97	0.43	53,53,53,53	0
56	MG	DA	3153	1/1	0.97	0.23	52,52,52,52	0
56	MG	DA	3154	1/1	0.97	0.20	59,59,59,59	0
56	MG	BA	1605	1/1	0.97	0.07	107,107,107,107	0
56	MG	AA	1633	1/1	0.97	0.06	123,123,123,123	0
56	MG	BA	1617	1/1	0.97	0.05	131,131,131,131	0
56	MG	DB	210	1/1	0.97	0.13	97,97,97,97	0
56	MG	AA	1610	1/1	0.97	0.21	90,90,90,90	0
56	MG	CA	3086	1/1	0.97	0.05	68,68,68,68	0
56	MG	DA	3135	1/1	0.97	0.14	72,72,72,72	0
56	MG	BA	1632	1/1	0.97	0.09	75,75,75,75	0
56	MG	CA	3089	1/1	0.97	0.11	68,68,68,68	0
56	MG	BA	1631	1/1	0.98	0.03	55,55,55,55	0
56	MG	DA	3117	1/1	0.98	0.03	56,56,56,56	0
56	MG	BA	1613	1/1	0.98	0.08	73,73,73,73	0
56	MG	AA	1613	1/1	0.98	0.35	65,65,65,65	0
56	MG	CA	3042	1/1	0.98	0.04	88,88,88,88	0
56	MG	BA	1601	1/1	0.98	0.06	106,106,106,106	0
58	MPD	DS	203	8/8	0.98	0.11	48,52,58,59	0
56	MG	BA	1602	1/1	0.98	0.04	68,68,68,68	0
56	MG	CA	3097	1/1	0.98	0.05	90,90,90,90	0
56	MG	CA	3098	1/1	0.98	0.04	77,77,77,77	0
56	MG	AA	1651	1/1	0.98	0.05	76,76,76,76	0
56	MG	CA	3100	1/1	0.98	0.12	92,92,92,92	0
56	MG	AA	1638	1/1	0.98	0.05	114,114,114,114	0
56	MG	CA	3053	1/1	0.98	0.09	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3024	1/1	0.98	0.08	102,102,102,102	0
56	MG	AA	1639	1/1	0.98	0.05	118,118,118,118	0
56	MG	AA	1641	1/1	0.98	0.05	67,67,67,67	0
56	MG	AA	1667	1/1	0.98	0.07	47,47,47,47	0
59	PUT	DA	3001	6/6	0.98	0.09	46,50,58,60	0
56	MG	BA	1608	1/1	0.98	0.06	102,102,102,102	0
56	MG	DA	3134	1/1	0.98	0.04	96,96,96,96	0
56	MG	CA	3059	1/1	0.98	0.04	86,86,86,86	0
56	MG	AA	1629	1/1	0.98	0.07	93,93,93,93	0
56	MG	CA	3081	1/1	0.98	0.04	104,104,104,104	0
56	MG	DA	3005	1/1	0.98	0.05	94,94,94,94	0
56	MG	DA	3139	1/1	0.98	0.11	67,67,67,67	0
56	MG	DA	3007	1/1	0.98	0.05	82,82,82,82	0
56	MG	CA	3033	1/1	0.98	0.14	110,110,110,110	0
56	MG	AA	1634	1/1	0.98	0.07	130,130,130,130	0
65	SPD	DA	3187	10/10	0.98	0.10	34,42,45,48	0
56	MG	DA	3042	1/1	0.98	0.09	40,40,40,40	0
56	MG	DA	3043	1/1	0.98	0.08	80,80,80,80	0
56	MG	DA	3053	1/1	0.98	0.07	89,89,89,89	0
56	MG	AA	1645	1/1	0.98	0.06	66,66,66,66	0
56	MG	DA	3079	1/1	0.98	0.07	119,119,119,119	0
56	MG	DA	3148	1/1	0.98	0.06	61,61,61,61	0
56	MG	DA	3149	1/1	0.98	0.07	62,62,62,62	0
56	MG	CA	3085	1/1	0.98	0.04	74,74,74,74	0
56	MG	CA	3013	1/1	0.98	0.04	86,86,86,86	0
56	MG	AA	1640	1/1	0.99	0.05	73,73,73,73	0
56	MG	CA	3025	1/1	0.99	0.04	82,82,82,82	0
56	MG	DA	3003	1/1	0.99	0.05	85,85,85,85	0
56	MG	DA	3004	1/1	0.99	0.09	77,77,77,77	0
56	MG	AA	1648	1/1	0.99	0.05	70,70,70,70	0
56	MG	DA	3006	1/1	0.99	0.03	87,87,87,87	0
56	MG	CA	3091	1/1	0.99	0.06	68,68,68,68	0
56	MG	BA	1634	1/1	0.99	0.08	99,99,99,99	0
56	MG	DA	3014	1/1	0.99	0.03	45,45,45,45	0
56	MG	DA	3025	1/1	0.99	0.06	108,108,108,108	0
56	MG	DA	3027	1/1	0.99	0.05	94,94,94,94	0
56	MG	DA	3029	1/1	0.99	0.04	46,46,46,46	0
56	MG	AA	1649	1/1	0.99	0.04	68,68,68,68	0
56	MG	CA	3030	1/1	0.99	0.05	78,78,78,78	0
56	MG	CA	3095	1/1	0.99	0.07	63,63,63,63	0
56	MG	DA	3048	1/1	0.99	0.04	57,57,57,57	0
56	MG	DA	3051	1/1	0.99	0.03	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3096	1/1	0.99	0.02	61,61,61,61	0
56	MG	DA	3159	1/1	0.99	0.07	72,72,72,72	0
56	MG	AA	1662	1/1	0.99	0.05	79,79,79,79	0
56	MG	DA	3063	1/1	0.99	0.12	72,72,72,72	0
56	MG	DA	3064	1/1	0.99	0.03	25,25,25,25	0
56	MG	DA	3069	1/1	0.99	0.08	79,79,79,79	0
56	MG	DA	3071	1/1	0.99	0.07	68,68,68,68	0
56	MG	DA	3073	1/1	0.99	0.04	45,45,45,45	0
56	MG	DA	3077	1/1	0.99	0.04	63,63,63,63	0
56	MG	DA	3078	1/1	0.99	0.04	96,96,96,96	0
56	MG	AA	1650	1/1	0.99	0.04	114,114,114,114	0
56	MG	DA	3080	1/1	0.99	0.03	44,44,44,44	0
56	MG	DA	3081	1/1	0.99	0.04	65,65,65,65	0
56	MG	DA	3084	1/1	0.99	0.07	54,54,54,54	0
56	MG	DA	3092	1/1	0.99	0.09	35,35,35,35	0
56	MG	DA	3093	1/1	0.99	0.05	20,20,20,20	0
56	MG	DA	3094	1/1	0.99	0.09	80,80,80,80	0
56	MG	DA	3175	1/1	0.99	0.06	63,63,63,63	0
56	MG	BA	1620	1/1	0.99	0.03	94,94,94,94	0
56	MG	BA	1621	1/1	0.99	0.12	33,33,33,33	0
56	MG	AA	1635	1/1	0.99	0.04	104,104,104,104	0
56	MG	CA	3011	1/1	0.99	0.03	59,59,59,59	0
56	MG	CA	3103	1/1	0.99	0.06	82,82,82,82	0
56	MG	AA	1632	1/1	0.99	0.04	94,94,94,94	0
56	MG	AA	1666	1/1	0.99	0.04	57,57,57,57	0
56	MG	DA	3230	1/1	0.99	0.05	55,55,55,55	0
56	MG	DA	3231	1/1	0.99	0.12	39,39,39,39	0
56	MG	AA	1643	1/1	0.99	0.03	65,65,65,65	0
56	MG	CA	3040	1/1	0.99	0.05	76,76,76,76	0
56	MG	CA	3144	1/1	0.99	0.03	49,49,49,49	0
56	MG	CA	3041	1/1	0.99	0.05	55,55,55,55	0
56	MG	CA	3015	1/1	0.99	0.13	51,51,51,51	0
56	MG	CA	3043	1/1	0.99	0.05	81,81,81,81	0
56	MG	CA	3044	1/1	0.99	0.06	57,57,57,57	0
56	MG	CA	3045	1/1	0.99	0.06	84,84,84,84	0
56	MG	BA	1626	1/1	0.99	0.03	102,102,102,102	0
56	MG	AA	1668	1/1	0.99	0.09	75,75,75,75	0
56	MG	BA	1628	1/1	0.99	0.05	89,89,89,89	0
56	MG	CA	3049	1/1	0.99	0.03	48,48,48,48	0
56	MG	CA	3050	1/1	0.99	0.04	54,54,54,54	0
56	MG	CA	3020	1/1	0.99	0.06	86,86,86,86	0
56	MG	CA	3052	1/1	0.99	0.06	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	1620	1/1	0.99	0.25	78,78,78,78	0
56	MG	DB	202	1/1	0.99	0.06	62,62,62,62	0
56	MG	AA	1631	1/1	0.99	0.05	53,53,53,53	0
56	MG	AA	1646	1/1	0.99	0.05	66,66,66,66	0
56	MG	CA	3087	1/1	0.99	0.05	77,77,77,77	0
56	MG	DA	3085	1/1	1.00	0.01	31,31,31,31	0
56	MG	DA	3086	1/1	1.00	0.01	34,34,34,34	0
56	MG	DA	3087	1/1	1.00	0.02	54,54,54,54	0
56	MG	DA	3088	1/1	1.00	0.03	24,24,24,24	0
56	MG	DA	3089	1/1	1.00	0.02	26,26,26,26	0
56	MG	DA	3090	1/1	1.00	0.04	24,24,24,24	0
56	MG	DA	3228	1/1	1.00	0.04	41,41,41,41	0
56	MG	DA	3229	1/1	1.00	0.02	54,54,54,54	0
56	MG	DA	3091	1/1	1.00	0.02	30,30,30,30	0
56	MG	DA	3019	1/1	1.00	0.03	65,65,65,65	0
56	MG	DA	3020	1/1	1.00	0.04	31,31,31,31	0
56	MG	DA	3021	1/1	1.00	0.05	34,34,34,34	0
56	MG	DA	3095	1/1	1.00	0.05	36,36,36,36	0
56	MG	DA	3096	1/1	1.00	0.03	33,33,33,33	0
56	MG	DA	3022	1/1	1.00	0.05	36,36,36,36	0
56	MG	DA	3098	1/1	1.00	0.03	23,23,23,23	0
56	MG	DA	3099	1/1	1.00	0.01	31,31,31,31	0
56	MG	DA	3100	1/1	1.00	0.03	61,61,61,61	0
56	MG	DA	3101	1/1	1.00	0.02	42,42,42,42	0
56	MG	DA	3102	1/1	1.00	0.05	34,34,34,34	0
56	MG	DA	3103	1/1	1.00	0.05	30,30,30,30	0
56	MG	DA	3104	1/1	1.00	0.03	29,29,29,29	0
56	MG	DA	3105	1/1	1.00	0.10	37,37,37,37	0
56	MG	DA	3106	1/1	1.00	0.02	36,36,36,36	0
56	MG	DA	3107	1/1	1.00	0.02	39,39,39,39	0
56	MG	DA	3108	1/1	1.00	0.02	30,30,30,30	0
56	MG	DA	3109	1/1	1.00	0.03	26,26,26,26	0
56	MG	DA	3023	1/1	1.00	0.04	29,29,29,29	0
56	MG	DA	3111	1/1	1.00	0.02	25,25,25,25	0
56	MG	DA	3112	1/1	1.00	0.04	83,83,83,83	0
56	MG	DA	3113	1/1	1.00	0.05	37,37,37,37	0
56	MG	DA	3114	1/1	1.00	0.01	31,31,31,31	0
56	MG	DA	3115	1/1	1.00	0.01	32,32,32,32	0
56	MG	DA	3024	1/1	1.00	0.01	39,39,39,39	0
56	MG	AA	1653	1/1	1.00	0.03	50,50,50,50	0
56	MG	DA	3026	1/1	1.00	0.03	51,51,51,51	0
56	MG	CA	3027	1/1	1.00	0.07	73,73,73,73	0

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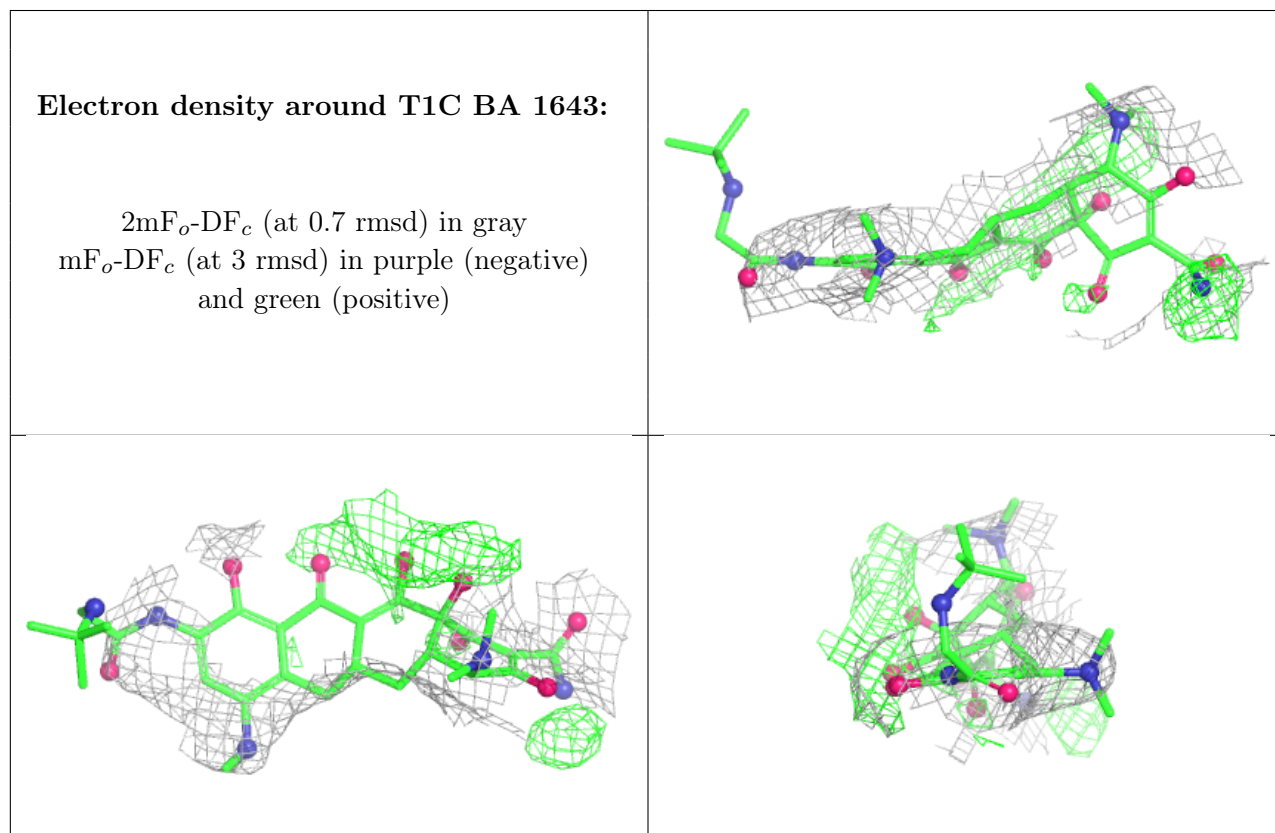
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3028	1/1	1.00	0.08	27,27,27,27	0
56	MG	AA	1637	1/1	1.00	0.03	51,51,51,51	0
56	MG	DA	3030	1/1	1.00	0.02	22,22,22,22	0
56	MG	DA	3031	1/1	1.00	0.07	29,29,29,29	0
56	MG	DA	3032	1/1	1.00	0.02	27,27,27,27	0
56	MG	DA	3033	1/1	1.00	0.01	13,13,13,13	0
56	MG	DA	3034	1/1	1.00	0.06	35,35,35,35	0
56	MG	DA	3035	1/1	1.00	0.04	34,34,34,34	0
56	MG	AA	1652	1/1	1.00	0.14	25,25,25,25	0
56	MG	DA	3037	1/1	1.00	0.03	30,30,30,30	0
56	MG	DA	3038	1/1	1.00	0.07	35,35,35,35	0
56	MG	DA	3039	1/1	1.00	0.07	55,55,55,55	0
56	MG	DA	3040	1/1	1.00	0.14	24,24,24,24	0
56	MG	DA	3041	1/1	1.00	0.03	52,52,52,52	0
61	ZN	D5	101	1/1	1.00	0.02	66,66,66,66	0
56	MG	CA	3017	1/1	1.00	0.08	88,88,88,88	0
56	MG	DD	301	1/1	1.00	0.03	35,35,35,35	0
56	MG	DA	3044	1/1	1.00	0.03	53,53,53,53	0
56	MG	DA	3045	1/1	1.00	0.03	24,24,24,24	0
56	MG	DA	3046	1/1	1.00	0.02	47,47,47,47	0
56	MG	DA	3047	1/1	1.00	0.05	36,36,36,36	0
56	MG	DM	201	1/1	1.00	0.04	56,56,56,56	0
56	MG	DA	3049	1/1	1.00	0.02	20,20,20,20	0
56	MG	DA	3050	1/1	1.00	0.02	24,24,24,24	0
56	MG	BA	1615	1/1	1.00	0.03	72,72,72,72	0
56	MG	DA	3052	1/1	1.00	0.03	41,41,41,41	0
56	MG	BA	1611	1/1	1.00	0.04	53,53,53,53	0
56	MG	DA	3054	1/1	1.00	0.04	30,30,30,30	0
56	MG	DA	3055	1/1	1.00	0.02	34,34,34,34	0
56	MG	DA	3056	1/1	1.00	0.04	23,23,23,23	0
56	MG	DA	3057	1/1	1.00	0.01	27,27,27,27	0
56	MG	DA	3058	1/1	1.00	0.03	27,27,27,27	0
56	MG	DA	3059	1/1	1.00	0.03	33,33,33,33	0
56	MG	DA	3060	1/1	1.00	0.04	41,41,41,41	0
56	MG	DB	203	1/1	1.00	0.04	41,41,41,41	0
56	MG	DA	3062	1/1	1.00	0.04	73,73,73,73	0
56	MG	DA	3008	1/1	1.00	0.03	27,27,27,27	0
56	MG	DA	3009	1/1	1.00	0.04	27,27,27,27	0
56	MG	DA	3065	1/1	1.00	0.06	45,45,45,45	0
56	MG	DA	3066	1/1	1.00	0.03	49,49,49,49	0
56	MG	DA	3067	1/1	1.00	0.06	46,46,46,46	0
56	MG	DA	3068	1/1	1.00	0.09	59,59,59,59	0

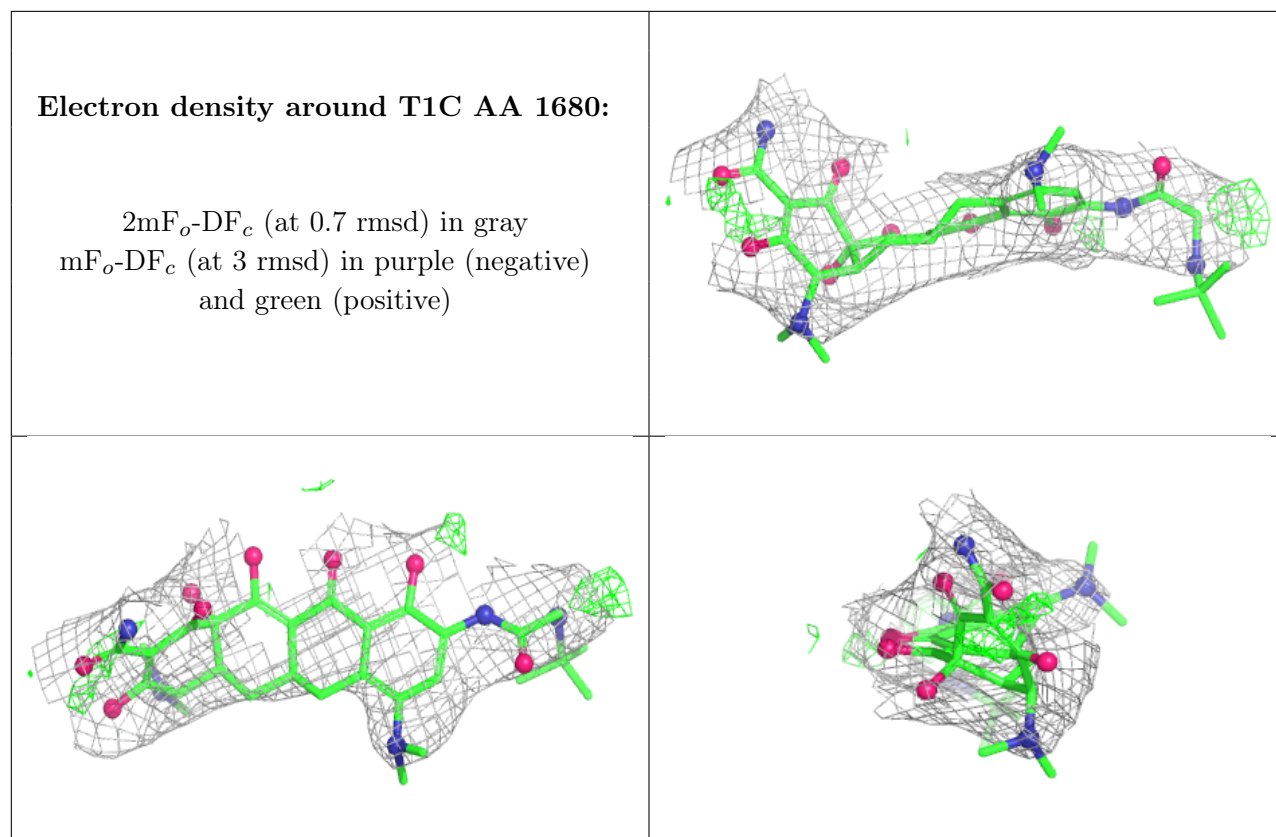
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3010	1/1	1.00	0.02	26,26,26,26	0
56	MG	DA	3070	1/1	1.00	0.05	55,55,55,55	0
56	MG	DB	204	1/1	1.00	0.06	37,37,37,37	0
56	MG	DA	3072	1/1	1.00	0.01	38,38,38,38	0
56	MG	DA	3012	1/1	1.00	0.03	25,25,25,25	0
56	MG	DA	3074	1/1	1.00	0.02	33,33,33,33	0
56	MG	DA	3075	1/1	1.00	0.03	40,40,40,40	0
56	MG	DA	3076	1/1	1.00	0.03	31,31,31,31	0
56	MG	DA	3013	1/1	1.00	0.02	20,20,20,20	0
56	MG	DB	205	1/1	1.00	0.04	63,63,63,63	0
56	MG	DA	3015	1/1	1.00	0.03	72,72,72,72	0
56	MG	DA	3016	1/1	1.00	0.01	26,26,26,26	0
56	MG	DA	3017	1/1	1.00	0.04	44,44,44,44	0
56	MG	DA	3082	1/1	1.00	0.06	56,56,56,56	0
56	MG	DA	3083	1/1	1.00	0.06	30,30,30,30	0
56	MG	DA	3018	1/1	1.00	0.11	8,8,8,8	0

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





6.5 Other polymers [i](#)

There are no such residues in this entry.