



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 09:09 PM EDT

PDB ID : 5J8A
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 Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

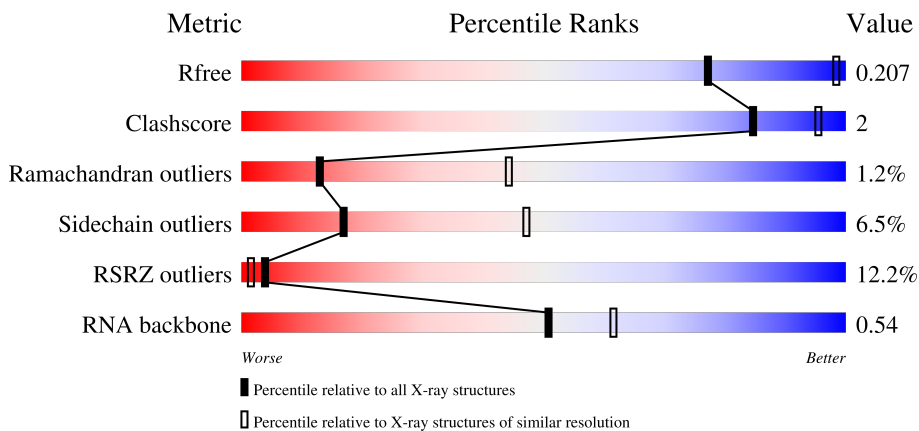
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

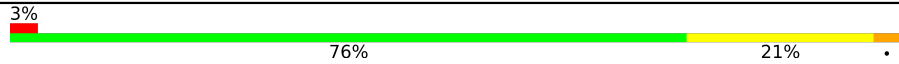
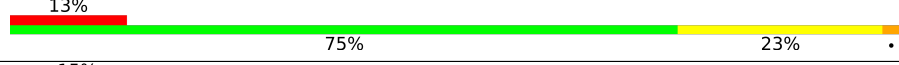
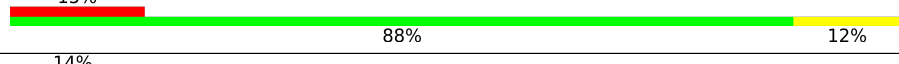

The reported resolution of this entry is 3.10 Å.

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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	
1	BA	1534	
2	AB	224	
2	BB	224	

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Mol	Chain	Length	Quality of chain
3	AC	206	4% 85% 15%
3	BC	206	27% 83% 17%
4	AD	205	90% 10%
4	BD	205	87% 13%
5	AE	155	81% 17% .
5	BE	155	% 71% 20% 5% . .
6	AF	106	3% 84% 16%
6	BF	106	3% 75% 19% 6%
7	AG	151	23% 87% 12% .
7	BG	151	58% 87% 13%
8	AH	129	2% 78% 20% .
8	BH	129	3% 79% 20% .
9	AI	127	26% 86% 13% .
9	BI	127	36% 84% 14% .
10	AJ	99	24% 81% 17% .
10	BJ	99	53% 75% 20% . .
11	AK	117	12% 86% 13% .
11	BK	117	11% 79% 20% .
12	AL	123	2% 89% 11% .
12	BL	123	4% 84% 15% .
13	AM	114	25% 80% 18% .
13	BM	114	69% 75% 21% .
14	AN	100	21% 91% 8% .
14	BN	100	52% 92% 8%
15	AO	88	2% 94% 6%

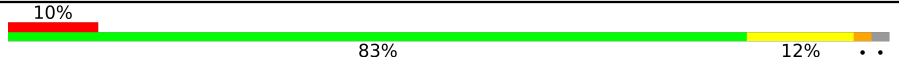








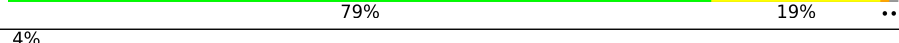
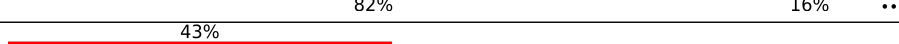






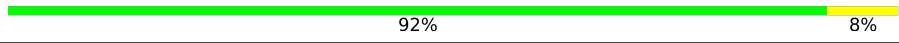



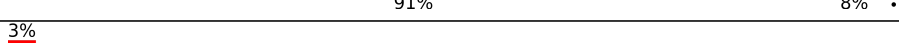
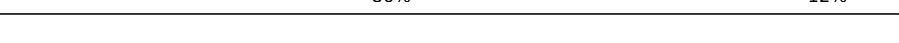


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Mol	Chain	Length	Quality of chain
15	BO	88	5% 91% 7% ..
16	AP	82	9% 85% 15%
16	BP	82	13% 80% 18% .
17	AQ	80	% 80% 19% .
17	BQ	80	15% 64% 31% ..
18	AR	55	7% 87% 13%
18	BR	55	5% 89% 11%
19	AS	79	8% 81% 18% .
19	BS	79	71% 84% 13% ..
20	AT	86	% 93% 6% .
20	BT	86	16% 78% 17% ..
21	AU	56	7% 86% 14%
21	BU	56	7% 88% 12%
22	C1	56	30% 82% 14% .
22	D1	56	82% 18%
23	C2	51	61% 65% 31% ..
23	D2	51	73% 25% .
24	C3	46	41% 85% 15%
24	D3	46	2% 93% 7%
25	C4	64	12% 92% 8%
25	D4	64	94% 5% .
26	C5	38	26% 71% 29%
26	D5	38	87% 13%
27	C0	58	33% 78% 19% .
27	D0	58	93% 7%

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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	15% 80% 14% . .
42	DO	125	88% 12%
43	CP	117	51% 87% 10% ..
43	DP	117	91% 6% .
44	CQ	114	15% 89% 10% .
44	DQ	114	% 88% 11% .
45	CR	117	10% 85% 15%
45	DR	117	86% 14%
46	CS	103	27% 84% 14% ..
46	DS	103	94% 6%
47	CT	110	13% 79% 21%
47	DT	110	85% 15%
48	CU	93	35% 83% 15% .
48	DU	93	3% 90% 10%
49	CV	103	53% 81% 17% ..
49	DV	103	7% 84% 14% ..
50	CW	94	30% 86% 14%
50	DW	94	88% 12%
51	CX	83	12% 82% 8% 10%
51	DX	83	83% 7% . 8%
52	CY	77	6% 87% 13%
52	DY	77	91% 9%
53	CZ	62	61% 92% 8%
53	DZ	62	3% 95% 5%
54	DI	135	24% 69% 27% .

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Mol	Chain	Length	Quality of chain
55	DA	2904	 3% 78% 19%

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	AA	1603	-	-	-	X
56	MG	AA	1612	-	-	-	X
56	MG	AA	1613	-	-	-	X
56	MG	AA	1615	-	-	-	X
56	MG	AA	1616	-	-	-	X
56	MG	AA	1618	-	-	-	X
56	MG	AA	1622	-	-	-	X
56	MG	AA	1626	-	-	-	X
56	MG	AA	1628	-	-	-	X
56	MG	BA	1612	-	-	-	X
56	MG	BA	1623	-	-	-	X
56	MG	BA	1624	-	-	-	X
56	MG	BA	1639	-	-	-	X
56	MG	BA	1647	-	-	-	X
56	MG	CA	3003	-	-	-	X
56	MG	CA	3047	-	-	-	X
56	MG	CA	3075	-	-	-	X
56	MG	CA	3077	-	-	-	X
56	MG	CA	3114	-	-	-	X
56	MG	CA	3122	-	-	-	X
56	MG	CA	3123	-	-	-	X
56	MG	CA	3132	-	-	-	X
56	MG	CA	3136	-	-	-	X
56	MG	CA	3139	-	-	-	X
56	MG	CA	3154	-	-	-	X
56	MG	CA	3156	-	-	-	X
56	MG	DA	3122	-	-	-	X
56	MG	DA	3129	-	-	-	X
56	MG	DA	3166	-	-	-	X
56	MG	DA	3167	-	-	-	X
56	MG	DA	3176	-	-	-	X
56	MG	DA	3179	-	-	-	X
56	MG	DA	3180	-	-	-	X
56	MG	DA	3181	-	-	-	X
56	MG	DB	206	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	DB	207	-	-	-	X
58	MPD	DA	3204	-	-	-	X
58	MPD	DE	301	-	-	-	X
59	PUT	AA	1672	-	-	-	X
59	PUT	AA	1674	-	-	-	X
59	PUT	AA	1675	-	-	-	X
59	PUT	DA	3195	-	-	-	X
62	PEG	D3	102	-	-	-	X
62	PEG	DA	3199	-	-	-	X
62	PEG	DA	3200	-	-	-	X
62	PEG	DP	201	-	-	-	X
62	PEG	DQ	201	-	-	-	X
64	PGE	D1	102	-	-	-	X
67	ACY	DA	3196	-	X	-	-
69	TRS	DA	3220	-	-	-	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
26	C5	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			
26	D5	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			

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

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

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

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

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

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

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

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

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

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

- 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	Total 857	C 532	N 166	O 156	S 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	Total 739	C 466	N 139	O 132	S 2	0	0	0
48	DU	93	Total 738	C 466	N 139	O 131	S 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	Total 779	C 492	N 146	O 141	0	0	0
49	DV	102	Total 779	C 492	N 146	O 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	Total 753	C 479	N 137	O 134	S 3	0	0	0
50	DW	94	Total 753	C 479	N 137	O 134	S 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	Total 569	C 353	N 113	O 102	S 1	0	0	0
51	DX	76	Total 591	C 365	N 121	O 104	S 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	Total 625	C 388	N 129	O 106	S 2	0	0	0
52	DY	77	Total 625	C 388	N 129	O 106	S 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 (three-letter code: MG) (formula: Mg).

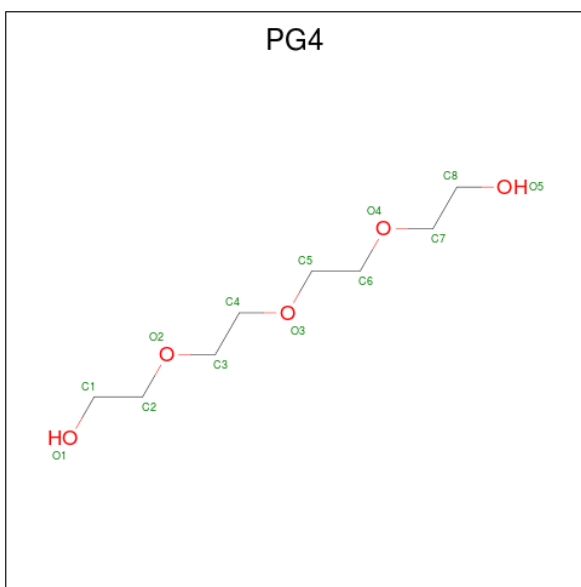
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	72	Total	Mg	0	0
			72	72		
56	BA	45	Total	Mg	0	0
			45	45		
56	CB	3	Total	Mg	0	0
			3	3		
56	CA	156	Total	Mg	0	0
			156	156		
56	DD	1	Total	Mg	0	0
			1	1		
56	DM	1	Total	Mg	0	0
			1	1		
56	DR	1	Total	Mg	0	0
			1	1		

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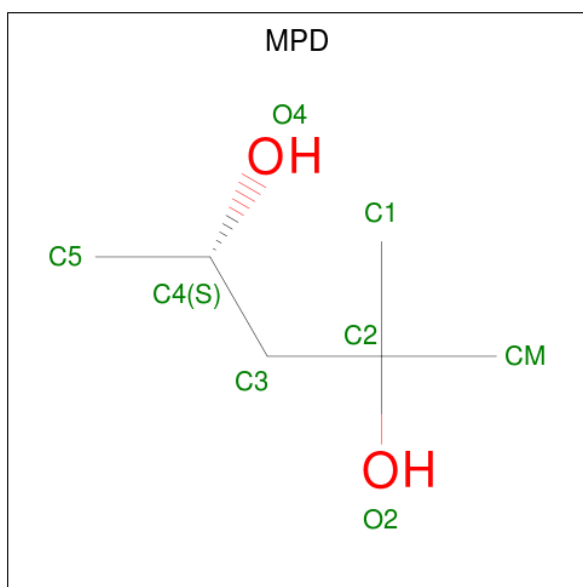
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	DB	9	Total Mg 9 9	0	0
56	DA	184	Total Mg 184 184	0	0

- Molecule 57 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



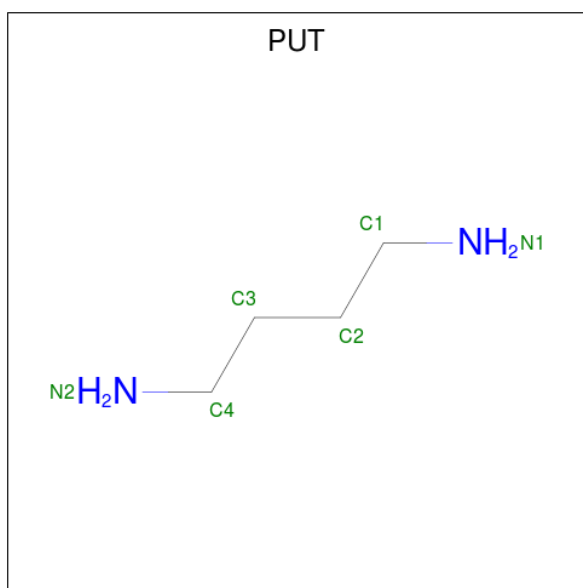
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AA	1	Total C O 13 8 5	0	0
57	BA	1	Total C O 13 8 5	0	0
57	DQ	1	Total C O 13 8 5	0	0
57	DR	1	Total C O 13 8 5	0	0
57	DS	1	Total C O 13 8 5	0	0
57	DA	1	Total C O 13 8 5	0	0
57	DA	1	Total C O 13 8 5	0	0

- Molecule 58 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: 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 (three-letter code: PUT) (formula: C₄H₁₂N₂).



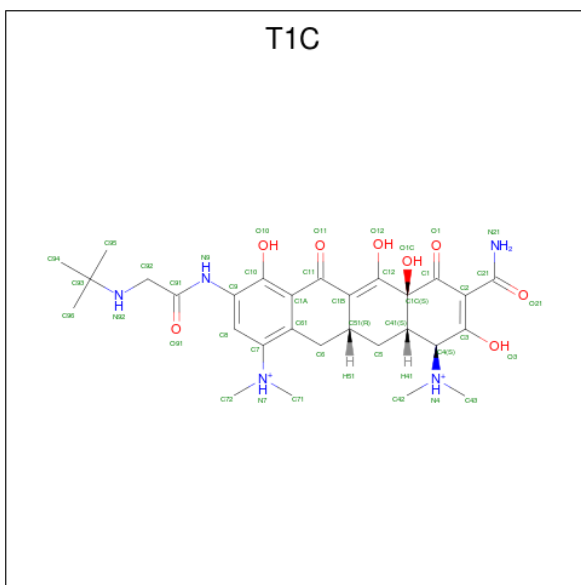
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	AA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	Total C N 6 4 2	0	0
59	DA	1	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 (three-letter code: T1C) (formula: C₂₉H₄₁N₅O₈).



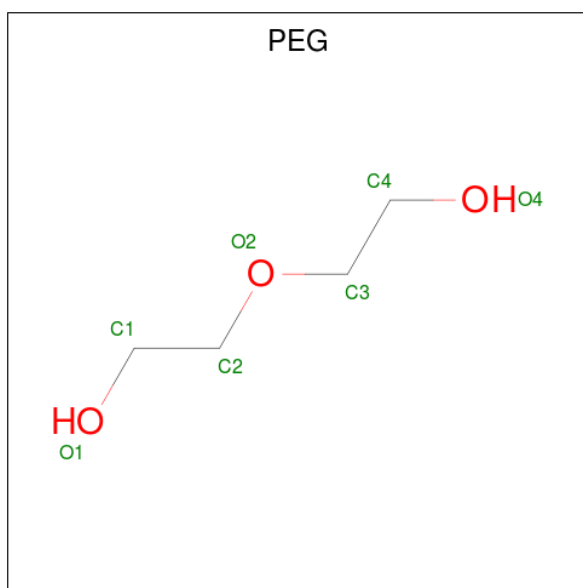
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
60	AA	1	Total	C	N	O	0	0
			42	29	5	8		
60	BA	1	Total	C	N	O	0	0
			42	29	5	8		

- Molecule 61 is ZINC ION (three-letter code: 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		

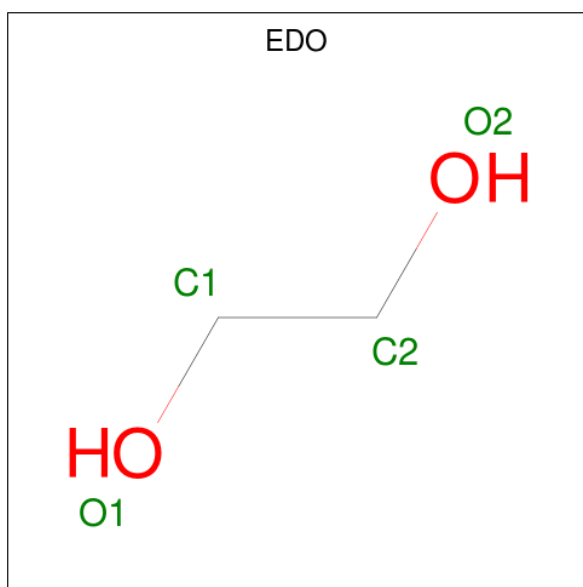
- Molecule 62 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:

C₄H₁₀O₃).



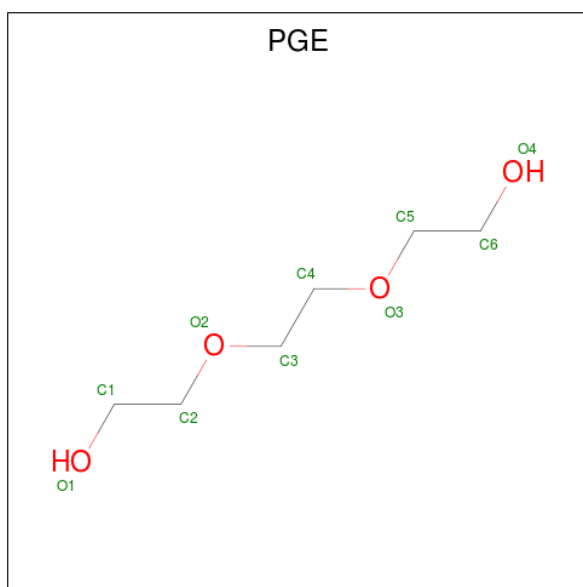
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	AL	1	Total C O 7 4 3	0	0
62	D1	1	Total C O 7 4 3	0	0
62	D3	1	Total C O 7 4 3	0	0
62	DL	1	Total C O 7 4 3	0	0
62	DP	1	Total C O 7 4 3	0	0
62	DQ	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	Total C O 7 4 3	0	0
62	DA	1	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 (three-letter code: EDO) (formula: C₂H₆O₂).



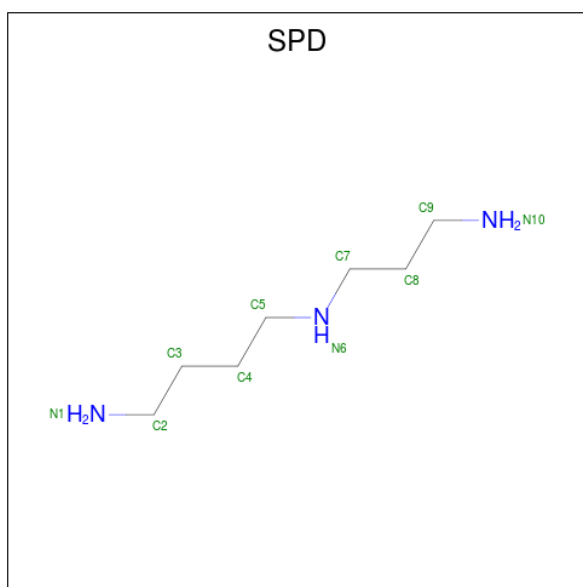
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	D1	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DB	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	Total C O 4 2 2	0	0
63	DA	1	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 (three-letter code: PGE) (formula: C₆H₁₄O₄).



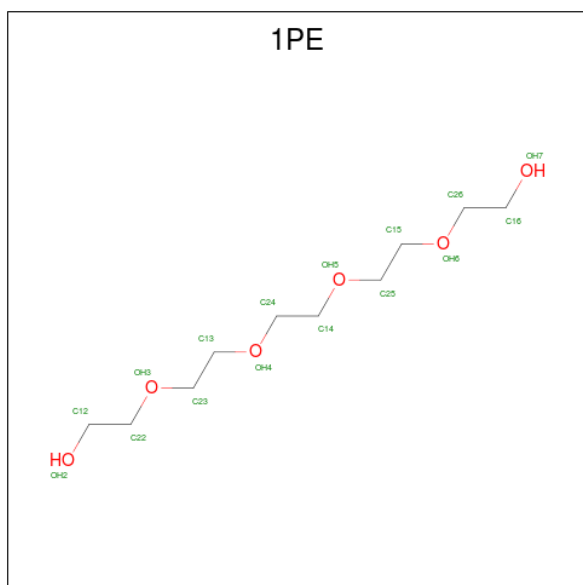
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	D1	1	Total C O 10 6 4	0	0
64	D3	1	Total C O 10 6 4	0	0
64	DS	1	Total C O 10 6 4	0	0
64	DU	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0
64	DA	1	Total C O 10 6 4	0	0

- Molecule 65 is SPERMIDINE (three-letter code: SPD) (formula: C₇H₁₉N₃).



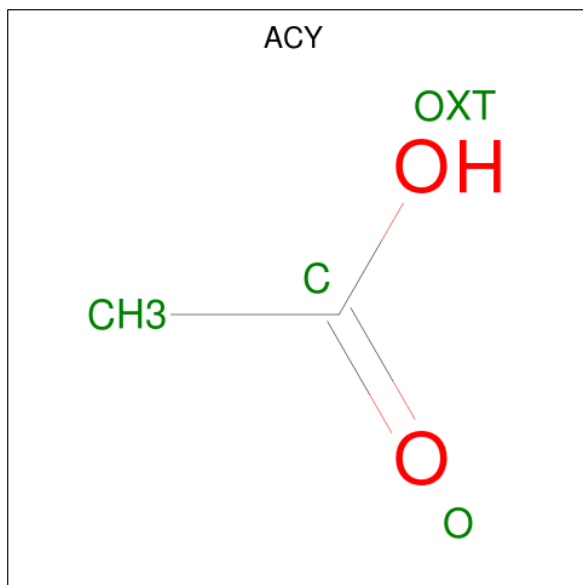
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
65	DA	1	Total C N 10 7 3	0	0
65	DA	1	Total C N 10 7 3	0	0
65	DA	1	Total C N 10 7 3	0	0
65	DA	1	Total C N 10 7 3	0	0

- Molecule 66 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



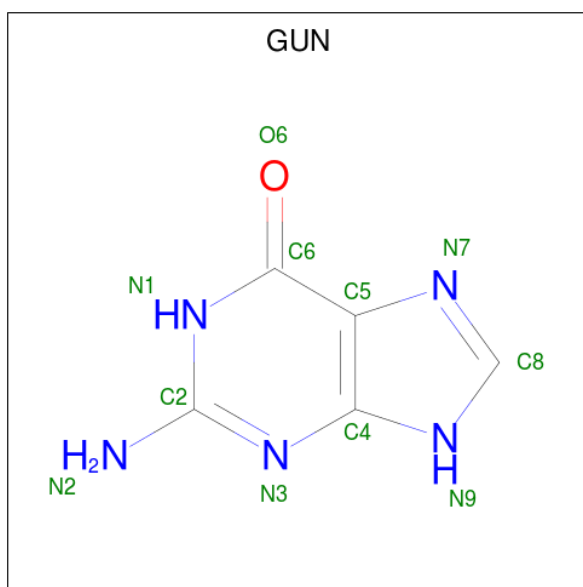
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
66	DA	1	Total	C	O	0	0
			16	10	6		
66	DA	1	Total	C	O	0	0
			16	10	6		

- Molecule 67 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



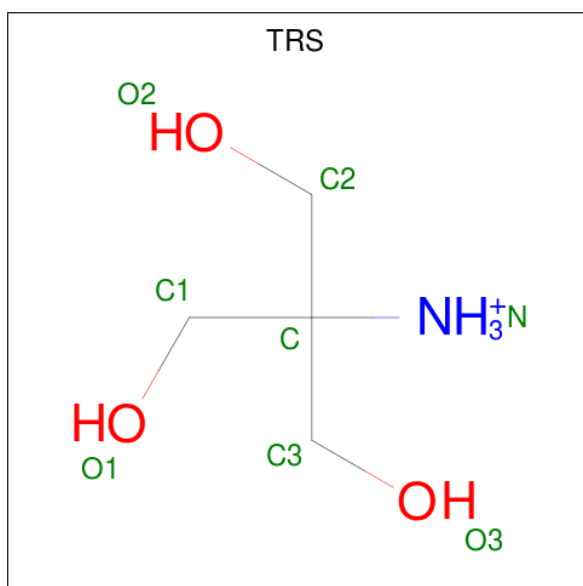
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
67	DA	1	Total	C	O	0	0
			4	2	2		
67	DA	1	Total	C	O	0	0
			4	2	2		
67	DA	1	Total	C	O	0	0
			4	2	2		

- Molecule 68 is GUANINE (three-letter code: 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 (three-letter code: 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 O 1 1	0	0
70	CM	4	Total O 4 4	0	0
70	CO	1	Total O 1 1	0	0
70	CU	3	Total O 3 3	0	0
70	CV	1	Total O 1 1	0	0
70	CW	1	Total O 1 1	0	0
70	CY	1	Total O 1 1	0	0
70	DE	60	Total O 60 60	0	0
70	DF	15	Total O 15 15	0	0
70	DG	6	Total O 6 6	0	0
70	DH	2	Total O 2 2	0	0
70	DK	64	Total O 64 64	0	0
70	DL	51	Total O 51 51	0	0
70	DM	64	Total O 64 64	0	0
70	DN	73	Total O 73 73	0	0
70	DO	46	Total O 46 46	0	0
70	DP	40	Total O 40 40	0	0
70	DQ	32	Total O 32 32	0	0
70	DR	63	Total O 63 63	0	0
70	DS	44	Total O 44 44	0	0
70	DT	69	Total O 69 69	0	0

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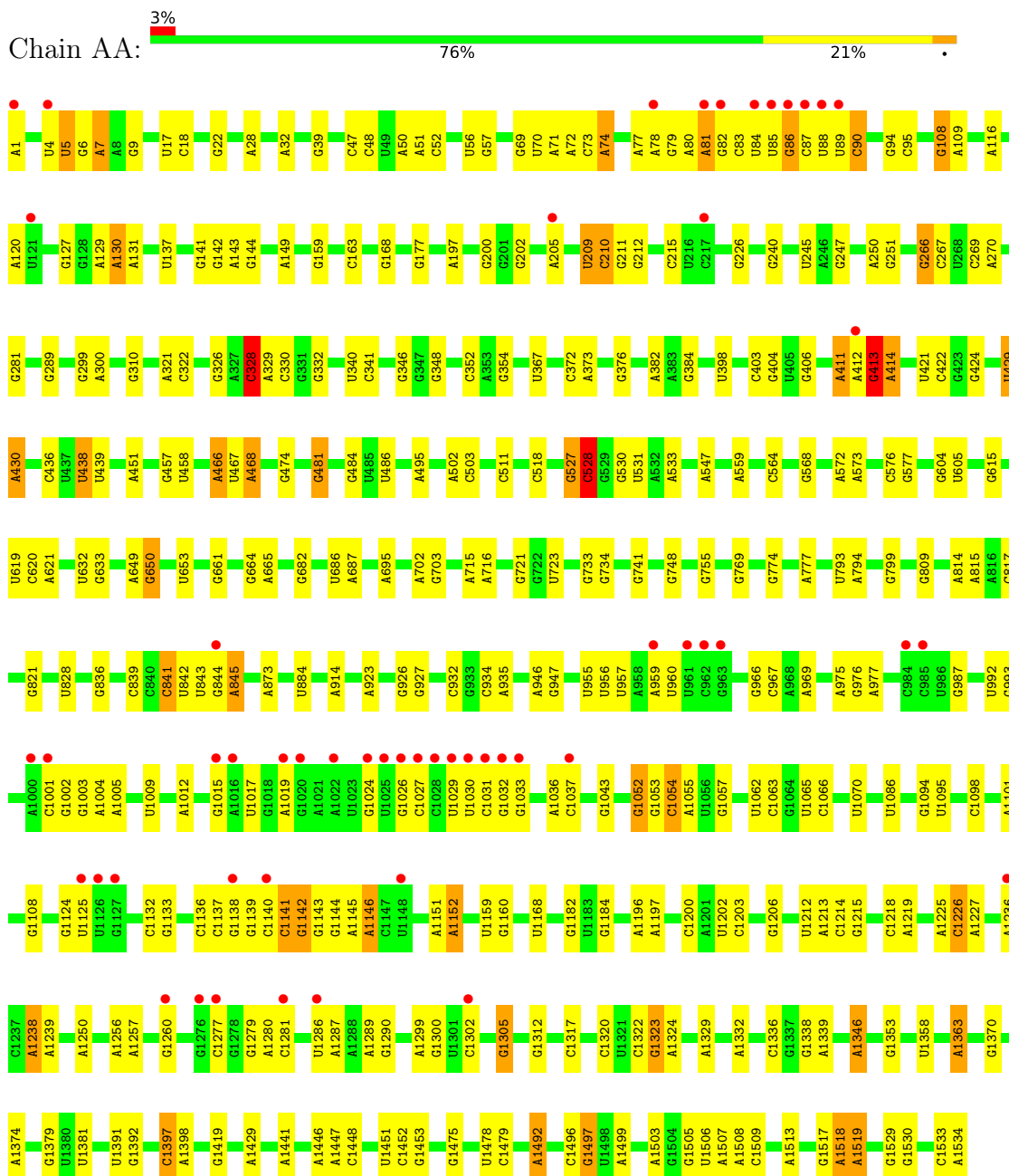
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
70	DU	21	Total 21	O 21	0	0
70	DV	20	Total 20	O 20	0	0
70	DW	31	Total 31	O 31	0	0
70	DX	26	Total 26	O 26	0	0
70	DY	11	Total 11	O 11	0	0
70	DZ	7	Total 7	O 7	0	0
70	DB	213	Total 213	O 213	0	0
70	DA	4829	Total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

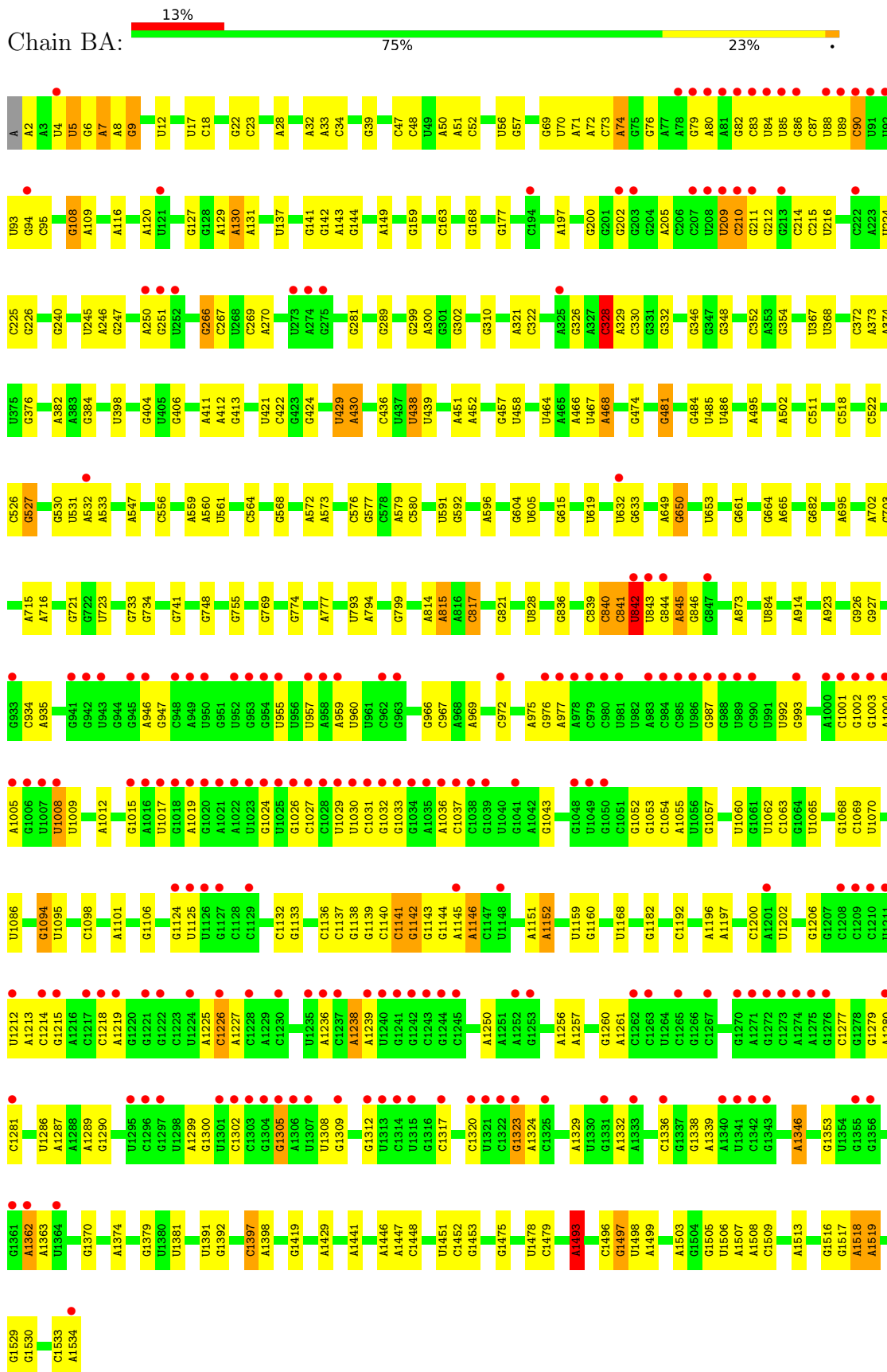
3 Residue-property plots [i](#)

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.

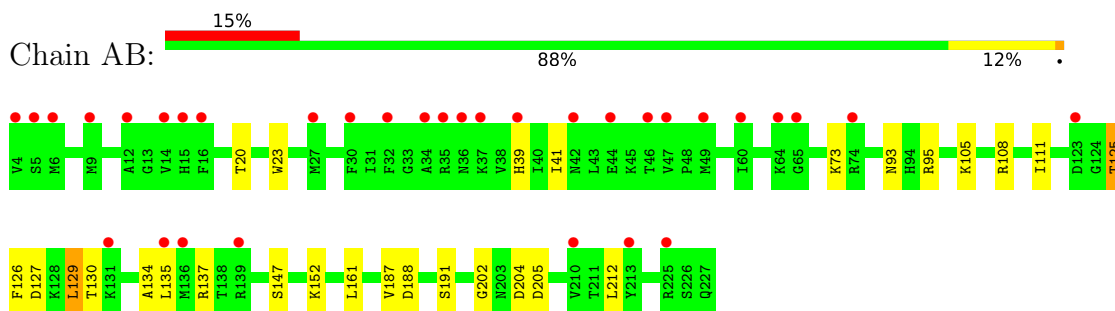
- Molecule 1: 16S rRNA



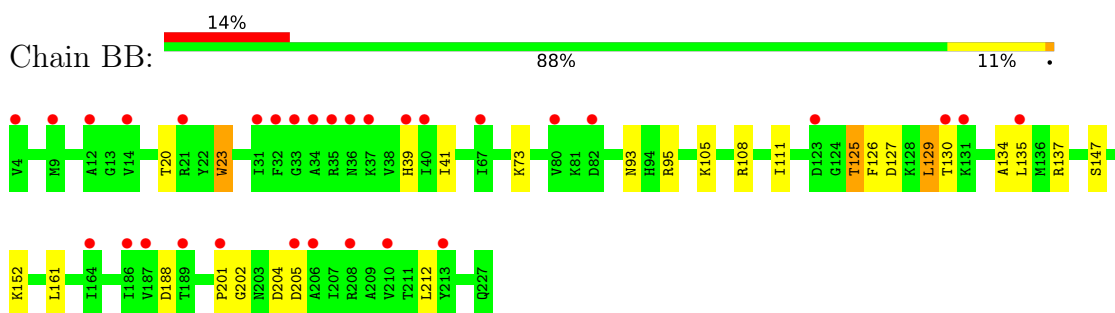
● Molecule 1: 16S rRNA



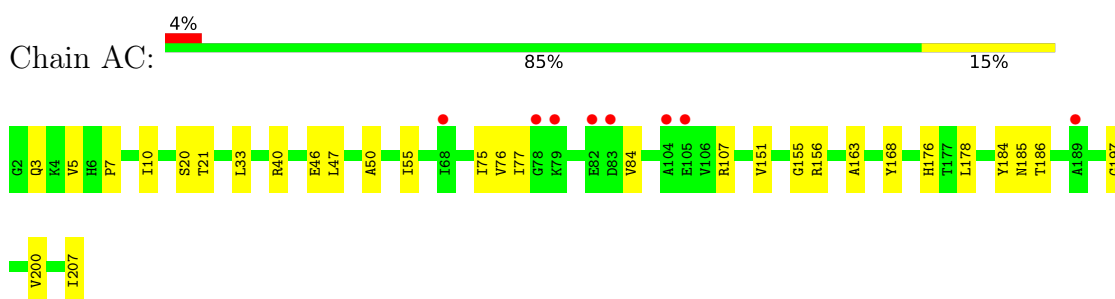
- Molecule 2: 30S ribosomal protein S2



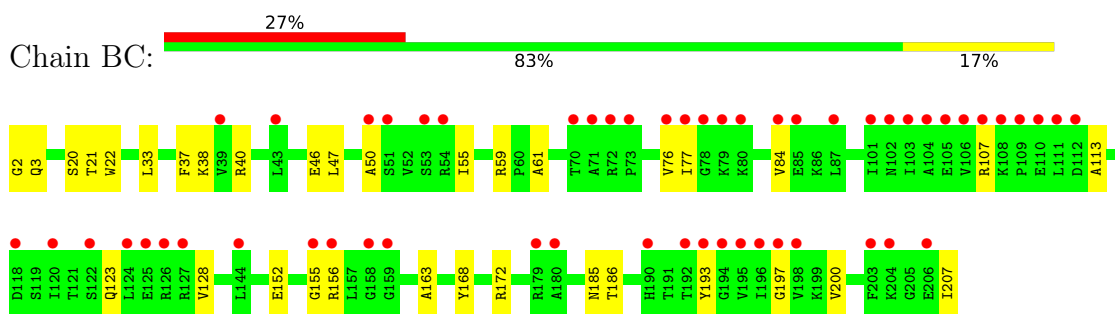
- Molecule 2: 30S ribosomal protein S2



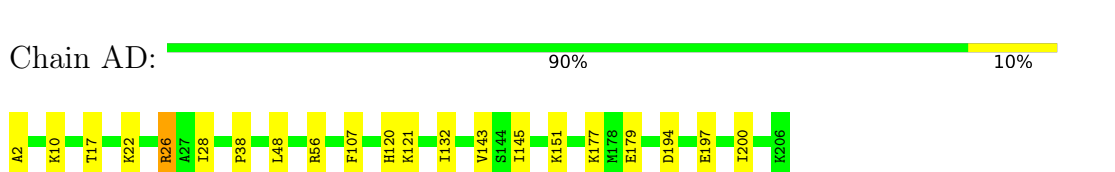
- Molecule 3: 30S ribosomal protein S3



- Molecule 3: 30S ribosomal protein S3



- Molecule 4: 30S ribosomal protein S4



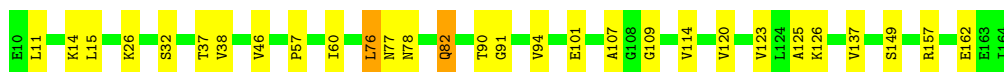
- Molecule 4: 30S ribosomal protein S4

Chain BD: 87% 13%



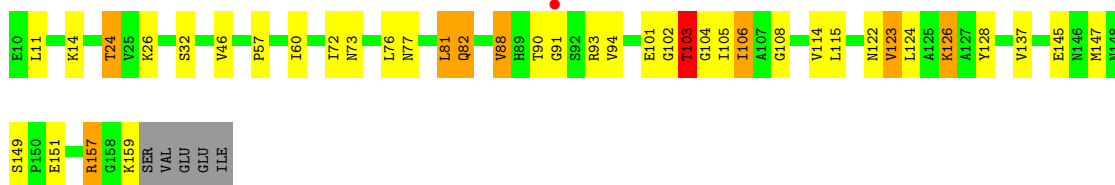
- Molecule 5: 30S ribosomal protein S5

Chain AE: 81% 17%



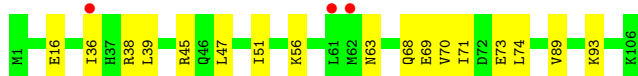
- Molecule 5: 30S ribosomal protein S5

Chain BE: 71% 20% 5%



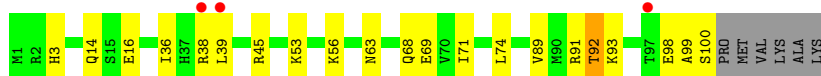
- Molecule 6: 30S ribosomal protein S6

Chain AF: 3% 84% 16%



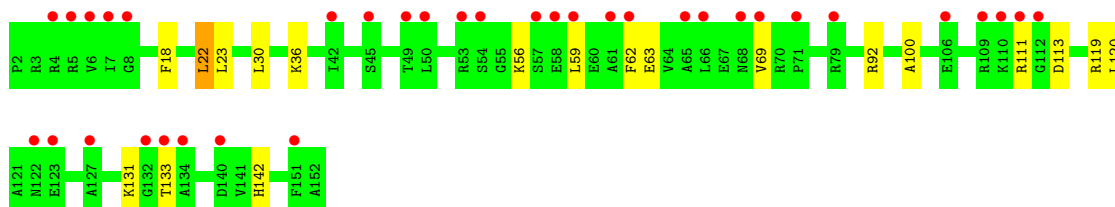
- Molecule 6: 30S ribosomal protein S6

Chain BF: 3% 75% 19% 6%

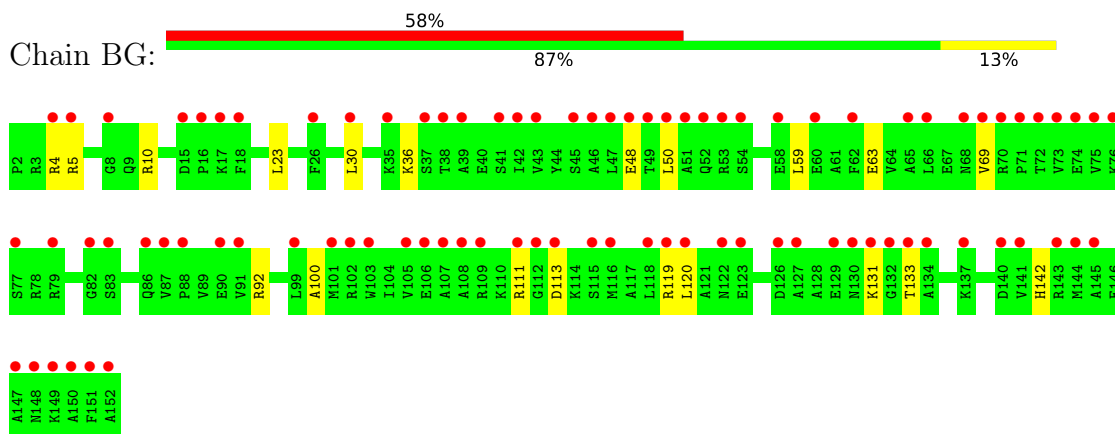


- Molecule 7: 30S ribosomal protein S7

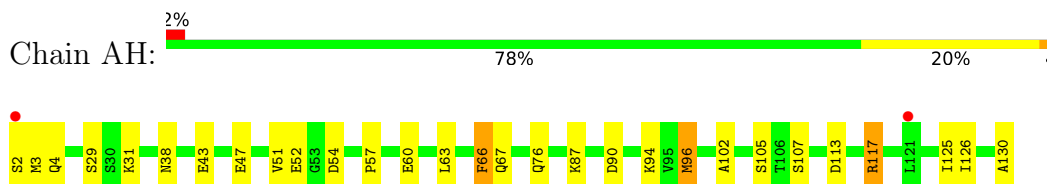
Chain AG: 23% 87% 12%



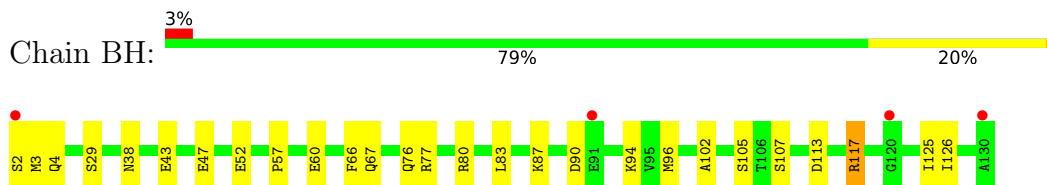
- Molecule 7: 30S ribosomal protein S7



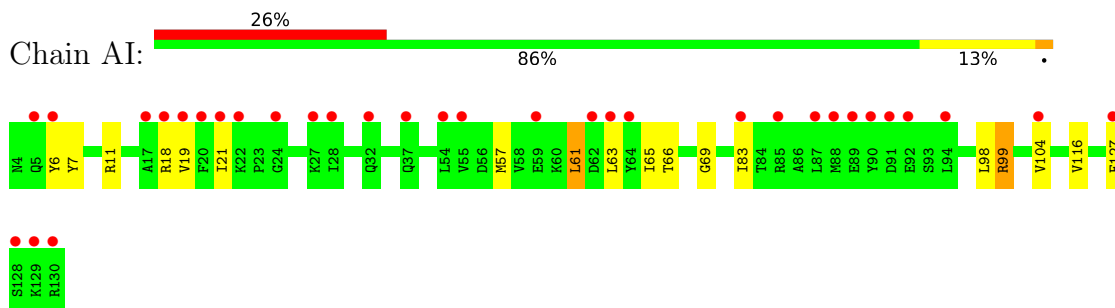
- Molecule 8: 30S ribosomal protein S8



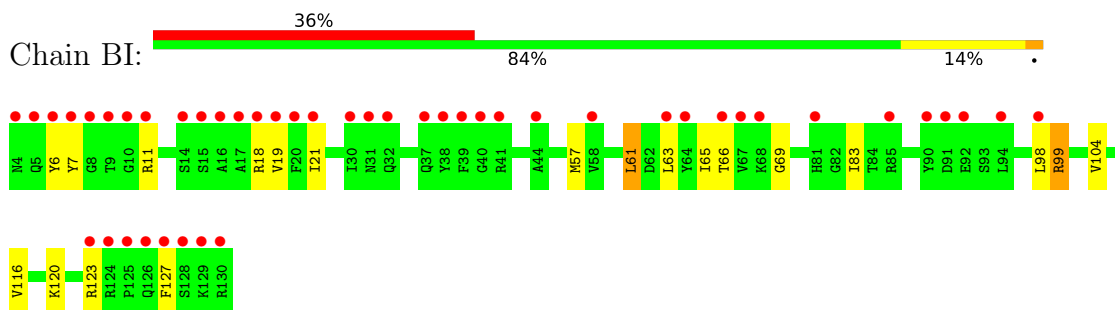
- Molecule 8: 30S ribosomal protein S8



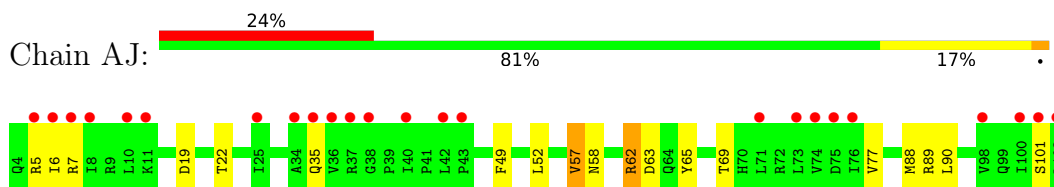
- Molecule 9: 30S ribosomal protein S9



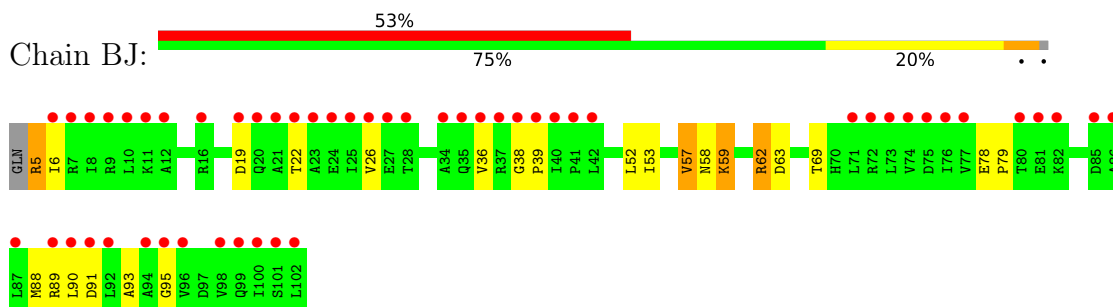
- Molecule 9: 30S ribosomal protein S9



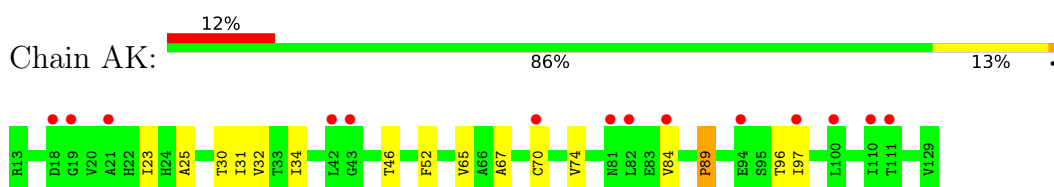
- Molecule 10: 30S ribosomal protein S10



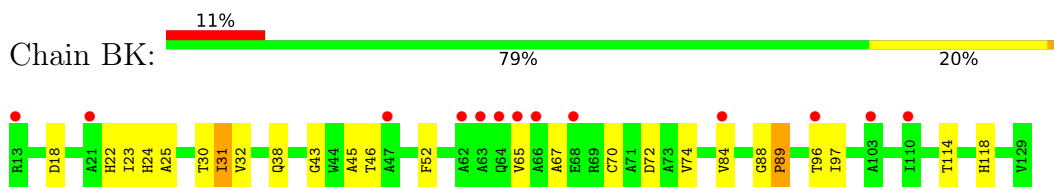
- Molecule 10: 30S ribosomal protein S10



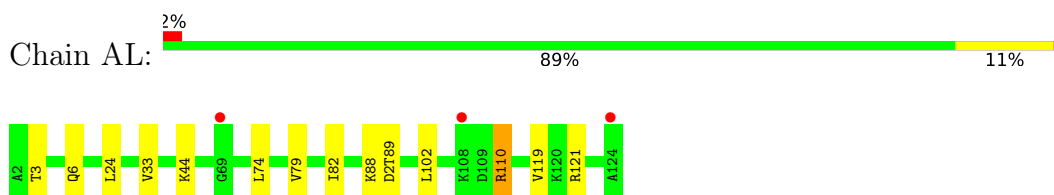
- Molecule 11: 30S ribosomal protein S11



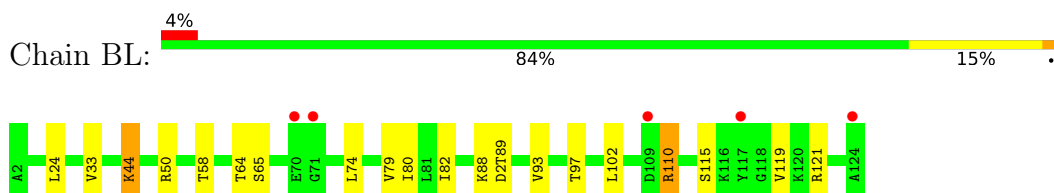
- Molecule 11: 30S ribosomal protein S11



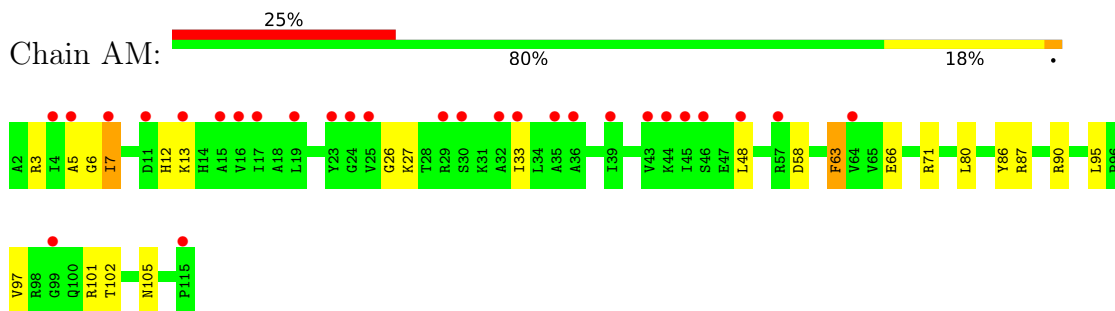
- Molecule 12: 30S ribosomal protein S12



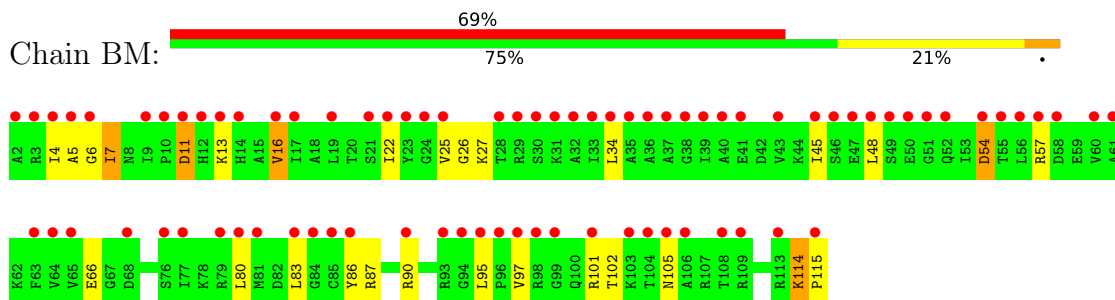
- Molecule 12: 30S ribosomal protein S12



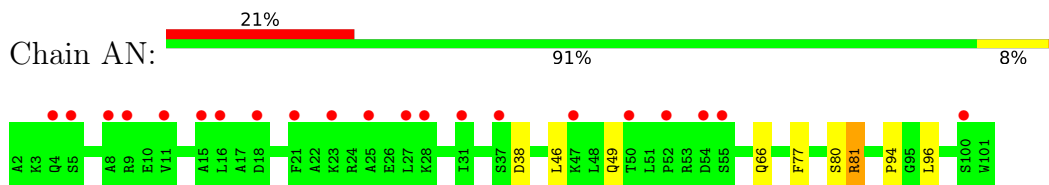
- Molecule 13: 30S ribosomal protein S13



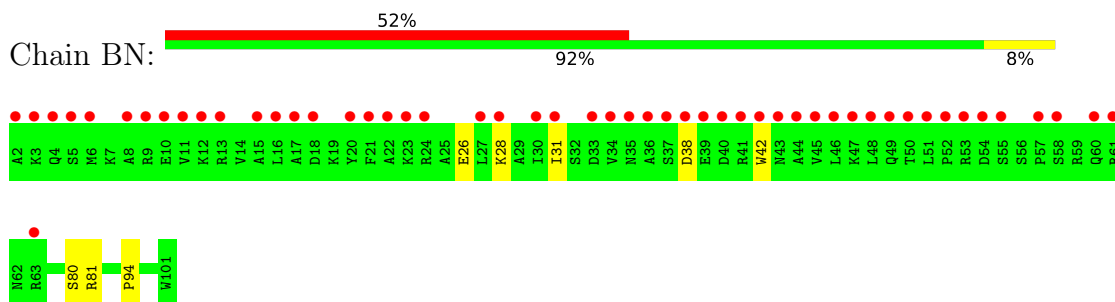
- Molecule 13: 30S ribosomal protein S13



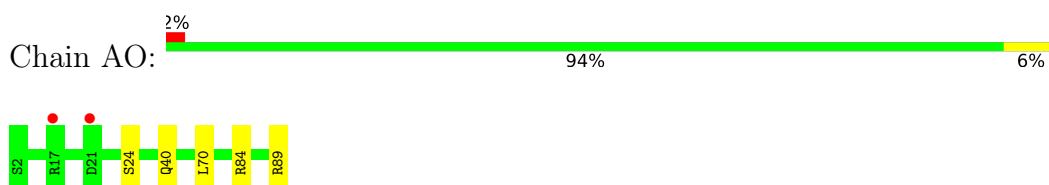
- Molecule 14: 30S ribosomal protein S14



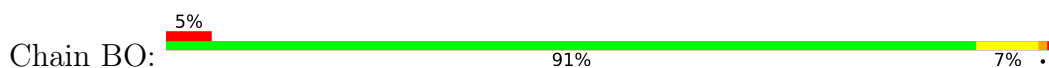
- Molecule 14: 30S ribosomal protein S14

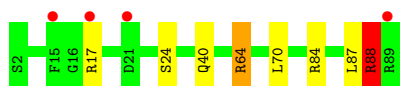


- Molecule 15: 30S ribosomal protein S15

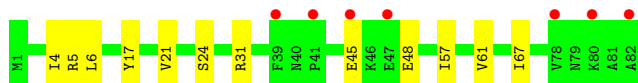
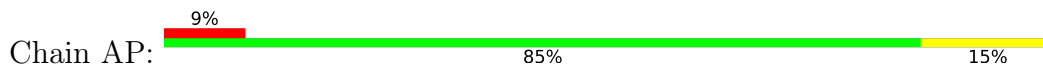


- Molecule 15: 30S ribosomal protein S15

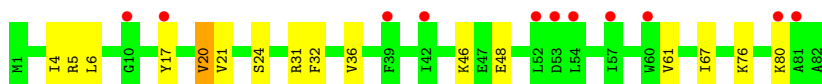
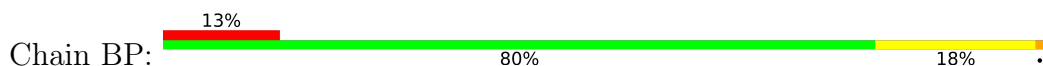




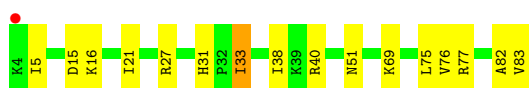
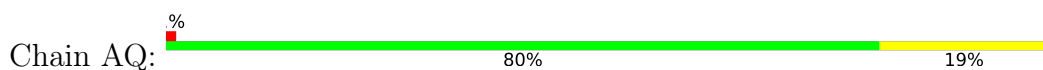
- Molecule 16: 30S ribosomal protein S16



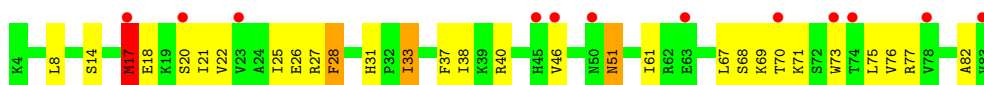
- Molecule 16: 30S ribosomal protein S16



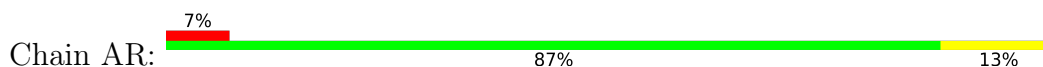
- Molecule 17: 30S ribosomal protein S17



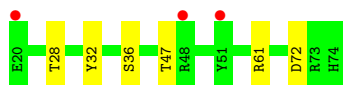
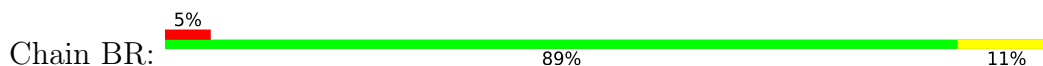
- Molecule 17: 30S ribosomal protein S17



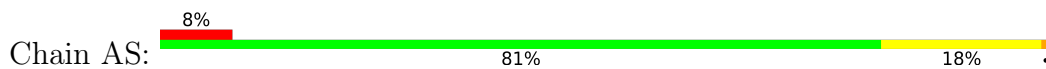
- Molecule 18: 30S ribosomal protein S18



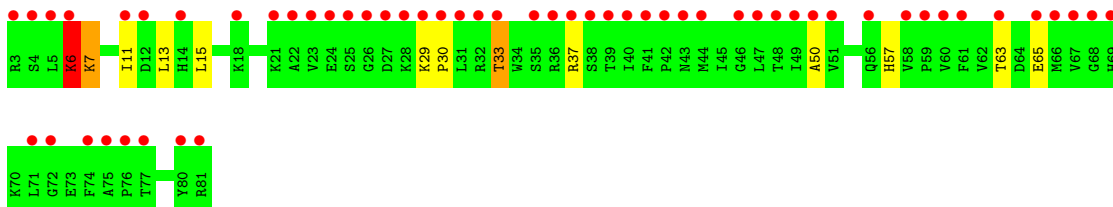
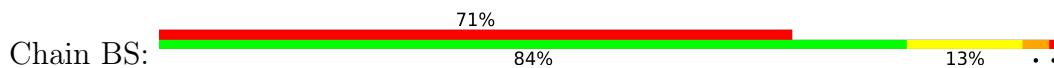
- Molecule 18: 30S ribosomal protein S18



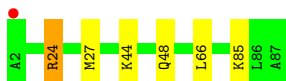
- Molecule 19: 30S ribosomal protein S19



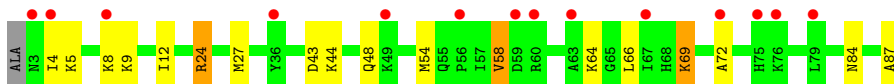
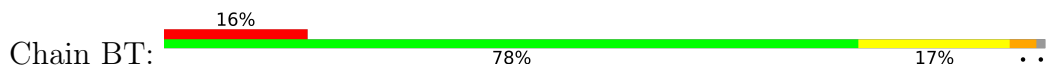
- Molecule 19: 30S ribosomal protein S19



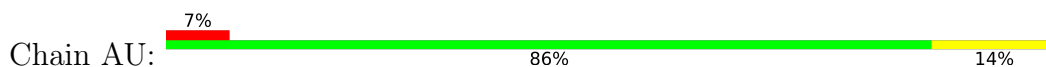
- Molecule 20: 30S ribosomal protein S20



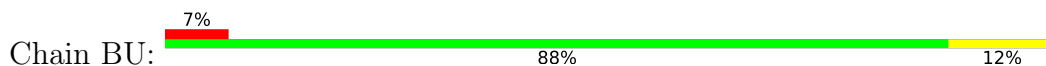
- Molecule 20: 30S ribosomal protein S20



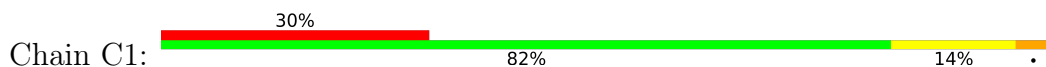
- Molecule 21: 30S ribosomal protein S21

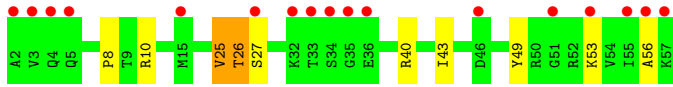


- Molecule 21: 30S ribosomal protein S21

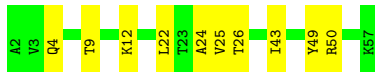
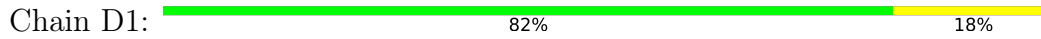


- Molecule 22: 50S ribosomal protein L32

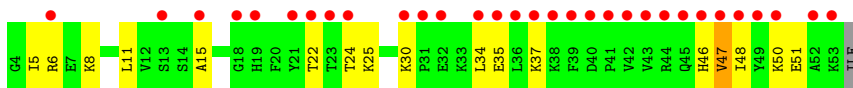




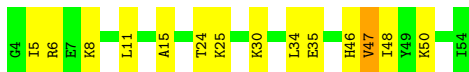
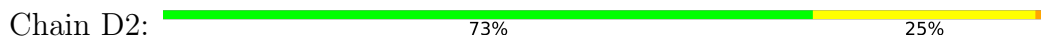
- Molecule 22: 50S ribosomal protein L32



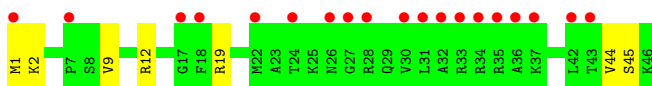
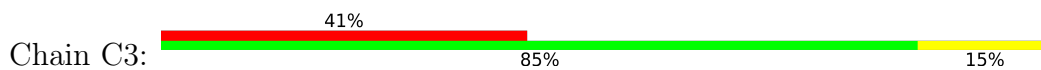
- Molecule 23: 50S ribosomal protein L33



- Molecule 23: 50S ribosomal protein L33



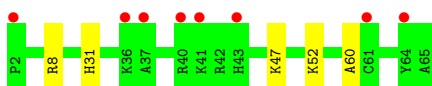
- Molecule 24: 50S ribosomal protein L34



- Molecule 24: 50S ribosomal protein L34

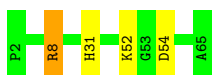


- Molecule 25: 50S ribosomal protein L35




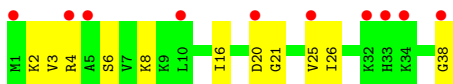
- Molecule 25: 50S ribosomal protein L35

Chain D4:  94% 5%




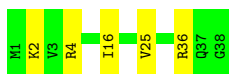
- Molecule 26: 50S ribosomal protein L36

Chain C5:  26% 71% 29%




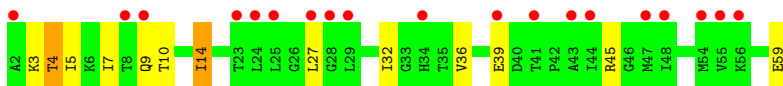
- Molecule 26: 50S ribosomal protein L36

Chain D5:  87% 13%



- Molecule 27: 50S ribosomal protein L30

Chain C0:  33% 78% 19%




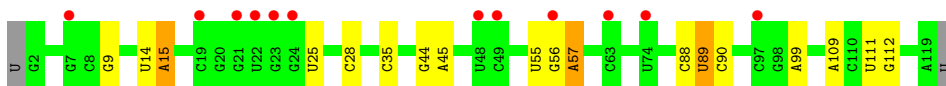
- Molecule 27: 50S ribosomal protein L30

Chain D0:  93% 7%



- Molecule 28: 5S rRNA

Chain CB:  10% 83% 12%

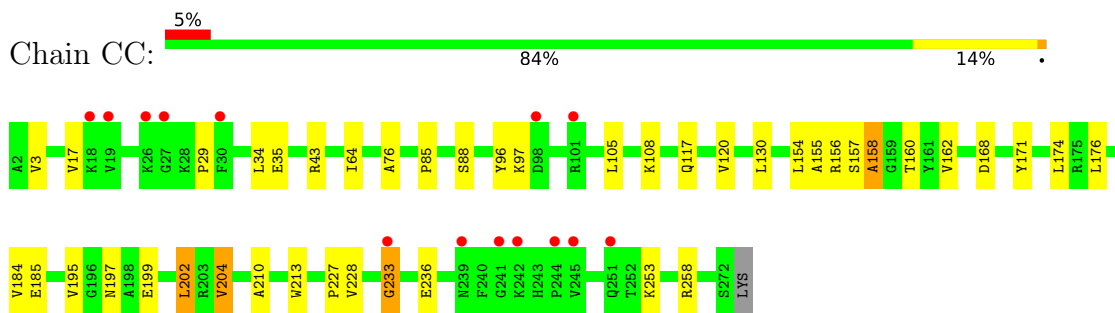


- Molecule 28: 5S rRNA

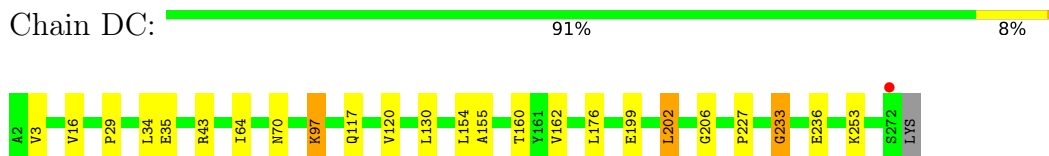
Chain DB:  91% 8%



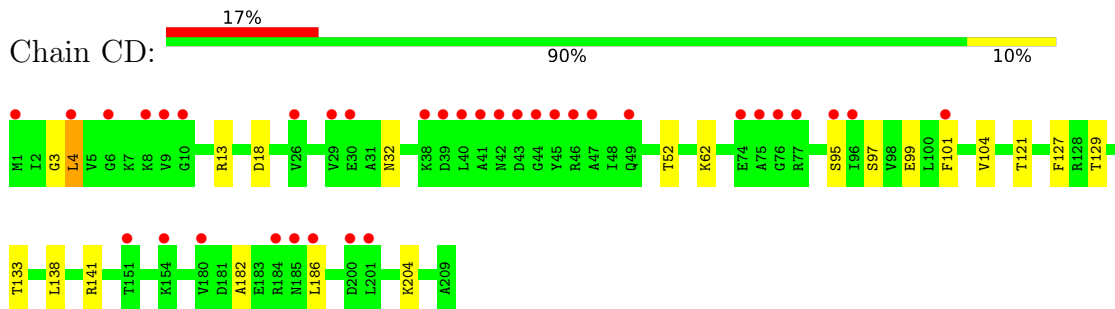
- Molecule 29: 50S ribosomal protein L2



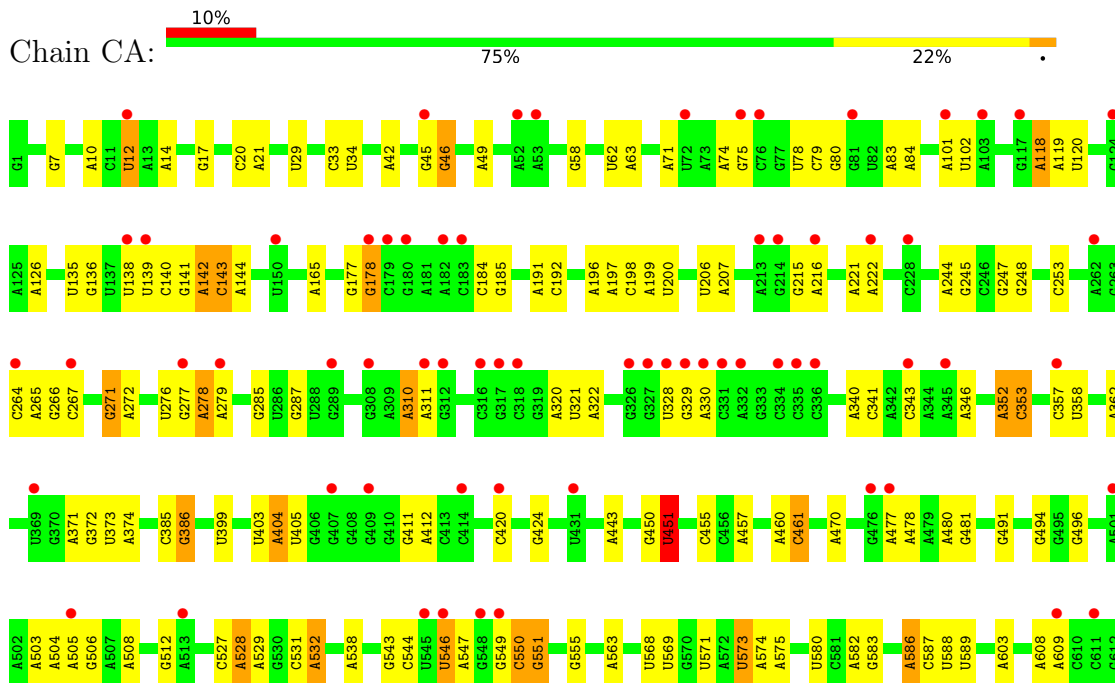
• Molecule 29: 50S ribosomal protein L2

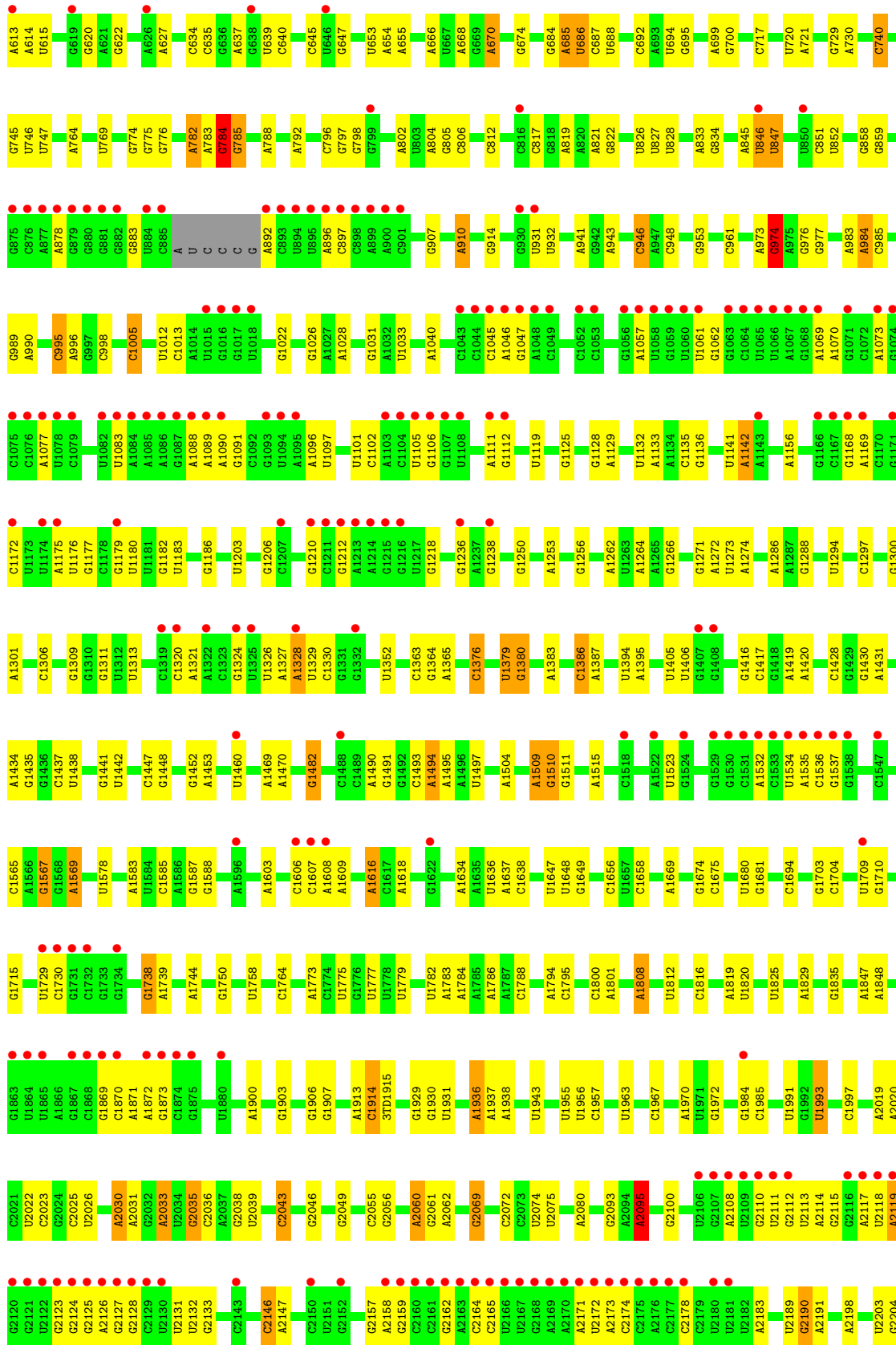


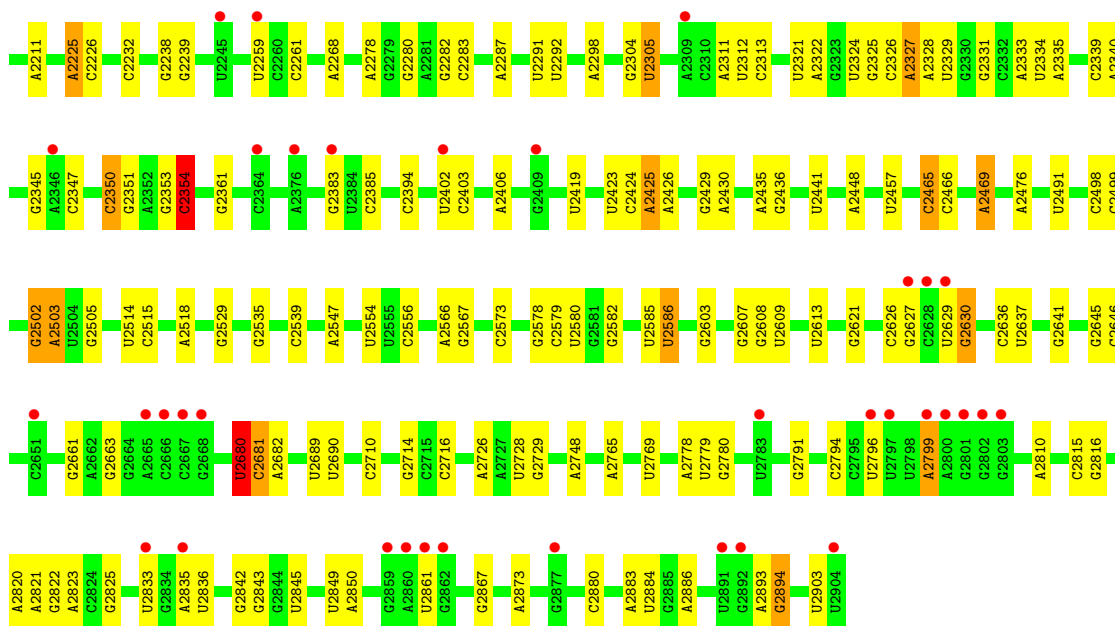
• Molecule 30: 50S ribosomal protein L3



• Molecule 31: 23S rRNA



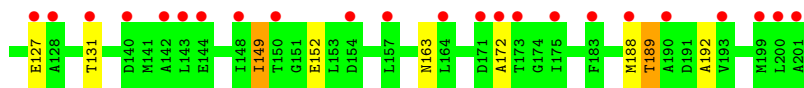
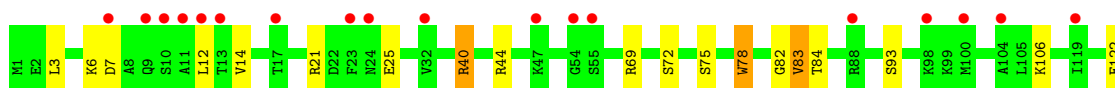




• Molecule 32: 50S ribosomal protein L3



• Molecule 33: 50S ribosomal protein L4

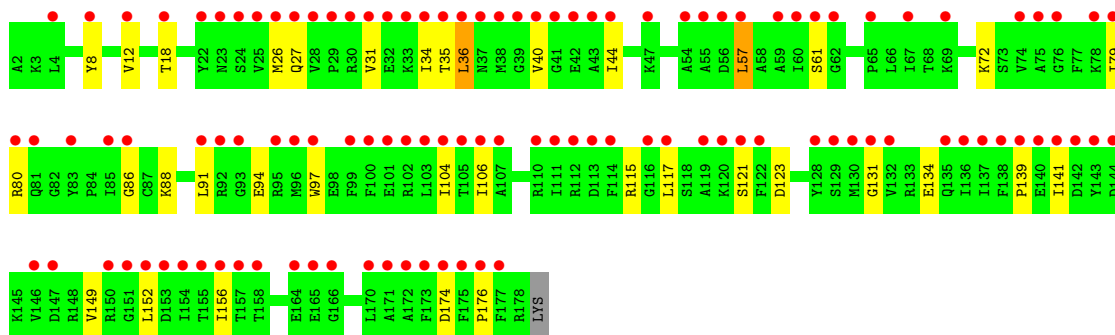


• Molecule 33: 50S ribosomal protein L4

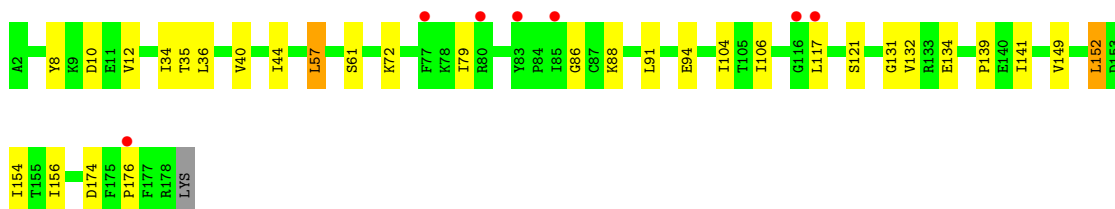
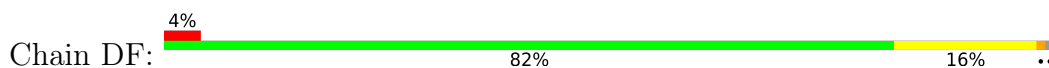


• Molecule 34: 50S ribosomal protein L5

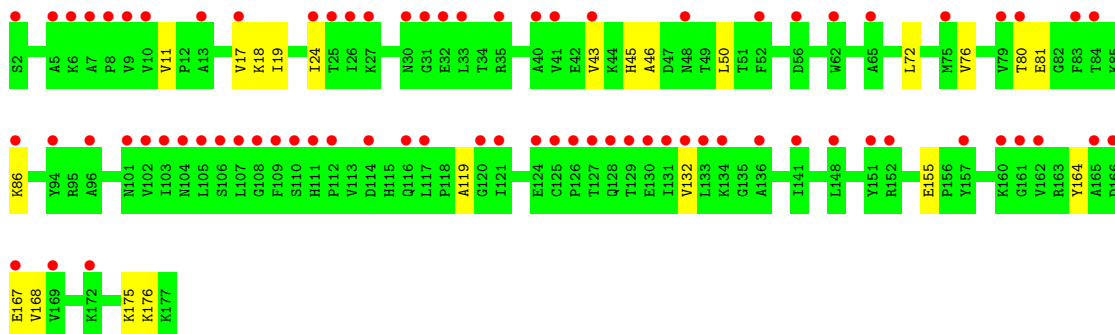
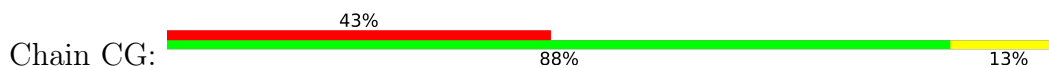




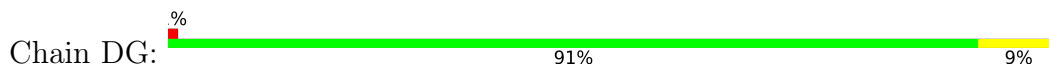
• Molecule 34: 50S ribosomal protein L5



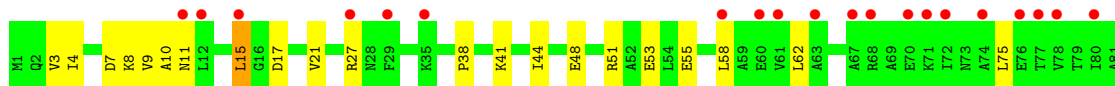
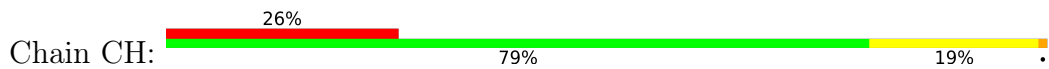
• Molecule 35: 50S ribosomal protein L6

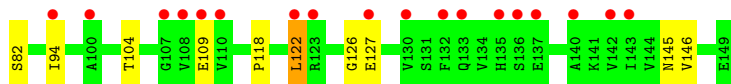


• Molecule 35: 50S ribosomal protein L6

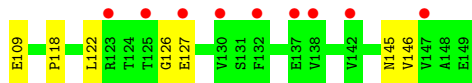
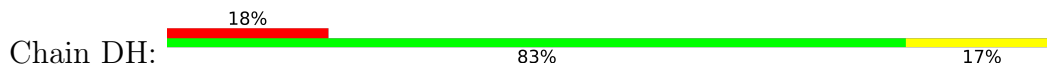


• Molecule 36: 50S ribosomal protein L9

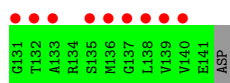
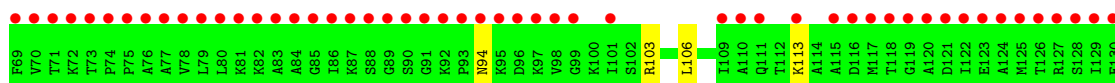
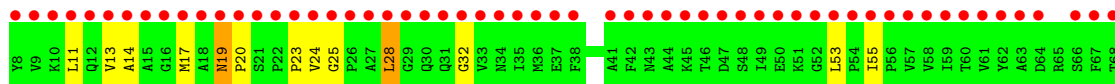
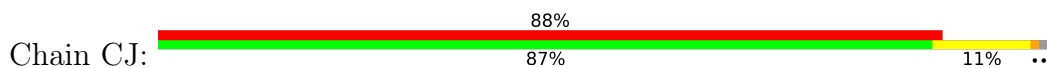




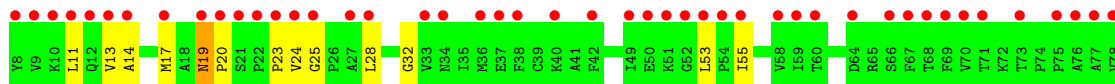
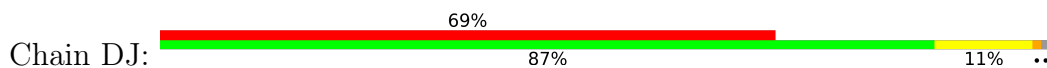
- Molecule 36: 50S ribosomal protein L9



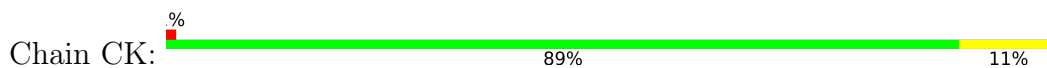
- Molecule 37: 50S ribosomal protein L11



- Molecule 37: 50S ribosomal protein L11



- Molecule 38: 50S ribosomal protein L13

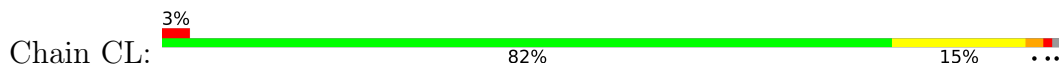


- Molecule 38: 50S ribosomal protein L13

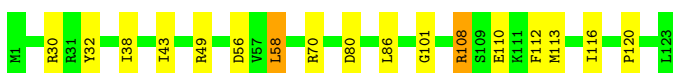
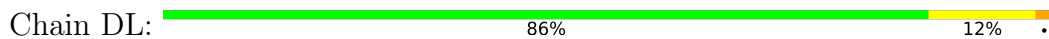




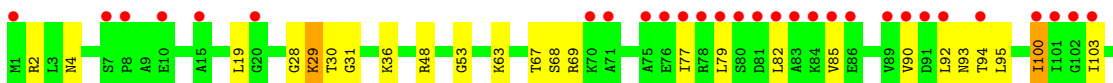
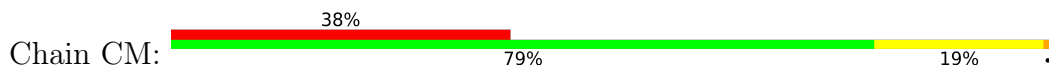
- Molecule 39: 50S ribosomal protein L14



- Molecule 39: 50S ribosomal protein L14



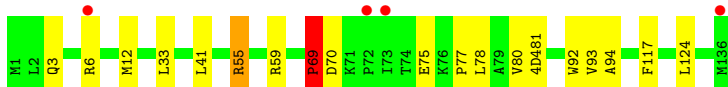
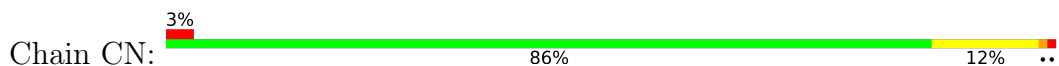
- Molecule 40: 50S ribosomal protein L15



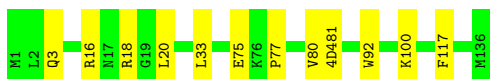
- Molecule 40: 50S ribosomal protein L15



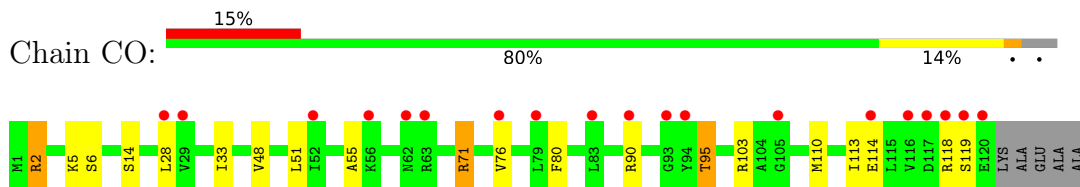
- Molecule 41: 50S ribosomal protein L16



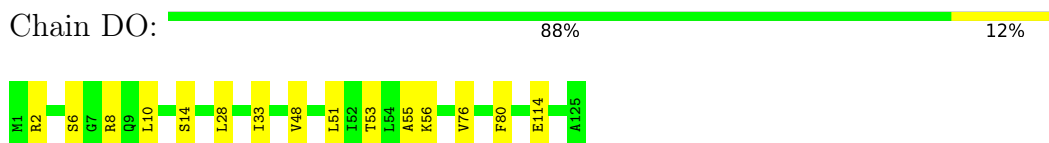
- Molecule 41: 50S ribosomal protein L16



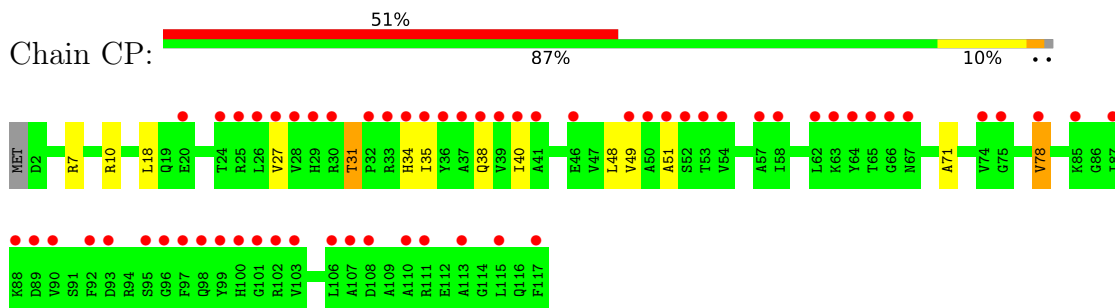
- Molecule 42: 50S ribosomal protein L17



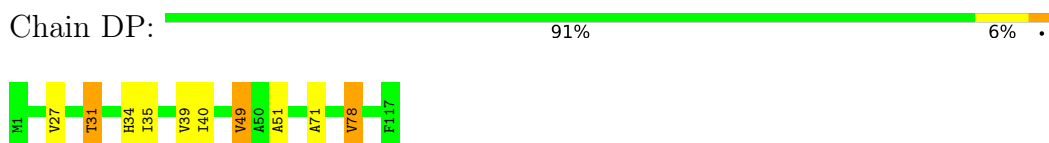
- Molecule 42: 50S ribosomal protein L17



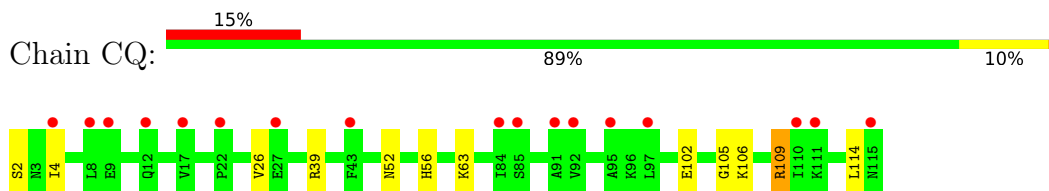
- Molecule 43: 50S ribosomal protein L18



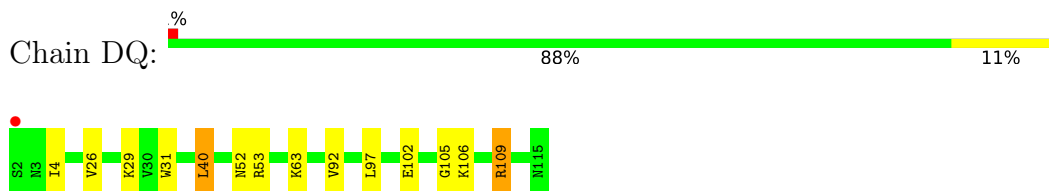
- Molecule 43: 50S ribosomal protein L18



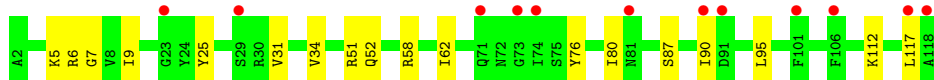
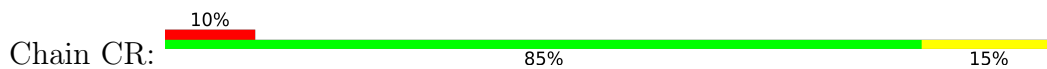
- Molecule 44: 50S ribosomal protein L19



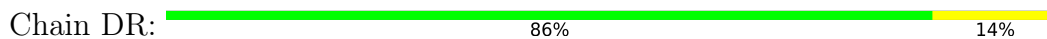
- Molecule 44: 50S ribosomal protein L19



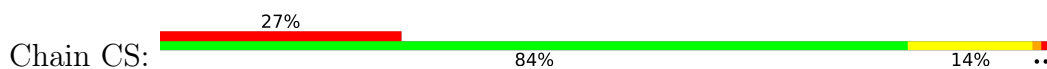
- Molecule 45: 50S ribosomal protein L20



- Molecule 45: 50S ribosomal protein L20



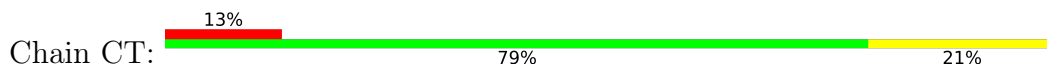
- Molecule 46: 50S ribosomal protein L21



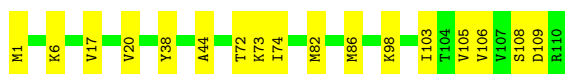
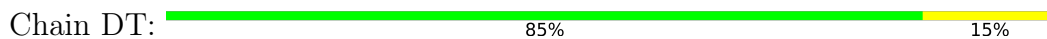
- Molecule 46: 50S ribosomal protein L21



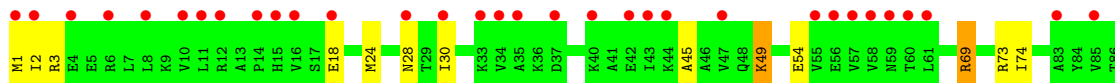
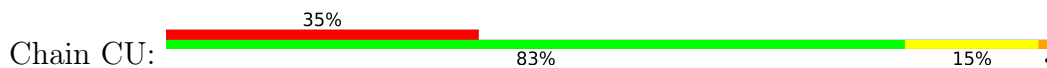
- Molecule 47: 50S ribosomal protein L22

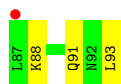


- Molecule 47: 50S ribosomal protein L22

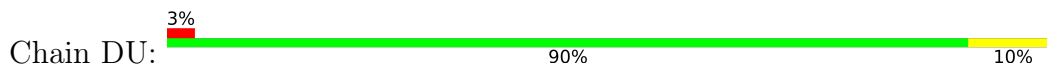


- Molecule 48: 50S ribosomal protein L23

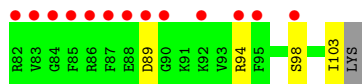
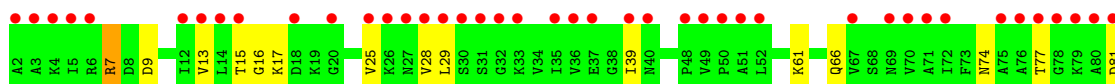
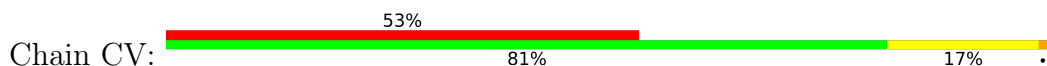




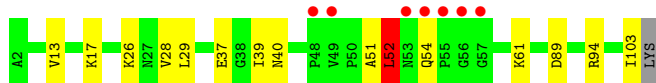
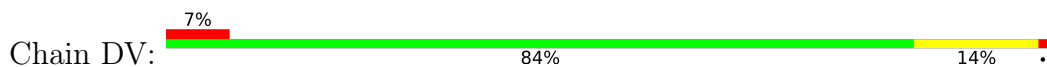
- Molecule 48: 50S ribosomal protein L23



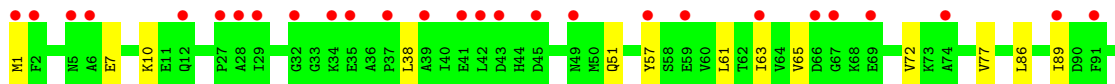
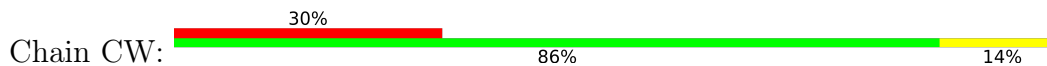
- Molecule 49: 50S ribosomal protein L24



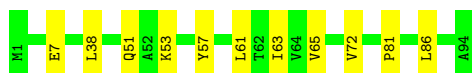
- Molecule 49: 50S ribosomal protein L24



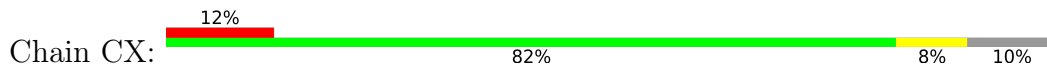
- Molecule 50: 50S ribosomal protein L25

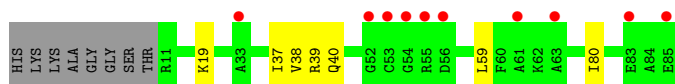


- Molecule 50: 50S ribosomal protein L25

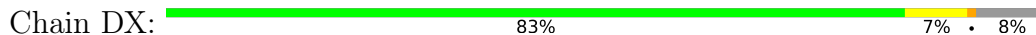


- Molecule 51: 50S ribosomal protein L27

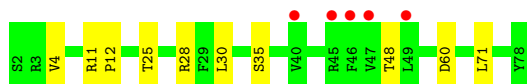
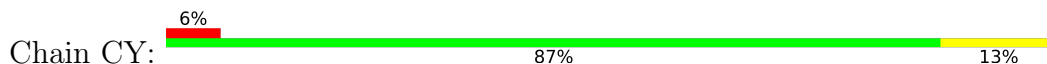




- Molecule 51: 50S ribosomal protein L27



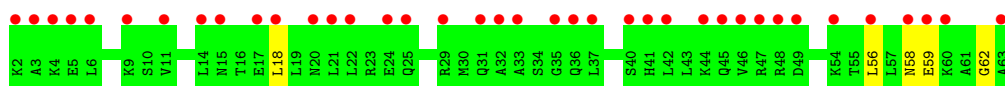
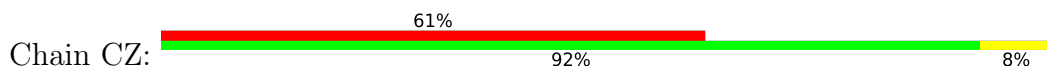
- Molecule 52: 50S ribosomal protein L28



- Molecule 52: 50S ribosomal protein L28



- Molecule 53: 50S ribosomal protein L29

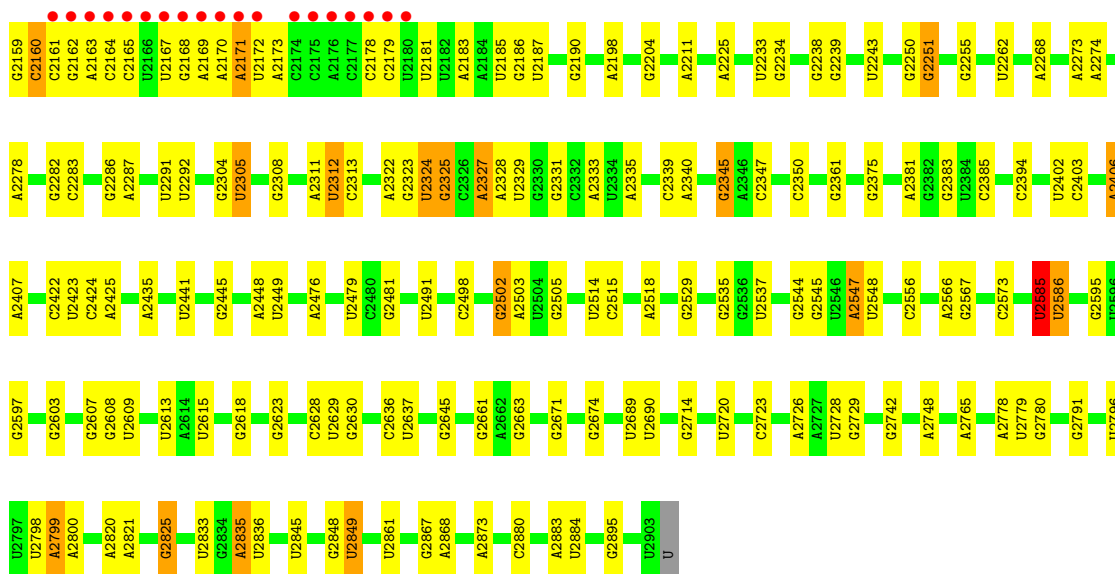


- Molecule 53: 50S ribosomal protein L29



- Molecule 54: 50S ribosomal protein L10





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)	0.27 , 91.1	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, ACY, 4OC, UR3, D2T, H2U, T1C, 5MU, 3TD, OMU, 4D4, PSU, PEG, 6MZ, MEQ, 5MC, ZN, 1MG, PUT, OMG, PG4, 1PE, GUN, MA6, EDO, OMC, 2MG, 2MA, SPD, 7MG, MG, TRS, PGE

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	0.95	7/36597 (0.0%)	0.85	6/57088 (0.0%)
1	BA	0.96	5/36572 (0.0%)	0.85	6/57049 (0.0%)
2	AB	0.43	0/1784	0.62	0/2403
2	BB	0.42	0/1784	0.63	0/2403
3	AC	0.45	0/1652	0.65	0/2225
3	BC	0.44	0/1652	0.65	0/2225
4	AD	0.41	0/1665	0.65	0/2227
4	BD	0.41	0/1665	0.66	0/2227
5	AE	0.44	0/1157	0.74	0/1557
5	BE	0.47	0/1118	0.77	0/1504
6	AF	0.42	0/881	0.66	0/1189
6	BF	0.44	0/835	0.74	0/1128
7	AG	0.44	0/1196	0.61	0/1602
7	BG	0.44	0/1196	0.62	0/1602
8	AH	0.40	0/989	0.66	0/1326
8	BH	0.40	0/989	0.66	0/1326
9	AI	0.42	0/1034	0.64	0/1375
9	BI	0.42	0/1034	0.64	0/1375
10	AJ	0.41	0/806	0.64	0/1089
10	BJ	0.46	0/797	0.69	0/1077
11	AK	0.43	0/893	0.61	0/1205
11	BK	0.41	0/893	0.65	0/1205
12	AL	0.42	0/960	0.69	0/1286
12	BL	0.42	0/960	0.70	0/1286
13	AM	0.47	0/893	0.70	0/1193
13	BM	0.48	0/893	0.70	0/1193
14	AN	0.44	0/817	0.63	0/1088
14	BN	0.42	0/817	0.62	0/1088
15	AO	0.43	0/722	0.59	0/964
15	BO	0.42	0/722	0.59	0/964

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	AP	0.43	0/659	0.68	0/884
16	BP	0.46	0/659	0.74	0/884
17	AQ	0.44	0/658	0.70	0/881
17	BQ	0.48	0/658	0.74	0/881
18	AR	0.46	0/463	0.63	0/621
18	BR	0.46	0/463	0.62	0/621
19	AS	0.46	0/653	0.59	0/877
19	BS	0.46	0/653	0.60	0/877
20	AT	0.45	0/676	0.64	0/895
20	BT	0.49	0/671	0.67	0/888
21	AU	0.40	0/472	0.60	0/627
21	BU	0.37	0/472	0.61	0/627
22	C1	0.48	0/450	0.66	0/599
22	D1	0.51	0/450	0.72	0/599
23	C2	0.44	0/416	0.68	0/554
23	D2	0.45	0/421	0.66	0/561
24	C3	0.40	0/380	0.67	0/498
24	D3	0.50	0/380	0.70	0/498
25	C4	0.41	0/513	0.62	0/676
25	D4	0.47	0/513	0.65	0/676
26	C5	0.41	0/303	0.76	0/397
26	D5	0.46	0/303	0.72	0/397
27	C0	0.47	0/453	0.79	0/605
27	D0	0.53	0/467	0.78	0/623
28	CB	0.92	0/2828	0.87	2/4410 (0.0%)
28	DB	0.94	0/2872	0.86	0/4478
29	CC	0.41	0/2121	0.70	0/2852
29	DC	0.43	0/2121	0.70	0/2852
30	CD	0.40	0/1586	0.65	0/2134
31	CA	0.97	29/69165 (0.0%)	0.86	10/107896 (0.0%)
32	DD	0.44	0/1576	0.65	0/2119
33	CE	0.42	0/1571	0.68	0/2113
33	DE	0.44	0/1570	0.66	0/2113
34	CF	0.40	0/1434	0.65	0/1926
34	DF	0.43	0/1434	0.67	0/1926
35	CG	0.39	0/1343	0.64	0/1816
35	DG	0.41	0/1343	0.62	0/1816
36	CH	0.45	0/1121	0.67	0/1515
36	DH	0.45	0/1121	0.66	0/1515
37	CJ	0.48	0/993	0.62	0/1341
37	DJ	0.48	0/993	0.62	0/1341
38	CK	0.39	0/1152	0.65	0/1551
38	DK	0.47	0/1152	0.66	0/1551

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	CL	0.43	0/947	0.69	0/1268
39	DL	0.46	0/955	0.68	0/1279
40	CM	0.42	0/1062	0.71	2/1413 (0.1%)
40	DM	0.42	0/1062	0.67	0/1413
41	CN	0.42	0/1081	0.71	1/1443 (0.1%)
41	DN	0.47	0/1092	0.71	0/1457
42	CO	0.41	0/973	0.67	0/1301
42	DO	0.48	0/1006	0.72	0/1345
43	CP	0.41	0/902	0.68	0/1209
43	DP	0.44	0/910	0.68	0/1219
44	CQ	0.38	0/929	0.68	0/1242
44	DQ	0.43	0/929	0.66	0/1242
45	CR	0.43	0/960	0.64	0/1278
45	DR	0.49	0/960	0.65	0/1278
46	CS	0.39	0/829	0.71	0/1107
46	DS	0.43	0/829	0.75	0/1107
47	CT	0.38	0/864	0.70	0/1156
47	DT	0.45	0/864	0.70	0/1156
48	CU	0.41	0/745	0.67	0/994
48	DU	0.43	0/744	0.68	0/994
49	CV	0.42	0/787	0.72	0/1051
49	DV	0.42	0/787	0.71	0/1051
50	CW	0.38	0/766	0.62	0/1025
50	DW	0.44	0/766	0.65	0/1025
51	CX	0.36	0/576	0.59	0/762
51	DX	0.43	0/598	0.63	0/790
52	CY	0.40	0/635	0.70	0/848
52	DY	0.44	0/635	0.69	0/848
53	CZ	0.40	0/502	0.60	0/667
53	DZ	0.42	0/502	0.59	0/667
54	DI	0.49	0/1037	0.73	1/1402 (0.1%)
55	DA	1.02	20/69364 (0.0%)	0.88	10/108207 (0.0%)
All	All	0.86	61/309273 (0.0%)	0.81	38/462224 (0.0%)

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

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	CA	2095	A	O5'-C5'	-9.11	1.28	1.42
31	CA	2425	A	C3'-O3'	8.77	1.54	1.42
55	DA	12	U	C1'-N1	8.01	1.60	1.48
31	CA	1936	A	N9-C4	-7.92	1.33	1.37
55	DA	2097	A	O5'-C5'	-7.38	1.31	1.42
55	DA	2585	U	C1'-N1	7.24	1.59	1.48
1	BA	5	U	C1'-N1	7.08	1.59	1.48
31	CA	2225	A	C3'-O3'	7.02	1.51	1.42
1	AA	1397	C	N1-C6	6.75	1.41	1.37
31	CA	12	U	C1'-N1	6.66	1.58	1.48
1	AA	5	U	C1'-N1	6.42	1.58	1.48
31	CA	769	U	C1'-N1	6.35	1.58	1.48
31	CA	451	U	C1'-N1	6.31	1.58	1.48
31	CA	546	U	C1'-N1	6.16	1.57	1.48
1	BA	1008	U	O5'-C5'	-6.08	1.33	1.42
1	BA	1493	A	C3'-O3'	6.08	1.50	1.42
55	DA	1306	C	C1'-N1	6.04	1.57	1.48
31	CA	2465	C	C1'-N1	5.96	1.57	1.48
55	DA	2585	U	N1-C2	5.93	1.43	1.38
31	CA	2354	C	C1'-N1	5.88	1.57	1.48
55	DA	2127	G	C3'-O3'	5.88	1.50	1.42
55	DA	784	G	C3'-O3'	5.86	1.50	1.42
31	CA	1379	U	C3'-O3'	5.79	1.50	1.42
1	BA	1397	C	N1-C2	5.78	1.46	1.40
31	CA	1825	U	C1'-N1	5.76	1.57	1.48
55	DA	1170	C	C1'-N1	5.75	1.57	1.48
55	DA	12	U	P-O5'	5.71	1.65	1.59
31	CA	692	C	C1'-N1	5.70	1.57	1.48
31	CA	995	C	O5'-C5'	-5.67	1.33	1.42
55	DA	1534	U	C1'-N1	5.57	1.57	1.48
31	CA	404	A	C3'-O3'	5.57	1.50	1.42
1	AA	528	C	C1'-N1	5.56	1.57	1.48
31	CA	1376	C	C1'-N1	5.53	1.57	1.48
55	DA	1920	C	C1'-N1	5.52	1.57	1.48
1	AA	932	C	C1'-N1	5.52	1.57	1.48
31	CA	946	C	C1'-N1	5.52	1.57	1.48
31	CA	1777	U	C1'-N1	5.47	1.56	1.48
31	CA	2232	C	C1'-N1	5.40	1.56	1.48
31	CA	1306	C	C1'-N1	5.38	1.56	1.48
31	CA	2146	C	C3'-O3'	5.38	1.49	1.42
1	AA	955	U	C1'-N1	5.37	1.56	1.48
55	DA	2586	U	C1'-N1	5.35	1.56	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	DA	613	A	N9-C4	5.35	1.41	1.37
31	CA	1658	C	C1'-N1	5.32	1.56	1.48
31	CA	2586	U	C1'-N1	5.28	1.56	1.48
1	BA	955	U	C1'-N1	5.25	1.56	1.48
1	AA	956	U	C1'-N1	5.24	1.56	1.48
31	CA	817	C	C1'-N1	5.22	1.56	1.48
55	DA	1020	A	N3-C4	5.21	1.38	1.34
55	DA	271	G	C3'-O3'	5.19	1.49	1.42
55	DA	2158	A	C3'-O3'	5.19	1.49	1.42
31	CA	1788	C	C1'-N1	5.16	1.56	1.48
55	DA	12	U	N1-C2	5.15	1.43	1.38
31	CA	461	C	C1'-N1	5.15	1.56	1.48
55	DA	140	C	C1'-N1	5.13	1.56	1.48
55	DA	578	G	N7-C5	-5.11	1.36	1.39
55	DA	2585	U	C3'-O3'	5.08	1.49	1.42
31	CA	29	U	C1'-N1	5.06	1.56	1.48
1	AA	1203	C	C1'-N1	5.05	1.56	1.48
31	CA	784	G	C3'-O3'	5.04	1.49	1.42
31	CA	2680	U	C3'-O3'	5.01	1.49	1.42

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	CB	15	A	O4'-C1'-N9	9.58	115.86	108.20
55	DA	1936	A	O4'-C1'-N9	7.65	114.32	108.20
1	AA	1	A	OP1-P-OP2	-7.18	108.83	119.60
54	DI	132	TYR	C-N-CA	7.11	139.46	121.70
1	AA	413	G	C1'-O4'-C4'	-7.07	104.24	109.90
55	DA	892	A	OP1-P-OP2	-7.02	109.07	119.60
31	CA	892	A	OP1-P-OP2	-7.01	109.09	119.60
55	DA	1	G	OP1-P-OP2	-6.89	109.27	119.60
55	DA	784	G	P-O3'-C3'	6.89	127.96	119.70
1	BA	1362	A	C1'-O4'-C4'	-6.76	104.49	109.90
31	CA	271	G	P-O3'-C3'	6.72	127.76	119.70
1	BA	2	A	OP1-P-OP2	-6.57	109.75	119.60
55	DA	271	G	P-O3'-C3'	6.53	127.53	119.70
55	DA	512	G	O4'-C1'-N9	6.29	113.23	108.20
31	CA	974	G	N9-C1'-C2'	6.25	122.12	114.00
31	CA	784	G	P-O3'-C3'	6.24	127.19	119.70
55	DA	2825	G	O4'-C1'-N9	6.13	113.11	108.20
1	BA	485	U	O4'-C1'-N1	6.01	113.01	108.20
31	CA	451	U	C1'-O4'-C4'	-6.01	105.09	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	CA	2035	G	C1'-O4'-C4'	-5.78	105.28	109.90
55	DA	2406	A	C5'-C4'-O4'	-5.66	102.31	109.10
1	BA	7	A	C1'-O4'-C4'	-5.54	105.47	109.90
41	CN	69	PRO	C-N-CA	5.52	135.49	121.70
28	CB	89	U	O4'-C1'-N1	5.45	112.56	108.20
31	CA	2225	A	P-O3'-C3'	5.41	126.19	119.70
55	DA	1266	G	C3'-C2'-C1'	-5.38	97.19	101.50
1	BA	328	C	C1'-O4'-C4'	-5.35	105.62	109.90
40	CM	68	SER	C-N-CA	5.29	134.92	121.70
1	AA	328	C	C1'-O4'-C4'	-5.25	105.70	109.90
1	AA	841	C	P-O3'-C3'	5.21	125.95	119.70
31	CA	2095	A	C5'-C4'-C3'	-5.16	107.75	116.00
1	BA	842	U	P-O3'-C3'	5.14	125.86	119.70
31	CA	2425	A	P-O3'-C3'	5.12	125.84	119.70
40	CM	30	THR	N-CA-CB	5.11	120.01	110.30
55	DA	1936	A	C1'-O4'-C4'	-5.11	105.81	109.90
1	AA	7	A	C1'-O4'-C4'	-5.11	105.81	109.90
31	CA	512	G	O4'-C1'-N9	5.09	112.27	108.20
1	AA	413	G	O4'-C1'-N9	5.02	112.22	108.20

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	CN	69	PRO	Mainchain
55	DA	1324	G	Sidechain
55	DA	1425	G	Sidechain
55	DA	15	G	Sidechain
55	DA	1753	G	Sidechain
55	DA	177	G	Sidechain
55	DA	1938	A	Sidechain
55	DA	1954	G	Sidechain
55	DA	2048	G	Sidechain
55	DA	221	A	Sidechain
55	DA	2250	G	Sidechain
55	DA	2323	G	Sidechain
55	DA	2375	G	Sidechain
55	DA	2481	G	Sidechain
55	DA	249	C	Sidechain
55	DA	250	G	Sidechain
55	DA	2595	G	Sidechain
55	DA	2597	G	Sidechain

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Mol	Chain	Res	Type	Group
55	DA	2645	G	Sidechain
55	DA	2835	A	Sidechain
55	DA	2848	G	Sidechain
55	DA	512	G	Sidechain
55	DA	555	G	Sidechain
55	DA	726	G	Sidechain
55	DA	858	G	Sidechain
55	DA	956	G	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	81	0
1	BA	32911	0	16582	95	0
2	AB	1753	0	1780	7	0
2	BB	1753	0	1780	8	0
3	AC	1625	0	1696	12	0
3	BC	1625	0	1696	13	0
4	AD	1643	0	1707	11	0
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	6	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	8	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	13	0
12	AL	957	0	1017	6	0
12	BL	957	0	1017	8	0
13	AM	884	0	941	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	BM	884	0	941	15	0
14	AN	805	0	844	6	0
14	BN	805	0	844	5	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	2	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	6	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
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	10	0
30	CD	1565	0	1616	12	0
31	CA	62229	0	31319	205	0
32	DD	1576	0	1627	11	0
33	CE	1552	0	1619	13	0
33	DE	1551	0	1619	10	0
34	CF	1410	0	1444	18	0
34	DF	1410	0	1444	13	0
35	CG	1323	0	1371	7	0
35	DG	1323	0	1371	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	6	0
39	CL	938	0	1012	8	0
39	DL	946	0	1023	7	0
40	CM	1053	0	1129	15	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
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	3	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	164	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	1128	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.

All (1128) 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
46:CS:14:VAL:CG2	46:CS:98:ILE:HG13	2.05	0.87
14:AN:66:GLN:HB2	70:AN:207:HOH:O	1.74	0.87
31:CA:1005:C:O2'	38:CK:30:THR:HG21	1.73	0.87
46:CS:14:VAL:HG21	46:CS:98:ILE:CG1	2.05	0.86
1:BA:1052:G:N2	1:BA:1206:G:H1	1.75	0.85
31:CA:2796:U:H3	31:CA:2799:A:H61	1.23	0.85
4:BD:85:ASN:HA	5:BE:102:GLY:HA2	1.60	0.84
40:CM:77:ILE:HD11	40:CM:108:ALA:HB1	1.60	0.84
31:CA:528:A:C2	31:CA:2043:C:H4'	2.13	0.83
13:AM:6:GLY:HA3	13:AM:66:GLU:HG3	1.61	0.82
1:BA:664:G:H22	1:BA:741:G:H1	1.28	0.81
18:AR:21:ILE:HG21	18:AR:54:GLN:HB3	1.64	0.80
11:BK:88:GLY:H	11:BK:114:THR:HG22	1.46	0.80
55:DA:135:U:H3	55:DA:144:A:H61	1.30	0.80
13:BM:6:GLY:HA3	13:BM:66:GLU:HG3	1.62	0.80
31:CA:568:U:H1'	31:CA:2030:6MZ:H9C1	1.63	0.80
31:CA:135:U:H3	31:CA:144:A:H61	1.30	0.79
1:AA:1492:A:H5''	12:AL:44:LYS:HG2	1.65	0.78
1:AA:664:G:H22	1:AA:741:G:H1	1.29	0.78
40:CM:82:LEU:HD11	40:CM:116:VAL:HG23	1.64	0.78
1:AA:1305:G:H21	1:AA:1332:A:H2	1.30	0.78
13:BM:114:LYS:HB3	13:BM:115:PRO:HD3	1.65	0.78
12:BL:80:ILE:HD12	12:BL:97:THR:HG22	1.66	0.78
1:BA:1305:G:H21	1:BA:1332:A:H2	1.30	0.76
1:BA:841:C:H3'	1:BA:842:U:H5''	1.66	0.76
3:BC:123:GLN:HB3	3:BC:128:VAL:HG21	1.69	0.75
31:CA:740:C:H5'	31:CA:1784:A:H3'	1.68	0.74
35:CG:80:THR:HG23	35:CG:81:GLU:H	1.52	0.74
1:BA:9:G:H5'	5:BE:108:GLY:HA3	1.70	0.73
1:AA:1518:MA6:H103	1:AA:1519:MA6:H102	1.70	0.73
10:AJ:7:ARG:HB3	10:AJ:101:SER:HB2	1.71	0.73
31:CA:846:U:H1'	31:CA:847:U:H5	1.52	0.73
45:DR:20:GLN:HG3	57:DR:202:PG4:H42	1.70	0.73
4:AD:107:PHE:HB3	4:AD:145:ILE:HD11	1.70	0.72
45:DR:20:GLN:CG	57:DR:202:PG4:H42	2.20	0.72
1:BA:1518:MA6:H103	1:BA:1519:MA6:H102	1.71	0.72
4:BD:107:PHE:HB3	4:BD:145:ILE:HD11	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:CD:133:THR:HG22	31:CA:1993:U:H4'	1.70	0.72
35:CG:24:ILE:HD11	35:CG:43:VAL:HG11	1.72	0.72
55:DA:2127:G:H4'	55:DA:2128:G:OP1	1.90	0.71
31:CA:1936:A:H2	31:CA:1943:U:N3	1.83	0.71
8:BH:87:LYS:HB2	8:BH:125:ILE:HD11	1.73	0.71
31:CA:1779:U:H5	31:CA:1784:A:N7	1.89	0.70
6:BF:38:ARG:HH12	6:BF:99:ALA:HB3	1.55	0.70
1:BA:522:C:H5	12:BL:50:ARG:HH12	1.37	0.70
13:AM:33:ILE:HD11	13:AM:63:PHE:HE1	1.57	0.69
1:BA:841:C:H3'	1:BA:842:U:C5'	2.22	0.69
2:BB:20:THR:HA	2:BB:39:HIS:HE1	1.55	0.69
3:BC:40:ARG:HH11	3:BC:55:ILE:HG23	1.56	0.69
47:CT:73:LYS:HB2	47:CT:106:VAL:HB	1.75	0.69
1:AA:73:C:HO2'	1:AA:74:A:H8	1.40	0.68
55:DA:1105:U:H2'	55:DA:1106:G:H8	1.58	0.68
55:DA:2033:A:H5'	70:DA:3343:HOH:O	1.92	0.68
48:CU:28:ASN:HD21	48:CU:91:GLN:HB3	1.58	0.68
35:DG:24:ILE:HD11	35:DG:43:VAL:HG11	1.74	0.68
13:BM:83:LEU:HD21	19:BS:65:GLU:HB2	1.74	0.68
43:DP:39:VAL:HB	43:DP:49:VAL:HG23	1.74	0.68
31:CA:1105:U:H2'	31:CA:1106:G:H8	1.58	0.68
55:DA:568:U:H1'	55:DA:2030:6MZ:H9C1	1.76	0.67
36:DH:41:LYS:HA	36:DH:44:ILE:HG12	1.76	0.67
1:BA:202:G:HO2'	1:BA:468:A:H8	1.42	0.67
33:CE:149:ILE:HG12	33:CE:188:MET:HG2	1.76	0.67
39:CL:38:ILE:HD11	39:CL:112:PHE:HZ	1.59	0.67
24:C3:12:ARG:HD2	24:C3:44:VAL:HG11	1.75	0.67
11:BK:89:PRO:HG3	21:BU:32:VAL:HG11	1.77	0.67
31:CA:1847:A:HO2'	31:CA:1848:A:H8	1.41	0.67
1:BA:451:A:H2'	70:BA:1701:HOH:O	1.95	0.66
31:CA:910:A:H62	41:CN:12:MET:HA	1.60	0.66
8:AH:87:LYS:HB2	8:AH:125:ILE:HD11	1.75	0.66
1:BA:619:U:H3	4:BD:131:ASN:HB3	1.60	0.66
55:DA:1913:A:H4'	55:DA:1913:A:OP1	1.96	0.66
36:CH:41:LYS:HA	36:CH:44:ILE:HG12	1.77	0.66
12:BL:65:SER:HB2	12:BL:82:ILE:HD11	1.77	0.66
31:CA:1105:U:H2'	31:CA:1106:G:C8	2.30	0.65
11:AK:89:PRO:HG3	21:AU:32:VAL:HG11	1.79	0.65
55:DA:1105:U:H2'	55:DA:1106:G:C8	2.30	0.65
47:DT:73:LYS:HB2	47:DT:106:VAL:HB	1.77	0.65
55:DA:1847:A:HO2'	55:DA:1848:A:H8	1.43	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BT:9:LYS:O	20:BT:12:ILE:HG13	1.96	0.65
31:CA:1311:G:H21	31:CA:1603:A:H62	1.43	0.65
55:DA:1853:A:N1	55:DA:2087:G:H1'	2.12	0.65
47:CT:86:MET:HB2	47:CT:96:ILE:HD11	1.77	0.65
31:CA:2291:U:H2'	31:CA:2292:U:C6	2.31	0.65
36:CH:15:LEU:HD22	36:CH:15:LEU:H	1.62	0.64
31:CA:699:A:H2'	31:CA:700:G:O4'	1.96	0.64
39:DL:38:ILE:HD11	39:DL:112:PHE:HZ	1.63	0.64
5:BE:72:ILE:HG12	5:BE:145:GLU:HG3	1.81	0.63
45:DR:31:VAL:HG13	55:DA:580:U:O3'	1.99	0.63
55:DA:1746:A:H2'	55:DA:1747:U:C6	2.34	0.63
5:AE:77:ASN:HB2	5:AE:82:GLN:NE2	2.14	0.63
55:DA:2628:C:H5'	59:DA:3195:PUT:H12	1.81	0.63
2:AB:20:THR:HG22	2:AB:39:HIS:CE1	2.34	0.63
26:C5:16:ILE:HD13	26:C5:25:VAL:HG22	1.81	0.63
11:BK:23:ILE:HG22	11:BK:32:VAL:HG13	1.81	0.63
17:BQ:8:LEU:HD23	17:BQ:25:ILE:HG21	1.80	0.63
22:D1:9:THR:CG2	55:DA:2020:A:H5'	2.28	0.62
11:AK:31:ILE:HG12	11:AK:46:THR:HG22	1.79	0.62
25:D4:8:ARG:HD3	55:DA:245:G:O6	1.99	0.62
11:AK:23:ILE:HG22	11:AK:32:VAL:HG13	1.80	0.62
33:DE:33:VAL:HG22	58:DA:3192:MPD:H12	1.81	0.62
22:C1:43:ILE:HG22	22:C1:49:TYR:HB2	1.81	0.62
55:DA:2291:U:H2'	55:DA:2292:U:C6	2.34	0.62
5:BE:77:ASN:HB2	5:BE:82:GLN:NE2	2.15	0.61
55:DA:2128:G:H1	55:DA:2160:C:H42	1.48	0.61
7:AG:22:LEU:HD12	7:AG:62:PHE:HE2	1.65	0.61
22:D1:43:ILE:HG22	22:D1:49:TYR:HB2	1.82	0.61
54:DI:69:PHE:HB3	54:DI:72:LEU:HD12	1.82	0.61
1:AA:1012:A:H61	1:AA:1017:U:H3	1.48	0.61
1:BA:1012:A:H61	1:BA:1017:U:H3	1.48	0.61
1:BA:1060:U:C5	3:BC:2:GLY:HA3	2.34	0.61
2:BB:23:TRP:HB3	2:BB:39:HIS:CE1	2.35	0.61
1:BA:73:C:HO2'	1:BA:74:A:H8	1.47	0.61
1:AA:81:A:H61	1:AA:86:G:H1	1.49	0.61
23:C2:22:THR:HG21	31:CA:2419:U:H5''	1.82	0.61
34:CF:36:LEU:HD21	34:CF:91:LEU:HD11	1.81	0.61
16:AP:4:ILE:HG12	16:AP:21:VAL:HG22	1.83	0.61
29:DC:29:PRO:HG2	29:DC:34:LEU:HD11	1.83	0.61
32:DD:140:HIS:HB3	70:DD:481:HOH:O	2.01	0.61
6:BF:38:ARG:NH1	6:BF:99:ALA:HB3	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:209:U:H4'	1:AA:210:C:OP2	2.01	0.60
29:CC:210:ALA:HA	29:CC:213:TRP:CE2	2.37	0.60
1:AA:412:A:H3'	1:AA:413:G:H5'	1.84	0.60
1:AA:774:G:H21	57:AA:1670:PG4:H51	1.67	0.60
48:CU:18:GLU:H	48:CU:18:GLU:CD	2.05	0.60
7:BG:113:ASP:HB2	7:BG:119:ARG:HG3	1.84	0.59
6:AF:38:ARG:HB3	6:AF:63:ASN:HB2	1.83	0.59
16:BP:4:ILE:HG12	16:BP:21:VAL:HG22	1.84	0.59
26:D5:16:ILE:HD13	26:D5:25:VAL:HG22	1.82	0.59
29:CC:29:PRO:HG2	29:CC:34:LEU:HD11	1.83	0.59
1:AA:1144:G:H21	1:AA:1146:A:H62	1.50	0.59
1:BA:1151:A:HO2'	1:BA:1152:A:H8	1.50	0.59
25:C4:60:ALA:O	40:CM:48:ARG:HD2	2.03	0.59
40:DM:53:GLY:HA3	55:DA:826:U:O2'	2.03	0.59
44:DQ:29:LYS:HB3	44:DQ:40:LEU:HD13	1.83	0.59
7:AG:113:ASP:HB2	7:AG:119:ARG:HG3	1.83	0.59
1:BA:209:U:H4'	1:BA:210:C:OP2	2.02	0.59
31:CA:450:G:H2'	31:CA:451:U:H5''	1.82	0.59
46:CS:78:ARG:HB2	46:CS:83:TYR:HD1	1.66	0.59
1:BA:1144:G:H21	1:BA:1146:A:H62	1.50	0.59
1:BA:1226:C:H2'	13:BM:102:THR:HB	1.85	0.59
33:DE:189:THR:HG22	33:DE:192:ALA:H	1.68	0.59
54:DI:57:ASN:HB3	54:DI:76:PHE:HB3	1.85	0.59
1:AA:1226:C:H2'	13:AM:102:THR:HB	1.85	0.59
31:CA:1394:U:H4'	31:CA:1603:A:H4'	1.85	0.59
45:DR:28:ARG:HD3	70:DR:306:HOH:O	2.02	0.59
46:DS:83:TYR:CE1	55:DA:1187:G:H5''	2.38	0.59
1:BA:1323:G:H2'	1:BA:1324:A:C8	2.38	0.58
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.39	0.58
19:AS:15:LEU:HD13	19:AS:33:THR:HG21	1.85	0.58
11:BK:88:GLY:N	11:BK:114:THR:HG22	2.16	0.58
29:CC:227:PRO:HA	29:CC:233:GLY:HA2	1.85	0.58
17:BQ:17:MET:HB3	17:BQ:20:SER:HB3	1.85	0.58
47:CT:59:GLU:HA	47:CT:64:ALA:HA	1.84	0.58
55:DA:1028:A:N6	55:DA:1125:G:H2'	2.18	0.58
34:CF:31:VAL:CG1	34:CF:97:TRP:CH2	2.86	0.58
45:CR:58:ARG:HH11	45:CR:62:ILE:HD11	1.69	0.58
31:CA:674:G:H1'	33:CE:69:ARG:HH11	1.68	0.58
50:CW:63:ILE:HD12	50:CW:72:VAL:HG21	1.86	0.58
29:DC:227:PRO:HA	29:DC:233:GLY:HA2	1.84	0.58
6:BF:38:ARG:HB3	6:BF:63:ASN:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:CA:1847:A:O2'	31:CA:1848:A:H8	1.86	0.58
54:DI:64:VAL:HG22	54:DI:69:PHE:HB2	1.85	0.57
51:CX:37:ILE:HG21	51:CX:80:ILE:HG21	1.85	0.57
51:DX:37:ILE:HG21	51:DX:80:ILE:HG21	1.87	0.57
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.87	0.57
55:DA:62:U:O4'	58:DA:3204:MPD:H31	2.04	0.57
47:CT:17:VAL:HG11	47:CT:103:ILE:HG12	1.86	0.57
25:D4:54:ASP:HB3	40:DM:57:LEU:HD22	1.87	0.57
45:CR:58:ARG:NH1	45:CR:62:ILE:HD11	2.19	0.57
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.87	0.57
28:CB:55:U:H1'	34:CF:26:MET:HG3	1.87	0.57
31:CA:1936:A:N6	31:CA:1963:U:H3	2.02	0.57
17:BQ:68:SER:OG	17:BQ:71:LYS:HB3	2.04	0.56
19:BS:50:ALA:HB1	19:BS:57:HIS:HB3	1.86	0.56
32:DD:99:GLU:HG2	32:DD:182:ALA:HB2	1.87	0.56
32:DD:150[A]:MEQ:HG2	70:DA:3371:HOH:O	2.05	0.56
36:CH:4:ILE:HD11	36:CH:44:ILE:HG22	1.87	0.56
17:BQ:14:SER:HB3	17:BQ:22:VAL:HG12	1.87	0.56
19:BS:6:LYS:HD2	19:BS:7:LYS:H	1.69	0.56
30:CD:4:LEU:HD22	30:CD:101:PHE:CE2	2.40	0.56
5:AE:38:VAL:HG11	5:AE:114:VAL:HG22	1.87	0.56
3:BC:77:ILE:HA	3:BC:84:VAL:HG23	1.87	0.56
31:CA:457:A:N1	31:CA:470:A:H5''	2.21	0.56
31:CA:2019:A:H4'	45:CR:34:VAL:HG21	1.88	0.56
33:CE:189:THR:HG22	33:CE:192:ALA:H	1.69	0.56
39:DL:113:MET:CE	39:DL:116:ILE:HD11	2.35	0.56
47:CT:69:LEU:HG	47:CT:107:VAL:HG22	1.88	0.56
55:DA:1847:A:O2'	55:DA:1848:A:H8	1.88	0.56
1:AA:451:A:H61	1:AA:481:G:H5'	1.71	0.56
29:CC:17:VAL:HB	29:CC:204:VAL:HG13	1.88	0.56
32:DD:150[A]:MEQ:HE3	55:DA:2032:G:C8	2.41	0.56
44:DQ:53:ARG:NH2	55:DA:2720:U:OP1	2.39	0.56
13:AM:33:ILE:HD11	13:AM:63:PHE:CE1	2.40	0.55
5:BE:90:THR:HG22	5:BE:91:GLY:H	1.70	0.55
1:BA:769:G:H4'	1:BA:1513:A:H4'	1.87	0.55
37:CJ:19:ASN:H	37:CJ:20:PRO:HD2	1.72	0.55
49:CV:74:ASN:HD22	49:CV:77:THR:H	1.53	0.55
34:DF:61:SER:HB2	34:DF:91:LEU:HD21	1.88	0.55
10:AJ:35:GLN:HB2	10:AJ:77:VAL:HB	1.88	0.55
47:DT:72:THR:HG21	47:DT:108:SER:HB3	1.89	0.55
55:DA:793:A:OP1	65:DA:3224:SPD:H81	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:34:ILE:HB	11:AK:74:VAL:HG11	1.87	0.55
39:CL:43:ILE:HD12	39:CL:56:ASP:HB2	1.88	0.55
49:DV:52:LEU:HB3	49:DV:54:GLN:HB2	1.89	0.55
55:DA:1482:G:H1'	55:DA:1509:A:H61	1.71	0.55
55:DA:2304:G:H22	55:DA:2312:U:H3	1.55	0.55
30:CD:99:GLU:HG2	30:CD:182:ALA:HB2	1.87	0.55
31:CA:2502:G:H5''	31:CA:2503:2MA:H5''	1.88	0.55
47:DT:17:VAL:HG11	47:DT:103:ILE:HG12	1.88	0.55
4:BD:197:GLU:HA	4:BD:200:ILE:HD12	1.87	0.55
31:CA:1779:U:C5	31:CA:1784:A:N7	2.72	0.55
47:DT:6:LYS:HB2	55:DA:494:G:H4'	1.89	0.55
47:CT:66:ILE:HA	47:CT:69:LEU:HD22	1.89	0.55
43:DP:31:THR:HG22	43:DP:34:HIS:H	1.72	0.55
50:DW:63:ILE:HD12	50:DW:72:VAL:HG21	1.87	0.55
31:CA:796:C:H2'	31:CA:797:G:C8	2.41	0.55
4:AD:197:GLU:HA	4:AD:200:ILE:HD12	1.88	0.54
26:C5:2:LYS:HE3	26:C5:4:ARG:HH11	1.70	0.54
31:CA:118:A:N3	31:CA:178:G:H1'	2.22	0.54
41:CN:41:LEU:HD21	41:CN:124:LEU:HD22	1.88	0.54
42:CO:95:THR:HG21	42:CO:113:ILE:HD11	1.89	0.54
52:CY:12:PRO:HB3	52:CY:30:LEU:HD23	1.90	0.54
16:BP:20:VAL:HG13	16:BP:32:PHE:HB2	1.88	0.54
31:CA:2304:G:H22	31:CA:2312:U:H3	1.55	0.54
37:DJ:19:ASN:H	37:DJ:20:PRO:HD2	1.72	0.54
22:D1:25:VAL:HG11	47:DT:38:TYR:HB2	1.90	0.54
23:D2:35:GLU:HG2	23:D2:50:LYS:HG2	1.89	0.54
43:CP:31:THR:HG22	43:CP:34:HIS:H	1.72	0.54
34:DF:131:GLY:HA3	55:DA:2305:U:H5''	1.90	0.54
31:CA:1482:G:H1'	31:CA:1509:A:H61	1.72	0.54
3:AC:40:ARG:HG2	3:AC:55:ILE:HG21	1.90	0.54
13:AM:12:HIS:HB3	70:AM:303:HOH:O	2.08	0.54
31:CA:833:A:H2'	31:CA:834:G:C8	2.42	0.54
39:DL:43:ILE:HD12	39:DL:56:ASP:HB2	1.88	0.54
49:DV:26:LYS:HE2	49:DV:37:GLU:HG3	1.89	0.54
12:BL:110:ARG:HB2	12:BL:119:VAL:HG21	1.89	0.54
31:CA:1936:A:H62	31:CA:1963:U:H3	1.54	0.54
31:CA:206:U:H2'	31:CA:207:A:H8	1.73	0.54
2:AB:129:LEU:HD13	2:AB:134:ALA:HB2	1.90	0.54
2:BB:129:LEU:HD13	2:BB:134:ALA:HB2	1.90	0.54
29:CC:174:LEU:CD2	29:CC:184:VAL:HB	2.38	0.54
5:AE:90:THR:HG22	5:AE:91:GLY:H	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DP:51:ALA:HB3	43:DP:78:VAL:HG13	1.90	0.53
55:DA:1026:G:H2'	55:DA:1027:A:C8	2.43	0.53
1:AA:1054:C:O2'	60:AA:1680:T1C:H921	2.08	0.53
11:AK:67:ALA:HB2	11:AK:96:THR:HG23	1.90	0.53
11:AK:84:VAL:HG21	11:AK:97:ILE:HG23	1.90	0.53
26:C5:3:VAL:HG11	31:CA:2539:C:C5'	2.38	0.53
1:BA:451:A:H61	1:BA:481:G:H5'	1.73	0.53
47:CT:82:MET:HB2	47:CT:98:LYS:HB2	1.89	0.53
1:AA:1218:C:H2'	1:AA:1219:A:C8	2.44	0.53
66:DA:3202:1PE:H231	70:DA:3315:HOH:O	2.08	0.53
23:C2:35:GLU:HG2	23:C2:50:LYS:HG2	1.91	0.53
31:CA:694:U:OP1	31:CA:1569:A:H1'	2.08	0.53
34:DF:88:LYS:HD3	55:DA:2313:C:H5''	1.91	0.53
1:AA:412:A:H3'	1:AA:413:G:C5'	2.39	0.53
43:CP:51:ALA:HB3	43:CP:78:VAL:HG13	1.90	0.53
1:AA:86:G:H21	1:AA:87:C:H41	1.57	0.53
1:AA:1141:C:HO2'	1:AA:1142:G:H8	1.56	0.53
1:BA:1218:C:H2'	1:BA:1219:A:C8	2.44	0.53
32:DD:186:LEU:HD21	44:DQ:4:ILE:HG21	1.90	0.53
31:CA:1738:G:HO2'	31:CA:1739:A:H8	1.57	0.52
26:C5:3:VAL:HG11	31:CA:2539:C:H5'	1.91	0.52
31:CA:2728:U:HO2'	31:CA:2729:G:H8	1.56	0.52
45:DR:20:GLN:HG2	57:DR:202:PG4:H42	1.91	0.52
3:AC:77:ILE:HA	3:AC:84:VAL:CG2	2.39	0.52
7:AG:22:LEU:HD12	7:AG:62:PHE:CE2	2.43	0.52
31:CA:2498:OMC:HM22	31:CA:2499:C:H5'	1.91	0.52
36:DH:4:ILE:HD11	36:DH:44:ILE:HG22	1.91	0.52
44:DQ:52:ASN:O	55:DA:2845:U:H5''	2.09	0.52
52:DY:12:PRO:HB3	52:DY:30:LEU:HD23	1.91	0.52
55:DA:2623:G:OP1	64:DA:3203:PGE:H12	2.08	0.52
31:CA:674:G:H1'	33:CE:69:ARG:HD2	1.91	0.52
49:CV:13:VAL:HG21	49:CV:39:ILE:HG21	1.92	0.52
31:CA:320:A:H2'	33:CE:131:THR:HG21	1.92	0.52
39:CL:121:GLU:HG2	39:CL:122:VAL:HG23	1.91	0.52
40:CM:79:LEU:HD11	40:CM:112:LEU:HD12	1.91	0.52
22:D1:9:THR:HG22	55:DA:2020:A:H5'	1.91	0.52
29:CC:105:LEU:H	29:CC:105:LEU:HD12	1.75	0.52
36:CH:27:ARG:HH11	52:CY:60:ASP:HA	1.75	0.52
47:DT:82:MET:HB2	47:DT:98:LYS:HB2	1.90	0.52
9:AI:19:VAL:HG22	9:AI:65:ILE:HG22	1.92	0.52
11:BK:67:ALA:HB2	11:BK:96:THR:HG23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:CF:61:SER:HB2	34:CF:91:LEU:HD21	1.89	0.52
1:AA:299:G:H2'	1:AA:300:A:C8	2.43	0.52
43:DP:31:THR:HG21	28:DB:28:C:OP1	2.08	0.52
48:DU:80:TRP:HB3	64:DU:101:PGE:H32	1.91	0.52
55:DA:551:G:H8	55:DA:551:G:H5''	1.75	0.52
13:BM:22:ILE:HB	13:BM:25:VAL:CG1	2.40	0.52
7:AG:69:VAL:HG23	7:AG:100:ALA:HB1	1.92	0.52
7:BG:69:VAL:HG23	7:BG:100:ALA:HB1	1.92	0.52
11:BK:84:VAL:HG21	11:BK:97:ILE:HG23	1.92	0.52
40:CM:77:ILE:CD1	40:CM:108:ALA:HB1	2.37	0.52
12:AL:33:VAL:HG22	12:AL:79:VAL:HG22	1.92	0.51
54:DI:44:ALA:HB1	54:DI:95:LEU:HD11	1.92	0.51
8:AH:2:SER:HB2	8:AH:4:GLN:HE21	1.75	0.51
1:BA:518:C:H2'	1:BA:530:G:C8	2.45	0.51
31:CA:639:U:H2'	31:CA:640:C:C6	2.45	0.51
40:CM:19:LEU:HD23	40:CM:31:GLY:O	2.10	0.51
1:AA:518:C:H2'	1:AA:530:G:C8	2.45	0.51
1:BA:299:G:H2'	1:BA:300:A:C8	2.44	0.51
8:BH:87:LYS:HB2	8:BH:125:ILE:CD1	2.38	0.51
1:AA:528:C:H5''	1:AA:528:C:H6	1.75	0.51
10:AJ:5:ARG:HE	10:AJ:77:VAL:HG22	1.75	0.51
31:CA:528:A:H8	31:CA:528:A:H3'	1.76	0.51
48:CU:54:GLU:HB3	48:CU:88:LYS:HD2	1.91	0.51
55:DA:102:U:H2'	55:DA:102:U:O2	2.11	0.51
55:DA:639:U:H2'	55:DA:640:C:C6	2.46	0.51
1:BA:8:A:C6	4:BD:206:LYS:HB3	2.46	0.51
3:BC:77:ILE:HA	3:BC:84:VAL:CG2	2.41	0.51
9:BI:19:VAL:HG22	9:BI:65:ILE:HG22	1.92	0.51
31:CA:1447:C:H2'	31:CA:1448:G:C8	2.46	0.51
42:CO:33:ILE:HD12	42:CO:114:GLU:HB3	1.92	0.51
34:DF:106:ILE:HD12	34:DF:139:PRO:HG2	1.93	0.51
16:AP:6:LEU:HB3	16:AP:17:TYR:HB3	1.92	0.51
1:BA:845:A:O5'	1:BA:845:A:H8	1.94	0.51
6:BF:45:ARG:O	6:BF:56:LYS:HA	2.11	0.51
17:BQ:8:LEU:HD13	17:BQ:73:TRP:CH2	2.46	0.51
29:CC:154:LEU:HD13	29:CC:176:LEU:HD21	1.92	0.51
31:CA:320:A:H4'	31:CA:322:A:N7	2.25	0.51
1:BA:374:A:OP1	1:BA:452:A:N1	2.44	0.51
55:DA:1509:A:HO2'	55:DA:1510:G:H8	1.57	0.51
1:AA:1277:C:HO2'	1:AA:1279:G:H8	1.58	0.51
2:AB:41:ILE:HD13	2:AB:202:GLY:HA2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:202:G:H1	1:BA:215:C:H42	1.58	0.51
2:BB:41:ILE:HD13	2:BB:202:GLY:HA2	1.93	0.51
47:CT:72:THR:HG21	47:CT:108:SER:HB3	1.92	0.51
50:CW:51:GLN:HG2	50:CW:86:LEU:HD11	1.93	0.51
47:DT:74:ILE:HD12	47:DT:105:VAL:HG22	1.91	0.51
1:BA:269:C:H2'	1:BA:270:A:C8	2.46	0.51
48:DU:54:GLU:HB3	48:DU:88:LYS:HD2	1.92	0.51
1:BA:1141:C:HO2'	1:BA:1142:G:H8	1.58	0.50
16:BP:6:LEU:HB3	16:BP:17:TYR:HB3	1.93	0.50
6:AF:45:ARG:O	6:AF:56:LYS:HA	2.10	0.50
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.93	0.50
5:BE:72:ILE:HG13	5:BE:73:ASN:N	2.25	0.50
10:BJ:5:ARG:HG2	10:BJ:79:PRO:HG3	1.93	0.50
30:CD:133:THR:CG2	31:CA:1993:U:H4'	2.41	0.50
49:CV:7:ARG:O	49:CV:25:VAL:HB	2.10	0.50
47:CT:74:ILE:HD12	47:CT:105:VAL:HG22	1.93	0.50
42:DO:33:ILE:HD12	42:DO:114:GLU:HB3	1.92	0.50
12:BL:33:VAL:HG22	12:BL:79:VAL:HG22	1.93	0.50
55:DA:1554:U:H1'	59:DA:3219:PUT:H32	1.94	0.50
1:AA:269:C:H2'	1:AA:270:A:C8	2.46	0.50
8:AH:87:LYS:HB2	8:AH:125:ILE:CD1	2.41	0.50
12:AL:110:ARG:HB2	12:AL:119:VAL:HG21	1.91	0.50
29:CC:158:ALA:HB3	31:CA:1820:U:O2'	2.11	0.50
31:CA:634:C:H2'	31:CA:635:C:C6	2.47	0.50
31:CA:974:G:H8	31:CA:990:A:H62	1.60	0.50
29:DC:154:LEU:HD13	29:DC:176:LEU:HD21	1.94	0.50
31:CA:784:G:H5'	31:CA:785:G:OP1	2.12	0.50
29:DC:16:VAL:HG22	29:DC:206:GLY:HA3	1.94	0.50
1:AA:845:A:O4'	1:AA:845:A:P	2.69	0.50
21:AU:51:SER:HA	21:AU:54:LYS:HE3	1.94	0.50
33:DE:189:THR:HG21	70:DE:441:HOH:O	2.11	0.50
1:AA:619:U:C2	4:AD:132:ILE:HD11	2.47	0.49
22:D1:4:GLN:HA	55:DA:2615:U:C2	2.47	0.49
23:D2:25:LYS:HE2	23:D2:30:LYS:O	2.12	0.49
31:CA:551:G:H5''	31:CA:551:G:H8	1.76	0.49
31:CA:2043:C:C6	31:CA:2043:C:H5''	2.47	0.49
31:CA:2189:U:H2'	31:CA:2190:G:H8	1.77	0.49
26:C5:6:SER:HB3	31:CA:2466:C:H5''	1.94	0.49
31:CA:2796:U:H3	31:CA:2799:A:N6	2.02	0.49
34:CF:106:ILE:HD12	34:CF:139:PRO:HG2	1.94	0.49
55:DA:118:A:N3	55:DA:178:G:H1'	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:DA:136:G:H1	55:DA:143:C:H42	1.60	0.49
5:AE:157:ARG:HD2	8:AH:43:GLU:O	2.13	0.49
8:BH:2:SER:HB2	8:BH:4:GLN:HE21	1.77	0.49
55:DA:12:U:O2	55:DA:12:U:H2'	2.12	0.49
55:DA:2273:A:H2'	55:DA:2274:A:C8	2.47	0.49
55:DA:2796:U:H3	55:DA:2799:A:N6	1.99	0.49
3:AC:155:GLY:HA2	3:AC:163:ALA:HB1	1.94	0.49
9:AI:116:VAL:HG21	10:AJ:62:ARG:HB2	1.94	0.49
18:AR:36:SER:HA	18:AR:72:ASP:HB3	1.94	0.49
24:C3:2:LYS:HE2	31:CA:687:C:H5''	1.94	0.49
39:CL:103:VAL:O	39:CL:122:VAL:HB	2.12	0.49
13:AM:90:ARG:HH21	13:AM:95:LEU:HB3	1.77	0.49
11:BK:43:GLY:HA3	11:BK:74:VAL:HG12	1.93	0.49
31:CA:2822:G:H2'	31:CA:2823:A:H5''	1.95	0.49
49:DV:13:VAL:HG21	49:DV:39:ILE:HG21	1.93	0.49
50:DW:63:ILE:HG22	50:DW:65:VAL:HG23	1.94	0.49
3:AC:47:LEU:HD22	3:AC:76:VAL:HG22	1.95	0.49
3:AC:151:VAL:HG12	3:AC:200:VAL:HG22	1.94	0.49
55:DA:1180:U:H5''	55:DA:1180:U:H6	1.78	0.49
13:BM:90:ARG:HH21	13:BM:95:LEU:HB3	1.78	0.49
31:CA:2394:C:H5''	40:CM:63:LYS:HE2	1.94	0.49
40:CM:28:GLY:O	40:CM:29:LYS:O	2.30	0.49
54:DI:132:TYR:H	54:DI:133:GLU:HB2	1.77	0.49
12:AL:79:VAL:HG12	12:AL:102:LEU:HD23	1.94	0.49
32:DD:121:THR:HB	32:DD:127:PHE:CD2	2.48	0.49
48:CU:69:ARG:HB2	48:CU:74:ILE:HG22	1.95	0.49
37:DJ:103:ARG:HA	37:DJ:106:LEU:HD12	1.94	0.49
39:DL:30:ARG:HD2	55:DA:2674:G:H4'	1.94	0.49
40:DM:21:ARG:HA	55:DA:811:U:H2'	1.93	0.49
13:AM:86:TYR:CZ	13:AM:90:ARG:HD2	2.47	0.49
3:BC:47:LEU:HD22	3:BC:76:VAL:HG22	1.95	0.49
5:BE:90:THR:HG22	5:BE:91:GLY:N	2.28	0.49
31:CA:2095:A:H8	31:CA:2095:A:H5''	1.78	0.49
35:CG:17:VAL:HG11	35:CG:50:LEU:HD21	1.95	0.49
37:CJ:103:ARG:HA	37:CJ:106:LEU:HD12	1.93	0.49
35:DG:19:ILE:HG12	35:DG:24:ILE:HG12	1.94	0.49
55:DA:1417:C:H5'	55:DA:1588:G:H1'	1.95	0.49
1:AA:1492:A:C5'	12:AL:44:LYS:HG2	2.39	0.49
1:BA:404:G:N7	4:BD:2:ALA:HB3	2.28	0.49
13:BM:86:TYR:CZ	13:BM:90:ARG:HD2	2.47	0.49
31:CA:2074:U:H2'	31:CA:2075:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:CA:136:G:H1	31:CA:143:C:H42	1.61	0.48
33:CE:21:ARG:HD3	33:CE:106:LYS:HB3	1.95	0.48
34:CF:44:ILE:HG21	34:CF:79:ILE:HG22	1.95	0.48
70:DK:307:HOH:O	45:DR:93:LYS:HD2	2.13	0.48
54:DI:23:LEU:HD13	54:DI:89:PRO:HD3	1.94	0.48
1:BA:266:G:H3'	17:BQ:69:LYS:HB2	1.95	0.48
3:BC:155:GLY:HA2	3:BC:163:ALA:HB1	1.95	0.48
19:BS:15:LEU:HD13	19:BS:33:THR:HG21	1.94	0.48
31:CA:1703:G:H2'	31:CA:1704:C:C6	2.48	0.48
31:CA:1794:A:H2'	31:CA:1795:C:C6	2.49	0.48
33:DE:21:ARG:HD2	70:DE:416:HOH:O	2.13	0.48
50:DW:51:GLN:HG2	50:DW:86:LEU:HD11	1.94	0.48
1:BA:209:U:H2'	1:BA:209:U:O2	2.13	0.48
5:BE:105:ILE:H	5:BE:123:VAL:H	1.61	0.48
31:CA:1274:A:N3	31:CA:1297:C:H1'	2.28	0.48
31:CA:2630:G:O4'	31:CA:2894:G:H1'	2.13	0.48
29:DC:199:GLU:O	29:DC:202:LEU:HB2	2.13	0.48
54:DI:31:ARG:HB2	54:DI:79:PRO:HG2	1.93	0.48
1:AA:266:G:H3'	17:AQ:69:LYS:HB2	1.95	0.48
1:AA:413:G:H5''	1:AA:414:A:H5'	1.96	0.48
10:AJ:52:LEU:HB2	14:AN:81:ARG:HD2	1.96	0.48
5:BE:106:ILE:HD11	5:BE:124:LEU:HD23	1.95	0.48
31:CA:45:G:H5''	31:CA:46:G:H5'	1.96	0.48
31:CA:668:A:H2'	31:CA:670:A:H62	1.78	0.48
31:CA:2327:A:H2'	31:CA:2328:A:C8	2.49	0.48
54:DI:26:VAL:HB	54:DI:83:ALA:HB3	1.95	0.48
55:DA:2187:U:H5''	70:DA:4577:HOH:O	2.12	0.48
55:DA:2728:U:O2'	55:DA:2729:G:H5''	2.13	0.48
50:CW:63:ILE:HG22	50:CW:65:VAL:HG23	1.95	0.48
52:CY:4:VAL:HG22	52:CY:11:ARG:HG3	1.95	0.48
55:DA:45:G:H5''	55:DA:46:G:H5'	1.95	0.48
1:AA:202:G:H21	1:AA:466:A:H61	1.60	0.48
1:AA:404:G:N7	4:AD:2:ALA:HB3	2.28	0.48
27:C0:9:GLN:HB3	27:C0:32:ILE:HA	1.95	0.48
6:BF:3:HIS:H	6:BF:92:THR:HG23	1.78	0.48
31:CA:586:A:H5'	33:CE:84:THR:HG21	1.96	0.48
31:CA:822:G:O6	31:CA:943:A:H2	1.96	0.48
31:CA:948:C:H1'	31:CA:984:A:C8	2.48	0.48
45:CR:87:SER:HB3	46:CS:52:PRO:HD3	1.94	0.48
19:BS:29:LYS:HB3	19:BS:30:PRO:HD2	1.96	0.48
31:CA:2636:C:H2'	31:CA:2637:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DK:9:GLU:HG2	70:DA:5165:HOH:O	2.13	0.48
1:AA:202:G:H1	1:AA:215:C:H42	1.62	0.48
24:D3:19:ARG:HG3	55:DA:126:A:O5'	2.14	0.48
31:CA:528:A:H3'	31:CA:528:A:C8	2.48	0.48
53:CZ:56:LEU:HA	53:CZ:59:GLU:HG2	1.96	0.48
55:DA:1975:G:H21	64:DA:3225:PGE:H22	1.79	0.48
32:DD:3:GLY:HA3	32:DD:204:LYS:HG2	1.95	0.48
39:CL:58:LEU:HD11	39:CL:86:LEU:HD13	1.96	0.48
41:DN:92:TRP:HE1	58:DN:201:MPD:HM1	1.78	0.48
22:C1:53:LYS:HE3	22:C1:56:ALA:HA	1.95	0.48
43:DP:35:ILE:HG21	43:DP:71:ALA:HA	1.96	0.48
51:DX:59:LEU:HD12	51:DX:80:ILE:HD12	1.96	0.48
55:DA:1536:C:H4'	55:DA:1537:G:H5''	1.95	0.48
17:AQ:15:ASP:HA	17:AQ:21:ILE:HG22	1.95	0.47
19:AS:29:LYS:HB3	19:AS:30:PRO:HD2	1.96	0.47
31:CA:1709:U:H2'	31:CA:1710:G:C8	2.49	0.47
34:CF:36:LEU:HD21	34:CF:91:LEU:CD1	2.45	0.47
40:DM:85:VAL:HB	40:DM:94:THR:HG22	1.96	0.47
8:AH:105:SER:HB2	8:AH:126:ILE:HD11	1.96	0.47
11:BK:24:HIS:HB3	11:BK:31:ILE:HG23	1.96	0.47
48:CU:28:ASN:ND2	48:CU:91:GLN:HB3	2.28	0.47
55:DA:2636:C:H2'	55:DA:2637:U:C6	2.49	0.47
65:DA:3224:SPD:H82	70:DA:4835:HOH:O	2.14	0.47
1:BA:108:G:H5''	1:BA:108:G:N3	2.30	0.47
13:BM:22:ILE:HB	13:BM:25:VAL:HG12	1.97	0.47
17:BQ:51:ASN:N	17:BQ:51:ASN:HD22	2.13	0.47
31:CA:532:A:N3	31:CA:532:A:H2'	2.30	0.47
35:CG:19:ILE:HG12	35:CG:24:ILE:HG12	1.96	0.47
42:CO:103:ARG:HD3	42:CO:110:MET:SD	2.55	0.47
3:BC:20:SER:HB3	14:BN:94:PRO:HG3	1.96	0.47
30:CD:3:GLY:HA3	30:CD:204:LYS:HG2	1.97	0.47
34:DF:44:ILE:HG21	34:DF:79:ILE:HG22	1.96	0.47
5:AE:90:THR:HG22	5:AE:91:GLY:N	2.29	0.47
23:C2:25:LYS:HE2	23:C2:30:LYS:O	2.14	0.47
31:CA:373:U:H2'	31:CA:374:A:H8	1.78	0.47
31:CA:782:A:H5'	31:CA:783:A:C2	2.50	0.47
51:CX:37:ILE:HG22	51:CX:38:VAL:HG23	1.94	0.47
35:DG:86:LYS:HG2	35:DG:132:VAL:HG22	1.96	0.47
41:DN:3:GLN:HG3	41:DN:92:TRP:CD1	2.49	0.47
55:DA:2547:A:H2'	55:DA:2548:U:C6	2.50	0.47
22:C1:8:PRO:HG2	31:CA:1264:A:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:BI:116:VAL:HG21	10:BJ:62:ARG:HB2	1.97	0.47
20:BT:4:ILE:HA	20:BT:8:LYS:HE2	1.96	0.47
23:D2:6:ARG:HG2	23:D2:24:THR:HB	1.96	0.47
29:CC:3:VAL:HG21	29:CC:202:LEU:HD23	1.97	0.47
41:CN:3:GLN:HG3	41:CN:92:TRP:CD1	2.49	0.47
42:CO:71:ARG:HG3	42:CO:71:ARG:O	2.15	0.47
43:CP:7:ARG:HA	43:CP:10:ARG:HE	1.80	0.47
38:DK:39:LYS:HZ1	55:DA:1007:C:P	2.37	0.47
1:AA:946:A:H2'	1:AA:947:G:C8	2.50	0.47
22:C1:25:VAL:HG13	22:C1:26:THR:H	1.78	0.47
4:BD:201:VAL:HG11	5:BE:103:THR:HB	1.96	0.47
10:BJ:57:VAL:HG22	10:BJ:58:ASN:H	1.79	0.47
29:CC:174:LEU:HD21	29:CC:184:VAL:HB	1.95	0.47
29:CC:199:GLU:O	29:CC:202:LEU:HB2	2.13	0.47
31:CA:1936:A:C2	31:CA:1943:U:N3	2.62	0.47
51:CX:59:LEU:HD12	51:CX:80:ILE:HD12	1.96	0.47
53:DZ:56:LEU:HA	53:DZ:59:GLU:HG2	1.96	0.47
55:DA:851:C:H2'	55:DA:852:U:C6	2.50	0.47
55:DA:2502:G:H5''	55:DA:2503:2MA:H5''	1.95	0.47
12:BL:79:VAL:HG12	12:BL:102:LEU:HD23	1.95	0.47
35:DG:17:VAL:HG11	35:DG:50:LEU:HD21	1.96	0.47
35:DG:164:TYR:HB2	35:DG:167:GLU:HB2	1.96	0.47
55:DA:1416:G:HO2'	55:DA:1417:C:H6	1.61	0.47
23:C2:6:ARG:HG2	23:C2:24:THR:HB	1.97	0.47
25:C4:8:ARG:HG3	31:CA:253:C:N4	2.30	0.47
1:BA:376:G:H5''	16:BP:5:ARG:HB2	1.97	0.47
22:D1:24:ALA:HB3	64:D1:102:PGE:H5	1.96	0.47
30:CD:121:THR:HB	30:CD:127:PHE:CD2	2.50	0.47
31:CA:12:U:H2'	31:CA:12:U:O2	2.15	0.47
31:CA:17:G:H4'	45:CR:25:TYR:HE2	1.80	0.47
31:CA:1956:U:O2	31:CA:1985:C:H4'	2.15	0.47
29:DC:160:THR:HG21	55:DA:1819:A:H5''	1.96	0.47
35:CG:164:TYR:HB2	35:CG:167:GLU:HB2	1.96	0.47
41:DN:33:LEU:HD13	41:DN:117:PHE:HB3	1.97	0.47
1:AA:411:A:P	4:AD:26:ARG:HH12	2.38	0.47
5:AE:57:PRO:O	5:AE:60:ILE:HG13	2.15	0.47
5:AE:107:ALA:HB2	5:AE:125:ALA:HB3	1.96	0.47
17:BQ:76:VAL:HG12	17:BQ:77:ARG:HG3	1.97	0.47
31:CA:1441:G:H2'	31:CA:1442:U:C6	2.50	0.47
35:CG:86:LYS:HG2	35:CG:132:VAL:HG22	1.97	0.47
33:DE:21:ARG:HD3	33:DE:106:LYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DL:58:LEU:HD11	39:DL:86:LEU:HD13	1.96	0.47
39:DL:101:GLY:O	39:DL:120:PRO:HD2	2.15	0.47
8:AH:66:PHE:CD2	8:AH:67:GLN:HG2	2.51	0.46
24:C3:19:ARG:HG3	31:CA:126:A:O5'	2.15	0.46
1:BA:946:A:H2'	1:BA:947:G:C8	2.50	0.46
20:BT:44:LYS:HB3	20:BT:87:ALA:HB2	1.96	0.46
31:CA:321:U:H5''	33:CE:131:THR:HG23	1.98	0.46
31:CA:851:C:H2'	31:CA:852:U:C6	2.50	0.46
31:CA:2845:U:H5''	44:CQ:52:ASN:O	2.15	0.46
1:AA:604:G:H2'	1:AA:605:U:O4'	2.15	0.46
23:C2:37:LYS:HG2	23:C2:48:ILE:HG13	1.97	0.46
20:BT:24:ARG:O	20:BT:27:MET:HG3	2.15	0.46
30:CD:13:ARG:HH11	44:CQ:56:HIS:HA	1.79	0.46
47:DT:20:VAL:HG11	47:DT:44:ALA:HA	1.97	0.46
10:AJ:57:VAL:HG22	10:AJ:58:ASN:H	1.81	0.46
17:AQ:76:VAL:HG12	17:AQ:77:ARG:HG3	1.96	0.46
5:BE:105:ILE:HA	5:BE:123:VAL:HG23	1.98	0.46
31:CA:608:A:H2'	31:CA:609:A:C8	2.50	0.46
31:CA:998:C:OP2	45:CR:58:ARG:NH2	2.48	0.46
43:CP:35:ILE:HG21	43:CP:71:ALA:HA	1.98	0.46
41:DN:18[B]:ARG:HG3	28:DB:90:C:H5''	1.97	0.46
1:AA:108:G:N3	1:AA:108:G:H5''	2.29	0.46
2:AB:129:LEU:H	2:AB:129:LEU:HG	1.53	0.46
3:AC:20:SER:HB3	14:AN:94:PRO:HG3	1.96	0.46
1:BA:1001:C:H2'	1:BA:1002:G:H8	1.81	0.46
31:CA:2842:G:H2'	31:CA:2843:G:O4'	2.15	0.46
29:DC:3:VAL:HG21	29:DC:202:LEU:HD23	1.97	0.46
55:DA:1014:A:H1'	70:DA:6962:HOH:O	2.14	0.46
55:DA:1999:C:H5''	55:DA:2723:C:O2'	2.15	0.46
9:AI:7:TYR:HE1	9:AI:18:ARG:HB2	1.80	0.46
8:BH:105:SER:HB2	8:BH:126:ILE:HD11	1.97	0.46
31:CA:1509:A:HO2'	31:CA:1510:G:H8	1.63	0.46
47:CT:20:VAL:HG11	47:CT:44:ALA:HA	1.98	0.46
40:DM:63:LYS:HE2	55:DA:2394:C:H5''	1.98	0.46
55:DA:858:G:H3'	55:DA:859:G:C8	2.51	0.46
8:AH:29:SER:HB3	8:AH:57:PRO:HB2	1.97	0.46
9:AI:98:LEU:HB3	9:AI:104:VAL:HG13	1.97	0.46
12:AL:3:THR:HB	12:AL:6:GLN:HG3	1.98	0.46
27:C0:14:ILE:HG12	31:CA:989:G:C8	2.50	0.46
1:BA:73:C:O2'	1:BA:74:A:H8	1.98	0.46
18:BR:36:SER:HA	18:BR:72:ASP:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:CA:1783:A:H5'	31:CA:2608:G:H4'	1.97	0.46
55:DA:287:G:H1	55:DA:353:C:H42	1.64	0.46
1:AA:79:G:H22	1:AA:90:C:H42	1.64	0.46
1:AA:1001:C:H2'	1:AA:1002:G:H8	1.81	0.46
1:BA:374:A:H5''	1:BA:452:A:C2	2.51	0.46
1:BA:374:A:H5''	1:BA:452:A:N1	2.29	0.46
29:CC:228:VAL:HG21	70:CA:3406:HOH:O	2.16	0.46
31:CA:7:G:H4'	38:CK:15:TRP:CZ2	2.50	0.46
42:CO:2:ARG:HA	42:CO:5:LYS:HD2	1.98	0.46
45:CR:90:ILE:HG22	45:CR:95:LEU:HG	1.97	0.46
41:DN:16:ARG:HG3	41:DN:18[B]:ARG:HH11	1.81	0.46
1:BA:604:G:H2'	1:BA:605:U:O4'	2.16	0.46
5:BE:88:VAL:HG12	5:BE:93:ARG:HG2	1.97	0.46
10:BJ:52:LEU:HB2	14:BN:81:ARG:HD2	1.98	0.46
31:CA:2815:C:H2'	31:CA:2816:G:O4'	2.15	0.46
39:CL:101:GLY:O	39:CL:120:PRO:HD2	2.15	0.46
41:DN:20:LEU:HD22	50:DW:81:PRO:HG2	1.98	0.46
45:DR:4:VAL:HG22	55:DA:1199:U:H1'	1.98	0.46
1:AA:56:U:H2'	1:AA:57:G:C8	2.51	0.46
31:CA:443:A:H2'	33:CE:40:ARG:NH1	2.30	0.46
31:CA:532:A:N1	31:CA:2020:A:H1'	2.31	0.46
31:CA:1028:A:N6	31:CA:1125:G:H2'	2.30	0.46
31:CA:1587:G:H2'	31:CA:1588:G:H8	1.81	0.46
40:CM:85:VAL:HG11	40:CM:90:VAL:HG22	1.98	0.46
45:CR:76:TYR:CZ	45:CR:80:ILE:HG13	2.51	0.46
55:DA:2133:G:H21	55:DA:2158:A:N6	2.13	0.46
1:AA:967:5MC:O3'	9:AI:127:PHE:HE1	1.98	0.46
4:AD:177:LYS:HB3	4:AD:179:GLU:HG2	1.98	0.46
1:BA:1478:U:H2'	1:BA:1479:C:C6	2.51	0.46
31:CA:1405:U:H2'	31:CA:1406:U:C6	2.51	0.46
31:CA:1430:G:H2'	31:CA:1431:A:O4'	2.15	0.46
41:CN:33:LEU:HD13	41:CN:117:PHE:HB3	1.98	0.46
38:DK:7:LYS:HG2	55:DA:538:A:H4'	1.97	0.46
55:DA:1794:A:H2'	55:DA:1795:C:C6	2.50	0.46
5:AE:76:LEU:HD11	5:AE:120:VAL:HG22	1.99	0.45
1:BA:972:C:H4'	10:BJ:59:LYS:HG2	1.98	0.45
2:BB:111:ILE:HD12	2:BB:152:LYS:HA	1.97	0.45
30:CD:186:LEU:HD21	44:CQ:4:ILE:HG21	1.98	0.45
33:CE:75:SER:O	33:CE:78:TRP:HB2	2.15	0.45
45:DR:6:ARG:HD3	55:DA:1250:G:C5'	2.46	0.45
55:DA:191:A:H2'	55:DA:192:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1478:U:H2'	1:AA:1479:C:C6	2.51	0.45
4:BD:177:LYS:HB3	4:BD:179:GLU:HG2	1.97	0.45
5:BE:57:PRO:O	5:BE:60:ILE:HG13	2.16	0.45
9:BI:7:TYR:HE1	9:BI:18:ARG:HB2	1.79	0.45
31:CA:244:A:H5''	40:CM:67:THR:HG21	1.98	0.45
31:CA:2305:U:H5''	34:CF:131:GLY:HA3	1.97	0.45
1:AA:403:C:H5'	4:AD:132:ILE:HG23	1.97	0.45
26:C5:3:VAL:CG1	31:CA:2539:C:H5'	2.46	0.45
1:BA:774:G:H21	57:BA:1642:PG4:H62	1.81	0.45
31:CA:804:A:H2'	31:CA:806:C:C4	2.51	0.45
33:CE:149:ILE:HD12	33:CE:172:ALA:HA	1.98	0.45
40:DM:32:GLY:HA2	55:DA:1190:G:H5''	1.98	0.45
55:DA:1587:G:H2'	55:DA:1588:G:H8	1.82	0.45
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.98	0.45
1:AA:923:A:OP1	5:AE:26:LYS:HG2	2.16	0.45
31:CA:1380:G:H1'	31:CA:1569:A:N6	2.32	0.45
31:CA:2350:C:H2'	31:CA:2351:G:O4'	2.17	0.45
45:DR:76:TYR:CZ	45:DR:80:ILE:HG13	2.52	0.45
22:D1:22:LEU:HD23	62:D1:103:PEG:H31	1.99	0.45
31:CA:310:A:H5''	49:CV:15:THR:HG23	1.97	0.45
43:DP:27:VAL:HG21	43:DP:40:ILE:HD12	1.98	0.45
55:DA:2128:G:H1	55:DA:2160:C:N4	2.13	0.45
2:AB:111:ILE:HD12	2:AB:152:LYS:HA	1.98	0.45
28:CB:57:A:C4'	34:CF:27:GLN:HG3	2.47	0.45
44:DQ:106:LYS:HA	44:DQ:109:ARG:HD3	1.99	0.45
55:DA:1424:G:H21	64:DA:3214:PGE:H32	1.82	0.45
14:BN:31:ILE:HG23	14:BN:42:TRP:HZ2	1.81	0.45
30:CD:62:LYS:HE2	31:CA:2810:A:H5''	1.99	0.45
31:CA:720:U:H2'	31:CA:721:A:C8	2.52	0.45
55:DA:742:A:H2'	55:DA:743:A:C8	2.52	0.45
2:AB:188:ASP:HB2	2:AB:204:ASP:OD2	2.16	0.45
1:BA:56:U:H2'	1:BA:57:G:C8	2.52	0.45
45:DR:16:LYS:HE2	63:DA:3209:EDO:H21	1.98	0.45
55:DA:2233:U:H2'	55:DA:2234:G:C8	2.52	0.45
1:AA:73:C:O2'	1:AA:74:A:H8	1.98	0.45
21:AU:4:ILE:HG13	21:AU:19:PHE:HA	1.99	0.45
1:BA:1003:G:H21	1:BA:1005:A:H5'	1.82	0.45
9:BI:57:MET:HG3	9:BI:61:LEU:HG	1.99	0.45
24:D3:12:ARG:HB2	55:DA:686:U:O4	2.17	0.45
38:DK:46:PRO:HD2	70:DK:360:HOH:O	2.17	0.45
41:DN:77:PRO:HG2	41:DN:80:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:188:ASP:HB2	2:BB:204:ASP:OD2	2.17	0.45
32:DD:150[B]:MEQ:HG3	55:DA:2032:G:N3	2.31	0.45
46:CS:49:ILE:HB	46:CS:51:VAL:O	2.17	0.45
54:DI:126:LEU:HA	54:DI:129:LEU:HD12	1.98	0.45
55:DA:31:C:O3'	55:DA:1238:G:H5''	2.17	0.45
1:AA:109:A:H2'	1:AA:326:G:N2	2.31	0.44
5:BE:157:ARG:HG3	8:BH:43:GLU:O	2.17	0.44
31:CA:191:A:H2'	31:CA:192:C:C6	2.52	0.44
42:DO:55:ALA:HA	42:DO:80:PHE:CE2	2.53	0.44
66:DA:3202:1PE:H162	70:DA:3315:HOH:O	2.16	0.44
11:AK:52:PHE:HE2	11:AK:65:VAL:HG21	1.82	0.44
1:BA:109:A:H2'	1:BA:326:G:N2	2.32	0.44
1:BA:1106:G:H5''	3:BC:172:ARG:HG3	1.99	0.44
2:BB:129:LEU:H	2:BB:129:LEU:HG	1.53	0.44
11:BK:52:PHE:HE2	11:BK:65:VAL:HG21	1.81	0.44
28:CB:28:C:OP1	43:CP:31:THR:HG21	2.16	0.44
31:CA:247:G:H4'	31:CA:386:G:C5	2.52	0.44
31:CA:287:G:H1	31:CA:353:C:H42	1.65	0.44
41:CN:69:PRO:HA	41:CN:94:ALA:HB2	1.99	0.44
43:CP:27:VAL:HG21	43:CP:40:ILE:HD12	2.00	0.44
1:BA:322:C:H5	1:BA:328:C:C5	2.36	0.44
13:BM:16:VAL:HG13	13:BM:34:LEU:HD12	1.98	0.44
31:CA:1434:A:H2'	31:CA:1435:G:C8	2.52	0.44
31:CA:2298:A:C2	31:CA:2321:U:N3	2.85	0.44
31:CA:2607:G:H2'	31:CA:2608:G:O4'	2.16	0.44
50:CW:38:LEU:HD21	50:CW:65:VAL:HG11	1.99	0.44
1:AA:715:A:H2'	1:AA:716:A:C8	2.53	0.44
1:AA:1329:A:H5''	13:AM:26:GLY:H	1.81	0.44
1:BA:328:C:H2'	1:BA:328:C:O2	2.17	0.44
1:BA:923:A:OP1	5:BE:26:LYS:HG2	2.18	0.44
1:BA:1329:A:H5''	13:BM:26:GLY:H	1.82	0.44
17:BQ:31:HIS:HE1	17:BQ:33:ILE:HD12	1.82	0.44
20:BT:69:LYS:H	20:BT:69:LYS:HG3	1.57	0.44
21:BU:4:ILE:HG13	21:BU:19:PHE:HA	1.99	0.44
31:CA:1638:C:H4'	31:CA:2710:C:O2	2.17	0.44
50:CW:63:ILE:CD1	50:CW:72:VAL:HG21	2.47	0.44
50:DW:63:ILE:CD1	50:DW:72:VAL:HG21	2.47	0.44
20:BT:58:VAL:HG13	20:BT:72:ALA:HB1	1.98	0.44
28:CB:14:U:H2'	28:CB:15:A:C2	2.52	0.44
31:CA:582:A:H2'	31:CA:583:G:C8	2.53	0.44
31:CA:588:U:H2'	31:CA:589:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:CG:76:VAL:O	35:CG:80:THR:HG22	2.18	0.44
44:DQ:31:TRP:CE2	44:DQ:40:LEU:HD21	2.52	0.44
55:DA:2324:U:H3'	55:DA:2325:G:H5''	2.00	0.44
8:AH:94:LYS:HB3	8:AH:117:ARG:HH22	1.82	0.44
9:AI:57:MET:HG3	9:AI:61:LEU:HG	1.99	0.44
13:AM:90:ARG:HD3	13:AM:97:VAL:HA	1.99	0.44
1:BA:439:U:H5''	4:BD:121:LYS:HD2	1.99	0.44
1:BA:1496:C:H2'	1:BA:1497:G:O4'	2.17	0.44
13:BM:90:ARG:HD3	13:BM:97:VAL:HA	1.99	0.44
21:BU:51:SER:HA	21:BU:54:LYS:HE3	2.00	0.44
29:CC:155:ALA:HB2	29:CC:162:VAL:HG23	1.98	0.44
31:CA:686:U:H2'	31:CA:788:A:N1	2.32	0.44
31:CA:1327:A:H2'	31:CA:1328:A:O4'	2.17	0.44
31:CA:1636:U:H2'	31:CA:1637:A:C8	2.52	0.44
45:CR:112:LYS:HD3	46:CS:48:LYS:HG3	2.00	0.44
55:DA:136:G:H1	55:DA:143:C:N4	2.16	0.44
55:DA:783:A:N3	55:DA:783:A:H2'	2.33	0.44
55:DA:2262:U:H4'	55:DA:2328:A:C2	2.53	0.44
3:AC:47:LEU:HB3	3:AC:50:ALA:HB3	2.00	0.44
17:AQ:31:HIS:HE1	17:AQ:33:ILE:HD12	1.83	0.44
27:C0:7:ILE:HD13	27:C0:27:LEU:HD22	2.00	0.44
7:BG:111:ARG:HB3	7:BG:119:ARG:HG2	2.00	0.44
8:BH:29:SER:HB3	8:BH:57:PRO:HB2	2.00	0.44
26:C5:38:GLY:HA2	31:CA:1125:G:H5'	1.99	0.44
1:BA:967:5MC:O3'	9:BI:127:PHE:HE1	2.00	0.44
9:BI:98:LEU:HB3	9:BI:104:VAL:HG13	1.98	0.44
31:CA:587:C:O2'	40:CM:19:LEU:HD13	2.17	0.44
31:CA:1680:U:H2'	31:CA:1681:G:O4'	2.18	0.44
31:CA:2190:G:H2'	31:CA:2191:A:H8	1.83	0.44
29:DC:97:LYS:HA	29:DC:97:LYS:HD3	1.68	0.44
47:DT:73:LYS:HD3	66:DA:3185:1PE:H232	2.00	0.44
50:DW:38:LEU:HD21	50:DW:65:VAL:HG11	1.99	0.44
1:AA:328:C:H2'	1:AA:328:C:O2	2.17	0.44
1:AA:439:U:H5''	4:AD:121:LYS:HD2	1.99	0.44
1:AA:1003:G:H21	1:AA:1005:A:H5'	1.82	0.44
24:C3:9:VAL:HG23	31:CA:1309:G:H5''	2.00	0.44
29:CC:160:THR:HG21	31:CA:1819:A:H5''	2.00	0.44
31:CA:826:U:O2'	40:CM:53:GLY:HA3	2.17	0.44
31:CA:1363:C:H2'	31:CA:1364:G:C8	2.53	0.44
34:CF:31:VAL:HG11	34:CF:97:TRP:CH2	2.53	0.44
37:DJ:14:ALA:HB3	37:DJ:17:MET:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:DI:3:LEU:HD12	54:DI:56:ARG:NH2	2.33	0.44
55:DA:720:U:H2'	55:DA:721:A:C8	2.53	0.44
55:DA:1101:U:H2'	55:DA:1102:C:C6	2.53	0.44
55:DA:1328:A:H2'	55:DA:1330:C:C5	2.53	0.44
55:DA:1975:G:H21	64:DA:3225:PGE:C2	2.31	0.44
6:AF:38:ARG:HE	6:AF:63:ASN:ND2	2.16	0.43
8:BH:102:ALA:HB3	8:BH:113:ASP:HB3	2.00	0.43
12:BL:64:THR:HG23	12:BL:93:VAL:HA	1.99	0.43
14:BN:31:ILE:HG23	14:BN:42:TRP:CZ2	2.53	0.43
22:D1:9:THR:HG21	55:DA:2020:A:H5'	2.00	0.43
26:D5:2:LYS:HE2	26:D5:4:ARG:HH11	1.83	0.43
31:CA:328:U:O3'	49:CV:66:GLN:HG3	2.18	0.43
31:CA:729:G:H2'	31:CA:1775:U:H1'	1.99	0.43
31:CA:1324:G:H1'	31:CA:1616:A:N6	2.33	0.43
29:DC:155:ALA:HB2	29:DC:162:VAL:HG23	2.00	0.43
36:CH:82:SER:HB2	36:CH:94:ILE:HD11	2.00	0.43
38:CK:117:ALA:HA	38:CK:120:ARG:HD2	2.00	0.43
44:CQ:106:LYS:HA	44:CQ:109:ARG:HD3	1.99	0.43
55:DA:588:U:H2'	55:DA:589:U:C6	2.53	0.43
55:DA:2607:G:H2'	55:DA:2608:G:O4'	2.17	0.43
1:BA:438:U:H5'	4:BD:120:HIS:HB3	1.99	0.43
9:BI:120:LYS:HB2	9:BI:123:ARG:HB3	2.00	0.43
38:DK:117:ALA:HA	38:DK:120:ARG:HD2	2.00	0.43
55:DA:1637:A:H5'	55:DA:1760:C:O2'	2.18	0.43
1:AA:438:U:H5'	4:AD:120:HIS:HB3	2.00	0.43
10:AJ:49:PHE:CE1	14:AN:77:PHE:HZ	2.36	0.43
4:BD:85:ASN:HA	5:BE:102:GLY:CA	2.41	0.43
14:BN:28:LYS:HA	14:BN:31:ILE:HG22	1.99	0.43
31:CA:357:C:H2'	31:CA:358:U:C6	2.53	0.43
31:CA:2190:G:H2'	31:CA:2191:A:C8	2.54	0.43
34:CF:36:LEU:HB2	34:CF:57:LEU:HD21	2.00	0.43
51:DX:41[A]:ARG:HH12	55:DA:2262:U:H5''	1.84	0.43
55:DA:357:C:H2'	55:DA:358:U:C6	2.53	0.43
55:DA:1433:A:O2'	55:DA:1434:A:H5'	2.19	0.43
1:BA:79:G:H22	1:BA:90:C:H42	1.65	0.43
1:BA:1493:A:H1'	31:CA:1913:A:H61	1.82	0.43
3:BC:113:ALA:O	3:BC:200:VAL:HG11	2.18	0.43
26:D5:36:ARG:HD3	55:DA:2742:G:OP1	2.19	0.43
31:CA:373:U:H2'	31:CA:374:A:C8	2.53	0.43
31:CA:460:A:H2'	31:CA:461:C:O4'	2.18	0.43
45:DR:19:LYS:HB3	57:DR:202:PG4:H41	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DR:90:ILE:HG22	45:DR:95:LEU:HG	2.00	0.43
54:DI:27:VAL:HG13	54:DI:80:THR:HG23	2.00	0.43
55:DA:138:U:H5'	55:DA:139:U:H5'	1.99	0.43
55:DA:278:A:N3	55:DA:278:A:H2'	2.33	0.43
55:DA:686:U:H2'	55:DA:788:A:N1	2.33	0.43
1:AA:649:A:H2'	1:AA:650:G:O4'	2.17	0.43
8:AH:102:ALA:HB3	8:AH:113:ASP:HB3	2.01	0.43
1:BA:1062:U:H2'	1:BA:1063:C:C6	2.54	0.43
17:BQ:28:PHE:HD2	17:BQ:37:PHE:HB3	1.84	0.43
30:CD:101:PHE:O	30:CD:104:VAL:HG22	2.19	0.43
30:CD:141:ARG:HB2	31:CA:1656:C:H5''	2.01	0.43
31:CA:278:A:N3	31:CA:278:A:H2'	2.33	0.43
32:DD:155:VAL:HG21	55:DA:2618:G:H21	1.84	0.43
36:DH:104:THR:HG22	36:DH:109:GLU:HA	1.99	0.43
55:DA:2800:A:C2	55:DA:2895:G:H1'	2.53	0.43
1:AA:1496:C:H2'	1:AA:1497:G:O4'	2.18	0.43
9:AI:99:ARG:HG2	9:AI:104:VAL:HG21	2.01	0.43
31:CA:20:C:H2'	31:CA:21:A:C8	2.53	0.43
31:CA:136:G:H1	31:CA:143:C:N4	2.17	0.43
42:DO:51:LEU:HD23	42:DO:51:LEU:HA	1.88	0.43
55:DA:57:C:H2'	55:DA:58:G:O4'	2.19	0.43
55:DA:340:A:H2'	55:DA:341:C:O4'	2.19	0.43
55:DA:2031:A:C6	55:DA:2498:OMC:H1'	2.53	0.43
55:DA:2251:OMG:H1'	55:DA:2251:OMG:HM23	1.73	0.43
55:DA:2479:U:OP1	55:DA:2537:U:H1'	2.19	0.43
1:AA:202:G:O2'	1:AA:468:A:H8	2.02	0.43
7:AG:111:ARG:HB3	7:AG:119:ARG:HG2	2.00	0.43
1:BA:649:A:H2'	1:BA:650:G:O4'	2.18	0.43
1:BA:840:C:H2'	1:BA:841:C:O4'	2.19	0.43
28:CB:57:A:O4'	34:CF:27:GLN:HG3	2.18	0.43
31:CA:1101:U:H2'	31:CA:1102:C:C6	2.53	0.43
36:DH:82:SER:HB2	36:DH:94:ILE:HD11	1.99	0.43
55:DA:784:G:H5'	55:DA:785:G:OP1	2.18	0.43
11:BK:84:VAL:HG11	11:BK:97:ILE:HG12	2.01	0.43
31:CA:2031:A:C6	31:CA:2498:OMC:H1'	2.54	0.43
33:DE:32:VAL:HG21	40:DM:6:LEU:HD13	2.00	0.43
49:DV:51:ALA:O	49:DV:52:LEU:HB2	2.18	0.43
54:DI:132:TYR:N	54:DI:133:GLU:HB2	2.33	0.43
55:DA:142:A:H2'	55:DA:143:C:C6	2.53	0.43
55:DA:184:C:H2'	55:DA:185:G:H8	1.84	0.43
55:DA:2849:U:H4'	55:DA:2868:A:C2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:957:U:O2	1:AA:959:A:H8	2.02	0.43
3:BC:22:TRP:HB3	3:BC:59:ARG:H	1.84	0.43
5:BE:104:GLY:HA3	5:BE:122:ASN:HA	2.01	0.43
8:BH:94:LYS:HB3	8:BH:117:ARG:HH22	1.84	0.43
22:D1:12:LYS:HD2	22:D1:12:LYS:HA	1.85	0.43
22:D1:50:ARG:NH2	55:DA:2884[A]:U:H4'	2.33	0.43
29:CC:88:SER:HB2	29:CC:158:ALA:HB2	2.01	0.43
29:DC:35:GLU:HG3	29:DC:64:ILE:HD11	2.00	0.43
42:CO:55:ALA:HA	42:CO:80:PHE:CE2	2.53	0.43
46:CS:38:VAL:HG22	46:CS:57:GLY:HA3	2.01	0.43
33:DE:3:LEU:HD12	33:DE:14:VAL:HG11	2.00	0.43
55:DA:526:A:H2'	70:DA:3565:HOH:O	2.19	0.43
1:AA:1358:U:H3	1:AA:1363:A:H62	1.67	0.43
20:AT:24:ARG:HD3	20:AT:24:ARG:N	2.34	0.43
13:BM:11:ASP:HA	13:BM:45:ILE:HD13	1.99	0.43
31:CA:2025:C:H2'	31:CA:2026:U:C6	2.54	0.43
31:CA:2469:A:H4'	41:CN:55:ARG:HD3	2.00	0.43
31:CA:2514:U:H2'	31:CA:2515:C:C6	2.54	0.43
47:DT:72:THR:CG2	47:DT:108:SER:HB3	2.48	0.43
48:DU:28:ASN:OD1	48:DU:91:GLN:HB3	2.19	0.43
52:DY:7:VAL:HG23	52:DY:51:VAL:HG12	2.01	0.43
53:DZ:47:ARG:HD3	70:DZ:102:HOH:O	2.19	0.43
1:BA:12:U:H4'	1:BA:526:C:H4'	1.99	0.42
3:BC:47:LEU:HB3	3:BC:50:ALA:HB3	2.01	0.42
32:DD:150[A]:MEQ:OE1	55:DA:2032:G:H1'	2.19	0.42
41:CN:69:PRO:O	41:CN:93:VAL:O	2.37	0.42
51:DX:21:LEU:HD11	51:DX:41[A]:ARG:HE	1.83	0.42
1:BA:957:U:O2	1:BA:959:A:H8	2.02	0.42
28:CB:14:U:H2'	28:CB:15:A:H2	1.84	0.42
31:CA:184:C:H2'	31:CA:185:G:H8	1.83	0.42
37:CJ:14:ALA:HB3	37:CJ:17:MET:HB2	2.00	0.42
1:AA:1346:A:H61	1:AA:1374:A:H3'	1.84	0.42
11:AK:84:VAL:HG11	11:AK:97:ILE:HG12	2.00	0.42
13:AM:80:LEU:HD22	13:AM:87:ARG:HB3	2.01	0.42
1:BA:429:U:H1'	1:BA:430:A:H5''	2.01	0.42
9:BI:19:VAL:HG11	9:BI:83:ILE:HA	2.01	0.42
31:CA:685:A:H1'	31:CA:688:U:O4	2.20	0.42
31:CA:1182:G:H2'	31:CA:1183:U:O4'	2.19	0.42
31:CA:2261:C:H5''	51:CX:19:LYS:HZ1	1.84	0.42
36:CH:3:VAL:HG12	36:CH:38:PRO:HA	2.01	0.42
39:CL:35:VAL:HG12	39:CL:106:GLU:HG2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:CN:77:PRO:HG2	41:CN:80:VAL:HG21	2.02	0.42
48:DU:11:LEU:HD22	48:DU:32:LEU:HD13	2.01	0.42
55:DA:745:1MG:HN21	55:DA:745:1MG:HM11	1.74	0.42
6:AF:16:GLU:HB3	4:BD:189:SER:HA	2.01	0.42
1:BA:1068:G:N7	1:BA:1094:G:H2'	2.35	0.42
4:BD:48:LEU:HD21	4:BD:56:ARG:HG3	2.01	0.42
13:BM:54:ASP:HA	13:BM:57:ARG:HD2	2.01	0.42
29:CC:35:GLU:HG3	29:CC:64:ILE:HD11	2.01	0.42
31:CA:571:U:H4'	31:CA:573:U:H5	1.84	0.42
31:CA:1250:G:C5'	45:CR:6:ARG:HD3	2.49	0.42
31:CA:2339:C:H2'	31:CA:2340:A:C8	2.55	0.42
33:CE:3:LEU:HD12	33:CE:14:VAL:HG11	2.01	0.42
36:CH:104:THR:HG22	36:CH:109:GLU:HA	1.99	0.42
38:CK:58:ASN:HA	38:CK:126:ALA:O	2.19	0.42
37:DJ:11:LEU:HD22	37:DJ:24:VAL:HG23	2.01	0.42
54:DI:50:VAL:HG11	54:DI:92:ALA:HB2	2.00	0.42
10:AJ:19:ASP:HA	10:AJ:22:THR:HB	2.02	0.42
10:BJ:26:VAL:HG21	10:BJ:39:PRO:HD3	2.02	0.42
31:CA:142:A:H2'	31:CA:143:C:C6	2.54	0.42
40:CM:95:LEU:HD22	40:CM:100:ILE:HG12	2.01	0.42
44:DQ:92:VAL:HG21	44:DQ:97:LEU:HD11	2.02	0.42
46:DS:79:ARG:NH2	55:DA:572:A:H5'	2.34	0.42
55:DA:634:C:H2'	55:DA:635:C:C6	2.55	0.42
55:DA:2327:A:H5''	70:DA:7160:HOH:O	2.19	0.42
55:DA:2328:A:H2'	55:DA:2329:U:C6	2.54	0.42
23:D2:15:ALA:HB2	23:D2:47:VAL:HG21	2.02	0.42
31:CA:580:U:O3'	45:CR:31:VAL:HG13	2.20	0.42
31:CA:976:G:H2'	31:CA:977:G:H8	1.84	0.42
31:CA:1386:C:H2'	31:CA:1387:A:C8	2.55	0.42
34:CF:104:ILE:HG23	34:CF:176:PRO:HD3	2.01	0.42
1:AA:1289:A:H3'	1:AA:1290:G:H8	1.85	0.42
4:AD:48:LEU:HD21	4:AD:56:ARG:HG3	2.02	0.42
26:C5:4:ARG:HB2	31:CA:2466:C:OP1	2.19	0.42
1:BA:76:G:H1	1:BA:93:U:H3	1.68	0.42
1:BA:1508:A:H2'	1:BA:1509:C:O4'	2.20	0.42
30:CD:3:GLY:O	30:CD:4:LEU:HD13	2.20	0.42
31:CA:2060:A:N6	33:CE:69:ARG:NH2	2.67	0.42
31:CA:2328:A:H2'	31:CA:2329:U:C6	2.55	0.42
49:CV:94:ARG:HB3	49:CV:103:ILE:HD12	2.02	0.42
41:DN:16:ARG:HG3	41:DN:18[B]:ARG:NH1	2.34	0.42
54:DI:12:VAL:O	54:DI:16:SER:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:DA:1381:G:H1'	55:DA:1571:A:N1	2.34	0.42
11:AK:31:ILE:HG12	11:AK:46:THR:CG2	2.47	0.42
1:BA:1346:A:H61	1:BA:1374:A:H3'	1.85	0.42
37:CJ:11:LEU:HD22	37:CJ:24:VAL:HG23	2.02	0.42
37:CJ:19:ASN:N	37:CJ:20:PRO:HD2	2.34	0.42
55:DA:476:G:H4'	55:DA:502:A:N1	2.35	0.42
55:DA:644:A:H2'	55:DA:645:C:O4'	2.20	0.42
1:AA:429:U:H1'	1:AA:430:A:H5''	2.01	0.42
1:AA:1250:A:O3'	9:AI:69:GLY:HA2	2.20	0.42
6:AF:47:LEU:HD13	6:AF:51:ILE:HG12	2.01	0.42
16:AP:61:VAL:HG21	16:AP:67:ILE:HD11	2.01	0.42
26:C5:8:LYS:HE3	31:CA:1031:G:H5''	2.02	0.42
1:BA:214:C:H2'	1:BA:215:C:H6	1.85	0.42
5:BE:81:LEU:HB3	5:BE:147:MET:SD	2.60	0.42
31:CA:1077:A:H4'	37:CJ:94:ASN:HB2	2.02	0.42
37:CJ:24:VAL:HG22	37:CJ:28:LEU:HD22	2.02	0.42
37:DJ:19:ASN:N	37:DJ:20:PRO:HD2	2.34	0.42
50:DW:51:GLN:HB2	50:DW:57:TYR:OH	2.19	0.42
55:DA:624:C:O2'	55:DA:657:U:H5''	2.20	0.42
55:DA:2262:U:H4'	55:DA:2328:A:H2	1.85	0.42
55:DA:2514:U:H2'	55:DA:2515:C:C6	2.54	0.42
1:AA:1057:G:O3'	3:AC:197:GLY:HA3	2.20	0.42
1:AA:1238:A:H5'	1:AA:1336:C:H41	1.84	0.42
10:AJ:5:ARG:HG3	10:AJ:77:VAL:HA	2.02	0.42
1:BA:17:U:H2'	1:BA:18:C:C6	2.55	0.42
9:BI:6:TYR:HB2	9:BI:21:ILE:HB	2.02	0.42
31:CA:782:A:H4'	31:CA:783:A:O5'	2.19	0.42
31:CA:2626:C:H2'	31:CA:2627:G:O4'	2.19	0.42
33:DE:131:THR:HG23	33:DE:160:ALA:O	2.19	0.42
45:DR:6:ARG:NH1	55:DA:585:G:N7	2.67	0.42
55:DA:1353:A:O4'	55:DA:1569:A:H2	2.01	0.42
55:DA:2339:C:H2'	55:DA:2340:A:C8	2.55	0.42
55:DA:2585:U:O2'	55:DA:2586:U:H5'	2.20	0.42
1:AA:322:C:H5	1:AA:328:C:C5	2.37	0.41
1:AA:1108:G:H5''	3:AC:176:HIS:ND1	2.35	0.41
4:BD:130:VAL:HG11	4:BD:135:TYR:CG	2.54	0.41
5:BE:126:LYS:HG2	5:BE:128:TYR:CZ	2.55	0.41
13:BM:6:GLY:O	13:BM:7:ILE:HG13	2.20	0.41
29:CC:85:PRO:HG3	31:CA:1567:G:H3'	2.02	0.41
31:CA:538:A:H4'	38:CK:7:LYS:HG2	2.02	0.41
42:DO:28:LEU:HD23	42:DO:48:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DS:21:ARG:HH21	57:DS:202:PG4:H71	1.85	0.41
49:DV:17:LYS:HE3	49:DV:40:ASN:HA	2.02	0.41
55:DA:503:A:H5'	55:DA:505:A:OP1	2.20	0.41
1:AA:77:A:H2'	1:AA:78:A:C8	2.55	0.41
3:AC:7:PRO:HD2	3:AC:184:TYR:CD1	2.55	0.41
11:AK:25:ALA:HA	11:AK:30:THR:HG22	2.02	0.41
1:BA:1308:U:H2'	1:BA:1309:G:H8	1.85	0.41
6:BF:99:ALA:O	6:BF:100:SER:HB3	2.19	0.41
31:CA:340:A:H2'	31:CA:341:C:O4'	2.20	0.41
31:CA:2313:C:H5''	34:CF:88:LYS:HD3	2.02	0.41
31:CA:2728:U:O2'	31:CA:2729:G:H5''	2.20	0.41
70:DD:411:HOH:O	55:DA:1671:U:H4'	2.20	0.41
42:CO:28:LEU:HD23	42:CO:48:VAL:HG21	2.01	0.41
50:CW:77:VAL:HG23	50:CW:89:ILE:HG12	2.02	0.41
1:AA:1151:A:O2'	1:AA:1152:A:H8	2.02	0.41
1:AA:1338:G:H2'	1:AA:1339:A:C8	2.56	0.41
9:AI:19:VAL:HG11	9:AI:83:ILE:HA	2.02	0.41
1:BA:1277:C:HO2'	1:BA:1279:G:H8	1.67	0.41
10:BJ:19:ASP:HA	10:BJ:22:THR:HB	2.02	0.41
31:CA:78:U:H2'	31:CA:79:C:C6	2.56	0.41
31:CA:550:C:H2'	31:CA:551:G:H5''	2.03	0.41
48:CU:45:ALA:O	48:CU:49:LYS:HG2	2.19	0.41
50:CW:51:GLN:HB2	50:CW:57:TYR:OH	2.21	0.41
38:DK:58:ASN:HA	38:DK:126:ALA:O	2.21	0.41
54:DI:94:ARG:HG2	54:DI:127:ALA:HA	2.01	0.41
55:DA:825:A:H5''	59:DA:3223:PUT:H12	2.02	0.41
1:AA:1508:A:H2'	1:AA:1509:C:O4'	2.21	0.41
8:AH:96:MET:HE2	8:AH:130:ALA:HB1	2.01	0.41
31:CA:1101:U:H2'	31:CA:1102:C:H6	1.86	0.41
31:CA:1326:U:H2'	31:CA:1327:A:H8	1.85	0.41
34:CF:40:VAL:HG23	34:CF:86:GLY:HA2	2.02	0.41
34:DF:34:ILE:HG12	34:DF:156:ILE:HG12	2.02	0.41
34:DF:36:LEU:HB2	34:DF:57:LEU:HD21	2.02	0.41
55:DA:825:A:H2'	55:DA:826:U:O4'	2.21	0.41
55:DA:1515:A:H2'	55:DA:1516:G:O4'	2.20	0.41
55:DA:2255:G:H21	69:DA:3220:TRS:H12	1.85	0.41
55:DA:2324:U:H3'	55:DA:2325:G:C5'	2.51	0.41
2:AB:187:VAL:HG13	2:AB:191:SER:HB2	2.03	0.41
14:AN:46:LEU:HA	14:AN:49:GLN:HE21	1.85	0.41
16:AP:57:ILE:O	16:AP:61:VAL:HG23	2.20	0.41
23:C2:15:ALA:HB2	23:C2:47:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:1238:A:H5'	1:BA:1336:C:H41	1.85	0.41
13:BM:80:LEU:HD22	13:BM:87:ARG:HB3	2.02	0.41
31:CA:2579:C:H2'	31:CA:2580:PSU:O4'	2.20	0.41
5:AE:15:LEU:HA	5:AE:37:THR:HG22	2.03	0.41
8:AH:96:MET:CE	8:AH:130:ALA:HB1	2.49	0.41
1:BA:715:A:H2'	1:BA:716:A:C8	2.54	0.41
31:CA:477:A:H2'	31:CA:478:A:C8	2.55	0.41
31:CA:784:G:H3'	70:CA:3540:HOH:O	2.20	0.41
31:CA:1141:U:H4'	31:CA:1142:A:O4'	2.20	0.41
31:CA:1363:C:H2'	31:CA:1364:G:H8	1.85	0.41
36:CH:27:ARG:HA	36:CH:27:ARG:HD3	1.92	0.41
33:DE:45:ALA:HB3	55:DA:38:A:H5'	2.02	0.41
52:DY:29:PHE:HB3	55:DA:396:G:H1'	2.02	0.41
54:DI:130:PRO:HG2	54:DI:134:GLU:HG2	2.02	0.41
55:DA:68:G:H2'	55:DA:69:C:O4'	2.19	0.41
55:DA:572:A:H5''	55:DA:573:U:OP2	2.21	0.41
55:DA:1386:C:H2'	55:DA:1387:A:C8	2.55	0.41
55:DA:2117:A:H61	55:DA:2171:A:H61	1.69	0.41
1:BA:216:U:H4'	1:BA:464:U:H4'	2.02	0.41
1:BA:310:G:H5''	16:BP:31:ARG:HB2	2.02	0.41
1:BA:1250:A:O3'	9:BI:69:GLY:HA2	2.21	0.41
9:BI:99:ARG:HG2	9:BI:104:VAL:HG21	2.01	0.41
11:BK:45:ALA:HB3	11:BK:70:CYS:HB2	2.03	0.41
19:BS:30:PRO:HB2	19:BS:50:ALA:HB2	2.03	0.41
31:CA:1294:U:H5''	31:CA:1294:U:H6	1.85	0.41
31:CA:1311:G:N2	31:CA:1603:A:H62	2.14	0.41
31:CA:1638:C:H5''	31:CA:2710:C:O2'	2.21	0.41
31:CA:2641:G:H5''	38:CK:78:THR:HB	2.02	0.41
34:DF:132:VAL:HG22	34:DF:152:LEU:HG	2.03	0.41
35:DG:52:PHE:CD1	35:DG:52:PHE:N	2.89	0.41
36:DH:126:GLY:H	36:DH:146:VAL:HB	1.85	0.41
49:DV:94:ARG:HB3	49:DV:103:ILE:HD12	2.01	0.41
55:DA:1804:C:H6	55:DA:1804:C:O5'	2.03	0.41
1:AA:1052:G:H22	1:AA:1206:G:H1	1.69	0.41
1:BA:815:A:H4'	1:BA:817:C:C4	2.56	0.41
1:BA:1289:A:H3'	1:BA:1290:G:H8	1.85	0.41
1:BA:1391:U:H2'	1:BA:1392:G:C8	2.56	0.41
23:D2:11:LEU:HD21	23:D2:34:LEU:HD23	2.03	0.41
31:CA:184:C:H2'	31:CA:185:G:C8	2.55	0.41
36:CH:126:GLY:H	36:CH:146:VAL:HB	1.86	0.41
33:DE:49:ARG:O	33:DE:74:LYS:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:17:U:H2'	1:AA:18:C:C6	2.56	0.41
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.56	0.41
11:AK:34:ILE:HG12	11:AK:70:CYS:SG	2.61	0.41
1:BA:23:C:H5	1:BA:561:U:O4	2.04	0.41
1:BA:129:A:H1'	1:BA:130:A:C8	2.56	0.41
6:BF:91:ARG:HD2	18:BR:61:ARG:HH22	1.85	0.41
11:BK:31:ILE:HB	11:BK:46:THR:HG22	2.03	0.41
16:BP:61:VAL:HG21	16:BP:67:ILE:HD11	2.03	0.41
31:CA:685:A:H5''	31:CA:774:G:O6	2.21	0.41
31:CA:1808:A:N1	52:CY:28:ARG:HD2	2.35	0.41
31:CA:1957:C:H5'	31:CA:1984:G:O2'	2.21	0.41
31:CA:2114:A:N6	31:CA:2119:A:H62	2.18	0.41
31:CA:2304:G:H5'	34:CF:121:SER:HB2	2.02	0.41
34:DF:104:ILE:HG23	34:DF:176:PRO:HD3	2.02	0.41
36:DH:3:VAL:HG12	36:DH:38:PRO:HA	2.03	0.41
42:DO:8:ARG:HB3	42:DO:10:LEU:HG	2.03	0.41
42:DO:53:THR:HA	42:DO:56:LYS:HD2	2.03	0.41
55:DA:839:U:H2'	55:DA:840:C:C6	2.56	0.41
55:DA:1321:A:C2	64:DA:3217:PGE:H12	2.56	0.41
55:DA:1604:C:H5'	70:DA:3811:HOH:O	2.21	0.41
55:DA:2345:G:N3	55:DA:2381:A:H2'	2.36	0.41
1:AA:686:U:HO2'	1:AA:687:A:H8	1.68	0.41
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.55	0.41
6:AF:70:VAL:HA	6:AF:73:GLU:HG2	2.04	0.41
1:BA:502:A:OP1	12:BL:115:SER:HB2	2.21	0.41
1:BA:1060:U:H4'	10:BJ:53:ILE:HG23	2.03	0.41
4:BD:10:LYS:HG2	4:BD:38:PRO:HB3	2.03	0.41
11:BK:25:ALA:HA	11:BK:30:THR:HG22	2.03	0.41
31:CA:574:A:C6	31:CA:2033:A:H5'	2.55	0.41
31:CA:666:A:H4'	40:CM:48:ARG:HD3	2.02	0.41
31:CA:1203:U:H1'	40:CM:4:ASN:HB3	2.03	0.41
31:CA:1494:A:H2'	31:CA:1495:A:C8	2.55	0.41
31:CA:2038:G:H2'	31:CA:2039:U:O4'	2.21	0.41
32:DD:152:PRO:HG3	32:DD:156:PHE:CZ	2.56	0.41
55:DA:78:U:H2'	55:DA:79:C:C6	2.56	0.41
55:DA:1802:A:N1	55:DA:1822:C:H1'	2.35	0.41
55:DA:2422:C:H1'	70:DA:3441:HOH:O	2.20	0.41
60:AA:1680:T1C:O1C	60:AA:1680:T1C:H422	2.21	0.40
1:BA:302:G:N3	1:BA:556:C:H4'	2.36	0.40
1:BA:1069:C:H4'	1:BA:1192:C:O2	2.20	0.40
29:CC:171:TYR:CD1	29:CC:185:GLU:HA	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:CA:494:G:H4'	47:CT:6:LYS:HB2	2.02	0.40
31:CA:2680:U:H2'	31:CA:2681:C:C6	2.56	0.40
34:CF:8:TYR:HA	34:CF:12:VAL:HB	2.03	0.40
36:CH:94:ILE:HB	36:CH:122:LEU:HB2	2.03	0.40
34:DF:121:SER:HB2	55:DA:2304:G:H5'	2.02	0.40
54:DI:70:GLU:HG2	54:DI:73:LYS:HE3	2.02	0.40
55:DA:281:C:H2'	55:DA:282:A:C8	2.56	0.40
55:DA:455:C:N3	55:DA:472:A:H2'	2.36	0.40
55:DA:837:C:H5	70:DA:6009:HOH:O	2.04	0.40
55:DA:2544:G:H2'	55:DA:2545:G:O4'	2.22	0.40
1:AA:129:A:H1'	1:AA:130:A:C8	2.57	0.40
1:AA:310:G:H5''	16:AP:31:ARG:HB2	2.03	0.40
1:AA:340:U:H2'	1:AA:341:C:C6	2.57	0.40
1:AA:502:A:H2'	1:AA:503:C:O4'	2.22	0.40
9:AI:6:TYR:HB2	9:AI:21:ILE:HB	2.02	0.40
4:BD:102:VAL:HG13	4:BD:107:PHE:HB2	2.03	0.40
15:BO:64:ARG:HH22	15:BO:88:ARG:NH2	2.19	0.40
31:CA:1469:A:H2'	31:CA:1470:A:C8	2.57	0.40
54:DI:28:ALA:HA	54:DI:109:LYS:H	1.86	0.40
54:DI:29:ASP:HB3	54:DI:106:PHE:HB2	2.03	0.40
54:DI:56:ARG:HA	55:DA:1107:G:OP1	2.22	0.40
55:DA:481:G:C4	55:DA:507:A:C2	3.09	0.40
1:AA:1322:C:P	19:AS:78:ARG:HH22	2.44	0.40
23:C2:11:LEU:HD21	23:C2:34:LEU:HD23	2.03	0.40
1:BA:579:A:H2'	1:BA:580:C:C6	2.56	0.40
1:BA:1057:G:O3'	3:BC:197:GLY:HA3	2.21	0.40
17:BQ:46:VAL:HG11	17:BQ:61:ILE:CG2	2.52	0.40
31:CA:352:A:H8	31:CA:352:A:H5''	1.87	0.40
31:CA:1914:C:H2'	31:CA:1915:3TD:H6	2.02	0.40
34:CF:34:ILE:HG12	34:CF:156:ILE:HG12	2.03	0.40
34:DF:40:VAL:HG23	34:DF:86:GLY:HA2	2.03	0.40
55:DA:612:G:H4'	55:DA:613:A:C2	2.56	0.40
1:AA:620:C:H2'	1:AA:621:A:O4'	2.21	0.40
10:AJ:65:TYR:HB2	14:AN:96:LEU:HD11	2.04	0.40
1:BA:224:U:H2'	1:BA:225:C:C6	2.57	0.40
1:BA:368:U:O4	36:DH:83:LYS:HB2	2.21	0.40
64:D1:102:PGE:H4	70:DT:319:HOH:O	2.21	0.40
29:CC:76:ALA:HB2	29:CC:96:TYR:CD1	2.56	0.40
29:CC:105:LEU:HD12	29:CC:105:LEU:N	2.36	0.40
31:CA:2353:G:H2'	31:CA:2354:C:O4'	2.20	0.40
34:DF:8:TYR:HA	34:DF:12:VAL:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DF:36:LEU:HD22	34:DF:154:ILE:HG12	2.02	0.40
39:DL:113:MET:O	39:DL:116:ILE:HG13	2.22	0.40
55:DA:1441:G:H2'	55:DA:1442:U:C6	2.55	0.40
55:DA:1532:A:H8	55:DA:1532:A:H5''	1.85	0.40
3:AC:5:VAL:HG21	3:AC:10:ILE:HD13	2.04	0.40
4:AD:10:LYS:HG2	4:AD:38:PRO:HB3	2.03	0.40
1:BA:33:A:H2'	1:BA:34:C:C6	2.56	0.40
1:BA:202:G:H21	1:BA:466:A:H61	1.68	0.40
1:BA:591:U:H2'	1:BA:592:G:C8	2.57	0.40
1:BA:1338:G:H2'	1:BA:1339:A:C8	2.56	0.40
18:BR:28:THR:HG22	18:BR:32:TYR:HE1	1.87	0.40
28:CB:111:U:H2'	28:CB:112:G:H8	1.87	0.40
31:CA:569:U:H5''	31:CA:821:A:C2	2.56	0.40
31:CA:1510:G:H2'	31:CA:1511:G:O4'	2.22	0.40
39:CL:113:MET:O	39:CL:116:ILE:HG13	2.21	0.40
47:CT:69:LEU:HG	47:CT:107:VAL:CG2	2.50	0.40
46:DS:24:LYS:HD2	64:DS:201:PGE:H22	2.03	0.40
55:DA:352:A:H8	55:DA:352:A:H5''	1.86	0.40
55:DA:2038:G:H2'	55:DA:2039:U:O4'	2.22	0.40

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%)	8	34
2	BB	222/224 (99%)	207 (93%)	11 (5%)	4 (2%)	8	34
3	AC	204/206 (99%)	194 (95%)	9 (4%)	1 (0%)	29	64
3	BC	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	15	49
4	AD	203/205 (99%)	197 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BD	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
5	AE	153/155 (99%)	144 (94%)	7 (5%)	2 (1%)	12	42
5	BE	148/155 (96%)	131 (88%)	14 (10%)	3 (2%)	7	31
6	AF	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
6	BF	98/106 (92%)	91 (93%)	5 (5%)	2 (2%)	7	31
7	AG	149/151 (99%)	135 (91%)	13 (9%)	1 (1%)	22	57
7	BG	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
8	AH	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19	54
8	BH	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	9	37
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%)	15	49
10	BJ	96/99 (97%)	77 (80%)	13 (14%)	6 (6%)	1	8
11	AK	115/117 (98%)	105 (91%)	9 (8%)	1 (1%)	17	52
11	BK	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	17	52
12	AL	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
12	BL	120/123 (98%)	111 (92%)	8 (7%)	1 (1%)	19	54
13	AM	112/114 (98%)	102 (91%)	7 (6%)	3 (3%)	5	25
13	BM	112/114 (98%)	101 (90%)	6 (5%)	5 (4%)	2	15
14	AN	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	7	31
14	BN	98/100 (98%)	87 (89%)	10 (10%)	1 (1%)	15	49
15	AO	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
15	BO	86/88 (98%)	83 (96%)	2 (2%)	1 (1%)	13	44
16	AP	80/82 (98%)	73 (91%)	5 (6%)	2 (2%)	5	27
16	BP	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	5	27
17	AQ	78/80 (98%)	71 (91%)	6 (8%)	1 (1%)	12	42
17	BQ	78/80 (98%)	67 (86%)	7 (9%)	4 (5%)	2	13
18	AR	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
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%)	12	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AT	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
20	BT	83/86 (96%)	79 (95%)	3 (4%)	1 (1%)	13	44
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%)	2	11
22	D1	54/56 (96%)	54 (100%)	0	0	100	100
23	C2	48/51 (94%)	43 (90%)	3 (6%)	2 (4%)	3	16
23	D2	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
24	C3	44/46 (96%)	42 (96%)	1 (2%)	1 (2%)	6	28
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%)	5	25
26	D5	36/38 (95%)	36 (100%)	0	0	100	100
27	C0	56/58 (97%)	51 (91%)	3 (5%)	2 (4%)	3	20
27	D0	57/58 (98%)	53 (93%)	4 (7%)	0	100	100
29	CC	269/272 (99%)	249 (93%)	15 (6%)	5 (2%)	8	33
29	DC	269/272 (99%)	251 (93%)	16 (6%)	2 (1%)	22	57
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%)	10	39
33	DE	199/201 (99%)	191 (96%)	7 (4%)	1 (0%)	29	64
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%)	4	24
35	DG	174/176 (99%)	165 (95%)	7 (4%)	2 (1%)	14	46
36	CH	147/149 (99%)	130 (88%)	11 (8%)	6 (4%)	3	16
36	DH	147/149 (99%)	133 (90%)	11 (8%)	3 (2%)	7	31
37	CJ	132/135 (98%)	125 (95%)	3 (2%)	4 (3%)	4	23
37	DJ	132/135 (98%)	125 (95%)	3 (2%)	4 (3%)	4	23
38	CK	140/142 (99%)	135 (96%)	2 (1%)	3 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	DK	140/142 (99%)	136 (97%)	2 (1%)	2 (1%)	11	40
39	CL	120/123 (98%)	114 (95%)	4 (3%)	2 (2%)	9	36
39	DL	121/123 (98%)	116 (96%)	4 (3%)	1 (1%)	19	54
40	CM	142/144 (99%)	132 (93%)	7 (5%)	3 (2%)	7	30
40	DM	142/144 (99%)	136 (96%)	5 (4%)	1 (1%)	22	57
41	CN	133/136 (98%)	125 (94%)	7 (5%)	1 (1%)	19	54
41	DN	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
42	CO	118/125 (94%)	110 (93%)	6 (5%)	2 (2%)	9	36
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%)	17	52
44	DQ	112/114 (98%)	107 (96%)	4 (4%)	1 (1%)	17	52
45	CR	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	17	52
45	DR	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	17	52
46	CS	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	4	23
46	DS	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	15	49
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%)	3	17
49	DV	100/103 (97%)	96 (96%)	2 (2%)	2 (2%)	7	31
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
52	DY	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
53	CZ	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	9	36
53	DZ	60/62 (97%)	59 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	DI	133/135 (98%)	112 (84%)	15 (11%)	6 (4%)	2	15
All	All	11407/11651 (98%)	10682 (94%)	590 (5%)	135 (1%)	13	44

All (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
23	C2	5	ILE
2	BB	126	PHE
3	BC	156	ARG
6	BF	98	GLU
10	BJ	38	GLY
10	BJ	91	ASP
13	BM	7	ILE
17	BQ	82	ALA
20	BT	5	LYS
29	CC	158	ALA
33	CE	83	VAL
35	CG	119	ALA
35	CG	175	LYS
35	CG	176	LYS
36	CH	10	ALA
37	CJ	19	ASN
38	CK	81	ILE
39	CL	35	VAL
40	CM	29	LYS
41	CN	70	ASP
49	CV	7	ARG
36	DH	11	ASN
37	DJ	19	ASN
49	DV	52	LEU
54	DI	91	ALA
5	AE	109	GLY
7	AG	56	LYS
10	AJ	57	VAL
13	AM	105	ASN
14	AN	38	ASP
27	C0	14	ILE

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Mol	Chain	Res	Type
3	BC	61	ALA
10	BJ	57	VAL
13	BM	5	ALA
13	BM	105	ASN
13	BM	114	LYS
14	BN	38	ASP
16	BP	80	LYS
17	BQ	70	THR
19	BS	6	LYS
29	CC	233	GLY
29	DC	233	GLY
33	CE	6	LYS
33	CE	82	GLY
35	CG	46	ALA
37	CJ	25	GLY
39	CL	108	ARG
40	CM	69	ARG
49	CV	16	GLY
49	CV	17	LYS
33	DE	6	LYS
35	DG	46	ALA
37	DJ	25	GLY
44	DQ	105	GLY
2	AB	95	ARG
2	AB	125	THR
11	AK	89	PRO
22	C1	26	THR
22	C1	27	SER
24	C3	45	SER
2	BB	95	ARG
2	BB	125	THR
5	BE	103	THR
10	BJ	95	GLY
11	BK	89	PRO
12	BL	44	LYS
15	BO	88	ARG
29	CC	197	ASN
29	CC	253	LYS
29	DC	253	LYS
36	CH	11	ASN
36	CH	122	LEU
38	CK	95	ARG

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Mol	Chain	Res	Type
40	CM	36	LYS
42	CO	118	ARG
42	CO	119	SER
49	CV	89	ASP
36	DH	122	LEU
38	DK	95	ARG
40	DM	36	LYS
49	DV	89	ASP
54	DI	130	PRO
2	AB	127	ASP
8	AH	66	PHE
16	AP	24	SER
23	C2	51	GLU
26	C5	21	GLY
27	C0	4	THR
2	BB	127	ASP
5	BE	24	THR
5	BE	157	ARG
8	BH	66	PHE
8	BH	67	GLN
10	BJ	36	VAL
13	BM	4	ILE
16	BP	24	SER
36	CH	9	VAL
38	CK	25	LEU
46	CS	43	ASN
46	CS	48	LYS
38	DK	25	LEU
46	DS	44	GLY
54	DI	70	GLU
54	DI	88	HIS
5	AE	162	GLU
13	AM	7	ILE
16	AP	45	GLU
17	BQ	17	MET
17	BQ	18	GLU
29	CC	108	LYS
35	CG	45	HIS
37	CJ	23	PRO
35	DG	45	HIS
37	DJ	23	PRO
39	DL	108	ARG

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Mol	Chain	Res	Type
54	DI	108	VAL
14	AN	81	ARG
6	BF	92	THR
10	BJ	93	ALA
36	CH	8	LYS
37	CJ	32	GLY
44	CQ	105	GLY
46	CS	53	PHE
53	CZ	62	GLY
37	DJ	32	GLY
45	DR	7	GLY
54	DI	109	LYS
36	DH	118	PRO
36	CH	118	PRO
45	CR	7	GLY

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%)	172 (92%)	14 (8%)	13	42
2	BB	186/186 (100%)	171 (92%)	15 (8%)	11	39
3	AC	170/170 (100%)	159 (94%)	11 (6%)	17	47
3	BC	170/170 (100%)	157 (92%)	13 (8%)	13	41
4	AD	172/172 (100%)	165 (96%)	7 (4%)	30	64
4	BD	172/172 (100%)	165 (96%)	7 (4%)	30	64
5	AE	118/118 (100%)	105 (89%)	13 (11%)	6	25
5	BE	113/118 (96%)	92 (81%)	21 (19%)	1	7
6	AF	92/92 (100%)	84 (91%)	8 (9%)	10	36
6	BF	87/92 (95%)	76 (87%)	11 (13%)	4	18
7	AG	124/124 (100%)	112 (90%)	12 (10%)	8	30
7	BG	124/124 (100%)	109 (88%)	15 (12%)	5	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AH	104/104 (100%)	90 (86%)	14 (14%)	4	16
8	BH	104/104 (100%)	91 (88%)	13 (12%)	4	18
9	AI	105/105 (100%)	100 (95%)	5 (5%)	25	58
9	BI	105/105 (100%)	100 (95%)	5 (5%)	25	58
10	AJ	87/87 (100%)	80 (92%)	7 (8%)	12	40
10	BJ	86/87 (99%)	76 (88%)	10 (12%)	5	22
11	AK	90/90 (100%)	90 (100%)	0	100	100
11	BK	90/90 (100%)	84 (93%)	6 (7%)	16	46
12	AL	102/102 (100%)	96 (94%)	6 (6%)	19	50
12	BL	102/102 (100%)	95 (93%)	7 (7%)	15	45
13	AM	92/92 (100%)	83 (90%)	9 (10%)	8	29
13	BM	92/92 (100%)	85 (92%)	7 (8%)	13	41
14	AN	83/83 (100%)	82 (99%)	1 (1%)	71	88
14	BN	83/83 (100%)	81 (98%)	2 (2%)	49	76
15	AO	76/76 (100%)	71 (93%)	5 (7%)	16	47
15	BO	76/76 (100%)	68 (90%)	8 (10%)	7	26
16	AP	65/65 (100%)	64 (98%)	1 (2%)	65	85
16	BP	65/65 (100%)	60 (92%)	5 (8%)	13	41
17	AQ	74/74 (100%)	65 (88%)	9 (12%)	5	19
17	BQ	74/74 (100%)	63 (85%)	11 (15%)	3	13
18	AR	48/48 (100%)	45 (94%)	3 (6%)	18	48
18	BR	48/48 (100%)	47 (98%)	1 (2%)	53	79
19	AS	70/70 (100%)	61 (87%)	9 (13%)	4	18
19	BS	70/70 (100%)	63 (90%)	7 (10%)	7	28
20	AT	65/65 (100%)	59 (91%)	6 (9%)	9	33
20	BT	65/65 (100%)	56 (86%)	9 (14%)	3	16
21	AU	48/48 (100%)	45 (94%)	3 (6%)	18	48
21	BU	48/48 (100%)	46 (96%)	2 (4%)	30	62
22	C1	47/47 (100%)	45 (96%)	2 (4%)	29	62
22	D1	47/47 (100%)	46 (98%)	1 (2%)	53	79
23	C2	45/46 (98%)	42 (93%)	3 (7%)	16	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	D2	45/46 (98%)	40 (89%)	5 (11%)	6	24
24	C3	38/38 (100%)	37 (97%)	1 (3%)	46	74
24	D3	38/38 (100%)	37 (97%)	1 (3%)	46	74
25	C4	51/51 (100%)	48 (94%)	3 (6%)	19	50
25	D4	51/51 (100%)	48 (94%)	3 (6%)	19	50
26	C5	34/34 (100%)	32 (94%)	2 (6%)	19	50
26	D5	34/34 (100%)	34 (100%)	0	100	100
27	C0	48/48 (100%)	40 (83%)	8 (17%)	2	9
27	D0	49/48 (102%)	45 (92%)	4 (8%)	11	38
29	CC	216/217 (100%)	203 (94%)	13 (6%)	19	49
29	DC	216/217 (100%)	208 (96%)	8 (4%)	34	66
30	CD	164/164 (100%)	156 (95%)	8 (5%)	25	57
32	DD	163/163 (100%)	157 (96%)	6 (4%)	34	66
33	CE	165/165 (100%)	150 (91%)	15 (9%)	9	33
33	DE	165/165 (100%)	160 (97%)	5 (3%)	41	71
34	CF	148/149 (99%)	133 (90%)	15 (10%)	7	28
34	DF	148/149 (99%)	137 (93%)	11 (7%)	13	42
35	CG	137/137 (100%)	132 (96%)	5 (4%)	35	67
35	DG	137/137 (100%)	133 (97%)	4 (3%)	42	72
36	CH	114/114 (100%)	101 (89%)	13 (11%)	5	23
36	DH	114/114 (100%)	104 (91%)	10 (9%)	10	36
37	CJ	104/105 (99%)	99 (95%)	5 (5%)	25	58
37	DJ	104/105 (99%)	99 (95%)	5 (5%)	25	58
38	CK	116/116 (100%)	112 (97%)	4 (3%)	37	69
38	DK	116/116 (100%)	114 (98%)	2 (2%)	60	83
39	CL	103/104 (99%)	95 (92%)	8 (8%)	12	40
39	DL	104/104 (100%)	97 (93%)	7 (7%)	16	46
40	CM	103/103 (100%)	95 (92%)	8 (8%)	12	40
40	DM	103/103 (100%)	98 (95%)	5 (5%)	25	57
41	CN	108/108 (100%)	103 (95%)	5 (5%)	27	59
41	DN	109/108 (101%)	107 (98%)	2 (2%)	59	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	CO	100/102 (98%)	92 (92%)	8 (8%)	12	40
42	DO	102/102 (100%)	98 (96%)	4 (4%)	32	65
43	CP	86/87 (99%)	80 (93%)	6 (7%)	15	45
43	DP	87/87 (100%)	84 (97%)	3 (3%)	37	69
44	CQ	99/99 (100%)	92 (93%)	7 (7%)	14	44
44	DQ	99/99 (100%)	94 (95%)	5 (5%)	24	56
45	CR	89/89 (100%)	84 (94%)	5 (6%)	21	52
45	DR	89/89 (100%)	86 (97%)	3 (3%)	37	69
46	CS	84/84 (100%)	78 (93%)	6 (7%)	14	44
46	DS	84/84 (100%)	83 (99%)	1 (1%)	71	88
47	CT	93/93 (100%)	90 (97%)	3 (3%)	39	69
47	DT	93/93 (100%)	90 (97%)	3 (3%)	39	69
48	CU	80/80 (100%)	71 (89%)	9 (11%)	6	23
48	DU	80/80 (100%)	78 (98%)	2 (2%)	47	75
49	CV	83/84 (99%)	77 (93%)	6 (7%)	14	44
49	DV	83/84 (99%)	79 (95%)	4 (5%)	25	58
50	CW	78/78 (100%)	74 (95%)	4 (5%)	24	56
50	DW	78/78 (100%)	75 (96%)	3 (4%)	33	66
51	CX	56/62 (90%)	54 (96%)	2 (4%)	35	67
51	DX	58/62 (94%)	54 (93%)	4 (7%)	15	45
52	CY	67/67 (100%)	63 (94%)	4 (6%)	19	49
52	DY	67/67 (100%)	65 (97%)	2 (3%)	41	71
53	CZ	54/54 (100%)	52 (96%)	2 (4%)	34	66
53	DZ	54/54 (100%)	54 (100%)	0	100	100
54	DI	103/103 (100%)	97 (94%)	6 (6%)	20	51
All	All	9461/9494 (100%)	8844 (94%)	617 (6%)	17	47

All (617) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	23	TRP
2	AB	73	LYS
2	AB	93	ASN

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Mol	Chain	Res	Type
2	AB	105	LYS
2	AB	108	ARG
2	AB	125	THR
2	AB	129	LEU
2	AB	130	THR
2	AB	135	LEU
2	AB	137	ARG
2	AB	147	SER
2	AB	161	LEU
2	AB	205	ASP
2	AB	212	LEU
3	AC	3	GLN
3	AC	21	THR
3	AC	33	LEU
3	AC	46	GLU
3	AC	75	ILE
3	AC	107	ARG
3	AC	168	TYR
3	AC	178	LEU
3	AC	185	ASN
3	AC	186	THR
3	AC	207	ILE
4	AD	17	THR
4	AD	22	LYS
4	AD	26	ARG
4	AD	28	ILE
4	AD	143	VAL
4	AD	151	LYS
4	AD	194	ASP
5	AE	11	LEU
5	AE	14	LYS
5	AE	32	SER
5	AE	46	VAL
5	AE	76	LEU
5	AE	78	ASN
5	AE	82	GLN
5	AE	94	VAL
5	AE	101	GLU
5	AE	123	VAL
5	AE	126	LYS
5	AE	137	VAL
5	AE	149	SER

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Mol	Chain	Res	Type
6	AF	36	ILE
6	AF	39	LEU
6	AF	68	GLN
6	AF	69	GLU
6	AF	71	ILE
6	AF	74	LEU
6	AF	89	VAL
6	AF	93	LYS
7	AG	18	PHE
7	AG	22	LEU
7	AG	23	LEU
7	AG	30	LEU
7	AG	36	LYS
7	AG	59	LEU
7	AG	63	GLU
7	AG	92	ARG
7	AG	120	LEU
7	AG	131	LYS
7	AG	133	THR
7	AG	142	HIS
8	AH	3	MET
8	AH	31	LYS
8	AH	38	ASN
8	AH	47	GLU
8	AH	51	VAL
8	AH	52	GLU
8	AH	54	ASP
8	AH	60	GLU
8	AH	63	LEU
8	AH	76	GLN
8	AH	90	ASP
8	AH	96	MET
8	AH	107	SER
8	AH	117	ARG
9	AI	11	ARG
9	AI	61	LEU
9	AI	63	LEU
9	AI	66	THR
9	AI	99	ARG
10	AJ	6	ILE
10	AJ	62	ARG
10	AJ	63	ASP

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Mol	Chain	Res	Type
10	AJ	69	THR
10	AJ	88	MET
10	AJ	89	ARG
10	AJ	90	LEU
12	AL	24	LEU
12	AL	74	LEU
12	AL	82	ILE
12	AL	88	LYS
12	AL	110	ARG
12	AL	121	ARG
13	AM	3	ARG
13	AM	7	ILE
13	AM	13	LYS
13	AM	27	LYS
13	AM	48	LEU
13	AM	58	ASP
13	AM	63	PHE
13	AM	71	ARG
13	AM	101	ARG
14	AN	80	SER
15	AO	24	SER
15	AO	40	GLN
15	AO	70	LEU
15	AO	84	ARG
15	AO	89	ARG
16	AP	48	GLU
17	AQ	5	ILE
17	AQ	16	LYS
17	AQ	27	ARG
17	AQ	33	ILE
17	AQ	38	ILE
17	AQ	40	ARG
17	AQ	51	ASN
17	AQ	75	LEU
17	AQ	83	VAL
18	AR	34	THR
18	AR	47	THR
18	AR	66	SER
19	AS	5	LEU
19	AS	7	LYS
19	AS	11	ILE
19	AS	13	LEU

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Mol	Chain	Res	Type
19	AS	27	ASP
19	AS	33	THR
19	AS	37	ARG
19	AS	56	GLN
19	AS	63	THR
20	AT	24	ARG
20	AT	27	MET
20	AT	44	LYS
20	AT	48	GLN
20	AT	66	LEU
20	AT	85	LYS
21	AU	13	ASP
21	AU	16	LEU
21	AU	56	HIS
22	C1	10	ARG
22	C1	40	ARG
23	C2	8	LYS
23	C2	46	HIS
23	C2	47	VAL
24	C3	1	MET
25	C4	31	HIS
25	C4	47	LYS
25	C4	52	LYS
26	C5	20	ASP
26	C5	26	ILE
27	C0	3	LYS
27	C0	4	THR
27	C0	5	ILE
27	C0	10	THR
27	C0	36	VAL
27	C0	39	GLU
27	C0	45	ARG
27	C0	59	GLU
2	BB	23	TRP
2	BB	73	LYS
2	BB	93	ASN
2	BB	105	LYS
2	BB	108	ARG
2	BB	125	THR
2	BB	129	LEU
2	BB	130	THR
2	BB	135	LEU

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Mol	Chain	Res	Type
2	BB	137	ARG
2	BB	147	SER
2	BB	161	LEU
2	BB	201	PRO
2	BB	205	ASP
2	BB	212	LEU
3	BC	3	GLN
3	BC	21	THR
3	BC	33	LEU
3	BC	37	PHE
3	BC	38	LYS
3	BC	46	GLU
3	BC	107	ARG
3	BC	152	GLU
3	BC	168	TYR
3	BC	185	ASN
3	BC	186	THR
3	BC	193	TYR
3	BC	207	ILE
4	BD	17	THR
4	BD	22	LYS
4	BD	28	ILE
4	BD	47	ARG
4	BD	143	VAL
4	BD	194	ASP
4	BD	206	LYS
5	BE	11	LEU
5	BE	14	LYS
5	BE	24	THR
5	BE	32	SER
5	BE	46	VAL
5	BE	76	LEU
5	BE	81	LEU
5	BE	82	GLN
5	BE	88	VAL
5	BE	94	VAL
5	BE	101	GLU
5	BE	103	THR
5	BE	106	ILE
5	BE	114	VAL
5	BE	115	LEU
5	BE	123	VAL

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Mol	Chain	Res	Type
5	BE	126	LYS
5	BE	137	VAL
5	BE	149	SER
5	BE	151	GLU
5	BE	159	LYS
6	BF	14	GLN
6	BF	16	GLU
6	BF	36	ILE
6	BF	39	LEU
6	BF	53	LYS
6	BF	68	GLN
6	BF	69	GLU
6	BF	71	ILE
6	BF	74	LEU
6	BF	89	VAL
6	BF	93	LYS
7	BG	4	ARG
7	BG	5	ARG
7	BG	10	ARG
7	BG	23	LEU
7	BG	30	LEU
7	BG	36	LYS
7	BG	48	GLU
7	BG	50	LEU
7	BG	59	LEU
7	BG	63	GLU
7	BG	92	ARG
7	BG	120	LEU
7	BG	131	LYS
7	BG	133	THR
7	BG	142	HIS
8	BH	3	MET
8	BH	38	ASN
8	BH	47	GLU
8	BH	52	GLU
8	BH	60	GLU
8	BH	76	GLN
8	BH	77	ARG
8	BH	80	ARG
8	BH	83	LEU
8	BH	90	ASP
8	BH	96	MET

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Mol	Chain	Res	Type
8	BH	107	SER
8	BH	117	ARG
9	BI	11	ARG
9	BI	61	LEU
9	BI	63	LEU
9	BI	66	THR
9	BI	99	ARG
10	BJ	5	ARG
10	BJ	6	ILE
10	BJ	59	LYS
10	BJ	62	ARG
10	BJ	63	ASP
10	BJ	69	THR
10	BJ	78	GLU
10	BJ	88	MET
10	BJ	89	ARG
10	BJ	90	LEU
11	BK	18	ASP
11	BK	22	HIS
11	BK	31	ILE
11	BK	38	GLN
11	BK	72	ASP
11	BK	118	HIS
12	BL	24	LEU
12	BL	44	LYS
12	BL	58	THR
12	BL	74	LEU
12	BL	88	LYS
12	BL	110	ARG
12	BL	121	ARG
13	BM	11	ASP
13	BM	13	LYS
13	BM	16	VAL
13	BM	27	LYS
13	BM	48	LEU
13	BM	54	ASP
13	BM	101	ARG
14	BN	26	GLU
14	BN	80	SER
15	BO	17	ARG
15	BO	24	SER
15	BO	40	GLN

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Mol	Chain	Res	Type
15	BO	64	ARG
15	BO	70	LEU
15	BO	84	ARG
15	BO	87	LEU
15	BO	88	ARG
16	BP	20	VAL
16	BP	36	VAL
16	BP	46	LYS
16	BP	48	GLU
16	BP	76	LYS
17	BQ	17	MET
17	BQ	21	ILE
17	BQ	26	GLU
17	BQ	27	ARG
17	BQ	28	PHE
17	BQ	33	ILE
17	BQ	38	ILE
17	BQ	40	ARG
17	BQ	51	ASN
17	BQ	67	LEU
17	BQ	75	LEU
18	BR	47	THR
19	BS	6	LYS
19	BS	7	LYS
19	BS	11	ILE
19	BS	13	LEU
19	BS	33	THR
19	BS	37	ARG
19	BS	63	THR
20	BT	24	ARG
20	BT	43	ASP
20	BT	48	GLN
20	BT	54	MET
20	BT	58	VAL
20	BT	64	LYS
20	BT	66	LEU
20	BT	69	LYS
20	BT	84	ASN
21	BU	13	ASP
21	BU	56	HIS
22	D1	26	THR
23	D2	5	ILE

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Mol	Chain	Res	Type
23	D2	8	LYS
23	D2	46	HIS
23	D2	47	VAL
23	D2	48	ILE
24	D3	1	MET
25	D4	8	ARG
25	D4	31	HIS
25	D4	52	LYS
27	D0	10	THR
27	D0	25	LEU
27	D0	36	VAL
27	D0	39	GLU
29	CC	43	ARG
29	CC	97	LYS
29	CC	117	GLN
29	CC	120	VAL
29	CC	130	LEU
29	CC	156	ARG
29	CC	157	SER
29	CC	168	ASP
29	CC	195	VAL
29	CC	202	LEU
29	CC	204	VAL
29	CC	236	GLU
29	CC	258	ARG
30	CD	4	LEU
30	CD	18	ASP
30	CD	32	ASN
30	CD	52	THR
30	CD	95	SER
30	CD	97	SER
30	CD	129	THR
30	CD	138	LEU
29	DC	43	ARG
29	DC	70	ASN
29	DC	97	LYS
29	DC	117	GLN
29	DC	120	VAL
29	DC	130	LEU
29	DC	202	LEU
29	DC	236	GLU
32	DD	18	ASP

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Mol	Chain	Res	Type
32	DD	32	ASN
32	DD	52	THR
32	DD	95	SER
32	DD	97	SER
32	DD	138	LEU
33	CE	7	ASP
33	CE	12	LEU
33	CE	25	GLU
33	CE	40	ARG
33	CE	44	ARG
33	CE	72	SER
33	CE	78	TRP
33	CE	83	VAL
33	CE	93	SER
33	CE	122	GLU
33	CE	127	GLU
33	CE	149	ILE
33	CE	152	GLU
33	CE	163	ASN
33	CE	189	THR
34	CF	18	THR
34	CF	35	THR
34	CF	36	LEU
34	CF	57	LEU
34	CF	72	LYS
34	CF	80	ARG
34	CF	94	GLU
34	CF	115	ARG
34	CF	117	LEU
34	CF	123	ASP
34	CF	134	GLU
34	CF	141	ILE
34	CF	149	VAL
34	CF	152	LEU
34	CF	174	ASP
35	CG	11	VAL
35	CG	18	LYS
35	CG	72	LEU
35	CG	155	GLU
35	CG	168	VAL
36	CH	7	ASP
36	CH	15	LEU

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Mol	Chain	Res	Type
36	CH	17	ASP
36	CH	21	VAL
36	CH	48	GLU
36	CH	51	ARG
36	CH	53	GLU
36	CH	55	GLU
36	CH	58	LEU
36	CH	62	LEU
36	CH	75	LEU
36	CH	127	GLU
36	CH	145	ASN
37	CJ	13	VAL
37	CJ	28	LEU
37	CJ	53	LEU
37	CJ	55	ILE
37	CJ	113	LYS
38	CK	5	THR
38	CK	106	LYS
38	CK	124	VAL
38	CK	142	ILE
39	CL	32	TYR
39	CL	35	VAL
39	CL	49	ARG
39	CL	58	LEU
39	CL	70	ARG
39	CL	76	VAL
39	CL	80	ASP
39	CL	113	MET
40	CM	2	ARG
40	CM	92	LEU
40	CM	93	ASN
40	CM	94	THR
40	CM	100	ILE
40	CM	103	ILE
40	CM	107	PHE
40	CM	120	VAL
41	CN	6	ARG
41	CN	55	ARG
41	CN	59	ARG
41	CN	75	GLU
41	CN	78	LEU
42	CO	2	ARG

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Mol	Chain	Res	Type
42	CO	6	SER
42	CO	14	SER
42	CO	51	LEU
42	CO	71	ARG
42	CO	76	VAL
42	CO	90	ARG
42	CO	95	THR
43	CP	18	LEU
43	CP	31	THR
43	CP	38	GLN
43	CP	48	LEU
43	CP	49	VAL
43	CP	78	VAL
44	CQ	2	SER
44	CQ	26	VAL
44	CQ	39	ARG
44	CQ	63	LYS
44	CQ	102	GLU
44	CQ	109	ARG
44	CQ	114	LEU
45	CR	5	LYS
45	CR	9	ILE
45	CR	51	ARG
45	CR	52	GLN
45	CR	117	LEU
46	CS	12	HIS
46	CS	45	GLU
46	CS	46	GLU
46	CS	48	LYS
46	CS	51	VAL
46	CS	102	SER
47	CT	7	HIS
47	CT	97	LEU
47	CT	109	ASP
48	CU	1	MET
48	CU	2	ILE
48	CU	3	ARG
48	CU	24	MET
48	CU	30	ILE
48	CU	49	LYS
48	CU	69	ARG
48	CU	73	ARG

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Mol	Chain	Res	Type
48	CU	93	LEU
49	CV	9	ASP
49	CV	28	VAL
49	CV	29	LEU
49	CV	61	LYS
49	CV	81	ASP
49	CV	98	SER
50	CW	1	MET
50	CW	7	GLU
50	CW	10	LYS
50	CW	61	LEU
51	CX	39	ARG
51	CX	40	GLN
52	CY	25	THR
52	CY	35	SER
52	CY	48	THR
52	CY	71	LEU
53	CZ	18	LEU
53	CZ	58	ASN
33	DE	12	LEU
33	DE	80	SER
33	DE	127	GLU
33	DE	163	ASN
33	DE	189	THR
34	DF	10	ASP
34	DF	35	THR
34	DF	57	LEU
34	DF	72	LYS
34	DF	94	GLU
34	DF	117	LEU
34	DF	134	GLU
34	DF	141	ILE
34	DF	149	VAL
34	DF	152	LEU
34	DF	174	ASP
35	DG	11	VAL
35	DG	18	LYS
35	DG	72	LEU
35	DG	155	GLU
36	DH	7	ASP
36	DH	15	LEU
36	DH	17	ASP

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Mol	Chain	Res	Type
36	DH	21	VAL
36	DH	48	GLU
36	DH	53	GLU
36	DH	58	LEU
36	DH	75	LEU
36	DH	127	GLU
36	DH	145	ASN
37	DJ	13	VAL
37	DJ	28	LEU
37	DJ	53	LEU
37	DJ	55	ILE
37	DJ	113	LYS
38	DK	124	VAL
38	DK	142	ILE
39	DL	32	TYR
39	DL	49	ARG
39	DL	58	LEU
39	DL	70	ARG
39	DL	80	ASP
39	DL	108	ARG
39	DL	110	GLU
40	DM	2	ARG
40	DM	92	LEU
40	DM	94	THR
40	DM	107	PHE
40	DM	120	VAL
41	DN	75	GLU
41	DN	100	LYS
42	DO	2	ARG
42	DO	6	SER
42	DO	14	SER
42	DO	76	VAL
43	DP	31	THR
43	DP	49	VAL
43	DP	78	VAL
44	DQ	26	VAL
44	DQ	40	LEU
44	DQ	63	LYS
44	DQ	102	GLU
44	DQ	109	ARG
45	DR	5	LYS
45	DR	9	ILE

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Mol	Chain	Res	Type
45	DR	51	ARG
46	DS	102	SER
47	DT	1	MET
47	DT	86	MET
47	DT	109	ASP
48	DU	1	MET
48	DU	3	ARG
49	DV	28	VAL
49	DV	29	LEU
49	DV	52	LEU
49	DV	61	LYS
50	DW	7	GLU
50	DW	53	LYS
50	DW	61	LEU
51	DX	11	ARG
51	DX	39	ARG
51	DX	41[A]	ARG
51	DX	41[B]	ARG
52	DY	25	THR
52	DY	35	SER
54	DI	7	ASP
54	DI	16	SER
54	DI	53	ARG
54	DI	60	LEU
54	DI	64	VAL
54	DI	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	93	ASN
2	AB	120	GLN
6	AF	63	ASN
7	AG	97	ASN
7	AG	142	HIS
8	AH	4	GLN
10	AJ	58	ASN
16	AP	9	HIS
20	AT	48	GLN
2	BB	39	HIS
2	BB	93	ASN
2	BB	120	GLN

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Mol	Chain	Res	Type
5	BE	70	ASN
7	BG	97	ASN
8	BH	4	GLN
16	BP	9	HIS
17	BQ	51	ASN
20	BT	3	ASN
35	CG	38	ASN
43	CP	29	HIS
46	CS	12	HIS
48	CU	28	ASN
49	CV	74	ASN
53	CZ	45	GLN
35	DG	116	GLN
38	DK	47	HIS
54	DI	122	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1530/1534 (99%)	263 (17%)	31 (2%)
1	BA	1529/1534 (99%)	264 (17%)	36 (2%)
28	CB	117/120 (97%)	12 (10%)	0
28	DB	119/120 (99%)	10 (8%)	0
31	CA	2892/2904 (99%)	466 (16%)	78 (2%)
55	DA	2880/2904 (99%)	404 (14%)	62 (2%)
All	All	9067/9116 (99%)	1419 (15%)	207 (2%)

All (1419) 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
1	AA	28	A
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A

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Mol	Chain	Res	Type
1	AA	51	A
1	AA	52	C
1	AA	69	G
1	AA	70	U
1	AA	71	A
1	AA	72	A
1	AA	74	A
1	AA	80	A
1	AA	81	A
1	AA	82	G
1	AA	83	C
1	AA	84	U
1	AA	85	U
1	AA	86	G
1	AA	88	U
1	AA	89	U
1	AA	90	C
1	AA	94	G
1	AA	95	C
1	AA	108	G
1	AA	116	A
1	AA	120	A
1	AA	127	G
1	AA	130	A
1	AA	131	A
1	AA	137	U
1	AA	141	G
1	AA	142	G
1	AA	143	A
1	AA	144	G
1	AA	149	A
1	AA	159	G
1	AA	163	C
1	AA	168	G
1	AA	177	G
1	AA	197	A
1	AA	200	G
1	AA	205	A
1	AA	210	C
1	AA	211	G
1	AA	212	G
1	AA	226	G

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Mol	Chain	Res	Type
1	AA	240	G
1	AA	245	U
1	AA	247	G
1	AA	250	A
1	AA	251	G
1	AA	266	G
1	AA	267	C
1	AA	281	G
1	AA	289	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	330	C
1	AA	332	G
1	AA	346	G
1	AA	348	G
1	AA	352	C
1	AA	354	G
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	398	U
1	AA	406	G
1	AA	411	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	436	C
1	AA	457	G
1	AA	458	U
1	AA	466	A
1	AA	467	U
1	AA	468	A
1	AA	474	G
1	AA	481	G
1	AA	484	G

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Mol	Chain	Res	Type
1	AA	486	U
1	AA	495	A
1	AA	511	C
1	AA	527	7MG
1	AA	528	C
1	AA	531	U
1	AA	533	A
1	AA	547	A
1	AA	559	A
1	AA	564	C
1	AA	568	G
1	AA	572	A
1	AA	573	A
1	AA	576	C
1	AA	577	G
1	AA	615	G
1	AA	632	U
1	AA	633	G
1	AA	650	G
1	AA	653	U
1	AA	661	G
1	AA	665	A
1	AA	682	G
1	AA	695	A
1	AA	702	A
1	AA	703	G
1	AA	721	G
1	AA	723	U
1	AA	734	G
1	AA	748	G
1	AA	755	G
1	AA	777	A
1	AA	793	U
1	AA	794	A
1	AA	799	G
1	AA	809	G
1	AA	814	A
1	AA	815	A
1	AA	817	C
1	AA	821	G
1	AA	828	U
1	AA	836	G

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Mol	Chain	Res	Type
1	AA	839	C
1	AA	841	C
1	AA	842	U
1	AA	843	U
1	AA	844	G
1	AA	845	A
1	AA	873	A
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	966	2MG
1	AA	969	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	987	G
1	AA	992	U
1	AA	993	G
1	AA	1004	A
1	AA	1009	U
1	AA	1015	G
1	AA	1019	A
1	AA	1024	G
1	AA	1026	G
1	AA	1027	C
1	AA	1029	U
1	AA	1030	U
1	AA	1031	C
1	AA	1032	G
1	AA	1033	G
1	AA	1036	A
1	AA	1037	C
1	AA	1043	G
1	AA	1052	G
1	AA	1053	G
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C

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Mol	Chain	Res	Type
1	AA	1070	U
1	AA	1086	U
1	AA	1094	G
1	AA	1095	U
1	AA	1098	C
1	AA	1101	A
1	AA	1124	G
1	AA	1125	U
1	AA	1132	C
1	AA	1133	G
1	AA	1136	C
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1142	G
1	AA	1143	G
1	AA	1145	A
1	AA	1146	A
1	AA	1152	A
1	AA	1159	U
1	AA	1160	G
1	AA	1168	U
1	AA	1182	G
1	AA	1184	G
1	AA	1196	A
1	AA	1197	A
1	AA	1200	C
1	AA	1202	U
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1215	G
1	AA	1225	A
1	AA	1226	C
1	AA	1227	A
1	AA	1236	A
1	AA	1238	A
1	AA	1239	A
1	AA	1256	A
1	AA	1257	A

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Mol	Chain	Res	Type
1	AA	1260	G
1	AA	1280	A
1	AA	1281	C
1	AA	1286	U
1	AA	1287	A
1	AA	1300	G
1	AA	1302	C
1	AA	1305	G
1	AA	1312	G
1	AA	1317	C
1	AA	1320	C
1	AA	1323	G
1	AA	1346	A
1	AA	1353	G
1	AA	1363	A
1	AA	1370	G
1	AA	1379	G
1	AA	1381	U
1	AA	1397	C
1	AA	1398	A
1	AA	1419	G
1	AA	1429	A
1	AA	1441	A
1	AA	1446	A
1	AA	1447	A
1	AA	1448	C
1	AA	1451	U
1	AA	1452	C
1	AA	1453	G
1	AA	1475	G
1	AA	1492	A
1	AA	1497	G
1	AA	1499	A
1	AA	1503	A
1	AA	1505	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1529	G
1	AA	1530	G
1	AA	1533	C
1	AA	1534	A

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Mol	Chain	Res	Type
1	BA	4	U
1	BA	5	U
1	BA	6	G
1	BA	9	G
1	BA	22	G
1	BA	28	A
1	BA	32	A
1	BA	39	G
1	BA	47	C
1	BA	48	C
1	BA	50	A
1	BA	51	A
1	BA	52	C
1	BA	69	G
1	BA	70	U
1	BA	71	A
1	BA	72	A
1	BA	74	A
1	BA	80	A
1	BA	82	G
1	BA	83	C
1	BA	84	U
1	BA	85	U
1	BA	86	G
1	BA	87	C
1	BA	88	U
1	BA	89	U
1	BA	90	C
1	BA	94	G
1	BA	95	C
1	BA	108	G
1	BA	116	A
1	BA	120	A
1	BA	127	G
1	BA	130	A
1	BA	131	A
1	BA	137	U
1	BA	141	G
1	BA	142	G
1	BA	143	A
1	BA	144	G
1	BA	149	A

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Mol	Chain	Res	Type
1	BA	159	G
1	BA	163	C
1	BA	168	G
1	BA	177	G
1	BA	197	A
1	BA	200	G
1	BA	205	A
1	BA	210	C
1	BA	211	G
1	BA	212	G
1	BA	226	G
1	BA	240	G
1	BA	245	U
1	BA	247	G
1	BA	250	A
1	BA	251	G
1	BA	266	G
1	BA	267	C
1	BA	281	G
1	BA	289	G
1	BA	321	A
1	BA	328	C
1	BA	329	A
1	BA	330	C
1	BA	332	G
1	BA	346	G
1	BA	348	G
1	BA	352	C
1	BA	354	G
1	BA	367	U
1	BA	372	C
1	BA	373	A
1	BA	382	A
1	BA	384	G
1	BA	398	U
1	BA	406	G
1	BA	411	A
1	BA	412	A
1	BA	413	G
1	BA	421	U
1	BA	422	C
1	BA	424	G

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Mol	Chain	Res	Type
1	BA	429	U
1	BA	430	A
1	BA	436	C
1	BA	457	G
1	BA	458	U
1	BA	467	U
1	BA	468	A
1	BA	474	G
1	BA	481	G
1	BA	484	G
1	BA	486	U
1	BA	495	A
1	BA	511	C
1	BA	527	7MG
1	BA	531	U
1	BA	532	A
1	BA	533	A
1	BA	547	A
1	BA	559	A
1	BA	564	C
1	BA	568	G
1	BA	572	A
1	BA	573	A
1	BA	576	C
1	BA	577	G
1	BA	596	A
1	BA	615	G
1	BA	632	U
1	BA	633	G
1	BA	650	G
1	BA	653	U
1	BA	661	G
1	BA	665	A
1	BA	682	G
1	BA	695	A
1	BA	702	A
1	BA	703	G
1	BA	721	G
1	BA	723	U
1	BA	734	G
1	BA	748	G
1	BA	755	G

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Mol	Chain	Res	Type
1	BA	777	A
1	BA	793	U
1	BA	794	A
1	BA	799	G
1	BA	814	A
1	BA	815	A
1	BA	817	C
1	BA	821	G
1	BA	828	U
1	BA	836	G
1	BA	839	C
1	BA	840	C
1	BA	841	C
1	BA	842	U
1	BA	843	U
1	BA	844	G
1	BA	845	A
1	BA	846	G
1	BA	873	A
1	BA	914	A
1	BA	926	G
1	BA	927	G
1	BA	934	C
1	BA	935	A
1	BA	960	U
1	BA	966	2MG
1	BA	969	A
1	BA	975	A
1	BA	976	G
1	BA	977	A
1	BA	987	G
1	BA	992	U
1	BA	993	G
1	BA	1004	A
1	BA	1008	U
1	BA	1009	U
1	BA	1015	G
1	BA	1019	A
1	BA	1024	G
1	BA	1026	G
1	BA	1027	C
1	BA	1029	U

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Mol	Chain	Res	Type
1	BA	1030	U
1	BA	1031	C
1	BA	1032	G
1	BA	1033	G
1	BA	1036	A
1	BA	1037	C
1	BA	1043	G
1	BA	1053	G
1	BA	1054	C
1	BA	1055	A
1	BA	1065	U
1	BA	1070	U
1	BA	1086	U
1	BA	1094	G
1	BA	1095	U
1	BA	1098	C
1	BA	1101	A
1	BA	1124	G
1	BA	1125	U
1	BA	1132	C
1	BA	1133	G
1	BA	1136	C
1	BA	1137	C
1	BA	1138	G
1	BA	1139	G
1	BA	1140	C
1	BA	1141	C
1	BA	1142	G
1	BA	1143	G
1	BA	1145	A
1	BA	1146	A
1	BA	1152	A
1	BA	1159	U
1	BA	1160	G
1	BA	1168	U
1	BA	1182	G
1	BA	1196	A
1	BA	1197	A
1	BA	1200	C
1	BA	1202	U
1	BA	1212	U
1	BA	1213	A

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Mol	Chain	Res	Type
1	BA	1214	C
1	BA	1215	G
1	BA	1225	A
1	BA	1226	C
1	BA	1227	A
1	BA	1236	A
1	BA	1238	A
1	BA	1239	A
1	BA	1256	A
1	BA	1257	A
1	BA	1260	G
1	BA	1261	A
1	BA	1280	A
1	BA	1281	C
1	BA	1286	U
1	BA	1287	A
1	BA	1300	G
1	BA	1302	C
1	BA	1305	G
1	BA	1312	G
1	BA	1317	C
1	BA	1320	C
1	BA	1323	G
1	BA	1346	A
1	BA	1353	G
1	BA	1362	A
1	BA	1363	A
1	BA	1370	G
1	BA	1379	G
1	BA	1381	U
1	BA	1397	C
1	BA	1398	A
1	BA	1419	G
1	BA	1429	A
1	BA	1441	A
1	BA	1446	A
1	BA	1447	A
1	BA	1448	C
1	BA	1451	U
1	BA	1452	C
1	BA	1453	G
1	BA	1475	G

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Mol	Chain	Res	Type
1	BA	1493	A
1	BA	1497	G
1	BA	1499	A
1	BA	1503	A
1	BA	1505	G
1	BA	1506	U
1	BA	1507	A
1	BA	1517	G
1	BA	1529	G
1	BA	1530	G
1	BA	1533	C
1	BA	1534	A
28	CB	9	G
28	CB	25	U
28	CB	35	C
28	CB	44	G
28	CB	45	A
28	CB	56	G
28	CB	57	A
28	CB	88	C
28	CB	89	U
28	CB	90	C
28	CB	99	A
28	CB	109	A
31	CA	10	A
31	CA	14	A
31	CA	33	C
31	CA	34	U
31	CA	42	A
31	CA	46	G
31	CA	49	A
31	CA	58	G
31	CA	63	A
31	CA	71	A
31	CA	74	A
31	CA	75	G
31	CA	80	G
31	CA	83	A
31	CA	84	A
31	CA	101	A
31	CA	102	U
31	CA	118	A

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Mol	Chain	Res	Type
31	CA	119	A
31	CA	120	U
31	CA	138	U
31	CA	139	U
31	CA	140	C
31	CA	141	G
31	CA	142	A
31	CA	143	C
31	CA	165	A
31	CA	177	G
31	CA	178	G
31	CA	196	A
31	CA	197	A
31	CA	198	C
31	CA	199	A
31	CA	200	U
31	CA	215	G
31	CA	216	A
31	CA	221	A
31	CA	222	A
31	CA	245	G
31	CA	248	G
31	CA	264	C
31	CA	265	A
31	CA	266	G
31	CA	267	C
31	CA	272	A
31	CA	276	U
31	CA	277	G
31	CA	278	A
31	CA	279	A
31	CA	285	G
31	CA	310	A
31	CA	311	A
31	CA	329	G
31	CA	330	A
31	CA	343	C
31	CA	346	A
31	CA	352	A
31	CA	353	C
31	CA	362	A
31	CA	371	A

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Mol	Chain	Res	Type
31	CA	372	G
31	CA	385	C
31	CA	386	G
31	CA	399	U
31	CA	403	U
31	CA	404	A
31	CA	405	U
31	CA	411	G
31	CA	412	A
31	CA	420	C
31	CA	424	G
31	CA	451	U
31	CA	480	A
31	CA	481	G
31	CA	491	G
31	CA	496	G
31	CA	503	A
31	CA	504	A
31	CA	505	A
31	CA	508	A
31	CA	528	A
31	CA	529	A
31	CA	531	C
31	CA	532	A
31	CA	543	G
31	CA	544	C
31	CA	546	U
31	CA	547	A
31	CA	549	G
31	CA	550	C
31	CA	551	G
31	CA	555	G
31	CA	563	A
31	CA	573	U
31	CA	575	A
31	CA	586	A
31	CA	603	A
31	CA	613	A
31	CA	614	A
31	CA	615	U
31	CA	622	G
31	CA	627	A

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Mol	Chain	Res	Type
31	CA	637	A
31	CA	645	C
31	CA	647	G
31	CA	653	U
31	CA	654	A
31	CA	655	A
31	CA	670	A
31	CA	684	G
31	CA	685	A
31	CA	686	U
31	CA	695	G
31	CA	717	C
31	CA	730	A
31	CA	740	C
31	CA	747	5MU
31	CA	764	A
31	CA	775	G
31	CA	776	G
31	CA	782	A
31	CA	784	G
31	CA	785	G
31	CA	792	A
31	CA	798	G
31	CA	802	A
31	CA	805	G
31	CA	812	C
31	CA	819	A
31	CA	827	U
31	CA	828	U
31	CA	845	A
31	CA	846	U
31	CA	847	U
31	CA	858	G
31	CA	859	G
31	CA	878	A
31	CA	883	G
31	CA	896	A
31	CA	897	C
31	CA	907	G
31	CA	910	A
31	CA	914	G
31	CA	931	U

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Mol	Chain	Res	Type
31	CA	932	U
31	CA	941	A
31	CA	946	C
31	CA	953	G
31	CA	961	C
31	CA	973	A
31	CA	974	G
31	CA	983	A
31	CA	984	A
31	CA	985	C
31	CA	995	C
31	CA	996	A
31	CA	1005	C
31	CA	1012	U
31	CA	1013	C
31	CA	1022	G
31	CA	1026	G
31	CA	1033	U
31	CA	1040	A
31	CA	1045	C
31	CA	1046	A
31	CA	1047	G
31	CA	1057	A
31	CA	1061	U
31	CA	1062	G
31	CA	1070	A
31	CA	1073	A
31	CA	1083	U
31	CA	1088	A
31	CA	1089	A
31	CA	1090	A
31	CA	1091	G
31	CA	1096	A
31	CA	1097	U
31	CA	1111	A
31	CA	1112	G
31	CA	1119	U
31	CA	1128	G
31	CA	1129	A
31	CA	1132	U
31	CA	1133	A
31	CA	1135	C

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Mol	Chain	Res	Type
31	CA	1136	G
31	CA	1142	A
31	CA	1156	A
31	CA	1168	G
31	CA	1169	A
31	CA	1172	C
31	CA	1175	A
31	CA	1176	U
31	CA	1177	G
31	CA	1179	G
31	CA	1180	U
31	CA	1186	G
31	CA	1206	G
31	CA	1210	G
31	CA	1212	G
31	CA	1218	G
31	CA	1236	G
31	CA	1238	G
31	CA	1253	A
31	CA	1256	G
31	CA	1262	A
31	CA	1266	G
31	CA	1271	G
31	CA	1272	A
31	CA	1273	U
31	CA	1300	G
31	CA	1301	A
31	CA	1313	U
31	CA	1320	C
31	CA	1321	A
31	CA	1328	A
31	CA	1329	U
31	CA	1330	C
31	CA	1352	U
31	CA	1365	A
31	CA	1376	C
31	CA	1379	U
31	CA	1380	G
31	CA	1383	A
31	CA	1386	C
31	CA	1395	A
31	CA	1416	G

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Mol	Chain	Res	Type
31	CA	1417	C
31	CA	1419	A
31	CA	1420	A
31	CA	1428	C
31	CA	1437	C
31	CA	1438	U
31	CA	1452	G
31	CA	1453	A
31	CA	1460	U
31	CA	1482	G
31	CA	1490	A
31	CA	1491	G
31	CA	1493	C
31	CA	1494	A
31	CA	1497	U
31	CA	1504	A
31	CA	1509	A
31	CA	1510	G
31	CA	1515	A
31	CA	1523	U
31	CA	1532	A
31	CA	1534	U
31	CA	1535	A
31	CA	1536	C
31	CA	1537	G
31	CA	1565	C
31	CA	1567	G
31	CA	1569	A
31	CA	1578	U
31	CA	1583	A
31	CA	1585	C
31	CA	1606	C
31	CA	1607	C
31	CA	1608	A
31	CA	1616	A
31	CA	1634	A
31	CA	1647	U
31	CA	1648	U
31	CA	1649	G
31	CA	1669	A
31	CA	1674	G
31	CA	1675	C

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Mol	Chain	Res	Type
31	CA	1694	C
31	CA	1715	G
31	CA	1729	U
31	CA	1730	C
31	CA	1738	G
31	CA	1744	A
31	CA	1750	G
31	CA	1758	U
31	CA	1764	C
31	CA	1773	A
31	CA	1782	U
31	CA	1800	C
31	CA	1801	A
31	CA	1808	A
31	CA	1812	U
31	CA	1816	C
31	CA	1829	A
31	CA	1869	G
31	CA	1870	C
31	CA	1871	A
31	CA	1872	A
31	CA	1873	G
31	CA	1900	A
31	CA	1903	G
31	CA	1906	G
31	CA	1907	G
31	CA	1914	C
31	CA	1929	G
31	CA	1930	G
31	CA	1931	U
31	CA	1937	A
31	CA	1938	A
31	CA	1955	U
31	CA	1967	C
31	CA	1970	A
31	CA	1972	G
31	CA	1991	U
31	CA	1993	U
31	CA	1997	C
31	CA	2022	U
31	CA	2023	C
31	CA	2033	A

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Mol	Chain	Res	Type
31	CA	2035	G
31	CA	2036	C
31	CA	2043	C
31	CA	2046	G
31	CA	2049	G
31	CA	2055	C
31	CA	2056	G
31	CA	2060	A
31	CA	2061	G
31	CA	2062	A
31	CA	2069	7MG
31	CA	2072	C
31	CA	2080	A
31	CA	2093	G
31	CA	2095	A
31	CA	2100	G
31	CA	2108	A
31	CA	2110	G
31	CA	2111	U
31	CA	2112	G
31	CA	2113	U
31	CA	2115	G
31	CA	2117	A
31	CA	2118	U
31	CA	2119	A
31	CA	2123	G
31	CA	2124	G
31	CA	2125	G
31	CA	2126	A
31	CA	2127	G
31	CA	2128	G
31	CA	2131	U
31	CA	2132	U
31	CA	2133	G
31	CA	2146	C
31	CA	2147	A
31	CA	2157	G
31	CA	2158	A
31	CA	2159	G
31	CA	2162	G
31	CA	2164	C
31	CA	2165	C

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Mol	Chain	Res	Type
31	CA	2171	A
31	CA	2172	U
31	CA	2173	A
31	CA	2174	C
31	CA	2178	C
31	CA	2183	A
31	CA	2190	G
31	CA	2198	A
31	CA	2203	U
31	CA	2204	G
31	CA	2211	A
31	CA	2225	A
31	CA	2226	C
31	CA	2238	G
31	CA	2239	G
31	CA	2259	U
31	CA	2268	A
31	CA	2278	A
31	CA	2280	G
31	CA	2282	G
31	CA	2283	C
31	CA	2287	A
31	CA	2305	U
31	CA	2311	A
31	CA	2322	A
31	CA	2324	U
31	CA	2325	G
31	CA	2326	C
31	CA	2327	A
31	CA	2331	G
31	CA	2333	A
31	CA	2334	U
31	CA	2335	A
31	CA	2345	G
31	CA	2347	C
31	CA	2350	C
31	CA	2354	C
31	CA	2361	G
31	CA	2383	G
31	CA	2385	C
31	CA	2402	U
31	CA	2403	C

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Mol	Chain	Res	Type
31	CA	2406	A
31	CA	2424	C
31	CA	2425	A
31	CA	2426	A
31	CA	2429	G
31	CA	2430	A
31	CA	2435	A
31	CA	2436	G
31	CA	2441	U
31	CA	2448	A
31	CA	2465	C
31	CA	2469	A
31	CA	2476	A
31	CA	2491	U
31	CA	2502	G
31	CA	2505	G
31	CA	2518	A
31	CA	2529	G
31	CA	2535	G
31	CA	2547	A
31	CA	2554	U
31	CA	2556	C
31	CA	2566	A
31	CA	2567	G
31	CA	2573	C
31	CA	2578	G
31	CA	2582	G
31	CA	2585	U
31	CA	2586	U
31	CA	2603	G
31	CA	2609	U
31	CA	2613	U
31	CA	2621	G
31	CA	2629	U
31	CA	2630	G
31	CA	2646	C
31	CA	2661	G
31	CA	2663	G
31	CA	2681	C
31	CA	2682	A
31	CA	2689	U
31	CA	2690	U

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Mol	Chain	Res	Type
31	CA	2714	G
31	CA	2716	C
31	CA	2726	A
31	CA	2748	A
31	CA	2765	A
31	CA	2769	U
31	CA	2778	A
31	CA	2779	U
31	CA	2780	G
31	CA	2791	G
31	CA	2794	C
31	CA	2799	A
31	CA	2820	A
31	CA	2821	A
31	CA	2825	G
31	CA	2833	U
31	CA	2835	A
31	CA	2836	U
31	CA	2850	A
31	CA	2861	U
31	CA	2867	G
31	CA	2880	C
31	CA	2883	A
31	CA	2884	U
31	CA	2886	A
31	CA	2893	A
31	CA	2894	G
31	CA	2903	U
28	DB	25	U
28	DB	35	C
28	DB	44	G
28	DB	45	A
28	DB	56	G
28	DB	57	A
28	DB	88	C
28	DB	89	U
28	DB	90	C
28	DB	109	A
55	DA	10	A
55	DA	12	U
55	DA	34	U
55	DA	42	A

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Mol	Chain	Res	Type
55	DA	46	G
55	DA	58	G
55	DA	63	A
55	DA	71	A
55	DA	74	A
55	DA	75	G
55	DA	80	G
55	DA	84	A
55	DA	101	A
55	DA	102	U
55	DA	118	A
55	DA	119	A
55	DA	120	U
55	DA	138	U
55	DA	139	U
55	DA	140	C
55	DA	141	G
55	DA	142	A
55	DA	143	C
55	DA	165	A
55	DA	196	A
55	DA	197	A
55	DA	199	A
55	DA	215	G
55	DA	216	A
55	DA	221	A
55	DA	222	A
55	DA	226	A
55	DA	248	G
55	DA	264	C
55	DA	265	A
55	DA	266	G
55	DA	267	C
55	DA	272	A
55	DA	276	U
55	DA	277	G
55	DA	278	A
55	DA	279	A
55	DA	285	G
55	DA	302	C
55	DA	310	A
55	DA	311	A

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Mol	Chain	Res	Type
55	DA	329	G
55	DA	330	A
55	DA	346	A
55	DA	352	A
55	DA	353	C
55	DA	362	A
55	DA	370	G
55	DA	371	A
55	DA	372	G
55	DA	386	G
55	DA	399	U
55	DA	411	G
55	DA	412	A
55	DA	420	C
55	DA	424	G
55	DA	454	A
55	DA	480	A
55	DA	481	G
55	DA	491	G
55	DA	496	G
55	DA	503	A
55	DA	504	A
55	DA	505	A
55	DA	508	A
55	DA	529	A
55	DA	531	C
55	DA	532	A
55	DA	533	G
55	DA	543	G
55	DA	544	C
55	DA	546	U
55	DA	547	A
55	DA	548	G
55	DA	549	G
55	DA	550	C
55	DA	551	G
55	DA	563	A
55	DA	573	U
55	DA	575	A
55	DA	586	A
55	DA	603	A
55	DA	613	A

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Mol	Chain	Res	Type
55	DA	614	A
55	DA	615	U
55	DA	627	A
55	DA	637	A
55	DA	645	C
55	DA	647	G
55	DA	653	U
55	DA	654	A
55	DA	655	A
55	DA	686	U
55	DA	702	U
55	DA	717	C
55	DA	730	A
55	DA	738	G
55	DA	747	5MU
55	DA	764	A
55	DA	765	C
55	DA	775	G
55	DA	776	G
55	DA	782	A
55	DA	783	A
55	DA	784	G
55	DA	785	G
55	DA	790	U
55	DA	805	G
55	DA	812	C
55	DA	827	U
55	DA	828	U
55	DA	858	G
55	DA	859	G
55	DA	878	A
55	DA	883	G
55	DA	885	C
55	DA	896	A
55	DA	897	C
55	DA	907	G
55	DA	910	A
55	DA	914	G
55	DA	931	U
55	DA	932	U
55	DA	946	C
55	DA	953	G

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Mol	Chain	Res	Type
55	DA	961	C
55	DA	974	G
55	DA	983	A
55	DA	984	A
55	DA	985	C
55	DA	996	A
55	DA	1005	C
55	DA	1012	U
55	DA	1013	C
55	DA	1022	G
55	DA	1026	G
55	DA	1033	U
55	DA	1040	A
55	DA	1047	G
55	DA	1057	A
55	DA	1061	U
55	DA	1062	G
55	DA	1070	A
55	DA	1073	A
55	DA	1083	U
55	DA	1088	A
55	DA	1089	A
55	DA	1090	A
55	DA	1091	G
55	DA	1096	A
55	DA	1097	U
55	DA	1112	G
55	DA	1119	U
55	DA	1128	G
55	DA	1129	A
55	DA	1132	U
55	DA	1133	A
55	DA	1135	C
55	DA	1136	G
55	DA	1142	A
55	DA	1156	A
55	DA	1168	G
55	DA	1172	C
55	DA	1174	U
55	DA	1175	A
55	DA	1176	U
55	DA	1177	G

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Mol	Chain	Res	Type
55	DA	1180	U
55	DA	1206	G
55	DA	1212	G
55	DA	1218	G
55	DA	1238	G
55	DA	1253	A
55	DA	1256	G
55	DA	1271	G
55	DA	1272	A
55	DA	1273	U
55	DA	1300	G
55	DA	1301	A
55	DA	1321	A
55	DA	1352	U
55	DA	1365	A
55	DA	1379	U
55	DA	1383	A
55	DA	1386	C
55	DA	1416	G
55	DA	1417	C
55	DA	1420	A
55	DA	1427	A
55	DA	1428	C
55	DA	1435	G
55	DA	1452	G
55	DA	1453	A
55	DA	1460	U
55	DA	1482	G
55	DA	1490	A
55	DA	1491	G
55	DA	1493	C
55	DA	1494	A
55	DA	1497	U
55	DA	1504	A
55	DA	1508	A
55	DA	1509	A
55	DA	1510	G
55	DA	1515	A
55	DA	1523	U
55	DA	1532	A
55	DA	1534	U
55	DA	1535	A

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Mol	Chain	Res	Type
55	DA	1537	G
55	DA	1569	A
55	DA	1578	U
55	DA	1583	A
55	DA	1585	C
55	DA	1606	C
55	DA	1607	C
55	DA	1608	A
55	DA	1634	A
55	DA	1647	U
55	DA	1648	U
55	DA	1649	G
55	DA	1674	G
55	DA	1694	C
55	DA	1715	G
55	DA	1729	U
55	DA	1730	C
55	DA	1738	G
55	DA	1744	A
55	DA	1758	U
55	DA	1764	C
55	DA	1773	A
55	DA	1782	U
55	DA	1800	C
55	DA	1801	A
55	DA	1808	A
55	DA	1812	U
55	DA	1816	C
55	DA	1829	A
55	DA	1839	G
55	DA	1869	G
55	DA	1870	C
55	DA	1871	A
55	DA	1872	A
55	DA	1873	G
55	DA	1900	A
55	DA	1906	G
55	DA	1907	G
55	DA	1913	A
55	DA	1914	C
55	DA	1929	G
55	DA	1930	G

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Mol	Chain	Res	Type
55	DA	1931	U
55	DA	1937	A
55	DA	1938	A
55	DA	1955	U
55	DA	1965	C
55	DA	1967	C
55	DA	1970	A
55	DA	1972	G
55	DA	1991	U
55	DA	1992	G
55	DA	1993	U
55	DA	1997	C
55	DA	2023	C
55	DA	2031	A
55	DA	2033	A
55	DA	2043	C
55	DA	2055	C
55	DA	2056	G
55	DA	2060	A
55	DA	2061	G
55	DA	2062	A
55	DA	2069	7MG
55	DA	2080	A
55	DA	2093	G
55	DA	2097	A
55	DA	2100	G
55	DA	2105	U
55	DA	2111	U
55	DA	2112	G
55	DA	2113	U
55	DA	2116	G
55	DA	2117	A
55	DA	2118	U
55	DA	2119	A
55	DA	2120	G
55	DA	2123	G
55	DA	2125	G
55	DA	2126	A
55	DA	2128	G
55	DA	2131	U
55	DA	2132	U
55	DA	2133	G

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Mol	Chain	Res	Type
55	DA	2134	A
55	DA	2135	A
55	DA	2145	C
55	DA	2146	C
55	DA	2148	G
55	DA	2158	A
55	DA	2159	G
55	DA	2160	C
55	DA	2161	C
55	DA	2162	G
55	DA	2163	A
55	DA	2164	C
55	DA	2165	C
55	DA	2167	U
55	DA	2168	G
55	DA	2169	A
55	DA	2170	A
55	DA	2171	A
55	DA	2172	U
55	DA	2173	A
55	DA	2178	C
55	DA	2179	C
55	DA	2181	U
55	DA	2183	A
55	DA	2185	U
55	DA	2186	G
55	DA	2190	G
55	DA	2198	A
55	DA	2204	G
55	DA	2211	A
55	DA	2225	A
55	DA	2238	G
55	DA	2239	G
55	DA	2243	U
55	DA	2268	A
55	DA	2278	A
55	DA	2283	C
55	DA	2286	G
55	DA	2287	A
55	DA	2305	U
55	DA	2308	G
55	DA	2312	U

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Mol	Chain	Res	Type
55	DA	2322	A
55	DA	2324	U
55	DA	2325	G
55	DA	2327	A
55	DA	2331	G
55	DA	2333	A
55	DA	2335	A
55	DA	2345	G
55	DA	2347	C
55	DA	2350	C
55	DA	2361	G
55	DA	2383	G
55	DA	2385	C
55	DA	2402	U
55	DA	2403	C
55	DA	2406	A
55	DA	2407	A
55	DA	2424	C
55	DA	2425	A
55	DA	2435	A
55	DA	2441	U
55	DA	2448	A
55	DA	2476	A
55	DA	2491	U
55	DA	2502	G
55	DA	2505	G
55	DA	2518	A
55	DA	2529	G
55	DA	2535	G
55	DA	2547	A
55	DA	2556	C
55	DA	2566	A
55	DA	2567	G
55	DA	2573	C
55	DA	2585	U
55	DA	2603	G
55	DA	2609	U
55	DA	2613	U
55	DA	2629	U
55	DA	2630	G
55	DA	2661	G
55	DA	2663	G

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Mol	Chain	Res	Type
55	DA	2671	G
55	DA	2689	U
55	DA	2690	U
55	DA	2714	G
55	DA	2726	A
55	DA	2748	A
55	DA	2765	A
55	DA	2778	A
55	DA	2780	G
55	DA	2791	G
55	DA	2798	U
55	DA	2799	A
55	DA	2820	A
55	DA	2821	A
55	DA	2825	G
55	DA	2833	U
55	DA	2835	A
55	DA	2836	U
55	DA	2861	U
55	DA	2867	G
55	DA	2880	C
55	DA	2883	A

All (207) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	7	A
1	AA	70	U
1	AA	88	U
1	AA	89	U
1	AA	209	U
1	AA	413	G
1	AA	422	C
1	AA	429	U
1	AA	438	U
1	AA	559	A
1	AA	576	C
1	AA	653	U
1	AA	702	A
1	AA	733	G
1	AA	793	U

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Mol	Chain	Res	Type
1	AA	841	C
1	AA	884	U
1	AA	992	U
1	AA	1086	U
1	AA	1137	C
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1196	A
1	AA	1225	A
1	AA	1281	C
1	AA	1299	A
1	AA	1397	C
1	AA	1447	A
1	AA	1452	C
1	BA	5	U
1	BA	7	A
1	BA	70	U
1	BA	86	G
1	BA	89	U
1	BA	209	U
1	BA	246	A
1	BA	422	C
1	BA	429	U
1	BA	438	U
1	BA	559	A
1	BA	560	A
1	BA	576	C
1	BA	653	U
1	BA	702	A
1	BA	733	G
1	BA	793	U
1	BA	842	U
1	BA	844	G
1	BA	884	U
1	BA	992	U
1	BA	1008	U
1	BA	1086	U
1	BA	1137	C
1	BA	1139	G
1	BA	1140	C
1	BA	1141	C

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Mol	Chain	Res	Type
1	BA	1196	A
1	BA	1225	A
1	BA	1281	C
1	BA	1299	A
1	BA	1362	A
1	BA	1363	A
1	BA	1397	C
1	BA	1447	A
1	BA	1452	C
31	CA	33	C
31	CA	62	U
31	CA	83	A
31	CA	138	U
31	CA	141	G
31	CA	177	G
31	CA	196	A
31	CA	199	A
31	CA	221	A
31	CA	271	G
31	CA	278	A
31	CA	310	A
31	CA	371	A
31	CA	403	U
31	CA	404	A
31	CA	451	U
31	CA	455	C
31	CA	503	A
31	CA	506	G
31	CA	527	C
31	CA	555	G
31	CA	620	G
31	CA	686	U
31	CA	764	A
31	CA	784	G
31	CA	846	U
31	CA	973	A
31	CA	984	A
31	CA	1045	C
31	CA	1046	A
31	CA	1061	U
31	CA	1069	A
31	CA	1070	A

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Mol	Chain	Res	Type
31	CA	1088	A
31	CA	1089	A
31	CA	1128	G
31	CA	1133	A
31	CA	1286	A
31	CA	1288	G
31	CA	1300	G
31	CA	1320	C
31	CA	1329	U
31	CA	1379	U
31	CA	1452	G
31	CA	1490	A
31	CA	1497	U
31	CA	1509	A
31	CA	1535	A
31	CA	1536	C
31	CA	1567	G
31	CA	1607	C
31	CA	1609	A
31	CA	1647	U
31	CA	1730	C
31	CA	1786	A
31	CA	1870	C
31	CA	1871	A
31	CA	1900	A
31	CA	2035	G
31	CA	2095	A
31	CA	2119	A
31	CA	2126	A
31	CA	2146	C
31	CA	2157	G
31	CA	2164	C
31	CA	2225	A
31	CA	2282	G
31	CA	2326	C
31	CA	2423	U
31	CA	2425	A
31	CA	2645	G
31	CA	2680	U
31	CA	2681	C
31	CA	2778	A
31	CA	2779	U

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Mol	Chain	Res	Type
31	CA	2849	U
31	CA	2873	A
31	CA	2893	A
55	DA	62	U
55	DA	138	U
55	DA	141	G
55	DA	196	A
55	DA	199	A
55	DA	271	G
55	DA	278	A
55	DA	310	A
55	DA	370	G
55	DA	371	A
55	DA	403	U
55	DA	503	A
55	DA	620	G
55	DA	764	A
55	DA	784	G
55	DA	961	C
55	DA	984	A
55	DA	1046	A
55	DA	1061	U
55	DA	1069	A
55	DA	1070	A
55	DA	1087	G
55	DA	1089	A
55	DA	1128	G
55	DA	1133	A
55	DA	1141	U
55	DA	1142	A
55	DA	1171	G
55	DA	1175	A
55	DA	1300	G
55	DA	1320	C
55	DA	1490	A
55	DA	1497	U
55	DA	1509	A
55	DA	1535	A
55	DA	1607	C
55	DA	1609	A
55	DA	1647	U
55	DA	1730	C

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Mol	Chain	Res	Type
55	DA	1800	C
55	DA	1870	C
55	DA	1871	A
55	DA	1900	A
55	DA	2097	A
55	DA	2119	A
55	DA	2127	G
55	DA	2146	C
55	DA	2157	G
55	DA	2158	A
55	DA	2164	C
55	DA	2282	G
55	DA	2286	G
55	DA	2311	A
55	DA	2324	U
55	DA	2406	A
55	DA	2423	U
55	DA	2585	U
55	DA	2779	U
55	DA	2798	U
55	DA	2820	A
55	DA	2849	U
55	DA	2873	A

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	PSU	DA	955	55	18,21,22	0.70	1 (5%)	22,30,33	0.51	0
55	OMU	DA	2552	55	19,22,23	0.53	0	26,31,34	0.29	0
1	4OC	AA	1402	1	20,23,24	0.38	0	26,32,35	0.45	0
1	2MG	AA	1516	1	18,26,27	0.79	0	16,38,41	0.54	0
55	6MZ	DA	2030	55	18,25,26	1.06	2 (11%)	16,36,39	0.99	2 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	PSU	CA	2605	31	18,21,22	0.48	0	22,30,33	0.56	0
55	5MC	DA	1962	55	18,22,23	0.65	1 (5%)	26,32,35	0.44	0
31	2MG	CA	1835	31	18,26,27	0.95	1 (5%)	16,38,41	0.45	0
1	2MG	BA	966	1	18,26,27	0.75	0	16,38,41	0.63	0
31	OMG	CA	2251	31	18,26,27	0.78	0	19,38,41	0.62	0
55	PSU	DA	746	55,56	18,21,22	0.99	1 (5%)	22,30,33	0.30	0
55	6MZ	DA	1618	55	18,25,26	0.73	0	16,36,39	2.09	2 (12%)
55	2MA	DA	2503	55,56	17,25,26	0.90	0	17,37,40	0.53	0
1	UR3	AA	1498	1	19,22,23	0.51	0	26,32,35	0.29	0
1	MA6	BA	1519	1	19,26,27	0.88	0	18,38,41	1.03	1 (5%)
55	PSU	DA	2504	55	18,21,22	0.50	0	22,30,33	0.42	0
1	UR3	BA	1498	1	19,22,23	0.85	0	26,32,35	0.65	1 (3%)
55	7MG	DA	2069	55	22,26,27	4.96	2 (9%)	29,39,42	2.05	6 (20%)
55	PSU	DA	2457	55	18,21,22	0.60	0	22,30,33	0.44	0
1	PSU	BA	516	1	18,21,22	0.40	0	22,30,33	0.46	0
1	2MG	AA	966	1	18,26,27	0.77	0	16,38,41	0.61	0
1	MA6	AA	1518	1	19,26,27	0.84	0	18,38,41	1.25	1 (5%)
31	5MC	CA	1962	31	18,22,23	0.35	0	26,32,35	0.37	0
31	5MU	CA	747	31	19,22,23	0.43	0	28,32,35	0.30	0
55	2MG	DA	1835	55	18,26,27	0.91	1 (5%)	16,38,41	0.55	0
55	PSU	DA	2580	55	18,21,22	0.80	0	22,30,33	0.62	0
31	PSU	CA	955	31	18,21,22	0.33	0	22,30,33	0.48	0
55	OMC	DA	2498	55,56	19,22,23	0.38	0	26,31,34	0.51	0
31	PSU	CA	2504	31	18,21,22	0.42	0	22,30,33	0.45	0
1	PSU	AA	516	1,56	18,21,22	0.36	0	22,30,33	0.47	0
1	4OC	BA	1402	1	20,23,24	0.36	0	26,32,35	0.46	0
1	2MG	BA	1516	1	18,26,27	0.79	1 (5%)	16,38,41	0.55	0
31	PSU	CA	1911	31	18,21,22	0.30	0	22,30,33	0.40	0
31	PSU	CA	1917	31	18,21,22	0.33	0	22,30,33	0.41	0
1	2MG	BA	1207	1	18,26,27	0.78	0	16,38,41	0.52	0
1	7MG	BA	527	1	22,26,27	4.94	2 (9%)	29,39,42	2.41	6 (20%)
12	D2T	BL	89	12	7,9,10	1.23	1 (14%)	6,11,13	1.32	1 (16%)
31	6MZ	CA	1618	31	18,25,26	0.89	0	16,36,39	0.93	1 (6%)
31	2MG	CA	2445	31	18,26,27	0.97	0	16,38,41	0.55	0
31	OMC	CA	2498	31,56	19,22,23	0.51	0	26,31,34	0.51	0
41	4D4	CN	81	41	9,11,12	2.20	2 (22%)	8,13,15	2.33	2 (25%)
55	5MU	DA	1939	55	19,22,23	0.53	0	28,32,35	0.41	0
32	MEQ	DD	150[B]	32	8,9,10	1.10	1 (12%)	5,10,12	0.73	0
55	OMG	DA	2251	55	18,26,27	1.01	1 (5%)	19,38,41	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	4D4	DN	81[B]	-	9,11,12	1.76	2 (22%)	8,13,15	2.46	2 (25%)
41	4D4	DN	81[A]	-	9,11,12	1.68	2 (22%)	8,13,15	2.40	3 (37%)
55	1MG	DA	745	55	18,26,27	1.06	2 (11%)	19,39,42	0.47	0
1	5MC	AA	1407	1	18,22,23	0.47	0	26,32,35	0.53	0
1	7MG	AA	527	1	22,26,27	4.98	2 (9%)	29,39,42	2.39	6 (20%)
31	3TD	CA	1915	31	18,22,23	0.50	0	22,32,35	0.48	0
32	MEQ	DD	150[A]	32	8,9,10	0.38	0	5,10,12	0.54	0
31	5MU	CA	1939	31	19,22,23	0.50	0	28,32,35	0.36	0
12	D2T	AL	89	12	7,9,10	1.39	2 (28%)	6,11,13	1.14	0
31	6MZ	CA	2030	31	18,25,26	0.86	0	16,36,39	0.78	1 (6%)
55	H2U	DA	2449	55	18,21,22	0.48	0	21,30,33	0.67	1 (4%)
55	PSU	DA	1911	55	18,21,22	0.30	0	22,30,33	0.39	0
31	PSU	CA	746	31,56	18,21,22	0.56	1 (5%)	22,30,33	0.42	0
55	PSU	DA	2604	55	18,21,22	0.85	0	22,30,33	0.52	0
31	2MA	CA	2503	31	17,25,26	0.87	1 (5%)	17,37,40	0.47	0
31	OMU	CA	2552	31	19,22,23	0.34	0	26,31,34	0.28	0
31	PSU	CA	2580	31	18,21,22	0.51	0	22,30,33	0.60	0
1	MA6	AA	1519	1	19,26,27	0.86	0	18,38,41	1.03	1 (5%)
1	5MC	BA	1407	1	18,22,23	0.49	0	26,32,35	0.51	0
1	MA6	BA	1518	1	19,26,27	0.80	0	18,38,41	1.26	1 (5%)
1	5MC	BA	967	1	18,22,23	0.36	0	26,32,35	0.41	0
55	3TD	DA	1915	55	18,22,23	0.46	0	22,32,35	0.50	0
55	PSU	DA	1917	55	18,21,22	0.38	0	22,30,33	0.41	0
55	2MG	DA	2445	55	18,26,27	0.96	1 (5%)	16,38,41	0.58	0
31	7MG	CA	2069	31	22,26,27	4.87	3 (13%)	29,39,42	2.16	6 (20%)
55	PSU	DA	2605	55	18,21,22	0.51	0	22,30,33	0.51	0
31	PSU	CA	2457	31	18,21,22	0.74	1 (5%)	22,30,33	0.46	0
55	5MU	DA	747	55	19,22,23	0.45	0	28,32,35	0.31	0
1	2MG	AA	1207	1	18,26,27	0.85	0	16,38,41	0.54	0
1	5MC	AA	967	1	18,22,23	0.38	0	26,32,35	0.42	0
31	1MG	CA	745	31	18,26,27	0.80	1 (5%)	19,39,42	0.47	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
55	PSU	DA	955	55	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	OMU	DA	2552	55	-	1/9/27/28	0/2/2/2
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
55	6MZ	DA	2030	55	-	2/5/27/28	0/3/3/3
31	PSU	CA	2605	31	-	0/7/25/26	0/2/2/2
55	5MC	DA	1962	55	-	2/7/25/26	0/2/2/2
31	2MG	CA	1835	31	-	1/5/27/28	0/3/3/3
1	2MG	BA	966	1	-	0/5/27/28	0/3/3/3
31	OMG	CA	2251	31	-	0/5/27/28	0/3/3/3
55	PSU	DA	746	55,56	-	1/7/25/26	0/2/2/2
55	6MZ	DA	1618	55	-	0/5/27/28	0/3/3/3
55	2MA	DA	2503	55,56	-	2/3/25/26	0/3/3/3
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
1	MA6	BA	1519	1	-	3/7/29/30	0/3/3/3
55	PSU	DA	2504	55	-	0/7/25/26	0/2/2/2
1	UR3	BA	1498	1	-	0/7/25/26	0/2/2/2
55	7MG	DA	2069	55	-	2/7/37/38	0/3/3/3
55	PSU	DA	2457	55	-	0/7/25/26	0/2/2/2
1	PSU	BA	516	1	-	0/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	0/5/27/28	0/3/3/3
1	MA6	AA	1518	1	-	0/7/29/30	0/3/3/3
31	5MC	CA	1962	31	-	0/7/25/26	0/2/2/2
31	5MU	CA	747	31	-	0/7/25/26	0/2/2/2
55	2MG	DA	1835	55	-	2/5/27/28	0/3/3/3
55	PSU	DA	2580	55	-	0/7/25/26	0/2/2/2
31	PSU	CA	955	31	-	0/7/25/26	0/2/2/2
55	OMC	DA	2498	55,56	-	0/9/27/28	0/2/2/2
31	PSU	CA	2504	31	-	0/7/25/26	0/2/2/2
1	PSU	AA	516	1,56	-	0/7/25/26	0/2/2/2
1	4OC	BA	1402	1	-	0/9/29/30	0/2/2/2
1	2MG	BA	1516	1	-	0/5/27/28	0/3/3/3
31	PSU	CA	1911	31	-	0/7/25/26	0/2/2/2
31	PSU	CA	1917	31	-	0/7/25/26	0/2/2/2
1	2MG	BA	1207	1	-	0/5/27/28	0/3/3/3
1	7MG	BA	527	1	-	2/7/37/38	0/3/3/3
12	D2T	BL	89	12	-	2/7/12/14	-
31	6MZ	CA	1618	31	-	1/5/27/28	0/3/3/3
31	2MG	CA	2445	31	-	0/5/27/28	0/3/3/3
31	OMC	CA	2498	31,56	-	0/9/27/28	0/2/2/2
41	4D4	CN	81	41	-	1/11/12/14	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	5MU	DA	1939	55	-	0/7/25/26	0/2/2/2
32	MEQ	DD	150[B]	32	-	4/8/9/11	-
55	OMG	DA	2251	55	-	1/5/27/28	0/3/3/3
41	4D4	DN	81[B]	-	-	3/11/12/14	-
41	4D4	DN	81[A]	-	-	1/11/12/14	-
55	1MG	DA	745	55	-	0/3/25/26	0/3/3/3
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
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
32	MEQ	DD	150[A]	32	-	4/8/9/11	-
31	5MU	CA	1939	31	-	0/7/25/26	0/2/2/2
12	D2T	AL	89	12	-	1/7/12/14	-
31	6MZ	CA	2030	31	-	2/5/27/28	0/3/3/3
55	H2U	DA	2449	55	-	0/7/38/39	0/2/2/2
55	PSU	DA	1911	55	-	0/7/25/26	0/2/2/2
31	PSU	CA	746	31,56	-	1/7/25/26	0/2/2/2
55	PSU	DA	2604	55	-	0/7/25/26	0/2/2/2
31	2MA	CA	2503	31	-	2/3/25/26	0/3/3/3
31	OMU	CA	2552	31	-	1/9/27/28	0/2/2/2
31	PSU	CA	2580	31	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	2/7/29/30	0/3/3/3
1	5MC	BA	1407	1	-	0/7/25/26	0/2/2/2
1	MA6	BA	1518	1	-	0/7/29/30	0/3/3/3
1	5MC	BA	967	1	-	0/7/25/26	0/2/2/2
55	3TD	DA	1915	55	-	0/7/25/26	0/2/2/2
55	PSU	DA	1917	55	-	0/7/25/26	0/2/2/2
55	2MG	DA	2445	55	-	2/5/27/28	0/3/3/3
31	7MG	CA	2069	31	-	1/7/37/38	0/3/3/3
55	PSU	DA	2605	55	-	0/7/25/26	0/2/2/2
31	PSU	CA	2457	31	-	0/7/25/26	0/2/2/2
55	5MU	DA	747	55	-	1/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
31	1MG	CA	745	31	-	0/3/25/26	0/3/3/3

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	527	7MG	C8-N9	-23.02	1.33	1.46
55	DA	2069	7MG	C8-N9	-22.88	1.33	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	527	7MG	C8-N9	-22.82	1.33	1.46
31	CA	2069	7MG	C8-N9	-22.47	1.33	1.46
41	CN	81	4D4	CZ-NE	6.09	1.45	1.33
41	DN	81[B]	4D4	CZ-NE	4.71	1.42	1.33
41	DN	81[A]	4D4	CZ-NE	4.39	1.42	1.33
55	DA	746	PSU	O4'-C1'	-3.14	1.39	1.43
32	DD	150[B]	MEQ	CB-CA	2.99	1.57	1.53
55	DA	2251	OMG	C5-C6	-2.87	1.41	1.47
12	AL	89	D2T	CB-SB	2.77	1.85	1.82
12	BL	89	D2T	CB-CG	2.74	1.56	1.52
55	DA	2069	7MG	C5-N7	2.74	1.38	1.35
1	AA	527	7MG	C5-N7	2.68	1.38	1.35
31	CA	2069	7MG	C1'-N9	-2.46	1.42	1.46
55	DA	2445	2MG	O5'-C5'	-2.34	1.39	1.44
31	CA	2069	7MG	C5-N7	2.26	1.38	1.35
1	BA	527	7MG	C5-N7	2.22	1.38	1.35
41	CN	81	4D4	CZ-NH1	2.22	1.43	1.34
31	CA	2457	PSU	O5'-C5'	-2.13	1.39	1.44
31	CA	2503	2MA	C8-N7	-2.11	1.31	1.35
55	DA	745	1MG	C8-N7	-2.11	1.31	1.35
41	DN	81[A]	4D4	CZ-NH1	2.09	1.43	1.34
31	CA	745	1MG	C8-N7	-2.08	1.31	1.35
41	DN	81[B]	4D4	CZ-NH1	2.08	1.43	1.34
12	AL	89	D2T	CB-CG	2.07	1.55	1.52
55	DA	1962	5MC	O5'-C5'	-2.07	1.39	1.44
55	DA	955	PSU	C2'-C1'	-2.07	1.51	1.53
31	CA	1835	2MG	C8-N7	-2.05	1.31	1.35
31	CA	746	PSU	O4'-C1'	-2.02	1.41	1.43
55	DA	745	1MG	O4'-C1'	2.02	1.43	1.41
55	DA	2030	6MZ	O3'-C3'	-2.01	1.38	1.43
1	BA	1516	2MG	C5-C4	-2.01	1.38	1.43
55	DA	2030	6MZ	C2'-C1'	-2.00	1.50	1.53
55	DA	1835	2MG	C5-C4	-2.00	1.38	1.43

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	DA	1618	6MZ	C9-N6-C6	-7.91	116.06	122.87
1	AA	527	7MG	O4'-C1'-N9	6.49	118.14	109.30
1	BA	527	7MG	C6-C5-N7	-6.45	121.78	131.91
1	BA	527	7MG	O4'-C1'-N9	6.34	117.94	109.30
55	DA	2069	7MG	O4'-C1'-N9	5.94	117.39	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	CA	2069	7MG	C6-C5-N7	-5.84	122.73	131.91
41	DN	81[B]	4D4	NE-CZ-NH2	5.78	130.85	120.70
1	AA	527	7MG	C6-C5-N7	-5.68	122.98	131.91
31	CA	2069	7MG	C6-C5-C4	-5.62	111.04	122.62
41	CN	81	4D4	NE-CZ-NH2	5.57	130.49	120.70
1	BA	527	7MG	C5-C4-N3	-5.52	117.60	128.13
1	AA	527	7MG	C5-C4-N3	-5.40	117.83	128.13
41	DN	81[A]	4D4	NE-CZ-NH2	5.20	129.84	120.70
1	AA	527	7MG	C6-C5-C4	-5.13	112.04	122.62
55	DA	2069	7MG	C6-C5-N7	-5.11	123.88	131.91
1	BA	527	7MG	C6-C5-C4	-4.95	112.42	122.62
1	AA	527	7MG	N9-C8-N7	4.58	109.92	103.38
31	CA	2069	7MG	O4'-C1'-N9	4.57	115.52	109.30
55	DA	2069	7MG	N9-C8-N7	4.57	109.91	103.38
31	CA	2069	7MG	N9-C8-N7	4.51	109.82	103.38
1	BA	527	7MG	N9-C8-N7	4.48	109.78	103.38
31	CA	2069	7MG	C5-C4-N3	-4.43	119.68	128.13
1	BA	1518	MA6	N1-C6-N6	-4.38	112.45	117.06
1	AA	1518	MA6	N1-C6-N6	-4.32	112.51	117.06
55	DA	2069	7MG	C6-C5-C4	-3.95	114.48	122.62
55	DA	2069	7MG	C5-C4-N3	-3.70	121.07	128.13
41	DN	81[B]	4D4	NH1-CZ-NE	-3.50	111.11	119.19
41	DN	81[A]	4D4	NH1-CZ-NE	-3.23	111.75	119.19
1	AA	1519	MA6	N1-C6-N6	-3.01	113.89	117.06
1	BA	1519	MA6	N1-C6-N6	-2.97	113.93	117.06
41	CN	81	4D4	NH1-CZ-NE	-2.76	112.82	119.19
1	BA	527	7MG	C4-C5-N7	-2.59	101.94	105.53
1	AA	527	7MG	C4-C5-N7	-2.55	102.00	105.53
55	DA	2030	6MZ	C2-N1-C6	2.48	118.71	116.59
55	DA	2069	7MG	C4-C5-N7	-2.46	102.11	105.53
55	DA	2449	H2U	O4'-C1'-N1	2.45	112.64	109.30
55	DA	2030	6MZ	O4'-C1'-C2'	-2.41	103.41	106.93
41	DN	81[A]	4D4	CB-CA-C	-2.33	108.05	111.77
31	CA	2030	6MZ	C2-N1-C6	2.27	118.53	116.59
12	BL	89	D2T	OD1-CG-CB	2.20	127.06	122.44
1	BA	1498	UR3	C4-N3-C2	-2.15	122.54	124.56
31	CA	2069	7MG	C4-C5-N7	-2.08	102.64	105.53
55	DA	1618	6MZ	C2-N1-C6	2.01	118.31	116.59
31	CA	1618	6MZ	C2-N1-C6	2.00	118.31	116.59

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	527	7MG	O4'-C4'-C5'-O5'
1	AA	527	7MG	C3'-C4'-C5'-O5'
1	BA	527	7MG	O4'-C4'-C5'-O5'
1	BA	527	7MG	C3'-C4'-C5'-O5'
31	CA	2030	6MZ	O4'-C4'-C5'-O5'
32	DD	150[A]	MEQ	N-CA-CB-CG
32	DD	150[A]	MEQ	C-CA-CB-CG
32	DD	150[B]	MEQ	N-CA-CB-CG
32	DD	150[B]	MEQ	O-C-CA-CB
55	DA	2030	6MZ	O4'-C4'-C5'-O5'
55	DA	2251	OMG	C1'-C2'-O2'-CM2
41	DN	81[B]	4D4	CA-CB-CG-CD
31	CA	2030	6MZ	C3'-C4'-C5'-O5'
55	DA	2030	6MZ	C3'-C4'-C5'-O5'
1	AA	1519	MA6	O4'-C4'-C5'-O5'
1	BA	1519	MA6	O4'-C4'-C5'-O5'
1	AA	1519	MA6	C3'-C4'-C5'-O5'
1	BA	1519	MA6	C3'-C4'-C5'-O5'
55	DA	2445	2MG	C3'-C4'-C5'-O5'
41	DN	81[B]	4D4	OB-CB-CG-CD
32	DD	150[B]	MEQ	C-CA-CB-CG
32	DD	150[B]	MEQ	CA-CB-CG-CD
32	DD	150[A]	MEQ	OE1-CD-CG-CB
12	AL	89	D2T	CG-CB-SB-CB1
12	BL	89	D2T	CG-CB-SB-CB1
55	DA	2445	2MG	O4'-C4'-C5'-O5'
1	BA	1519	MA6	C5-C6-N6-C9
55	DA	2069	7MG	C4'-C5'-O5'-P
32	DD	150[A]	MEQ	NE2-CD-CG-CB
41	DN	81[A]	4D4	CG-CD-NE-CZ
41	DN	81[B]	4D4	N-CA-CB-CG
55	DA	1962	5MC	O4'-C1'-N1-C6
55	DA	1962	5MC	C2'-C1'-N1-C6
55	DA	747	5MU	C3'-C4'-C5'-O5'
12	BL	89	D2T	SB-CB-CG-OD2
55	DA	1835	2MG	O4'-C4'-C5'-O5'
31	CA	746	PSU	O4'-C1'-C5-C6
55	DA	746	PSU	O4'-C1'-C5-C6
31	CA	2069	7MG	O4'-C4'-C5'-O5'
31	CA	2503	2MA	O4'-C4'-C5'-O5'
55	DA	2069	7MG	O4'-C4'-C5'-O5'
55	DA	2503	2MA	O4'-C4'-C5'-O5'
31	CA	2503	2MA	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
55	DA	2503	2MA	C4'-C5'-O5'-P
31	CA	2552	OMU	C3'-C2'-O2'-CM2
55	DA	2552	OMU	C3'-C2'-O2'-CM2
31	CA	1835	2MG	O4'-C4'-C5'-O5'
41	CN	81	4D4	O-C-CA-CB
31	CA	1618	6MZ	C4'-C5'-O5'-P
55	DA	1835	2MG	C3'-C4'-C5'-O5'

There are no ring outliers.

18 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	DA	2030	6MZ	1	0
55	DA	2503	2MA	1	0
1	BA	1519	MA6	1	0
1	AA	1518	MA6	1	0
55	DA	2498	OMC	1	0
31	CA	2498	OMC	2	0
32	DD	150[B]	MEQ	1	0
55	DA	2251	OMG	1	0
55	DA	745	1MG	1	0
31	CA	1915	3TD	1	0
32	DD	150[A]	MEQ	3	0
31	CA	2030	6MZ	1	0
31	CA	2503	2MA	1	0
31	CA	2580	PSU	1	0
1	AA	1519	MA6	1	0
1	BA	1518	MA6	1	0
1	BA	967	5MC	1	0
1	AA	967	5MC	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides 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
57	PG4	BA	1642	-	12,12,12	0.15	0	11,11,11	0.20	0
57	PG4	DA	3193	-	12,12,12	0.30	0	11,11,11	0.25	0
59	PUT	DA	3188	-	5,5,5	0.21	0	4,4,4	0.13	0
63	EDO	DA	3215	-	3,3,3	0.69	0	2,2,2	0.18	0
59	PUT	AA	1674	-	5,5,5	0.16	0	4,4,4	0.10	0
62	PEG	DA	3227	-	6,6,6	0.21	0	5,5,5	0.14	0
60	T1C	BA	1643	56	44,45,45	1.02	3 (6%)	53,72,72	1.52	3 (5%)
58	MPD	DA	3210	-	7,7,7	0.63	0	9,10,10	0.28	0
59	PUT	DA	3219	-	5,5,5	0.17	0	4,4,4	0.20	0
63	EDO	DB	211	-	3,3,3	0.71	0	2,2,2	0.13	0
64	PGE	D1	102	-	9,9,9	0.20	0	8,8,8	0.14	0
59	PUT	DA	3223	-	5,5,5	0.16	0	4,4,4	0.15	0
64	PGE	DU	101	-	9,9,9	0.23	0	8,8,8	0.12	0
64	PGE	DA	3214	-	9,9,9	0.19	0	8,8,8	0.27	0
63	EDO	DA	3209	-	3,3,3	0.61	0	2,2,2	0.28	0
66	1PE	DA	3185	-	15,15,15	0.19	0	14,14,14	0.21	0
57	PG4	DS	202	-	12,12,12	0.45	0	11,11,11	0.30	0
59	PUT	DA	3189	-	5,5,5	0.30	0	4,4,4	0.18	0
59	PUT	DA	3184	-	5,5,5	0.16	0	4,4,4	0.12	0
62	PEG	D1	103	-	6,6,6	0.30	0	5,5,5	0.16	0
57	PG4	AA	1670	-	12,12,12	0.31	0	11,11,11	0.28	0
62	PEG	D3	102	-	6,6,6	0.21	0	5,5,5	0.20	0
58	MPD	AA	1671	-	7,7,7	0.67	0	9,10,10	0.49	0
58	MPD	DN	201	-	7,7,7	0.87	0	9,10,10	0.54	0
62	PEG	DL	201	-	6,6,6	0.07	0	5,5,5	0.10	0
63	EDO	DA	3002	-	3,3,3	0.69	0	2,2,2	0.19	0
59	PUT	DA	3221	-	5,5,5	0.17	0	4,4,4	0.10	0
59	PUT	DA	3222	-	5,5,5	0.44	0	4,4,4	0.54	0
63	EDO	DA	3208	-	3,3,3	0.68	0	2,2,2	0.16	0
62	PEG	DA	3226	-	6,6,6	0.24	0	5,5,5	0.13	0
57	PG4	DQ	202	-	12,12,12	0.20	0	11,11,11	0.14	0
69	TRS	DA	3220	-	7,7,7	0.26	0	9,9,9	0.27	0
58	MPD	DT	201	-	7,7,7	0.52	0	9,10,10	0.30	0
59	PUT	DA	3212	-	5,5,5	0.18	0	4,4,4	0.04	0
58	MPD	DA	3192	-	7,7,7	0.52	0	9,10,10	0.54	0
59	PUT	AA	1673	-	5,5,5	0.12	0	4,4,4	0.10	0
64	PGE	DS	201	-	9,9,9	0.25	0	8,8,8	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	MPD	DK	201	-	7,7,7	0.66	0	9,10,10	0.30	0
59	PUT	AA	1672	-	5,5,5	0.20	0	4,4,4	0.20	0
64	PGE	DA	3186	-	9,9,9	0.24	0	8,8,8	0.29	0
58	MPD	DE	301	-	7,7,7	0.81	0	9,10,10	0.56	0
64	PGE	DA	3203	-	9,9,9	0.21	0	8,8,8	0.20	0
59	PUT	DA	3205	-	5,5,5	0.12	0	4,4,4	0.12	0
68	GUN	DA	3211	-	7,12,12	0.36	0	8,17,17	0.68	0
63	EDO	DA	3194	-	3,3,3	0.80	0	2,2,2	0.13	0
58	MPD	DT	202	-	7,7,7	0.70	0	9,10,10	0.39	0
58	MPD	DA	3207	-	7,7,7	0.76	0	9,10,10	0.51	0
63	EDO	DA	3198	-	3,3,3	0.66	0	2,2,2	0.20	0
65	SPD	DA	3183	-	9,9,9	0.11	0	8,8,8	0.10	0
64	PGE	DA	3217	-	9,9,9	0.16	0	8,8,8	0.14	0
59	PUT	DA	3213	-	5,5,5	0.17	0	4,4,4	0.17	0
63	EDO	DB	212	-	3,3,3	0.58	0	2,2,2	0.30	0
58	MPD	DS	203	-	7,7,7	0.37	0	9,10,10	0.49	0
67	ACY	DA	3191	-	3,3,3	0.58	0	3,3,3	1.02	0
62	PEG	DP	201	-	6,6,6	0.16	0	5,5,5	0.09	0
60	T1C	AA	1680	56	44,45,45	1.04	3 (6%)	53,72,72	1.53	3 (5%)
62	PEG	DQ	201	-	6,6,6	0.12	0	5,5,5	0.09	0
59	PUT	DA	3001	-	5,5,5	0.25	0	4,4,4	0.13	0
63	EDO	DB	201	-	3,3,3	0.68	0	2,2,2	0.13	0
62	PEG	DA	3199	-	6,6,6	0.24	0	5,5,5	0.15	0
59	PUT	DA	3195	-	5,5,5	0.31	0	4,4,4	0.32	0
57	PG4	DR	202	-	12,12,12	0.26	0	11,11,11	0.36	0
62	PEG	DA	3200	-	6,6,6	0.34	0	5,5,5	0.22	0
59	PUT	AA	1675	-	5,5,5	0.21	0	4,4,4	0.12	0
65	SPD	DA	3224	-	9,9,9	0.20	0	8,8,8	0.38	0
63	EDO	D1	101	-	3,3,3	0.62	0	2,2,2	0.09	0
58	MPD	DE	302	-	7,7,7	0.88	1 (14%)	9,10,10	0.56	0
64	PGE	D3	101	-	9,9,9	0.22	0	8,8,8	0.22	0
67	ACY	DA	3201	-	3,3,3	0.74	0	3,3,3	1.12	0
66	1PE	DA	3202	-	15,15,15	0.32	0	14,14,14	0.34	0
67	ACY	DA	3196	-	3,3,3	2.15	1 (33%)	3,3,3	2.36	2 (66%)
58	MPD	DA	3204	-	7,7,7	0.77	0	9,10,10	0.70	0
58	MPD	AA	1676	-	7,7,7	0.60	0	9,10,10	0.54	0
62	PEG	DA	3218	-	6,6,6	0.16	0	5,5,5	0.09	0
64	PGE	DA	3225	-	9,9,9	0.12	0	8,8,8	0.17	0
63	EDO	DA	3197	-	3,3,3	0.67	0	2,2,2	0.18	0
65	SPD	DA	3206	-	9,9,9	0.21	0	8,8,8	0.15	0
57	PG4	DA	3216	-	12,12,12	0.11	0	11,11,11	0.17	0
63	EDO	DB	213	-	3,3,3	0.74	0	2,2,2	0.03	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	MPD	DA	3190	-	7,7,7	0.37	0	9,10,10	0.48	0
65	SPD	DA	3187	-	9,9,9	0.21	0	8,8,8	0.17	0
62	PEG	AL	201	-	6,6,6	0.23	0	5,5,5	0.13	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
57	PG4	BA	1642	-	-	0/10/10/10	-
57	PG4	DA	3193	-	-	6/10/10/10	-
59	PUT	DA	3188	-	-	0/3/3/3	-
63	EDO	DA	3215	-	-	1/1/1/1	-
59	PUT	AA	1674	-	-	0/3/3/3	-
62	PEG	DA	3227	-	-	0/4/4/4	-
60	T1C	BA	1643	56	-	11/22/80/80	0/4/4/4
58	MPD	DA	3210	-	-	0/5/5/5	-
59	PUT	DA	3219	-	-	0/3/3/3	-
63	EDO	DB	211	-	-	0/1/1/1	-
64	PGE	D1	102	-	-	3/7/7/7	-
59	PUT	DA	3223	-	-	1/3/3/3	-
64	PGE	DU	101	-	-	3/7/7/7	-
64	PGE	DA	3214	-	-	2/7/7/7	-
63	EDO	DA	3209	-	-	0/1/1/1	-
66	1PE	DA	3185	-	-	5/13/13/13	-
57	PG4	DS	202	-	-	5/10/10/10	-
59	PUT	DA	3189	-	-	0/3/3/3	-
59	PUT	DA	3184	-	-	0/3/3/3	-
62	PEG	D1	103	-	-	0/4/4/4	-
57	PG4	AA	1670	-	-	3/10/10/10	-
62	PEG	D3	102	-	-	1/4/4/4	-
58	MPD	AA	1671	-	-	0/5/5/5	-
58	MPD	DN	201	-	-	2/5/5/5	-
62	PEG	DL	201	-	-	2/4/4/4	-
63	EDO	DA	3002	-	-	0/1/1/1	-
59	PUT	DA	3221	-	-	0/3/3/3	-
59	PUT	DA	3222	-	-	0/3/3/3	-
63	EDO	DA	3208	-	-	0/1/1/1	-
62	PEG	DA	3226	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PG4	DQ	202	-	-	1/10/10/10	-
69	TRS	DA	3220	-	-	0/9/9/9	-
58	MPD	DT	201	-	-	2/5/5/5	-
59	PUT	DA	3212	-	-	0/3/3/3	-
58	MPD	DA	3192	-	-	2/5/5/5	-
59	PUT	AA	1673	-	-	0/3/3/3	-
64	PGE	DS	201	-	-	3/7/7/7	-
58	MPD	DK	201	-	-	2/5/5/5	-
59	PUT	AA	1672	-	-	0/3/3/3	-
64	PGE	DA	3186	-	-	3/7/7/7	-
58	MPD	DE	301	-	-	2/5/5/5	-
64	PGE	DA	3203	-	-	5/7/7/7	-
59	PUT	DA	3205	-	-	0/3/3/3	-
68	GUN	DA	3211	-	-	-	0/2/2/2
63	EDO	DA	3194	-	-	0/1/1/1	-
58	MPD	DT	202	-	-	1/5/5/5	-
58	MPD	DA	3207	-	-	3/5/5/5	-
63	EDO	DA	3198	-	-	1/1/1/1	-
65	SPD	DA	3183	-	-	1/7/7/7	-
64	PGE	DA	3217	-	-	4/7/7/7	-
59	PUT	DA	3213	-	-	0/3/3/3	-
63	EDO	DB	212	-	-	1/1/1/1	-
58	MPD	DS	203	-	-	0/5/5/5	-
62	PEG	DP	201	-	-	2/4/4/4	-
60	T1C	AA	1680	56	-	6/22/80/80	0/4/4/4
62	PEG	DQ	201	-	-	1/4/4/4	-
59	PUT	DA	3001	-	-	0/3/3/3	-
63	EDO	DB	201	-	-	1/1/1/1	-
62	PEG	DA	3199	-	-	2/4/4/4	-
59	PUT	DA	3195	-	-	1/3/3/3	-
57	PG4	DR	202	-	-	5/10/10/10	-
62	PEG	DA	3200	-	-	2/4/4/4	-
59	PUT	AA	1675	-	-	1/3/3/3	-
65	SPD	DA	3224	-	-	3/7/7/7	-
63	EDO	D1	101	-	-	0/1/1/1	-
58	MPD	DE	302	-	-	3/5/5/5	-
64	PGE	D3	101	-	-	2/7/7/7	-
66	1PE	DA	3202	-	-	4/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	MPD	DA	3204	-	-	2/5/5/5	-
58	MPD	AA	1676	-	-	2/5/5/5	-
62	PEG	DA	3218	-	-	1/4/4/4	-
64	PGE	DA	3225	-	-	4/7/7/7	-
63	EDO	DA	3197	-	-	0/1/1/1	-
65	SPD	DA	3206	-	-	3/7/7/7	-
57	PG4	DA	3216	-	-	3/10/10/10	-
63	EDO	DB	213	-	-	0/1/1/1	-
58	MPD	DA	3190	-	-	2/5/5/5	-
65	SPD	DA	3187	-	-	2/7/7/7	-
62	PEG	AL	201	-	-	2/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	DA	3196	ACY	O-C	3.55	1.38	1.22
60	BA	1643	T1C	C4-C3	3.16	1.58	1.51
60	AA	1680	T1C	C4-C3	2.86	1.57	1.51
60	AA	1680	T1C	C7-C61	2.76	1.43	1.40
60	BA	1643	T1C	C7-C61	2.71	1.43	1.40
60	BA	1643	T1C	C7-N7	2.60	1.49	1.42
60	AA	1680	T1C	C7-N7	2.52	1.49	1.42
58	DE	302	MPD	C3-C2	2.07	1.59	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BA	1643	T1C	C92-N92-C93	7.94	125.80	115.84
60	AA	1680	T1C	C92-N92-C93	7.70	125.49	115.84
60	AA	1680	T1C	C8-C9-C10	-5.12	115.41	120.49
60	BA	1643	T1C	C8-C9-C10	-4.54	115.98	120.49
67	DA	3196	ACY	OXT-C-CH3	3.07	127.87	115.18
67	DA	3196	ACY	O-C-CH3	-2.64	112.04	122.33
60	BA	1643	T1C	C11-C1B-C12	2.16	120.51	118.80
60	AA	1680	T1C	O3-C3-C2	2.05	126.56	122.96

There are no chirality outliers.

All (132) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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
60	BA	1643	T1C	C1-C2-C21-O21
60	BA	1643	T1C	C1-C2-C21-N21
57	DR	202	PG4	O2-C3-C4-O3
66	DA	3202	1PE	OH5-C14-C24-OH4
66	DA	3202	1PE	OH4-C13-C23-OH3
60	AA	1680	T1C	C94-C93-N92-C92
64	DA	3203	PGE	O2-C3-C4-O3
64	DU	101	PGE	O3-C5-C6-O4
60	BA	1643	T1C	C92-C91-N9-C9
57	DS	202	PG4	O1-C1-C2-O2
64	DU	101	PGE	O1-C1-C2-O2
57	DQ	202	PG4	O1-C1-C2-O2
65	DA	3224	SPD	C7-C8-C9-N10
65	DA	3183	SPD	C2-C3-C4-C5
60	BA	1643	T1C	O91-C91-N9-C9
57	DS	202	PG4	O4-C7-C8-O5
64	DA	3186	PGE	O3-C5-C6-O4
66	DA	3202	1PE	OH2-C12-C22-OH3
65	DA	3224	SPD	C4-C5-N6-C7
57	DA	3193	PG4	O3-C5-C6-O4
60	BA	1643	T1C	O91-C91-C92-N92
65	DA	3187	SPD	C2-C3-C4-C5
65	DA	3206	SPD	C2-C3-C4-C5
64	DA	3225	PGE	O3-C5-C6-O4
58	DE	302	MPD	O2-C2-C3-C4
58	DT	201	MPD	O2-C2-C3-C4
64	DA	3225	PGE	O2-C3-C4-O3
59	DA	3223	PUT	C1-C2-C3-C4
57	DA	3216	PG4	C3-C4-O3-C5
62	DA	3200	PEG	C1-C2-O2-C3
62	DA	3199	PEG	C4-C3-O2-C2
60	BA	1643	T1C	N9-C91-C92-N92
64	DA	3186	PGE	C3-C4-O3-C5
66	DA	3185	1PE	C12-C22-OH3-C23
62	DA	3218	PEG	C1-C2-O2-C3
64	DA	3217	PGE	C3-C4-O3-C5
60	BA	1643	T1C	C91-C92-N92-C93
64	DA	3214	PGE	C4-C3-O2-C2
57	DR	202	PG4	C4-C3-O2-C2

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Mol	Chain	Res	Type	Atoms
57	DR	202	PG4	C6-C5-O3-C4
57	DA	3193	PG4	C4-C3-O2-C2
64	D3	101	PGE	C4-C3-O2-C2
66	DA	3185	1PE	C16-C26-OH6-C15
64	DU	101	PGE	C6-C5-O3-C4
66	DA	3185	1PE	C13-C23-OH3-C22
60	AA	1680	T1C	O91-C91-C92-N92
57	AA	1670	PG4	C4-C3-O2-C2
62	AL	201	PEG	C4-C3-O2-C2
62	D3	102	PEG	C1-C2-O2-C3
64	DA	3225	PGE	C1-C2-O2-C3
64	DA	3203	PGE	C3-C4-O3-C5
64	D1	102	PGE	C4-C3-O2-C2
58	DE	301	MPD	C2-C3-C4-C5
58	DT	202	MPD	C2-C3-C4-C5
58	DA	3190	MPD	C2-C3-C4-C5
62	DP	201	PEG	C4-C3-O2-C2
64	D3	101	PGE	C3-C4-O3-C5
64	DS	201	PGE	C4-C3-O2-C2
57	DS	202	PG4	C4-C3-O2-C2
60	BA	1643	T1C	C3-C2-C21-N21
64	DA	3186	PGE	O1-C1-C2-O2
64	DA	3225	PGE	O1-C1-C2-O2
57	DA	3216	PG4	C8-C7-O4-C6
66	DA	3202	1PE	C12-C22-OH3-C23
58	DE	302	MPD	C2-C3-C4-O4
58	DN	201	MPD	C2-C3-C4-O4
64	DA	3203	PGE	C4-C3-O2-C2
57	DA	3193	PG4	C6-C5-O3-C4
58	DT	201	MPD	C1-C2-C3-C4
58	DA	3207	MPD	C1-C2-C3-C4
65	DA	3187	SPD	N6-C7-C8-C9
62	DA	3200	PEG	C4-C3-O2-C2
60	AA	1680	T1C	N9-C91-C92-N92
62	DA	3226	PEG	C4-C3-O2-C2
59	AA	1675	PUT	C1-C2-C3-C4
62	DQ	201	PEG	C1-C2-O2-C3
59	DA	3195	PUT	C1-C2-C3-C4
57	DA	3193	PG4	C3-C4-O3-C5
65	DA	3206	SPD	C8-C7-N6-C5
63	DB	201	EDO	O1-C1-C2-O2
64	D1	102	PGE	C3-C4-O3-C5

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Mol	Chain	Res	Type	Atoms
57	DR	202	PG4	O3-C5-C6-O4
64	DA	3203	PGE	C1-C2-O2-C3
64	DA	3217	PGE	C6-C5-O3-C4
65	DA	3224	SPD	C8-C7-N6-C5
62	AL	201	PEG	C1-C2-O2-C3
62	DA	3226	PEG	O1-C1-C2-O2
63	DA	3198	EDO	O1-C1-C2-O2
62	DL	201	PEG	C1-C2-O2-C3
57	AA	1670	PG4	C1-C2-O2-C3
66	DA	3185	1PE	C24-C14-OH5-C25
57	AA	1670	PG4	C5-C6-O4-C7
64	DA	3217	PGE	C1-C2-O2-C3
57	DS	202	PG4	C5-C6-O4-C7
64	D1	102	PGE	O2-C3-C4-O3
63	DA	3215	EDO	O1-C1-C2-O2
58	AA	1676	MPD	O2-C2-C3-C4
58	DA	3207	MPD	O2-C2-C3-C4
64	DA	3217	PGE	C4-C3-O2-C2
62	DA	3199	PEG	C1-C2-O2-C3
66	DA	3185	1PE	C23-C13-OH4-C24
57	DS	202	PG4	C1-C2-O2-C3
62	DP	201	PEG	C1-C2-O2-C3
57	DA	3216	PG4	C1-C2-O2-C3
65	DA	3206	SPD	C4-C5-N6-C7
64	DA	3203	PGE	O3-C5-C6-O4
63	DB	212	EDO	O1-C1-C2-O2
60	BA	1643	T1C	C61-C7-N7-C71
58	DE	302	MPD	C2-C3-C4-C5
58	DK	201	MPD	C2-C3-C4-C5
58	DN	201	MPD	C2-C3-C4-C5
58	DA	3192	MPD	C2-C3-C4-C5
58	DA	3204	MPD	C2-C3-C4-C5
58	DA	3207	MPD	C2-C3-C4-C5
62	DL	201	PEG	C4-C3-O2-C2
60	BA	1643	T1C	C61-C7-N7-C72
64	DA	3214	PGE	O3-C5-C6-O4
57	DR	202	PG4	C8-C7-O4-C6
64	DS	201	PGE	C6-C5-O3-C4
64	DS	201	PGE	O2-C3-C4-O3
60	BA	1643	T1C	C3-C2-C21-O21
57	DA	3193	PG4	O1-C1-C2-O2
57	DA	3193	PG4	O2-C3-C4-O3

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Mol	Chain	Res	Type	Atoms
58	AA	1676	MPD	C2-C3-C4-O4
58	DE	301	MPD	C2-C3-C4-O4
58	DK	201	MPD	C2-C3-C4-O4
58	DA	3190	MPD	C2-C3-C4-O4
58	DA	3204	MPD	C2-C3-C4-O4

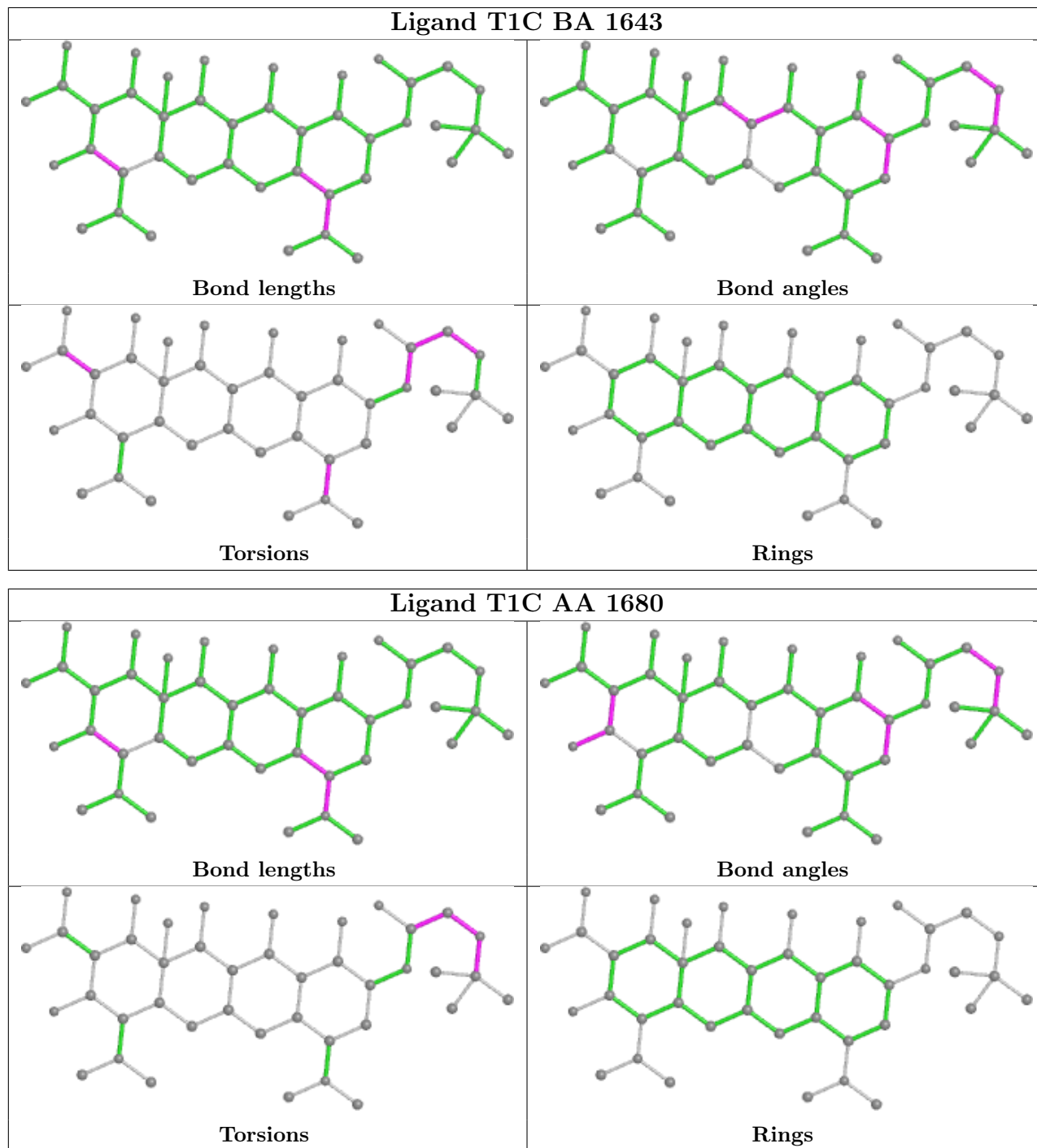
There are no ring outliers.

24 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	BA	1642	PG4	1	0
59	DA	3219	PUT	1	0
64	D1	102	PGE	2	0
59	DA	3223	PUT	1	0
64	DU	101	PGE	1	0
64	DA	3214	PGE	1	0
63	DA	3209	EDO	1	0
66	DA	3185	1PE	1	0
57	DS	202	PG4	1	0
62	D1	103	PEG	1	0
57	AA	1670	PG4	1	0
58	DN	201	MPD	1	0
69	DA	3220	TRS	1	0
58	DA	3192	MPD	1	0
64	DS	201	PGE	1	0
64	DA	3203	PGE	1	0
64	DA	3217	PGE	1	0
60	AA	1680	T1C	2	0
59	DA	3195	PUT	1	0
57	DR	202	PG4	4	0
65	DA	3224	SPD	2	0
66	DA	3202	1PE	2	0
58	DA	3204	MPD	1	0
64	DA	3225	PGE	2	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

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	53 (3%) 44 23	43, 96, 240, 296	0
1	BA	1522/1534 (99%)	0.59	195 (12%) 3 1	59, 109, 268, 280	0
2	AB	224/224 (100%)	0.69	33 (14%) 2 1	72, 125, 197, 249	0
2	BB	224/224 (100%)	0.65	31 (13%) 2 1	101, 143, 205, 240	0
3	AC	206/206 (100%)	0.13	8 (3%) 39 20	78, 108, 137, 154	0
3	BC	206/206 (100%)	1.33	55 (26%) 0 0	103, 151, 181, 204	0
4	AD	205/205 (100%)	-0.19	0 100 100	71, 104, 137, 164	0
4	BD	205/205 (100%)	-0.34	0 100 100	51, 77, 108, 132	0
5	AE	155/155 (100%)	0.02	0 100 100	59, 84, 116, 155	0
5	BE	150/155 (96%)	0.14	1 (0%) 87 75	68, 94, 135, 207	0
6	AF	106/106 (100%)	0.17	3 (2%) 53 30	78, 107, 128, 148	0
6	BF	100/106 (94%)	0.32	3 (3%) 50 27	88, 124, 147, 160	0
7	AG	151/151 (100%)	0.93	35 (23%) 0 0	108, 141, 166, 178	0
7	BG	151/151 (100%)	3.03	88 (58%) 0 0	145, 205, 222, 231	0
8	AH	129/129 (100%)	0.03	2 (1%) 72 51	67, 89, 116, 132	0
8	BH	129/129 (100%)	0.10	4 (3%) 49 26	90, 113, 141, 157	0
9	AI	127/127 (100%)	1.25	33 (25%) 0 0	86, 142, 167, 175	0
9	BI	127/127 (100%)	1.95	46 (36%) 0 0	141, 172, 209, 221	0
10	AJ	99/99 (100%)	1.14	24 (24%) 0 0	91, 129, 150, 161	0
10	BJ	98/99 (98%)	2.76	52 (53%) 0 0	144, 175, 196, 202	0
11	AK	117/117 (100%)	0.75	14 (11%) 4 2	59, 117, 141, 150	0
11	BK	117/117 (100%)	0.63	13 (11%) 5 2	69, 115, 149, 175	0
12	AL	122/123 (99%)	0.02	3 (2%) 57 34	50, 70, 99, 133	0
12	BL	122/123 (99%)	0.33	5 (4%) 37 18	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%)	1.30	28 (24%) 0 0	116, 139, 175, 182	0
13	BM	114/114 (100%)	3.30	79 (69%) 0 0	202, 239, 248, 254	0
14	AN	100/100 (100%)	1.03	21 (21%) 1 0	84, 124, 192, 203	0
14	BN	100/100 (100%)	2.33	52 (52%) 0 0	134, 185, 229, 236	0
15	AO	88/88 (100%)	0.17	2 (2%) 60 39	68, 92, 115, 136	0
15	BO	88/88 (100%)	0.44	4 (4%) 33 16	79, 113, 132, 152	0
16	AP	82/82 (100%)	0.54	7 (8%) 10 4	62, 86, 128, 142	0
16	BP	82/82 (100%)	0.76	11 (13%) 3 1	77, 94, 149, 159	0
17	AQ	80/80 (100%)	0.00	1 (1%) 77 59	64, 88, 118, 134	0
17	BQ	80/80 (100%)	0.77	12 (15%) 2 1	83, 120, 149, 157	0
18	AR	55/55 (100%)	0.36	4 (7%) 15 6	74, 101, 142, 166	0
18	BR	55/55 (100%)	0.52	3 (5%) 25 11	75, 97, 134, 166	0
19	AS	79/79 (100%)	0.76	6 (7%) 13 5	123, 139, 159, 165	0
19	BS	79/79 (100%)	3.47	56 (70%) 0 0	217, 233, 247, 254	0
20	AT	86/86 (100%)	0.22	1 (1%) 79 61	68, 86, 116, 133	0
20	BT	85/86 (98%)	0.89	14 (16%) 1 1	90, 119, 151, 161	0
21	AU	56/56 (100%)	0.50	4 (7%) 16 6	81, 118, 163, 176	0
21	BU	56/56 (100%)	0.30	4 (7%) 16 6	75, 110, 147, 155	0
22	C1	56/56 (100%)	1.53	17 (30%) 0 0	93, 147, 170, 185	0
22	D1	56/56 (100%)	-0.40	0 100 100	21, 47, 72, 112	0
23	C2	50/51 (98%)	2.71	31 (62%) 0 0	145, 160, 172, 198	0
23	D2	51/51 (100%)	0.03	0 100 100	56, 69, 100, 116	0
24	C3	46/46 (100%)	1.85	19 (41%) 0 0	102, 130, 139, 152	0
24	D3	46/46 (100%)	-0.10	1 (2%) 62 41	30, 40, 58, 116	0
25	C4	64/64 (100%)	1.00	8 (12%) 3 1	108, 134, 150, 160	0
25	D4	64/64 (100%)	-0.33	0 100 100	32, 41, 57, 75	0
26	C5	38/38 (100%)	1.54	10 (26%) 0 0	115, 134, 145, 151	0
26	D5	38/38 (100%)	-0.10	0 100 100	43, 55, 72, 99	0
27	C0	58/58 (100%)	1.69	19 (32%) 0 0	109, 132, 151, 162	0
27	D0	58/58 (100%)	-0.39	0 100 100	29, 39, 64, 83	0
28	CB	118/120 (98%)	0.63	12 (10%) 6 2	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%)	-0.14	0 100 100	34, 63, 99, 131	0
29	CC	271/272 (99%)	0.32	14 (5%) 27 12	73, 100, 126, 136	0
29	DC	271/272 (99%)	-0.32	1 (0%) 92 84	26, 57, 84, 99	0
30	CD	209/209 (100%)	0.91	35 (16%) 1 1	79, 116, 143, 158	0
31	CA	2876/2904 (99%)	0.70	304 (10%) 6 2	64, 133, 248, 291	0
32	DD	208/209 (99%)	-0.40	0 100 100	20, 41, 71, 100	0
33	CE	201/201 (100%)	1.05	41 (20%) 1 0	90, 160, 190, 200	0
33	DE	201/201 (100%)	-0.25	1 (0%) 91 81	25, 62, 104, 136	0
34	CF	177/178 (99%)	2.86	112 (63%) 0 0	201, 219, 227, 235	0
34	DF	177/178 (99%)	0.15	7 (3%) 38 19	54, 89, 132, 150	0
35	CG	176/176 (100%)	2.02	76 (43%) 0 0	140, 167, 194, 206	0
35	DG	176/176 (100%)	-0.11	1 (0%) 89 78	44, 75, 103, 136	0
36	CH	149/149 (100%)	1.24	38 (25%) 0 0	89, 149, 175, 187	0
36	DH	149/149 (100%)	0.90	27 (18%) 1 0	71, 150, 190, 207	0
37	CJ	134/135 (99%)	5.86	119 (88%) 0 0	241, 258, 269, 276	0
37	DJ	134/135 (99%)	3.91	93 (69%) 0 0	210, 234, 245, 252	0
38	CK	142/142 (100%)	0.31	1 (0%) 87 75	84, 109, 134, 142	0
38	DK	142/142 (100%)	-0.45	0 100 100	23, 37, 67, 88	0
39	CL	122/123 (99%)	0.23	4 (3%) 46 24	76, 99, 141, 159	0
39	DL	123/123 (100%)	-0.42	0 100 100	28, 44, 71, 110	0
40	CM	144/144 (100%)	1.98	55 (38%) 0 0	94, 152, 193, 222	0
40	DM	144/144 (100%)	-0.32	1 (0%) 87 75	18, 56, 88, 121	0
41	CN	135/136 (99%)	0.29	4 (2%) 50 27	76, 111, 139, 174	0
41	DN	135/136 (99%)	-0.54	0 100 100	26, 43, 73, 95	0
42	CO	120/125 (96%)	1.00	19 (15%) 2 1	93, 124, 143, 189	0
42	DO	125/125 (100%)	-0.38	0 100 100	27, 40, 76, 125	0
43	CP	116/117 (99%)	2.38	60 (51%) 0 0	142, 164, 181, 187	0
43	DP	117/117 (100%)	-0.16	0 100 100	42, 61, 90, 99	0
44	CQ	114/114 (100%)	0.83	17 (14%) 2 1	96, 114, 138, 154	0
44	DQ	114/114 (100%)	-0.32	1 (0%) 84 69	28, 52, 86, 125	0
45	CR	117/117 (100%)	0.73	12 (10%) 6 2	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%)	-0.30	0 100 100	19, 34, 52, 82	0
46	CS	103/103 (100%)	1.66	28 (27%) 0 0	101, 124, 166, 174	0
46	DS	103/103 (100%)	-0.36	0 100 100	22, 45, 74, 101	0
47	CT	110/110 (100%)	0.71	14 (12%) 3 1	99, 126, 157, 172	0
47	DT	110/110 (100%)	-0.45	0 100 100	26, 37, 67, 120	0
48	CU	93/93 (100%)	1.83	33 (35%) 0 0	124, 154, 178, 190	0
48	DU	93/93 (100%)	0.18	3 (3%) 47 25	41, 63, 120, 139	0
49	CV	102/103 (99%)	2.69	55 (53%) 0 0	132, 164, 197, 206	0
49	DV	102/103 (99%)	-0.04	7 (6%) 16 7	49, 67, 116, 143	0
50	CW	94/94 (100%)	1.35	28 (29%) 0 0	122, 144, 158, 167	0
50	DW	94/94 (100%)	-0.43	0 100 100	38, 58, 88, 96	0
51	CX	75/83 (90%)	0.74	10 (13%) 3 1	95, 126, 138, 176	0
51	DX	76/83 (91%)	-0.49	0 100 100	29, 43, 72, 108	0
52	CY	77/77 (100%)	0.35	5 (6%) 18 8	87, 116, 146, 163	0
52	DY	77/77 (100%)	-0.19	0 100 100	34, 58, 96, 112	0
53	CZ	62/62 (100%)	2.52	38 (61%) 0 0	139, 171, 185, 191	0
53	DZ	62/62 (100%)	0.32	2 (3%) 47 25	51, 81, 123, 140	0
54	DI	135/135 (100%)	1.33	33 (24%) 0 0	82, 161, 211, 226	1 (0%)
55	DA	2873/2904 (98%)	0.09	101 (3%) 44 23	22, 47, 217, 299	0
All	All	20634/20767 (99%)	0.59	2527 (12%) 4 1	18, 106, 237, 299	1 (0%)

All (2527) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
37	DJ	54	PRO	22.9
37	CJ	76	ALA	22.4
37	CJ	13	VAL	18.2
37	CJ	87	LYS	17.4
55	DA	2120	G	16.3
37	CJ	54	PRO	15.9
9	BI	128	SER	15.4
37	DJ	135	SER	15.4
37	CJ	12	GLN	14.6
37	CJ	69	PHE	14.4
37	CJ	14	ALA	14.2

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Mol	Chain	Res	Type	RSRZ
37	DJ	53	LEU	13.8
31	CA	2172	U	13.8
31	CA	1067	A	13.7
37	CJ	11	LEU	13.1
31	CA	1068	G	12.9
37	DJ	79	LEU	12.6
37	CJ	23	PRO	12.3
37	CJ	20	PRO	12.0
37	CJ	21	SER	12.0
40	CM	81	ASP	11.8
37	CJ	56	PRO	11.5
35	CG	32	GLU	11.4
9	AI	130	ARG	11.3
46	CS	50	GLY	11.3
31	CA	2174	C	11.2
37	DJ	67	PHE	11.1
37	DJ	94	ASN	11.1
7	BG	112	GLY	11.1
37	CJ	138	LEU	10.9
37	CJ	57	VAL	10.9
55	DA	2110	G	10.9
37	CJ	86	ILE	10.8
7	BG	52	GLN	10.7
1	BA	1302	C	10.7
37	CJ	22	PRO	10.6
37	CJ	80	LEU	10.5
37	DJ	80	LEU	10.2
37	CJ	51	LYS	10.1
37	DJ	55	ILE	10.1
37	CJ	82	LYS	10.1
54	DI	131	THR	10.0
10	BJ	41	PRO	9.8
10	BJ	74	VAL	9.8
9	BI	130	ARG	9.7
7	BG	62	PHE	9.6
37	DJ	96	ASP	9.5
1	BA	1030	U	9.5
19	BS	29	LYS	9.4
19	BS	74	PHE	9.4
37	CJ	89	GLY	9.3
31	CA	2110	G	9.3
37	CJ	75	PRO	9.3

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Mol	Chain	Res	Type	RSRZ
1	BA	82	G	9.2
1	BA	1024	G	9.2
19	BS	48	THR	9.2
13	BM	84	GLY	9.2
9	BI	16	ALA	9.2
37	DJ	88	SER	9.2
37	CJ	129	ILE	9.1
55	DA	2124	G	9.1
34	CF	155	THR	9.1
7	BG	49	THR	9.0
34	CF	106	ILE	9.0
49	CV	3	ALA	8.9
9	BI	17	ALA	8.9
18	BR	20	GLU	8.9
10	BJ	8	ILE	8.9
37	CJ	77	ALA	8.9
31	CA	2173	A	8.8
7	BG	45	SER	8.8
13	BM	45	ILE	8.8
31	CA	331	C	8.8
31	CA	1087	G	8.7
37	CJ	88	SER	8.7
37	DJ	116	ASP	8.6
31	CA	2126	A	8.6
19	BS	66	MET	8.5
37	CJ	131	GLY	8.5
1	BA	1020	G	8.5
37	CJ	79	LEU	8.4
55	DA	2127	G	8.4
37	DJ	131	GLY	8.4
37	CJ	55	ILE	8.3
1	BA	983	A	8.3
37	CJ	17	MET	8.3
31	CA	1537	G	8.3
34	CF	23	ASN	8.3
14	BN	35	ASN	8.2
7	BG	43	VAL	8.2
31	CA	2402	U	8.2
40	CM	80	SER	8.2
19	BS	49	ILE	8.1
7	BG	73	VAL	8.1
7	BG	134	ALA	8.1

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Mol	Chain	Res	Type	RSRZ
10	BJ	75	ASP	8.1
27	C0	48	ILE	8.0
37	DJ	12	GLN	8.0
1	BA	1242	G	8.0
9	BI	31	ASN	8.0
37	DJ	23	PRO	8.0
37	DJ	13	VAL	7.9
1	BA	1016	A	7.9
34	CF	128	TYR	7.9
7	BG	42	ILE	7.9
55	DA	2174	C	7.9
31	CA	1084	A	7.9
1	AA	1030	U	7.9
31	CA	931	U	7.9
37	DJ	78	VAL	7.8
1	BA	1241	G	7.8
37	CJ	42	PHE	7.8
37	DJ	138	LEU	7.8
1	BA	1022	A	7.8
37	DJ	87	LYS	7.7
31	CA	1103	A	7.7
55	DA	2111	U	7.7
37	CJ	99	GLY	7.7
13	BM	48	LEU	7.7
23	C2	47	VAL	7.7
1	BA	1025	U	7.7
48	CU	1	MET	7.6
55	DA	2121	G	7.6
7	BG	111	ARG	7.6
13	BM	64	VAL	7.5
55	DA	2175	C	7.5
37	CJ	52	GLY	7.5
37	CJ	78	VAL	7.5
14	BN	36	ALA	7.5
10	BJ	90	LEU	7.5
1	AA	86	G	7.5
9	BI	126	GLN	7.5
13	BM	46	SER	7.5
37	CJ	50	GLU	7.5
23	C2	52	ALA	7.4
37	CJ	73	THR	7.4
31	CA	1066	U	7.4

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Mol	Chain	Res	Type	RSRZ
37	CJ	83	ALA	7.4
34	CF	153	ASP	7.4
35	CG	103	ILE	7.4
31	CA	1057	A	7.4
19	BS	39	THR	7.3
40	CM	78	ARG	7.3
1	AA	87	C	7.3
37	DJ	114	ALA	7.3
53	CZ	45	GLN	7.3
31	CA	2125	G	7.3
55	DA	2123	G	7.3
55	DA	2163	A	7.3
31	CA	1065	U	7.2
55	DA	2167	U	7.2
37	CJ	120	ALA	7.2
37	DJ	24	VAL	7.2
49	CV	80	ALA	7.2
7	BG	133	THR	7.2
37	DJ	76	ALA	7.2
13	BM	104	THR	7.2
55	DA	2125	G	7.2
19	BS	30	PRO	7.2
20	BT	4	ILE	7.1
43	CP	64	TYR	7.1
31	CA	1085	A	7.1
13	BM	95	LEU	7.1
31	CA	1095	A	7.1
53	CZ	49	ASP	7.1
37	CJ	24	VAL	7.1
31	CA	1731	G	7.0
10	BJ	100	ILE	7.0
13	BM	105	ASN	7.0
49	CV	31	SER	7.0
37	CJ	53	LEU	6.9
10	BJ	91	ASP	6.9
13	BM	2	ALA	6.9
55	DA	2116	G	6.9
7	BG	65	ALA	6.9
20	BT	3	ASN	6.9
37	CJ	59	ILE	6.9
1	BA	1243	C	6.8
7	BG	116	MET	6.8

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Mol	Chain	Res	Type	RSRZ
34	CF	85	ILE	6.8
1	BA	1017	U	6.8
7	BG	129	GLU	6.8
31	CA	877	A	6.8
55	DA	884	U	6.8
37	CJ	45	LYS	6.8
13	BM	23	TYR	6.7
31	CA	1064	C	6.7
37	DJ	89	GLY	6.7
13	BM	83	LEU	6.7
37	CJ	85	GLY	6.7
1	AA	1032	G	6.7
54	DI	130	PRO	6.7
49	CV	33	LYS	6.7
43	CP	29	HIS	6.6
14	BN	37	SER	6.6
31	CA	2171	A	6.6
43	CP	117	PHE	6.6
43	CP	52	SER	6.6
13	BM	19	LEU	6.6
31	CA	1175	A	6.6
37	CJ	28	LEU	6.6
31	CA	2168	G	6.6
19	BS	60	VAL	6.6
37	CJ	61	VAL	6.5
14	AN	23	LYS	6.5
1	BA	1032	G	6.5
7	BG	53	ARG	6.5
14	BN	4	GLN	6.5
3	BC	196	ILE	6.5
37	DJ	38	PHE	6.5
48	CU	55	VAL	6.5
13	BM	22	ILE	6.5
13	BM	96	PRO	6.5
19	BS	28	LYS	6.5
37	CJ	60	THR	6.5
35	CG	2	SER	6.5
31	CA	1105	U	6.5
49	CV	89	ASP	6.4
37	CJ	81	LYS	6.4
37	CJ	90	SER	6.4
37	DJ	137	GLY	6.4

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Mol	Chain	Res	Type	RSRZ
10	BJ	6	ILE	6.4
55	DA	2118	U	6.4
37	DJ	77	ALA	6.4
41	CN	136	MET	6.4
14	BN	60	GLN	6.4
1	AA	1031	C	6.4
31	CA	1104	C	6.4
43	CP	37	ALA	6.3
37	CJ	96	ASP	6.3
34	CF	170	LEU	6.3
1	BA	1296	C	6.3
34	CF	40	VAL	6.3
31	CA	1536	C	6.3
31	CA	2119	A	6.3
37	CJ	121	ASP	6.3
9	AI	20	PHE	6.3
40	CM	77	ILE	6.3
35	CG	148	LEU	6.3
1	BA	1274	A	6.2
31	CA	1086	A	6.2
14	AN	21	PHE	6.2
1	AA	844	G	6.2
7	BG	66	LEU	6.2
55	DA	2168	G	6.2
7	BG	48	GLU	6.2
23	C2	36	LEU	6.2
1	BA	844	G	6.2
10	BJ	40	ILE	6.2
14	BN	30	ILE	6.2
1	BA	1305	G	6.2
31	CA	2123	G	6.2
1	BA	1314	C	6.2
31	CA	2169	A	6.2
34	CF	102	ARG	6.1
34	CF	97	TRP	6.1
1	BA	1031	C	6.1
55	DA	1065	U	6.1
55	DA	2172	U	6.1
48	CU	8	LEU	6.1
22	C1	27	SER	6.1
34	CF	107	ALA	6.1
50	CW	94	ALA	6.1

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Mol	Chain	Res	Type	RSRZ
42	CO	120	GLU	6.1
37	CJ	94	ASN	6.1
55	DA	1062	G	6.1
9	BI	67	VAL	6.0
48	CU	83	ALA	6.0
37	DJ	133	ALA	6.0
31	CA	2128	G	6.0
40	CM	82	LEU	6.0
31	CA	878	A	6.0
34	CF	175	PHE	6.0
46	CS	96	VAL	6.0
10	BJ	76	ILE	6.0
37	CJ	74	PRO	6.0
7	BG	148	ASN	6.0
37	CJ	67	PHE	6.0
7	BG	91	VAL	6.0
34	CF	173	PHE	6.0
37	CJ	98	VAL	5.9
17	BQ	70	THR	5.9
1	BA	1021	A	5.9
1	BA	1026	G	5.9
43	CP	65	THR	5.9
55	DA	1172	C	5.9
34	CF	147	ASP	5.9
13	BM	39	ILE	5.9
48	CU	43	ILE	5.9
55	DA	1731	G	5.9
1	BA	1240	U	5.9
46	CS	55	ASP	5.9
1	BA	1236	A	5.9
13	BM	10	PRO	5.9
49	CV	81	ASP	5.9
31	CA	2120	G	5.9
55	DA	2166	U	5.9
34	CF	131	GLY	5.8
37	CJ	116	ASP	5.8
50	CW	27	PRO	5.8
7	BG	54	SER	5.8
19	BS	71	LEU	5.8
31	CA	2175	C	5.8
13	BM	11	ASP	5.8
49	CV	69	ASN	5.8

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Mol	Chain	Res	Type	RSRZ
49	CV	87	PHE	5.8
23	C2	21	TYR	5.8
9	BI	32	GLN	5.8
7	BG	72	THR	5.8
10	BJ	7	ARG	5.8
37	CJ	15	ALA	5.8
37	CJ	126	THR	5.8
37	CJ	139	VAL	5.8
13	AM	44	LYS	5.8
37	DJ	69	PHE	5.8
40	CM	114	GLY	5.8
33	CE	143	LEU	5.8
7	BG	150	ALA	5.8
23	C2	24	THR	5.8
7	BG	151	PHE	5.8
13	BM	47	GLU	5.8
37	CJ	130	GLU	5.8
9	AI	129	LYS	5.8
49	DV	56	GLY	5.8
43	CP	38	GLN	5.8
37	CJ	68	THR	5.7
37	DJ	68	THR	5.7
48	CU	2	ILE	5.7
14	BN	43	ASN	5.7
37	CJ	38	PHE	5.7
54	DI	134	GLU	5.7
3	BC	197	GLY	5.7
54	DI	128	THR	5.7
13	BM	12	HIS	5.7
7	BG	41	SER	5.7
9	AI	90	TYR	5.7
31	CA	2170	A	5.7
37	DJ	134	ARG	5.7
34	CF	144	ASP	5.7
37	CJ	47	ASP	5.7
37	CJ	48	SER	5.7
40	CM	92	LEU	5.7
40	CM	120	VAL	5.7
31	CA	2124	G	5.7
48	CU	59	ASN	5.7
37	DJ	21	SER	5.7
27	C0	56	LYS	5.6

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Mol	Chain	Res	Type	RSRZ
55	DA	885	C	5.6
9	BI	38	TYR	5.6
34	CF	156	ILE	5.6
31	CA	2127	G	5.6
14	BN	54	ASP	5.6
19	BS	38	SER	5.6
34	CF	113	ASP	5.6
10	BJ	73	LEU	5.6
3	BC	193	TYR	5.6
31	CA	896	A	5.6
3	BC	79	LYS	5.6
23	C2	39	PHE	5.5
55	DA	879	G	5.5
35	CG	33	LEU	5.5
55	DA	881	G	5.5
43	CP	92	PHE	5.5
19	BS	37	ARG	5.5
31	CA	2162	G	5.5
19	BS	24	GLU	5.5
53	CZ	36	GLN	5.5
13	AM	33	ILE	5.5
1	BA	1018	G	5.5
7	BG	152	ALA	5.5
13	BM	108	THR	5.5
7	BG	39	ALA	5.5
19	BS	12	ASP	5.5
3	BC	71	ALA	5.5
31	CA	1061	U	5.5
37	CJ	25	GLY	5.5
24	C3	35	ARG	5.5
43	CP	40	ILE	5.5
55	DA	882	G	5.5
37	DJ	20	PRO	5.4
10	AJ	75	ASP	5.4
34	CF	92	ARG	5.4
54	DI	136	ILE	5.4
3	BC	159	GLY	5.4
7	BG	46	ALA	5.4
31	CA	329	G	5.4
54	DI	2	ALA	5.4
37	CJ	33	VAL	5.4
55	DA	896	A	5.4

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Mol	Chain	Res	Type	RSRZ
9	BI	127	PHE	5.4
7	BG	106	GLU	5.4
23	C2	37	LYS	5.4
55	DA	2176	A	5.3
53	CZ	15	ASN	5.3
13	BM	32	ALA	5.3
2	AB	123	ASP	5.3
7	BG	15	ASP	5.3
37	CJ	46	THR	5.3
37	CJ	132	THR	5.3
55	DA	2109	U	5.3
34	CF	76	GLY	5.3
7	BG	79	ARG	5.3
7	AG	4	ARG	5.3
1	BA	79	G	5.3
49	CV	70	VAL	5.3
10	BJ	26	VAL	5.3
10	BJ	72	ARG	5.3
49	CV	29	LEU	5.2
55	DA	2178	C	5.2
14	BN	52	PRO	5.2
31	CA	2109	U	5.2
37	DJ	59	ILE	5.2
43	CP	51	ALA	5.2
34	CF	34	ILE	5.2
26	C5	1	MET	5.2
35	CG	105	LEU	5.2
55	DA	2164	C	5.2
55	DA	1067	A	5.2
37	DJ	66	SER	5.2
34	CF	130	MET	5.2
19	BS	61	PHE	5.2
34	CF	86	GLY	5.2
31	CA	1083	U	5.2
1	BA	211	G	5.2
7	BG	103	TRP	5.2
49	CV	5	ILE	5.2
49	CV	32	GLY	5.2
1	BA	1028	C	5.2
49	CV	83	VAL	5.2
34	CF	35	THR	5.2
40	CM	100	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
35	CG	84	THR	5.2
7	BG	109	ARG	5.2
1	BA	1218	C	5.2
1	BA	954	G	5.1
1	BA	1004	A	5.1
37	DJ	52	GLY	5.1
31	CA	1535	A	5.1
31	CA	1078	U	5.1
14	BN	33	ASP	5.1
9	AI	128	SER	5.1
3	BC	53	SER	5.1
9	BI	9	THR	5.1
13	BM	94	GLY	5.1
37	DJ	95	LYS	5.1
3	BC	192	THR	5.0
34	CF	138	PHE	5.0
37	DJ	99	GLY	5.0
19	BS	41	PHE	5.0
40	CM	117	THR	5.0
55	DA	892	A	5.0
43	CP	66	GLY	5.0
7	BG	75	VAL	5.0
43	CP	36	TYR	5.0
19	BS	43	ASN	5.0
10	BJ	39	PRO	5.0
7	BG	137	LYS	5.0
37	DJ	113	LYS	5.0
55	DA	1064	C	5.0
46	CS	20	VAL	5.0
14	BN	39	GLU	5.0
13	BM	63	PHE	5.0
49	CV	4	LYS	5.0
10	BJ	102	LEU	5.0
34	CF	117	LEU	5.0
31	CA	2797	U	5.0
7	BG	69	VAL	4.9
1	BA	985	C	4.9
1	BA	989	U	4.9
49	CV	12	ILE	4.9
43	CP	30	ARG	4.9
37	CJ	18	ALA	4.9
37	CJ	8	TYR	4.9

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Mol	Chain	Res	Type	RSRZ
1	BA	1217	C	4.9
44	CQ	115	ASN	4.9
49	CV	79	LYS	4.9
10	BJ	87	LEU	4.9
19	BS	31	LEU	4.9
34	CF	75	ALA	4.9
35	CG	111	HIS	4.9
7	BG	71	PRO	4.9
31	CA	846	U	4.9
53	CZ	17	GLU	4.9
3	BC	195	VAL	4.9
19	BS	50	ALA	4.9
35	CG	151	TYR	4.9
43	CP	99	TYR	4.9
34	CF	60	ILE	4.9
35	CG	131	ILE	4.9
1	BA	1023	U	4.9
13	BM	55	THR	4.9
31	CA	876	C	4.9
31	CA	2161	C	4.9
19	BS	81	ARG	4.9
37	CJ	95	LYS	4.9
55	DA	1729	U	4.9
10	BJ	77	VAL	4.8
13	AM	43	VAL	4.8
31	CA	2121	G	4.8
23	C2	15	ALA	4.8
27	C0	24	LEU	4.8
31	CA	138	U	4.8
42	CO	63	ARG	4.8
13	AM	11	ASP	4.8
33	CE	144	GLU	4.8
55	DA	2171	A	4.8
49	CV	28	VAL	4.8
55	DA	883	G	4.8
55	DA	2119	A	4.8
31	CA	1870	C	4.8
9	BI	68	LYS	4.8
31	CA	546	U	4.8
37	CJ	62	TYR	4.8
31	CA	1107	G	4.8
48	DU	1	MET	4.8

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Mol	Chain	Res	Type	RSRZ
33	CE	119	ILE	4.8
19	BS	5	LEU	4.8
1	BA	1271	A	4.8
34	CF	174	ASP	4.8
9	BI	40	GLY	4.8
37	CJ	91	GLY	4.8
37	CJ	125	MET	4.8
49	CV	2	ALA	4.8
9	BI	14	SER	4.8
34	CF	136	ILE	4.8
46	CS	32	THR	4.8
24	C3	28	ARG	4.7
34	CF	154	ILE	4.7
37	CJ	43	ASN	4.7
10	BJ	35	GLN	4.7
9	BI	64	TYR	4.7
37	DJ	11	LEU	4.7
49	CV	88	GLU	4.7
23	C2	18	GLY	4.7
34	CF	37	ASN	4.7
37	DJ	92	LYS	4.7
11	AK	18	ASP	4.7
1	BA	1307	U	4.7
34	CF	177	PHE	4.7
55	DA	1066	U	4.7
9	BI	10	GLY	4.7
55	DA	1060	U	4.7
26	C5	38	GLY	4.7
49	CV	25	VAL	4.7
7	BG	131	LYS	4.7
1	BA	80	A	4.7
1	BA	1201	A	4.7
43	CP	103	VAL	4.7
1	AA	82	G	4.7
37	CJ	58	VAL	4.7
1	BA	81	A	4.7
55	DA	1077	A	4.7
40	CM	79	LEU	4.7
13	BM	29	ARG	4.7
7	BG	38	THR	4.7
10	BJ	37	ARG	4.7
51	CX	54	GLY	4.7

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Mol	Chain	Res	Type	RSRZ
26	C5	20	ASP	4.7
34	CF	132	VAL	4.7
34	CF	93	GLY	4.6
37	CJ	119	GLY	4.6
14	BN	22	ALA	4.6
31	CA	893	C	4.6
35	CG	162	VAL	4.6
37	DJ	22	PRO	4.6
1	BA	208	U	4.6
34	CF	122	PHE	4.6
9	BI	5	GLN	4.6
37	CJ	113	LYS	4.6
3	BC	198	VAL	4.6
43	CP	63	LYS	4.6
7	BG	88	PRO	4.6
14	AN	8	ALA	4.6
27	C0	44	ILE	4.6
9	BI	20	PHE	4.6
37	DJ	93	PRO	4.6
33	CE	104	ALA	4.6
13	BM	58	ASP	4.6
24	C3	22	MET	4.6
31	CA	1046	A	4.6
31	CA	2163	A	4.6
34	CF	135	GLN	4.6
31	CA	1106	G	4.6
11	AK	19	GLY	4.5
31	CA	2129	C	4.5
54	DI	96	PHE	4.5
37	CJ	31	GLN	4.5
53	CZ	42	LEU	4.5
19	BS	11	ILE	4.5
34	CF	99	PHE	4.5
10	BJ	10	LEU	4.5
19	BS	14	HIS	4.5
1	BA	959	A	4.5
1	BA	1275	A	4.5
10	BJ	38	GLY	4.5
13	AM	32	ALA	4.5
1	BA	984	C	4.5
7	BG	132	GLY	4.5
40	CM	118	THR	4.5

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Mol	Chain	Res	Type	RSRZ
10	BJ	19	ASP	4.5
19	BS	75	ALA	4.5
35	CG	102	VAL	4.5
31	CA	895	U	4.5
37	DJ	19	ASN	4.5
31	CA	2666	C	4.5
1	BA	1003	G	4.5
31	CA	879	G	4.5
37	CJ	123	GLU	4.5
37	CJ	124	ALA	4.5
31	CA	1094	U	4.5
7	BG	144	MET	4.5
19	BS	32	ARG	4.5
31	CA	2111	U	4.5
31	CA	1048	A	4.5
31	CA	1077	A	4.5
34	CF	105	THR	4.5
37	DJ	73	THR	4.5
7	AG	109	ARG	4.5
37	CJ	115	ALA	4.5
1	BA	962	C	4.5
40	CM	10	GLU	4.4
37	DJ	106	LEU	4.4
1	BA	1235	U	4.4
55	DA	893	C	4.4
13	AM	30	SER	4.4
14	BN	58	SER	4.4
3	BC	155	GLY	4.4
14	BN	45	VAL	4.4
1	BA	1126	U	4.4
14	BN	44	ALA	4.4
31	CA	1729	U	4.4
37	CJ	135	SER	4.4
40	CM	131	ALA	4.4
1	BA	958	A	4.4
14	BN	47	LYS	4.4
29	CC	27	GLY	4.4
23	C2	46	HIS	4.4
55	DA	2162	G	4.4
55	DA	2169	A	4.4
37	CJ	34	ASN	4.4
1	BA	1005	A	4.4

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Mol	Chain	Res	Type	RSRZ
2	AB	6	MET	4.4
2	AB	9	MET	4.4
7	BG	77	SER	4.4
37	CJ	92	LYS	4.4
31	CA	1167	C	4.4
9	AI	21	ILE	4.4
30	CD	10	GLY	4.4
43	CP	87	ILE	4.4
9	AI	19	VAL	4.4
14	BN	27	LEU	4.4
48	CU	10	VAL	4.4
10	AJ	74	VAL	4.4
1	BA	84	U	4.4
40	CM	115	GLU	4.4
10	BJ	25	ILE	4.3
35	CG	94	TYR	4.3
24	C3	31	LEU	4.3
37	DJ	36	MET	4.3
31	CA	2150	C	4.3
1	BA	1224	U	4.3
9	BI	129	LYS	4.3
37	CJ	64	ASP	4.3
31	CA	1047	G	4.3
37	CJ	137	GLY	4.3
36	DH	137	GLU	4.3
55	DA	1063	G	4.3
13	AM	24	GLY	4.3
43	CP	90	VAL	4.3
51	CX	52	GLY	4.3
14	BN	18	ASP	4.3
53	CZ	40	SER	4.3
7	BG	87	VAL	4.3
10	BJ	86	ALA	4.3
27	C0	47	MET	4.3
34	CF	152	LEU	4.3
1	BA	90	C	4.3
22	C1	33	THR	4.3
34	CF	43	ALA	4.3
37	CJ	122	ILE	4.3
14	BN	53	ARG	4.3
31	CA	2860	A	4.3
49	DV	53	ASN	4.3

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Mol	Chain	Res	Type	RSRZ
43	CP	115	LEU	4.3
54	DI	132	TYR	4.3
31	CA	613	A	4.3
31	CA	1089	A	4.3
37	CJ	110	ALA	4.3
13	AM	19	LEU	4.3
34	CF	100	PHE	4.2
7	BG	123	GLU	4.2
3	BC	73	PRO	4.2
13	BM	24	GLY	4.2
49	CV	13	VAL	4.2
7	BG	141	VAL	4.2
14	BN	20	TYR	4.2
33	CE	164	LEU	4.2
49	CV	35	ILE	4.2
1	BA	1237	C	4.2
13	BM	85	CYS	4.2
34	CF	112	ARG	4.2
13	AM	16	VAL	4.2
31	CA	81	G	4.2
49	CV	20	GLY	4.2
14	AN	31	ILE	4.2
12	BL	124	ALA	4.2
24	C3	18	PHE	4.2
31	CA	2667	C	4.2
35	CG	108	GLY	4.2
10	BJ	12	ALA	4.2
37	DJ	117	MET	4.2
13	BM	113	ARG	4.2
1	BA	250	A	4.2
10	AJ	6	ILE	4.2
55	DA	2122	U	4.2
2	BB	37	LYS	4.2
43	CP	35	ILE	4.2
34	CF	172	ALA	4.2
9	BI	66	THR	4.2
31	CA	2802	G	4.2
34	CF	139	PRO	4.2
35	CG	112	PRO	4.2
37	CJ	118	THR	4.2
1	AA	88	U	4.2
37	CJ	97	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
1	BA	78	A	4.2
31	CA	2118	U	4.2
2	BB	34	ALA	4.2
30	CD	4	LEU	4.2
36	CH	136	SER	4.2
46	CS	27	ILE	4.2
1	BA	4	U	4.1
14	BN	51	LEU	4.1
34	CF	47	LYS	4.1
53	CZ	14	LEU	4.1
19	BS	59	PRO	4.1
43	CP	97	PHE	4.1
13	BM	41	GLU	4.1
13	BM	40	ALA	4.1
1	BA	83	C	4.1
1	BA	950	U	4.1
34	CF	143	TYR	4.1
19	BS	76	PRO	4.1
1	AA	984	C	4.1
45	CR	74	ILE	4.1
34	CF	157	THR	4.1
48	CU	60	THR	4.1
48	CU	42	GLU	4.1
13	BM	52	GLN	4.1
35	CG	107	LEU	4.1
53	CZ	31	GLN	4.1
10	BJ	9	ARG	4.1
13	BM	101	ARG	4.1
43	CP	93	ASP	4.1
1	BA	1312	G	4.1
55	DA	1068	G	4.1
10	BJ	71	LEU	4.1
31	CA	1533	C	4.1
34	CF	32	GLU	4.1
10	BJ	42	LEU	4.1
13	BM	50	GLU	4.1
40	CM	121	THR	4.1
55	DA	2161	C	4.1
13	BM	54	ASP	4.1
13	BM	93	ARG	4.1
53	CZ	24	GLU	4.1
1	BA	949	A	4.1

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Mol	Chain	Res	Type	RSRZ
21	AU	2	PRO	4.1
31	CA	311	A	4.1
49	CV	51	ALA	4.1
1	AA	81	A	4.1
3	BC	156	ARG	4.1
12	AL	124	ALA	4.1
49	CV	36	VAL	4.1
31	CA	1534	U	4.0
15	AO	17	ARG	4.0
7	BG	107	ALA	4.0
1	BA	1209	C	4.0
25	C4	36	LYS	4.0
49	CV	95	PHE	4.0
14	BN	5	SER	4.0
40	CM	101	ILE	4.0
54	DI	121	SER	4.0
36	DH	142	VAL	4.0
53	CZ	32	ALA	4.0
13	BM	31	LYS	4.0
37	CJ	35	ILE	4.0
40	CM	90	VAL	4.0
10	AJ	8	ILE	4.0
53	CZ	59	GLU	4.0
13	AM	13	LYS	4.0
13	BM	56	LEU	4.0
37	CJ	19	ASN	4.0
37	DJ	120	ALA	4.0
43	CP	26	LEU	4.0
43	CP	107	ALA	4.0
35	CG	166	ASP	4.0
10	AJ	101	SER	4.0
19	BS	69	HIS	4.0
34	CF	28	VAL	4.0
35	CG	27	LYS	4.0
37	DJ	81	LYS	4.0
1	BA	89	U	4.0
14	BN	55	SER	4.0
9	BI	90	TYR	4.0
1	BA	85	U	4.0
31	CA	1058	U	4.0
48	CU	47	VAL	4.0
48	CU	15	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
54	DI	38	MET	4.0
15	BO	17	ARG	4.0
3	BC	78	GLY	4.0
22	C1	46	ASP	4.0
10	AJ	76	ILE	4.0
16	BP	57	ILE	4.0
1	BA	1033	G	3.9
24	C3	42	LEU	3.9
28	CB	24	G	3.9
31	CA	549	G	3.9
33	CE	200	LEU	3.9
37	DJ	97	LYS	3.9
14	BN	50	THR	3.9
36	CH	132	PHE	3.9
37	CJ	136	MET	3.9
19	BS	63	THR	3.9
23	C2	45	GLN	3.9
30	CD	6	GLY	3.9
10	AJ	7	ARG	3.9
31	CA	1075	C	3.9
53	CZ	37	LEU	3.9
1	BA	1276	G	3.9
1	BA	1029	U	3.9
54	DI	135	ALA	3.9
37	CJ	32	GLY	3.9
43	CP	101	GLY	3.9
3	BC	106	VAL	3.9
6	BF	39	LEU	3.9
7	BG	37	SER	3.9
2	BB	201	PRO	3.9
23	C2	53	LYS	3.9
7	BG	4	ARG	3.9
13	BM	98	ARG	3.9
37	CJ	84	ALA	3.9
10	AJ	36	VAL	3.9
13	BM	65	VAL	3.9
33	CE	157	LEU	3.9
13	BM	51	GLY	3.9
55	DA	138	U	3.9
26	C5	32	LYS	3.9
34	CF	95	ARG	3.9
49	CV	84	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
23	C2	19	HIS	3.9
30	CD	30	GLU	3.9
54	DI	104	ALA	3.9
34	CF	176	PRO	3.9
54	DI	124	ASP	3.9
3	BC	43	LEU	3.8
10	AJ	42	LEU	3.8
18	BR	48	ARG	3.8
31	CA	2122	U	3.8
22	C1	34	SER	3.8
7	BG	130	ASN	3.8
24	C3	32	ALA	3.8
13	BM	99	GLY	3.8
1	BA	1270	G	3.8
1	BA	1273	C	3.8
43	CP	24	THR	3.8
14	BN	40	ASP	3.8
19	BS	27	ASP	3.8
36	CH	11	ASN	3.8
34	CF	65	PRO	3.8
53	CZ	56	LEU	3.8
55	DA	880	G	3.8
55	DA	1072	C	3.8
55	DA	2115	G	3.8
19	BS	40	ILE	3.8
49	CV	30	SER	3.8
1	BA	1035	A	3.8
9	BI	37	GLN	3.8
42	CO	116	VAL	3.8
53	CZ	29	ARG	3.8
54	DI	133	GLU	3.8
35	CG	104	ASN	3.8
31	CA	75	G	3.8
49	CV	78	GLY	3.8
1	BA	1219	A	3.8
37	DJ	100	LYS	3.8
8	BH	2	SER	3.8
53	CZ	41	HIS	3.8
55	DA	1078	U	3.8
40	CM	91	ASP	3.8
19	BS	23	VAL	3.8
36	CH	130	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
35	CG	157	TYR	3.8
1	BA	953	G	3.8
9	BI	39	PHE	3.8
14	BN	38	ASP	3.8
33	DE	7	ASP	3.8
25	C4	37	ALA	3.8
10	BJ	82	LYS	3.8
35	DG	177	LYS	3.8
42	CO	28	LEU	3.8
43	CP	25	ARG	3.8
43	CP	106	LEU	3.8
48	CU	87	LEU	3.8
1	BA	955	U	3.8
13	BM	97	VAL	3.8
31	CA	312	G	3.8
37	DJ	104	ALA	3.8
34	CF	4	LEU	3.8
19	BS	35	SER	3.8
35	CG	9	VAL	3.8
1	BA	1148	U	3.7
30	CD	26	VAL	3.7
55	DA	141	G	3.7
24	C3	33	ARG	3.7
9	AI	32	GLN	3.7
49	CV	50	PRO	3.7
43	CP	39	VAL	3.7
31	CA	2117	A	3.7
34	CF	26	MET	3.7
23	C2	41	PRO	3.7
30	CD	200	ASP	3.7
31	CA	2181	U	3.7
39	CL	110	GLU	3.7
33	CE	172	ALA	3.7
42	CO	119	SER	3.7
50	CW	6	ALA	3.7
10	BJ	99	GLN	3.7
31	CA	2116	G	3.7
36	CH	72	ILE	3.7
19	BS	58	VAL	3.7
14	BN	16	LEU	3.7
40	CM	89	VAL	3.7
40	CM	84	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
40	CM	102	GLY	3.7
31	CA	1059	G	3.7
31	CA	1063	G	3.7
3	BC	109	PRO	3.7
37	DJ	85	GLY	3.7
31	CA	1076	C	3.7
46	CS	49	ILE	3.7
10	AJ	73	LEU	3.7
31	CA	12	U	3.7
55	DA	1088	A	3.7
55	DA	2106	U	3.7
1	BA	948	C	3.7
19	AS	56	GLN	3.7
31	CA	885	C	3.7
55	DA	2177	C	3.7
31	CA	930	G	3.7
31	CA	1873	G	3.7
13	AM	15	ALA	3.7
13	BM	33	ILE	3.7
2	AB	14	VAL	3.7
35	CG	83	PHE	3.7
36	CH	133	GLN	3.7
31	CA	330	A	3.7
40	CM	113	ALA	3.7
43	CP	41	ALA	3.7
13	AM	64	VAL	3.7
10	AJ	35	GLN	3.7
31	CA	1532	A	3.7
31	CA	2178	C	3.7
55	DA	654	A	3.7
10	BJ	21	ALA	3.7
37	CJ	133	ALA	3.7
37	DJ	42	PHE	3.7
7	AG	8	GLY	3.6
1	BA	1006	G	3.6
30	CD	8	LYS	3.6
31	CA	1056	G	3.6
31	CA	1074	G	3.6
53	CZ	6	LEU	3.6
7	BG	113	ASP	3.6
43	CP	89	ASP	3.6
16	BP	80	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
7	AG	110	LYS	3.6
14	AN	4	GLN	3.6
31	CA	332	A	3.6
35	CG	40	ALA	3.6
37	CJ	44	ALA	3.6
1	BA	1049	U	3.6
49	CV	85	PHE	3.6
1	BA	842	U	3.6
9	BI	11	ARG	3.6
2	AB	37	LYS	3.6
17	BQ	17	MET	3.6
7	BG	60	GLU	3.6
53	CZ	5	GLU	3.6
1	BA	209	U	3.6
47	CT	94	ASP	3.6
37	CJ	9	VAL	3.6
23	C2	31	PRO	3.6
34	CF	41	GLY	3.6
37	DJ	128	SER	3.6
49	CV	77	THR	3.6
45	CR	90	ILE	3.6
55	DA	2114	A	3.6
55	DA	2132	U	3.6
10	BJ	20	GLN	3.6
38	CK	142	ILE	3.6
3	BC	104	ALA	3.6
31	CA	1518	C	3.6
13	BM	38	GLY	3.6
14	BN	48	LEU	3.6
18	BR	51	TYR	3.6
34	CF	91	LEU	3.6
29	CC	239	ASN	3.6
37	CJ	71	THR	3.6
7	BG	50	LEU	3.6
34	CF	151	GLY	3.6
24	C3	34	ARG	3.6
31	CA	1069	A	3.6
46	CS	35	PHE	3.6
1	AA	1020	G	3.6
30	CD	185	ASN	3.6
55	DA	2128	G	3.6
1	AA	121	U	3.5

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Mol	Chain	Res	Type	RSRZ
31	CA	1082	U	3.5
22	C1	53	LYS	3.5
14	BN	34	VAL	3.5
24	C3	30	VAL	3.5
31	CA	1872	A	3.5
31	CA	2108	A	3.5
27	C0	28	GLY	3.5
7	BG	5	ARG	3.5
31	CA	1407	G	3.5
31	CA	1538	G	3.5
14	BN	3	LYS	3.5
19	BS	65	GLU	3.5
31	CA	328	U	3.5
2	BB	135	LEU	3.5
55	DA	2165	C	3.5
1	BA	1019	A	3.5
43	CP	46	GLU	3.5
1	BA	843	U	3.5
45	CR	71	GLN	3.5
3	BC	111	LEU	3.5
13	AM	36	ALA	3.5
7	BG	35	LYS	3.5
1	BA	207	C	3.5
35	CG	56	ASP	3.5
7	AG	58	GLU	3.5
2	BB	35	ARG	3.5
34	CF	137	ILE	3.5
43	CP	102	ARG	3.5
50	CW	29	ILE	3.5
49	CV	26	LYS	3.5
1	AA	1025	U	3.5
1	BA	1297	G	3.5
55	DA	2105	U	3.5
7	AG	7	ILE	3.5
23	C2	23	THR	3.5
37	DJ	139	VAL	3.5
50	CW	89	ILE	3.5
40	CM	8	PRO	3.5
43	CP	88	LYS	3.5
1	BA	1321	U	3.5
49	CV	92	LYS	3.5
2	BB	9	MET	3.5

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Mol	Chain	Res	Type	RSRZ
24	C3	27	GLY	3.5
35	CG	132	VAL	3.5
37	CJ	49	ILE	3.5
10	BJ	22	THR	3.5
24	C3	36	ALA	3.5
35	CG	52	PHE	3.5
34	CF	74	VAL	3.5
55	DA	2126	A	3.5
34	CF	96	MET	3.5
3	BC	107	ARG	3.5
7	AG	62	PHE	3.5
40	CM	20	GLY	3.5
46	CS	52	PRO	3.5
1	BA	942	G	3.5
1	BA	1001	C	3.5
31	CA	335	C	3.5
7	BG	18	PHE	3.5
43	CP	50	ALA	3.5
49	CV	98	SER	3.5
49	CV	14	LEU	3.5
13	BM	3	ARG	3.5
37	DJ	40	LYS	3.5
13	AM	115	PRO	3.5
3	BC	76	VAL	3.5
46	CS	63	VAL	3.5
23	C2	44	ARG	3.5
37	CJ	117	MET	3.5
40	CM	130	GLY	3.5
7	BG	145	ALA	3.5
53	CZ	33	ALA	3.5
31	CA	2107	G	3.4
10	AJ	5	ARG	3.4
1	BA	1341	U	3.4
35	CG	133	LEU	3.4
2	AB	27	MET	3.4
31	CA	1168	G	3.4
19	BS	42	PRO	3.4
35	CG	141	ILE	3.4
44	CQ	110	ILE	3.4
13	BM	6	GLY	3.4
34	CF	39	GLY	3.4
20	BT	49	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
40	CM	132	ARG	3.4
40	CM	133	ALA	3.4
1	BA	1331	G	3.4
1	AA	1302	C	3.4
3	BC	206	GLU	3.4
13	BM	4	ILE	3.4
14	BN	31	ILE	3.4
7	AG	151	PHE	3.4
14	BN	61	ARG	3.4
28	CB	23	G	3.4
16	BP	17	TYR	3.4
31	CA	336	C	3.4
35	CG	121	ILE	3.4
13	BM	21	SER	3.4
33	CE	201	ALA	3.4
1	BA	1048	G	3.4
1	BA	1222	G	3.4
31	CA	880	G	3.4
34	CF	36	LEU	3.4
37	DJ	9	VAL	3.4
3	BC	179	ARG	3.4
1	BA	1303	C	3.4
2	BB	82	ASP	3.4
50	CW	43	ASP	3.4
13	BM	80	LEU	3.4
40	CM	122	VAL	3.4
1	BA	1002	G	3.4
1	AA	1027	C	3.4
9	BI	125	PRO	3.4
24	C3	37	LYS	3.4
36	DH	74	ALA	3.4
37	CJ	127	ARG	3.4
37	DJ	110	ALA	3.4
54	DI	84	TYR	3.4
24	C3	43	THR	3.4
31	CA	2176	A	3.4
19	BS	22	ALA	3.4
49	CV	6	ARG	3.4
3	BC	103	ILE	3.4
7	AG	79	ARG	3.4
55	DA	1089	A	3.4
43	CP	108	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
53	CZ	63	ALA	3.4
34	CF	27	GLN	3.4
7	AG	133	THR	3.4
46	CS	7	SER	3.4
31	CA	2180	U	3.3
31	CA	2665	A	3.3
34	CF	119	ALA	3.3
30	CD	9	VAL	3.3
31	CA	882	G	3.3
13	BM	109	ARG	3.3
30	CD	44	GLY	3.3
13	AM	5	ALA	3.3
14	BN	23	LYS	3.3
1	BA	1280	A	3.3
54	DI	129	LEU	3.3
3	BC	39	VAL	3.3
7	AG	6	VAL	3.3
7	BG	102	ARG	3.3
14	BN	8	ALA	3.3
34	CF	18	THR	3.3
37	CJ	26	PRO	3.3
54	DI	40	GLU	3.3
37	DJ	98	VAL	3.3
49	CV	40	ASN	3.3
2	BB	40	ILE	3.3
3	BC	122	SER	3.3
30	CD	47	ALA	3.3
9	AI	6	TYR	3.3
37	CJ	93	PRO	3.3
11	BK	68	GLU	3.3
13	BM	35	ALA	3.3
23	C2	22	THR	3.3
31	CA	892	A	3.3
27	C0	29	LEU	3.3
47	CT	97	LEU	3.3
24	C3	1	MET	3.3
1	BA	1320	C	3.3
16	AP	82	ALA	3.3
35	CG	136	ALA	3.3
40	CM	108	ALA	3.3
14	AN	47	LYS	3.3
37	DJ	60	THR	3.3

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Mol	Chain	Res	Type	RSRZ
55	DA	2141	G	3.3
44	CQ	95	ALA	3.3
54	DI	98	GLU	3.3
19	BS	21	LYS	3.3
33	CE	12	LEU	3.3
44	DQ	2	SER	3.3
14	BN	10	GLU	3.3
34	CF	69	LYS	3.3
1	BA	1221	G	3.3
19	BS	3	ARG	3.3
14	BN	21	PHE	3.3
44	CQ	22	PRO	3.3
34	CF	80	ARG	3.3
31	CA	1088	A	3.3
1	AA	1127	G	3.3
34	CF	24	SER	3.3
35	CG	5	ALA	3.3
53	CZ	22	LEU	3.3
35	CG	6	LYS	3.3
11	AK	110	ILE	3.2
35	CG	106	SER	3.2
1	BA	1034	G	3.2
1	BA	1039	G	3.2
9	BI	6	TYR	3.2
53	CZ	21	LEU	3.2
2	BB	14	VAL	3.2
43	CP	54	VAL	3.2
40	CM	76	GLU	3.2
49	CV	72	ILE	3.2
2	BB	12	ALA	3.2
31	CA	1460	U	3.2
7	AG	5	ARG	3.2
44	CQ	85	SER	3.2
45	CR	118	ALA	3.2
1	BA	1027	C	3.2
1	BA	1038	C	3.2
31	CA	1044	C	3.2
13	BM	77	ILE	3.2
7	AG	59	LEU	3.2
22	C1	57	LYS	3.2
43	CP	98	GLN	3.2
31	CA	1071	G	3.2

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Mol	Chain	Res	Type	RSRZ
49	CV	27	ASN	3.2
40	CM	135	ILE	3.2
10	AJ	102	LEU	3.2
1	BA	1244	G	3.2
13	BM	103	LYS	3.2
42	CO	56	LYS	3.2
7	AG	65	ALA	3.2
37	DJ	14	ALA	3.2
48	CU	85	VAL	3.2
7	BG	76	LYS	3.2
49	CV	82	ARG	3.2
22	C1	15	MET	3.2
31	CA	1060	U	3.2
49	CV	18	ASP	3.2
1	BA	94	G	3.2
31	CA	327	G	3.2
31	CA	476	G	3.2
43	CP	100	HIS	3.2
13	BM	25	VAL	3.2
35	CG	172	LYS	3.2
40	CM	86	GLU	3.2
7	BG	115	SER	3.2
13	BM	30	SER	3.2
33	CE	173	THR	3.2
33	CE	98	LYS	3.2
43	CP	49	VAL	3.2
3	BC	85	GLU	3.2
10	BJ	80	THR	3.2
36	CH	135	HIS	3.2
43	CP	34	HIS	3.2
31	CA	2106	U	3.2
34	CF	22	TYR	3.2
30	CD	186	LEU	3.2
14	AN	5	SER	3.2
23	C2	38	LYS	3.2
13	BM	5	ALA	3.2
31	CA	1169	A	3.2
31	CA	139	U	3.2
55	DA	1061	U	3.2
37	CJ	10	LYS	3.2
9	AI	5	GLN	3.2
14	BN	17	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
18	AR	20	GLU	3.2
46	CS	28	ALA	3.2
31	CA	1112	G	3.2
13	AM	39	ILE	3.1
31	CA	183	C	3.1
31	CA	1606	C	3.1
29	CC	233	GLY	3.1
10	BJ	94	ALA	3.1
11	BK	21	ALA	3.1
35	CG	110	SER	3.1
40	CM	144	GLU	3.1
44	CQ	111	LYS	3.1
11	AK	82	LEU	3.1
49	DV	55	PRO	3.1
55	DA	2108	A	3.1
1	BA	1214	C	3.1
9	AI	127	PHE	3.1
31	CA	1049	C	3.1
7	BG	17	LYS	3.1
33	CE	10	SER	3.1
44	CQ	84	ILE	3.1
9	AI	89	GLU	3.1
31	CA	2383	G	3.1
10	BJ	89	ARG	3.1
13	BM	79	ARG	3.1
34	CF	116	GLY	3.1
1	AA	85	U	3.1
34	CF	141	ILE	3.1
20	BT	59	ASP	3.1
10	BJ	36	VAL	3.1
49	CV	71	ALA	3.1
49	CV	52	LEU	3.1
1	BA	88	U	3.1
1	AA	1019	A	3.1
37	CJ	66	SER	3.1
9	BI	92	GLU	3.1
40	CM	1	MET	3.1
22	C1	2	ALA	3.1
31	CA	1210	G	3.1
34	CF	171	ALA	3.1
53	DZ	63	ALA	3.1
55	DA	1087	G	3.1

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Mol	Chain	Res	Type	RSRZ
34	CF	83	TYR	3.1
7	BG	105	VAL	3.1
14	AN	11	VAL	3.1
23	C2	43	VAL	3.1
1	AA	1281	C	3.1
31	CA	2309	A	3.1
3	BC	108	LYS	3.1
13	BM	34	LEU	3.1
37	CJ	27	ALA	3.1
1	AA	1026	G	3.1
7	BG	8	GLY	3.1
35	CG	35	ARG	3.1
7	AG	106	GLU	3.1
21	AU	9	ASN	3.1
2	AB	131	LYS	3.1
7	AG	54	SER	3.1
46	CS	18	GLN	3.1
7	BG	118	LEU	3.1
14	AN	15	ALA	3.1
48	DU	92	ASN	3.1
40	CM	142	ILE	3.1
16	AP	47	GLU	3.1
35	CG	86	LYS	3.1
34	CF	29	PRO	3.1
14	BN	42	TRP	3.1
31	CA	646	U	3.1
2	AB	4	VAL	3.1
9	AI	27	LYS	3.1
13	AM	29	ARG	3.1
37	DJ	28	LEU	3.1
10	BJ	85	ASP	3.0
54	DI	103	ASN	3.0
1	AA	84	U	3.0
14	BN	49	GLN	3.0
36	CH	127	GLU	3.0
31	CA	1073	A	3.0
2	BB	36	ASN	3.0
36	CH	142	VAL	3.0
37	CJ	70	VAL	3.0
55	DA	546	U	3.0
7	BG	108	ALA	3.0
13	BM	14	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
36	CH	140	ALA	3.0
34	CF	67	ILE	3.0
55	DA	2133	G	3.0
31	CA	1214	A	3.0
13	BM	13	LYS	3.0
53	CZ	44	LYS	3.0
35	CG	31	GLY	3.0
23	C2	42	VAL	3.0
34	CF	110	ARG	3.0
35	CG	17	VAL	3.0
42	CO	118	ARG	3.0
13	BM	49	SER	3.0
33	CE	171	ASP	3.0
16	AP	80	LYS	3.0
35	CG	30	ASN	3.0
37	CJ	128	SER	3.0
37	DJ	10	LYS	3.0
2	AB	30	PHE	3.0
7	BG	51	ALA	3.0
43	CP	113	ALA	3.0
10	BJ	81	GLU	3.0
49	CV	94	ARG	3.0
36	DH	138	VAL	3.0
34	CF	61	SER	3.0
14	BN	13	ARG	3.0
31	CA	2164	C	3.0
36	CH	74	ALA	3.0
36	DH	105	ALA	3.0
37	DJ	118	THR	3.0
2	BB	67	ILE	3.0
31	CA	894	U	3.0
42	CO	29	VAL	3.0
54	DI	5	LEU	3.0
33	CE	140	ASP	3.0
37	CJ	36	MET	3.0
50	CW	5	ASN	3.0
36	DH	94	ILE	3.0
1	BA	1125	U	3.0
31	CA	1531	C	3.0
35	CG	169	VAL	3.0
2	AB	139	ARG	3.0
23	C2	49	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
39	CL	111	LYS	3.0
50	CW	42	LEU	3.0
1	BA	1272	G	3.0
31	CA	1093	G	3.0
33	CE	7	ASP	3.0
14	BN	9	ARG	3.0
7	BG	86	GLN	3.0
1	BA	1211	U	3.0
9	AI	17	ALA	3.0
27	C0	43	ALA	3.0
31	CA	1052	C	3.0
33	CE	154	ASP	3.0
34	CF	111	ILE	3.0
7	AG	57	SER	3.0
34	CF	31	VAL	3.0
48	CU	44	LYS	3.0
3	AC	82	GLU	3.0
43	CP	20	GLU	3.0
43	CP	110	ALA	3.0
31	CA	1320	C	3.0
34	CF	38	MET	3.0
1	BA	1343	G	2.9
55	DA	1094	U	2.9
19	BS	25	SER	2.9
37	CJ	29	GLY	2.9
55	DA	2117	A	2.9
1	AA	1125	U	2.9
31	CA	2167	U	2.9
40	CM	126	ARG	2.9
2	BB	130	THR	2.9
27	C0	41	THR	2.9
40	CM	94	THR	2.9
49	DV	48	PRO	2.9
55	DA	2170	A	2.9
3	BC	127	ARG	2.9
30	CD	77	ARG	2.9
31	CA	150	U	2.9
31	CA	545	U	2.9
55	DA	1059	G	2.9
3	BC	70	THR	2.9
13	BM	37	ALA	2.9
34	CF	54	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
35	CG	127	THR	2.9
25	C4	40	ARG	2.9
35	CG	152	ARG	2.9
37	DJ	51	LYS	2.9
13	BM	43	VAL	2.9
14	AN	55	SER	2.9
41	CN	73	ILE	2.9
40	CM	75	ALA	2.9
53	CZ	18	LEU	2.9
54	DI	55	VAL	2.9
9	AI	22	LYS	2.9
10	BJ	24	GLU	2.9
31	CA	2177	C	2.9
7	BG	140	ASP	2.9
46	CS	30	GLY	2.9
40	CM	15	ALA	2.9
35	CG	62	TRP	2.9
44	CQ	9	GLU	2.9
31	CA	2803	G	2.9
16	BP	52	LEU	2.9
22	C1	3	VAL	2.9
1	BA	1036	A	2.9
35	CG	80	THR	2.9
13	AM	48	LEU	2.9
14	BN	28	LYS	2.9
31	CA	897	C	2.9
31	CA	1179	G	2.9
31	CA	2796	U	2.9
41	CN	72	PRO	2.9
55	DA	1175	A	2.9
7	BG	119	ARG	2.9
22	C1	51	GLY	2.9
46	CS	19	THR	2.9
53	CZ	48	ARG	2.9
37	DJ	140	VAL	2.9
43	CP	78	VAL	2.9
12	BL	109	ASP	2.9
50	CW	59	GLU	2.9
9	BI	18	ARG	2.9
53	CZ	47	ARG	2.9
31	CA	431	U	2.9
31	CA	1880	U	2.9

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Mol	Chain	Res	Type	RSRZ
31	CA	2112	G	2.9
1	AA	1022	A	2.9
31	CA	103	A	2.9
40	CM	85	VAL	2.9
52	CY	47	VAL	2.9
7	BG	127	ALA	2.9
34	CF	8	TYR	2.9
34	CF	121	SER	2.9
42	CO	62	ASN	2.9
1	BA	252	U	2.9
2	BB	32	PHE	2.9
11	AK	111	THR	2.9
10	AJ	37	ARG	2.9
44	CQ	27	GLU	2.9
13	AM	7	ILE	2.8
7	BG	68	ASN	2.8
14	AN	37	SER	2.8
34	CF	104	ILE	2.8
36	CH	94	ILE	2.8
1	AA	1286	U	2.8
1	BA	1322	C	2.8
18	AR	51	TYR	2.8
31	CA	1734	G	2.8
36	CH	12	LEU	2.8
2	BB	21	ARG	2.8
49	CV	15	THR	2.8
40	CM	116	VAL	2.8
1	BA	86	G	2.8
10	BJ	27	GLU	2.8
31	CA	1215	G	2.8
31	CA	1530	G	2.8
13	AM	23	TYR	2.8
30	CD	45	TYR	2.8
35	CG	116	GLN	2.8
37	DJ	84	ALA	2.8
33	CE	150	THR	2.8
27	C0	25	LEU	2.8
37	CJ	16	GLY	2.8
7	AG	53	ARG	2.8
15	BO	89	ARG	2.8
31	CA	2165	C	2.8
34	CF	165	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	BA	1050	G	2.8
31	CA	2877	G	2.8
37	DJ	71	THR	2.8
35	CG	126	PRO	2.8
36	DH	63	ALA	2.8
7	BG	47	LEU	2.8
19	BS	68	GLY	2.8
19	BS	72	GLY	2.8
20	BT	60	ARG	2.8
35	CG	128	GLN	2.8
17	BQ	78	VAL	2.8
1	BA	1309	G	2.8
14	AN	52	PRO	2.8
31	CA	1108	U	2.8
31	CA	1325	U	2.8
19	AS	55	ARG	2.8
6	AF	61	LEU	2.8
43	CP	27	VAL	2.8
14	AN	9	ARG	2.8
31	CA	1864	U	2.8
31	CA	1865	U	2.8
40	CM	119	PRO	2.8
55	DA	1071	G	2.8
10	AJ	100	ILE	2.8
35	CG	26	ILE	2.8
12	BL	70	GLU	2.8
2	BB	131	LYS	2.8
10	BJ	28	THR	2.8
2	AB	135	LEU	2.8
7	BG	82	GLY	2.8
33	CE	9	GLN	2.8
33	CE	193	VAL	2.8
1	BA	1323	G	2.8
2	AB	42	ASN	2.8
2	AB	136	MET	2.8
27	C0	39	GLU	2.8
31	CA	881	G	2.8
31	CA	1524	G	2.8
48	CU	4	GLU	2.8
53	CZ	54	LYS	2.8
55	DA	283	G	2.8
54	DI	72	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
16	AP	39	PHE	2.8
31	CA	1090	A	2.8
46	CS	38	VAL	2.8
47	CT	101	SER	2.8
1	BA	1210	C	2.8
14	BN	46	LEU	2.8
37	DJ	83	ALA	2.8
37	DJ	115	ALA	2.8
1	AA	963	G	2.8
1	BA	945	G	2.8
2	AB	39	HIS	2.8
31	CA	2801	G	2.8
34	CF	25	VAL	2.8
34	CF	142	ASP	2.8
53	CZ	35	GLY	2.8
10	BJ	98	VAL	2.8
35	CG	24	ILE	2.8
1	BA	1212	U	2.8
31	CA	262	A	2.8
2	BB	33	GLY	2.8
10	BJ	23	ALA	2.8
1	BA	194	C	2.8
31	CA	1607	C	2.8
1	BA	1253	G	2.7
1	BA	1333	A	2.7
1	BA	1362	A	2.7
10	AJ	34	ALA	2.7
10	BJ	95	GLY	2.7
19	BS	80	TYR	2.7
40	CM	70	LYS	2.7
55	DA	2147	A	2.7
21	BU	12	PHE	2.7
50	CW	35	GLU	2.7
1	AA	1277	C	2.7
31	CA	898	C	2.7
21	BU	16	LEU	2.7
1	BA	121	U	2.7
1	BA	987	G	2.7
3	BC	77	ILE	2.7
7	AG	49	THR	2.7
7	BG	58	GLU	2.7
31	CA	899	A	2.7

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Mol	Chain	Res	Type	RSRZ
37	DJ	34	ASN	2.7
49	CV	39	ILE	2.7
49	CV	48	PRO	2.7
53	CZ	20	ASN	2.7
11	BK	84	VAL	2.7
13	BM	36	ALA	2.7
50	CW	67	GLY	2.7
31	CA	1171	G	2.7
31	CA	2159	G	2.7
25	C4	64	TYR	2.7
33	CE	142	ALA	2.7
35	CG	10	VAL	2.7
36	CH	78	VAL	2.7
1	BA	1364	U	2.7
2	AB	5	SER	2.7
35	CG	130	GLU	2.7
55	DA	2131	U	2.7
2	AB	225	ARG	2.7
7	AG	68	ASN	2.7
20	BT	56	PRO	2.7
30	CD	43	ASP	2.7
45	CR	91	ASP	2.7
49	DV	57	GLY	2.7
37	CJ	63	ALA	2.7
40	CM	83	ALA	2.7
40	CM	138	ALA	2.7
44	CQ	91	ALA	2.7
10	AJ	25	ILE	2.7
14	AN	28	LYS	2.7
35	CG	167	GLU	2.7
42	CO	52	ILE	2.7
31	CA	2904	U	2.7
55	DA	897	C	2.7
9	AI	24	GLY	2.7
48	CU	58	VAL	2.7
50	CW	57	TYR	2.7
31	CA	277	G	2.7
37	DJ	136	MET	2.7
5	BE	91	GLY	2.7
10	BJ	11	LYS	2.7
16	BP	53	ASP	2.7
42	CO	117	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
49	CV	86	ARG	2.7
54	DI	36	ASP	2.7
6	AF	36	ILE	2.7
7	AG	50	LEU	2.7
22	C1	5	GLN	2.7
54	DI	3	LEU	2.7
50	CW	1	MET	2.7
1	AA	1024	G	2.7
1	BA	1015	G	2.7
3	BC	102	ASN	2.7
31	CA	619	G	2.7
37	DJ	103	ARG	2.7
55	DA	277	G	2.7
11	AK	94	GLU	2.7
34	CF	164	GLU	2.7
36	CH	60	GLU	2.7
37	DJ	49	ILE	2.7
30	CD	201	LEU	2.7
45	CR	117	LEU	2.7
33	CE	23	PHE	2.7
37	DJ	25	GLY	2.7
1	BA	532	A	2.7
3	BC	50	ALA	2.7
55	DA	1847	A	2.7
51	CX	56	ASP	2.7
1	AA	962	C	2.7
1	AA	1015	G	2.7
31	CA	45	G	2.7
31	CA	2668	G	2.7
33	CE	54	GLY	2.7
34	CF	12	VAL	2.7
34	CF	166	GLY	2.7
30	CD	41	ALA	2.7
34	CF	79	ILE	2.7
36	CH	67	ALA	2.7
25	C4	61	CYS	2.7
1	BA	1007	U	2.7
1	BA	1245	C	2.7
1	AA	1276	G	2.7
22	C1	35	GLY	2.7
37	DJ	33	VAL	2.7
37	DJ	58	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
13	BM	9	ILE	2.7
9	AI	87	LEU	2.6
31	CA	1213	A	2.6
31	CA	2861	U	2.6
13	AM	25	VAL	2.6
9	AI	83	ILE	2.6
28	CB	49	C	2.6
33	CE	190	ALA	2.6
19	BS	4	SER	2.6
31	CA	117	G	2.6
1	BA	92	U	2.6
2	AB	46	THR	2.6
9	AI	55	VAL	2.6
43	CP	53	THR	2.6
49	CV	67	VAL	2.6
53	CZ	25	GLN	2.6
10	AJ	43	PRO	2.6
34	DF	117	LEU	2.6
35	CG	117	LEU	2.6
37	DJ	75	PRO	2.6
10	BJ	101	SER	2.6
1	BA	976	G	2.6
10	BJ	16	ARG	2.6
27	C0	9	GLN	2.6
31	CA	180	G	2.6
31	CA	1869	G	2.6
43	CP	67	ASN	2.6
45	CR	23	GLY	2.6
26	C5	10	LEU	2.6
1	BA	1239	A	2.6
55	DA	1057	A	2.6
1	AA	1037	C	2.6
3	BC	194	GLY	2.6
30	CD	95	SER	2.6
2	BB	123	ASP	2.6
37	DJ	127	ARG	2.6
3	BC	120	ILE	2.6
37	DJ	132	THR	2.6
1	AA	4	U	2.6
1	BA	632	U	2.6
31	CA	1324	G	2.6
31	CA	2891	U	2.6

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Mol	Chain	Res	Type	RSRZ
47	CT	10	ALA	2.6
3	BC	80	LYS	2.6
31	CA	213	A	2.6
37	DJ	70	VAL	2.6
9	AI	62	ASP	2.6
9	AI	63	LEU	2.6
9	BI	21	ILE	2.6
13	BM	28	THR	2.6
27	C0	23	THR	2.6
2	AB	35	ARG	2.6
19	AS	57	HIS	2.6
7	BG	90	GLU	2.6
31	CA	1875	G	2.6
53	CZ	46	VAL	2.6
1	AA	78	A	2.6
37	CJ	101	ILE	2.6
1	BA	1230	C	2.6
2	AB	12	ALA	2.6
9	AI	64	TYR	2.6
10	BJ	34	ALA	2.6
50	CW	28	ALA	2.6
7	BG	16	PRO	2.6
30	CD	74	GLU	2.6
34	CF	42	GLU	2.6
48	CU	34	VAL	2.6
14	AN	54	ASP	2.6
40	CM	71	ALA	2.6
31	CA	1111	A	2.6
36	DH	66	ASN	2.6
2	AB	210	VAL	2.6
36	DH	147	VAL	2.6
37	DJ	50	GLU	2.6
19	BS	18	LYS	2.6
3	BC	144	LEU	2.6
47	CT	86	MET	2.6
13	BM	17	ILE	2.6
36	CH	143	ILE	2.6
43	CP	58	ILE	2.6
46	CS	101	ILE	2.6
36	DH	56	ALA	2.6
53	CZ	3	ALA	2.6
44	CQ	92	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	BA	1306	A	2.6
1	BA	1208	C	2.6
1	BA	1317	C	2.6
1	BA	1342	C	2.6
8	AH	121	LEU	2.6
36	CH	15	LEU	2.6
52	CY	45	ARG	2.6
9	BI	7	TYR	2.6
13	BM	61	ALA	2.6
36	CH	110	VAL	2.6
36	DH	107	GLY	2.6
28	CB	21	G	2.6
31	CA	101	A	2.6
31	CA	1596	A	2.6
1	BA	91	U	2.6
14	BN	2	ALA	2.6
19	AS	50	ALA	2.6
7	AG	123	GLU	2.6
3	BC	72	ARG	2.6
43	CP	74	VAL	2.6
22	C1	32	LYS	2.5
37	CJ	41	ALA	2.5
40	CM	134	ALA	2.5
1	AA	959	A	2.5
1	AA	1000	A	2.5
1	BA	210	C	2.5
2	BB	210	VAL	2.5
7	BG	143	ARG	2.5
9	BI	124	ARG	2.5
12	BL	71	GLY	2.5
31	CA	900	A	2.5
33	CE	127	GLU	2.5
31	CA	289	G	2.5
31	CA	369	U	2.5
36	CH	61	VAL	2.5
43	CP	62	LEU	2.5
6	AF	62	MET	2.5
11	AK	81	ASN	2.5
3	BC	180	ALA	2.5
50	CW	69	GLU	2.5
1	BA	1336	C	2.5
31	CA	318	C	2.5

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Mol	Chain	Res	Type	RSRZ
31	CA	345	A	2.5
31	CA	1732	C	2.5
55	DA	878	A	2.5
25	C4	43	HIS	2.5
34	DF	80	ARG	2.5
36	CH	76	GLU	2.5
7	AG	42	ILE	2.5
15	BO	21	ASP	2.5
1	BA	1000	A	2.5
31	CA	334	C	2.5
31	CA	513	A	2.5
31	CA	1045	C	2.5
31	CA	1868	C	2.5
31	CA	1874	C	2.5
13	BM	16	VAL	2.5
48	CU	16	VAL	2.5
2	AB	32	PHE	2.5
2	BB	31	ILE	2.5
3	AC	68	ILE	2.5
13	AM	46	SER	2.5
31	CA	884	U	2.5
43	CP	32	PRO	2.5
2	AB	47	VAL	2.5
35	CG	25	THR	2.5
48	CU	33	LYS	2.5
1	BA	1355	G	2.5
31	CA	1238	G	2.5
50	CW	91	PHE	2.5
35	CG	8	PRO	2.5
2	AB	34	ALA	2.5
29	CC	245	VAL	2.5
37	DJ	8	TYR	2.5
53	CZ	4	LYS	2.5
36	DH	72	ILE	2.5
23	C2	35	GLU	2.5
1	BA	981	U	2.5
9	BI	94	LEU	2.5
31	CA	1863	G	2.5
30	CD	101	PHE	2.5
1	BA	1252	A	2.5
31	CA	2800	A	2.5
55	DA	613	A	2.5

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Mol	Chain	Res	Type	RSRZ
36	CH	68	ARG	2.5
46	CS	12	HIS	2.5
1	BA	1313	U	2.5
11	BK	110	ILE	2.5
13	AM	17	ILE	2.5
24	D3	46	LYS	2.5
9	BI	98	LEU	2.5
11	AK	84	VAL	2.5
36	CH	108	VAL	2.5
42	CO	94	TYR	2.5
31	CA	505	A	2.5
33	CE	55	SER	2.5
49	DV	54	GLN	2.5
17	BQ	45	HIS	2.5
47	CT	48	LYS	2.5
33	CE	175	ILE	2.5
3	BC	126	ARG	2.5
19	BS	33	THR	2.5
43	CP	33	ARG	2.5
1	BA	847	G	2.5
20	AT	2	ALA	2.5
31	CA	1166	G	2.5
31	CA	2627	G	2.5
37	DJ	27	ALA	2.5
30	CD	154	LYS	2.5
34	CF	140	GLU	2.5
1	BA	273	U	2.5
1	BA	1315	U	2.5
11	BK	96	THR	2.5
24	C3	24	THR	2.5
28	CB	74	U	2.5
42	CO	105	GLY	2.5
20	BT	36	TYR	2.5
34	DF	83	TYR	2.5
48	CU	14	PRO	2.5
3	BC	190	HIS	2.5
19	BS	36	ARG	2.5
46	CS	59	ILE	2.5
2	AB	64	LYS	2.4
10	AJ	10	LEU	2.4
35	CG	101	ASN	2.4
2	BB	205	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
35	CG	124	GLU	2.4
7	AG	66	LEU	2.4
7	BG	30	LEU	2.4
14	BN	15	ALA	2.4
31	CA	316	C	2.4
36	DH	67	ALA	2.4
1	BA	1534	A	2.4
30	CD	184	ARG	2.4
31	CA	501	A	2.4
34	DF	85	ILE	2.4
3	BC	118	ASP	2.4
29	CC	98	ASP	2.4
19	BS	26	GLY	2.4
14	BN	24	ARG	2.4
1	BA	202	G	2.4
1	BA	1304	G	2.4
1	BA	1356	G	2.4
48	CU	30	ILE	2.4
31	CA	182	A	2.4
31	CA	216	A	2.4
3	AC	78	GLY	2.4
3	BC	158	GLY	2.4
7	AG	112	GLY	2.4
40	CM	127	VAL	2.4
46	CS	66	HIS	2.4
54	DI	126	LEU	2.4
7	BG	122	ASN	2.4
9	AI	92	GLU	2.4
12	AL	108	LYS	2.4
33	CE	24	ASN	2.4
53	CZ	9	LYS	2.4
1	BA	1265	C	2.4
31	CA	357	C	2.4
31	CA	1174	U	2.4
1	BA	946	A	2.4
3	BC	112	ASP	2.4
13	BM	68	ASP	2.4
31	CA	53	A	2.4
48	CU	12	ARG	2.4
13	BM	57	ARG	2.4
17	BQ	46	VAL	2.4
17	BQ	83	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
36	CH	27	ARG	2.4
44	CQ	8	LEU	2.4
47	CT	84	ARG	2.4
1	BA	979	C	2.4
13	AM	35	ALA	2.4
2	AB	44	GLU	2.4
9	BI	15	SER	2.4
7	BG	149	LYS	2.4
34	DF	176	PRO	2.4
36	DH	125	THR	2.4
1	AA	1029	U	2.4
27	C0	2	ALA	2.4
31	CA	179	C	2.4
7	AG	45	SER	2.4
19	AS	25	SER	2.4
1	BA	1340	A	2.4
9	BI	63	LEU	2.4
21	AU	16	LEU	2.4
1	BA	203	G	2.4
1	BA	1124	G	2.4
17	AQ	4	LYS	2.4
23	C2	30	LYS	2.4
31	CA	2409	G	2.4
45	CR	73	GLY	2.4
33	CE	131	THR	2.4
40	CM	107	PHE	2.4
45	CR	81	ASN	2.4
2	BB	208	ARG	2.4
1	BA	986	U	2.4
1	BA	1228	C	2.4
1	BA	1281	C	2.4
31	CA	2628	C	2.4
34	CF	57	LEU	2.4
11	BK	64	GLN	2.4
46	CS	24	LYS	2.4
55	DA	2153	C	2.4
1	AA	1260	G	2.4
31	CA	317	G	2.4
34	CF	33	LYS	2.4
13	BM	76	SER	2.4
22	C1	4	GLN	2.4
35	CG	161	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
46	CS	31	GLU	2.4
51	CX	85	GLU	2.4
54	DI	119	PRO	2.4
3	BC	101	ILE	2.4
3	BC	204	LYS	2.4
31	CA	52	A	2.4
37	DJ	82	LYS	2.4
30	CD	39	ASP	2.4
44	CQ	97	LEU	2.4
54	DI	29	ASP	2.4
9	BI	123	ARG	2.4
16	BP	39	PHE	2.4
31	CA	850	U	2.4
35	CG	75	MET	2.4
34	CF	78	LYS	2.4
50	CW	41	GLU	2.4
2	AB	213	TYR	2.4
2	BB	206	ALA	2.4
11	BK	62	ALA	2.4
13	AM	45	ILE	2.4
49	CV	76	ALA	2.4
14	AN	27	LEU	2.4
1	AA	205	A	2.3
50	CW	32	GLY	2.3
19	BS	56	GLN	2.3
1	BA	943	U	2.3
7	BG	74	GLU	2.3
21	AU	8	GLU	2.3
47	CT	85	ILE	2.3
48	CU	11	LEU	2.3
31	CA	1207	C	2.3
43	CP	111	ARG	2.3
14	AN	18	ASP	2.3
17	BQ	73	TRP	2.3
46	CS	14	VAL	2.3
49	CV	90	GLY	2.3
35	CG	134	LYS	2.3
7	AG	71	PRO	2.3
11	BK	66	ALA	2.3
16	BP	42	ILE	2.3
35	CG	7	ALA	2.3
29	CC	101	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
40	CM	110	VAL	2.3
1	BA	933	G	2.3
11	AK	70	CYS	2.3
27	C0	8	THR	2.3
55	DA	2112	G	2.3
9	AI	91	ASP	2.3
16	AP	45	GLU	2.3
31	CA	1488	C	2.3
2	AB	60	ILE	2.3
11	AK	21	ALA	2.3
11	BK	13	ARG	2.3
21	BU	2	PRO	2.3
31	CA	609	A	2.3
34	CF	30	ARG	2.3
34	CF	59	ALA	2.3
28	CB	22	U	2.3
2	AB	65	GLY	2.3
9	BI	8	GLY	2.3
10	AJ	38	GLY	2.3
11	AK	43	GLY	2.3
13	BM	60	VAL	2.3
19	BS	6	LYS	2.3
31	CA	2166	U	2.3
37	CJ	140	VAL	2.3
9	AI	88	MET	2.3
22	C1	36	GLU	2.3
35	CG	129	THR	2.3
35	CG	125	CYS	2.3
1	BA	1226	C	2.3
14	AN	25	ALA	2.3
31	CA	414	C	2.3
31	CA	1211	C	2.3
31	CA	1236	G	2.3
55	DA	1093	G	2.3
7	AG	69	VAL	2.3
9	BI	58	VAL	2.3
29	CC	242	LYS	2.3
43	CP	85	LYS	2.3
47	CT	47	VAL	2.3
1	AA	412	A	2.3
12	AL	69	GLY	2.3
31	CA	1608	A	2.3

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Mol	Chain	Res	Type	RSRZ
34	DF	116	GLY	2.3
55	DA	1103	A	2.3
46	CS	62	GLU	2.3
10	AJ	11	LYS	2.3
34	CF	44	ILE	2.3
16	AP	78	VAL	2.3
1	BA	251	G	2.3
24	C3	7	PRO	2.3
48	CU	57	VAL	2.3
31	CA	409	G	2.3
1	BA	274	A	2.3
11	BK	63	ALA	2.3
35	CG	96	ALA	2.3
40	CM	103	ILE	2.3
40	CM	111	ILE	2.3
52	CY	40	VAL	2.3
3	BC	125	GLU	2.3
7	BG	83	SER	2.3
36	CH	137	GLU	2.3
51	CX	55	ARG	2.3
22	C1	55	ILE	2.3
31	CA	1212	G	2.3
31	CA	1529	G	2.3
31	CA	2862	G	2.3
9	BI	91	ASP	2.3
36	CH	77	THR	2.3
36	CH	100	ALA	2.3
53	CZ	11	VAL	2.3
36	CH	70	GLU	2.3
51	CX	83	GLU	2.3
53	CZ	2	LYS	2.3
1	AA	1028	C	2.3
10	BJ	92	LEU	2.3
34	CF	81	GLN	2.3
3	BC	203	PHE	2.3
8	BH	130	ALA	2.3
16	BP	81	ALA	2.3
29	CC	19	VAL	2.3
35	CG	165	ALA	2.3
36	DH	132	PHE	2.3
1	BA	988	G	2.3
1	BA	1127	G	2.3

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Mol	Chain	Res	Type	RSRZ
31	CA	214	G	2.3
31	CA	1408	G	2.3
46	CS	46	GLU	2.3
48	CU	40	LYS	2.3
36	CH	122	LEU	2.3
2	BB	39	HIS	2.3
33	CE	11	ALA	2.3
35	CG	13	ALA	2.3
1	AA	961	U	2.3
1	AA	1001	C	2.3
1	BA	1295	U	2.3
28	CB	63	C	2.3
44	CQ	17	VAL	2.3
55	DA	1870	C	2.3
6	BF	97	THR	2.3
36	CH	109	GLU	2.3
2	AB	74	ARG	2.3
48	CU	6	ARG	2.3
2	AB	16	PHE	2.3
3	AC	104	ALA	2.3
11	BK	65	VAL	2.3
30	CD	180	VAL	2.3
1	AA	217	C	2.3
1	BA	990	C	2.3
55	DA	1176	U	2.3
23	C2	34	LEU	2.3
33	CE	199	MET	2.3
36	DH	12	LEU	2.3
50	CW	37	PRO	2.3
9	AI	104	VAL	2.3
29	CC	30	PHE	2.3
34	CF	120	LYS	2.3
37	CJ	30	GLN	2.3
31	CA	1216	G	2.2
31	CA	2859	G	2.2
37	CJ	37	GLU	2.2
1	BA	1301	U	2.2
3	AC	83	ASP	2.2
9	AI	94	LEU	2.2
9	BI	85	ARG	2.2
31	CA	1015	U	2.2
36	CH	58	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
42	CO	90	ARG	2.2
52	CY	49	LEU	2.2
1	BA	1037	C	2.2
2	BB	164	ILE	2.2
14	BN	57	PRO	2.2
27	C0	55	VAL	2.2
8	BH	120	GLY	2.2
11	BK	103	ALA	2.2
53	DZ	39	GLN	2.2
42	CO	114	GLU	2.2
1	BA	977	A	2.2
9	BI	41	ARG	2.2
31	CA	1522	A	2.2
7	BG	99	LEU	2.2
1	BA	1215	G	2.2
14	BN	6	MET	2.2
15	AO	21	ASP	2.2
33	CE	47	LYS	2.2
1	AA	1148	U	2.2
2	BB	186	ILE	2.2
36	CH	80	ILE	2.2
24	C3	17	GLY	2.2
29	CC	241	GLY	2.2
42	CO	93	GLY	2.2
48	CU	56	GLU	2.2
9	BI	81	HIS	2.2
17	BQ	20	SER	2.2
13	BM	81	MET	2.2
35	CG	109	PHE	2.2
36	DH	98	ASP	2.2
1	BA	993	G	2.2
3	AC	105	GLU	2.2
9	AI	37	GLN	2.2
19	BS	46	GLY	2.2
29	CC	251	GLN	2.2
31	CA	1867	G	2.2
34	CF	62	GLY	2.2
37	DJ	107	GLN	2.2
43	CP	96	GLY	2.2
50	CW	74	ALA	2.2
51	CX	33	ALA	2.2
1	BA	1325	C	2.2

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Mol	Chain	Res	Type	RSRZ
14	AN	100	SER	2.2
28	CB	19	C	2.2
31	CA	267	C	2.2
31	CA	901	C	2.2
47	CT	7	HIS	2.2
9	AI	28	ILE	2.2
35	CG	41	VAL	2.2
43	CP	28	VAL	2.2
2	BB	213	TYR	2.2
13	BM	86	TYR	2.2
17	BQ	63	GLU	2.2
30	CD	75	ALA	2.2
31	CA	222	A	2.2
36	CH	107	GLY	2.2
36	DH	70	GLU	2.2
37	DJ	124	ALA	2.2
51	CX	61	ALA	2.2
1	AA	1126	U	2.2
31	CA	1018	U	2.2
31	CA	1017	G	2.2
31	CA	1053	C	2.2
31	CA	2364	C	2.2
37	DJ	17	MET	2.2
39	CL	14	SER	2.2
2	BB	187	VAL	2.2
30	CD	29	VAL	2.2
13	AM	99	GLY	2.2
36	DH	87	GLU	2.2
50	CW	45	ASP	2.2
53	CZ	60	LYS	2.2
30	CD	40	LEU	2.2
7	BG	70	ARG	2.2
8	AH	2	SER	2.2
23	C2	6	ARG	2.2
34	CF	150	ARG	2.2
34	DF	77	PHE	2.2
36	CH	35	LYS	2.2
50	CW	34	LYS	2.2
50	CW	63	ILE	2.2
46	CS	103	ALA	2.2
47	CT	5	ALA	2.2
2	AB	36	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
11	AK	42	LEU	2.2
2	AB	49	MET	2.2
23	C2	50	LYS	2.2
31	CA	2783	U	2.2
33	CE	188	MET	2.2
40	CM	7	SER	2.2
43	CP	95	SER	2.2
18	AR	23	TYR	2.2
31	CA	420	C	2.2
44	CQ	12	GLN	2.2
36	CH	123	ARG	2.2
48	CU	28	ASN	2.2
55	DA	1076	C	2.2
1	BA	275	G	2.2
30	CD	151	THR	2.2
31	CA	326	G	2.2
34	CF	146	VAL	2.2
49	DV	49	VAL	2.2
1	BA	1008	U	2.2
31	CA	2245	U	2.2
1	AA	1	A	2.2
1	AA	1016	A	2.2
31	CA	279	A	2.2
6	BF	38	ARG	2.2
13	BM	115	PRO	2.2
36	DH	86	ASP	2.2
1	BA	1129	C	2.2
10	AJ	98	VAL	2.2
31	CA	1079	C	2.2
31	CA	1319	C	2.2
31	CA	1016	G	2.2
3	BC	54	ARG	2.2
7	AG	111	ARG	2.2
35	CG	65	ALA	2.2
31	CA	1143	A	2.2
3	BC	105	GLU	2.2
10	AJ	40	ILE	2.2
19	BS	51	VAL	2.2
19	BS	77	THR	2.2
42	CO	76	VAL	2.2
10	AJ	71	LEU	2.2
30	CD	38	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
34	CF	55	ALA	2.2
1	BA	213	G	2.2
28	CB	56	G	2.2
30	CD	49	GLN	2.2
31	CA	308	G	2.2
34	CF	101	GLU	2.2
36	DH	88	GLY	2.2
43	CP	75	GLY	2.2
54	DI	67	THR	2.2
31	CA	343	C	2.1
14	BN	12	LYS	2.1
25	C4	41	LYS	2.1
30	CD	1	MET	2.1
31	CA	2892	G	2.1
12	BL	117	TYR	2.1
14	AN	50	THR	2.1
36	DH	6	LEU	2.1
20	BT	63	ALA	2.1
45	CR	101	PHE	2.1
3	BC	51	SER	2.1
11	AK	97	ILE	2.1
41	CN	6	ARG	2.1
46	CS	45	GLU	2.1
54	DI	47	GLU	2.1
37	DJ	91	GLY	2.1
47	CT	82	MET	2.1
11	BK	47	ALA	2.1
20	BT	75	HIS	2.1
24	C3	26	ASN	2.1
30	CD	42	ASN	2.1
15	BO	15	PHE	2.1
36	DH	65	ALA	2.1
54	DI	127	ALA	2.1
9	AI	18	ARG	2.1
13	BM	90	ARG	2.1
31	CA	1984	G	2.1
26	C5	25	VAL	2.1
33	CE	148	ILE	2.1
37	CJ	111	GLN	2.1
50	CW	12	GLN	2.1
29	CC	244	PRO	2.1
1	AA	1140	C	2.1

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Mol	Chain	Res	Type	RSRZ
1	BA	957	U	2.1
1	BA	980	C	2.1
19	BS	47	LEU	2.1
31	CA	2833	U	2.1
2	AB	15	HIS	2.1
7	BG	147	ALA	2.1
26	C5	5	ALA	2.1
33	CE	13	THR	2.1
35	CG	160	LYS	2.1
44	CQ	43	PHE	2.1
3	BC	84	VAL	2.1
48	CU	18	GLU	2.1
49	CV	49	VAL	2.1
54	DI	114	GLU	2.1
1	AA	1033	G	2.1
20	BT	79	LEU	2.1
31	CA	1328	A	2.1
47	CT	87	PRO	2.1
7	BG	26	PHE	2.1
13	AM	57	ARG	2.1
28	CB	48	U	2.1
48	CU	37	ASP	2.1
36	DH	64	ALA	2.1
7	AG	122	ASN	2.1
10	BJ	96	VAL	2.1
17	BQ	50	ASN	2.1
35	CG	48	ASN	2.1
13	AM	4	ILE	2.1
9	AI	54	LEU	2.1
11	AK	100	LEU	2.1
23	C2	13	SER	2.1
29	DC	272	SER	2.1
1	AA	1138	G	2.1
1	BA	941	G	2.1
7	AG	61	ALA	2.1
7	AG	134	ALA	2.1
9	BI	44	ALA	2.1
20	BT	72	ALA	2.1
31	CA	626	A	2.1
34	CF	56	ASP	2.1
35	CG	114	ASP	2.1
43	CP	57	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
27	C0	34	HIS	2.1
31	CA	2629	U	2.1
55	DA	2152	G	2.1
1	BA	1267	C	2.1
3	BC	110	GLU	2.1
31	CA	1172	C	2.1
33	CE	32	VAL	2.1
3	BC	124	LEU	2.1
25	C4	2	PRO	2.1
8	BH	91	GLU	2.1
22	C1	56	ALA	2.1
23	C2	32	GLU	2.1
1	BA	1145	A	2.1
31	CA	477	A	2.1
31	CA	1322	A	2.1
31	CA	2130	U	2.1
44	CQ	4	ILE	2.1
1	AA	985	C	2.1
1	BA	1041	G	2.1
7	BG	101	MET	2.1
9	AI	85	ARG	2.1
19	BS	44	MET	2.1
20	BT	76	LYS	2.1
48	DU	91	GLN	2.1
54	DI	101	LYS	2.1
31	CA	2143	C	2.1
55	DA	2179	C	2.1
9	BI	30	ILE	2.1
36	DH	130	VAL	2.1
1	BA	325	A	2.1
31	CA	1709	U	2.1
50	CW	49	ASN	2.1
55	DA	1083	U	2.1
55	DA	2180	U	2.1
52	CY	46	PHE	2.1
1	BA	1262	C	2.1
31	CA	228	C	2.1
31	CA	1730	C	2.1
7	AG	127	ALA	2.1
37	DJ	37	GLU	2.1
2	BB	4	VAL	2.1
26	C5	34	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
7	AG	140	ASP	2.1
50	CW	66	ASP	2.1
51	CX	53	CYS	2.1
16	BP	10	GLY	2.1
33	CE	17	THR	2.1
1	BA	978	A	2.1
3	AC	79	LYS	2.1
31	CA	2376	A	2.1
2	BB	80	VAL	2.1
33	CE	128	ALA	2.1
35	CG	43	VAL	2.1
36	DH	123	ARG	2.1
28	CB	97	C	2.1
31	CA	264	C	2.1
7	BG	120	LEU	2.1
39	CL	28	SER	2.1
7	BG	126	ASP	2.1
23	C2	40	ASP	2.1
31	CA	124	G	2.1
46	CS	56	GLY	2.1
34	CF	114	PHE	2.1
9	AI	59	GLU	2.1
29	CC	26	LYS	2.1
19	AS	39	THR	2.1
16	AP	41	PRO	2.1
55	DA	1058	U	2.1
23	C2	48	ILE	2.1
34	CF	103	LEU	2.1
35	CG	120	GLY	2.1
42	CO	83	LEU	2.1
55	DA	1073	A	2.1
1	BA	972	C	2.1
31	CA	1043	C	2.1
31	CA	2651	C	2.1
45	CR	29	SER	2.1
36	CH	29	PHE	2.0
37	DJ	64	ASP	2.1
14	BN	63	ARG	2.0
1	BA	1361	G	2.0
31	CA	799	G	2.0
31	CA	1332	G	2.0
31	CA	1622	G	2.0

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Mol	Chain	Res	Type	RSRZ
9	BI	19	VAL	2.0
48	CU	35	ALA	2.0
51	CX	63	ALA	2.0
14	AN	16	LEU	2.0
30	CD	76	GLY	2.0
1	AA	1236	A	2.0
20	BT	8	LYS	2.0
26	C5	33	HIS	2.0
31	CA	2158	A	2.0
31	CA	2346	A	2.0
31	CA	2799	A	2.0
40	DM	104	GLN	2.0
1	BA	222	C	2.0
31	CA	611	C	2.0
31	CA	1547	C	2.0
14	BN	11	VAL	2.0
47	CT	43	ALA	2.0
3	BC	87	LEU	2.0
9	BI	4	ASN	2.0
18	AR	55	LEU	2.0
30	CD	96	ILE	2.0
37	CJ	109	ILE	2.0
48	CU	61	LEU	2.0
31	CA	548	G	2.0
31	CA	638	G	2.0
31	CA	875	G	2.0
31	CA	2152	G	2.0
21	BU	19	PHE	2.0
33	CE	100	MET	2.0
33	CE	183	PHE	2.0
45	CR	106	PHE	2.0
50	CW	2	PHE	2.0
55	DA	2151	U	2.0
30	CD	46	ARG	2.0
54	DI	122	GLN	2.0
31	CA	2835	A	2.0
3	AC	189	ALA	2.0
13	BM	106	ALA	2.0
36	CH	63	ALA	2.0
40	CM	137	ALA	2.0
50	CW	39	ALA	2.0
7	AG	132	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
37	CJ	72	LYS	2.0
31	CA	72	U	2.0
28	CB	7	G	2.0
31	CA	178	G	2.0
34	CF	129	SER	2.0
55	DA	2140	G	2.0
17	BQ	23	VAL	2.0
19	BS	67	VAL	2.0
20	BT	67	ILE	2.0
29	CC	18	LYS	2.0
36	CH	71	LYS	2.0
42	CO	79	LEU	2.0
37	DJ	119	GLY	2.0
1	BA	1263	C	2.0
2	BB	189	THR	2.0
17	BQ	74	THR	2.0
31	CA	2160	C	2.0
36	DH	127	GLU	2.0
1	AA	89	U	2.0
1	BA	952	U	2.0
31	CA	2259	U	2.0
16	BP	60	TRP	2.0
26	C5	4	ARG	2.0
27	C0	27	LEU	2.0
49	CV	75	ALA	2.0
1	BA	963	G	2.0
31	CA	407	G	2.0
27	C0	54	MET	2.0
34	CF	158	THR	2.0
37	DJ	126	THR	2.0
49	CV	37	GLU	2.0
31	CA	76	C	2.0
31	CA	816	C	2.0
53	CZ	58	ASN	2.0
14	BN	41	ARG	2.0
16	BP	54	LEU	2.0
33	CE	88	ARG	2.0
35	CG	79	VAL	2.0

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	5MC	BA	967	21/22	0.78	0.38	156,162,165,165	0
1	2MG	BA	966	24/25	0.79	0.31	161,163,169,169	0
1	2MG	BA	1207	24/25	0.85	0.27	169,172,175,177	0
31	PSU	CA	1917	20/21	0.89	0.20	106,115,121,121	0
31	PSU	CA	2504	20/21	0.90	0.24	87,89,95,96	0
1	5MC	AA	967	21/22	0.91	0.21	90,100,103,105	0
1	2MG	AA	1207	24/25	0.91	0.17	124,129,130,132	0
31	PSU	CA	955	20/21	0.91	0.19	92,93,95,95	0
31	3TD	CA	1915	21/22	0.91	0.23	132,137,140,141	0
1	PSU	BA	516	20/21	0.91	0.18	93,98,101,102	0
1	2MG	AA	966	24/25	0.91	0.21	84,94,103,105	0
31	2MA	CA	2503	23/24	0.92	0.23	90,95,99,100	0
31	PSU	CA	1911	20/21	0.92	0.18	112,123,126,126	0
41	4D4	CN	81	12/13	0.92	0.32	85,88,108,110	0
31	5MU	CA	747	21/22	0.93	0.20	95,101,103,106	0
31	7MG	CA	2069	24/25	0.93	0.21	84,89,94,94	0
55	PSU	DA	1911	20/21	0.93	0.20	82,85,87,88	0
31	PSU	CA	2457	20/21	0.93	0.20	83,88,93,96	0
12	D2T	AL	89	10/11	0.94	0.22	61,65,85,86	0
1	5MC	BA	1407	21/22	0.94	0.17	81,92,94,95	0
31	6MZ	CA	2030	23/24	0.94	0.20	82,91,100,102	0
31	OMU	CA	2552	21/22	0.94	0.32	80,82,86,88	0
12	D2T	BL	89	10/11	0.94	0.26	77,82,93,93	0
55	3TD	DA	1915	21/22	0.94	0.19	105,109,117,117	0
31	2MG	CA	2445	24/25	0.94	0.24	74,83,85,89	0
31	PSU	CA	746	20/21	0.95	0.17	98,101,104,104	0
31	OMG	CA	2251	24/25	0.95	0.18	69,79,82,84	0
1	MA6	BA	1519	24/25	0.95	0.24	74,77,81,83	0
1	2MG	BA	1516	24/25	0.95	0.17	67,75,78,81	0
31	6MZ	CA	1618	23/24	0.95	0.29	112,116,119,120	0
31	1MG	CA	745	24/25	0.96	0.20	92,96,97,98	0
31	2MG	CA	1835	24/25	0.96	0.17	61,72,77,78	0
1	MA6	BA	1518	24/25	0.96	0.18	67,73,76,77	0
31	PSU	CA	2580	20/21	0.96	0.18	86,88,93,94	0
1	7MG	BA	527	24/25	0.96	0.18	76,81,88,89	0
1	4OC	BA	1402	22/23	0.96	0.17	79,83,83,84	0
55	PSU	DA	1917	20/21	0.96	0.18	79,84,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
31	OMC	CA	2498	21/22	0.96	0.25	82,84,89,92	0
41	4D4	DN	81[A]	12/13	0.96	0.22	32,40,49,51	9
41	4D4	DN	81[B]	12/13	0.96	0.22	12,25,36,36	9
1	4OC	AA	1402	22/23	0.97	0.17	53,61,66,66	0
31	PSU	CA	2605	20/21	0.97	0.15	73,75,78,80	0
55	2MG	DA	1835	24/25	0.97	0.20	41,47,52,52	0
1	5MC	AA	1407	21/22	0.97	0.15	55,57,60,62	0
1	UR3	BA	1498	21/22	0.97	0.15	81,84,87,88	0
1	UR3	AA	1498	21/22	0.97	0.16	58,63,67,70	0
31	5MC	CA	1962	21/22	0.97	0.19	67,69,73,76	0
1	2MG	AA	1516	24/25	0.97	0.16	58,62,63,63	0
1	PSU	AA	516	20/21	0.97	0.14	81,85,86,87	0
1	MA6	AA	1519	24/25	0.98	0.17	53,56,61,64	0
1	7MG	AA	527	24/25	0.98	0.15	60,65,72,74	0
31	5MU	CA	1939	21/22	0.98	0.17	70,73,82,85	0
55	5MC	DA	1962	21/22	0.98	0.23	36,44,48,49	0
55	PSU	DA	2604	20/21	0.98	0.17	41,46,56,56	0
32	MEQ	DD	150[A]	10/11	0.98	0.23	7,15,29,31	10
32	MEQ	DD	150[B]	10/11	0.98	0.23	23,32,41,41	10
1	MA6	AA	1518	24/25	0.98	0.17	51,55,58,61	0
55	5MU	DA	1939	21/22	0.99	0.19	35,37,41,47	0
55	6MZ	DA	1618	23/24	0.99	0.18	26,33,36,36	0
55	7MG	DA	2069	24/25	0.99	0.18	32,37,41,43	0
55	OMG	DA	2251	24/25	0.99	0.18	27,32,37,42	0
55	2MG	DA	2445	24/25	0.99	0.19	26,29,35,37	0
55	H2U	DA	2449	20/21	0.99	0.19	25,29,31,32	0
55	PSU	DA	2457	20/21	0.99	0.18	27,31,37,37	0
55	OMC	DA	2498	21/22	0.99	0.19	21,26,29,30	0
55	2MA	DA	2503	23/24	0.99	0.19	21,35,41,42	0
55	PSU	DA	2504	20/21	0.99	0.20	37,40,44,44	0
55	OMU	DA	2552	21/22	0.99	0.20	31,34,39,46	0
55	PSU	DA	2580	20/21	0.99	0.19	20,25,32,34	0
55	1MG	DA	745	24/25	0.99	0.18	25,29,37,41	0
55	PSU	DA	2605	20/21	0.99	0.15	31,41,43,43	0
55	PSU	DA	746	20/21	0.99	0.17	21,28,31,35	0
55	5MU	DA	747	21/22	0.99	0.18	28,33,36,41	0
55	PSU	DA	955	20/21	0.99	0.19	25,27,30,30	0
55	6MZ	DA	2030	23/24	1.00	0.19	22,25,29,34	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands i

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	AA	1628	1/1	-0.13	0.61	159,159,159,159	0
56	MG	CA	3154	1/1	0.03	0.72	147,147,147,147	0
56	MG	BA	1639	1/1	0.19	0.63	94,94,94,94	0
56	MG	BA	1625	1/1	0.38	0.16	256,256,256,256	0
56	MG	CA	3122	1/1	0.39	1.73	126,126,126,126	0
56	MG	CA	3123	1/1	0.40	0.90	113,113,113,113	0
56	MG	DA	3168	1/1	0.43	0.19	141,141,141,141	0
56	MG	CA	3139	1/1	0.44	0.47	87,87,87,87	0
56	MG	DA	3167	1/1	0.46	0.55	102,102,102,102	0
56	MG	CA	3075	1/1	0.46	1.38	230,230,230,230	0
59	PUT	AA	1674	6/6	0.51	0.87	133,134,135,135	0
56	MG	CA	3077	1/1	0.52	0.44	249,249,249,249	0
56	MG	AA	1603	1/1	0.55	0.52	83,83,83,83	0
56	MG	CA	3060	1/1	0.55	0.28	234,234,234,234	0
56	MG	DA	3129	1/1	0.55	0.67	102,102,102,102	0
56	MG	AA	1615	1/1	0.56	0.84	83,83,83,83	0
56	MG	AA	1622	1/1	0.56	0.89	100,100,100,100	0
56	MG	DA	3136	1/1	0.57	0.33	77,77,77,77	0
56	MG	BA	1647	1/1	0.58	0.60	91,91,91,91	0
56	MG	CA	3028	1/1	0.59	0.37	278,278,278,278	0
56	MG	CA	3140	1/1	0.59	0.29	84,84,84,84	0
56	MG	CA	3132	1/1	0.60	0.59	105,105,105,105	0
56	MG	AA	1618	1/1	0.61	0.50	92,92,92,92	0
56	MG	CA	3124	1/1	0.62	0.20	118,118,118,118	0
56	MG	CB	201	1/1	0.62	0.07	168,168,168,168	0
56	MG	CA	3156	1/1	0.64	0.51	232,232,232,232	0
56	MG	CA	3136	1/1	0.64	0.52	84,84,84,84	0
56	MG	CA	3047	1/1	0.64	0.45	229,229,229,229	0
62	PEG	D3	102	7/7	0.64	1.36	114,119,124,125	0
56	MG	AA	1626	1/1	0.66	1.61	99,99,99,99	0
56	MG	DA	3163	1/1	0.66	0.38	91,91,91,91	0
56	MG	CA	3114	1/1	0.66	0.48	66,66,66,66	0
56	MG	CA	3131	1/1	0.67	0.34	78,78,78,78	0
59	PUT	AA	1672	6/6	0.67	0.69	99,100,102,103	0
56	MG	AA	1614	1/1	0.68	0.13	85,85,85,85	0
56	MG	BA	1612	1/1	0.68	0.46	182,182,182,182	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
62	PEG	DQ	201	7/7	0.68	0.97	124,127,128,129	0
56	MG	DA	3128	1/1	0.69	0.17	72,72,72,72	0
62	PEG	DP	201	7/7	0.69	0.79	126,127,131,132	0
56	MG	CA	3094	1/1	0.69	0.15	105,105,105,105	0
56	MG	CA	3006	1/1	0.70	0.08	155,155,155,155	0
56	MG	DA	3151	1/1	0.70	0.25	82,82,82,82	0
63	EDO	DB	212	4/4	0.72	0.39	115,115,116,116	0
56	MG	DA	3176	1/1	0.73	0.42	98,98,98,98	0
58	MPD	DE	301	8/8	0.73	1.08	139,140,142,142	0
56	MG	CA	3129	1/1	0.73	0.18	104,104,104,104	0
56	MG	CA	3130	1/1	0.73	0.35	89,89,89,89	0
59	PUT	DA	3195	6/6	0.73	0.63	87,91,91,92	0
56	MG	CA	3002	1/1	0.73	0.23	265,265,265,265	0
56	MG	BA	1623	1/1	0.73	0.59	248,248,248,248	0
56	MG	DA	3122	1/1	0.73	0.87	100,100,100,100	0
56	MG	BA	1624	1/1	0.73	0.82	262,262,262,262	0
65	SPD	DA	3206	10/10	0.73	0.36	87,102,109,110	0
69	TRS	DA	3220	8/8	0.73	0.56	125,128,134,134	0
56	MG	DA	3179	1/1	0.74	0.51	104,104,104,104	0
56	MG	DA	3181	1/1	0.74	0.58	83,83,83,83	0
56	MG	DB	206	1/1	0.74	1.11	80,80,80,80	0
62	PEG	DA	3200	7/7	0.75	0.50	83,85,95,96	0
59	PUT	AA	1675	6/6	0.75	0.48	106,109,109,109	0
62	PEG	DA	3218	7/7	0.76	0.36	123,129,133,134	0
56	MG	CA	3141	1/1	0.76	0.31	80,80,80,80	0
56	MG	CA	3135	1/1	0.76	0.38	101,101,101,101	0
56	MG	CA	3034	1/1	0.76	0.19	246,246,246,246	0
56	MG	DA	3165	1/1	0.77	0.30	62,62,62,62	0
56	MG	DA	3166	1/1	0.77	1.04	81,81,81,81	0
62	PEG	DA	3199	7/7	0.77	0.48	80,89,93,95	0
56	MG	BA	1641	1/1	0.77	0.20	120,120,120,120	0
56	MG	CA	3111	1/1	0.77	0.25	83,83,83,83	0
56	MG	AA	1613	1/1	0.77	1.07	65,65,65,65	0
56	MG	CA	3055	1/1	0.77	0.14	169,169,169,169	0
56	MG	DA	3180	1/1	0.77	2.06	106,106,106,106	0
56	MG	CA	3003	1/1	0.78	1.90	278,278,278,278	0
56	MG	AA	1612	1/1	0.78	0.43	77,77,77,77	0
56	MG	CA	3115	1/1	0.78	0.35	84,84,84,84	0
56	MG	CA	3127	1/1	0.78	0.14	73,73,73,73	0
59	PUT	DA	3219	6/6	0.78	0.37	70,75,78,79	0
64	PGE	D1	102	10/10	0.78	0.50	122,127,128,128	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	DB	207	1/1	0.78	0.56	92,92,92,92	0
58	MPD	DT	202	8/8	0.78	0.38	128,128,130,130	0
56	MG	CA	3007	1/1	0.79	0.32	214,214,214,214	0
56	MG	BA	1606	1/1	0.79	0.19	227,227,227,227	0
56	MG	DA	3142	1/1	0.79	0.31	62,62,62,62	0
56	MG	CA	3031	1/1	0.79	0.08	64,64,64,64	0
56	MG	BA	1603	1/1	0.79	0.20	263,263,263,263	0
63	EDO	DB	211	4/4	0.80	0.39	88,90,92,92	0
58	MPD	DA	3204	8/8	0.80	0.61	112,114,117,117	0
63	EDO	DA	3209	4/4	0.80	0.28	135,136,137,138	0
57	PG4	DR	202	13/13	0.80	0.35	109,117,120,121	0
64	PGE	DS	201	10/10	0.80	0.37	77,89,91,92	0
56	MG	CA	3125	1/1	0.80	0.33	89,89,89,89	0
56	MG	AA	1616	1/1	0.80	0.97	85,85,85,85	0
56	MG	DA	3172	1/1	0.81	0.34	103,103,103,103	0
56	MG	DA	3152	1/1	0.81	0.42	66,66,66,66	0
56	MG	CA	3080	1/1	0.81	0.17	151,151,151,151	0
56	MG	DA	3137	1/1	0.81	0.68	37,37,37,37	1
56	MG	CA	3145	1/1	0.81	0.79	73,73,73,73	0
56	MG	DA	3143	1/1	0.81	0.59	114,114,114,114	0
61	ZN	C5	101	1/1	0.81	0.06	149,149,149,149	0
56	MG	AA	1617	1/1	0.81	0.32	96,96,96,96	0
58	MPD	DK	201	8/8	0.81	0.29	120,121,123,124	0
56	MG	DA	3171	1/1	0.81	0.69	73,73,73,73	0
56	MG	DA	3123	1/1	0.82	0.19	62,62,62,62	0
56	MG	DA	3147	1/1	0.82	0.24	65,65,65,65	0
56	MG	CA	3038	1/1	0.82	0.28	263,263,263,263	0
56	MG	AA	1624	1/1	0.82	0.44	95,95,95,95	0
60	T1C	BA	1643	42/42	0.82	0.23	170,174,179,179	0
56	MG	AA	1606	1/1	0.82	0.28	91,91,91,91	0
62	PEG	D1	103	7/7	0.82	0.38	85,90,91,91	0
56	MG	AA	1627	1/1	0.82	0.54	91,91,91,91	0
56	MG	CA	3128	1/1	0.82	0.28	75,75,75,75	0
67	ACY	DA	3196	4/4	0.82	0.30	84,85,87,87	0
59	PUT	AA	1673	6/6	0.82	0.64	100,102,103,104	0
56	MG	CA	3146	1/1	0.83	0.15	144,144,144,144	0
56	MG	DA	3160	1/1	0.83	0.61	74,74,74,74	0
56	MG	DA	3162	1/1	0.83	0.34	85,85,85,85	0
59	PUT	DA	3221	6/6	0.83	0.48	138,140,141,141	0
59	PUT	DA	3222	6/6	0.83	0.34	48,52,57,58	0
58	MPD	DN	201	8/8	0.83	0.36	106,111,116,117	0
56	MG	CA	3078	1/1	0.83	0.16	149,149,149,149	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3113	1/1	0.83	0.41	71,71,71,71	0
56	MG	CA	3005	1/1	0.83	0.60	237,237,237,237	0
56	MG	BA	1640	1/1	0.83	0.42	124,124,124,124	0
57	PG4	AA	1670	13/13	0.83	0.25	78,87,97,97	0
56	MG	CA	3149	1/1	0.84	0.31	67,67,67,67	0
56	MG	CA	3119	1/1	0.84	0.43	89,89,89,89	0
56	MG	BA	1644	1/1	0.84	0.13	133,133,133,133	0
56	MG	DA	3182	1/1	0.84	0.32	61,61,61,61	0
56	MG	CA	3106	1/1	0.84	0.24	83,83,83,83	0
56	MG	DA	3153	1/1	0.84	0.45	52,52,52,52	0
56	MG	DA	3177	1/1	0.84	0.41	77,77,77,77	0
62	PEG	DA	3227	7/7	0.84	0.38	97,99,103,104	0
56	MG	DB	208	1/1	0.85	0.71	76,76,76,76	0
58	MPD	DT	201	8/8	0.85	0.34	102,108,109,109	0
63	EDO	DB	201	4/4	0.85	0.31	94,97,98,99	0
56	MG	CA	3116	1/1	0.85	0.34	95,95,95,95	0
56	MG	BA	1637	1/1	0.85	0.66	85,85,85,85	0
56	MG	CA	3152	1/1	0.85	0.35	151,151,151,151	0
56	MG	BA	1646	1/1	0.85	0.11	108,108,108,108	0
64	PGE	D3	101	10/10	0.85	0.61	97,99,102,103	0
56	MG	CA	3063	1/1	0.85	0.17	125,125,125,125	0
57	PG4	DA	3193	13/13	0.85	0.84	85,95,100,101	0
56	MG	CA	3070	1/1	0.85	0.09	91,91,91,91	0
56	MG	CA	3071	1/1	0.85	0.13	166,166,166,166	0
56	MG	CA	3126	1/1	0.86	0.20	86,86,86,86	0
56	MG	CA	3105	1/1	0.86	0.31	262,262,262,262	0
56	MG	CA	3142	1/1	0.86	0.42	78,78,78,78	0
56	MG	AA	1661	1/1	0.86	0.24	173,173,173,173	0
56	MG	DA	3170	1/1	0.86	0.40	77,77,77,77	0
59	PUT	DA	3205	6/6	0.86	0.37	108,109,111,111	0
57	PG4	DA	3216	13/13	0.86	0.32	99,104,109,110	0
56	MG	DA	3131	1/1	0.86	0.21	62,62,62,62	0
63	EDO	DA	3002	4/4	0.86	0.71	93,94,95,95	0
63	EDO	DA	3194	4/4	0.86	0.27	76,77,78,78	0
56	MG	DA	3133	1/1	0.86	0.41	91,91,91,91	0
56	MG	DA	3155	1/1	0.86	0.38	58,58,58,58	0
56	MG	AA	1621	1/1	0.86	0.51	77,77,77,77	0
56	MG	CA	3022	1/1	0.86	0.83	195,195,195,195	0
58	MPD	DA	3190	8/8	0.86	0.32	95,97,99,102	0
62	PEG	DL	201	7/7	0.86	0.28	82,85,87,87	0
56	MG	DA	3140	1/1	0.86	0.27	54,54,54,54	0
56	MG	CA	3076	1/1	0.87	0.19	182,182,182,182	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	AA	1625	1/1	0.87	0.35	86,86,86,86	0
56	MG	CB	203	1/1	0.87	0.08	145,145,145,145	0
56	MG	CA	3056	1/1	0.87	0.35	71,71,71,71	0
56	MG	AA	1609	1/1	0.87	0.33	89,89,89,89	0
56	MG	DA	3146	1/1	0.87	0.19	122,122,122,122	0
59	PUT	DA	3189	6/6	0.87	0.43	45,54,56,56	0
58	MPD	DE	302	8/8	0.88	0.68	93,97,102,102	0
56	MG	DA	3132	1/1	0.88	0.31	70,70,70,70	0
59	PUT	DA	3184	6/6	0.88	0.26	78,80,81,82	0
56	MG	CA	3001	1/1	0.88	0.18	296,296,296,296	0
56	MG	DR	201	1/1	0.88	0.57	42,42,42,42	0
56	MG	AA	1601	1/1	0.88	0.68	67,67,67,67	0
59	PUT	DA	3213	6/6	0.88	0.32	105,107,110,110	0
57	PG4	DS	202	13/13	0.88	0.34	43,51,72,73	0
56	MG	CA	3057	1/1	0.88	0.17	133,133,133,133	0
65	SPD	DA	3224	10/10	0.88	0.28	50,54,66,68	0
56	MG	DA	3141	1/1	0.88	0.32	86,86,86,86	0
56	MG	CA	3108	1/1	0.88	0.22	83,83,83,83	0
56	MG	AA	1605	1/1	0.89	0.64	89,89,89,89	0
56	MG	CA	3059	1/1	0.89	0.10	86,86,86,86	0
62	PEG	DA	3226	7/7	0.89	0.24	89,91,98,98	0
56	MG	AA	1642	1/1	0.89	0.25	158,158,158,158	0
56	MG	CA	3061	1/1	0.89	0.11	247,247,247,247	0
56	MG	CA	3151	1/1	0.89	0.42	71,71,71,71	0
56	MG	BA	1609	1/1	0.89	0.12	166,166,166,166	0
56	MG	CA	3133	1/1	0.89	0.33	72,72,72,72	0
60	T1C	AA	1680	42/42	0.89	0.26	96,107,123,124	0
63	EDO	DA	3208	4/4	0.89	0.22	89,90,90,91	0
56	MG	CA	3064	1/1	0.89	0.36	249,249,249,249	0
58	MPD	DA	3192	8/8	0.89	0.49	95,100,104,105	0
56	MG	CA	3068	1/1	0.89	0.38	216,216,216,216	0
56	MG	CA	3019	1/1	0.89	0.16	58,58,58,58	0
57	PG4	DQ	202	13/13	0.89	0.21	60,63,76,76	0
56	MG	AA	1620	1/1	0.89	0.25	78,78,78,78	0
66	1PE	DA	3202	16/16	0.89	0.29	61,64,72,73	0
56	MG	BA	1614	1/1	0.89	0.18	171,171,171,171	0
56	MG	DA	3110	1/1	0.89	0.34	295,295,295,295	0
56	MG	DB	209	1/1	0.90	0.37	66,66,66,66	0
56	MG	CA	3048	1/1	0.90	0.12	76,76,76,76	0
56	MG	DA	3121	1/1	0.90	0.59	68,68,68,68	0
56	MG	CA	3112	1/1	0.90	0.24	75,75,75,75	0
56	MG	CA	3134	1/1	0.90	0.17	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3009	1/1	0.90	0.19	243,243,243,243	0
56	MG	CA	3072	1/1	0.90	0.64	249,249,249,249	0
56	MG	DA	3130	1/1	0.90	0.24	54,54,54,54	0
56	MG	AA	1608	1/1	0.90	0.47	96,96,96,96	0
56	MG	BA	1645	1/1	0.90	0.15	102,102,102,102	0
64	PGE	DU	101	10/10	0.90	0.55	89,97,104,105	0
64	PGE	DA	3214	10/10	0.90	0.38	72,73,77,78	0
59	PUT	DA	3212	6/6	0.90	0.23	81,84,85,85	0
56	MG	AA	1638	1/1	0.90	0.07	114,114,114,114	0
56	MG	CA	3120	1/1	0.90	0.17	102,102,102,102	0
56	MG	CA	3110	1/1	0.90	0.19	93,93,93,93	0
63	EDO	D1	101	4/4	0.90	0.24	59,60,60,60	0
56	MG	BA	1638	1/1	0.91	0.58	78,78,78,78	0
56	MG	CA	3012	1/1	0.91	0.17	95,95,95,95	0
56	MG	CA	3053	1/1	0.91	0.16	65,65,65,65	0
56	MG	AA	1654	1/1	0.91	0.39	262,262,262,262	0
56	MG	DA	3174	1/1	0.91	0.24	74,74,74,74	0
58	MPD	DA	3207	8/8	0.91	0.40	77,78,80,80	0
56	MG	BA	1608	1/1	0.91	0.11	102,102,102,102	0
56	MG	CA	3023	1/1	0.91	0.08	158,158,158,158	0
56	MG	DA	3178	1/1	0.91	0.45	88,88,88,88	0
56	MG	BA	1635	1/1	0.91	0.10	102,102,102,102	0
56	MG	DA	3145	1/1	0.91	0.25	79,79,79,79	0
56	MG	CB	202	1/1	0.91	0.10	116,116,116,116	0
56	MG	DB	210	1/1	0.91	0.46	97,97,97,97	0
56	MG	DA	3061	1/1	0.91	0.15	233,233,233,233	0
57	PG4	BA	1642	13/13	0.91	0.58	88,89,99,100	0
56	MG	CA	3137	1/1	0.91	0.20	106,106,106,106	0
56	MG	CA	3090	1/1	0.91	0.25	185,185,185,185	0
56	MG	CA	3093	1/1	0.91	0.11	88,88,88,88	0
56	MG	AA	1659	1/1	0.91	0.10	115,115,115,115	0
64	PGE	DA	3203	10/10	0.91	0.31	83,85,88,90	0
56	MG	CA	3036	1/1	0.91	0.17	193,193,193,193	0
65	SPD	DA	3183	10/10	0.91	0.61	79,83,87,87	0
58	MPD	AA	1676	8/8	0.91	0.42	95,99,100,101	0
56	MG	CA	3008	1/1	0.91	0.10	136,136,136,136	0
66	1PE	DA	3185	16/16	0.91	0.24	50,55,84,87	0
56	MG	CA	3107	1/1	0.91	0.35	83,83,83,83	0
56	MG	CA	3046	1/1	0.91	0.13	111,111,111,111	0
68	GUN	DA	3211	11/11	0.91	0.29	98,100,101,102	0
56	MG	CA	3109	1/1	0.91	0.25	62,62,62,62	0
56	MG	BA	1617	1/1	0.92	0.12	131,131,131,131	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3086	1/1	0.92	0.07	68,68,68,68	0
56	MG	BA	1619	1/1	0.92	0.19	96,96,96,96	0
63	EDO	DA	3215	4/4	0.92	0.25	65,66,68,70	0
56	MG	CA	3026	1/1	0.92	0.87	173,173,173,173	0
56	MG	CA	3150	1/1	0.92	0.96	75,75,75,75	0
56	MG	CA	3051	1/1	0.92	0.20	80,80,80,80	0
56	MG	CA	3101	1/1	0.92	0.15	151,151,151,151	0
59	PUT	DA	3188	6/6	0.92	0.26	50,53,55,56	0
56	MG	AA	1658	1/1	0.92	0.08	98,98,98,98	0
64	PGE	DA	3217	10/10	0.92	0.34	85,88,91,92	0
56	MG	DA	3175	1/1	0.92	0.48	63,63,63,63	0
56	MG	CA	3054	1/1	0.92	0.15	156,156,156,156	0
56	MG	CA	3029	1/1	0.92	0.20	143,143,143,143	0
56	MG	AA	1623	1/1	0.92	0.37	69,69,69,69	0
56	MG	DA	3157	1/1	0.92	0.54	73,73,73,73	0
56	MG	AA	1602	1/1	0.92	0.30	78,78,78,78	0
56	MG	AA	1665	1/1	0.92	0.30	161,161,161,161	0
56	MG	AA	1604	1/1	0.92	0.39	70,70,70,70	0
56	MG	CA	3014	1/1	0.93	0.18	216,216,216,216	0
56	MG	CA	3018	1/1	0.93	0.08	85,85,85,85	0
56	MG	DA	3126	1/1	0.93	0.22	61,61,61,61	0
56	MG	CA	3148	1/1	0.93	0.48	51,51,51,51	1
56	MG	BA	1629	1/1	0.93	0.45	168,168,168,168	0
63	EDO	DA	3197	4/4	0.93	0.23	65,67,68,69	0
56	MG	CA	3079	1/1	0.93	0.07	115,115,115,115	0
56	MG	CA	3021	1/1	0.93	1.26	264,264,264,264	0
56	MG	CA	3082	1/1	0.93	0.24	114,114,114,114	0
56	MG	CA	3083	1/1	0.93	0.16	204,204,204,204	0
56	MG	CA	3155	1/1	0.93	0.17	156,156,156,156	0
56	MG	BA	1630	1/1	0.93	0.05	153,153,153,153	0
62	PEG	AL	201	7/7	0.93	0.34	83,85,94,95	0
56	MG	CA	3089	1/1	0.93	0.19	68,68,68,68	0
56	MG	AA	1677	1/1	0.93	0.10	194,194,194,194	0
56	MG	CA	3092	1/1	0.93	0.12	152,152,152,152	0
64	PGE	DA	3225	10/10	0.93	0.23	73,83,94,96	0
56	MG	BA	1605	1/1	0.93	0.09	107,107,107,107	0
56	MG	CA	3138	1/1	0.93	0.08	66,66,66,66	0
56	MG	AA	1678	1/1	0.93	0.17	78,78,78,78	0
56	MG	DA	3011	1/1	0.93	0.18	115,115,115,115	0
56	MG	CA	3010	1/1	0.93	0.13	234,234,234,234	0
56	MG	BA	1627	1/1	0.93	0.53	124,124,124,124	0
56	MG	DA	3120	1/1	0.93	0.21	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3032	1/1	0.93	0.17	241,241,241,241	0
56	MG	CA	3040	1/1	0.94	0.08	76,76,76,76	0
56	MG	BA	1602	1/1	0.94	0.10	68,68,68,68	0
56	MG	AA	1656	1/1	0.94	0.19	196,196,196,196	0
56	MG	BA	1604	1/1	0.94	0.17	153,153,153,153	0
56	MG	DA	3124	1/1	0.94	0.22	65,65,65,65	0
56	MG	CA	3050	1/1	0.94	0.13	54,54,54,54	0
56	MG	CA	3143	1/1	0.94	0.18	70,70,70,70	0
58	MPD	DA	3210	8/8	0.94	0.29	87,89,90,91	0
56	MG	AA	1632	1/1	0.94	0.05	94,94,94,94	0
56	MG	CA	3020	1/1	0.94	0.10	86,86,86,86	0
56	MG	AA	1611	1/1	0.94	0.24	108,108,108,108	0
56	MG	BA	1633	1/1	0.94	0.11	229,229,229,229	0
63	EDO	DA	3198	4/4	0.94	0.38	78,81,83,83	0
56	MG	CA	3084	1/1	0.94	0.47	174,174,174,174	0
56	MG	AA	1641	1/1	0.94	0.07	67,67,67,67	0
56	MG	AA	1663	1/1	0.94	0.10	90,90,90,90	0
56	MG	DA	3138	1/1	0.94	0.18	59,59,59,59	0
56	MG	CA	3004	1/1	0.94	0.07	159,159,159,159	0
56	MG	BA	1610	1/1	0.94	0.05	93,93,93,93	0
56	MG	AA	1664	1/1	0.94	0.49	212,212,212,212	0
56	MG	AA	1610	1/1	0.94	0.24	90,90,90,90	0
56	MG	AA	1667	1/1	0.94	0.11	47,47,47,47	0
56	MG	CA	3104	1/1	0.94	0.37	258,258,258,258	0
56	MG	CA	3066	1/1	0.94	0.18	89,89,89,89	0
56	MG	CA	3067	1/1	0.94	0.32	277,277,277,277	0
56	MG	AA	1645	1/1	0.94	0.13	66,66,66,66	0
56	MG	CA	3069	1/1	0.94	0.19	88,88,88,88	0
58	MPD	AA	1671	8/8	0.94	0.55	88,88,90,92	0
56	MG	DA	3036	1/1	0.94	0.22	24,24,24,24	0
56	MG	DA	3156	1/1	0.94	0.23	62,62,62,62	0
56	MG	CA	3037	1/1	0.94	0.40	189,189,189,189	0
56	MG	AA	1619	1/1	0.94	0.23	92,92,92,92	0
56	MG	DA	3161	1/1	0.95	0.22	61,61,61,61	0
56	MG	DA	3116	1/1	0.95	0.14	72,72,72,72	0
56	MG	CA	3044	1/1	0.95	0.09	57,57,57,57	0
56	MG	CA	3065	1/1	0.95	0.19	109,109,109,109	0
56	MG	CA	3058	1/1	0.95	0.16	98,98,98,98	0
56	MG	CA	3099	1/1	0.95	0.28	160,160,160,160	0
56	MG	AA	1655	1/1	0.95	0.17	163,163,163,163	0
56	MG	DA	3169	1/1	0.95	0.20	69,69,69,69	0
59	PUT	DA	3001	6/6	0.95	0.17	46,50,58,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	1616	1/1	0.95	0.10	122,122,122,122	0
56	MG	CA	3088	1/1	0.95	0.08	62,62,62,62	0
56	MG	CA	3016	1/1	0.95	0.29	107,107,107,107	0
56	MG	CA	3035	1/1	0.95	0.19	91,91,91,91	0
56	MG	DA	3043	1/1	0.95	0.07	80,80,80,80	0
56	MG	DA	3154	1/1	0.95	0.14	59,59,59,59	0
56	MG	DA	3053	1/1	0.95	0.13	89,89,89,89	0
56	MG	CA	3117	1/1	0.95	0.35	67,67,67,67	0
56	MG	DA	3064	1/1	0.95	0.14	25,25,25,25	0
63	EDO	DB	213	4/4	0.95	0.19	82,82,84,84	0
56	MG	CA	3118	1/1	0.95	0.39	59,59,59,59	0
59	PUT	DA	3223	6/6	0.95	0.27	61,62,65,67	0
56	MG	CA	3081	1/1	0.96	0.07	104,104,104,104	0
56	MG	AA	1650	1/1	0.96	0.07	114,114,114,114	0
56	MG	CA	3033	1/1	0.96	0.09	110,110,110,110	0
56	MG	BA	1628	1/1	0.96	0.15	89,89,89,89	0
56	MG	AA	1636	1/1	0.96	0.22	97,97,97,97	0
56	MG	CA	3144	1/1	0.96	0.06	49,49,49,49	0
56	MG	AA	1630	1/1	0.96	0.12	134,134,134,134	0
56	MG	DA	3135	1/1	0.96	0.20	72,72,72,72	0
56	MG	DA	3042	1/1	0.96	0.16	40,40,40,40	0
64	PGE	DA	3186	10/10	0.96	0.18	39,48,55,57	0
56	MG	AA	1639	1/1	0.96	0.11	118,118,118,118	0
56	MG	CA	3147	1/1	0.96	0.56	58,58,58,58	1
56	MG	BA	1634	1/1	0.96	0.06	99,99,99,99	0
56	MG	CA	3039	1/1	0.96	0.20	175,175,175,175	0
56	MG	AA	1657	1/1	0.96	0.38	136,136,136,136	0
56	MG	CA	3015	1/1	0.96	0.19	51,51,51,51	0
56	MG	CA	3098	1/1	0.96	0.07	77,77,77,77	0
56	MG	BA	1626	1/1	0.96	0.09	102,102,102,102	0
56	MG	DA	3173	1/1	0.96	0.33	98,98,98,98	0
56	MG	CA	3062	1/1	0.96	0.12	175,175,175,175	0
67	ACY	DA	3201	4/4	0.96	0.21	78,79,79,79	0
56	MG	CA	3030	1/1	0.96	0.07	78,78,78,78	0
56	MG	CA	3017	1/1	0.96	0.09	88,88,88,88	0
56	MG	AA	1644	1/1	0.97	0.17	106,106,106,106	0
56	MG	CA	3087	1/1	0.97	0.13	77,77,77,77	0
56	MG	CA	3042	1/1	0.97	0.08	88,88,88,88	0
56	MG	DA	3125	1/1	0.97	0.34	59,59,59,59	0
56	MG	CA	3043	1/1	0.97	0.07	81,81,81,81	0
56	MG	DA	3127	1/1	0.97	0.92	53,53,53,53	0
56	MG	CA	3121	1/1	0.97	0.13	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	1621	1/1	0.97	0.21	33,33,33,33	0
56	MG	CA	3091	1/1	0.97	0.08	68,68,68,68	0
56	MG	BA	1622	1/1	0.97	0.07	85,85,85,85	0
56	MG	CA	3024	1/1	0.97	0.05	102,102,102,102	0
56	MG	AA	1634	1/1	0.97	0.12	130,130,130,130	0
56	MG	DA	3134	1/1	0.97	0.07	96,96,96,96	0
56	MG	CA	3097	1/1	0.97	0.09	90,90,90,90	0
56	MG	AA	1666	1/1	0.97	0.06	57,57,57,57	0
56	MG	DB	202	1/1	0.97	0.09	62,62,62,62	0
56	MG	AA	1649	1/1	0.97	0.07	68,68,68,68	0
56	MG	DA	3139	1/1	0.97	0.17	67,67,67,67	0
56	MG	CA	3052	1/1	0.97	0.10	68,68,68,68	0
56	MG	CA	3102	1/1	0.97	0.17	113,113,113,113	0
56	MG	CA	3073	1/1	0.97	0.28	222,222,222,222	0
56	MG	CA	3074	1/1	0.97	0.24	131,131,131,131	0
56	MG	DA	3144	1/1	0.97	0.12	72,72,72,72	0
56	MG	BA	1607	1/1	0.97	0.35	207,207,207,207	0
56	MG	DA	3027	1/1	0.97	0.11	94,94,94,94	0
56	MG	AA	1668	1/1	0.97	0.11	75,75,75,75	0
56	MG	DA	3148	1/1	0.97	0.15	61,61,61,61	0
56	MG	CA	3013	1/1	0.97	0.10	86,86,86,86	0
56	MG	AA	1669	1/1	0.97	0.27	134,134,134,134	0
56	MG	DA	3048	1/1	0.97	0.14	57,57,57,57	0
56	MG	AA	1640	1/1	0.97	0.11	73,73,73,73	0
56	MG	AA	1607	1/1	0.97	0.45	65,65,65,65	0
56	MG	AA	1679	1/1	0.97	0.16	77,77,77,77	0
56	MG	DA	3066	1/1	0.97	0.07	49,49,49,49	0
56	MG	DA	3158	1/1	0.97	0.28	191,191,191,191	0
56	MG	DA	3073	1/1	0.97	0.05	45,45,45,45	0
56	MG	DA	3080	1/1	0.97	0.08	44,44,44,44	0
56	MG	DA	3088	1/1	0.97	0.17	24,24,24,24	0
65	SPD	DA	3187	10/10	0.97	0.25	34,42,45,48	0
56	MG	DA	3106	1/1	0.97	0.15	36,36,36,36	0
56	MG	DA	3164	1/1	0.97	0.53	71,71,71,71	0
56	MG	BA	1601	1/1	0.97	0.22	106,106,106,106	0
56	MG	AA	1629	1/1	0.97	0.18	93,93,93,93	0
67	ACY	DA	3191	4/4	0.97	0.20	68,70,70,71	0
56	MG	DA	3117	1/1	0.97	0.09	56,56,56,56	0
56	MG	DA	3119	1/1	0.97	0.40	57,57,57,57	0
56	MG	BA	1636	1/1	0.97	0.43	72,72,72,72	0
56	MG	CA	3085	1/1	0.97	0.08	74,74,74,74	0
56	MG	DA	3102	1/1	0.98	0.07	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	CA	3103	1/1	0.98	0.15	82,82,82,82	0
56	MG	DA	3109	1/1	0.98	0.13	26,26,26,26	0
56	MG	AA	1637	1/1	0.98	0.05	51,51,51,51	0
56	MG	AA	1631	1/1	0.98	0.11	53,53,53,53	0
56	MG	AA	1647	1/1	0.98	0.24	179,179,179,179	0
56	MG	DA	3118	1/1	0.98	0.41	68,68,68,68	0
61	ZN	AB	301	1/1	0.98	0.19	171,171,171,171	0
56	MG	BA	1613	1/1	0.98	0.16	73,73,73,73	0
56	MG	AA	1648	1/1	0.98	0.07	70,70,70,70	0
56	MG	DA	3003	1/1	0.98	0.11	85,85,85,85	0
56	MG	DA	3005	1/1	0.98	0.06	94,94,94,94	0
56	MG	DA	3006	1/1	0.98	0.07	87,87,87,87	0
56	MG	DA	3008	1/1	0.98	0.08	27,27,27,27	0
56	MG	BA	1615	1/1	0.98	0.06	72,72,72,72	0
56	MG	DA	3021	1/1	0.98	0.14	34,34,34,34	0
56	MG	DA	3025	1/1	0.98	0.10	108,108,108,108	0
56	MG	AA	1633	1/1	0.98	0.14	123,123,123,123	0
56	MG	DA	3029	1/1	0.98	0.20	46,46,46,46	0
56	MG	DA	3030	1/1	0.98	0.13	22,22,22,22	0
56	MG	DA	3031	1/1	0.98	0.20	29,29,29,29	0
56	MG	DA	3032	1/1	0.98	0.15	27,27,27,27	0
56	MG	AA	1643	1/1	0.98	0.11	65,65,65,65	0
56	MG	DA	3039	1/1	0.98	0.11	55,55,55,55	0
56	MG	CA	3027	1/1	0.98	0.18	73,73,73,73	0
56	MG	BA	1631	1/1	0.98	0.07	55,55,55,55	0
56	MG	BA	1632	1/1	0.98	0.12	75,75,75,75	0
56	MG	DA	3051	1/1	0.98	0.10	73,73,73,73	0
56	MG	CA	3096	1/1	0.98	0.06	61,61,61,61	0
56	MG	BA	1618	1/1	0.98	0.11	129,129,129,129	0
56	MG	CA	3153	1/1	0.98	0.11	64,64,64,64	0
56	MG	DA	3065	1/1	0.98	0.14	45,45,45,45	0
56	MG	AA	1660	1/1	0.98	0.15	284,284,284,284	0
58	MPD	DS	203	8/8	0.98	0.19	48,52,58,59	0
56	MG	DA	3068	1/1	0.98	0.14	59,59,59,59	0
56	MG	DA	3069	1/1	0.98	0.10	79,79,79,79	0
56	MG	DA	3071	1/1	0.98	0.23	68,68,68,68	0
56	MG	CA	3049	1/1	0.98	0.11	48,48,48,48	0
56	MG	DA	3076	1/1	0.98	0.09	31,31,31,31	0
56	MG	DA	3150	1/1	0.98	0.31	51,51,51,51	0
56	MG	DA	3077	1/1	0.98	0.05	63,63,63,63	0
56	MG	DA	3078	1/1	0.98	0.22	96,96,96,96	0
56	MG	DA	3079	1/1	0.98	0.11	119,119,119,119	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	AA	1653	1/1	0.98	0.05	50,50,50,50	0
56	MG	DA	3087	1/1	0.98	0.08	54,54,54,54	0
56	MG	AA	1662	1/1	0.98	0.15	79,79,79,79	0
56	MG	DA	3091	1/1	0.98	0.11	30,30,30,30	0
56	MG	DA	3092	1/1	0.98	0.20	35,35,35,35	0
56	MG	DA	3093	1/1	0.98	0.13	20,20,20,20	0
56	MG	DA	3096	1/1	0.98	0.07	33,33,33,33	0
56	MG	DA	3097	1/1	0.98	0.13	128,128,128,128	0
56	MG	DA	3098	1/1	0.98	0.14	23,23,23,23	0
56	MG	AA	1635	1/1	0.99	0.10	104,104,104,104	0
56	MG	DA	3049	1/1	0.99	0.16	20,20,20,20	0
56	MG	DA	3050	1/1	0.99	0.10	24,24,24,24	0
56	MG	DA	3004	1/1	0.99	0.13	77,77,77,77	0
56	MG	DA	3052	1/1	0.99	0.09	41,41,41,41	0
56	MG	BA	1620	1/1	0.99	0.09	94,94,94,94	0
56	MG	DA	3054	1/1	0.99	0.18	30,30,30,30	0
56	MG	DA	3055	1/1	0.99	0.20	34,34,34,34	0
56	MG	DA	3056	1/1	0.99	0.11	23,23,23,23	0
56	MG	DA	3058	1/1	0.99	0.06	27,27,27,27	0
56	MG	DA	3059	1/1	0.99	0.13	33,33,33,33	0
56	MG	CA	3100	1/1	0.99	0.22	92,92,92,92	0
56	MG	DA	3063	1/1	0.99	0.12	72,72,72,72	0
56	MG	DA	3007	1/1	0.99	0.07	82,82,82,82	0
56	MG	AA	1646	1/1	0.99	0.11	66,66,66,66	0
56	MG	DA	3009	1/1	0.99	0.12	27,27,27,27	0
56	MG	DA	3067	1/1	0.99	0.18	46,46,46,46	0
56	MG	DD	301	1/1	0.99	0.15	35,35,35,35	0
56	MG	DA	3012	1/1	0.99	0.18	25,25,25,25	0
56	MG	DA	3070	1/1	0.99	0.07	55,55,55,55	0
56	MG	DA	3014	1/1	0.99	0.12	45,45,45,45	0
56	MG	DA	3015	1/1	0.99	0.17	72,72,72,72	0
56	MG	DA	3075	1/1	0.99	0.15	40,40,40,40	0
56	MG	DA	3017	1/1	0.99	0.10	44,44,44,44	0
56	MG	DA	3149	1/1	0.99	0.09	62,62,62,62	0
56	MG	DA	3018	1/1	0.99	0.24	8,8,8,8	0
56	MG	DA	3019	1/1	0.99	0.07	65,65,65,65	0
56	MG	DM	201	1/1	0.99	0.05	56,56,56,56	0
56	MG	DA	3022	1/1	0.99	0.18	36,36,36,36	0
61	ZN	D5	101	1/1	0.99	0.10	66,66,66,66	0
56	MG	DA	3081	1/1	0.99	0.06	65,65,65,65	0
56	MG	DA	3082	1/1	0.99	0.12	56,56,56,56	0
56	MG	DA	3083	1/1	0.99	0.13	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3084	1/1	0.99	0.08	54,54,54,54	0
56	MG	DA	3085	1/1	0.99	0.11	31,31,31,31	0
56	MG	DA	3086	1/1	0.99	0.14	34,34,34,34	0
56	MG	DA	3024	1/1	0.99	0.07	39,39,39,39	0
56	MG	BA	1611	1/1	0.99	0.11	53,53,53,53	0
56	MG	DA	3089	1/1	0.99	0.13	26,26,26,26	0
56	MG	DA	3090	1/1	0.99	0.16	24,24,24,24	0
56	MG	DA	3026	1/1	0.99	0.20	51,51,51,51	0
56	MG	CA	3041	1/1	0.99	0.07	55,55,55,55	0
56	MG	DA	3028	1/1	0.99	0.17	27,27,27,27	0
56	MG	DA	3094	1/1	0.99	0.12	80,80,80,80	0
56	MG	DA	3095	1/1	0.99	0.14	36,36,36,36	0
56	MG	DB	203	1/1	0.99	0.11	41,41,41,41	0
56	MG	DB	204	1/1	0.99	0.08	37,37,37,37	0
56	MG	DB	205	1/1	0.99	0.18	63,63,63,63	0
56	MG	DA	3099	1/1	0.99	0.15	31,31,31,31	0
56	MG	DA	3100	1/1	0.99	0.11	61,61,61,61	0
56	MG	DA	3101	1/1	0.99	0.11	42,42,42,42	0
56	MG	CA	3025	1/1	0.99	0.07	82,82,82,82	0
56	MG	DA	3104	1/1	0.99	0.14	29,29,29,29	0
56	MG	DA	3105	1/1	0.99	0.17	37,37,37,37	0
56	MG	DA	3035	1/1	0.99	0.16	34,34,34,34	0
56	MG	DA	3107	1/1	0.99	0.09	39,39,39,39	0
56	MG	CA	3011	1/1	0.99	0.11	59,59,59,59	0
56	MG	DA	3037	1/1	0.99	0.10	30,30,30,30	0
56	MG	DA	3229	1/1	0.99	0.06	54,54,54,54	0
56	MG	DA	3230	1/1	0.99	0.05	55,55,55,55	0
56	MG	DA	3231	1/1	0.99	0.28	39,39,39,39	0
56	MG	DA	3113	1/1	0.99	0.14	37,37,37,37	0
56	MG	DA	3114	1/1	0.99	0.14	31,31,31,31	0
56	MG	DA	3115	1/1	0.99	0.12	32,32,32,32	0
56	MG	DA	3038	1/1	0.99	0.14	35,35,35,35	0
56	MG	AA	1651	1/1	0.99	0.11	76,76,76,76	0
56	MG	DA	3040	1/1	0.99	0.23	24,24,24,24	0
56	MG	DA	3041	1/1	0.99	0.08	52,52,52,52	0
56	MG	CA	3045	1/1	0.99	0.07	84,84,84,84	0
56	MG	AA	1652	1/1	0.99	0.23	25,25,25,25	0
56	MG	DA	3045	1/1	0.99	0.17	24,24,24,24	0
56	MG	DA	3046	1/1	0.99	0.08	47,47,47,47	0
56	MG	DA	3047	1/1	0.99	0.15	36,36,36,36	0
56	MG	DA	3020	1/1	1.00	0.14	31,31,31,31	0
56	MG	DA	3072	1/1	1.00	0.10	38,38,38,38	0

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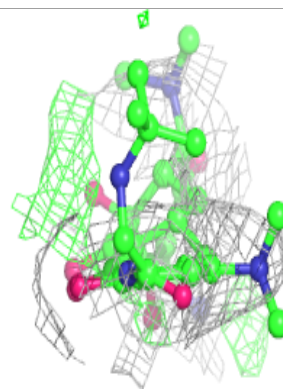
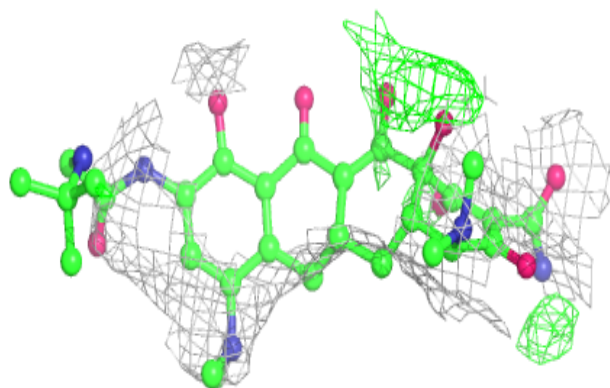
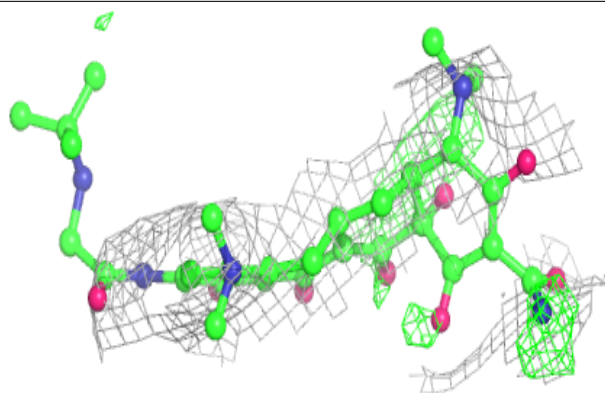
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3060	1/1	1.00	0.16	41,41,41,41	0
56	MG	DA	3074	1/1	1.00	0.13	33,33,33,33	0
56	MG	DA	3103	1/1	1.00	0.18	30,30,30,30	0
56	MG	DA	3033	1/1	1.00	0.12	13,13,13,13	0
56	MG	DA	3159	1/1	1.00	0.13	72,72,72,72	0
56	MG	DA	3062	1/1	1.00	0.09	73,73,73,73	0
56	MG	DA	3034	1/1	1.00	0.18	35,35,35,35	0
56	MG	DA	3016	1/1	1.00	0.15	26,26,26,26	0
56	MG	DA	3108	1/1	1.00	0.18	30,30,30,30	0
56	MG	DA	3228	1/1	1.00	0.13	41,41,41,41	0
56	MG	DA	3044	1/1	1.00	0.08	53,53,53,53	0
56	MG	DA	3013	1/1	1.00	0.17	20,20,20,20	0
56	MG	DA	3111	1/1	1.00	0.17	25,25,25,25	0
56	MG	DA	3112	1/1	1.00	0.08	83,83,83,83	0
56	MG	DA	3023	1/1	1.00	0.16	29,29,29,29	0
56	MG	CA	3095	1/1	1.00	0.06	63,63,63,63	0
56	MG	DA	3057	1/1	1.00	0.08	27,27,27,27	0
56	MG	DA	3010	1/1	1.00	0.10	26,26,26,26	0

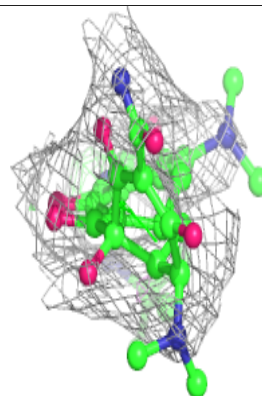
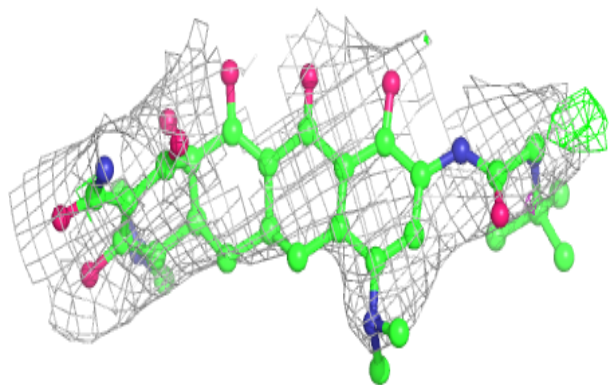
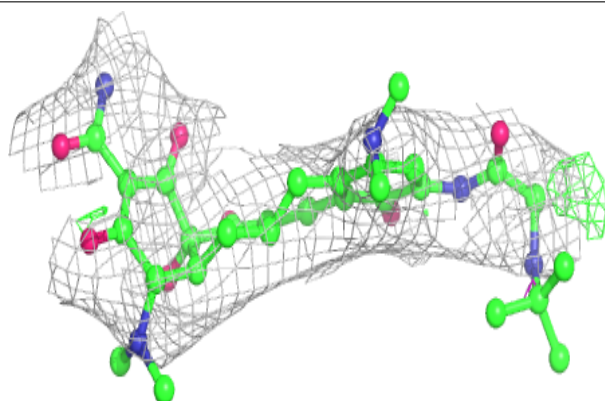
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around T1C BA 1643:

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

**Electron density around T1C AA 1680:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.