



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 12:44 PM UTC

PDB ID : 5MC6 / pdb_00005mc6
EMDB ID : EMD-3461
Title : Cryo-EM structure of a native ribosome-Ski2-Ski3-Ski8 complex from *S. cerevisiae*
Authors : Schmidt, C.; Kowalinski, E.; Shanmuganathan, V.; Defenouillere, Q.; Braunger, K.; Heuer, A.; Pech, M.; Namane, A.; Berninghausen, O.; Fromont-Racine, M.; Jacquier, A.; Conti, E.; Becker, T.; Beckmann, R.
Deposited on : 2016-11-09
Resolution : 3.80 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

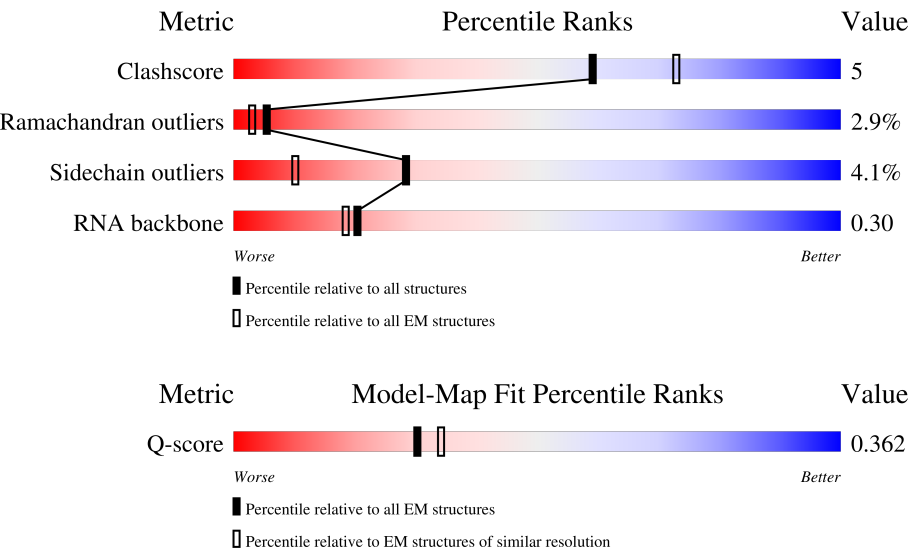
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1800	12% 49% 39% 9% ••
2	A	240	27% 78% 14% • 7%
3	B	225	39% 73% 17% • 8%

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Mol	Chain	Length	Quality of chain
4	C	105	
5	D	143	
6	E	142	
7	F	143	
8	G	136	
9	H	146	
10	I	144	
11	J	121	
12	K	108	
13	L	67	
14	M	56	
15	N	152	
16	O	319	
17	P	252	
18	Q	255	
19	R	254	
20	S	261	
21	T	236	
22	U	190	
23	V	200	
24	W	197	
25	X	156	
26	Y	151	
27	Z	137	
28	a	87	

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Mol	Chain	Length	Quality of chain
29	b	130	
30	c	145	
31	d	135	
32	e	119	
33	f	82	
34	g	63	
35	l	34	
36	m	76	
37	n	77	
38	h	1287	
39	i	1432	
40	j	397	
40	k	397	
41	AA	256	
42	AB	137	
43	AC	100	
44	AD	191	
45	AE	155	
46	AF	88	
47	AG	174	
48	AH	142	
49	AI	78	
50	AJ	199	
51	AK	127	
52	AL	51	

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Mol	Chain	Length	Quality of chain
53	AM	138	
54	AN	136	
55	AO	128	
56	AP	106	
57	AQ	204	
58	AR	149	
59	AS	25	
60	AT	92	
61	AU	199	
62	AV	59	
63	AW	254	
64	AX	184	
65	AY	105	
66	AZ	210	
67	BA	387	
68	BB	186	
69	BC	113	
70	BD	221	
71	BE	362	
72	BF	189	
73	BG	130	
74	BH	172	
75	BI	297	
76	BJ	160	
77	BK	107	

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Mol	Chain	Length	Quality of chain
78	BL	121	
79	BM	176	
80	BN	121	
81	BO	244	
82	BP	120	
83	BQ	3396	
84	BR	121	
85	BS	158	
86	BT	157	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 229285 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1767	Total	C	N	O	P	0	0
			37645	16830	6656	12392	1767		

- Molecule 2 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	96	Total	C	N	O	S	0	0
			813	527	133	151	2		

- Molecule 5 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	121	Total	C	N	O	S	0	0
			877	552	153	170	2		

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	91	Total	C	N	O	S	0	0
			746	467	144	133	2		

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 11 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	K	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 13 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 19 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	178	Total	C	N	O	S	0	0
			1434	905	276	252	1		

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 26 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 27 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	132	Total	C	N	O		0	0
			1060	669	206	185			

- Molecule 32 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	34	Total	C	N	O	P	0	0
			692	311	84	263	34		

- Molecule 36 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 37 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 38 is a protein called Antiviral helicase SKI2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	1121	Total	C	N	O	S	0	0
			8814	5643	1504	1625	42		

- Molecule 39 is a protein called Superkiller protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	1365	Total	C	N	O	S	0	0
			9827	6302	1663	1825	37		

- Molecule 40 is a protein called Antiviral protein SKI8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	392	Total	C	N	O	S	0	0
			2933	1861	500	558	14		
40	k	388	Total	C	N	O	S	0	0
			2919	1851	502	552	14		

- Molecule 41 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 42 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AB	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AC	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AD	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AE	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AF	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 47 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 48 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AH	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 49 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	AI	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	AJ	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 51 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	AK	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 52 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AL	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	AN	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 55 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AO	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 56 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 57 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 58 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 59 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 60 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 61 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	AV	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 63 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 64 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AX	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AY	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 66 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 67 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BA	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 68 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BC	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 70 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BD	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 71 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BE	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 72 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BF	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 73 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 74 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 75 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BI	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 76 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 77 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 78 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BL	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 79 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BM	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 80 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 81 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BO	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 82 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BP	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 83 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BQ	3165	Total	C	N	O	P	0	0
			67695	30238	12201	22091	3165		

- Molecule 84 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BR	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BS	158	Total	C	N	O	P	0	0
			3352	1500	586	1108	158		

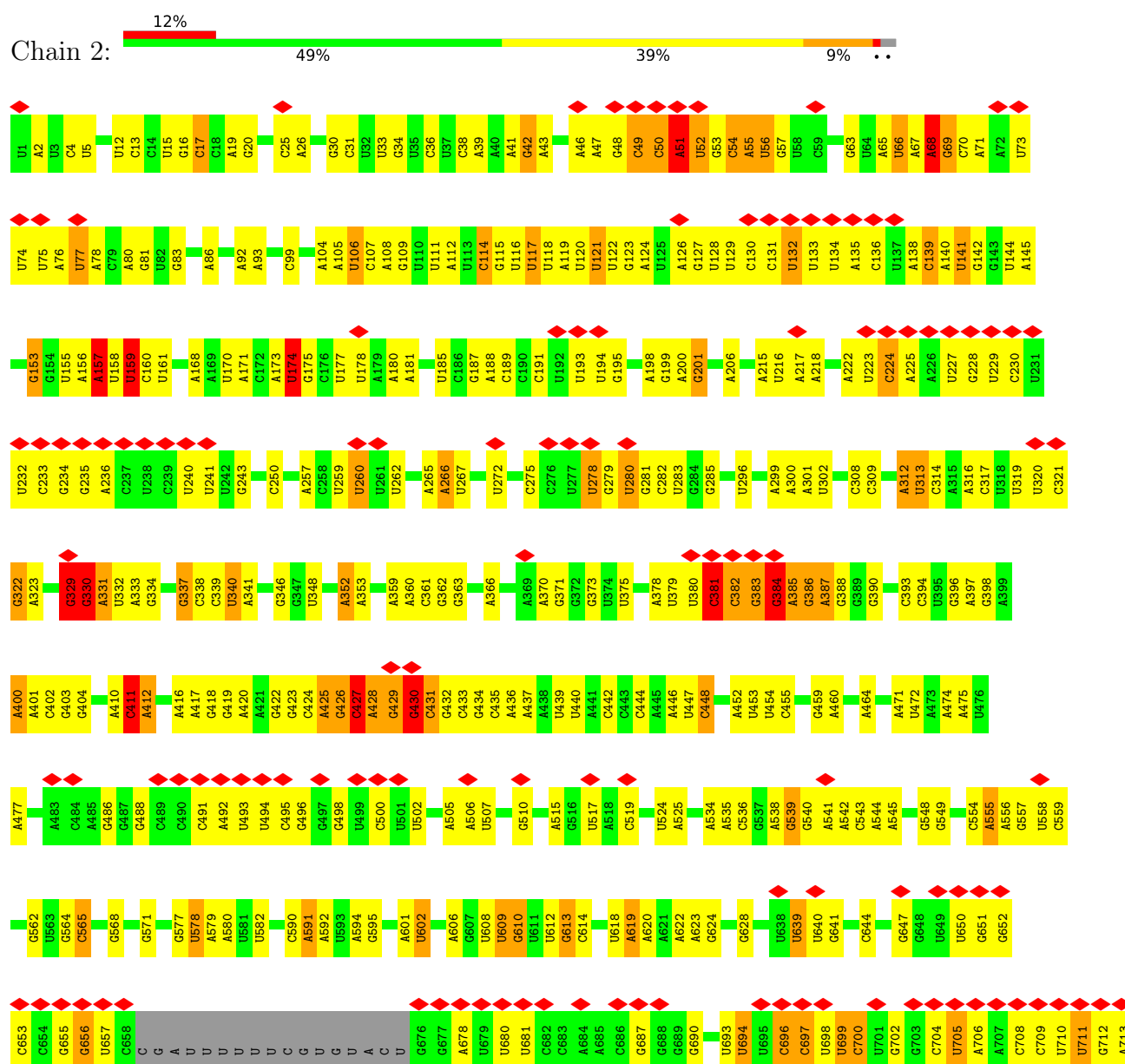
- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

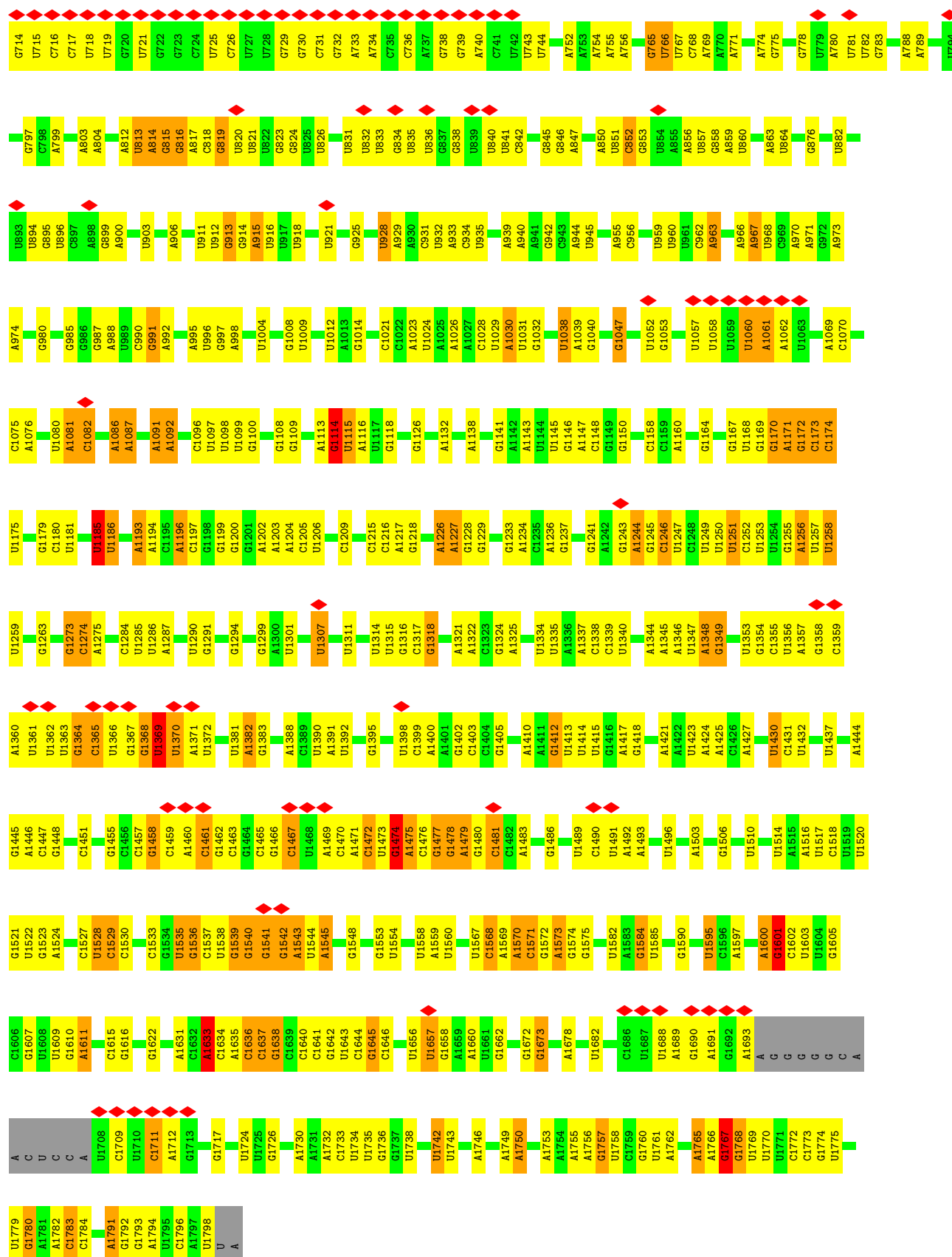
Mol	Chain	Residues	Atoms					AltConf	Trace
86	BT	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

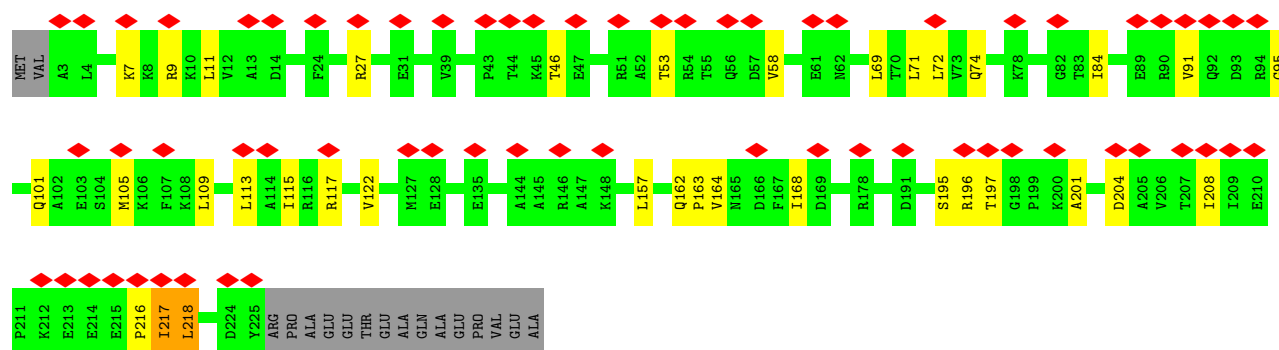
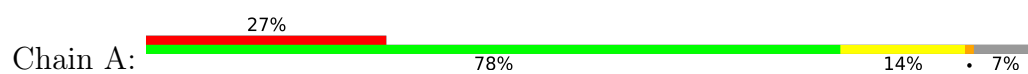
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

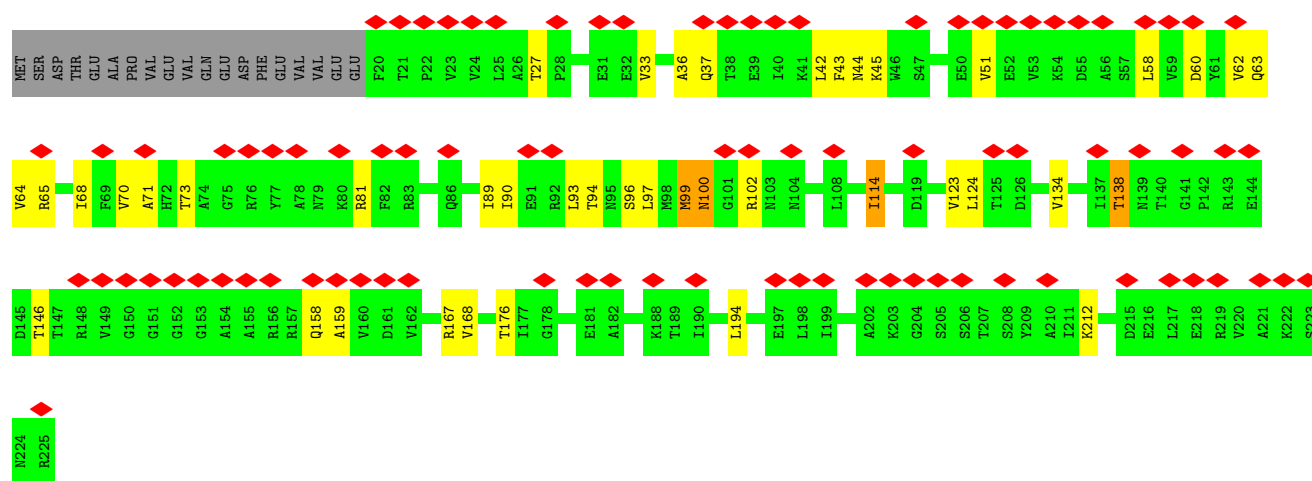
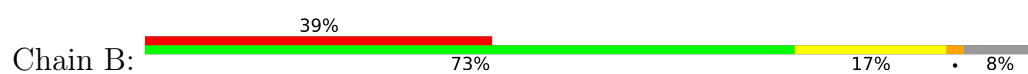
• Molecule 1: 18S ribosomal RNA



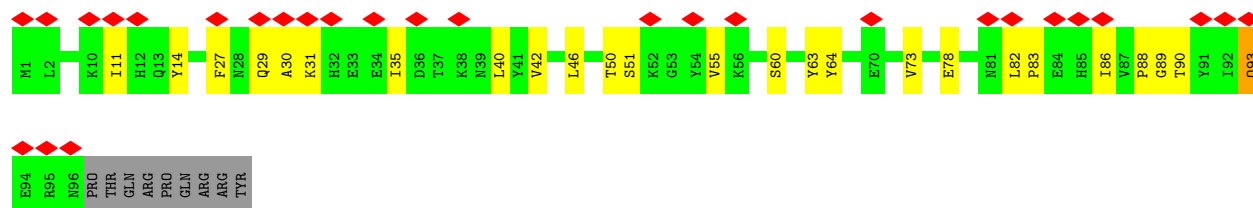




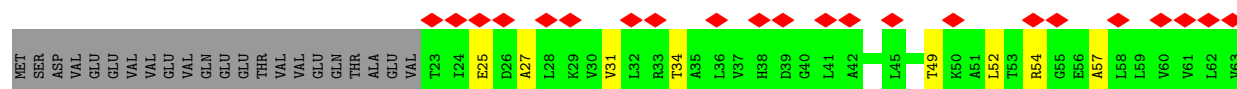
• Molecule 3: 40S ribosomal protein S5



• Molecule 4: 40S ribosomal protein S10-A

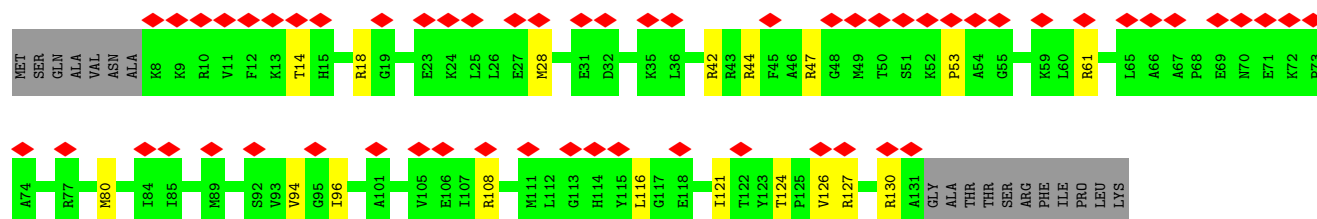
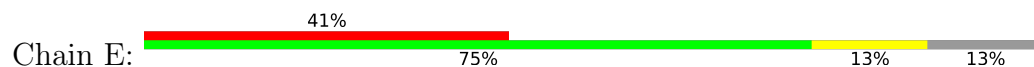


• Molecule 5: 40S ribosomal protein S12

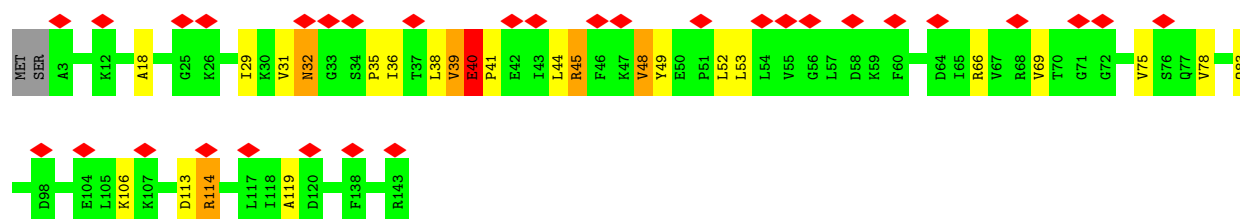
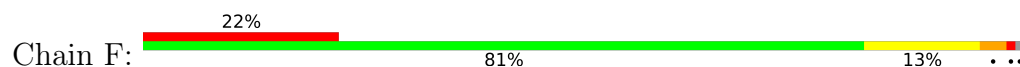




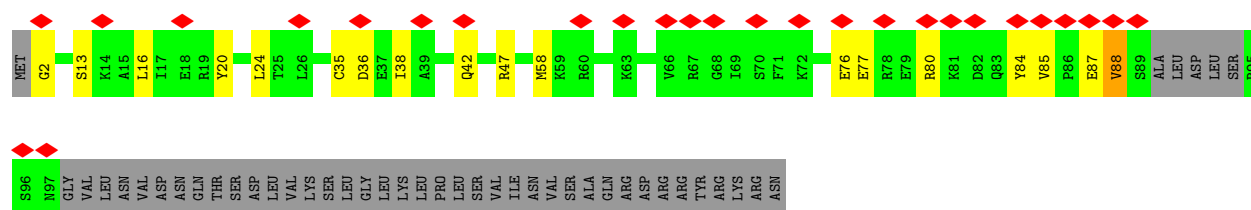
• Molecule 6: 40S ribosomal protein S15



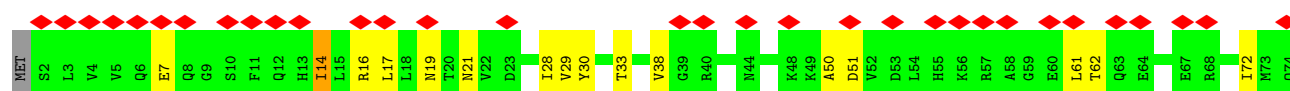
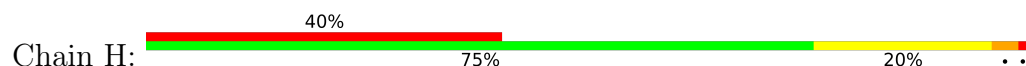
• Molecule 7: 40S ribosomal protein S16-A

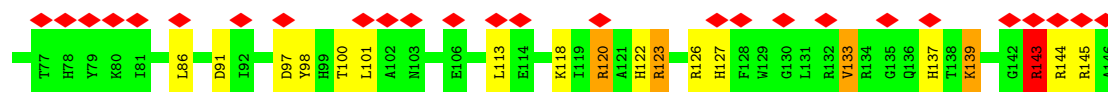


• Molecule 8: 40S ribosomal protein S17-B

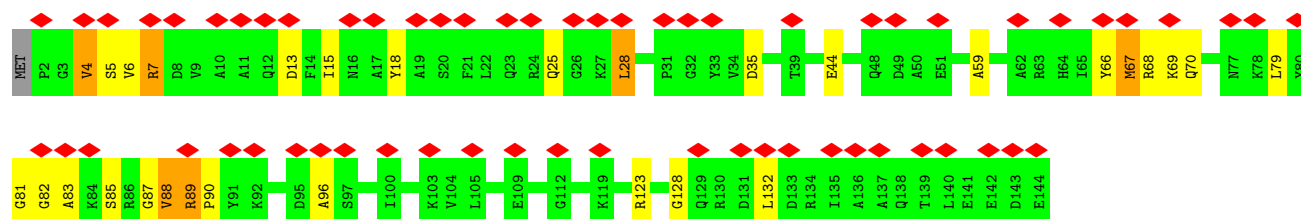
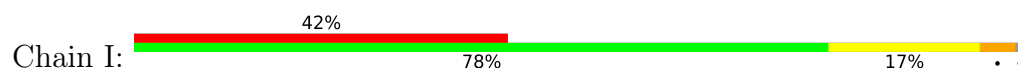


• Molecule 9: 40S ribosomal protein S18-A

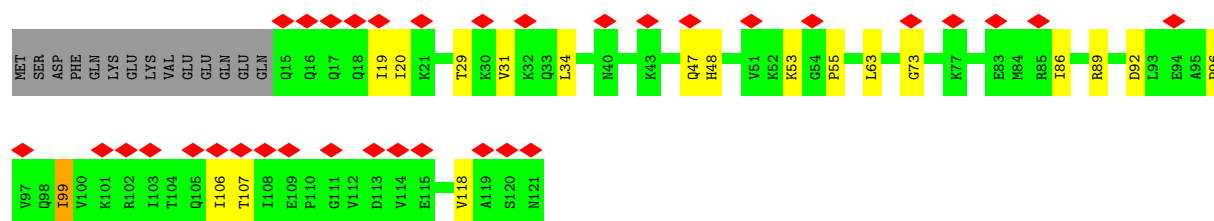




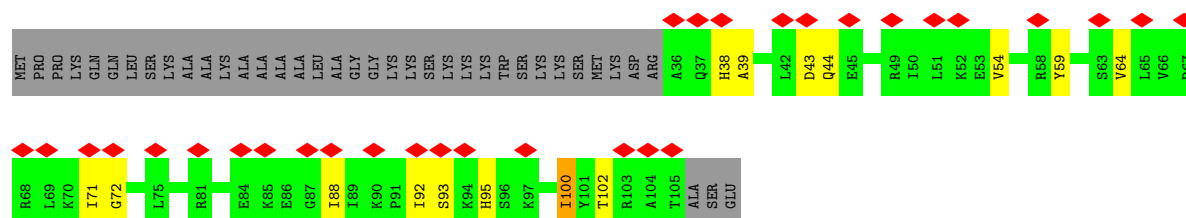
• Molecule 10: 40S ribosomal protein S19-A



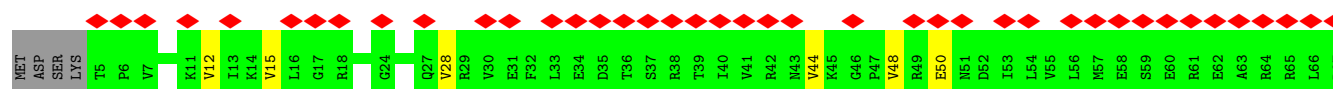
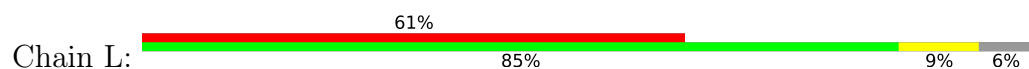
• Molecule 11: 40S ribosomal protein S20



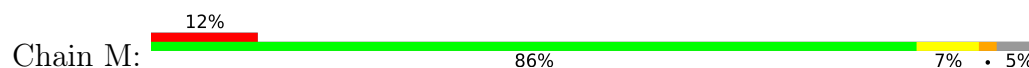
• Molecule 12: 40S ribosomal protein S25-A

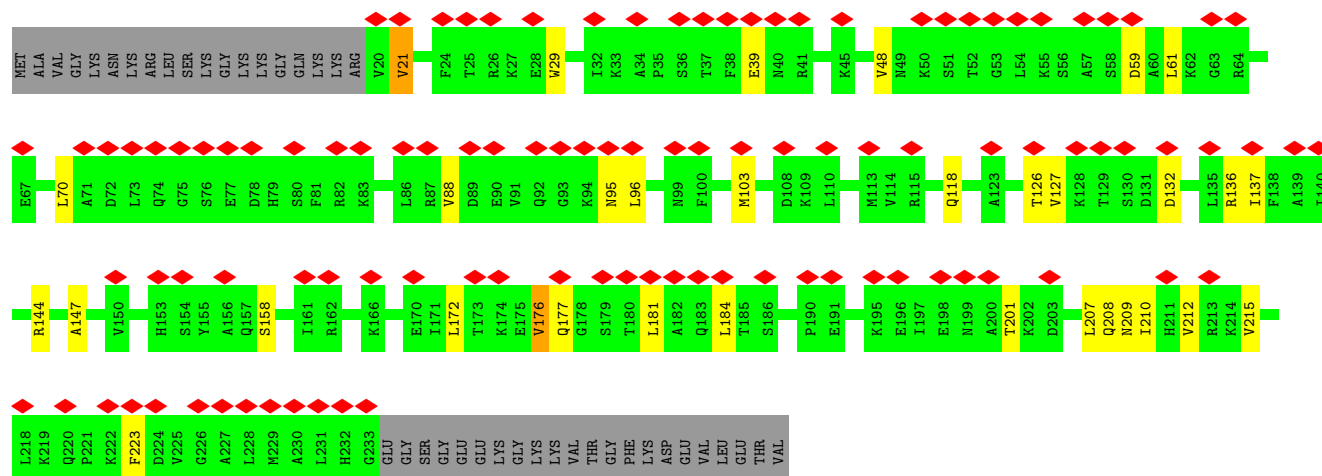
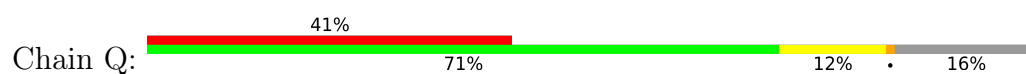


• Molecule 13: 40S ribosomal protein S28-B

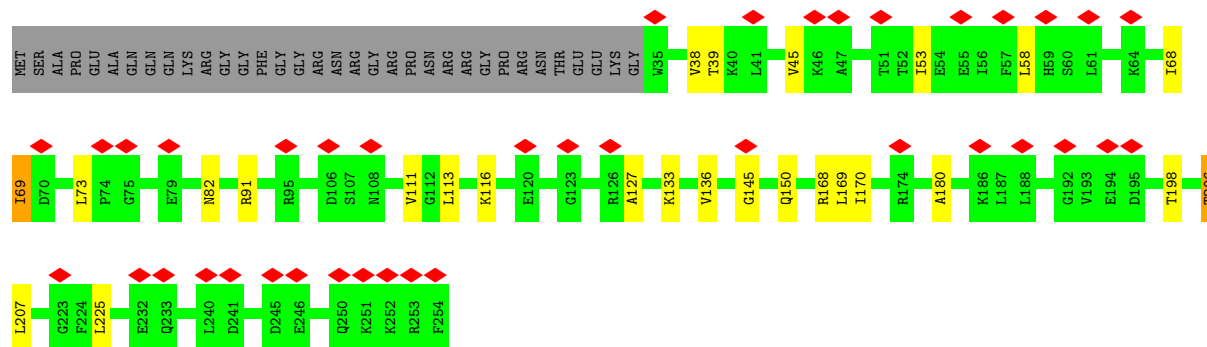
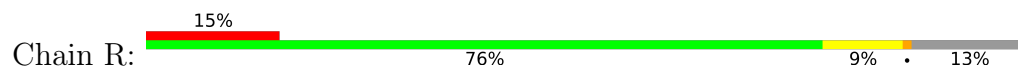


• Molecule 14: 40S ribosomal protein S29-A

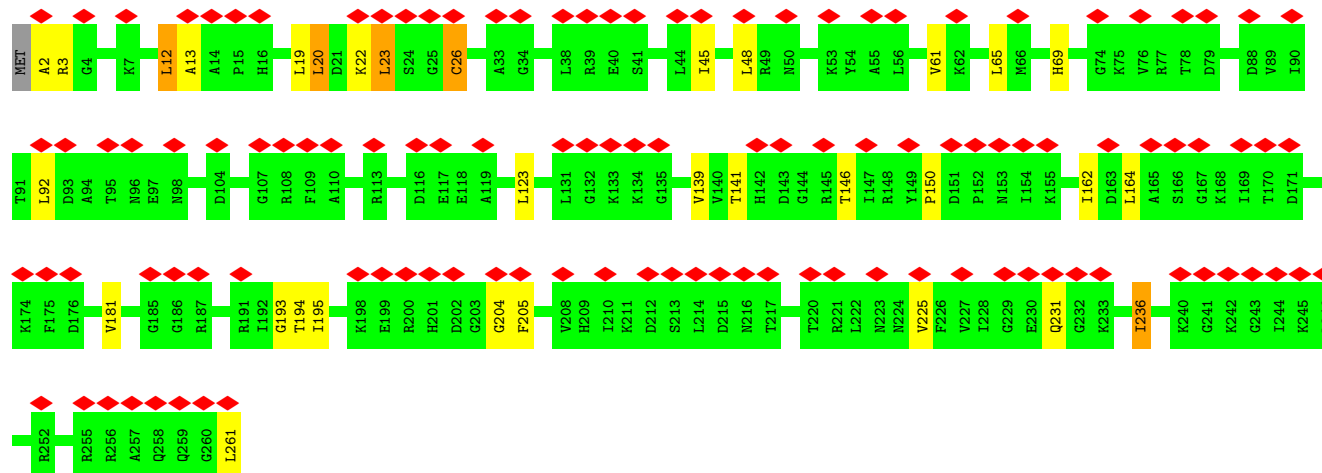
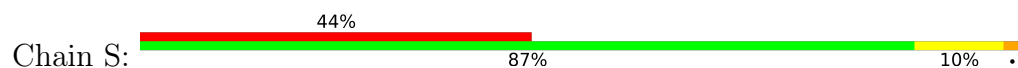




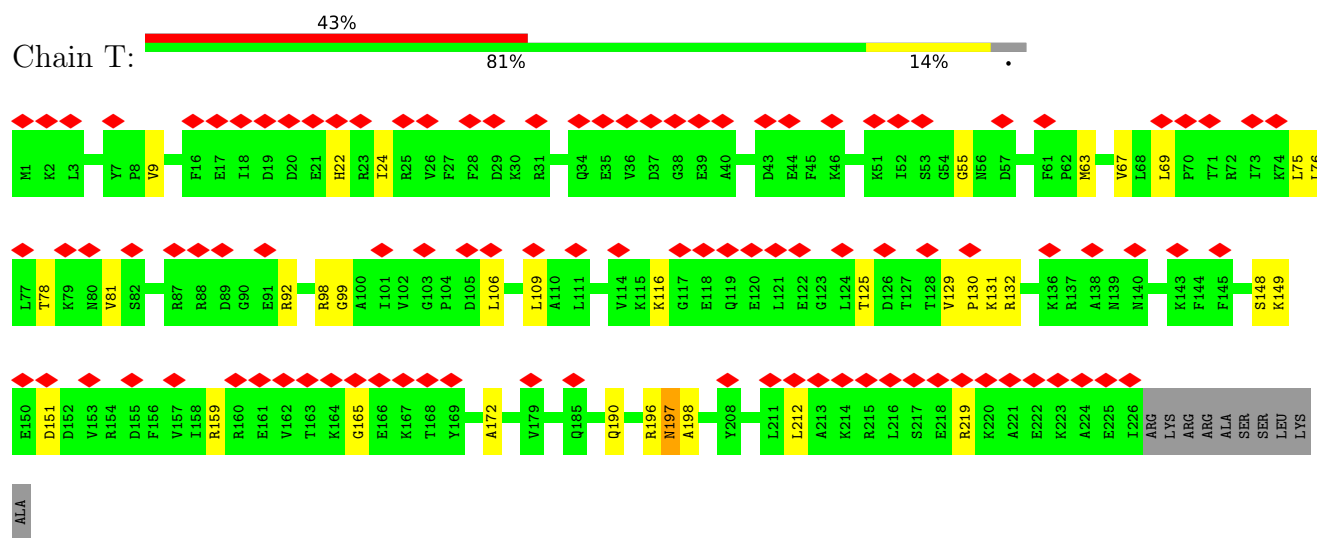
• Molecule 19: 40S ribosomal protein S2



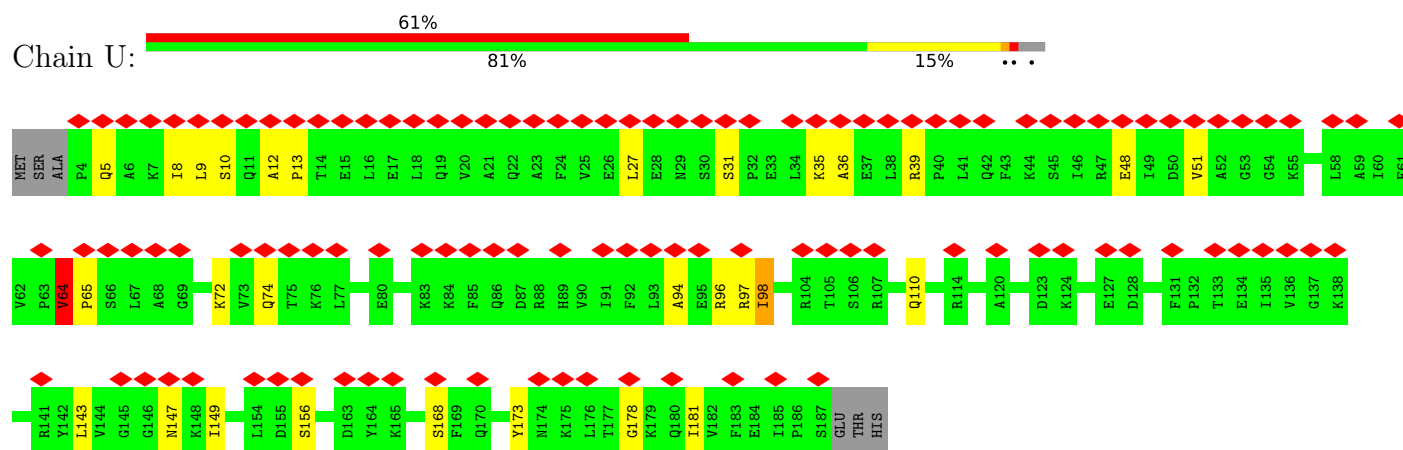
• Molecule 20: 40S ribosomal protein S4-A



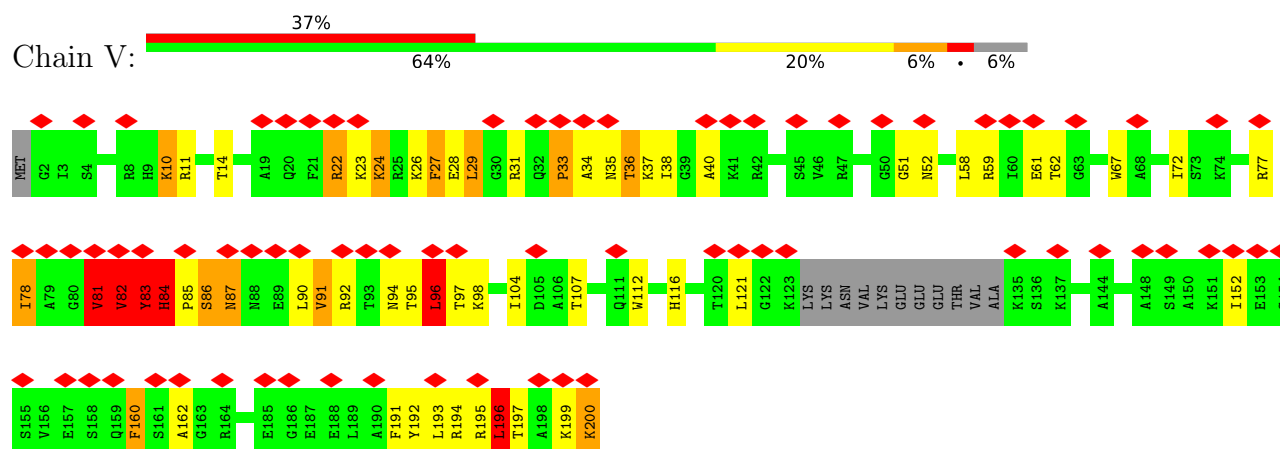
- Molecule 21: 40S ribosomal protein S6-A



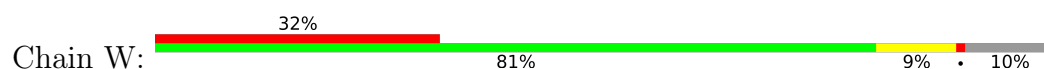
- Molecule 22: 40S ribosomal protein S7-A

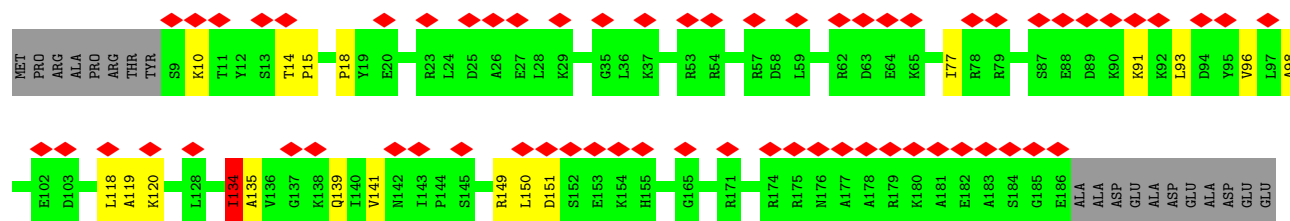


- Molecule 23: 40S ribosomal protein S8-A

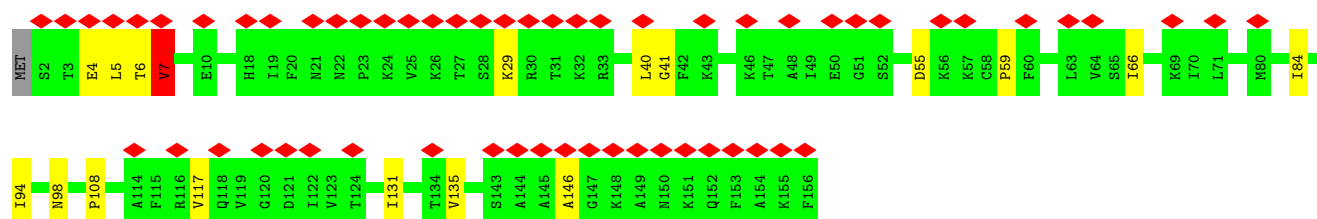
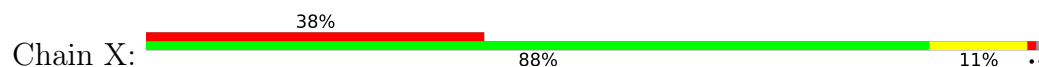


- Molecule 24: 40S ribosomal protein S9-A

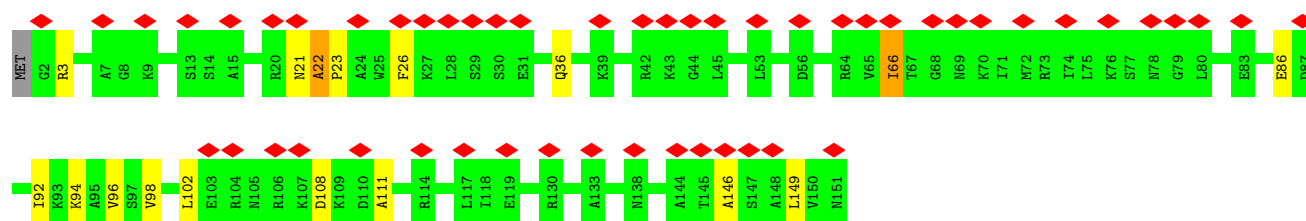
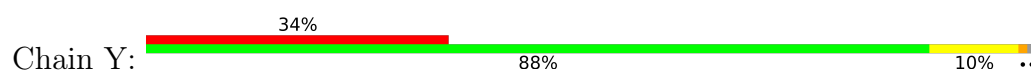




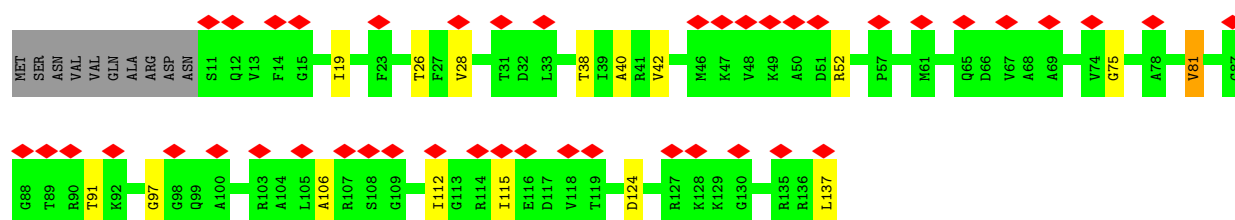
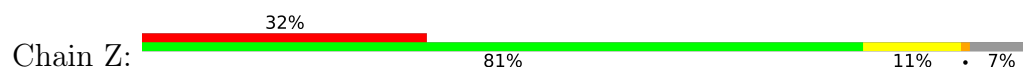
• Molecule 25: 40S ribosomal protein S11-A



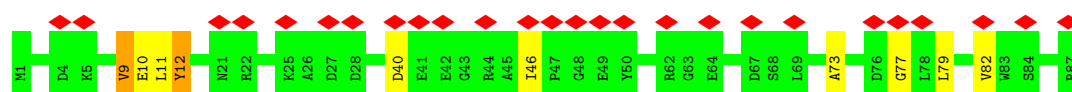
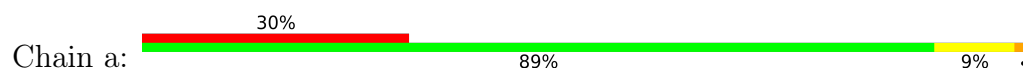
• Molecule 26: 40S ribosomal protein S13



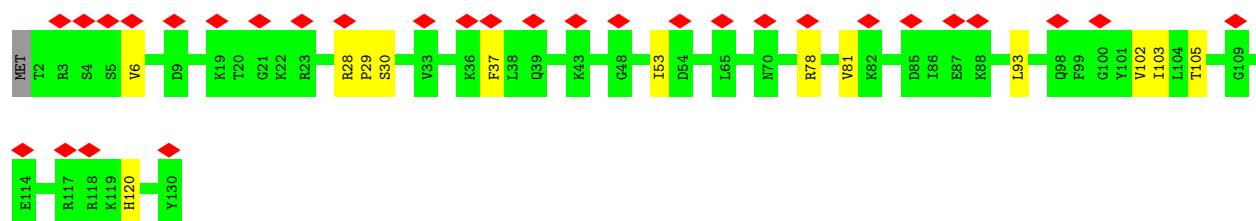
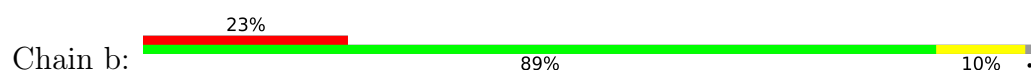
• Molecule 27: 40S ribosomal protein S14-A



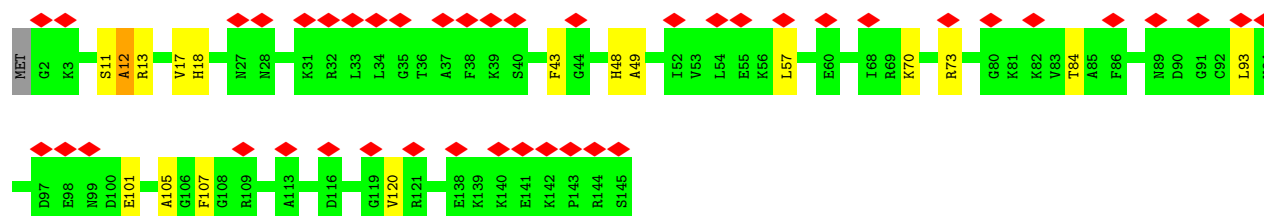
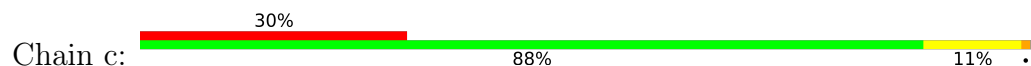
• Molecule 28: 40S ribosomal protein S21-A



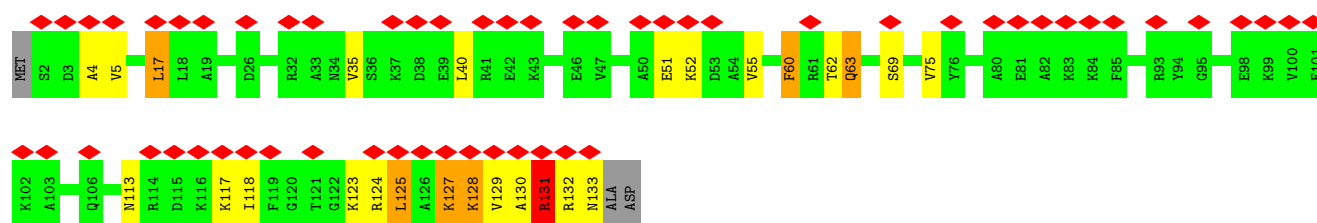
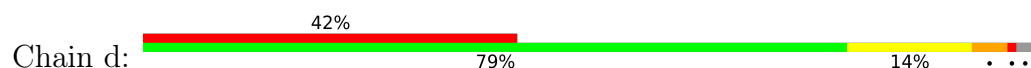
• Molecule 29: 40S ribosomal protein S22-A



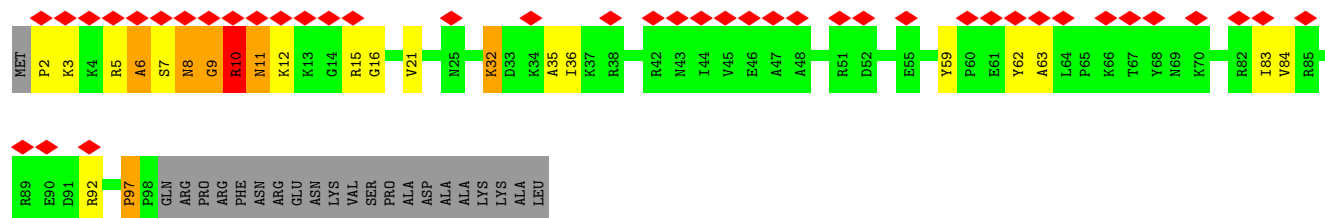
• Molecule 30: 40S ribosomal protein S23-A



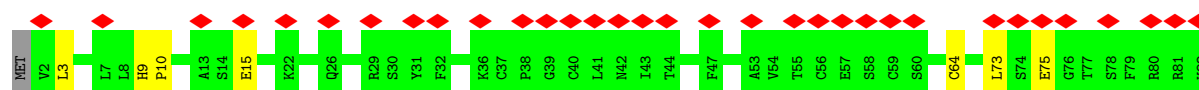
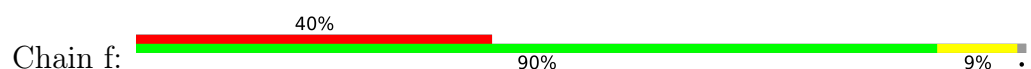
• Molecule 31: 40S ribosomal protein S24-A



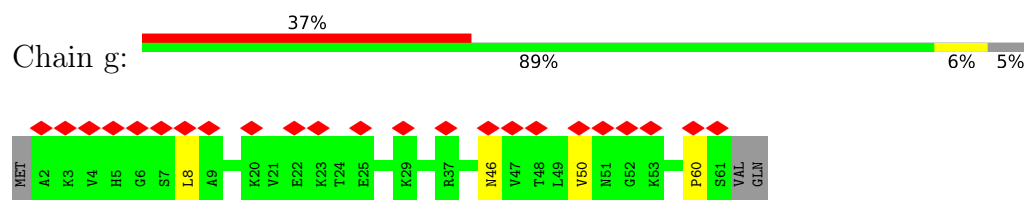
• Molecule 32: 40S ribosomal protein S26-A



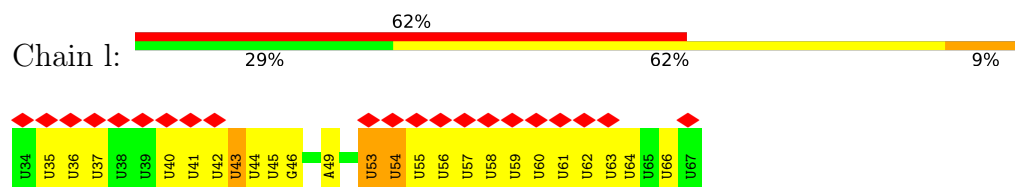
• Molecule 33: 40S ribosomal protein S27-A



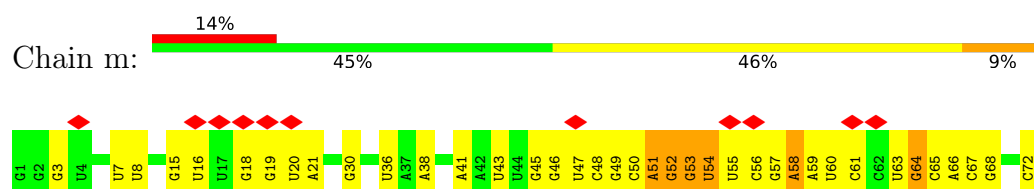
- Molecule 34: 40S ribosomal protein S30-A



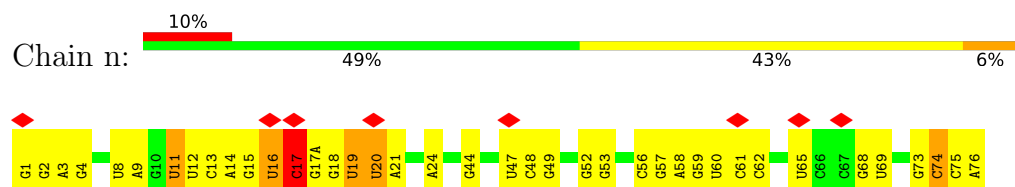
- Molecule 35: mRNA



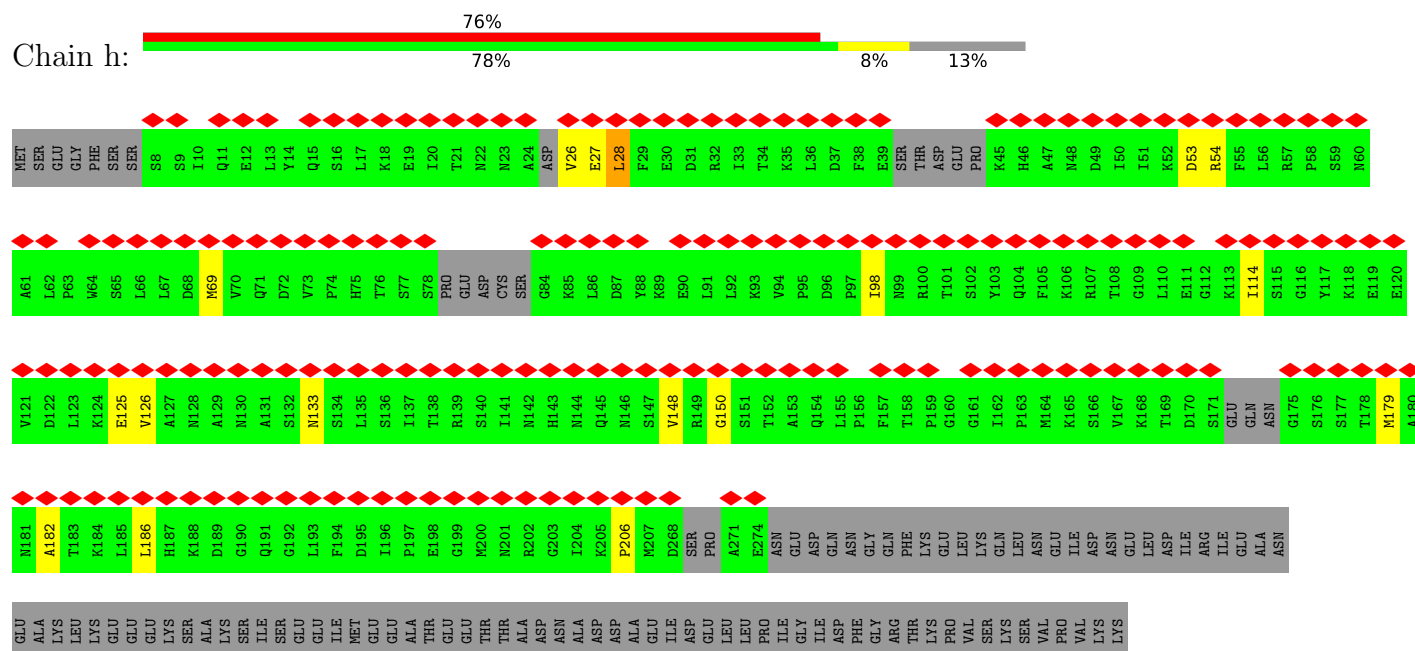
- Molecule 36: A-site tRNA



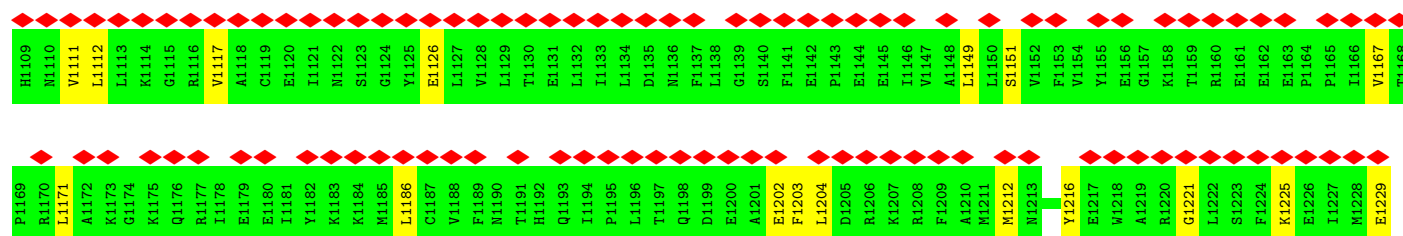
- Molecule 37: P-site tRNA



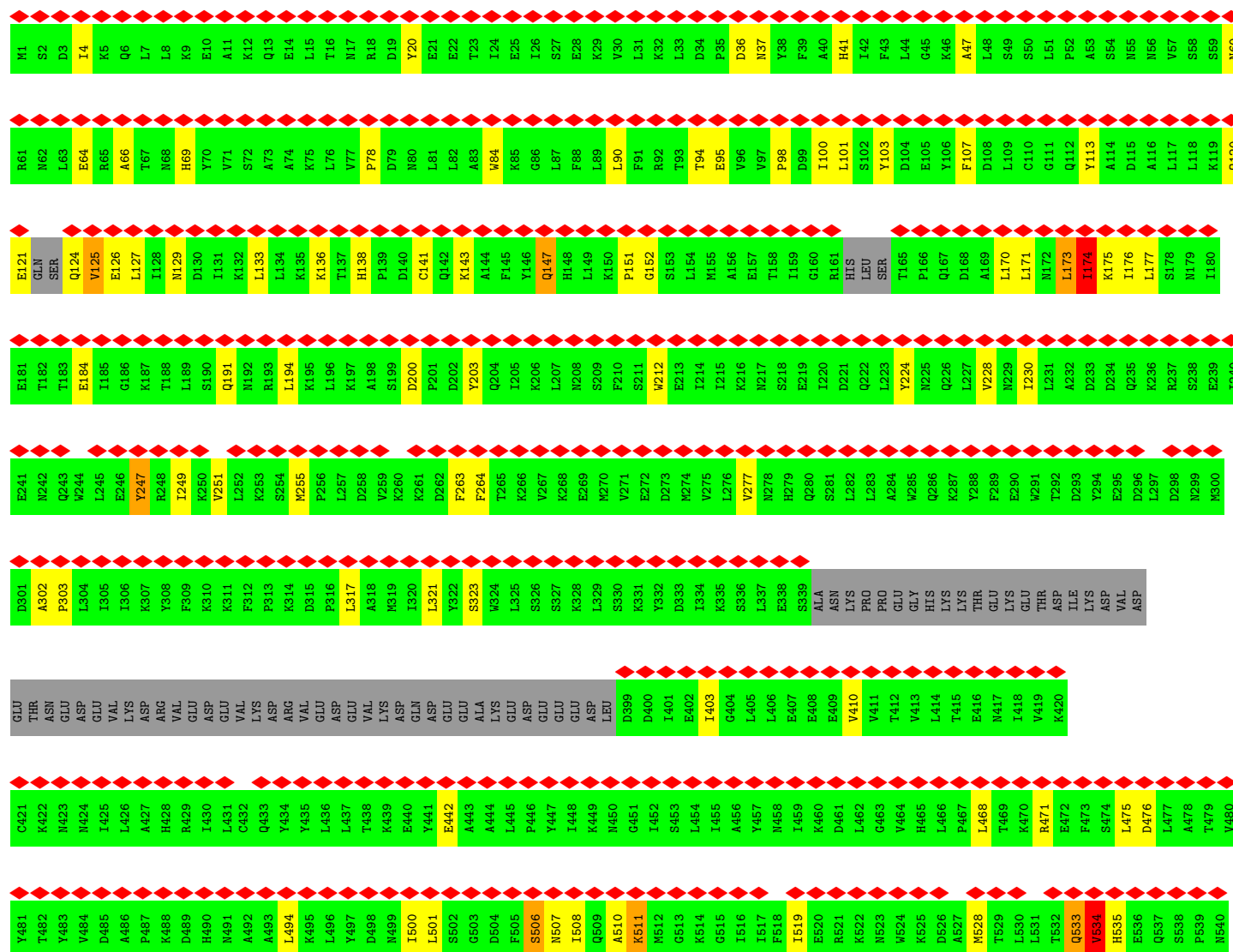
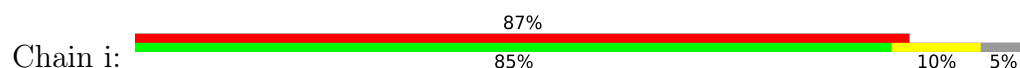
- Molecule 38: Antiviral helicase SKI2



E301	W302	A303	H304	V305	V306	D307	L308	N309	H310	K311	I312	E313	N314	F315	D316	E317	L318	I319	P320	N321	P322	A323	R324	S325	W326	P327	F328	E329	L330	D331	T332	F333	Q334	K335	E336	A337	V338	Y339		E342	Q343	G344	D345	S346	V347	F348	V349	A350	A351	H352	T353	S354	A355	G356	K357	T358	V359	V360	A361
E362	Y363	A364	I365	A366	M367	A368	H369	R370	N371	M372	T373	T375	K374	T376	T377	T378	S379	P380	I381	K382	A383	L384	S385	N386	Q387	K388	F389	R390	D391	F392	K393	E394	T395	F396	D397	D398	V399		C402	L403	I404	T405	G406	D407	V408	Q409	I410	N411	P412	D413	A414	N415	C416	I418	M419	T420	T421	E422	
I423	L424	R425	S426	M427	L428	Y429	G430	G431	A432	D433	L434	I435	R436	D437	V438	E439	F440	V441	I442	F443	D444	E445	V446	H447	Y448	V449	N450	D451	Q452	D453	R454	G455	V456	V457	V458	E459	V460	V461	I462	I463	M464	L465	P466	Q467	H468	V469	K470	F471	I472	D473	L474	A475	T477	V478	P479	N480	T481	Y482	
E483	F484	A485	M486	W487	I488	G489	R490	T491	K492	Q493	K494	N495	I496	Y497	V498	I499	S500	T501	P502	I503	R504	E505	V506	P507	L508	E509	I510	N511	I512	N513	A514	K515	K516	E517	L518	I519	P520	V521	I522	N523	Q524	N525	S526	E527	F528	L529	E530	A531	N532	F533	R534	K535	H536	K537	E538	I539	L540	N541	GLY
GLU	SER	ALA	LYS	GLY	ALA	PRO	SER	LYS	THR	ASP	ASN	GLY	ARG	GLY	SER	THR	ALA	ARG	GLY	ARG	THR	ASP	GLY	ARG	GLY	ARG	GLY	ASN	SER	THR	ARG	GLY	ALA	ASN	ARG	GLY	SER	ARG	GLY	ALA	GLY	ILE	G597	S598	N599	K600	R601	K602											
F603	F604	T605	Q606	D607	K611	T612	T613	E616	Y620	L621	R622	K623	R624	E625	L626	L627	P628	N629	F632	V633	E641	Y642	A643	D644	V645	L646	E647	G648	I649	N650	F651	G652	K655	S658	H661	F662	F663	I664	E665	K666	S667	T668	T669	R670	L671	K672	K673	E674	D675	R676	D677								
L678	P679	Q680	K683	T684	R685	S686	L687	L688	E689	R690	A693	V694	G697	G698	L699	L700	P701	I702	V703	K704	E705	L706	I707	E708	I709	F711	S712	L713	G714	F715	I716	K717	V718	L719	F720	A721	T722	E723	T724	F725	A726	M727	G728	L729	N730	L731	P732	T733	R734	V735	I737	F738	S739	S740					
I741	R742	K743	H744	G746	W747	G748	L749	R750	E751	L752	G755	E756	M760	A761	G762	R763	A764	G765	R766	R767	G768	L769	D770	S771	T772	G773	T774	V775	I776	V777	M778	A779	T780	N781	S782	P783	L784	S785	I786	A787	T788	F789	K790	E791	V792	T793	W794	G795	V796	F797	T798	R799	L800	Q801	S802	Q803			
F804	R805	L806	T807	Y808	N809	H810	T811	L812	N813	L814	L815	R816	T817	E818	A819	L820	R821	V822	E823	E824	M825	I826	K827	Y828	S829	F830	S831	E832	K835	R836	T837	L838	Q839	P840	E841	H842	E843	K844	Q845	I846	K847	V848	L849	Q850	E851	E852	L853	Q854	T855	I856	E857	Y858	K859	S860	C861	E862	T863	C864	
D865	N866	D867	T868	E869	K870	F871	L872	E873	L874	M875	L876	A877	Y878	K879	E880	A881	T882	V883	N884	L885	N886	Q887	E888	N889	W890	K891	S892	P893	S894	I895	L896	H897	I898	L899	K900	E901	G902	R903	L904	Y905	A906	F907	R908	D909	P910	N911	D912	C913	L914	K915	L916	G917	F918	V919	S860	C861	E862	T863	C864
K925	D926	A927	V928	C929	V930	L931	N932	T933	F934	T935	K936	P937	Y938	K939	L940	P941	N942	G943	E944	P945	I1070	N1007	A1008	I1072	I1074	Y1075	E1076	L1077	K953	A954	D955	Q956	Y957	R958	R959	R960	F963	K964	P965	Q966	K967	T968	D969	F970	Y971	N972	E973	E974	V975	P976	Y977	T978	A979	I980	E981	V982	I983	T984	K985
R986	K987	F988	A989	A990	P991	L992	G993	K994	V995	I996	K997	K998	D999	V1000	A1001	A1002	A1003	N1004	E1005	F1006	I1070	N1007	A1008	I1072	I1074	Y1075	E1076	L1077	K953	A954	D955	Q956	Y957	R958	R959	R960	F963	K964	P965	Q966	K967	T968	D969	F970	Y971	N972	E973	E974	V975	P976	Y977	T978	A979	I980	E981	V982	I983	T984	K985
I1046	F1047	K1048	L1049	K1050	S1051	I1052	K1053	C1054	P1055	N1056	H1060	P1063	K1064	F1065	K1066	A1067	H1068	V1069	I1070	K1071	K1072	K1073	I1074	N1011	N1012	I1013	L1014	D1015	G1016	M1081	S1082	D1083	L1019	K1020	E1021	A1022	I1023	N1024	I1025	E1026	I1027	Q1028	G1029	L1030	K1031	R1032	L1033	Q1034	L1035	K1100	D1101	T1102	R1039	F1104	I1105	D1106	Q1107	N1108	



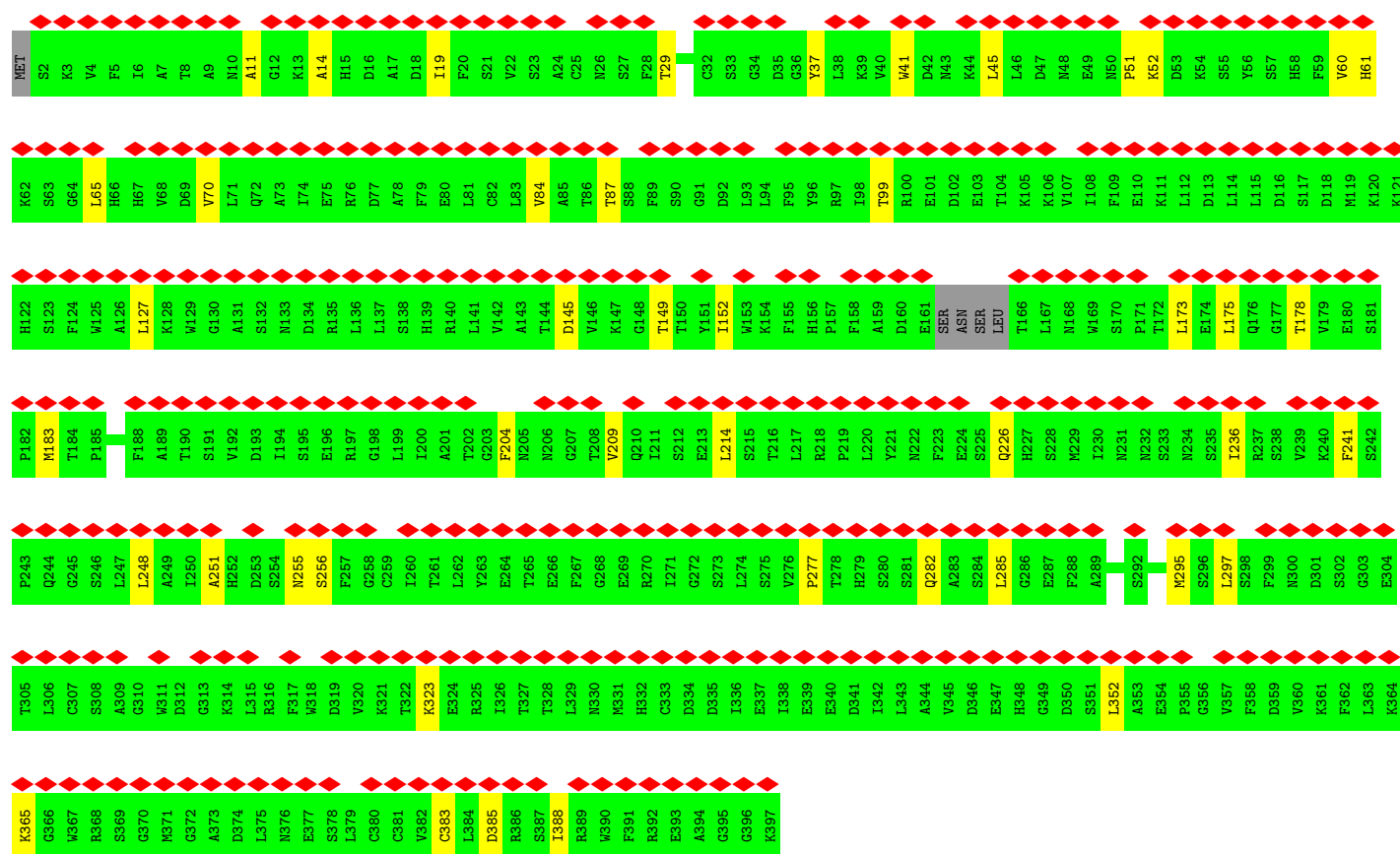
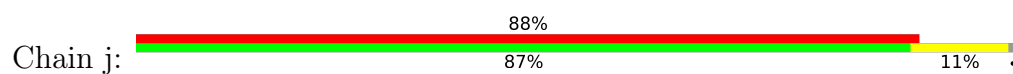
● Molecule 39: Supercollider protein 3



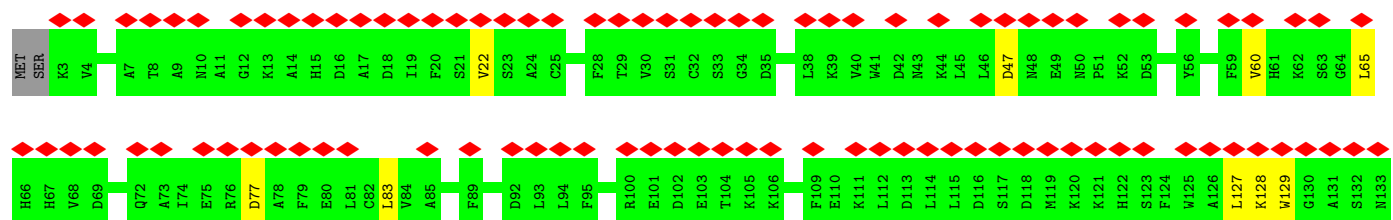
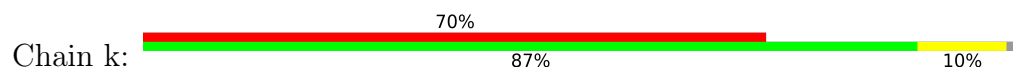


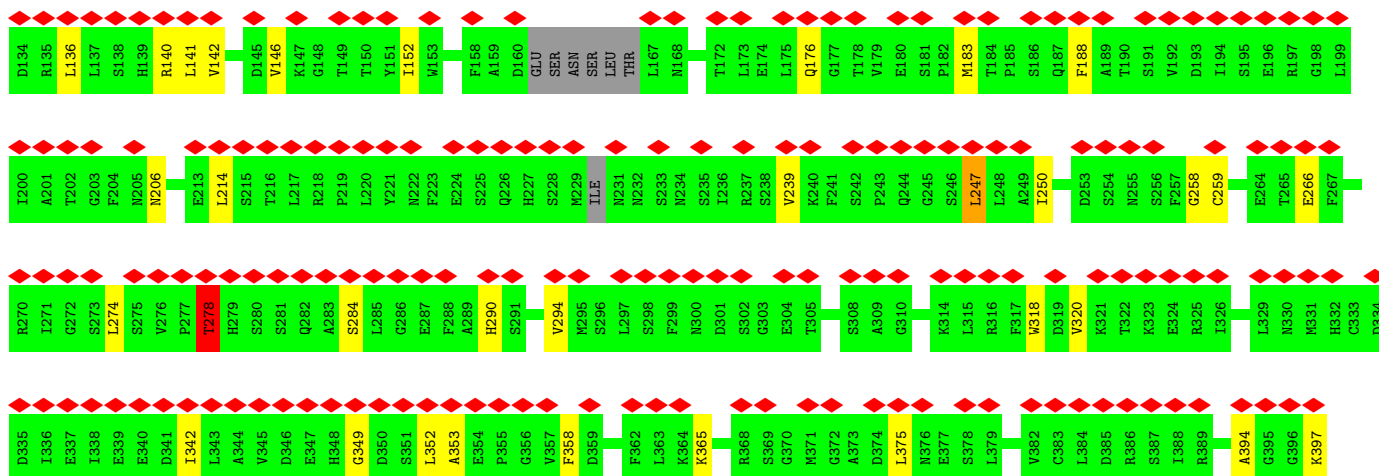


• Molecule 40: Antiviral protein SKI8



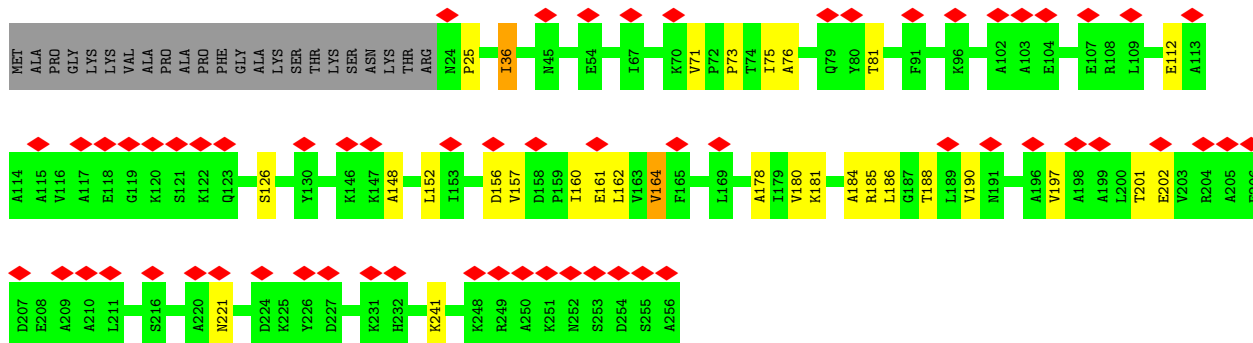
• Molecule 40: Antiviral protein SKI8





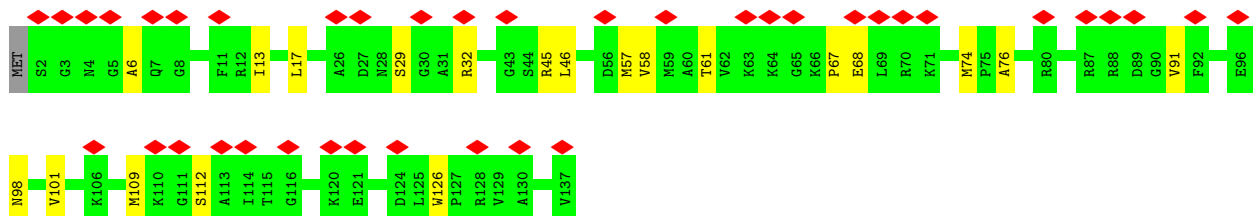
• Molecule 41: 60S ribosomal protein L8-A

Chain AA:



• Molecule 42: 60S ribosomal protein L23-A

Chain AB:

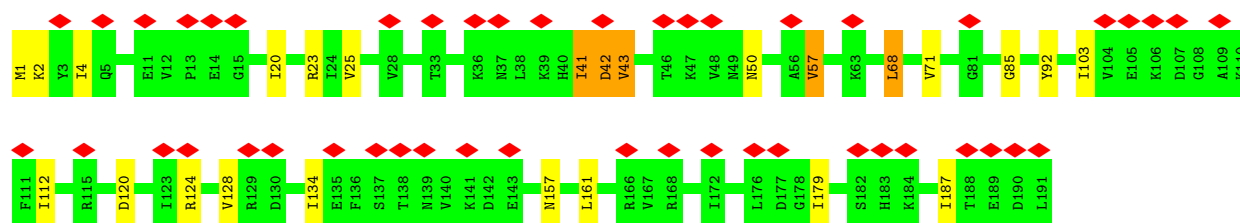
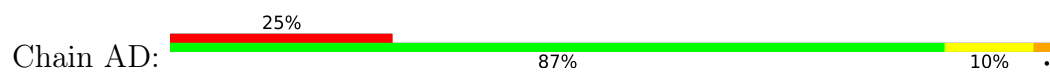


• Molecule 43: 60S ribosomal protein L36-A

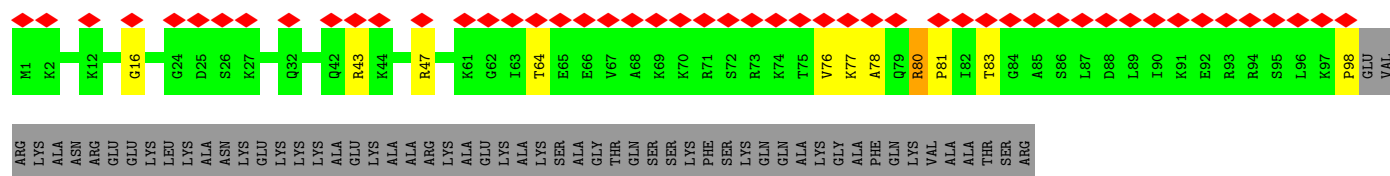
Chain AC:



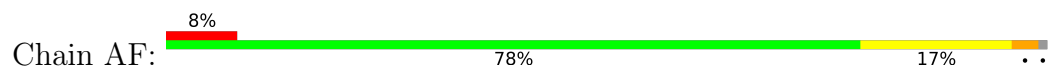
• Molecule 44: 60S ribosomal protein L9-A



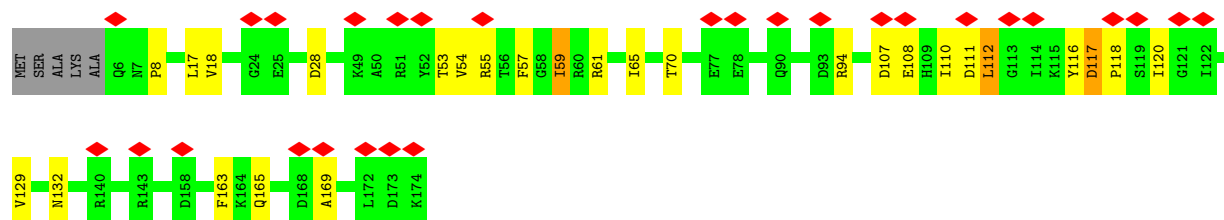
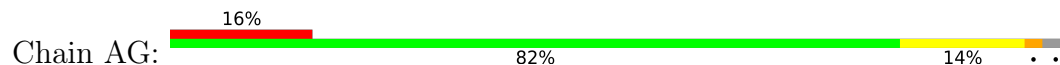
- Molecule 45: 60S ribosomal protein L24-A



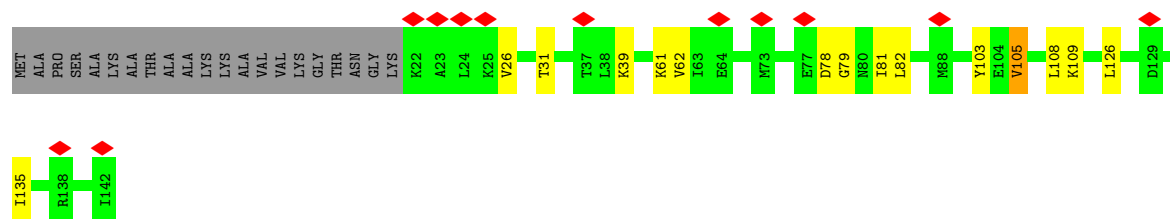
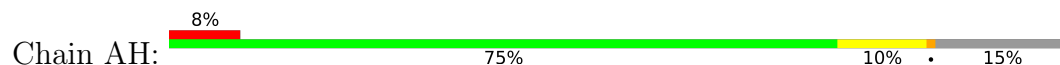
- Molecule 46: 60S ribosomal protein L37-A



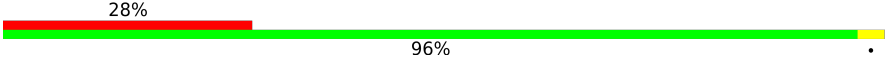
- Molecule 47: 60S ribosomal protein L11-A



- Molecule 48: 60S ribosomal protein L25



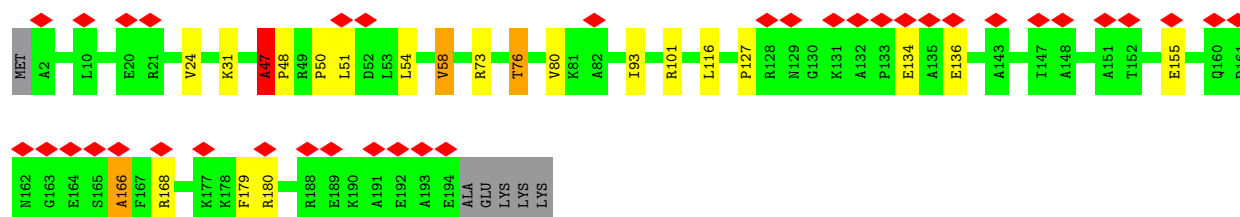
- Molecule 49: 60S ribosomal protein L38

Chain AI: 

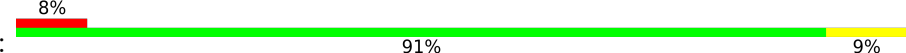


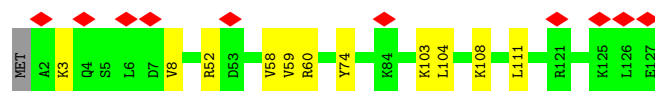
- Molecule 50: 60S ribosomal protein L13-A

Chain AJ: 



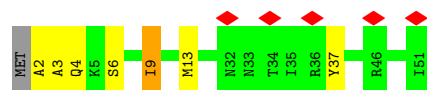
- Molecule 51: 60S ribosomal protein L26-A

Chain AK: 



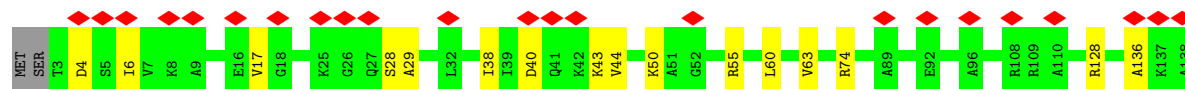
- Molecule 52: 60S ribosomal protein L39

Chain AL: 



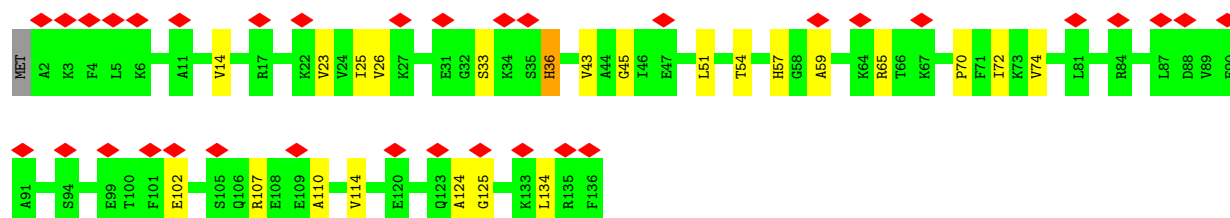
- Molecule 53: 60S ribosomal protein L14-A

Chain AM: 

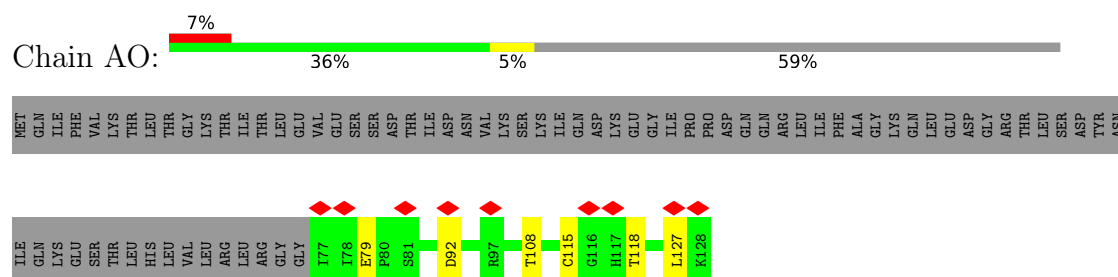


- Molecule 54: 60S ribosomal protein L27-A

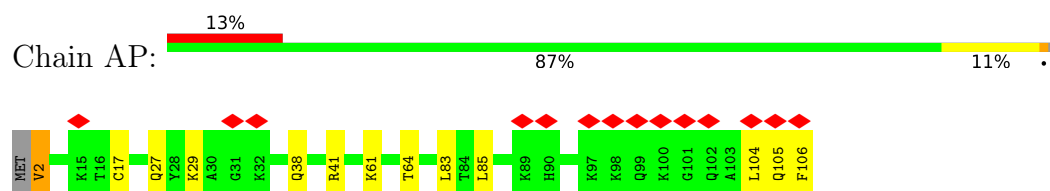
Chain AN: 



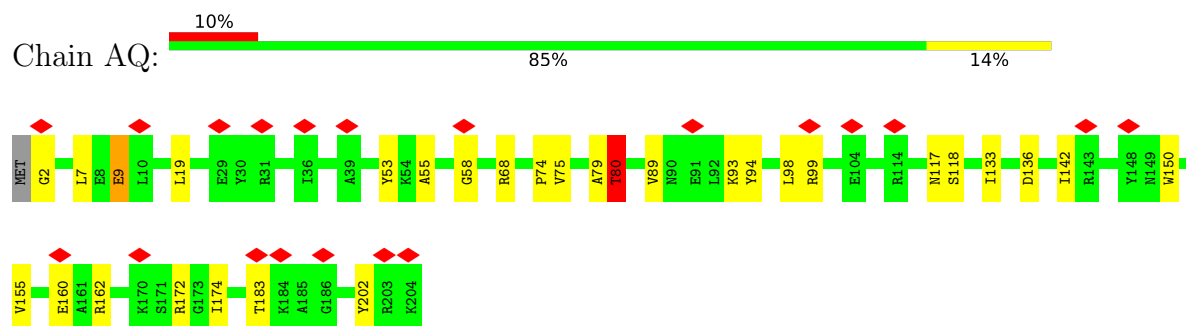
- Molecule 55: Ubiquitin-60S ribosomal protein L40



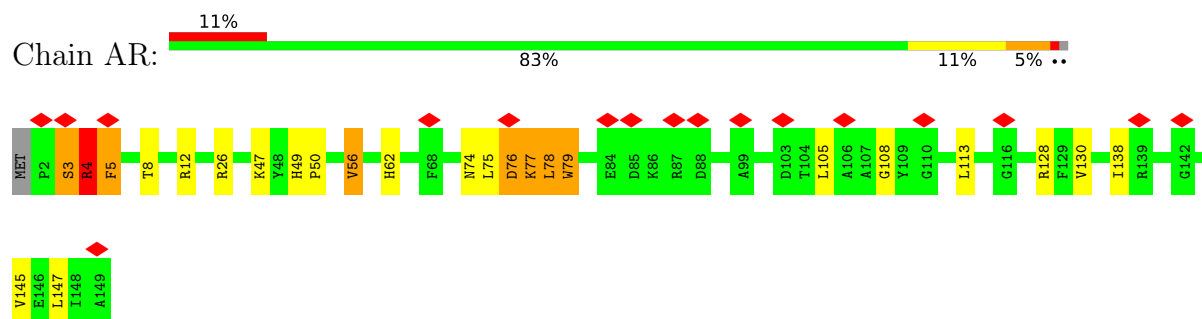
- Molecule 56: 60S ribosomal protein L42-A



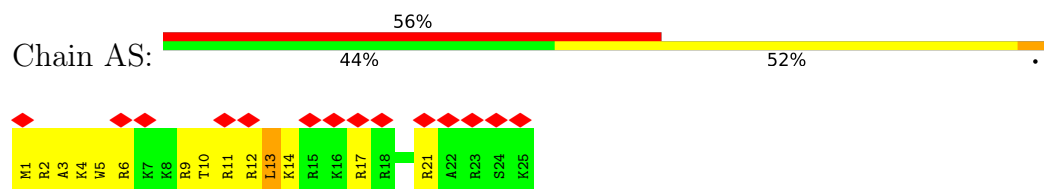
- Molecule 57: 60S ribosomal protein L15-A



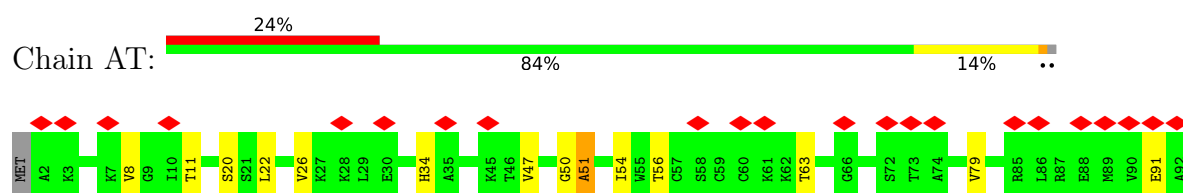
- Molecule 58: 60S ribosomal protein L28



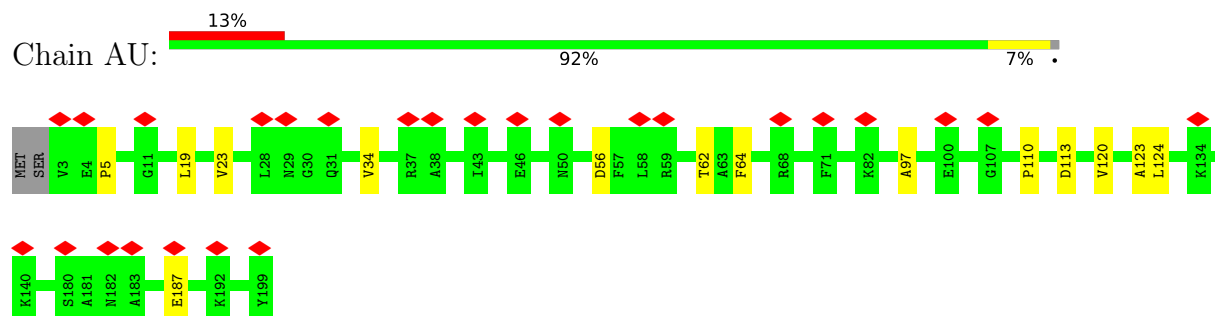
- Molecule 59: 60S ribosomal protein L41-A



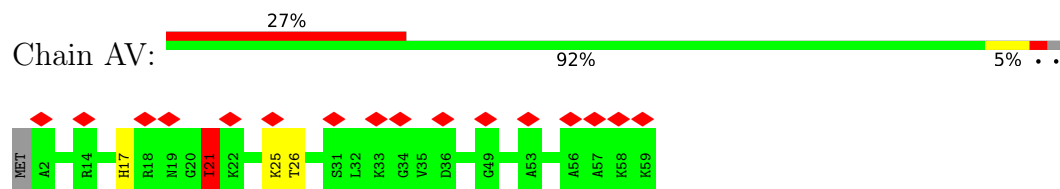
- Molecule 60: 60S ribosomal protein L43-A



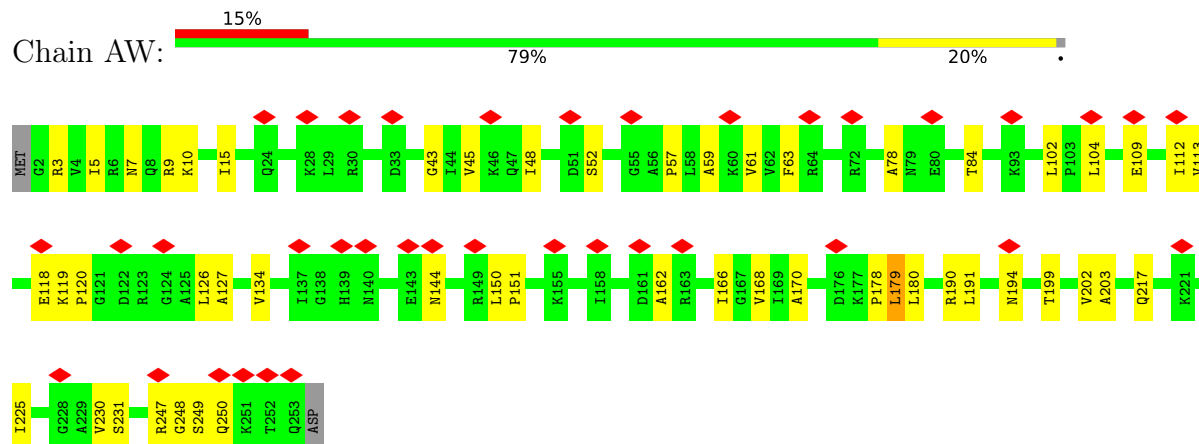
- Molecule 61: 60S ribosomal protein L16-A



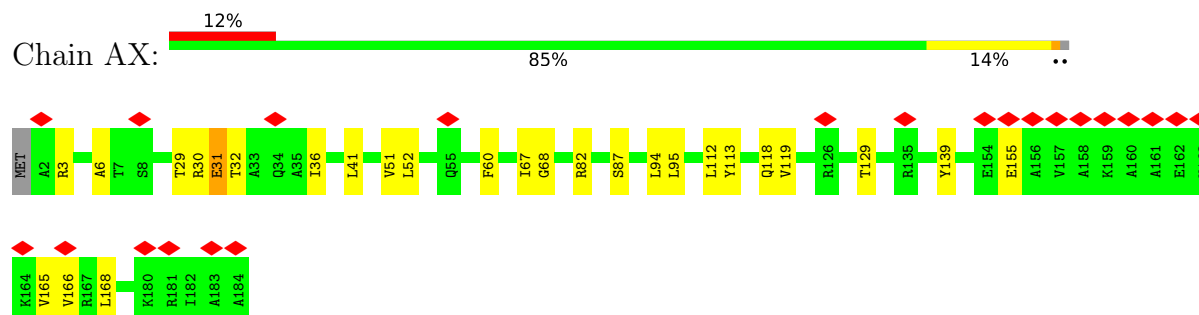
- Molecule 62: 60S ribosomal protein L29



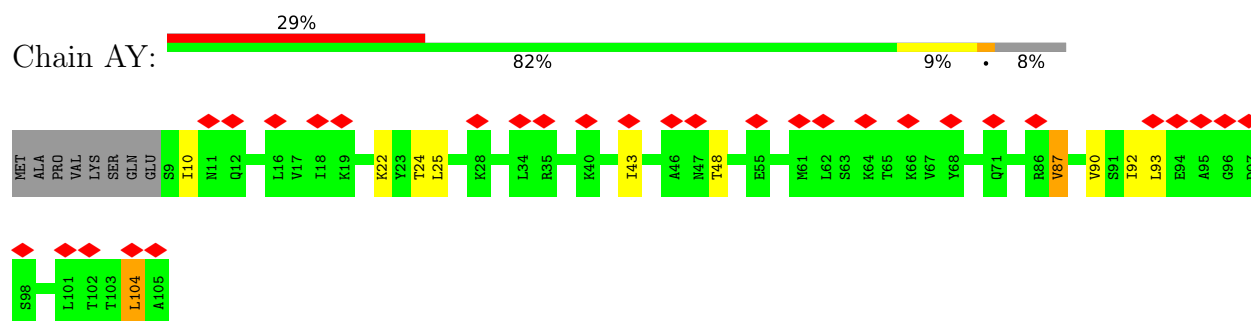
- Molecule 63: 60S ribosomal protein L2-A



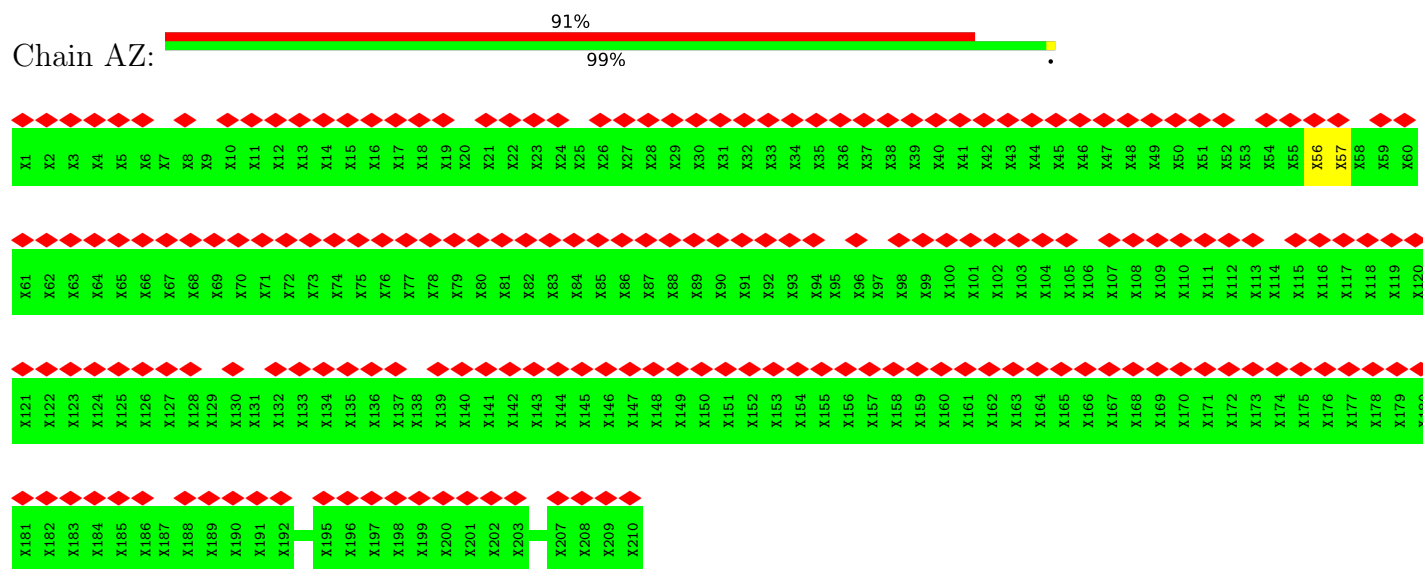
- Molecule 64: 60S ribosomal protein L17-A



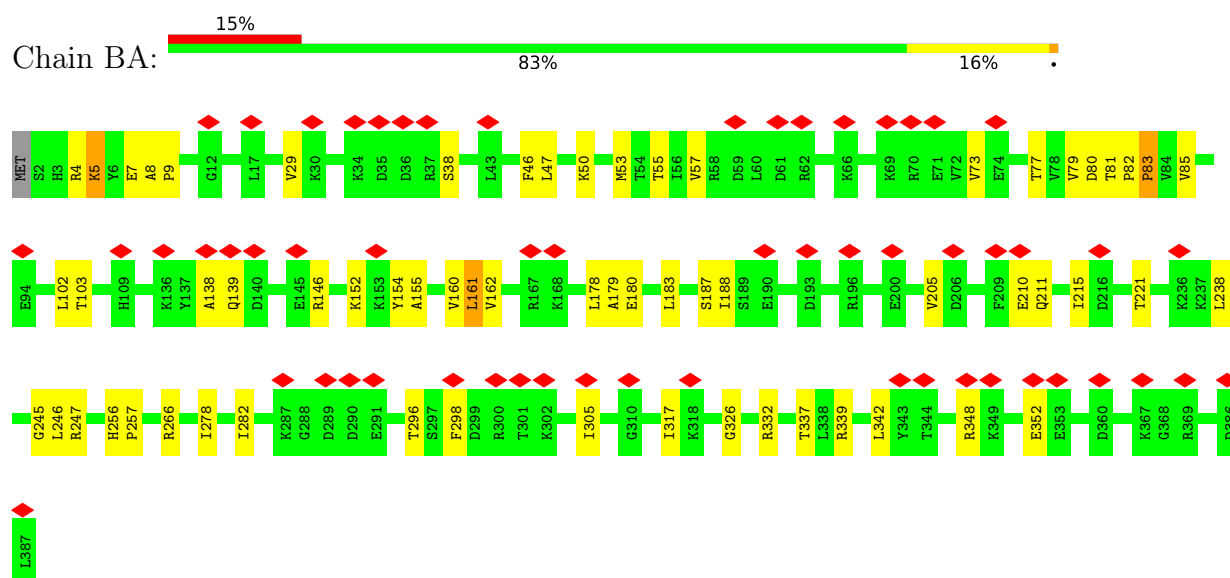
- Molecule 65: 60S ribosomal protein L30



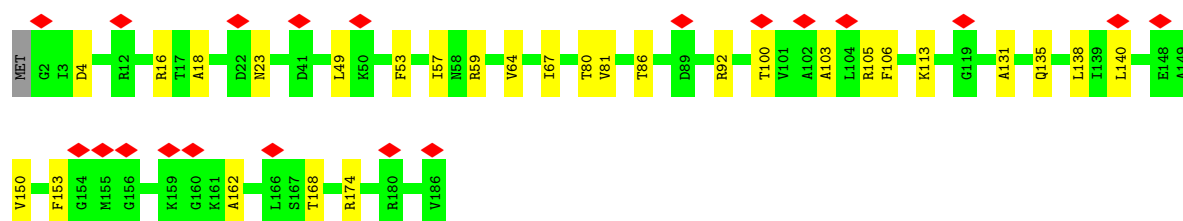
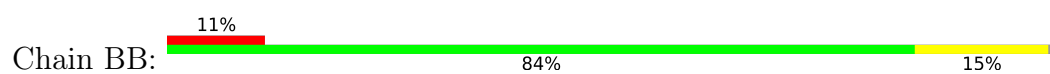
- Molecule 66: uL1



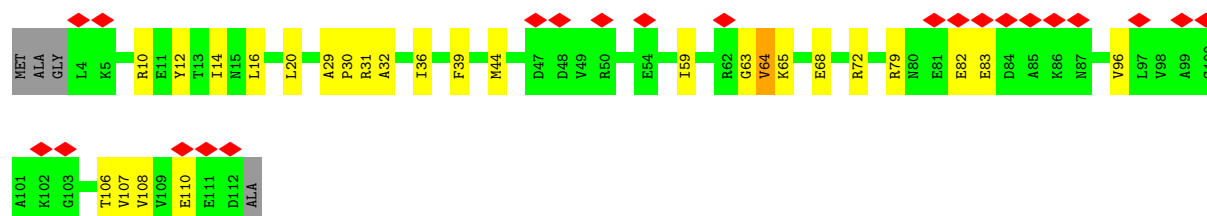
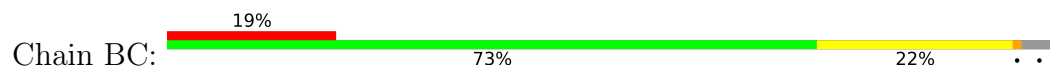
- Molecule 67: 60S ribosomal protein L3



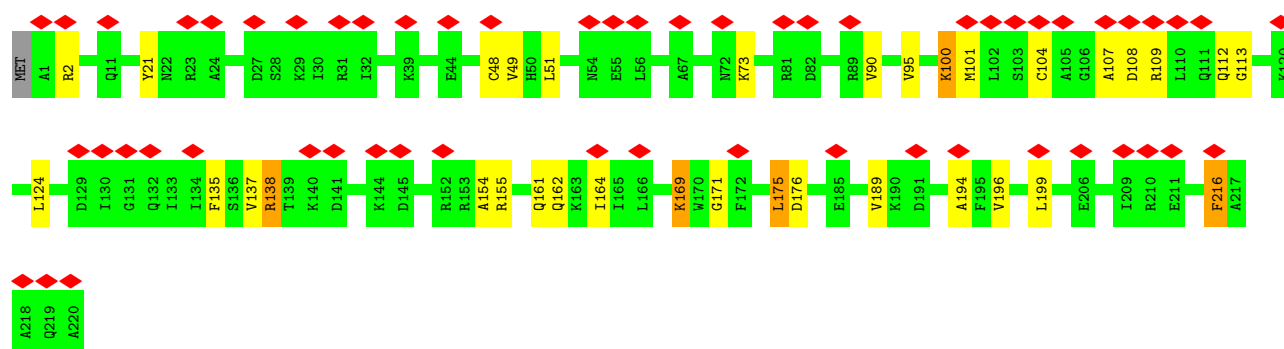
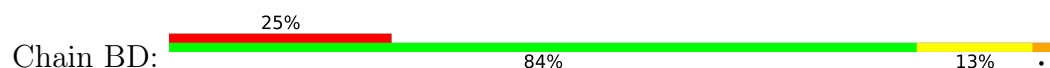
- Molecule 68: 60S ribosomal protein L18-A



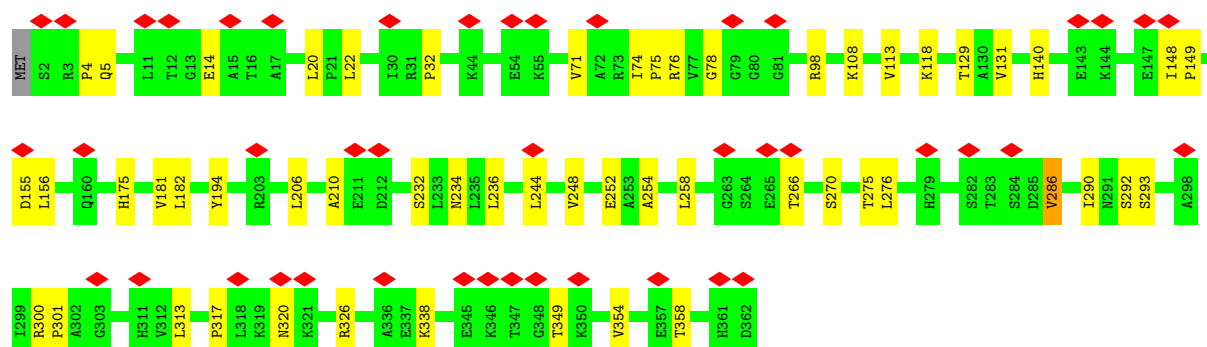
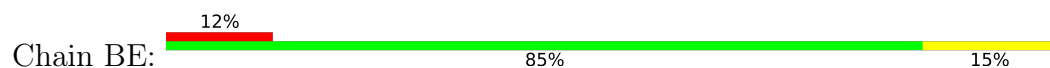
- Molecule 69: 60S ribosomal protein L31-A



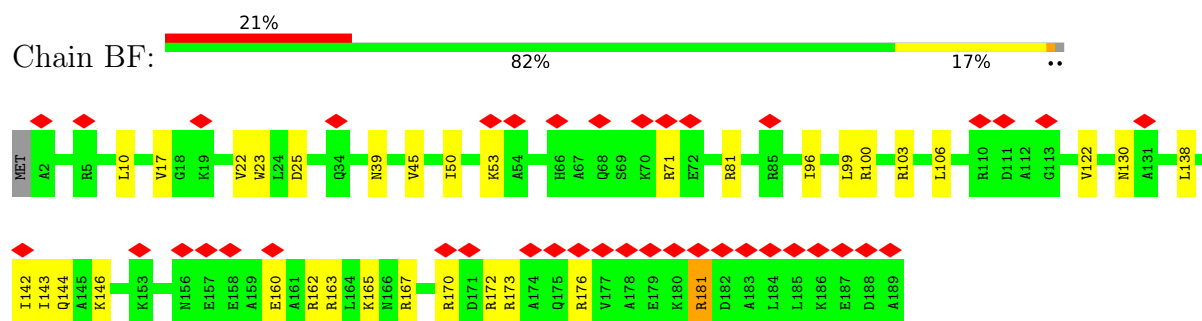
- Molecule 70: 60S ribosomal protein L10



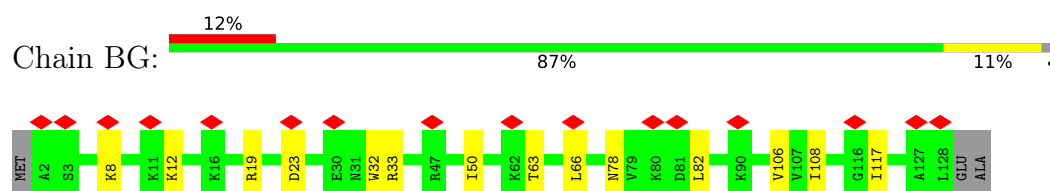
- Molecule 71: 60S ribosomal protein L4-A



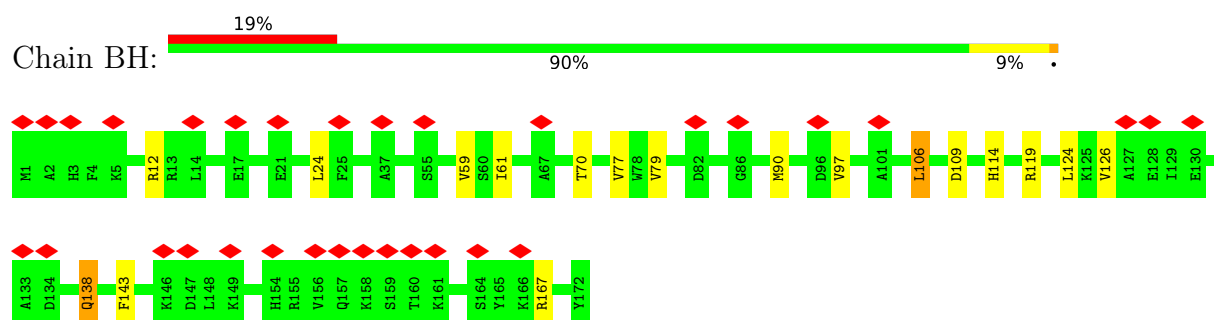
- Molecule 72: 60S ribosomal protein L19-A



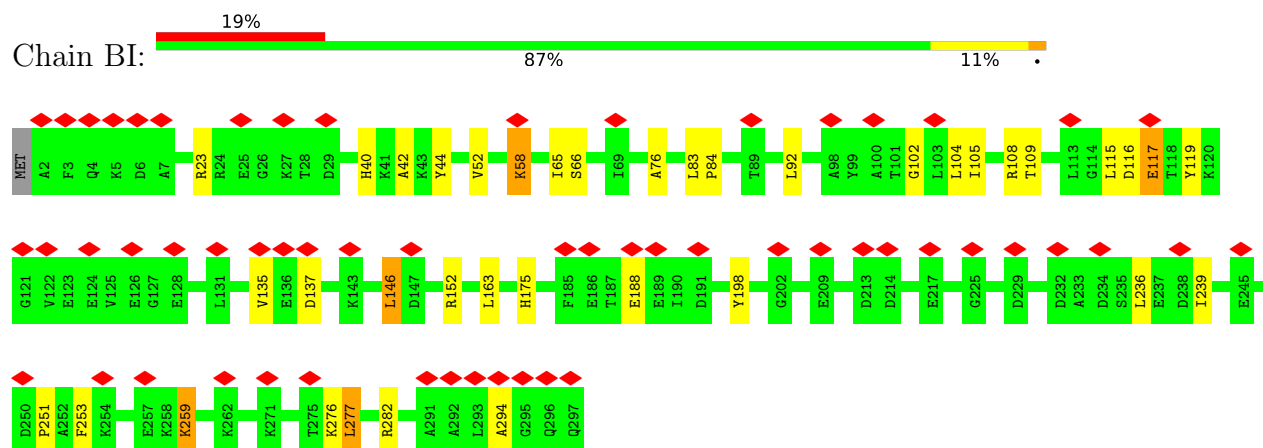
- Molecule 73: 60S ribosomal protein L32



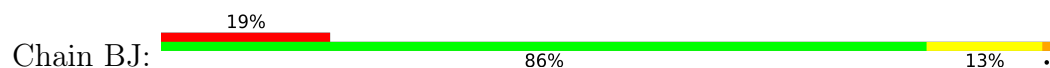
- Molecule 74: 60S ribosomal protein L20-A

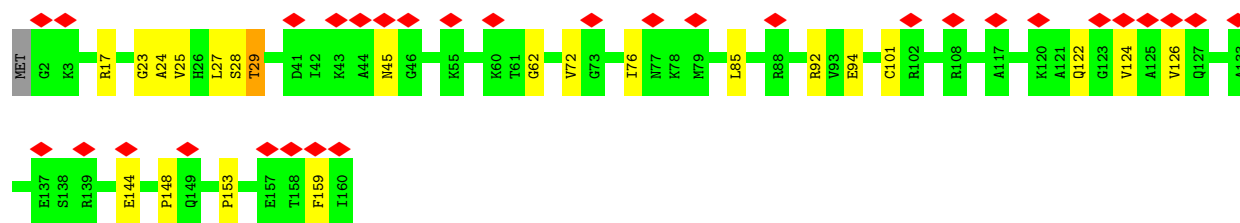


- Molecule 75: 60S ribosomal protein L5

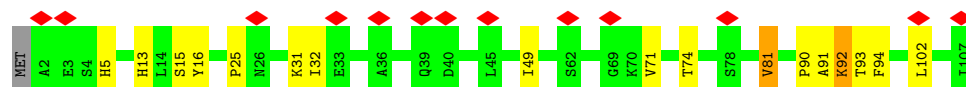
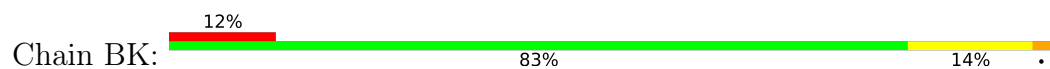


- Molecule 76: 60S ribosomal protein L21-A

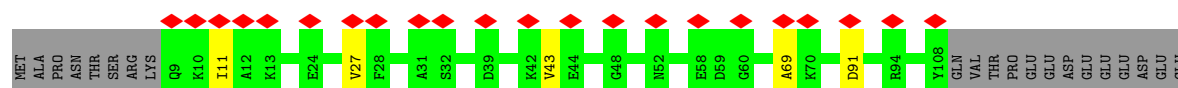
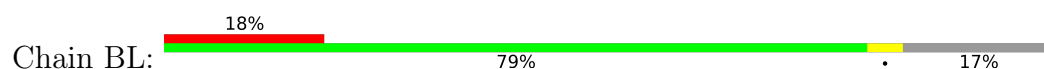




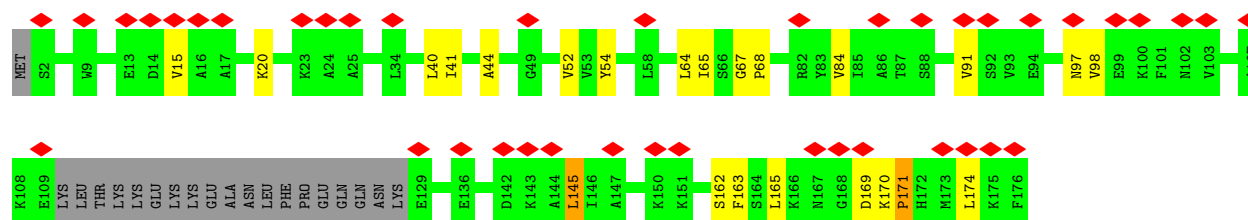
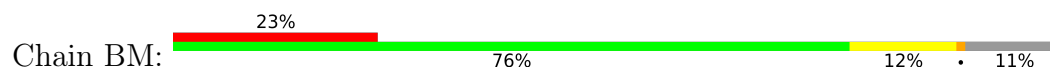
- Molecule 77: 60S ribosomal protein L33-A



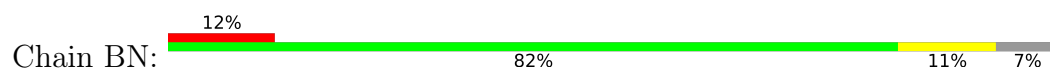
- Molecule 78: 60S ribosomal protein L22-A



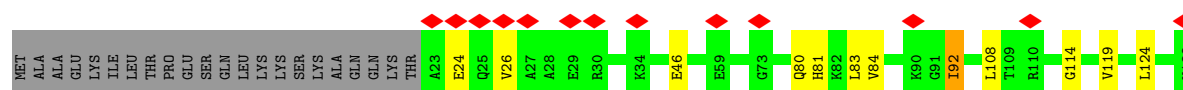
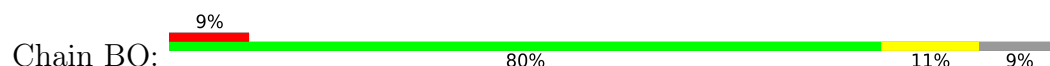
- Molecule 79: 60S ribosomal protein L6-A

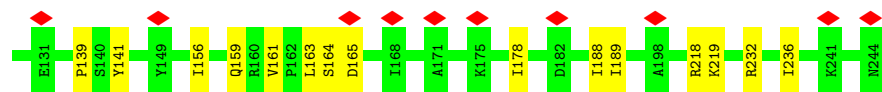


- Molecule 80: 60S ribosomal protein L34-A

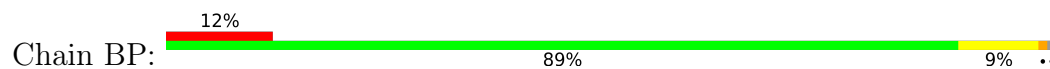


- Molecule 81: 60S ribosomal protein L7-A

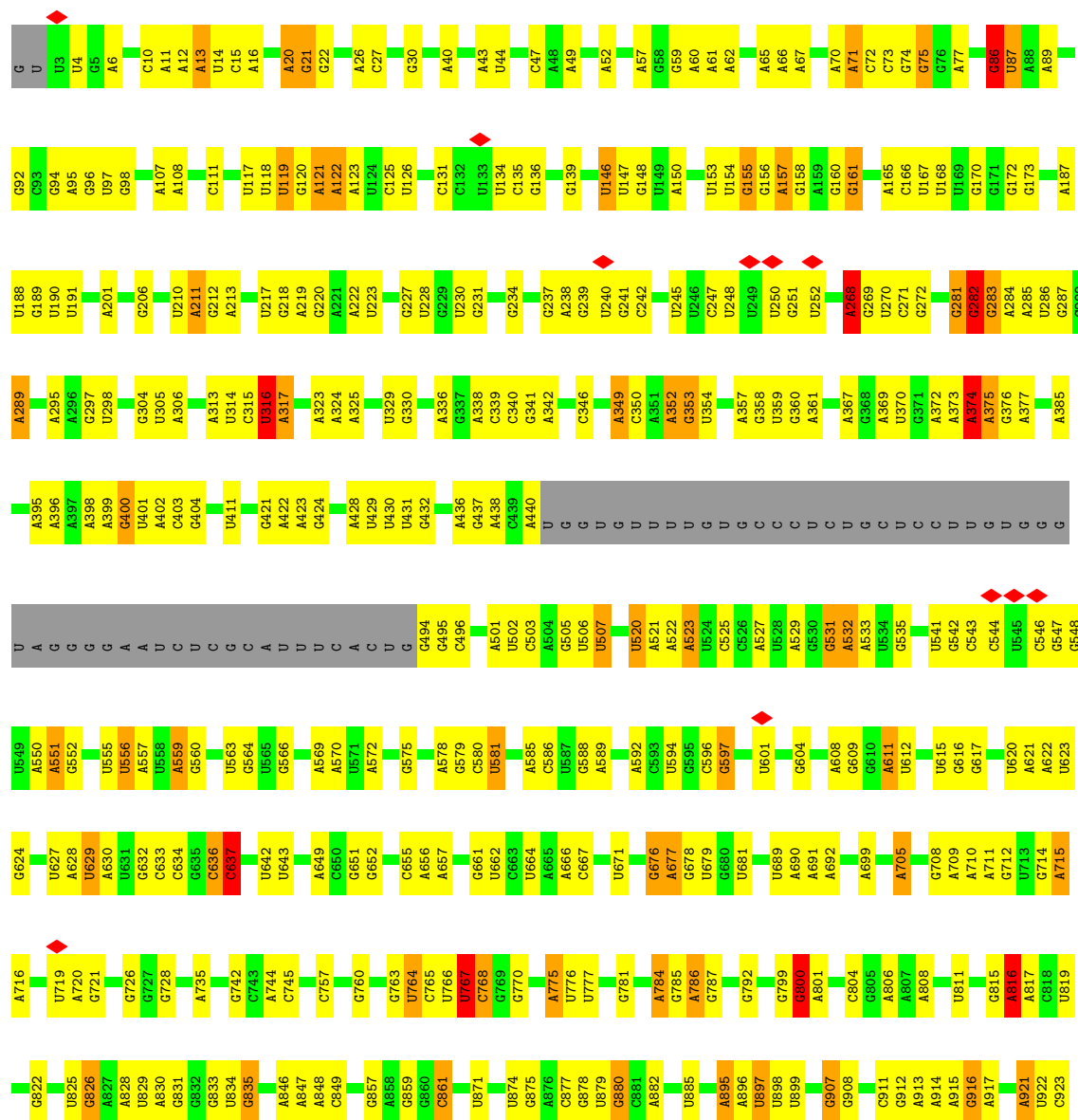




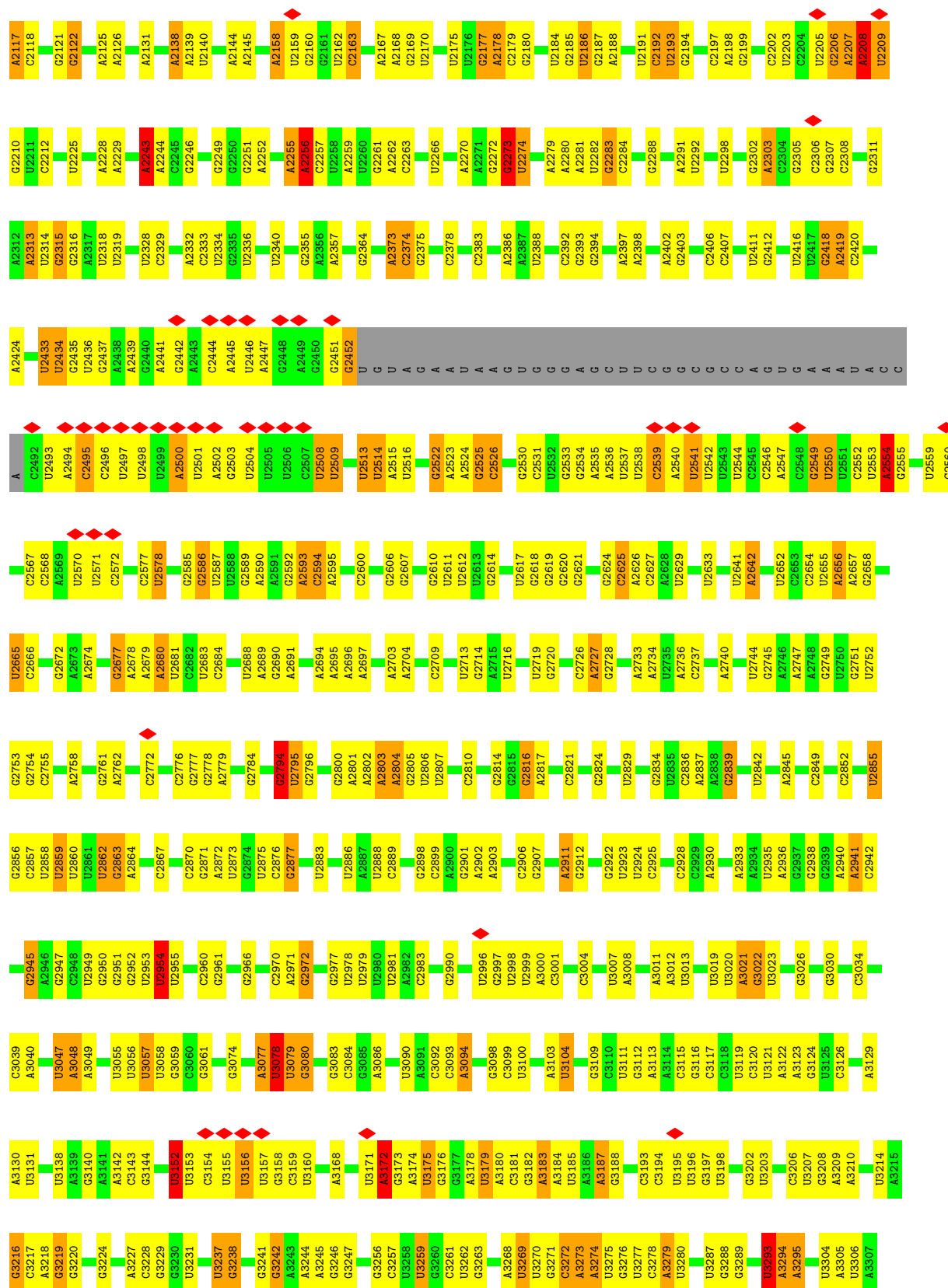
• Molecule 82: 60S ribosomal protein L35-A

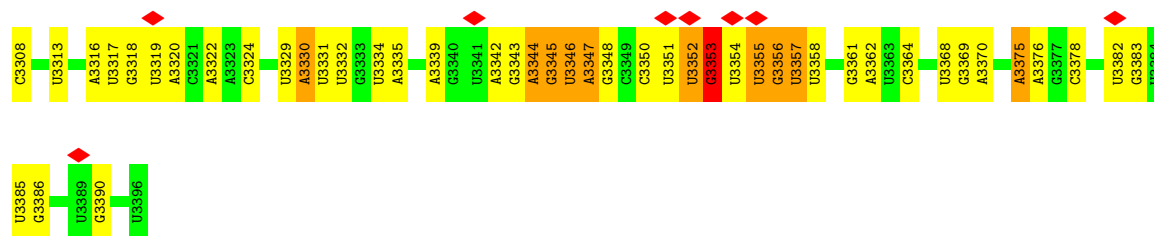


• Molecule 83: 25S ribosomal RNA





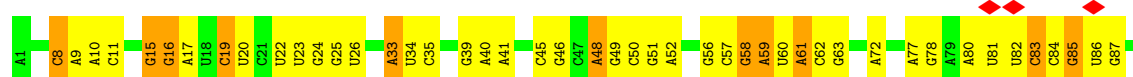




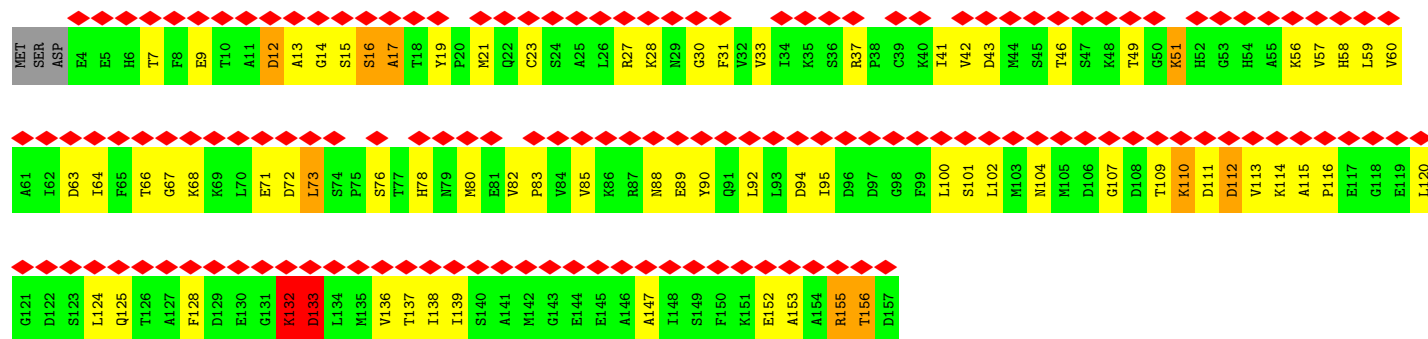
• Molecule 84: 5S ribosomal RNA



• Molecule 85: 5.8S ribosomal RNA



• Molecule 86: Eukaryotic translation initiation factor 5A-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.075	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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	2	0.41	1/42103 (0.0%)	0.78	99/65603 (0.2%)
2	A	0.54	0/1759	0.83	0/2368
3	B	0.58	0/1629	0.91	0/2202
4	C	0.55	0/833	0.81	0/1126
5	D	0.63	0/885	0.89	0/1202
6	E	0.58	0/998	0.84	0/1341
7	F	0.59	0/1125	0.92	1/1510 (0.1%)
8	G	0.67	2/754 (0.3%)	0.96	0/1005
9	H	0.62	0/1211	0.95	2/1628 (0.1%)
10	I	0.63	0/1130	0.95	3/1517 (0.2%)
11	J	0.55	0/865	0.84	1/1169 (0.1%)
12	K	0.61	0/571	0.90	0/768
13	L	0.54	0/499	0.70	0/670
14	M	0.50	0/452	0.74	0/600
15	N	0.58	0/404	0.79	0/542
16	O	0.52	0/2489	0.66	0/3389
17	P	0.56	0/1617	0.86	0/2215
18	Q	0.62	0/1735	0.84	0/2335
19	R	0.51	0/1702	0.80	0/2310
20	S	0.60	1/2109 (0.0%)	0.80	1/2839 (0.0%)
21	T	0.57	0/1823	0.78	1/2439 (0.0%)
22	U	0.61	0/1506	0.81	2/2028 (0.1%)
23	V	0.69	0/1514	0.99	5/2021 (0.2%)
24	W	0.60	0/1456	0.87	0/1949
25	X	0.55	0/1239	0.72	0/1673
26	Y	0.58	0/1215	0.96	0/1638
27	Z	0.64	0/901	0.91	0/1217
28	a	0.57	0/693	0.80	0/935
29	b	0.49	0/1038	0.88	1/1395 (0.1%)
30	c	0.51	0/1139	0.77	0/1518
31	d	0.62	0/1074	0.91	3/1431 (0.2%)
32	e	1.01	5/782 (0.6%)	1.06	5/1047 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.55	0/620	0.74	0/838
34	g	0.63	1/481 (0.2%)	0.79	0/640
35	l	0.41	0/764	0.85	1/1179 (0.1%)
36	m	0.40	0/1799	0.80	4/2801 (0.1%)
37	n	0.39	0/1835	0.75	4/2858 (0.1%)
38	h	0.57	0/8985	0.84	3/12155 (0.0%)
39	i	0.55	1/10027 (0.0%)	0.87	6/13707 (0.0%)
40	j	0.54	0/3001	0.69	0/4083
40	k	0.52	0/2988	0.70	0/4060
41	AA	0.64	0/1836	0.90	1/2481 (0.0%)
42	AB	0.57	0/1018	0.89	1/1369 (0.1%)
43	AC	0.63	0/778	0.93	0/1034
44	AD	0.58	0/1539	0.85	0/2073
45	AE	0.61	0/712	1.26	2/958 (0.2%)
46	AF	0.63	0/696	0.88	1/923 (0.1%)
47	AG	0.61	0/1374	0.88	2/1842 (0.1%)
48	AH	0.52	0/979	0.83	0/1321
49	AI	0.61	0/618	0.77	0/826
50	AJ	0.63	0/1568	0.92	2/2106 (0.1%)
51	AK	0.59	0/1004	0.89	0/1341
52	AL	0.55	0/443	0.82	0/588
53	AM	0.60	0/1068	0.94	0/1438
54	AN	0.57	0/1118	0.88	0/1497
55	AO	0.62	0/423	0.90	0/562
56	AP	0.53	0/860	0.80	0/1136
57	AQ	0.58	0/1757	0.89	1/2354 (0.0%)
58	AR	0.57	0/1204	0.90	2/1612 (0.1%)
59	AS	0.67	0/234	1.01	0/300
60	AT	0.56	0/701	0.87	0/934
61	AU	0.58	0/1585	0.89	1/2128 (0.0%)
62	AV	0.52	0/473	0.88	0/629
63	AW	0.54	0/1948	0.85	1/2617 (0.0%)
64	AX	0.58	0/1443	0.89	0/1944
65	AY	0.57	0/750	0.88	0/1008
67	BA	0.56	0/3146	0.83	0/4228
68	BB	0.56	0/1465	0.90	0/1965
69	BC	0.53	0/890	0.79	0/1196
70	BD	0.59	0/1807	0.89	2/2425 (0.1%)
71	BE	0.59	0/2800	0.92	0/3790
72	BF	0.64	0/1538	0.94	3/2050 (0.1%)
73	BG	0.55	0/1041	0.80	0/1394
74	BH	0.54	0/1481	0.83	0/1990
75	BI	0.58	0/2425	0.86	0/3271

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	BJ	0.53	0/1300	0.83	0/1743
77	BK	0.56	0/868	0.80	0/1168
78	BL	0.62	0/812	0.82	0/1099
79	BM	0.57	0/1260	0.87	2/1694 (0.1%)
80	BN	0.57	0/890	0.89	2/1189 (0.2%)
81	BO	0.59	0/1821	0.92	0/2451
82	BP	0.55	0/978	0.91	0/1301
83	BQ	0.42	0/75774	0.83	160/118137 (0.1%)
84	BR	0.40	0/2883	0.79	5/4491 (0.1%)
85	BS	0.41	0/3745	0.80	4/5829 (0.1%)
86	BT	0.30	0/1142	0.75	0/1537
All	All	0.50	11/243945 (0.0%)	0.83	334/355920 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	H	0	1
10	I	0	2
21	T	0	2
22	U	0	1
23	V	0	3
32	e	0	2
57	AQ	0	1
58	AR	0	2
63	AW	0	1
69	BC	0	1
70	BD	0	1
86	BT	0	1
All	All	0	18

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	52	U	O3'-P	18.60	1.89	1.61
32	e	8	ASN	CA-C	8.98	1.61	1.53
8	G	36	ASP	CG-OD1	7.28	1.39	1.25
8	G	36	ASP	CG-OD2	6.06	1.36	1.25
39	i	147	GLN	C-O	-5.92	1.16	1.24
34	g	46	ASN	CA-C	5.74	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	e	10	ARG	N-CA	5.67	1.52	1.45
32	e	7	SER	N-CA	5.59	1.52	1.45
32	e	9	GLY	N-CA	5.58	1.53	1.45
32	e	6	ALA	CA-C	5.16	1.59	1.52
20	S	26	CYS	CA-C	5.10	1.55	1.52

All (334) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	AE	80	ARG	CA-C-N	19.43	144.12	119.84
45	AE	80	ARG	C-N-CA	19.43	144.12	119.84
83	BQ	933	A	C2'-C3'-O3'	14.27	130.90	109.50
83	BQ	1808	G	C2'-C3'-O3'	13.57	129.86	109.50
83	BQ	1429	G	C2'-C3'-O3'	11.78	127.17	109.50
83	BQ	1511	U	C2'-C3'-O3'	11.74	127.11	109.50
1	2	52	U	P-O3'-C3'	-11.54	102.89	120.20
83	BQ	2116	G	C2'-C3'-O3'	11.30	126.45	109.50
83	BQ	1241	U	C4'-C3'-O3'	11.26	126.29	109.40
83	BQ	316	U	C2'-C3'-O3'	10.49	125.23	109.50
1	2	52	U	C5'-C4'-O4'	-10.42	93.47	109.10
83	BQ	282	G	C2'-C3'-O3'	10.28	129.12	113.70
83	BQ	1913	A	C2'-C3'-O3'	10.14	124.71	109.50
1	2	49	C	C1'-C2'-O2'	-9.94	93.49	108.40
58	AR	4	ARG	N-CA-C	9.90	127.03	113.37
83	BQ	816	A	C2'-C3'-O3'	-9.70	99.15	113.70
83	BQ	2177	G	C2'-C3'-O3'	9.67	124.00	109.50
83	BQ	1724	U	C4'-C3'-O3'	9.47	123.60	109.40
83	BQ	2972	G	C4'-C3'-O3'	9.37	127.05	113.00
85	BS	33	A	C4'-C3'-O3'	9.34	123.40	109.40
83	BQ	1467	A	C2'-C3'-O3'	9.26	123.39	109.50
1	2	1274	C	C2'-C3'-O3'	9.24	123.36	109.50
32	e	7	SER	N-CA-C	9.24	124.13	110.17
1	2	428	A	C4'-C3'-O3'	9.22	126.83	113.00
83	BQ	2665	U	C4'-C3'-O3'	9.18	123.17	109.40
83	BQ	1483	G	C2'-C3'-O3'	9.17	123.26	109.50
83	BQ	611	A	C2'-C3'-O3'	8.92	122.89	109.50
83	BQ	2593	A	C2'-C3'-O3'	8.86	122.80	109.50
83	BQ	2972	G	C1'-C2'-O2'	-8.79	95.22	108.40
83	BQ	2273	G	C2'-C3'-O3'	8.68	122.52	109.50
31	d	128	LYS	N-CA-C	8.65	120.70	111.28
83	BQ	2727	A	C2'-C3'-O3'	8.57	122.36	109.50
1	2	384	G	C4'-C3'-O3'	8.56	125.84	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	BQ	2972	G	N9-C1'-C2'	-8.51	99.23	112.00
83	BQ	352	A	C4'-C3'-O3'	8.51	122.17	109.40
39	i	534	VAL	N-CA-C	-8.39	104.96	113.10
83	BQ	1900	A	C2'-C3'-O3'	8.36	122.04	109.50
83	BQ	1352	A	C4'-C3'-O3'	8.35	121.93	109.40
1	2	322	G	C2'-C3'-O3'	8.34	122.02	109.50
83	BQ	1418	A	C4'-C3'-O3'	8.26	121.78	109.40
83	BQ	3274	A	C4'-C3'-O3'	8.24	121.76	109.40
7	F	40	GLU	C-N-CD	-8.22	102.51	120.60
84	BR	77	G	C2'-C3'-O3'	8.21	121.81	109.50
83	BQ	921	A	C2'-C3'-O3'	8.12	121.69	109.50
1	2	578	U	C4'-C3'-O3'	8.11	121.56	109.40
83	BQ	1588	A	C2'-C3'-O3'	-8.07	101.59	113.70
83	BQ	3269	U	C4'-C3'-O3'	8.07	121.50	109.40
83	BQ	3021	A	C4'-C3'-O3'	8.03	121.44	109.40
83	BQ	3272	C	C4'-C3'-O3'	7.95	121.33	109.40
1	2	639	U	C2'-C3'-O3'	7.95	121.42	109.50
83	BQ	1815	U	C4'-C3'-O3'	7.93	121.30	109.40
85	BS	48	A	C2'-C3'-O3'	7.93	121.39	109.50
83	BQ	2941	A	C2'-C3'-O3'	7.92	121.39	109.50
83	BQ	353	G	C4'-C3'-O3'	7.90	121.25	109.40
84	BR	86	U	C2'-C3'-O3'	7.85	121.28	109.50
79	BM	170	LYS	CA-C-N	7.80	129.60	119.84
79	BM	170	LYS	C-N-CA	7.80	129.60	119.84
85	BS	58	G	C4'-C3'-O3'	7.69	120.94	109.40
1	2	66	U	C2'-C3'-O3'	7.68	121.02	109.50
1	2	609	U	C2'-C3'-O3'	7.64	120.96	109.50
1	2	1081	A	C4'-C3'-O3'	7.63	120.85	109.40
83	BQ	211	A	C2'-C3'-O3'	7.63	120.94	109.50
83	BQ	2954	U	C4'-C3'-O3'	-7.59	98.01	109.40
1	2	352	A	C2'-C3'-O3'	7.58	120.87	109.50
83	BQ	2680	A	C2'-C3'-O3'	7.57	120.86	109.50
1	2	428	A	N9-C1'-C2'	-7.56	100.66	112.00
83	BQ	3353	G	C4'-C3'-O3'	7.53	120.69	109.40
83	BQ	715	A	C2'-C3'-O3'	-7.47	102.49	113.70
83	BQ	1850	A	C4'-C3'-O3'	7.46	120.59	109.40
83	BQ	1481	A	C2'-C3'-O3'	7.45	120.68	109.50
1	2	114	C	C4'-C3'-O3'	7.42	120.54	109.40
83	BQ	916	G	C4'-C3'-O3'	7.38	124.06	113.00
83	BQ	677	A	C2'-C3'-O3'	7.37	120.55	109.50
83	BQ	146	U	C2'-C3'-O3'	-7.32	102.72	113.70
83	BQ	1307	G	C2'-C3'-O3'	7.26	120.39	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1273	G	C2'-C3'-O3'	7.25	120.38	109.50
83	BQ	1816	A	C4'-C3'-O3'	7.24	120.27	109.40
83	BQ	1199	C	C4'-C3'-O3'	7.21	120.22	109.40
1	2	613	G	C4'-C3'-O3'	7.21	120.22	109.40
83	BQ	2554	A	C4'-C3'-O3'	7.19	120.18	109.40
83	BQ	86	G	C4'-C3'-O3'	7.19	120.18	109.40
83	BQ	520	U	C4'-C3'-O3'	-7.19	102.22	113.00
84	BR	41	G	C2'-C3'-O3'	7.16	120.24	109.50
50	AJ	47	ALA	CA-C-N	-7.16	112.51	120.45
50	AJ	47	ALA	C-N-CA	-7.16	112.51	120.45
83	BQ	2940	A	C4'-C3'-O3'	-7.15	102.27	113.00
83	BQ	2178	A	C4'-C3'-O3'	7.15	120.12	109.40
32	e	97	PRO	N-CA-C	7.12	119.39	110.70
1	2	1256	A	C2'-C3'-O3'	7.09	120.14	109.50
1	2	1370	U	C4'-C3'-O3'	7.09	120.04	109.40
83	BQ	786	A	C4'-C3'-O3'	7.09	120.04	109.40
83	BQ	2945	G	C3'-C2'-O2'	7.07	121.30	110.70
1	2	313	U	C2'-C3'-O3'	7.07	120.10	109.50
83	BQ	1355	A	C2'-C3'-O3'	7.06	120.10	109.50
37	n	58	A	C4'-C3'-O3'	7.06	119.99	109.40
83	BQ	2283	G	C2'-C3'-O3'	7.05	120.08	109.50
1	2	329	G	C3'-C2'-O2'	7.02	121.23	110.70
1	2	312	A	C2'-C3'-O3'	7.00	120.00	109.50
10	I	4	VAL	N-CA-C	6.99	117.53	107.88
83	BQ	2111	G	C2'-C3'-O3'	-6.97	103.24	113.70
61	AU	110	PRO	N-CA-C	6.95	119.18	110.70
80	BN	58	ARG	CA-C-N	6.94	128.51	119.84
80	BN	58	ARG	C-N-CA	6.94	128.51	119.84
83	BQ	3022	G	C2'-C3'-O3'	6.93	119.89	109.50
83	BQ	3344	A	C2'-C3'-O3'	-6.93	103.31	113.70
1	2	711	U	C2'-C3'-O3'	6.90	119.85	109.50
83	BQ	1095	U	C2'-C3'-O3'	-6.88	103.37	113.70
1	2	141	U	C4'-C3'-O3'	6.88	123.32	113.00
1	2	1185	U	C2'-C3'-O3'	6.88	124.02	113.70
83	BQ	2539	C	C4'-C3'-O3'	6.87	119.71	109.40
32	e	11	ASN	N-CA-C	6.85	119.84	109.23
83	BQ	2434	U	C2'-C3'-O3'	6.82	119.72	109.50
1	2	765	G	C4'-C3'-O3'	6.78	119.57	109.40
1	2	278	U	C2'-C3'-O3'	6.77	119.66	109.50
84	BR	111	U	C4'-C3'-O3'	6.77	119.55	109.40
83	BQ	1144	U	C2'-C3'-O3'	6.76	119.65	109.50
83	BQ	979	U	C2'-C3'-O3'	6.75	119.63	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	BQ	2816	G	C4'-C3'-O3'	6.74	119.51	109.40
36	m	54	U	C4'-C3'-O3'	6.74	123.11	113.00
1	2	928	U	C2'-C3'-O3'	6.74	119.61	109.50
84	BR	41	G	C4'-C3'-O3'	6.73	119.50	109.40
1	2	77	U	C2'-C3'-O3'	6.67	119.50	109.50
83	BQ	1631	C	C2'-C3'-O3'	-6.65	103.72	113.70
83	BQ	2625	C	C4'-C3'-O3'	6.65	119.38	109.40
1	2	963	A	C4'-C3'-O3'	-6.64	103.04	113.00
83	BQ	1554	U	C4'-C3'-O3'	6.61	119.32	109.40
83	BQ	1850	A	C2'-C3'-O3'	6.60	119.40	109.50
1	2	819	G	C2'-C3'-O3'	6.57	119.35	109.50
83	BQ	3293	U	C4'-C3'-O3'	6.56	122.84	113.00
83	BQ	2256	A	C2'-C3'-O3'	6.53	119.30	109.50
83	BQ	1840	U	N1-C1'-C2'	6.50	121.75	112.00
83	BQ	374	A	C4'-C3'-O3'	6.50	119.15	109.40
83	BQ	1820	U	C2'-C3'-O3'	6.48	119.22	109.50
1	2	1474	G	C4'-C3'-O3'	-6.46	103.31	113.00
83	BQ	2243	A	C2'-C3'-O3'	-6.44	104.04	113.70
38	h	928	VAL	N-CA-C	6.43	113.09	106.21
83	BQ	3352	U	C2'-C3'-O3'	-6.41	104.08	113.70
1	2	1430	U	C2'-C3'-O3'	6.40	123.30	113.70
39	i	125	VAL	N-CA-C	6.40	122.64	109.34
31	d	131	ARG	N-CA-C	6.39	118.25	111.28
83	BQ	2112	U	C2'-C3'-O3'	6.39	119.08	109.50
83	BQ	2677	G	C4'-C3'-O3'	6.36	118.93	109.40
83	BQ	2803	A	C4'-C3'-O3'	6.35	122.52	113.00
1	2	157	A	N9-C1'-C2'	-6.35	102.48	112.00
58	AR	3	SER	N-CA-C	6.33	124.28	110.80
38	h	394	GLU	N-CA-C	6.31	117.85	110.97
21	T	198	ALA	N-CA-C	6.30	118.96	111.33
1	2	427	C	C1'-C2'-O2'	-6.30	98.96	108.40
1	2	1472	C	C4'-C3'-O3'	6.30	118.84	109.40
83	BQ	556	U	C4'-C3'-O3'	6.29	118.84	109.40
83	BQ	2541	U	C4'-C3'-O3'	6.29	118.83	109.40
83	BQ	1407	A	C4'-C3'-O3'	-6.27	103.60	113.00
1	2	429	G	C4'-C3'-O3'	-6.26	103.60	113.00
83	BQ	815	G	C2'-C3'-O3'	-6.25	104.32	113.70
83	BQ	1392	G	C4'-C3'-O3'	-6.24	103.64	113.00
1	2	1742	U	C2'-C3'-O3'	6.23	123.05	113.70
1	2	1369	U	C4'-C3'-O3'	6.20	118.69	109.40
1	2	1601	G	C2'-C3'-O3'	6.19	118.78	109.50
1	2	1412	G	C4'-C3'-O3'	6.18	118.67	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	e	10	ARG	N-CA-C	6.18	119.64	109.94
1	2	1765	A	C2'-C3'-O3'	-6.17	104.45	113.70
1	2	1573	A	C4'-C3'-O3'	6.16	118.64	109.40
46	AF	4	GLY	N-CA-C	6.16	115.81	110.21
39	i	533	GLN	N-CA-C	-6.13	106.47	112.97
1	2	1169	G	C2'-C3'-O3'	-6.13	104.51	113.70
1	2	159	U	C4'-C3'-O3'	6.12	118.58	109.40
1	2	387	A	C2'-C3'-O3'	6.12	118.68	109.50
1	2	1543	A	C3'-C2'-O2'	6.11	119.87	110.70
83	BQ	1840	U	C4'-C3'-O3'	-6.11	103.83	113.00
37	n	58	A	C2'-C3'-O3'	6.10	118.65	109.50
83	BQ	924	G	C4'-C3'-O3'	6.06	118.49	109.40
83	BQ	2970	C	N1-C1'-C2'	-6.04	102.93	112.00
83	BQ	2816	G	C2'-C3'-O3'	6.03	118.54	109.50
39	i	535	HIS	N-CA-C	6.03	118.34	111.11
83	BQ	1846	C	C2'-C3'-O3'	6.03	118.54	109.50
1	2	1251	U	C2'-C3'-O3'	6.01	122.71	113.70
83	BQ	2495	C	C2'-C3'-O3'	6.01	122.71	113.70
83	BQ	1558	A	C4'-C3'-O3'	-6.00	104.00	113.00
83	BQ	1839	A	C2'-C3'-O3'	6.00	122.69	113.70
1	2	381	C	N1-C1'-C2'	5.99	120.99	112.00
32	e	6	ALA	N-CA-C	5.98	123.54	110.80
11	J	73	GLY	N-CA-C	5.97	121.21	113.27
1	2	1636	C	C2'-C3'-O3'	5.96	118.45	109.50
83	BQ	1096	U	C4'-C3'-O3'	5.95	118.32	109.40
35	l	54	U	C4'-C3'-O3'	5.94	118.31	109.40
83	BQ	1751	G	C2'-C3'-O3'	5.94	122.61	113.70
83	BQ	2807	U	C4'-C3'-O3'	-5.93	104.10	113.00
83	BQ	2794	G	C2'-C3'-O3'	5.92	118.39	109.50
83	BQ	3172	A	C4'-C3'-O3'	5.89	118.23	109.40
42	AB	74	MET	N-CA-C	5.88	113.51	108.22
1	2	430	G	C3'-C2'-O2'	5.87	123.41	114.60
9	H	143	ARG	CA-C-N	5.87	132.76	121.54
9	H	143	ARG	C-N-CA	5.87	132.76	121.54
39	i	1001	PHE	N-CA-C	5.87	117.35	111.07
23	V	84	HIS	CA-C-N	5.86	127.17	119.84
23	V	84	HIS	C-N-CA	5.86	127.17	119.84
1	2	1791	A	C3'-C2'-O2'	5.86	119.49	110.70
1	2	224	C	C3'-C2'-O2'	5.85	119.48	110.70
83	BQ	3152	U	N1-C1'-C2'	5.85	120.77	112.00
83	BQ	767	U	C2'-C3'-O3'	5.85	118.27	109.50
83	BQ	2970	C	C4'-C3'-O3'	5.85	121.77	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	BQ	3140	G	C4'-C3'-O3'	-5.85	104.23	113.00
29	b	28	ARG	C-N-CD	-5.83	107.77	120.60
1	2	412	A	C3'-C2'-O2'	5.80	119.40	110.70
1	2	400	A	C2'-C3'-O3'	5.79	118.19	109.50
1	2	157	A	C4'-C3'-O3'	5.78	121.67	113.00
83	BQ	1729	A	C2'-C3'-O3'	5.78	118.17	109.50
83	BQ	1657	C	C2'-C3'-O3'	-5.78	105.03	113.70
83	BQ	2549	G	C2'-C3'-O3'	5.78	118.17	109.50
1	2	427	C	C4'-C3'-O3'	5.77	121.66	113.00
1	2	54	C	C3'-C2'-O2'	5.76	119.35	110.70
72	BF	142	ILE	N-CA-CB	5.76	118.37	110.54
83	BQ	2177	G	C4'-C3'-O3'	5.76	118.03	109.40
83	BQ	3156	U	C2'-C3'-O3'	5.75	122.33	113.70
1	2	280	U	C2'-C3'-O3'	5.74	118.12	109.50
1	2	52	U	O3'-P-O5'	-5.73	95.40	104.00
83	BQ	689	U	C2'-C3'-O3'	-5.73	105.10	113.70
83	BQ	1392	G	C2'-C3'-O3'	5.72	122.29	113.70
83	BQ	1417	G	C4'-C3'-O3'	5.72	121.58	113.00
1	2	696	C	C4'-C3'-O3'	5.72	121.58	113.00
83	BQ	3078	U	C2'-C3'-O3'	5.71	122.26	113.70
1	2	400	A	C4'-C3'-O3'	5.69	117.93	109.40
83	BQ	3219	G	C2'-C3'-O3'	5.68	122.22	113.70
1	2	1633	A	C4'-C3'-O3'	5.67	117.91	109.40
1	2	51	A	C4'-C3'-O3'	-5.66	100.92	109.40
83	BQ	400	G	C4'-C3'-O3'	5.64	121.46	113.00
83	BQ	1144	U	C4'-C3'-O3'	5.63	117.85	109.40
83	BQ	1816	A	C2'-C3'-O3'	5.63	117.95	109.50
1	2	1767	G	C4'-C3'-O3'	5.62	117.83	109.40
83	BQ	2593	A	C4'-C3'-O3'	5.61	117.82	109.40
83	BQ	2208	A	C3'-C2'-O2'	5.60	119.10	110.70
83	BQ	3179	U	C4'-C3'-O3'	5.60	117.80	109.40
83	BQ	2592	G	C4'-C3'-O3'	-5.60	104.60	113.00
1	2	132	U	C3'-C2'-O2'	5.59	119.09	110.70
83	BQ	935	U	C4'-C3'-O3'	-5.58	104.64	113.00
83	BQ	1695	U	C4'-C3'-O3'	-5.58	104.64	113.00
83	BQ	715	A	C4'-C3'-O3'	5.57	121.35	113.00
83	BQ	2178	A	C2'-C3'-O3'	5.57	117.85	109.50
83	BQ	2500	A	C2'-C3'-O3'	5.56	122.05	113.70
83	BQ	1482	A	C4'-C3'-O3'	5.56	117.74	109.40
1	2	928	U	C4'-C3'-O3'	5.55	117.73	109.40
1	2	139	C	C2'-C3'-O3'	5.55	117.83	109.50
1	2	1382	A	C2'-C3'-O3'	5.55	122.03	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	387	A	C4'-C3'-O3'	5.53	117.70	109.40
22	U	10	SER	N-CA-C	5.51	117.36	110.91
1	2	819	G	C4'-C3'-O3'	5.51	117.66	109.40
83	BQ	2981	U	C4'-C3'-O3'	-5.50	104.75	113.00
1	2	1244	A	C2'-C3'-O3'	5.49	121.93	113.70
83	BQ	223	U	C4'-C3'-O3'	-5.49	104.77	113.00
1	2	139	C	C4'-C3'-O3'	5.48	117.62	109.40
1	2	1114	G	C3'-C2'-O2'	5.48	118.92	110.70
83	BQ	2549	G	C4'-C3'-O3'	5.48	117.62	109.40
1	2	803	A	C4'-C3'-O3'	-5.48	104.78	113.00
1	2	1756	A	C2'-C3'-O3'	-5.47	105.50	113.70
83	BQ	3156	U	C3'-C2'-O2'	5.47	118.90	110.70
83	BQ	1455	U	C2'-C3'-O3'	-5.47	105.50	113.70
23	V	200	LYS	N-CA-C	5.46	126.30	111.00
83	BQ	349	A	C2'-C3'-O3'	5.46	117.69	109.50
1	2	68	A	C4'-C3'-O3'	5.45	121.18	113.00
1	2	803	A	C3'-C2'-O2'	5.45	118.87	110.70
1	2	1193	A	C4'-C3'-O3'	5.44	117.57	109.40
1	2	539	G	C2'-C3'-O3'	5.43	121.85	113.70
83	BQ	353	G	C2'-C3'-O3'	5.39	117.59	109.50
83	BQ	268	A	C4'-C3'-O3'	-5.36	104.95	113.00
1	2	1711	C	C2'-C3'-O3'	-5.36	105.66	113.70
72	BF	122	VAL	N-CA-C	5.36	115.50	110.30
1	2	1636	C	C4'-C3'-O3'	5.34	117.40	109.40
70	BD	169	LYS	N-CA-C	5.33	119.09	112.58
1	2	411	C	C3'-C2'-O2'	5.33	118.69	110.70
10	I	89	ARG	CA-C-N	5.33	126.50	119.84
10	I	89	ARG	C-N-CA	5.33	126.50	119.84
83	BQ	1538	G	C4'-C3'-O3'	-5.32	105.03	113.00
36	m	58	A	C4'-C3'-O3'	5.31	117.36	109.40
83	BQ	1900	A	C4'-C3'-O3'	5.30	117.35	109.40
83	BQ	3022	G	C4'-C3'-O3'	5.30	117.35	109.40
1	2	766	U	C2'-C3'-O3'	5.29	121.64	113.70
83	BQ	775	A	C4'-C3'-O3'	5.28	117.32	109.40
41	AA	164	VAL	N-CA-C	5.27	116.63	110.62
72	BF	142	ILE	CB-CA-C	-5.27	105.03	112.14
83	BQ	155	G	C2'-C3'-O3'	5.26	117.39	109.50
38	h	826	ILE	N-CA-C	5.26	115.88	110.36
1	2	1369	U	C2'-C3'-O3'	5.25	117.38	109.50
23	V	36	THR	N-CA-C	5.23	117.93	107.62
1	2	1791	A	C2'-C3'-O3'	5.22	121.54	113.70
83	BQ	3259	U	C2'-C3'-O3'	5.22	117.33	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	BQ	1064	A	C4'-C3'-O3'	5.22	117.23	109.40
1	2	705	U	C4'-C3'-O3'	5.21	120.82	113.00
1	2	174	U	C2'-C3'-O3'	5.21	121.52	113.70
57	AQ	93	LYS	N-CA-C	5.21	121.94	114.39
47	AG	117	ASP	CA-C-N	5.20	124.87	119.56
47	AG	117	ASP	C-N-CA	5.20	124.87	119.56
1	2	1193	A	C2'-C3'-O3'	5.20	117.30	109.50
83	BQ	2374	C	C4'-C3'-O3'	-5.18	105.22	113.00
83	BQ	953	G	C4'-C3'-O3'	-5.17	105.25	113.00
83	BQ	800	G	C2'-C3'-O3'	-5.17	105.95	113.70
83	BQ	1580	A	C3'-C2'-O2'	5.16	118.44	110.70
83	BQ	679	U	C4'-C3'-O3'	-5.15	105.27	113.00
83	BQ	2256	A	C4'-C3'-O3'	5.15	117.12	109.40
1	2	430	G	C2'-C3'-O3'	-5.15	101.78	109.50
83	BQ	3175	U	C2'-C3'-O3'	5.15	121.42	113.70
85	BS	19	C	C4'-C3'-O3'	-5.15	105.28	113.00
83	BQ	1113	G	C4'-C3'-O3'	-5.14	105.28	113.00
36	m	51	A	C3'-C2'-O2'	5.14	118.41	110.70
1	2	1573	A	C2'-C3'-O3'	5.14	117.21	109.50
1	2	411	C	C4'-C3'-O3'	5.12	120.68	113.00
1	2	1458	G	C2'-C3'-O3'	-5.12	106.02	113.70
83	BQ	1317	A	C4'-C3'-O3'	-5.12	105.32	113.00
83	BQ	2158	A	C2'-C3'-O3'	5.12	117.18	109.50
83	BQ	1103	A	C2'-C3'-O3'	5.12	117.18	109.50
83	BQ	3078	U	N1-C1'-C2'	5.10	119.65	112.00
83	BQ	2949	U	C4'-C3'-O3'	-5.10	105.35	113.00
39	i	147	GLN	N-CA-C	5.09	121.64	110.80
83	BQ	268	A	N9-C1'-C2'	5.09	119.63	112.00
23	V	83	TYR	N-CA-C	5.08	121.63	110.80
1	2	555	A	C2'-C3'-O3'	5.08	121.32	113.70
1	2	555	A	C3'-C2'-O2'	5.08	118.32	110.70
37	n	16	U	C2'-C3'-O3'	-5.08	106.08	113.70
70	BD	154	ALA	N-CA-C	5.08	116.89	111.36
31	d	118	ILE	N-CA-C	5.08	115.43	108.12
36	m	65	C	C2'-C3'-O3'	5.07	121.31	113.70
1	2	330	G	C3'-C2'-O2'	5.05	118.28	110.70
1	2	1273	G	C4'-C3'-O3'	5.05	116.97	109.40
37	n	17	C	N1-C1'-C2'	5.04	119.57	112.00
20	S	194	THR	N-CA-C	5.04	121.54	110.80
83	BQ	637	C	C4'-C3'-O3'	-5.04	105.44	113.00
63	AW	10	LYS	N-CA-C	5.04	118.20	111.75
1	2	313	U	C4'-C3'-O3'	5.03	116.95	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1226	A	C2'-C3'-O3'	5.03	121.25	113.70
83	BQ	2138	A	C2'-C3'-O3'	-5.03	106.15	113.70
83	BQ	1750	A	C4'-C3'-O3'	5.02	116.93	109.40
83	BQ	282	G	C3'-C2'-O2'	5.01	118.22	110.70
22	U	8	ILE	N-CA-C	5.01	115.96	111.90
83	BQ	1926	C	C4'-C3'-O3'	5.01	116.91	109.40
83	BQ	3179	U	C2'-C3'-O3'	5.00	117.01	109.50

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
57	AQ	202	TYR	Peptide
58	AR	3	SER	Peptide
58	AR	5	PHE	Peptide
63	AW	250	GLN	Peptide
69	BC	12	TYR	Peptide
70	BD	171	GLY	Peptide
86	BT	76	SER	Peptide
9	H	143	ARG	Peptide
10	I	88	VAL	Peptide
10	I	89	ARG	Peptide
21	T	196	ARG	Peptide
21	T	197	ASN	Peptide
22	U	64	VAL	Peptide
23	V	33	PRO	Peptide
23	V	82	VAL	Peptide
23	V	84	HIS	Peptide
32	e	5	ARG	Peptide
32	e	6	ALA	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37645	0	18938	405	0
2	A	1734	0	1817	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1609	0	1675	18	0
4	C	813	0	800	9	0
5	D	877	0	883	8	0
6	E	977	0	1002	7	0
7	F	1105	0	1166	14	0
8	G	746	0	781	11	0
9	H	1192	0	1220	50	0
10	I	1112	0	1124	12	0
11	J	855	0	917	8	0
12	K	563	0	603	9	0
13	L	497	0	535	2	0
14	M	442	0	428	2	0
15	N	397	0	399	2	0
16	O	2436	0	2386	12	0
17	P	1577	0	1567	4	0
18	Q	1709	0	1784	10	0
19	R	1671	0	1768	13	0
20	S	2068	0	2154	15	0
21	T	1799	0	1879	43	0
22	U	1481	0	1572	16	0
23	V	1489	0	1525	35	0
24	W	1434	0	1511	8	0
25	X	1213	0	1257	7	0
26	Y	1192	0	1255	8	0
27	Z	891	0	883	4	0
28	a	684	0	672	3	0
29	b	1021	0	1060	4	0
30	c	1121	0	1196	10	0
31	d	1060	0	1123	33	0
32	e	769	0	818	5	0
33	f	610	0	633	1	0
34	g	473	0	518	1	0
35	l	692	0	347	5	0
36	m	1611	0	817	55	0
37	n	1644	0	831	65	0
38	h	8814	0	8710	45	0
39	i	9827	0	8617	109	0
40	j	2933	0	2695	21	0
40	k	2919	0	2682	17	0
41	AA	1804	0	1877	14	0
42	AB	1003	0	1048	12	0
43	AC	771	0	849	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	AD	1518	0	1587	14	0
45	AE	699	0	638	38	0
46	AF	681	0	684	8	0
47	AG	1353	0	1381	43	0
48	AH	964	0	1025	4	0
49	AI	612	0	682	1	0
50	AJ	1543	0	1608	8	0
51	AK	993	0	1081	5	0
52	AL	436	0	475	2	0
53	AM	1053	0	1149	4	0
54	AN	1092	0	1155	9	0
55	AO	417	0	459	1	0
56	AP	847	0	918	35	0
57	AQ	1720	0	1779	15	0
58	AR	1173	0	1215	13	0
59	AS	233	0	282	57	0
60	AT	694	0	738	11	0
61	AU	1555	0	1659	3	0
62	AV	462	0	491	2	0
63	AW	1914	0	1980	53	0
64	AX	1420	0	1437	15	0
65	AY	742	0	797	4	0
66	AZ	1050	0	245	1	0
67	BA	3075	0	3142	35	0
68	BB	1441	0	1543	18	0
69	BC	876	0	912	10	0
70	BD	1770	0	1808	27	0
71	BE	2748	0	2859	18	0
72	BF	1521	0	1611	72	0
73	BG	1020	0	1090	5	0
74	BH	1445	0	1487	10	0
75	BI	2375	0	2325	15	0
76	BJ	1276	0	1323	7	0
77	BK	850	0	880	8	0
78	BL	796	0	812	2	0
79	BM	1239	0	1326	11	0
80	BN	880	0	945	5	0
81	BO	1784	0	1862	13	0
82	BP	969	0	1078	5	0
83	BQ	67695	0	34019	506	0
84	BR	2579	0	1304	16	0
85	BS	3352	0	1695	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	BT	1143	0	1103	99	0
All	All	229285	0	172911	1849	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 5.

All (1849) 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)
83:BQ:2418:G:C2	86:BT:73:LEU:HD11	1.29	1.63
39:i:147:GLN:NE2	39:i:177:LEU:CD1	1.68	1.52
31:d:125:LEU:CB	31:d:128:LYS:HE2	1.41	1.49
1:2:1645:G:C5'	83:BQ:2255:A:N6	1.76	1.47
1:2:815:G:N3	72:BF:162:ARG:CZ	1.82	1.42
56:AP:27:GLN:HE22	86:BT:14:GLY:N	1.03	1.40
39:i:151:PRO:C	39:i:230:ILE:HD12	1.46	1.39
39:i:151:PRO:C	39:i:230:ILE:CD1	1.96	1.39
1:2:987:G:C6	63:AW:249:SER:HA	1.58	1.38
31:d:125:LEU:HB3	31:d:128:LYS:CE	1.53	1.38
1:2:55:A:C2	1:2:403:G:N3	1.91	1.37
1:2:55:A:H2	1:2:403:G:C2	1.43	1.36
1:2:813:U:C1'	72:BF:163:ARG:NH1	1.71	1.36
39:i:147:GLN:NE2	39:i:177:LEU:HD11	1.29	1.36
9:H:16:ARG:NH1	47:AG:110:ILE:C	1.84	1.35
1:2:1645:G:H5''	83:BQ:2255:A:N6	1.03	1.34
1:2:815:G:N3	72:BF:162:ARG:NH2	1.74	1.33
1:2:1724:U:H4'	45:AE:47:ARG:NH2	1.43	1.33
36:m:53:G:O5'	70:BD:73:LYS:HD2	1.17	1.32
1:2:815:G:C2	72:BF:162:ARG:NH2	1.97	1.31
1:2:987:G:N1	63:AW:249:SER:HA	1.42	1.30
9:H:16:ARG:HH12	47:AG:111:ASP:N	1.29	1.30
1:2:987:G:C2	63:AW:249:SER:CA	2.15	1.29
37:n:74:C:N3	83:BQ:2621:G:C2	2.00	1.29
1:2:55:A:C2	1:2:403:G:C2	2.19	1.28
1:2:850:A:OP1	72:BF:165:LYS:NZ	1.65	1.28
21:T:151:ASP:OD2	45:AE:98:PRO:HG3	1.17	1.27
56:AP:27:GLN:NE2	86:BT:14:GLY:N	1.80	1.27
1:2:1779:U:O4	59:AS:12:ARG:NH1	1.66	1.26
1:2:1735:U:P	42:AB:32:ARG:HH12	1.58	1.25
83:BQ:2418:G:C2	86:BT:73:LEU:CD1	2.18	1.25
1:2:987:G:C2	63:AW:249:SER:N	2.05	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:BT:132:LYS:HB3	86:BT:152:GLU:OE2	1.14	1.23
39:i:151:PRO:O	39:i:230:ILE:CD1	1.86	1.23
1:2:1595:U:O4	1:2:1600:A:N1	1.71	1.23
21:T:9:VAL:CG1	45:AE:78:ALA:HB3	1.70	1.22
1:2:55:A:H2	1:2:403:G:N3	1.26	1.21
1:2:1080:U:O4	1:2:1091:A:N1	1.71	1.21
1:2:813:U:C2'	72:BF:163:ARG:NH1	2.03	1.20
21:T:22:HIS:NE2	67:BA:298:PHE:CD1	2.10	1.20
36:m:53:G:OP1	70:BD:73:LYS:CE	1.89	1.20
39:i:143:LYS:HG3	39:i:176:ILE:HA	1.24	1.20
1:2:1784:C:C5	59:AS:5:TRP:CZ2	2.10	1.19
39:i:151:PRO:O	39:i:230:ILE:HD11	1.41	1.18
36:m:74:C:C5	83:BQ:2924:U:C4	2.31	1.18
1:2:1118:G:P	59:AS:21:ARG:HH12	1.67	1.17
1:2:1724:U:C4'	45:AE:47:ARG:HH22	1.58	1.16
83:BQ:2433:U:O4	83:BQ:2595:A:N1	1.79	1.16
1:2:42:G:C2'	1:2:430:G:O6	1.93	1.16
36:m:53:G:P	70:BD:73:LYS:HD2	1.87	1.15
1:2:1642:G:H4'	59:AS:1:MET:SD	1.85	1.15
1:2:815:G:C1'	72:BF:162:ARG:NH1	2.07	1.14
83:BQ:1554:U:O4	83:BQ:1559:A:N1	1.79	1.14
1:2:1735:U:OP1	42:AB:32:ARG:NH1	1.80	1.13
37:n:20:U:O5'	47:AG:55:ARG:NH1	1.81	1.13
1:2:42:G:H2'	1:2:430:G:O6	0.97	1.13
39:i:147:GLN:NE2	39:i:177:LEU:HD12	1.50	1.13
1:2:816:G:N7	72:BF:170:ARG:NH2	1.96	1.12
1:2:153:G:C8	31:d:124:ARG:NH1	2.19	1.11
21:T:130:PRO:HA	45:AE:83:THR:CB	1.80	1.11
36:m:74:C:C6	83:BQ:2924:U:N3	2.19	1.10
9:H:120:ARG:HE	83:BQ:1025:A:H1'	1.16	1.09
86:BT:132:LYS:CB	86:BT:152:GLU:OE2	1.91	1.09
22:U:39:ARG:CZ	72:BF:181:ARG:O	1.99	1.09
37:n:74:C:N3	83:BQ:2621:G:N2	2.00	1.09
21:T:131:LYS:O	45:AE:83:THR:O	1.70	1.08
21:T:9:VAL:HG11	45:AE:78:ALA:CB	1.84	1.07
1:2:971:A:H61	83:BQ:846:A:N6	1.51	1.07
1:2:1057:U:O4	1:2:1062:A:N1	1.88	1.07
83:BQ:2418:G:N2	86:BT:73:LEU:HD11	1.67	1.07
21:T:22:HIS:NE2	67:BA:298:PHE:HD1	1.49	1.06
83:BQ:829:U:N3	83:BQ:895:A:N6	2.03	1.06
39:i:143:LYS:HG3	39:i:176:ILE:CA	1.83	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:125:LEU:HG	31:d:128:LYS:HZ3	1.18	1.06
1:2:1757:G:O2'	83:BQ:2255:A:O2'	1.73	1.06
1:2:815:G:H1'	72:BF:162:ARG:NH1	1.69	1.05
1:2:1585:U:C4	1:2:1611:A:N1	2.24	1.05
21:T:130:PRO:CA	45:AE:83:THR:CB	2.34	1.04
1:2:1784:C:H5	59:AS:5:TRP:CZ2	1.42	1.04
56:AP:64:THR:O	86:BT:17:ALA:CB	2.06	1.04
83:BQ:1554:U:C4	83:BQ:1559:A:N1	2.26	1.04
1:2:814:A:C2	72:BF:170:ARG:NH1	2.26	1.04
1:2:42:G:H2'	1:2:430:G:C6	1.93	1.03
1:2:850:A:H5''	72:BF:165:LYS:HZ1	1.20	1.03
1:2:850:A:H5''	72:BF:165:LYS:NZ	1.72	1.03
1:2:987:G:C2	63:AW:249:SER:HA	1.83	1.03
1:2:1735:U:P	42:AB:32:ARG:NH1	2.31	1.03
1:2:813:U:H1'	72:BF:163:ARG:NH1	1.68	1.03
1:2:971:A:N6	83:BQ:846:A:N6	2.04	1.03
36:m:53:G:OP1	70:BD:73:LYS:NZ	1.93	1.02
1:2:987:G:N2	63:AW:248:GLY:C	2.18	1.01
31:d:125:LEU:HG	31:d:128:LYS:NZ	1.75	1.00
38:h:27:GLU:O	40:j:37:TYR:OH	1.79	1.00
83:BQ:3047:U:C4	83:BQ:3094:A:N1	2.28	1.00
83:BQ:2418:G:N1	86:BT:73:LEU:CD1	2.24	1.00
1:2:1645:G:C5'	83:BQ:2255:A:C6	2.44	0.99
36:m:53:G:O5'	70:BD:73:LYS:CD	2.10	0.99
56:AP:27:GLN:HE22	86:BT:13:ALA:C	1.69	0.99
21:T:151:ASP:OD2	45:AE:98:PRO:CG	2.09	0.99
1:2:913:G:C6	83:BQ:2207:A:O2'	2.13	0.99
37:n:12:U:H1'	83:BQ:2266:U:O2'	1.63	0.99
1:2:1080:U:C4	1:2:1091:A:N1	2.30	0.98
83:BQ:1188:U:N3	83:BQ:1317:A:N6	2.10	0.98
1:2:816:G:O6	72:BF:170:ARG:NH2	1.95	0.98
83:BQ:2612:U:N3	83:BQ:2804:A:N6	2.10	0.98
1:2:1724:U:H4'	45:AE:47:ARG:HH22	0.91	0.98
83:BQ:2966:G:O6	86:BT:56:LYS:NZ	1.97	0.98
1:2:1038:U:O4	1:2:1092:A:N1	1.96	0.97
1:2:816:G:C6	72:BF:170:ARG:NH2	2.32	0.97
36:m:53:G:OP1	70:BD:73:LYS:HE2	1.63	0.97
1:2:55:A:N3	1:2:403:G:N2	2.13	0.97
1:2:814:A:N3	72:BF:170:ARG:NH1	2.12	0.96
1:2:815:G:C4	72:BF:162:ARG:CZ	2.48	0.95
21:T:22:HIS:NE2	67:BA:298:PHE:CE1	2.33	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:913:G:C5	83:BQ:2207:A:O2'	2.17	0.95
36:m:74:C:C5	83:BQ:2924:U:N3	2.33	0.95
39:i:151:PRO:CA	39:i:230:ILE:HD12	1.94	0.95
1:2:1585:U:O4	1:2:1611:A:N1	1.99	0.95
21:T:131:LYS:HE2	45:AE:81:PRO:HA	1.47	0.95
39:i:143:LYS:CG	39:i:176:ILE:CB	2.43	0.95
56:AP:64:THR:O	86:BT:17:ALA:HB3	1.64	0.94
1:2:987:G:N2	63:AW:249:SER:N	2.16	0.94
1:2:1012:U:H4'	63:AW:247:ARG:HB3	1.48	0.94
83:BQ:2612:U:N3	83:BQ:2804:A:C6	2.36	0.94
1:2:153:G:N7	31:d:124:ARG:NH1	2.15	0.94
1:2:987:G:H2'	63:AW:249:SER:CB	1.98	0.94
1:2:816:G:C5	72:BF:170:ARG:NH2	2.30	0.93
36:m:74:C:C2	83:BQ:2924:U:C2	2.57	0.93
9:H:16:ARG:HH12	47:AG:110:ILE:C	1.57	0.93
1:2:815:G:C1'	72:BF:162:ARG:HH11	1.80	0.93
9:H:16:ARG:HH11	47:AG:110:ILE:C	1.69	0.93
1:2:1645:G:H5''	83:BQ:2255:A:H62	1.12	0.92
1:2:1080:U:O4	1:2:1091:A:C2	2.23	0.92
1:2:1783:C:C5	59:AS:5:TRP:CD2	2.58	0.92
1:2:1645:G:H5''	83:BQ:2255:A:H61	1.10	0.92
56:AP:27:GLN:HE22	86:BT:14:GLY:H	1.11	0.92
83:BQ:1188:U:O4	83:BQ:1317:A:N1	2.02	0.92
1:2:1118:G:OP1	59:AS:21:ARG:NH1	2.03	0.91
1:2:850:A:C5'	72:BF:165:LYS:HZ1	1.84	0.91
1:2:55:A:OP2	31:d:113:ASN:ND2	2.04	0.91
83:BQ:2418:G:N1	86:BT:73:LEU:HD11	1.83	0.91
39:i:151:PRO:CB	39:i:230:ILE:HD12	2.01	0.91
83:BQ:3047:U:C5	83:BQ:3094:A:C2	2.58	0.91
36:m:76:A:O2'	83:BQ:2954:U:C5	2.24	0.91
9:H:16:ARG:NH1	47:AG:110:ILE:HG13	1.86	0.91
1:2:813:U:H2'	72:BF:163:ARG:NH1	1.82	0.90
36:m:76:A:N1	83:BQ:2952:G:O2'	2.04	0.90
1:2:55:A:O2'	1:2:56:U:OP1	1.90	0.90
9:H:16:ARG:NH1	47:AG:111:ASP:N	2.06	0.89
39:i:147:GLN:HE21	39:i:177:LEU:CD1	1.85	0.89
31:d:125:LEU:CB	31:d:128:LYS:CE	2.30	0.89
21:T:9:VAL:HG11	45:AE:78:ALA:HB3	0.92	0.89
21:T:131:LYS:N	45:AE:83:THR:CB	2.36	0.89
39:i:151:PRO:HB2	39:i:230:ILE:HD12	1.52	0.89
9:H:120:ARG:NE	83:BQ:1025:A:HI'	1.88	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:131:LYS:CE	45:AE:81:PRO:HA	2.03	0.88
56:AP:27:GLN:NE2	86:BT:14:GLY:CA	2.36	0.88
1:2:1772:C:H3'	59:AS:2:ARG:HH21	1.39	0.88
1:2:987:G:N1	63:AW:249:SER:CA	2.23	0.88
1:2:1185:U:O2'	1:2:1186:U:OP2	1.92	0.88
1:2:815:G:C4	72:BF:162:ARG:NH2	2.42	0.87
1:2:1038:U:C4	1:2:1092:A:N1	2.42	0.87
1:2:1126:G:C5'	59:AS:11:ARG:NH1	2.37	0.87
1:2:1311:U:HO2'	8:G:2:GLY:N	1.72	0.87
1:2:1783:C:H5	59:AS:5:TRP:CG	1.92	0.87
1:2:851:U:P	72:BF:165:LYS:HE3	2.15	0.87
36:m:74:C:C4	83:BQ:2924:U:C6	2.63	0.87
37:n:74:C:C2	83:BQ:2621:G:N2	2.42	0.87
39:i:143:LYS:HG3	39:i:176:ILE:CB	2.04	0.87
3:B:123:VAL:HG21	12:K:100:ILE:HD11	1.54	0.86
1:2:813:U:C2'	72:BF:163:ARG:HH11	1.83	0.86
1:2:1783:C:C5	59:AS:5:TRP:CG	2.63	0.86
1:2:987:G:C6	63:AW:249:SER:CA	2.53	0.86
36:m:72:C:HO2'	70:BD:104:CYS:HG	1.21	0.86
1:2:1126:G:H5'	59:AS:11:ARG:NH1	1.91	0.86
1:2:1660:A:H5'	42:AB:67:PRO:HG2	1.58	0.85
21:T:130:PRO:C	45:AE:83:THR:CB	2.48	0.85
83:BQ:2418:G:N2	86:BT:73:LEU:HD21	1.91	0.85
1:2:971:A:C6	83:BQ:846:A:N6	2.44	0.85
1:2:1113:A:H5''	59:AS:6:ARG:HH22	1.40	0.85
38:h:26:VAL:O	38:h:28:LEU:N	2.08	0.85
83:BQ:816:A:O2'	83:BQ:819:U:O4	1.94	0.85
56:AP:64:THR:O	86:BT:17:ALA:HB2	1.75	0.84
1:2:1757:G:HO2'	83:BQ:2255:A:HO2'	1.13	0.84
39:i:506:SER:HB2	39:i:510:ALA:HB3	1.59	0.84
37:n:56:C:C4	56:AP:104:LEU:HD22	2.13	0.84
1:2:1126:G:H4'	59:AS:11:ARG:HH12	1.40	0.84
1:2:1118:G:P	59:AS:21:ARG:NH1	2.51	0.84
83:BQ:2612:U:O2	83:BQ:2804:A:N7	2.11	0.83
1:2:1595:U:C4	1:2:1600:A:N1	2.46	0.83
1:2:1642:G:C4'	59:AS:1:MET:SD	2.65	0.83
1:2:987:G:H2'	63:AW:249:SER:HB3	1.59	0.83
1:2:1780:G:H1'	83:BQ:2262:A:O3'	1.79	0.83
37:n:12:U:HO2'	83:BQ:2266:U:HO2'	1.06	0.83
21:T:22:HIS:CD2	67:BA:298:PHE:CD1	2.66	0.83
21:T:22:HIS:CD2	67:BA:298:PHE:CE1	2.67	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:534:VAL:HG21	39:i:544:VAL:HG21	1.60	0.83
31:d:125:LEU:CA	31:d:128:LYS:HE2	2.08	0.82
1:2:1645:G:H5'	83:BQ:2255:A:N6	1.94	0.82
36:m:38:A:H5'	83:BQ:2256:A:C6	2.14	0.82
67:BA:305:ILE:HD11	67:BA:317:ILE:HG21	1.60	0.82
83:BQ:2612:U:C4	83:BQ:2804:A:N6	2.47	0.82
37:n:56:C:C4	56:AP:104:LEU:CD2	2.63	0.82
1:2:815:G:H1'	72:BF:162:ARG:HH11	1.37	0.82
22:U:39:ARG:NH2	72:BF:181:ARG:O	2.10	0.82
21:T:151:ASP:CG	45:AE:98:PRO:HG3	2.04	0.82
23:V:162:ALA:HA	83:BQ:3353:G:OP2	1.80	0.82
1:2:55:A:H2	1:2:403:G:C4	1.98	0.82
37:n:75:C:N3	83:BQ:2620:G:N2	2.27	0.82
1:2:987:G:C2	63:AW:248:GLY:C	2.55	0.81
36:m:53:G:P	70:BD:73:LYS:CD	2.69	0.81
37:n:12:U:C2'	83:BQ:2266:U:HO2'	1.93	0.81
9:H:16:ARG:HH11	47:AG:110:ILE:CB	1.94	0.81
26:Y:22:ALA:HB1	26:Y:23:PRO:HA	1.62	0.81
3:B:94:THR:HG22	3:B:114:ILE:HG13	1.63	0.81
31:d:125:LEU:HB3	31:d:128:LYS:HE2	0.82	0.81
56:AP:27:GLN:OE1	86:BT:12:ASP:O	1.99	0.80
83:BQ:1554:U:O4	83:BQ:1559:A:C2	2.35	0.80
37:n:56:C:C1'	47:AG:61:ARG:HD2	2.12	0.80
4:C:11:ILE:HD11	4:C:42:VAL:HG22	1.63	0.80
9:H:120:ARG:HE	83:BQ:1025:A:C1'	1.95	0.80
38:h:972:MET:HE3	38:h:996:ILE:HD11	1.63	0.79
83:BQ:2418:G:N1	86:BT:73:LEU:HD12	1.95	0.79
1:2:1724:U:H4'	45:AE:47:ARG:CZ	2.11	0.79
39:i:511:LYS:HE3	39:i:533:GLN:HB3	1.64	0.79
1:2:853:G:N7	72:BF:173:ARG:NH2	2.30	0.79
36:m:74:C:C2	83:BQ:2924:U:O2	2.36	0.79
1:2:1645:G:C4'	83:BQ:2255:A:C6	2.66	0.79
21:T:131:LYS:CD	45:AE:81:PRO:HA	2.12	0.79
37:n:20:U:C5'	47:AG:55:ARG:NH1	2.45	0.78
1:2:1113:A:H5''	59:AS:6:ARG:NH2	1.96	0.78
37:n:75:C:N3	83:BQ:2620:G:C2	2.51	0.78
1:2:1783:C:N4	59:AS:5:TRP:CE3	2.52	0.78
1:2:55:A:C2	1:2:403:G:C4	2.72	0.78
9:H:16:ARG:HH11	47:AG:110:ILE:HB	1.49	0.78
1:2:815:G:N9	72:BF:162:ARG:NH1	2.32	0.78
1:2:1660:A:H5'	42:AB:67:PRO:CG	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:15:ILE:HG23	10:I:59:ALA:HB3	1.65	0.77
37:n:56:C:H5'	47:AG:61:ARG:NH1	1.99	0.77
1:2:813:U:H2'	72:BF:163:ARG:HH11	1.42	0.77
36:m:74:C:N4	83:BQ:2924:U:C6	2.53	0.77
83:BQ:1524:A:O2'	83:BQ:1526:U:OP2	2.02	0.77
1:2:1642:G:C5'	59:AS:1:MET:SD	2.73	0.77
31:d:125:LEU:CG	31:d:128:LYS:HE2	2.15	0.77
37:n:74:C:N4	83:BQ:2621:G:N1	2.33	0.76
9:H:16:ARG:NH1	47:AG:110:ILE:CG1	2.48	0.76
31:d:125:LEU:HB3	31:d:128:LYS:HE3	1.64	0.76
1:2:1779:U:O4	59:AS:12:ARG:CZ	2.33	0.76
36:m:74:C:C5	83:BQ:2924:U:C5	2.74	0.76
83:BQ:1084:A:H2'	83:BQ:1085:A:C8	2.21	0.76
83:BQ:2273:G:O2'	83:BQ:2274:U:OP2	2.04	0.76
36:m:74:C:C6	83:BQ:2924:U:C2	2.73	0.76
58:AR:138:ILE:HD13	58:AR:145:VAL:HG22	1.66	0.75
1:2:815:G:C4	72:BF:162:ARG:NH1	2.55	0.75
1:2:1641:C:H4'	59:AS:1:MET:H2	1.52	0.75
86:BT:90:TYR:CE1	86:BT:104:ASN:OD1	2.39	0.75
1:2:815:G:N2	72:BF:162:ARG:HH21	1.85	0.75
36:m:74:C:C4	83:BQ:2924:U:C2	2.75	0.74
36:m:76:A:H2	83:BQ:2952:G:N3	1.84	0.74
1:2:1114:G:OP1	59:AS:6:ARG:NH1	2.19	0.74
83:BQ:2806:U:OP1	86:BT:49:THR:OG1	2.03	0.74
1:2:1656:U:HO2'	83:BQ:2292:U:HO2'	1.28	0.74
6:E:108:ARG:NH2	83:BQ:1025:A:C2	2.55	0.74
56:AP:64:THR:HG21	86:BT:19:TYR:HB3	1.69	0.74
37:n:24:A:O2'	83:BQ:2266:U:OP1	2.04	0.74
36:m:74:C:C4	83:BQ:2924:U:N1	2.56	0.74
37:n:56:C:H1'	47:AG:61:ARG:HD2	1.70	0.74
39:i:152:GLY:N	39:i:230:ILE:HD12	2.03	0.74
29:b:93:LEU:HD11	29:b:102:VAL:HG22	1.70	0.74
37:n:4:G:H4'	86:BT:27:ARG:NH2	2.02	0.74
1:2:153:G:N7	31:d:124:ARG:CZ	2.50	0.74
1:2:1038:U:H3	1:2:1092:A:N6	1.85	0.74
83:BQ:12:A:H2'	83:BQ:13:A:C8	2.22	0.74
1:2:157:A:H5''	31:d:130:ALA:HB1	1.69	0.73
1:2:300:A:H2'	1:2:301:A:C8	2.23	0.73
9:H:16:ARG:HH12	47:AG:111:ASP:CA	2.01	0.73
9:H:16:ARG:NH1	47:AG:110:ILE:CB	2.50	0.73
36:m:76:A:O2'	83:BQ:2954:U:C4	2.40	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:55:A:C2	1:2:403:G:N2	2.53	0.73
1:2:853:G:C8	72:BF:173:ARG:NH2	2.57	0.73
23:V:81:VAL:O	23:V:94:ASN:HA	1.89	0.73
86:BT:133:ASP:O	86:BT:152:GLU:HG3	1.88	0.73
1:2:850:A:C5'	72:BF:165:LYS:NZ	2.47	0.73
1:2:1750:A:P	59:AS:13:LEU:HD11	2.29	0.73
1:2:1645:G:C4'	83:BQ:2255:A:N6	2.50	0.73
1:2:1641:C:H4'	59:AS:1:MET:N	2.04	0.73
36:m:63:U:O2'	83:BQ:2852:C:H5'	1.89	0.73
67:BA:53:MET:HE2	67:BA:77:THR:HG22	1.70	0.73
39:i:1057:LEU:HD21	39:i:1089:ALA:HB3	1.71	0.73
63:AW:113:VAL:HG12	63:AW:166:ILE:HD13	1.71	0.72
1:2:1775:U:O4	59:AS:4:LYS:HE2	1.88	0.72
1:2:1118:G:OP2	59:AS:21:ARG:NH2	2.22	0.72
9:H:19:ASN:HA	47:AG:111:ASP:OD2	1.89	0.72
21:T:131:LYS:HE2	45:AE:81:PRO:CA	2.19	0.72
39:i:170:LEU:HD11	39:i:228:VAL:HA	1.72	0.72
36:m:38:A:H4'	83:BQ:2256:A:N6	2.04	0.72
1:2:1080:U:O4	1:2:1091:A:C6	2.42	0.72
31:d:125:LEU:CG	31:d:128:LYS:CE	2.68	0.72
56:AP:41:ARG:NH1	83:BQ:284:A:OP2	2.23	0.72
1:2:813:U:C5	72:BF:163:ARG:CD	2.72	0.72
1:2:851:U:C5'	72:BF:172:ARG:HH22	2.03	0.72
39:i:143:LYS:HG2	39:i:176:ILE:CB	2.18	0.72
86:BT:43:ASP:HB2	86:BT:60:VAL:HB	1.72	0.72
1:2:987:G:C5	63:AW:249:SER:HA	1.94	0.72
1:2:815:G:N3	72:BF:162:ARG:NE	2.37	0.71
1:2:1481:C:OP2	10:I:4:VAL:HA	1.91	0.71
1:2:1734:U:OP1	42:AB:32:ARG:NH2	2.24	0.71
9:H:118:LYS:O	83:BQ:1025:A:C2	2.43	0.71
37:n:56:C:C5'	47:AG:61:ARG:NH1	2.52	0.71
39:i:143:LYS:CG	39:i:176:ILE:HA	2.13	0.71
86:BT:155:ARG:C	86:BT:156:THR:HG23	2.16	0.71
7:F:44:LEU:HD11	7:F:75:VAL:HG22	1.73	0.71
1:2:1012:U:H4'	63:AW:247:ARG:CB	2.21	0.71
1:2:1773:C:OP2	59:AS:4:LYS:HB2	1.91	0.71
1:2:913:G:N1	83:BQ:2207:A:H1'	2.06	0.71
23:V:91:VAL:CG2	23:V:95:THR:HG21	2.20	0.71
41:AA:160:ILE:HG22	41:AA:164:VAL:HG13	1.73	0.71
83:BQ:3152:U:O2	83:BQ:3152:U:H2'	1.89	0.71
1:2:815:G:H1'	72:BF:162:ARG:CZ	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:851:U:OP2	72:BF:165:LYS:HE3	1.90	0.70
1:2:851:U:OP1	72:BF:165:LYS:HE3	1.89	0.70
1:2:1038:U:N3	1:2:1092:A:N6	2.38	0.70
8:G:20:TYR:CG	8:G:38:ILE:HD11	2.25	0.70
21:T:131:LYS:HD3	45:AE:81:PRO:N	2.07	0.70
1:2:987:G:H22	63:AW:248:GLY:C	1.97	0.70
86:BT:111:ASP:O	86:BT:112:ASP:O	2.09	0.70
1:2:853:G:P	72:BF:176:ARG:HE	2.14	0.70
41:AA:152:LEU:HD23	41:AA:178:ALA:HB3	1.73	0.70
36:m:76:A:C2	83:BQ:2952:G:N3	2.58	0.70
1:2:1116:A:OP2	59:AS:14:LYS:NZ	2.25	0.69
37:n:12:U:C1'	83:BQ:2266:U:O2'	2.38	0.69
9:H:16:ARG:NH1	47:AG:110:ILE:O	2.23	0.69
38:h:417:LEU:HD12	38:h:434:LEU:HD22	1.74	0.69
1:2:987:G:C2'	63:AW:249:SER:CB	2.71	0.69
1:2:1645:G:H5'	83:BQ:2255:A:C6	2.26	0.69
74:BH:77:VAL:HG13	74:BH:126:VAL:HG22	1.73	0.69
19:R:53:ILE:HD11	19:R:73:LEU:HB2	1.74	0.69
21:T:151:ASP:OD1	45:AE:98:PRO:HB3	1.93	0.69
31:d:125:LEU:CG	31:d:128:LYS:NZ	2.54	0.69
67:BA:215:ILE:HG21	67:BA:282:ILE:HD11	1.74	0.69
39:i:64:GLU:HG2	39:i:100:ILE:HD12	1.75	0.69
1:2:1724:U:C4'	45:AE:47:ARG:NH2	2.31	0.69
67:BA:46:PHE:CE2	67:BA:81:THR:HG23	2.28	0.68
1:2:1643:U:H5'	59:AS:9:ARG:HH12	1.58	0.68
86:BT:101:SER:HA	86:BT:111:ASP:HA	1.75	0.68
2:A:208:ILE:HD12	8:G:16:LEU:HD21	1.76	0.68
37:n:12:U:C1'	83:BQ:2266:U:HO2'	2.07	0.68
56:AP:27:GLN:NE2	86:BT:14:GLY:HA3	2.07	0.68
1:2:330:G:H2'	1:2:331:A:C8	2.29	0.68
36:m:74:C:N1	83:BQ:2924:U:C2	2.62	0.68
36:m:74:C:C5	83:BQ:2924:U:C2	2.81	0.68
31:d:131:ARG:HG2	31:d:131:ARG:HH21	1.58	0.68
71:BE:313:LEU:HD21	83:BQ:505:G:H4'	1.75	0.68
1:2:55:A:N3	1:2:403:G:C2	2.54	0.68
36:m:53:G:OP1	70:BD:73:LYS:CD	2.41	0.68
86:BT:33:VAL:HG23	86:BT:83:PRO:HD3	1.75	0.68
1:2:815:G:O4'	72:BF:162:ARG:NH1	2.27	0.68
37:n:4:G:H4'	86:BT:27:ARG:HH22	1.56	0.68
1:2:697:C:O2	1:2:697:C:H2'	1.94	0.68
1:2:850:A:P	72:BF:165:LYS:NZ	2.67	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:125:LEU:HG	31:d:128:LYS:CE	2.24	0.68
39:i:37:ASN:O	39:i:41:HIS:ND1	2.24	0.67
83:BQ:800:G:H2'	83:BQ:800:G:N3	2.09	0.67
83:BQ:2418:G:N2	86:BT:73:LEU:CG	2.57	0.67
31:d:131:ARG:HH21	31:d:131:ARG:CG	2.07	0.67
83:BQ:1188:U:C4	83:BQ:1317:A:N1	2.61	0.67
83:BQ:3047:U:O4	83:BQ:3094:A:N1	2.27	0.67
10:I:18:TYR:CD2	10:I:59:ALA:HB2	2.30	0.67
37:n:12:U:H1'	83:BQ:2266:U:HO2'	1.58	0.67
83:BQ:1898:G:O6	83:BQ:1899:G:N2	2.27	0.67
83:BQ:2418:G:N2	86:BT:73:LEU:CD1	2.41	0.67
1:2:1642:G:H5'	59:AS:1:MET:SD	2.33	0.67
74:BH:90:MET:HE1	74:BH:114:HIS:CE1	2.30	0.67
1:2:55:A:O2'	1:2:56:U:P	2.51	0.67
1:2:1080:U:N3	1:2:1091:A:N6	2.43	0.67
37:n:74:C:C4	83:BQ:2621:G:C2	2.79	0.67
1:2:851:U:H5'	72:BF:172:ARG:HH22	1.60	0.67
38:h:456:VAL:HG21	38:h:805:ARG:HB3	1.77	0.67
56:AP:27:GLN:NE2	86:BT:14:GLY:H	1.77	0.67
83:BQ:1188:U:C2	83:BQ:1317:A:N6	2.62	0.67
36:m:38:A:C4'	83:BQ:2256:A:N6	2.58	0.67
85:BS:145:U:H2'	85:BS:146:U:C6	2.30	0.67
1:2:1595:U:N3	1:2:1600:A:N6	2.42	0.66
18:Q:201:THR:HG21	18:Q:207:LEU:HD22	1.77	0.66
1:2:619:A:OP2	32:e:8:ASN:HB3	1.96	0.66
1:2:55:A:N3	1:2:55:A:H2'	2.09	0.66
83:BQ:3294:A:H2'	83:BQ:3295:A:O4'	1.96	0.66
16:O:180:ALA:HB3	16:O:190:ALA:HB3	1.78	0.66
1:2:383:G:O2'	1:2:384:G:O5'	2.12	0.66
22:U:39:ARG:NH2	72:BF:181:ARG:C	2.54	0.66
83:BQ:2418:G:N2	86:BT:73:LEU:CD2	2.59	0.66
83:BQ:430:U:H2'	83:BQ:431:U:O4'	1.95	0.65
36:m:52:G:P	83:BQ:2839:G:H4'	2.35	0.65
36:m:74:C:C6	83:BQ:2924:U:C4	2.75	0.65
1:2:1749:A:O3'	59:AS:13:LEU:HD11	1.96	0.65
1:2:1082:C:N4	1:2:1091:A:N7	2.44	0.65
1:2:1116:A:C5'	59:AS:17:ARG:NH1	2.60	0.65
38:h:26:VAL:C	38:h:28:LEU:N	2.53	0.65
56:AP:27:GLN:HE21	86:BT:14:GLY:HA3	1.59	0.65
83:BQ:559:A:H2'	83:BQ:560:G:O4'	1.97	0.65
1:2:987:G:C5	63:AW:249:SER:CA	2.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1783:C:OP2	59:AS:1:MET:HB2	1.97	0.65
39:i:171:LEU:HD12	39:i:171:LEU:N	2.11	0.65
1:2:1584:G:N2	1:2:1611:A:OP2	2.30	0.64
40:j:175:LEU:HD21	40:j:178:THR:HG23	1.79	0.64
37:n:1:G:OP2	70:BD:100:LYS:HE3	1.96	0.64
60:AT:79:VAL:HG22	63:AW:112:ILE:HD13	1.79	0.64
1:2:1540:G:H2'	1:2:1541:G:C4	2.32	0.64
19:R:180:ALA:HB2	19:R:198:THR:HG21	1.79	0.64
21:T:131:LYS:HD3	45:AE:81:PRO:HA	1.78	0.64
39:i:121:GLU:CB	39:i:124:GLN:HA	2.27	0.64
48:AH:103:TYR:HB3	48:AH:135:ILE:HD11	1.78	0.64
37:n:73:G:N3	70:BD:109:ARG:HD3	2.12	0.64
86:BT:132:LYS:HB3	86:BT:152:GLU:CD	2.17	0.64
1:2:1080:U:H3	1:2:1091:A:N6	1.95	0.64
83:BQ:3047:U:C4	83:BQ:3094:A:C2	2.82	0.64
83:BQ:3152:U:O2'	83:BQ:3294:A:C8	2.47	0.64
1:2:340:U:C2	23:V:86:SER:HB3	2.33	0.64
83:BQ:829:U:C2	83:BQ:895:A:N6	2.65	0.64
1:2:331:A:H2'	1:2:332:U:O4'	1.98	0.64
36:m:74:C:N3	83:BQ:2924:U:C2	2.65	0.64
67:BA:8:ALA:HB1	67:BA:9:PRO:HD2	1.78	0.64
83:BQ:708:G:O2'	83:BQ:710:A:N7	2.24	0.64
1:2:1645:G:O4'	83:BQ:2255:A:C5	2.51	0.64
37:n:56:C:O4'	47:AG:61:ARG:HD2	1.98	0.63
1:2:1645:G:O4'	83:BQ:2255:A:C6	2.51	0.63
26:Y:22:ALA:HB1	26:Y:23:PRO:CA	2.28	0.63
36:m:75:C:H42	83:BQ:2922:G:H1	1.46	0.63
86:BT:46:THR:HG22	86:BT:57:VAL:HG22	1.80	0.63
1:2:1126:G:C4'	59:AS:11:ARG:HH12	2.11	0.63
21:T:131:LYS:HD3	45:AE:81:PRO:CA	2.28	0.63
37:n:73:G:O3'	70:BD:108:ASP:HB3	1.98	0.63
39:i:113:TYR:CD2	39:i:127:LEU:HD22	2.34	0.63
54:AN:51:LEU:HD12	54:AN:65:ARG:HD2	1.79	0.63
83:BQ:2960:C:H2'	83:BQ:2961:G:C8	2.33	0.63
2:A:105:MET:HG2	2:A:122:VAL:HG21	1.80	0.63
21:T:9:VAL:HG13	45:AE:78:ALA:O	1.98	0.63
67:BA:256:HIS:HA	67:BA:257:PRO:C	2.24	0.63
83:BQ:1554:U:N3	83:BQ:1559:A:N6	2.46	0.63
86:BT:64:ILE:HG21	86:BT:139:ILE:HD11	1.78	0.63
86:BT:100:LEU:O	86:BT:111:ASP:O	2.16	0.63
36:m:38:A:C5'	83:BQ:2256:A:C6	2.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AH:105:VAL:HG11	48:AH:126:LEU:HD22	1.80	0.63
81:BO:156:ILE:HD12	81:BO:161:VAL:HG21	1.79	0.63
83:BQ:1188:U:H3	83:BQ:1317:A:N6	1.92	0.63
21:T:131:LYS:CE	45:AE:81:PRO:CA	2.75	0.63
39:i:533:GLN:HG2	39:i:533:GLN:O	1.98	0.63
54:AN:25:ILE:HA	54:AN:43:VAL:HG12	1.80	0.62
1:2:1116:A:H5'	59:AS:17:ARG:NH1	2.14	0.62
1:2:1132:A:OP1	32:e:2:PRO:N	2.32	0.62
42:AB:101:VAL:HG21	42:AB:109:MET:HE1	1.81	0.62
40:j:11:ALA:HB3	40:j:388:ILE:HG23	1.80	0.62
83:BQ:829:U:H3	83:BQ:895:A:N6	1.81	0.62
37:n:17:C:O2	37:n:17:C:H2'	1.97	0.62
83:BQ:1786:G:H2'	83:BQ:1787:A:C8	2.34	0.62
83:BQ:1808:G:O2'	83:BQ:1809:A:OP2	2.11	0.62
86:BT:138:ILE:HG22	86:BT:147:ALA:HA	1.80	0.62
1:2:851:U:C5'	72:BF:172:ARG:NH2	2.62	0.62
39:i:668:ILE:HG21	39:i:684:ILE:HD11	1.80	0.62
83:BQ:2333:C:H2'	83:BQ:2334:U:O2	2.00	0.62
86:BT:113:VAL:O	86:BT:115:ALA:N	2.33	0.62
37:n:73:G:N3	70:BD:109:ARG:CD	2.62	0.62
1:2:55:A:H2'	1:2:403:G:H21	1.65	0.62
1:2:1645:G:C5'	83:BQ:2255:A:H61	1.76	0.62
86:BT:109:THR:HG22	86:BT:110:LYS:N	2.13	0.62
1:2:1774:G:N7	59:AS:4:LYS:NZ	2.39	0.62
38:h:26:VAL:C	38:h:28:LEU:H	2.06	0.62
83:BQ:3047:U:C5	83:BQ:3048:A:C5	2.88	0.62
83:BQ:1188:U:N3	83:BQ:1317:A:C6	2.68	0.61
16:O:243:LEU:HD23	16:O:254:ALA:HB2	1.80	0.61
37:n:56:C:HO2'	47:AG:53:THR:CB	2.09	0.61
1:2:987:G:N2	63:AW:248:GLY:CA	2.63	0.61
1:2:1642:G:O3'	59:AS:9:ARG:NH2	2.33	0.61
22:U:12:ALA:HB3	22:U:13:PRO:HD3	1.82	0.61
9:H:16:ARG:NH1	47:AG:110:ILE:CA	2.63	0.61
64:AX:36:ILE:CD1	64:AX:95:LEU:HD11	2.31	0.61
57:AQ:58:GLY:HA3	57:AQ:142:ILE:HD11	1.81	0.61
3:B:96:SER:HB3	3:B:176:THR:HG21	1.83	0.61
37:n:56:C:N4	56:AP:104:LEU:CD2	2.64	0.61
40:k:60:VAL:HG11	40:k:65:LEU:HD11	1.81	0.61
83:BQ:2315:G:C2	83:BQ:2316:G:N7	2.69	0.61
36:m:74:C:C4	83:BQ:2924:U:C5	2.89	0.61
83:BQ:11:A:O4'	83:BQ:1558:A:N6	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:2433:U:C4	83:BQ:2595:A:N1	2.68	0.61
1:2:1080:U:C4	1:2:1091:A:C6	2.89	0.60
37:n:20:U:C5'	47:AG:55:ARG:HH12	2.13	0.60
39:i:151:PRO:HB2	39:i:230:ILE:CD1	2.29	0.60
83:BQ:1317:A:O2'	83:BQ:1318:A:H2'	2.01	0.60
1:2:1595:U:O4	1:2:1600:A:C2	2.53	0.60
1:2:1642:G:H5'	59:AS:1:MET:HG2	1.82	0.60
9:H:16:ARG:HH11	47:AG:110:ILE:CA	2.13	0.60
38:h:1117:VAL:HG23	38:h:1255:ALA:HB1	1.83	0.60
83:BQ:1073:U:H2'	83:BQ:1074:U:C6	2.36	0.60
39:i:66:ALA:HA	39:i:69:HIS:HD2	1.66	0.60
44:AD:43:VAL:HG12	44:AD:57:VAL:HG23	1.82	0.60
53:AM:17:VAL:HG21	53:AM:74:ARG:HB3	1.83	0.60
83:BQ:2273:G:HO2'	83:BQ:2311:G:H1	1.40	0.60
86:BT:88:ASN:HD22	86:BT:138:ILE:HD11	1.66	0.60
1:2:1541:G:C4	1:2:1570:A:N6	2.70	0.60
37:n:56:C:C2'	47:AG:53:THR:HG1	2.09	0.60
1:2:432:G:C6	1:2:433:C:C4	2.89	0.60
23:V:78:ILE:HD12	23:V:96:LEU:HD13	1.84	0.60
83:BQ:2683:U:H2'	83:BQ:2684:C:C6	2.36	0.60
37:n:56:C:C4	56:AP:104:LEU:HD21	2.36	0.60
77:BK:15:SER:HA	77:BK:94:PHE:CE1	2.37	0.59
86:BT:94:ASP:O	86:BT:101:SER:OG	2.14	0.59
39:i:147:GLN:HG3	39:i:173:LEU:HG	1.85	0.59
1:2:55:A:N7	1:2:426:G:N1	2.50	0.59
3:B:58:LEU:HD12	3:B:138:THR:HG22	1.84	0.59
5:D:57:ALA:HB2	5:D:122:VAL:HG13	1.84	0.59
10:I:81:GLY:N	10:I:96:ALA:HB2	2.17	0.59
38:h:1151:SER:HA	38:h:1245:LEU:HD21	1.82	0.59
68:BB:92:ARG:NH1	83:BQ:784:A:O2'	2.35	0.59
83:BQ:829:U:N3	83:BQ:895:A:C6	2.60	0.59
37:n:12:U:O2'	83:BQ:2266:U:O2'	1.87	0.59
39:i:151:PRO:CA	39:i:230:ILE:CD1	2.68	0.59
1:2:1642:G:H5'	59:AS:1:MET:CG	2.32	0.59
37:n:56:C:O2'	47:AG:53:THR:CB	2.50	0.59
38:h:1167:VAL:HG12	38:h:1171:LEU:HD12	1.84	0.59
37:n:19:U:O4	56:AP:104:LEU:C	2.45	0.59
79:BM:169:ASP:HB3	79:BM:174:LEU:HD11	1.85	0.59
83:BQ:2333:C:C2	83:BQ:2334:U:O2	2.56	0.59
32:e:32:LYS:HA	32:e:35:ALA:HB2	1.85	0.59
39:i:152:GLY:N	39:i:230:ILE:CD1	2.62	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:BF:99:LEU:HD21	72:BF:103:ARG:CZ	2.33	0.59
1:2:431:C:C4	1:2:432:G:C6	2.91	0.58
63:AW:15:ILE:HD12	63:AW:194:ASN:HD22	1.68	0.58
83:BQ:2416:U:H3	83:BQ:2804:A:H2	1.50	0.58
1:2:384:G:H2'	1:2:385:A:H4'	1.84	0.58
1:2:987:G:H2'	63:AW:249:SER:HB2	1.83	0.58
1:2:1057:U:C4	1:2:1062:A:N1	2.68	0.58
11:J:34:LEU:HD21	11:J:89:ARG:HG3	1.84	0.58
36:m:75:C:N4	83:BQ:2922:G:H1	2.00	0.58
38:h:1117:VAL:CG2	38:h:1255:ALA:HB1	2.34	0.58
83:BQ:1696:A:H2'	83:BQ:1697:A:C8	2.38	0.58
19:R:82:ASN:HB2	19:R:207:LEU:HD12	1.85	0.58
30:c:11:SER:O	30:c:13:ARG:N	2.36	0.58
37:n:74:C:OP2	70:BD:108:ASP:CG	2.46	0.58
86:BT:23:CYS:SG	86:BT:80:MET:N	2.76	0.58
86:BT:63:ASP:HB2	86:BT:67:GLY:H	1.68	0.58
1:2:813:U:C5	72:BF:163:ARG:HD2	2.37	0.58
65:AY:22:LYS:HB3	65:AY:93:LEU:HD11	1.84	0.58
83:BQ:2199:G:O2'	86:BT:71:GLU:OE2	2.18	0.58
75:BI:236:LEU:HA	75:BI:239:ILE:HD12	1.85	0.58
83:BQ:632:G:H2'	83:BQ:633:C:O4'	2.03	0.58
1:2:425:A:P	1:2:425:A:H3'	2.44	0.58
37:n:56:C:N3	56:AP:104:LEU:HD22	2.19	0.58
86:BT:155:ARG:O	86:BT:156:THR:HG23	2.02	0.58
57:AQ:2:GLY:N	83:BQ:117:U:OP2	2.37	0.57
1:2:851:U:OP1	72:BF:165:LYS:CD	2.52	0.57
83:BQ:550:A:H2'	83:BQ:551:A:C8	2.39	0.57
1:2:967:A:H2'	1:2:968:U:O4'	2.04	0.57
19:R:45:VAL:HG21	19:R:68:ILE:HG23	1.87	0.57
46:AF:19:CYS:SG	46:AF:22:CYS:N	2.75	0.57
50:AJ:166:ALA:HB1	58:AR:147:LEU:HD11	1.86	0.57
75:BI:104:LEU:HD11	75:BI:108:ARG:NH2	2.18	0.57
75:BI:277:LEU:HD23	75:BI:282:ARG:HG3	1.86	0.57
86:BT:89:GLU:HA	86:BT:137:THR:HG22	1.85	0.57
26:Y:108:ASP:OD2	26:Y:111:ALA:HB3	2.04	0.57
1:2:987:G:N2	63:AW:248:GLY:HA2	2.20	0.57
1:2:1585:U:O4	1:2:1611:A:C6	2.57	0.57
39:i:66:ALA:HA	39:i:69:HIS:CD2	2.40	0.57
67:BA:266:ARG:NH2	83:BQ:2392:C:O2'	2.37	0.57
83:BQ:628:A:H2'	83:BQ:629:U:O4'	2.04	0.57
83:BQ:3047:U:C4	83:BQ:3048:A:C6	2.92	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:697:C:O2	1:2:697:C:C2'	2.53	0.57
69:BC:36:ILE:CD1	69:BC:59:ILE:HD11	2.35	0.57
9:H:120:ARG:NE	83:BQ:1025:A:N3	2.53	0.57
83:BQ:107:A:O2'	83:BQ:324:A:N3	2.32	0.57
1:2:1474:G:H2'	1:2:1475:A:C8	2.40	0.57
83:BQ:1447:G:O2'	83:BQ:2355:G:N1	2.31	0.57
56:AP:64:THR:CG2	86:BT:19:TYR:HB3	2.33	0.57
85:BS:145:U:H2'	85:BS:146:U:O4'	2.04	0.57
9:H:50:ALA:HB2	9:H:72:ILE:HD12	1.87	0.56
47:AG:59:ILE:HG21	47:AG:65:ILE:HD12	1.86	0.56
83:BQ:2186:U:H2'	83:BQ:2187:G:O4'	2.05	0.56
23:V:81:VAL:HG13	23:V:82:VAL:N	2.19	0.56
43:AC:26:ILE:HD13	83:BQ:157:A:C8	2.40	0.56
77:BK:49:ILE:HD11	77:BK:71:VAL:HG23	1.86	0.56
1:2:815:G:H1'	72:BF:162:ARG:HD2	1.85	0.56
1:2:1780:G:N3	83:BQ:2262:A:O2'	2.35	0.56
9:H:14:ILE:CD1	47:AG:118:PRO:HB3	2.35	0.56
21:T:9:VAL:CG1	45:AE:78:ALA:CB	2.62	0.56
21:T:131:LYS:H	45:AE:83:THR:CB	2.14	0.56
39:i:173:LEU:CD2	39:i:224:TYR:HD2	2.18	0.56
39:i:774:TYR:CZ	39:i:778:ILE:HD11	2.40	0.56
1:2:1542:G:N2	1:2:1568:C:O2'	2.39	0.56
36:m:38:A:H5'	83:BQ:2256:A:N1	2.21	0.56
83:BQ:1554:U:O4	83:BQ:1559:A:C6	2.57	0.56
19:R:38:VAL:HG13	19:R:39:THR:HG23	1.87	0.56
56:AP:64:THR:HG22	86:BT:19:TYR:HA	1.86	0.56
86:BT:21:MET:HE2	86:BT:82:VAL:HG21	1.87	0.56
1:2:15:U:H2'	1:2:16:G:O4'	2.04	0.56
1:2:1773:C:OP1	59:AS:3:ALA:HB3	2.05	0.56
3:B:90:ILE:O	3:B:94:THR:HG23	2.05	0.56
9:H:143:ARG:HB3	9:H:144:ARG:HB2	1.88	0.56
26:Y:22:ALA:CB	26:Y:23:PRO:HA	2.35	0.56
68:BB:4:ASP:HB2	81:BO:92:ILE:HD13	1.86	0.56
69:BC:10:ARG:NH1	69:BC:44:MET:HE1	2.21	0.56
83:BQ:2612:U:O4	83:BQ:2805:G:O6	2.23	0.56
39:i:302:ALA:HB3	39:i:303:PRO:HD3	1.88	0.56
44:AD:4:ILE:HD12	74:BH:143:PHE:CE1	2.40	0.56
77:BK:102:LEU:HD11	79:BM:165:LEU:HD11	1.88	0.56
1:2:1779:U:O4	59:AS:12:ARG:NH2	2.39	0.56
31:d:40:LEU:HD13	31:d:60:PHE:CZ	2.41	0.56
39:i:120:GLN:O	39:i:121:GLU:C	2.49	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:90:THR:HG22	4:C:93:GLN:HE22	1.70	0.56
39:i:37:ASN:H	39:i:41:HIS:CE1	2.24	0.56
54:AN:54:THR:HG22	54:AN:57:HIS:CD2	2.41	0.56
84:BR:67:G:H2'	84:BR:68:C:O4'	2.05	0.56
1:2:1038:U:O4	1:2:1092:A:C2	2.58	0.55
5:D:74:LEU:HD11	15:N:106:TYR:HB3	1.88	0.55
16:O:89:LEU:HD21	16:O:110:VAL:HG11	1.87	0.55
51:AK:59:VAL:HG12	51:AK:103:LYS:O	2.06	0.55
83:BQ:2328:U:H2'	83:BQ:2329:C:C6	2.42	0.55
83:BQ:2612:U:C2	83:BQ:2804:A:N6	2.74	0.55
39:i:60:ASN:HA	39:i:64:GLU:HB2	1.87	0.55
16:O:83:ALA:HA	16:O:89:LEU:HD22	1.88	0.55
21:T:130:PRO:CB	45:AE:83:THR:CB	2.84	0.55
70:BD:189:VAL:HG13	70:BD:196:VAL:HG13	1.88	0.55
83:BQ:1241:U:H4'	83:BQ:1242:G:OP1	2.06	0.55
31:d:55:VAL:HG22	31:d:75:VAL:HG23	1.88	0.55
37:n:12:U:C2'	83:BQ:2266:U:O2'	2.48	0.55
83:BQ:3256:G:H2'	83:BQ:3257:C:O4'	2.06	0.55
1:2:852:C:H5'	72:BF:176:ARG:CD	2.37	0.55
54:AN:23:VAL:HG12	54:AN:45:GLY:HA3	1.89	0.55
83:BQ:656:A:H2'	83:BQ:657:A:C8	2.42	0.55
1:2:913:G:N2	83:BQ:2206:G:O2'	2.40	0.55
1:2:1030:A:N7	32:e:9:GLY:C	2.64	0.55
64:AX:36:ILE:HD12	64:AX:95:LEU:HD11	1.89	0.55
83:BQ:829:U:C4	83:BQ:895:A:N6	2.70	0.55
1:2:174:U:C4	1:2:266:A:N6	2.75	0.55
38:h:804:PHE:CD2	38:h:1088:LEU:HD22	2.41	0.55
56:AP:64:THR:HG21	86:BT:19:TYR:CB	2.36	0.55
79:BM:54:TYR:HA	79:BM:65:ILE:HG22	1.89	0.55
86:BT:16:SER:O	86:BT:17:ALA:HB2	2.06	0.55
2:A:201:ALA:HB3	8:G:42:GLN:NE2	2.22	0.55
20:S:92:LEU:HD23	31:d:17:LEU:HD22	1.88	0.55
37:n:74:C:N3	83:BQ:2621:G:N3	2.51	0.55
39:i:129:ASN:O	39:i:133:LEU:N	2.40	0.55
83:BQ:358:G:N2	83:BQ:361:A:OP2	2.39	0.55
83:BQ:1482:A:H2'	83:BQ:1482:A:N3	2.22	0.55
83:BQ:3047:U:O4	83:BQ:3094:A:C6	2.60	0.55
83:BQ:1554:U:C4	83:BQ:1559:A:C6	2.94	0.55
83:BQ:2452:G:N3	83:BQ:2452:G:H2'	2.22	0.55
39:i:171:LEU:CD1	39:i:171:LEU:H	2.20	0.54
81:BO:163:LEU:O	81:BO:165:ASP:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:1724:U:H4'	83:BQ:1725:C:OP1	2.07	0.54
83:BQ:3121:U:C4	83:BQ:3124:G:O6	2.60	0.54
86:BT:111:ASP:O	86:BT:112:ASP:C	2.50	0.54
1:2:107:C:OP1	1:2:382:C:O2'	2.24	0.54
1:2:851:U:OP1	72:BF:165:LYS:CE	2.56	0.54
1:2:851:U:H5''	72:BF:172:ARG:CZ	2.28	0.54
1:2:1672:G:H2'	1:2:1673:G:C8	2.42	0.54
67:BA:57:VAL:HG22	67:BA:73:VAL:HG12	1.89	0.54
14:M:21:CYS:SG	14:M:39:CYS:N	2.77	0.54
1:2:973:A:H5'	83:BQ:848:A:C2	2.43	0.54
1:2:1601:G:C4	10:I:88:VAL:HG11	2.43	0.54
6:E:121:ILE:HD12	9:H:122:HIS:CD2	2.43	0.54
41:AA:148:ALA:HA	41:AA:201:THR:HG22	1.90	0.54
42:AB:6:ALA:HB2	42:AB:126:TRP:CZ3	2.42	0.54
67:BA:8:ALA:HB1	67:BA:9:PRO:CD	2.37	0.54
75:BI:52:VAL:HG21	75:BI:65:ILE:HD12	1.90	0.54
6:E:108:ARG:NH2	83:BQ:1025:A:N1	2.54	0.54
25:X:94:ILE:HD13	30:c:12:ALA:HB1	1.88	0.54
38:h:934:PHE:CD1	38:h:1010:THR:HG23	2.43	0.54
77:BK:90:PRO:O	77:BK:92:LYS:N	2.40	0.54
86:BT:109:THR:O	86:BT:110:LYS:HB2	2.07	0.54
1:2:1012:U:C4'	63:AW:247:ARG:HB3	2.31	0.54
38:h:986:ARG:HD3	38:h:1019:LEU:HD11	1.90	0.54
83:BQ:2433:U:O4	83:BQ:2595:A:C2	2.58	0.54
83:BQ:2858:U:C4	83:BQ:2859:U:O4	2.61	0.54
1:2:1644:C:O2'	83:BQ:2255:A:N1	2.38	0.54
23:V:81:VAL:HG12	23:V:95:THR:C	2.32	0.54
77:BK:16:TYR:CD1	77:BK:25:PRO:HA	2.43	0.54
86:BT:94:ASP:HA	86:BT:128:PHE:CZ	2.43	0.54
4:C:11:ILE:HD13	4:C:35:ILE:HD13	1.90	0.54
36:m:52:G:OP1	83:BQ:2839:G:H4'	2.08	0.54
37:n:17:C:O2	37:n:17:C:C2'	2.56	0.54
83:BQ:3202:G:H2'	83:BQ:3203:U:O4'	2.08	0.54
83:BQ:3375:A:O2'	83:BQ:3376:A:O4'	2.21	0.54
1:2:1645:G:C4'	83:BQ:2255:A:C5	2.91	0.54
20:S:181:VAL:HG13	20:S:225:VAL:HG13	1.88	0.54
41:AA:162:LEU:HD23	57:AQ:7:LEU:HD21	1.90	0.54
78:BL:43:VAL:HG11	78:BL:69:ALA:HB1	1.90	0.54
83:BQ:1194:G:H2'	83:BQ:1195:A:C8	2.43	0.54
36:m:53:G:P	70:BD:73:LYS:CE	2.92	0.53
74:BH:77:VAL:HG11	74:BH:106:LEU:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:BK:13:HIS:ND1	77:BK:93:THR:O	2.42	0.53
86:BT:59:LEU:HB2	86:BT:72:ASP:OD1	2.08	0.53
26:Y:26:PHE:CE2	26:Y:66:ILE:HD11	2.42	0.53
39:i:173:LEU:C	39:i:175:LYS:H	2.17	0.53
83:BQ:2418:G:N3	86:BT:73:LEU:HD11	2.05	0.53
83:BQ:3152:U:H1'	83:BQ:3294:A:C4	2.43	0.53
39:i:95:GLU:OE2	39:i:138:HIS:NE2	2.41	0.53
56:AP:27:GLN:NE2	86:BT:13:ALA:C	2.46	0.53
3:B:123:VAL:HG13	12:K:102:THR:HG22	1.89	0.53
83:BQ:877:C:H2'	83:BQ:878:G:O4'	2.08	0.53
83:BQ:3237:U:H2'	83:BQ:3238:G:O4'	2.08	0.53
1:2:1783:C:C4	59:AS:5:TRP:CE3	2.97	0.53
9:H:16:ARG:NH1	47:AG:111:ASP:CA	2.66	0.53
36:m:74:C:N3	83:BQ:2924:U:N1	2.57	0.53
39:i:103:TYR:HA	39:i:107:PHE:CD2	2.44	0.53
39:i:171:LEU:HD12	39:i:171:LEU:H	1.73	0.53
1:2:1544:U:C5	1:2:1545:A:N7	2.77	0.53
42:AB:101:VAL:CG2	42:AB:109:MET:HE1	2.38	0.53
55:AO:115:CYS:SG	55:AO:118:THR:HG22	2.49	0.53
83:BQ:3055:U:O2'	83:BQ:3057:U:OP2	2.23	0.53
60:AT:26:VAL:HG22	63:AW:178:PRO:HD2	1.91	0.53
63:AW:5:ILE:HD11	63:AW:7:ASN:OD1	2.09	0.53
83:BQ:2418:G:H22	86:BT:73:LEU:CG	2.22	0.53
1:2:411:C:H2'	1:2:412:A:H8	1.74	0.53
1:2:1637:C:H3'	1:2:1638:G:H5'	1.91	0.53
44:AD:128:VAL:HA	44:AD:157:ASN:HD21	1.73	0.53
58:AR:77:LYS:O	58:AR:79:TRP:N	2.42	0.53
58:AR:105:LEU:HD21	58:AR:128:ARG:NH1	2.24	0.53
83:BQ:1046:A:H2'	83:BQ:1049:C:C5	2.44	0.53
1:2:591:A:H2'	1:2:592:A:C8	2.44	0.53
21:T:131:LYS:HB2	45:AE:81:PRO:HA	1.89	0.53
44:AD:23:ARG:NE	83:BQ:3187:A:OP1	2.40	0.53
5:D:52:LEU:HD22	5:D:85:LYS:HE3	1.89	0.53
19:R:180:ALA:HB2	19:R:198:THR:CG2	2.39	0.53
21:T:159:ARG:NE	21:T:172:ALA:HB2	2.24	0.53
61:AU:97:ALA:HB1	83:BQ:3172:A:O2'	2.08	0.53
1:2:1038:U:H3	1:2:1092:A:H61	1.43	0.52
86:BT:28:LYS:HE3	86:BT:42:VAL:HA	1.91	0.52
7:F:31:VAL:HG12	7:F:32:ASN:HD22	1.73	0.52
12:K:59:TYR:CE1	12:K:100:ILE:HD13	2.44	0.52
38:h:1242:ILE:HG21	38:h:1280:VAL:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:AW:52:SER:HB3	63:AW:191:LEU:HD23	1.91	0.52
73:BG:82:LEU:HD21	73:BG:117:ILE:HD12	1.92	0.52
83:BQ:531:G:H2'	83:BQ:532:A:C8	2.43	0.52
1:2:1571:C:O4'	1:2:1571:C:O2	2.25	0.52
7:F:32:ASN:HD21	7:F:69:VAL:HG13	1.74	0.52
31:d:131:ARG:NH2	31:d:131:ARG:CB	2.73	0.52
82:BP:53:CYS:O	82:BP:57:VAL:HG23	2.08	0.52
85:BS:41:A:N6	85:BS:103:G:O2'	2.38	0.52
1:2:329:G:O2'	23:V:84:HIS:CB	2.58	0.52
9:H:120:ARG:HG3	83:BQ:1025:A:C2	2.44	0.52
39:i:133:LEU:HA	39:i:136:LYS:CB	2.39	0.52
76:BJ:62:GLY:HA3	76:BJ:76:ILE:HD13	1.90	0.52
21:T:116:LYS:HD2	21:T:125:THR:HG21	1.90	0.52
76:BJ:92:ARG:NH1	83:BQ:2736:A:OP1	2.42	0.52
1:2:411:C:H2'	1:2:412:A:C8	2.45	0.52
1:2:1477:G:H2'	1:2:1478:G:O4'	2.09	0.52
39:i:103:TYR:CE1	39:i:141:CYS:HB3	2.45	0.52
75:BI:146:LEU:HD12	75:BI:163:LEU:HD12	1.91	0.52
1:2:850:A:P	72:BF:165:LYS:HZ1	2.33	0.52
29:b:37:PHE:CE1	29:b:103:ILE:HD11	2.44	0.52
63:AW:127:ALA:HB2	63:AW:134:VAL:HG13	1.91	0.52
69:BC:14:ILE:HD12	69:BC:39:PHE:CG	2.44	0.52
83:BQ:1784:G:H2'	83:BQ:1785:U:O4'	2.09	0.52
9:H:16:ARG:NH1	47:AG:110:ILE:HB	2.20	0.52
23:V:91:VAL:HG23	23:V:95:THR:HG21	1.90	0.52
68:BB:80:THR:HG22	68:BB:100:THR:HB	1.92	0.52
82:BP:48:ARG:HA	82:BP:51:ILE:HD12	1.89	0.52
83:BQ:2794:G:N7	83:BQ:2795:U:C4	2.78	0.52
83:BQ:2804:A:C2	83:BQ:2805:G:C8	2.97	0.52
83:BQ:2804:A:OP2	86:BT:78:HIS:CD2	2.63	0.52
1:2:565:C:H2'	1:2:577:G:N3	2.25	0.52
10:I:4:VAL:HG13	10:I:67:MET:HE1	1.92	0.52
21:T:22:HIS:NE2	67:BA:298:PHE:HE1	1.99	0.52
30:c:57:LEU:HD11	30:c:73:ARG:HG2	1.92	0.52
37:n:12:U:HO2'	83:BQ:2266:U:C2'	2.20	0.52
67:BA:160:VAL:HG12	67:BA:162:VAL:CG1	2.40	0.52
83:BQ:3187:A:H2'	83:BQ:3188:G:O4'	2.09	0.52
86:BT:116:PRO:HB3	86:BT:147:ALA:HB3	1.91	0.52
1:2:55:A:N7	1:2:426:G:C6	2.78	0.52
36:m:38:A:H4'	83:BQ:2256:A:C6	2.44	0.52
54:AN:14:VAL:HG21	80:BN:90:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:BH:12:ARG:HD3	74:BH:59:VAL:HG22	1.91	0.52
83:BQ:70:A:H2'	83:BQ:71:A:C8	2.45	0.52
85:BS:59:A:N3	85:BS:61:A:N6	2.58	0.52
1:2:1258:U:O2	1:2:1258:U:O4'	2.28	0.51
2:A:71:LEU:HD23	2:A:74:GLN:HE21	1.75	0.51
3:B:43:PHE:O	3:B:45:LYS:N	2.43	0.51
38:h:179:MET:HG2	38:h:182:ALA:HB3	1.91	0.51
64:AX:6:ALA:HB2	85:BS:11:C:H1'	1.91	0.51
83:BQ:1696:A:H2'	83:BQ:1697:A:H8	1.74	0.51
9:H:86:LEU:HD22	9:H:97:ASP:HB3	1.92	0.51
9:H:126:ARG:HB2	9:H:133:VAL:HG23	1.91	0.51
24:W:134:ILE:HD12	24:W:135:ALA:N	2.26	0.51
39:i:90:LEU:O	39:i:94:THR:N	2.43	0.51
39:i:1415:MET:SD	39:i:1428:LEU:HD22	2.50	0.51
56:AP:64:THR:CG2	86:BT:19:TYR:CB	2.87	0.51
1:2:1347:U:O2	1:2:1347:U:H2'	2.09	0.51
31:d:125:LEU:HD12	31:d:125:LEU:N	2.26	0.51
40:k:60:VAL:CG1	40:k:65:LEU:HD11	2.41	0.51
40:k:142:VAL:HG12	40:k:152:ILE:HD12	1.91	0.51
52:AL:9:ILE:HG22	52:AL:13:MET:HE3	1.91	0.51
83:BQ:708:G:N2	83:BQ:711:A:OP2	2.42	0.51
1:2:913:G:C6	83:BQ:2207:A:H1'	2.45	0.51
23:V:34:ALA:HB1	23:V:91:VAL:HG23	1.92	0.51
36:m:72:C:O2'	70:BD:104:CYS:SG	2.45	0.51
58:AR:4:ARG:NE	58:AR:4:ARG:O	2.43	0.51
72:BF:99:LEU:HD22	83:BQ:1722:U:H5''	1.92	0.51
83:BQ:1556:C:O2	83:BQ:1556:C:O4'	2.24	0.51
83:BQ:1661:G:H2'	83:BQ:1662:G:C8	2.45	0.51
1:2:1172:G:N2	1:2:1467:C:O2	2.43	0.51
13:L:44:VAL:HG21	13:L:48:VAL:HG21	1.91	0.51
51:AK:3:LYS:HG3	51:AK:8:VAL:HG13	1.92	0.51
53:AM:60:LEU:HA	53:AM:63:VAL:HG12	1.93	0.51
83:BQ:1203:A:N3	83:BQ:2855:U:O2'	2.41	0.51
83:BQ:1897:G:H2'	83:BQ:1898:G:O4'	2.11	0.51
83:BQ:2418:G:H21	86:BT:73:LEU:HD21	1.74	0.51
83:BQ:3214:U:O4'	83:BQ:3214:U:O2	2.27	0.51
83:BQ:3346:U:O2'	83:BQ:3347:A:H5'	2.10	0.51
38:h:378:THR:HG21	38:h:424:LEU:HD22	1.93	0.51
38:h:986:ARG:HG3	38:h:1019:LEU:HD21	1.93	0.51
39:i:838:ILE:HG21	39:i:881:LEU:HD11	1.93	0.51
67:BA:29:VAL:CG2	67:BA:337:THR:HG21	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:BA:47:LEU:HD21	67:BA:179:ALA:HB3	1.91	0.51
83:BQ:431:U:C2	83:BQ:432:G:C8	2.98	0.51
83:BQ:1160:C:O2	83:BQ:1160:C:H2'	2.11	0.51
83:BQ:1177:G:O2'	83:BQ:1178:G:O5'	2.27	0.51
1:2:1477:G:H2'	1:2:1478:G:C1'	2.41	0.51
1:2:1585:U:O2	1:2:1585:U:H2'	2.09	0.51
23:V:34:ALA:CB	23:V:91:VAL:HG23	2.40	0.51
35:l:53:U:O2	35:l:53:U:O4'	2.29	0.51
47:AG:59:ILE:HG21	47:AG:65:ILE:CD1	2.41	0.51
83:BQ:1817:G:H2'	83:BQ:1818:U:O4'	2.10	0.51
1:2:159:U:H5'	31:d:117:LYS:HD2	1.92	0.51
1:2:694:U:C5	22:U:98:ILE:HD12	2.46	0.51
35:l:63:U:O4'	35:l:63:U:O2	2.29	0.51
38:h:1167:VAL:HG11	38:h:1216:TYR:CD2	2.46	0.51
83:BQ:316:U:O2'	83:BQ:317:A:OP2	2.29	0.51
1:2:55:A:HO2'	1:2:56:U:P	2.31	0.51
22:U:173:TYR:CE2	22:U:181:ILE:HD11	2.46	0.51
1:2:1246:C:O2	1:2:1246:C:O4'	2.26	0.51
28:a:40:ASP:HB3	28:a:46:ILE:HD11	1.92	0.51
37:n:73:G:O3'	70:BD:108:ASP:CB	2.59	0.51
39:i:171:LEU:N	39:i:171:LEU:CD1	2.73	0.51
40:j:14:ALA:HB3	40:j:19:ILE:HD11	1.93	0.51
50:AJ:76:THR:HG22	50:AJ:101:ARG:HG3	1.93	0.51
53:AM:40:ASP:OD1	53:AM:43:LYS:N	2.44	0.51
63:AW:230:VAL:HG21	83:BQ:2424:A:N1	2.26	0.51
72:BF:96:ILE:HG12	83:BQ:1722:U:O4'	2.11	0.51
83:BQ:859:G:C5	83:BQ:861:C:C5	2.99	0.51
84:BR:75:G:C8	84:BR:76:A:H2'	2.46	0.51
86:BT:109:THR:CG2	86:BT:110:LYS:N	2.74	0.51
83:BQ:2508:U:H2'	83:BQ:2509:U:O4'	2.11	0.50
22:U:39:ARG:HD2	72:BF:181:ARG:HB2	1.94	0.50
39:i:37:ASN:H	39:i:41:HIS:HE1	1.59	0.50
39:i:534:VAL:HG11	39:i:544:VAL:HG13	1.91	0.50
68:BB:57:ILE:HD12	83:BQ:671:U:OP2	2.11	0.50
72:BF:106:LEU:HD11	72:BF:138:LEU:HD21	1.94	0.50
70:BD:169:LYS:HB3	70:BD:176:ASP:HA	1.93	0.50
37:n:20:U:H5'	47:AG:55:ARG:NH1	2.24	0.50
39:i:174:ILE:HG23	39:i:174:ILE:O	2.11	0.50
40:j:45:LEU:HD22	40:j:51:PRO:CG	2.41	0.50
76:BJ:94:GLU:OE1	76:BJ:94:GLU:N	2.44	0.50
83:BQ:1554:U:H3	83:BQ:1559:A:N6	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:2419:A:H1'	83:BQ:2804:A:C8	2.46	0.50
84:BR:11:A:O2'	84:BR:13:A:OP2	2.29	0.50
1:2:610:G:N3	1:2:610:G:H2'	2.26	0.50
38:h:932:MET:HE2	38:h:970:PHE:HB2	1.93	0.50
39:i:595:ILE:HD11	39:i:616:LEU:HD11	1.93	0.50
1:2:427:C:H2'	1:2:428:A:H8	1.76	0.50
1:2:1174:C:O2'	1:2:1196:A:N6	2.44	0.50
5:D:27:ALA:HB3	5:D:136:ILE:HG23	1.94	0.50
31:d:131:ARG:CG	31:d:131:ARG:NH2	2.72	0.50
39:i:103:TYR:HD1	39:i:107:PHE:CE2	2.30	0.50
43:AC:77:LEU:HD11	43:AC:86:LYS:HG2	1.93	0.50
51:AK:59:VAL:HG13	51:AK:60:ARG:HG2	1.93	0.50
39:i:1027:MET:HE2	39:i:1027:MET:HA	1.92	0.50
83:BQ:1632:A:H2'	83:BQ:1633:C:C6	2.47	0.50
1:2:1290:U:H2'	1:2:1291:G:C8	2.47	0.50
1:2:1362:U:O2	1:2:1362:U:O4'	2.30	0.50
1:2:1479:A:C2	1:2:1529:C:C2	3.00	0.50
68:BB:131:ALA:HB1	68:BB:135:GLN:H	1.76	0.50
73:BG:78:ASN:HA	73:BG:108:ILE:HD11	1.93	0.50
83:BQ:268:A:H2'	83:BQ:268:A:N3	2.27	0.50
83:BQ:1134:G:O2'	83:BQ:2642:A:N3	2.37	0.50
86:BT:90:TYR:CE1	86:BT:104:ASN:CG	2.89	0.50
86:BT:156:THR:O	86:BT:156:THR:OG1	2.30	0.50
4:C:83:PRO:HB2	4:C:86:ILE:HD12	1.93	0.50
18:Q:103:MET:HB3	18:Q:215:VAL:HG12	1.93	0.50
21:T:131:LYS:CB	45:AE:81:PRO:HA	2.42	0.50
23:V:162:ALA:HA	83:BQ:3353:G:P	2.52	0.50
35:l:45:U:O2	35:l:45:U:O4'	2.28	0.50
37:n:56:C:N4	56:AP:104:LEU:HD22	2.27	0.50
71:BE:71:VAL:HG22	71:BE:76:ARG:NH2	2.26	0.50
83:BQ:373:A:C6	83:BQ:375:A:C6	3.00	0.50
83:BQ:1326:A:H2'	83:BQ:1327:C:O4'	2.11	0.50
83:BQ:2836:C:O2	83:BQ:2836:C:O4'	2.30	0.50
1:2:337:G:O2'	23:V:10:LYS:NZ	2.44	0.49
1:2:987:G:N1	63:AW:248:GLY:C	2.70	0.49
1:2:1145:U:C5	1:2:1633:A:C2	2.97	0.49
58:AR:26:ARG:NH1	83:BQ:938:C:OP2	2.43	0.49
1:2:1185:U:O2'	1:2:1455:G:O2'	2.29	0.49
3:B:146:THR:HG22	3:B:159:ALA:HA	1.94	0.49
5:D:69:ALA:HA	5:D:72:ILE:HD12	1.93	0.49
9:H:118:LYS:O	83:BQ:1025:A:H2	1.89	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:BT:31:PHE:O	86:BT:82:VAL:HG13	2.12	0.49
24:W:134:ILE:HD11	24:W:141:VAL:HB	1.94	0.49
50:AJ:47:ALA:HB1	50:AJ:48:PRO:HD3	1.94	0.49
83:BQ:423:A:N6	83:BQ:637:C:OP1	2.45	0.49
1:2:1600:A:H2'	1:2:1600:A:N3	2.28	0.49
1:2:1784:C:C5	59:AS:5:TRP:HZ2	2.09	0.49
23:V:78:ILE:HD12	23:V:96:LEU:CD1	2.42	0.49
60:AT:79:VAL:HG21	63:AW:168:VAL:HG13	1.93	0.49
83:BQ:313:A:H2'	83:BQ:314:U:O4'	2.12	0.49
83:BQ:1188:U:OP1	83:BQ:1210:U:O2'	2.28	0.49
1:2:1461:C:C2	9:H:139:LYS:HD3	2.48	0.49
1:2:1750:A:OP1	59:AS:13:LEU:CD1	2.61	0.49
23:V:81:VAL:HG22	23:V:83:TYR:CD1	2.48	0.49
47:AG:163:PHE:CE2	47:AG:169:ALA:HB1	2.47	0.49
83:BQ:2577:C:C4	83:BQ:2578:U:C4	3.01	0.49
20:S:61:VAL:HG12	20:S:65:LEU:HD12	1.94	0.49
57:AQ:117:ASN:O	57:AQ:133:ILE:HG22	2.13	0.49
71:BE:286:VAL:HG12	71:BE:290:ILE:HD11	1.95	0.49
83:BQ:1188:U:C4	83:BQ:1317:A:N6	2.79	0.49
85:BS:83:C:O2'	85:BS:85:G:N2	2.46	0.49
86:BT:90:TYR:CD1	86:BT:104:ASN:OD1	2.65	0.49
1:2:1086:A:H2'	1:2:1087:A:C8	2.47	0.49
1:2:1560:U:O2	1:2:1560:U:O4'	2.29	0.49
8:G:24:LEU:HB2	8:G:58:MET:HE3	1.94	0.49
74:BH:90:MET:HE1	74:BH:114:HIS:NE2	2.28	0.49
83:BQ:2886:U:C4	83:BQ:2911:A:C6	3.01	0.49
1:2:1479:A:H2'	10:I:6:VAL:HG21	1.94	0.49
22:U:64:VAL:CG2	22:U:94:ALA:HB1	2.43	0.49
39:i:151:PRO:O	39:i:230:ILE:HD13	1.99	0.49
56:AP:64:THR:C	86:BT:17:ALA:HB3	2.36	0.49
64:AX:30:ARG:HA	64:AX:119:VAL:HG21	1.94	0.49
83:BQ:1625:A:N6	83:BQ:1818:U:O4	2.45	0.49
83:BQ:2328:U:H2'	83:BQ:2329:C:H6	1.77	0.49
18:Q:137:ILE:HD12	18:Q:172:LEU:HD22	1.94	0.49
31:d:131:ARG:NH2	31:d:131:ARG:HB3	2.28	0.49
40:k:239:VAL:HG12	40:k:250:ILE:HD12	1.94	0.49
67:BA:339:ARG:NE	67:BA:342:LEU:HD21	2.28	0.49
83:BQ:831:G:O2'	83:BQ:1864:A:N3	2.40	0.49
83:BQ:2418:G:N3	83:BQ:2418:G:H2'	2.26	0.49
85:BS:25:G:H2'	85:BS:26:U:C6	2.47	0.49
1:2:903:U:O2	1:2:906:A:N7	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AA:81:THR:HG21	41:AA:181:LYS:HD2	1.94	0.49
46:AF:31:LYS:HB2	46:AF:33:THR:HG22	1.94	0.49
69:BC:44:MET:HA	69:BC:44:MET:HE2	1.95	0.49
83:BQ:86:G:H1'	83:BQ:87:U:OP2	2.13	0.49
83:BQ:359:U:H2'	83:BQ:360:G:O4'	2.13	0.49
83:BQ:2162:U:H2'	83:BQ:2163:C:O4'	2.12	0.49
1:2:1116:A:H5'	59:AS:17:ARG:NH1	2.27	0.48
40:j:209:VAL:HG22	40:j:236:ILE:HD13	1.94	0.48
1:2:472:U:O2'	1:2:769:A:N3	2.42	0.48
3:B:123:VAL:CG2	12:K:92:ILE:HD11	2.43	0.48
9:H:14:ILE:HG23	9:H:14:ILE:O	2.13	0.48
20:S:141:THR:HG21	20:S:162:ILE:HD11	1.95	0.48
31:d:125:LEU:N	31:d:125:LEU:CD1	2.76	0.48
75:BI:76:ALA:HB3	75:BI:109:THR:HG22	1.94	0.48
16:O:222:LEU:CD2	16:O:265:LEU:HD21	2.44	0.48
37:n:73:G:O2'	70:BD:108:ASP:HB2	2.13	0.48
41:AA:184:ALA:O	41:AA:188:THR:HG23	2.13	0.48
83:BQ:10:C:O2'	83:BQ:1558:A:N6	2.47	0.48
2:A:162:GLN:N	2:A:163:PRO:CD	2.77	0.48
20:S:48:LEU:HD22	20:S:61:VAL:HG13	1.95	0.48
23:V:61:GLU:HG2	23:V:62:THR:HG23	1.95	0.48
36:m:38:A:C4'	83:BQ:2256:A:C6	2.96	0.48
54:AN:110:ALA:O	54:AN:114:VAL:HG23	2.13	0.48
68:BB:86:THR:HG22	68:BB:105:ARG:HB2	1.94	0.48
83:BQ:431:U:N3	83:BQ:628:A:C2	2.82	0.48
83:BQ:2418:G:C6	86:BT:73:LEU:HD12	2.48	0.48
1:2:804:A:N3	29:b:105:THR:HG22	2.28	0.48
1:2:1057:U:N3	1:2:1062:A:N6	2.60	0.48
1:2:1126:G:C4'	59:AS:11:ARG:NH1	2.74	0.48
1:2:1585:U:O4	1:2:1611:A:C2	2.63	0.48
9:H:120:ARG:CD	83:BQ:1025:A:N3	2.77	0.48
16:O:144:LEU:HD23	16:O:181:TRP:CD2	2.48	0.48
25:X:5:LEU:O	25:X:7:VAL:N	2.47	0.48
40:j:145:ASP:OD1	40:j:149:THR:N	2.46	0.48
51:AK:58:VAL:HG22	51:AK:104:LEU:HD22	1.96	0.48
57:AQ:53:TYR:CB	57:AQ:133:ILE:HD11	2.43	0.48
77:BK:49:ILE:HD11	77:BK:71:VAL:CG2	2.43	0.48
83:BQ:1110:U:H2'	83:BQ:1111:U:C6	2.49	0.48
83:BQ:3079:U:O2	83:BQ:3079:U:O4'	2.32	0.48
1:2:381:C:O2	1:2:381:C:C2'	2.61	0.48
1:2:788:A:C2	20:S:19:LEU:HD13	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:216:PRO:HB2	2:A:217:ILE:HD12	1.95	0.48
11:J:34:LEU:HD21	11:J:89:ARG:CG	2.43	0.48
13:L:12:VAL:HG13	13:L:28:VAL:HG13	1.94	0.48
21:T:131:LYS:O	45:AE:83:THR:C	2.49	0.48
38:h:417:LEU:CD1	38:h:434:LEU:HD22	2.42	0.48
38:h:456:VAL:HG21	38:h:805:ARG:CB	2.42	0.48
38:h:984:THR:HB	38:h:1019:LEU:HD13	1.95	0.48
83:BQ:2191:U:H2'	83:BQ:2192:C:O4'	2.12	0.48
1:2:260:U:O2	1:2:260:U:O4'	2.29	0.48
1:2:656:G:N3	1:2:656:G:H2'	2.27	0.48
3:B:62:VAL:HG13	3:B:89:ILE:HD13	1.95	0.48
4:C:11:ILE:HD13	4:C:35:ILE:HG21	1.95	0.48
19:R:69:ILE:HD11	19:R:133:LYS:HD3	1.94	0.48
25:X:94:ILE:HD13	30:c:12:ALA:CB	2.43	0.48
35:l:62:U:O2	35:l:62:U:O4'	2.32	0.48
46:AF:5:THR:HG22	46:AF:6:PRO:HD3	1.95	0.48
83:BQ:1580:A:O2'	83:BQ:1581:C:O5'	2.26	0.48
83:BQ:3182:G:C6	83:BQ:3183:A:N1	2.81	0.48
84:BR:113:C:H2'	84:BR:114:U:O4'	2.14	0.48
86:BT:132:LYS:HD2	86:BT:132:LYS:HA	1.58	0.48
1:2:1249:U:O4	1:2:1250:U:O4	2.32	0.48
9:H:16:ARG:HH12	47:AG:110:ILE:HG13	1.73	0.48
9:H:21:ASN:OD1	47:AG:116:TYR:CG	2.66	0.48
24:W:14:THR:HB	24:W:15:PRO:CD	2.43	0.48
37:n:19:U:O4	56:AP:106:PHE:N	2.47	0.48
72:BF:23:TRP:CZ3	72:BF:25:ASP:HB3	2.49	0.48
81:BO:84:VAL:HG13	81:BO:119:VAL:CG2	2.44	0.48
1:2:381:C:O2	1:2:381:C:H2'	2.14	0.48
1:2:850:A:H5''	72:BF:165:LYS:HZ2	1.68	0.48
1:2:1116:A:H5'	59:AS:17:ARG:HH12	1.79	0.48
2:A:69:LEU:HA	2:A:72:LEU:HD12	1.96	0.48
10:I:5:SER:CB	10:I:67:MET:HE3	2.44	0.48
36:m:64:G:H2'	36:m:64:G:N3	2.29	0.48
83:BQ:501:A:H2'	83:BQ:502:U:C6	2.49	0.48
86:BT:104:ASN:HB2	86:BT:107:GLY:O	2.13	0.48
86:BT:112:ASP:OD1	86:BT:113:VAL:HG13	2.13	0.48
1:2:93:A:O2'	20:S:3:ARG:O	2.27	0.48
30:c:57:LEU:HD11	30:c:73:ARG:CD	2.44	0.48
37:n:75:C:C2	83:BQ:2620:G:N2	2.81	0.48
38:h:364:ALA:CB	38:h:442:ILE:HD11	2.43	0.48
71:BE:4:PRO:HD2	71:BE:22:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:BO:218:ARG:HA	83:BQ:1170:A:OP1	2.14	0.48
83:BQ:1188:U:C4	83:BQ:1317:A:C6	3.02	0.48
83:BQ:1203:A:H2'	83:BQ:1204:A:C8	2.49	0.48
83:BQ:1302:A:N7	83:BQ:2857:C:O2'	2.45	0.48
83:BQ:3019:U:C4	83:BQ:3020:U:C4	3.01	0.48
1:2:300:A:H5''	20:S:2:ALA:HB2	1.96	0.47
1:2:329:G:O2'	23:V:84:HIS:HB2	2.13	0.47
1:2:1145:U:C4	1:2:1146:G:C5	3.02	0.47
11:J:106:ILE:HG23	11:J:107:THR:HG23	1.96	0.47
63:AW:9:ARG:NH1	83:BQ:912:G:OP2	2.40	0.47
68:BB:86:THR:HG21	83:BQ:676:G:O6	2.14	0.47
71:BE:210:ALA:HB2	71:BE:254:ALA:N	2.29	0.47
83:BQ:3329:U:H2'	83:BQ:3330:A:O4'	2.14	0.47
1:2:55:A:N3	1:2:55:A:C2'	2.75	0.47
1:2:1170:G:H2'	1:2:1170:G:N3	2.30	0.47
1:2:1772:C:O5'	59:AS:2:ARG:NE	2.47	0.47
39:i:501:LEU:HG	39:i:506:SER:N	2.29	0.47
44:AD:112:ILE:HG21	44:AD:161:LEU:HD11	1.96	0.47
63:AW:104:LEU:HD13	63:AW:162:ALA:O	2.14	0.47
69:BC:14:ILE:HG23	69:BC:16:LEU:CD1	2.44	0.47
69:BC:72:ARG:HB3	69:BC:96:VAL:CG2	2.44	0.47
83:BQ:2302:G:H2'	83:BQ:2303:A:O4'	2.14	0.47
83:BQ:2744:U:H2'	83:BQ:2745:G:O4'	2.13	0.47
1:2:995:A:H2'	1:2:996:U:O4'	2.14	0.47
9:H:123:ARG:HG3	9:H:133:VAL:HG22	1.97	0.47
16:O:22:SER:HB3	16:O:36:ALA:HB3	1.95	0.47
50:AJ:47:ALA:CB	50:AJ:48:PRO:CD	2.93	0.47
69:BC:36:ILE:HD12	69:BC:59:ILE:HD11	1.95	0.47
79:BM:68:PRO:HG3	79:BM:145:LEU:HD13	1.96	0.47
79:BM:162:SER:N	83:BQ:3216:G:OP1	2.48	0.47
83:BQ:629:U:C2	83:BQ:630:A:C8	3.02	0.47
83:BQ:1063:G:N7	83:BQ:1097:G:H2'	2.29	0.47
83:BQ:1719:G:H2'	83:BQ:1720:U:O4'	2.14	0.47
83:BQ:2656:A:C4	83:BQ:2658:G:N7	2.83	0.47
1:2:50:C:O2	1:2:50:C:H2'	2.15	0.47
1:2:382:C:O2	1:2:382:C:C2'	2.63	0.47
7:F:39:VAL:O	7:F:40:GLU:HB2	2.14	0.47
29:b:6:VAL:HG13	29:b:29:PRO:HD2	1.96	0.47
37:n:65:U:O2	37:n:65:U:O4'	2.32	0.47
41:AA:36:ILE:O	83:BQ:2550:U:N3	2.47	0.47
2:A:95:GLY:HA2	2:A:101:GLN:HE21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AT:63:THR:HG22	63:AW:48:ILE:HD11	1.95	0.47
67:BA:82:PRO:O	67:BA:83:PRO:C	2.57	0.47
72:BF:45:VAL:HG22	72:BF:50:ILE:HB	1.95	0.47
83:BQ:580:C:H2'	83:BQ:581:U:O4'	2.14	0.47
83:BQ:897:U:C2	83:BQ:898:U:C5	3.03	0.47
1:2:1533:C:H4'	1:2:1539:G:N1	2.29	0.47
2:A:46:THR:HB	2:A:84:ILE:HD12	1.96	0.47
10:I:5:SER:HB2	10:I:67:MET:HE3	1.95	0.47
18:Q:176:VAL:HG22	18:Q:184:LEU:HD21	1.96	0.47
64:AX:129:THR:HG22	83:BQ:1507:G:C8	2.49	0.47
69:BC:29:ALA:HB3	69:BC:30:PRO:HD3	1.97	0.47
83:BQ:436:A:H2'	83:BQ:437:G:O4'	2.14	0.47
83:BQ:1127:G:N2	83:BQ:1130:A:OP2	2.43	0.47
1:2:851:U:H4'	72:BF:172:ARG:NH2	2.27	0.47
1:2:987:G:N1	63:AW:248:GLY:O	2.48	0.47
9:H:113:LEU:HD21	9:H:127:HIS:HB3	1.97	0.47
16:O:225:LEU:HD12	16:O:228:LYS:HG3	1.97	0.47
17:P:139:VAL:O	17:P:139:VAL:HG22	2.15	0.47
26:Y:94:LYS:O	26:Y:98:VAL:HG23	2.14	0.47
30:c:70:LYS:HG3	30:c:93:LEU:HD22	1.97	0.47
35:l:43:U:O2	35:l:43:U:O4'	2.32	0.47
40:k:136:LEU:HD13	40:k:140:ARG:NH2	2.29	0.47
49:AI:53:THR:HG21	83:BQ:1747:G:O3'	2.14	0.47
58:AR:8:THR:HG21	83:BQ:662:U:OP1	2.14	0.47
83:BQ:1046:A:H2'	83:BQ:1049:C:H5	1.79	0.47
83:BQ:1282:G:H2'	83:BQ:1283:C:O4'	2.15	0.47
83:BQ:1494:U:O4'	83:BQ:1495:U:C5	2.68	0.47
83:BQ:1657:C:N4	83:BQ:1798:A:OP2	2.47	0.47
83:BQ:1834:U:H3'	83:BQ:1835:A:H5'	1.95	0.47
83:BQ:3078:U:O2	83:BQ:3078:U:C2'	2.63	0.47
83:BQ:3083:G:H2'	83:BQ:3084:C:O4'	2.15	0.47
2:A:113:LEU:HD22	2:A:117:ARG:HD2	1.97	0.47
8:G:20:TYR:CD1	8:G:38:ILE:HD11	2.50	0.47
42:AB:17:LEU:HD21	42:AB:98:ASN:CG	2.40	0.47
73:BG:63:THR:HA	73:BG:66:LEU:HD12	1.97	0.47
83:BQ:1224:C:H2'	83:BQ:1225:A:O4'	2.15	0.47
86:BT:42:VAL:HG13	86:BT:43:ASP:H	1.79	0.47
1:2:1597:A:C8	14:M:14:TYR:CD1	3.02	0.47
24:W:14:THR:HB	24:W:15:PRO:HD2	1.95	0.47
27:Z:26:THR:HG21	27:Z:97:GLY:HA3	1.96	0.47
47:AG:18:VAL:HG22	47:AG:70:THR:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:AW:202:VAL:HG23	83:BQ:2185:G:OP1	2.15	0.47
83:BQ:1462:A:H2'	83:BQ:1463:U:O4'	2.14	0.47
1:2:628:G:O2'	83:BQ:846:A:C4	2.68	0.47
1:2:1358:G:N3	1:2:1358:G:H2'	2.30	0.47
1:2:1595:U:C4	1:2:1600:A:N6	2.82	0.47
22:U:39:ARG:HH21	72:BF:181:ARG:HA	1.80	0.47
37:n:74:C:C4	83:BQ:2621:G:N1	2.82	0.47
43:AC:33:ALA:O	43:AC:37:THR:OG1	2.31	0.47
50:AJ:93:ILE:HG22	50:AJ:93:ILE:O	2.15	0.47
75:BI:146:LEU:HD12	75:BI:163:LEU:CD1	2.45	0.47
83:BQ:829:U:O4	83:BQ:895:A:N1	2.48	0.47
83:BQ:2696:A:H2'	83:BQ:2697:A:C8	2.50	0.47
1:2:1757:G:H4'	83:BQ:2256:A:H2'	1.97	0.46
22:U:143:LEU:HD11	22:U:149:ILE:CD1	2.45	0.46
40:j:352:LEU:HD13	40:j:385:ASP:HB3	1.96	0.46
42:AB:46:LEU:HD22	67:BA:8:ALA:HB2	1.97	0.46
57:AQ:94:TYR:O	83:BQ:289:A:O2'	2.33	0.46
58:AR:4:ARG:NH2	58:AR:5:PHE:HA	2.31	0.46
60:AT:54:ILE:HG23	63:AW:48:ILE:HD11	1.97	0.46
75:BI:83:LEU:N	75:BI:84:PRO:HD2	2.30	0.46
83:BQ:1748:G:C6	83:BQ:1749:A:C6	3.04	0.46
1:2:382:C:O2'	1:2:383:G:N7	2.42	0.46
1:2:1236:A:H2'	1:2:1237:G:H8	1.79	0.46
1:2:1585:U:C4	1:2:1611:A:C2	3.00	0.46
39:i:147:GLN:HE21	39:i:177:LEU:HD12	1.52	0.46
79:BM:40:LEU:HD11	79:BM:54:TYR:HB2	1.97	0.46
83:BQ:506:U:C4	83:BQ:507:U:C5	3.03	0.46
1:2:1060:U:H3'	1:2:1061:A:H5''	1.97	0.46
1:2:1172:G:O2'	1:2:1173:C:O4'	2.33	0.46
1:2:1775:U:O4	59:AS:4:LYS:CE	2.59	0.46
10:I:18:TYR:CE2	10:I:59:ALA:HB2	2.49	0.46
11:J:63:LEU:HD11	11:J:86:ILE:HD11	1.98	0.46
18:Q:126:THR:HG22	18:Q:136:ARG:CG	2.45	0.46
31:d:131:ARG:HH21	31:d:131:ARG:CB	2.28	0.46
38:h:1018:THR:O	38:h:1018:THR:HG23	2.15	0.46
40:k:146:VAL:HG12	40:k:188:PHE:CE1	2.49	0.46
44:AD:1:MET:HE1	74:BH:138:GLN:HB3	1.98	0.46
44:AD:20:ILE:HG12	44:AD:25:VAL:HG22	1.96	0.46
46:AF:34:CYS:SG	46:AF:35:SER:N	2.88	0.46
63:AW:118:GLU:CG	63:AW:126:LEU:HD21	2.46	0.46
79:BM:40:LEU:HB3	79:BM:84:VAL:CG1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:BR:80:G:H2'	84:BR:81:U:O4'	2.14	0.46
3:B:73:THR:HG23	7:F:114:ARG:HD2	1.97	0.46
39:i:323:SER:CB	39:i:410:VAL:HG22	2.45	0.46
44:AD:85:GLY:HA3	44:AD:187:ILE:HD12	1.98	0.46
64:AX:67:ILE:HD12	64:AX:82:ARG:NE	2.31	0.46
68:BB:81:VAL:HG21	68:BB:140:LEU:HD12	1.96	0.46
83:BQ:523:A:N6	83:BQ:570:A:C2	2.83	0.46
84:BR:62:U:O4	84:BR:63:A:N6	2.49	0.46
1:2:1236:A:H2'	1:2:1237:G:C8	2.50	0.46
37:n:75:C:H42	83:BQ:2620:G:H1	1.59	0.46
39:i:36:ASP:HA	39:i:41:HIS:HE1	1.80	0.46
67:BA:161:LEU:N	67:BA:161:LEU:HD23	2.30	0.46
71:BE:98:ARG:NH2	83:BQ:804:C:OP1	2.49	0.46
80:BN:38:LEU:N	80:BN:38:LEU:HD12	2.30	0.46
83:BQ:542:G:H2'	83:BQ:542:G:N3	2.31	0.46
83:BQ:2612:U:O2	83:BQ:2804:A:C5	2.69	0.46
9:H:14:ILE:HG21	47:AG:118:PRO:HD3	1.97	0.46
21:T:9:VAL:CG1	45:AE:78:ALA:O	2.63	0.46
37:n:12:U:H5''	83:BQ:2251:G:O2'	2.16	0.46
81:BO:232:ARG:HD2	81:BO:236:ILE:HD12	1.96	0.46
1:2:42:G:C2'	1:2:430:G:C6	2.74	0.46
1:2:1570:A:C5	1:2:1570:A:OP2	2.68	0.46
10:I:4:VAL:HG12	10:I:79:LEU:HD21	1.97	0.46
39:i:566:ASP:HA	39:i:569:ILE:HD12	1.97	0.46
40:j:87:THR:HG23	40:j:127:LEU:HD23	1.98	0.46
40:j:152:ILE:HD11	40:j:214:LEU:HD11	1.98	0.46
40:k:375:LEU:HD13	40:k:397:LYS:CB	2.46	0.46
44:AD:161:LEU:CD2	44:AD:179:ILE:HG21	2.45	0.46
69:BC:63:GLY:O	69:BC:65:LYS:N	2.49	0.46
70:BD:21:TYR:CZ	83:BQ:1048:A:H2'	2.51	0.46
83:BQ:563:U:H2'	83:BQ:564:G:O4'	2.15	0.46
83:BQ:898:U:H2'	83:BQ:899:U:O4'	2.15	0.46
83:BQ:2117:A:H2'	83:BQ:2118:C:O4'	2.16	0.46
1:2:393:C:H2'	1:2:394:C:C6	2.51	0.46
1:2:1535:U:O2'	1:2:1536:G:O5'	2.26	0.46
1:2:1641:C:O2'	59:AS:1:MET:HB3	2.15	0.46
1:2:1657:U:O2	83:BQ:2125:A:O4'	2.34	0.46
9:H:29:VAL:O	9:H:33:THR:HG23	2.15	0.46
38:h:1151:SER:CA	38:h:1245:LEU:HD21	2.46	0.46
68:BB:131:ALA:HB1	68:BB:135:GLN:N	2.30	0.46
83:BQ:20:A:C6	83:BQ:21:G:C6	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:2862:U:C2	83:BQ:2863:G:C8	3.04	0.46
83:BQ:2906:C:H2'	83:BQ:2907:G:O4'	2.15	0.46
86:BT:7:THR:O	86:BT:9:GLU:N	2.46	0.46
1:2:1553:G:N7	6:E:47:ARG:NH2	2.63	0.46
7:F:83:GLN:HE22	7:F:119:ALA:HB2	1.81	0.46
70:BD:216:PHE:CD1	75:BI:294:ALA:HB1	2.50	0.46
75:BI:119:TYR:CE1	75:BI:135:VAL:HG23	2.51	0.46
83:BQ:1448:U:O2	83:BQ:1448:U:H2'	2.15	0.46
83:BQ:2418:G:H22	86:BT:73:LEU:HG	1.80	0.46
86:BT:7:THR:C	86:BT:9:GLU:H	2.24	0.46
1:2:1038:U:O4	1:2:1092:A:C6	2.67	0.46
1:2:1724:U:C4'	45:AE:47:ARG:NH1	2.79	0.46
4:C:27:PHE:CD1	4:C:40:LEU:HD13	2.51	0.46
31:d:125:LEU:HA	31:d:128:LYS:HE2	1.93	0.46
68:BB:64:VAL:HA	68:BB:67:ILE:HD12	1.98	0.46
71:BE:354:VAL:O	71:BE:358:THR:HG23	2.16	0.46
79:BM:41:ILE:HG21	79:BM:163:PHE:CD2	2.50	0.46
83:BQ:357:A:H2'	83:BQ:358:G:O4'	2.16	0.46
83:BQ:877:C:O2'	83:BQ:880:G:H1'	2.16	0.46
83:BQ:942:U:OP1	83:BQ:1434:G:N7	2.49	0.46
1:2:348:U:H4'	23:V:14:THR:HG22	1.96	0.45
1:2:1368:G:N2	1:2:1369:U:O4'	2.49	0.45
2:A:201:ALA:HB3	8:G:42:GLN:HE22	1.81	0.45
23:V:36:THR:HG23	23:V:36:THR:O	2.16	0.45
16:O:103:PHE:HB3	16:O:134:TRP:CZ3	2.51	0.45
57:AQ:79:ALA:O	57:AQ:80:THR:HG23	2.16	0.45
81:BO:83:LEU:CD2	81:BO:139:PRO:HG3	2.46	0.45
83:BQ:1337:A:H2'	83:BQ:1338:C:O4'	2.16	0.45
83:BQ:2998:U:H2'	83:BQ:2999:U:O4'	2.16	0.45
8:G:84:TYR:CD2	8:G:85:VAL:HG23	2.51	0.45
21:T:151:ASP:CG	45:AE:98:PRO:CG	2.80	0.45
37:n:19:U:O4	56:AP:104:LEU:O	2.33	0.45
40:k:128:LYS:O	40:k:141:LEU:HD12	2.16	0.45
41:AA:241:LYS:HB3	83:BQ:2586:G:N7	2.31	0.45
61:AU:120:VAL:O	61:AU:124:LEU:HD13	2.16	0.45
71:BE:148:ILE:HA	71:BE:149:PRO:C	2.41	0.45
83:BQ:3306:U:O2	83:BQ:3306:U:O4'	2.33	0.45
19:R:168:ARG:HD3	19:R:170:ILE:HD11	1.99	0.45
23:V:26:LYS:O	23:V:28:GLU:N	2.49	0.45
23:V:121:LEU:HD23	23:V:160:PHE:CG	2.51	0.45
36:m:74:C:N1	83:BQ:2924:U:O2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:899:LEU:HD22	38:h:900:LYS:N	2.31	0.45
39:i:534:VAL:CG2	39:i:544:VAL:HG21	2.37	0.45
40:j:45:LEU:HD22	40:j:51:PRO:HG2	1.99	0.45
40:k:258:GLY:HA3	40:k:294:VAL:HG23	1.98	0.45
60:AT:8:VAL:O	60:AT:11:THR:HG22	2.17	0.45
63:AW:59:ALA:HB2	63:AW:78:ALA:HB2	1.98	0.45
83:BQ:623:U:H2'	83:BQ:624:G:O4'	2.16	0.45
83:BQ:1520:G:H2'	83:BQ:1521:G:O4'	2.16	0.45
83:BQ:2228:A:H2'	83:BQ:2229:A:C8	2.51	0.45
36:m:75:C:O2	83:BQ:2876:C:O2'	2.32	0.45
74:BH:77:VAL:HG13	74:BH:126:VAL:CG2	2.43	0.45
1:2:987:G:H22	63:AW:248:GLY:CA	2.28	0.45
7:F:18:ALA:HA	7:F:69:VAL:HG12	1.99	0.45
9:H:143:ARG:HB3	9:H:144:ARG:CB	2.46	0.45
20:S:139:VAL:HG13	20:S:150:PRO:HG3	1.97	0.45
37:n:74:C:C2	83:BQ:2621:G:C2	2.89	0.45
64:AX:60:PHE:CE2	64:AX:82:ARG:HB3	2.51	0.45
68:BB:16:ARG:HD2	68:BB:53:PHE:O	2.17	0.45
68:BB:103:ALA:HB3	68:BB:106:PHE:CE2	2.51	0.45
71:BE:210:ALA:HB2	71:BE:254:ALA:CA	2.46	0.45
75:BI:115:LEU:O	75:BI:117:GLU:N	2.50	0.45
79:BM:52:VAL:HG23	79:BM:67:GLY:HA2	1.98	0.45
83:BQ:1055:A:N3	84:BR:81:U:O2'	2.46	0.45
83:BQ:1077:U:O2	83:BQ:1083:G:C2	2.70	0.45
83:BQ:1192:C:N4	83:BQ:1302:A:OP1	2.50	0.45
83:BQ:3077:A:N6	83:BQ:3080:G:C5	2.84	0.45
1:2:1118:G:OP2	59:AS:21:ARG:NH1	2.48	0.45
39:i:1166:LEU:HD13	39:i:1182:PHE:CD1	2.52	0.45
62:AV:26:THR:HG23	83:BQ:1065:A:N1	2.31	0.45
71:BE:181:VAL:O	71:BE:182:LEU:HB2	2.16	0.45
83:BQ:1696:A:C2	83:BQ:1697:A:C5	3.05	0.45
83:BQ:3007:U:C2	83:BQ:3008:A:C8	3.05	0.45
1:2:699:U:H2'	1:2:700:C:C5	2.51	0.45
11:J:19:ILE:HA	11:J:96:PRO:HA	1.99	0.45
23:V:72:ILE:HG21	23:V:112:TRP:CE2	2.52	0.45
24:W:93:LEU:O	24:W:96:VAL:HG22	2.17	0.45
31:d:62:THR:HG22	31:d:69:SER:OG	2.17	0.45
37:n:74:C:C4	83:BQ:2621:G:N2	2.78	0.45
39:i:4:ILE:HG21	39:i:37:ASN:HD21	1.81	0.45
39:i:247:TYR:O	39:i:251:VAL:HG23	2.17	0.45
40:k:290:HIS:CD2	40:k:294:VAL:HG22	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AA:81:THR:HG21	41:AA:181:LYS:CD	2.47	0.45
64:AX:67:ILE:HG23	64:AX:82:ARG:HE	1.82	0.45
83:BQ:118:U:C5	83:BQ:119:U:C5	3.04	0.45
83:BQ:2610:G:H2'	83:BQ:2611:U:O4'	2.17	0.45
85:BS:8:C:H2'	85:BS:9:A:C8	2.52	0.45
9:H:120:ARG:NH1	83:BQ:1025:A:O2'	2.50	0.45
39:i:471:ARG:HH22	39:i:507:ASN:HD22	1.65	0.45
64:AX:41:LEU:HD13	64:AX:112:LEU:HD23	1.99	0.45
75:BI:102:GLY:O	75:BI:105:ILE:HG22	2.17	0.45
83:BQ:908:G:N3	83:BQ:925:A:N7	2.64	0.45
83:BQ:989:A:H2'	83:BQ:990:U:O4'	2.17	0.45
83:BQ:1105:A:H2'	83:BQ:1106:G:O4'	2.17	0.45
83:BQ:2612:U:C2	83:BQ:2804:A:C6	3.04	0.45
86:BT:58:HIS:ND1	86:BT:72:ASP:O	2.50	0.45
1:2:1116:A:OP1	59:AS:14:LYS:HG2	2.17	0.45
1:2:1126:G:O5'	59:AS:11:ARG:NH1	2.48	0.45
1:2:1732:A:H2'	1:2:1733:C:C6	2.52	0.45
7:F:18:ALA:CB	7:F:69:VAL:HG12	2.47	0.45
38:h:621:LEU:HB2	38:h:629:MET:HE1	1.99	0.45
40:k:274:LEU:HD13	40:k:318:TRP:CG	2.51	0.45
64:AX:139:TYR:CE1	83:BQ:2355:G:H4'	2.52	0.45
68:BB:150:VAL:HG23	68:BB:153:PHE:CD2	2.52	0.45
73:BG:23:ASP:OD1	73:BG:23:ASP:N	2.50	0.45
83:BQ:125:C:H2'	83:BQ:126:U:C6	2.52	0.45
83:BQ:1782:U:H2'	83:BQ:1783:U:O4'	2.17	0.45
83:BQ:1914:G:C8	83:BQ:2115:G:C2	3.05	0.45
83:BQ:2373:A:N3	83:BQ:2824:G:O2'	2.42	0.45
83:BQ:2886:U:C4	83:BQ:2911:A:C5	3.05	0.45
86:BT:51:5CT:H10	86:BT:51:5CT:H3	1.58	0.45
1:2:55:A:H2'	1:2:403:G:N2	2.32	0.44
1:2:385:A:H2'	1:2:386:G:C8	2.53	0.44
21:T:131:LYS:NZ	45:AE:81:PRO:CB	2.80	0.44
38:h:678:LEU:HD23	38:h:1225:LYS:HG2	2.00	0.44
46:AF:22:CYS:HB3	46:AF:37:CYS:HB3	1.85	0.44
56:AP:85:LEU:N	56:AP:85:LEU:HD12	2.31	0.44
57:AQ:99:ARG:NH2	57:AQ:118:SER:O	2.50	0.44
72:BF:100:ARG:NH1	83:BQ:1722:U:OP1	2.51	0.44
83:BQ:1185:C:C4	83:BQ:1186:G:N7	2.85	0.44
50:AJ:58:VAL:HG13	83:BQ:75:G:H5'	1.98	0.44
52:AL:2:ALA:O	52:AL:4:GLN:N	2.51	0.44
83:BQ:907:G:N2	83:BQ:925:A:O2'	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:m:19:G:O4'	36:m:57:G:N2	2.50	0.44
39:i:675:LYS:N	39:i:676:PRO:HA	2.32	0.44
67:BA:161:LEU:HD22	67:BA:180:GLU:HG2	1.98	0.44
2:A:164:VAL:HG13	2:A:168:ILE:HD11	1.98	0.44
9:H:143:ARG:HG2	9:H:144:ARG:HD2	1.99	0.44
12:K:93:SER:HA	12:K:100:ILE:HG23	1.99	0.44
19:R:169:LEU:HD23	19:R:198:THR:HG22	1.99	0.44
26:Y:96:VAL:HG22	26:Y:146:ALA:HB1	1.99	0.44
30:c:84:THR:HB	30:c:120:VAL:HG22	1.99	0.44
37:n:73:G:H1'	70:BD:109:ARG:HD3	1.99	0.44
39:i:78:PRO:HA	39:i:84:TRP:CZ2	2.52	0.44
50:AJ:179:PHE:O	50:AJ:180:ARG:C	2.61	0.44
71:BE:20:LEU:HD11	71:BE:252:GLU:HG3	1.99	0.44
71:BE:74:ILE:HB	71:BE:75:PRO:HD2	2.00	0.44
83:BQ:3343:G:C2	83:BQ:3361:G:C2	3.05	0.44
1:2:360:A:O2'	1:2:362:G:OP1	2.29	0.44
1:2:851:U:OP1	72:BF:165:LYS:HD2	2.16	0.44
1:2:851:U:H5''	72:BF:172:ARG:NH2	2.30	0.44
4:C:46:LEU:O	4:C:50:THR:HG23	2.17	0.44
17:P:157:ASP:O	17:P:158:VAL:C	2.60	0.44
38:h:680:GLN:HE22	38:h:699:LEU:HA	1.82	0.44
39:i:277:VAL:HG13	39:i:277:VAL:O	2.18	0.44
40:j:29:THR:O	40:j:41:TRP:N	2.51	0.44
40:j:183:MET:HE3	40:j:204:PHE:CD2	2.53	0.44
64:AX:51:VAL:O	64:AX:52:LEU:C	2.59	0.44
66:AZ:56:UNK:O	66:AZ:57:UNK:CB	2.65	0.44
83:BQ:1317:A:O2'	83:BQ:1318:A:C2'	2.66	0.44
83:BQ:1481:A:H2'	83:BQ:1481:A:N3	2.32	0.44
83:BQ:1930:A:C8	83:BQ:1932:A:O4'	2.70	0.44
83:BQ:2612:U:C2	83:BQ:2804:A:C5	3.05	0.44
86:BT:152:GLU:HG2	86:BT:153:ALA:O	2.17	0.44
1:2:19:A:H2'	1:2:20:G:O4'	2.17	0.44
20:S:123:LEU:HD13	20:S:236:ILE:HD11	1.99	0.44
24:W:77:ILE:HG21	24:W:91:LYS:HG3	1.99	0.44
63:AW:230:VAL:HG22	63:AW:231:SER:H	1.83	0.44
6:E:96:ILE:HD13	6:E:116:LEU:O	2.17	0.44
8:G:35:CYS:HA	8:G:38:ILE:HG22	2.00	0.44
9:H:16:ARG:HD2	47:AG:110:ILE:HB	2.00	0.44
26:Y:26:PHE:CD2	26:Y:66:ILE:HD11	2.52	0.44
37:n:56:C:C5	56:AP:104:LEU:HD21	2.52	0.44
39:i:103:TYR:HA	39:i:107:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:j:175:LEU:HD21	40:j:178:THR:CG2	2.45	0.44
56:AP:64:THR:O	86:BT:16:SER:O	2.34	0.44
83:BQ:2243:A:H1'	83:BQ:2313:A:H2'	1.99	0.44
83:BQ:2535:A:H2'	83:BQ:2536:A:O4'	2.18	0.44
83:BQ:2902:A:H2'	83:BQ:2903:A:O4'	2.18	0.44
1:2:339:C:O2'	23:V:87:ASN:CG	2.61	0.44
25:X:59:PRO:HG3	25:X:66:ILE:HD11	1.99	0.44
41:AA:75:ILE:O	41:AA:76:ALA:HB3	2.18	0.44
64:AX:29:THR:HA	64:AX:32:THR:HG22	2.00	0.44
83:BQ:160:G:H2'	83:BQ:161:G:O4'	2.18	0.44
83:BQ:2193:U:O2	83:BQ:2193:U:O4'	2.35	0.44
83:BQ:3078:U:O2	83:BQ:3078:U:H2'	2.17	0.44
1:2:330:G:H1'	23:V:200:LYS:O	2.18	0.44
1:2:973:A:H5'	83:BQ:848:A:H2	1.82	0.44
30:c:93:LEU:HD21	34:g:8:LEU:HD13	2.00	0.44
39:i:173:LEU:CD2	39:i:224:TYR:CD2	2.99	0.44
39:i:500:ILE:HD12	39:i:507:ASN:HB2	1.99	0.44
60:AT:54:ILE:HG23	63:AW:48:ILE:CD1	2.48	0.44
83:BQ:283:G:OP2	83:BQ:285:A:H4'	2.18	0.44
83:BQ:3084:C:O2'	83:BQ:3332:U:H5''	2.18	0.44
86:BT:66:THR:HG22	86:BT:68:LYS:HG2	1.99	0.44
1:2:813:U:H5	72:BF:163:ARG:HD2	1.79	0.43
1:2:1114:G:HO2'	1:2:1115:U:P	2.41	0.43
1:2:1545:A:H5'	9:H:133:VAL:HG12	1.99	0.43
40:k:247:LEU:HD13	40:k:320:VAL:HG11	1.99	0.43
43:AC:6:GLY:O	43:AC:7:ILE:HG23	2.18	0.43
56:AP:2:VAL:HG11	83:BQ:2654:C:C5	2.52	0.43
83:BQ:2208:A:O2'	83:BQ:2209:U:OP1	2.26	0.43
1:2:42:G:O2'	1:2:430:G:N1	2.51	0.43
1:2:1147:A:H2'	1:2:1148:C:O4'	2.17	0.43
1:2:1595:U:C4	1:2:1600:A:C6	3.04	0.43
37:n:73:G:H21	70:BD:109:ARG:NE	2.16	0.43
39:i:143:LYS:CD	39:i:176:ILE:CB	2.95	0.43
54:AN:54:THR:HG22	54:AN:57:HIS:CG	2.53	0.43
58:AR:49:HIS:N	58:AR:50:PRO:CD	2.80	0.43
83:BQ:632:G:H2'	83:BQ:633:C:C6	2.53	0.43
83:BQ:2433:U:H3	83:BQ:2595:A:N6	2.16	0.43
83:BQ:2503:G:H2'	83:BQ:2504:U:O4'	2.18	0.43
83:BQ:2733:A:H2'	83:BQ:2734:A:O4'	2.18	0.43
83:BQ:2873:U:O4'	83:BQ:2873:U:O2	2.33	0.43
1:2:173:A:H2'	1:2:174:U:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:432:G:C6	1:2:433:C:N3	2.86	0.43
1:2:1475:A:O2'	1:2:1540:G:O3'	2.37	0.43
22:U:143:LEU:HD12	22:U:147:ASN:HB2	1.99	0.43
38:h:779:ALA:HB2	38:h:784:LEU:HD11	2.00	0.43
41:AA:180:VAL:HG11	41:AA:186:LEU:HD21	2.01	0.43
64:AX:165:VAL:O	64:AX:165:VAL:HG13	2.18	0.43
86:BT:95:ILE:HG13	86:BT:95:ILE:O	2.18	0.43
1:2:16:G:H2'	1:2:17:C:C6	2.54	0.43
1:2:1171:A:O2'	1:2:1172:G:P	2.77	0.43
9:H:21:ASN:OD1	47:AG:116:TYR:CB	2.67	0.43
17:P:146:LEU:HD22	17:P:173:ILE:HG21	2.00	0.43
21:T:55:GLY:HA3	21:T:63:MET:HE2	2.00	0.43
25:X:108:PRO:HB2	25:X:135:VAL:HG22	1.99	0.43
27:Z:106:ALA:HA	27:Z:112:ILE:HD11	1.99	0.43
31:d:123:LYS:C	31:d:125:LEU:N	2.73	0.43
39:i:528:MET:SD	39:i:555:MET:HE3	2.59	0.43
39:i:1398:MET:HE3	39:i:1402:TYR:CE2	2.52	0.43
83:BQ:3375:A:H2'	83:BQ:3375:A:N3	2.33	0.43
84:BR:13:A:OP1	84:BR:111:U:H1'	2.18	0.43
1:2:990:C:H2'	1:2:991:G:O4'	2.18	0.43
1:2:1038:U:C4	1:2:1092:A:C6	3.06	0.43
1:2:1145:U:C4	1:2:1146:G:C4	3.06	0.43
3:B:36:ALA:HB1	3:B:42:LEU:HD11	1.99	0.43
3:B:97:LEU:HD21	3:B:194:LEU:HD22	2.01	0.43
5:D:125:ASN:O	5:D:127:GLY:N	2.49	0.43
18:Q:88:VAL:HG13	18:Q:96:LEU:HD13	2.00	0.43
23:V:72:ILE:HG21	23:V:112:TRP:CZ2	2.53	0.43
36:m:76:A:O2'	83:BQ:2954:U:H5	1.94	0.43
37:n:74:C:N4	83:BQ:2620:G:H1	2.16	0.43
38:h:1202:GLU:O	38:h:1204:LEU:N	2.51	0.43
40:k:129:TRP:CD2	40:k:141:LEU:HD13	2.52	0.43
43:AC:44:VAL:HG21	57:AQ:9:GLU:HB3	2.00	0.43
57:AQ:117:ASN:C	57:AQ:133:ILE:HG22	2.43	0.43
81:BO:84:VAL:HG13	81:BO:119:VAL:HG21	2.00	0.43
83:BQ:1064:A:N6	83:BQ:1096:U:O4	2.52	0.43
83:BQ:1319:G:C6	83:BQ:1320:C:C4	3.07	0.43
83:BQ:2696:A:N7	83:BQ:2758:A:N6	2.66	0.43
1:2:601:A:H2'	1:2:602:U:O4'	2.18	0.43
1:2:814:A:C2	72:BF:170:ARG:CZ	2.99	0.43
1:2:1227:A:C8	1:2:1229:G:N2	2.86	0.43
19:R:116:LYS:HG2	19:R:127:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:181:VAL:CG1	20:S:225:VAL:HG13	2.48	0.43
23:V:195:ARG:HB2	23:V:196:LEU:HD13	2.01	0.43
36:m:74:C:H5	83:BQ:2924:U:C4	2.17	0.43
37:n:56:C:C5'	47:AG:61:ARG:HH12	2.30	0.43
38:h:404:ILE:HD12	38:h:419:MET:HE2	2.01	0.43
40:j:70:VAL:HG23	40:j:84:VAL:HG22	2.00	0.43
40:j:251:ALA:HB2	40:j:297:LEU:HD13	2.00	0.43
65:AY:10:ILE:HD11	65:AY:104:LEU:HD23	2.01	0.43
83:BQ:2855:U:H2'	83:BQ:2856:G:O4'	2.18	0.43
85:BS:15:G:C2	85:BS:16:G:N2	2.87	0.43
1:2:1535:U:O2'	1:2:1536:G:N3	2.51	0.43
10:I:82:GLY:O	10:I:83:ALA:HB3	2.18	0.43
12:K:39:ALA:O	12:K:72:GLY:N	2.51	0.43
38:h:98:ILE:HD11	39:i:987:GLU:HG2	2.00	0.43
39:i:113:TYR:CE2	39:i:127:LEU:HD22	2.53	0.43
47:AG:17:LEU:HD13	47:AG:129:VAL:HG22	2.00	0.43
60:AT:34:HIS:NE2	83:BQ:1792:C:OP2	2.50	0.43
80:BN:41:ARG:HG2	80:BN:56:THR:HG21	2.00	0.43
83:BQ:1481:A:O2'	83:BQ:1482:A:OP2	2.37	0.43
1:2:30:G:H2'	1:2:31:C:C6	2.54	0.43
1:2:329:G:O2'	23:V:84:HIS:HB3	2.19	0.43
1:2:1746:A:N1	83:BQ:2302:G:O2'	2.47	0.43
2:A:109:LEU:HD21	2:A:115:ILE:CD1	2.49	0.43
7:F:35:PRO:CG	7:F:38:LEU:HD12	2.48	0.43
37:n:75:C:N4	83:BQ:2620:G:N1	2.64	0.43
38:h:365:ILE:HD12	38:h:396:PHE:CZ	2.54	0.43
38:h:380:PRO:HG2	38:h:381:ILE:HD12	2.00	0.43
39:i:317:LEU:HD21	39:i:321:LEU:HD13	2.00	0.43
83:BQ:431:U:N3	83:BQ:432:G:N7	2.66	0.43
83:BQ:2433:U:N3	83:BQ:2595:A:N6	2.67	0.43
84:BR:8:G:H2'	84:BR:9:C:O4'	2.19	0.43
1:2:1646:C:OP1	83:BQ:2259:A:C2	2.72	0.43
11:J:48:HIS:NE2	11:J:99:ILE:HD13	2.34	0.43
16:O:67:ILE:HD12	16:O:85:TRP:CE3	2.54	0.43
38:h:365:ILE:HD12	38:h:396:PHE:CE2	2.54	0.43
38:h:741:ILE:HD11	38:h:777:VAL:HG13	2.00	0.43
44:AD:112:ILE:HG21	44:AD:161:LEU:CD1	2.49	0.43
57:AQ:133:ILE:HG23	57:AQ:133:ILE:O	2.18	0.43
63:AW:179:LEU:HD13	83:BQ:1793:C:C5	2.53	0.43
68:BB:4:ASP:CB	81:BO:92:ILE:HD13	2.49	0.43
81:BO:141:TYR:HA	81:BO:189:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:324:A:H2'	83:BQ:325:A:C8	2.53	0.43
83:BQ:859:G:C6	83:BQ:861:C:C4	3.07	0.43
83:BQ:2525:G:O2'	83:BQ:2526:C:OP2	2.30	0.43
83:BQ:3000:A:H2'	83:BQ:3001:C:C6	2.53	0.43
85:BS:45:C:H2'	85:BS:46:G:O4'	2.19	0.43
1:2:121:U:C4	1:2:122:U:C4	3.07	0.43
1:2:123:G:O2'	20:S:146:THR:N	2.52	0.43
1:2:1317:C:H2'	1:2:1318:G:O4'	2.19	0.43
9:H:30:TYR:O	9:H:33:THR:OG1	2.30	0.43
39:i:500:ILE:HD12	39:i:507:ASN:CB	2.49	0.43
46:AF:12:HIS:O	46:AF:12:HIS:ND1	2.52	0.43
57:AQ:160:GLU:OE1	57:AQ:160:GLU:N	2.52	0.43
72:BF:99:LEU:HD21	72:BF:103:ARG:NE	2.34	0.43
83:BQ:1047:A:N3	83:BQ:2633:U:O2'	2.51	0.43
83:BQ:1286:A:O2'	83:BQ:1287:A:H4'	2.19	0.43
1:2:106:U:H2'	1:2:107:C:O4'	2.18	0.42
38:h:986:ARG:CD	38:h:1019:LEU:HD11	2.48	0.42
39:i:151:PRO:C	39:i:230:ILE:HD13	2.21	0.42
39:i:1301:LEU:HD22	39:i:1339:ALA:CB	2.50	0.42
67:BA:29:VAL:HG22	67:BA:337:THR:HG21	1.99	0.42
67:BA:247:ARG:HD2	83:BQ:1888:U:OP1	2.19	0.42
83:BQ:2612:U:C2	83:BQ:2804:A:N7	2.85	0.42
86:BT:30:GLY:O	86:BT:41:ILE:HD12	2.19	0.42
1:2:50:C:O2	1:2:50:C:C2'	2.67	0.42
1:2:955:A:H2'	1:2:956:C:O4'	2.19	0.42
1:2:956:C:O3'	1:2:1047:G:N2	2.52	0.42
3:B:68:ILE:HD12	3:B:71:ALA:HA	2.01	0.42
3:B:123:VAL:HG22	12:K:92:ILE:HD11	2.01	0.42
22:U:143:LEU:HD11	22:U:149:ILE:HD12	2.01	0.42
27:Z:81:VAL:HB	27:Z:115:ILE:HG22	2.01	0.42
39:i:668:ILE:HD13	39:i:684:ILE:HD11	2.01	0.42
57:AQ:172:ARG:NE	57:AQ:174:ILE:HD11	2.34	0.42
63:AW:57:PRO:HD2	63:AW:170:ALA:HB3	2.00	0.42
63:AW:203:ALA:HA	63:AW:217:GLN:HE21	1.84	0.42
67:BA:53:MET:HE2	67:BA:77:THR:CG2	2.46	0.42
82:BP:9:LEU:HB3	82:BP:17:LEU:HD21	2.01	0.42
83:BQ:281:G:C6	83:BQ:282:G:C6	3.07	0.42
83:BQ:828:A:N1	83:BQ:895:A:N6	2.67	0.42
83:BQ:2167:A:N6	83:BQ:2168:A:N1	2.67	0.42
83:BQ:2794:G:C8	83:BQ:2795:U:C4	3.07	0.42
85:BS:77:A:H2'	85:BS:78:G:O4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:12:U:H2'	1:2:13:C:C6	2.54	0.42
11:J:53:LYS:HB2	11:J:92:ASP:HB2	2.02	0.42
23:V:29:LEU:HD21	23:V:31:ARG:CZ	2.49	0.42
38:h:1167:VAL:CG1	38:h:1171:LEU:HD12	2.49	0.42
39:i:811:VAL:HG13	39:i:841:ILE:HD11	2.01	0.42
56:AP:38:GLN:OE1	56:AP:41:ARG:NH1	2.52	0.42
57:AQ:155:VAL:O	57:AQ:162:ARG:NH2	2.52	0.42
63:AW:150:LEU:HB3	63:AW:151:PRO:HD2	2.01	0.42
83:BQ:1064:A:H4'	83:BQ:1065:A:O5'	2.19	0.42
83:BQ:2273:G:O2'	83:BQ:2274:U:P	2.77	0.42
83:BQ:2886:U:C5	83:BQ:2911:A:C5	3.07	0.42
1:2:68:A:H4'	1:2:69:G:OP2	2.19	0.42
1:2:1030:A:C8	32:e:10:ARG:O	2.72	0.42
9:H:120:ARG:HG3	83:BQ:1025:A:H2	1.84	0.42
39:i:878:VAL:HB	39:i:881:LEU:HD12	2.01	0.42
75:BI:40:HIS:CD2	75:BI:42:ALA:HB3	2.55	0.42
81:BO:219:LYS:HD3	83:BQ:1169:A:H4'	2.02	0.42
83:BQ:767:U:C2	83:BQ:768:C:C6	3.08	0.42
83:BQ:3159:C:H2'	83:BQ:3160:U:O4'	2.19	0.42
84:BR:84:A:H2'	84:BR:85:G:C8	2.54	0.42
1:2:371:G:N2	1:2:612:U:O2	2.53	0.42
1:2:1233:G:H2'	1:2:1234:A:O4'	2.19	0.42
33:f:64:CYS:HB3	33:f:73:LEU:HD23	2.01	0.42
60:AT:47:VAL:HA	60:AT:56:THR:O	2.19	0.42
64:AX:31:GLU:N	64:AX:31:GLU:OE1	2.53	0.42
69:BC:20:LEU:HD11	69:BC:32:ALA:HB2	2.01	0.42
83:BQ:94:G:H2'	83:BQ:95:A:C8	2.54	0.42
83:BQ:1721:U:O2'	83:BQ:1723:A:N7	2.38	0.42
85:BS:19:C:C4	85:BS:20:U:C4	3.07	0.42
86:BT:42:VAL:HG13	86:BT:43:ASP:N	2.35	0.42
1:2:1069:A:H2'	1:2:1070:C:O4'	2.19	0.42
1:2:1767:G:H4'	1:2:1768:G:O5'	2.20	0.42
1:2:1783:C:C5	59:AS:5:TRP:CE2	3.07	0.42
23:V:77:ARG:O	23:V:104:ILE:HG22	2.19	0.42
38:h:148:VAL:HG13	38:h:427:MET:HG2	2.01	0.42
39:i:534:VAL:HG11	39:i:544:VAL:CG1	2.49	0.42
39:i:1264:VAL:HG13	39:i:1298:LEU:HD23	2.02	0.42
48:AH:79:GLY:HA3	48:AH:81:ILE:HD12	2.02	0.42
58:AR:74:ASN:HA	58:AR:113:LEU:O	2.20	0.42
83:BQ:833:G:H2'	83:BQ:834:U:O4'	2.19	0.42
83:BQ:1481:A:O2'	83:BQ:1858:A:C2	2.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:1856:C:H2'	83:BQ:1857:C:C6	2.55	0.42
83:BQ:1912:U:N3	83:BQ:2122:G:OP2	2.47	0.42
83:BQ:2193:U:C5	83:BQ:2313:A:N7	2.87	0.42
83:BQ:2406:C:H2'	83:BQ:2407:C:C6	2.54	0.42
83:BQ:2516:U:O2	83:BQ:2594:C:N4	2.53	0.42
83:BQ:3357:U:H2'	83:BQ:3358:U:C6	2.54	0.42
1:2:431:C:H2'	1:2:432:G:C8	2.54	0.42
1:2:962:C:C4	1:2:963:A:C2	3.08	0.42
1:2:1784:C:H5	59:AS:5:TRP:CE2	2.17	0.42
5:D:31:VAL:HG21	5:D:136:ILE:HD11	2.02	0.42
20:S:12:LEU:HD23	20:S:13:ALA:N	2.35	0.42
22:U:39:ARG:NH1	72:BF:181:ARG:O	2.49	0.42
36:m:76:A:O2'	83:BQ:2954:U:O4	2.36	0.42
39:i:468:LEU:HD23	39:i:471:ARG:HD3	2.01	0.42
39:i:841:ILE:HG21	39:i:859:LEU:HD12	2.01	0.42
41:AA:185:ARG:CZ	85:BS:155:A:H4'	2.49	0.42
44:AD:41:ILE:O	44:AD:42:ASP:HB2	2.20	0.42
46:AF:21:ARG:NH2	46:AF:41:ALA:O	2.53	0.42
51:AK:52:ARG:NH2	85:BS:72:A:N7	2.68	0.42
63:AW:3:ARG:HD3	83:BQ:911:C:N4	2.34	0.42
67:BA:77:THR:HG23	67:BA:326:GLY:O	2.20	0.42
74:BH:124:LEU:HD23	76:BJ:153:PRO:HB2	2.01	0.42
80:BN:56:THR:O	80:BN:57:LEU:HD23	2.19	0.42
83:BQ:636:C:C3'	83:BQ:637:C:H5'	2.50	0.42
83:BQ:1504:A:C5	83:BQ:1505:C:C5	3.08	0.42
83:BQ:1532:C:H2'	83:BQ:1533:U:O4'	2.20	0.42
23:V:162:ALA:CA	83:BQ:3353:G:OP2	2.60	0.42
37:n:75:C:N4	83:BQ:2620:G:H1	2.18	0.42
40:k:140:ARG:NE	40:k:214:LEU:HD21	2.34	0.42
63:AW:43:GLY:HA3	63:AW:63:PHE:CD1	2.55	0.42
85:BS:115:C:H2'	85:BS:116:G:O4'	2.20	0.42
85:BS:149:A:H2'	85:BS:150:G:C8	2.54	0.42
86:BT:124:LEU:HD11	86:BT:136:VAL:HG21	2.00	0.42
1:2:200:A:H2'	1:2:201:G:O4'	2.20	0.42
1:2:628:G:O2'	83:BQ:846:A:C5	2.73	0.42
1:2:1147:A:H2'	1:2:1148:C:C6	2.55	0.42
1:2:1530:C:OP2	12:K:95:HIS:HB2	2.20	0.42
7:F:45:ARG:O	7:F:48:VAL:HG12	2.19	0.42
8:G:87:GLU:O	8:G:88:VAL:HG12	2.18	0.42
38:h:384:LEU:HD21	38:h:727:MET:HB3	2.01	0.42
39:i:20:TYR:HB3	39:i:47:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:774:TYR:CE1	39:i:778:ILE:HD11	2.55	0.42
45:AE:16:GLY:N	67:BA:73:VAL:HG11	2.35	0.42
58:AR:75:LEU:HD23	58:AR:78:LEU:HD13	2.00	0.42
81:BO:108:LEU:HD22	81:BO:114:GLY:HA2	2.02	0.42
83:BQ:271:C:H2'	83:BQ:272:G:O4'	2.20	0.42
83:BQ:340:C:N4	83:BQ:341:G:O6	2.53	0.42
83:BQ:1624:G:H2'	83:BQ:1625:A:C8	2.55	0.42
83:BQ:3385:U:H2'	83:BQ:3386:G:O4'	2.20	0.42
1:2:156:A:C2'	1:2:157:A:H5'	2.49	0.42
3:B:99:MET:O	3:B:100:ASN:HB2	2.19	0.42
22:U:51:VAL:HG11	22:U:168:SER:HA	2.02	0.42
24:W:139:GLN:HE22	31:d:63:GLN:HG3	1.85	0.42
39:i:173:LEU:C	39:i:175:LYS:N	2.77	0.42
40:k:278:THR:HB	40:k:342:ILE:HD12	2.00	0.42
54:AN:36:HIS:NE2	54:AN:74:VAL:HG11	2.35	0.42
57:AQ:136:ASP:O	57:AQ:142:ILE:HD13	2.19	0.42
58:AR:62:HIS:CG	58:AR:62:HIS:O	2.72	0.42
62:AV:17:HIS:CD2	62:AV:21:ILE:HD11	2.55	0.42
71:BE:129:THR:HG21	71:BE:248:VAL:HG21	2.02	0.42
80:BN:107:GLU:O	80:BN:111:ALA:HB3	2.20	0.42
83:BQ:61:A:H2'	83:BQ:62:A:O4'	2.19	0.42
83:BQ:339:C:OP1	83:BQ:1380:G:O2'	2.36	0.42
83:BQ:423:A:H2'	83:BQ:424:G:O4'	2.20	0.42
83:BQ:988:U:H2'	83:BQ:989:A:O4'	2.20	0.42
16:O:222:LEU:HD21	16:O:265:LEU:HD21	2.02	0.41
23:V:23:LYS:O	23:V:24:LYS:C	2.62	0.41
23:V:95:THR:O	23:V:97:THR:HG23	2.20	0.41
36:m:74:C:N4	83:BQ:2924:U:C5	2.87	0.41
39:i:98:PRO:O	39:i:101:LEU:N	2.53	0.41
39:i:1360:TRP:CE3	39:i:1373:VAL:HG23	2.54	0.41
50:AJ:48:PRO:HB2	82:BP:117:ALA:HB2	2.02	0.41
65:AY:43:ILE:CD1	65:AY:92:ILE:HD11	2.50	0.41
78:BL:43:VAL:HG11	78:BL:69:ALA:CB	2.49	0.41
83:BQ:651:G:H2'	83:BQ:652:G:O4'	2.19	0.41
83:BQ:2332:A:C6	83:BQ:2333:C:C2	3.08	0.41
83:BQ:3346:U:H1'	83:BQ:3347:A:H5''	2.02	0.41
83:BQ:3355:U:H3'	83:BQ:3356:G:C5'	2.50	0.41
84:BR:86:U:O2'	84:BR:87:G:P	2.77	0.41
86:BT:102:LEU:HD23	86:BT:113:VAL:HG21	2.02	0.41
1:2:915:A:H2'	1:2:915:A:N3	2.35	0.41
1:2:1609:U:H2'	1:2:1610:G:O4'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1746:A:H2	83:BQ:2302:G:N3	2.17	0.41
1:2:1783:C:C4	59:AS:5:TRP:CD2	3.07	0.41
4:C:29:GLN:O	4:C:30:ALA:HB3	2.21	0.41
36:m:63:U:O2'	83:BQ:2852:C:C5'	2.64	0.41
39:i:121:GLU:CB	39:i:124:GLN:CA	2.97	0.41
39:i:1042:LEU:HD23	39:i:1045:LEU:HD12	2.02	0.41
39:i:1397:GLU:O	39:i:1401:LEU:HG	2.21	0.41
53:AM:55:ARG:HD3	74:BH:70:THR:HB	2.00	0.41
64:AX:32:THR:HG21	64:AX:87:SER:HB3	2.02	0.41
68:BB:103:ALA:HB3	68:BB:106:PHE:CZ	2.55	0.41
70:BD:95:VAL:HG22	70:BD:124:LEU:HD21	2.01	0.41
83:BQ:655:C:H2'	83:BQ:656:A:H8	1.85	0.41
83:BQ:763:G:C2	83:BQ:764:U:H1'	2.55	0.41
83:BQ:835:G:H2'	83:BQ:857:G:N2	2.35	0.41
83:BQ:1260:A:C2	83:BQ:1261:G:N7	2.89	0.41
83:BQ:2577:C:N4	83:BQ:2578:U:C4	2.88	0.41
84:BR:113:C:C4	84:BR:114:U:C4	3.08	0.41
6:E:108:ARG:NH2	83:BQ:1025:A:H2	2.15	0.41
7:F:29:ILE:HG22	7:F:36:ILE:HD12	2.02	0.41
15:N:132:LEU:HD13	15:N:139:LEU:HD23	2.00	0.41
18:Q:126:THR:HG22	18:Q:136:ARG:HG3	2.02	0.41
18:Q:144:ARG:HB3	18:Q:208:GLN:HB3	2.02	0.41
22:U:35:LYS:O	22:U:36:ALA:HB3	2.20	0.41
68:BB:18:ALA:HA	68:BB:53:PHE:CE1	2.55	0.41
71:BE:234:ASN:HD21	71:BE:236:LEU:HD12	1.85	0.41
71:BE:300:ARG:HB2	71:BE:301:PRO:CD	2.51	0.41
76:BJ:17:ARG:NH1	76:BJ:45:ASN:OD1	2.52	0.41
76:BJ:23:GLY:O	76:BJ:24:ALA:C	2.63	0.41
83:BQ:825:U:C2	83:BQ:826:G:C8	3.09	0.41
83:BQ:1238:C:H2'	83:BQ:1239:C:C6	2.55	0.41
83:BQ:1447:G:O2'	83:BQ:1448:U:P	2.78	0.41
83:BQ:1668:G:H2'	83:BQ:1669:C:O4'	2.20	0.41
83:BQ:2513:U:O2'	83:BQ:2514:U:C6	2.72	0.41
83:BQ:3103:A:H2'	83:BQ:3104:U:O4'	2.20	0.41
83:BQ:3279:A:H2'	83:BQ:3280:U:O4'	2.19	0.41
84:BR:24:A:H2'	84:BR:25:G:O4'	2.21	0.41
86:BT:92:LEU:HD12	86:BT:101:SER:O	2.20	0.41
1:2:425:A:H3'	1:2:425:A:OP1	2.21	0.41
1:2:1180:C:H2'	1:2:1181:U:O4'	2.20	0.41
1:2:1533:C:H4'	1:2:1539:G:C6	2.55	0.41
1:2:1780:G:C1'	83:BQ:2262:A:O3'	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:56:LYS:HZ2	17:P:158:VAL:HA	1.85	0.41
19:R:53:ILE:HD11	19:R:73:LEU:HD22	2.02	0.41
20:S:45:ILE:HA	20:S:61:VAL:HG11	2.02	0.41
23:V:95:THR:O	23:V:95:THR:HG22	2.20	0.41
28:a:73:ALA:HB1	28:a:79:LEU:CD1	2.50	0.41
36:m:53:G:P	70:BD:73:LYS:HE2	2.56	0.41
38:h:1266:MET:HB3	40:j:285:LEU:HD12	2.01	0.41
39:i:143:LYS:CG	39:i:176:ILE:CA	2.68	0.41
39:i:1398:MET:HE3	39:i:1402:TYR:CZ	2.56	0.41
40:j:45:LEU:HD22	40:j:51:PRO:HG3	2.01	0.41
65:AY:25:LEU:HD23	65:AY:90:VAL:HG13	2.01	0.41
67:BA:152:LYS:O	67:BA:188:ILE:HD11	2.20	0.41
75:BI:58:LYS:HD2	84:BR:49:G:C8	2.55	0.41
77:BK:32:ILE:HD12	77:BK:81:VAL:HG21	2.02	0.41
81:BO:80:GLN:O	81:BO:81:HIS:C	2.64	0.41
83:BQ:1003:A:N1	83:BQ:1049:C:O2'	2.53	0.41
83:BQ:2719:U:C2	83:BQ:2720:G:C8	3.08	0.41
83:BQ:3293:U:H4'	83:BQ:3294:A:OP1	2.20	0.41
86:BT:95:ILE:HD11	86:BT:125:GLN:HE22	1.85	0.41
1:2:51:A:O4'	1:2:51:A:P	2.79	0.41
1:2:117:U:H2'	1:2:118:U:O4'	2.21	0.41
1:2:447:U:H2'	1:2:448:C:O4'	2.21	0.41
1:2:987:G:C2'	63:AW:249:SER:HB2	2.45	0.41
1:2:1724:U:H4'	45:AE:47:ARG:NH1	2.35	0.41
12:K:59:TYR:HE1	12:K:100:ILE:HD13	1.84	0.41
40:j:241:PHE:CE1	40:j:248:LEU:HD13	2.54	0.41
42:AB:58:VAL:HG23	42:AB:76:ALA:HB3	2.01	0.41
63:AW:102:LEU:HD12	63:AW:102:LEU:N	2.35	0.41
83:BQ:13:A:C6	83:BQ:15:C:C5	3.08	0.41
1:2:1334:U:H2'	1:2:1335:U:O4'	2.20	0.41
1:2:1364:G:N7	1:2:1365:C:C2	2.89	0.41
22:U:64:VAL:O	22:U:64:VAL:HG12	2.20	0.41
25:X:84:ILE:HD13	25:X:117:VAL:HG11	2.01	0.41
39:i:475:LEU:HD22	39:i:508:ILE:HD11	2.02	0.41
40:j:60:VAL:HG11	40:j:65:LEU:HD21	2.01	0.41
54:AN:72:ILE:HD11	54:AN:107:ARG:HD3	2.02	0.41
61:AU:19:LEU:O	61:AU:23:VAL:HG23	2.21	0.41
63:AW:45:VAL:HG13	63:AW:84:THR:HA	2.02	0.41
79:BM:44:ALA:HB1	83:BQ:3273:A:H4'	2.01	0.41
83:BQ:227:G:C2	83:BQ:228:U:C2	3.09	0.41
83:BQ:238:A:H2'	83:BQ:239:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:108:A:H2'	1:2:109:G:C8	2.56	0.41
1:2:1348:A:H2'	1:2:1349:G:O4'	2.21	0.41
1:2:1585:U:O2	1:2:1585:U:C2'	2.68	0.41
4:C:14:TYR:CD2	4:C:35:ILE:HD11	2.55	0.41
9:H:28:ILE:HD12	9:H:61:LEU:CD1	2.51	0.41
27:Z:19:ILE:HG23	27:Z:28:VAL:HG22	2.03	0.41
30:c:43:PHE:CZ	30:c:49:ALA:HB3	2.56	0.41
39:i:125:VAL:O	39:i:126:GLU:C	2.63	0.41
46:AF:64:MET:O	46:AF:68:LYS:HB2	2.21	0.41
63:AW:119:LYS:HB2	63:AW:120:PRO:CD	2.51	0.41
70:BD:48:CYS:SG	70:BD:49:VAL:N	2.93	0.41
71:BE:286:VAL:HG12	71:BE:290:ILE:CD1	2.51	0.41
79:BM:52:VAL:HG21	79:BM:65:ILE:HD13	2.02	0.41
83:BQ:374:A:H4'	83:BQ:375:A:OP1	2.21	0.41
83:BQ:945:C:H2'	83:BQ:946:U:C6	2.55	0.41
83:BQ:1227:C:N4	83:BQ:1281:G:O6	2.54	0.41
83:BQ:1562:C:C4	83:BQ:1563:C:N4	2.89	0.41
83:BQ:2416:U:O4	83:BQ:2804:A:N1	2.53	0.41
83:BQ:3047:U:C5	83:BQ:3094:A:H2	2.29	0.41
85:BS:56:G:H2'	85:BS:57:C:O4'	2.20	0.41
85:BS:147:U:N3	85:BS:148:G:C8	2.88	0.41
86:BT:31:PHE:CE2	86:BT:85:VAL:HG21	2.56	0.41
1:2:853:G:P	72:BF:176:ARG:NE	2.79	0.41
7:F:49:TYR:HA	7:F:52:LEU:HD12	2.03	0.41
19:R:133:LYS:O	19:R:136:VAL:HG23	2.19	0.41
25:X:94:ILE:N	25:X:94:ILE:HD12	2.36	0.41
39:i:138:HIS:HB2	39:i:141:CYS:SG	2.61	0.41
44:AD:57:VAL:HB	44:AD:68:LEU:HD13	2.03	0.41
44:AD:120:ASP:OD2	44:AD:124:ARG:NH2	2.51	0.41
67:BA:102:LEU:O	67:BA:103:THR:HG23	2.20	0.41
83:BQ:705:A:N1	83:BQ:714:G:O2'	2.48	0.41
83:BQ:1160:C:O2	83:BQ:1160:C:C2'	2.69	0.41
86:BT:33:VAL:HA	86:BT:37:ARG:O	2.21	0.41
1:2:51:A:OP2	1:2:51:A:C4'	2.69	0.41
1:2:1365:C:C2'	1:2:1366:U:O5'	2.69	0.41
3:B:58:LEU:HD12	3:B:138:THR:CG2	2.49	0.41
18:Q:61:LEU:HD11	18:Q:96:LEU:HD21	2.01	0.41
19:R:69:ILE:HD12	19:R:69:ILE:C	2.46	0.41
20:S:22:LYS:O	20:S:23:LEU:C	2.63	0.41
21:T:76:LEU:HD22	21:T:92:ARG:HB3	2.01	0.41
28:a:9:VAL:HG22	28:a:10:GLU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AA:241:LYS:CB	83:BQ:2586:G:N7	2.83	0.41
47:AG:54:VAL:HG11	47:AG:57:PHE:CD2	2.55	0.41
48:AH:82:LEU:HD21	48:AH:135:ILE:HG23	2.03	0.41
56:AP:27:GLN:OE1	86:BT:12:ASP:C	2.63	0.41
60:AT:22:LEU:O	60:AT:26:VAL:HG23	2.20	0.41
68:BB:81:VAL:CG2	68:BB:140:LEU:HD12	2.51	0.41
68:BB:150:VAL:HG23	68:BB:153:PHE:CE2	2.56	0.41
73:BG:32:TRP:O	73:BG:33:ARG:HG2	2.21	0.41
83:BQ:121:A:H3'	83:BQ:122:A:C5'	2.51	0.41
83:BQ:585:A:H2'	83:BQ:586:C:C6	2.56	0.41
83:BQ:1617:G:H2'	83:BQ:1618:G:O4'	2.21	0.41
83:BQ:2513:U:H4'	83:BQ:2514:U:OP1	2.21	0.41
83:BQ:2522:G:C2'	83:BQ:2522:G:N3	2.84	0.41
83:BQ:3183:A:C6	83:BQ:3184:A:N1	2.89	0.41
84:BR:109:G:C6	84:BR:110:G:N7	2.89	0.41
1:2:1307:U:O2	1:2:1307:U:O4'	2.39	0.41
1:2:1746:A:H1'	83:BQ:2291:A:H1'	2.01	0.41
2:A:11:LEU:HD13	11:J:29:THR:HG23	2.02	0.41
2:A:53:THR:HA	2:A:91:VAL:HG12	2.02	0.41
37:n:11:U:H4'	83:BQ:2252:A:O2'	2.20	0.41
39:i:127:LEU:HG	39:i:127:LEU:O	2.20	0.41
67:BA:50:LYS:NZ	83:BQ:3048:A:OP1	2.54	0.41
71:BE:32:PRO:HA	71:BE:244:LEU:HD11	2.03	0.41
75:BI:163:LEU:HD21	75:BI:175:HIS:CE1	2.56	0.41
83:BQ:423:A:H2'	83:BQ:424:G:C8	2.56	0.41
83:BQ:1332:A:H2'	83:BQ:1333:C:C6	2.55	0.41
83:BQ:2419:A:C2	83:BQ:2420:C:C4	3.09	0.41
1:2:1423:U:H2'	1:2:1424:A:O4'	2.21	0.40
2:A:217:ILE:HG22	2:A:218:LEU:N	2.36	0.40
21:T:63:MET:SD	21:T:106:LEU:HD21	2.61	0.40
21:T:67:VAL:HG23	21:T:99:GLY:HA2	2.02	0.40
38:h:376:ILE:HG13	38:h:438:VAL:HG21	2.03	0.40
44:AD:103:ILE:HD11	44:AD:134:ILE:HB	2.03	0.40
58:AR:76:ASP:OD1	58:AR:76:ASP:N	2.53	0.40
67:BA:154:TYR:CE1	83:BQ:3242:G:H5''	2.56	0.40
76:BJ:28:SER:O	76:BJ:29:THR:C	2.64	0.40
83:BQ:1444:G:C6	83:BQ:1445:U:O2	2.74	0.40
83:BQ:3331:U:H2'	83:BQ:3332:U:O4'	2.21	0.40
1:2:1145:U:O2	1:2:1145:U:O4'	2.39	0.40
2:A:195:SER:O	2:A:197:THR:N	2.54	0.40
5:D:52:LEU:HD21	5:D:57:ALA:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:83:TYR:CB	23:V:84:HIS:HA	2.51	0.40
39:i:1416:PHE:CZ	40:j:295:MET:HE2	2.56	0.40
40:k:352:LEU:HD12	40:k:353:ALA:N	2.35	0.40
67:BA:4:ARG:O	67:BA:5:LYS:CB	2.69	0.40
83:BQ:744:A:H2'	83:BQ:745:C:O4'	2.20	0.40
83:BQ:1049:C:H2'	83:BQ:1050:U:C6	2.56	0.40
83:BQ:1051:U:C5	83:BQ:1052:U:C6	3.10	0.40
83:BQ:1479:U:O4	83:BQ:1480:G:C2	2.74	0.40
83:BQ:1676:A:C6	83:BQ:1677:G:N7	2.89	0.40
83:BQ:1840:U:O2	83:BQ:1840:U:C2'	2.69	0.40
83:BQ:2202:C:H2'	83:BQ:2203:U:O4'	2.21	0.40
86:BT:92:LEU:HA	86:BT:102:LEU:HD13	2.03	0.40
1:2:93:A:O2'	1:2:398:G:N2	2.54	0.40
1:2:119:A:H1'	1:2:397:A:C8	2.57	0.40
1:2:144:U:H2'	1:2:145:A:O4'	2.21	0.40
1:2:816:G:N7	72:BF:170:ARG:CZ	2.76	0.40
1:2:1479:A:N6	1:2:1528:U:O4	2.51	0.40
16:O:38:ARG:HA	16:O:67:ILE:HG23	2.04	0.40
30:c:48:HIS:CD2	30:c:105:ALA:HB2	2.56	0.40
38:h:1149:LEU:HD12	38:h:1212:MET:HE2	2.02	0.40
40:k:183:MET:HE1	40:k:206:ASN:HD21	1.86	0.40
60:AT:50:GLY:O	60:AT:51:ALA:HB3	2.22	0.40
67:BA:278:ILE:HD11	83:BQ:3098:G:H4'	2.02	0.40
83:BQ:1047:A:H2'	83:BQ:1048:A:C8	2.57	0.40
83:BQ:1765:U:H2'	83:BQ:1766:G:O4'	2.22	0.40
1:2:107:C:H2'	1:2:108:A:C8	2.57	0.40
6:E:18:ARG:NH1	9:H:91:ASP:O	2.54	0.40
7:F:41:PRO:HD2	7:F:44:LEU:HB2	2.04	0.40
9:H:21:ASN:OD1	47:AG:116:TYR:CD2	2.74	0.40
21:T:159:ARG:HE	21:T:172:ALA:HB2	1.86	0.40
23:V:91:VAL:HG13	23:V:200:LYS:HA	2.02	0.40
24:W:149:ARG:O	24:W:151:ASP:N	2.53	0.40
83:BQ:52:A:N3	83:BQ:811:U:O2'	2.52	0.40
83:BQ:306:A:N6	83:BQ:2784:G:C2	2.89	0.40
83:BQ:2553:U:H3'	83:BQ:2554:A:H5''	2.02	0.40
83:BQ:3345:G:H2'	83:BQ:3346:U:C6	2.56	0.40
84:BR:48:U:N3	84:BR:49:G:N7	2.69	0.40
85:BS:9:A:H2'	85:BS:10:A:C8	2.56	0.40
1:2:1126:G:O3'	59:AS:11:ARG:NH2	2.54	0.40
3:B:37:GLN:HB3	7:F:53:LEU:HD22	2.03	0.40
8:G:24:LEU:CB	8:G:58:MET:HE3	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:127:VAL:HG11	18:Q:176:VAL:HG21	2.03	0.40
39:i:251:VAL:HG12	39:i:255:MET:HE3	2.03	0.40
41:AA:160:ILE:HG22	41:AA:164:VAL:CG1	2.46	0.40
67:BA:81:THR:HG21	67:BA:205:VAL:CG1	2.52	0.40
71:BE:275:THR:HG22	71:BE:276:LEU:O	2.21	0.40
82:BP:100:VAL:HG22	82:BP:104:GLN:HB3	2.03	0.40
83:BQ:596:C:H2'	83:BQ:597:G:O4'	2.21	0.40
83:BQ:949:C:H2'	83:BQ:950:G:O4'	2.21	0.40
83:BQ:1230:G:C6	83:BQ:1231:A:C6	3.09	0.40
83:BQ:1290:A:H2'	83:BQ:1291:A:C8	2.57	0.40
83:BQ:2876:C:H2'	83:BQ:2877:G:O4'	2.21	0.40
86:BT:16:SER:O	86:BT:17:ALA:CB	2.69	0.40
86:BT:27:ARG:HA	86:BT:27:ARG:HD3	1.93	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 PDB entries followed by that with respect to all EM entries.

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	A	221/240 (92%)	194 (88%)	24 (11%)	3 (1%)	9	37
3	B	204/225 (91%)	172 (84%)	24 (12%)	8 (4%)	2	20
4	C	94/105 (90%)	72 (77%)	16 (17%)	6 (6%)	1	14
5	D	119/143 (83%)	92 (77%)	17 (14%)	10 (8%)	0	9
6	E	122/142 (86%)	101 (83%)	18 (15%)	3 (2%)	4	28
7	F	139/143 (97%)	119 (86%)	15 (11%)	5 (4%)	2	22
8	G	87/136 (64%)	73 (84%)	11 (13%)	3 (3%)	3	23
9	H	143/146 (98%)	123 (86%)	17 (12%)	3 (2%)	5	31
10	I	141/144 (98%)	112 (79%)	21 (15%)	8 (6%)	1	15
11	J	105/121 (87%)	94 (90%)	10 (10%)	1 (1%)	12	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	K	68/108 (63%)	54 (79%)	9 (13%)	5 (7%)	1	11
13	L	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
14	M	51/56 (91%)	41 (80%)	10 (20%)	0	100	100
15	N	49/152 (32%)	40 (82%)	6 (12%)	3 (6%)	1	14
16	O	316/319 (99%)	274 (87%)	37 (12%)	5 (2%)	7	35
17	P	204/252 (81%)	176 (86%)	20 (10%)	8 (4%)	2	20
18	Q	212/255 (83%)	170 (80%)	31 (15%)	11 (5%)	1	17
19	R	218/254 (86%)	184 (84%)	30 (14%)	4 (2%)	6	33
20	S	258/261 (99%)	213 (83%)	36 (14%)	9 (4%)	3	23
21	T	224/236 (95%)	188 (84%)	29 (13%)	7 (3%)	3	25
22	U	182/190 (96%)	142 (78%)	31 (17%)	9 (5%)	1	17
23	V	184/200 (92%)	128 (70%)	30 (16%)	26 (14%)	0	3
24	W	176/197 (89%)	149 (85%)	21 (12%)	6 (3%)	3	23
25	X	153/156 (98%)	129 (84%)	17 (11%)	7 (5%)	2	18
26	Y	148/151 (98%)	134 (90%)	11 (7%)	3 (2%)	6	32
27	Z	125/137 (91%)	103 (82%)	17 (14%)	5 (4%)	2	20
28	a	85/87 (98%)	67 (79%)	14 (16%)	4 (5%)	2	18
29	b	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	4	29
30	c	142/145 (98%)	120 (84%)	21 (15%)	1 (1%)	18	51
31	d	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	1	16
32	e	95/119 (80%)	70 (74%)	17 (18%)	8 (8%)	0	9
33	f	79/82 (96%)	61 (77%)	14 (18%)	4 (5%)	1	17
34	g	58/63 (92%)	48 (83%)	8 (14%)	2 (3%)	3	23
38	h	1107/1287 (86%)	965 (87%)	124 (11%)	18 (2%)	7	35
39	i	1355/1432 (95%)	1158 (86%)	172 (13%)	25 (2%)	6	33
40	j	388/397 (98%)	335 (86%)	46 (12%)	7 (2%)	6	33
40	k	382/397 (96%)	333 (87%)	40 (10%)	9 (2%)	4	29
41	AA	231/256 (90%)	194 (84%)	32 (14%)	5 (2%)	5	30
42	AB	134/137 (98%)	117 (87%)	14 (10%)	3 (2%)	5	30
43	AC	97/100 (97%)	80 (82%)	13 (13%)	4 (4%)	2	20
44	AD	189/191 (99%)	166 (88%)	19 (10%)	4 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	AE	96/155 (62%)	73 (76%)	18 (19%)	5 (5%)	1	17
46	AF	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	10	40
47	AG	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	2	22
48	AH	119/142 (84%)	103 (87%)	14 (12%)	2 (2%)	7	34
49	AI	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	9	38
50	AJ	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	3	25
51	AK	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
52	AL	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	5	31
53	AM	134/138 (97%)	119 (89%)	12 (9%)	3 (2%)	5	30
54	AN	133/136 (98%)	118 (89%)	10 (8%)	5 (4%)	2	21
55	AO	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	2	20
56	AP	103/106 (97%)	86 (84%)	16 (16%)	1 (1%)	12	43
57	AQ	201/204 (98%)	175 (87%)	21 (10%)	5 (2%)	4	28
58	AR	146/149 (98%)	118 (81%)	21 (14%)	7 (5%)	2	17
59	AS	23/25 (92%)	23 (100%)	0	0	100	100
60	AT	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	11	41
61	AU	195/199 (98%)	177 (91%)	15 (8%)	3 (2%)	8	36
62	AV	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	6	33
63	AW	250/254 (98%)	218 (87%)	31 (12%)	1 (0%)	30	62
64	AX	181/184 (98%)	158 (87%)	19 (10%)	4 (2%)	5	30
65	AY	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	11	41
67	BA	384/387 (99%)	332 (86%)	41 (11%)	11 (3%)	3	25
68	BB	183/186 (98%)	163 (89%)	17 (9%)	3 (2%)	7	35
69	BC	107/113 (95%)	94 (88%)	11 (10%)	2 (2%)	6	32
70	BD	218/221 (99%)	185 (85%)	24 (11%)	9 (4%)	2	20
71	BE	359/362 (99%)	306 (85%)	38 (11%)	15 (4%)	2	19
72	BF	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	7	35
73	BG	125/130 (96%)	110 (88%)	13 (10%)	2 (2%)	7	35
74	BH	170/172 (99%)	151 (89%)	16 (9%)	3 (2%)	6	33
75	BI	294/297 (99%)	263 (90%)	22 (8%)	9 (3%)	3	25
76	BJ	157/160 (98%)	133 (85%)	18 (12%)	6 (4%)	2	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	BK	104/107 (97%)	93 (89%)	9 (9%)	2 (2%)	6	32
78	BL	98/121 (81%)	79 (81%)	16 (16%)	3 (3%)	3	25
79	BM	152/176 (86%)	137 (90%)	11 (7%)	4 (3%)	4	27
80	BN	110/121 (91%)	104 (94%)	3 (3%)	3 (3%)	4	27
81	BO	220/244 (90%)	199 (90%)	16 (7%)	5 (2%)	5	30
82	BP	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	45
86	BT	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	13
All	All	14299/15550 (92%)	12246 (86%)	1644 (12%)	409 (3%)	5	25

All (409) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	196	ARG
3	B	100	ASN
5	D	115	VAL
5	D	126	TRP
7	F	32	ASN
7	F	40	GLU
7	F	45	ARG
7	F	113	ASP
10	I	69	LYS
17	P	110	TYR
18	Q	132	ASP
18	Q	176	VAL
20	S	12	LEU
20	S	69	HIS
20	S	231	GLN
23	V	11	ARG
23	V	27	PHE
23	V	33	PRO
23	V	35	ASN
23	V	83	TYR
23	V	85	PRO
23	V	192	TYR
23	V	193	LEU
23	V	194	ARG
24	W	98	ALA
24	W	134	ILE
25	X	7	VAL
26	Y	22	ALA

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Mol	Chain	Res	Type
27	Z	91	THR
27	Z	124	ASP
30	c	12	ALA
38	h	126	VAL
38	h	900	LYS
38	h	1203	PHE
39	i	203	TYR
39	i	1032	LYS
40	k	278	THR
40	k	365	LYS
42	AB	29	SER
44	AD	42	ASP
44	AD	50	ASN
45	AE	64	THR
47	AG	8	PRO
50	AJ	47	ALA
50	AJ	166	ALA
53	AM	136	ALA
57	AQ	75	VAL
58	AR	12	ARG
58	AR	78	LEU
62	AV	21	ILE
63	AW	144	ASN
67	BA	5	LYS
67	BA	138	ALA
69	BC	64	VAL
70	BD	135	PHE
70	BD	138	ARG
71	BE	292	SER
75	BI	116	ASP
76	BJ	25	VAL
76	BJ	124	VAL
76	BJ	144	GLU
76	BJ	159	PHE
77	BK	92	LYS
79	BM	171	PRO
81	BO	164	SER
86	BT	110	LYS
86	BT	112	ASP
86	BT	133	ASP
2	A	217	ILE
2	A	218	LEU

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Mol	Chain	Res	Type
3	B	44	ASN
3	B	60	ASP
4	C	60	SER
4	C	64	TYR
5	D	25	GLU
5	D	91	VAL
5	D	106	ILE
7	F	39	VAL
8	G	76	GLU
8	G	77	GLU
8	G	88	VAL
9	H	7	GLU
9	H	51	ASP
10	I	7	ARG
11	J	55	PRO
12	K	71	ILE
15	N	107	LYS
15	N	146	SER
17	P	21	ASN
17	P	39	ASN
17	P	169	SER
18	Q	158	SER
19	R	91	ARG
19	R	145	GLY
19	R	206	THR
20	S	23	LEU
21	T	148	SER
21	T	219	ARG
22	U	74	GLN
22	U	110	GLN
23	V	10	LYS
23	V	24	LYS
23	V	52	ASN
23	V	86	SER
23	V	152	ILE
23	V	191	PHE
24	W	119	ALA
25	X	6	THR
27	Z	42	VAL
29	b	78	ARG
31	d	35	VAL
31	d	51	GLU

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Mol	Chain	Res	Type
31	d	52	LYS
31	d	60	PHE
31	d	127	LYS
32	e	36	ILE
32	e	63	ALA
38	h	649	ILE
38	h	986	ARG
38	h	1052	ILE
39	i	200	ASP
39	i	264	PHE
39	i	624	ASP
40	j	255	ASN
40	j	323	LYS
40	k	266	GLU
41	AA	156	ASP
42	AB	45	ARG
43	AC	99	ARG
45	AE	77	LYS
48	AH	109	LYS
50	AJ	51	LEU
52	AL	3	ALA
57	AQ	55	ALA
58	AR	47	LYS
61	AU	123	ALA
61	AU	187	GLU
64	AX	68	GLY
64	AX	166	VAL
67	BA	38	SER
67	BA	332	ARG
67	BA	348	ARG
67	BA	352	GLU
70	BD	113	GLY
70	BD	194	ALA
71	BE	131	VAL
71	BE	140	HIS
71	BE	293	SER
72	BF	130	ASN
73	BG	50	ILE
74	BH	24	LEU
74	BH	97	VAL
75	BI	276	LYS
82	BP	90	ARG

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Mol	Chain	Res	Type
86	BT	15	SER
86	BT	132	LYS
86	BT	156	THR
3	B	81	ARG
4	C	93	GLN
5	D	87	PRO
9	H	139	LYS
10	I	28	LEU
10	I	67	MET
10	I	128	GLY
17	P	35	PRO
18	Q	177	GLN
18	Q	209	ASN
18	Q	223	PHE
20	S	20	LEU
20	S	205	PHE
22	U	97	ARG
22	U	156	SER
23	V	96	LEU
23	V	98	LYS
23	V	116	HIS
23	V	196	LEU
24	W	120	LYS
24	W	150	LEU
25	X	55	ASP
29	b	30	SER
31	d	4	ALA
32	e	83	ILE
33	f	3	LEU
33	f	10	PRO
38	h	28	LEU
38	h	53	ASP
38	h	769	LEU
39	i	442	GLU
39	i	494	LEU
39	i	506	SER
39	i	621	LYS
39	i	658	ASP
39	i	1254	SER
40	j	365	LYS
40	k	77	ASP
42	AB	112	SER

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Mol	Chain	Res	Type
43	AC	27	SER
47	AG	112	LEU
49	AI	33	LYS
54	AN	59	ALA
54	AN	102	GLU
54	AN	125	GLY
57	AQ	80	THR
58	AR	77	LYS
58	AR	108	GLY
61	AU	5	PRO
64	AX	155	GLU
67	BA	7	GLU
68	BB	23	ASN
70	BD	2	ARG
71	BE	232	SER
71	BE	338	LYS
72	BF	53	LYS
76	BJ	29	THR
77	BK	91	ALA
78	BL	91	ASP
79	BM	20	LYS
79	BM	97	ASN
81	BO	159	GLN
86	BT	16	SER
86	BT	17	ALA
86	BT	114	LYS
3	B	63	GLN
3	B	64	VAL
5	D	93	ASP
10	I	132	LEU
12	K	44	GLN
15	N	118	ARG
17	P	103	THR
18	Q	39	GLU
18	Q	147	ALA
21	T	132	ARG
21	T	197	ASN
23	V	22	ARG
23	V	37	LYS
23	V	81	VAL
23	V	87	ASN
25	X	29	LYS

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Mol	Chain	Res	Type
26	Y	3	ARG
27	Z	75	GLY
28	a	9	VAL
32	e	59	TYR
32	e	62	TYR
33	f	15	GLU
34	g	60	PRO
38	h	125	GLU
38	h	133	ASN
39	i	174	ILE
39	i	212	TRP
39	i	939	ILE
39	i	1175	ASP
40	j	282	GLN
40	k	47	ASP
40	k	284	SER
44	AD	2	LYS
44	AD	41	ILE
46	AF	11	ARG
48	AH	62	VAL
53	AM	29	ALA
55	AO	79	GLU
55	AO	92	ASP
56	AP	17	CYS
57	AQ	150	TRP
67	BA	187	SER
68	BB	162	ALA
70	BD	100	LYS
70	BD	107	ALA
71	BE	14	GLU
71	BE	266	THR
71	BE	270	SER
71	BE	320	ASN
72	BF	81	ARG
75	BI	188	GLU
75	BI	259	LYS
79	BM	98	VAL
3	B	65	ARG
5	D	111	ASN
5	D	119	SER
6	E	28	MET
6	E	53	PRO

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Mol	Chain	Res	Type
6	E	127	ARG
10	I	90	PRO
12	K	38	HIS
12	K	43	ASP
12	K	88	ILE
16	O	120	SER
16	O	162	ALA
16	O	283	LYS
17	P	111	ILE
18	Q	210	ILE
19	R	150	GLN
20	S	195	ILE
21	T	69	LEU
23	V	40	ALA
23	V	51	GLY
25	X	146	ALA
26	Y	21	ASN
27	Z	40	ALA
29	b	120	HIS
31	d	5	VAL
32	e	97	PRO
38	h	767	ARG
39	i	263	PHE
39	i	1177	ARG
40	j	256	SER
40	k	22	VAL
45	AE	43	ARG
47	AG	94	ARG
47	AG	108	GLU
50	AJ	155	GLU
54	AN	70	PRO
54	AN	124	ALA
58	AR	56	VAL
58	AR	79	TRP
64	AX	3	ARG
67	BA	155	ALA
69	BC	83	GLU
70	BD	112	GLN
70	BD	175	LEU
71	BE	5	GLN
71	BE	155	ASP
71	BE	175	HIS

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Mol	Chain	Res	Type
71	BE	317	PRO
73	BG	12	LYS
75	BI	44	TYR
75	BI	137	ASP
75	BI	253	PHE
75	BI	277	LEU
78	BL	11	ILE
80	BN	59	PRO
86	BT	12	ASP
4	C	51	SER
10	I	87	GLY
21	T	149	LYS
22	U	64	VAL
22	U	96	ARG
22	U	98	ILE
23	V	82	VAL
25	X	4	GLU
28	a	12	TYR
28	a	82	VAL
33	f	75	GLU
38	h	114	ILE
38	h	150	GLY
39	i	403	ILE
39	i	570	LYS
39	i	876	LEU
39	i	1067	GLY
39	i	1213	ILE
40	j	52	LYS
40	k	394	ALA
41	AA	25	PRO
41	AA	36	ILE
41	AA	157	VAL
43	AC	3	VAL
45	AE	80	ARG
47	AG	120	ILE
50	AJ	50	PRO
60	AT	51	ALA
76	BJ	148	PRO
80	BN	77	GLY
81	BO	178	ILE
5	D	66	VAL
18	Q	21	VAL

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Mol	Chain	Res	Type
22	U	178	GLY
32	e	16	GLY
34	g	50	VAL
38	h	1029	GLY
39	i	1197	GLY
39	i	1203	ILE
43	AC	9	ILE
47	AG	117	ASP
53	AM	6	ILE
67	BA	245	GLY
78	BL	27	VAL
81	BO	188	ILE
16	O	63	GLY
21	T	165	GLY
32	e	84	VAL
57	AQ	74	PRO
71	BE	78	GLY
75	BI	251	PRO
4	C	88	PRO
4	C	89	GLY
16	O	105	GLY
28	a	77	GLY
38	h	206	PRO
38	h	1232	PRO
40	k	349	GLY
65	AY	87	VAL
74	BH	167	ARG
81	BO	26	VAL
17	P	158	VAL
20	S	204	GLY
22	U	65	PRO
38	h	1221	GLY
41	AA	73	PRO
50	AJ	127	PRO
68	BB	59	ARG
80	BN	12	PRO
3	B	51	VAL
18	Q	48	VAL
20	S	193	GLY
24	W	18	PRO
25	X	41	GLY
39	i	1192	ILE

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Mol	Chain	Res	Type
40	j	277	PRO
45	AE	76	VAL
67	BA	83	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	A	182/195 (93%)	176 (97%)	6 (3%)	33	56
3	B	173/191 (91%)	159 (92%)	14 (8%)	11	35
4	C	88/98 (90%)	82 (93%)	6 (7%)	14	40
5	D	89/119 (75%)	83 (93%)	6 (7%)	15	41
6	E	101/118 (86%)	92 (91%)	9 (9%)	9	32
7	F	117/119 (98%)	112 (96%)	5 (4%)	26	50
8	G	80/124 (64%)	77 (96%)	3 (4%)	29	53
9	H	128/129 (99%)	116 (91%)	12 (9%)	8	30
10	I	115/116 (99%)	104 (90%)	11 (10%)	8	29
11	J	100/114 (88%)	95 (95%)	5 (5%)	22	47
12	K	61/89 (68%)	58 (95%)	3 (5%)	22	47
13	L	56/60 (93%)	54 (96%)	2 (4%)	31	54
14	M	47/49 (96%)	44 (94%)	3 (6%)	16	42
15	N	43/135 (32%)	41 (95%)	2 (5%)	23	48
16	O	259/262 (99%)	252 (97%)	7 (3%)	39	59
17	P	164/210 (78%)	159 (97%)	5 (3%)	36	57
18	Q	191/224 (85%)	183 (96%)	8 (4%)	26	50
19	R	180/205 (88%)	174 (97%)	6 (3%)	33	56
20	S	221/222 (100%)	216 (98%)	5 (2%)	44	63
21	T	188/201 (94%)	179 (95%)	9 (5%)	23	47
22	U	165/170 (97%)	159 (96%)	6 (4%)	31	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	V	150/161 (93%)	131 (87%)	19 (13%)	4	21
24	W	152/166 (92%)	149 (98%)	3 (2%)	48	65
25	X	129/137 (94%)	125 (97%)	4 (3%)	35	57
26	Y	127/128 (99%)	121 (95%)	6 (5%)	23	48
27	Z	81/105 (77%)	77 (95%)	4 (5%)	22	47
28	a	74/74 (100%)	72 (97%)	2 (3%)	39	59
29	b	110/111 (99%)	108 (98%)	2 (2%)	51	67
30	c	119/120 (99%)	115 (97%)	4 (3%)	32	55
31	d	111/113 (98%)	103 (93%)	8 (7%)	13	39
32	e	83/101 (82%)	75 (90%)	8 (10%)	8	29
33	f	70/71 (99%)	69 (99%)	1 (1%)	59	70
34	g	50/54 (93%)	50 (100%)	0	100	100
38	h	936/1139 (82%)	900 (96%)	36 (4%)	29	53
39	i	849/1279 (66%)	830 (98%)	19 (2%)	45	63
40	j	296/347 (85%)	291 (98%)	5 (2%)	53	67
40	k	295/347 (85%)	288 (98%)	7 (2%)	43	62
41	AA	187/208 (90%)	179 (96%)	8 (4%)	26	50
42	AB	104/105 (99%)	99 (95%)	5 (5%)	23	47
43	AC	81/82 (99%)	75 (93%)	6 (7%)	13	38
44	AD	171/171 (100%)	166 (97%)	5 (3%)	37	58
45	AE	57/129 (44%)	57 (100%)	0	100	100
46	AF	70/71 (99%)	65 (93%)	5 (7%)	13	39
47	AG	147/150 (98%)	141 (96%)	6 (4%)	27	51
48	AH	104/118 (88%)	97 (93%)	7 (7%)	15	41
49	AI	68/69 (99%)	68 (100%)	0	100	100
50	AJ	154/159 (97%)	143 (93%)	11 (7%)	13	39
51	AK	109/110 (99%)	106 (97%)	3 (3%)	38	58
52	AL	45/46 (98%)	42 (93%)	3 (7%)	15	41
53	AM	107/109 (98%)	101 (94%)	6 (6%)	19	45
54	AN	115/116 (99%)	111 (96%)	4 (4%)	32	54
55	AO	47/116 (40%)	45 (96%)	2 (4%)	26	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	AP	90/91 (99%)	85 (94%)	5 (6%)	19	45
57	AQ	175/176 (99%)	168 (96%)	7 (4%)	28	52
58	AR	118/119 (99%)	114 (97%)	4 (3%)	32	55
59	AS	23/23 (100%)	21 (91%)	2 (9%)	9	33
60	AT	71/72 (99%)	69 (97%)	2 (3%)	38	58
61	AU	160/162 (99%)	155 (97%)	5 (3%)	35	57
62	AV	46/47 (98%)	44 (96%)	2 (4%)	26	50
63	AW	193/196 (98%)	186 (96%)	7 (4%)	31	54
64	AX	140/146 (96%)	135 (96%)	5 (4%)	31	54
65	AY	81/88 (92%)	77 (95%)	4 (5%)	22	47
67	BA	320/323 (99%)	305 (95%)	15 (5%)	23	48
68	BB	150/151 (99%)	145 (97%)	5 (3%)	33	56
69	BC	92/97 (95%)	83 (90%)	9 (10%)	7	29
70	BD	184/187 (98%)	172 (94%)	12 (6%)	15	42
71	BE	288/289 (100%)	278 (96%)	10 (4%)	32	54
72	BF	153/154 (99%)	142 (93%)	11 (7%)	13	39
73	BG	109/111 (98%)	106 (97%)	3 (3%)	38	58
74	BH	156/156 (100%)	150 (96%)	6 (4%)	29	53
75	BI	244/245 (100%)	235 (96%)	9 (4%)	30	54
76	BJ	136/137 (99%)	130 (96%)	6 (4%)	25	49
77	BK	90/91 (99%)	86 (96%)	4 (4%)	25	49
78	BL	87/107 (81%)	87 (100%)	0	100	100
79	BM	134/153 (88%)	129 (96%)	5 (4%)	30	54
80	BN	95/103 (92%)	93 (98%)	2 (2%)	47	64
81	BO	186/205 (91%)	182 (98%)	4 (2%)	45	63
82	BP	104/105 (99%)	101 (97%)	3 (3%)	37	58
86	BT	118/132 (89%)	113 (96%)	5 (4%)	26	50
All	All	11689/13228 (88%)	11205 (96%)	484 (4%)	28	51

All (484) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	7	LYS

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Mol	Chain	Res	Type
2	A	9	ARG
2	A	27	ARG
2	A	58	VAL
2	A	157	LEU
2	A	204	ASP
3	B	27	THR
3	B	33	VAL
3	B	70	VAL
3	B	93	LEU
3	B	99	MET
3	B	102	ARG
3	B	114	ILE
3	B	124	LEU
3	B	134	VAL
3	B	138	THR
3	B	158	GLN
3	B	167	ARG
3	B	168	VAL
3	B	212	LYS
4	C	31	LYS
4	C	55	VAL
4	C	63	TYR
4	C	73	VAL
4	C	78	GLU
4	C	82	LEU
5	D	34	THR
5	D	49	THR
5	D	54	ARG
5	D	74	LEU
5	D	121	VAL
5	D	122	VAL
6	E	14	THR
6	E	42	ARG
6	E	44	ARG
6	E	61	ARG
6	E	80	MET
6	E	94	VAL
6	E	124	THR
6	E	126	VAL
6	E	130	ARG
7	F	48	VAL
7	F	66	ARG

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Mol	Chain	Res	Type
7	F	78	VAL
7	F	106	LYS
7	F	114	ARG
8	G	13	SER
8	G	47	ARG
8	G	80	ARG
9	H	14	ILE
9	H	17	LEU
9	H	38	VAL
9	H	62	THR
9	H	98	TYR
9	H	100	THR
9	H	101	LEU
9	H	120	ARG
9	H	123	ARG
9	H	133	VAL
9	H	137	HIS
9	H	145	ARG
10	I	7	ARG
10	I	13	ASP
10	I	25	GLN
10	I	28	LEU
10	I	35	ASP
10	I	44	GLU
10	I	66	TYR
10	I	68	ARG
10	I	70	GLN
10	I	85	SER
10	I	123	ARG
11	J	20	ILE
11	J	31	VAL
11	J	47	GLN
11	J	99	ILE
11	J	118	VAL
12	K	54	VAL
12	K	64	VAL
12	K	100	ILE
13	L	15	VAL
13	L	50	GLU
14	M	19	ARG
14	M	28	THR
14	M	39	CYS

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Mol	Chain	Res	Type
15	N	103	LEU
15	N	108	VAL
16	O	58	VAL
16	O	114	ASP
16	O	185	GLN
16	O	202	LEU
16	O	228	LYS
16	O	274	LEU
16	O	308	ASN
17	P	103	THR
17	P	113	ARG
17	P	135	GLU
17	P	148	ASP
17	P	198	MET
18	Q	21	VAL
18	Q	29	TRP
18	Q	59	ASP
18	Q	70	LEU
18	Q	95	ASN
18	Q	118	GLN
18	Q	181	LEU
18	Q	212	VAL
19	R	58	LEU
19	R	69	ILE
19	R	111	VAL
19	R	113	LEU
19	R	206	THR
19	R	225	LEU
20	S	20	LEU
20	S	26	CYS
20	S	164	LEU
20	S	236	ILE
20	S	261	LEU
21	T	24	ILE
21	T	75	LEU
21	T	78	THR
21	T	81	VAL
21	T	98	ARG
21	T	109	LEU
21	T	129	VAL
21	T	190	GLN
21	T	212	LEU

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Mol	Chain	Res	Type
22	U	5	GLN
22	U	9	LEU
22	U	27	LEU
22	U	31	SER
22	U	48	GLU
22	U	72	LYS
23	V	22	ARG
23	V	27	PHE
23	V	29	LEU
23	V	38	ILE
23	V	58	LEU
23	V	59	ARG
23	V	67	TRP
23	V	78	ILE
23	V	81	VAL
23	V	82	VAL
23	V	90	LEU
23	V	91	VAL
23	V	92	ARG
23	V	96	LEU
23	V	107	THR
23	V	160	PHE
23	V	196	LEU
23	V	197	THR
23	V	199	LYS
24	W	10	LYS
24	W	118	LEU
24	W	134	ILE
25	X	7	VAL
25	X	40	LEU
25	X	98	ASN
25	X	131	ILE
26	Y	36	GLN
26	Y	66	ILE
26	Y	86	GLU
26	Y	92	ILE
26	Y	102	LEU
26	Y	149	LEU
27	Z	38	THR
27	Z	52	ARG
27	Z	81	VAL
27	Z	137	LEU

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Mol	Chain	Res	Type
28	a	11	LEU
28	a	12	TYR
29	b	53	ILE
29	b	81	VAL
30	c	17	VAL
30	c	18	HIS
30	c	101	GLU
30	c	107	PHE
31	d	17	LEU
31	d	63	GLN
31	d	125	LEU
31	d	127	LYS
31	d	129	VAL
31	d	131	ARG
31	d	132	ARG
31	d	133	ASN
32	e	3	LYS
32	e	10	ARG
32	e	11	ASN
32	e	12	LYS
32	e	15	ARG
32	e	21	VAL
32	e	32	LYS
32	e	92	ARG
33	f	9	HIS
38	h	54	ARG
38	h	69	MET
38	h	186	LEU
38	h	434	LEU
38	h	446	VAL
38	h	464	MET
38	h	669	THR
38	h	694	VAL
38	h	709	ILE
38	h	710	LEU
38	h	731	LEU
38	h	742	ARG
38	h	756	GLU
38	h	769	LEU
38	h	770	ASP
38	h	772	THR
38	h	788	THR

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Mol	Chain	Res	Type
38	h	798	THR
38	h	824	GLU
38	h	847	LYS
38	h	856	ILE
38	h	892	SER
38	h	899	LEU
38	h	900	LYS
38	h	905	VAL
38	h	908	ARG
38	h	1000	VAL
38	h	1036	LEU
38	h	1049	LEU
38	h	1089	LEU
38	h	1111	VAL
38	h	1112	LEU
38	h	1126	GLU
38	h	1186	LEU
38	h	1229	GLU
38	h	1280	VAL
39	i	173	LEU
39	i	174	ILE
39	i	184	GLU
39	i	191	GLN
39	i	194	LEU
39	i	247	TYR
39	i	249	ILE
39	i	476	ASP
39	i	511	LYS
39	i	519	ILE
39	i	534	VAL
39	i	558	MET
39	i	596	MET
39	i	636	ILE
39	i	644	HIS
39	i	646	ARG
39	i	687	ARG
39	i	718	GLU
39	i	1323	LEU
40	j	61	HIS
40	j	99	THR
40	j	173	LEU
40	j	226	GLN

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Mol	Chain	Res	Type
40	j	383	CYS
40	k	83	LEU
40	k	127	LEU
40	k	176	GLN
40	k	247	LEU
40	k	259	CYS
40	k	278	THR
40	k	358	PHE
41	AA	71	VAL
41	AA	112	GLU
41	AA	126	SER
41	AA	161	GLU
41	AA	190	VAL
41	AA	197	VAL
41	AA	202	GLU
41	AA	221	ASN
42	AB	13	ILE
42	AB	57	MET
42	AB	61	THR
42	AB	68	GLU
42	AB	91	VAL
43	AC	7	ILE
43	AC	20	MET
43	AC	29	LYS
43	AC	46	GLU
43	AC	71	LYS
43	AC	88	GLU
44	AD	43	VAL
44	AD	57	VAL
44	AD	68	LEU
44	AD	71	VAL
44	AD	92	TYR
46	AF	5	THR
46	AF	13	ASN
46	AF	17	THR
46	AF	19	CYS
46	AF	37	CYS
47	AG	28	ASP
47	AG	59	ILE
47	AG	107	ASP
47	AG	112	LEU
47	AG	132	ASN

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Mol	Chain	Res	Type
47	AG	165	GLN
48	AH	26	VAL
48	AH	31	THR
48	AH	39	LYS
48	AH	61	LYS
48	AH	78	ASP
48	AH	105	VAL
48	AH	108	LEU
50	AJ	24	VAL
50	AJ	31	LYS
50	AJ	54	LEU
50	AJ	58	VAL
50	AJ	73	ARG
50	AJ	76	THR
50	AJ	80	VAL
50	AJ	116	LEU
50	AJ	134	GLU
50	AJ	136	GLU
50	AJ	168	ARG
51	AK	74	TYR
51	AK	108	LYS
51	AK	111	LEU
52	AL	6	SER
52	AL	9	ILE
52	AL	37	TYR
53	AM	4	ASP
53	AM	28	SER
53	AM	38	ILE
53	AM	44	VAL
53	AM	50	LYS
53	AM	128	ARG
54	AN	26	VAL
54	AN	33	SER
54	AN	36	HIS
54	AN	134	LEU
55	AO	108	THR
55	AO	127	LEU
56	AP	2	VAL
56	AP	29	LYS
56	AP	61	LYS
56	AP	83	LEU
56	AP	105	GLN

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Mol	Chain	Res	Type
57	AQ	9	GLU
57	AQ	19	LEU
57	AQ	68	ARG
57	AQ	80	THR
57	AQ	89	VAL
57	AQ	98	LEU
57	AQ	183	THR
58	AR	4	ARG
58	AR	56	VAL
58	AR	76	ASP
58	AR	130	VAL
59	AS	10	THR
59	AS	13	LEU
60	AT	20	SER
60	AT	91	GLU
61	AU	34	VAL
61	AU	56	ASP
61	AU	62	THR
61	AU	64	PHE
61	AU	113	ASP
62	AV	21	ILE
62	AV	25	LYS
63	AW	61	VAL
63	AW	109	GLU
63	AW	179	LEU
63	AW	180	LEU
63	AW	190	ARG
63	AW	199	THR
63	AW	225	ILE
64	AX	31	GLU
64	AX	94	LEU
64	AX	113	TYR
64	AX	118	GLN
64	AX	168	LEU
65	AY	24	THR
65	AY	48	THR
65	AY	87	VAL
65	AY	104	LEU
67	BA	55	THR
67	BA	79	VAL
67	BA	80	ASP
67	BA	85	VAL

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Mol	Chain	Res	Type
67	BA	139	GLN
67	BA	146	ARG
67	BA	161	LEU
67	BA	178	LEU
67	BA	183	LEU
67	BA	210	GLU
67	BA	211	GLN
67	BA	221	THR
67	BA	238	LEU
67	BA	246	LEU
67	BA	296	THR
68	BB	49	LEU
68	BB	113	LYS
68	BB	138	LEU
68	BB	168	THR
68	BB	174	ARG
69	BC	31	ARG
69	BC	64	VAL
69	BC	68	GLU
69	BC	79	ARG
69	BC	82	GLU
69	BC	106	THR
69	BC	107	VAL
69	BC	108	VAL
69	BC	110	GLU
70	BD	51	LEU
70	BD	90	VAL
70	BD	101	MET
70	BD	137	VAL
70	BD	138	ARG
70	BD	155	ARG
70	BD	161	GLN
70	BD	162	GLN
70	BD	164	ILE
70	BD	175	LEU
70	BD	199	LEU
70	BD	216	PHE
71	BE	108	LYS
71	BE	113	VAL
71	BE	118	LYS
71	BE	156	LEU
71	BE	194	TYR

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Mol	Chain	Res	Type
71	BE	206	LEU
71	BE	258	LEU
71	BE	286	VAL
71	BE	326	ARG
71	BE	349	THR
72	BF	10	LEU
72	BF	17	VAL
72	BF	22	VAL
72	BF	39	ASN
72	BF	71	ARG
72	BF	143	ILE
72	BF	144	GLN
72	BF	146	LYS
72	BF	160	GLU
72	BF	167	ARG
72	BF	181	ARG
73	BG	8	LYS
73	BG	19	ARG
73	BG	106	VAL
74	BH	61	ILE
74	BH	79	VAL
74	BH	106	LEU
74	BH	109	ASP
74	BH	119	ARG
74	BH	138	GLN
75	BI	23	ARG
75	BI	58	LYS
75	BI	66	SER
75	BI	92	LEU
75	BI	117	GLU
75	BI	146	LEU
75	BI	152	ARG
75	BI	198	TYR
75	BI	259	LYS
76	BJ	27	LEU
76	BJ	72	VAL
76	BJ	85	LEU
76	BJ	101	CYS
76	BJ	122	GLN
76	BJ	126	VAL
77	BK	5	HIS
77	BK	31	LYS

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Mol	Chain	Res	Type
77	BK	74	THR
77	BK	81	VAL
79	BM	15	VAL
79	BM	64	LEU
79	BM	91	VAL
79	BM	145	LEU
79	BM	171	PRO
80	BN	23	VAL
80	BN	98	GLN
81	BO	24	GLU
81	BO	46	GLU
81	BO	92	ILE
81	BO	124	LEU
82	BP	20	GLN
82	BP	27	GLU
82	BP	53	CYS
86	BT	73	LEU
86	BT	120	LEU
86	BT	132	LYS
86	BT	133	ASP
86	BT	155	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (215) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	22	ASN
2	A	74	GLN
2	A	101	GLN
3	B	131	GLN
3	B	139	ASN
3	B	170	GLN
3	B	186	ASN
3	B	224	ASN
4	C	13	GLN
4	C	29	GLN
4	C	85	HIS
7	F	32	ASN
7	F	83	GLN
7	F	103	ASN
8	G	31	ASN
8	G	42	GLN
8	G	48	ASN

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Mol	Chain	Res	Type
9	H	44	ASN
9	H	71	GLN
9	H	78	HIS
9	H	136	GLN
10	I	25	GLN
10	I	43	ASN
10	I	129	GLN
11	J	17	GLN
11	J	49	ASN
13	L	27	GLN
13	L	51	ASN
14	M	37	ASN
14	M	53	ASN
15	N	123	ASN
16	O	31	ASN
16	O	66	HIS
16	O	185	GLN
16	O	198	ASN
16	O	288	HIS
17	P	131	GLN
17	P	140	ASN
18	Q	49	ASN
18	Q	79	HIS
18	Q	95	ASN
18	Q	99	ASN
18	Q	146	GLN
18	Q	183	GLN
19	R	89	GLN
20	S	17	HIS
20	S	67	GLN
20	S	96	ASN
20	S	98	ASN
20	S	142	HIS
21	T	34	GLN
21	T	176	GLN
21	T	201	GLN
21	T	210	GLN
22	U	29	ASN
22	U	161	GLN
23	V	20	GLN
23	V	32	GLN
23	V	64	ASN

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Mol	Chain	Res	Type
23	V	88	ASN
23	V	119	GLN
25	X	106	ASN
26	Y	36	GLN
29	b	12	ASN
29	b	15	ASN
29	b	39	GLN
29	b	64	GLN
29	b	80	ASN
29	b	113	HIS
30	c	75	GLN
30	c	99	ASN
31	d	22	GLN
31	d	63	GLN
32	e	43	ASN
33	f	26	GLN
34	g	17	GLN
34	g	51	ASN
38	h	15	GLN
38	h	314	ASN
38	h	334	GLN
38	h	387	GLN
38	h	511	ASN
38	h	680	GLN
38	h	695	HIS
38	h	809	ASN
38	h	839	GLN
38	h	897	HIS
38	h	961	ASN
38	h	1056	ASN
38	h	1059	GLN
38	h	1122	ASN
39	i	69	HIS
39	i	172	ASN
39	i	424	ASN
39	i	507	ASN
39	i	701	ASN
39	i	773	GLN
39	i	853	GLN
39	i	1046	GLN
39	i	1066	GLN
39	i	1150	HIS

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Mol	Chain	Res	Type
39	i	1151	HIS
39	i	1156	ASN
39	i	1228	ASN
39	i	1250	GLN
39	i	1358	GLN
39	i	1361	GLN
39	i	1382	GLN
40	j	66	HIS
40	j	226	GLN
40	j	279	HIS
40	j	348	HIS
40	k	156	HIS
40	k	176	GLN
40	k	187	GLN
40	k	300	ASN
41	AA	24	ASN
41	AA	45	ASN
41	AA	77	GLN
41	AA	192	GLN
41	AA	243	GLN
42	AB	47	ASN
44	AD	49	ASN
44	AD	51	GLN
44	AD	77	ASN
44	AD	157	ASN
44	AD	183	HIS
46	AF	13	ASN
46	AF	57	HIS
47	AG	39	GLN
47	AG	68	HIS
47	AG	132	ASN
49	AI	28	ASN
49	AI	67	GLN
50	AJ	37	ASN
50	AJ	137	GLN
51	AK	4	GLN
51	AK	91	ASN
51	AK	98	ASN
52	AL	19	GLN
52	AL	32	ASN
52	AL	33	ASN
52	AL	50	ASN

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Mol	Chain	Res	Type
53	AM	56	GLN
53	AM	62	GLN
54	AN	57	HIS
55	AO	109	ASN
56	AP	3	ASN
56	AP	27	GLN
56	AP	47	GLN
57	AQ	57	GLN
57	AQ	90	ASN
58	AR	44	ASN
58	AR	62	HIS
58	AR	67	HIS
58	AR	89	GLN
61	AU	14	HIS
61	AU	26	GLN
61	AU	193	GLN
62	AV	17	HIS
62	AV	48	HIS
63	AW	8	GLN
63	AW	24	GLN
63	AW	47	GLN
63	AW	194	ASN
63	AW	205	ASN
63	AW	209	HIS
63	AW	211	HIS
63	AW	217	GLN
64	AX	28	ASN
64	AX	97	ASN
65	AY	11	ASN
65	AY	47	ASN
65	AY	71	GLN
67	BA	68	HIS
67	BA	224	HIS
68	BB	9	GLN
68	BB	158	HIS
70	BD	22	ASN
70	BD	94	HIS
70	BD	161	GLN
70	BD	207	ASN
70	BD	208	ASN
71	BE	48	GLN
71	BE	59	GLN

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Mol	Chain	Res	Type
71	BE	110	ASN
71	BE	116	ASN
71	BE	260	GLN
71	BE	291	ASN
71	BE	296	GLN
71	BE	304	GLN
71	BE	316	ASN
72	BF	39	ASN
72	BF	144	GLN
72	BF	166	ASN
73	BG	98	HIS
74	BH	108	GLN
75	BI	90	HIS
75	BI	151	GLN
76	BJ	16	GLN
76	BJ	82	ASN
76	BJ	98	HIS
76	BJ	146	ASN
76	BJ	149	GLN
77	BK	42	GLN
79	BM	4	GLN
79	BM	57	HIS
79	BM	167	ASN
80	BN	83	ASN
81	BO	146	GLN
81	BO	157	ASN
82	BP	16	GLN
82	BP	20	GLN
82	BP	99	GLN
86	BT	125	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1800 (98%)	729 (41%)	100 (5%)
35	l	33/34 (97%)	21 (63%)	0
36	m	75/76 (98%)	34 (45%)	0
37	n	76/77 (98%)	30 (39%)	0
83	BQ	3162/3396 (93%)	1076 (34%)	177 (5%)
84	BR	120/121 (99%)	35 (29%)	7 (5%)
85	BS	157/158 (99%)	50 (31%)	10 (6%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5387/5662 (95%)	1975 (36%)	294 (5%)

All (1975) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	17	C
1	2	25	C
1	2	26	A
1	2	33	U
1	2	34	G
1	2	36	C
1	2	38	C
1	2	39	A
1	2	41	A
1	2	42	G
1	2	43	A
1	2	46	A
1	2	47	A
1	2	48	G
1	2	49	C
1	2	50	C
1	2	51	A
1	2	52	U
1	2	53	G
1	2	54	C
1	2	55	A
1	2	56	U
1	2	57	G
1	2	63	G
1	2	65	A
1	2	66	U
1	2	67	A
1	2	68	A
1	2	69	G
1	2	70	C
1	2	71	A
1	2	73	U
1	2	74	U
1	2	75	U

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Mol	Chain	Res	Type
1	2	76	A
1	2	78	A
1	2	80	A
1	2	81	G
1	2	83	G
1	2	86	A
1	2	92	A
1	2	99	C
1	2	104	A
1	2	105	A
1	2	106	U
1	2	111	U
1	2	112	A
1	2	114	C
1	2	115	G
1	2	116	U
1	2	117	U
1	2	120	U
1	2	121	U
1	2	124	A
1	2	127	G
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	138	A
1	2	139	C
1	2	140	A
1	2	141	U
1	2	142	G
1	2	153	G
1	2	155	U
1	2	157	A
1	2	158	U
1	2	159	U
1	2	160	C
1	2	161	U
1	2	168	A

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Mol	Chain	Res	Type
1	2	170	U
1	2	171	A
1	2	174	U
1	2	175	G
1	2	177	U
1	2	178	U
1	2	180	A
1	2	181	A
1	2	185	U
1	2	187	G
1	2	188	A
1	2	189	C
1	2	191	C
1	2	193	U
1	2	194	U
1	2	195	G
1	2	198	A
1	2	199	G
1	2	201	G
1	2	206	A
1	2	215	A
1	2	216	U
1	2	217	A
1	2	218	A
1	2	222	A
1	2	223	U
1	2	224	C
1	2	225	A
1	2	227	U
1	2	228	G
1	2	229	U
1	2	230	C
1	2	232	U
1	2	233	C
1	2	234	G
1	2	235	G
1	2	236	A
1	2	240	U
1	2	241	U
1	2	243	G
1	2	250	C
1	2	257	A

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Mol	Chain	Res	Type
1	2	259	U
1	2	260	U
1	2	262	U
1	2	265	A
1	2	266	A
1	2	267	U
1	2	272	U
1	2	275	C
1	2	278	U
1	2	279	G
1	2	280	U
1	2	281	G
1	2	282	C
1	2	283	U
1	2	285	G
1	2	296	U
1	2	299	A
1	2	302	U
1	2	308	C
1	2	309	C
1	2	312	A
1	2	313	U
1	2	314	C
1	2	316	A
1	2	317	C
1	2	319	U
1	2	320	U
1	2	321	C
1	2	322	G
1	2	323	A
1	2	329	G
1	2	330	G
1	2	331	A
1	2	333	A
1	2	334	G
1	2	337	G
1	2	338	C
1	2	340	U
1	2	341	A
1	2	346	G
1	2	352	A
1	2	353	A

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Mol	Chain	Res	Type
1	2	359	A
1	2	361	C
1	2	363	G
1	2	366	A
1	2	370	A
1	2	373	G
1	2	375	U
1	2	378	A
1	2	380	U
1	2	381	C
1	2	382	C
1	2	383	G
1	2	384	G
1	2	385	A
1	2	386	G
1	2	387	A
1	2	388	G
1	2	390	G
1	2	396	G
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	411	C
1	2	416	A
1	2	417	A
1	2	418	G
1	2	419	G
1	2	420	A
1	2	422	G
1	2	423	G
1	2	424	C
1	2	425	A
1	2	426	G
1	2	427	C
1	2	429	G
1	2	430	G
1	2	431	C
1	2	434	G
1	2	435	C
1	2	436	A
1	2	437	A

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Mol	Chain	Res	Type
1	2	439	U
1	2	440	U
1	2	442	C
1	2	444	C
1	2	446	A
1	2	448	C
1	2	452	A
1	2	453	U
1	2	454	U
1	2	455	C
1	2	459	G
1	2	460	A
1	2	464	A
1	2	471	A
1	2	474	A
1	2	475	A
1	2	477	A
1	2	486	G
1	2	488	G
1	2	491	C
1	2	492	A
1	2	493	U
1	2	494	U
1	2	495	C
1	2	496	G
1	2	498	G
1	2	500	C
1	2	502	U
1	2	505	A
1	2	506	A
1	2	507	U
1	2	510	G
1	2	515	A
1	2	517	U
1	2	519	C
1	2	524	U
1	2	525	A
1	2	534	A
1	2	535	A
1	2	536	C
1	2	538	A
1	2	540	G

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Mol	Chain	Res	Type
1	2	541	A
1	2	542	A
1	2	543	C
1	2	544	A
1	2	545	A
1	2	548	G
1	2	549	G
1	2	554	C
1	2	555	A
1	2	556	A
1	2	557	G
1	2	558	U
1	2	559	C
1	2	562	G
1	2	564	G
1	2	565	C
1	2	568	G
1	2	571	G
1	2	578	U
1	2	579	A
1	2	580	A
1	2	582	U
1	2	590	C
1	2	591	A
1	2	594	A
1	2	595	G
1	2	602	U
1	2	606	A
1	2	608	U
1	2	610	G
1	2	614	C
1	2	618	U
1	2	619	A
1	2	620	A
1	2	622	A
1	2	623	A
1	2	624	G
1	2	639	U
1	2	640	U
1	2	641	G
1	2	644	C
1	2	647	G

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Mol	Chain	Res	Type
1	2	650	U
1	2	651	G
1	2	652	G
1	2	653	C
1	2	655	G
1	2	656	G
1	2	657	U
1	2	678	A
1	2	680	U
1	2	681	U
1	2	687	G
1	2	690	G
1	2	693	U
1	2	694	U
1	2	696	C
1	2	697	C
1	2	698	U
1	2	699	U
1	2	700	C
1	2	702	G
1	2	704	C
1	2	705	U
1	2	706	A
1	2	708	C
1	2	709	C
1	2	710	U
1	2	711	U
1	2	712	G
1	2	713	A
1	2	714	G
1	2	715	U
1	2	716	C
1	2	717	C
1	2	718	U
1	2	719	U
1	2	721	U
1	2	725	U
1	2	726	C
1	2	729	G
1	2	730	G
1	2	731	C
1	2	732	G

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Mol	Chain	Res	Type
1	2	733	A
1	2	734	A
1	2	736	C
1	2	738	G
1	2	739	G
1	2	740	A
1	2	743	U
1	2	744	U
1	2	752	A
1	2	754	A
1	2	755	A
1	2	756	A
1	2	765	G
1	2	766	U
1	2	767	U
1	2	768	C
1	2	771	A
1	2	774	A
1	2	775	G
1	2	778	G
1	2	780	A
1	2	781	U
1	2	782	U
1	2	783	G
1	2	789	A
1	2	797	G
1	2	799	A
1	2	812	A
1	2	813	U
1	2	814	A
1	2	815	G
1	2	816	G
1	2	817	A
1	2	818	C
1	2	819	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	824	G
1	2	826	U
1	2	831	U
1	2	832	U

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Mol	Chain	Res	Type
1	2	833	U
1	2	834	G
1	2	835	U
1	2	836	U
1	2	838	G
1	2	840	U
1	2	841	U
1	2	842	C
1	2	845	G
1	2	846	G
1	2	847	A
1	2	852	C
1	2	856	A
1	2	857	U
1	2	858	G
1	2	859	A
1	2	860	U
1	2	863	A
1	2	864	U
1	2	876	G
1	2	882	U
1	2	894	U
1	2	895	G
1	2	896	U
1	2	899	G
1	2	900	A
1	2	911	U
1	2	912	U
1	2	913	G
1	2	914	G
1	2	915	A
1	2	916	U
1	2	918	U
1	2	921	U
1	2	925	G
1	2	929	A
1	2	931	C
1	2	932	U
1	2	933	A
1	2	934	C
1	2	935	U
1	2	939	A

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Mol	Chain	Res	Type
1	2	940	A
1	2	942	G
1	2	944	A
1	2	945	U
1	2	959	U
1	2	960	U
1	2	966	A
1	2	967	A
1	2	970	A
1	2	974	A
1	2	980	G
1	2	985	G
1	2	988	A
1	2	991	G
1	2	992	A
1	2	997	G
1	2	998	A
1	2	1004	U
1	2	1008	G
1	2	1009	U
1	2	1014	G
1	2	1021	C
1	2	1023	A
1	2	1024	U
1	2	1026	A
1	2	1028	C
1	2	1029	U
1	2	1030	A
1	2	1031	U
1	2	1032	G
1	2	1038	U
1	2	1039	A
1	2	1040	G
1	2	1047	G
1	2	1052	U
1	2	1053	G
1	2	1058	U
1	2	1060	U
1	2	1061	A
1	2	1075	C
1	2	1076	A
1	2	1081	A

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Mol	Chain	Res	Type
1	2	1082	C
1	2	1086	A
1	2	1087	A
1	2	1091	A
1	2	1092	A
1	2	1096	C
1	2	1097	U
1	2	1098	U
1	2	1099	U
1	2	1100	G
1	2	1108	G
1	2	1109	G
1	2	1114	G
1	2	1115	U
1	2	1138	A
1	2	1141	G
1	2	1143	A
1	2	1150	G
1	2	1158	C
1	2	1160	A
1	2	1164	G
1	2	1167	G
1	2	1168	U
1	2	1170	G
1	2	1171	A
1	2	1172	G
1	2	1173	C
1	2	1174	C
1	2	1175	U
1	2	1179	G
1	2	1185	U
1	2	1186	U
1	2	1193	A
1	2	1194	A
1	2	1196	A
1	2	1197	C
1	2	1199	G
1	2	1200	G
1	2	1202	A
1	2	1203	A
1	2	1204	A
1	2	1205	C

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Mol	Chain	Res	Type
1	2	1206	U
1	2	1209	C
1	2	1215	C
1	2	1216	C
1	2	1217	A
1	2	1218	G
1	2	1227	A
1	2	1228	G
1	2	1241	G
1	2	1243	G
1	2	1244	A
1	2	1245	G
1	2	1246	C
1	2	1247	U
1	2	1251	U
1	2	1252	C
1	2	1253	U
1	2	1255	G
1	2	1256	A
1	2	1257	U
1	2	1258	U
1	2	1259	U
1	2	1263	G
1	2	1273	G
1	2	1274	C
1	2	1275	A
1	2	1284	C
1	2	1285	U
1	2	1286	U
1	2	1287	A
1	2	1294	G
1	2	1299	G
1	2	1301	U
1	2	1307	U
1	2	1314	U
1	2	1315	U
1	2	1316	G
1	2	1318	G
1	2	1321	A
1	2	1322	A
1	2	1324	G
1	2	1325	A

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Mol	Chain	Res	Type
1	2	1337	A
1	2	1338	C
1	2	1339	C
1	2	1340	U
1	2	1344	A
1	2	1345	A
1	2	1346	A
1	2	1348	A
1	2	1349	G
1	2	1353	U
1	2	1354	G
1	2	1355	C
1	2	1356	U
1	2	1359	C
1	2	1360	A
1	2	1361	U
1	2	1363	U
1	2	1364	G
1	2	1365	C
1	2	1367	G
1	2	1368	G
1	2	1369	U
1	2	1370	U
1	2	1371	A
1	2	1372	U
1	2	1381	U
1	2	1382	A
1	2	1383	G
1	2	1388	A
1	2	1390	U
1	2	1391	A
1	2	1392	U
1	2	1395	G
1	2	1398	U
1	2	1399	C
1	2	1400	A
1	2	1402	G
1	2	1403	C
1	2	1405	G
1	2	1410	A
1	2	1413	U
1	2	1414	U

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Mol	Chain	Res	Type
1	2	1415	U
1	2	1417	A
1	2	1418	G
1	2	1421	A
1	2	1425	A
1	2	1427	A
1	2	1431	C
1	2	1432	U
1	2	1437	U
1	2	1444	A
1	2	1445	G
1	2	1446	A
1	2	1447	C
1	2	1448	G
1	2	1451	C
1	2	1458	G
1	2	1459	C
1	2	1460	A
1	2	1461	C
1	2	1462	G
1	2	1463	C
1	2	1465	C
1	2	1466	G
1	2	1467	C
1	2	1469	A
1	2	1470	C
1	2	1471	A
1	2	1472	C
1	2	1473	U
1	2	1474	G
1	2	1475	A
1	2	1476	C
1	2	1477	G
1	2	1478	G
1	2	1479	A
1	2	1480	G
1	2	1481	C
1	2	1483	A
1	2	1486	G
1	2	1489	U
1	2	1490	C
1	2	1491	U

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Mol	Chain	Res	Type
1	2	1492	A
1	2	1493	A
1	2	1496	U
1	2	1503	A
1	2	1506	G
1	2	1510	U
1	2	1514	U
1	2	1516	A
1	2	1517	U
1	2	1518	C
1	2	1520	U
1	2	1521	G
1	2	1522	U
1	2	1523	G
1	2	1524	A
1	2	1527	C
1	2	1528	U
1	2	1529	C
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1538	U
1	2	1540	G
1	2	1541	G
1	2	1542	G
1	2	1543	A
1	2	1545	A
1	2	1548	G
1	2	1554	U
1	2	1558	U
1	2	1559	A
1	2	1567	U
1	2	1568	C
1	2	1569	A
1	2	1570	A
1	2	1571	C
1	2	1572	G
1	2	1573	A
1	2	1574	G
1	2	1575	G
1	2	1582	U
1	2	1584	G

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Mol	Chain	Res	Type
1	2	1590	G
1	2	1595	U
1	2	1600	A
1	2	1601	G
1	2	1602	C
1	2	1603	U
1	2	1605	G
1	2	1607	G
1	2	1611	A
1	2	1616	G
1	2	1622	G
1	2	1631	A
1	2	1633	A
1	2	1634	C
1	2	1635	A
1	2	1636	C
1	2	1637	C
1	2	1638	G
1	2	1640	C
1	2	1645	G
1	2	1657	U
1	2	1658	G
1	2	1662	G
1	2	1673	G
1	2	1678	A
1	2	1682	U
1	2	1688	U
1	2	1689	A
1	2	1690	G
1	2	1691	A
1	2	1693	A
1	2	1709	C
1	2	1711	C
1	2	1712	A
1	2	1717	G
1	2	1726	G
1	2	1730	A
1	2	1736	G
1	2	1738	U
1	2	1742	U
1	2	1743	U
1	2	1750	A

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Mol	Chain	Res	Type
1	2	1753	A
1	2	1755	A
1	2	1757	G
1	2	1758	U
1	2	1760	G
1	2	1762	A
1	2	1765	A
1	2	1766	A
1	2	1767	G
1	2	1768	G
1	2	1769	U
1	2	1770	U
1	2	1780	G
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1793	G
1	2	1794	A
1	2	1796	C
1	2	1798	U
35	1	35	U
35	1	36	U
35	1	37	U
35	1	40	U
35	1	41	U
35	1	42	U
35	1	43	U
35	1	44	U
35	1	46	G
35	1	49	A
35	1	53	U
35	1	54	U
35	1	55	U
35	1	56	U
35	1	57	U
35	1	58	U
35	1	59	U
35	1	60	U
35	1	61	U
35	1	64	U
35	1	66	U
36	m	3	G

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Mol	Chain	Res	Type
36	m	7	U
36	m	8	U
36	m	15	G
36	m	16	U
36	m	18	G
36	m	20	U
36	m	21	A
36	m	30	G
36	m	36	U
36	m	41	A
36	m	43	U
36	m	45	G
36	m	46	G
36	m	47	U
36	m	48	C
36	m	49	G
36	m	50	C
36	m	51	A
36	m	52	G
36	m	53	G
36	m	54	U
36	m	55	U
36	m	56	C
36	m	58	A
36	m	59	A
36	m	60	U
36	m	61	C
36	m	64	G
36	m	66	A
36	m	67	C
36	m	68	G
36	m	73	A
36	m	74	C
37	n	2	G
37	n	3	A
37	n	8	U
37	n	9	A
37	n	11	U
37	n	13	C
37	n	14	A
37	n	15	G
37	n	16	U

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Mol	Chain	Res	Type
37	n	17	C
37	n	17(A)	G
37	n	18	G
37	n	19	U
37	n	20	U
37	n	21	A
37	n	44	G
37	n	47	U
37	n	48	C
37	n	49	G
37	n	52	G
37	n	53	G
37	n	57	G
37	n	59	G
37	n	60	U
37	n	61	C
37	n	62	C
37	n	68	G
37	n	69	U
37	n	74	C
37	n	76	A
83	BQ	4	U
83	BQ	6	A
83	BQ	13	A
83	BQ	14	U
83	BQ	16	A
83	BQ	20	A
83	BQ	21	G
83	BQ	22	G
83	BQ	26	A
83	BQ	27	C
83	BQ	30	G
83	BQ	40	A
83	BQ	43	A
83	BQ	44	U
83	BQ	47	C
83	BQ	49	A
83	BQ	57	A
83	BQ	59	G
83	BQ	60	A
83	BQ	65	A
83	BQ	66	A

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Mol	Chain	Res	Type
83	BQ	67	A
83	BQ	71	A
83	BQ	72	C
83	BQ	73	C
83	BQ	74	G
83	BQ	75	G
83	BQ	77	A
83	BQ	86	G
83	BQ	87	U
83	BQ	89	A
83	BQ	92	G
83	BQ	96	G
83	BQ	97	U
83	BQ	98	G
83	BQ	108	A
83	BQ	111	C
83	BQ	119	U
83	BQ	120	G
83	BQ	121	A
83	BQ	122	A
83	BQ	123	A
83	BQ	131	C
83	BQ	134	U
83	BQ	135	C
83	BQ	136	G
83	BQ	139	G
83	BQ	146	U
83	BQ	147	U
83	BQ	148	G
83	BQ	150	A
83	BQ	153	U
83	BQ	154	U
83	BQ	155	G
83	BQ	156	G
83	BQ	157	A
83	BQ	158	G
83	BQ	161	G
83	BQ	165	A
83	BQ	166	C
83	BQ	167	U
83	BQ	168	U
83	BQ	170	G

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Mol	Chain	Res	Type
83	BQ	172	G
83	BQ	173	G
83	BQ	187	A
83	BQ	188	U
83	BQ	189	G
83	BQ	190	U
83	BQ	191	U
83	BQ	201	A
83	BQ	206	G
83	BQ	210	U
83	BQ	211	A
83	BQ	212	G
83	BQ	213	A
83	BQ	217	U
83	BQ	218	G
83	BQ	219	A
83	BQ	220	G
83	BQ	222	A
83	BQ	230	U
83	BQ	231	G
83	BQ	234	G
83	BQ	237	G
83	BQ	240	U
83	BQ	241	G
83	BQ	242	C
83	BQ	245	U
83	BQ	247	C
83	BQ	248	U
83	BQ	250	U
83	BQ	251	G
83	BQ	252	U
83	BQ	268	A
83	BQ	269	G
83	BQ	270	U
83	BQ	281	G
83	BQ	282	G
83	BQ	283	G
83	BQ	286	U
83	BQ	287	G
83	BQ	289	A
83	BQ	295	A
83	BQ	297	G

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Mol	Chain	Res	Type
83	BQ	298	U
83	BQ	304	G
83	BQ	305	U
83	BQ	315	C
83	BQ	317	A
83	BQ	323	A
83	BQ	329	U
83	BQ	330	G
83	BQ	336	A
83	BQ	338	A
83	BQ	342	A
83	BQ	346	C
83	BQ	349	A
83	BQ	350	C
83	BQ	353	G
83	BQ	354	U
83	BQ	367	A
83	BQ	370	U
83	BQ	372	A
83	BQ	375	A
83	BQ	376	G
83	BQ	377	A
83	BQ	385	A
83	BQ	395	A
83	BQ	396	A
83	BQ	398	A
83	BQ	399	A
83	BQ	400	G
83	BQ	401	U
83	BQ	402	A
83	BQ	403	C
83	BQ	404	G
83	BQ	421	G
83	BQ	422	A
83	BQ	428	A
83	BQ	429	U
83	BQ	438	A
83	BQ	440	A
83	BQ	495	G
83	BQ	496	C
83	BQ	503	C
83	BQ	507	U

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Mol	Chain	Res	Type
83	BQ	520	U
83	BQ	521	A
83	BQ	522	A
83	BQ	523	A
83	BQ	525	C
83	BQ	527	A
83	BQ	529	A
83	BQ	531	G
83	BQ	532	A
83	BQ	533	A
83	BQ	535	G
83	BQ	541	U
83	BQ	543	C
83	BQ	544	C
83	BQ	546	C
83	BQ	547	G
83	BQ	548	G
83	BQ	551	A
83	BQ	552	G
83	BQ	555	U
83	BQ	557	A
83	BQ	559	A
83	BQ	566	G
83	BQ	569	A
83	BQ	572	A
83	BQ	575	G
83	BQ	578	A
83	BQ	579	G
83	BQ	581	U
83	BQ	588	G
83	BQ	589	A
83	BQ	592	A
83	BQ	594	U
83	BQ	597	G
83	BQ	601	U
83	BQ	604	G
83	BQ	608	A
83	BQ	609	G
83	BQ	611	A
83	BQ	612	U
83	BQ	615	U
83	BQ	616	G

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Mol	Chain	Res	Type
83	BQ	617	G
83	BQ	620	U
83	BQ	621	A
83	BQ	622	A
83	BQ	627	U
83	BQ	629	U
83	BQ	634	C
83	BQ	636	C
83	BQ	637	C
83	BQ	642	U
83	BQ	643	U
83	BQ	649	A
83	BQ	661	G
83	BQ	664	U
83	BQ	666	A
83	BQ	667	C
83	BQ	676	G
83	BQ	677	A
83	BQ	678	G
83	BQ	681	U
83	BQ	690	A
83	BQ	691	A
83	BQ	692	A
83	BQ	699	A
83	BQ	705	A
83	BQ	709	A
83	BQ	712	G
83	BQ	715	A
83	BQ	716	A
83	BQ	719	U
83	BQ	720	A
83	BQ	721	G
83	BQ	726	G
83	BQ	728	G
83	BQ	735	A
83	BQ	742	G
83	BQ	757	C
83	BQ	760	G
83	BQ	764	U
83	BQ	765	C
83	BQ	766	U
83	BQ	767	U

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Mol	Chain	Res	Type
83	BQ	768	C
83	BQ	770	G
83	BQ	776	U
83	BQ	777	U
83	BQ	781	G
83	BQ	784	A
83	BQ	785	G
83	BQ	787	G
83	BQ	792	G
83	BQ	799	G
83	BQ	800	G
83	BQ	801	A
83	BQ	806	A
83	BQ	808	A
83	BQ	816	A
83	BQ	817	A
83	BQ	826	G
83	BQ	830	A
83	BQ	835	G
83	BQ	847	A
83	BQ	849	C
83	BQ	861	C
83	BQ	871	U
83	BQ	874	U
83	BQ	875	G
83	BQ	879	U
83	BQ	880	G
83	BQ	882	A
83	BQ	885	U
83	BQ	895	A
83	BQ	896	A
83	BQ	897	U
83	BQ	907	G
83	BQ	913	A
83	BQ	914	A
83	BQ	915	A
83	BQ	916	G
83	BQ	917	A
83	BQ	921	A
83	BQ	922	U
83	BQ	923	C
83	BQ	924	G

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Mol	Chain	Res	Type
83	BQ	925	A
83	BQ	926	A
83	BQ	933	A
83	BQ	934	G
83	BQ	937	G
83	BQ	938	C
83	BQ	939	U
83	BQ	944	C
83	BQ	953	G
83	BQ	954	U
83	BQ	959	C
83	BQ	960	U
83	BQ	961	C
83	BQ	962	A
83	BQ	964	G
83	BQ	974	G
83	BQ	977	C
83	BQ	979	U
83	BQ	980	A
83	BQ	981	U
83	BQ	984	G
83	BQ	991	G
83	BQ	993	G
83	BQ	994	G
83	BQ	995	U
83	BQ	996	A
83	BQ	1001	G
83	BQ	1005	G
83	BQ	1007	U
83	BQ	1008	U
83	BQ	1010	G
83	BQ	1013	G
83	BQ	1015	U
83	BQ	1016	C
83	BQ	1017	C
83	BQ	1018	G
83	BQ	1019	G
83	BQ	1020	G
83	BQ	1023	C
83	BQ	1025	A
83	BQ	1028	U
83	BQ	1029	G

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Mol	Chain	Res	Type
83	BQ	1030	A
83	BQ	1032	C
83	BQ	1033	U
83	BQ	1036	A
83	BQ	1038	C
83	BQ	1042	U
83	BQ	1043	C
83	BQ	1045	C
83	BQ	1047	A
83	BQ	1049	C
83	BQ	1050	U
83	BQ	1063	G
83	BQ	1065	A
83	BQ	1071	U
83	BQ	1076	C
83	BQ	1077	U
83	BQ	1081	U
83	BQ	1083	G
83	BQ	1087	G
83	BQ	1092	C
83	BQ	1093	A
83	BQ	1094	U
83	BQ	1095	U
83	BQ	1096	U
83	BQ	1097	G
83	BQ	1098	A
83	BQ	1102	A
83	BQ	1103	A
83	BQ	1104	G
83	BQ	1117	G
83	BQ	1125	U
83	BQ	1128	U
83	BQ	1131	G
83	BQ	1140	G
83	BQ	1142	G
83	BQ	1143	A
83	BQ	1144	U
83	BQ	1145	G
83	BQ	1149	G
83	BQ	1150	A
83	BQ	1151	U
83	BQ	1153	A

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Mol	Chain	Res	Type
83	BQ	1154	A
83	BQ	1155	C
83	BQ	1159	A
83	BQ	1171	G
83	BQ	1172	G
83	BQ	1177	G
83	BQ	1178	G
83	BQ	1180	A
83	BQ	1181	U
83	BQ	1182	A
83	BQ	1186	G
83	BQ	1191	U
83	BQ	1192	C
83	BQ	1193	A
83	BQ	1197	A
83	BQ	1199	C
83	BQ	1200	A
83	BQ	1201	C
83	BQ	1202	A
83	BQ	1206	G
83	BQ	1213	G
83	BQ	1217	A
83	BQ	1220	U
83	BQ	1222	G
83	BQ	1223	A
83	BQ	1225	A
83	BQ	1228	C
83	BQ	1230	G
83	BQ	1233	G
83	BQ	1234	G
83	BQ	1235	U
83	BQ	1236	G
83	BQ	1237	G
83	BQ	1238	C
83	BQ	1239	C
83	BQ	1240	A
83	BQ	1241	U
83	BQ	1242	G
83	BQ	1243	G
83	BQ	1245	A
83	BQ	1246	G
83	BQ	1247	U

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Mol	Chain	Res	Type
83	BQ	1248	C
83	BQ	1249	G
83	BQ	1251	A
83	BQ	1252	A
83	BQ	1253	U
83	BQ	1254	C
83	BQ	1256	G
83	BQ	1257	C
83	BQ	1260	A
83	BQ	1262	G
83	BQ	1263	A
83	BQ	1264	G
83	BQ	1265	U
83	BQ	1266	G
83	BQ	1267	U
83	BQ	1270	A
83	BQ	1271	A
83	BQ	1272	C
83	BQ	1273	A
83	BQ	1274	A
83	BQ	1275	C
83	BQ	1276	U
83	BQ	1277	C
83	BQ	1278	A
83	BQ	1279	C
83	BQ	1280	C
83	BQ	1281	G
83	BQ	1282	G
83	BQ	1285	G
83	BQ	1286	A
83	BQ	1287	A
83	BQ	1294	A
83	BQ	1301	A
83	BQ	1303	A
83	BQ	1305	U
83	BQ	1308	A
83	BQ	1309	U
83	BQ	1313	G
83	BQ	1315	U
83	BQ	1316	C
83	BQ	1317	A
83	BQ	1318	A

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Mol	Chain	Res	Type
83	BQ	1321	G
83	BQ	1325	U
83	BQ	1329	U
83	BQ	1330	A
83	BQ	1332	A
83	BQ	1334	U
83	BQ	1345	G
83	BQ	1348	U
83	BQ	1349	G
83	BQ	1351	U
83	BQ	1353	U
83	BQ	1354	G
83	BQ	1355	A
83	BQ	1356	U
83	BQ	1357	G
83	BQ	1359	C
83	BQ	1364	C
83	BQ	1382	G
83	BQ	1386	A
83	BQ	1391	C
83	BQ	1392	G
83	BQ	1393	A
83	BQ	1399	A
83	BQ	1400	G
83	BQ	1408	G
83	BQ	1418	A
83	BQ	1419	A
83	BQ	1424	C
83	BQ	1429	G
83	BQ	1430	U
83	BQ	1432	C
83	BQ	1434	G
83	BQ	1435	A
83	BQ	1437	C
83	BQ	1446	A
83	BQ	1447	G
83	BQ	1448	U
83	BQ	1450	G
83	BQ	1452	A
83	BQ	1456	A
83	BQ	1464	G
83	BQ	1468	A

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Mol	Chain	Res	Type
83	BQ	1480	G
83	BQ	1481	A
83	BQ	1482	A
83	BQ	1483	G
83	BQ	1484	U
83	BQ	1485	G
83	BQ	1487	G
83	BQ	1508	C
83	BQ	1511	U
83	BQ	1512	U
83	BQ	1514	G
83	BQ	1523	U
83	BQ	1527	C
83	BQ	1533	U
83	BQ	1536	G
83	BQ	1539	A
83	BQ	1542	G
83	BQ	1549	U
83	BQ	1554	U
83	BQ	1555	U
83	BQ	1556	C
83	BQ	1557	A
83	BQ	1558	A
83	BQ	1559	A
83	BQ	1560	G
83	BQ	1561	G
83	BQ	1563	C
83	BQ	1567	U
83	BQ	1568	U
83	BQ	1569	U
83	BQ	1570	U
83	BQ	1571	A
83	BQ	1572	U
83	BQ	1576	G
83	BQ	1577	G
83	BQ	1578	C
83	BQ	1579	C
83	BQ	1580	A
83	BQ	1581	C
83	BQ	1582	C
83	BQ	1583	A
83	BQ	1587	A

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Mol	Chain	Res	Type
83	BQ	1588	A
83	BQ	1589	A
83	BQ	1593	A
83	BQ	1596	C
83	BQ	1597	C
83	BQ	1602	A
83	BQ	1603	A
83	BQ	1605	A
83	BQ	1613	A
83	BQ	1619	A
83	BQ	1620	U
83	BQ	1621	A
83	BQ	1630	U
83	BQ	1631	C
83	BQ	1632	A
83	BQ	1645	U
83	BQ	1646	G
83	BQ	1656	A
83	BQ	1657	C
83	BQ	1658	G
83	BQ	1659	U
83	BQ	1662	G
83	BQ	1683	A
83	BQ	1684	U
83	BQ	1692	U
83	BQ	1694	U
83	BQ	1696	A
83	BQ	1697	A
83	BQ	1702	U
83	BQ	1704	A
83	BQ	1708	C
83	BQ	1713	G
83	BQ	1714	A
83	BQ	1717	U
83	BQ	1718	G
83	BQ	1724	U
83	BQ	1725	C
83	BQ	1728	G
83	BQ	1729	A
83	BQ	1730	G
83	BQ	1731	A
83	BQ	1735	G

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Mol	Chain	Res	Type
83	BQ	1740	U
83	BQ	1741	A
83	BQ	1750	A
83	BQ	1751	G
83	BQ	1752	A
83	BQ	1760	A
83	BQ	1761	C
83	BQ	1762	C
83	BQ	1763	U
83	BQ	1765	U
83	BQ	1769	G
83	BQ	1770	G
83	BQ	1775	G
83	BQ	1780	G
83	BQ	1785	U
83	BQ	1788	C
83	BQ	1794	G
83	BQ	1797	A
83	BQ	1809	A
83	BQ	1813	A
83	BQ	1814	A
83	BQ	1815	U
83	BQ	1816	A
83	BQ	1817	G
83	BQ	1819	U
83	BQ	1820	U
83	BQ	1821	U
83	BQ	1822	C
83	BQ	1834	U
83	BQ	1835	A
83	BQ	1839	A
83	BQ	1840	U
83	BQ	1841	A
83	BQ	1842	A
83	BQ	1845	G
83	BQ	1846	C
83	BQ	1847	A
83	BQ	1848	G
83	BQ	1849	C
83	BQ	1851	G
83	BQ	1854	C
83	BQ	1855	U

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Mol	Chain	Res	Type
83	BQ	1856	C
83	BQ	1866	C
83	BQ	1868	G
83	BQ	1871	U
83	BQ	1877	U
83	BQ	1879	A
83	BQ	1880	U
83	BQ	1881	A
83	BQ	1884	A
83	BQ	1885	U
83	BQ	1886	A
83	BQ	1893	A
83	BQ	1894	U
83	BQ	1895	A
83	BQ	1899	G
83	BQ	1900	A
83	BQ	1901	A
83	BQ	1905	G
83	BQ	1906	G
83	BQ	1914	G
83	BQ	1918	C
83	BQ	1927	G
83	BQ	1930	A
83	BQ	1931	U
83	BQ	1932	A
83	BQ	1936	A
83	BQ	1942	U
83	BQ	1947	G
83	BQ	1948	G
83	BQ	1949	G
83	BQ	1952	G
83	BQ	1953	G
83	BQ	1954	G
83	BQ	2095	G
83	BQ	2099	A
83	BQ	2100	A
83	BQ	2101	C
83	BQ	2102	U
83	BQ	2106	A
83	BQ	2107	A
83	BQ	2108	C
83	BQ	2111	G

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Mol	Chain	Res	Type
83	BQ	2112	U
83	BQ	2113	A
83	BQ	2116	G
83	BQ	2117	A
83	BQ	2121	G
83	BQ	2122	G
83	BQ	2126	A
83	BQ	2131	A
83	BQ	2138	A
83	BQ	2139	A
83	BQ	2140	U
83	BQ	2144	A
83	BQ	2145	A
83	BQ	2158	A
83	BQ	2159	U
83	BQ	2160	G
83	BQ	2163	C
83	BQ	2169	G
83	BQ	2170	U
83	BQ	2175	U
83	BQ	2177	G
83	BQ	2178	A
83	BQ	2179	C
83	BQ	2180	G
83	BQ	2184	U
83	BQ	2186	U
83	BQ	2188	A
83	BQ	2192	C
83	BQ	2193	U
83	BQ	2194	G
83	BQ	2197	C
83	BQ	2198	A
83	BQ	2205	U
83	BQ	2206	G
83	BQ	2207	A
83	BQ	2208	A
83	BQ	2209	U
83	BQ	2210	G
83	BQ	2212	C
83	BQ	2225	U
83	BQ	2243	A
83	BQ	2244	A

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Mol	Chain	Res	Type
83	BQ	2246	G
83	BQ	2249	G
83	BQ	2255	A
83	BQ	2256	A
83	BQ	2257	C
83	BQ	2261	G
83	BQ	2263	C
83	BQ	2270	A
83	BQ	2272	G
83	BQ	2274	U
83	BQ	2279	A
83	BQ	2280	A
83	BQ	2281	A
83	BQ	2282	U
83	BQ	2283	G
83	BQ	2284	C
83	BQ	2288	G
83	BQ	2298	U
83	BQ	2303	A
83	BQ	2306	C
83	BQ	2307	G
83	BQ	2308	C
83	BQ	2313	A
83	BQ	2314	U
83	BQ	2315	G
83	BQ	2318	U
83	BQ	2319	U
83	BQ	2336	U
83	BQ	2340	U
83	BQ	2357	A
83	BQ	2364	G
83	BQ	2373	A
83	BQ	2374	C
83	BQ	2375	G
83	BQ	2378	C
83	BQ	2383	C
83	BQ	2386	A
83	BQ	2388	U
83	BQ	2393	G
83	BQ	2394	G
83	BQ	2397	A
83	BQ	2398	A

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Mol	Chain	Res	Type
83	BQ	2402	A
83	BQ	2403	G
83	BQ	2411	U
83	BQ	2412	G
83	BQ	2418	G
83	BQ	2419	A
83	BQ	2433	U
83	BQ	2435	G
83	BQ	2436	U
83	BQ	2437	G
83	BQ	2439	A
83	BQ	2441	A
83	BQ	2442	G
83	BQ	2444	C
83	BQ	2445	A
83	BQ	2446	U
83	BQ	2447	A
83	BQ	2451	G
83	BQ	2452	G
83	BQ	2493	U
83	BQ	2494	A
83	BQ	2496	C
83	BQ	2497	U
83	BQ	2498	U
83	BQ	2501	U
83	BQ	2502	A
83	BQ	2508	U
83	BQ	2509	U
83	BQ	2514	U
83	BQ	2515	A
83	BQ	2522	G
83	BQ	2523	A
83	BQ	2524	A
83	BQ	2526	C
83	BQ	2530	G
83	BQ	2531	C
83	BQ	2533	G
83	BQ	2534	G
83	BQ	2537	U
83	BQ	2538	U
83	BQ	2539	C
83	BQ	2540	A

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Mol	Chain	Res	Type
83	BQ	2541	U
83	BQ	2542	U
83	BQ	2544	U
83	BQ	2546	C
83	BQ	2547	A
83	BQ	2550	U
83	BQ	2552	C
83	BQ	2554	A
83	BQ	2555	G
83	BQ	2559	U
83	BQ	2560	C
83	BQ	2567	C
83	BQ	2568	C
83	BQ	2570	U
83	BQ	2571	U
83	BQ	2572	C
83	BQ	2578	U
83	BQ	2585	G
83	BQ	2587	U
83	BQ	2589	G
83	BQ	2590	A
83	BQ	2593	A
83	BQ	2594	C
83	BQ	2600	C
83	BQ	2606	G
83	BQ	2607	G
83	BQ	2614	G
83	BQ	2617	U
83	BQ	2618	G
83	BQ	2619	G
83	BQ	2624	G
83	BQ	2626	A
83	BQ	2627	C
83	BQ	2629	U
83	BQ	2641	U
83	BQ	2642	A
83	BQ	2652	U
83	BQ	2655	U
83	BQ	2656	A
83	BQ	2657	A
83	BQ	2666	C
83	BQ	2672	G

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Mol	Chain	Res	Type
83	BQ	2674	A
83	BQ	2678	A
83	BQ	2679	A
83	BQ	2681	U
83	BQ	2688	U
83	BQ	2689	A
83	BQ	2690	G
83	BQ	2691	A
83	BQ	2694	A
83	BQ	2695	A
83	BQ	2703	A
83	BQ	2704	A
83	BQ	2709	C
83	BQ	2713	U
83	BQ	2714	G
83	BQ	2716	U
83	BQ	2726	C
83	BQ	2727	A
83	BQ	2728	G
83	BQ	2737	C
83	BQ	2740	A
83	BQ	2747	A
83	BQ	2749	G
83	BQ	2751	G
83	BQ	2752	U
83	BQ	2753	G
83	BQ	2754	G
83	BQ	2755	C
83	BQ	2761	G
83	BQ	2762	A
83	BQ	2772	C
83	BQ	2776	C
83	BQ	2777	G
83	BQ	2778	G
83	BQ	2779	A
83	BQ	2795	U
83	BQ	2796	G
83	BQ	2800	G
83	BQ	2801	A
83	BQ	2802	A
83	BQ	2803	A
83	BQ	2804	A

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Mol	Chain	Res	Type
83	BQ	2810	C
83	BQ	2814	G
83	BQ	2816	G
83	BQ	2817	A
83	BQ	2821	C
83	BQ	2829	U
83	BQ	2834	G
83	BQ	2837	A
83	BQ	2839	G
83	BQ	2842	U
83	BQ	2845	A
83	BQ	2849	C
83	BQ	2855	U
83	BQ	2859	U
83	BQ	2860	U
83	BQ	2862	U
83	BQ	2863	G
83	BQ	2864	A
83	BQ	2867	C
83	BQ	2870	C
83	BQ	2871	G
83	BQ	2872	A
83	BQ	2875	U
83	BQ	2877	G
83	BQ	2883	U
83	BQ	2888	U
83	BQ	2889	C
83	BQ	2898	G
83	BQ	2899	C
83	BQ	2901	G
83	BQ	2911	A
83	BQ	2912	G
83	BQ	2923	U
83	BQ	2925	C
83	BQ	2928	C
83	BQ	2930	A
83	BQ	2933	A
83	BQ	2935	U
83	BQ	2936	A
83	BQ	2938	G
83	BQ	2941	A
83	BQ	2942	C

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Mol	Chain	Res	Type
83	BQ	2945	G
83	BQ	2947	G
83	BQ	2950	G
83	BQ	2951	G
83	BQ	2953	U
83	BQ	2954	U
83	BQ	2955	U
83	BQ	2971	A
83	BQ	2972	G
83	BQ	2977	G
83	BQ	2978	U
83	BQ	2979	U
83	BQ	2983	C
83	BQ	2990	G
83	BQ	2996	U
83	BQ	2997	G
83	BQ	3004	C
83	BQ	3012	A
83	BQ	3013	U
83	BQ	3022	G
83	BQ	3023	U
83	BQ	3026	G
83	BQ	3030	G
83	BQ	3034	C
83	BQ	3039	C
83	BQ	3040	A
83	BQ	3047	U
83	BQ	3048	A
83	BQ	3049	A
83	BQ	3056	U
83	BQ	3057	U
83	BQ	3058	U
83	BQ	3059	G
83	BQ	3061	G
83	BQ	3074	G
83	BQ	3077	A
83	BQ	3078	U
83	BQ	3079	U
83	BQ	3080	G
83	BQ	3086	A
83	BQ	3090	U
83	BQ	3092	C

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Mol	Chain	Res	Type
83	BQ	3093	C
83	BQ	3094	A
83	BQ	3099	C
83	BQ	3100	U
83	BQ	3104	U
83	BQ	3109	G
83	BQ	3111	U
83	BQ	3112	G
83	BQ	3113	A
83	BQ	3115	C
83	BQ	3116	G
83	BQ	3117	C
83	BQ	3119	U
83	BQ	3120	C
83	BQ	3122	A
83	BQ	3123	A
83	BQ	3126	C
83	BQ	3129	A
83	BQ	3130	A
83	BQ	3131	U
83	BQ	3138	U
83	BQ	3142	A
83	BQ	3143	C
83	BQ	3144	G
83	BQ	3152	U
83	BQ	3153	U
83	BQ	3154	C
83	BQ	3155	U
83	BQ	3156	U
83	BQ	3157	U
83	BQ	3158	G
83	BQ	3168	A
83	BQ	3171	U
83	BQ	3172	A
83	BQ	3173	G
83	BQ	3174	A
83	BQ	3175	U
83	BQ	3176	G
83	BQ	3178	A
83	BQ	3179	U
83	BQ	3180	A
83	BQ	3181	C

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Mol	Chain	Res	Type
83	BQ	3183	A
83	BQ	3185	U
83	BQ	3187	A
83	BQ	3193	C
83	BQ	3194	C
83	BQ	3195	U
83	BQ	3196	U
83	BQ	3197	G
83	BQ	3198	U
83	BQ	3206	C
83	BQ	3207	U
83	BQ	3208	G
83	BQ	3209	A
83	BQ	3210	A
83	BQ	3216	G
83	BQ	3217	C
83	BQ	3218	A
83	BQ	3220	G
83	BQ	3224	G
83	BQ	3227	A
83	BQ	3228	C
83	BQ	3229	G
83	BQ	3231	U
83	BQ	3237	U
83	BQ	3238	G
83	BQ	3241	G
83	BQ	3242	G
83	BQ	3244	A
83	BQ	3245	A
83	BQ	3246	G
83	BQ	3247	G
83	BQ	3259	U
83	BQ	3261	C
83	BQ	3262	U
83	BQ	3263	G
83	BQ	3268	A
83	BQ	3269	U
83	BQ	3270	U
83	BQ	3271	G
83	BQ	3272	C
83	BQ	3273	A
83	BQ	3274	A

Continued on next page...

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Mol	Chain	Res	Type
83	BQ	3275	U
83	BQ	3276	G
83	BQ	3277	U
83	BQ	3278	C
83	BQ	3279	A
83	BQ	3287	U
83	BQ	3288	G
83	BQ	3289	G
83	BQ	3294	A
83	BQ	3295	A
83	BQ	3304	U
83	BQ	3305	A
83	BQ	3308	C
83	BQ	3313	U
83	BQ	3316	A
83	BQ	3317	U
83	BQ	3318	G
83	BQ	3319	U
83	BQ	3320	A
83	BQ	3322	A
83	BQ	3324	C
83	BQ	3330	A
83	BQ	3334	U
83	BQ	3335	A
83	BQ	3339	A
83	BQ	3342	A
83	BQ	3345	G
83	BQ	3346	U
83	BQ	3347	A
83	BQ	3348	G
83	BQ	3351	U
83	BQ	3352	U
83	BQ	3353	G
83	BQ	3354	U
83	BQ	3355	U
83	BQ	3356	G
83	BQ	3357	U
83	BQ	3362	A
83	BQ	3364	C
83	BQ	3368	U
83	BQ	3369	G
83	BQ	3370	A

Continued on next page...

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Mol	Chain	Res	Type
83	BQ	3375	A
83	BQ	3378	C
83	BQ	3382	U
83	BQ	3383	G
83	BQ	3390	G
84	BR	10	C
84	BR	11	A
84	BR	13	A
84	BR	14	U
84	BR	19	C
84	BR	20	A
84	BR	22	A
84	BR	23	A
84	BR	26	C
84	BR	29	C
84	BR	32	U
84	BR	33	U
84	BR	41	G
84	BR	42	A
84	BR	49	G
84	BR	53	U
84	BR	54	U
84	BR	55	A
84	BR	56	A
84	BR	65	G
84	BR	71	G
84	BR	73	C
84	BR	74	C
84	BR	77	G
84	BR	78	U
84	BR	79	A
84	BR	87	G
84	BR	91	G
84	BR	99	G
84	BR	101	G
84	BR	102	A
84	BR	103	A
84	BR	111	U
84	BR	112	G
84	BR	121	U
85	BS	8	C
85	BS	15	G

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Mol	Chain	Res	Type
85	BS	16	G
85	BS	17	A
85	BS	22	U
85	BS	23	U
85	BS	24	G
85	BS	34	U
85	BS	35	C
85	BS	39	G
85	BS	40	A
85	BS	49	G
85	BS	50	C
85	BS	51	G
85	BS	52	A
85	BS	59	A
85	BS	60	U
85	BS	61	A
85	BS	62	C
85	BS	63	G
85	BS	80	A
85	BS	81	U
85	BS	82	U
85	BS	83	C
85	BS	84	C
85	BS	85	G
85	BS	86	U
85	BS	87	G
85	BS	90	U
85	BS	91	C
85	BS	95	G
85	BS	97	A
85	BS	102	U
85	BS	104	A
85	BS	106	C
85	BS	110	C
85	BS	112	U
85	BS	113	U
85	BS	115	C
85	BS	116	G
85	BS	125	U
85	BS	126	A
85	BS	127	U
85	BS	129	C

Continued on next page...

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Mol	Chain	Res	Type
85	BS	144	G
85	BS	148	G
85	BS	151	C
85	BS	152	G
85	BS	154	C
85	BS	158	U

All (294) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	42	G
1	2	51	A
1	2	52	U
1	2	53	G
1	2	54	C
1	2	55	A
1	2	66	U
1	2	68	A
1	2	77	U
1	2	104	A
1	2	114	C
1	2	115	G
1	2	126	A
1	2	128	U
1	2	132	U
1	2	139	C
1	2	141	U
1	2	158	U
1	2	159	U
1	2	174	U
1	2	224	C
1	2	266	A
1	2	278	U
1	2	280	U
1	2	312	A
1	2	313	U
1	2	322	G
1	2	352	A
1	2	379	U
1	2	380	U
1	2	381	C
1	2	385	A

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Mol	Chain	Res	Type
1	2	387	A
1	2	400	A
1	2	410	A
1	2	411	C
1	2	425	A
1	2	429	G
1	2	430	G
1	2	439	U
1	2	454	U
1	2	539	G
1	2	541	A
1	2	555	A
1	2	578	U
1	2	609	U
1	2	613	G
1	2	619	A
1	2	639	U
1	2	696	C
1	2	699	U
1	2	705	U
1	2	711	U
1	2	754	A
1	2	765	G
1	2	766	U
1	2	782	U
1	2	819	G
1	2	913	G
1	2	928	U
1	2	944	A
1	2	1023	A
1	2	1081	A
1	2	1092	A
1	2	1108	G
1	2	1114	G
1	2	1173	C
1	2	1185	U
1	2	1193	A
1	2	1226	A
1	2	1244	A
1	2	1245	G
1	2	1251	U
1	2	1256	A

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Mol	Chain	Res	Type
1	2	1273	G
1	2	1274	C
1	2	1314	U
1	2	1344	A
1	2	1357	A
1	2	1369	U
1	2	1370	U
1	2	1382	A
1	2	1399	C
1	2	1412	G
1	2	1430	U
1	2	1457	C
1	2	1472	C
1	2	1481	C
1	2	1520	U
1	2	1539	G
1	2	1570	A
1	2	1573	A
1	2	1601	G
1	2	1615	C
1	2	1633	A
1	2	1636	C
1	2	1742	U
1	2	1761	U
1	2	1767	G
1	2	1791	A
83	BQ	13	A
83	BQ	21	G
83	BQ	40	A
83	BQ	43	A
83	BQ	66	A
83	BQ	71	A
83	BQ	86	G
83	BQ	97	U
83	BQ	154	U
83	BQ	155	G
83	BQ	189	G
83	BQ	211	A
83	BQ	269	G
83	BQ	282	G
83	BQ	316	U
83	BQ	349	A

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Mol	Chain	Res	Type
83	BQ	352	A
83	BQ	353	G
83	BQ	369	A
83	BQ	374	A
83	BQ	376	G
83	BQ	400	G
83	BQ	411	U
83	BQ	494	G
83	BQ	547	G
83	BQ	556	U
83	BQ	588	G
83	BQ	611	A
83	BQ	621	A
83	BQ	677	A
83	BQ	715	A
83	BQ	764	U
83	BQ	767	U
83	BQ	775	A
83	BQ	786	A
83	BQ	806	A
83	BQ	816	A
83	BQ	822	G
83	BQ	895	A
83	BQ	896	A
83	BQ	916	G
83	BQ	921	A
83	BQ	923	C
83	BQ	924	G
83	BQ	933	A
83	BQ	961	C
83	BQ	978	G
83	BQ	979	U
83	BQ	980	A
83	BQ	993	G
83	BQ	1064	A
83	BQ	1095	U
83	BQ	1096	U
83	BQ	1103	A
83	BQ	1116	G
83	BQ	1144	U
83	BQ	1152	G
83	BQ	1154	A

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Mol	Chain	Res	Type
83	BQ	1177	G
83	BQ	1222	G
83	BQ	1241	U
83	BQ	1253	U
83	BQ	1307	G
83	BQ	1352	A
83	BQ	1355	A
83	BQ	1392	G
83	BQ	1417	G
83	BQ	1418	A
83	BQ	1429	G
83	BQ	1467	A
83	BQ	1481	A
83	BQ	1482	A
83	BQ	1483	G
83	BQ	1511	U
83	BQ	1554	U
83	BQ	1568	U
83	BQ	1580	A
83	BQ	1607	U
83	BQ	1695	U
83	BQ	1724	U
83	BQ	1729	A
83	BQ	1730	G
83	BQ	1751	G
83	BQ	1808	G
83	BQ	1815	U
83	BQ	1816	A
83	BQ	1820	U
83	BQ	1839	A
83	BQ	1840	U
83	BQ	1846	C
83	BQ	1847	A
83	BQ	1849	C
83	BQ	1850	A
83	BQ	1885	U
83	BQ	1900	A
83	BQ	1913	A
83	BQ	2101	C
83	BQ	2112	U
83	BQ	2116	G
83	BQ	2138	A

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Mol	Chain	Res	Type
83	BQ	2144	A
83	BQ	2159	U
83	BQ	2177	G
83	BQ	2178	A
83	BQ	2198	A
83	BQ	2208	A
83	BQ	2256	A
83	BQ	2273	G
83	BQ	2279	A
83	BQ	2281	A
83	BQ	2282	U
83	BQ	2283	G
83	BQ	2305	G
83	BQ	2313	A
83	BQ	2433	U
83	BQ	2434	U
83	BQ	2445	A
83	BQ	2493	U
83	BQ	2495	C
83	BQ	2500	A
83	BQ	2501	U
83	BQ	2513	U
83	BQ	2514	U
83	BQ	2525	G
83	BQ	2539	C
83	BQ	2541	U
83	BQ	2549	G
83	BQ	2554	A
83	BQ	2586	G
83	BQ	2593	A
83	BQ	2617	U
83	BQ	2625	C
83	BQ	2665	U
83	BQ	2677	G
83	BQ	2680	A
83	BQ	2689	A
83	BQ	2703	A
83	BQ	2727	A
83	BQ	2754	G
83	BQ	2794	G
83	BQ	2801	A
83	BQ	2803	A

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Mol	Chain	Res	Type
83	BQ	2816	G
83	BQ	2898	G
83	BQ	2911	A
83	BQ	2941	A
83	BQ	2950	G
83	BQ	2953	U
83	BQ	2954	U
83	BQ	2971	A
83	BQ	3011	A
83	BQ	3021	A
83	BQ	3022	G
83	BQ	3047	U
83	BQ	3048	A
83	BQ	3057	U
83	BQ	3078	U
83	BQ	3093	C
83	BQ	3143	C
83	BQ	3156	U
83	BQ	3172	A
83	BQ	3175	U
83	BQ	3179	U
83	BQ	3196	U
83	BQ	3216	G
83	BQ	3219	G
83	BQ	3241	G
83	BQ	3269	U
83	BQ	3272	C
83	BQ	3274	A
83	BQ	3293	U
83	BQ	3317	U
83	BQ	3344	A
83	BQ	3345	G
83	BQ	3350	C
83	BQ	3353	G
83	BQ	3382	U
84	BR	12	U
84	BR	32	U
84	BR	41	G
84	BR	54	U
84	BR	77	G
84	BR	86	U
84	BR	111	U

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Mol	Chain	Res	Type
85	BS	22	U
85	BS	23	U
85	BS	33	A
85	BS	34	U
85	BS	39	G
85	BS	48	A
85	BS	58	G
85	BS	85	G
85	BS	112	U
85	BS	125	U

5.4 Non-standard residues in protein, DNA, RNA chains

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	5CT	BT	51	86	13,14,15	0.32	0	8,15,17	1.21	2 (25%)

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
86	5CT	BT	51	86	-	7/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	BT	51	5CT	C1-NZ-CE	-2.34	108.27	113.38
86	BT	51	5CT	C4-C3-C2	-2.03	109.19	113.47

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	BT	51	5CT	O-C-CA-CB
86	BT	51	5CT	C2-C1-NZ-CE
86	BT	51	5CT	C2-C3-C4-N1
86	BT	51	5CT	CD-CE-NZ-C1
86	BT	51	5CT	C-CA-CB-CG
86	BT	51	5CT	CG-CD-CE-NZ
86	BT	51	5CT	NZ-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	BT	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	52:U	O3'	53:G	P	1.89

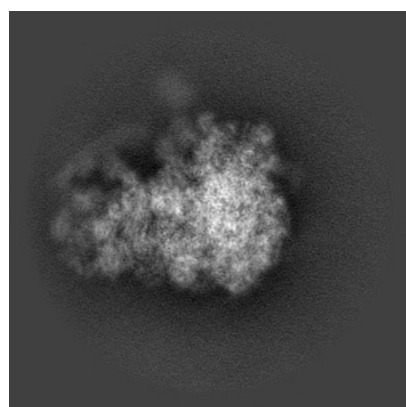
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3461. These allow visual inspection of the internal detail of the map and identification of artifacts.

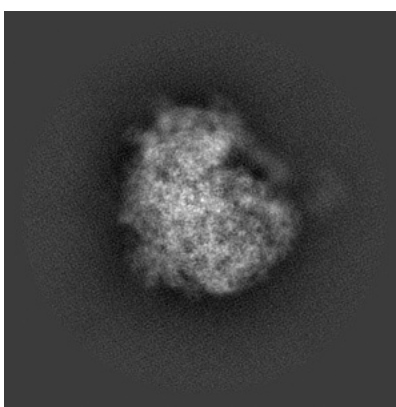
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

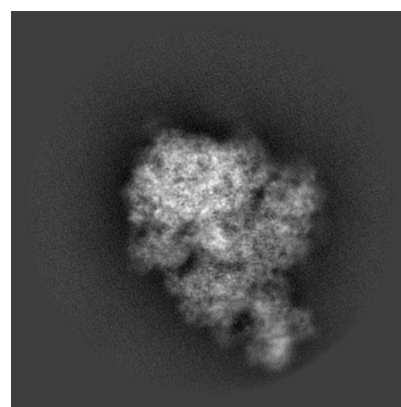
6.1.1 Primary map



X



Y

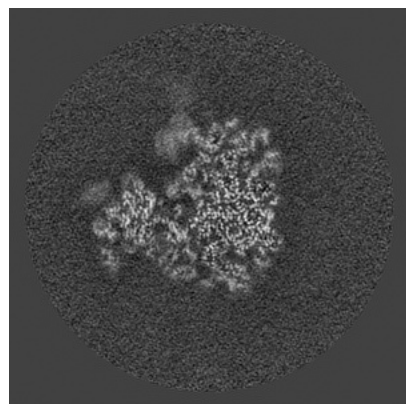


Z

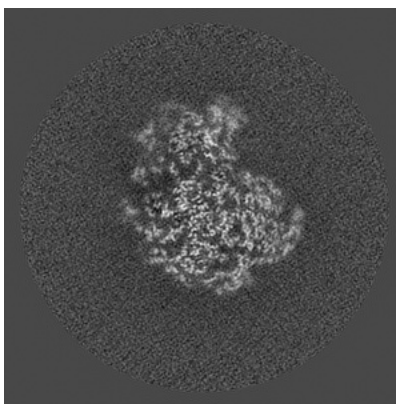
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

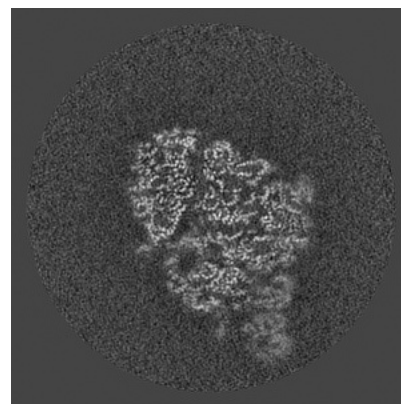
6.2.1 Primary map



X Index: 240



Y Index: 240

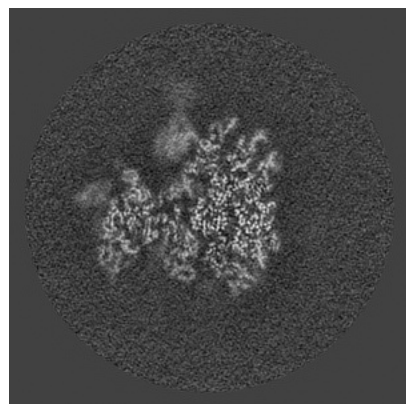


Z Index: 240

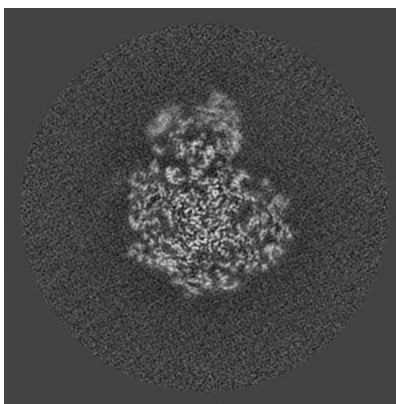
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

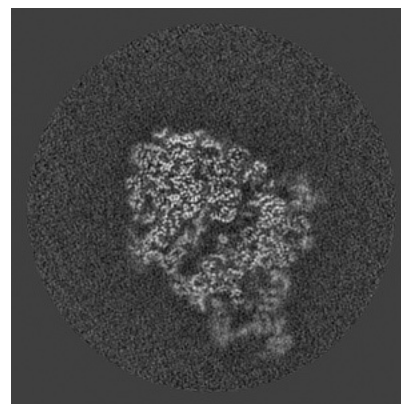
6.3.1 Primary map



X Index: 245



Y Index: 253

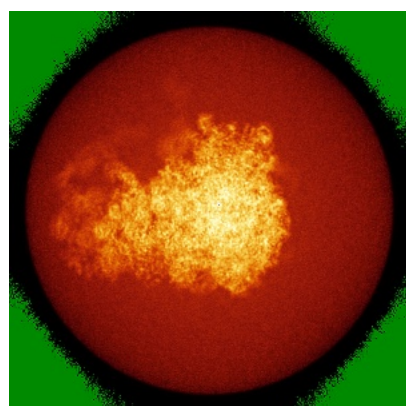


Z Index: 247

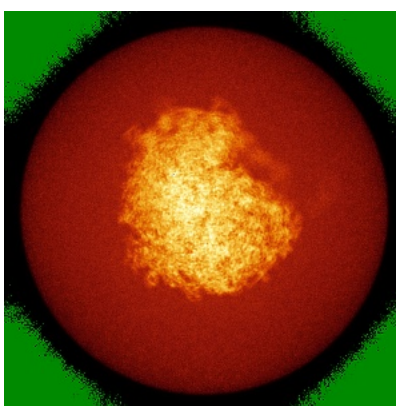
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

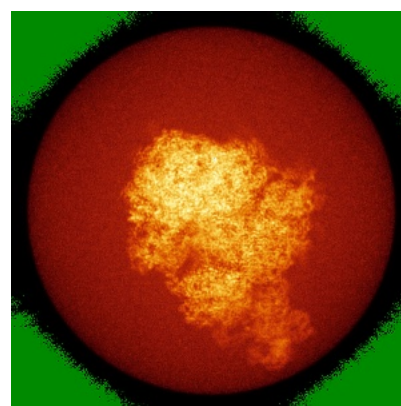
6.4.1 Primary map



X



Y



Z

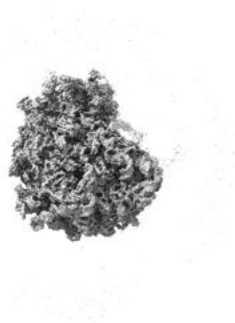
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

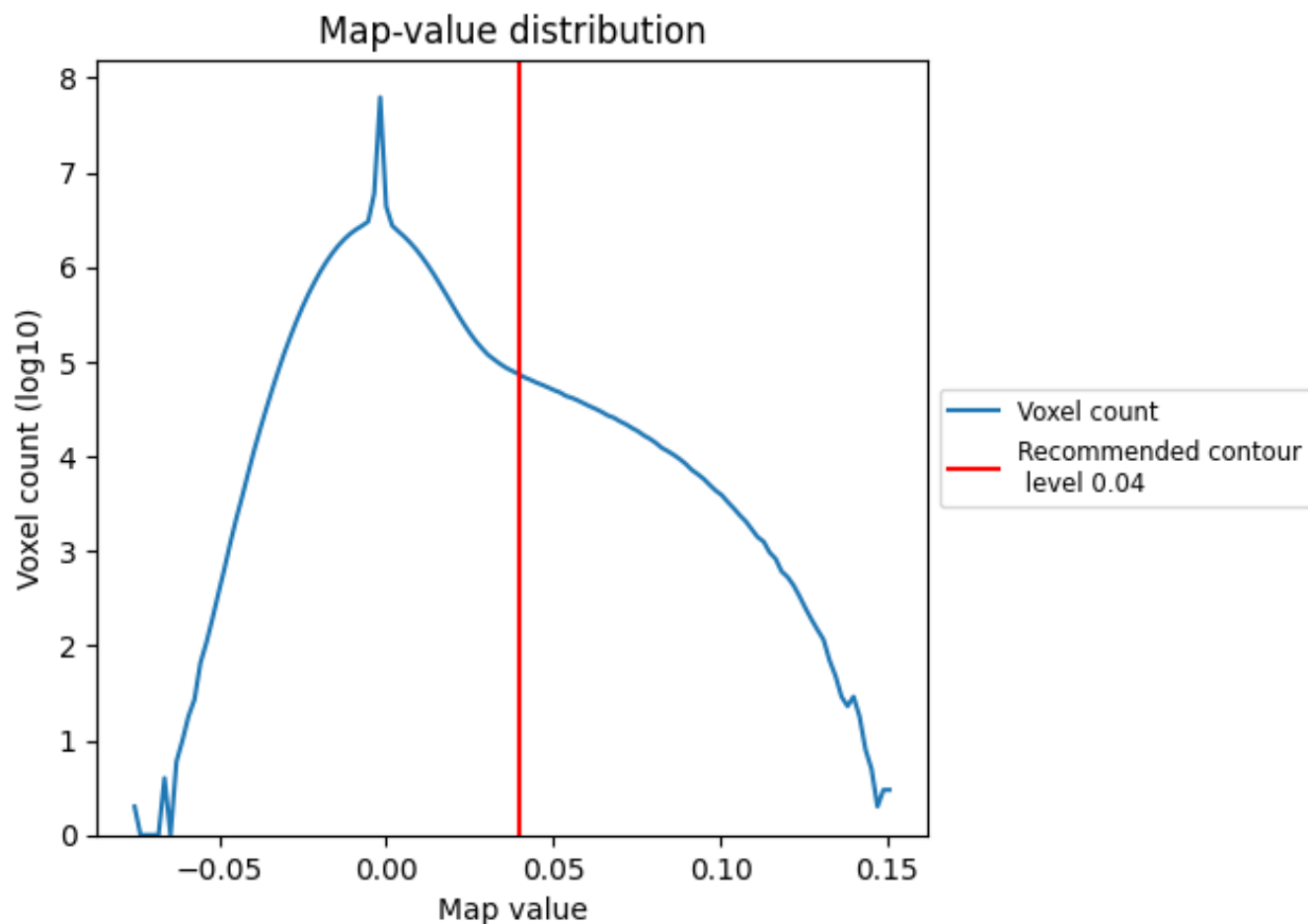
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

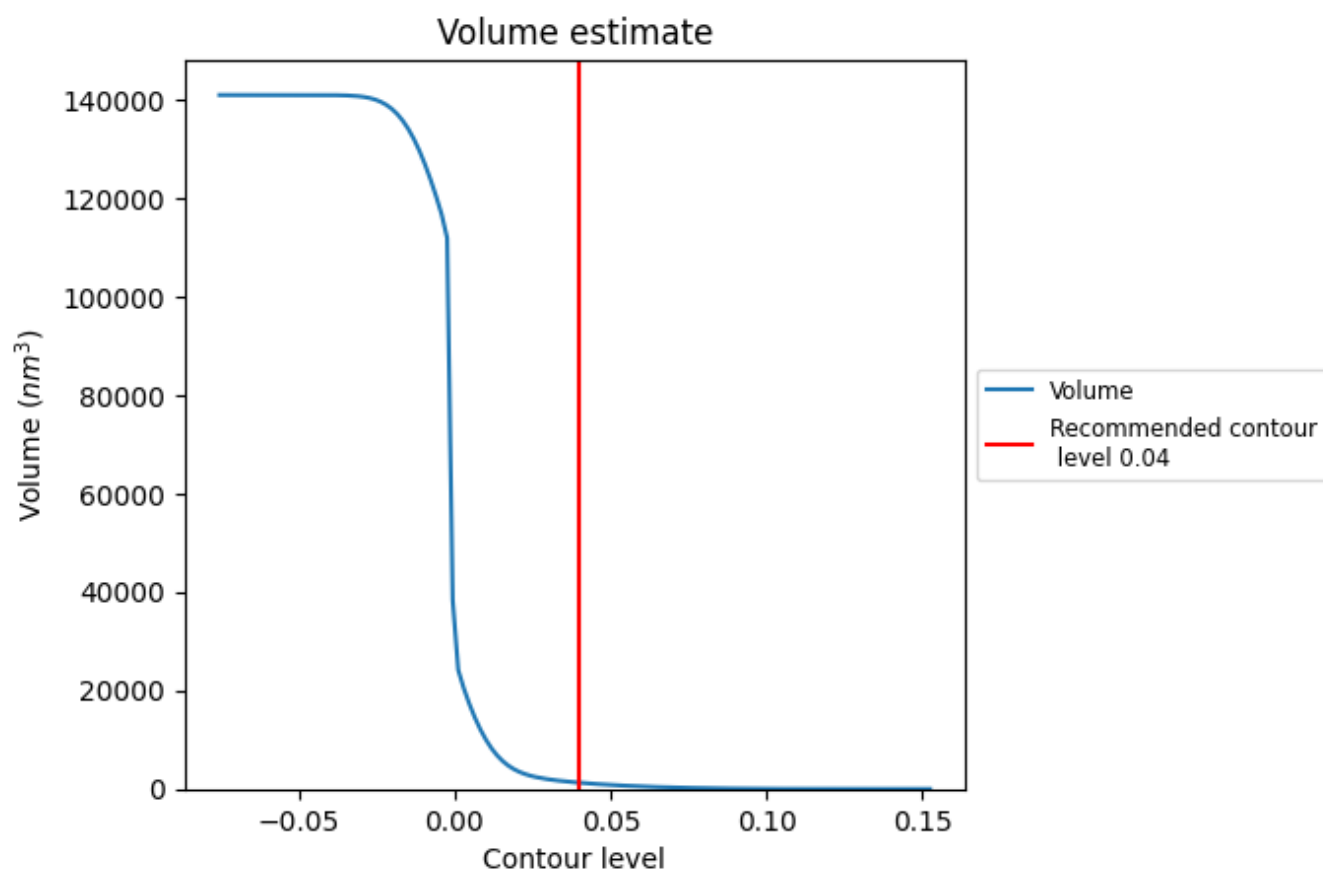
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

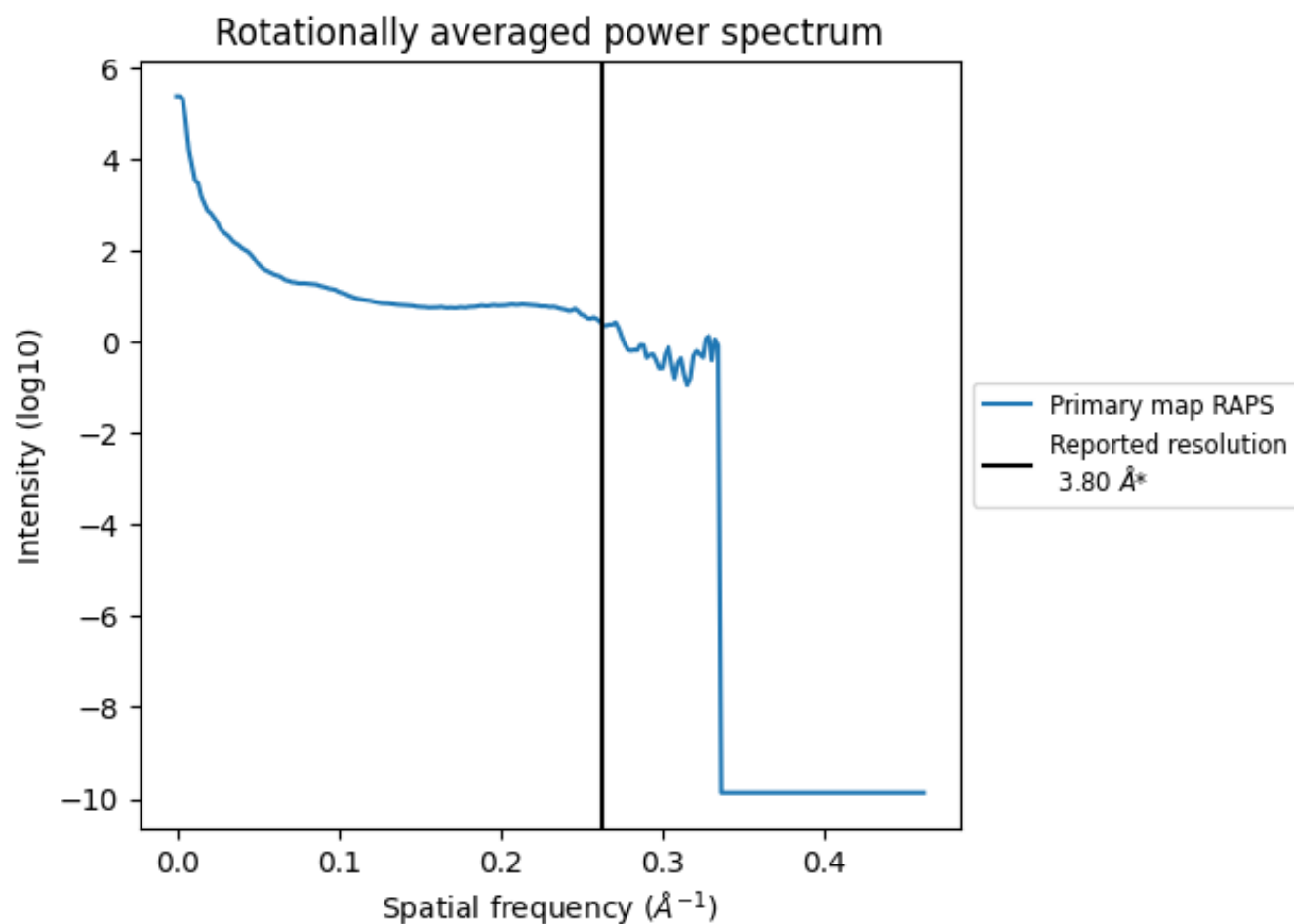
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1270 nm³; this corresponds to an approximate mass of 1147 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

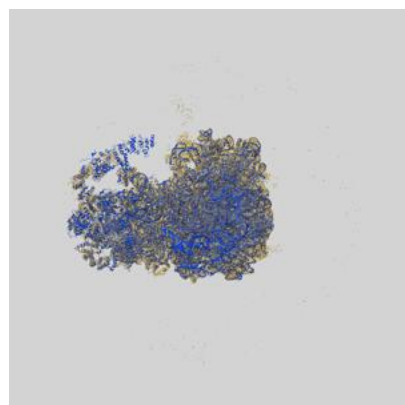
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

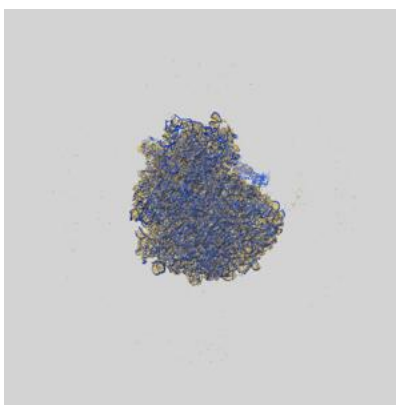
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3461 and PDB model 5MC6. Per-residue inclusion information can be found in section 3 on page 20.

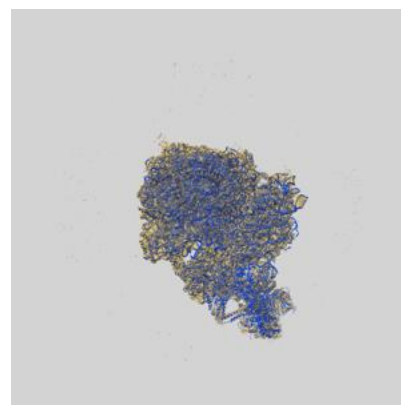
9.1 Map-model overlay [i](#)



X



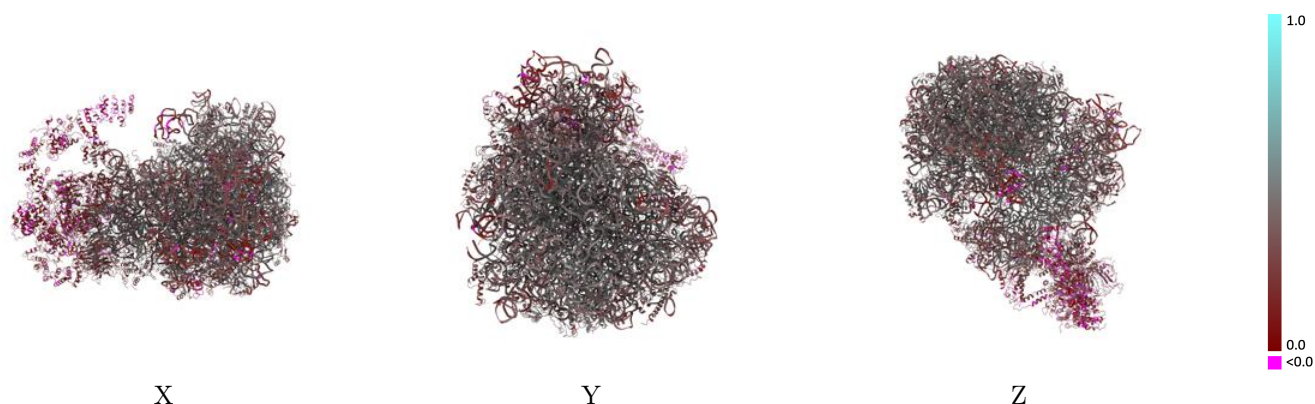
Y



Z

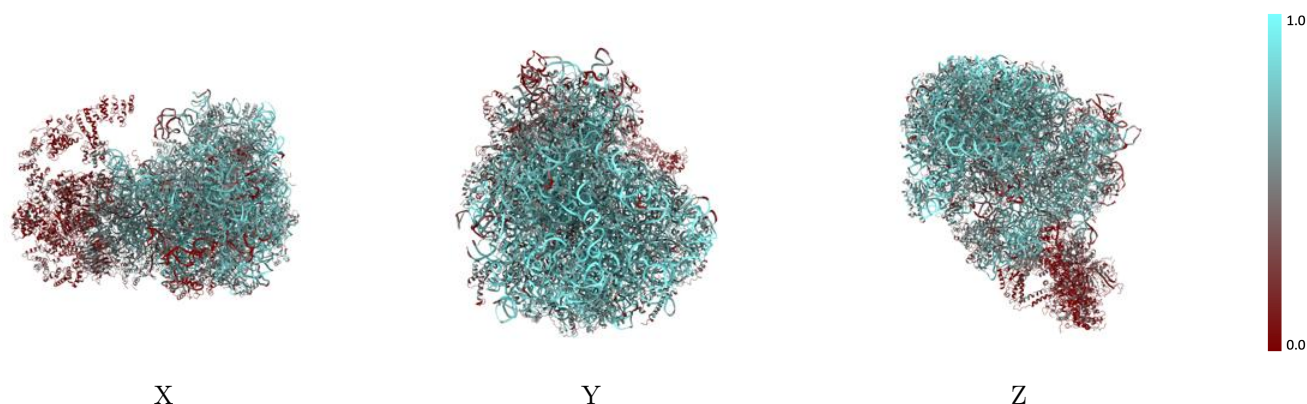
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



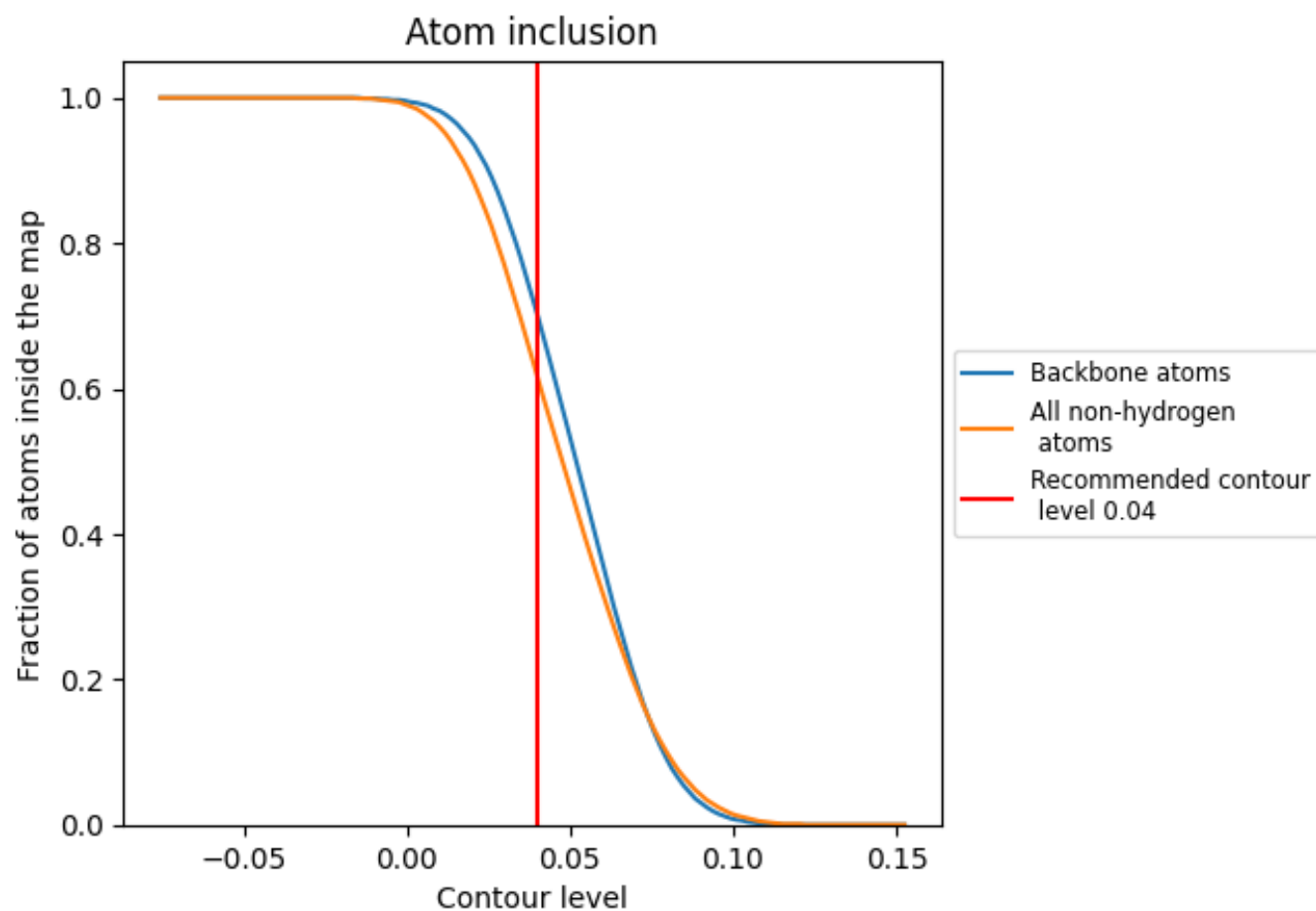
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6170	 0.3620
2	 0.7280	 0.3590
A	 0.4940	 0.3910
AA	 0.5150	 0.3680
AB	 0.5170	 0.4220
AC	 0.5580	 0.3700
AD	 0.5210	 0.3780
AE	 0.4080	 0.3450
AF	 0.6690	 0.4610
AG	 0.5800	 0.3740
AH	 0.6240	 0.4290
AI	 0.5160	 0.3720
AJ	 0.5990	 0.3970
AK	 0.6430	 0.4260
AL	 0.6240	 0.4640
AM	 0.5590	 0.3630
AN	 0.5400	 0.3760
AO	 0.5860	 0.4030
AP	 0.5880	 0.4350
AQ	 0.6360	 0.4330
AR	 0.6320	 0.4220
AS	 0.4010	 0.3980
AT	 0.5590	 0.4280
AU	 0.5950	 0.4140
AV	 0.5690	 0.3950
AW	 0.5980	 0.4500
AX	 0.6260	 0.4410
AY	 0.5160	 0.3840
AZ	 0.1600	 0.3360
B	 0.4320	 0.3190
BA	 0.6070	 0.4230
BB	 0.6190	 0.4260
BC	 0.5780	 0.4330
BD	 0.5240	 0.3950
BE	 0.6270	 0.4240



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Chain	Atom inclusion	Q-score
BF	 0.5680	 0.3980
BG	 0.6020	 0.4350
BH	 0.5740	 0.4020
BI	 0.5980	 0.3630
BJ	 0.5690	 0.4280
BK	 0.6130	 0.4340
BL	 0.5360	 0.3630
BM	 0.5600	 0.3760
BN	 0.5850	 0.4230
BO	 0.6060	 0.3950
BP	 0.6190	 0.3980
BQ	 0.8210	 0.4040
BR	 0.8840	 0.4050
BS	 0.8620	 0.4220
BT	 0.1120	 0.2900
C	 0.4710	 0.3480
D	 0.2720	 0.2450
E	 0.4300	 0.2960
F	 0.5130	 0.3470
G	 0.4920	 0.3700
H	 0.4700	 0.3120
I	 0.4420	 0.2390
J	 0.4860	 0.3610
K	 0.4520	 0.2770
L	 0.3310	 0.3320
M	 0.6290	 0.4270
N	 0.2970	 0.1920
O	 0.4580	 0.3280
P	 0.5110	 0.3600
Q	 0.4160	 0.3170
R	 0.5480	 0.4150
S	 0.4370	 0.3460
T	 0.4160	 0.3090
U	 0.3130	 0.2740
V	 0.4670	 0.2950
W	 0.5200	 0.3250
X	 0.4480	 0.3800
Y	 0.4980	 0.3600
Z	 0.4840	 0.3360
a	 0.5000	 0.3860
b	 0.5380	 0.4090
c	 0.4940	 0.4090

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Chain	Atom inclusion	Q-score
d	 0.4220	 0.2950
e	 0.4360	 0.3140
f	 0.4360	 0.3540
g	 0.4420	 0.3550
h	 0.1760	 0.2120
i	 0.1490	 0.1490
j	 0.1570	 0.1890
k	 0.2920	 0.2970
l	 0.3370	 0.3130
m	 0.6030	 0.3250
n	 0.6440	 0.3480