



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 09:30 PM UTC

PDB ID : 6GQ1 / pdb_00006gq1
EMDB ID : EMD-0047
Title : Cryo-EM reconstruction of yeast 80S ribosome in complex with mRNA, tRNA and eEF2 (GMPPCP/sordarin)
Authors : Pellegrino, S.; Demeshkina, N.; Mancera-Martinez, E.; Melnikov, S.; Simonetti, A.; Myasnikov, A.; Yusupov, M.; Yusupova, G.; Hashem, Y.
Deposited on : 2018-06-07
Resolution : 4.40 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:

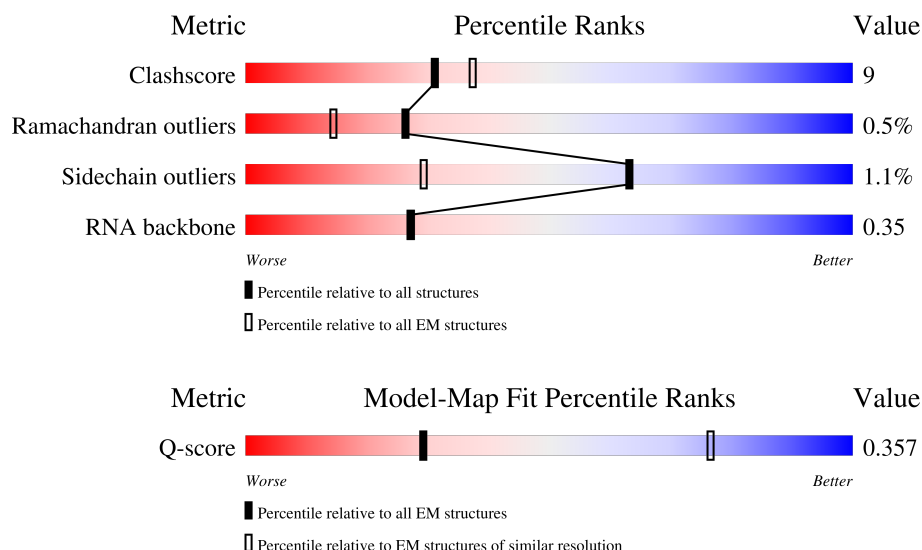
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 4.40 Å.

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



Metric	Whole archive (#Entries)	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	3132 (3.91 - 4.90)

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	1	3396	
2	3	121	
3	4	158	

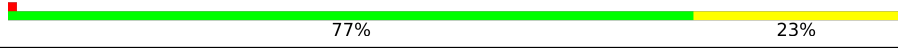
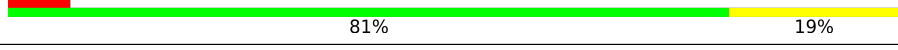
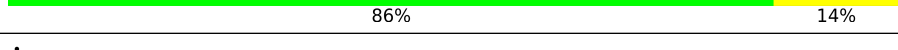
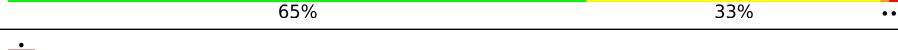
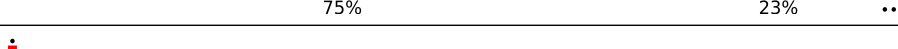
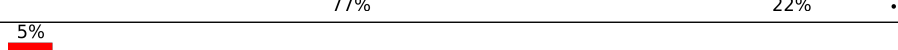
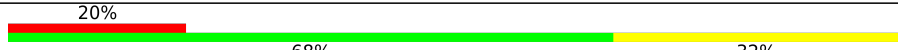
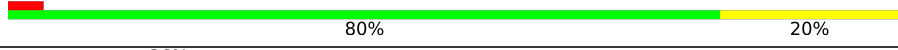
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Mol	Chain	Length	Quality of chain
4	P0	189	
5	P2	94	
6	A	252	
7	B	386	
8	C	361	
9	D	296	
10	E	175	
11	F	222	
12	G	233	
13	H	191	
14	I	220	
15	J	169	
16	L	193	
17	M	136	
18	N	203	
19	O	197	
20	P	183	
21	Q	185	
22	R	188	
23	S	172	
24	T	159	
25	U	100	
26	V	136	
27	W	63	
28	X	121	

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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	135	
31	a	148	
32	b	58	
33	c	97	
34	d	109	
35	e	127	
36	f	106	
37	g	112	
38	h	119	
39	i	99	
40	j	87	
41	k	77	
42	l	50	
43	m	52	
44	n	25	
45	o	105	
46	p	91	
47	2	1797	
48	q	206	
49	r	214	
50	s	217	
51	t	223	
52	u	260	
53	v	206	

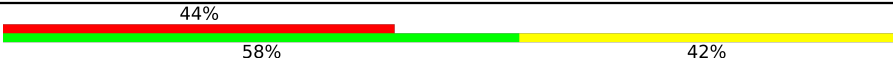
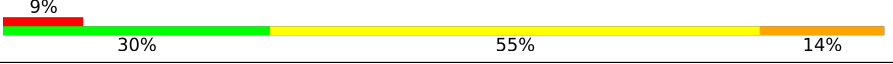
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Mol	Chain	Length	Quality of chain
54	w	223	
55	x	184	
56	y	199	
57	z	185	
58	AA	105	
59	AB	153	
60	AC	124	
61	AD	150	
62	AE	127	
63	AF	124	
64	AG	141	
65	AH	125	
66	AI	145	
67	AJ	143	
68	AK	107	
69	AL	87	
70	AM	129	
71	AN	144	
72	AO	134	
73	AP	70	
74	AQ	97	
75	AR	81	
76	AS	63	
77	AT	53	
78	AU	60	

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Mol	Chain	Length	Quality of chain
79	AV	318	
80	AW	37	
81	AX	76	
82	AY	8	
83	AZ	840	

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 210540 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 *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3223	Total	C	N	O	P	0	0
			68931	30790	12416	22502	3223		

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 5 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L3.

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

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L5.

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

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 15 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 28 is a protein called 60S ribosomal protein L25.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L28.

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

- Molecule 32 is a protein called 60S ribosomal protein L29.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

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

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	25	Total	C	N	O	S	0	0
			227	139	60	27	1		

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1776	Total	C	N	O	P	0	0
			37845	16918	6702	12449	1776		

- Molecule 48 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 49 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 51 is a protein called 40S ribosomal protein S3.

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

- Molecule 52 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 53 is a protein called 40S ribosomal protein S5.

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

- Molecule 54 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 55 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	x	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 56 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 57 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	z	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 58 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AA	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 59 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AB	153	Total	C	N	O	S	0	0
			1220	780	231	206	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AC	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 61 is a protein called 40S ribosomal protein S13.

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

- Molecule 62 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 63 is a protein called 40S ribosomal protein S15.

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

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AG	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 65 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AH	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 66 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 68 is a protein called 40S ribosomal protein S20.

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

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 71 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 72 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AO	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 73 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 74 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 76 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 77 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 78 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AU	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AV	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AW	37	Total	C	N	O	S	0	0
			287	177	57	49	4		

- Molecule 81 is a RNA chain called Transfer RNA - Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AX	76	Total	C	N	O	P	0	0
			1626	725	293	532	76		

- Molecule 82 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	AY	8	Total	C	N	O	P	0	0
			164	74	23	59	8		

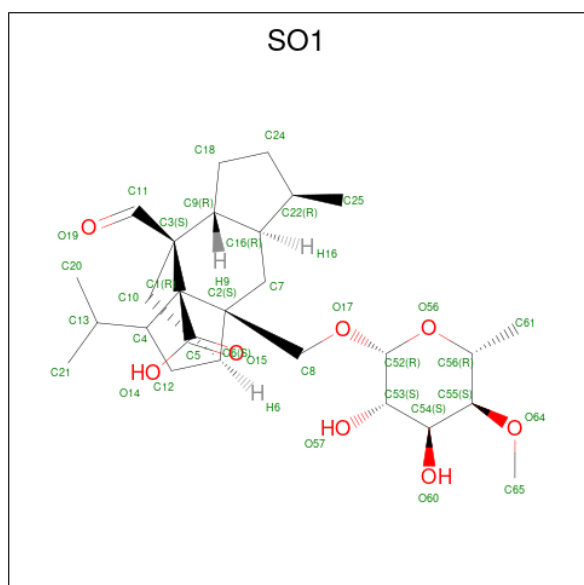
- Molecule 83 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	AZ	840	Total	C	N	O	S	0	0
			6551	4161	1124	1237	29		

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	j	1	Total	Zn	0
			1	1	
84	m	1	Total	Zn	0
			1	1	
84	o	1	Total	Zn	0
			1	1	
84	p	1	Total	Zn	0
			1	1	
84	AQ	1	Total	Zn	0
			1	1	
84	AR	1	Total	Zn	0
			1	1	
84	AT	1	Total	Zn	0
			1	1	
84	AW	1	Total	Zn	0
			1	1	

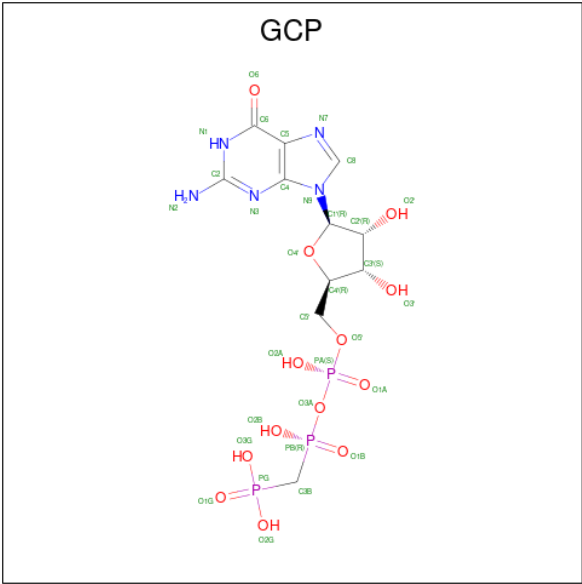
- Molecule 85 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: $C_{27}H_{42}O_8$).



Mol	Chain	Residues	Atoms			AltConf
85	AZ	1	Total	C	O	0
			35	27	8	

- Molecule 86 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD

ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

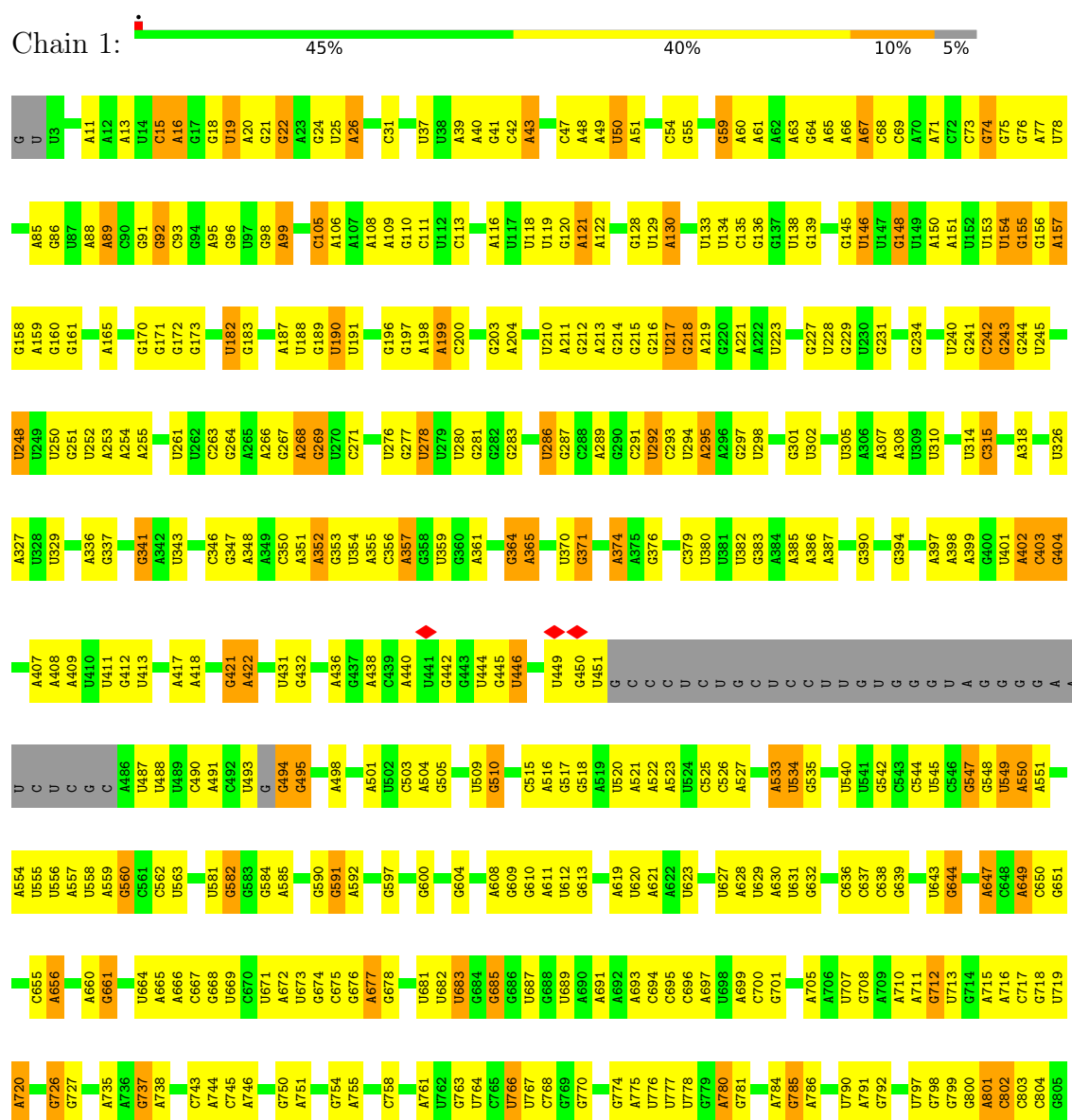


Mol	Chain	Residues	Atoms					AltConf
86	AZ	1	Total	C	N	O	P	0
			32	11	5	13	3	

3 Residue-property plots

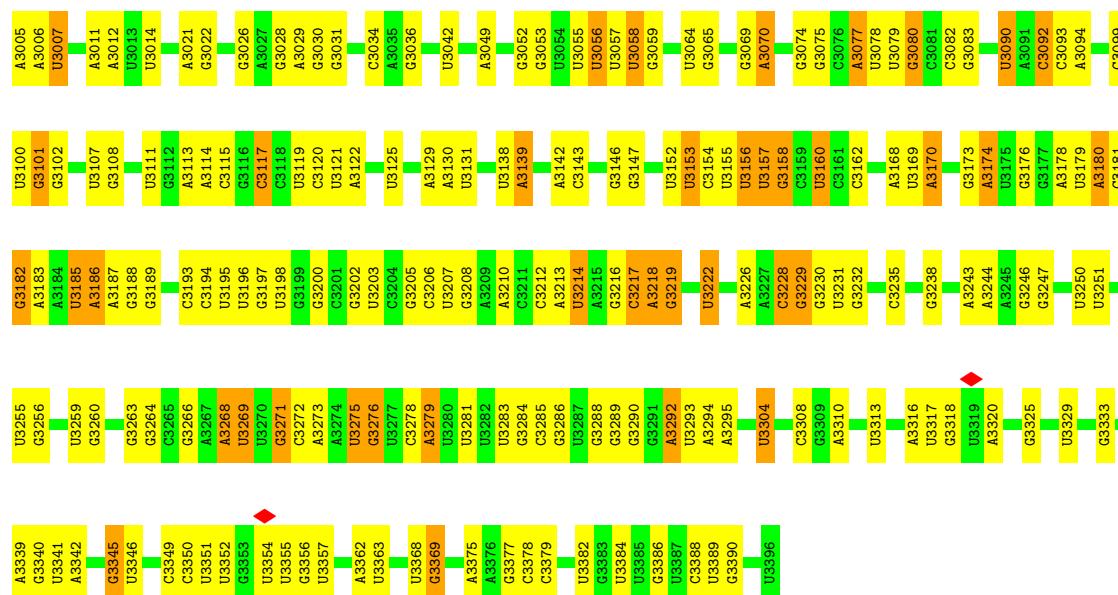
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA



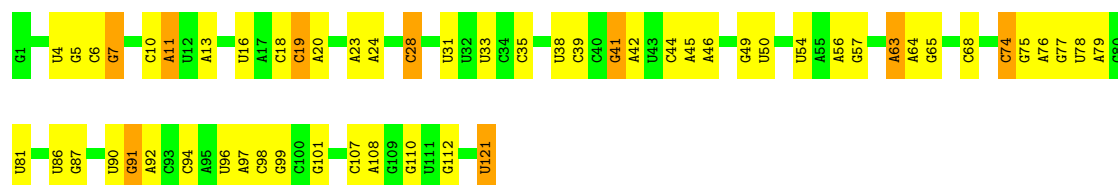
A1839	A1840	A1841	C1771	G1770	C1671	G1592	G1510	A1435	U1347	U1269	C1198	G1126	U1041	A967	A806
A1842	C1772	A1843	C1773	U1672	A1593	A1592	U1511	U1436	U1348	A1270	C1201	G1127	U1041	G894	A807
A1844	C1774	C1843	U1595	A1683	U1594	A1594	U1512	U1438	A1350	C1272	A1202	A1129	U1044	C969	A808
C1844	G1775	C1596	C1516	G1517	U1596	C1596	U1517	G1440	U1351	A1274	A1203	A1130	C1045	U897	A816
G1845	U1687	G1604	G1521	U1687	U1521	G1521	U1510	U1443	U1354	C1276	A1205	C1132	A1046	G900	A817
A1846	C1693	A1605	U1522	G1693	U1522	U1522	U1522	U1446	G1354	C1277	G1206	A1133	U1047	U976	U821
C1848	U1694	U1606	U1523	U1694	U1523	U1606	U1524	U1447	A1355	A1278	G1209	G1134	A1053	U903	G822
A1849	U1695	U1607	G1524	U1695	U1524	U1607	U1525	U1448	G1356	C1279	U1210	A1135	A1054	A904	C923
A1850	U1782	C1608	A1525	U1782	A1525	C1608	U1526	U1449	G1357	C1280	U1211	C1136	A1055	A980	G826
C1850	C1706	G1609	U1526	C1706	U1526	G1609	U1526	A1449	A1362	G1281	A1212	C1137	A1062	U981	G826
G1851	A1707	G1610	A1529	A1707	U1529	G1610	U1529	U1450	A1363	C1282	G1213	G1142	G1063	G908	G908
U1855	C1710	A1613	U1530	C1710	U1530	A1613	U1530	C1451	U1363	C1283	U1214	A1143	A1064	G909	A830
A1859	G1711	G1618	U1533	G1711	U1533	G1618	U1533	U1455	U1368	G1284	A1217	G1145	A1065	C911	G833
C1859	G1712	A1619	A1534	G1712	A1534	A1619	A1534	U1456	A1369	A1286	C1218	G1148	C1069	A914	U834
G1860	C1713	U1620	A1535	C1713	A1535	U1620	A1535	U1457	G1370	A1287	U1219	G1149	U1070	A915	G835
C1863	A1714	A1621	U1541	A1714	U1541	A1621	U1541	U1458	G1371	A1287	U1220	G1149	G933	G916	A836
A1864	C1715	G1622	G1541	C1715	U1541	G1622	G1541	U1459	A1372	A1290	G1222	G1152	U1071	A917	A837
A1865	U1716	G1623	U1541	U1716	U1541	G1623	U1541	U1459	A1373	A1291	A1223	A1153	G1072	U995	G838
C1866	G1717	G1624	G1551	G1717	U1551	G1624	G1551	U1460	G1374	C1292	C1224	A1154	A920	A921	G842
A1867	U1718	A1625	U1552	U1718	U1552	A1625	U1552	G1464	G1382	G1295	A1225	C1076	A998	A921	G842
G1868	C1719	G1626	U1553	C1719	U1553	G1626	U1553	U1468	G1383	C1296	A1229	A1155	C1086	A920	A843
U1871	U1720	U1627	U1554	U1720	U1554	U1627	U1554	C1469	U1384	C1297	G1230	G1156	A1079	G999	A843
A1872	A1723	U1628	U1555	A1723	U1555	U1628	U1555	U1470	C1385	A1297	G1231	A1158	U1081	G1001	A846
C1872	U1724	U1629	C1562	C1724	U1562	A1637	C1562	U1471	A1386	U1301	A1231	G1159	U1082	A1002	A847
A1874	U1725	U1630	U1556	U1725	U1556	U1630	U1556	U1472	G1387	A1302	G1232	G1160	G1083	A929	C928
C1805	G1727	U1634	U1557	G1727	U1557	U1634	U1557	U1473	U1388	U1303	G1233	G1161	A1084	G1005	U850
A1806	U1728	G1635	U1558	U1728	U1558	G1635	U1558	A1474	G1389	U1305	U1235	A1165	A1085	A1006	C851
A1807	C1730	C1636	U1560	C1730	U1560	C1636	U1560	U1475	C1391	G1306	G1236	G1166	C1086	U932	U852
G1808	A1731	A1637	C1562	A1731	U1562	A1637	C1562	U1482	G1392	A1308	G1237	U1167	G1087	G934	G853
A1881	G1736	C1638	U1563	G1736	U1563	C1638	U1563	U1483	A1393	U1309	C1238	U1094	G1013	G937	U855
A1883	U1737	C1639	U1564	U1737	U1564	C1639	U1564	U1484	A1394	G1313	G1243	U1095	U1014	U939	G856
A1884	C1738	G1640	U1565	C1738	U1565	G1640	U1565	G1485	U1399	G1314	A1244	U1173	G1097	G857	A858
U1815	U1739	A1643	U1566	U1739	U1566	A1643	U1566	G1486	G1400	U1315	G1245	G1174	A1098	C941	G859
A1816	C1740	C1644	U1567	C1740	U1567	C1644	U1567	G1487	U1405	C1316	G1246	C1175	A1099	U942	C860
A1817	U1741	U1645	U1568	U1741	U1568	U1645	U1568	U1488	U1405	A1317	C1176	G1177	U1100	U943	G860
U1818	U1742	G1646	U1569	U1742	U1569	G1646	U1569	A1489	U1405	U1317	G1246	G1178	G1101	C944	C861
C1819	G1748	G1653	U1570	C1819	U1570	G1653	U1570	A1491	G1408	G1321	G1249	A1179	A1103	G944	G864
A1820	A1749	A1654	A1571	A1820	U1571	A1654	A1571	G1492	C1411	U1322	A1252	C1181	G1021	U946	U865
U1821	C1750	G1655	U1572	C1750	U1572	G1655	U1572	G1493	G1411	G1323	U1253	A1180	G1020	U946	U865
C1822	G1751	A1656	C1573	C1822	U1573	A1656	C1573	U1494	G1417	U1324	C1254	G1104	G1021	G947	A866
A1896	C1756	C1657	U1574	A1896	U1574	C1657	U1574	U1497	G1408	U1325	G1255	A1106	C948	C948	U871
A1900	U1757	G1658	U1577	U1757	U1577	G1658	U1577	U1498	A1419	A1330	C1257	C1185	U1110	G950	U874
C1904	A1757	U1659	C1578	A1757	U1578	U1659	C1578	C1499	A1419	A1330	G1257	G1186	A1025	A951	G875
G1905	C1760	C1660	C1579	C1760	U1579	C1660	C1579	G1500	G1421	U1336	U1258	C1187	A1026	A952	A876
C1906	G1761	G1661	U1580	G1761	U1580	G1661	U1580	U1501	G1422	U1337	A1260	G1115	A1027	C959	C877
C1907	C1762	C1662	C1581	C1762	U1581	C1662	C1581	C1502	C1423	G1261	A1261	G1116	U1028	U960	G878
A1908	U1763	C1663	C1582	U1763	U1582	C1663	C1582	A1503	U1425	G1340	G1262	C1118	G1029	C961	U879
C1835	C1764	G1664	U1583	C1835	U1583	G1664	U1583	U1425	U1425	C1341	G1263	C1119	U1028	A962	G880
U1912	U1764	C1665	U1584	U1764	U1584	C1665	U1584	A1506	U1430	C1342	G1264	A1120	A1030	G963	C881
U1837	U1765	G1666	U1587	U1837	U1587	G1666	U1587	U1507	G1431	A1343	U1265	U1121	C1031	A882	A882
A1915	G1769	G1668	A1588	A1915	U1588	G1668	U1588	A1509	G1434	G1344	G1268	A1197	U1125	U966	A888





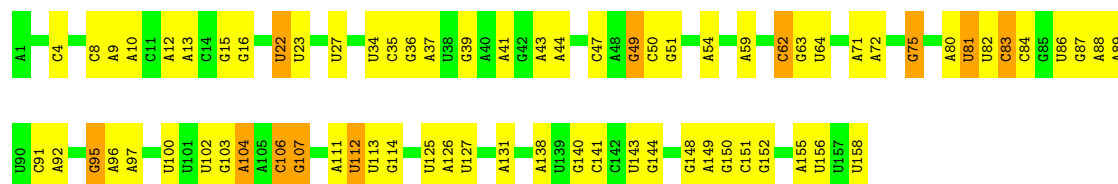
• Molecule 2: 5.8S ribosomal RNA

Chain 3: 54% 39% 7%



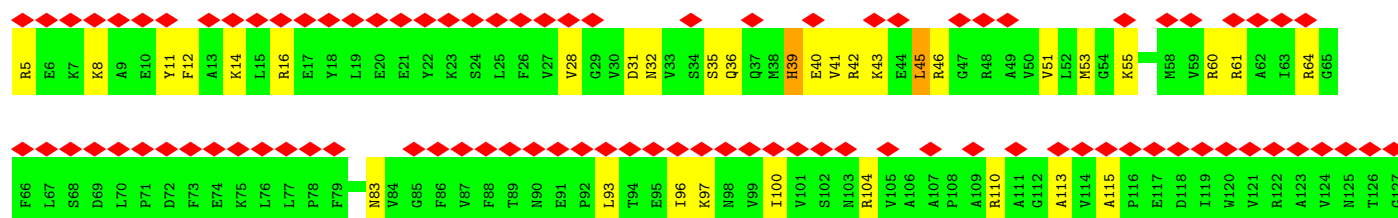
• Molecule 3: 5S ribosomal RNA

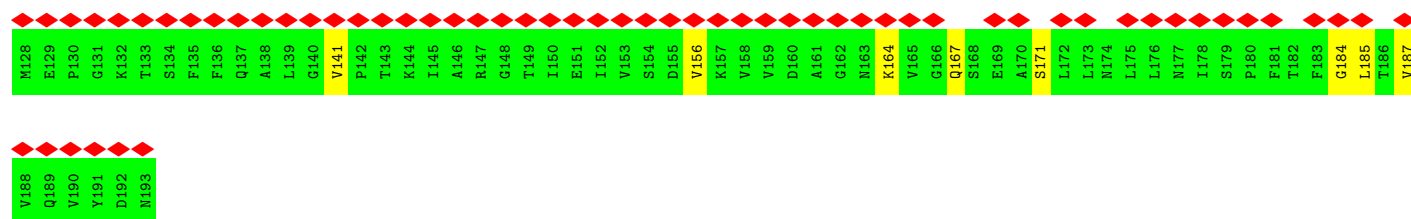
Chain 4: 54% 39% 7%



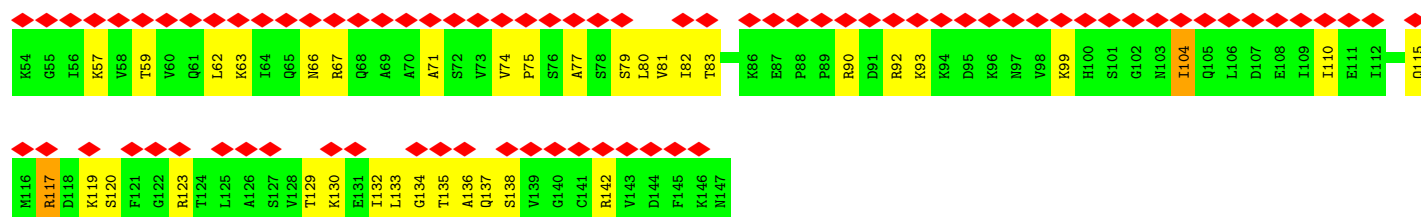
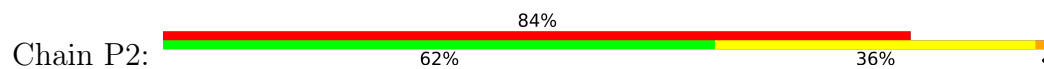
• Molecule 4: 60S acidic ribosomal protein P0

Chain P0: 80% 78% 21%

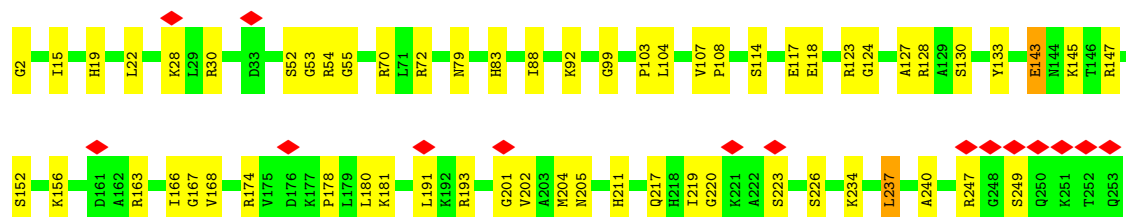
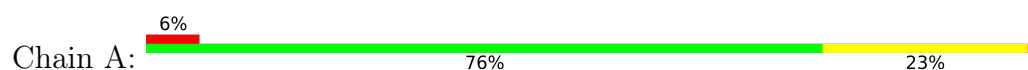




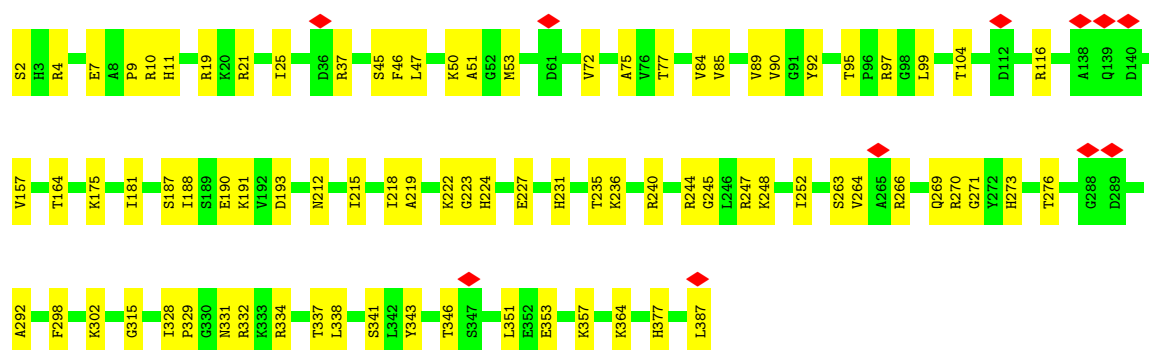
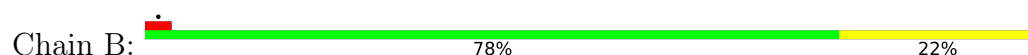
• Molecule 5: 60S ribosomal protein L12-A



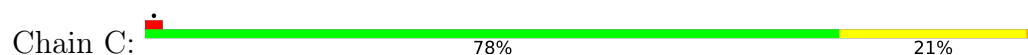
• Molecule 6: 60S ribosomal protein L2-A

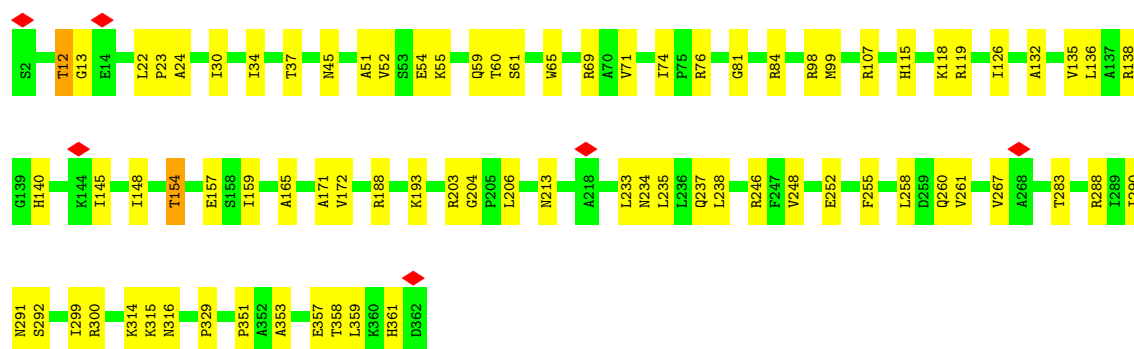


• Molecule 7: 60S ribosomal protein L3

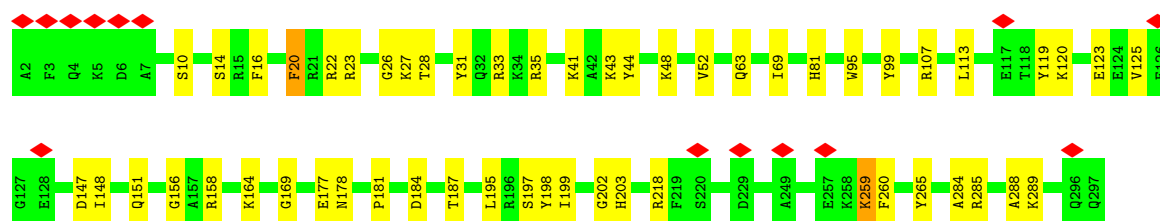
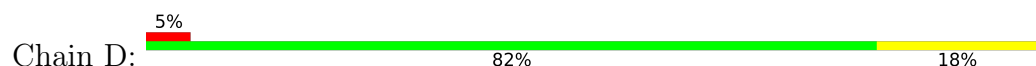


• Molecule 8: 60S ribosomal protein L4-A

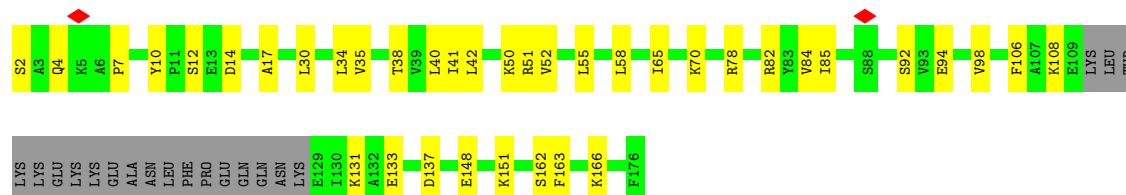




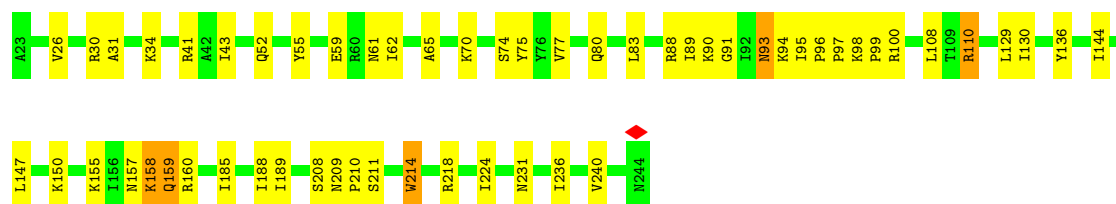
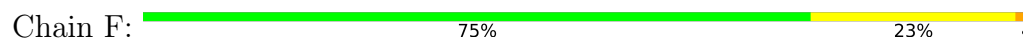
• Molecule 9: 60S ribosomal protein L5



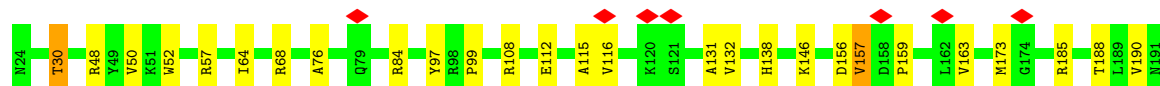
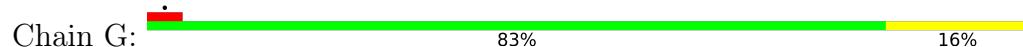
• Molecule 10: 60S ribosomal protein L6-A

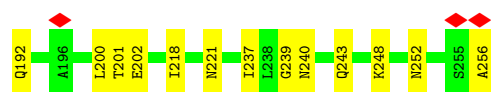


• Molecule 11: 60S ribosomal protein L7-A

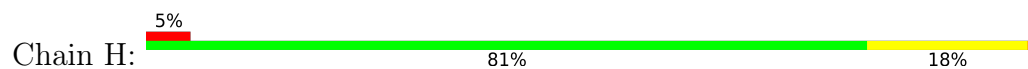


• Molecule 12: 60S ribosomal protein L8-A

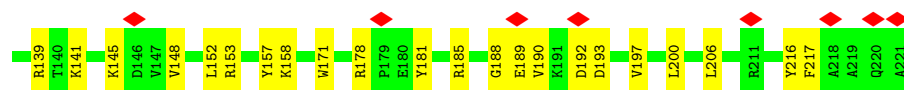
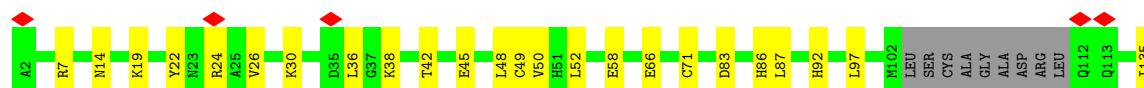
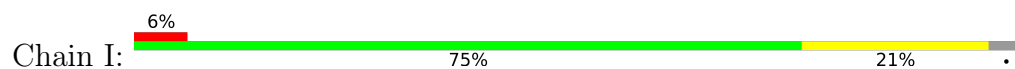




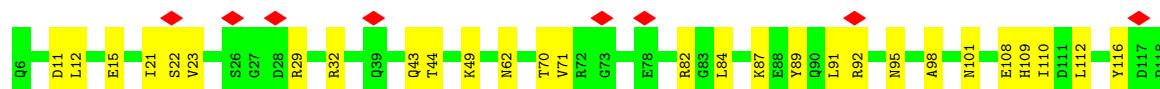
- Molecule 13: 60S ribosomal protein L9-A



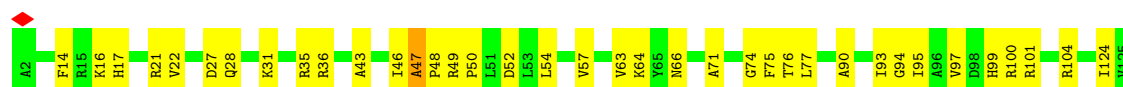
- Molecule 14: 60S ribosomal protein L10



- Molecule 15: 60S ribosomal protein L11-B

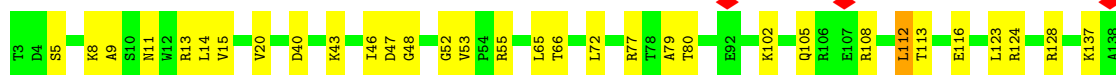


- Molecule 16: 60S ribosomal protein L13-A



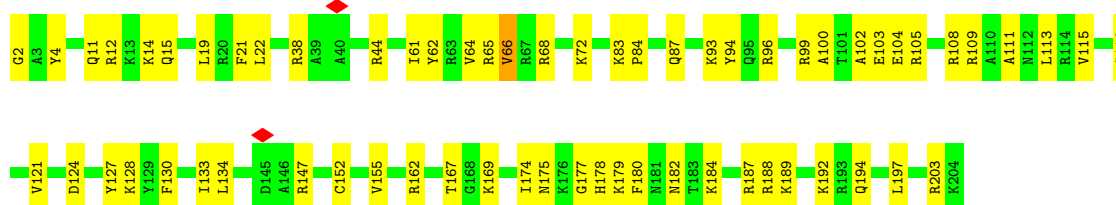
- Molecule 17: 60S ribosomal protein L14-A

Chain M:  76% 23%



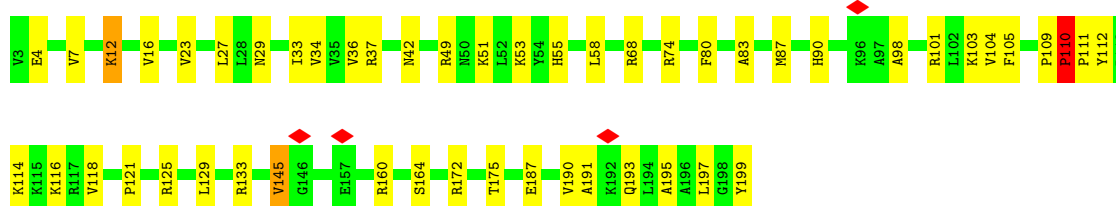
- Molecule 18: 60S ribosomal protein L15-A

Chain N:  68% 31%



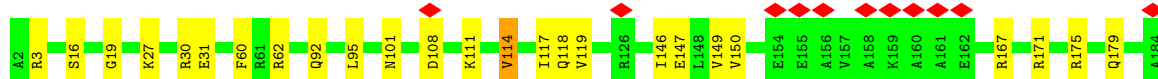
- Molecule 19: 60S ribosomal protein L16-A

Chain O:  74% 24%



- Molecule 20: 60S ribosomal protein L17-A

Chain P:  6% 86% 13%



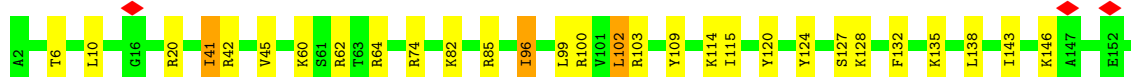
- Molecule 21: 60S ribosomal protein L18-A

Chain Q:  84% 16%



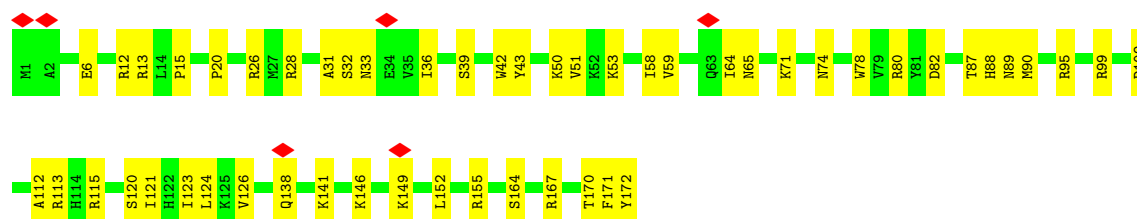
- Molecule 22: 60S ribosomal protein L19-A

Chain R:  81% 18%

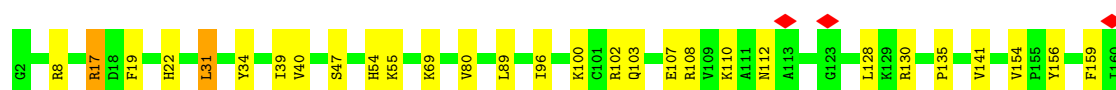
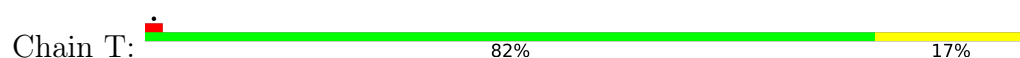




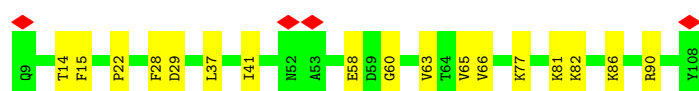
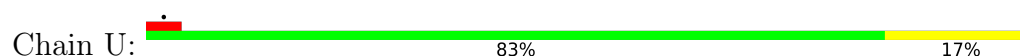
- Molecule 23: 60S ribosomal protein L20-A



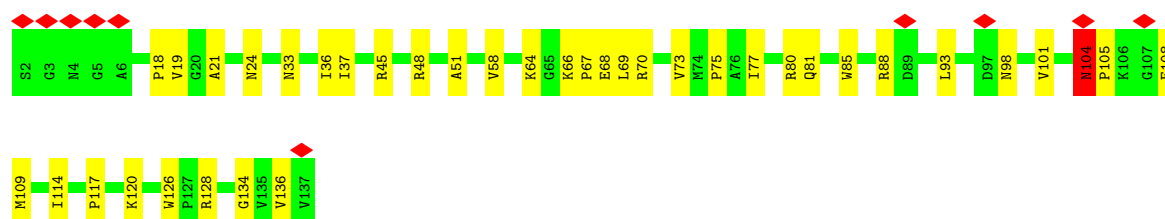
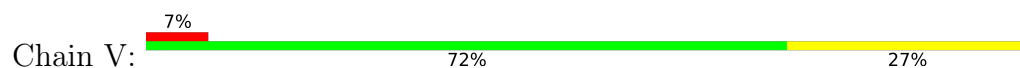
- Molecule 24: 60S ribosomal protein L21-A



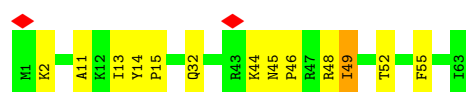
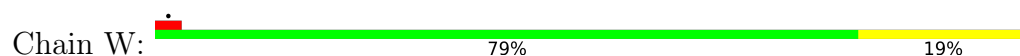
- Molecule 25: 60S ribosomal protein L22-A



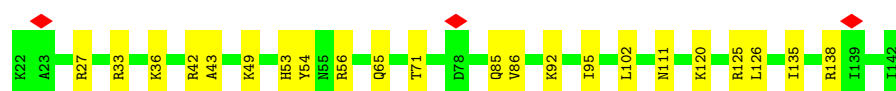
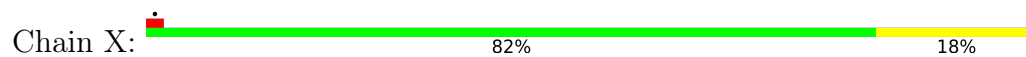
- Molecule 26: 60S ribosomal protein L23-A



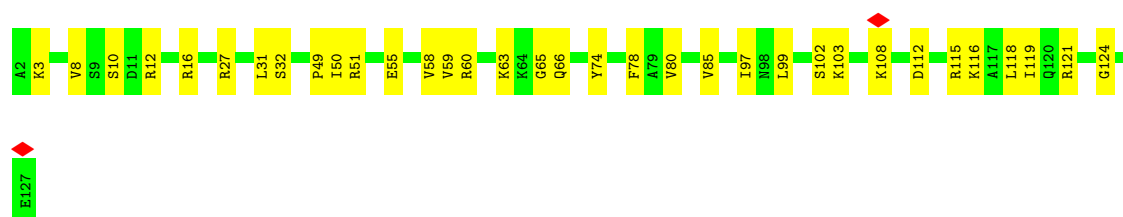
- Molecule 27: 60S ribosomal protein L24-A



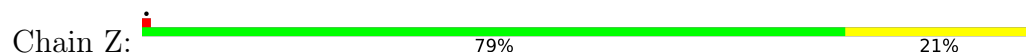
- Molecule 28: 60S ribosomal protein L25



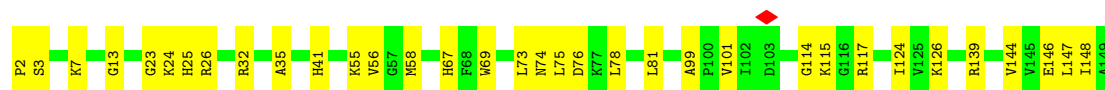
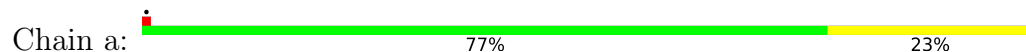
- Molecule 29: 60S ribosomal protein L26-A



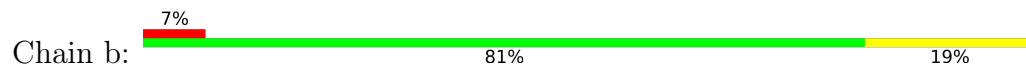
- Molecule 30: 60S ribosomal protein L27-A



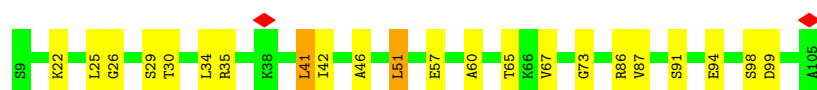
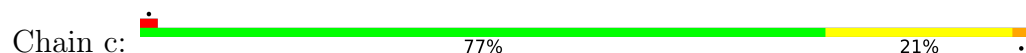
- Molecule 31: 60S ribosomal protein L28



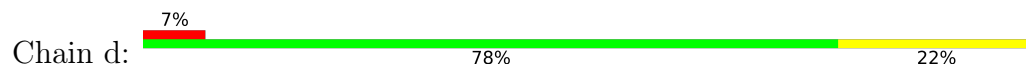
- Molecule 32: 60S ribosomal protein L29



- Molecule 33: 60S ribosomal protein L30

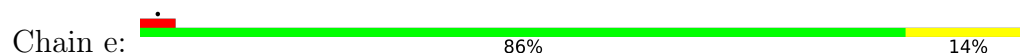


- Molecule 34: 60S ribosomal protein L31-A

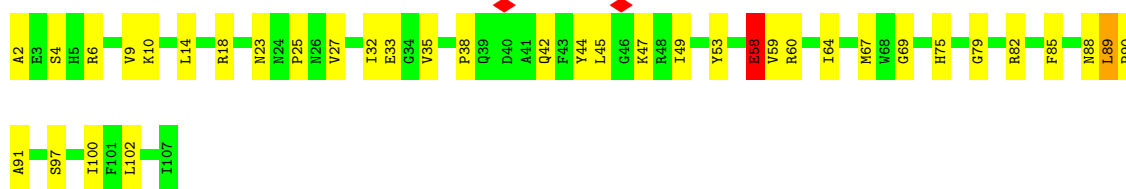




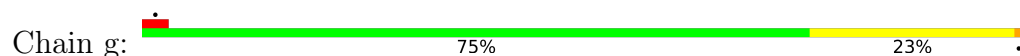
- Molecule 35: 60S ribosomal protein L32



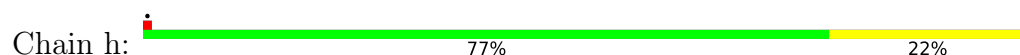
- Molecule 36: 60S ribosomal protein L33-A



- Molecule 37: 60S ribosomal protein L34-A



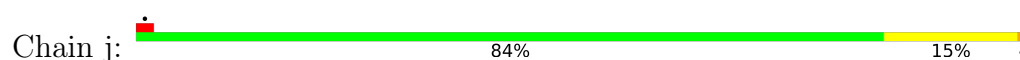
- Molecule 38: 60S ribosomal protein L35-A

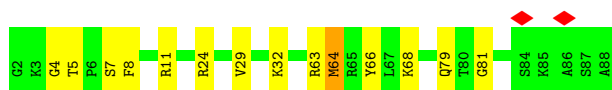


- Molecule 39: 60S ribosomal protein L36-A

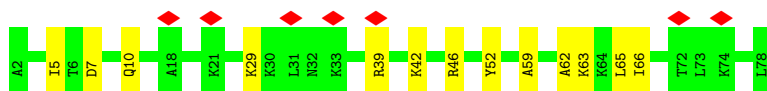
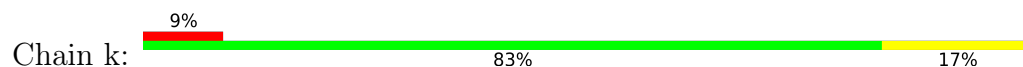


- Molecule 40: 60S ribosomal protein L37-A

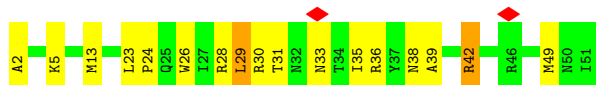




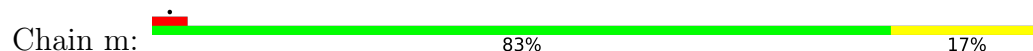
- Molecule 41: 60S ribosomal protein L38



- Molecule 42: 60S ribosomal protein L39



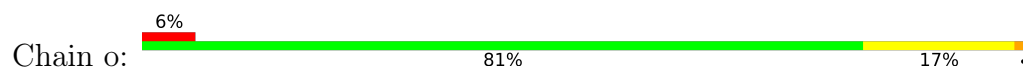
- Molecule 43: Ubiquitin-60S ribosomal protein L40



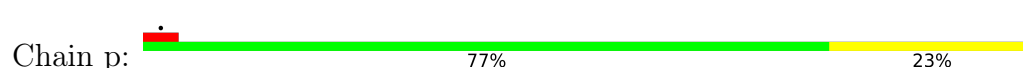
- Molecule 44: 60S ribosomal protein L41-B



- Molecule 45: 60S ribosomal protein L42-A

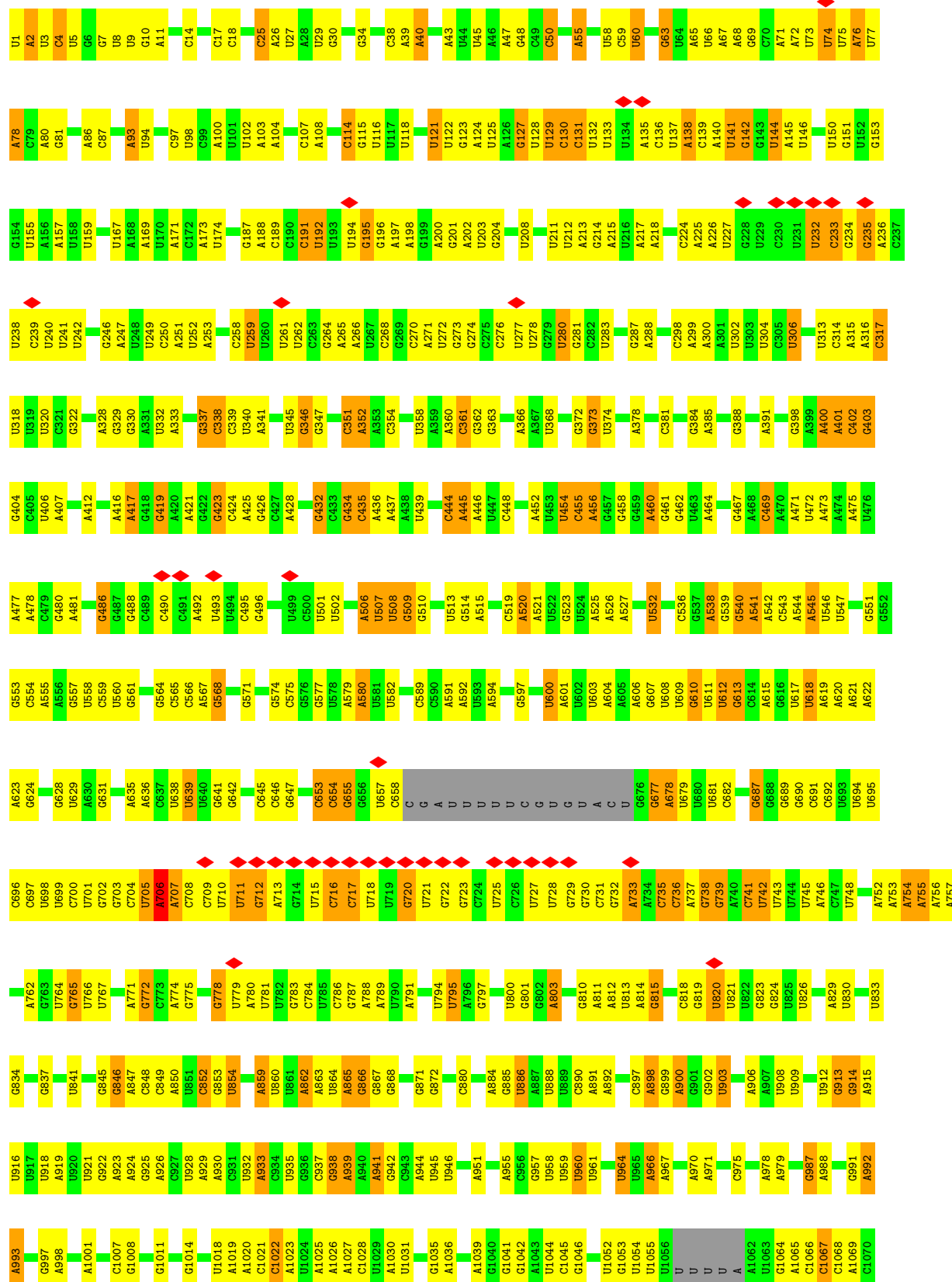


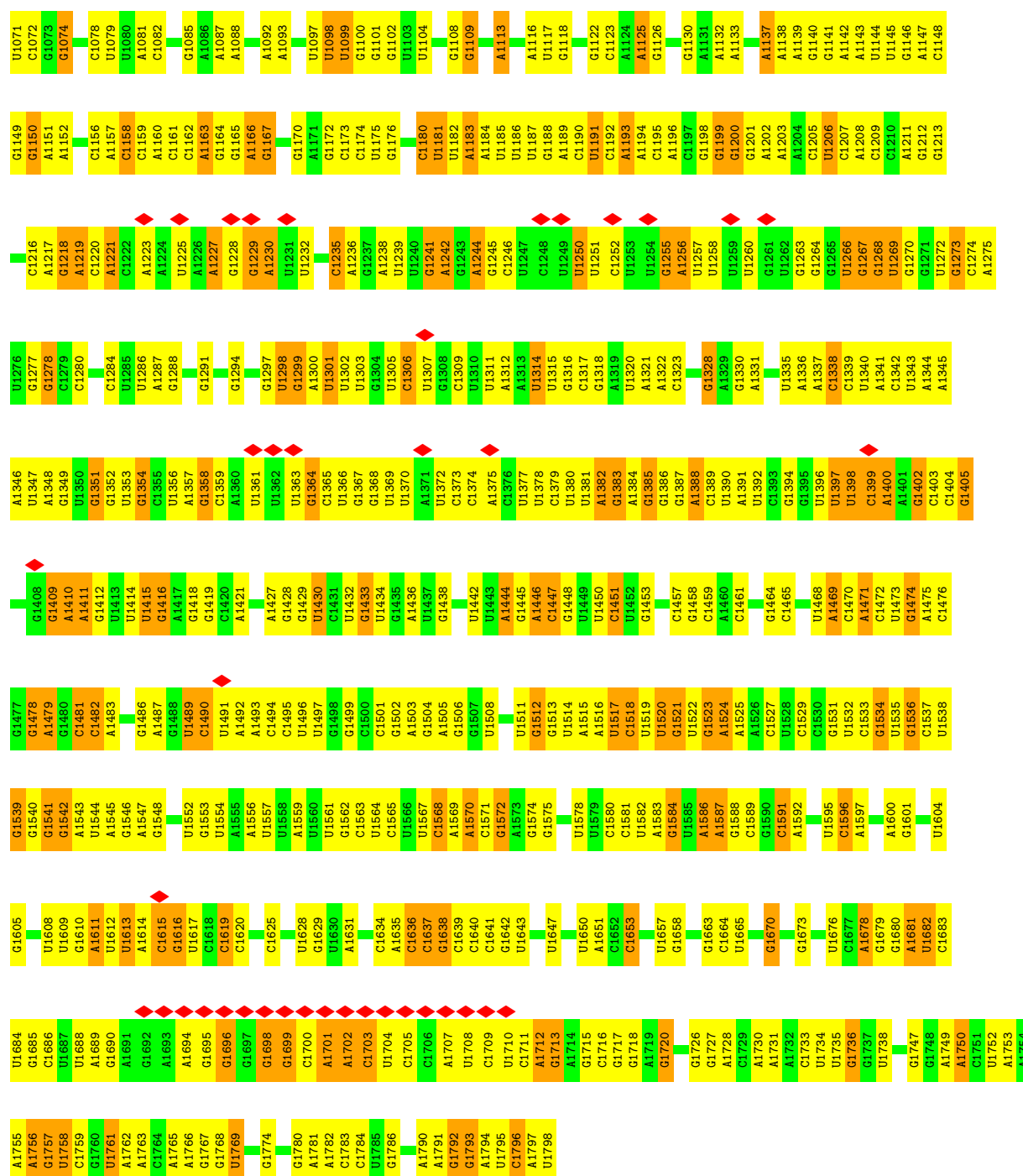
- Molecule 46: 60S ribosomal protein L43-A



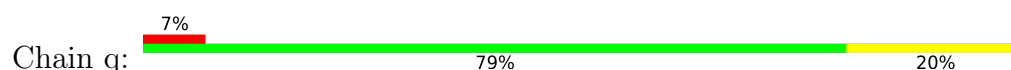
- Molecule 47: 18S ribosomal RNA

Chain 2:  39% 45% 15%



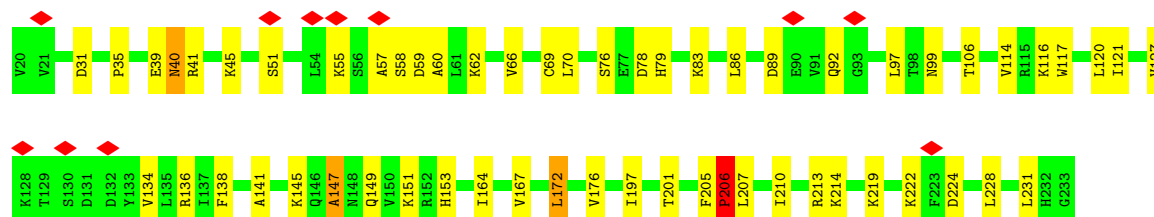
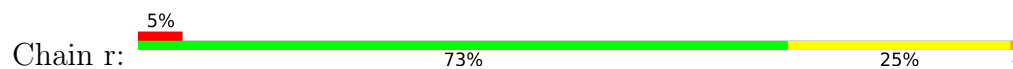


• Molecule 48: 40S ribosomal protein S0-A

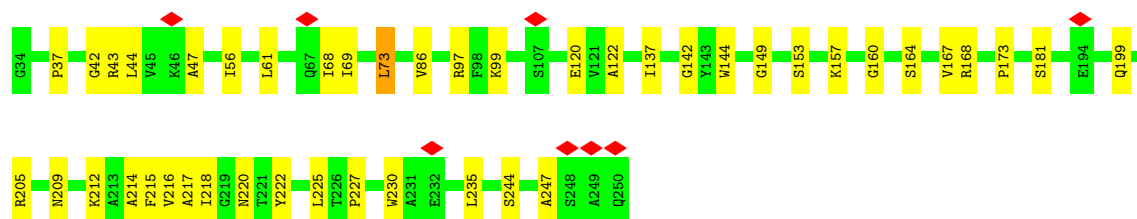
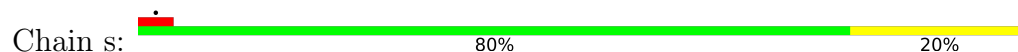




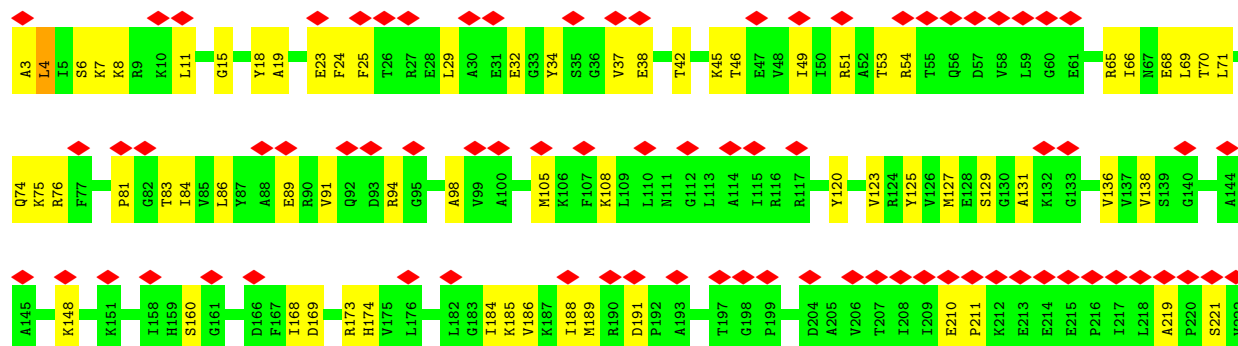
- Molecule 49: 40S ribosomal protein S1-A



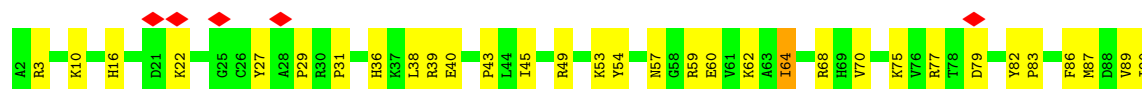
- Molecule 50: 40S ribosomal protein S2

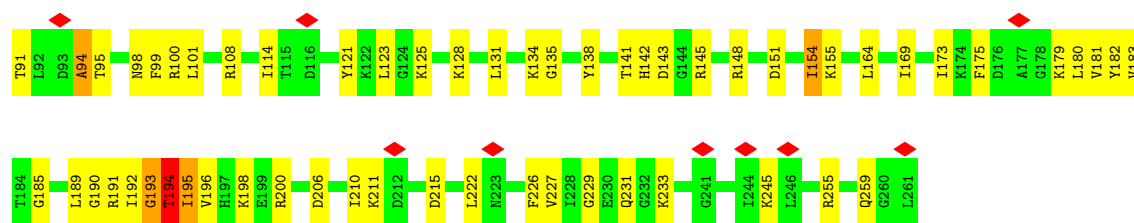


- Molecule 51: 40S ribosomal protein S3

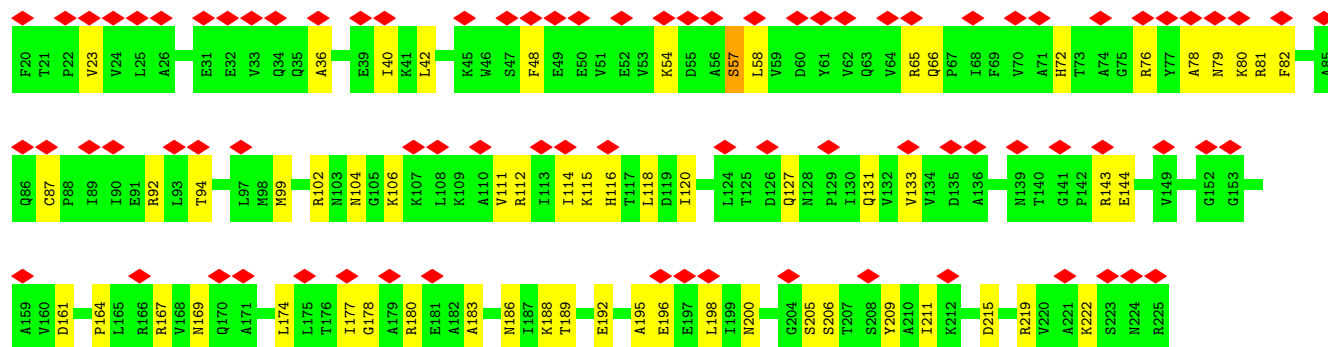
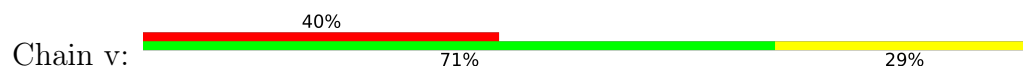


- Molecule 52: 40S ribosomal protein S4-A

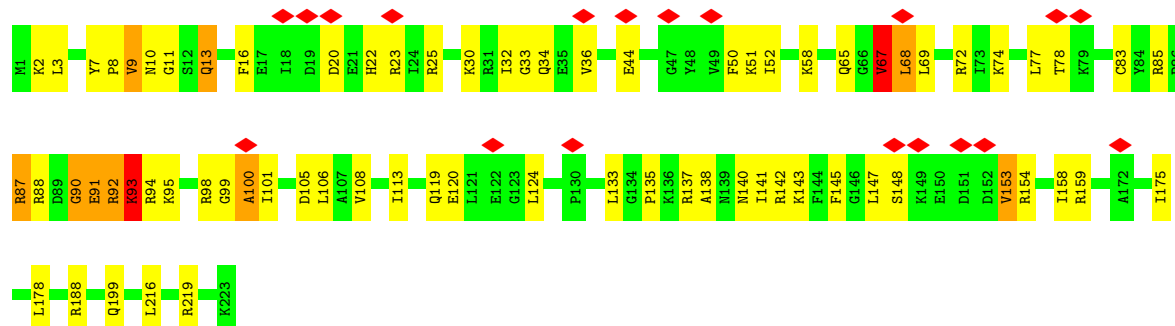




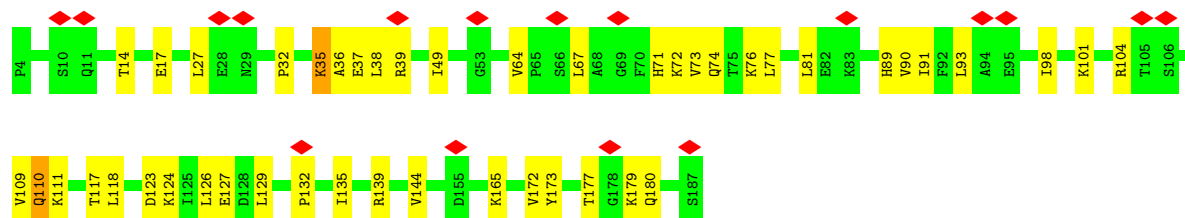
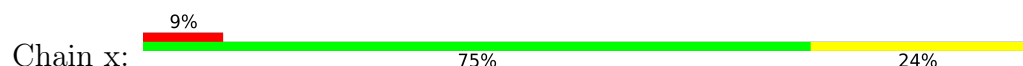
• Molecule 53: 40S ribosomal protein S5



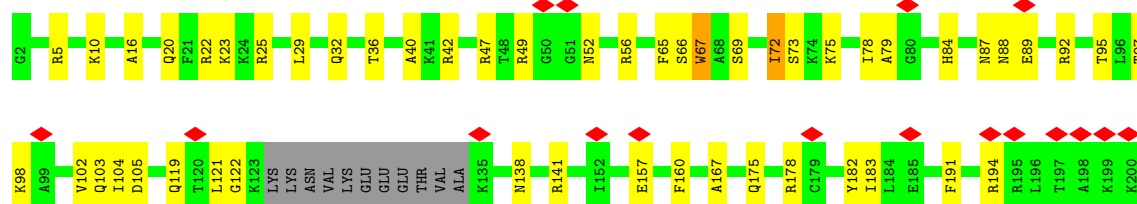
• Molecule 54: 40S ribosomal protein S6-A



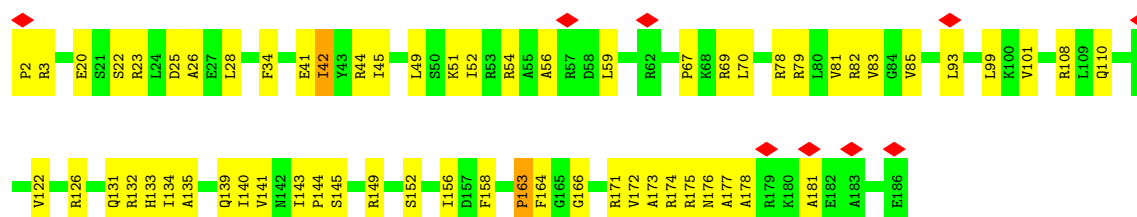
• Molecule 55: 40S ribosomal protein S7-A



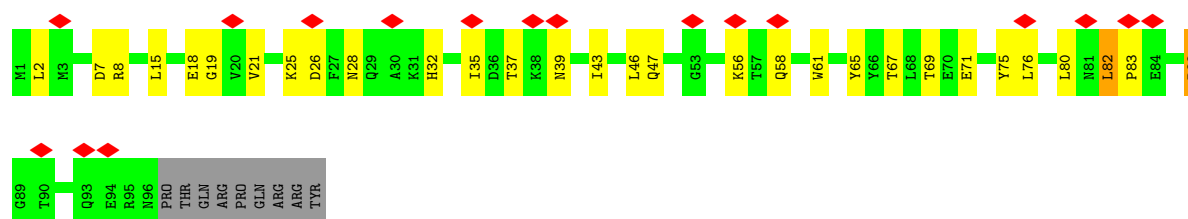
• Molecule 56: 40S ribosomal protein S8-A



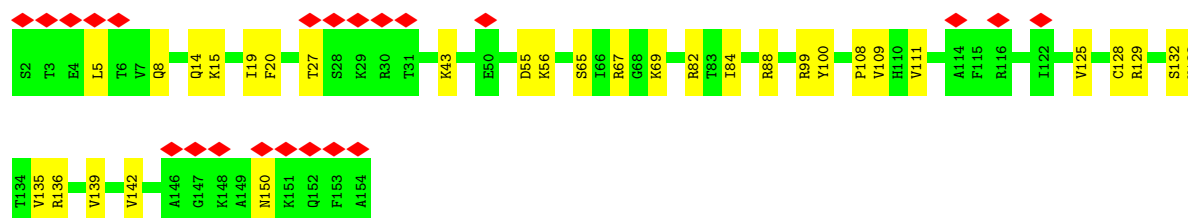
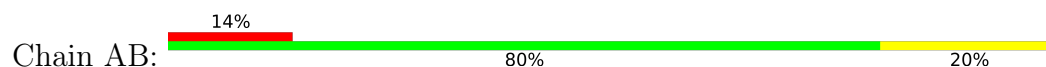
- Molecule 57: 40S ribosomal protein S9-A



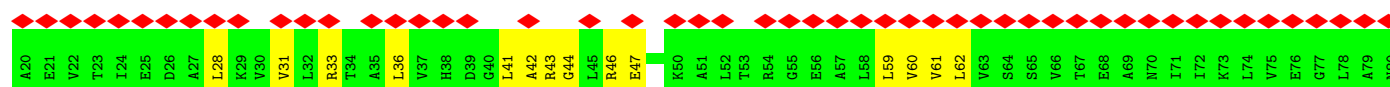
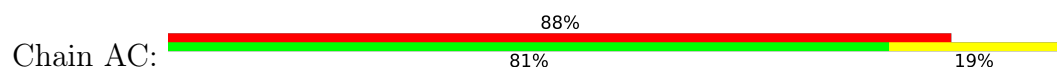
- Molecule 58: 40S ribosomal protein S10-A

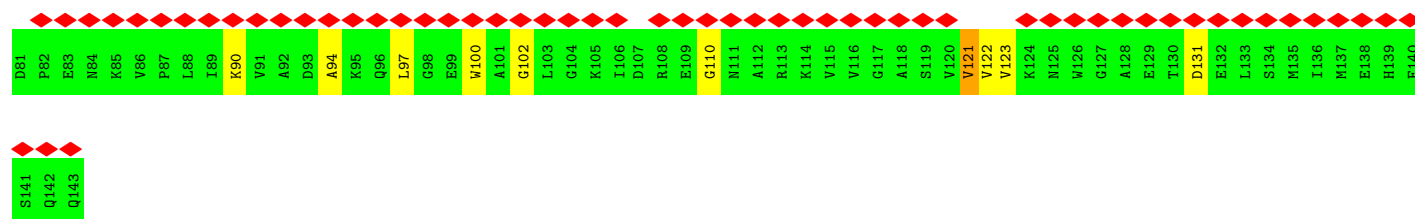


- Molecule 59: 40S ribosomal protein S11-A

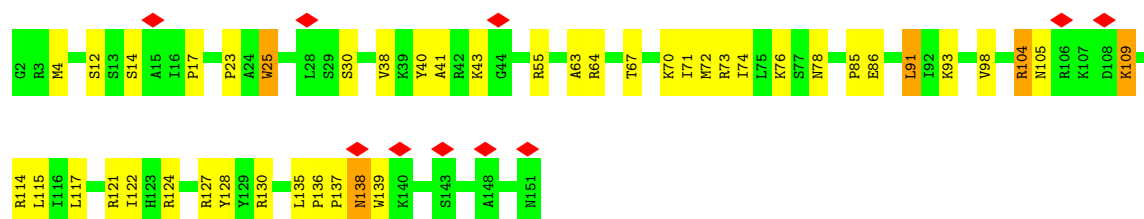
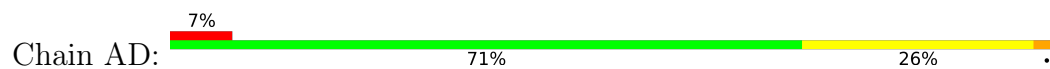


- Molecule 60: 40S ribosomal protein S12

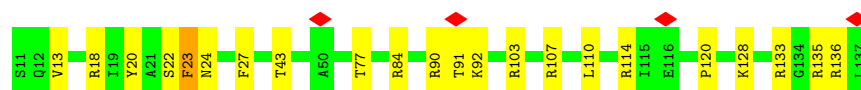
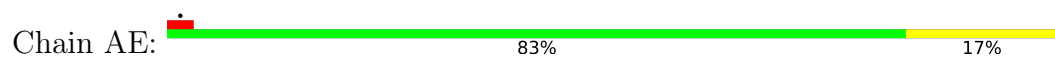




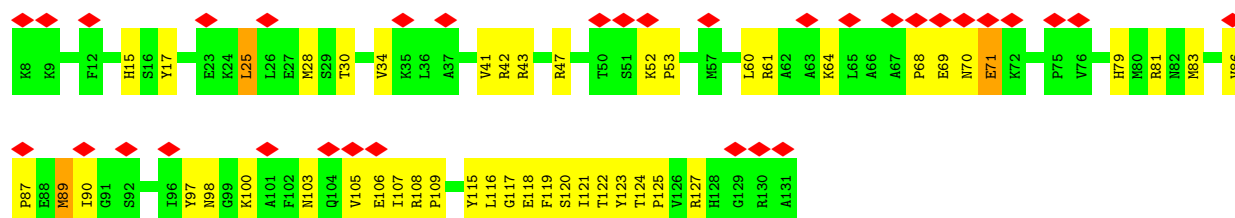
- Molecule 61: 40S ribosomal protein S13



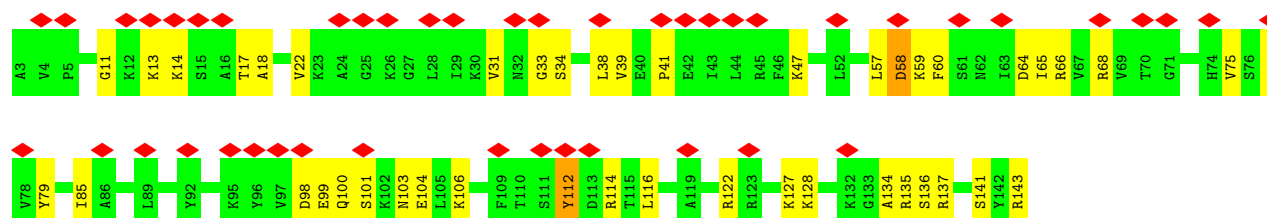
- Molecule 62: 40S ribosomal protein S14-B



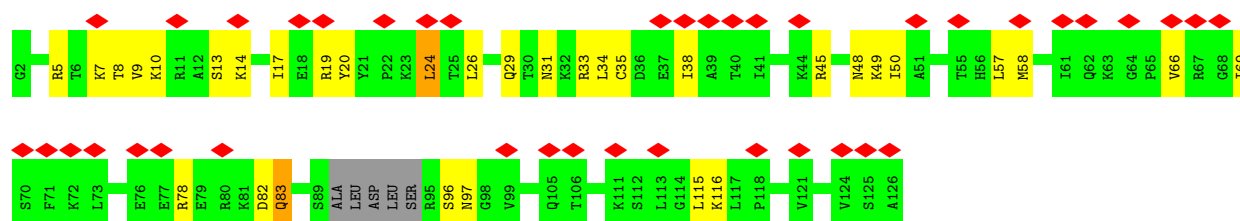
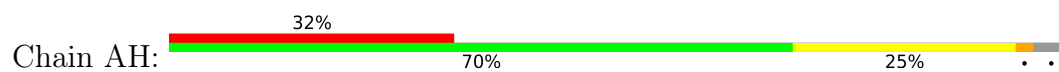
- Molecule 63: 40S ribosomal protein S15



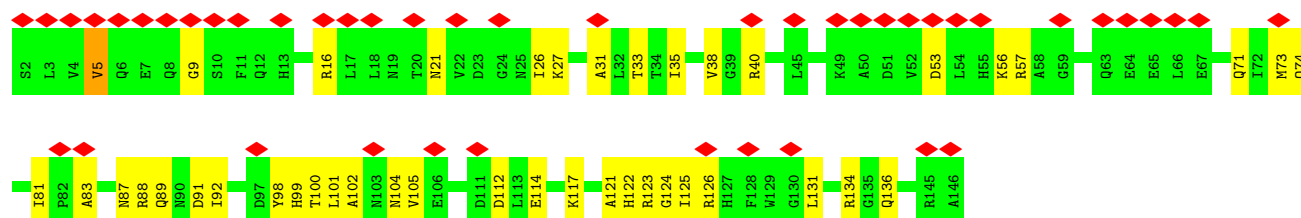
- Molecule 64: 40S ribosomal protein S16-A



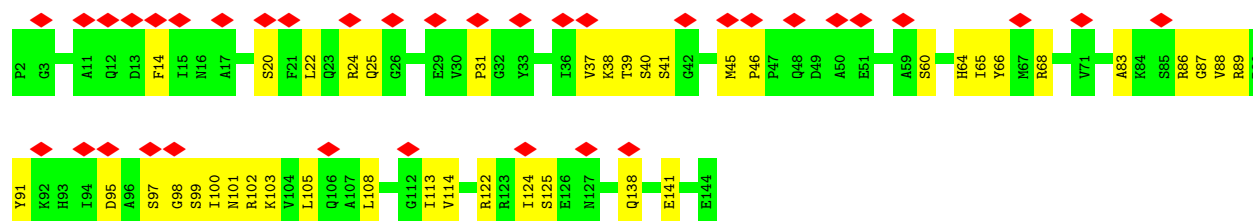
- Molecule 65: 40S ribosomal protein S17-B



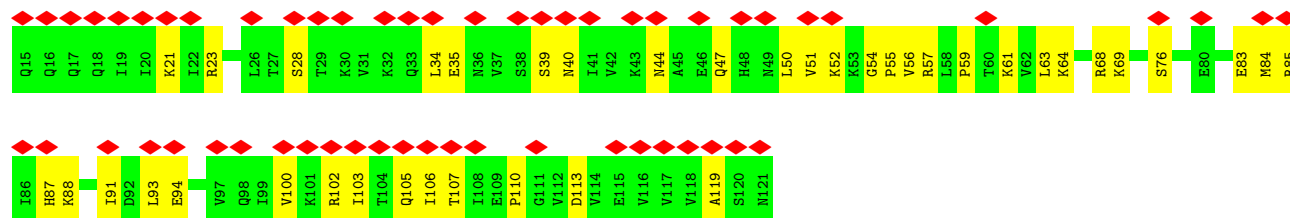
- Molecule 66: 40S ribosomal protein S18-A



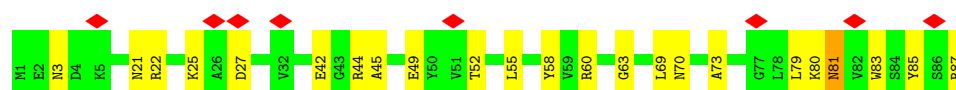
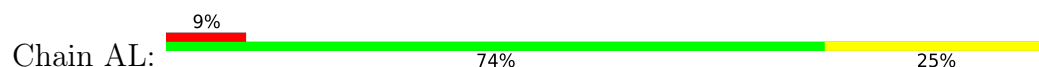
- Molecule 67: 40S ribosomal protein S19-A



- Molecule 68: 40S ribosomal protein S20



- Molecule 69: 40S ribosomal protein S21-A



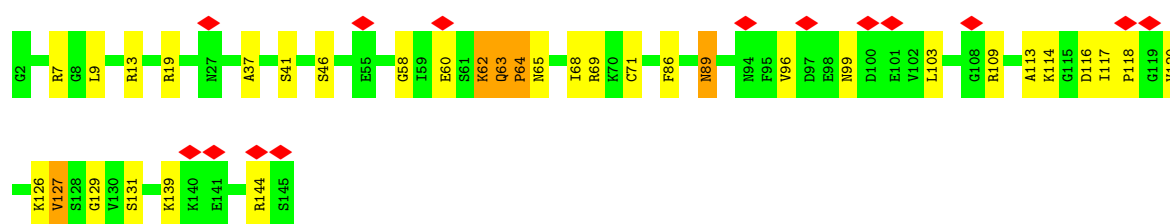
- Molecule 70: 40S ribosomal protein S22-A

Chain AM:  72% 26%



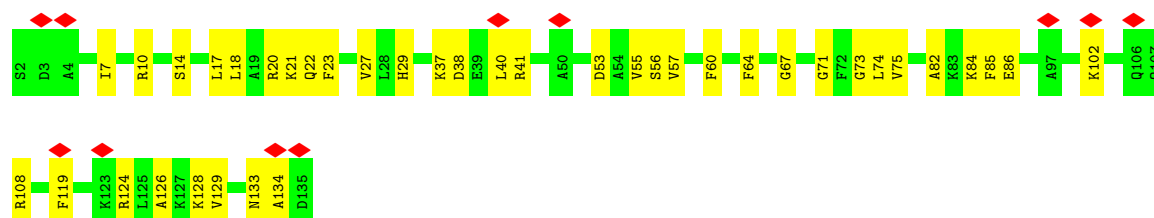
- Molecule 71: 40S ribosomal protein S23-A

Chain AN:  10% 76% 20%

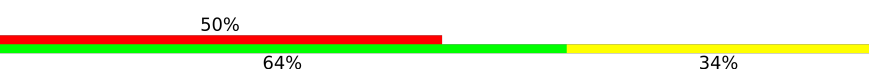


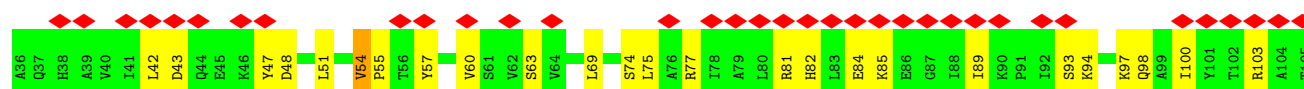
- Molecule 72: 40S ribosomal protein S24-A

Chain AO:  8% 71% 29%



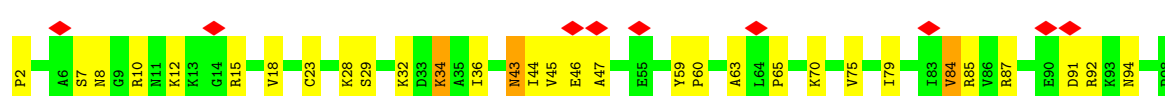
- Molecule 73: 40S ribosomal protein S25-A

Chain AP:  50% 64% 34%

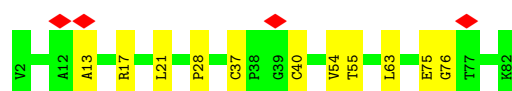
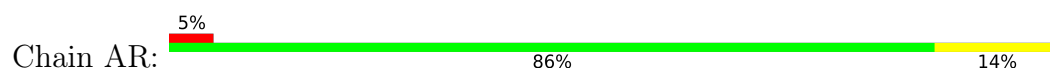


- Molecule 74: 40S ribosomal protein S26-B

Chain AQ:  9% 68% 29%



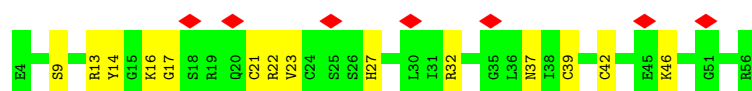
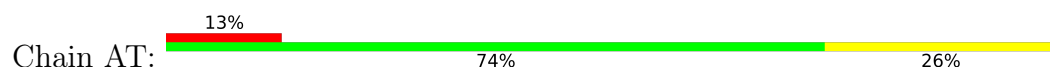
- Molecule 75: 40S ribosomal protein S27-A



- Molecule 76: 40S ribosomal protein S28-A



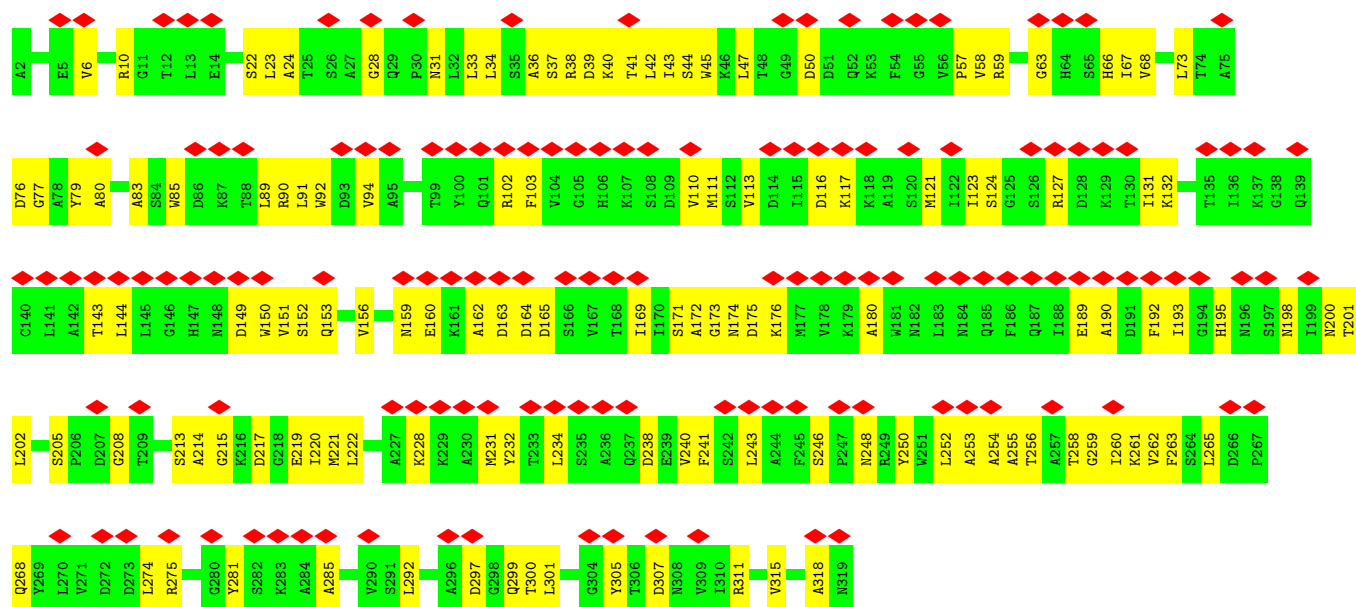
- Molecule 77: 40S ribosomal protein S29-A



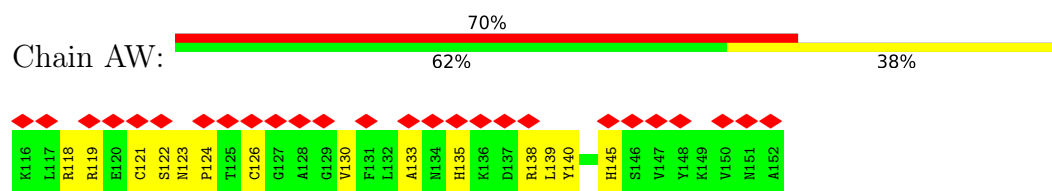
- Molecule 78: 40S ribosomal protein S30-A



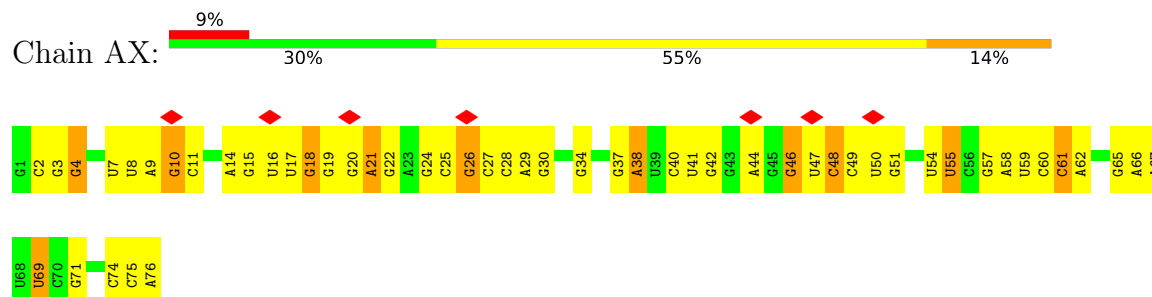
- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein



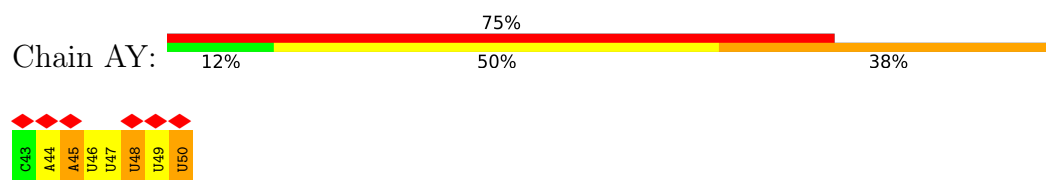
- Molecule 80: Ubiquitin-40S ribosomal protein S31



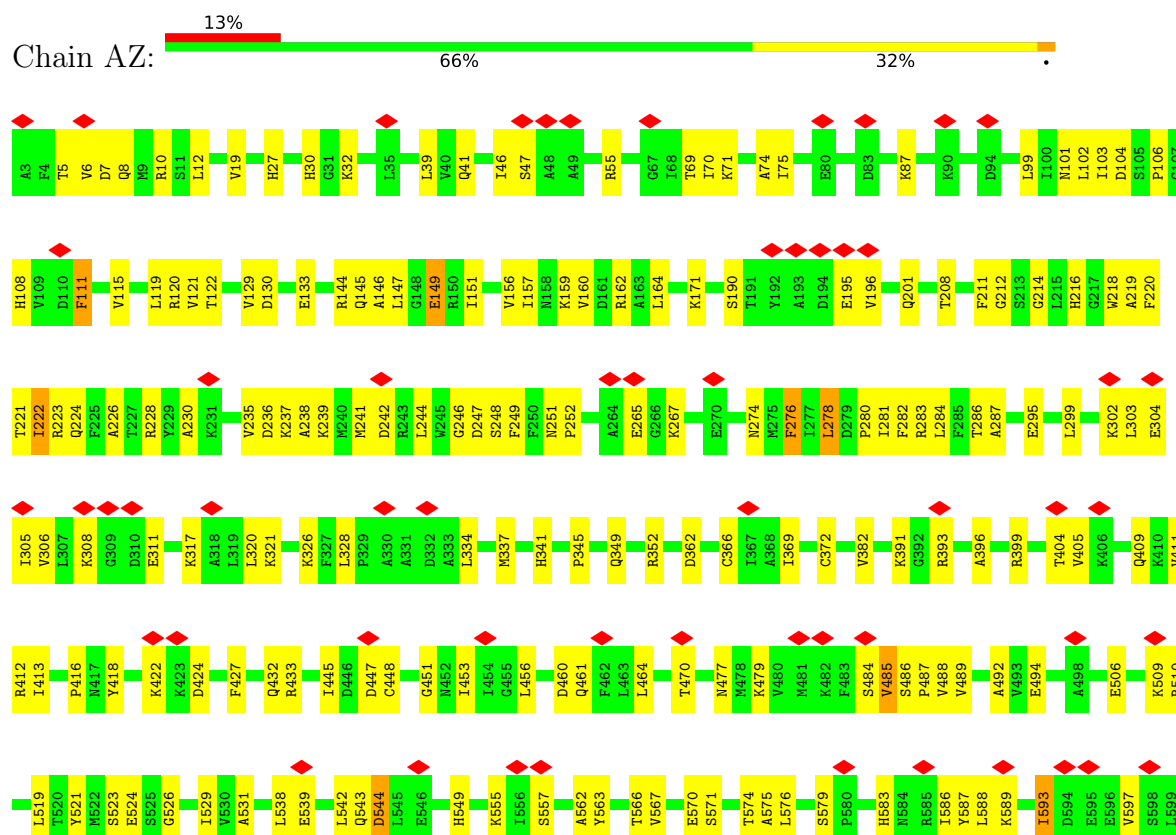
- Molecule 81: Transfer RNA - Phe

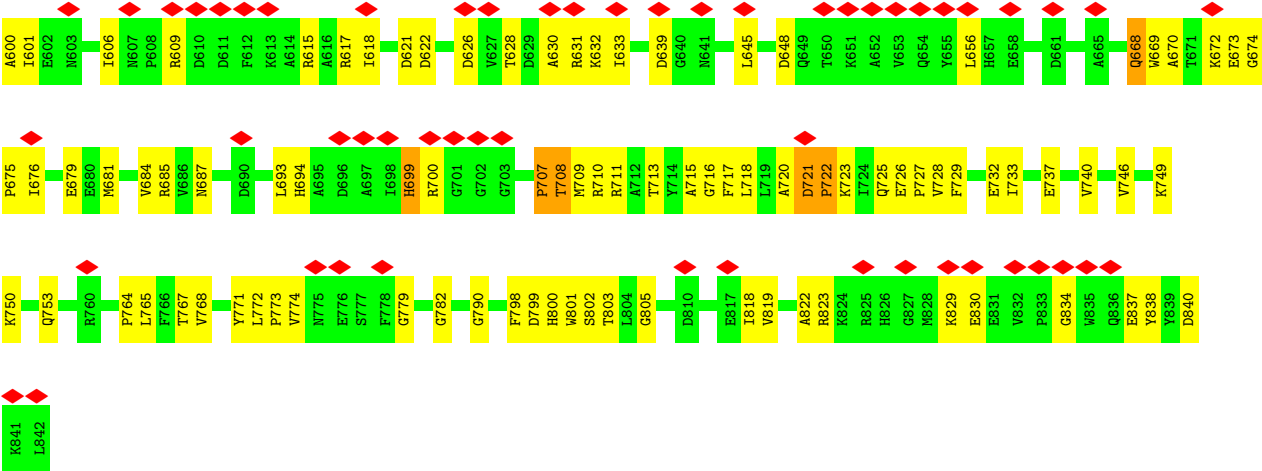


- Molecule 82: Messenger RNA



- Molecule 83: Elongation factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	189700	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	0.347	Depositor
Minimum map value	-0.197	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, DDE, ZN, SO1

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	1	0.30	0/77157	0.47	1/120295 (0.0%)
2	3	0.26	0/2883	0.42	0/4491
3	4	0.29	0/3746	0.46	0/5832
4	P0	0.25	0/1498	0.70	1/2025 (0.0%)
5	P2	0.27	0/728	0.80	0/975
6	A	0.37	0/1948	0.72	0/2617
7	B	0.32	0/3146	0.68	0/4228
8	C	0.30	0/2800	0.67	0/3790
9	D	0.27	0/2425	0.66	0/3271
10	E	0.23	0/1260	0.59	0/1694
11	F	0.31	0/1821	0.71	0/2451
12	G	0.28	0/1836	0.72	0/2481
13	H	0.27	0/1539	0.70	0/2073
14	I	0.31	0/1741	0.70	0/2335
15	J	0.27	0/1374	0.78	0/1842
16	L	0.31	0/1568	0.79	3/2106 (0.1%)
17	M	0.26	0/1068	0.61	0/1438
18	N	0.35	0/1757	0.79	0/2354
19	O	0.33	0/1585	0.73	1/2128 (0.0%)
20	P	0.29	0/1443	0.64	0/1944
21	Q	0.28	0/1465	0.66	0/1965
22	R	0.28	0/1538	0.65	0/2050
23	S	0.29	0/1481	0.66	0/1990
24	T	0.30	0/1300	0.73	2/1743 (0.1%)
25	U	0.25	0/812	0.65	2/1099 (0.2%)
26	V	0.31	0/1018	0.72	1/1369 (0.1%)
27	W	0.31	0/533	0.70	0/707
28	X	0.27	0/979	0.65	0/1321
29	Y	0.27	0/1004	0.66	0/1341
30	Z	0.28	0/1118	0.68	3/1497 (0.2%)
31	a	0.32	0/1204	0.70	0/1612
32	b	0.24	0/473	0.67	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.27	0/751	0.62	0/1008
34	d	0.31	0/897	0.65	0/1205
35	e	0.28	0/1041	0.67	0/1394
36	f	0.34	0/868	0.81	2/1168 (0.2%)
37	g	0.32	0/890	0.77	1/1189 (0.1%)
38	h	0.29	0/978	0.71	1/1301 (0.1%)
39	i	0.28	0/778	0.74	0/1034
40	j	0.36	0/696	0.85	1/923 (0.1%)
41	k	0.24	0/618	0.66	0/826
42	l	0.45	0/443	1.02	0/588
43	m	0.28	0/423	0.64	0/562
44	n	0.26	0/228	0.71	0/293
45	o	0.29	0/860	0.72	0/1136
46	p	0.32	0/701	0.76	0/934
47	2	0.26	0/42328	0.48	3/65955 (0.0%)
48	q	0.26	0/1617	0.70	0/2215
49	r	0.30	0/1735	0.83	4/2335 (0.2%)
50	s	0.27	0/1665	0.68	0/2263
51	t	0.29	0/1759	0.74	1/2368 (0.0%)
52	u	0.29	0/2109	0.83	8/2839 (0.3%)
53	v	0.29	0/1629	0.77	2/2202 (0.1%)
54	w	0.30	0/1814	0.90	7/2425 (0.3%)
55	x	0.31	0/1506	0.80	2/2028 (0.1%)
56	y	0.29	0/1514	0.79	5/2021 (0.2%)
57	z	0.28	0/1519	0.78	3/2035 (0.1%)
58	AA	0.31	0/789	0.78	1/1067 (0.1%)
59	AB	0.27	0/1247	0.72	1/1681 (0.1%)
60	AC	0.26	0/898	0.73	0/1220
61	AD	0.29	0/1215	0.80	2/1638 (0.1%)
62	AE	0.28	0/901	0.73	2/1217 (0.2%)
63	AF	0.34	0/998	0.91	4/1341 (0.3%)
64	AG	0.28	0/1125	0.81	0/1510
65	AH	0.27	0/935	0.72	1/1254 (0.1%)
66	AI	0.25	0/1211	0.70	0/1628
67	AJ	0.26	0/1130	0.70	0/1517
68	AK	0.28	0/865	0.70	0/1169
69	AL	0.34	0/693	0.87	2/935 (0.2%)
70	AM	0.33	0/1038	0.73	1/1395 (0.1%)
71	AN	0.33	0/1139	0.82	0/1518
72	AO	0.25	0/1087	0.67	0/1449
73	AP	0.31	0/571	0.76	0/768
74	AQ	0.34	0/782	0.98	4/1047 (0.4%)
75	AR	0.31	0/620	0.86	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	AS	0.25	0/499	0.70	0/670
77	AT	0.22	0/452	0.67	0/600
78	AU	0.24	0/483	0.65	0/643
79	AV	0.26	0/2490	0.70	4/3389 (0.1%)
80	AW	0.23	0/292	0.76	3/390 (0.8%)
81	AX	0.22	0/1818	0.48	0/2831
82	AY	0.32	0/181	0.64	0/278
83	AZ	0.31	0/6655	0.82	10/9009 (0.1%)
All	All	0.29	0/225729	0.59	89/330942 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	P0	0	2
5	P2	0	1
6	A	0	1
7	B	0	1
9	D	0	5
10	E	0	1
11	F	0	3
12	G	0	3
13	H	0	2
14	I	0	2
15	J	0	1
16	L	0	1
19	O	0	2
21	Q	0	1
24	T	0	2
26	V	0	2
27	W	0	1
31	a	0	1
34	d	0	2
35	e	0	2
36	f	0	1
37	g	0	3
38	h	0	1
39	i	0	3
40	j	0	1
42	l	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	o	0	3
48	q	0	4
49	r	0	4
51	t	0	1
52	u	0	5
53	v	0	2
54	w	0	11
55	x	0	2
56	y	0	1
57	z	0	2
59	AB	0	1
60	AC	0	1
61	AD	0	3
63	AF	0	2
64	AG	0	3
65	AH	0	2
66	AI	0	1
69	AL	0	2
71	AN	0	1
72	AO	0	1
73	AP	0	1
74	AQ	0	7
75	AR	0	2
79	AV	0	1
83	AZ	0	14
All	All	0	123

There are no bond length outliers.

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	z	164	PHE	N-CA-C	-8.78	100.04	111.02
63	AF	71	GLU	CA-C-N	8.65	132.41	120.39
63	AF	71	GLU	C-N-CA	8.65	132.41	120.39
63	AF	69	GLU	CA-C-N	7.75	136.35	121.54
63	AF	69	GLU	C-N-CA	7.75	136.35	121.54
83	AZ	247	ASP	CA-C-N	7.48	135.17	121.70
83	AZ	247	ASP	C-N-CA	7.48	135.17	121.70
83	AZ	721	ASP	CA-C-N	7.47	129.18	119.84
83	AZ	721	ASP	C-N-CA	7.47	129.18	119.84
58	AA	88	PRO	N-CA-CB	7.46	111.08	103.25
74	AQ	60	PRO	CA-C-N	7.16	135.22	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	AQ	60	PRO	C-N-CA	7.16	135.22	121.54
54	w	92	ARG	CA-C-N	7.06	135.02	121.54
54	w	92	ARG	C-N-CA	7.06	135.02	121.54
1	1	1636	U	C1'-C2'-O2'	-6.70	101.75	111.80
54	w	67	VAL	CA-C-N	6.45	133.85	121.54
54	w	67	VAL	C-N-CA	6.45	133.85	121.54
56	y	119	GLN	CA-C-N	6.41	133.24	121.70
56	y	119	GLN	C-N-CA	6.41	133.24	121.70
19	O	145	VAL	N-CA-C	-6.23	107.22	113.20
37	g	81	CYS	CA-CB-SG	6.15	128.54	114.40
83	AZ	709	MET	CA-C-N	6.02	129.17	120.38
83	AZ	709	MET	C-N-CA	6.02	129.17	120.38
30	Z	103	GLN	CA-CB-CG	6.01	126.13	114.10
56	y	67	TRP	CA-C-N	5.90	132.33	121.70
56	y	67	TRP	C-N-CA	5.90	132.33	121.70
16	L	47	ALA	CA-C-N	5.83	127.13	119.84
16	L	47	ALA	C-N-CA	5.83	127.13	119.84
38	h	91	ALA	N-CA-C	5.82	118.29	111.02
52	u	154	ILE	CA-C-N	5.81	132.63	121.54
52	u	154	ILE	C-N-CA	5.81	132.63	121.54
52	u	193	GLY	CA-C-N	5.77	132.56	121.54
52	u	193	GLY	C-N-CA	5.77	132.56	121.54
83	AZ	149	GLU	CA-C-N	5.77	132.09	121.70
83	AZ	149	GLU	C-N-CA	5.77	132.09	121.70
74	AQ	18	VAL	CA-C-N	5.74	135.81	121.80
74	AQ	18	VAL	C-N-CA	5.74	135.81	121.80
49	r	147	ALA	CA-C-N	5.73	132.48	121.54
49	r	147	ALA	C-N-CA	5.73	132.48	121.54
51	t	76	ARG	N-CA-C	-5.71	106.97	114.04
49	r	206	PRO	CA-C-N	5.65	132.33	121.54
49	r	206	PRO	C-N-CA	5.65	132.33	121.54
52	u	194	THR	CA-C-N	5.62	132.09	121.97
52	u	194	THR	C-N-CA	5.62	132.09	121.97
47	2	706	A	C2'-C3'-O3'	5.60	117.90	109.50
56	y	40	ALA	N-CA-C	5.54	117.39	110.91
69	AL	44	ARG	CA-C-N	5.53	132.09	121.54
69	AL	44	ARG	C-N-CA	5.53	132.09	121.54
79	AV	164	ASP	CA-C-N	5.52	132.09	121.54
79	AV	164	ASP	C-N-CA	5.52	132.09	121.54
57	z	101	VAL	CA-C-N	5.49	135.47	126.86
57	z	101	VAL	C-N-CA	5.49	135.47	126.86
80	AW	119	ARG	N-CA-C	5.48	118.02	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	w	90	GLY	CA-C-N	5.47	131.56	121.70
54	w	90	GLY	C-N-CA	5.47	131.56	121.70
53	v	57	SER	CA-C-N	5.43	130.34	122.36
53	v	57	SER	C-N-CA	5.43	130.34	122.36
47	2	706	A	P-O3'-C3'	5.38	128.27	120.20
40	j	64	MET	CA-CB-CG	5.37	124.84	114.10
24	T	19	PHE	CA-C-N	5.36	135.57	125.66
24	T	19	PHE	C-N-CA	5.36	135.57	125.66
80	AW	118	ARG	CA-C-N	5.36	129.29	121.31
80	AW	118	ARG	C-N-CA	5.36	129.29	121.31
52	u	94	ALA	CA-C-N	5.36	135.93	126.45
52	u	94	ALA	C-N-CA	5.36	135.93	126.45
25	U	90	ARG	CA-C-N	5.25	131.57	121.54
25	U	90	ARG	C-N-CA	5.25	131.57	121.54
16	L	93	ILE	N-CA-C	-5.24	107.72	112.12
36	f	58	GLU	CA-C-N	5.22	131.37	121.97
36	f	58	GLU	C-N-CA	5.22	131.37	121.97
70	AM	28	ARG	C-N-CD	-5.20	109.17	120.60
30	Z	102	GLU	CA-C-N	5.18	134.45	121.80
30	Z	102	GLU	C-N-CA	5.18	134.45	121.80
47	2	1338	C	P-O3'-C3'	5.18	127.97	120.20
83	AZ	424	ASP	CA-C-N	5.18	131.44	121.54
83	AZ	424	ASP	C-N-CA	5.18	131.44	121.54
26	V	104	ASN	N-CA-C	5.17	121.23	109.81
59	AB	5	LEU	CA-CB-CG	5.16	134.35	116.30
62	AE	23	PHE	CA-C-N	5.16	131.39	121.54
62	AE	23	PHE	C-N-CA	5.16	131.39	121.54
4	P0	45	LEU	CA-CB-CG	5.15	134.32	116.30
61	AD	137	PRO	CA-C-N	5.12	131.33	121.54
61	AD	137	PRO	C-N-CA	5.12	131.33	121.54
54	w	93	LYS	N-CA-C	-5.11	99.91	110.80
55	x	35	LYS	CA-C-N	5.08	131.24	121.54
55	x	35	LYS	C-N-CA	5.08	131.24	121.54
65	AH	24	LEU	CA-CB-CG	5.07	134.03	116.30
79	AV	162	ALA	CA-C-N	5.07	131.21	121.54
79	AV	162	ALA	C-N-CA	5.07	131.21	121.54

There are no chirality outliers.

All (123) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A	143	GLU	Peptide

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Mol	Chain	Res	Type	Group
59	AB	27	THR	Peptide
60	AC	110	GLY	Peptide
61	AD	104	ARG	Peptide
61	AD	138	ASN	Peptide
61	AD	25	TRP	Peptide
63	AF	100	LYS	Peptide
63	AF	89	MET	Peptide
64	AG	112	TYR	Peptide
64	AG	58	ASP	Peptide
64	AG	68	ARG	Peptide
65	AH	78	ARG	Peptide
65	AH	83	GLN	Peptide
66	AI	91	ASP	Peptide
69	AL	49	GLU	Peptide
69	AL	52	THR	Peptide
71	AN	113	ALA	Peptide
72	AO	37	LYS	Peptide
73	AP	54	VAL	Peptide
74	AQ	34	LYS	Peptide
74	AQ	43	ASN	Peptide
74	AQ	46	GLU	Peptide
74	AQ	47	ALA	Peptide
74	AQ	59	TYR	Peptide
74	AQ	63	ALA	Peptide
74	AQ	7	SER	Peptide
75	AR	55	THR	Peptide
75	AR	75	GLU	Peptide
79	AV	275	ARG	Peptide
83	AZ	111	PHE	Peptide
83	AZ	244	LEU	Peptide
83	AZ	246	GLY	Peptide
83	AZ	251	ASN	Peptide
83	AZ	276	PHE	Peptide
83	AZ	485	VAL	Peptide
83	AZ	487	PRO	Peptide
83	AZ	544	ASP	Peptide
83	AZ	645	LEU	Peptide
83	AZ	656	LEU	Peptide
83	AZ	668	GLN	Peptide
83	AZ	707	PRO	Peptide
83	AZ	721	ASP	Peptide
83	AZ	790	GLY	Peptide

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Mol	Chain	Res	Type	Group
7	B	25	ILE	Peptide
9	D	177	GLU	Peptide
9	D	20	PHE	Peptide
9	D	260	PHE	Peptide
9	D	43	LYS	Peptide
9	D	81	HIS	Peptide
10	E	58	LEU	Peptide
11	F	110	ARG	Peptide
11	F	157	ASN	Peptide
11	F	214	TRP	Peptide
12	G	156	ASP	Peptide
12	G	30	THR	Peptide
12	G	76	ALA	Peptide
13	H	20	ILE	Peptide
13	H	21	LYS	Peptide
14	I	217	PHE	Peptide
14	I	58	GLU	Peptide
15	J	167	TYR	Peptide
16	L	47	ALA	Peptide
19	O	110	PRO	Peptide
19	O	36	VAL	Peptide
4	P0	39	HIS	Peptide
4	P0	41	VAL	Peptide
5	P2	117	ARG	Peptide
21	Q	59	ARG	Peptide
24	T	103	GLN	Peptide
24	T	17	ARG	Peptide
26	V	104	ASN	Peptide
26	V	93	LEU	Peptide
27	W	14	TYR	Peptide
31	a	23	GLY	Peptide
34	d	56	ASN	Peptide
34	d	87	ASN	Peptide
35	e	20	HIS	Peptide
35	e	39	ASP	Peptide
36	f	58	GLU	Peptide
37	g	66	SER	Peptide
37	g	80	ARG	Peptide
37	g	82	ALA	Peptide
38	h	90	ARG	Peptide
39	i	12	ASN	Peptide
39	i	63	ASN	Peptide

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Mol	Chain	Res	Type	Group
39	i	97	SER	Peptide
40	j	5	THR	Peptide
42	l	29	LEU	Peptide
45	o	28	TYR	Peptide
45	o	34	SER	Peptide
45	o	7	THR	Peptide
48	q	107	PHE	Peptide
48	q	111	ILE	Peptide
48	q	112	THR	Peptide
48	q	192	THR	Peptide
49	r	147	ALA	Peptide
49	r	205	PHE	Peptide
49	r	206	PRO	Peptide
49	r	40	ASN	Peptide
51	t	219	ALA	Peptide
52	u	154	ILE	Peptide
52	u	194	THR	Peptide
52	u	195	ILE	Peptide
52	u	233	LYS	Peptide
52	u	94	ALA	Peptide
53	v	127	GLN	Peptide
53	v	57	SER	Peptide
54	w	100	ALA	Peptide
54	w	119	GLN	Peptide
54	w	13	GLN	Peptide
54	w	148	SER	Peptide
54	w	153	VAL	Peptide
54	w	67	VAL	Peptide
54	w	88	ARG	Peptide
54	w	9	VAL	Peptide
54	w	91	GLU	Peptide
54	w	92	ARG	Peptide
54	w	93	LYS	Peptide
55	x	110	GLN	Peptide
55	x	36	ALA	Peptide
56	y	20	GLN	Peptide
57	z	133	HIS	Peptide
57	z	163	PRO	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	1	68931	0	34637	848	0
2	3	2579	0	1304	32	0
3	4	3353	0	1695	32	0
4	P0	1473	0	1514	39	0
5	P2	723	0	774	31	0
6	A	1914	0	1981	47	0
7	B	3075	0	3142	57	0
8	C	2748	0	2859	57	0
9	D	2375	0	2325	34	0
10	E	1239	0	1326	24	0
11	F	1784	0	1862	38	0
12	G	1804	0	1877	26	0
13	H	1518	0	1587	28	0
14	I	1705	0	1736	30	0
15	J	1353	0	1383	29	0
16	L	1543	0	1608	41	0
17	M	1053	0	1149	25	0
18	N	1720	0	1779	51	0
19	O	1555	0	1659	30	0
20	P	1420	0	1437	17	0
21	Q	1441	0	1543	26	0
22	R	1521	0	1617	28	0
23	S	1445	0	1487	44	0
24	T	1276	0	1323	23	0
25	U	796	0	812	9	0
26	V	1003	0	1048	20	0
27	W	521	0	551	6	0
28	X	964	0	1025	19	0
29	Y	993	0	1081	25	0
30	Z	1092	0	1155	20	0
31	a	1173	0	1215	31	0
32	b	462	0	491	8	0
33	c	743	0	797	13	0
34	d	883	0	918	19	0
35	e	1020	0	1090	11	0
36	f	850	0	880	24	0
37	g	880	0	941	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	h	969	0	1078	19	0
39	i	771	0	849	19	0
40	j	681	0	683	9	0
41	k	612	0	682	7	0
42	l	436	0	475	14	0
43	m	417	0	458	6	0
44	n	227	0	273	9	0
45	o	847	0	915	15	0
46	p	694	0	734	20	0
47	2	37845	0	19040	632	0
48	q	1577	0	1567	24	0
49	r	1709	0	1784	31	0
50	s	1635	0	1723	29	0
51	t	1734	0	1817	47	0
52	u	2068	0	2154	60	0
53	v	1609	0	1675	49	0
54	w	1790	0	1881	48	0
55	x	1481	0	1572	31	0
56	y	1489	0	1525	37	0
57	z	1494	0	1573	40	0
58	AA	772	0	727	20	0
59	AB	1220	0	1281	21	0
60	AC	890	0	887	14	0
61	AD	1192	0	1255	30	0
62	AE	891	0	883	15	0
63	AF	977	0	1002	42	0
64	AG	1105	0	1166	29	0
65	AH	926	0	930	23	0
66	AI	1192	0	1222	34	0
67	AJ	1112	0	1124	32	0
68	AK	855	0	917	27	0
69	AL	684	0	672	17	0
70	AM	1021	0	1060	26	0
71	AN	1121	0	1196	32	0
72	AO	1073	0	1132	26	0
73	AP	563	0	603	17	0
74	AQ	769	0	816	23	0
75	AR	610	0	632	5	0
76	AS	497	0	535	19	0
77	AT	442	0	431	18	0
78	AU	475	0	525	4	0
79	AV	2437	0	2386	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	AW	287	0	287	8	0
81	AX	1626	0	820	24	0
82	AY	164	0	84	10	0
83	AZ	6551	0	6613	194	0
84	AQ	1	0	0	0	0
84	AR	1	0	0	0	0
84	AT	1	0	0	0	0
84	AW	1	0	0	0	0
84	j	1	0	0	0	0
84	m	1	0	0	0	0
84	o	1	0	0	0	0
84	p	1	0	0	0	0
85	AZ	35	0	41	13	0
86	AZ	32	0	14	5	0
All	All	210540	0	157307	3106	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 9.

All (3106) 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)
47:2:40:A:H62	47:2:467:G:N2	1.55	1.03
47:2:214:G:N2	47:2:251:A:H62	1.55	1.03
1:1:1636:U:H5'	1:1:1636:U:H6	1.24	1.02
1:1:1636:U:H5'	1:1:1636:U:C6	1.94	1.02
47:2:214:G:H21	47:2:251:A:N6	1.59	0.99
47:2:993:A:H62	47:2:1011:G:N2	1.61	0.98
1:1:1257:C:H42	1:1:1261:G:N2	1.63	0.97
2:3:79:A:H62	2:3:101:G:N2	1.62	0.97
47:2:1542:G:H21	47:2:1569:A:H62	1.04	0.97
83:AZ:317:LYS:O	83:AZ:321:LYS:HB2	1.64	0.97
47:2:628:G:H21	47:2:971:A:H62	1.11	0.96
1:1:1257:C:N4	1:1:1261:G:H22	1.63	0.96
85:AZ:901:SO1:H203	85:AZ:901:SO1:C11	1.96	0.96
1:1:1071:U:H3	1:1:1087:G:H1	1.12	0.95
1:1:2465:G:H21	1:1:2491:A:N6	1.64	0.95
1:1:2465:G:H21	1:1:2491:A:H62	1.08	0.94
83:AZ:576:LEU:HA	83:AZ:586:ILE:O	1.68	0.94
47:2:1588:G:H1	47:2:1608:U:H3	0.95	0.94
1:1:355:A:H62	1:1:364:G:H21	1.13	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:40:A:N6	47:2:467:G:H21	1.66	0.93
47:2:993:A:N6	47:2:1011:G:H21	1.66	0.93
47:2:1356:U:H3	47:2:1367:G:H1	0.97	0.92
47:2:629:U:H3	47:2:970:A:H62	1.03	0.92
81:AX:4:G:H1	81:AX:69:U:H3	0.99	0.92
2:3:79:A:N6	2:3:101:G:H21	1.68	0.92
47:2:1663:G:H1	47:2:1738:U:H3	0.96	0.91
47:2:826:U:H3	47:2:846:G:H1	0.92	0.91
47:2:486:G:H1	47:2:501:U:H3	0.94	0.90
47:2:1203:A:H61	47:2:1553:G:H21	1.13	0.90
1:1:3222:U:H3	1:1:3263:G:H1	0.95	0.90
47:2:1542:G:N2	47:2:1569:A:H62	1.67	0.90
1:1:3189:G:H1	1:1:3203:U:H3	1.15	0.89
1:1:1257:C:H42	1:1:1261:G:H22	0.90	0.88
1:1:1533:U:H3	1:1:1587:A:N6	1.70	0.88
1:1:3160:U:H3	1:1:3290:G:H1	1.20	0.87
47:2:1499:G:H1	47:2:1508:U:H3	0.91	0.87
47:2:1335:U:H3	47:2:1416:G:H1	1.16	0.87
47:2:1542:G:H21	47:2:1569:A:N6	1.73	0.87
47:2:40:A:H62	47:2:467:G:H21	0.87	0.86
2:3:79:A:H62	2:3:101:G:H21	0.87	0.86
1:1:1896:A:H61	1:1:2339:C:N4	1.73	0.85
83:AZ:74:ALA:HA	83:AZ:102:LEU:O	1.76	0.85
47:2:1203:A:H61	47:2:1553:G:N2	1.75	0.85
47:2:1490:C:HO2'	51:t:3:ALA:N	1.75	0.84
83:AZ:75:ILE:O	83:AZ:101:ASN:HA	1.76	0.84
83:AZ:404:THR:HA	83:AZ:448:CYS:O	1.77	0.84
1:1:355:A:H62	1:1:364:G:N2	1.77	0.83
1:1:182:U:H3	1:1:234:G:H1	1.28	0.82
2:3:81:U:H3	2:3:99:G:H1	1.27	0.82
1:1:355:A:N6	1:1:364:G:H21	1.77	0.81
47:2:752:A:H2	47:2:797:G:H1	1.24	0.81
47:2:478:A:H2	47:2:510:G:H1	1.25	0.81
47:2:1213:G:H1	47:2:1450:U:H3	1.28	0.81
1:1:2465:G:N2	1:1:2491:A:H62	1.79	0.80
47:2:628:G:H21	47:2:971:A:N6	1.78	0.80
83:AZ:538:LEU:O	83:AZ:542:LEU:HB2	1.81	0.80
1:1:1193:A:H62	1:1:1314:C:N4	1.80	0.80
1:1:2696:A:C6	1:1:2758:A:N1	2.49	0.79
83:AZ:713:THR:O	83:AZ:717:PHE:HB2	1.82	0.79
47:2:628:G:N2	47:2:971:A:H62	1.79	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:774:VAL:HG11	85:AZ:901:SO1:H202	1.64	0.79
1:1:2565:U:H3	1:1:2576:G:H1	1.31	0.79
83:AZ:226:ALA:O	83:AZ:230:ALA:HB2	1.83	0.79
47:2:629:U:H3	47:2:970:A:N6	1.80	0.78
83:AZ:539:GLU:O	83:AZ:543:GLN:HB2	1.83	0.78
1:1:1533:U:H3	1:1:1587:A:H62	0.85	0.78
47:2:752:A:C2	47:2:797:G:N1	2.51	0.78
83:AZ:280:PRO:O	83:AZ:284:LEU:HB2	1.83	0.78
47:2:1203:A:N6	47:2:1553:G:H21	1.81	0.77
1:1:1234:G:H21	5:P2:132:ILE:HG12	1.49	0.77
47:2:174:U:H3	47:2:266:A:H62	1.31	0.75
1:1:754:G:H1	1:1:778:U:H3	1.35	0.75
1:1:2844:C:N4	1:1:2898:G:H22	1.86	0.74
1:1:2256:A:H2	47:2:1757:G:P	2.12	0.73
49:r:145:LYS:HB3	49:r:149:GLN:HG3	1.70	0.73
36:f:38:PRO:HG3	36:f:79:GLY:H	1.52	0.73
83:AZ:345:PRO:O	83:AZ:349:GLN:HB2	1.88	0.73
83:AZ:492:ALA:HB3	83:AZ:557:SER:O	1.89	0.73
83:AZ:818:ILE:O	83:AZ:822:ALA:HB3	1.89	0.72
47:2:273:G:H1	47:2:283:U:H3	0.81	0.72
1:1:2696:A:N6	1:1:2758:A:C6	2.57	0.72
47:2:1316:G:H5''	65:AH:7:LYS:HG3	1.72	0.71
34:d:6:ASP:H	34:d:77:ARG:HH21	1.37	0.71
47:2:752:A:H2	47:2:797:G:N1	1.88	0.71
51:t:38:GLU:HB2	68:AK:110:PRO:HG3	1.73	0.71
1:1:354:U:H3	1:1:365:A:H62	1.38	0.71
1:1:2256:A:C2	47:2:1757:G:O5'	2.43	0.71
1:1:2635:A:N7	1:1:2642:A:N6	2.39	0.71
1:1:1257:C:H5'	4:P0:46:ARG:HH12	1.54	0.70
10:E:51:ARG:HH21	10:E:163:PHE:HB2	1.54	0.70
31:a:124:ILE:HG22	31:a:144:VAL:H	1.56	0.70
47:2:993:A:H62	47:2:1011:G:H21	0.81	0.70
3:4:95:G:N3	40:j:79:GLN:NE2	2.39	0.70
71:AN:62:LYS:HD2	71:AN:118:PRO:HD3	1.73	0.70
83:AZ:305:ILE:HG23	83:AZ:306:VAL:HG13	1.71	0.70
1:1:1636:U:OP1	30:Z:36:HIS:CE1	2.44	0.70
1:1:2256:A:H2	47:2:1757:G:O5'	1.73	0.70
47:2:902:G:N7	62:AE:24:ASN:ND2	2.39	0.70
83:AZ:115:VAL:O	83:AZ:119:LEU:HB2	1.91	0.70
7:B:95:THR:HG23	7:B:97:ARG:H	1.56	0.70
52:u:151:ASP:H	52:u:169:ILE:HD11	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:238:ALA:O	83:AZ:242:ASP:HB2	1.92	0.70
58:AA:7:ASP:HB3	58:AA:37:THR:HG22	1.73	0.69
4:P0:40:GLU:HG3	4:P0:43:LYS:HD2	1.73	0.69
67:AJ:37:VAL:HG13	67:AJ:39:THR:H	1.57	0.69
80:AW:135:HIS:HB2	80:AW:138:ARG:HB3	1.75	0.69
45:o:7:THR:HA	45:o:24:LYS:HA	1.74	0.69
6:A:55:GLY:HA3	6:A:174:ARG:HH12	1.56	0.69
28:X:49:LYS:HD2	38:h:78:LYS:HZ1	1.58	0.69
1:1:1195:A:H61	1:1:1313:G:H1	1.40	0.69
47:2:1433:G:N2	77:AT:42:CYS:SG	2.66	0.69
47:2:1580:C:H4'	64:AG:137:ARG:HB2	1.73	0.69
47:2:1388:A:C2	47:2:1409:G:N2	2.61	0.69
70:AM:3:ARG:HE	70:AM:28:ARG:HH12	1.41	0.69
1:1:2844:C:H42	1:1:2898:G:N2	1.92	0.68
83:AZ:405:VAL:O	83:AZ:447:ASP:HA	1.93	0.68
79:AV:37:SER:HB3	79:AV:41:THR:H	1.59	0.68
79:AV:80:ALA:HB3	79:AV:92:TRP:HB2	1.74	0.68
83:AZ:733:ILE:O	83:AZ:767:THR:HA	1.94	0.68
20:P:31:GLU:HG2	20:P:60:PHE:HA	1.76	0.68
47:2:214:G:H21	47:2:251:A:H62	0.78	0.68
1:1:1231:A:N6	4:P0:110:ARG:HH12	1.92	0.68
54:w:25:ARG:HH22	54:w:106:LEU:HB3	1.59	0.68
79:AV:131:ILE:HD11	79:AV:171:SER:HB2	1.75	0.68
1:1:1805:C:H2'	1:1:1806:A:H8	1.60	0.67
1:1:3113:A:H4'	13:H:69:ARG:HD2	1.75	0.67
5:P2:77:ALA:O	5:P2:117:ARG:NH1	2.27	0.67
18:N:103:GLU:HG3	18:N:118:SER:HB3	1.75	0.67
47:2:478:A:C2	47:2:510:G:N1	2.57	0.67
54:w:77:LEU:HD23	54:w:95:LYS:HB3	1.77	0.67
69:AL:22:ARG:HH22	69:AL:58:TYR:HB3	1.58	0.67
47:2:788:A:N7	52:u:108:ARG:NH1	2.43	0.67
66:AI:126:ARG:HD3	66:AI:131:LEU:HD22	1.77	0.67
83:AZ:144:ARG:HA	83:AZ:147:LEU:HG	1.76	0.67
47:2:903:U:O2	47:2:906:A:N7	2.28	0.67
1:1:2844:C:N4	1:1:2898:G:N2	2.42	0.66
14:I:188:GLY:HA3	14:I:216:TYR:HB2	1.77	0.66
47:2:507:U:C6	47:2:507:U:H5''	2.30	0.66
85:AZ:901:SO1:O15	85:AZ:901:SO1:H212	1.95	0.66
52:u:181:VAL:H	52:u:194:THR:HA	1.61	0.66
16:L:90:ALA:HB1	16:L:95:ILE:HB	1.76	0.66
53:v:177:ILE:HD13	53:v:180:ARG:HH12	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:396:ALA:HB3	83:AZ:456:LEU:HB3	1.78	0.66
5:P2:134:GLY:H	5:P2:137:GLN:HB3	1.61	0.66
7:B:10:ARG:NH1	7:B:11:HIS:O	2.29	0.66
47:2:227:U:O2	47:2:834:G:N2	2.28	0.66
1:1:1259:A:OP2	4:P0:14:LYS:NZ	2.27	0.66
47:2:1346:A:H5''	47:2:1348:A:H62	1.60	0.66
8:C:258:LEU:HA	8:C:261:VAL:HG12	1.77	0.65
30:Z:22:LYS:NZ	30:Z:129:TRP:O	2.29	0.65
47:2:1167:G:H1	47:2:1578:U:H3	1.43	0.65
1:1:2769:A:H1'	45:o:82:GLN:HE22	1.62	0.65
1:1:1347:U:H3'	21:Q:38:ARG:HH22	1.60	0.65
4:P0:97:LYS:HZ2	4:P0:187:VAL:HG22	1.60	0.65
44:n:5:TRP:HE1	47:2:1784:C:H41	1.44	0.65
83:AZ:713:THR:O	83:AZ:717:PHE:CB	2.44	0.65
1:1:1195:A:N6	1:1:1313:G:H1	1.95	0.65
22:R:167:ARG:HG2	22:R:170:ARG:HE	1.61	0.65
47:2:1116:A:H62	47:2:1130:G:H21	1.43	0.65
1:1:3158:G:C6	1:1:3292:A:N1	2.65	0.65
4:P0:60:ARG:HH21	4:P0:64:ARG:HD3	1.60	0.65
53:v:92:ARG:NH2	53:v:169:ASN:OD1	2.30	0.65
54:w:67:VAL:HG21	54:w:99:GLY:HA3	1.79	0.65
70:AM:28:ARG:HB3	70:AM:60:LYS:HG2	1.79	0.65
6:A:28:LYS:HG3	6:A:123:ARG:HD2	1.79	0.65
81:AX:18:G:H22	81:AX:57:G:H2'	1.62	0.65
39:i:34:SER:HG	39:i:37:THR:HG1	1.40	0.65
7:B:10:ARG:NH2	7:B:263:SER:O	2.29	0.65
1:1:1257:C:N3	1:1:1261:G:N1	2.41	0.65
1:1:1405:U:H3	35:e:55:ILE:HD12	1.62	0.65
1:1:1231:A:H62	4:P0:110:ARG:HH12	1.43	0.64
1:1:412:G:N3	20:P:118:GLN:NE2	2.44	0.64
1:1:510:G:H1	1:1:581:U:H3	1.46	0.64
47:2:195:G:N7	56:y:141:ARG:NH2	2.46	0.64
47:2:1157:A:H3'	47:2:1160:A:H62	1.62	0.64
57:z:163:PRO:HA	57:z:166:GLY:H	1.62	0.64
57:z:143:ILE:HG22	57:z:145:SER:H	1.62	0.64
21:Q:171:LYS:H	31:a:56:VAL:HG11	1.61	0.64
34:d:44:MET:HG2	34:d:77:ARG:HH11	1.61	0.64
47:2:1294:G:H1	47:2:1303:U:H3	1.43	0.64
1:1:995:U:H3	1:1:1054:A:H62	1.43	0.64
52:u:68:ARG:NH1	52:u:70:VAL:O	2.30	0.64
53:v:80:LYS:HE3	53:v:82:PHE:HB2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:282:PHE:O	83:AZ:286:THR:HB	1.98	0.64
85:AZ:901:SO1:H203	85:AZ:901:SO1:O19	1.97	0.64
12:G:190:VAL:HG13	12:G:192:GLN:H	1.63	0.64
19:O:190:VAL:HA	19:O:193:GLN:HE21	1.63	0.64
5:P2:110:ILE:HD13	5:P2:130:LYS:HZ2	1.63	0.64
31:a:74:ASN:HD22	31:a:114:GLY:HA2	1.62	0.64
1:1:2114:C:O2'	1:1:2116:G:N2	2.31	0.64
79:AV:250:TYR:HB3	79:AV:265:LEU:HB2	1.80	0.64
1:1:2176:U:OP1	6:A:54:ARG:NH2	2.31	0.63
11:F:90:LYS:HD2	11:F:95:ILE:HD11	1.80	0.63
47:2:1256:A:H3'	60:AC:43:ARG:HE	1.63	0.63
85:AZ:901:SO1:H212	85:AZ:901:SO1:O19	1.97	0.63
14:I:71:CYS:SG	14:I:158:LYS:NZ	2.71	0.63
47:2:715:U:H3'	47:2:720:G:H21	1.63	0.63
1:1:351:A:H61	42:l:38:ASN:HA	1.61	0.63
52:u:79:ASP:HB3	52:u:82:TYR:HB2	1.80	0.63
52:u:191:ARG:HG3	52:u:245:LYS:HG2	1.80	0.63
79:AV:202:LEU:HA	79:AV:243:LEU:HD12	1.80	0.63
1:1:1213:G:O2'	23:S:90:MET:SD	2.56	0.63
47:2:1673:G:N1	47:2:1728:A:C2	2.65	0.63
11:F:98:LYS:HG3	11:F:129:LEU:HD11	1.80	0.63
74:AQ:12:LYS:HD2	74:AQ:15:ARG:HB2	1.81	0.63
1:1:1062:A:N3	24:T:130:ARG:NH2	2.46	0.63
1:1:3158:G:O6	1:1:3292:A:N1	2.31	0.63
23:S:138:GLN:HA	23:S:141:LYS:HG2	1.80	0.63
79:AV:172:ALA:HB1	79:AV:201:THR:HA	1.79	0.63
1:1:1132:C:H2'	1:1:1133:A:H8	1.62	0.63
17:M:47:ASP:OD2	17:M:55:ARG:NH1	2.32	0.63
47:2:55:A:H3'	47:2:403:G:H22	1.64	0.63
2:3:28:C:OP1	15:J:137:ARG:NH1	2.31	0.62
30:Z:50:PRO:HG3	30:Z:131:PHE:HB3	1.80	0.62
39:i:58:ILE:HA	39:i:61:ILE:HD12	1.79	0.62
43:m:96:CYS:SG	43:m:97:ARG:N	2.72	0.62
50:s:137:ILE:HD12	69:AL:27:ASP:HB2	1.80	0.62
83:AZ:412:ARG:HB2	83:AZ:470:THR:O	1.99	0.62
1:1:2898:G:OP2	13:H:173:ARG:NH2	2.31	0.62
1:1:3138:U:H2'	1:1:3139:A:H8	1.64	0.62
1:1:3213:A:N7	17:M:124:ARG:NH1	2.46	0.62
47:2:1227:A:H1'	60:AC:44:GLY:HA2	1.81	0.62
1:1:2256:A:C2	47:2:1757:G:OP1	2.52	0.62
1:1:2838:A:H62	1:1:2850:G:H21	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1354:G:H1	47:2:1369:U:H3	1.43	0.62
56:y:72:ILE:HD12	56:y:73:SER:H	1.63	0.62
79:AV:156:VAL:HA	79:AV:169:ILE:HG22	1.79	0.62
80:AW:133:ALA:HB3	80:AW:140:TYR:HB3	1.80	0.62
59:AB:8:GLN:NE2	59:AB:14:GLN:O	2.31	0.62
1:1:1015:U:H3	1:1:1035:G:H22	1.46	0.62
47:2:1150:G:N1	82:AY:46:U:OP2	2.26	0.62
50:s:225:LEU:HB3	50:s:230:TRP:HE1	1.64	0.62
79:AV:83:ALA:HB2	79:AV:113:VAL:HG12	1.82	0.62
1:1:98:G:O3'	18:N:194:GLN:NE2	2.32	0.62
71:AN:96:VAL:HG22	71:AN:127:VAL:HG11	1.80	0.62
83:AZ:615:ARG:HH22	83:AZ:630:ALA:HA	1.65	0.62
1:1:1350:A:N6	1:1:1353:U:O2'	2.33	0.62
47:2:553:G:N2	47:2:571:G:N7	2.47	0.62
63:AF:98:ASN:HB2	63:AF:122:THR:HG22	1.81	0.62
24:T:17:ARG:HE	24:T:22:HIS:HA	1.65	0.62
85:AZ:901:SO1:O60	85:AZ:901:SO1:H652	1.99	0.62
1:1:1348:U:OP2	21:Q:38:ARG:NH2	2.33	0.62
1:1:1491:A:N7	42:l:2:ALA:N	2.47	0.62
47:2:1352:G:OP1	64:AG:66:ARG:NH2	2.33	0.62
47:2:1529:C:OP1	53:v:112:ARG:NH1	2.33	0.62
47:2:1727:G:N2	56:y:32:GLN:OE1	2.30	0.62
1:1:1127:G:H21	1:1:1129:A:H8	1.46	0.61
1:1:2256:A:H2	47:2:1757:G:OP1	1.81	0.61
7:B:190:GLU:HA	7:B:193:ASP:HB2	1.82	0.61
16:L:76:THR:HG23	16:L:101:ARG:HE	1.65	0.61
41:k:29:LYS:HE3	41:k:39:ARG:HH22	1.64	0.61
51:t:49:ILE:HG23	51:t:89:GLU:HG3	1.82	0.61
51:t:53:THR:HG23	51:t:54:ARG:HD2	1.81	0.61
1:1:562:C:OP2	17:M:77:ARG:NH1	2.33	0.61
5:P2:62:LEU:HB2	5:P2:75:PRO:HG3	1.83	0.61
14:I:189:GLU:HG2	14:I:200:LEU:HB3	1.82	0.61
21:Q:82:VAL:HA	21:Q:102:ALA:HB3	1.82	0.61
63:AF:98:ASN:ND2	63:AF:120:SER:OG	2.33	0.61
73:AP:54:VAL:HG13	73:AP:60:VAL:HG21	1.82	0.61
1:1:1383:G:OP1	8:C:203:ARG:NH1	2.34	0.61
1:1:1671:C:OP1	22:R:60:LYS:NZ	2.33	0.61
47:2:78:A:OP2	54:w:159:ARG:NH2	2.32	0.61
54:w:113:ILE:HG13	54:w:124:LEU:HD21	1.82	0.61
1:1:542:G:H1	1:1:549:U:H3	1.48	0.61
1:1:1896:A:N6	1:1:2339:C:N4	2.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:x:27:LEU:HD12	55:x:32:PRO:HG3	1.83	0.61
1:1:1029:G:H2'	1:1:1030:A:H8	1.66	0.61
38:h:85:THR:HG22	38:h:87:ALA:H	1.65	0.61
47:2:7:G:N7	50:s:205:ARG:NH1	2.49	0.61
47:2:647:G:H1	47:2:687:G:H22	1.46	0.61
47:2:1140:G:H2'	47:2:1141:G:H8	1.66	0.61
63:AF:90:ILE:HD11	63:AF:109:PRO:HA	1.83	0.61
83:AZ:171:LYS:HA	83:AZ:274:ASN:HD22	1.66	0.61
16:L:74:GLY:O	16:L:101:ARG:NH2	2.34	0.61
47:2:862:A:OP2	61:AD:64:ARG:NH2	2.33	0.61
47:2:1614:A:N6	53:v:78:ALA:O	2.34	0.61
54:w:67:VAL:HG22	54:w:69:LEU:H	1.65	0.61
83:AZ:727:PRO:HG3	83:AZ:801:TRP:HE1	1.66	0.61
15:J:98:ALA:HA	15:J:156:LYS:HB2	1.82	0.61
47:2:1678:A:OP2	56:y:42:ARG:NH1	2.34	0.61
54:w:68:LEU:H	54:w:100:ALA:HB2	1.64	0.61
83:AZ:488:VAL:HG13	83:AZ:489:VAL:HG13	1.81	0.61
1:1:1636:U:OP1	30:Z:36:HIS:HE1	1.83	0.61
47:2:354:C:H5''	56:y:16:ALA:HB2	1.83	0.61
57:z:25:ASP:HA	57:z:28:LEU:HB2	1.82	0.61
1:1:269:G:O6	18:N:15:GLN:NE2	2.33	0.61
16:L:128:ARG:HE	38:h:114:ARG:HD2	1.66	0.61
22:R:167:ARG:HA	22:R:170:ARG:HB2	1.82	0.61
31:a:75:LEU:H	31:a:114:GLY:HA3	1.64	0.61
1:1:1126:G:OP2	14:I:14:ASN:ND2	2.33	0.60
9:D:289:LYS:HD2	14:I:206:LEU:HD23	1.83	0.60
33:c:22:LYS:HB2	33:c:94:GLU:HB3	1.82	0.60
57:z:135:ALA:HB2	57:z:140:ILE:HD13	1.83	0.60
1:1:3283:U:H2'	1:1:3284:G:H8	1.66	0.60
33:c:46:ALA:H	33:c:73:GLY:HA2	1.66	0.60
47:2:1681:A:N7	54:w:65:GLN:NE2	2.49	0.60
60:AC:36:LEU:HD11	60:AC:102:GLY:HA3	1.84	0.60
83:AZ:829:LYS:HD3	83:AZ:830:GLU:H	1.66	0.60
47:2:509:G:C5'	47:2:509:G:H8	2.14	0.60
47:2:1793:G:H1	74:AQ:75:VAL:HG21	1.65	0.60
60:AC:94:ALA:HA	60:AC:97:LEU:HD13	1.82	0.60
1:1:1261:G:O2'	1:1:1262:G:N7	2.34	0.60
6:A:166:ILE:HD12	46:p:83:ILE:HG21	1.84	0.60
52:u:31:PRO:HG2	52:u:39:ARG:HG3	1.82	0.60
79:AV:73:LEU:HB3	79:AV:77:GLY:HA2	1.83	0.60
8:C:358:THR:O	23:S:26:ARG:NH1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:52:VAL:HG12	9:D:147:ASP:HB2	1.82	0.60
47:2:1588:G:O6	47:2:1608:U:O4	2.20	0.60
50:s:149:GLY:HA2	69:AL:3:ASN:HB2	1.82	0.60
50:s:157:LYS:HE2	70:AM:95:PRO:HA	1.83	0.60
19:O:4:GLU:HB2	19:O:7:VAL:HG12	1.82	0.60
34:d:49:VAL:HG12	34:d:91:SER:HB2	1.83	0.60
56:y:167:ALA:HA	56:y:183:ILE:HA	1.82	0.60
83:AZ:208:THR:HA	83:AZ:337:MET:HE3	1.83	0.60
83:AZ:729:PHE:CZ	85:AZ:901:SO1:H122	2.36	0.60
1:1:3042:U:OP2	1:1:3092:C:N4	2.33	0.60
2:3:86:U:O2'	11:F:218:ARG:NH1	2.34	0.60
5:P2:79:SER:HA	5:P2:82:ILE:HD12	1.84	0.60
14:I:192:ASP:HA	14:I:197:VAL:HG22	1.83	0.60
15:J:12:LEU:HD23	15:J:133:ARG:HE	1.66	0.60
18:N:155:VAL:O	18:N:162:ARG:NH1	2.34	0.60
58:AA:8:ARG:HH12	58:AA:46:LEU:HD22	1.66	0.60
58:AA:58:GLN:HB3	58:AA:65:TYR:HB2	1.84	0.60
66:AI:101:LEU:H	66:AI:104:ASN:HB3	1.66	0.60
1:1:1712:G:N1	1:1:1731:A:OP2	2.34	0.60
1:1:215:G:OP1	29:Y:12:ARG:NH1	2.35	0.60
1:1:1533:U:O4	1:1:1587:A:N7	2.35	0.60
4:P0:35:SER:O	4:P0:39:HIS:ND1	2.35	0.60
17:M:124:ARG:NH2	19:O:199:TYR:OH	2.35	0.60
44:n:21:ARG:HH12	47:2:1653:C:H4'	1.66	0.60
47:2:933:A:OP1	49:r:116:LYS:NZ	2.32	0.60
52:u:181:VAL:HG12	52:u:227:VAL:HG12	1.82	0.60
1:1:353:G:H22	1:1:364:G:H3'	1.67	0.60
1:1:1475:A:H4'	34:d:57:GLN:HE22	1.67	0.60
16:L:75:PHE:HB2	16:L:97:VAL:HG12	1.84	0.60
37:g:44:CYS:SG	37:g:45:GLY:N	2.74	0.60
38:h:83:LYS:NZ	40:j:66:TYR:OH	2.31	0.60
53:v:112:ARG:O	53:v:116:HIS:ND1	2.35	0.60
1:1:278:U:H3	1:1:287:G:H1	1.50	0.59
18:N:68:ARG:HG3	18:N:128:LYS:HG3	1.84	0.59
37:g:42:PRO:HB2	37:g:51:LEU:HD12	1.83	0.59
47:2:472:U:H2'	47:2:473:A:H8	1.67	0.59
57:z:41:GLU:OE1	57:z:44:ARG:NE	2.35	0.59
42:l:28:ARG:NH2	42:l:36:ARG:O	2.33	0.59
1:1:874:U:N3	1:1:2978:U:OP1	2.35	0.59
9:D:107:ARG:NH2	9:D:169:GLY:O	2.35	0.59
12:G:157:VAL:HG22	12:G:159:PRO:HD2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:S:109:ASP:OD1	23:S:113:ARG:NH1	2.35	0.59
54:w:2:LYS:HB2	54:w:108:VAL:HG12	1.82	0.59
54:w:85:ARG:NH2	72:AO:119:PHE:O	2.35	0.59
60:AC:62:LEU:H	60:AC:90:LYS:HG3	1.68	0.59
83:AZ:399:ARG:HE	83:AZ:451:GLY:HA2	1.66	0.59
1:1:1233:G:O2'	4:P0:43:LYS:NZ	2.26	0.59
1:1:1714:A:H62	1:1:1730:G:N2	2.00	0.59
1:1:2487:U:H3'	1:1:2488:A:H8	1.68	0.59
13:H:115:ARG:NH2	13:H:120:ASP:O	2.34	0.59
47:2:752:A:N1	47:2:797:G:O6	2.35	0.59
47:2:803:A:N7	55:x:104:ARG:NH2	2.50	0.59
48:q:33:GLN:NE2	69:AL:63:GLY:O	2.35	0.59
83:AZ:212:GLY:HA3	83:AZ:218:TRP:O	2.02	0.59
83:AZ:588:LEU:HD11	83:AZ:716:GLY:HA3	1.83	0.59
1:1:3092:C:O2'	1:1:3094:A:OP2	2.21	0.59
16:L:140:SER:HB2	16:L:143:ALA:HB3	1.84	0.59
47:2:960:U:OP2	61:AD:55:ARG:NH1	2.35	0.59
83:AZ:149:GLU:OE1	83:AZ:352:ARG:NH2	2.35	0.59
1:1:668:G:O2'	21:Q:164:ARG:NH1	2.35	0.59
1:1:683:U:OP2	16:L:28:GLN:NE2	2.35	0.59
1:1:696:C:OP2	8:C:119:ARG:NH2	2.32	0.59
1:1:1106:G:O2'	32:b:25:LYS:NZ	2.36	0.59
1:1:1281:G:N2	4:P0:31:ASP:OD1	2.35	0.59
1:1:1420:C:OP2	8:C:193:LYS:NZ	2.36	0.59
47:2:1299:G:OP1	50:s:212:LYS:NZ	2.35	0.59
69:AL:70:ASN:HB3	69:AL:83:TRP:HB2	1.84	0.59
1:1:1194:G:H2'	1:1:1195:A:H8	1.68	0.59
1:1:3056:U:O2	34:d:28:ARG:NH2	2.35	0.59
1:1:3185:U:HO2'	23:S:170:THR:HG1	1.48	0.59
47:2:197:A:N1	56:y:138:ASN:ND2	2.51	0.59
47:2:478:A:N1	47:2:510:G:O6	2.35	0.59
47:2:508:U:H2'	47:2:509:G:H5''	1.85	0.59
51:t:120:TYR:HA	51:t:123:VAL:HG22	1.85	0.59
52:u:183:VAL:HB	52:u:190:GLY:H	1.68	0.59
25:U:58:GLU:HG3	25:U:63:VAL:HG22	1.84	0.59
47:2:1354:G:N1	47:2:1369:U:N3	2.46	0.59
54:w:175:ILE:HD11	54:w:178:LEU:HD12	1.85	0.59
68:AK:55:PRO:HA	68:AK:91:ILE:HG23	1.85	0.59
83:AZ:416:PRO:O	83:AZ:477:ASN:ND2	2.35	0.59
1:1:1523:U:O2	28:X:111:ASN:ND2	2.35	0.59
1:1:1739:U:O2	37:g:41:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1863:G:O2'	22:R:82:LYS:NZ	2.35	0.59
1:1:2947:G:OP1	1:1:2982:A:N6	2.36	0.59
13:H:90:MET:N	13:H:90:MET:SD	2.72	0.59
47:2:1533:C:O2'	47:2:1539:G:N7	2.34	0.59
48:q:53:THR:HG22	48:q:161:PRO:HG2	1.85	0.59
1:1:1145:G:OP1	35:e:44:ARG:NH1	2.36	0.59
1:1:1723:A:OP1	22:R:128:LYS:NZ	2.35	0.59
7:B:269:GLN:NE2	7:B:270:ARG:O	2.36	0.59
16:L:27:ASP:OD2	16:L:31:LYS:NZ	2.34	0.59
47:2:1158:C:OP2	47:2:1161:C:N4	2.36	0.59
83:AZ:27:HIS:O	83:AZ:32:LYS:NZ	2.36	0.59
1:1:2981:U:OP2	7:B:244:ARG:NH2	2.36	0.58
7:B:219:ALA:HB3	7:B:329:PRO:HG2	1.85	0.58
42:l:28:ARG:HA	42:l:33:ASN:HA	1.84	0.58
47:2:2:A:O2'	50:s:199:GLN:NE2	2.36	0.58
47:2:1187:U:H2'	47:2:1188:G:H8	1.67	0.58
47:2:1572:G:OP1	47:2:1574:G:N2	2.36	0.58
1:1:908:G:N2	1:1:2609:A:OP1	2.36	0.58
16:L:170:LEU:HD21	31:a:147:LEU:HD22	1.85	0.58
47:2:868:G:OP1	61:AD:121:ARG:NH1	2.36	0.58
47:2:1311:U:N3	47:2:1314:U:OP2	2.35	0.58
47:2:1790:A:OP1	74:AQ:10:ARG:NH1	2.37	0.58
83:AZ:237:LYS:O	83:AZ:241:MET:HB3	2.03	0.58
1:1:280:U:O2'	18:N:182:ASN:ND2	2.36	0.58
1:1:608:A:OP1	8:C:315:LYS:NZ	2.35	0.58
64:AG:39:VAL:HG12	64:AG:41:PRO:HD3	1.85	0.58
26:V:81:GLN:O	26:V:98:ASN:ND2	2.36	0.58
47:2:1022:C:O2'	47:2:1125:A:N1	2.36	0.58
47:2:1638:G:O5'	47:2:1638:G:H8	1.85	0.58
1:1:1336:U:H2'	1:1:1337:A:H8	1.68	0.58
11:F:97:PRO:HA	11:F:100:ARG:HG2	1.85	0.58
44:n:21:ARG:NH2	47:2:1653:C:O3'	2.36	0.58
47:2:778:G:H22	72:AO:10:ARG:HH12	1.51	0.58
47:2:1211:A:N3	63:AF:97:TYR:OH	2.33	0.58
47:2:1301:U:OP2	50:s:97:ARG:NH2	2.36	0.58
58:AA:76:LEU:HD12	58:AA:80:LEU:HB2	1.85	0.58
83:AZ:618:ILE:O	83:AZ:622:ASP:HB2	2.03	0.58
1:1:713:U:H5''	16:L:171:ARG:HH12	1.68	0.58
1:1:1492:G:N7	42:l:2:ALA:N	2.52	0.58
1:1:3200:G:OP2	17:M:8:LYS:NZ	2.37	0.58
47:2:639:U:OP1	55:x:117:THR:OG1	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:815:G:N2	59:AB:150:ASN:OD1	2.37	0.58
47:2:1166:A:H4'	47:2:1587:A:H4'	1.84	0.58
47:2:1181:U:O2	63:AF:127:ARG:NH1	2.36	0.58
47:2:1397:U:H5''	47:2:1399:C:H42	1.68	0.58
47:2:1552:U:OP2	63:AF:43:ARG:NH2	2.37	0.58
70:AM:15:ASN:HD21	70:AM:72:CYS:H	1.52	0.58
1:1:816:A:H5''	1:1:920:A:H62	1.69	0.58
1:1:1193:A:N6	1:1:1314:C:N4	2.49	0.58
1:1:2701:U:OP1	24:T:17:ARG:NH2	2.37	0.58
20:P:30:ARG:HA	20:P:119:VAL:HG21	1.85	0.58
47:2:819:G:H1'	47:2:820:U:H2'	1.85	0.58
47:2:1489:U:OP2	47:2:1515:A:N6	2.36	0.58
51:t:211:PRO:HG3	65:AH:19:ARG:HD3	1.85	0.58
83:AZ:521:TYR:HE2	85:AZ:901:SO1:O14	1.86	0.58
1:1:31:C:OP2	18:N:187:ARG:NH2	2.35	0.58
1:1:1125:U:H2'	1:1:1126:G:H8	1.69	0.58
5:P2:66:ASN:HD21	5:P2:67:ARG:NH1	2.02	0.58
10:E:41:ILE:HD13	10:E:51:ARG:HB3	1.86	0.58
34:d:13:THR:OG1	34:d:72:ARG:NH1	2.37	0.58
47:2:1102:G:OP2	71:AN:7:ARG:NH2	2.37	0.58
53:v:143:ARG:HA	53:v:167:ARG:HH12	1.69	0.58
83:AZ:676:ILE:O	83:AZ:823:ARG:NH2	2.37	0.58
1:1:436:A:OP2	1:1:621:A:N6	2.36	0.58
1:1:3070:A:OP1	22:R:62:ARG:NH1	2.37	0.58
30:Z:12:VAL:HB	30:Z:81:LEU:HB3	1.86	0.58
47:2:1288:G:N7	47:2:1314:U:O2'	2.32	0.58
56:y:191:PHE:HA	56:y:194:ARG:HG2	1.86	0.58
83:AZ:220:PHE:HB3	83:AZ:328:LEU:HD11	1.84	0.58
1:1:2655:U:O4	45:o:8:ARG:NH1	2.37	0.58
3:4:156:U:OP2	12:G:84:ARG:NH2	2.36	0.58
6:A:180:LEU:HD21	46:p:26:VAL:HG21	1.86	0.58
13:H:47:LYS:HD3	13:H:50:ASN:H	1.67	0.58
14:I:38:LYS:NZ	14:I:83:ASP:O	2.36	0.58
47:2:1230:A:H8	47:2:1255:G:H21	1.52	0.58
47:2:1346:A:OP2	47:2:1348:A:N6	2.37	0.58
47:2:1497:U:N3	47:2:1511:U:O2	2.37	0.58
83:AZ:631:ARG:HH11	83:AZ:648:ASP:HB3	1.68	0.58
1:1:1238:C:H1'	5:P2:138:SER:HB2	1.84	0.57
1:1:2386:A:H62	1:1:2993:G:H21	1.52	0.57
1:1:2647:A:H4'	14:I:22:TYR:HB2	1.86	0.57
1:1:2664:C:OP2	15:J:142:LYS:NZ	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:133:TYR:HB3	6:A:168:VAL:HG12	1.85	0.57
31:a:101:VAL:HG22	31:a:124:ILE:HD11	1.86	0.57
83:AZ:819:VAL:O	83:AZ:823:ARG:HB2	2.04	0.57
1:1:2562:A:H1'	12:G:30:THR:HG22	1.85	0.57
5:P2:74:VAL:HB	5:P2:80:LEU:HD23	1.85	0.57
7:B:4:ARG:HD2	7:B:7:GLU:HA	1.86	0.57
47:2:18:C:O3'	71:AN:109:ARG:NH2	2.37	0.57
47:2:304:U:O2	59:AB:69:LYS:NZ	2.37	0.57
47:2:328:A:OP1	59:AB:56:LYS:NZ	2.37	0.57
64:AG:114:ARG:H	64:AG:116:LEU:HD23	1.69	0.57
83:AZ:732:GLU:HA	83:AZ:768:VAL:O	2.05	0.57
1:1:943:U:N3	1:1:1431:G:OP1	2.37	0.57
5:P2:77:ALA:H	5:P2:80:LEU:HD22	1.68	0.57
7:B:346:THR:HG23	7:B:351:LEU:HD21	1.85	0.57
23:S:12:ARG:HH12	23:S:15:PRO:HD3	1.70	0.57
47:2:127:G:O6	54:w:199:GLN:NE2	2.34	0.57
47:2:215:A:H62	47:2:242:U:H2'	1.68	0.57
51:t:7:LYS:HD2	68:AK:88:LYS:HE2	1.85	0.57
63:AF:123:TYR:OH	66:AI:126:ARG:NH2	2.37	0.57
83:AZ:728:VAL:HA	83:AZ:773:PRO:HA	1.86	0.57
10:E:30:LEU:HD11	10:E:34:LEU:HD12	1.86	0.57
46:p:38:ASP:HB3	46:p:45:LYS:HB3	1.87	0.57
55:x:98:ILE:HD11	55:x:118:LEU:HA	1.85	0.57
83:AZ:725:GLN:NE2	83:AZ:726:GLU:O	2.38	0.57
14:I:30:LYS:NZ	14:I:66:GLU:OE2	2.37	0.57
47:2:129:U:OP1	47:2:131:C:N4	2.38	0.57
48:q:112:THR:OG1	48:q:113:ARG:N	2.37	0.57
1:1:75:G:H3'	1:1:76:G:H8	1.70	0.57
1:1:157:A:H62	1:1:264:G:H21	1.51	0.57
1:1:286:U:H2'	1:1:287:G:H8	1.69	0.57
1:1:1874:A:N7	22:R:20:ARG:NH1	2.52	0.57
4:P0:11:TYR:OH	4:P0:61:ARG:NH2	2.37	0.57
44:n:7:LYS:NZ	47:2:1774:G:OP1	2.36	0.57
47:2:540:G:OP1	47:2:541:A:N6	2.37	0.57
47:2:1229:G:H21	47:2:1256:A:H62	1.51	0.57
1:1:1282:G:O4'	4:P0:83:ASN:ND2	2.38	0.57
8:C:107:ARG:O	18:N:203:ARG:NH2	2.38	0.57
13:H:1:MET:SD	23:S:113:ARG:NH2	2.77	0.57
15:J:108:GLU:HG2	15:J:122:ILE:HD11	1.87	0.57
23:S:28:ARG:HH21	23:S:99:ARG:HH22	1.53	0.57
29:Y:49:PRO:O	29:Y:115:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Y:59:VAL:HG13	29:Y:60:ARG:HG2	1.87	0.57
46:p:10:ILE:HD13	46:p:31:ILE:HB	1.87	0.57
54:w:216:LEU:HA	54:w:219:ARG:HB3	1.87	0.57
83:AZ:746:VAL:HA	83:AZ:749:LYS:HG2	1.86	0.57
1:1:1119:C:H2'	1:1:1120:A:H8	1.69	0.57
1:1:2417:U:O2'	1:1:2966:G:N2	2.37	0.57
10:E:52:VAL:HG21	10:E:65:ILE:HG23	1.87	0.57
47:2:639:U:H5''	55:x:101:LYS:HD2	1.86	0.57
47:2:1220:C:H2'	47:2:1221:A:H8	1.70	0.57
51:t:225:TYR:HB2	79:AV:189:GLU:HA	1.85	0.57
52:u:10:LYS:HA	52:u:27:TYR:HA	1.86	0.57
1:1:780:A:N7	21:Q:178:ARG:NH2	2.50	0.57
7:B:222:LYS:HD2	7:B:331:ASN:HB3	1.87	0.57
16:L:22:VAL:HG12	18:N:197:LEU:HB2	1.86	0.57
17:M:108:ARG:NH1	19:O:195:ALA:O	2.36	0.57
26:V:36:ILE:HD11	26:V:58:VAL:HG11	1.87	0.57
47:2:706:A:N6	47:2:733:A:OP1	2.38	0.57
51:t:105:MET:HA	51:t:108:LYS:HD3	1.87	0.57
83:AZ:539:GLU:O	83:AZ:543:GLN:CB	2.52	0.57
1:1:2351:U:H2'	1:1:2352:A:H8	1.70	0.57
6:A:180:LEU:HD12	46:p:18:TYR:HB3	1.87	0.57
36:f:25:PRO:O	36:f:88:ASN:ND2	2.36	0.57
47:2:1665:U:O2	47:2:1736:G:N2	2.37	0.57
47:2:50:C:OP1	47:2:423:G:N2	2.37	0.56
47:2:862:A:H62	61:AD:70:LYS:HE2	1.69	0.56
47:2:1539:G:H21	67:AJ:45:MET:HG3	1.69	0.56
51:t:173:ARG:HB2	51:t:184:ILE:HB	1.87	0.56
63:AF:98:ASN:ND2	63:AF:121:ILE:O	2.38	0.56
66:AI:53:ASP:HB3	66:AI:56:LYS:HG3	1.86	0.56
5:P2:66:ASN:HD21	5:P2:67:ARG:HH11	1.52	0.56
20:P:167:ARG:O	36:f:60:ARG:NH2	2.38	0.56
23:S:80:ARG:NH2	24:T:154:VAL:O	2.38	0.56
45:o:24:LYS:N	45:o:73:GLU:O	2.38	0.56
47:2:774:A:N6	47:2:786:C:O2	2.37	0.56
48:q:84:ARG:NH2	65:AH:82:ASP:O	2.37	0.56
58:AA:26:ASP:O	58:AA:39:ASN:ND2	2.38	0.56
83:AZ:711:ARG:NH1	83:AZ:837:GLU:OE2	2.34	0.56
1:1:67:A:O2'	1:1:315:C:O2	2.23	0.56
1:1:203:G:H2'	1:1:204:A:H8	1.70	0.56
1:1:1221:A:N3	4:P0:5:ARG:NH2	2.51	0.56
1:1:3379:C:H4'	7:B:315:GLY:HA2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:74:ILE:HG22	8:C:76:ARG:HH21	1.69	0.56
21:Q:38:ARG:HG3	21:Q:39:ARG:HG3	1.87	0.56
29:Y:63:LYS:HB3	29:Y:66:GLN:HE22	1.70	0.56
44:n:21:ARG:NH1	47:2:1117:U:OP1	2.38	0.56
47:2:705:U:O4	47:2:707:A:N6	2.39	0.56
47:2:705:U:H2'	47:2:706:A:H2'	1.88	0.56
47:2:800:U:H2'	47:2:801:G:H8	1.71	0.56
47:2:1471:A:H1'	47:2:1540:G:H1'	1.86	0.56
47:2:1611:A:H8	53:v:99:MET:HE1	1.70	0.56
52:u:255:ARG:O	52:u:259:GLN:NE2	2.38	0.56
67:AJ:31:PRO:HG2	67:AJ:100:ILE:HG23	1.87	0.56
67:AJ:86:ARG:O	67:AJ:89:ARG:NE	2.36	0.56
73:AP:81:ARG:HH22	73:AP:94:LYS:HZ3	1.53	0.56
79:AV:240:VAL:HG22	79:AV:256:THR:HG22	1.87	0.56
83:AZ:708:THR:O	83:AZ:710:ARG:NH1	2.38	0.56
1:1:302:U:O3'	18:N:179:LYS:NZ	2.36	0.56
1:1:1268:G:N3	1:1:1274:A:N6	2.53	0.56
1:1:1566:A:O2'	1:1:1573:G:O6	2.20	0.56
8:C:359:LEU:HD11	23:S:64:ILE:HG21	1.88	0.56
36:f:85:PHE:HE2	36:f:89:LEU:HD23	1.69	0.56
39:i:91:ASN:HA	39:i:94:ILE:HG22	1.88	0.56
40:j:8:PHE:HD1	40:j:11:ARG:HE	1.51	0.56
47:2:1132:A:H2'	47:2:1133:A:H8	1.70	0.56
47:2:1765:A:H62	47:2:1768:G:H1	1.52	0.56
63:AF:43:ARG:HE	63:AF:47:ARG:HD2	1.71	0.56
71:AN:62:LYS:HE3	71:AN:118:PRO:HD3	1.87	0.56
83:AZ:519:LEU:O	83:AZ:531:ALA:HB3	2.05	0.56
83:AZ:681:MET:N	83:AZ:681:MET:SD	2.79	0.56
1:1:677:A:N6	1:1:785:G:O2'	2.36	0.56
1:1:852:U:H2'	1:1:853:G:H8	1.69	0.56
1:1:2301:U:H2'	1:1:2302:G:H8	1.69	0.56
1:1:2435:G:N2	1:1:2514:U:O4	2.39	0.56
2:3:5:G:O2'	9:D:63:GLN:NE2	2.39	0.56
47:2:1099:U:O4	50:s:168:ARG:NH1	2.39	0.56
47:2:1242:A:N6	47:2:1244:A:N7	2.54	0.56
57:z:178:ALA:HA	57:z:181:ALA:HB3	1.87	0.56
68:AK:102:ARG:HB2	68:AK:105:GLN:HE21	1.71	0.56
1:1:1055:A:N3	2:3:81:U:O2'	2.39	0.56
1:1:2828:G:OP2	14:I:7:ARG:NH2	2.39	0.56
1:1:3082:C:H2'	1:1:3083:G:H8	1.71	0.56
8:C:235:LEU:HA	8:C:238:LEU:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:155:LYS:HE3	11:F:158:LYS:HG3	1.86	0.56
27:W:2:LYS:HB3	27:W:15:PRO:HG2	1.88	0.56
47:2:1476:C:O2'	47:2:1539:G:N2	2.39	0.56
50:s:37:PRO:HG2	50:s:43:ARG:HG2	1.86	0.56
52:u:179:LYS:O	52:u:194:THR:OG1	2.20	0.56
62:AE:20:TYR:HD1	62:AE:84:ARG:HE	1.51	0.56
1:1:151:A:OP2	18:N:147:ARG:NH2	2.38	0.56
1:1:1639:C:H2'	1:1:1640:G:H8	1.70	0.56
1:1:2756:C:O2	24:T:8:ARG:NH2	2.39	0.56
1:1:3158:G:N1	1:1:3292:A:C2	2.64	0.56
47:2:58:U:OP1	47:2:456:A:O2'	2.23	0.56
47:2:513:U:O2'	57:z:131:GLN:OE1	2.23	0.56
47:2:753:A:N1	47:2:754:A:N6	2.53	0.56
49:r:213:ARG:HD3	49:r:214:LYS:HG2	1.86	0.56
65:AH:31:ASN:O	65:AH:35:CYS:N	2.37	0.56
1:1:1560:G:O6	28:X:33:ARG:NH1	2.38	0.56
1:1:2162:U:OP1	6:A:234:LYS:NZ	2.38	0.56
12:G:239:GLY:O	12:G:243:GLN:N	2.38	0.56
12:G:252:ASN:HA	12:G:256:ALA:HB2	1.87	0.56
28:X:125:ARG:NH2	28:X:126:LEU:O	2.38	0.56
47:2:167:U:H1'	54:w:133:LEU:HB3	1.87	0.56
47:2:865:A:OP1	70:AM:3:ARG:NH2	2.39	0.56
63:AF:115:TYR:HB2	63:AF:118:GLU:HG3	1.87	0.56
71:AN:62:LYS:HD3	71:AN:116:ASP:O	2.05	0.56
79:AV:66:HIS:HD2	79:AV:85:TRP:HB2	1.71	0.56
83:AZ:544:ASP:O	83:AZ:549:HIS:ND1	2.39	0.56
1:1:865:U:H2'	1:1:866:A:H8	1.71	0.56
47:2:444:C:OP2	72:AO:108:ARG:NH2	2.35	0.56
66:AI:99:HIS:O	66:AI:104:ASN:ND2	2.39	0.56
71:AN:99:ASN:ND2	83:AZ:526:GLY:O	2.39	0.56
77:AT:21:CYS:SG	77:AT:22:ARG:N	2.79	0.56
79:AV:85:TRP:HA	79:AV:110:VAL:H	1.71	0.56
83:AZ:718:LEU:HA	83:AZ:722:PRO:HG2	1.87	0.56
1:1:655:C:H2'	1:1:656:A:H8	1.71	0.56
39:i:93:ILE:O	39:i:97:SER:N	2.37	0.56
47:2:388:G:OP2	47:2:423:G:O2'	2.24	0.56
47:2:547:U:OP1	71:AN:139:LYS:NZ	2.38	0.56
53:v:178:GLY:HA2	53:v:209:TYR:HD2	1.69	0.56
63:AF:124:THR:O	63:AF:127:ARG:NH2	2.39	0.56
68:AK:50:LEU:HD21	68:AK:93:LEU:HB2	1.88	0.56
83:AZ:283:ARG:O	83:AZ:287:ALA:CB	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1541:G:C6	1:1:1555:U:N3	2.73	0.55
1:1:1561:G:N7	28:X:36:LYS:NZ	2.46	0.55
1:1:2245:C:O2'	6:A:220:GLY:O	2.23	0.55
1:1:2723:U:H4'	24:T:89:LEU:HD12	1.87	0.55
1:1:2772:C:H4'	1:1:2773:C:H5'	1.87	0.55
8:C:140:HIS:HE1	8:C:204:GLY:HA2	1.71	0.55
30:Z:88:ASP:O	30:Z:121:ARG:NH2	2.39	0.55
47:2:93:A:O2'	47:2:398:G:N2	2.38	0.55
63:AF:60:LEU:HD12	63:AF:61:ARG:HH11	1.71	0.55
83:AZ:30:HIS:O	83:AZ:159:LYS:NZ	2.39	0.55
83:AZ:228:ARG:NH1	83:AZ:304:GLU:OE1	2.39	0.55
83:AZ:228:ARG:HH12	83:AZ:303:LEU:HD11	1.70	0.55
1:1:105:C:H2'	1:1:106:A:H8	1.71	0.55
2:3:46:A:OP2	9:D:158:ARG:NH1	2.40	0.55
36:f:27:VAL:HG11	36:f:82:ARG:HD2	1.88	0.55
47:2:478:A:H2	47:2:510:G:N1	2.01	0.55
47:2:867:G:H1	47:2:961:U:H3	1.53	0.55
47:2:938:G:N2	47:2:941:A:OP2	2.38	0.55
47:2:1008:G:OP1	62:AE:135:ARG:NH1	2.38	0.55
47:2:1267:G:H21	47:2:1448:G:H5'	1.70	0.55
47:2:1542:G:H3'	67:AJ:87:GLY:HA2	1.89	0.55
47:2:1575:G:N2	81:AX:41:U:O2'	2.38	0.55
47:2:1637:C:C5'	82:AY:48:U:C4	2.89	0.55
83:AZ:574:THR:HA	83:AZ:588:LEU:O	2.06	0.55
1:1:768:C:O2'	16:L:183:ARG:NH2	2.39	0.55
1:1:2471:U:O2	1:1:2473:C:N4	2.39	0.55
9:D:69:ILE:HG23	24:T:31:LEU:HD12	1.88	0.55
19:O:74:ARG:NH1	19:O:145:VAL:O	2.39	0.55
47:2:1055:U:H3	47:2:1064:G:H1	1.55	0.55
52:u:54:TYR:O	72:AO:20:ARG:NH1	2.38	0.55
79:AV:10:ARG:NH1	79:AV:50:ASP:O	2.40	0.55
1:1:627:U:H2'	1:1:628:A:C8	2.41	0.55
1:1:3213:A:OP1	17:M:128:ARG:NH2	2.39	0.55
21:Q:182:LYS:HD3	31:a:55:LYS:H	1.71	0.55
23:S:13:ARG:HD3	23:S:51:VAL:HG23	1.89	0.55
47:2:939:A:OP1	61:AD:114:ARG:NH2	2.37	0.55
47:2:1345:A:N6	47:2:1377:U:O2'	2.36	0.55
47:2:1354:G:O6	47:2:1369:U:O4	2.25	0.55
47:2:1471:A:N1	47:2:1474:G:N2	2.54	0.55
57:z:108:ARG:NH2	57:z:144:PRO:O	2.39	0.55
64:AG:100:GLN:O	64:AG:104:GLU:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:7:PRO:HG2	10:E:10:TYR:HE1	1.71	0.55
12:G:68:ARG:NH1	12:G:237:ILE:O	2.39	0.55
47:2:958:U:O2'	61:AD:55:ARG:NH1	2.39	0.55
52:u:57:ASN:HB2	52:u:60:GLU:HB2	1.89	0.55
83:AZ:382:VAL:HG21	83:AZ:396:ALA:HB1	1.88	0.55
1:1:92:G:OP2	45:o:42:ARG:NH2	2.40	0.55
1:1:1233:G:OP1	4:P0:36:GLN:NE2	2.40	0.55
1:1:2673:A:N6	1:1:2681:U:O4	2.39	0.55
35:e:60:ASN:HB3	35:e:63:THR:HG22	1.87	0.55
47:2:385:A:H5''	56:y:22:ARG:HB3	1.87	0.55
47:2:699:U:O2	47:2:739:G:N2	2.35	0.55
55:x:35:LYS:HA	55:x:38:LEU:HB2	1.88	0.55
1:1:2528:G:H5''	12:G:248:LYS:HD2	1.89	0.55
1:1:2553:U:O4	37:g:98:GLN:NE2	2.39	0.55
1:1:3266:G:OP2	10:E:70:LYS:NZ	2.32	0.55
18:N:94:TYR:OH	18:N:96:ARG:NH2	2.40	0.55
23:S:112:ALA:O	23:S:115:ARG:NH1	2.40	0.55
24:T:39:ILE:HD12	24:T:102:ARG:HB2	1.89	0.55
29:Y:112:ASP:O	29:Y:116:LYS:NZ	2.35	0.55
47:2:151:G:N3	54:w:13:GLN:NE2	2.55	0.55
47:2:1280:C:H5''	68:AK:69:LYS:HE2	1.89	0.55
49:r:134:VAL:HG12	49:r:219:LYS:HB2	1.89	0.55
79:AV:124:SER:O	79:AV:132:LYS:N	2.38	0.55
1:1:281:G:N7	18:N:182:ASN:ND2	2.51	0.55
1:1:1785:U:H5''	37:g:38:LEU:HD11	1.87	0.55
1:1:3333:G:H22	1:1:3369:G:H1'	1.71	0.55
6:A:79:ASN:HD21	6:A:99:GLY:HA2	1.72	0.55
14:I:48:LEU:HA	14:I:178:ARG:HH22	1.71	0.55
16:L:144:THR:OG1	38:h:119:LYS:NZ	2.40	0.55
47:2:259:U:O2	56:y:178:ARG:NH1	2.40	0.55
47:2:486:G:O6	47:2:501:U:O4	2.24	0.55
47:2:1035:G:H2'	47:2:1036:A:H8	1.72	0.55
47:2:1236:A:N6	47:2:1250:U:O2	2.40	0.55
77:AT:21:CYS:SG	77:AT:39:CYS:N	2.77	0.55
1:1:877:C:O2'	1:1:880:G:O2'	2.23	0.55
1:1:916:G:OP2	6:A:205:ASN:ND2	2.40	0.55
1:1:2131:A:H61	46:p:18:TYR:HD1	1.55	0.55
1:1:3325:G:OP1	34:d:70:ARG:NH2	2.40	0.55
10:E:42:LEU:HA	10:E:84:VAL:HG23	1.88	0.55
12:G:64:ILE:HD11	12:G:68:ARG:HH21	1.72	0.55
24:T:112:ASN:HB3	24:T:128:LEU:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:v:200:ASN:HB3	53:v:205:SER:HB2	1.89	0.55
70:AM:24:GLN:HE21	70:AM:62:VAL:HG23	1.70	0.55
1:1:894:G:H4'	1:1:895:A:H5'	1.89	0.55
1:1:3080:G:OP1	34:d:65:LYS:NZ	2.37	0.55
3:4:81:U:O2'	3:4:83:C:OP2	2.21	0.55
51:t:71:LEU:HA	51:t:74:GLN:HB3	1.89	0.55
59:AB:111:VAL:HG23	59:AB:139:VAL:HG11	1.89	0.55
62:AE:22:SER:OG	62:AE:23:PHE:N	2.39	0.55
83:AZ:675:PRO:HG2	83:AZ:676:ILE:HD12	1.89	0.55
1:1:348:A:N3	1:1:352:A:O2'	2.38	0.54
1:1:903:U:H2'	1:1:904:A:H8	1.72	0.54
1:1:2167:A:OP1	18:N:72:LYS:NZ	2.39	0.54
1:1:3153:U:OP2	1:1:3293:U:O2'	2.25	0.54
2:3:38:U:N3	2:3:41:G:OP2	2.40	0.54
5:P2:77:ALA:HB3	5:P2:80:LEU:HD13	1.89	0.54
47:2:795:U:OP1	70:AM:82:LYS:NZ	2.39	0.54
53:v:196:GLU:O	53:v:200:ASN:ND2	2.37	0.54
47:2:1341:A:O2'	79:AV:102:ARG:NH1	2.39	0.54
66:AI:33:THR:HA	66:AI:38:VAL:HG11	1.89	0.54
66:AI:88:ARG:HD3	66:AI:98:TYR:HD2	1.72	0.54
79:AV:28:GLY:HA3	79:AV:76:ASP:HA	1.90	0.54
1:1:2179:C:O2'	6:A:130:SER:O	2.23	0.54
6:A:30:ARG:O	6:A:163:ARG:NH1	2.39	0.54
47:2:1067:C:OP1	49:r:151:LYS:NZ	2.40	0.54
66:AI:81:ILE:HG22	66:AI:83:ALA:H	1.72	0.54
68:AK:68:ARG:NH2	68:AK:76:SER:O	2.40	0.54
1:1:785:G:H1	21:Q:90:ASP:HA	1.72	0.54
1:1:2150:G:O6	1:1:2187:G:N2	2.40	0.54
47:2:416:A:OP2	47:2:417:A:N6	2.40	0.54
47:2:1191:U:O2'	47:2:1193:A:N7	2.41	0.54
49:r:76:SER:OG	49:r:78:ASP:OD1	2.25	0.54
57:z:34:PHE:HD1	57:z:122:VAL:HG11	1.72	0.54
74:AQ:28:LYS:NZ	74:AQ:29:SER:O	2.35	0.54
79:AV:252:LEU:O	79:AV:263:PHE:N	2.34	0.54
1:1:445:G:O6	1:1:490:C:O2'	2.24	0.54
1:1:677:A:OP2	21:Q:88:THR:OG1	2.25	0.54
1:1:1363:A:OP1	11:F:160:ARG:NH1	2.40	0.54
1:1:1789:G:H2'	1:1:1790:G:H8	1.72	0.54
1:1:3174:A:OP1	36:f:97:SER:OG	2.26	0.54
1:1:3217:C:H5'	1:1:3219:G:H21	1.72	0.54
11:F:88:ARG:HB2	11:F:108:LEU:HD23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L:161:ASP:OD2	31:a:139:ARG:NH1	2.40	0.54
19:O:121:PRO:HG3	23:S:164:SER:HB3	1.90	0.54
25:U:22:PRO:HB2	25:U:28:PHE:HB2	1.90	0.54
33:c:26:GLY:O	33:c:30:THR:OG1	2.25	0.54
47:2:859:A:O2'	61:AD:73:ARG:NH2	2.37	0.54
47:2:1586:A:H62	47:2:1610:G:N2	2.06	0.54
72:AO:57:VAL:HA	72:AO:73:GLY:HA2	1.90	0.54
83:AZ:211:PHE:O	83:AZ:219:ALA:HA	2.06	0.54
83:AZ:710:ARG:O	83:AZ:711:ARG:NE	2.40	0.54
1:1:1388:U:O2'	35:e:99:ASN:O	2.23	0.54
1:1:2361:A:HO2'	35:e:25:TYR:HH	1.49	0.54
1:1:2362:C:O2	1:1:2377:G:N2	2.40	0.54
3:4:36:G:O2'	3:4:104:A:N1	2.41	0.54
47:2:868:G:H22	47:2:960:U:H3	1.56	0.54
47:2:1398:U:OP1	47:2:1400:A:N6	2.40	0.54
47:2:1544:U:O4	47:2:1545:A:N6	2.41	0.54
47:2:1596:C:OP2	77:AT:32:ARG:NH2	2.41	0.54
1:1:700:C:H2'	1:1:701:G:H8	1.72	0.54
1:1:726:G:N1	1:1:743:C:OP2	2.38	0.54
1:1:975:C:O2'	21:Q:144:ARG:NH1	2.40	0.54
17:M:112:LEU:HD12	17:M:116:GLU:HB2	1.90	0.54
20:P:118:GLN:HB3	20:P:147:GLU:HG3	1.88	0.54
24:T:17:ARG:HD3	24:T:47:SER:HB3	1.89	0.54
47:2:932:U:O3'	74:AQ:32:LYS:NZ	2.39	0.54
64:AG:128:LYS:HE2	64:AG:135:ARG:HD2	1.90	0.54
83:AZ:120:ARG:HD3	83:AZ:479:LYS:HZ1	1.73	0.54
1:1:347:G:H21	8:C:59:GLN:HG3	1.73	0.54
6:A:83:HIS:HA	46:p:64:VAL:HA	1.89	0.54
8:C:353:ALA:O	8:C:357:GLU:N	2.41	0.54
47:2:140:A:N6	47:2:280:U:O2'	2.41	0.54
47:2:1591:C:H2'	47:2:1592:A:H8	1.72	0.54
48:q:36:TYR:HB3	48:q:48:ILE:HG23	1.89	0.54
51:t:53:THR:OG1	51:t:94:ARG:NH1	2.41	0.54
57:z:174:ARG:O	57:z:178:ALA:N	2.41	0.54
85:AZ:901:SO1:C21	85:AZ:901:SO1:C5	2.85	0.54
1:1:1019:G:H2'	1:1:1020:G:H8	1.72	0.54
1:1:1524:A:O2'	1:1:1526:U:OP2	2.25	0.54
5:P2:59:THR:HG23	5:P2:80:LEU:HD11	1.90	0.54
47:2:997:G:H2'	47:2:998:A:H8	1.73	0.54
47:2:1483:A:OP1	47:2:1521:G:N2	2.41	0.54
49:r:51:SER:HA	49:r:57:ALA:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:50:U:OP1	18:N:188:ARG:NH1	2.41	0.54
1:1:71:A:OP1	31:a:67:HIS:NE2	2.39	0.54
1:1:210:U:HO2'	1:1:229:G:HO2'	1.53	0.54
1:1:1948:G:H2'	1:1:1949:G:H8	1.73	0.54
1:1:3090:U:OP1	7:B:270:ARG:NH2	2.41	0.54
4:P0:93:LEU:HG	4:P0:96:ILE:HD11	1.90	0.54
7:B:245:GLY:HA3	7:B:248:LYS:HE3	1.89	0.54
16:L:17:HIS:O	16:L:21:ARG:NH2	2.41	0.54
47:2:866:G:H2'	47:2:867:G:H8	1.72	0.54
47:2:961:U:H5''	61:AD:71:ILE:HD13	1.90	0.54
47:2:1670:G:H21	47:2:1731:A:H62	1.56	0.54
57:z:45:ILE:O	57:z:49:LEU:N	2.39	0.54
66:AI:71:GLN:HA	66:AI:74:GLN:HG2	1.88	0.54
72:AO:14:SER:HA	72:AO:21:LYS:HA	1.90	0.54
83:AZ:237:LYS:O	83:AZ:241:MET:CB	2.56	0.54
83:AZ:588:LEU:HA	83:AZ:687:ASN:O	2.08	0.54
1:1:943:U:H3'	31:a:13:GLY:HA2	1.89	0.53
2:3:81:U:O2	2:3:99:G:N2	2.37	0.53
12:G:146:LYS:NZ	12:G:173:MET:O	2.41	0.53
33:c:98:SER:OG	33:c:99:ASP:N	2.41	0.53
39:i:20:MET:HG3	39:i:22:PRO:HD3	1.89	0.53
47:2:615:A:O2'	47:2:621:A:N6	2.42	0.53
51:t:221:SER:HB2	51:t:223:LYS:HG2	1.90	0.53
1:1:1237:G:N2	5:P2:138:SER:OG	2.40	0.53
1:1:2640:A:OP1	24:T:55:LYS:NZ	2.40	0.53
1:1:3304:U:O3'	7:B:334:ARG:NH2	2.41	0.53
38:h:31:LEU:HA	38:h:34:GLN:HB2	1.90	0.53
47:2:17:C:O2'	47:2:1137:A:N6	2.41	0.53
47:2:975:C:H5''	61:AD:109:LYS:HE2	1.90	0.53
47:2:1586:A:H1'	47:2:1611:A:H61	1.73	0.53
59:AB:15:LYS:NZ	59:AB:19:ILE:O	2.39	0.53
63:AF:60:LEU:HG	63:AF:89:MET:HG3	1.89	0.53
1:1:326:U:H2'	1:1:327:A:H8	1.74	0.53
1:1:687:U:OP2	16:L:36:ARG:NH2	2.42	0.53
1:1:804:C:OP1	8:C:98:ARG:NH2	2.42	0.53
8:C:22:LEU:HD13	8:C:24:ALA:H	1.72	0.53
9:D:22:ARG:O	9:D:26:GLY:N	2.38	0.53
15:J:49:LYS:HD3	15:J:62:ASN:HB2	1.89	0.53
20:P:175:ARG:NH2	20:P:179:GLN:OE1	2.40	0.53
29:Y:27:ARG:HD3	29:Y:78:PHE:HE1	1.74	0.53
35:e:18:LYS:HE2	35:e:30:GLU:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:29:U:H2'	47:2:30:G:H8	1.72	0.53
47:2:107:C:H2'	47:2:108:A:C8	2.44	0.53
80:AW:140:TYR:OH	80:AW:145:HIS:O	2.27	0.53
1:1:2956:A:H62	1:1:2977:G:H21	1.56	0.53
1:1:3231:U:H2'	1:1:3232:G:H8	1.73	0.53
2:3:39:C:N3	15:J:70:THR:OG1	2.33	0.53
22:R:186:LYS:O	55:x:35:LYS:NZ	2.40	0.53
47:2:1553:G:N7	63:AF:47:ARG:NH2	2.45	0.53
47:2:1769:U:O2	62:AE:136:ARG:NH1	2.40	0.53
57:z:82:ARG:HH21	57:z:149:ARG:HH21	1.57	0.53
83:AZ:32:LYS:HE3	83:AZ:106:PRO:HA	1.88	0.53
83:AZ:484:SER:OG	83:AZ:485:VAL:N	2.39	0.53
83:AZ:772:LEU:HD22	83:AZ:773:PRO:HD2	1.90	0.53
1:1:821:U:H2'	1:1:822:G:H8	1.73	0.53
1:1:1389:G:OP1	35:e:104:ASN:ND2	2.39	0.53
1:1:1634:G:OP1	30:Z:107:ARG:NH1	2.41	0.53
4:P0:100:ILE:HB	4:P0:185:LEU:HD23	1.91	0.53
8:C:300:ARG:HE	21:Q:39:ARG:HA	1.73	0.53
47:2:957:G:N7	61:AD:12:SER:OG	2.40	0.53
54:w:142:ARG:HH21	54:w:153:VAL:H	1.54	0.53
72:AO:55:VAL:HA	72:AO:75:VAL:HA	1.90	0.53
73:AP:57:TYR:O	73:AP:103:ARG:NH2	2.38	0.53
83:AZ:510:ARG:NH2	83:AZ:549:HIS:O	2.42	0.53
83:AZ:723:LYS:HD3	83:AZ:805:GLY:HA2	1.89	0.53
83:AZ:729:PHE:HZ	85:AZ:901:SO1:H122	1.73	0.53
1:1:15:C:OP1	28:X:42:ARG:NH1	2.41	0.53
1:1:2256:A:C2	47:2:1757:G:P	2.97	0.53
1:1:2742:C:O5'	45:o:19:LYS:NZ	2.41	0.53
1:1:3064:U:H2'	1:1:3065:G:H8	1.74	0.53
11:F:59:GLU:HA	11:F:62:ILE:HG12	1.90	0.53
13:H:18:VAL:HG12	13:H:27:VAL:HG22	1.90	0.53
23:S:74:ASN:OD1	23:S:95:ARG:NH1	2.42	0.53
26:V:45:ARG:HB3	26:V:48:ARG:HG2	1.90	0.53
47:2:589:C:OP1	78:AU:42:ARG:NH1	2.42	0.53
47:2:1595:U:OP2	77:AT:32:ARG:NH1	2.41	0.53
47:2:1757:G:O5'	47:2:1757:G:H8	1.92	0.53
55:x:73:VAL:HB	55:x:77:LEU:HD23	1.90	0.53
1:1:148:G:O6	12:G:138:HIS:N	2.37	0.53
1:1:2696:A:C5	1:1:2758:A:N1	2.77	0.53
6:A:117:GLU:OE2	6:A:124:GLY:N	2.41	0.53
7:B:84:VAL:HG12	7:B:164:THR:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1098:U:OP2	50:s:168:ARG:NE	2.41	0.53
47:2:1205:C:O2	77:AT:17:GLY:N	2.39	0.53
47:2:1682:U:O4	47:2:1720:G:N2	2.40	0.53
52:u:180:LEU:HB2	52:u:229:GLY:H	1.73	0.53
57:z:152:SER:O	57:z:156:ILE:N	2.40	0.53
72:AO:38:ASP:OD1	72:AO:41:ARG:NH1	2.35	0.53
1:1:43:A:OP1	18:N:83:LYS:NZ	2.40	0.53
1:1:91:G:N2	1:1:95:A:OP2	2.42	0.53
1:1:944:C:OP1	35:e:33:ARG:NH1	2.42	0.53
1:1:1306:G:N2	1:1:1307:G:N7	2.56	0.53
1:1:1464:G:H21	1:1:1511:U:H3	1.56	0.53
1:1:2746:A:H5''	9:D:178:ASN:HD22	1.73	0.53
10:E:166:LYS:HE2	36:f:4:SER:HB2	1.91	0.53
11:F:31:ALA:HA	11:F:34:LYS:HB2	1.91	0.53
26:V:80:ARG:NH1	26:V:117:PRO:O	2.36	0.53
30:Z:27:LYS:NZ	30:Z:96:VAL:O	2.42	0.53
41:k:5:ILE:HD12	41:k:52:TYR:HB3	1.91	0.53
71:AN:126:LYS:HA	71:AN:131:SER:HA	1.91	0.53
79:AV:253:ALA:HA	79:AV:262:VAL:HA	1.90	0.53
1:1:2202:C:H5''	6:A:226:SER:HB3	1.91	0.53
1:1:2216:G:H22	1:1:2229:A:H2	1.55	0.53
9:D:22:ARG:HG2	9:D:28:THR:HG23	1.90	0.53
13:H:91:ARG:HG2	13:H:143:GLU:HG3	1.89	0.53
16:L:153:ASP:OD2	31:a:126:LYS:NZ	2.40	0.53
23:S:6:GLU:OE2	23:S:64:ILE:N	2.42	0.53
47:2:25:C:O2'	47:2:366:A:O2'	2.26	0.53
49:r:69:CYS:SG	49:r:70:LEU:N	2.82	0.53
83:AZ:115:VAL:O	83:AZ:119:LEU:CB	2.57	0.53
1:1:1220:U:O4'	1:1:1286:A:N6	2.42	0.53
1:1:1223:A:OP2	1:1:1285:G:N2	2.42	0.53
1:1:1232:C:H2'	1:1:1233:G:H8	1.74	0.53
1:1:1382:G:OP2	8:C:188:ARG:NH1	2.41	0.53
1:1:3214:U:OP2	17:M:128:ARG:NH1	2.38	0.53
4:P0:115:ALA:H	4:P0:164:LYS:HD3	1.74	0.53
5:P2:83:THR:HA	5:P2:90:ARG:HG2	1.91	0.53
9:D:197:SER:O	9:D:202:GLY:N	2.40	0.53
15:J:141:ARG:HD2	15:J:145:LYS:HA	1.91	0.53
48:q:69:ASN:ND2	48:q:71:GLU:OE2	2.41	0.53
49:r:89:ASP:OD2	49:r:99:ASN:ND2	2.39	0.53
52:u:91:THR:OG1	52:u:98:ASN:ND2	2.42	0.53
83:AZ:216:HIS:NE2	83:AZ:320:LEU:O	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:494:G:N2	1:1:495:G:O6	2.42	0.52
1:1:665:A:OP1	18:N:203:ARG:NH1	2.41	0.52
1:1:962:A:N6	1:1:2408:U:O2	2.42	0.52
1:1:1487:G:H1'	37:g:6:THR:HG21	1.91	0.52
1:1:2471:U:N3	1:1:2474:G:N7	2.57	0.52
1:1:2787:G:O2'	31:a:58:MET:SD	2.66	0.52
6:A:147:ARG:NH1	47:2:892:A:O2'	2.43	0.52
8:C:52:VAL:HG21	8:C:99:MET:HE2	1.90	0.52
22:R:96:ILE:O	22:R:100:ARG:N	2.41	0.52
47:2:174:U:O4	47:2:266:A:N7	2.42	0.52
47:2:959:U:H5''	61:AD:14:SER:HB3	1.90	0.52
47:2:1615:C:N4	53:v:79:ASN:O	2.42	0.52
51:t:42:THR:OG1	51:t:45:LYS:O	2.27	0.52
53:v:112:ARG:HA	53:v:115:LYS:HG2	1.90	0.52
53:v:133:VAL:HG12	53:v:198:LEU:HD23	1.91	0.52
55:x:64:VAL:HA	55:x:67:LEU:HD23	1.89	0.52
1:1:86:G:N2	1:1:99:A:OP2	2.43	0.52
1:1:1149:G:H21	1:1:1198:C:H42	1.56	0.52
1:1:1541:G:N1	1:1:1555:U:N3	2.57	0.52
1:1:2154:U:H2'	1:1:2155:G:C8	2.45	0.52
6:A:247:ARG:NE	6:A:249:SER:OG	2.42	0.52
8:C:361:HIS:O	23:S:26:ARG:NH2	2.42	0.52
47:2:1216:C:O2	47:2:1446:A:N6	2.40	0.52
47:2:1503:A:H4'	67:AJ:97:SER:HB2	1.91	0.52
79:AV:79:TYR:HB3	79:AV:91:LEU:HD11	1.90	0.52
79:AV:299:GLN:O	79:AV:315:VAL:N	2.39	0.52
83:AZ:12:LEU:HB3	83:AZ:99:LEU:HD22	1.91	0.52
83:AZ:725:GLN:NE2	83:AZ:802:SER:O	2.39	0.52
1:1:74:G:H5''	16:L:104:ARG:HD2	1.91	0.52
1:1:708:G:N2	1:1:711:A:OP2	2.37	0.52
1:1:1613:A:OP2	41:k:46:ARG:NH1	2.42	0.52
1:1:2160:G:H2'	1:1:2161:G:H8	1.75	0.52
2:3:7:G:O5'	9:D:33:ARG:NH1	2.43	0.52
9:D:31:TYR:O	9:D:35:ARG:NH1	2.42	0.52
13:H:115:ARG:HE	13:H:116:ASN:H	1.56	0.52
15:J:82:ARG:HG3	15:J:112:LEU:HD12	1.90	0.52
15:J:84:LEU:HD12	15:J:89:TYR:HA	1.91	0.52
47:2:741:C:OP1	59:AB:43:LYS:NZ	2.43	0.52
47:2:1330:G:N2	65:AH:8:THR:OG1	2.40	0.52
79:AV:132:LYS:HG2	79:AV:143:THR:HG23	1.91	0.52
79:AV:200:ASN:H	79:AV:215:GLY:HA2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:408:A:N3	1:1:655:C:O2'	2.41	0.52
1:1:1383:G:O3'	8:C:138:ARG:NH2	2.43	0.52
1:1:2374:C:O2'	1:1:2941:A:N6	2.42	0.52
1:1:3189:G:O6	1:1:3203:U:O4	2.27	0.52
9:D:198:TYR:HE1	9:D:203:HIS:HB3	1.74	0.52
33:c:41:LEU:N	33:c:65:THR:OG1	2.39	0.52
47:2:400:A:H62	56:y:29:LEU:HG	1.73	0.52
47:2:1482:C:H4'	64:AG:77:GLN:HE22	1.75	0.52
47:2:1587:A:O2'	53:v:104:ASN:ND2	2.36	0.52
49:r:222:LYS:HD2	49:r:224:ASP:H	1.75	0.52
63:AF:106:GLU:O	63:AF:108:ARG:NH1	2.43	0.52
66:AI:16:ARG:NH2	66:AI:21:ASN:OD1	2.42	0.52
74:AQ:43:ASN:ND2	74:AQ:65:PRO:O	2.41	0.52
1:1:98:G:OP1	16:L:16:LYS:NZ	2.36	0.52
1:1:413:U:OP1	20:P:30:ARG:NH2	2.42	0.52
1:1:2988:C:OP1	19:O:68:ARG:NH2	2.43	0.52
26:V:114:ILE:HD11	26:V:134:GLY:H	1.73	0.52
47:2:401:A:OP1	56:y:23:LYS:NZ	2.38	0.52
47:2:509:G:C5'	47:2:509:G:C8	2.93	0.52
52:u:189:LEU:O	52:u:191:ARG:NH1	2.42	0.52
65:AH:66:VAL:HB	65:AH:69:ILE:HB	1.92	0.52
71:AN:37:ALA:HA	71:AN:41:SER:HB3	1.91	0.52
1:1:148:G:OP2	18:N:4:TYR:OH	2.28	0.52
1:1:1071:U:O2	1:1:1087:G:N2	2.38	0.52
1:1:1529:A:OP2	1:1:1592:G:N2	2.40	0.52
1:1:1886:A:H2'	1:1:1887:A:H8	1.74	0.52
1:1:2696:A:N6	1:1:2758:A:N1	2.58	0.52
12:G:132:VAL:HG12	12:G:200:LEU:HD23	1.91	0.52
47:2:610:G:O2'	47:2:613:G:O2'	2.20	0.52
52:u:173:ILE:HG21	52:u:229:GLY:HA2	1.92	0.52
54:w:32:ILE:H	54:w:34:GLN:HE22	1.57	0.52
64:AG:31:VAL:HB	64:AG:34:SER:HB2	1.92	0.52
67:AJ:99:SER:OG	67:AJ:102:ARG:NH2	2.42	0.52
68:AK:28:SER:HB3	68:AK:34:LEU:HB2	1.92	0.52
70:AM:40:VAL:HA	70:AM:43:LYS:HZ3	1.75	0.52
71:AN:103:LEU:N	71:AN:126:LYS:O	2.41	0.52
83:AZ:617:ARG:O	83:AZ:621:ASP:HB2	2.10	0.52
1:1:1222:G:HO2'	1:1:1285:G:H1	1.54	0.52
1:1:2180:G:OP1	6:A:174:ARG:NH2	2.43	0.52
7:B:212:ASN:ND2	7:B:353:GLU:OE1	2.42	0.52
10:E:92:SER:OG	10:E:94:GLU:OE1	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:52:LEU:HD12	14:I:135:ILE:HB	1.91	0.52
15:J:21:ILE:HD13	15:J:23:VAL:HG12	1.92	0.52
40:j:63:ARG:O	40:j:68:LYS:NZ	2.35	0.52
47:2:1553:G:N1	47:2:1556:A:OP2	2.35	0.52
47:2:1752:U:H2'	47:2:1753:A:H8	1.74	0.52
52:u:86:PHE:HA	52:u:101:LEU:HD12	1.90	0.52
52:u:182:TYR:N	52:u:226:PHE:O	2.42	0.52
53:v:114:ILE:O	53:v:118:LEU:N	2.41	0.52
54:w:140:ASN:HA	54:w:143:LYS:HB2	1.91	0.52
64:AG:11:GLY:N	64:AG:18:ALA:O	2.42	0.52
69:AL:85:TYR:O	69:AL:87:ARG:NH1	2.41	0.52
85:AZ:901:SO1:H212	85:AZ:901:SO1:C5	2.40	0.52
1:1:764:U:O2'	1:1:766:U:OP2	2.28	0.52
1:1:1604:G:H4'	1:1:1835:A:H4'	1.92	0.52
13:H:10:ILE:HD12	13:H:55:VAL:HG21	1.92	0.52
47:2:653:C:H3'	47:2:654:C:H4'	1.92	0.52
47:2:961:U:O2'	61:AD:86:GLU:OE2	2.24	0.52
55:x:71:HIS:HA	55:x:74:GLN:HG2	1.92	0.52
74:AQ:87:ARG:NH2	74:AQ:91:ASP:OD2	2.43	0.52
79:AV:22:SER:HB3	79:AV:36:ALA:HB3	1.92	0.52
1:1:150:A:OP1	18:N:147:ARG:NH1	2.43	0.52
1:1:754:G:N2	1:1:778:U:O2	2.35	0.52
1:1:1459:C:H2'	1:1:1460:A:H8	1.74	0.52
1:1:1793:C:OP2	46:p:49:ARG:NH2	2.43	0.52
1:1:3049:A:H4'	7:B:364:LYS:HD2	1.92	0.52
1:1:3219:G:O6	36:f:2:ALA:N	2.43	0.52
7:B:224:HIS:HB2	7:B:270:ARG:HD2	1.91	0.52
12:G:50:VAL:HG11	28:X:27:ARG:HD2	1.92	0.52
19:O:23:VAL:O	19:O:27:LEU:N	2.42	0.52
25:U:82:LYS:O	25:U:86:LYS:N	2.43	0.52
47:2:4:C:OP1	50:s:181:SER:OG	2.27	0.52
47:2:1344:A:H4'	68:AK:54:GLY:HA3	1.91	0.52
47:2:1421:A:H4'	51:t:160:SER:HB3	1.92	0.52
47:2:1504:G:N3	47:2:1563:C:O2'	2.43	0.52
55:x:81:LEU:HD13	55:x:90:VAL:HG11	1.92	0.52
60:AC:42:ALA:HB2	60:AC:122:VAL:HB	1.90	0.52
79:AV:307:ASP:OD2	79:AV:311:ARG:NH1	2.42	0.52
83:AZ:195:GLU:HG2	83:AZ:196:VAL:HG23	1.92	0.52
1:1:1156:C:OP2	11:F:94:LYS:NZ	2.34	0.52
1:1:1832:C:OP1	28:X:120:LYS:NZ	2.40	0.52
1:1:2415:C:OP1	6:A:2:GLY:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3188:G:OP1	13:H:22:SER:OG	2.27	0.52
3:4:141:C:OP1	18:N:109:ARG:NH2	2.43	0.52
8:C:12:THR:HA	8:C:171:ALA:HB1	1.92	0.52
11:F:75:TYR:HB2	24:T:141:VAL:HB	1.92	0.52
28:X:53:HIS:ND1	28:X:54:TYR:O	2.37	0.52
49:r:164:ILE:HA	49:r:167:VAL:HG22	1.92	0.52
53:v:58:LEU:HD11	53:v:167:ARG:HG2	1.92	0.52
53:v:188:LYS:HZ1	53:v:192:GLU:HB2	1.75	0.52
59:AB:128:CYS:SG	59:AB:129:ARG:N	2.83	0.52
1:1:1233:G:N3	5:P2:120:SER:OG	2.43	0.51
1:1:1523:U:O2'	28:X:111:ASN:ND2	2.43	0.51
1:1:2168:A:N6	1:1:2170:U:O2	2.43	0.51
1:1:2818:U:OP1	32:b:2:ALA:N	2.43	0.51
1:1:3146:G:H2'	1:1:3147:G:H8	1.74	0.51
11:F:224:ILE:HA	23:S:36:ILE:HG22	1.92	0.51
36:f:10:LYS:HB2	36:f:33:GLU:HB2	1.92	0.51
47:2:897:C:N4	47:2:914:G:O2'	2.42	0.51
47:2:1541:G:N2	47:2:1569:A:OP2	2.42	0.51
47:2:1637:C:H5'	82:AY:48:U:C4	2.45	0.51
71:AN:62:LYS:CD	71:AN:118:PRO:HD3	2.40	0.51
83:AZ:295:GLU:O	83:AZ:299:LEU:HB2	2.09	0.51
1:1:278:U:O4	1:1:287:G:O6	2.28	0.51
1:1:584:G:H2'	1:1:585:A:H8	1.74	0.51
1:1:1372:C:O5'	31:a:7:LYS:NZ	2.42	0.51
1:1:1786:G:H2'	1:1:1787:A:C8	2.45	0.51
3:4:49:G:H5'	38:h:44:ILE:HD11	1.91	0.51
19:O:12:LYS:HE2	23:S:167:ARG:HD3	1.92	0.51
47:2:144:U:O4	54:w:137:ARG:NH2	2.43	0.51
47:2:406:U:H5''	54:w:94:ARG:HB2	1.92	0.51
51:t:211:PRO:HB3	65:AH:19:ARG:HB2	1.91	0.51
69:AL:21:ASN:HB2	70:AM:67:GLY:HA3	1.92	0.51
79:AV:6:VAL:HB	79:AV:318:ALA:HB3	1.93	0.51
1:1:799:G:OP1	31:a:32:ARG:NH1	2.44	0.51
1:1:941:G:H1'	1:1:1435:A:H1'	1.91	0.51
1:1:2828:G:H22	1:1:2863:G:H1'	1.75	0.51
1:1:3058:U:O4	34:d:65:LYS:NZ	2.41	0.51
33:c:30:THR:HG23	33:c:91:SER:HB2	1.92	0.51
39:i:19:SER:OG	39:i:20:MET:N	2.43	0.51
47:2:506:A:O2'	47:2:507:U:H5''	2.11	0.51
47:2:1213:G:N2	47:2:1450:U:O2	2.41	0.51
47:2:1786:G:OP2	62:AE:133:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:v:23:VAL:HG12	64:AG:57:LEU:HD23	1.92	0.51
53:v:94:THR:HG22	53:v:114:ILE:HG13	1.92	0.51
81:AX:8:U:O2'	81:AX:21:A:N1	2.37	0.51
83:AZ:160:VAL:O	83:AZ:164:LEU:HB2	2.10	0.51
83:AZ:399:ARG:HB2	83:AZ:453:ILE:HG22	1.91	0.51
83:AZ:728:VAL:HG22	83:AZ:773:PRO:HB3	1.91	0.51
1:1:2713:U:O2'	45:o:8:ARG:NH2	2.43	0.51
16:L:126:PHE:HB2	38:h:115:LYS:HG3	1.92	0.51
48:q:127:ARG:HD3	48:q:151:SER:HA	1.92	0.51
53:v:72:HIS:O	64:AG:79:TYR:OH	2.26	0.51
56:y:79:ALA:HB3	56:y:103:GLN:HG3	1.91	0.51
83:AZ:32:LYS:N	86:AZ:902:GCP:O1B	2.39	0.51
83:AZ:129:VAL:HB	83:AZ:157:ILE:HG22	1.92	0.51
83:AZ:494:GLU:HB3	83:AZ:555:LYS:HE3	1.93	0.51
1:1:138:U:H2'	1:1:139:G:H8	1.74	0.51
1:1:1516:C:H2'	1:1:1517:G:H8	1.76	0.51
1:1:1923:C:OP1	44:n:25:LYS:NZ	2.42	0.51
1:1:2338:C:H3'	1:1:2339:C:H2'	1.91	0.51
1:1:3174:A:N1	1:1:3279:A:O2'	2.39	0.51
10:E:50:LYS:NZ	10:E:162:SER:OG	2.42	0.51
38:h:38:ARG:NH1	38:h:40:SER:O	2.44	0.51
45:o:6:LYS:NZ	45:o:93:LEU:O	2.38	0.51
47:2:448:C:OP1	52:u:49:ARG:NH1	2.44	0.51
47:2:733:A:O2'	47:2:736:C:N4	2.44	0.51
47:2:1268:G:N3	47:2:1447:C:O2'	2.44	0.51
47:2:1474:G:H2'	47:2:1475:A:H8	1.76	0.51
47:2:1520:U:H5'	47:2:1523:G:H22	1.75	0.51
47:2:1637:C:H5''	82:AY:48:U:C4	2.46	0.51
58:AA:28:ASN:ND2	77:AT:9:SER:OG	2.44	0.51
66:AI:35:ILE:HG23	66:AI:102:ALA:HB2	1.93	0.51
1:1:693:A:OP1	8:C:45:ASN:ND2	2.42	0.51
1:1:775:A:OP2	32:b:44:LYS:NZ	2.42	0.51
1:1:990:U:H4'	24:T:100:LYS:HG3	1.92	0.51
1:1:1194:G:H2'	1:1:1195:A:C8	2.45	0.51
1:1:1530:U:HO2'	3:4:114:G:HO2'	1.53	0.51
1:1:2960:C:H2'	1:1:2961:G:C8	2.46	0.51
8:C:159:ILE:HG21	8:C:165:ALA:HB2	1.92	0.51
33:c:25:LEU:O	33:c:29:SER:OG	2.29	0.51
47:2:211:U:H5''	59:AB:20:PHE:HB2	1.93	0.51
47:2:923:A:H2'	47:2:924:A:C8	2.45	0.51
47:2:1527:C:OP1	53:v:106:LYS:NZ	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:z:59:LEU:HD12	57:z:69:ARG:HG2	1.92	0.51
64:AG:58:ASP:O	64:AG:60:PHE:N	2.44	0.51
75:AR:37:CYS:HB3	75:AR:40:CYS:HB2	1.92	0.51
82:AY:48:U:H4'	82:AY:48:U:OP1	2.11	0.51
1:1:356:C:O2'	8:C:81:GLY:O	2.28	0.51
1:1:638:C:N4	1:1:639:G:O6	2.44	0.51
1:1:938:C:OP1	1:1:962:A:O2'	2.26	0.51
1:1:1201:C:N4	1:1:2858:U:OP1	2.44	0.51
19:O:98:ALA:HA	19:O:101:ARG:HE	1.75	0.51
47:2:60:U:N3	47:2:63:G:OP1	2.36	0.51
47:2:564:G:N2	47:2:577:G:OP1	2.36	0.51
47:2:1180:C:O2'	63:AF:127:ARG:O	2.27	0.51
51:t:23:GLU:OE1	58:AA:61:TRP:NE1	2.43	0.51
56:y:36:THR:O	56:y:95:THR:OG1	2.22	0.51
79:AV:255:ALA:HA	79:AV:260:ILE:HA	1.93	0.51
83:AZ:413:ILE:HB	83:AZ:427:PHE:HB2	1.92	0.51
1:1:560:G:H5'	17:M:80:THR:HG23	1.92	0.51
1:1:1592:G:OP1	37:g:58:ARG:NH2	2.43	0.51
1:1:1783:U:H2'	1:1:1784:G:H8	1.76	0.51
1:1:2270:A:H2'	1:1:2271:A:C8	2.46	0.51
1:1:2347:U:H3'	1:1:2348:A:H8	1.75	0.51
1:1:2468:A:O2'	1:1:2478:C:O2	2.28	0.51
1:1:2812:C:H2'	1:1:2813:A:C8	2.45	0.51
1:1:2812:C:H2'	1:1:2813:A:H8	1.76	0.51
1:1:2960:C:H2'	1:1:2961:G:H8	1.76	0.51
8:C:54:GLU:OE2	8:C:55:LYS:NZ	2.40	0.51
18:N:61:ILE:HG22	18:N:133:ILE:HA	1.92	0.51
21:Q:185:LYS:HG2	21:Q:186:VAL:HG22	1.93	0.51
47:2:351:C:O4'	71:AN:13:ARG:NH1	2.44	0.51
47:2:922:G:H2'	47:2:923:A:C8	2.46	0.51
53:v:111:VAL:O	53:v:115:LYS:N	2.37	0.51
56:y:49:ARG:O	56:y:52:ASN:ND2	2.43	0.51
70:AM:55:ASP:OD2	70:AM:57:ARG:NH1	2.41	0.51
79:AV:150:TRP:HB2	79:AV:174:ASN:HB2	1.91	0.51
80:AW:121:CYS:SG	80:AW:122:SER:N	2.84	0.51
1:1:365:A:OP1	8:C:84:ARG:NH1	2.44	0.51
1:1:707:U:OP1	1:1:780:A:O2'	2.27	0.51
1:1:911:C:H5''	6:A:15:ILE:HD13	1.91	0.51
1:1:1459:C:H2'	1:1:1460:A:C8	2.45	0.51
1:1:1831:U:OP2	28:X:92:LYS:NZ	2.33	0.51
1:1:1868:G:HO2'	1:1:2118:C:HO2'	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:107:C:H2'	2:3:108:A:H8	1.75	0.51
7:B:51:ALA:O	7:B:332:ARG:NH1	2.40	0.51
22:R:99:LEU:HD23	22:R:103:ARG:HH21	1.75	0.51
47:2:332:U:OP1	56:y:56:ARG:NH2	2.35	0.51
47:2:1396:U:O2	47:2:1402:G:O6	2.28	0.51
47:2:1733:C:H2'	47:2:1734:U:H6	1.75	0.51
50:s:44:LEU:HA	50:s:47:ALA:HB3	1.93	0.51
83:AZ:601:ILE:HA	83:AZ:606:ILE:HD11	1.92	0.51
1:1:293:C:O3'	39:i:76:ARG:NH2	2.44	0.51
1:1:799:G:H2'	1:1:801:A:H62	1.75	0.51
9:D:10:SER:O	9:D:14:SER:N	2.39	0.51
47:2:810:G:N2	55:x:109:VAL:O	2.44	0.51
47:2:1272:U:O2	47:2:1438:G:O6	2.29	0.51
47:2:1481:C:N4	47:2:1525:A:OP2	2.44	0.51
60:AC:41:LEU:O	60:AC:46:ARG:NH2	2.43	0.51
68:AK:44:ASN:OD1	68:AK:47:GLN:NE2	2.37	0.51
72:AO:82:ALA:O	72:AO:86:GLU:N	2.43	0.51
79:AV:116:ASP:HB2	79:AV:121:MET:HB3	1.92	0.51
83:AZ:226:ALA:O	83:AZ:230:ALA:CB	2.55	0.51
83:AZ:248:SER:OG	83:AZ:249:PHE:N	2.44	0.51
1:1:155:G:H1'	39:i:26:ILE:HD11	1.94	0.50
1:1:297:G:O2'	39:i:32:ALA:O	2.27	0.50
7:B:116:ARG:HG3	7:B:175:LYS:HG3	1.92	0.50
9:D:22:ARG:HD2	9:D:27:LYS:HB2	1.92	0.50
42:l:24:PRO:HB2	42:l:26:TRP:HB3	1.93	0.50
47:2:227:U:H3	47:2:834:G:H1	1.58	0.50
47:2:283:U:OP2	54:w:188:ARG:NH2	2.43	0.50
47:2:1470:C:OP1	47:2:1471:A:O2'	2.29	0.50
51:t:138:VAL:O	51:t:148:LYS:NZ	2.40	0.50
61:AD:30:SER:HB3	61:AD:67:THR:HG22	1.92	0.50
65:AH:9:VAL:HG23	65:AH:50:ILE:HA	1.93	0.50
67:AJ:86:ARG:HH21	67:AJ:89:ARG:HB3	1.77	0.50
72:AO:60:PHE:H	72:AO:71:GLY:HA2	1.76	0.50
79:AV:123:ILE:HD11	79:AV:169:ILE:HD13	1.92	0.50
83:AZ:337:MET:HE2	83:AZ:341:HIS:HB3	1.93	0.50
83:AZ:819:VAL:O	83:AZ:823:ARG:CB	2.58	0.50
1:1:544:C:N3	1:1:547:G:N1	2.60	0.50
1:1:2918:G:H2'	1:1:2919:A:H8	1.75	0.50
3:4:75:G:OP2	29:Y:74:TYR:OH	2.22	0.50
14:I:49:CYS:SG	14:I:50:VAL:N	2.83	0.50
23:S:82:ASP:OD1	23:S:120:SER:OG	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:67:LYS:HA	37:g:70:LYS:HB2	1.93	0.50
47:2:1547:A:O2'	66:AI:89:GLN:O	2.29	0.50
47:2:1641:C:H2'	47:2:1642:G:C8	2.46	0.50
47:2:1797:A:H61	74:AQ:84:VAL:HG21	1.75	0.50
53:v:206:SER:H	53:v:211:ILE:HG13	1.74	0.50
63:AF:121:ILE:HD11	66:AI:125:ILE:HD11	1.92	0.50
68:AK:106:ILE:HG13	68:AK:107:THR:HG23	1.93	0.50
83:AZ:162:ARG:HH11	86:AZ:902:GCP:HN22	1.58	0.50
1:1:1635:G:N7	30:Z:73:LYS:NZ	2.47	0.50
1:1:2351:U:H2'	1:1:2352:A:C8	2.46	0.50
1:1:2392:C:O2	7:B:266:ARG:NH2	2.45	0.50
4:P0:46:ARG:NH1	5:P2:123:ARG:NH1	2.59	0.50
8:C:34:ILE:HA	8:C:37:THR:HG22	1.93	0.50
14:I:141:LYS:O	14:I:145:LYS:NZ	2.34	0.50
37:g:58:ARG:H	37:g:61:GLN:HE21	1.59	0.50
45:o:74:CYS:SG	45:o:75:VAL:N	2.84	0.50
47:2:1213:G:O6	47:2:1450:U:O4	2.28	0.50
57:z:110:GLN:OE1	57:z:126:ARG:NH2	2.44	0.50
83:AZ:69:THR:HB	83:AZ:106:PRO:HB3	1.94	0.50
83:AZ:149:GLU:HB3	83:AZ:352:ARG:HH12	1.77	0.50
83:AZ:566:THR:OG1	83:AZ:723:LYS:O	2.26	0.50
1:1:501:A:OP1	10:E:82:ARG:NH1	2.32	0.50
1:1:2675:C:N4	15:J:22:SER:O	2.43	0.50
7:B:341:SER:OG	7:B:343:TYR:O	2.30	0.50
12:G:112:GLU:HA	12:G:115:ALA:HB3	1.93	0.50
14:I:19:LYS:HG2	14:I:26:VAL:HG11	1.94	0.50
29:Y:3:LYS:HG2	29:Y:8:VAL:HG11	1.93	0.50
30:Z:26:VAL:O	30:Z:93:LYS:NZ	2.34	0.50
38:h:92:LEU:HD12	38:h:96:GLU:HG3	1.94	0.50
47:2:1616:G:OP1	76:AS:18:ARG:NH2	2.44	0.50
48:q:183:ARG:NE	69:AL:42:GLU:OE2	2.44	0.50
56:y:84:HIS:NE2	56:y:97:THR:OG1	2.42	0.50
64:AG:99:GLU:N	79:AV:58:VAL:O	2.43	0.50
83:AZ:715:ALA:HB2	83:AZ:838:TYR:HB2	1.92	0.50
1:1:2588:U:OP1	12:G:48:ARG:NH2	2.44	0.50
1:1:3208:G:O6	19:O:116:LYS:NZ	2.42	0.50
39:i:4:LYS:HB2	39:i:16:LYS:HA	1.94	0.50
42:l:23:LEU:HD21	42:l:35:ILE:HG22	1.92	0.50
46:p:20:SER:HA	46:p:23:ARG:HG2	1.94	0.50
47:2:1216:C:H5''	58:AA:2:LEU:HD11	1.94	0.50
49:r:138:PHE:HB2	49:r:214:LYS:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:210:GLU:O	65:AH:20:TYR:OH	2.28	0.50
52:u:206:ASP:HB2	52:u:222:LEU:HB2	1.92	0.50
56:y:67:TRP:HD1	56:y:69:SER:H	1.60	0.50
83:AZ:265:GLU:OE2	83:AZ:267:LYS:NZ	2.41	0.50
83:AZ:349:GLN:NE2	83:AZ:369:ILE:O	2.35	0.50
1:1:547:G:H2'	1:1:548:G:C8	2.47	0.50
47:2:78:A:H5'	54:w:154:ARG:HG3	1.94	0.50
47:2:86:A:H2'	47:2:87:C:H6	1.76	0.50
47:2:478:A:N1	47:2:510:G:C6	2.80	0.50
47:2:1147:A:O2'	47:2:1636:C:OP2	2.29	0.50
57:z:134:ILE:HG22	57:z:158:PHE:HA	1.94	0.50
63:AF:68:PRO:HG2	63:AF:71:GLU:HB3	1.93	0.50
64:AG:103:ASN:HA	64:AG:106:LYS:HB3	1.92	0.50
67:AJ:14:PHE:HE2	67:AJ:60:SER:HA	1.77	0.50
70:AM:38:LEU:HA	70:AM:41:MET:HE3	1.92	0.50
71:AN:60:GLU:HA	71:AN:68:ILE:HA	1.92	0.50
79:AV:152:SER:OG	79:AV:172:ALA:O	2.26	0.50
79:AV:201:THR:HG23	79:AV:214:ALA:HB3	1.93	0.50
1:1:370:U:H4'	1:1:404:G:H5''	1.92	0.50
1:1:851:C:OP2	46:p:6:LYS:NZ	2.41	0.50
1:1:1921:A:H2'	1:1:1922:A:H8	1.77	0.50
1:1:2841:G:N2	1:1:2898:G:O6	2.45	0.50
9:D:156:GLY:HA2	9:D:181:PRO:HB3	1.93	0.50
15:J:11:ASP:OD1	15:J:11:ASP:N	2.42	0.50
15:J:15:GLU:OE1	15:J:132:ASN:ND2	2.41	0.50
22:R:115:ILE:HD13	22:R:120:TYR:HB2	1.92	0.50
22:R:143:ILE:HA	22:R:146:LYS:HG2	1.92	0.50
47:2:757:A:O3'	52:u:22:LYS:NZ	2.44	0.50
47:2:1536:G:O2'	47:2:1572:G:O6	2.29	0.50
47:2:1542:G:H22	47:2:1568:C:H1'	1.75	0.50
47:2:1619:C:H2'	47:2:1620:C:H6	1.77	0.50
50:s:244:SER:HA	50:s:247:ALA:HB3	1.94	0.50
51:t:70:THR:HA	51:t:86:LEU:HD11	1.93	0.50
53:v:144:GLU:HB2	53:v:161:ASP:HA	1.94	0.50
55:x:64:VAL:HG13	55:x:67:LEU:HB2	1.94	0.50
65:AH:34:LEU:O	65:AH:38:ILE:N	2.45	0.50
69:AL:55:LEU:HD21	69:AL:69:LEU:HD21	1.93	0.50
83:AZ:10:ARG:HD2	83:AZ:445:ILE:HG22	1.93	0.50
83:AZ:121:VAL:O	83:AZ:399:ARG:NH1	2.42	0.50
83:AZ:597:VAL:HA	83:AZ:600:ALA:HB3	1.93	0.50
1:1:1229:G:H4'	4:P0:32:ASN:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1237:G:N2	5:P2:135:THR:O	2.44	0.50
1:1:1618:G:H2'	1:1:1619:A:H8	1.77	0.50
8:C:288:ARG:HA	8:C:291:ASN:HB2	1.93	0.50
13:H:156:GLN:NE2	13:H:160:ASP:OD2	2.40	0.50
39:i:7:ILE:O	39:i:13:LYS:NZ	2.39	0.50
47:2:853:G:H2'	47:2:854:U:H6	1.77	0.50
47:2:1796:C:OP2	74:AQ:92:ARG:NH1	2.44	0.50
50:s:142:GLY:N	50:s:153:SER:O	2.45	0.50
83:AZ:235:VAL:HG13	83:AZ:236:ASP:HB3	1.93	0.50
1:1:952:A:O2'	1:1:968:G:N2	2.42	0.50
1:1:1342:C:H2'	1:1:1343:A:H8	1.77	0.50
1:1:3188:G:H2'	1:1:3189:G:H8	1.76	0.50
2:3:35:C:O2	2:3:45:A:O2'	2.30	0.50
17:M:48:GLY:O	17:M:52:GLY:N	2.43	0.50
47:2:30:G:OP1	71:AN:126:LYS:NZ	2.36	0.50
47:2:114:C:N4	47:2:247:A:N7	2.60	0.50
47:2:273:G:O6	47:2:283:U:O4	2.28	0.50
1:1:121:A:N1	12:G:108:ARG:NH1	2.59	0.49
1:1:122:A:N7	1:1:146:U:N3	2.60	0.49
30:Z:78:ASN:HA	33:c:35:ARG:HH22	1.77	0.49
33:c:25:LEU:HD12	33:c:87:VAL:HG21	1.93	0.49
46:p:24:ARG:NH2	47:2:1123:C:O2	2.44	0.49
47:2:509:G:H8	47:2:509:G:H5''	1.77	0.49
47:2:1586:A:H62	47:2:1610:G:H21	1.59	0.49
57:z:52:ILE:O	57:z:56:ALA:N	2.44	0.49
60:AC:61:VAL:HG23	60:AC:90:LYS:HA	1.92	0.49
68:AK:51:VAL:HB	68:AK:94:GLU:HB2	1.94	0.49
72:AO:29:HIS:N	72:AO:67:GLY:O	2.38	0.49
74:AQ:23:CYS:HB3	74:AQ:28:LYS:H	1.76	0.49
79:AV:153:GLN:HB2	79:AV:172:ALA:HB3	1.93	0.49
1:1:68:C:OP2	1:1:301:G:N2	2.43	0.49
1:1:422:A:N1	1:1:2362:C:O2'	2.37	0.49
1:1:631:U:H2'	1:1:632:G:H8	1.76	0.49
1:1:2218:G:H2'	1:1:2219:A:H8	1.77	0.49
2:3:121:U:OP2	9:D:265:TYR:OH	2.25	0.49
6:A:92:LYS:HA	6:A:103:PRO:HD2	1.93	0.49
47:2:372:G:H1'	47:2:612:U:H3	1.75	0.49
72:AO:40:LEU:HD11	72:AO:57:VAL:HG21	1.93	0.49
1:1:938:C:O2	1:1:2813:A:O2'	2.30	0.49
1:1:1408:G:OP2	35:e:33:ARG:NH2	2.40	0.49
5:P2:92:ARG:HD3	5:P2:93:LYS:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:110:ILE:HG21	15:J:116:TYR:HD1	1.76	0.49
33:c:86:ARG:HH12	46:p:44:LYS:HA	1.77	0.49
47:2:138:A:O2'	47:2:141:U:OP1	2.30	0.49
47:2:332:U:OP2	56:y:175:GLN:NE2	2.43	0.49
51:t:8:LYS:HG2	68:AK:61:LYS:HD2	1.94	0.49
57:z:34:PHE:O	57:z:110:GLN:NE2	2.45	0.49
79:AV:33:LEU:O	79:AV:45:TRP:N	2.46	0.49
1:1:307:A:H2'	1:1:308:A:H8	1.77	0.49
1:1:383:G:O2'	1:1:385:A:N7	2.43	0.49
1:1:1883:A:H2'	1:1:1884:A:H8	1.78	0.49
11:F:26:VAL:O	11:F:30:ARG:N	2.45	0.49
47:2:937:C:H41	74:AQ:15:ARG:HG3	1.78	0.49
47:2:1218:G:O4'	47:2:1444:A:N6	2.46	0.49
47:2:1294:G:N2	47:2:1303:U:O2	2.32	0.49
47:2:1695:G:O6	47:2:1696:G:N2	2.45	0.49
49:r:197:ILE:HG21	49:r:210:ILE:HG21	1.95	0.49
57:z:139:GLN:HE22	72:AO:64:PHE:HB3	1.78	0.49
83:AZ:711:ARG:O	83:AZ:715:ALA:HB2	2.11	0.49
1:1:2446:U:H1'	1:1:2502:A:H61	1.78	0.49
8:C:329:PRO:HG3	11:F:41:ARG:HD2	1.95	0.49
9:D:259:LYS:O	9:D:265:TYR:OH	2.31	0.49
17:M:112:LEU:HD13	17:M:113:THR:H	1.76	0.49
33:c:42:ILE:HB	33:c:67:VAL:HG22	1.94	0.49
45:o:23:HIS:HA	45:o:74:CYS:HA	1.93	0.49
47:2:235:G:H2'	47:2:236:A:H8	1.78	0.49
47:2:1174:C:H42	47:2:1465:C:H42	1.61	0.49
67:AJ:38:LYS:HA	67:AJ:46:PRO:HB3	1.93	0.49
68:AK:63:LEU:HD12	68:AK:84:MET:HB3	1.94	0.49
74:AQ:44:ILE:N	74:AQ:65:PRO:O	2.41	0.49
83:AZ:41:GLN:HA	83:AZ:46:ILE:HG12	1.94	0.49
1:1:1727:G:OP2	46:p:44:LYS:NZ	2.35	0.49
1:1:2744:U:H2'	1:1:2745:G:C8	2.48	0.49
1:1:2889:C:O2'	1:1:2934:A:O2'	2.25	0.49
1:1:3065:G:O6	1:1:3077:A:N6	2.45	0.49
6:A:211:HIS:HB3	6:A:219:ILE:HG22	1.94	0.49
23:S:33:ASN:HB2	23:S:36:ILE:HG12	1.94	0.49
25:U:37:LEU:O	25:U:41:ILE:N	2.46	0.49
26:V:120:LYS:HE2	26:V:136:VAL:HG12	1.94	0.49
36:f:75:HIS:HB2	36:f:82:ARG:HG3	1.93	0.49
47:2:306:U:OP2	59:AB:88:ARG:NH2	2.34	0.49
47:2:629:U:O4	47:2:970:A:N7	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:898:A:N6	47:2:912:U:O4'	2.46	0.49
47:2:922:G:H2'	47:2:923:A:H8	1.77	0.49
47:2:1160:A:O2'	47:2:1620:C:N3	2.42	0.49
47:2:1298:U:O2	50:s:209:ASN:ND2	2.33	0.49
48:q:88:LYS:NZ	65:AH:83:GLN:OE1	2.35	0.49
49:r:58:SER:O	49:r:62:LYS:NZ	2.45	0.49
75:AR:13:ALA:HB1	75:AR:17:ARG:HH21	1.77	0.49
79:AV:37:SER:OG	79:AV:39:ASP:OD1	2.24	0.49
1:1:67:A:N6	1:1:271:C:O2'	2.45	0.49
1:1:1193:A:N6	1:1:1314:C:C4	2.80	0.49
1:1:1822:C:H2'	1:1:1823:A:H8	1.76	0.49
1:1:2992:U:OP1	7:B:21:ARG:NH1	2.40	0.49
27:W:11:ALA:HB3	27:W:32:GLN:HG3	1.94	0.49
37:g:3:GLN:HE21	37:g:29:ILE:HG23	1.77	0.49
47:2:174:U:H3	47:2:266:A:N6	2.06	0.49
47:2:891:A:H2'	47:2:892:A:H8	1.77	0.49
47:2:1328:G:H5'	51:t:160:SER:H	1.77	0.49
47:2:1356:U:H2'	47:2:1357:A:C8	2.47	0.49
47:2:1765:A:N6	47:2:1768:G:H1	2.10	0.49
49:r:57:ALA:HA	49:r:60:ALA:HB2	1.94	0.49
54:w:3:LEU:N	54:w:16:PHE:O	2.44	0.49
58:AA:21:VAL:HB	58:AA:67:THR:HA	1.95	0.49
68:AK:35:GLU:O	68:AK:39:SER:N	2.44	0.49
83:AZ:30:HIS:N	86:AZ:902:GCP:O2B	2.43	0.49
1:1:150:A:H5'	18:N:147:ARG:HH22	1.77	0.49
1:1:1148:G:H21	1:1:1197:A:H61	1.60	0.49
1:1:1167:U:O2'	11:F:210:PRO:O	2.30	0.49
1:1:2526:C:H2'	1:1:2527:G:H8	1.77	0.49
8:C:145:ILE:HD11	8:C:172:VAL:HG22	1.95	0.49
14:I:145:LYS:HA	14:I:148:VAL:HG12	1.95	0.49
34:d:62:ARG:NH1	34:d:66:GLY:O	2.45	0.49
39:i:2:THR:OG1	39:i:12:ASN:ND2	2.45	0.49
47:2:337:G:H3'	59:AB:133:LYS:HB2	1.95	0.49
47:2:400:A:H4'	47:2:401:A:H5''	1.95	0.49
47:2:520:A:H2'	47:2:521:A:C8	2.48	0.49
47:2:1358:G:H2'	47:2:1359:C:C6	2.48	0.49
53:v:192:GLU:HA	53:v:195:ALA:HB3	1.95	0.49
83:AZ:345:PRO:O	83:AZ:349:GLN:CB	2.59	0.49
1:1:158:G:H2'	1:1:159:A:H8	1.78	0.49
1:1:354:U:O4	1:1:365:A:N7	2.46	0.49
1:1:671:U:H2'	1:1:672:A:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1026:A:H2'	1:1:1027:A:H4'	1.93	0.49
1:1:1748:G:OP2	41:k:42:LYS:NZ	2.41	0.49
1:1:2211:U:O2	81:AX:71:G:O2'	2.31	0.49
1:1:2703:A:H5''	1:1:2704:A:H5'	1.95	0.49
1:1:2760:C:N4	1:1:2796:G:O6	2.46	0.49
20:P:108:ASP:HB3	20:P:111:LYS:HG2	1.94	0.49
25:U:15:PHE:HB2	25:U:65:VAL:HG23	1.94	0.49
47:2:467:G:O2'	47:2:469:C:OP2	2.27	0.49
47:2:872:G:O6	47:2:955:A:N1	2.46	0.49
47:2:908:U:H5''	47:2:909:U:H5	1.78	0.49
47:2:1381:U:H4'	68:AK:59:PRO:HG3	1.95	0.49
50:s:42:GLY:HA2	50:s:68:ILE:HD11	1.95	0.49
52:u:181:VAL:HA	52:u:227:VAL:HA	1.95	0.49
54:w:83:CYS:SG	54:w:95:LYS:NZ	2.81	0.49
55:x:144:VAL:HG13	70:AM:42:GLN:HE22	1.77	0.49
68:AK:103:ILE:HA	68:AK:106:ILE:HG22	1.95	0.49
79:AV:111:MET:HE1	79:AV:127:ARG:HA	1.94	0.49
83:AZ:668:GLN:O	83:AZ:672:LYS:N	2.42	0.49
1:1:197:G:H21	1:1:218:G:H21	1.59	0.49
1:1:664:U:H2'	1:1:665:A:C8	2.47	0.49
1:1:1167:U:H4'	11:F:211:SER:HA	1.94	0.49
1:1:1595:U:O2'	1:1:1606:U:O2	2.31	0.49
7:B:53:MET:HG2	7:B:77:THR:HG22	1.94	0.49
47:2:1044:U:O2	47:2:1074:G:O6	2.31	0.49
47:2:1464:G:O2'	64:AG:141:SER:OG	2.31	0.49
49:r:69:CYS:HB3	62:AE:114:ARG:HH21	1.77	0.49
52:u:90:ILE:HG23	52:u:99:PHE:HB2	1.95	0.49
57:z:2:PRO:HD2	57:z:3:ARG:HH21	1.78	0.49
64:AG:13:LYS:HG3	64:AG:14:LYS:H	1.78	0.49
65:AH:35:CYS:HA	65:AH:38:ILE:HG22	1.94	0.49
79:AV:176:LYS:NZ	79:AV:198:ASN:OD1	2.46	0.49
81:AX:4:G:O6	81:AX:69:U:O4	2.30	0.49
83:AZ:235:VAL:HA	83:AZ:236:ASP:HA	1.71	0.49
1:1:509:U:O2	1:1:582:G:O6	2.31	0.48
1:1:525:C:H5''	17:M:79:ALA:HB2	1.95	0.48
1:1:3058:U:H5''	34:d:28:ARG:HH12	1.77	0.48
1:1:3228:C:OP1	17:M:137:LYS:NZ	2.40	0.48
15:J:133:ARG:NH1	15:J:152:HIS:O	2.46	0.48
47:2:340:U:H2'	47:2:341:A:C8	2.48	0.48
47:2:1489:U:H1'	47:2:1494:C:C2	2.48	0.48
81:AX:15:G:N2	81:AX:48:C:O2	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:294:U:OP2	18:N:15:GLN:NE2	2.46	0.48
11:F:185:ILE:HA	11:F:188:ILE:HG22	1.96	0.48
14:I:181:TYR:HE2	14:I:185:ARG:HH11	1.60	0.48
25:U:58:GLU:HG2	25:U:60:GLY:H	1.79	0.48
29:Y:112:ASP:OD1	29:Y:115:ARG:N	2.45	0.48
36:f:32:ILE:HD13	36:f:44:TYR:HE2	1.79	0.48
47:2:140:A:H61	47:2:281:G:H5''	1.77	0.48
47:2:235:G:H2'	47:2:236:A:C8	2.48	0.48
47:2:1183:A:N6	63:AF:122:THR:O	2.46	0.48
51:t:127:MET:HA	51:t:131:ALA:H	1.77	0.48
51:t:136:VAL:HG22	51:t:186:VAL:HG22	1.95	0.48
57:z:141:VAL:HG12	57:z:143:ILE:H	1.78	0.48
60:AC:31:VAL:HG12	60:AC:123:VAL:HG21	1.95	0.48
74:AQ:91:ASP:OD1	74:AQ:94:ASN:ND2	2.39	0.48
79:AV:31:ASN:HA	79:AV:47:LEU:HB2	1.94	0.48
83:AZ:570:GLU:O	83:AZ:589:LYS:NZ	2.38	0.48
1:1:2458:A:H2	1:1:2480:A:H61	1.61	0.48
1:1:2768:U:O2'	45:o:71:ARG:NH1	2.36	0.48
11:F:236:ILE:HG22	11:F:240:VAL:HG23	1.95	0.48
26:V:75:PRO:HD2	26:V:104:ASN:HB2	1.95	0.48
47:2:1041:G:H2'	47:2:1042:G:C8	2.48	0.48
53:v:58:LEU:HD21	53:v:167:ARG:HB3	1.96	0.48
66:AI:122:HIS:CE1	66:AI:126:ARG:HE	2.31	0.48
76:AS:42:ARG:HG3	76:AS:43:ASN:H	1.78	0.48
79:AV:34:LEU:HA	79:AV:44:SER:HA	1.94	0.48
79:AV:299:GLN:OE1	79:AV:300:THR:OG1	2.31	0.48
81:AX:55:U:N3	81:AX:58:A:OP2	2.46	0.48
1:1:129:U:H2'	1:1:130:A:C8	2.49	0.48
1:1:371:G:N1	1:1:374:A:OP2	2.42	0.48
1:1:790:U:H2'	1:1:791:A:H8	1.77	0.48
1:1:2257:C:H4'	1:1:2257:C:OP1	2.12	0.48
1:1:3180:A:C6	19:O:114:LYS:HD2	2.49	0.48
1:1:3345:G:OP1	56:y:92:ARG:NH1	2.41	0.48
9:D:95:TRP:O	9:D:99:TYR:N	2.39	0.48
12:G:201:THR:HG23	12:G:202:GLU:HG3	1.95	0.48
16:L:99:HIS:CE1	16:L:100:ARG:HE	2.31	0.48
16:L:157:ARG:HH21	31:a:124:ILE:HD13	1.78	0.48
47:2:400:A:H5''	56:y:25:ARG:HA	1.95	0.48
47:2:689:G:H2'	47:2:690:G:H8	1.78	0.48
47:2:1727:G:H2'	47:2:1728:A:C8	2.48	0.48
63:AF:98:ASN:ND2	63:AF:103:ASN:OD1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:802:SER:OG	83:AZ:803:THR:N	2.46	0.48
1:1:361:A:OP1	40:j:24:ARG:NH1	2.46	0.48
1:1:650:C:H2'	1:1:651:G:C8	2.49	0.48
1:1:2519:A:H2'	1:1:2520:A:H8	1.77	0.48
1:1:2583:C:N4	1:1:2584:G:O6	2.46	0.48
1:1:3114:A:OP2	1:1:3115:C:O2'	2.27	0.48
8:C:206:LEU:HB3	8:C:248:VAL:HG12	1.96	0.48
18:N:14:LYS:HA	18:N:19:LEU:HD11	1.94	0.48
22:R:103:ARG:NH1	22:R:124:TYR:OH	2.46	0.48
51:t:74:GLN:HB2	51:t:84:ILE:HG21	1.95	0.48
52:u:211:LYS:HE2	52:u:215:ASP:HA	1.94	0.48
54:w:33:GLY:N	54:w:52:ILE:O	2.46	0.48
54:w:78:THR:O	54:w:87:ARG:NH2	2.47	0.48
56:y:78:ILE:HD12	56:y:104:ILE:HG22	1.95	0.48
65:AH:66:VAL:N	65:AH:69:ILE:O	2.45	0.48
68:AK:40:ASN:O	68:AK:44:ASN:N	2.42	0.48
76:AS:19:THR:OG1	76:AS:27:GLN:NE2	2.34	0.48
83:AZ:432:GLN:HG3	83:AZ:433:ARG:HG3	1.94	0.48
4:P0:141:VAL:HG12	4:P0:156:VAL:HB	1.95	0.48
47:2:655:G:N2	47:2:679:U:OP2	2.47	0.48
47:2:1142:A:H5''	74:AQ:2:PRO:HB3	1.95	0.48
49:r:117:TRP:HB3	49:r:153:HIS:HA	1.95	0.48
63:AF:25:LEU:HD12	63:AF:87:PRO:HB2	1.96	0.48
71:AN:126:LYS:HD3	71:AN:129:GLY:HA2	1.96	0.48
73:AP:82:HIS:O	73:AP:85:LYS:NZ	2.43	0.48
1:1:1488:G:H21	37:g:12:PRO:HG3	1.79	0.48
1:1:2458:A:H62	1:1:2475:G:H2'	1.78	0.48
1:1:2531:C:H42	1:1:2548:C:H42	1.60	0.48
2:3:74:C:H2'	2:3:75:G:C8	2.49	0.48
2:3:96:U:OP1	23:S:43:TYR:OH	2.25	0.48
7:B:50:LYS:HG3	7:B:328:ILE:HD11	1.95	0.48
8:C:252:GLU:HA	8:C:255:PHE:HB3	1.96	0.48
46:p:56:THR:HG23	46:p:63:THR:HG22	1.95	0.48
47:2:1152:A:H4'	74:AQ:85:ARG:HG2	1.94	0.48
47:2:1201:G:H21	47:2:1600:A:H5'	1.79	0.48
47:2:1305:U:OP2	47:2:1306:C:N4	2.43	0.48
48:q:143:VAL:HG23	48:q:157:ASP:H	1.78	0.48
63:AF:52:LYS:HE2	63:AF:83:MET:HA	1.96	0.48
65:AH:26:LEU:HD23	65:AH:58:MET:HB3	1.96	0.48
67:AJ:108:LEU:HB2	67:AJ:113:ILE:HD12	1.95	0.48
67:AJ:114:VAL:HG23	67:AJ:124:ILE:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:120:ARG:HB2	83:AZ:479:LYS:HZ1	1.79	0.48
83:AZ:798:PHE:N	85:AZ:901:SO1:O57	2.47	0.48
1:1:39:A:H5''	31:a:35:ALA:HB2	1.96	0.48
1:1:542:G:O6	1:1:549:U:O4	2.32	0.48
1:1:802:C:H41	31:a:25:HIS:HB3	1.79	0.48
1:1:1029:G:H2'	1:1:1030:A:C8	2.48	0.48
1:1:2555:G:H1'	37:g:92:ALA:HB2	1.96	0.48
5:P2:133:LEU:HD22	5:P2:137:GLN:HB2	1.96	0.48
15:J:109:HIS:CD2	15:J:123:PHE:H	2.32	0.48
18:N:66:VAL:HG22	18:N:102:ALA:HB2	1.95	0.48
28:X:86:VAL:HG21	28:X:95:ILE:HD11	1.95	0.48
47:2:1756:A:H2	82:AY:50:U:OP2	1.96	0.48
48:q:13:ASP:HB3	48:q:17:LEU:HD13	1.95	0.48
49:r:92:GLN:HE22	49:r:228:LEU:HD11	1.79	0.48
56:y:87:ASN:ND2	56:y:89:GLU:OE2	2.47	0.48
57:z:22:SER:O	57:z:26:ALA:N	2.46	0.48
65:AH:17:ILE:HG22	65:AH:24:LEU:HD11	1.96	0.48
67:AJ:105:LEU:HD13	67:AJ:122:ARG:HH22	1.79	0.48
83:AZ:840:ASP:N	83:AZ:840:ASP:OD1	2.46	0.48
1:1:411:U:H2'	1:1:412:G:H8	1.79	0.48
11:F:110:ARG:HH21	21:Q:3:ILE:HG23	1.79	0.48
16:L:52:ASP:HB3	16:L:141:ALA:HB3	1.96	0.48
47:2:445:A:H61	47:2:462:G:H1'	1.79	0.48
47:2:507:U:O2	47:2:507:U:H2'	2.13	0.48
47:2:1219:A:O2'	58:AA:47:GLN:O	2.29	0.48
47:2:1512:G:N3	47:2:1518:C:O2'	2.34	0.48
47:2:1641:C:H2'	47:2:1642:G:H8	1.79	0.48
47:2:1688:U:H3	47:2:1713:G:H1	1.62	0.48
50:s:227:PRO:HA	50:s:230:TRP:CD2	2.49	0.48
57:z:20:GLU:OE1	57:z:23:ARG:N	2.42	0.48
65:AH:5:ARG:NH1	65:AH:49:LYS:O	2.47	0.48
66:AI:100:THR:HB	66:AI:105:VAL:HA	1.96	0.48
67:AJ:65:ILE:HA	67:AJ:68:ARG:HH21	1.78	0.48
1:1:68:C:N4	1:1:314:U:O2'	2.46	0.48
1:1:69:C:OP1	18:N:178:HIS:ND1	2.37	0.48
1:1:417:A:H2'	1:1:418:A:C8	2.49	0.48
1:1:2248:C:N4	1:1:2312:A:OP2	2.46	0.48
8:C:55:LYS:HB3	8:C:59:GLN:HE21	1.79	0.48
8:C:299:ILE:HG23	21:Q:39:ARG:HB3	1.95	0.48
19:O:110:PRO:O	19:O:112:TYR:N	2.46	0.48
23:S:89:ASN:ND2	24:T:156:TYR:O	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:69:GLY:HA2	36:f:85:PHE:HA	1.96	0.48
46:p:38:ASP:OD1	46:p:38:ASP:N	2.47	0.48
47:2:538:A:OP2	57:z:175:ARG:NH1	2.47	0.48
47:2:631:G:N2	47:2:1104:U:OP1	2.47	0.48
47:2:732:G:O2'	47:2:733:A:O4'	2.31	0.48
47:2:1101:G:H21	70:AM:4:SER:HG	1.58	0.48
47:2:1411:A:O2'	47:2:1415:U:O2	2.30	0.48
47:2:1499:G:O6	47:2:1508:U:O4	2.32	0.48
52:u:128:LYS:NZ	52:u:138:TYR:OH	2.47	0.48
68:AK:85:ARG:HE	68:AK:87:HIS:HD2	1.62	0.48
1:1:297:G:OP2	1:1:297:G:N2	2.37	0.47
6:A:201:GLY:HA2	6:A:204:MET:HE2	1.96	0.47
7:B:215:ILE:HD13	7:B:338:LEU:HD12	1.96	0.47
12:G:112:GLU:HB2	12:G:116:VAL:HG23	1.95	0.47
17:M:9:ALA:HB1	17:M:11:ASN:HB2	1.96	0.47
30:Z:95:VAL:HG23	30:Z:96:VAL:HG23	1.95	0.47
34:d:8:VAL:HG23	34:d:10:ARG:HH11	1.78	0.47
39:i:8:ALA:HA	39:i:13:LYS:HD2	1.96	0.47
47:2:1389:C:N4	47:2:1391:A:O4'	2.47	0.47
47:2:1534:G:N1	73:AP:98:GLN:OE1	2.47	0.47
57:z:67:PRO:HA	57:z:70:LEU:HB2	1.95	0.47
58:AA:71:GLU:O	58:AA:75:TYR:N	2.47	0.47
63:AF:90:ILE:HG13	63:AF:107:ILE:HG22	1.96	0.47
79:AV:248:ASN:ND2	79:AV:297:ASP:O	2.47	0.47
83:AZ:626:ASP:OD2	83:AZ:628:THR:OG1	2.30	0.47
1:1:89:A:OP2	21:Q:170:ARG:NH1	2.46	0.47
1:1:612:U:H2'	1:1:613:G:H8	1.79	0.47
1:1:655:C:H2'	1:1:656:A:C8	2.48	0.47
1:1:1232:C:H2'	1:1:1233:G:C8	2.49	0.47
1:1:1483:G:O6	1:1:1873:U:O4	2.33	0.47
1:1:1622:U:H2'	1:1:1623:G:H8	1.79	0.47
1:1:1834:U:OP1	42:l:5:LYS:NZ	2.39	0.47
1:1:2703:A:N1	9:D:23:ARG:NH2	2.62	0.47
1:1:2945:G:O2'	1:1:2948:C:OP2	2.24	0.47
1:1:3152:U:H5''	1:1:3293:U:H1'	1.95	0.47
11:F:158:LYS:H	11:F:158:LYS:HD2	1.79	0.47
36:f:6:ARG:HH12	36:f:10:LYS:HE3	1.78	0.47
41:k:59:ALA:O	41:k:63:LYS:N	2.46	0.47
52:u:125:LYS:HD3	52:u:226:PHE:HD1	1.79	0.47
53:v:174:LEU:HA	53:v:177:ILE:HB	1.96	0.47
58:AA:21:VAL:HG11	58:AA:46:LEU:HG	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AB:65:SER:H	59:AB:67:ARG:HH22	1.62	0.47
67:AJ:22:LEU:HD13	67:AJ:25:GLN:HG3	1.95	0.47
79:AV:305:TYR:HE2	79:AV:311:ARG:HB2	1.79	0.47
83:AZ:304:GLU:O	83:AZ:326:LYS:NZ	2.40	0.47
1:1:591:G:O2'	10:E:17:ALA:O	2.29	0.47
1:1:1175:C:O2'	19:O:87:MET:O	2.29	0.47
3:4:8:C:H2'	3:4:9:A:C8	2.50	0.47
7:B:45:SER:HB2	7:B:181:ILE:HG22	1.95	0.47
10:E:35:VAL:O	10:E:38:THR:OG1	2.30	0.47
16:L:50:PRO:HG3	38:h:118:ILE:HD11	1.96	0.47
19:O:34:VAL:HG22	19:O:103:LYS:H	1.79	0.47
47:2:432:G:OP1	83:AZ:391:LYS:NZ	2.37	0.47
47:2:811:A:C5	55:x:110:GLN:HB3	2.49	0.47
47:2:925:G:H2'	47:2:926:A:H8	1.79	0.47
47:2:1208:A:H1'	47:2:1269:U:H1'	1.96	0.47
47:2:1673:G:H1	47:2:1728:A:H2	1.54	0.47
61:AD:135:LEU:HD13	61:AD:136:PRO:HD2	1.96	0.47
1:1:196:G:N1	1:1:199:A:OP2	2.35	0.47
1:1:860:G:H5'	1:1:861:C:H5''	1.95	0.47
1:1:1354:G:H1	1:1:1357:G:HO2'	1.59	0.47
1:1:1942:U:HO2'	1:1:3345:G:HO2'	1.61	0.47
1:1:2748:A:O3'	9:D:48:LYS:NZ	2.46	0.47
2:3:63:A:OP1	9:D:285:ARG:NH1	2.48	0.47
6:A:178:PRO:HB2	6:A:180:LEU:HD22	1.96	0.47
7:B:218:ILE:HB	7:B:276:THR:HG23	1.97	0.47
15:J:43:GLN:HE22	15:J:71:VAL:HG13	1.79	0.47
23:S:32:SER:H	23:S:36:ILE:HD11	1.79	0.47
47:2:762:A:H5''	57:z:79:ARG:HH12	1.79	0.47
47:2:1148:C:H2'	47:2:1149:G:H8	1.79	0.47
47:2:1548:G:H1'	66:Al:89:GLN:HE21	1.79	0.47
53:v:189:THR:OG1	53:v:192:GLU:OE1	2.32	0.47
67:AJ:83:ALA:HB1	67:AJ:91:TYR:HB3	1.97	0.47
73:AP:48:ASP:HA	73:AP:51:LEU:HD13	1.96	0.47
79:AV:252:LEU:N	79:AV:263:PHE:O	2.47	0.47
83:AZ:393:ARG:NH1	83:AZ:461:GLN:OE1	2.40	0.47
1:1:292:U:OP2	18:N:68:ARG:NH2	2.48	0.47
1:1:661:G:OP2	1:1:661:G:N2	2.42	0.47
1:1:1666:G:H2'	1:1:1667:A:H8	1.80	0.47
1:1:2340:U:H2'	1:1:2341:A:H8	1.79	0.47
1:1:3114:A:OP1	13:H:69:ARG:NH1	2.48	0.47
23:S:123:ILE:HG21	23:S:126:VAL:HG13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:142:G:H22	47:2:173:A:H2	1.62	0.47
48:q:57:LEU:O	48:q:61:ALA:N	2.47	0.47
52:u:200:ARG:NH2	52:u:206:ASP:OD1	2.47	0.47
81:AX:54:U:C2	81:AX:58:A:N7	2.82	0.47
1:1:836:A:O2'	46:p:9:GLY:O	2.26	0.47
1:1:1827:C:H2'	1:1:1828:A:C8	2.50	0.47
1:1:2424:A:H3'	1:1:2425:G:H8	1.79	0.47
1:1:2899:C:O2	13:H:173:ARG:NH2	2.48	0.47
3:4:8:C:H2'	3:4:9:A:H8	1.79	0.47
7:B:223:GLY:HA2	7:B:271:GLY:HA3	1.97	0.47
8:C:288:ARG:O	8:C:292:SER:N	2.47	0.47
20:P:30:ARG:NH1	20:P:31:GLU:OE1	2.44	0.47
47:2:406:U:O2'	54:w:94:ARG:NH2	2.48	0.47
47:2:756:A:O3'	52:u:16:HIS:NE2	2.48	0.47
47:2:818:C:N3	47:2:819:G:N1	2.62	0.47
47:2:1642:G:N3	47:2:1781:A:O2'	2.41	0.47
51:t:51:ARG:HG2	51:t:91:VAL:HG23	1.97	0.47
71:AN:86:PHE:HB2	71:AN:120:VAL:HG11	1.97	0.47
71:AN:103:LEU:HB3	71:AN:126:LYS:HB3	1.96	0.47
83:AZ:524:GLU:HG2	83:AZ:562:ALA:HB2	1.96	0.47
83:AZ:571:SER:H	83:AZ:720:ALA:HB2	1.78	0.47
83:AZ:818:ILE:O	83:AZ:822:ALA:CB	2.61	0.47
1:1:707:U:H2'	1:1:708:G:C8	2.50	0.47
1:1:1350:A:N6	1:1:1354:G:OP2	2.47	0.47
1:1:1551:C:HO2'	1:1:2170:U:HO2'	1.59	0.47
1:1:2178:A:O2'	6:A:152:SER:OG	2.33	0.47
1:1:2207:A:H61	1:1:2236:G:H1	1.63	0.47
1:1:2519:A:H2'	1:1:2520:A:C8	2.50	0.47
1:1:2666:C:OP2	1:1:2687:G:N1	2.37	0.47
1:1:2916:U:H2'	1:1:2917:G:H8	1.80	0.47
1:1:3304:U:H4'	7:B:331:ASN:HD21	1.79	0.47
2:3:11:A:N6	9:D:16:PHE:O	2.48	0.47
5:P2:115:GLN:HA	5:P2:119:LYS:NZ	2.30	0.47
6:A:247:ARG:HE	6:A:249:SER:HG	1.60	0.47
9:D:125:VAL:HG22	9:D:199:ILE:HD13	1.96	0.47
16:L:124:ILE:HD11	38:h:117:ALA:HB3	1.97	0.47
20:P:16:SER:O	20:P:101:ASN:ND2	2.48	0.47
20:P:92:GLN:HA	20:P:95:LEU:HG	1.96	0.47
34:d:72:ARG:NH1	34:d:104:LEU:O	2.48	0.47
47:2:629:U:H5''	61:AD:127:ARG:HH22	1.80	0.47
47:2:1181:U:O2'	63:AF:127:ARG:NE	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1517:U:OP2	47:2:1518:C:N4	2.38	0.47
51:t:34:TYR:HE1	51:t:37:VAL:HG13	1.78	0.47
51:t:168:ILE:HA	51:t:189:MET:HA	1.97	0.47
54:w:20:ASP:HB3	54:w:23:ARG:HB2	1.96	0.47
55:x:127:GLU:HG2	55:x:135:ILE:HD13	1.97	0.47
58:AA:82:LEU:HD22	58:AA:83:PRO:HD2	1.96	0.47
61:AD:17:PRO:HG3	75:AR:28:PRO:HG3	1.97	0.47
72:AO:126:ALA:HA	72:AO:129:VAL:HG12	1.97	0.47
79:AV:34:LEU:HD11	79:AV:42:LEU:HB3	1.95	0.47
83:AZ:103:ILE:HD11	83:AZ:122:THR:HB	1.97	0.47
83:AZ:575:ALA:O	83:AZ:587:TYR:HA	2.14	0.47
1:1:355:A:O2'	42:l:39:ALA:O	2.33	0.47
1:1:713:U:O2'	1:1:754:G:OP1	2.29	0.47
1:1:2750:U:OP2	24:T:69:LYS:NZ	2.43	0.47
1:1:3004:C:O2'	7:B:99:LEU:N	2.48	0.47
15:J:91:LEU:HD13	15:J:95:ASN:HD22	1.79	0.47
21:Q:51:ALA:HB1	21:Q:84:VAL:HG11	1.96	0.47
22:R:169:ALA:O	22:R:173:ARG:NE	2.41	0.47
22:R:172:ARG:HH21	47:2:852:C:H5''	1.80	0.47
47:2:1108:G:H4'	47:2:1109:G:H5''	1.96	0.47
47:2:1192:C:H3'	47:2:1193:A:C8	2.50	0.47
47:2:1584:G:N7	53:v:76:ARG:NH1	2.62	0.47
53:v:116:HIS:NE2	73:AP:93:SER:OG	2.46	0.47
55:x:35:LYS:HD2	55:x:39:ARG:HB2	1.96	0.47
71:AN:62:LYS:CE	71:AN:118:PRO:HD3	2.45	0.47
76:AS:49:ARG:N	76:AS:52:ASP:OD2	2.47	0.47
79:AV:159:ASN:HB3	79:AV:163:ASP:HA	1.96	0.47
1:1:216:G:OP1	29:Y:16:ARG:NH1	2.48	0.47
1:1:242:C:O2'	1:1:243:G:N7	2.40	0.47
1:1:846:A:H2'	1:1:847:A:C8	2.50	0.47
1:1:1497:C:H2'	1:1:1498:A:H8	1.80	0.47
1:1:1863:G:N1	1:1:1866:C:OP2	2.46	0.47
3:4:64:U:O2'	38:h:52:ALA:O	2.32	0.47
8:C:351:PRO:HB3	11:F:70:LYS:HD2	1.96	0.47
11:F:96:PRO:HB2	11:F:99:PRO:HD2	1.97	0.47
12:G:240:ASN:HA	12:G:243:GLN:HB3	1.97	0.47
13:H:173:ARG:HB2	43:m:127:LEU:HD22	1.95	0.47
14:I:171:TRP:HE3	14:I:178:ARG:HG3	1.79	0.47
24:T:34:TYR:OH	24:T:96:ILE:O	2.33	0.47
47:2:513:U:H2'	47:2:514:G:C8	2.50	0.47
47:2:1030:A:N6	47:2:1792:G:N7	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1156:C:H2'	47:2:1157:A:H8	1.80	0.47
48:q:27:ARG:NH1	48:q:43:ASP:O	2.48	0.47
49:r:114:VAL:HG12	49:r:120:LEU:HD21	1.97	0.47
53:v:188:LYS:HA	73:AP:63:SER:HB3	1.96	0.47
54:w:72:ARG:HA	54:w:98:ARG:HA	1.96	0.47
83:AZ:593:ILE:HD11	83:AZ:685:ARG:HB2	1.96	0.47
1:1:644:G:N2	1:1:2372:A:O4'	2.47	0.47
1:1:1203:A:H4'	2:3:91:G:H22	1.80	0.47
12:G:97:TYR:HB3	12:G:131:ALA:HA	1.97	0.47
19:O:51:LYS:O	19:O:55:HIS:N	2.48	0.47
47:2:318:U:O2	47:2:346:G:O6	2.33	0.47
47:2:568:G:N7	71:AN:69:ARG:NH1	2.63	0.47
47:2:1165:G:O2'	47:2:1166:A:O5'	2.31	0.47
52:u:89:VAL:HB	52:u:100:ARG:HE	1.79	0.47
58:AA:56:LYS:H	58:AA:69:THR:HG21	1.80	0.47
69:AL:21:ASN:OD1	70:AM:23:ARG:NH1	2.44	0.47
81:AX:10:G:O6	81:AX:44:A:N6	2.48	0.47
1:1:286:U:H2'	1:1:287:G:C8	2.49	0.46
1:1:837:A:N6	1:1:856:G:O2'	2.48	0.46
1:1:1231:A:O2'	1:1:1278:A:N6	2.49	0.46
1:1:1336:U:H2'	1:1:1337:A:C8	2.50	0.46
1:1:1836:C:H2'	1:1:1837:U:H6	1.80	0.46
3:4:9:A:H2'	3:4:10:A:C8	2.50	0.46
3:4:91:C:H2'	3:4:92:A:C8	2.50	0.46
8:C:154:THR:OG1	8:C:252:GLU:OE2	2.33	0.46
9:D:284:ALA:O	9:D:288:ALA:N	2.47	0.46
19:O:160:ARG:O	19:O:164:SER:N	2.48	0.46
47:2:1045:C:H2'	47:2:1046:G:C8	2.50	0.46
47:2:1320:U:N3	47:2:1323:C:OP1	2.47	0.46
47:2:1382:A:H1'	68:AK:57:ARG:HH21	1.81	0.46
47:2:1533:C:OP2	73:AP:77:ARG:NH2	2.48	0.46
47:2:1544:U:OP1	66:AI:136:GLN:NE2	2.48	0.46
51:t:29:LEU:HG	51:t:32:GLU:HB3	1.98	0.46
54:w:135:PRO:HD2	54:w:158:ILE:HG13	1.97	0.46
61:AD:38:VAL:HA	61:AD:41:ALA:HB3	1.97	0.46
79:AV:292:LEU:HD12	79:AV:301:LEU:HD11	1.96	0.46
80:AW:123:ASN:HB3	80:AW:126:CYS:HB2	1.96	0.46
83:AZ:278:LEU:HD12	83:AZ:281:ILE:HB	1.96	0.46
83:AZ:409:GLN:HE22	83:AZ:411:VAL:HB	1.80	0.46
1:1:3255:U:H2'	1:1:3256:G:H8	1.80	0.46
12:G:97:TYR:HB2	12:G:132:VAL:HG13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Z:76:ASN:HD21	30:Z:78:ASN:HD22	1.63	0.46
31:a:73:LEU:HD21	31:a:81:LEU:HD11	1.97	0.46
38:h:67:ARG:HG2	38:h:80:LEU:HD21	1.96	0.46
47:2:416:A:N6	83:AZ:47:SER:OG	2.48	0.46
47:2:477:A:OP1	78:AU:31:LYS:N	2.45	0.46
54:w:145:PHE:HB2	54:w:147:LEU:HG	1.97	0.46
71:AN:144:ARG:HH11	83:AZ:464:LEU:HD23	1.79	0.46
79:AV:66:HIS:CD2	79:AV:85:TRP:HB2	2.49	0.46
83:AZ:283:ARG:O	83:AZ:287:ALA:HB2	2.16	0.46
1:1:214:G:H2'	1:1:215:G:C8	2.50	0.46
1:1:399:A:HO2'	1:1:403:C:HO2'	1.57	0.46
1:1:836:A:N7	1:1:856:G:N2	2.64	0.46
1:1:1717:U:H2'	1:1:1718:G:H8	1.80	0.46
1:1:2112:U:O2	1:1:2113:A:N6	2.49	0.46
1:1:2526:C:H2'	1:1:2527:G:C8	2.50	0.46
16:L:71:ALA:HB2	16:L:147:ILE:HD11	1.97	0.46
27:W:52:THR:HG23	27:W:55:PHE:H	1.80	0.46
29:Y:60:ARG:HB2	29:Y:103:LYS:HD2	1.97	0.46
47:2:107:C:H2'	47:2:108:A:H8	1.80	0.46
47:2:1546:G:OP2	66:AI:134:ARG:NE	2.46	0.46
53:v:222:LYS:NZ	76:AS:57:MET:O	2.49	0.46
71:AN:96:VAL:HG13	71:AN:127:VAL:HG21	1.97	0.46
81:AX:21:A:N6	81:AX:48:C:OP2	2.47	0.46
1:1:647:A:O2'	1:1:649:A:OP1	2.33	0.46
1:1:951:A:O2'	1:1:969:C:O2'	2.33	0.46
1:1:1236:G:H1'	1:1:1245:A:H1'	1.98	0.46
1:1:2802:A:H4'	45:o:58:PHE:HA	1.97	0.46
1:1:3250:U:H2'	1:1:3251:U:H6	1.80	0.46
9:D:120:LYS:NZ	9:D:123:GLU:OE1	2.47	0.46
10:E:12:SER:OG	10:E:14:ASP:OD1	2.33	0.46
10:E:131:LYS:HG3	10:E:133:GLU:H	1.80	0.46
47:2:717:C:N4	47:2:723:G:O6	2.48	0.46
47:2:1547:A:OP2	66:AI:123:ARG:NH2	2.49	0.46
47:2:1616:G:N2	76:AS:22:ARG:O	2.35	0.46
48:q:167:LYS:HE3	48:q:203:PHE:HB3	1.96	0.46
59:AB:132:SER:HG	59:AB:135:VAL:H	1.60	0.46
62:AE:92:LYS:NZ	62:AE:120:PRO:O	2.49	0.46
67:AJ:20:SER:O	67:AJ:24:ARG:NH1	2.46	0.46
79:AV:59:ARG:HH21	79:AV:94:VAL:HG12	1.80	0.46
83:AZ:563:TYR:HE2	83:AZ:818:ILE:HD12	1.81	0.46
83:AZ:711:ARG:O	83:AZ:715:ALA:CB	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1348:U:O2	1:1:1349:G:N2	2.37	0.46
1:1:2154:U:H2'	1:1:2155:G:H8	1.80	0.46
1:1:2661:G:H2'	1:1:2662:G:H8	1.80	0.46
1:1:2918:G:H2'	1:1:2919:A:C8	2.50	0.46
1:1:3058:U:OP2	34:d:28:ARG:NH2	2.49	0.46
1:1:3222:U:O2	1:1:3263:G:N2	2.35	0.46
2:3:18:C:OP2	15:J:150:ASN:ND2	2.47	0.46
3:4:41:A:H62	3:4:103:G:H21	1.64	0.46
6:A:108:PRO:HG2	46:p:86:LEU:HD11	1.98	0.46
11:F:80:GLN:HB3	24:T:135:PRO:HB2	1.96	0.46
38:h:17:LEU:HD22	38:h:58:ILE:HG23	1.98	0.46
47:2:118:U:H3	47:2:298:C:H42	1.63	0.46
47:2:299:A:H2'	47:2:300:A:H8	1.81	0.46
47:2:748:U:O2	47:2:801:G:O6	2.33	0.46
47:2:864:U:H5	70:AM:28:ARG:HE	1.63	0.46
47:2:1149:G:N3	47:2:1765:A:O2'	2.46	0.46
47:2:1277:G:H21	51:t:174:HIS:HE1	1.64	0.46
47:2:1524:A:H2'	47:2:1525:A:C8	2.51	0.46
47:2:1591:C:H2'	47:2:1592:A:C8	2.50	0.46
83:AZ:669:TRP:HA	83:AZ:670:ALA:HA	1.66	0.46
1:1:213:A:O2'	29:Y:3:LYS:NZ	2.46	0.46
1:1:673:U:H2'	1:1:674:G:H8	1.81	0.46
1:1:964:G:OP2	1:1:1115:G:N1	2.46	0.46
1:1:1187:C:OP1	13:H:2:LYS:NZ	2.42	0.46
1:1:1783:U:H2'	1:1:1784:G:C8	2.51	0.46
2:3:107:C:H2'	2:3:108:A:C8	2.50	0.46
10:E:55:LEU:HD21	10:E:98:VAL:HG22	1.96	0.46
38:h:44:ILE:HA	38:h:47:VAL:HG12	1.97	0.46
38:h:93:THR:N	38:h:96:GLU:OE2	2.48	0.46
47:2:609:U:O2'	71:AN:19:ARG:NH2	2.45	0.46
47:2:1758:U:C4	47:2:1759:C:C4	3.04	0.46
54:w:7:TYR:HD1	54:w:113:ILE:HB	1.81	0.46
55:x:14:THR:HG23	55:x:17:GLU:H	1.80	0.46
57:z:78:ARG:O	57:z:82:ARG:N	2.49	0.46
74:AQ:79:ILE:HB	74:AQ:85:ARG:HA	1.97	0.46
1:1:1119:C:H2'	1:1:1120:A:C8	2.50	0.46
1:1:1695:U:O2'	1:1:1749:A:N1	2.38	0.46
1:1:3229:G:H2'	1:1:3230:G:H8	1.80	0.46
47:2:645:C:H2'	47:2:646:C:H6	1.80	0.46
47:2:1068:C:H2'	47:2:1069:A:H8	1.80	0.46
47:2:1113:A:H62	47:2:1132:A:H62	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1532:U:OP2	73:AP:77:ARG:NH1	2.49	0.46
66:AI:73:MET:O	66:AI:99:HIS:NE2	2.48	0.46
83:AZ:6:VAL:HA	83:AZ:7:ASP:HA	1.68	0.46
1:1:63:A:N3	1:1:78:U:O2'	2.42	0.46
1:1:1018:G:H22	1:1:1034:U:H3	1.64	0.46
1:1:1019:G:H2'	1:1:1020:G:C8	2.50	0.46
3:4:95:G:H1'	40:j:81:GLY:HA2	1.98	0.46
18:N:84:PRO:HA	18:N:87:GLN:HB2	1.96	0.46
23:S:155:ARG:NE	23:S:171:PHE:O	2.49	0.46
47:2:610:G:HO2'	47:2:613:G:HO2'	1.58	0.46
47:2:918:U:H2'	47:2:919:A:C8	2.50	0.46
47:2:1148:C:H2'	47:2:1149:G:C8	2.50	0.46
47:2:1235:C:H1'	80:AW:138:ARG:HH12	1.81	0.46
47:2:1524:A:H2'	47:2:1525:A:H8	1.80	0.46
47:2:1761:U:C5	82:AY:47:U:H5''	2.50	0.46
47:2:1792:G:OP1	74:AQ:8:ASN:ND2	2.45	0.46
51:t:75:LYS:HZ3	51:t:81:PRO:HD3	1.80	0.46
53:v:183:ALA:HA	53:v:186:ASN:HD21	1.80	0.46
63:AF:118:GLU:O	66:AI:122:HIS:N	2.45	0.46
72:AO:41:ARG:HH22	72:AO:53:ASP:HA	1.81	0.46
76:AS:10:ALA:HA	76:AS:32:PHE:HA	1.97	0.46
1:1:157:A:N7	39:i:26:ILE:HD13	2.31	0.46
1:1:609:G:OP2	8:C:315:LYS:NZ	2.44	0.46
1:1:952:A:N7	1:1:1142:G:N2	2.64	0.46
1:1:2366:C:H2'	1:1:2367:A:H8	1.80	0.46
1:1:2696:A:C6	1:1:2758:A:C2	3.03	0.46
18:N:11:GLN:OE1	18:N:44:ARG:NE	2.42	0.46
20:P:19:GLY:N	20:P:146:ILE:O	2.43	0.46
26:V:101:VAL:HG11	26:V:109:MET:HE2	1.98	0.46
47:2:826:U:O2	47:2:846:G:N2	2.33	0.46
47:2:884:A:H2'	47:2:885:G:C8	2.51	0.46
50:s:167:VAL:HG21	50:s:214:ALA:HA	1.98	0.46
72:AO:56:SER:O	72:AO:74:LEU:N	2.49	0.46
83:AZ:506:GLU:HA	83:AZ:509:LYS:HG2	1.98	0.46
1:1:13:A:O2'	1:1:15:C:OP2	2.30	0.46
1:1:1618:G:H2'	1:1:1619:A:C8	2.51	0.46
1:1:2158:A:O2'	6:A:118:GLU:OE2	2.33	0.46
1:1:2950:G:H22	1:1:2979:U:H2'	1.80	0.46
2:3:31:U:O2'	9:D:218:ARG:NH2	2.36	0.46
7:B:46:PHE:O	7:B:337:THR:OG1	2.32	0.46
14:I:42:THR:OG1	14:I:45:GLU:OE1	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:42:THR:N	14:I:45:GLU:OE2	2.49	0.46
47:2:454:U:O2'	47:2:455:C:O4'	2.31	0.46
47:2:1001:A:OP1	81:AX:38:A:O2'	2.31	0.46
47:2:1474:G:H2'	47:2:1475:A:C8	2.51	0.46
47:2:1673:G:C6	47:2:1728:A:N1	2.84	0.46
48:q:72:ASP:OD2	48:q:119:ARG:N	2.49	0.46
52:u:193:GLY:HA3	52:u:210:ILE:HG23	1.98	0.46
54:w:98:ARG:NH2	54:w:105:ASP:OD2	2.49	0.46
79:AV:131:ILE:HB	79:AV:144:LEU:HD13	1.98	0.46
79:AV:241:PHE:N	79:AV:255:ALA:O	2.49	0.46
1:1:1158:A:OP1	11:F:91:GLY:N	2.46	0.45
1:1:1342:C:H2'	1:1:1343:A:C8	2.51	0.45
1:1:1785:U:H2'	1:1:1786:G:C8	2.51	0.45
1:1:2521:U:O2'	1:1:2524:A:OP1	2.27	0.45
1:1:2586:G:O2'	1:1:2588:U:OP2	2.31	0.45
14:I:36:LEU:HG	14:I:87:LEU:HB2	1.97	0.45
22:R:162:ARG:NH1	47:2:815:G:N3	2.64	0.45
28:X:53:HIS:CE1	28:X:56:ARG:HE	2.34	0.45
42:l:29:LEU:O	42:l:31:THR:N	2.49	0.45
47:2:689:G:H2'	47:2:690:G:C8	2.51	0.45
47:2:733:A:O2'	47:2:735:C:N4	2.48	0.45
47:2:964:U:OP1	61:AD:128:TYR:OH	2.33	0.45
47:2:1374:C:H2'	47:2:1375:A:C8	2.52	0.45
47:2:1501:C:H2'	47:2:1502:G:C8	2.51	0.45
49:r:39:GLU:HG3	49:r:40:ASN:H	1.80	0.45
52:u:180:LEU:HG	52:u:231:GLN:HA	1.98	0.45
58:AA:32:HIS:HD2	58:AA:35:ILE:HB	1.80	0.45
83:AZ:39:LEU:HD21	83:AZ:334:LEU:HD12	1.99	0.45
1:1:402:A:OP2	42:l:36:ARG:NH2	2.49	0.45
1:1:1231:A:H62	4:P0:110:ARG:HH22	1.63	0.45
1:1:1344:G:N3	11:F:159:GLN:NE2	2.64	0.45
1:1:2222:A:H2'	1:1:2223:A:C8	2.51	0.45
15:J:165:GLN:CD	15:J:166:LYS:H	2.24	0.45
23:S:82:ASP:HA	23:S:87:THR:HA	1.98	0.45
44:n:9:ARG:NH2	47:2:1642:G:O2'	2.49	0.45
47:2:381:C:O2'	47:2:755:A:N1	2.45	0.45
47:2:891:A:H2'	47:2:892:A:C8	2.51	0.45
47:2:1167:G:OP2	53:v:102:ARG:NH2	2.40	0.45
61:AD:63:ALA:HB3	61:AD:71:ILE:HD11	1.98	0.45
64:AG:127:LYS:HG3	64:AG:134:ALA:HA	1.98	0.45
76:AS:41:VAL:HG12	76:AS:62:GLU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AX:50:U:H2'	81:AX:51:G:H8	1.80	0.45
1:1:116:A:OP2	18:N:2:GLY:N	2.50	0.45
1:1:590:G:C2	1:1:610:G:H2'	2.52	0.45
1:1:842:G:H2'	1:1:843:A:H8	1.81	0.45
1:1:966:U:H2'	1:1:967:A:C8	2.51	0.45
1:1:2273:G:O2'	1:1:2311:G:O6	2.27	0.45
1:1:2943:G:C8	7:B:2:SER:HB3	2.52	0.45
1:1:3101:G:H2'	1:1:3102:G:H8	1.82	0.45
8:C:260:GLN:HA	8:C:267:VAL:HG11	1.97	0.45
17:M:123:LEU:HB3	19:O:193:GLN:HE22	1.82	0.45
29:Y:58:VAL:HG13	29:Y:65:GLY:H	1.80	0.45
37:g:41:ARG:NH2	37:g:51:LEU:O	2.49	0.45
47:2:677:G:H21	47:2:678:A:H62	1.64	0.45
47:2:991:G:H1'	47:2:1014:G:H22	1.82	0.45
48:q:184:LEU:HD12	69:AL:45:ALA:HB2	1.97	0.45
67:AJ:97:SER:O	67:AJ:101:ASN:ND2	2.35	0.45
83:AZ:238:ALA:O	83:AZ:242:ASP:CB	2.63	0.45
83:AZ:583:HIS:HA	83:AZ:694:HIS:HE1	1.81	0.45
1:1:50:U:H2'	1:1:51:A:H8	1.82	0.45
1:1:417:A:H2'	1:1:418:A:H8	1.82	0.45
1:1:534:U:H1'	23:S:146:LYS:HE2	1.98	0.45
1:1:671:U:H2'	1:1:672:A:C8	2.52	0.45
1:1:1231:A:H62	4:P0:110:ARG:NH1	2.12	0.45
1:1:3119:U:O3'	43:m:111:ARG:NH1	2.50	0.45
6:A:202:VAL:HG12	6:A:217:GLN:HB3	1.97	0.45
7:B:19:ARG:HB2	7:B:273:HIS:CE1	2.51	0.45
10:E:41:ILE:N	10:E:85:ILE:O	2.48	0.45
15:J:32:ARG:HB2	15:J:120:ILE:HG23	1.97	0.45
18:N:65:ARG:HD3	18:N:127:TYR:CD1	2.52	0.45
45:o:65:THR:HG21	45:o:87:ARG:HB3	1.99	0.45
47:2:641:G:H2'	47:2:642:G:H8	1.81	0.45
47:2:711:U:H2'	47:2:712:G:C8	2.52	0.45
47:2:1018:U:H2'	47:2:1019:A:H8	1.81	0.45
47:2:1698:G:N2	47:2:1703:C:N3	2.65	0.45
52:u:131:LEU:HD11	52:u:135:GLY:HA2	1.99	0.45
62:AE:13:VAL:N	62:AE:77:THR:OG1	2.50	0.45
63:AF:105:VAL:HG12	63:AF:108:ARG:HH12	1.81	0.45
63:AF:119:PHE:HA	66:AI:121:ALA:HA	1.97	0.45
67:AJ:113:ILE:O	67:AJ:125:SER:OG	2.31	0.45
79:AV:232:TYR:HE1	79:AV:268:GLN:HE21	1.64	0.45
79:AV:254:ALA:HB3	79:AV:261:LYS:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:418:TYR:OH	83:AZ:422:LYS:O	2.34	0.45
1:1:86:G:H22	1:1:98:G:H3'	1.82	0.45
1:1:878:G:H1'	1:1:880:G:H21	1.82	0.45
1:1:1063:G:O2'	1:1:1097:G:N2	2.50	0.45
1:1:1609:C:H2'	1:1:1610:G:H8	1.82	0.45
1:1:2412:G:H2'	1:1:2413:A:H8	1.80	0.45
1:1:2968:G:H2'	1:1:2969:A:H8	1.81	0.45
4:P0:8:LYS:HG2	4:P0:55:LYS:HE3	1.98	0.45
4:P0:60:ARG:HH21	4:P0:64:ARG:HH11	1.64	0.45
23:S:13:ARG:NH1	23:S:50:LYS:O	2.48	0.45
47:2:716:C:OP2	47:2:717:C:N4	2.49	0.45
49:r:41:ARG:NH2	49:r:231:LEU:O	2.50	0.45
64:AG:100:GLN:HG2	64:AG:104:GLU:HG2	1.97	0.45
66:AI:5:VAL:HG11	73:AP:75:LEU:HD12	1.98	0.45
70:AM:2:THR:O	70:AM:3:ARG:NH1	2.44	0.45
71:AN:65:ASN:ND2	71:AN:116:ASP:OD1	2.47	0.45
71:AN:126:LYS:HG3	71:AN:131:SER:H	1.81	0.45
77:AT:13:ARG:HG3	77:AT:14:TYR:HD1	1.82	0.45
79:AV:24:ALA:HB3	79:AV:34:LEU:HB3	1.97	0.45
1:1:672:A:OP2	21:Q:55:SER:OG	2.35	0.45
1:1:881:C:H2'	1:1:882:A:H8	1.82	0.45
1:1:928:C:H2'	1:1:929:A:H8	1.82	0.45
36:f:49:ILE:HD13	36:f:100:ILE:HD13	1.99	0.45
47:2:446:A:OP1	52:u:59:ARG:NE	2.43	0.45
47:2:764:U:O2	47:2:772:G:O6	2.34	0.45
47:2:937:C:H2'	47:2:938:G:C8	2.52	0.45
47:2:1150:G:H1	82:AY:46:U:P	2.39	0.45
50:s:69:ILE:HG23	50:s:73:LEU:HD11	1.99	0.45
57:z:78:ARG:HA	57:z:81:VAL:HG22	1.97	0.45
63:AF:81:ARG:NH1	63:AF:117:GLY:O	2.50	0.45
68:AK:113:ASP:N	68:AK:113:ASP:OD1	2.48	0.45
83:AZ:737:GLU:HA	83:AZ:740:VAL:HG23	1.98	0.45
1:1:1636:U:H6	1:1:1636:U:C5'	2.12	0.45
1:1:1943:C:H5	22:R:74:ARG:HH12	1.65	0.45
1:1:3049:A:C6	7:B:75:ALA:HB2	2.52	0.45
1:1:3155:U:H3'	1:1:3156:U:H4'	1.98	0.45
1:1:3222:U:O4	1:1:3263:G:O6	2.34	0.45
7:B:292:ALA:HB2	7:B:302:LYS:HE3	1.98	0.45
10:E:2:SER:OG	10:E:4:GLN:O	2.33	0.45
12:G:218:ILE:HA	12:G:221:ASN:HB2	1.99	0.45
19:O:58:LEU:HD21	19:O:74:ARG:HH22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1241:G:H1'	63:AF:79:HIS:H	1.80	0.45
81:AX:28:C:H2'	81:AX:29:A:H8	1.82	0.45
83:AZ:221:THR:HG23	83:AZ:223:ARG:H	1.82	0.45
1:1:563:U:OP1	23:S:71:LYS:NZ	2.48	0.45
1:1:631:U:H2'	1:1:632:G:C8	2.51	0.45
1:1:737:G:H2'	1:1:738:A:C8	2.52	0.45
1:1:1062:A:O2'	1:1:1098:A:OP2	2.30	0.45
1:1:1301:A:H4'	1:1:1302:A:H5''	1.97	0.45
1:1:2280:A:N6	1:1:2282:U:O2'	2.49	0.45
1:1:3052:G:H2'	1:1:3053:G:H8	1.82	0.45
1:1:3108:G:OP2	1:1:3120:C:N4	2.49	0.45
9:D:164:LYS:HE2	9:D:195:LEU:HD11	1.98	0.45
10:E:78:ARG:HH21	10:E:106:PHE:HB2	1.82	0.45
18:N:21:PHE:HD2	18:N:22:LEU:HD22	1.82	0.45
23:S:155:ARG:HD3	23:S:172:TYR:HD1	1.82	0.45
47:2:76:A:O2'	47:2:80:A:N6	2.48	0.45
47:2:1267:G:O6	47:2:1442:U:O2	2.35	0.45
47:2:1469:A:OP1	67:AJ:91:TYR:OH	2.26	0.45
61:AD:130:ARG:HD2	61:AD:138:ASN:HA	1.98	0.45
79:AV:259:GLY:HA3	79:AV:274:LEU:H	1.82	0.45
1:1:118:U:N3	1:1:122:A:OP2	2.37	0.45
1:1:928:C:H2'	1:1:929:A:C8	2.52	0.45
1:1:1262:G:N2	1:1:1265:U:OP1	2.49	0.45
1:1:1882:G:O3'	34:d:34:LYS:NZ	2.42	0.45
1:1:2176:U:OP2	6:A:128:ARG:NH2	2.50	0.45
1:1:2272:G:OP2	1:1:2272:G:N2	2.50	0.45
1:1:2999:U:H2'	1:1:3000:A:H8	1.81	0.45
1:1:3285:C:H2'	1:1:3286:G:C8	2.52	0.45
2:3:78:U:H2'	2:3:79:A:H8	1.81	0.45
10:E:133:GLU:O	10:E:137:ASP:N	2.48	0.45
11:F:208:SER:OG	11:F:209:ASN:N	2.50	0.45
18:N:104:GLU:OE2	18:N:108:ARG:NH2	2.50	0.45
21:Q:92:ARG:NE	31:a:76:ASP:OD1	2.50	0.45
47:2:129:U:O4'	47:2:264:G:N1	2.50	0.45
47:2:232:U:H3'	47:2:233:C:H4'	1.98	0.45
47:2:1613:U:H6	53:v:81:ARG:HH12	1.65	0.45
47:2:1797:A:C6	74:AQ:87:ARG:HD2	2.51	0.45
60:AC:33:ARG:HE	60:AC:36:LEU:HD12	1.81	0.45
66:AI:57:ARG:NH2	73:AP:74:SER:OG	2.49	0.45
67:AJ:98:GLY:O	67:AJ:102:ARG:N	2.50	0.45
76:AS:9:LEU:HA	76:AS:55:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:220:PHE:HA	83:AZ:224:GLN:HE21	1.80	0.45
1:1:1439:U:H2'	1:1:1440:G:H8	1.81	0.45
1:1:1907:C:O2	7:B:240:ARG:NH2	2.50	0.45
1:1:2423:U:H2'	1:1:2424:A:H8	1.82	0.45
1:1:2579:G:H3'	1:1:2580:A:H8	1.81	0.45
6:A:70:ARG:HE	6:A:72:ARG:HB3	1.81	0.45
17:M:13:ARG:NH1	17:M:65:LEU:O	2.50	0.45
22:R:42:ARG:HA	22:R:45:VAL:HG13	1.99	0.45
22:R:109:TYR:HD1	22:R:114:LYS:HB2	1.82	0.45
23:S:31:ALA:HB1	23:S:36:ILE:HG13	1.99	0.45
47:2:629:U:C2	47:2:970:A:N6	2.84	0.45
47:2:1758:U:O4	47:2:1759:C:N4	2.50	0.45
51:t:98:ALA:N	51:t:169:ASP:OD2	2.46	0.45
54:w:138:ALA:HA	54:w:141:ILE:HD12	1.99	0.45
72:AO:124:ARG:HH12	72:AO:128:LYS:HB2	1.80	0.45
75:AR:13:ALA:O	75:AR:17:ARG:NE	2.44	0.45
79:AV:220:ILE:N	79:AV:234:LEU:O	2.49	0.45
83:AZ:130:ASP:HB2	83:AZ:133:GLU:HB2	1.99	0.45
83:AZ:631:ARG:NH1	83:AZ:648:ASP:O	2.50	0.45
1:1:754:G:H2'	1:1:755:A:H8	1.82	0.44
1:1:1447:G:C8	20:P:27:LYS:HB2	2.52	0.44
1:1:1785:U:H2'	1:1:1786:G:H8	1.82	0.44
1:1:2897:A:OP2	43:m:124:LYS:NZ	2.40	0.44
1:1:2986:U:H2'	1:1:2987:A:H8	1.82	0.44
1:1:3185:U:OP1	13:H:23:ARG:NH1	2.50	0.44
2:3:23:A:H2'	2:3:24:A:C8	2.51	0.44
2:3:77:G:O2'	2:3:101:G:O6	2.32	0.44
12:G:64:ILE:HG13	12:G:68:ARG:HE	1.81	0.44
15:J:92:ARG:HA	15:J:172:LEU:HD12	1.99	0.44
37:g:67:LYS:HB2	37:g:71:THR:HG22	1.98	0.44
47:2:1405:G:O4'	76:AS:49:ARG:NH2	2.50	0.44
53:v:215:ASP:O	53:v:219:ARG:N	2.40	0.44
56:y:121:LEU:HA	56:y:122:GLY:HA2	1.76	0.44
58:AA:61:TRP:HA	77:AT:23:VAL:HG23	1.99	0.44
83:AZ:7:ASP:HB3	83:AZ:10:ARG:HH12	1.81	0.44
83:AZ:282:PHE:O	83:AZ:286:THR:CB	2.64	0.44
1:1:673:U:H2'	1:1:674:G:C8	2.52	0.44
1:1:1922:A:H62	1:1:1929:G:H21	1.64	0.44
1:1:2111:G:C8	27:W:49:ILE:HG22	2.53	0.44
1:1:3271:G:H2'	10:E:108:LYS:HE3	1.98	0.44
1:1:3275:U:C4	36:f:64:ILE:HG12	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:98:C:OP1	23:S:39:SER:OG	2.30	0.44
4:P0:5:ARG:HH11	4:P0:8:LYS:CD	2.30	0.44
7:B:92:TYR:HB2	7:B:157:VAL:HG23	1.99	0.44
16:L:46:ILE:HG13	16:L:49:ARG:HB2	1.99	0.44
16:L:157:ARG:O	31:a:99:ALA:N	2.46	0.44
16:L:177:LYS:HA	16:L:180:ARG:HB2	1.99	0.44
24:T:54:HIS:CE1	24:T:55:LYS:HG2	2.52	0.44
47:2:702:G:H2'	47:2:703:G:C8	2.52	0.44
52:u:77:ARG:HD3	52:u:82:TYR:CZ	2.53	0.44
59:AB:55:ASP:OD1	59:AB:82:ARG:NH1	2.50	0.44
64:AG:22:VAL:HG23	64:AG:64:ASP:H	1.81	0.44
81:AX:54:U:O2	81:AX:58:A:N7	2.51	0.44
1:1:158:G:N2	1:1:264:G:H1'	2.31	0.44
1:1:1340:G:H2'	1:1:1341:U:C6	2.52	0.44
1:1:2697:A:H2'	1:1:2698:G:H8	1.82	0.44
3:4:97:A:O2'	38:h:59:ASN:ND2	2.50	0.44
30:Z:111:LYS:HA	30:Z:114:VAL:HG12	1.99	0.44
39:i:18:THR:OG1	39:i:19:SER:N	2.49	0.44
43:m:109:ASN:ND2	43:m:117:HIS:O	2.41	0.44
47:2:150:U:H2'	47:2:151:G:C8	2.53	0.44
47:2:435:C:N4	71:AN:46:SER:OG	2.51	0.44
47:2:454:U:H4'	52:u:62:LYS:HE3	1.98	0.44
47:2:1117:U:H2'	47:2:1118:G:H8	1.83	0.44
47:2:1468:U:H2'	47:2:1469:A:C8	2.53	0.44
47:2:1642:G:H2'	47:2:1643:U:H6	1.81	0.44
49:r:172:LEU:HD22	49:r:172:LEU:HA	1.83	0.44
63:AF:34:VAL:HG22	63:AF:42:ARG:HG2	2.00	0.44
66:AI:26:ILE:HG22	66:AI:27:LYS:H	1.81	0.44
66:AI:114:GLU:HA	66:AI:117:LYS:HB2	2.00	0.44
70:AM:23:ARG:NH1	70:AM:66:ASN:O	2.50	0.44
71:AN:69:ARG:HB3	71:AN:86:PHE:HE1	1.82	0.44
76:AS:11:LYS:HG2	76:AS:53:ILE:HA	1.98	0.44
79:AV:117:LYS:HE3	79:AV:160:GLU:HA	1.98	0.44
79:AV:151:VAL:HA	79:AV:173:GLY:HA2	1.99	0.44
83:AZ:5:THR:O	83:AZ:8:GLN:N	2.50	0.44
83:AZ:220:PHE:HZ	83:AZ:278:LEU:HD21	1.82	0.44
1:1:379:C:H2'	1:1:380:U:H6	1.82	0.44
1:1:768:C:H4'	16:L:183:ARG:HH21	1.83	0.44
1:1:1258:U:O2'	1:1:1260:A:N7	2.39	0.44
1:1:2268:U:H3'	1:1:2269:U:H5''	2.00	0.44
1:1:2830:G:H2'	1:1:2831:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:223:SER:O	6:A:237:LEU:N	2.50	0.44
7:B:37:ARG:HE	7:B:187:SER:H	1.66	0.44
18:N:68:ARG:NH1	18:N:124:ASP:O	2.49	0.44
47:2:506:A:O2'	47:2:507:U:C5'	2.66	0.44
47:2:1163:A:N3	47:2:1613:U:O2'	2.32	0.44
47:2:1356:U:O4	47:2:1367:G:O6	2.36	0.44
47:2:1554:U:H6	77:AT:13:ARG:HH12	1.65	0.44
55:x:179:LYS:HG3	55:x:180:GLN:H	1.83	0.44
59:AB:108:PRO:HB2	59:AB:135:VAL:HG22	2.00	0.44
65:AH:45:ARG:HA	65:AH:48:ASN:HD22	1.83	0.44
79:AV:85:TRP:NE1	79:AV:111:MET:HA	2.32	0.44
83:AZ:108:HIS:O	83:AZ:111:PHE:N	2.50	0.44
1:1:190:U:O2'	29:Y:60:ARG:NH2	2.48	0.44
1:1:421:G:N1	1:1:2383:C:O2	2.50	0.44
1:1:650:C:H2'	1:1:651:G:H8	1.83	0.44
1:1:998:A:H2'	1:1:999:G:H8	1.83	0.44
1:1:3283:U:H2'	1:1:3284:G:C8	2.50	0.44
4:P0:97:LYS:HA	4:P0:100:ILE:HG12	1.98	0.44
7:B:46:PHE:HB3	7:B:338:LEU:HB2	2.00	0.44
11:F:93:ASN:HD22	11:F:94:LYS:H	1.64	0.44
16:L:63:VAL:HA	16:L:66:ASN:HB2	2.00	0.44
21:Q:170:ARG:NH2	31:a:58:MET:O	2.38	0.44
25:U:77:LYS:HG2	25:U:81:LYS:HE2	2.00	0.44
26:V:18:PRO:HA	26:V:51:ALA:HA	1.99	0.44
47:2:434:G:N2	47:2:437:A:OP2	2.50	0.44
47:2:1235:C:H2'	47:2:1236:A:H8	1.83	0.44
47:2:1335:U:O4	47:2:1416:G:O6	2.34	0.44
47:2:1486:G:H2'	47:2:1487:A:C8	2.52	0.44
48:q:70:PRO:HB2	48:q:95:ALA:H	1.82	0.44
51:t:24:PHE:HE1	58:AA:58:GLN:HG2	1.83	0.44
53:v:54:LYS:HB3	53:v:131:GLN:HE22	1.81	0.44
53:v:65:ARG:HA	53:v:66:GLN:HA	1.76	0.44
55:x:49:ILE:HD11	55:x:172:VAL:HG22	1.99	0.44
55:x:173:TYR:O	55:x:177:THR:OG1	2.29	0.44
83:AZ:631:ARG:HH12	83:AZ:632:LYS:HZ3	1.64	0.44
1:1:627:U:H2'	1:1:628:A:H8	1.80	0.44
1:1:707:U:O2	1:1:712:G:O6	2.36	0.44
1:1:1211:U:H2'	1:1:1212:A:H8	1.82	0.44
1:1:2218:G:H2'	1:1:2219:A:C8	2.53	0.44
2:3:96:U:H2'	2:3:97:A:H8	1.83	0.44
7:B:227:GLU:HG2	7:B:231:HIS:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:13:GLY:N	8:C:171:ALA:O	2.50	0.44
36:f:18:ARG:HA	36:f:23:ASN:HA	2.00	0.44
47:2:741:C:O2'	47:2:742:U:O4'	2.33	0.44
47:2:1502:G:N2	47:2:1505:A:OP2	2.42	0.44
47:2:1752:U:H2'	47:2:1753:A:C8	2.52	0.44
49:r:127:VAL:HG11	49:r:176:VAL:HG11	1.98	0.44
50:s:215:PHE:HA	50:s:218:ILE:HG22	2.00	0.44
53:v:111:VAL:HA	53:v:114:ILE:HB	2.00	0.44
1:1:694:C:OP1	8:C:118:LYS:NZ	2.51	0.44
1:1:1069:C:H2'	1:1:1070:U:H6	1.82	0.44
3:4:41:A:H62	3:4:103:G:N2	2.16	0.44
5:P2:63:LYS:HE3	5:P2:71:ALA:H	1.83	0.44
6:A:114:SER:OG	6:A:127:ALA:O	2.34	0.44
8:C:237:GLN:HG3	8:C:246:ARG:HH21	1.83	0.44
29:Y:118:LEU:HA	29:Y:121:ARG:HE	1.82	0.44
30:Z:43:VAL:HG22	30:Z:73:LYS:H	1.82	0.44
36:f:89:LEU:HD13	36:f:91:ALA:H	1.81	0.44
47:2:187:G:H21	47:2:198:A:H62	1.66	0.44
50:s:216:VAL:O	50:s:220:ASN:ND2	2.51	0.44
62:AE:133:ARG:HD2	62:AE:136:ARG:NH2	2.33	0.44
70:AM:11:LEU:HD11	70:AM:37:PHE:HE2	1.83	0.44
1:1:966:U:H2'	1:1:967:A:H8	1.83	0.44
1:1:1636:U:C6	1:1:1636:U:C5'	2.85	0.44
1:1:1667:A:H2'	1:1:1668:G:C8	2.52	0.44
1:1:2382:G:OP2	19:O:90:HIS:NE2	2.41	0.44
1:1:2502:A:H2'	1:1:2503:G:H8	1.83	0.44
7:B:252:ILE:HG23	7:B:264:VAL:HG11	2.00	0.44
7:B:252:ILE:HG23	7:B:264:VAL:HG21	2.00	0.44
8:C:71:VAL:HG12	8:C:76:ARG:HH22	1.82	0.44
8:C:283:THR:HG21	8:C:288:ARG:HD2	1.99	0.44
9:D:184:ASP:OD2	9:D:187:THR:OG1	2.36	0.44
23:S:15:PRO:HB3	23:S:20:PRO:HA	1.99	0.44
28:X:135:ILE:HA	28:X:138:ARG:HB2	2.00	0.44
31:a:126:LYS:HD2	31:a:148:ILE:HG12	2.00	0.44
42:l:42:ARG:HH21	42:l:49:MET:HB3	1.83	0.44
47:2:130:C:O2'	47:2:131:C:O4'	2.35	0.44
47:2:1278:G:H5'	51:t:185:LYS:HE2	1.99	0.44
47:2:1464:G:HO2'	64:AG:141:SER:HG	1.64	0.44
47:2:1756:A:C2	82:AY:50:U:OP2	2.70	0.44
49:r:55:LYS:NZ	49:r:59:ASP:O	2.47	0.44
57:z:172:VAL:O	57:z:176:ASN:ND2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AX:21:A:O4'	81:AX:48:C:N4	2.51	0.44
1:1:122:A:N6	1:1:146:U:O4'	2.51	0.44
1:1:700:C:H2'	1:1:701:G:C8	2.51	0.44
1:1:1355:A:H4'	1:1:1356:U:H5''	2.00	0.44
1:1:1439:U:H2'	1:1:1440:G:C8	2.53	0.44
1:1:1622:U:H2'	1:1:1623:G:C8	2.53	0.44
1:1:1821:U:O3'	37:g:66:SER:OG	2.32	0.44
1:1:1859:A:H2'	1:1:1860:G:H8	1.83	0.44
1:1:2213:A:H2'	1:1:2214:A:C8	2.53	0.44
1:1:3119:U:H4'	43:m:104:PRO:HG2	1.98	0.44
3:4:143:U:H2'	3:4:144:G:C8	2.53	0.44
8:C:135:VAL:HG11	8:C:148:ILE:HD13	2.00	0.44
11:F:52:GLN:HA	11:F:55:TYR:HB2	2.00	0.44
22:R:6:THR:O	22:R:10:LEU:N	2.51	0.44
33:c:57:GLU:HA	33:c:60:ALA:HB3	1.99	0.44
47:2:1064:G:H2'	47:2:1065:A:C8	2.53	0.44
47:2:1478:G:H2'	47:2:1479:A:H8	1.83	0.44
49:r:121:ILE:HB	49:r:141:ALA:HB3	1.99	0.44
73:AP:43:ASP:O	73:AP:47:TYR:N	2.51	0.44
81:AX:25:C:H2'	81:AX:26:G:H8	1.83	0.44
83:AZ:222:ILE:H	83:AZ:222:ILE:HG13	1.40	0.44
1:1:16:A:OP2	28:X:42:ARG:NH1	2.51	0.43
1:1:61:A:N1	18:N:189:LYS:NZ	2.65	0.43
1:1:64:G:OP2	18:N:169:LYS:NZ	2.37	0.43
1:1:268:A:N7	18:N:12:ARG:NE	2.65	0.43
1:1:1010:G:N2	14:I:193:ASP:OD2	2.51	0.43
1:1:1871:U:H2'	1:1:1872:C:H6	1.83	0.43
1:1:2335:G:N2	1:1:2339:C:O2	2.52	0.43
1:1:2534:G:H2'	1:1:2535:A:C8	2.53	0.43
1:1:2687:G:O2'	1:1:2690:G:O6	2.36	0.43
1:1:2972:G:H2'	1:1:2973:G:H8	1.83	0.43
12:G:99:PRO:HG2	12:G:190:VAL:HA	2.00	0.43
23:S:42:TRP:CG	23:S:53:LYS:HB3	2.53	0.43
29:Y:85:VAL:HG12	29:Y:97:ILE:HD11	2.00	0.43
35:e:81:ASP:O	35:e:84:THR:OG1	2.36	0.43
47:2:29:U:H2'	47:2:30:G:C8	2.52	0.43
47:2:208:U:N3	47:2:258:C:O2	2.51	0.43
47:2:351:C:H5'	47:2:352:A:N7	2.32	0.43
47:2:1198:G:H5''	47:2:1199:G:C8	2.53	0.43
47:2:1609:U:H5''	64:AG:75:VAL:HB	1.98	0.43
52:u:175:PHE:HD2	52:u:198:LYS:HE3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:AI:40:ARG:NH2	67:AJ:45:MET:SD	2.91	0.43
81:AX:61:C:H2'	81:AX:62:A:C8	2.53	0.43
83:AZ:104:ASP:OD1	83:AZ:104:ASP:N	2.51	0.43
83:AZ:485:VAL:HG22	83:AZ:486:SER:HB3	1.99	0.43
83:AZ:718:LEU:HD11	83:AZ:838:TYR:CZ	2.53	0.43
1:1:835:G:N2	1:1:857:G:O2'	2.51	0.43
1:1:1916:U:O3'	22:R:85:ARG:NH2	2.42	0.43
1:1:2894:C:H2'	1:1:2895:G:H8	1.83	0.43
1:1:2936:A:H2'	1:1:2937:G:H8	1.82	0.43
3:4:47:C:O2'	3:4:62:C:OP2	2.36	0.43
18:N:100:ALA:O	18:N:104:GLU:N	2.51	0.43
26:V:77:ILE:HD11	26:V:126:TRP:CD1	2.53	0.43
47:2:1145:U:H2'	47:2:1146:G:H8	1.81	0.43
51:t:125:TYR:O	51:t:129:SER:N	2.49	0.43
53:v:87:CYS:HB2	53:v:92:ARG:HD2	2.00	0.43
61:AD:72:MET:O	61:AD:76:LYS:N	2.51	0.43
61:AD:74:ILE:O	61:AD:78:ASN:ND2	2.50	0.43
63:AF:15:HIS:HD2	63:AF:17:TYR:HB2	1.83	0.43
63:AF:83:MET:HE2	63:AF:116:LEU:HD12	1.99	0.43
68:AK:21:LYS:HA	68:AK:94:GLU:HG2	2.00	0.43
1:1:940:G:OP2	31:a:24:LYS:NZ	2.47	0.43
1:1:1098:A:P	24:T:108:ARG:HH12	2.42	0.43
1:1:1778:G:O2'	1:1:1780:G:OP2	2.31	0.43
1:1:3157:U:H4'	1:1:3158:G:H5'	2.01	0.43
1:1:3186:A:H8	13:H:44:THR:HG23	1.83	0.43
3:4:27:U:H4'	8:C:51:ALA:HB3	2.00	0.43
6:A:167:GLY:HA2	46:p:79:VAL:HG21	1.99	0.43
44:n:15:ARG:O	44:n:19:LYS:N	2.47	0.43
47:2:317:C:O2'	47:2:354:C:O2'	2.33	0.43
47:2:406:U:H2'	47:2:407:A:C8	2.53	0.43
47:2:885:G:H2'	47:2:886:U:C6	2.53	0.43
52:u:100:ARG:HB2	52:u:114:ILE:HD13	2.00	0.43
59:AB:132:SER:O	59:AB:136:ARG:NH2	2.47	0.43
63:AF:83:MET:O	63:AF:116:LEU:N	2.51	0.43
67:AJ:138:GLN:HA	67:AJ:141:GLU:HB2	2.01	0.43
79:AV:37:SER:H	79:AV:68:VAL:HG23	1.83	0.43
83:AZ:19:VAL:HG22	83:AZ:99:LEU:HD21	2.00	0.43
83:AZ:523:SER:OG	83:AZ:524:GLU:N	2.50	0.43
1:1:1225:A:O2'	1:1:3117:C:N3	2.51	0.43
1:1:1373:A:H2'	1:1:1374:G:H8	1.84	0.43
1:1:1661:G:H2'	1:1:1662:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1672:U:OP1	22:R:64:ARG:NH2	2.51	0.43
1:1:1717:U:H2'	1:1:1718:G:C8	2.54	0.43
1:1:1831:U:OP1	28:X:92:LYS:N	2.50	0.43
1:1:2173:U:O3'	6:A:193:ARG:NH1	2.51	0.43
1:1:2205:U:O2	47:2:913:G:N2	2.51	0.43
1:1:3153:U:H3	1:1:3293:U:H2'	1.84	0.43
1:1:3186:A:C8	13:H:44:THR:HG23	2.52	0.43
6:A:88:ILE:HD12	6:A:88:ILE:HA	1.87	0.43
14:I:48:LEU:HD23	14:I:145:LYS:HE2	2.00	0.43
19:O:105:PHE:CE2	19:O:109:PRO:HG3	2.53	0.43
27:W:45:ASN:HA	27:W:46:PRO:HD3	1.92	0.43
32:b:33:LYS:O	32:b:40:ARG:NH2	2.51	0.43
46:p:24:ARG:HH22	47:2:1123:C:H1'	1.84	0.43
47:2:368:U:O4	47:2:373:G:O6	2.37	0.43
47:2:545:A:H4'	47:2:546:U:H5'	1.99	0.43
47:2:702:G:H2'	47:2:703:G:H8	1.83	0.43
47:2:1142:A:H2'	47:2:1143:A:C8	2.54	0.43
47:2:1587:A:H2'	47:2:1588:G:C8	2.53	0.43
49:r:66:VAL:HB	49:r:86:LEU:HB2	2.00	0.43
56:y:65:PHE:HE2	56:y:104:ILE:HG21	1.83	0.43
65:AH:96:SER:HA	65:AH:97:ASN:HA	1.74	0.43
70:AM:111:MET:HE1	70:AM:121:VAL:HG23	1.99	0.43
71:AN:58:GLY:HA2	71:AN:71:CYS:H	1.84	0.43
75:AR:54:VAL:HG13	75:AR:63:LEU:HB2	2.01	0.43
83:AZ:74:ALA:CA	83:AZ:102:LEU:O	2.59	0.43
83:AZ:567:VAL:HG12	83:AZ:684:VAL:HG12	2.00	0.43
1:1:19:U:H3	3:4:140:G:H1	1.66	0.43
1:1:522:A:O2'	23:S:65:ASN:O	2.35	0.43
1:1:720:A:OP2	31:a:117:ARG:NH2	2.48	0.43
1:1:2386:A:H62	1:1:2993:G:N2	2.14	0.43
1:1:3229:G:H2'	1:1:3230:G:C8	2.54	0.43
3:4:149:A:H2'	3:4:150:G:C8	2.53	0.43
47:2:339:C:OP2	56:y:10:LYS:NZ	2.51	0.43
47:2:532:U:OP1	57:z:132:ARG:NH2	2.51	0.43
47:2:992:A:H3'	47:2:993:A:H8	1.84	0.43
47:2:1064:G:H2'	47:2:1065:A:H8	1.84	0.43
47:2:1502:G:OP2	67:AJ:103:LYS:NZ	2.48	0.43
47:2:1596:C:OP1	77:AT:16:LYS:NZ	2.46	0.43
47:2:1712:A:H3'	47:2:1713:G:H8	1.82	0.43
50:s:120:GLU:OE1	50:s:122:ALA:N	2.46	0.43
50:s:160:GLY:HA3	50:s:217:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:u:180:LEU:HD22	52:u:192:ILE:HD11	1.99	0.43
54:w:7:TYR:HA	54:w:8:PRO:HD3	1.89	0.43
67:AJ:45:MET:HE3	67:AJ:46:PRO:HD2	1.99	0.43
79:AV:195:HIS:HD2	79:AV:219:GLU:HG2	1.84	0.43
1:1:154:U:H4'	1:1:155:G:H5'	1.99	0.43
1:1:310:U:O4	1:1:2780:A:N6	2.52	0.43
1:1:1100:U:H2'	1:1:1101:G:H8	1.83	0.43
1:1:1693:C:O2'	1:1:1772:U:O2'	2.32	0.43
1:1:2158:A:OP2	6:A:156:LYS:NZ	2.41	0.43
1:1:2959:C:OP1	6:A:217:GLN:NE2	2.51	0.43
11:F:130:ILE:HD12	11:F:130:ILE:HG23	1.85	0.43
16:L:57:VAL:HG22	16:L:147:ILE:HG23	2.00	0.43
18:N:108:ARG:HA	18:N:111:ALA:HB2	2.00	0.43
47:2:38:C:H5	47:2:39:A:C5	2.37	0.43
47:2:73:U:O2'	47:2:74:U:O4'	2.30	0.43
47:2:97:C:H2'	47:2:98:U:C6	2.53	0.43
47:2:1175:U:H3	47:2:1464:G:H1	1.65	0.43
47:2:1242:A:N1	47:2:1451:C:O2'	2.51	0.43
47:2:1351:G:H5''	64:AG:66:ARG:HH22	1.83	0.43
52:u:95:THR:HG21	72:AO:17:LEU:HD23	1.99	0.43
52:u:141:THR:OG1	52:u:145:ARG:N	2.51	0.43
59:AB:109:VAL:HG21	59:AB:125:VAL:HG11	2.00	0.43
61:AD:98:VAL:HG13	61:AD:115:LEU:HD23	2.00	0.43
83:AZ:299:LEU:HA	83:AZ:302:LYS:HB2	2.01	0.43
83:AZ:764:PRO:HB2	83:AZ:765:LEU:HD12	2.00	0.43
1:1:16:A:H5'	28:X:43:ALA:HB3	2.00	0.43
1:1:516:A:H2'	1:1:517:G:C8	2.54	0.43
1:1:526:C:H2'	1:1:527:A:H8	1.84	0.43
1:1:533:A:H2'	1:1:535:G:C8	2.54	0.43
1:1:1799:A:H2'	1:1:1800:A:C8	2.54	0.43
1:1:2252:A:H2'	1:1:2253:G:H8	1.84	0.43
3:4:143:U:H2'	3:4:144:G:H8	1.84	0.43
23:S:82:ASP:HB3	23:S:87:THR:HG22	2.00	0.43
25:U:14:THR:HG23	25:U:66:VAL:HG22	2.01	0.43
26:V:19:VAL:HG23	26:V:37:ILE:HA	2.01	0.43
29:Y:51:ARG:HB2	29:Y:115:ARG:HH12	1.83	0.43
40:j:4:GLY:O	40:j:7:SER:OG	2.25	0.43
46:p:83:ILE:O	46:p:87:ARG:N	2.51	0.43
47:2:155:U:H4'	54:w:58:LYS:HG3	1.99	0.43
47:2:212:U:H2'	47:2:213:A:C8	2.54	0.43
47:2:919:A:OP1	62:AE:18:ARG:NH1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1192:C:OP2	47:2:1193:A:O2'	2.34	0.43
47:2:1495:C:O2'	47:2:1519:U:O2	2.32	0.43
47:2:1698:G:O2'	47:2:1699:G:O4'	2.34	0.43
51:t:71:LEU:HD11	58:AA:18:GLU:HB3	2.01	0.43
52:u:38:LEU:HB3	52:u:40:GLU:HG3	2.01	0.43
66:AI:26:ILE:HB	66:AI:31:ALA:HB2	2.01	0.43
76:AS:11:LYS:HB3	76:AS:33:LEU:HD13	2.00	0.43
76:AS:13:ILE:HD12	76:AS:14:LYS:HG2	2.01	0.43
79:AV:238:ASP:OD2	79:AV:258:THR:OG1	2.29	0.43
1:1:354:U:H3	1:1:365:A:N6	2.12	0.43
1:1:504:A:H2'	1:1:505:G:H8	1.84	0.43
1:1:1259:A:OP1	4:P0:53:MET:N	2.52	0.43
1:1:1657:C:O2'	1:1:1797:A:OP2	2.34	0.43
1:1:1714:A:H62	1:1:1730:G:H21	1.66	0.43
1:1:1831:U:O2'	3:4:114:G:OP1	2.30	0.43
1:1:2697:A:H2'	1:1:2698:G:C8	2.53	0.43
1:1:2999:U:H2'	1:1:3000:A:C8	2.53	0.43
4:P0:28:VAL:HG23	4:P0:53:MET:HE1	2.00	0.43
8:C:132:ALA:HB1	8:C:136:LEU:HD23	2.01	0.43
16:L:27:ASP:HB2	16:L:31:LYS:HG2	2.00	0.43
16:L:54:LEU:N	16:L:94:GLY:O	2.51	0.43
21:Q:27:LYS:HA	21:Q:30:VAL:HG12	2.00	0.43
27:W:45:ASN:HD21	27:W:48:ARG:HD3	1.84	0.43
47:2:121:U:H2'	47:2:122:U:H6	1.84	0.43
47:2:591:A:H2'	47:2:592:A:C8	2.53	0.43
47:2:762:A:OP1	57:z:79:ARG:NH2	2.39	0.43
47:2:923:A:H2'	47:2:924:A:H8	1.84	0.43
47:2:1595:U:H3'	77:AT:32:ARG:HH22	1.82	0.43
47:2:1756:A:H2'	47:2:1757:G:H5''	2.00	0.43
53:v:42:LEU:HA	53:v:48:PHE:HB3	2.00	0.43
54:w:74:LYS:HD3	54:w:94:ARG:HD2	2.00	0.43
55:x:37:GLU:HB2	55:x:73:VAL:HG11	2.01	0.43
57:z:85:VAL:HG11	57:z:99:LEU:HD11	2.01	0.43
59:AB:99:ARG:NE	71:AN:7:ARG:O	2.43	0.43
63:AF:25:LEU:HD23	63:AF:28:MET:HE2	2.01	0.43
73:AP:84:GLU:HA	73:AP:89:ILE:HD11	2.00	0.43
79:AV:38:ARG:HD3	79:AV:67:ILE:HG21	2.00	0.43
79:AV:246:SER:OG	79:AV:248:ASN:OD1	2.36	0.43
83:AZ:283:ARG:O	83:AZ:287:ALA:HB3	2.18	0.43
83:AZ:305:ILE:HA	83:AZ:306:VAL:HA	1.82	0.43
83:AZ:670:ALA:HB1	83:AZ:674:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:26:A:N1	1:1:59:G:O6	2.52	0.43
1:1:254:A:H2'	1:1:255:A:H8	1.83	0.43
1:1:336:A:OP2	29:Y:10:SER:OG	2.32	0.43
1:1:1035:G:H2'	1:1:1036:A:C8	2.54	0.43
1:1:1079:A:C4	9:D:113:LEU:HD21	2.54	0.43
1:1:1888:U:H5''	7:B:247:ARG:HB2	1.99	0.43
1:1:2374:C:OP1	1:1:2823:G:O2'	2.35	0.43
1:1:2442:G:H2'	1:1:2443:A:H8	1.83	0.43
1:1:2701:U:P	24:T:17:ARG:HH22	2.41	0.43
5:P2:129:THR:HA	5:P2:132:ILE:HD12	2.00	0.43
30:Z:22:LYS:HZ3	30:Z:129:TRP:CD1	2.37	0.43
40:j:29:VAL:O	40:j:32:LYS:NZ	2.38	0.43
47:2:299:A:H2'	47:2:300:A:C8	2.54	0.43
47:2:419:G:H5'	54:w:72:ARG:HH21	1.84	0.43
47:2:600:U:H2'	47:2:601:A:C8	2.53	0.43
47:2:1564:U:H2'	47:2:1565:C:C6	2.54	0.43
47:2:1735:U:H2'	47:2:1736:G:C8	2.54	0.43
56:y:102:VAL:HG23	56:y:167:ALA:HB3	2.01	0.43
68:AK:100:VAL:HG13	68:AK:103:ILE:HD12	2.01	0.43
76:AS:19:THR:HG21	76:AS:65:ARG:HA	2.00	0.43
78:AU:13:LYS:HD2	83:AZ:609:ARG:HG2	2.00	0.43
79:AV:63:GLY:O	79:AV:90:ARG:NH2	2.51	0.43
83:AZ:214:GLY:N	86:AZ:902:GCP:O6	2.49	0.43
1:1:970:A:OP2	32:b:18:ARG:NE	2.52	0.43
4:P0:104:ARG:HE	4:P0:184:GLY:HA3	1.84	0.43
12:G:52:TRP:H	12:G:57:ARG:HH21	1.64	0.43
26:V:21:ALA:H	26:V:36:ILE:HG22	1.84	0.43
63:AF:103:ASN:OD1	63:AF:120:SER:OG	2.37	0.43
76:AS:12:VAL:HG22	76:AS:30:VAL:HG12	2.01	0.43
1:1:715:A:C8	31:a:115:LYS:HG2	2.54	0.42
1:1:1044:U:H1'	14:I:92:HIS:CE1	2.54	0.42
1:1:1280:C:H2'	1:1:1281:G:H8	1.83	0.42
1:1:1457:U:H5	1:1:1877:U:H2'	1.83	0.42
1:1:1523:U:OP1	1:1:1834:U:O2'	2.36	0.42
4:P0:167:GLN:O	4:P0:171:SER:OG	2.33	0.42
5:P2:110:ILE:HD13	5:P2:130:LYS:NZ	2.32	0.42
11:F:77:VAL:HG12	23:S:59:VAL:HA	2.01	0.42
19:O:29:ASN:HD21	36:f:14:LEU:HD13	1.82	0.42
19:O:172:ARG:HA	19:O:175:THR:HG22	2.01	0.42
32:b:47:LEU:HA	32:b:50:THR:HG22	2.01	0.42
47:2:434:G:O2'	47:2:436:A:N7	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:477:A:OP2	78:AU:28:LYS:NZ	2.51	0.42
47:2:1200:G:OP2	47:2:1595:U:O2'	2.33	0.42
47:2:1561:U:H2'	47:2:1562:G:H8	1.83	0.42
52:u:121:TYR:HA	52:u:164:LEU:HD23	2.01	0.42
56:y:104:ILE:HG13	56:y:105:ASP:H	1.83	0.42
83:AZ:799:ASP:N	83:AZ:799:ASP:OD1	2.50	0.42
1:1:146:U:O2	1:1:148:G:C2	2.72	0.42
1:1:518:G:OP2	1:1:518:G:N2	2.35	0.42
1:1:797:U:H2'	1:1:798:G:C8	2.54	0.42
1:1:1100:U:H2'	1:1:1101:G:C8	2.54	0.42
1:1:3107:U:H2'	1:1:3108:G:C8	2.54	0.42
4:P0:110:ARG:HB3	4:P0:113:ALA:HB2	2.01	0.42
7:B:364:LYS:HA	7:B:364:LYS:HD3	1.90	0.42
14:I:190:VAL:HG13	14:I:197:VAL:HG11	2.00	0.42
20:P:3:ARG:HD3	20:P:3:ARG:HA	1.89	0.42
47:2:258:C:H5''	56:y:75:LYS:HD2	2.01	0.42
47:2:1595:U:H6	77:AT:32:ARG:HH12	1.67	0.42
53:v:40:ILE:HG23	53:v:42:LEU:HD22	2.00	0.42
54:w:9:VAL:O	54:w:11:GLY:N	2.52	0.42
58:AA:25:LYS:HB3	58:AA:43:ILE:HD12	2.00	0.42
68:AK:64:LYS:NZ	68:AK:83:GLU:OE2	2.39	0.42
76:AS:30:VAL:HG21	76:AS:56:LEU:HD11	2.00	0.42
81:AX:28:C:H2'	81:AX:29:A:C8	2.54	0.42
83:AZ:707:PRO:O	83:AZ:710:ARG:N	2.52	0.42
1:1:737:G:H2'	1:1:738:A:H8	1.84	0.42
1:1:823:C:H4'	6:A:19:HIS:HD2	1.85	0.42
1:1:1238:C:OP1	5:P2:79:SER:OG	2.29	0.42
1:1:1257:C:H5'	4:P0:46:ARG:NH1	2.28	0.42
1:1:1262:G:C4	1:1:1264:G:H1'	2.54	0.42
1:1:1284:C:H2'	1:1:1285:G:C8	2.54	0.42
1:1:1710:C:OP1	30:Z:79:HIS:NE2	2.53	0.42
1:1:2256:A:H3'	1:1:2256:A:H8	1.85	0.42
1:1:2295:A:C4	26:V:37:ILE:HD11	2.54	0.42
1:1:3111:U:OP1	13:H:184:LYS:NZ	2.42	0.42
8:C:234:ASN:OD1	8:C:234:ASN:N	2.49	0.42
44:n:17:ARG:NH2	47:2:1750:A:O2'	2.52	0.42
47:2:124:A:O2'	52:u:148:ARG:NE	2.52	0.42
47:2:384:G:H2'	47:2:385:A:C8	2.55	0.42
47:2:564:G:N1	47:2:580:A:OP2	2.49	0.42
47:2:603:U:H2'	47:2:604:A:C8	2.54	0.42
47:2:924:A:O2'	47:2:987:G:OP1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1140:G:H2'	47:2:1141:G:C8	2.51	0.42
47:2:1512:G:H2'	47:2:1513:G:C8	2.54	0.42
55:x:91:ILE:HD11	55:x:129:LEU:HA	2.02	0.42
61:AD:91:LEU:HD22	61:AD:122:ILE:HG12	2.00	0.42
81:AX:21:A:N6	81:AX:46:G:N3	2.67	0.42
83:AZ:55:ARG:HH12	86:AZ:902:GCP:H5'2	1.83	0.42
83:AZ:673:GLU:HA	83:AZ:679:GLU:HA	2.01	0.42
1:1:446:U:N3	1:1:490:C:O2	2.53	0.42
1:1:629:U:H2'	1:1:630:A:C8	2.54	0.42
1:1:784:A:C5	21:Q:93:ILE:HD11	2.55	0.42
1:1:860:G:O4'	6:A:181:LYS:NZ	2.51	0.42
1:1:1206:G:OP1	14:I:157:TYR:OH	2.28	0.42
1:1:1411:C:OP1	35:e:98:HIS:ND1	2.40	0.42
1:1:1750:A:H4'	1:1:1751:G:H5'	2.00	0.42
1:1:2246:G:H2'	1:1:2247:G:C8	2.54	0.42
1:1:2618:G:O2'	1:1:2865:U:OP1	2.37	0.42
3:4:106:C:H4'	3:4:107:G:H5''	2.00	0.42
6:A:52:SER:OG	6:A:53:GLY:N	2.50	0.42
17:M:48:GLY:HA3	17:M:53:VAL:HG22	2.01	0.42
18:N:177:GLY:O	18:N:184:LYS:NZ	2.42	0.42
21:Q:16:ARG:O	21:Q:50:LYS:NZ	2.53	0.42
29:Y:55:GLU:HB2	29:Y:108:LYS:H	1.84	0.42
36:f:35:VAL:HG21	36:f:79:GLY:HA3	2.01	0.42
45:o:34:SER:OG	45:o:35:LEU:O	2.37	0.42
47:2:225:A:H2'	47:2:226:A:C8	2.55	0.42
47:2:1638:G:O5'	47:2:1638:G:C8	2.70	0.42
64:AG:98:ASP:O	64:AG:101:SER:OG	2.29	0.42
65:AH:10:LYS:HA	65:AH:13:SER:HB2	2.01	0.42
66:AI:101:LEU:N	66:AI:104:ASN:HB3	2.33	0.42
68:AK:52:LYS:HE2	68:AK:52:LYS:HB3	1.89	0.42
79:AV:89:LEU:O	79:AV:103:PHE:N	2.52	0.42
81:AX:2:C:H2'	81:AX:3:G:C8	2.54	0.42
81:AX:7:U:O4	81:AX:67:A:N6	2.53	0.42
83:AZ:221:THR:H	83:AZ:224:GLN:NE2	2.18	0.42
83:AZ:538:LEU:O	83:AZ:542:LEU:CB	2.60	0.42
1:1:294:U:O2'	1:1:295:A:O4'	2.34	0.42
1:1:315:C:OP2	39:i:28:TYR:OH	2.30	0.42
1:1:1203:A:H2'	1:1:1204:A:C8	2.54	0.42
1:1:1258:U:H2'	1:1:1259:A:H3'	2.01	0.42
1:1:2202:C:O2'	6:A:240:ALA:O	2.27	0.42
1:1:2268:U:O4	1:1:2272:G:O6	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2900:A:H61	1:1:3029:A:H61	1.67	0.42
4:P0:42:ARG:NH2	4:P0:51:VAL:HG11	2.33	0.42
7:B:377:HIS:CD2	7:B:387:LEU:HG	2.55	0.42
20:P:114:VAL:HA	20:P:150:VAL:HA	2.02	0.42
23:S:155:ARG:HD3	23:S:172:TYR:CD1	2.54	0.42
33:c:51:LEU:HD21	37:g:91:ARG:HA	2.01	0.42
42:l:13:MET:HE1	42:l:49:MET:HE3	2.02	0.42
47:2:250:C:H2'	47:2:251:A:C8	2.54	0.42
47:2:884:A:H2'	47:2:885:G:H8	1.84	0.42
47:2:1365:C:H2'	47:2:1366:U:C6	2.53	0.42
47:2:1486:G:O6	47:2:1520:U:O4	2.37	0.42
52:u:75:LYS:HD3	52:u:77:ARG:HH21	1.83	0.42
83:AZ:145:GLN:HA	83:AZ:146:ALA:HA	1.73	0.42
1:1:214:G:O6	1:1:227:G:N2	2.52	0.42
1:1:980:A:H2	1:1:1104:G:H21	1.65	0.42
1:1:1541:G:N1	1:1:1555:U:C2	2.87	0.42
1:1:1624:G:H2'	1:1:1625:A:H8	1.83	0.42
1:1:1655:G:N2	1:1:1801:U:O4	2.53	0.42
1:1:1816:A:H2'	1:1:1817:G:C8	2.54	0.42
1:1:2412:G:H2'	1:1:2413:A:C8	2.55	0.42
1:1:3101:G:H2'	1:1:3102:G:C8	2.54	0.42
1:1:3268:A:O2'	1:1:3269:U:O2	2.37	0.42
6:A:143:GLU:O	6:A:145:LYS:N	2.53	0.42
10:E:82:ARG:HH11	10:E:82:ARG:HD3	1.71	0.42
26:V:64:LYS:HA	26:V:70:ARG:HD3	2.01	0.42
47:2:400:A:N6	56:y:29:LEU:HG	2.34	0.42
47:2:460:A:O2'	52:u:27:TYR:OH	2.33	0.42
47:2:1071:U:H2'	47:2:1072:C:C6	2.55	0.42
47:2:1352:G:O6	47:2:1373:C:N4	2.49	0.42
47:2:1354:G:N2	47:2:1369:U:O2	2.50	0.42
47:2:1366:U:O2	67:AJ:66:TYR:OH	2.29	0.42
47:2:1387:G:O2'	47:2:1410:A:N6	2.53	0.42
47:2:1490:C:H2'	51:t:4:LEU:HB2	2.00	0.42
47:2:1690:G:N2	47:2:1712:A:O2'	2.51	0.42
51:t:65:ARG:HH21	51:t:68:GLU:CD	2.28	0.42
51:t:66:ILE:HA	51:t:69:LEU:HB2	2.02	0.42
55:x:126:LEU:HD13	55:x:129:LEU:HD12	2.01	0.42
61:AD:23:PRO:HB2	61:AD:25:TRP:CD1	2.54	0.42
66:AI:88:ARG:NH2	66:AI:112:ASP:OD2	2.52	0.42
70:AM:3:ARG:HE	70:AM:28:ARG:NH1	2.15	0.42
74:AQ:23:CYS:HB3	74:AQ:28:LYS:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:AZ:362:ASP:N	83:AZ:366:CYS:SG	2.93	0.42
1:1:695:C:OP2	8:C:115:HIS:NE2	2.42	0.42
1:1:846:A:N6	47:2:971:A:N1	2.68	0.42
1:1:2340:U:H2'	1:1:2341:A:C8	2.55	0.42
1:1:3158:G:H1	1:1:3292:A:H2	1.52	0.42
2:3:68:C:OP1	9:D:14:SER:OG	2.33	0.42
4:P0:42:ARG:HA	4:P0:45:LEU:HB3	2.00	0.42
14:I:48:LEU:HA	14:I:178:ARG:NH2	2.35	0.42
18:N:102:ALA:HA	18:N:105:ARG:HG2	2.02	0.42
23:S:88:HIS:HB3	23:S:90:MET:HE2	2.00	0.42
26:V:24:ASN:HA	26:V:33:ASN:HA	2.01	0.42
47:2:122:U:H4'	52:u:77:ARG:HH12	1.84	0.42
47:2:1711:C:C2	47:2:1712:A:H1'	2.55	0.42
62:AE:103:ARG:NH2	62:AE:107:ARG:HB2	2.34	0.42
63:AF:61:ARG:HA	63:AF:64:LYS:HB3	2.02	0.42
69:AL:25:LYS:HA	69:AL:25:LYS:HD2	1.87	0.42
69:AL:73:ALA:HB1	69:AL:79:LEU:HD13	2.00	0.42
70:AM:36:LYS:HG3	70:AM:39:GLN:HE21	1.85	0.42
83:AZ:693:LEU:HD21	83:AZ:700:ARG:HB3	2.00	0.42
83:AZ:800:HIS:HE2	83:AZ:802:SER:HB2	1.85	0.42
1:1:182:U:O4	1:1:234:G:O6	2.38	0.42
1:1:408:A:H2'	1:1:409:A:C8	2.55	0.42
1:1:915:A:OP1	1:1:2145:A:O2'	2.28	0.42
1:1:1883:A:H2'	1:1:1884:A:C8	2.54	0.42
1:1:2618:G:N2	1:1:2645:G:OP1	2.52	0.42
3:4:4:C:OP1	20:P:62:ARG:NH2	2.52	0.42
3:4:140:G:O2'	18:N:109:ARG:O	2.37	0.42
6:A:22:LEU:HD23	6:A:191:LEU:HD11	2.00	0.42
6:A:247:ARG:HH12	47:2:987:G:H1	1.68	0.42
7:B:264:VAL:HG13	7:B:266:ARG:HG3	2.02	0.42
7:B:377:HIS:HD2	7:B:387:LEU:HG	1.85	0.42
11:F:74:SER:OG	24:T:141:VAL:O	2.31	0.42
13:H:46:THR:O	13:H:54:LYS:N	2.47	0.42
16:L:64:LYS:HG3	31:a:69:TRP:CG	2.55	0.42
17:M:20:VAL:O	17:M:66:THR:OG1	2.37	0.42
37:g:49:SER:OG	37:g:50:ALA:N	2.52	0.42
37:g:74:ARG:HD3	37:g:85:VAL:HG11	2.01	0.42
41:k:62:ALA:HA	41:k:65:LEU:HD23	2.02	0.42
47:2:645:C:H2'	47:2:646:C:C6	2.55	0.42
47:2:1195:C:H42	64:AG:143:ARG:HA	1.84	0.42
47:2:1266:U:H2'	47:2:1267:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AB:100:TYR:N	71:AN:9:LEU:O	2.42	0.42
81:AX:50:U:H2'	81:AX:51:G:C8	2.54	0.42
83:AZ:834:GLY:HA3	83:AZ:838:TYR:CE2	2.54	0.42
1:1:157:A:H62	1:1:264:G:N2	2.16	0.42
1:1:1084:A:H2'	1:1:1085:A:C8	2.55	0.42
1:1:1165:A:H2'	1:1:1166:G:H8	1.84	0.42
1:1:1259:A:C5	4:P0:53:MET:HB3	2.55	0.42
1:1:1497:C:H2'	1:1:1498:A:C8	2.54	0.42
1:1:1827:C:H2'	1:1:1828:A:H8	1.85	0.42
1:1:2389:C:H2'	1:1:2390:A:C8	2.55	0.42
1:1:2632:G:O6	1:1:2647:A:N6	2.53	0.42
2:3:19:C:H2'	2:3:20:A:H8	1.85	0.42
4:P0:46:ARG:NH1	5:P2:123:ARG:HH11	2.18	0.42
5:P2:81:VAL:HG13	5:P2:142:ARG:HH22	1.85	0.42
7:B:188:ILE:HA	7:B:191:LYS:HD2	2.02	0.42
13:H:47:LYS:HA	13:H:53:ILE:HG13	2.02	0.42
15:J:29:ARG:HA	15:J:32:ARG:HG2	2.01	0.42
23:S:42:TRP:HE1	23:S:58:ILE:HD11	1.84	0.42
25:U:29:ASP:OD1	25:U:29:ASP:N	2.49	0.42
29:Y:55:GLU:HG3	29:Y:108:LYS:HB2	2.01	0.42
47:2:618:U:H5'	47:2:1030:A:C5	2.55	0.42
47:2:679:U:O4	47:2:682:C:N4	2.52	0.42
47:2:752:A:N1	47:2:797:G:C6	2.88	0.42
49:r:78:ASP:OD1	49:r:79:HIS:ND1	2.53	0.42
51:t:6:SER:OG	51:t:7:LYS:N	2.53	0.42
55:x:89:HIS:CE1	55:x:165:LYS:HG2	2.55	0.42
57:z:51:LYS:HA	57:z:54:ARG:HB3	2.02	0.42
60:AC:43:ARG:HH11	60:AC:46:ARG:NH2	2.18	0.42
63:AF:79:HIS:HA	63:AF:97:TYR:HB3	2.02	0.42
66:AI:5:VAL:HG22	73:AP:42:LEU:HD13	2.02	0.42
72:AO:27:VAL:HG12	72:AO:29:HIS:HD2	1.85	0.42
74:AQ:87:ARG:NH2	74:AQ:91:ASP:O	2.43	0.42
79:AV:22:SER:OG	79:AV:23:LEU:N	2.50	0.42
1:1:276:U:H2'	1:1:277:G:H8	1.85	0.42
1:1:431:U:H2'	1:1:432:G:H8	1.84	0.42
1:1:685:G:OP2	16:L:35:ARG:NH2	2.53	0.42
1:1:790:U:H2'	1:1:791:A:C8	2.54	0.42
1:1:1917:C:P	22:R:85:ARG:HH22	2.43	0.42
1:1:2611:U:H2'	1:1:2612:U:C6	2.54	0.42
1:1:2642:A:H5'	32:b:7:HIS:CD2	2.55	0.42
1:1:2662:G:H2'	1:1:2663:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:126:ILE:HD11	8:C:233:LEU:HD11	2.02	0.42
13:H:18:VAL:O	17:M:5:SER:OG	2.29	0.42
18:N:113:LEU:HB2	18:N:134:LEU:HD23	2.01	0.42
26:V:66:LYS:HA	26:V:67:PRO:HD3	1.87	0.42
30:Z:25:ILE:HG23	30:Z:41:ALA:HB1	2.02	0.42
36:f:9:VAL:HG12	36:f:100:ILE:HB	2.02	0.42
39:i:13:LYS:HA	39:i:13:LYS:HD3	1.86	0.42
47:2:1541:G:N2	47:2:1570:A:H62	2.18	0.42
47:2:1701:A:C5	47:2:1702:A:H1'	2.55	0.42
48:q:9:LEU:HD23	48:q:54:TRP:CD2	2.54	0.42
48:q:17:LEU:HD11	48:q:176:LEU:HD11	2.01	0.42
48:q:74:VAL:HB	48:q:121:VAL:HG12	2.02	0.42
48:q:163:ASN:HB2	48:q:165:ARG:HG2	2.01	0.42
49:r:83:LYS:HE2	49:r:106:THR:HG22	2.01	0.42
52:u:87:MET:HB2	52:u:87:MET:HE3	1.84	0.42
53:v:76:ARG:HE	64:AG:122:ARG:HD3	1.84	0.42
77:AT:21:CYS:SG	77:AT:23:VAL:N	2.84	0.42
79:AV:192:PHE:HZ	79:AV:228:LYS:HB3	1.85	0.42
83:AZ:70:ILE:HG22	83:AZ:71:LYS:HG3	2.02	0.42
1:1:504:A:H2'	1:1:505:G:C8	2.55	0.41
1:1:1621:A:H2'	1:1:1622:U:C6	2.55	0.41
1:1:1665:C:H2'	1:1:1666:G:H8	1.85	0.41
1:1:1896:A:N6	1:1:2339:C:H42	2.17	0.41
17:M:14:LEU:HD13	23:S:149:LYS:HD2	2.02	0.41
18:N:100:ALA:HB2	18:N:167:THR:HG21	2.02	0.41
47:2:338:C:H1'	56:y:5:ARG:HG3	2.02	0.41
47:2:898:A:H62	47:2:914:G:N2	2.18	0.41
47:2:1066:C:H2'	47:2:1067:C:C6	2.55	0.41
50:s:144:TRP:CD2	50:s:173:PRO:HG3	2.55	0.41
52:u:125:LYS:H	52:u:142:HIS:CD2	2.38	0.41
55:x:173:TYR:HE2	55:x:179:LYS:HB3	1.85	0.41
57:z:42:ILE:H	57:z:42:ILE:HG13	1.76	0.41
69:AL:80:LYS:HB3	69:AL:81:ASN:H	1.60	0.41
74:AQ:43:ASN:HB3	74:AQ:45:VAL:HG22	2.01	0.41
80:AW:123:ASN:HD22	80:AW:124:PRO:HD2	1.85	0.41
85:AZ:901:SO1:H4	85:AZ:901:SO1:H81	1.76	0.41
1:1:549:U:H2'	1:1:550:A:C8	2.55	0.41
1:1:710:A:H2'	1:1:711:A:C8	2.55	0.41
1:1:939:U:OP2	31:a:26:ARG:NH2	2.53	0.41
1:1:1349:G:H2'	1:1:1350:A:H4'	2.01	0.41
1:1:2261:G:O2'	1:1:2263:C:N4	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2456:A:O2'	1:1:2457:G:O4'	2.38	0.41
1:1:2674:A:H62	15:J:22:SER:H	1.67	0.41
1:1:3181:C:H2'	1:1:3182:G:C8	2.55	0.41
1:1:3198:U:HO2'	13:H:19:SER:HG	1.67	0.41
1:1:3218:A:H5''	1:1:3219:G:C8	2.55	0.41
7:B:72:VAL:HG22	26:V:88:ARG:HB3	2.02	0.41
9:D:107:ARG:NH2	9:D:119:TYR:O	2.48	0.41
13:H:104:VAL:N	13:H:111:PHE:O	2.52	0.41
15:J:84:LEU:HA	15:J:87:LYS:HB2	2.01	0.41
18:N:152:CYS:HB3	38:h:92:LEU:HD21	2.01	0.41
22:R:127:SER:HB2	22:R:132:PHE:HD2	1.84	0.41
37:g:57:LEU:HB2	37:g:61:GLN:HE21	1.85	0.41
47:2:14:C:H5''	50:s:164:SER:HB2	2.02	0.41
47:2:402:C:OP1	52:u:3:ARG:NH1	2.53	0.41
47:2:899:G:H2'	47:2:900:A:H8	1.85	0.41
47:2:903:U:C2	47:2:906:A:N7	2.87	0.41
47:2:930:A:H5''	74:AQ:70:LYS:HZ1	1.85	0.41
52:u:29:PRO:HB3	52:u:45:ILE:HD11	2.01	0.41
53:v:94:THR:HG21	53:v:111:VAL:HG22	2.02	0.41
57:z:171:ARG:NH1	57:z:174:ARG:HE	2.18	0.41
64:AG:47:LYS:HZ1	64:AG:112:TYR:HH	1.65	0.41
64:AG:65:ILE:HG13	64:AG:85:ILE:HG23	2.02	0.41
71:AN:89:ASN:HD22	71:AN:89:ASN:HA	1.60	0.41
80:AW:121:CYS:HB3	80:AW:130:VAL:HG23	2.02	0.41
83:AZ:190:SER:OG	83:AZ:201:GLN:NE2	2.47	0.41
1:1:21:G:H3'	1:1:22:G:H8	1.85	0.41
1:1:171:G:N1	1:1:248:U:N3	2.69	0.41
1:1:1135:A:H1'	1:1:2642:A:H2	1.85	0.41
1:1:1192:C:N4	1:1:1302:A:O5'	2.54	0.41
1:1:1510:G:H2'	1:1:1512:U:C4	2.55	0.41
1:1:1756:C:H2'	1:1:1757:A:H8	1.84	0.41
1:1:2597:U:H2'	1:1:2598:G:H8	1.85	0.41
1:1:3022:G:O2'	1:1:3031:G:O6	2.35	0.41
11:F:89:ILE:HD11	11:F:214:TRP:HH2	1.85	0.41
14:I:153:ARG:HH11	14:I:157:TYR:HE2	1.68	0.41
18:N:175:ASN:HB2	18:N:180:PHE:CE2	2.55	0.41
21:Q:62:VAL:HG13	21:Q:87:VAL:HG12	2.02	0.41
29:Y:119:ILE:O	29:Y:124:GLY:N	2.52	0.41
47:2:398:G:OP2	56:y:47:ARG:NH1	2.37	0.41
47:2:925:G:H2'	47:2:926:A:C8	2.55	0.41
47:2:1552:U:H2'	47:2:1553:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1561:U:H2'	47:2:1562:G:C8	2.55	0.41
47:2:1640:C:O2	47:2:1763:A:C6	2.73	0.41
51:t:46:THR:N	51:t:83:THR:O	2.42	0.41
63:AF:15:HIS:CD2	63:AF:17:TYR:HB2	2.55	0.41
65:AH:14:LYS:HZ1	65:AH:57:LEU:HD11	1.85	0.41
68:AK:23:ARG:HG3	68:AK:119:ALA:HB3	2.03	0.41
71:AN:63:GLN:HA	71:AN:64:PRO:HA	1.73	0.41
1:1:217:U:O2'	29:Y:102:SER:OG	2.38	0.41
1:1:341:G:O2'	3:4:22:U:O4	2.38	0.41
1:1:353:G:N2	1:1:365:A:OP2	2.53	0.41
1:1:407:A:H2'	1:1:408:A:H8	1.85	0.41
1:1:1257:C:O2	1:1:1261:G:O6	2.38	0.41
1:1:1262:G:H8	1:1:1262:G:H2'	1.72	0.41
1:1:1949:G:OP2	22:R:135:LYS:NZ	2.52	0.41
1:1:2294:U:H2'	1:1:2295:A:H3'	2.02	0.41
1:1:2565:U:O2	1:1:2576:G:N2	2.39	0.41
1:1:3064:U:H2'	1:1:3065:G:C8	2.55	0.41
5:P2:99:LYS:HE2	5:P2:99:LYS:HB3	1.87	0.41
7:B:187:SER:O	7:B:190:GLU:N	2.51	0.41
8:C:22:LEU:HA	8:C:23:PRO:HD3	1.79	0.41
8:C:316:ASN:HD22	11:F:150:LYS:HE2	1.84	0.41
11:F:136:TYR:CZ	11:F:231:ASN:HB3	2.55	0.41
17:M:40:ASP:OD1	17:M:43:LYS:N	2.45	0.41
19:O:129:LEU:HD21	19:O:133:ARG:HB3	2.03	0.41
22:R:10:LEU:HD12	22:R:10:LEU:HA	1.88	0.41
22:R:102:LEU:HD21	22:R:138:LEU:HB2	2.03	0.41
23:S:78:TRP:HB2	23:S:124:LEU:HB2	2.02	0.41
41:k:7:ASP:OD1	41:k:10:GLN:NE2	2.53	0.41
47:2:361:C:H2'	47:2:362:G:H8	1.84	0.41
47:2:384:G:H2'	47:2:385:A:H8	1.85	0.41
47:2:526:A:H2'	47:2:527:A:C4	2.56	0.41
51:t:7:LYS:HA	51:t:11:LEU:HD13	2.02	0.41
52:u:36:HIS:HA	52:u:143:ASP:HA	2.01	0.41
53:v:36:ALA:HB1	53:v:42:LEU:HD21	2.02	0.41
54:w:100:ALA:HB1	54:w:101:ILE:HD12	2.01	0.41
55:x:71:HIS:CD2	55:x:132:PRO:HG3	2.56	0.41
59:AB:8:GLN:HE21	59:AB:14:GLN:H	1.69	0.41
60:AC:97:LEU:HG	60:AC:100:TRP:HB2	2.01	0.41
61:AD:93:LYS:HE2	61:AD:93:LYS:HB3	1.95	0.41
79:AV:180:ALA:HB3	79:AV:190:ALA:HB3	2.03	0.41
1:1:939:U:H2'	1:1:940:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1243:G:N2	1:1:1270:A:O2'	2.53	0.41
1:1:1521:G:H5'	28:X:71:THR:HG21	2.03	0.41
1:1:2368:A:H2'	1:1:2369:G:C8	2.55	0.41
1:1:2916:U:H2'	1:1:2917:G:C8	2.56	0.41
4:P0:5:ARG:HD2	4:P0:8:LYS:HB2	2.03	0.41
5:P2:104:ILE:H	5:P2:104:ILE:HG13	1.64	0.41
6:A:104:LEU:HA	6:A:107:VAL:HG22	2.02	0.41
7:B:10:ARG:HH21	7:B:263:SER:HG	1.65	0.41
29:Y:80:VAL:O	29:Y:99:LEU:N	2.51	0.41
34:d:9:THR:HG21	34:d:74:ARG:HH21	1.85	0.41
47:2:872:G:C6	47:2:955:A:N1	2.89	0.41
49:r:31:ASP:HA	49:r:45:LYS:HA	2.01	0.41
49:r:35:PRO:HB3	49:r:231:LEU:HD13	2.03	0.41
52:u:64:ILE:HG13	72:AO:18:LEU:HD21	2.02	0.41
52:u:185:GLY:H	52:u:189:LEU:HB2	1.86	0.41
54:w:74:LYS:HD3	54:w:94:ARG:HH11	1.85	0.41
64:AG:136:SER:OG	64:AG:137:ARG:N	2.49	0.41
76:AS:43:ASN:HD22	76:AS:66:LEU:HD12	1.85	0.41
83:AZ:235:VAL:O	83:AZ:239:LYS:NZ	2.54	0.41
83:AZ:236:ASP:HB2	83:AZ:237:LYS:H	1.73	0.41
1:1:307:A:H2'	1:1:308:A:C8	2.54	0.41
1:1:356:C:H2'	1:1:357:A:H8	1.86	0.41
1:1:798:G:O2'	16:L:14:PHE:O	2.34	0.41
1:1:1627:U:H2'	1:1:1814:A:H62	1.85	0.41
1:1:1653:G:H2'	1:1:1654:A:C8	2.55	0.41
1:1:2098:C:H2'	1:1:2099:A:C8	2.54	0.41
1:1:2331:C:H2'	1:1:2332:A:C8	2.55	0.41
1:1:2440:G:H2'	1:1:2441:A:C8	2.55	0.41
3:4:141:C:O3'	18:N:62:TYR:OH	2.39	0.41
9:D:148:ILE:O	9:D:151:GLN:NE2	2.46	0.41
11:F:89:ILE:HD12	11:F:89:ILE:HA	1.82	0.41
14:I:36:LEU:HD11	14:I:87:LEU:HD12	2.02	0.41
16:L:167:PHE:HZ	16:L:171:ARG:HH11	1.69	0.41
17:M:105:GLN:NE2	19:O:199:TYR:O	2.53	0.41
18:N:99:ARG:HA	18:N:130:PHE:CE2	2.55	0.41
28:X:65:GLN:HB2	28:X:85:GLN:HB3	2.02	0.41
30:Z:90:GLU:HA	30:Z:93:LYS:HB2	2.03	0.41
39:i:20:MET:HE3	39:i:22:PRO:HG3	2.02	0.41
39:i:51:SER:O	39:i:55:ARG:N	2.52	0.41
47:2:97:C:H2'	47:2:98:U:H6	1.84	0.41
47:2:506:A:H4'	47:2:507:U:H5	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1087:A:H2'	47:2:1088:A:C8	2.55	0.41
47:2:1144:U:H2'	47:2:1145:U:H6	1.86	0.41
47:2:1158:C:H41	47:2:1581:C:H2'	1.85	0.41
47:2:1175:U:H2'	47:2:1176:G:C8	2.56	0.41
47:2:1330:G:H3'	47:2:1331:A:H8	1.86	0.41
47:2:1364:G:H2'	47:2:1365:C:C6	2.55	0.41
47:2:1595:U:H3'	77:AT:32:ARG:NH2	2.36	0.41
50:s:222:TYR:HB2	69:AL:25:LYS:HE3	2.02	0.41
51:t:15:GLY:HA2	51:t:18:TYR:CE2	2.55	0.41
51:t:191:ASP:OD1	51:t:191:ASP:N	2.50	0.41
52:u:64:ILE:HD11	72:AO:18:LEU:HD11	2.01	0.41
54:w:33:GLY:HA2	54:w:51:LYS:HA	2.03	0.41
57:z:34:PHE:HA	57:z:122:VAL:HG21	2.02	0.41
60:AC:42:ALA:HA	60:AC:47:GLU:HB2	2.03	0.41
61:AD:40:TYR:HA	61:AD:43:LYS:HE2	2.01	0.41
65:AH:29:GLN:HG3	65:AH:33:ARG:HH22	1.85	0.41
66:AI:74:GLN:HA	66:AI:99:HIS:HE2	1.85	0.41
74:AQ:10:ARG:HB2	74:AQ:34:LYS:HA	2.03	0.41
81:AX:65:G:H2'	81:AX:66:A:C8	2.56	0.41
83:AZ:349:GLN:HE21	83:AZ:372:CYS:HB3	1.86	0.41
1:1:276:U:H2'	1:1:277:G:C8	2.56	0.41
1:1:584:G:H2'	1:1:585:A:C8	2.54	0.41
1:1:1756:C:H2'	1:1:1757:A:C8	2.55	0.41
1:1:2562:A:H3'	1:1:2563:G:H8	1.85	0.41
12:G:185:ARG:O	12:G:188:THR:OG1	2.31	0.41
22:R:10:LEU:HD23	22:R:41:ILE:HD13	2.02	0.41
24:T:107:GLU:HA	24:T:110:LYS:HB3	2.02	0.41
26:V:108:GLU:HA	26:V:128:ARG:HG2	2.03	0.41
29:Y:32:SER:HA	29:Y:50:ILE:HD11	2.02	0.41
31:a:35:ALA:O	31:a:41:HIS:ND1	2.54	0.41
34:d:25:PHE:HB3	34:d:65:LYS:HG2	2.03	0.41
47:2:890:C:H2'	47:2:891:A:C8	2.56	0.41
47:2:1133:A:N3	47:2:1650:U:O2'	2.54	0.41
47:2:1220:C:H2'	47:2:1221:A:C8	2.52	0.41
47:2:1481:C:OP2	67:AJ:64:HIS:ND1	2.53	0.41
47:2:1503:A:H2'	47:2:1504:G:C8	2.56	0.41
47:2:1517:U:P	47:2:1518:C:H41	2.43	0.41
48:q:11:PRO:HG3	65:AH:115:LEU:HD22	2.02	0.41
50:s:86:VAL:HG21	50:s:99:LYS:HE3	2.03	0.41
56:y:66:SER:H	56:y:182:TYR:HA	1.84	0.41
56:y:67:TRP:CD1	56:y:69:SER:H	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:157:GLU:HA	56:y:160:PHE:HD2	1.86	0.41
57:z:69:ARG:HH21	57:z:93:LEU:HD12	1.86	0.41
63:AF:25:LEU:HD22	63:AF:25:LEU:HA	1.90	0.41
67:AJ:41:SER:OG	67:AJ:95:ASP:O	2.28	0.41
69:AL:69:LEU:O	69:AL:73:ALA:N	2.54	0.41
72:AO:102:LYS:H	72:AO:102:LYS:HD2	1.85	0.41
76:AS:36:THR:OG1	76:AS:37:SER:N	2.53	0.41
79:AV:281:TYR:HB3	79:AV:285:ALA:HB3	2.02	0.41
1:1:76:G:N7	16:L:101:ARG:HG2	2.36	0.41
1:1:431:U:OP1	36:f:53:TYR:OH	2.37	0.41
1:1:946:U:H2'	1:1:947:G:H8	1.85	0.41
1:1:1009:A:H2'	1:1:1010:G:C8	2.56	0.41
1:1:1392:G:N1	1:1:1417:G:N7	2.69	0.41
1:1:2252:A:H2'	1:1:2253:G:C8	2.55	0.41
1:1:2409:G:H3'	1:1:2410:U:H4'	2.01	0.41
7:B:298:PHE:HD2	7:B:357:LYS:HG3	1.85	0.41
19:O:187:GLU:HA	19:O:191:ALA:HB2	2.03	0.41
36:f:47:LYS:HZ2	36:f:102:LEU:HA	1.85	0.41
47:2:358:U:H2'	47:2:360:A:H8	1.85	0.41
47:2:641:G:H2'	47:2:642:G:C8	2.56	0.41
47:2:846:G:H2'	47:2:847:A:H8	1.85	0.41
47:2:871:G:H2'	47:2:872:G:C8	2.56	0.41
47:2:885:G:OP1	49:r:136:ARG:NH1	2.54	0.41
53:v:164:PRO:HG3	76:AS:52:ASP:HB3	2.03	0.41
54:w:90:GLY:H	54:w:91:GLU:HB3	1.85	0.41
55:x:72:LYS:O	55:x:76:LYS:NZ	2.54	0.41
60:AC:59:LEU:HD22	60:AC:121:VAL:H	1.85	0.41
63:AF:34:VAL:HG23	63:AF:41:VAL:HG12	2.03	0.41
67:AJ:40:SER:OG	67:AJ:41:SER:N	2.53	0.41
72:AO:23:PHE:HE1	72:AO:75:VAL:HG12	1.85	0.41
77:AT:22:ARG:N	77:AT:37:ASN:O	2.54	0.41
79:AV:213:SER:N	79:AV:221:MET:O	2.54	0.41
83:AZ:151:ILE:HD12	83:AZ:151:ILE:HA	1.97	0.41
1:1:54:C:H2'	1:1:55:G:H8	1.86	0.41
1:1:385:A:O2'	1:1:386:A:O4'	2.36	0.41
1:1:835:G:O2'	1:1:857:G:N2	2.44	0.41
1:1:900:G:N3	1:1:1589:A:N6	2.69	0.41
1:1:949:C:O2'	21:Q:8:LYS:NZ	2.39	0.41
1:1:1023:C:N4	1:1:1024:G:N3	2.69	0.41
1:1:2563:G:O5'	30:Z:55:LYS:NZ	2.50	0.41
1:1:3007:U:OP1	19:O:74:ARG:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3049:A:OP1	7:B:332:ARG:NH2	2.54	0.41
1:1:3255:U:H2'	1:1:3256:G:C8	2.56	0.41
1:1:3276:G:O6	20:P:171:ARG:NE	2.54	0.41
1:1:3325:G:H5''	34:d:103:GLY:HA2	2.02	0.41
3:4:95:G:H21	40:j:79:GLN:HE22	1.69	0.41
4:P0:12:PHE:O	4:P0:16:ARG:N	2.49	0.41
5:P2:57:LYS:HE3	5:P2:79:SER:HB2	2.02	0.41
7:B:235:THR:OG1	7:B:236:LYS:N	2.51	0.41
10:E:148:GLU:O	10:E:151:LYS:NZ	2.54	0.41
13:H:92:TYR:HB2	13:H:142:ASP:HB3	2.03	0.41
15:J:101:ASN:HD22	15:J:130:VAL:HA	1.86	0.41
26:V:81:GLN:HB3	26:V:85:TRP:HZ3	1.86	0.41
31:a:2:PRO:HB2	31:a:3:SER:H	1.76	0.41
47:2:201:G:H2'	47:2:202:A:C8	2.56	0.41
47:2:358:U:H2'	47:2:360:A:C8	2.56	0.41
47:2:560:U:H2'	47:2:561:G:H8	1.85	0.41
47:2:636:A:H5''	70:AM:31:SER:HB3	2.02	0.41
47:2:1018:U:H2'	47:2:1019:A:C8	2.55	0.41
47:2:1158:C:H5	47:2:1582:U:H5''	1.86	0.41
47:2:1206:U:H4'	77:AT:27:HIS:NE2	2.36	0.41
47:2:1273:G:O2'	47:2:1430:U:OP2	2.37	0.41
47:2:1344:A:N6	47:2:1377:U:O2'	2.54	0.41
47:2:1379:C:H4'	64:AG:17:THR:HG21	2.03	0.41
47:2:1385:G:H2'	47:2:1386:G:C8	2.56	0.41
47:2:1587:A:H2'	47:2:1588:G:H8	1.86	0.41
51:t:19:ALA:HB1	77:AT:46:LYS:HG2	2.03	0.41
51:t:169:ASP:N	51:t:188:ILE:O	2.54	0.41
54:w:94:ARG:HD3	54:w:94:ARG:HA	1.88	0.41
57:z:173:ALA:O	57:z:177:ALA:N	2.49	0.41
61:AD:4:MET:HE2	61:AD:4:MET:HB2	1.89	0.41
62:AE:27:PHE:HB3	62:AE:43:THR:HA	2.02	0.41
63:AF:60:LEU:O	63:AF:64:LYS:N	2.46	0.41
79:AV:40:LYS:HG2	79:AV:67:ILE:HA	2.02	0.41
83:AZ:567:VAL:HG23	83:AZ:722:PRO:HG3	2.02	0.41
83:AZ:699:DDE:HAU3	83:AZ:699:DDE:HAB2	1.85	0.41
83:AZ:753:GLN:HB2	83:AZ:771:TYR:HB2	2.02	0.41
1:1:2129:U:H2'	1:1:2130:G:C8	2.55	0.41
1:1:2724:U:H4'	24:T:54:HIS:CE1	2.56	0.41
1:1:3003:G:O2'	7:B:92:TYR:OH	2.30	0.41
1:1:3205:G:H5''	17:M:102:LYS:NZ	2.36	0.41
8:C:157:GLU:HB3	8:C:213:ASN:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:42:GLN:HA	36:f:45:LEU:HG	2.03	0.41
47:2:1078:C:H2'	47:2:1079:U:H6	1.86	0.41
47:2:1676:U:C2	47:2:1726:G:N1	2.89	0.41
47:2:1758:U:C4	47:2:1759:C:N4	2.88	0.41
52:u:43:PRO:HA	52:u:83:PRO:HA	2.03	0.41
52:u:123:LEU:HD12	52:u:123:LEU:HA	1.90	0.41
55:x:123:ASP:OD1	55:x:124:LYS:N	2.53	0.41
55:x:139:ARG:HG3	70:AM:53:ILE:HD12	2.03	0.41
58:AA:15:LEU:O	58:AA:19:GLY:N	2.54	0.41
67:AJ:65:ILE:HG12	67:AJ:68:ARG:HH21	1.86	0.41
83:AZ:75:ILE:HB	83:AZ:102:LEU:HB3	2.03	0.41
83:AZ:75:ILE:HD12	83:AZ:102:LEU:HD23	2.01	0.41
83:AZ:130:ASP:OD1	83:AZ:159:LYS:NZ	2.40	0.41
83:AZ:779:GLY:O	83:AZ:782:GLY:N	2.53	0.41
1:1:41:G:H21	1:1:2803:A:H62	1.69	0.40
1:1:289:A:O2'	18:N:93:LYS:O	2.36	0.40
1:1:842:G:H2'	1:1:843:A:C8	2.56	0.40
1:1:852:U:H2'	1:1:853:G:C8	2.54	0.40
1:1:903:U:H2'	1:1:904:A:C8	2.53	0.40
1:1:1485:G:N3	37:g:4:ARG:NH2	2.69	0.40
1:1:2545:C:H2'	1:1:2546:C:C6	2.56	0.40
1:1:3185:U:O2'	23:S:170:THR:OG1	2.25	0.40
8:C:65:TRP:CG	8:C:69:ARG:HH22	2.39	0.40
8:C:314:LYS:NZ	8:C:315:LYS:O	2.42	0.40
11:F:144:ILE:HG21	11:F:189:ILE:HD11	2.03	0.40
13:H:80:THR:HG23	13:H:84:LYS:HD2	2.03	0.40
14:I:86:HIS:HB3	14:I:139:ARG:HG2	2.03	0.40
19:O:49:ARG:O	19:O:53:LYS:N	2.44	0.40
19:O:80:PHE:HA	19:O:83:ALA:HB3	2.02	0.40
31:a:126:LYS:HG2	31:a:146:GLU:HB3	2.02	0.40
47:2:97:C:O2	47:2:425:A:O2'	2.33	0.40
47:2:114:C:O2'	59:AB:67:ARG:NH2	2.34	0.40
47:2:253:A:H5'	52:u:134:LYS:HA	2.03	0.40
47:2:520:A:H2'	47:2:521:A:H8	1.87	0.40
47:2:765:G:H1	57:z:149:ARG:HB2	1.86	0.40
47:2:1022:C:H5	47:2:1023:A:C6	2.39	0.40
47:2:1172:G:N2	67:AJ:88:VAL:HG11	2.36	0.40
47:2:1303:U:O2'	47:2:1322:A:OP2	2.29	0.40
47:2:1470:C:OP1	47:2:1540:G:O2'	2.34	0.40
48:q:155:PHE:O	69:AL:60:ARG:NH1	2.54	0.40
53:v:76:ARG:HD3	53:v:76:ARG:HA	1.82	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w:30:LYS:HE3	54:w:34:GLN:HG2	2.02	0.40
54:w:36:VAL:HB	54:w:50:PHE:HB2	2.03	0.40
55:x:98:ILE:HD12	55:x:98:ILE:HA	1.96	0.40
63:AF:86:VAL:HA	63:AF:87:PRO:HD3	1.80	0.40
66:AI:87:ASN:OD1	66:AI:87:ASN:N	2.53	0.40
66:AI:121:ALA:HB3	66:AI:124:GLY:H	1.85	0.40
67:AJ:65:ILE:HA	67:AJ:68:ARG:HE	1.86	0.40
70:AM:20:THR:OG1	70:AM:22:LYS:NZ	2.39	0.40
83:AZ:308:LYS:O	83:AZ:311:GLU:HB2	2.21	0.40
1:1:720:A:H5'	21:Q:69:ARG:HH22	1.86	0.40
1:1:1263:A:H61	5:P2:136:ALA:HB2	1.86	0.40
1:1:1628:C:H4'	1:1:1629:U:H3'	2.02	0.40
1:1:2228:A:H2'	1:1:2229:A:H8	1.86	0.40
1:1:2815:G:N7	1:1:2870:C:O2'	2.52	0.40
11:F:43:ILE:H	11:F:43:ILE:HG13	1.69	0.40
13:H:34:LEU:HD21	13:H:78:MET:HB2	2.04	0.40
32:b:32:LEU:O	32:b:40:ARG:NH2	2.54	0.40
47:2:737:A:O2'	47:2:738:G:O5'	2.37	0.40
47:2:899:G:H2'	47:2:900:A:C8	2.56	0.40
47:2:966:A:OP1	61:AD:124:ARG:NE	2.53	0.40
47:2:1150:G:N2	82:AY:45:A:O2'	2.54	0.40
47:2:1673:G:O6	47:2:1728:A:N1	2.54	0.40
50:s:56:ILE:HD11	50:s:61:LEU:HB2	2.02	0.40
52:u:53:LYS:O	72:AO:22:GLN:NE2	2.43	0.40
54:w:44:GLU:HB2	54:w:120:GLU:HB2	2.04	0.40
56:y:98:LYS:HE3	56:y:98:LYS:HB3	1.97	0.40
57:z:83:VAL:HG23	57:z:85:VAL:HG23	2.03	0.40
65:AH:115:LEU:HB3	65:AH:116:LYS:H	1.77	0.40
72:AO:84:LYS:HE3	72:AO:85:PHE:HE2	1.86	0.40
79:AV:43:ILE:HG23	79:AV:57:PRO:HB3	2.03	0.40
83:AZ:574:THR:HG22	83:AZ:589:LYS:HB2	2.02	0.40
1:1:160:G:H1	1:1:261:U:H3	1.68	0.40
1:1:1084:A:H4'	9:D:44:TYR:HE2	1.86	0.40
1:1:1276:U:P	4:P0:110:ARG:HH11	2.44	0.40
1:1:1348:U:H2'	8:C:290:ILE:HD13	2.04	0.40
1:1:1881:A:H2'	1:1:1882:G:H8	1.86	0.40
1:1:2591:A:H2'	1:1:2592:G:C8	2.56	0.40
1:1:2816:G:N2	1:1:2819:A:OP2	2.41	0.40
3:4:111:A:O2'	3:4:112:U:OP1	2.38	0.40
3:4:143:U:OP1	18:N:38:ARG:NH2	2.54	0.40
8:C:60:THR:OG1	8:C:61:SER:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:61:ASN:O	11:F:65:ALA:N	2.49	0.40
15:J:62:ASN:ND2	45:o:101:GLY:O	2.54	0.40
16:L:21:ARG:HB3	18:N:192:LYS:NZ	2.37	0.40
17:M:15:VAL:HG11	23:S:152:LEU:HD23	2.02	0.40
19:O:42:ASN:ND2	19:O:125:ARG:HG3	2.37	0.40
26:V:68:GLU:HG2	26:V:69:LEU:HD22	2.03	0.40
34:d:61:LYS:HE2	34:d:61:LYS:HB3	1.96	0.40
42:l:49:MET:HE2	42:l:49:MET:HB2	1.91	0.40
47:2:86:A:H2'	47:2:87:C:C6	2.55	0.40
47:2:142:G:H1	47:2:173:A:H2	1.57	0.40
47:2:975:C:H5''	61:AD:109:LYS:HG2	2.02	0.40
47:2:978:A:H2'	47:2:979:A:H8	1.87	0.40
47:2:1474:G:N7	73:AP:97:LYS:NZ	2.57	0.40
53:v:120:ILE:HD13	73:AP:100:ILE:HD11	2.02	0.40
62:AE:90:ARG:HB3	62:AE:91:THR:H	1.72	0.40
70:AM:101:TYR:HA	70:AM:113:HIS:HE1	1.86	0.40
79:AV:149:ASP:HB2	79:AV:175:ASP:HA	2.03	0.40
79:AV:205:SER:OG	79:AV:208:GLY:N	2.50	0.40
1:1:49:A:H61	1:1:287:G:H21	1.69	0.40
1:1:1224:C:H2'	1:1:1225:A:H8	1.87	0.40
1:1:1370:G:H2'	1:1:1371:G:C8	2.56	0.40
1:1:2367:A:H2'	1:1:2368:A:C8	2.57	0.40
1:1:2661:G:H2'	1:1:2662:G:C8	2.56	0.40
1:1:2914:G:H5'	7:B:9:PRO:HG3	2.03	0.40
10:E:38:THR:HG22	10:E:40:LEU:HB3	2.02	0.40
16:L:43:ALA:HA	16:L:46:ILE:HG22	2.02	0.40
29:Y:31:LEU:HD11	29:Y:78:PHE:HA	2.04	0.40
36:f:67:MET:HE1	36:f:90:PRO:HD3	2.04	0.40
47:2:1316:G:H2'	47:2:1317:C:C6	2.56	0.40
47:2:1383:G:N7	68:AK:57:ARG:NH2	2.70	0.40
56:y:52:ASN:N	56:y:52:ASN:OD1	2.54	0.40
62:AE:103:ARG:HH22	62:AE:107:ARG:HB2	1.85	0.40
70:AM:51:GLU:HB3	70:AM:62:VAL:HG13	2.04	0.40
83:AZ:579:SER:N	83:AZ:710:ARG:HH21	2.19	0.40
1:1:39:A:H61	1:1:42:C:H3'	1.86	0.40
1:1:88:A:H62	1:1:98:G:N2	2.19	0.40
1:1:720:A:OP1	31:a:117:ARG:NH1	2.42	0.40
1:1:745:C:H2'	1:1:746:A:C8	2.57	0.40
1:1:915:A:H2'	1:1:916:G:H4'	2.04	0.40
1:1:992:A:N6	1:1:993:G:O6	2.54	0.40
1:1:3169:U:H2'	1:1:3170:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3340:G:O2'	1:1:3342:A:OP2	2.35	0.40
2:3:39:C:O2'	15:J:44:THR:O	2.39	0.40
47:2:191:C:O2'	47:2:192:U:O4'	2.38	0.40
47:2:546:U:H2'	47:2:547:U:C6	2.56	0.40
47:2:1628:U:H2'	47:2:1629:G:C8	2.56	0.40
48:q:150:ASP:OD1	48:q:150:ASP:N	2.51	0.40
51:t:25:PHE:HD1	51:t:29:LEU:HD22	1.87	0.40
54:w:22:HIS:HA	54:w:25:ARG:HB2	2.03	0.40
72:AO:133:ASN:HA	72:AO:134:ALA:HA	1.76	0.40
79:AV:217:ASP:OD1	79:AV:217:ASP:N	2.54	0.40
79:AV:222:LEU:HB2	79:AV:231:MET:HB2	2.04	0.40
83:AZ:460:ASP:OD1	83:AZ:460:ASP:N	2.54	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	
4	P0	187/189 (99%)	151 (81%)	36 (19%)	0	100	100
5	P2	92/94 (98%)	71 (77%)	21 (23%)	0	100	100
6	A	250/252 (99%)	212 (85%)	38 (15%)	0	100	100
7	B	384/386 (100%)	337 (88%)	47 (12%)	0	100	100
8	C	359/361 (99%)	307 (86%)	52 (14%)	0	100	100
9	D	294/296 (99%)	257 (87%)	35 (12%)	2 (1%)	18	55
10	E	152/175 (87%)	135 (89%)	17 (11%)	0	100	100
11	F	220/222 (99%)	184 (84%)	34 (16%)	2 (1%)	14	49
12	G	231/233 (99%)	199 (86%)	31 (13%)	1 (0%)	30	66
13	H	189/191 (99%)	159 (84%)	30 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	I	207/220 (94%)	182 (88%)	24 (12%)	1 (0%)	24	62
15	J	167/169 (99%)	135 (81%)	31 (19%)	1 (1%)	21	58
16	L	191/193 (99%)	155 (81%)	34 (18%)	2 (1%)	12	47
17	M	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
18	N	201/203 (99%)	171 (85%)	30 (15%)	0	100	100
19	O	195/197 (99%)	170 (87%)	22 (11%)	3 (2%)	8	38
20	P	181/183 (99%)	161 (89%)	20 (11%)	0	100	100
21	Q	183/185 (99%)	162 (88%)	21 (12%)	0	100	100
22	R	186/188 (99%)	173 (93%)	13 (7%)	0	100	100
23	S	170/172 (99%)	147 (86%)	23 (14%)	0	100	100
24	T	157/159 (99%)	137 (87%)	19 (12%)	1 (1%)	21	58
25	U	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
26	V	134/136 (98%)	114 (85%)	19 (14%)	1 (1%)	18	55
27	W	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
28	X	119/121 (98%)	103 (87%)	16 (13%)	0	100	100
29	Y	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
30	Z	133/135 (98%)	111 (84%)	22 (16%)	0	100	100
31	a	146/148 (99%)	117 (80%)	28 (19%)	1 (1%)	18	55
32	b	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
33	c	95/97 (98%)	84 (88%)	11 (12%)	0	100	100
34	d	107/109 (98%)	91 (85%)	16 (15%)	0	100	100
35	e	125/127 (98%)	111 (89%)	12 (10%)	2 (2%)	7	36
36	f	104/106 (98%)	82 (79%)	20 (19%)	2 (2%)	6	32
37	g	110/112 (98%)	99 (90%)	9 (8%)	2 (2%)	6	33
38	h	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
39	i	97/99 (98%)	78 (80%)	19 (20%)	0	100	100
40	j	85/87 (98%)	65 (76%)	19 (22%)	1 (1%)	10	42
41	k	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
42	l	48/50 (96%)	36 (75%)	11 (23%)	1 (2%)	5	29
43	m	50/52 (96%)	45 (90%)	5 (10%)	0	100	100
44	n	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	o	103/105 (98%)	78 (76%)	25 (24%)	0	100	100
46	p	89/91 (98%)	78 (88%)	11 (12%)	0	100	100
48	q	204/206 (99%)	169 (83%)	33 (16%)	2 (1%)	12	47
49	r	212/214 (99%)	161 (76%)	49 (23%)	2 (1%)	14	49
50	s	215/217 (99%)	183 (85%)	32 (15%)	0	100	100
51	t	221/223 (99%)	182 (82%)	39 (18%)	0	100	100
52	u	258/260 (99%)	200 (78%)	56 (22%)	2 (1%)	16	52
53	v	204/206 (99%)	164 (80%)	40 (20%)	0	100	100
54	w	221/223 (99%)	157 (71%)	61 (28%)	3 (1%)	9	39
55	x	182/184 (99%)	150 (82%)	31 (17%)	1 (0%)	24	62
56	y	184/199 (92%)	141 (77%)	43 (23%)	0	100	100
57	z	183/185 (99%)	153 (84%)	30 (16%)	0	100	100
58	AA	94/105 (90%)	77 (82%)	16 (17%)	1 (1%)	11	45
59	AB	151/153 (99%)	125 (83%)	26 (17%)	0	100	100
60	AC	122/124 (98%)	98 (80%)	23 (19%)	1 (1%)	16	52
61	AD	148/150 (99%)	129 (87%)	15 (10%)	4 (3%)	4	25
62	AE	125/127 (98%)	105 (84%)	20 (16%)	0	100	100
63	AF	122/124 (98%)	85 (70%)	33 (27%)	4 (3%)	3	21
64	AG	139/141 (99%)	111 (80%)	26 (19%)	2 (1%)	9	39
65	AH	116/125 (93%)	97 (84%)	19 (16%)	0	100	100
66	AI	143/145 (99%)	122 (85%)	19 (13%)	2 (1%)	9	39
67	AJ	141/143 (99%)	124 (88%)	17 (12%)	0	100	100
68	AK	105/107 (98%)	91 (87%)	14 (13%)	0	100	100
69	AL	85/87 (98%)	64 (75%)	20 (24%)	1 (1%)	10	42
70	AM	127/129 (98%)	114 (90%)	12 (9%)	1 (1%)	16	52
71	AN	142/144 (99%)	114 (80%)	26 (18%)	2 (1%)	9	39
72	AO	132/134 (98%)	112 (85%)	20 (15%)	0	100	100
73	AP	68/70 (97%)	46 (68%)	21 (31%)	1 (2%)	8	38
74	AQ	95/97 (98%)	65 (68%)	30 (32%)	0	100	100
75	AR	79/81 (98%)	57 (72%)	21 (27%)	1 (1%)	9	41
76	AS	61/63 (97%)	54 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	AT	51/53 (96%)	46 (90%)	5 (10%)	0	100	100
78	AU	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
79	AV	316/318 (99%)	254 (80%)	61 (19%)	1 (0%)	36	71
80	AW	35/37 (95%)	26 (74%)	9 (26%)	0	100	100
83	AZ	837/840 (100%)	676 (81%)	157 (19%)	4 (0%)	24	62
All	All	12005/12221 (98%)	10010 (83%)	1937 (16%)	58 (0%)	26	62

All (58) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	O	111	PRO
48	q	113	ARG
49	r	207	LEU
54	w	10	ASN
54	w	68	LEU
58	AA	88	PRO
61	AD	105	ASN
64	AG	59	LYS
16	L	48	PRO
16	L	77	LEU
26	V	105	PRO
35	e	79	VAL
36	f	58	GLU
36	f	59	VAL
42	l	30	ARG
49	r	206	PRO
52	u	195	ILE
54	w	93	LYS
71	AN	114	LYS
75	AR	76	GLY
11	F	159	GLN
24	T	159	PHE
48	q	112	THR
55	x	111	LYS
61	AD	85	PRO
63	AF	30	THR
63	AF	53	PRO
73	AP	55	PRO
83	AZ	252	PRO
83	AZ	708	THR

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Mol	Chain	Res	Type
83	AZ	722	PRO
11	F	158	LYS
14	I	24	ARG
19	O	37	ARG
31	a	78	LEU
37	g	66	SER
40	j	64	MET
52	u	155	LYS
61	AD	139	TRP
69	AL	81	ASN
79	AV	165	ASP
9	D	259	LYS
19	O	110	PRO
35	e	78	ASN
37	g	67	LYS
60	AC	131	ASP
61	AD	104	ARG
63	AF	125	PRO
83	AZ	639	ASP
9	D	20	PHE
15	J	165	GLN
63	AF	70	ASN
66	AI	9	GLY
12	G	157	VAL
71	AN	64	PRO
64	AG	33	GLY
66	AI	92	ILE
70	AM	67	GLY

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	
4	P0	160/160 (100%)	160 (100%)	0	100	100
5	P2	81/81 (100%)	80 (99%)	1 (1%)	63	73
6	A	193/194 (100%)	192 (100%)	1 (0%)	81	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	B	321/322 (100%)	316 (98%)	5 (2%)	55	69
8	C	288/288 (100%)	285 (99%)	3 (1%)	68	76
9	D	244/244 (100%)	243 (100%)	1 (0%)	84	82
10	E	134/152 (88%)	134 (100%)	0	100	100
11	F	186/186 (100%)	183 (98%)	3 (2%)	55	69
12	G	187/191 (98%)	186 (100%)	1 (0%)	81	81
13	H	171/171 (100%)	170 (99%)	1 (1%)	78	80
14	I	177/186 (95%)	175 (99%)	2 (1%)	65	74
15	J	147/147 (100%)	147 (100%)	0	100	100
16	L	154/154 (100%)	154 (100%)	0	100	100
17	M	107/107 (100%)	104 (97%)	3 (3%)	38	59
18	N	175/175 (100%)	170 (97%)	5 (3%)	37	58
19	O	160/160 (100%)	154 (96%)	6 (4%)	29	50
20	P	140/145 (97%)	137 (98%)	3 (2%)	47	65
21	Q	150/150 (100%)	149 (99%)	1 (1%)	76	79
22	R	153/153 (100%)	150 (98%)	3 (2%)	48	66
23	S	156/156 (100%)	155 (99%)	1 (1%)	78	80
24	T	136/136 (100%)	133 (98%)	3 (2%)	45	64
25	U	87/87 (100%)	87 (100%)	0	100	100
26	V	104/104 (100%)	103 (99%)	1 (1%)	68	76
27	W	55/55 (100%)	52 (94%)	3 (6%)	19	42
28	X	104/105 (99%)	103 (99%)	1 (1%)	68	76
29	Y	109/109 (100%)	109 (100%)	0	100	100
30	Z	115/115 (100%)	115 (100%)	0	100	100
31	a	118/118 (100%)	118 (100%)	0	100	100
32	b	46/46 (100%)	45 (98%)	1 (2%)	45	64
33	c	81/81 (100%)	78 (96%)	3 (4%)	30	51
34	d	94/96 (98%)	94 (100%)	0	100	100
35	e	109/109 (100%)	108 (99%)	1 (1%)	70	76
36	f	90/90 (100%)	89 (99%)	1 (1%)	65	74
37	g	95/95 (100%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	h	104/104 (100%)	102 (98%)	2 (2%)	50	66
39	i	81/81 (100%)	81 (100%)	0	100	100
40	j	70/70 (100%)	70 (100%)	0	100	100
41	k	68/68 (100%)	67 (98%)	1 (2%)	57	70
42	l	45/45 (100%)	44 (98%)	1 (2%)	45	64
43	m	47/47 (100%)	46 (98%)	1 (2%)	47	65
44	n	22/23 (96%)	22 (100%)	0	100	100
45	o	90/90 (100%)	90 (100%)	0	100	100
46	p	71/71 (100%)	70 (99%)	1 (1%)	59	71
48	q	164/173 (95%)	163 (99%)	1 (1%)	78	80
49	r	191/191 (100%)	188 (98%)	3 (2%)	55	69
50	s	176/176 (100%)	174 (99%)	2 (1%)	65	74
51	t	182/182 (100%)	181 (100%)	1 (0%)	81	81
52	u	221/221 (100%)	219 (99%)	2 (1%)	70	76
53	v	173/173 (100%)	173 (100%)	0	100	100
54	w	189/191 (99%)	188 (100%)	1 (0%)	81	81
55	x	165/165 (100%)	164 (99%)	1 (1%)	78	80
56	y	150/160 (94%)	148 (99%)	2 (1%)	61	72
57	z	158/158 (100%)	157 (99%)	1 (1%)	78	80
58	AA	77/98 (79%)	76 (99%)	1 (1%)	61	72
59	AB	133/134 (99%)	131 (98%)	2 (2%)	57	70
60	AC	88/100 (88%)	85 (97%)	3 (3%)	32	54
61	AD	127/127 (100%)	124 (98%)	3 (2%)	43	63
62	AE	81/96 (84%)	79 (98%)	2 (2%)	42	62
63	AF	101/104 (97%)	100 (99%)	1 (1%)	68	76
64	AG	117/117 (100%)	116 (99%)	1 (1%)	70	76
65	AH	94/113 (83%)	94 (100%)	0	100	100
66	AI	128/128 (100%)	127 (99%)	1 (1%)	73	77
67	AJ	115/115 (100%)	115 (100%)	0	100	100
68	AK	100/100 (100%)	99 (99%)	1 (1%)	68	76
69	AL	74/74 (100%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	AM	110/110 (100%)	107 (97%)	3 (3%)	39	59
71	AN	119/119 (100%)	114 (96%)	5 (4%)	26	48
72	AO	112/112 (100%)	111 (99%)	1 (1%)	70	76
73	AP	61/61 (100%)	60 (98%)	1 (2%)	55	69
74	AQ	83/83 (100%)	81 (98%)	2 (2%)	43	63
75	AR	70/70 (100%)	69 (99%)	1 (1%)	59	71
76	AS	56/56 (100%)	56 (100%)	0	100	100
77	AT	47/47 (100%)	47 (100%)	0	100	100
78	AU	51/51 (100%)	51 (100%)	0	100	100
79	AV	259/261 (99%)	258 (100%)	1 (0%)	84	82
80	AW	31/31 (100%)	30 (97%)	1 (3%)	34	55
83	AZ	711/712 (100%)	702 (99%)	9 (1%)	61	72
All	All	10139/10276 (99%)	10026 (99%)	113 (1%)	63	74

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	P2	104	ILE
6	A	237	LEU
7	B	47	LEU
7	B	85	VAL
7	B	89	VAL
7	B	90	VAL
7	B	104	THR
8	C	12	THR
8	C	30	ILE
8	C	154	THR
9	D	41	LYS
11	F	83	LEU
11	F	93	ASN
11	F	147	LEU
12	G	163	VAL
13	H	53	ILE
14	I	97	LEU
14	I	152	LEU
17	M	46	ILE
17	M	72	LEU
17	M	112	LEU

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Mol	Chain	Res	Type
18	N	64	VAL
18	N	66	VAL
18	N	115	VAL
18	N	121	VAL
18	N	174	ILE
19	O	12	LYS
19	O	16	VAL
19	O	33	ILE
19	O	104	VAL
19	O	118	VAL
19	O	197	LEU
20	P	114	VAL
20	P	117	ILE
20	P	149	VAL
21	Q	127	LEU
22	R	41	ILE
22	R	96	ILE
22	R	102	LEU
23	S	121	ILE
24	T	31	LEU
24	T	40	VAL
24	T	80	VAL
26	V	73	VAL
27	W	13	ILE
27	W	44	LYS
27	W	49	ILE
28	X	102	LEU
32	b	58	LYS
33	c	34	LEU
33	c	41	LEU
33	c	51	LEU
35	e	28	VAL
36	f	89	LEU
38	h	58	ILE
38	h	88	LEU
41	k	66	ILE
42	l	42	ARG
43	m	78	ILE
46	p	8	VAL
48	q	188	LEU
49	r	97	LEU
49	r	172	LEU

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Mol	Chain	Res	Type
49	r	201	THR
50	s	73	LEU
50	s	235	LEU
51	t	4	LEU
52	u	64	ILE
52	u	196	VAL
54	w	87	ARG
55	x	93	LEU
56	y	72	ILE
56	y	88	ASN
57	z	42	ILE
58	AA	82	LEU
59	AB	84	ILE
59	AB	142	VAL
60	AC	28	LEU
60	AC	60	VAL
60	AC	121	VAL
61	AD	91	LEU
61	AD	109	LYS
61	AD	117	LEU
62	AE	110	LEU
62	AE	128	LYS
63	AF	25	LEU
64	AG	38	LEU
66	AI	5	VAL
68	AK	56	VAL
70	AM	34	ILE
70	AM	62	VAL
70	AM	93	LEU
71	AN	62	LYS
71	AN	63	GLN
71	AN	89	ASN
71	AN	117	ILE
71	AN	127	VAL
72	AO	7	ILE
73	AP	69	LEU
74	AQ	36	ILE
74	AQ	84	VAL
75	AR	21	LEU
79	AV	193	ILE
80	AW	139	LEU
83	AZ	87	LYS

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Mol	Chain	Res	Type
83	AZ	156	VAL
83	AZ	222	ILE
83	AZ	276	PHE
83	AZ	278	LEU
83	AZ	529	ILE
83	AZ	593	ILE
83	AZ	633	ILE
83	AZ	750	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (167) such sidechains are listed below:

Mol	Chain	Res	Type
4	P0	98	ASN
5	P2	66	ASN
5	P2	105	GLN
6	A	24	GLN
6	A	132	ASN
6	A	205	ASN
6	A	209	HIS
7	B	68	HIS
7	B	109	HIS
7	B	163	HIS
7	B	177	HIS
7	B	345	ASN
7	B	377	HIS
8	C	43	ASN
8	C	59	GLN
8	C	140	HIS
8	C	291	ASN
9	D	39	GLN
9	D	57	ASN
9	D	63	GLN
9	D	90	HIS
9	D	178	ASN
9	D	206	GLN
9	D	244	HIS
9	D	297	GLN
11	F	93	ASN
11	F	104	GLN
11	F	199	ASN
13	H	37	ASN
13	H	58	HIS

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Mol	Chain	Res	Type
13	H	162	GLN
14	I	14	ASN
14	I	133	GLN
15	J	6	GLN
15	J	43	GLN
15	J	101	ASN
15	J	150	ASN
16	L	114	GLN
17	M	27	GLN
17	M	105	GLN
17	M	126	GLN
18	N	37	HIS
18	N	156	HIS
18	N	195	ASN
19	O	29	ASN
19	O	31	GLN
19	O	193	GLN
20	P	72	GLN
20	P	92	GLN
20	P	97	ASN
20	P	145	HIS
21	Q	5	HIS
21	Q	9	GLN
21	Q	45	ASN
22	R	39	ASN
22	R	166	ASN
23	S	49	HIS
23	S	88	HIS
24	T	90	ASN
24	T	127	GLN
24	T	131	GLN
25	U	87	ASN
26	V	98	ASN
28	X	85	GLN
29	Y	120	GLN
30	Z	36	HIS
30	Z	57	HIS
30	Z	78	ASN
30	Z	127	ASN
31	a	14	HIS
31	a	38	GLN
31	a	74	ASN

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Mol	Chain	Res	Type
32	b	19	ASN
32	b	42	ASN
32	b	45	HIS
34	d	21	HIS
34	d	57	GLN
34	d	87	ASN
36	f	77	ASN
37	g	61	GLN
37	g	69	HIS
38	h	104	GLN
39	i	12	ASN
40	j	79	GLN
42	l	4	GLN
45	o	47	GLN
45	o	82	GLN
46	p	33	GLN
48	q	39	ASN
48	q	46	HIS
48	q	131	GLN
49	r	42	ASN
49	r	92	GLN
49	r	199	ASN
49	r	209	ASN
50	s	199	GLN
50	s	233	GLN
51	t	159	HIS
51	t	174	HIS
52	u	8	HIS
52	u	98	ASN
52	u	209	HIS
52	u	223	ASN
52	u	259	GLN
53	v	86	GLN
53	v	95	ASN
53	v	104	ASN
53	v	131	GLN
54	w	56	ASN
54	w	139	ASN
54	w	182	GLN
55	x	71	HIS
55	x	86	GLN
55	x	174	ASN

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Mol	Chain	Res	Type
56	y	88	ASN
57	z	139	GLN
58	AA	12	HIS
58	AA	28	ASN
58	AA	62	GLN
59	AB	8	GLN
59	AB	81	HIS
60	AC	142	GLN
63	AF	15	HIS
63	AF	98	ASN
63	AF	103	ASN
64	AG	77	GLN
64	AG	103	ASN
65	AH	31	ASN
65	AH	48	ASN
66	AI	19	ASN
66	AI	44	ASN
66	AI	63	GLN
67	AJ	43	ASN
68	AK	36	ASN
68	AK	48	HIS
68	AK	105	GLN
69	AL	33	GLN
69	AL	35	ASN
69	AL	70	ASN
70	AM	16	ASN
70	AM	24	GLN
70	AM	42	GLN
71	AN	79	ASN
72	AO	113	ASN
74	AQ	43	ASN
77	AT	20	GLN
78	AU	17	GLN
78	AU	46	ASN
79	AV	66	HIS
79	AV	148	ASN
79	AV	184	ASN
79	AV	195	HIS
79	AV	237	GLN
80	AW	123	ASN
80	AW	145	HIS
83	AZ	27	HIS

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Mol	Chain	Res	Type
83	AZ	176	GLN
83	AZ	201	GLN
83	AZ	224	GLN
83	AZ	259	ASN
83	AZ	274	ASN
83	AZ	355	GLN
83	AZ	409	GLN
83	AZ	414	GLN
83	AZ	452	ASN
83	AZ	528	HIS
83	AZ	583	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3220/3396 (94%)	1049 (32%)	18 (0%)
2	3	120/121 (99%)	31 (25%)	0
3	4	157/158 (99%)	50 (31%)	2 (1%)
47	2	1774/1797 (98%)	665 (37%)	23 (1%)
81	AX	75/76 (98%)	33 (44%)	1 (1%)
82	AY	7/8 (87%)	5 (71%)	0
All	All	5353/5556 (96%)	1833 (34%)	44 (0%)

All (1833) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	11	A
1	1	15	C
1	1	16	A
1	1	18	G
1	1	19	U
1	1	20	A
1	1	22	G
1	1	24	G
1	1	25	U
1	1	26	A
1	1	37	U
1	1	40	A
1	1	43	A
1	1	47	C
1	1	48	A

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Mol	Chain	Res	Type
1	1	50	U
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	73	C
1	1	74	G
1	1	77	A
1	1	85	A
1	1	89	A
1	1	92	G
1	1	93	C
1	1	96	G
1	1	99	A
1	1	105	C
1	1	108	A
1	1	109	A
1	1	110	G
1	1	111	C
1	1	113	C
1	1	119	U
1	1	120	G
1	1	121	A
1	1	128	G
1	1	130	A
1	1	133	U
1	1	134	U
1	1	135	C
1	1	136	G
1	1	145	G
1	1	146	U
1	1	148	G
1	1	153	U
1	1	154	U
1	1	155	G
1	1	156	G
1	1	157	A
1	1	161	G
1	1	165	A
1	1	170	G
1	1	172	G

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Mol	Chain	Res	Type
1	1	173	G
1	1	182	U
1	1	183	G
1	1	187	A
1	1	188	U
1	1	189	G
1	1	190	U
1	1	191	U
1	1	198	A
1	1	199	A
1	1	200	C
1	1	211	A
1	1	212	G
1	1	217	U
1	1	218	G
1	1	219	A
1	1	221	A
1	1	223	U
1	1	228	U
1	1	231	G
1	1	240	U
1	1	241	G
1	1	242	C
1	1	243	G
1	1	244	G
1	1	245	U
1	1	248	U
1	1	250	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	263	C
1	1	266	A
1	1	267	G
1	1	268	A
1	1	269	G
1	1	278	U
1	1	283	G
1	1	286	U
1	1	291	C
1	1	292	U
1	1	295	A

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Mol	Chain	Res	Type
1	1	298	U
1	1	305	U
1	1	315	C
1	1	318	A
1	1	329	U
1	1	337	G
1	1	341	G
1	1	343	U
1	1	346	C
1	1	350	C
1	1	352	A
1	1	357	A
1	1	359	U
1	1	364	G
1	1	365	A
1	1	371	G
1	1	374	A
1	1	376	G
1	1	382	U
1	1	387	A
1	1	390	G
1	1	394	G
1	1	397	A
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	421	G
1	1	422	A
1	1	438	A
1	1	440	A
1	1	442	G
1	1	444	U
1	1	446	U
1	1	449	U
1	1	450	G
1	1	451	U
1	1	487	U
1	1	488	U
1	1	491	A
1	1	493	U

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Mol	Chain	Res	Type
1	1	494	G
1	1	495	G
1	1	498	A
1	1	503	C
1	1	510	G
1	1	515	C
1	1	520	U
1	1	521	A
1	1	523	A
1	1	533	A
1	1	534	U
1	1	540	U
1	1	545	U
1	1	547	G
1	1	549	U
1	1	550	A
1	1	551	A
1	1	554	A
1	1	555	U
1	1	556	U
1	1	557	A
1	1	558	U
1	1	559	A
1	1	560	G
1	1	582	G
1	1	591	G
1	1	592	A
1	1	597	G
1	1	600	G
1	1	604	G
1	1	611	A
1	1	619	A
1	1	620	U
1	1	623	U
1	1	636	C
1	1	637	C
1	1	643	U
1	1	644	G
1	1	647	A
1	1	649	A
1	1	656	A
1	1	660	A

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Mol	Chain	Res	Type
1	1	661	G
1	1	666	A
1	1	667	C
1	1	669	U
1	1	675	C
1	1	676	G
1	1	677	A
1	1	678	G
1	1	681	U
1	1	682	U
1	1	683	U
1	1	685	G
1	1	689	U
1	1	691	A
1	1	697	A
1	1	699	A
1	1	705	A
1	1	712	G
1	1	716	A
1	1	717	C
1	1	718	G
1	1	719	U
1	1	720	A
1	1	726	G
1	1	727	G
1	1	735	A
1	1	737	G
1	1	744	A
1	1	750	G
1	1	751	A
1	1	758	C
1	1	761	A
1	1	763	G
1	1	766	U
1	1	767	U
1	1	770	G
1	1	774	G
1	1	776	U
1	1	777	U
1	1	780	A
1	1	781	G
1	1	785	G

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Mol	Chain	Res	Type
1	1	786	A
1	1	792	G
1	1	800	G
1	1	801	A
1	1	802	C
1	1	803	C
1	1	806	A
1	1	807	A
1	1	808	A
1	1	816	A
1	1	817	A
1	1	826	G
1	1	827	A
1	1	830	A
1	1	833	G
1	1	836	A
1	1	838	G
1	1	849	C
1	1	854	G
1	1	855	U
1	1	857	G
1	1	859	G
1	1	860	G
1	1	861	C
1	1	864	G
1	1	871	U
1	1	874	U
1	1	875	G
1	1	879	U
1	1	880	G
1	1	888	A
1	1	896	A
1	1	897	U
1	1	907	G
1	1	908	G
1	1	909	G
1	1	914	A
1	1	915	A
1	1	916	G
1	1	917	A
1	1	921	A
1	1	924	G

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Mol	Chain	Res	Type
1	1	925	A
1	1	932	U
1	1	934	G
1	1	937	G
1	1	939	U
1	1	941	G
1	1	943	U
1	1	944	C
1	1	949	C
1	1	951	A
1	1	959	C
1	1	960	U
1	1	962	A
1	1	967	A
1	1	970	A
1	1	977	C
1	1	979	U
1	1	980	A
1	1	981	U
1	1	984	G
1	1	985	U
1	1	991	G
1	1	994	G
1	1	1000	C
1	1	1002	A
1	1	1004	U
1	1	1006	A
1	1	1010	G
1	1	1013	G
1	1	1014	U
1	1	1016	C
1	1	1017	C
1	1	1018	G
1	1	1021	G
1	1	1024	G
1	1	1026	A
1	1	1027	A
1	1	1028	U
1	1	1029	G
1	1	1031	C
1	1	1033	U
1	1	1041	U

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Mol	Chain	Res	Type
1	1	1046	A
1	1	1047	A
1	1	1054	A
1	1	1063	G
1	1	1064	A
1	1	1065	A
1	1	1066	G
1	1	1072	G
1	1	1076	C
1	1	1081	U
1	1	1083	G
1	1	1086	C
1	1	1087	G
1	1	1094	U
1	1	1095	U
1	1	1097	G
1	1	1098	A
1	1	1102	A
1	1	1103	A
1	1	1106	G
1	1	1110	U
1	1	1116	G
1	1	1117	G
1	1	1121	U
1	1	1127	G
1	1	1129	A
1	1	1131	G
1	1	1137	C
1	1	1143	A
1	1	1144	U
1	1	1152	G
1	1	1153	A
1	1	1155	C
1	1	1158	A
1	1	1159	A
1	1	1161	G
1	1	1171	G
1	1	1172	G
1	1	1174	G
1	1	1177	G
1	1	1178	G
1	1	1180	A

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Mol	Chain	Res	Type
1	1	1181	U
1	1	1182	A
1	1	1185	C
1	1	1191	U
1	1	1192	C
1	1	1193	A
1	1	1194	G
1	1	1196	C
1	1	1197	A
1	1	1201	C
1	1	1209	G
1	1	1210	U
1	1	1213	G
1	1	1214	U
1	1	1217	A
1	1	1219	C
1	1	1221	A
1	1	1222	G
1	1	1230	G
1	1	1232	C
1	1	1236	G
1	1	1237	G
1	1	1245	A
1	1	1246	G
1	1	1249	G
1	1	1252	A
1	1	1253	U
1	1	1254	C
1	1	1255	C
1	1	1256	G
1	1	1258	U
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1264	G
1	1	1268	G
1	1	1269	U
1	1	1270	A
1	1	1272	C
1	1	1273	A
1	1	1276	U
1	1	1277	C

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Mol	Chain	Res	Type
1	1	1281	G
1	1	1282	G
1	1	1284	C
1	1	1285	G
1	1	1286	A
1	1	1287	A
1	1	1290	A
1	1	1292	C
1	1	1295	G
1	1	1297	C
1	1	1302	A
1	1	1305	U
1	1	1307	G
1	1	1308	A
1	1	1309	U
1	1	1313	G
1	1	1316	C
1	1	1317	A
1	1	1321	G
1	1	1323	G
1	1	1324	U
1	1	1325	U
1	1	1330	A
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1355	A
1	1	1356	U
1	1	1357	G
1	1	1362	G
1	1	1368	U
1	1	1372	C
1	1	1382	G
1	1	1385	C
1	1	1386	A
1	1	1391	C
1	1	1392	G
1	1	1394	A
1	1	1399	A

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Mol	Chain	Res	Type
1	1	1400	G
1	1	1408	G
1	1	1418	A
1	1	1419	A
1	1	1422	G
1	1	1424	C
1	1	1425	U
1	1	1430	U
1	1	1434	G
1	1	1436	U
1	1	1437	C
1	1	1443	G
1	1	1446	A
1	1	1448	U
1	1	1450	G
1	1	1451	C
1	1	1455	U
1	1	1456	A
1	1	1457	U
1	1	1458	U
1	1	1468	A
1	1	1470	U
1	1	1471	U
1	1	1473	G
1	1	1482	A
1	1	1483	G
1	1	1485	G
1	1	1488	G
1	1	1489	A
1	1	1494	U
1	1	1500	G
1	1	1501	U
1	1	1503	A
1	1	1507	G
1	1	1508	C
1	1	1511	U
1	1	1522	U
1	1	1523	U
1	1	1524	A
1	1	1525	G
1	1	1526	U
1	1	1533	U

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Mol	Chain	Res	Type
1	1	1535	A
1	1	1553	U
1	1	1554	U
1	1	1555	U
1	1	1556	C
1	1	1557	A
1	1	1558	A
1	1	1559	A
1	1	1560	G
1	1	1562	C
1	1	1563	C
1	1	1565	G
1	1	1566	A
1	1	1570	U
1	1	1573	G
1	1	1574	C
1	1	1577	G
1	1	1579	C
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1583	A
1	1	1584	U
1	1	1587	A
1	1	1588	A
1	1	1589	A
1	1	1593	A
1	1	1595	U
1	1	1596	C
1	1	1605	A
1	1	1606	U
1	1	1607	U
1	1	1613	A
1	1	1620	U
1	1	1628	C
1	1	1630	U
1	1	1635	G
1	1	1636	U
1	1	1637	A
1	1	1638	A
1	1	1643	A
1	1	1645	U

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Mol	Chain	Res	Type
1	1	1646	G
1	1	1657	C
1	1	1659	U
1	1	1662	G
1	1	1664	G
1	1	1683	A
1	1	1687	U
1	1	1706	C
1	1	1707	A
1	1	1712	G
1	1	1713	G
1	1	1714	A
1	1	1716	U
1	1	1717	U
1	1	1720	U
1	1	1724	U
1	1	1728	G
1	1	1729	A
1	1	1730	G
1	1	1736	G
1	1	1737	U
1	1	1740	U
1	1	1741	A
1	1	1742	U
1	1	1750	A
1	1	1751	G
1	1	1756	C
1	1	1760	A
1	1	1761	C
1	1	1763	U
1	1	1764	U
1	1	1765	U
1	1	1769	G
1	1	1770	G
1	1	1773	C
1	1	1775	G
1	1	1780	G
1	1	1781	C
1	1	1788	C
1	1	1793	C
1	1	1794	G
1	1	1795	U

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Mol	Chain	Res	Type
1	1	1797	A
1	1	1808	G
1	1	1812	G
1	1	1813	A
1	1	1814	A
1	1	1815	U
1	1	1818	U
1	1	1820	U
1	1	1821	U
1	1	1835	A
1	1	1838	G
1	1	1840	U
1	1	1841	A
1	1	1842	A
1	1	1843	C
1	1	1844	C
1	1	1846	C
1	1	1848	G
1	1	1850	A
1	1	1851	G
1	1	1855	U
1	1	1863	G
1	1	1865	A
1	1	1874	A
1	1	1878	G
1	1	1879	A
1	1	1880	U
1	1	1881	A
1	1	1884	A
1	1	1886	A
1	1	1889	G
1	1	1893	A
1	1	1896	A
1	1	1900	A
1	1	1904	C
1	1	1905	G
1	1	1906	G
1	1	1908	A
1	1	1912	U
1	1	1915	A
1	1	1926	C
1	1	1927	G

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Mol	Chain	Res	Type
1	1	1928	G
1	1	1930	A
1	1	1931	U
1	1	1932	A
1	1	1935	G
1	1	1948	G
1	1	1953	G
1	1	1954	G
1	1	2094	C
1	1	2101	C
1	1	2102	U
1	1	2107	A
1	1	2111	G
1	1	2114	C
1	1	2116	G
1	1	2117	A
1	1	2118	C
1	1	2119	A
1	1	2122	G
1	1	2131	A
1	1	2134	G
1	1	2136	C
1	1	2137	U
1	1	2138	A
1	1	2139	A
1	1	2143	A
1	1	2145	A
1	1	2148	U
1	1	2157	G
1	1	2158	A
1	1	2160	G
1	1	2166	A
1	1	2167	A
1	1	2168	A
1	1	2169	G
1	1	2170	U
1	1	2172	A
1	1	2176	U
1	1	2177	G
1	1	2178	A
1	1	2180	G
1	1	2184	U

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Mol	Chain	Res	Type
1	1	2185	G
1	1	2186	U
1	1	2187	G
1	1	2188	A
1	1	2189	U
1	1	2194	G
1	1	2205	U
1	1	2206	G
1	1	2207	A
1	1	2223	A
1	1	2231	C
1	1	2239	G
1	1	2255	A
1	1	2257	C
1	1	2263	C
1	1	2269	U
1	1	2270	A
1	1	2271	A
1	1	2273	G
1	1	2279	A
1	1	2281	A
1	1	2285	C
1	1	2286	U
1	1	2288	G
1	1	2295	A
1	1	2296	A
1	1	2303	A
1	1	2304	C
1	1	2306	C
1	1	2307	G
1	1	2309	A
1	1	2310	U
1	1	2312	A
1	1	2313	A
1	1	2315	G
1	1	2327	U
1	1	2334	U
1	1	2335	G
1	1	2336	U
1	1	2339	C
1	1	2344	U
1	1	2345	A

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Mol	Chain	Res	Type
1	1	2347	U
1	1	2357	A
1	1	2361	A
1	1	2363	A
1	1	2364	G
1	1	2365	C
1	1	2370	G
1	1	2372	A
1	1	2373	A
1	1	2374	C
1	1	2375	G
1	1	2376	G
1	1	2383	C
1	1	2385	G
1	1	2388	U
1	1	2393	G
1	1	2397	A
1	1	2400	G
1	1	2401	A
1	1	2402	A
1	1	2403	G
1	1	2404	A
1	1	2410	U
1	1	2411	U
1	1	2415	C
1	1	2417	U
1	1	2418	G
1	1	2419	A
1	1	2422	C
1	1	2424	A
1	1	2429	G
1	1	2432	A
1	1	2434	U
1	1	2438	A
1	1	2439	A
1	1	2452	G
1	1	2455	U
1	1	2456	A
1	1	2459	A
1	1	2460	U
1	1	2461	A
1	1	2462	A

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Mol	Chain	Res	Type
1	1	2468	A
1	1	2469	G
1	1	2471	U
1	1	2474	G
1	1	2476	C
1	1	2479	C
1	1	2480	A
1	1	2482	U
1	1	2483	G
1	1	2486	A
1	1	2487	U
1	1	2488	A
1	1	2490	C
1	1	2491	A
1	1	2492	C
1	1	2494	A
1	1	2495	C
1	1	2496	C
1	1	2497	U
1	1	2500	A
1	1	2501	U
1	1	2502	A
1	1	2505	U
1	1	2507	C
1	1	2510	U
1	1	2514	U
1	1	2515	A
1	1	2522	G
1	1	2524	A
1	1	2525	G
1	1	2526	C
1	1	2532	U
1	1	2537	U
1	1	2538	U
1	1	2540	A
1	1	2541	U
1	1	2542	U
1	1	2543	U
1	1	2549	G
1	1	2550	U
1	1	2552	C
1	1	2555	G

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Mol	Chain	Res	Type
1	1	2557	A
1	1	2558	U
1	1	2559	U
1	1	2560	C
1	1	2561	A
1	1	2569	A
1	1	2570	U
1	1	2573	G
1	1	2575	G
1	1	2583	C
1	1	2584	G
1	1	2585	G
1	1	2593	A
1	1	2595	A
1	1	2606	G
1	1	2614	G
1	1	2615	G
1	1	2617	U
1	1	2618	G
1	1	2619	G
1	1	2620	G
1	1	2625	C
1	1	2628	A
1	1	2635	A
1	1	2639	G
1	1	2648	G
1	1	2649	A
1	1	2652	U
1	1	2655	U
1	1	2656	A
1	1	2658	G
1	1	2669	G
1	1	2672	G
1	1	2674	A
1	1	2676	A
1	1	2677	G
1	1	2678	A
1	1	2680	A
1	1	2681	U
1	1	2686	A
1	1	2688	U
1	1	2689	A

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Mol	Chain	Res	Type
1	1	2690	G
1	1	2691	A
1	1	2692	A
1	1	2701	U
1	1	2703	A
1	1	2704	A
1	1	2705	A
1	1	2712	U
1	1	2714	G
1	1	2716	U
1	1	2717	U
1	1	2719	U
1	1	2725	U
1	1	2726	C
1	1	2728	G
1	1	2729	U
1	1	2741	C
1	1	2749	G
1	1	2753	G
1	1	2755	C
1	1	2759	U
1	1	2760	C
1	1	2762	A
1	1	2765	C
1	1	2769	A
1	1	2771	U
1	1	2772	C
1	1	2773	C
1	1	2777	G
1	1	2780	A
1	1	2787	G
1	1	2795	U
1	1	2796	G
1	1	2798	C
1	1	2799	A
1	1	2800	G
1	1	2801	A
1	1	2803	A
1	1	2804	A
1	1	2808	A
1	1	2809	C
1	1	2810	C

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Mol	Chain	Res	Type
1	1	2816	G
1	1	2817	A
1	1	2818	U
1	1	2821	C
1	1	2827	U
1	1	2838	A
1	1	2843	U
1	1	2844	C
1	1	2845	A
1	1	2847	A
1	1	2852	C
1	1	2858	U
1	1	2859	U
1	1	2860	U
1	1	2861	U
1	1	2863	G
1	1	2869	U
1	1	2871	G
1	1	2872	A
1	1	2873	U
1	1	2875	U
1	1	2886	U
1	1	2887	A
1	1	2889	C
1	1	2899	C
1	1	2901	G
1	1	2904	U
1	1	2905	U
1	1	2907	G
1	1	2911	A
1	1	2912	G
1	1	2914	G
1	1	2925	C
1	1	2932	U
1	1	2934	A
1	1	2935	U
1	1	2936	A
1	1	2941	A
1	1	2942	C
1	1	2945	G
1	1	2946	A
1	1	2947	G

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Mol	Chain	Res	Type
1	1	2954	U
1	1	2955	U
1	1	2968	G
1	1	2971	A
1	1	2978	U
1	1	2979	U
1	1	2981	U
1	1	2983	C
1	1	2984	C
1	1	2988	C
1	1	2992	U
1	1	2996	U
1	1	2997	G
1	1	3001	C
1	1	3003	G
1	1	3005	A
1	1	3006	A
1	1	3007	U
1	1	3011	A
1	1	3012	A
1	1	3014	U
1	1	3021	A
1	1	3026	G
1	1	3028	G
1	1	3030	G
1	1	3034	C
1	1	3036	G
1	1	3055	U
1	1	3056	U
1	1	3057	U
1	1	3058	U
1	1	3059	G
1	1	3069	G
1	1	3070	A
1	1	3074	G
1	1	3075	G
1	1	3077	A
1	1	3078	U
1	1	3079	U
1	1	3080	G
1	1	3090	U
1	1	3092	C

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Mol	Chain	Res	Type
1	1	3093	C
1	1	3099	C
1	1	3100	U
1	1	3101	G
1	1	3117	C
1	1	3122	A
1	1	3125	U
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3139	A
1	1	3142	A
1	1	3143	C
1	1	3153	U
1	1	3154	C
1	1	3156	U
1	1	3157	U
1	1	3158	G
1	1	3160	U
1	1	3162	C
1	1	3168	A
1	1	3170	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3178	A
1	1	3179	U
1	1	3180	A
1	1	3182	G
1	1	3183	A
1	1	3185	U
1	1	3186	A
1	1	3187	A
1	1	3193	C
1	1	3194	C
1	1	3195	U
1	1	3196	U
1	1	3197	G
1	1	3202	G
1	1	3206	C
1	1	3207	U
1	1	3210	A

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Mol	Chain	Res	Type
1	1	3212	C
1	1	3214	U
1	1	3216	G
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3222	U
1	1	3226	A
1	1	3228	C
1	1	3229	G
1	1	3235	C
1	1	3238	G
1	1	3243	A
1	1	3244	A
1	1	3246	G
1	1	3247	G
1	1	3259	U
1	1	3260	G
1	1	3264	G
1	1	3268	A
1	1	3269	U
1	1	3271	G
1	1	3272	C
1	1	3273	A
1	1	3275	U
1	1	3276	G
1	1	3278	C
1	1	3279	A
1	1	3281	U
1	1	3288	G
1	1	3289	G
1	1	3292	A
1	1	3294	A
1	1	3295	A
1	1	3304	U
1	1	3308	C
1	1	3310	A
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3318	G
1	1	3320	A

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Mol	Chain	Res	Type
1	1	3329	U
1	1	3339	A
1	1	3341	U
1	1	3345	G
1	1	3346	U
1	1	3349	C
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3357	U
1	1	3362	A
1	1	3363	U
1	1	3368	U
1	1	3369	G
1	1	3375	A
1	1	3377	G
1	1	3378	C
1	1	3382	U
1	1	3384	U
1	1	3386	G
1	1	3388	C
1	1	3389	U
1	1	3390	G
2	3	4	U
2	3	6	C
2	3	7	G
2	3	10	C
2	3	11	A
2	3	13	A
2	3	16	U
2	3	19	C
2	3	28	C
2	3	33	U
2	3	41	G
2	3	42	A
2	3	44	C
2	3	49	G
2	3	50	U
2	3	54	U

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Mol	Chain	Res	Type
2	3	56	A
2	3	57	G
2	3	63	A
2	3	64	A
2	3	65	G
2	3	74	C
2	3	76	A
2	3	87	G
2	3	90	U
2	3	91	G
2	3	92	A
2	3	94	C
2	3	110	G
2	3	112	G
2	3	121	U
3	4	12	A
3	4	13	A
3	4	15	G
3	4	16	G
3	4	22	U
3	4	23	U
3	4	34	U
3	4	35	C
3	4	37	A
3	4	39	G
3	4	43	A
3	4	44	A
3	4	49	G
3	4	50	C
3	4	51	G
3	4	54	A
3	4	59	A
3	4	62	C
3	4	63	G
3	4	71	A
3	4	72	A
3	4	75	G
3	4	80	A
3	4	81	U
3	4	82	U
3	4	83	C
3	4	84	C

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Mol	Chain	Res	Type
3	4	86	U
3	4	87	G
3	4	88	A
3	4	89	A
3	4	95	G
3	4	96	A
3	4	100	U
3	4	102	U
3	4	104	A
3	4	106	C
3	4	107	G
3	4	112	U
3	4	113	U
3	4	125	U
3	4	126	A
3	4	127	U
3	4	131	A
3	4	138	A
3	4	148	G
3	4	151	C
3	4	152	G
3	4	155	A
3	4	158	U
47	2	2	A
47	2	3	U
47	2	4	C
47	2	5	U
47	2	8	U
47	2	9	U
47	2	10	G
47	2	11	A
47	2	25	C
47	2	26	A
47	2	27	U
47	2	34	G
47	2	40	A
47	2	43	A
47	2	45	U
47	2	47	A
47	2	48	G
47	2	50	C
47	2	55	A

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Mol	Chain	Res	Type
47	2	59	C
47	2	60	U
47	2	63	G
47	2	65	A
47	2	66	U
47	2	67	A
47	2	68	A
47	2	69	G
47	2	71	A
47	2	72	A
47	2	74	U
47	2	75	U
47	2	76	A
47	2	77	U
47	2	78	A
47	2	81	G
47	2	93	A
47	2	94	U
47	2	100	A
47	2	102	U
47	2	103	A
47	2	104	A
47	2	114	C
47	2	115	G
47	2	116	U
47	2	121	U
47	2	123	G
47	2	125	U
47	2	127	G
47	2	128	U
47	2	129	U
47	2	130	C
47	2	131	C
47	2	132	U
47	2	133	U
47	2	135	A
47	2	136	C
47	2	137	U
47	2	138	A
47	2	139	C
47	2	141	U
47	2	142	G

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Mol	Chain	Res	Type
47	2	144	U
47	2	145	A
47	2	146	U
47	2	153	G
47	2	157	A
47	2	159	U
47	2	169	A
47	2	171	A
47	2	188	A
47	2	189	C
47	2	191	C
47	2	192	U
47	2	194	U
47	2	195	G
47	2	196	G
47	2	200	A
47	2	203	U
47	2	204	G
47	2	217	A
47	2	218	A
47	2	224	C
47	2	232	U
47	2	233	C
47	2	234	G
47	2	235	G
47	2	238	U
47	2	239	C
47	2	240	U
47	2	241	U
47	2	246	G
47	2	249	U
47	2	252	U
47	2	259	U
47	2	261	U
47	2	262	U
47	2	265	A
47	2	268	C
47	2	270	C
47	2	271	A
47	2	272	U
47	2	274	G
47	2	276	C

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Mol	Chain	Res	Type
47	2	277	U
47	2	278	U
47	2	280	U
47	2	287	G
47	2	288	A
47	2	302	U
47	2	306	U
47	2	313	U
47	2	314	C
47	2	316	A
47	2	317	C
47	2	320	U
47	2	322	G
47	2	329	G
47	2	330	G
47	2	333	A
47	2	337	G
47	2	338	C
47	2	345	U
47	2	346	G
47	2	347	G
47	2	351	C
47	2	352	A
47	2	361	C
47	2	363	G
47	2	373	G
47	2	374	U
47	2	378	A
47	2	391	A
47	2	400	A
47	2	401	A
47	2	402	C
47	2	403	G
47	2	404	G
47	2	412	A
47	2	417	A
47	2	419	G
47	2	421	A
47	2	423	G
47	2	424	C
47	2	426	G
47	2	428	A

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Mol	Chain	Res	Type
47	2	432	G
47	2	434	G
47	2	435	C
47	2	439	U
47	2	444	C
47	2	445	A
47	2	452	A
47	2	454	U
47	2	455	C
47	2	456	A
47	2	458	G
47	2	460	A
47	2	461	G
47	2	464	A
47	2	469	C
47	2	471	A
47	2	475	A
47	2	480	G
47	2	481	A
47	2	486	G
47	2	488	G
47	2	490	C
47	2	492	A
47	2	493	U
47	2	495	C
47	2	496	G
47	2	502	U
47	2	506	A
47	2	507	U
47	2	508	U
47	2	509	G
47	2	515	A
47	2	519	C
47	2	520	A
47	2	523	G
47	2	525	A
47	2	532	U
47	2	536	C
47	2	538	A
47	2	539	G
47	2	540	G
47	2	541	A

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Mol	Chain	Res	Type
47	2	542	A
47	2	543	C
47	2	544	A
47	2	545	A
47	2	551	G
47	2	554	C
47	2	555	A
47	2	557	G
47	2	558	U
47	2	559	C
47	2	565	C
47	2	566	C
47	2	567	A
47	2	568	G
47	2	574	G
47	2	575	C
47	2	579	A
47	2	580	A
47	2	582	U
47	2	594	A
47	2	597	G
47	2	600	U
47	2	606	A
47	2	607	G
47	2	608	U
47	2	610	G
47	2	611	U
47	2	612	U
47	2	613	G
47	2	617	U
47	2	618	U
47	2	619	A
47	2	620	A
47	2	622	A
47	2	623	A
47	2	624	G
47	2	635	A
47	2	638	U
47	2	639	U
47	2	653	C
47	2	654	C
47	2	655	G

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Mol	Chain	Res	Type
47	2	657	U
47	2	658	C
47	2	677	G
47	2	678	A
47	2	681	U
47	2	687	G
47	2	691	C
47	2	692	C
47	2	694	U
47	2	695	U
47	2	696	C
47	2	697	C
47	2	698	U
47	2	700	C
47	2	701	U
47	2	704	C
47	2	705	U
47	2	706	A
47	2	707	A
47	2	708	C
47	2	709	C
47	2	710	U
47	2	711	U
47	2	712	G
47	2	713	A
47	2	716	C
47	2	717	C
47	2	718	U
47	2	720	G
47	2	721	U
47	2	722	G
47	2	725	U
47	2	727	U
47	2	728	U
47	2	729	G
47	2	730	G
47	2	731	C
47	2	733	A
47	2	735	C
47	2	736	C
47	2	738	G
47	2	739	G

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Mol	Chain	Res	Type
47	2	741	C
47	2	742	U
47	2	743	U
47	2	745	U
47	2	746	A
47	2	754	A
47	2	755	A
47	2	765	G
47	2	766	U
47	2	767	U
47	2	771	A
47	2	772	G
47	2	775	G
47	2	778	G
47	2	779	U
47	2	780	A
47	2	781	U
47	2	783	G
47	2	784	C
47	2	787	G
47	2	789	A
47	2	791	A
47	2	794	U
47	2	795	U
47	2	803	A
47	2	812	A
47	2	813	U
47	2	814	A
47	2	815	G
47	2	820	U
47	2	821	U
47	2	823	G
47	2	824	G
47	2	829	A
47	2	830	U
47	2	833	U
47	2	837	G
47	2	841	U
47	2	845	G
47	2	846	G
47	2	848	C
47	2	849	C

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Mol	Chain	Res	Type
47	2	850	A
47	2	852	C
47	2	854	U
47	2	859	A
47	2	860	U
47	2	862	A
47	2	863	A
47	2	865	A
47	2	866	G
47	2	880	C
47	2	886	U
47	2	888	U
47	2	898	A
47	2	900	A
47	2	903	U
47	2	913	G
47	2	914	G
47	2	915	A
47	2	916	U
47	2	921	U
47	2	928	U
47	2	929	A
47	2	933	A
47	2	935	U
47	2	938	G
47	2	939	A
47	2	942	G
47	2	944	A
47	2	945	U
47	2	946	U
47	2	951	A
47	2	960	U
47	2	964	U
47	2	966	A
47	2	967	A
47	2	987	G
47	2	988	A
47	2	992	A
47	2	993	A
47	2	1007	C
47	2	1020	A
47	2	1021	C

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Mol	Chain	Res	Type
47	2	1022	C
47	2	1025	A
47	2	1026	A
47	2	1027	A
47	2	1028	C
47	2	1031	U
47	2	1039	A
47	2	1052	U
47	2	1053	G
47	2	1054	U
47	2	1067	C
47	2	1074	G
47	2	1081	A
47	2	1082	C
47	2	1085	G
47	2	1092	A
47	2	1093	A
47	2	1097	U
47	2	1098	U
47	2	1099	U
47	2	1100	G
47	2	1109	G
47	2	1113	A
47	2	1122	G
47	2	1125	A
47	2	1126	G
47	2	1137	A
47	2	1138	A
47	2	1139	A
47	2	1150	G
47	2	1151	A
47	2	1158	C
47	2	1159	C
47	2	1162	C
47	2	1163	A
47	2	1164	G
47	2	1166	A
47	2	1167	G
47	2	1170	G
47	2	1173	C
47	2	1180	C
47	2	1181	U

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Mol	Chain	Res	Type
47	2	1182	U
47	2	1183	A
47	2	1184	A
47	2	1185	U
47	2	1186	U
47	2	1189	A
47	2	1190	C
47	2	1191	U
47	2	1193	A
47	2	1194	A
47	2	1196	A
47	2	1199	G
47	2	1200	G
47	2	1202	A
47	2	1206	U
47	2	1207	C
47	2	1209	C
47	2	1212	G
47	2	1217	A
47	2	1218	G
47	2	1219	A
47	2	1221	A
47	2	1223	A
47	2	1225	U
47	2	1227	A
47	2	1228	G
47	2	1229	G
47	2	1230	A
47	2	1232	U
47	2	1235	C
47	2	1238	A
47	2	1239	U
47	2	1241	G
47	2	1242	A
47	2	1244	A
47	2	1245	G
47	2	1246	C
47	2	1250	U
47	2	1251	U
47	2	1252	C
47	2	1255	G
47	2	1256	A

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Mol	Chain	Res	Type
47	2	1257	U
47	2	1258	U
47	2	1260	U
47	2	1263	G
47	2	1264	G
47	2	1266	U
47	2	1267	G
47	2	1268	G
47	2	1269	U
47	2	1270	G
47	2	1273	G
47	2	1274	C
47	2	1275	A
47	2	1278	G
47	2	1284	C
47	2	1286	U
47	2	1287	A
47	2	1291	G
47	2	1297	G
47	2	1298	U
47	2	1299	G
47	2	1300	A
47	2	1301	U
47	2	1302	U
47	2	1306	C
47	2	1307	U
47	2	1309	C
47	2	1312	A
47	2	1314	U
47	2	1315	U
47	2	1318	G
47	2	1321	A
47	2	1328	G
47	2	1336	A
47	2	1337	A
47	2	1339	C
47	2	1340	U
47	2	1342	C
47	2	1343	U
47	2	1347	U
47	2	1349	G
47	2	1351	G

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Mol	Chain	Res	Type
47	2	1353	U
47	2	1354	G
47	2	1358	G
47	2	1361	U
47	2	1363	U
47	2	1364	G
47	2	1368	G
47	2	1370	U
47	2	1372	U
47	2	1378	U
47	2	1380	U
47	2	1382	A
47	2	1383	G
47	2	1384	A
47	2	1385	G
47	2	1388	A
47	2	1390	U
47	2	1392	U
47	2	1394	G
47	2	1397	U
47	2	1398	U
47	2	1399	C
47	2	1400	A
47	2	1402	G
47	2	1403	C
47	2	1404	C
47	2	1405	G
47	2	1409	G
47	2	1410	A
47	2	1411	A
47	2	1412	G
47	2	1414	U
47	2	1415	U
47	2	1416	G
47	2	1418	G
47	2	1419	G
47	2	1427	A
47	2	1428	G
47	2	1429	G
47	2	1430	U
47	2	1432	U
47	2	1433	G

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Mol	Chain	Res	Type
47	2	1434	U
47	2	1436	A
47	2	1444	A
47	2	1445	G
47	2	1446	A
47	2	1447	C
47	2	1451	C
47	2	1453	G
47	2	1457	C
47	2	1458	G
47	2	1459	C
47	2	1461	C
47	2	1469	A
47	2	1471	A
47	2	1472	C
47	2	1473	U
47	2	1474	G
47	2	1478	G
47	2	1479	A
47	2	1481	C
47	2	1482	C
47	2	1489	U
47	2	1490	C
47	2	1491	U
47	2	1492	A
47	2	1493	A
47	2	1496	U
47	2	1506	G
47	2	1512	G
47	2	1514	U
47	2	1516	A
47	2	1517	U
47	2	1518	C
47	2	1520	U
47	2	1521	G
47	2	1522	U
47	2	1523	G
47	2	1524	A
47	2	1531	G
47	2	1534	G
47	2	1535	U
47	2	1536	G

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Mol	Chain	Res	Type
47	2	1537	C
47	2	1538	U
47	2	1539	G
47	2	1541	G
47	2	1542	G
47	2	1543	A
47	2	1557	U
47	2	1559	A
47	2	1567	U
47	2	1568	C
47	2	1570	A
47	2	1571	C
47	2	1572	G
47	2	1583	A
47	2	1584	G
47	2	1586	A
47	2	1587	A
47	2	1589	C
47	2	1591	C
47	2	1596	C
47	2	1597	A
47	2	1601	G
47	2	1604	U
47	2	1605	G
47	2	1612	U
47	2	1613	U
47	2	1615	C
47	2	1616	G
47	2	1617	U
47	2	1619	C
47	2	1625	C
47	2	1631	A
47	2	1634	C
47	2	1635	A
47	2	1636	C
47	2	1637	C
47	2	1638	G
47	2	1639	C
47	2	1647	U
47	2	1651	A
47	2	1653	C
47	2	1657	U

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Mol	Chain	Res	Type
47	2	1658	G
47	2	1664	C
47	2	1670	G
47	2	1678	A
47	2	1679	G
47	2	1680	G
47	2	1681	A
47	2	1682	U
47	2	1683	C
47	2	1684	U
47	2	1685	G
47	2	1686	C
47	2	1689	A
47	2	1694	A
47	2	1696	G
47	2	1698	G
47	2	1699	G
47	2	1700	C
47	2	1701	A
47	2	1702	A
47	2	1703	C
47	2	1704	U
47	2	1705	C
47	2	1707	A
47	2	1708	U
47	2	1709	C
47	2	1710	U
47	2	1712	A
47	2	1713	G
47	2	1715	G
47	2	1716	C
47	2	1717	G
47	2	1718	G
47	2	1720	G
47	2	1730	A
47	2	1736	G
47	2	1747	G
47	2	1749	A
47	2	1750	A
47	2	1755	A
47	2	1756	A
47	2	1757	G

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Mol	Chain	Res	Type
47	2	1758	U
47	2	1761	U
47	2	1762	A
47	2	1766	A
47	2	1767	G
47	2	1769	U
47	2	1780	G
47	2	1782	A
47	2	1783	C
47	2	1791	A
47	2	1792	G
47	2	1793	G
47	2	1794	A
47	2	1795	U
47	2	1796	C
47	2	1798	U
81	AX	4	G
81	AX	9	A
81	AX	10	G
81	AX	11	C
81	AX	14	A
81	AX	16	U
81	AX	17	U
81	AX	18	G
81	AX	19	G
81	AX	20	G
81	AX	21	A
81	AX	22	G
81	AX	24	G
81	AX	26	G
81	AX	27	C
81	AX	30	G
81	AX	34	G
81	AX	37	G
81	AX	38	A
81	AX	40	C
81	AX	42	G
81	AX	46	G
81	AX	47	U
81	AX	48	C
81	AX	49	C
81	AX	55	U

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Mol	Chain	Res	Type
81	AX	59	U
81	AX	60	C
81	AX	61	C
81	AX	69	U
81	AX	74	C
81	AX	75	C
81	AX	76	A
82	AY	44	A
82	AY	45	A
82	AY	48	U
82	AY	49	U
82	AY	50	U

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	980	A
1	1	1053	A
1	1	1283	C
1	1	1285	G
1	1	1506	A
1	1	1562	C
1	1	1594	A
1	1	1629	U
1	1	2270	A
1	1	2295	A
1	1	2306	C
1	1	2461	A
1	1	2541	U
1	1	2549	G
1	1	2874	G
1	1	3004	C
1	1	3078	U
1	1	3121	U
3	4	22	U
3	4	88	A
47	2	1	U
47	2	74	U
47	2	315	A
47	2	507	U
47	2	611	U
47	2	706	A

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Mol	Chain	Res	Type
47	2	779	U
47	2	780	A
47	2	865	A
47	2	941	A
47	2	1138	A
47	2	1244	A
47	2	1273	G
47	2	1274	C
47	2	1298	U
47	2	1338	C
47	2	1399	C
47	2	1491	U
47	2	1536	G
47	2	1611	A
47	2	1637	C
47	2	1684	U
47	2	1756	A
81	AX	19	G

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
83	DDE	AZ	699	83	18,20,21	2.05	5 (27%)	17,28,30	1.43	3 (17%)

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
83	DDE	AZ	699	83	-	6/20/21/23	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	AZ	699	DDE	CBI-NAD	6.09	1.47	1.32
83	AZ	699	DDE	CAT-CE1	3.06	1.54	1.49
83	AZ	699	DDE	CG-ND1	-3.04	1.32	1.38
83	AZ	699	DDE	OAG-CBI	-2.22	1.19	1.23
83	AZ	699	DDE	CBW-NCB	-2.15	1.49	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	AZ	699	DDE	OAG-CBI-NAD	-2.78	118.14	123.04
83	AZ	699	DDE	CAC-NCB-CAB	2.58	117.80	107.99
83	AZ	699	DDE	CAU-CBW-CBI	-2.31	106.70	111.22

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
83	AZ	699	DDE	N-CA-CB-CG
83	AZ	699	DDE	C-CA-CB-CG
83	AZ	699	DDE	CAT-CAU-CBW-CBI
83	AZ	699	DDE	CAT-CAU-CBW-NCB
83	AZ	699	DDE	NAD-CBI-CBW-NCB
83	AZ	699	DDE	CE1-CAT-CAU-CBW

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	AZ	699	DDE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
85	SO1	AZ	901	-	34,39,39	0.19	0	38,64,64	0.90	2 (5%)
86	GCP	AZ	902	-	32,34,34	0.84	3 (9%)	49,54,54	0.96	5 (10%)

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
85	SO1	AZ	901	-	-	8/21/104/104	0/7/5/5
86	GCP	AZ	902	-	-	5/19/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AZ	902	GCP	PB-O2B	-2.63	1.50	1.56
86	AZ	902	GCP	PG-O1G	2.25	1.54	1.50
86	AZ	902	GCP	PG-O3G	-2.22	1.50	1.55

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	AZ	901	SO1	C18-C9-C16	-4.39	97.73	103.72
86	AZ	902	GCP	O2B-PB-C3B	3.85	122.68	106.73
86	AZ	902	GCP	O3G-PG-C3B	2.58	112.66	106.40
86	AZ	902	GCP	O1G-PG-C3B	-2.44	106.06	111.37
85	AZ	901	SO1	C7-C2-C6	2.31	116.47	112.05
86	AZ	902	GCP	PB-O3A-PA	-2.13	125.41	132.37
86	AZ	902	GCP	O2G-PG-O1G	-2.10	106.95	112.39

There are no chirality outliers.

All (13) torsion outliers are listed below:

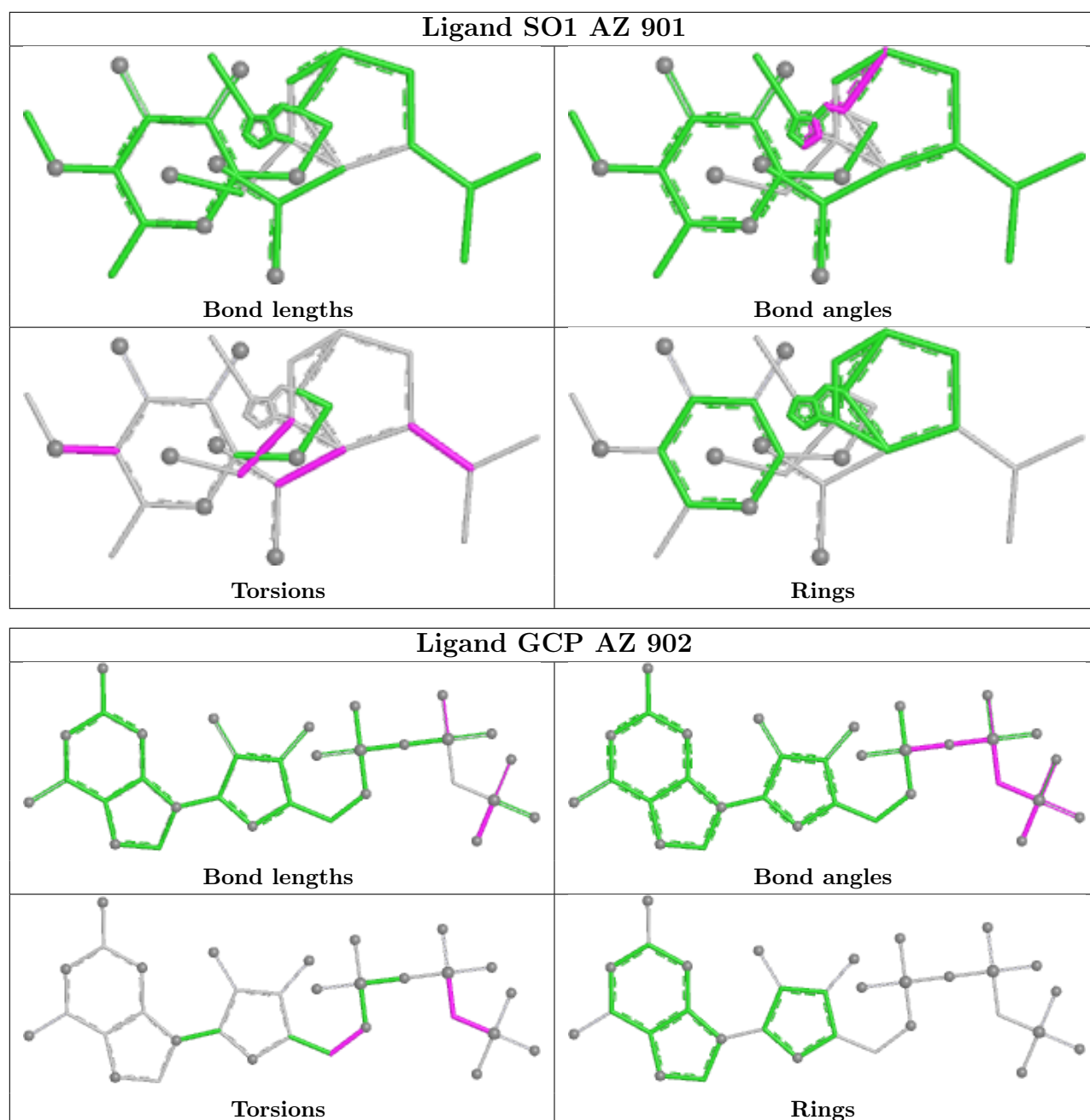
Mol	Chain	Res	Type	Atoms
86	AZ	902	GCP	PG-C3B-PB-O1B
86	AZ	902	GCP	PG-C3B-PB-O3A
85	AZ	901	SO1	C56-C55-O64-C65
85	AZ	901	SO1	C2-C1-C5-O14
85	AZ	901	SO1	C2-C1-C5-O15
86	AZ	902	GCP	PG-C3B-PB-O2B
86	AZ	902	GCP	C4'-C5'-O5'-PA
85	AZ	901	SO1	O19-C11-C3-C1
85	AZ	901	SO1	C3-C1-C5-O15
86	AZ	902	GCP	PB-C3B-PG-O1G
85	AZ	901	SO1	C20-C13-C4-C1
85	AZ	901	SO1	C54-C55-O64-C65
85	AZ	901	SO1	O19-C11-C3-C9

There are no ring outliers.

2 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	AZ	901	SO1	13	0
86	AZ	902	GCP	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

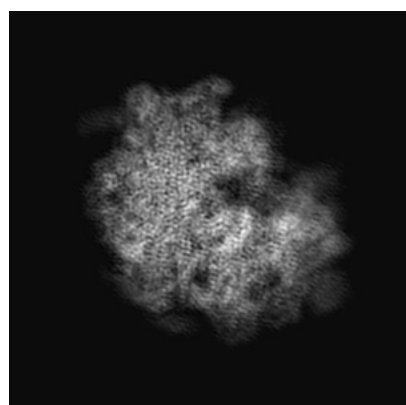
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0047. These allow visual inspection of the internal detail of the map and identification of artifacts.

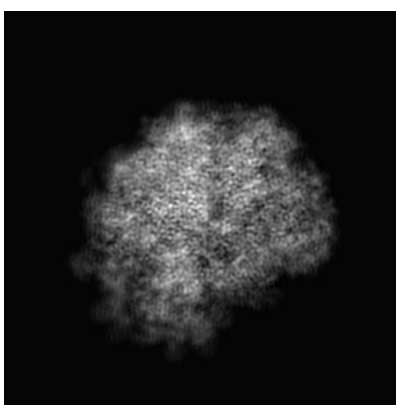
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

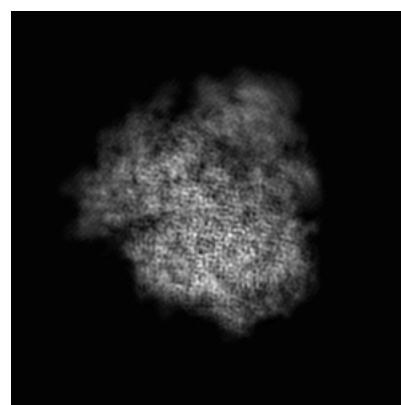
6.1.1 Primary map



X



Y

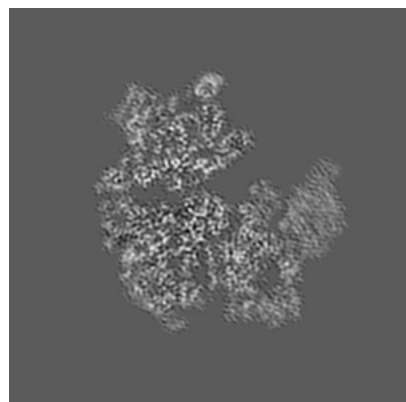


Z

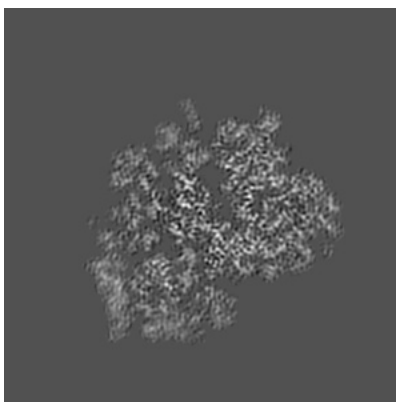
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

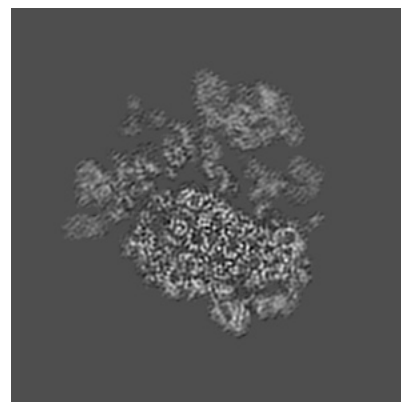
6.2.1 Primary map



X Index: 180



Y Index: 180

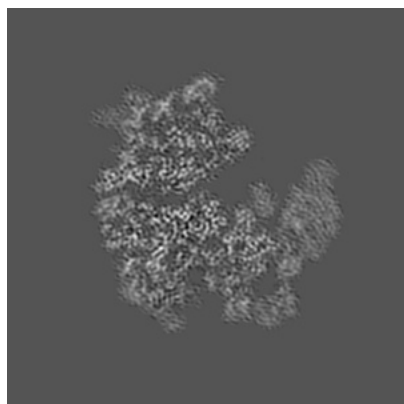


Z Index: 180

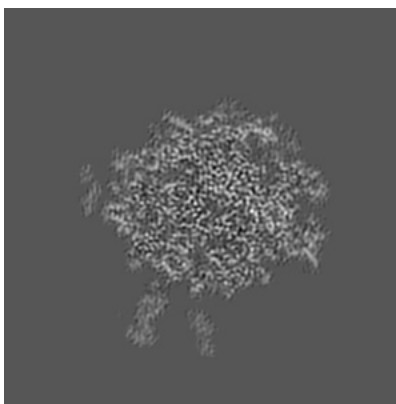
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

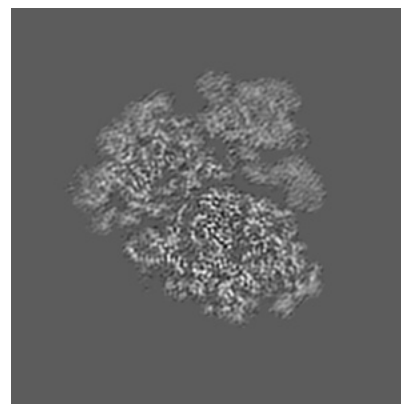
6.3.1 Primary map



X Index: 183



Y Index: 156

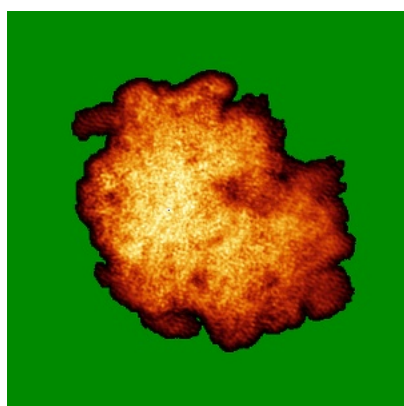


Z Index: 166

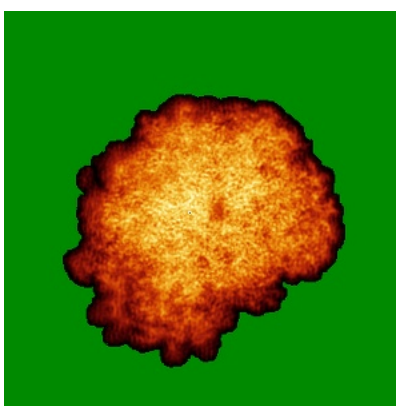
The images above show the largest variance slices of the map in three orthogonal directions.

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

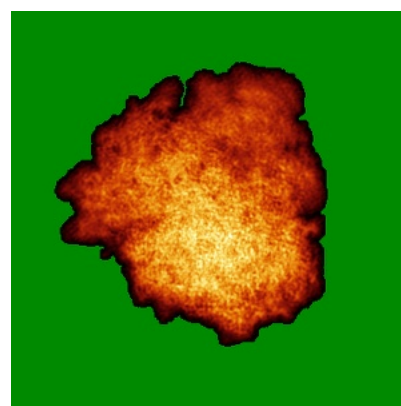
6.4.1 Primary map



X



Y



Z

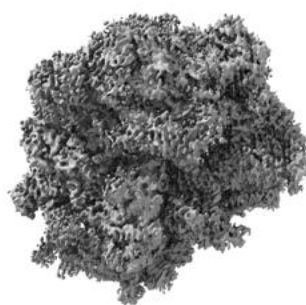
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

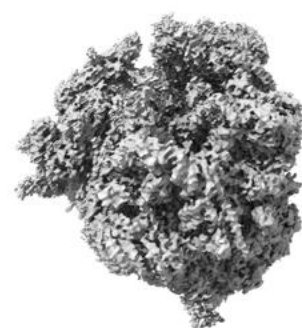
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

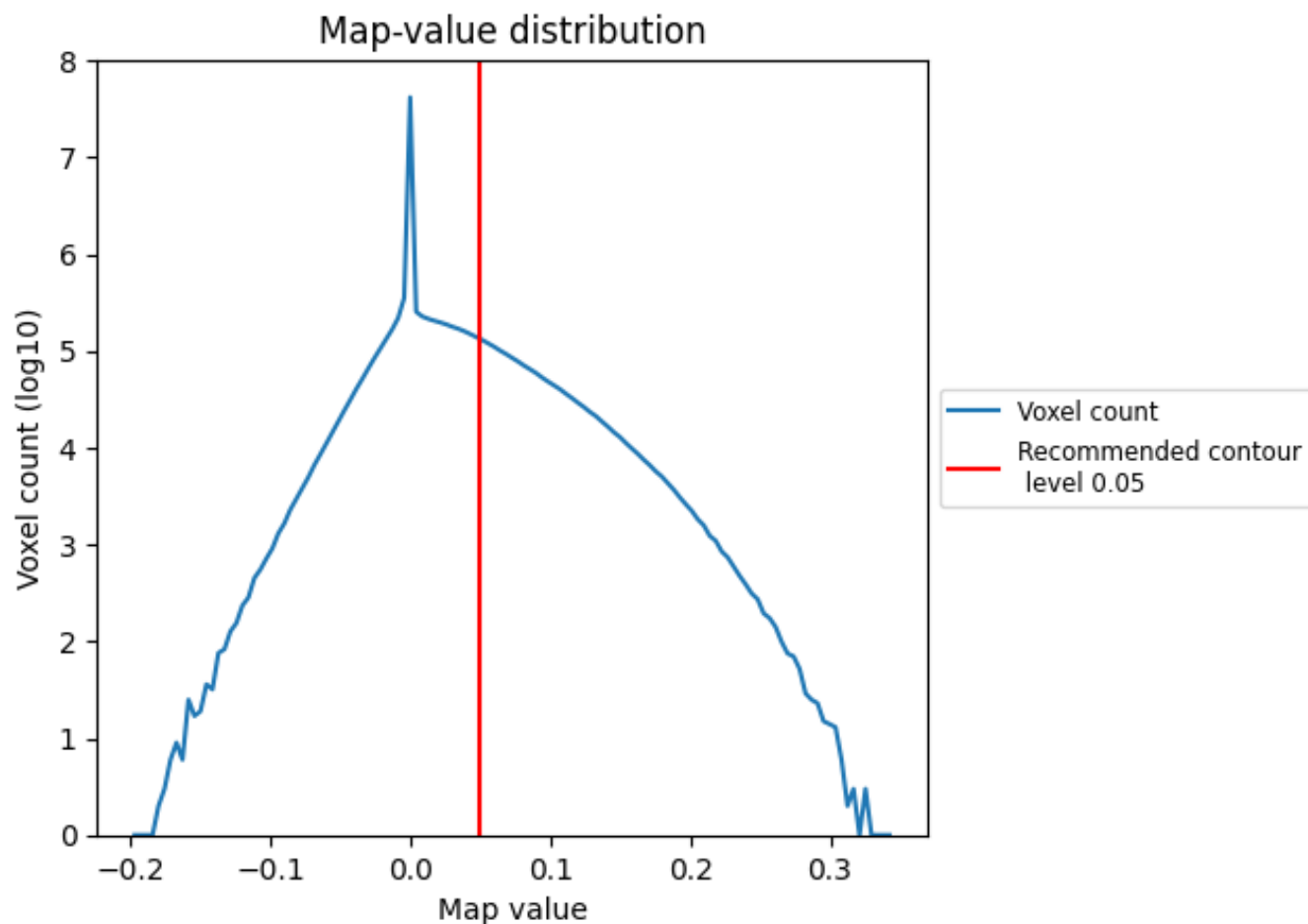
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

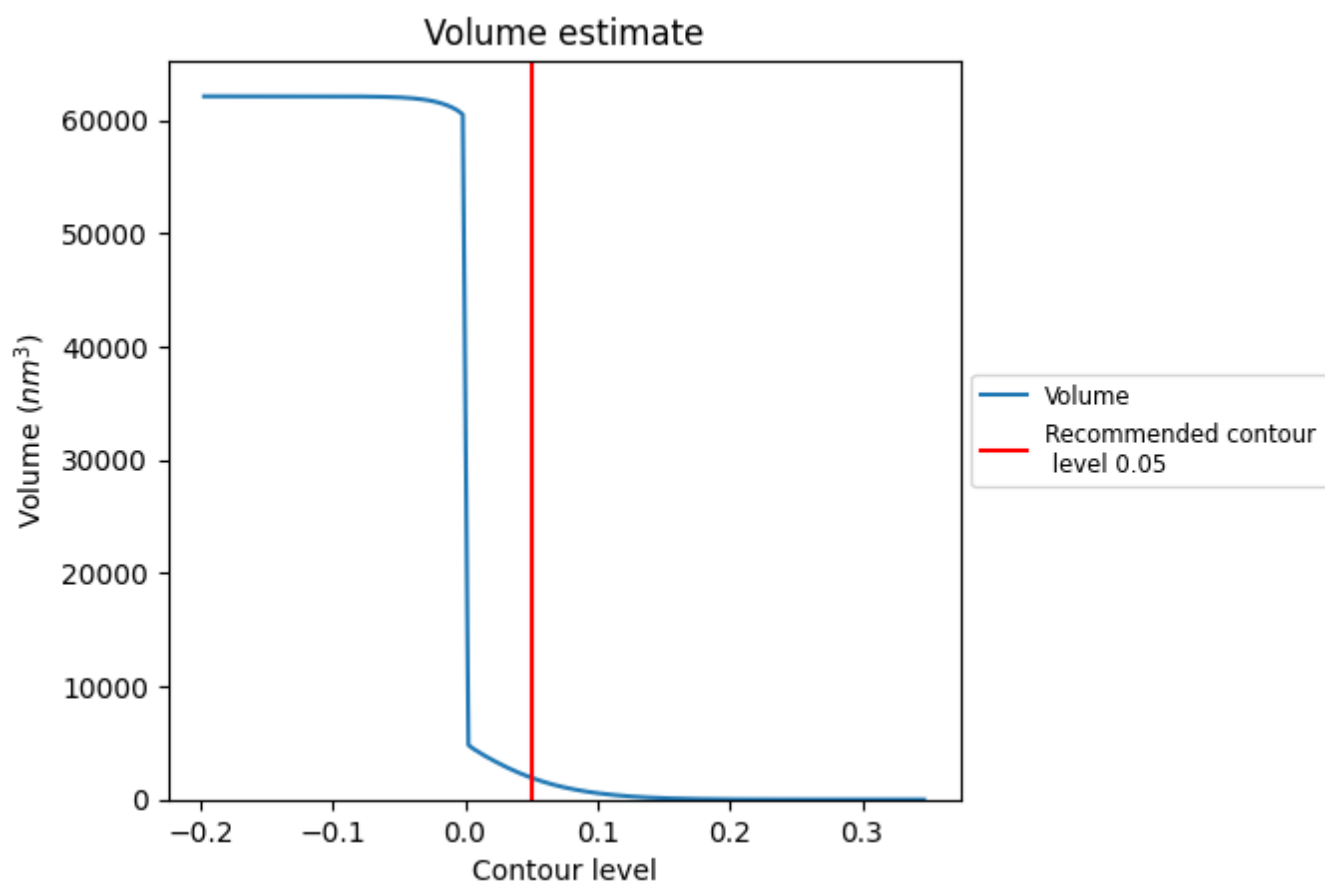
This section contains the results of statistical analysis of the map.

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.

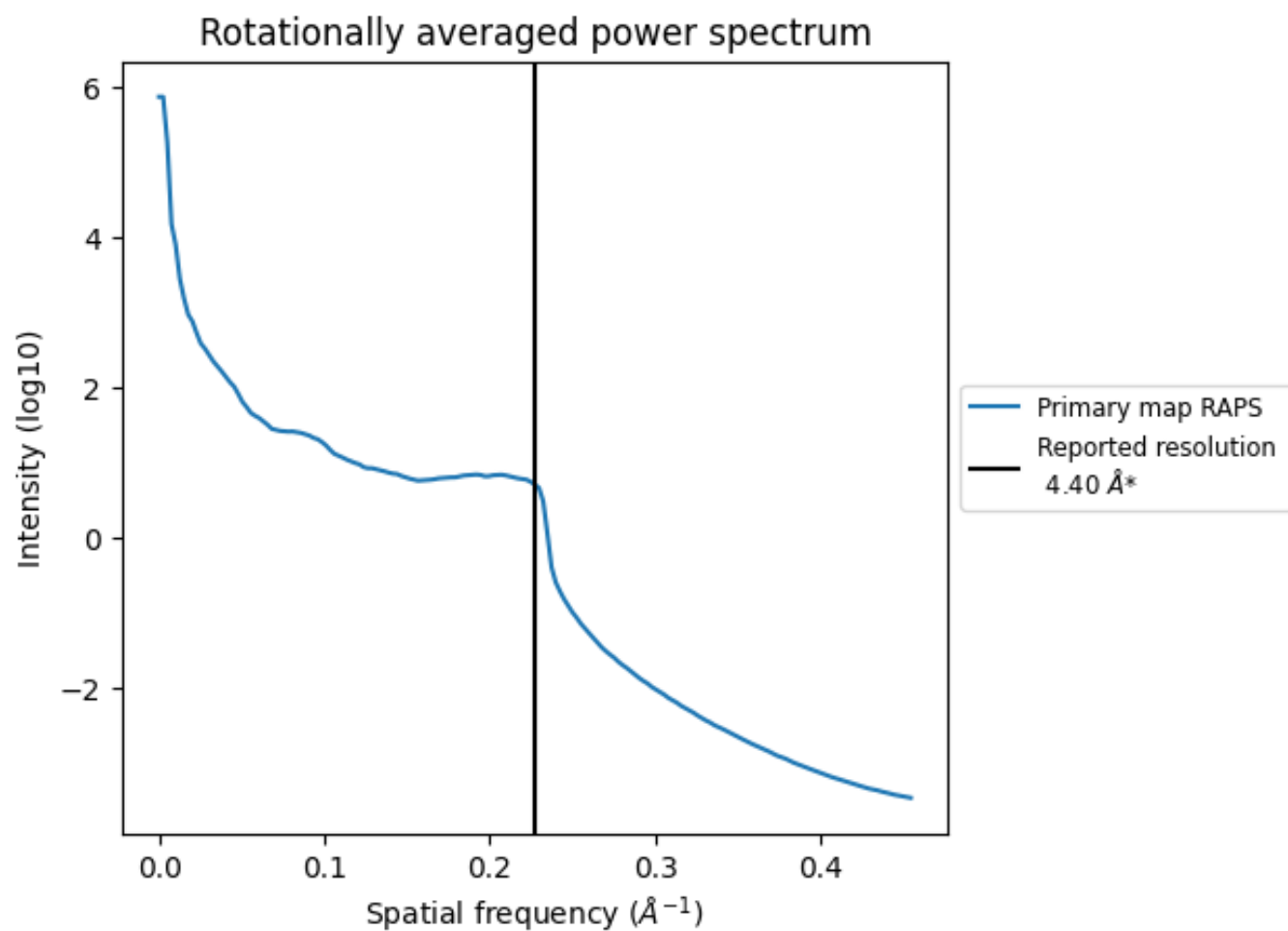
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1936 nm³; this corresponds to an approximate mass of 1749 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 0.227 Å⁻¹

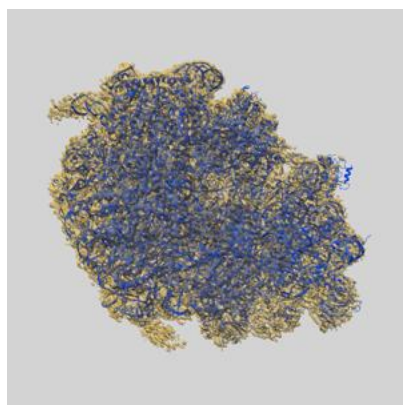
8 Fourier-Shell correlation

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

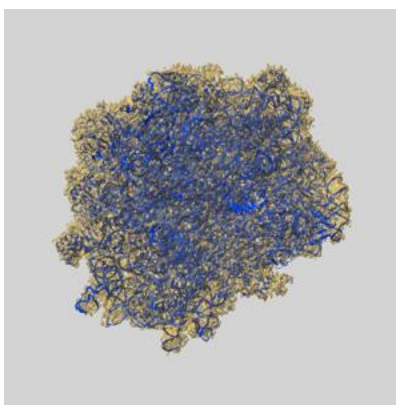
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0047 and PDB model 6GQ1. Per-residue inclusion information can be found in section 3 on page 21.

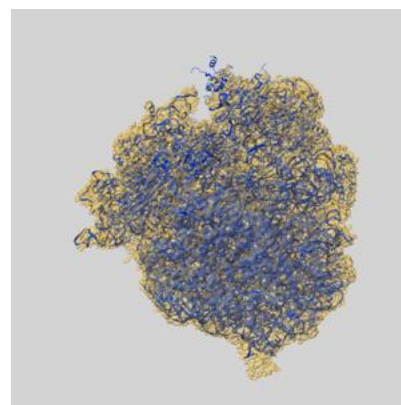
9.1 Map-model overlay [i](#)



X



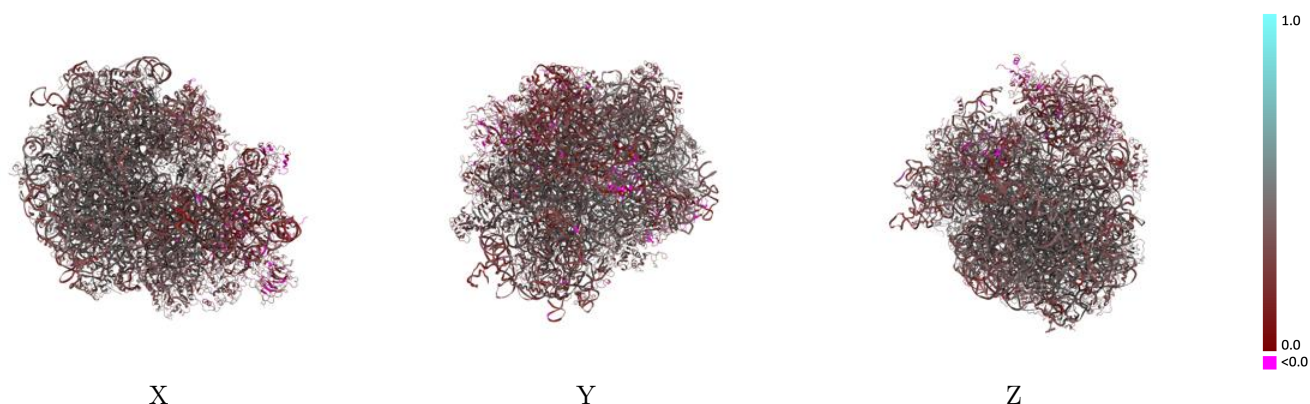
Y



Z

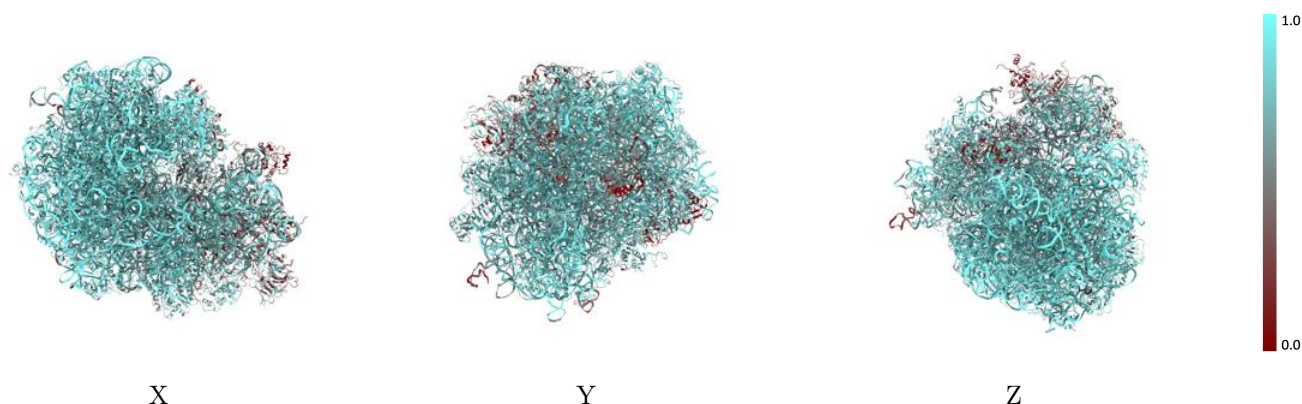
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



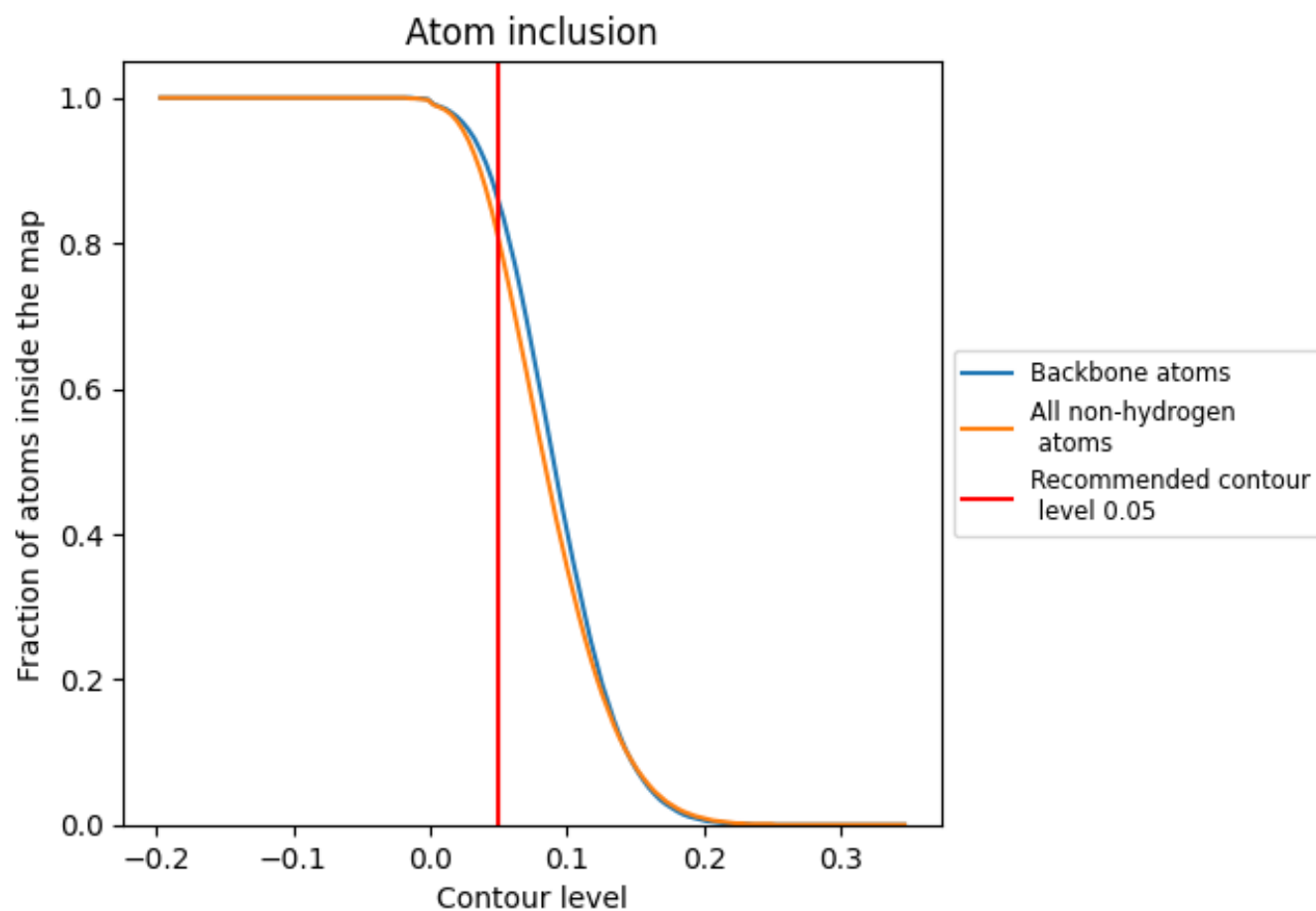
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.3570
1	 0.9110	 0.3810
2	 0.8440	 0.3240
3	 0.9360	 0.3530
4	 0.9340	 0.3930
A	 0.7740	 0.4380
AA	 0.6570	 0.2610
AB	 0.6780	 0.3880
AC	 0.1070	 0.1250
AD	 0.7700	 0.3720
AE	 0.7990	 0.3800
AF	 0.6000	 0.2770
AG	 0.5530	 0.2570
AH	 0.5300	 0.2530
AI	 0.5570	 0.2540
AJ	 0.5780	 0.2420
AK	 0.3580	 0.2170
AL	 0.7110	 0.3380
AM	 0.7650	 0.3910
AN	 0.6980	 0.3920
AO	 0.7460	 0.3370
AP	 0.3710	 0.1990
AQ	 0.7460	 0.3600
AR	 0.7480	 0.3620
AS	 0.4110	 0.2240
AT	 0.7030	 0.2720
AU	 0.6250	 0.3360
AV	 0.4710	 0.2100
AW	 0.3210	 0.1830
AX	 0.6670	 0.2570
AY	 0.2990	 0.3080
AZ	 0.6610	 0.3520
B	 0.8060	 0.4140
C	 0.8280	 0.4080
D	 0.7760	 0.3260



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Chain	Atom inclusion	Q-score
E	 0.8090	 0.3660
F	 0.8180	 0.3970
G	 0.7980	 0.3630
H	 0.7720	 0.3940
I	 0.7780	 0.4000
J	 0.7450	 0.3430
L	 0.8120	 0.3950
M	 0.8110	 0.3730
N	 0.8330	 0.4160
O	 0.8140	 0.3990
P	 0.8200	 0.4120
P0	 0.1920	 0.1770
P2	 0.1750	 0.1800
Q	 0.8150	 0.4190
R	 0.7980	 0.3970
S	 0.8030	 0.4050
T	 0.7980	 0.4070
U	 0.7560	 0.3640
V	 0.7370	 0.4370
W	 0.7860	 0.4210
X	 0.7830	 0.4060
Y	 0.8320	 0.4070
Z	 0.8170	 0.3910
a	 0.8350	 0.4160
b	 0.7630	 0.4150
c	 0.7970	 0.3830
d	 0.7530	 0.4080
e	 0.8160	 0.4230
f	 0.8030	 0.4150
g	 0.7860	 0.4240
h	 0.7840	 0.3870
i	 0.7950	 0.3630
j	 0.8550	 0.4370
k	 0.7460	 0.3910
l	 0.7900	 0.4110
m	 0.7770	 0.4180
n	 0.6300	 0.4360
o	 0.7720	 0.4100
p	 0.7630	 0.4320
q	 0.7250	 0.3320
r	 0.7530	 0.3650
s	 0.7290	 0.3740

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Chain	Atom inclusion	Q-score
t	 0.5030	 0.2530
u	 0.7380	 0.3500
v	 0.4740	 0.2470
w	 0.7180	 0.3120
x	 0.7030	 0.3170
y	 0.7330	 0.3570
z	 0.7560	 0.3450