



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2016 – 01:10 AM EST

PDB ID : 5DGV
Title : Complex of yeast 80S ribosome with hypusine-containing/non-modified eIF5A and/or a peptidyl-tRNA analog
Authors : Melnikov, S.; Mailliot, J.; Shin, B.-S.; Rigger, L.; Yusupova, G.; Micura, R.; Dever, T.E.; Yusupov, M.
Deposited on : 2015-08-28
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

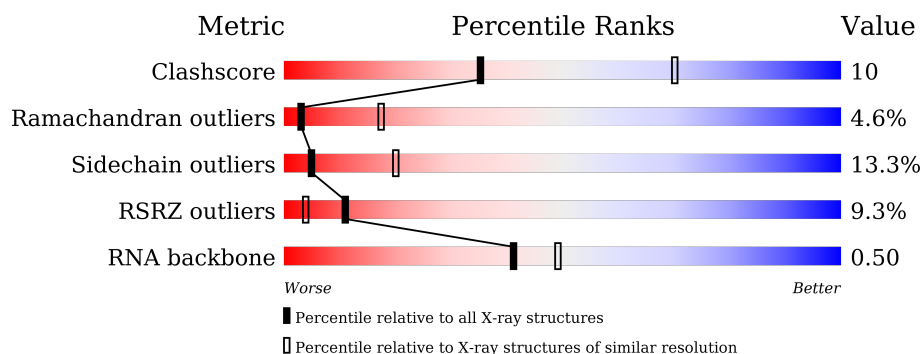
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)
RNA backbone	2183	1010 (3.52-2.68)

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

Mol	Chain	Length	Quality of chain
1	2	1800	<div> <div>8%</div> <div>48%</div> <div>38%</div> <div>12%</div> <div>..</div> </div>
1	6	1800	<div> <div>6%</div> <div>51%</div> <div>37%</div> <div>11%</div> </div>
2	S0	251	<div> <div>27%</div> <div>32%</div> <div>44%</div> <div>6%</div> <div>18%</div> </div>
2	s0	251	<div> <div>12%</div> <div>66%</div> <div>15%</div> <div>18%</div> </div>
3	S1	254	<div> <div>20%</div> <div>27%</div> <div>44%</div> <div>11%</div> <div>16%</div> </div>
3	s1	254	<div> <div>15%</div> <div>70%</div> <div>14%</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
4	S2	253	
4	s2	253	
5	S3	239	
5	s3	239	
6	S4	260	
6	s4	260	
7	S5	224	
7	s5	224	
8	S6	236	
8	s6	236	
9	S7	189	
9	s7	189	
10	S8	200	
10	s8	200	
11	S9	196	
11	s9	196	
12	C0	105	
12	c0	105	
13	C1	155	
13	c1	155	
14	C2	142	
14	c2	142	
15	C3	150	
15	c3	150	
16	C4	136	

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Mol	Chain	Length	Quality of chain
16	c4	136	
17	C5	141	
17	c5	141	
18	C6	142	
18	c6	142	
19	C7	136	
19	c7	136	
20	C8	145	
20	c8	145	
21	C9	143	
21	c9	143	
22	D0	120	
22	d0	120	
23	D1	87	
23	d1	87	
24	D2	129	
24	d2	129	
25	D3	144	
25	d3	144	
26	D4	134	
26	d4	134	
27	D5	107	
27	d5	107	
28	D6	97	
28	d6	97	



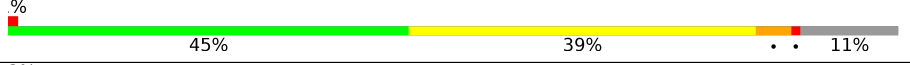


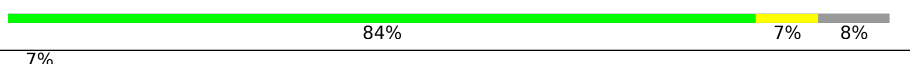


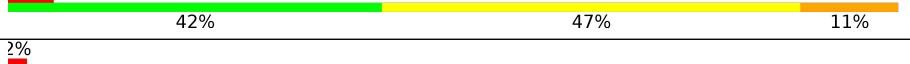



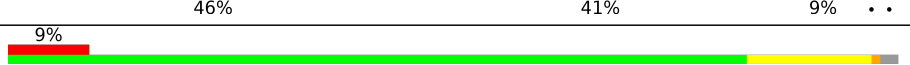
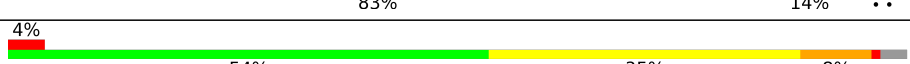


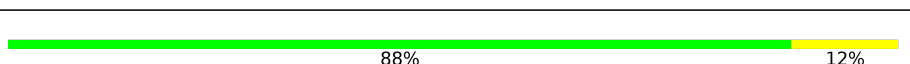

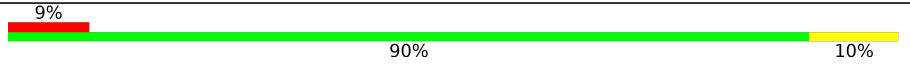


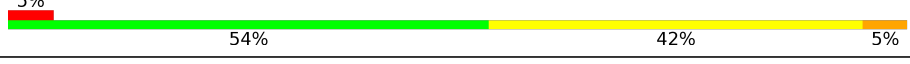
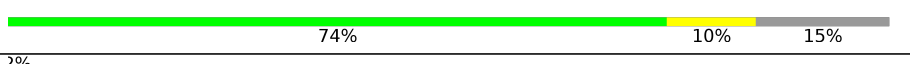


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Mol	Chain	Length	Quality of chain
29	D7	81	
29	d7	81	
30	D8	66	
30	d8	66	
31	D9	55	
31	d9	55	
32	E0	60	
33	E1	76	
33	e1	76	
34	SR	318	
34	sR	318	
35	SM	263	
35	sM	263	
36	1	3396	
36	5	3396	
37	3	121	
37	7	121	
38	4	158	
38	8	158	
39	L2	253	
39	l2	253	
40	L3	386	
40	l3	386	
41	L4	361	
41	l4	361	






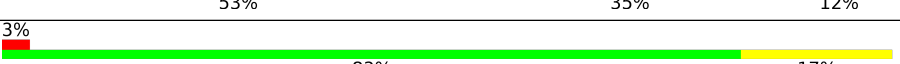
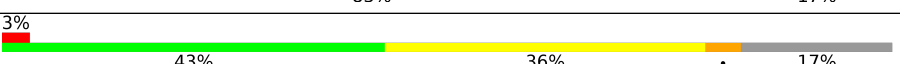
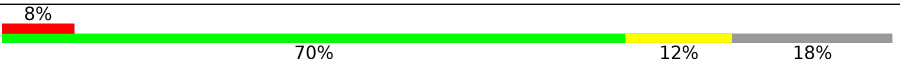

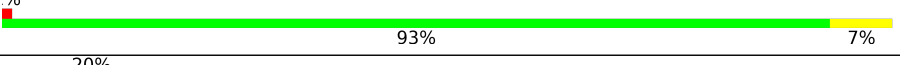
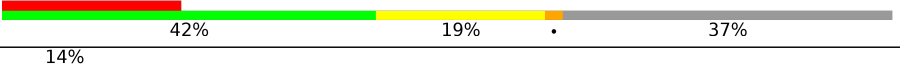
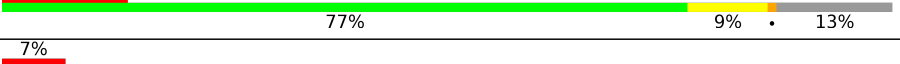

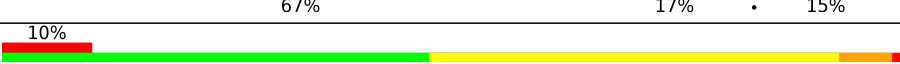
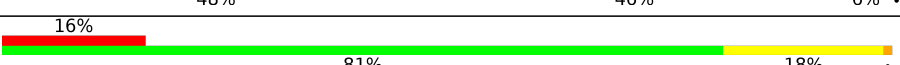
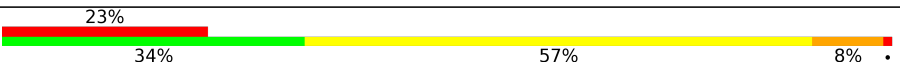

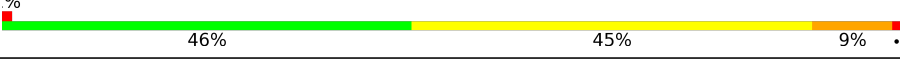







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Mol	Chain	Length	Quality of chain
42	L5	296	
42	l5	296	
43	L6	175	
43	l6	175	
44	L7	243	
44	l7	243	
45	L8	255	
45	l8	255	
46	L9	191	
46	l9	191	
47	M0	220	
47	m0	220	
48	M1	173	
48	m1	173	
49	M3	198	
49	m3	198	
50	M4	137	
50	m4	137	
51	M5	203	
51	m5	203	
52	M6	198	
52	m6	198	
53	M7	183	
53	m7	183	
54	M8	185	

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Mol	Chain	Length	Quality of chain
54	m8	185	
55	M9	188	
55	m9	188	
56	N0	172	
56	n0	172	
57	N1	159	
57	n1	159	
58	N2	120	
58	n2	120	
59	N3	136	
59	n3	136	
60	N4	155	
60	n4	155	
61	N5	141	
61	n5	141	
62	N6	126	
62	n6	126	
63	N7	135	
63	n7	135	
64	N8	148	
64	n8	148	
65	N9	58	
65	n9	58	
66	O0	104	
66	o0	104	

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Mol	Chain	Length	Quality of chain
67	O1	112	
67	o1	112	
68	O2	129	
68	o2	129	
69	O3	106	
69	o3	106	
70	O4	119	
70	o4	119	
71	O5	119	
71	o5	119	
72	O6	99	
72	o6	99	
73	O7	87	
73	o7	87	
74	O8	77	
74	o8	77	
75	O9	50	
75	o9	50	
76	Q0	52	
76	q0	52	
77	Q1	25	
77	q1	25	
78	Q2	105	
78	q2	105	
79	Q3	91	

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Mol	Chain	Length	Quality of chain
79	q3	91	
80	e0	62	
81	m2	160	
82	p0	311	
83	p1	47	
84	p2	46	
85	C	5	
85	D	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
88	MG	C	3402	-	-	-	X
88	MG	D	3402	-	-	-	X

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 402683 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called *Saccharomyces cerevisiae* S288c RDN37-1 miscRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	2	1781	Total	C	N	O	P	0	1	0
			37970	16975	6720	12493	1782			
1	6	1795	Total	C	N	O	P	0	1	0
			38260	17105	6763	12596	1796			

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S0	206	Total	C	N	O	S	0	0	0
			1577	1014	278	283	2			
2	s0	206	Total	C	N	O	S	0	0	0
			1583	1017	281	283	2			

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S1	214	Total	C	N	O	S	0	0	0
			1709	1084	310	311	4			
3	s1	216	Total	C	N	O	S	0	0	0
			1722	1091	312	315	4			

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	S2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			
4	s2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	S3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			
5	s3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	S4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			
6	s4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	S5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			
7	s5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	S6	226	Total	C	N	O	S	0	0	0
			1799	1129	346	321	3			
8	s6	218	Total	C	N	O	S	0	0	0
			1755	1102	337	313	3			

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	S7	184	Total	C	N	O	0	0	0
			1481	951	265	265			
9	s7	186	Total	C	N	O	0	0	0
			1491	957	267	267			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	S8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	s8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	S9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			
11	s9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	C0	96	Total	C	N	O	S	0	0	0
			773	500	126	145	2			
12	c0	96	Total	C	N	O	S	0	0	0
			762	491	125	144	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C0	89	ALA	GLY	conflict	UNP Q08745
c0	91	ALA	GLY	conflict	UNP Q08745

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	C1	155	Total	C	N	O	S	0	0	0
			1213	774	230	206	3			
13	c1	146	Total	C	N	O	S	0	0	0
			1168	747	221	197	3			

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	C2	124	Total	C	N	O	S	0	0	0
			892	562	156	172	2			
14	c2	124	Total	C	N	O	S	0	0	0
			892	562	156	172	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C2	104	ALA	GLY	conflict	UNP P48589
C2	110	ALA	GLY	conflict	UNP P48589
c2	104	ALA	GLY	conflict	UNP P48589
c2	110	ALA	GLY	conflict	UNP P48589

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	C3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			
15	c3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			

- Molecule 16 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	C4	127	Total	C	N	O	S	0	0	0
			891	545	182	163	1			
16	c4	128	Total	C	N	O	S	0	0	0
			949	582	188	176	3			

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	C5	124	Total	C	N	O	S	0	0	0
			977	622	182	166	7			
17	c5	135	Total	C	N	O	S	0	0	0
			1039	658	196	178	7			

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	C6	141	Total	C	N	O	0	0	0
			1105	708	203	194			
18	c6	142	Total	C	N	O	0	0	0
			1111	711	204	196			

- Molecule 19 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	C7	120	Total	C	N	O	S	0	0	0
			926	577	177	170	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	c7	117	Total	C	N	O	S	0	0	0
			906	563	174	167	2			

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	C8	145	Total	C	N	O	S	0	0	0
			1192	743	237	210	2			
20	c8	145	Total	C	N	O	S	0	0	0
			1192	743	237	210	2			

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	C9	143	Total	C	N	O	S	0	0	0
			1112	694	208	208	2			
21	c9	143	Total	C	N	O	S	0	0	0
			1112	694	208	208	2			

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	D0	107	Total	C	N	O	S	0	0	0
			855	539	156	159	1			
22	d0	110	Total	C	N	O	S	0	0	0
			882	554	161	166	1			

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	D1	87	Total	C	N	O	S	0	0	0
			684	420	125	137	2			
23	d1	87	Total	C	N	O	S	0	0	0
			684	420	125	137	2			

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	D2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			
24	d2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	D3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			
25	d3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	D4	134	Total	C	N	O	0	0	0
			1073	676	208	189			
26	d4	134	Total	C	N	O	0	0	0
			1073	676	208	189			

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	D5	70	Total	C	N	O	0	0	0
			563	360	104	99			
27	d5	69	Total	C	N	O	0	0	0
			558	357	103	98			

- Molecule 28 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	D6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			
28	d6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	D7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			
29	d7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			

- Molecule 30 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	D8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			
30	d8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			

- Molecule 31 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	D9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			
31	d9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	E0	60	Total	C	N	O	S	0	0	0
			475	299	98	77	1			

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	E1	71	Total	C	N	O	S	0	0	0
			566	362	106	94	4			
33	e1	76	Total	C	N	O	S	0	0	0
			608	388	117	99	4			

- Molecule 34 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	SR	318	Total	C	N	O	S	0	0	0
			2437	1541	418	470	8			
34	sR	318	Total	C	N	O	S	0	0	0
			2442	1544	418	472	8			

- Molecule 35 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	SM	159	Total	C	N	O		0	0	0
			1104	652	221	231				
35	sM	104	Total	C	N	O		0	0	0
			681	404	140	137				

- Molecule 36 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1	3148	Total	C	N	O	P	0	0	0
			67333	30076	12137	21972	3148			
36	5	3149	Total	C	N	O	P	0	0	0
			67354	30085	12140	21981	3148			

- Molecule 37 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	3	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			
37	7	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	4	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			
38	8	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	L2	252	Total	C	N	O	S	0	0	0
			1914	1191	388	334	1			
39	12	252	Total	C	N	O	S	0	0	0
			1912	1190	388	333	1			

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	L3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			
40	13	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	L4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			
41	14	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	L5	296	Total	C	N	O	S	0	0	0
			2375	1501	414	458	2			
42	15	294	Total	C	N	O	S	0	0	0
			2359	1489	412	456	2			

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	L6	156	Total	C	N	O	S	0	0	0
			1239	800	222	216	1			
43	16	157	Total	C	N	O	S	0	0	0
			1248	806	224	217	1			

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	L7	222	Total	C	N	O	S	0	0	0
			1784	1151	324	308	1			
44	17	223	Total	C	N	O	S	0	0	0
			1791	1155	325	310	1			

- Molecule 45 is a protein called 60S ribosomal protein L8-A (eL8).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	L8	233	Total	C	N	O	S	0	0	0
			1804	1151	323	327	3			
45	18	231	Total	C	N	O	S	0	0	0
			1764	1131	316	314	3			

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	L9	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	19	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	M0	211	Total	C	N	O	S	0	0	0
			1705	1083	322	294	6			
47	m0	213	Total	C	N	O	S	0	0	0
			1722	1094	325	297	6			

- Molecule 48 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	M1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			
48	m1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	M3	193	Total	C	N	O		0	0	0
			1543	962	315	266				
49	m3	194	Total	C	N	O		0	0	0
			1548	965	316	267				

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	M4	136	Total	C	N	O	S	0	0	0
			1053	675	199	177	2			
50	m4	137	Total	C	N	O	S	0	0	0
			1059	678	200	179	2			

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	M5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			
51	m5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	M6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			
52	m6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	M7	183	Total	C	N	O		0	0	0
			1420	882	281	257				
53	m7	155	Total	C	N	O		0	0	0
			1227	764	238	225				

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	M8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			
54	m8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	M9	188	Total	C	N	O		0	0	0
			1521	935	326	260				
55	m9	188	Total	C	N	O		0	0	0
			1521	935	326	260				

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	N0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			
56	n0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	N1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			
57	n1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	N2	100	Total	C	N	O	S	0	0	0
			796	516	131	149				
58	n2	98	Total	C	N	O	S	0	0	0
			778	505	127	146				

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	N3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			
59	n3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	N4	98	Total	C	N	O	S	0	0	0
			699	443	137	118	1			
60	n4	135	Total	C	N	O	S	0	0	0
			1038	651	206	180	1			

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	N5	121	Total	C	N	O	S	0	0	0
			964	620	169	173	2			
61	n5	120	Total	C	N	O	S	0	0	0
			959	617	168	172	2			

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
62	N6	126	Total	C	N	O	S	0	0	0
			993	625	192	176				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
62	n6	126	Total	C	N	O	0	0	0
			993	625	192	176			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
63	N7	135	Total	C	N	O	0	0	0
			1092	710	202	180			
63	n7	135	Total	C	N	O	0	0	0
			1092	710	202	180			

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	N8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			
64	n8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
65	N9	58	Total	C	N	O	0	0	0
			462	289	100	73			
65	n9	58	Total	C	N	O	0	0	0
			462	289	100	73			

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	O0	97	Total	C	N	O	S	0	0	0
			743	479	124	139	1			
66	o0	100	Total	C	N	O	S	0	0	0
			767	492	128	146	1			

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	O1	109	Total	C	N	O	S	0	0	0
			876	556	167	152	1			
67	o1	109	Total	C	N	O	S	0	0	0
			883	559	167	156	1			

- Molecule 68 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	O2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			
68	o2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	O3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			
69	o3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	O4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			
70	o4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O4	?	-	LYS	deletion	UNP P87262
o4	?	-	LYS	deletion	UNP P87262

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
71	O5	119	Total	C	N	O	S	0	0	0
			969	615	186	167	1			
71	o5	119	Total	C	N	O	S	0	0	0
			965	612	185	167	1			

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	O6	99	Total	C	N	O	S	0	0	0
			771	481	156	132	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	o6	99	Total	C	N	O	S	0	0	0
			770	481	156	131	2			

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	O7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			
73	o7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			

- Molecule 74 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	O8	77	Total	C	N	O	S	0	0	0
			612	391	115	106				
74	o8	77	Total	C	N	O	S	0	0	0
			608	388	114	106				

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	O9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			
75	o9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	Q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			
76	q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	Q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			
77	q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
78	Q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			
78	q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	Q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			
79	q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			

- Molecule 80 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	e0	62	Total	C	N	O	S	0	0	0
			491	309	101	80	1			

- Molecule 81 is a protein called 60S ribosomal protein L12-A (uL11).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
81	m2	150	Total	C	N	O	0	0	0
			750	450	150	150			

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	p0	143	Total	C	N	O	S	0	0	0
			1076	686	192	195	3			

- Molecule 83 is a protein called 60S ribosomal protein P1 alpha/P2 beta.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
83	p1	47	Total	C	N	O	0	0	0
			235	141	47	47			

- Molecule 84 is a protein called 60S ribosomal protein P1 alpha/P2 beta.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
84	p2	46	Total	C	N	O	0	0	0
			230	138	46	46			

- Molecule 85 is a RNA chain called DNA (5'-R(*CP*CP*(8AN)*(Pro)*(Pro))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
85	C	5	Total	C	N	O	P	0	0	0
			73	38	14	19	2			
85	D	5	Total	C	N	O	P	0	0	0
			76	38	14	21	3			

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

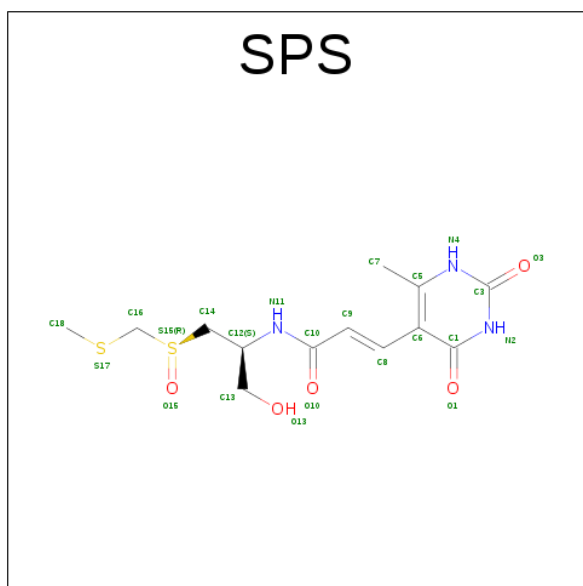
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	q0	1	Total	Zn	0	0
			1	1		
86	D6	1	Total	Zn	0	0
			1	1		
86	Q2	1	Total	Zn	0	0
			1	1		
86	e1	1	Total	Zn	0	0
			1	1		
86	Q3	1	Total	Zn	0	0
			1	1		
86	D9	1	Total	Zn	0	0
			1	1		
86	E1	1	Total	Zn	0	0
			1	1		
86	Q0	1	Total	Zn	0	0
			1	1		
86	d7	1	Total	Zn	0	0
			1	1		
86	q3	1	Total	Zn	0	0
			1	1		
86	d9	1	Total	Zn	0	0
			1	1		
86	D7	1	Total	Zn	0	0
			1	1		
86	d6	1	Total	Zn	0	0
			1	1		
86	o7	1	Total	Zn	0	0
			1	1		
86	O7	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	q2	1	Total	Zn	0	0
			1	1		

- Molecule 87 is SPARSOMYCIN (three-letter code: SPS) (formula: $C_{13}H_{19}N_3O_5S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
87	C	1	Total	C	N	O	S	0	0
			23	13	3	5	2		
87	D	1	Total	C	N	O	S	0	0
			23	13	3	5	2		

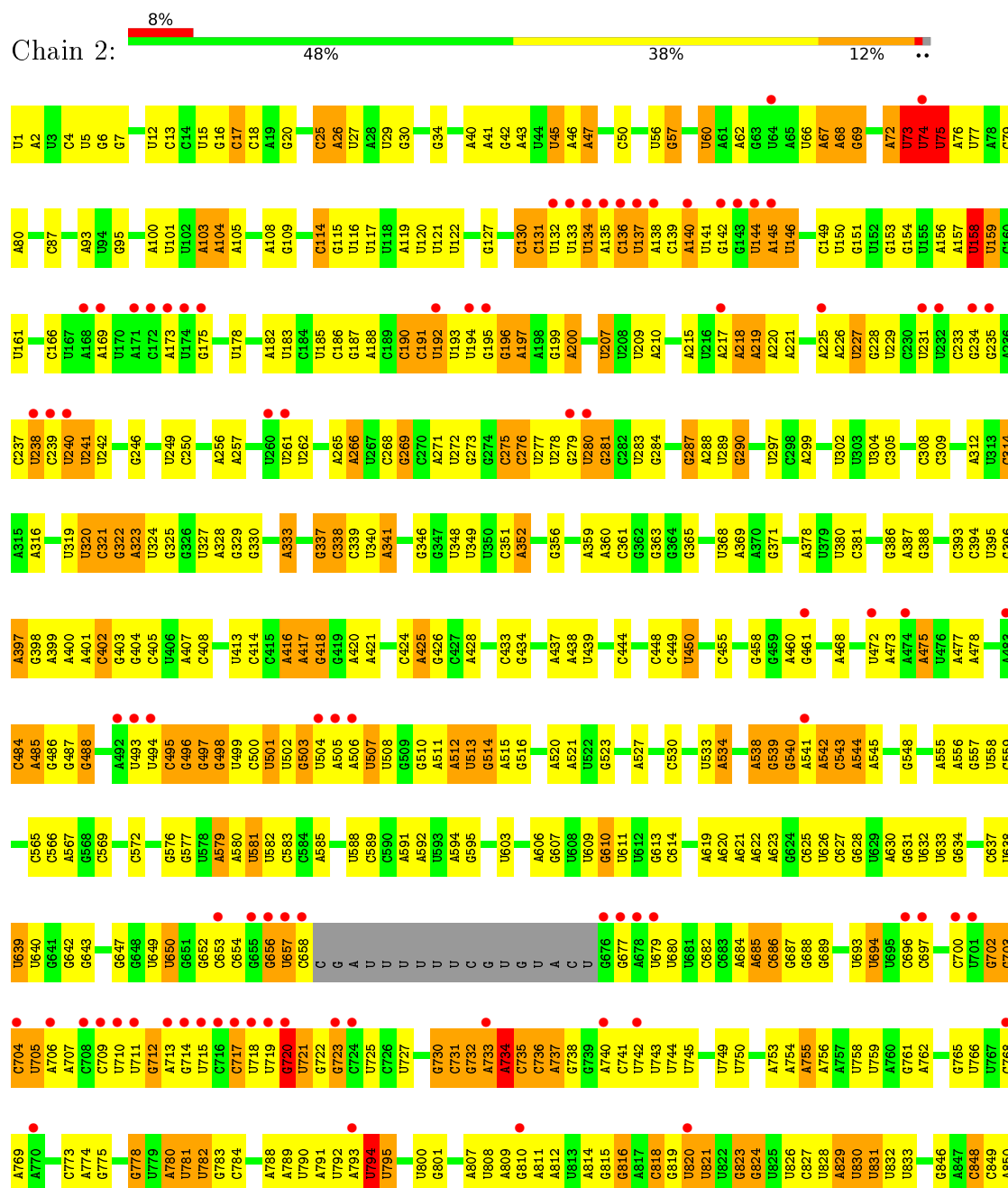
- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

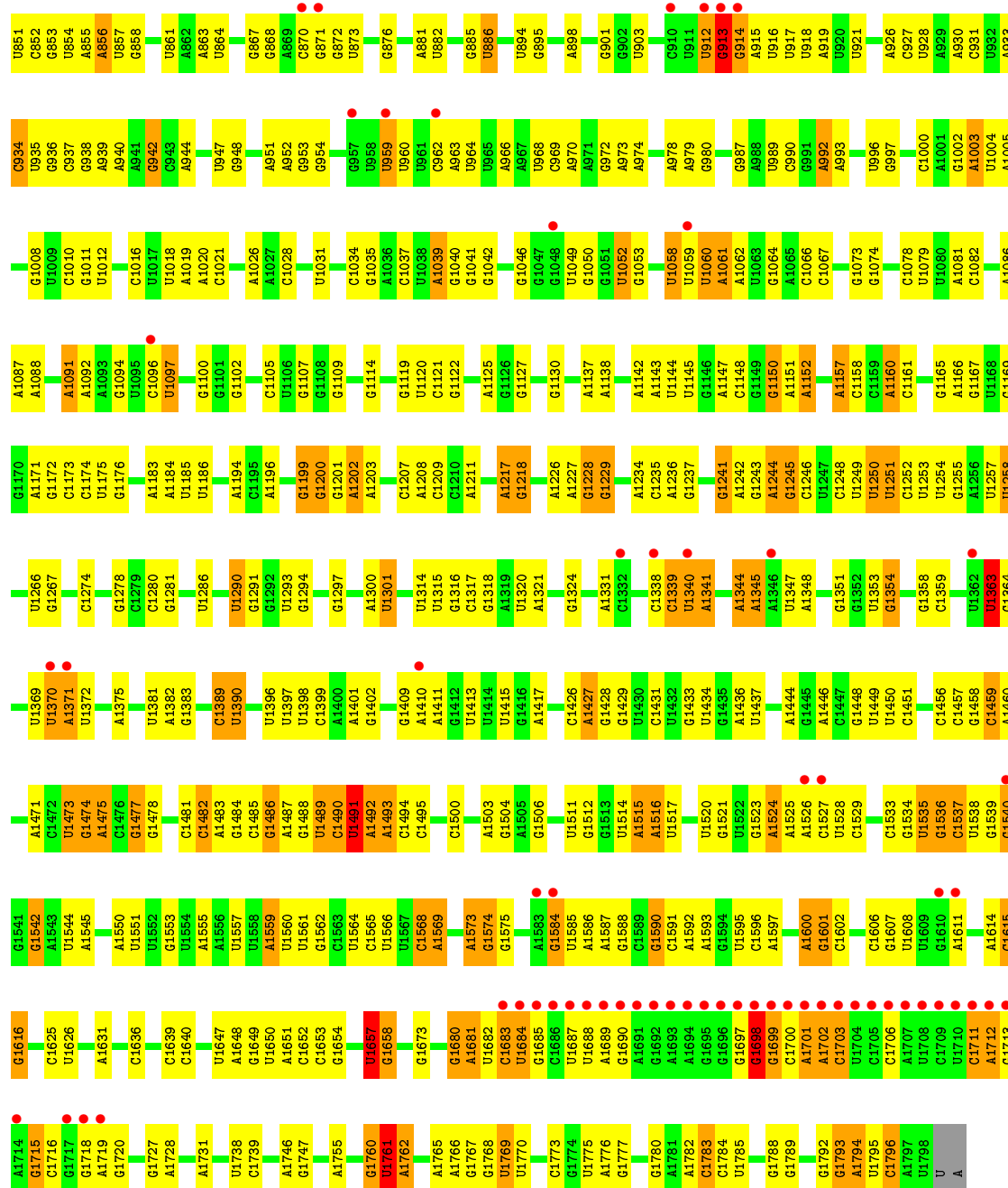
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
88	D	1	Total	Mg	0	0
			1	1		
88	C	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

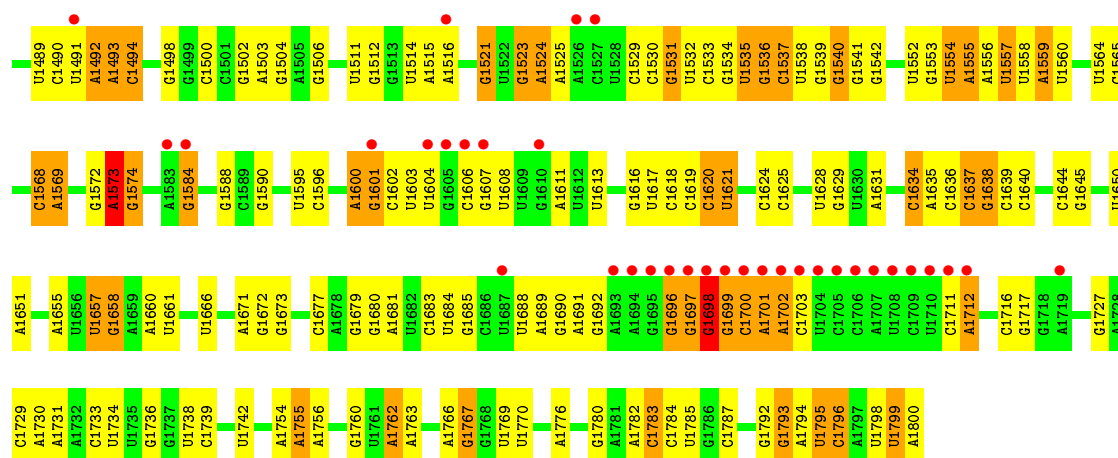
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: *Saccharomyces cerevisiae* S288c RDN37-1 miscRNA

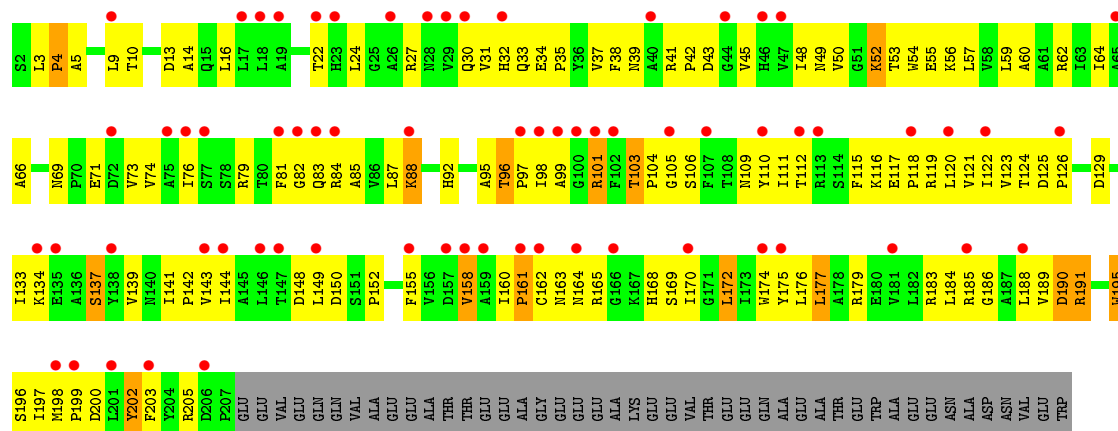




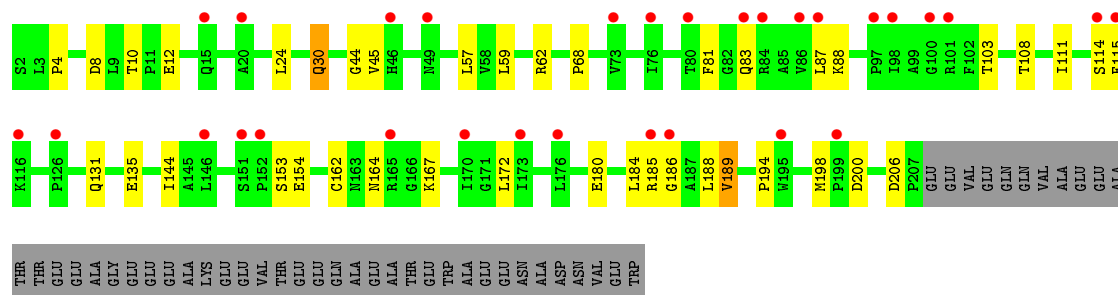




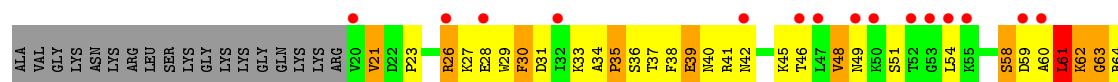
• Molecule 2: 40S ribosomal protein S0-A

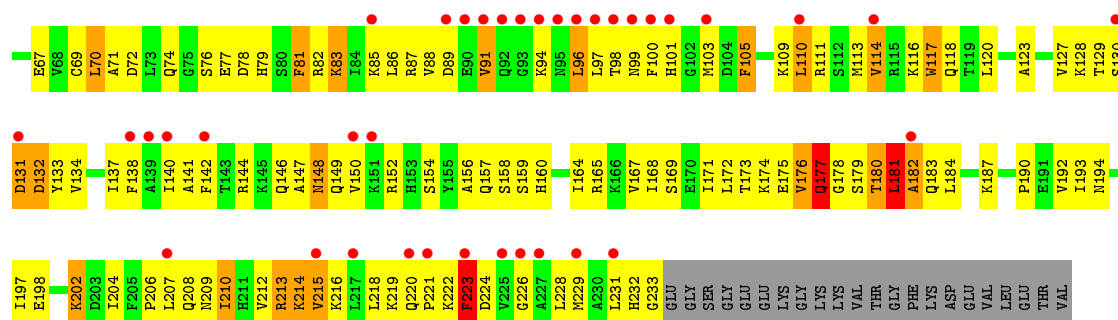


• Molecule 2: 40S ribosomal protein S0-A

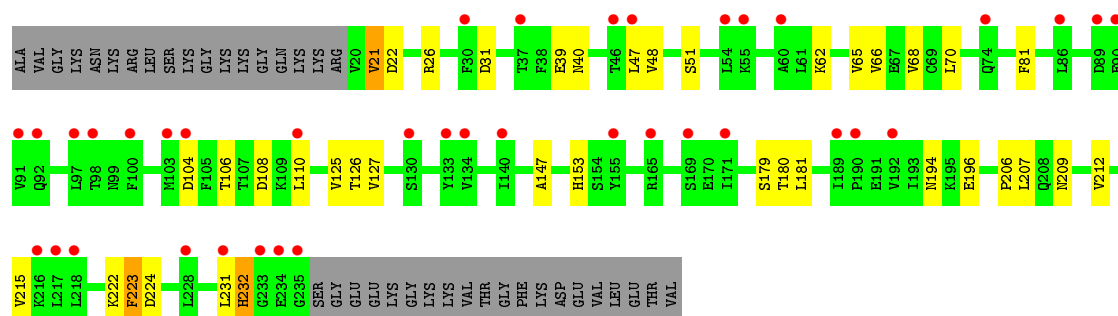


• Molecule 3: 40S ribosomal protein S1-A

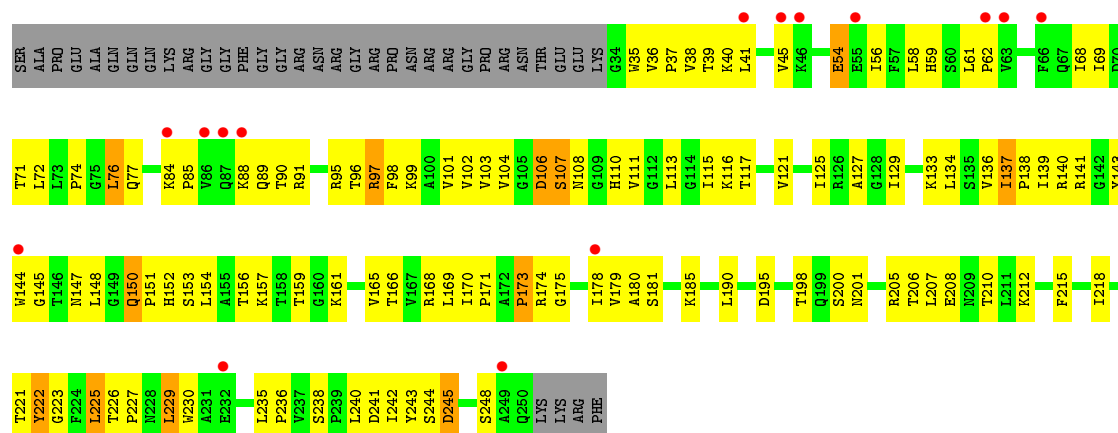
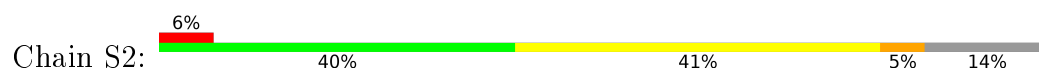




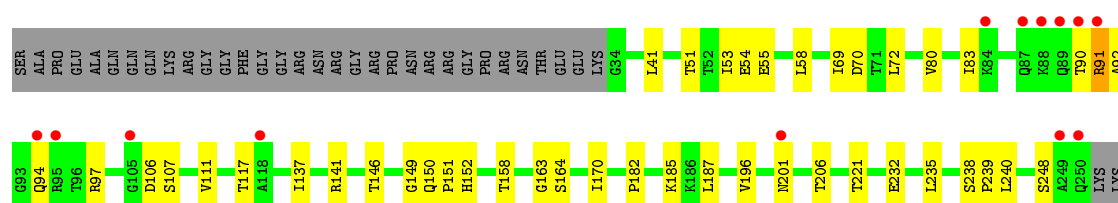
• Molecule 3: 40S ribosomal protein S1-A



• Molecule 4: 40S ribosomal protein S2

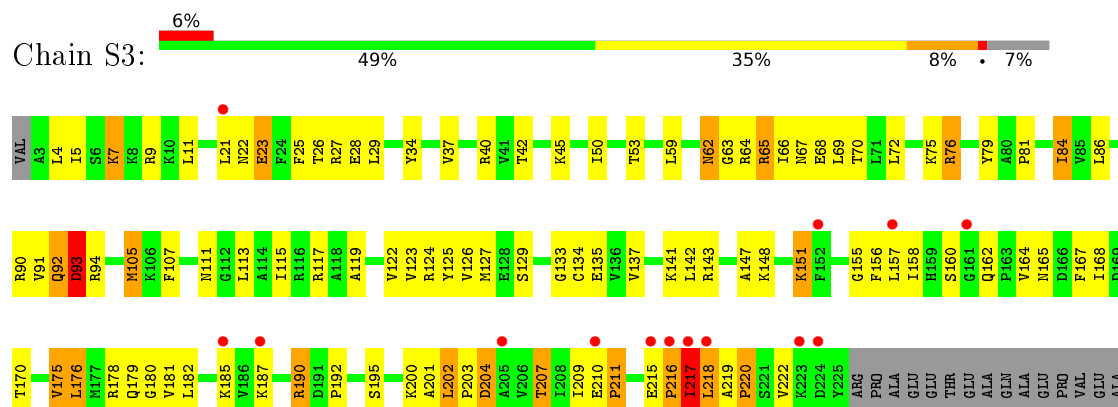


• Molecule 4: 40S ribosomal protein S2

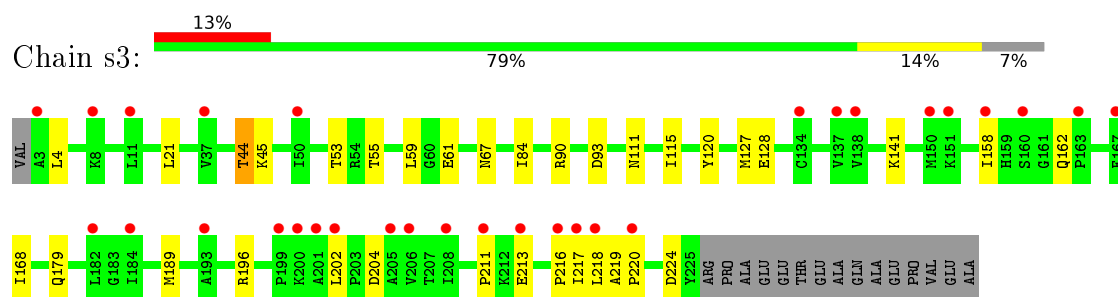


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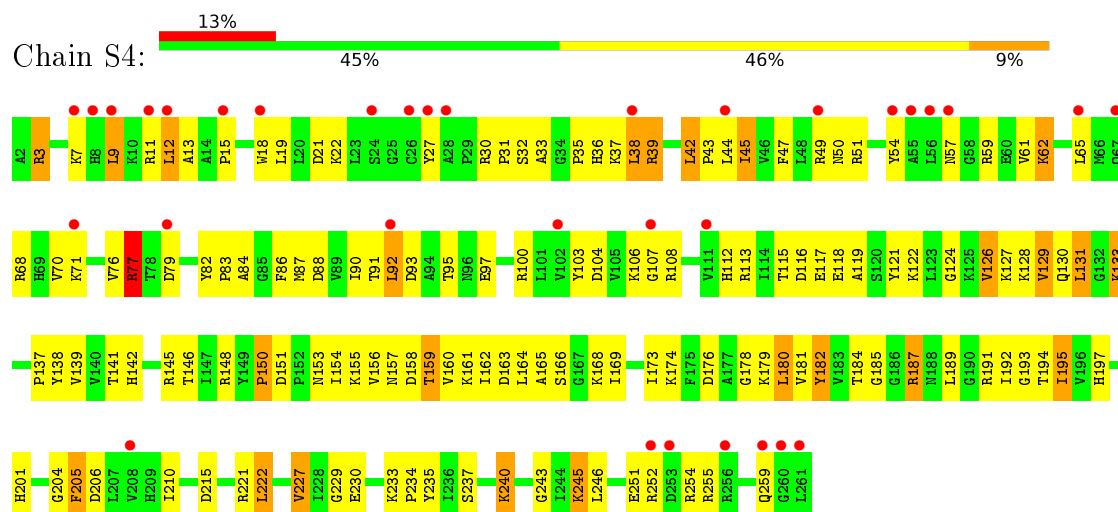
- Molecule 5: 40S ribosomal protein S3



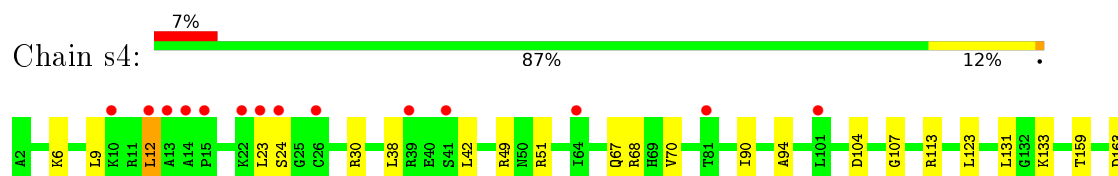
- Molecule 5: 40S ribosomal protein S3

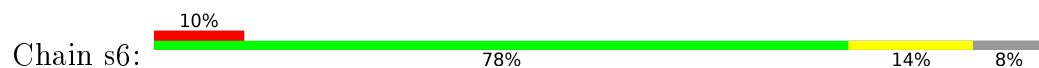


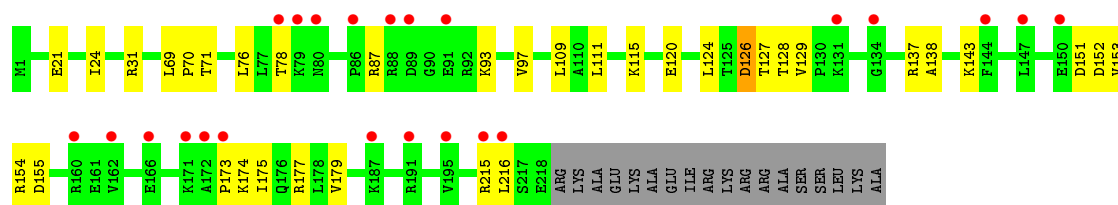
- Molecule 6: 40S ribosomal protein S4-A



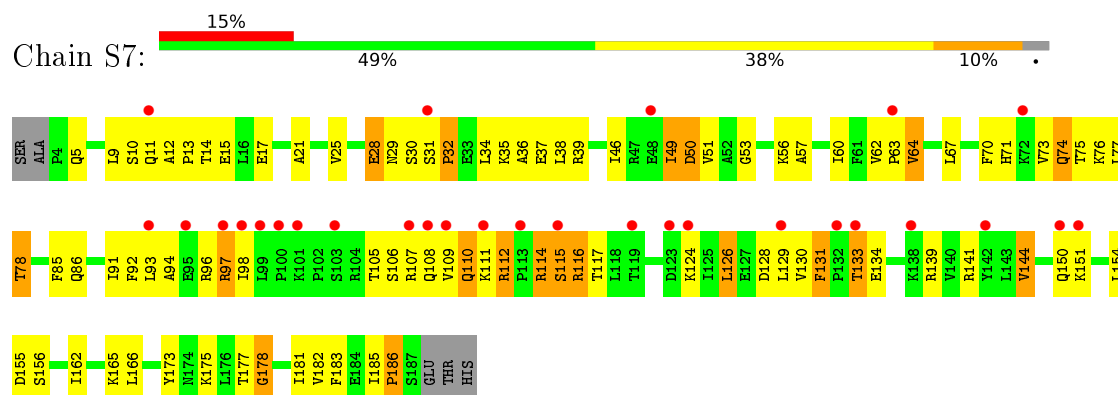
- Molecule 6: 40S ribosomal protein S4-A



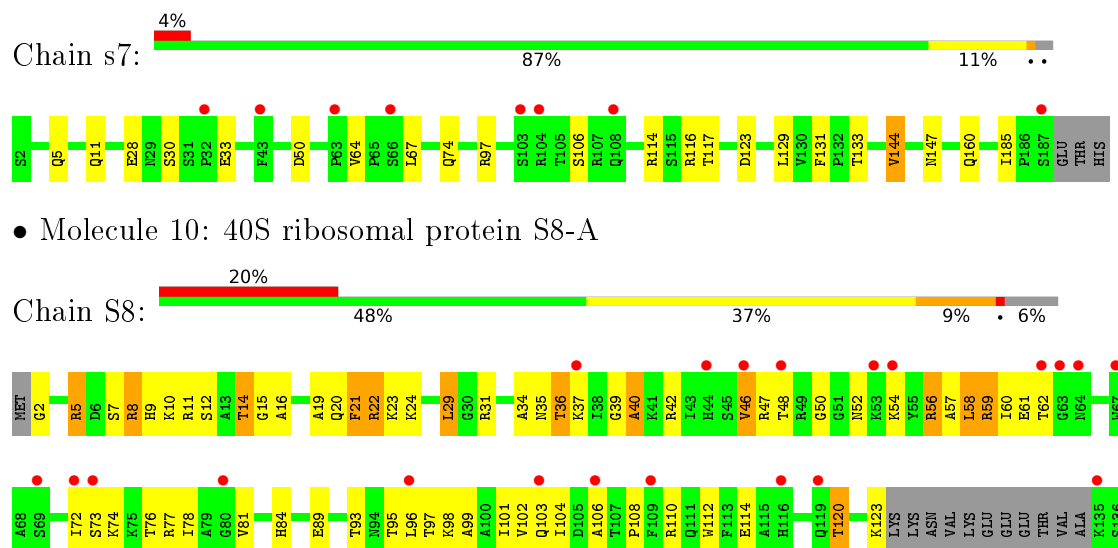




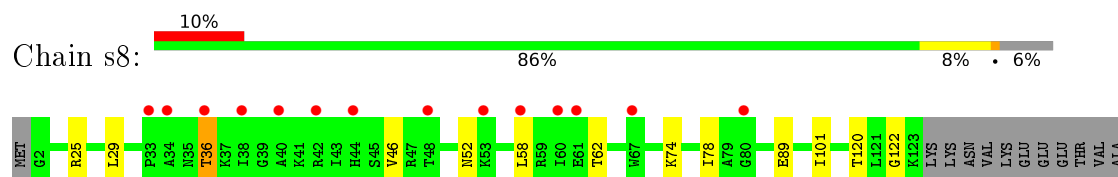
• Molecule 9: 40S ribosomal protein S7-A

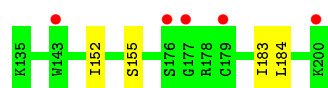


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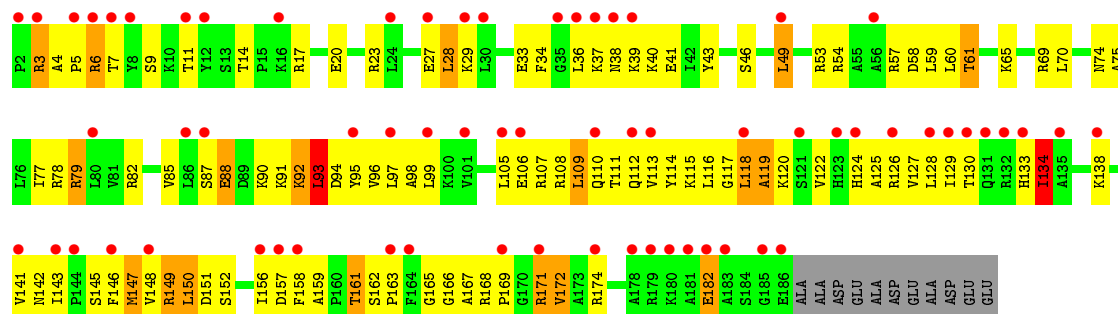
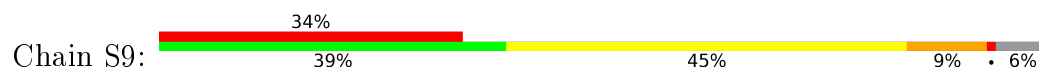


• Molecule 10: 40S ribosomal protein S8-A

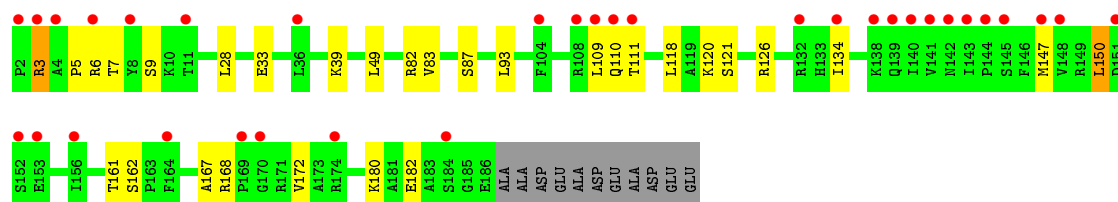
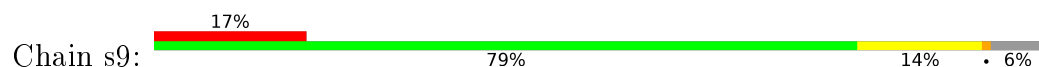




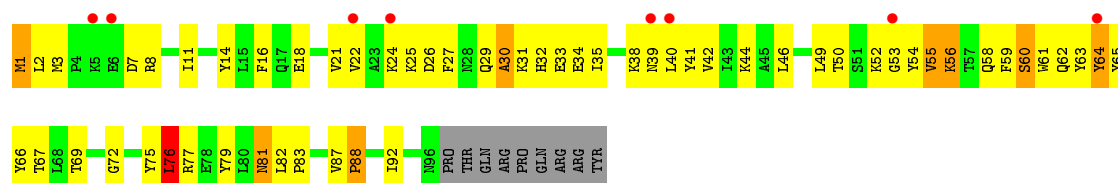
- Molecule 11: 40S ribosomal protein S9-A



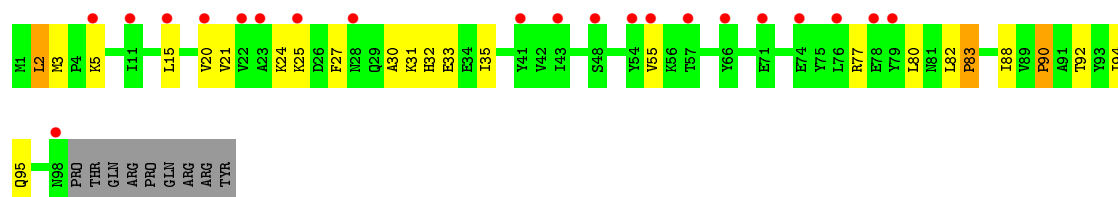
- Molecule 11: 40S ribosomal protein S9-A



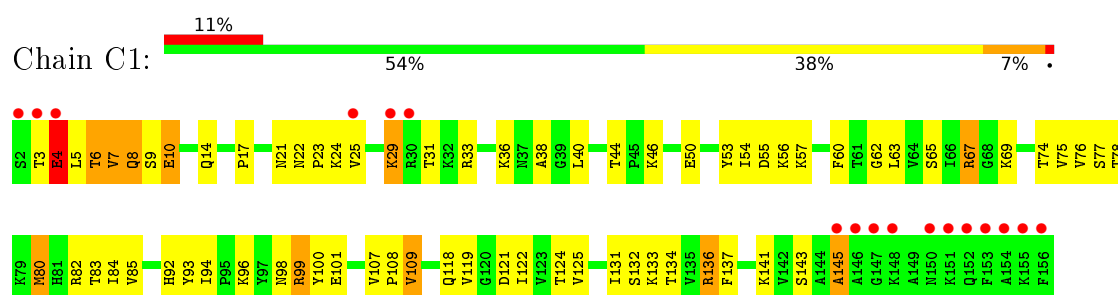
- Molecule 12: 40S ribosomal protein S10-A



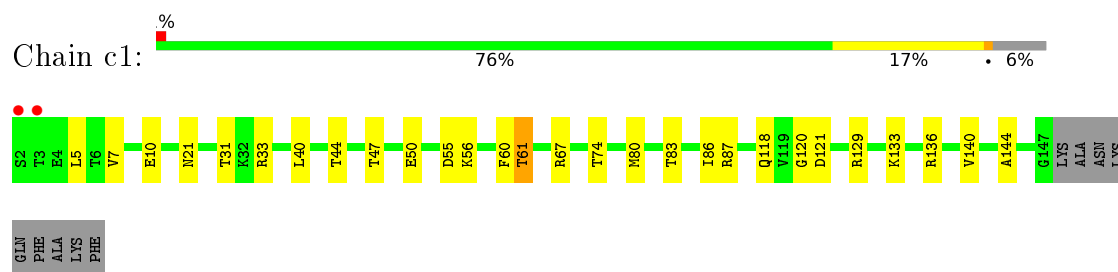
- Molecule 12: 40S ribosomal protein S10-A



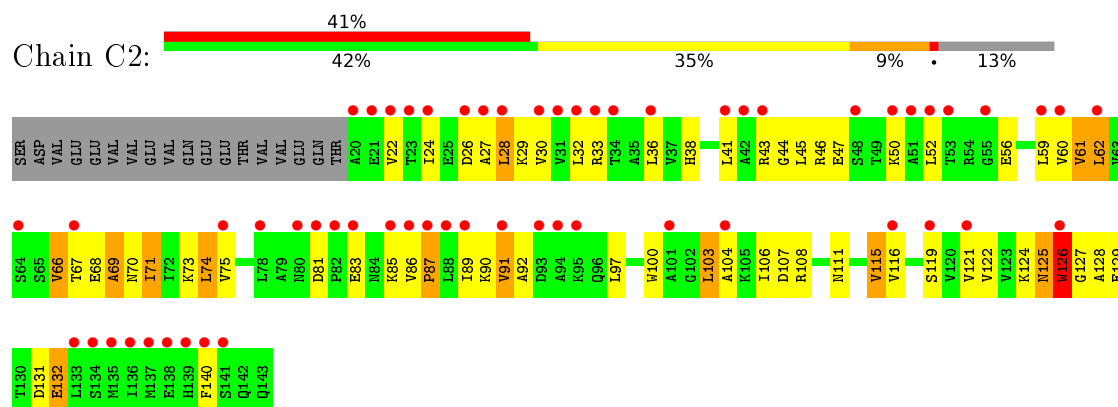
- Molecule 13: 40S ribosomal protein S11-A



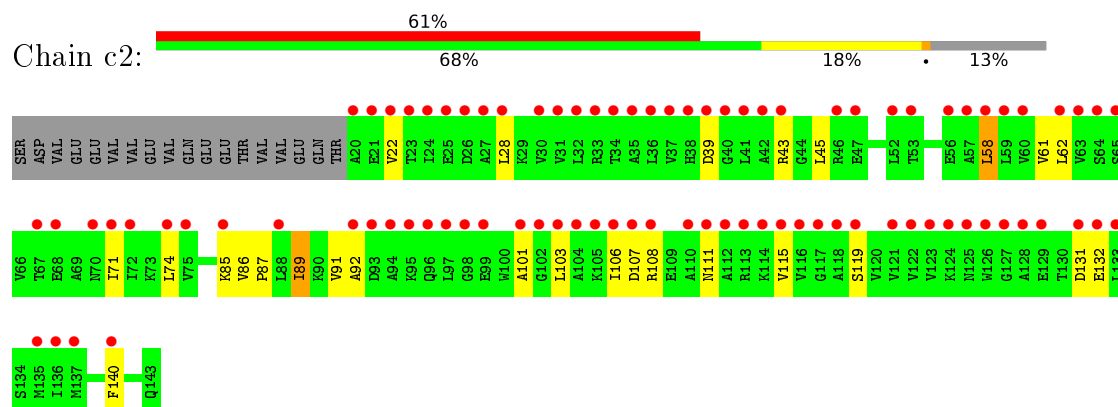
- Molecule 13: 40S ribosomal protein S11-A



- Molecule 14: 40S ribosomal protein S12

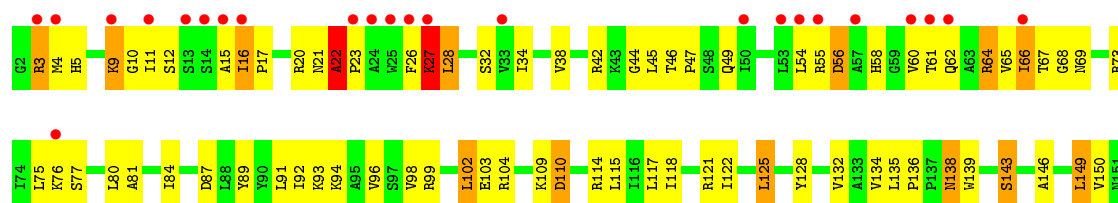


- Molecule 14: 40S ribosomal protein S12

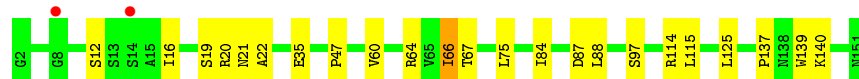
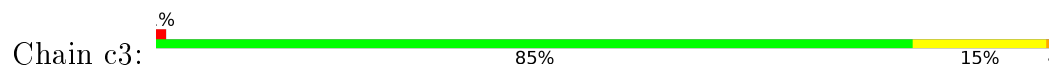


- Molecule 15: 40S ribosomal protein S13

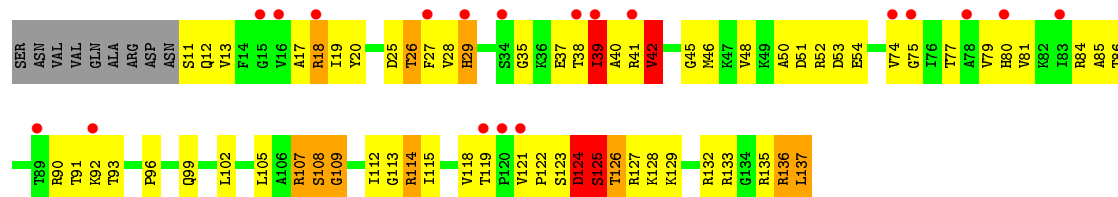
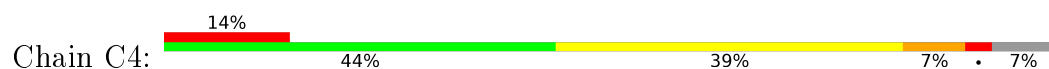




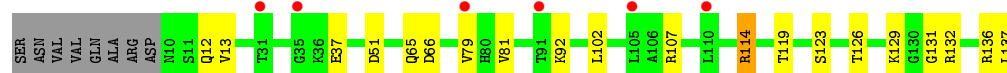
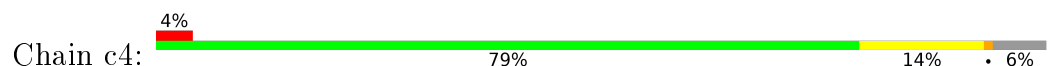
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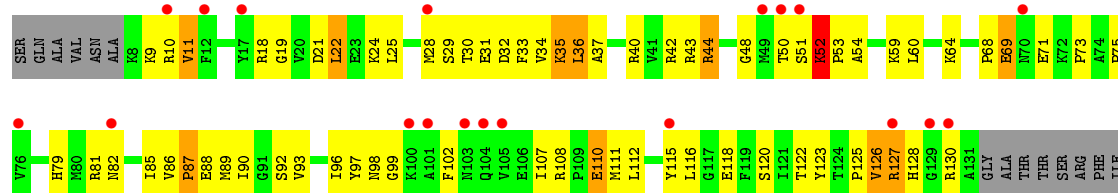
- Molecule 16: 40S ribosomal protein S14-A



- Molecule 16: 40S ribosomal protein S14-A

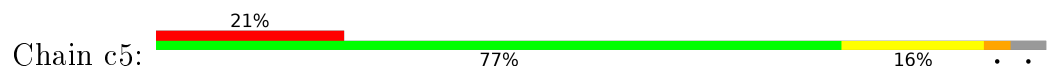


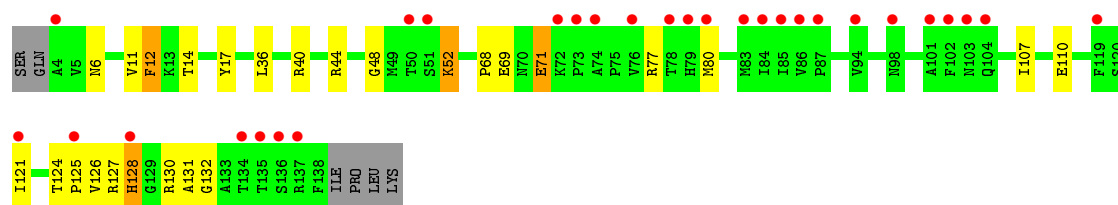
- Molecule 17: 40S ribosomal protein S15



PRO
LEU
LYS

- Molecule 17: 40S ribosomal protein S15

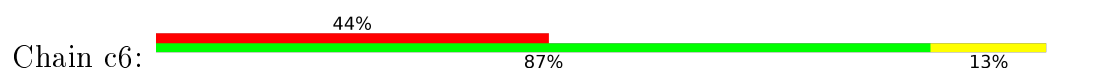




• Molecule 18: 40S ribosomal protein S16-A



• Molecule 18: 40S ribosomal protein S16-A

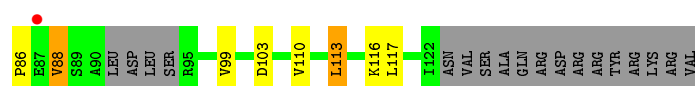


• Molecule 19: 40S ribosomal protein S17-A

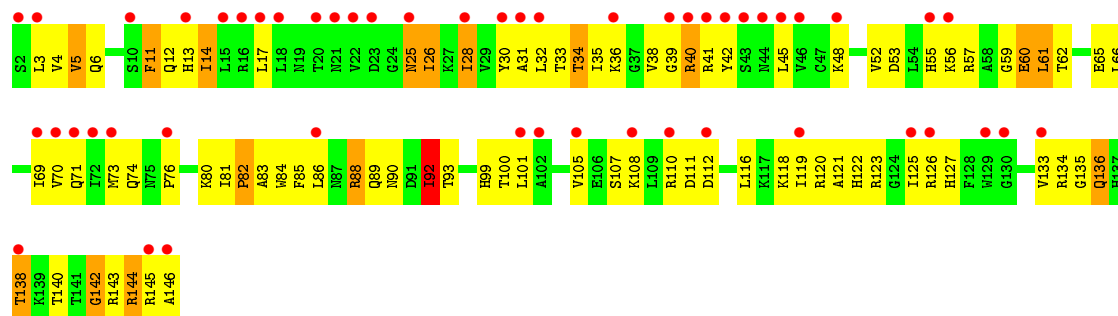
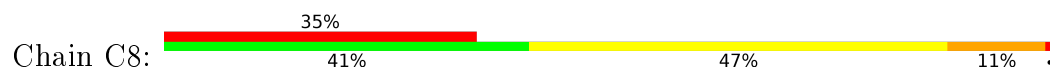


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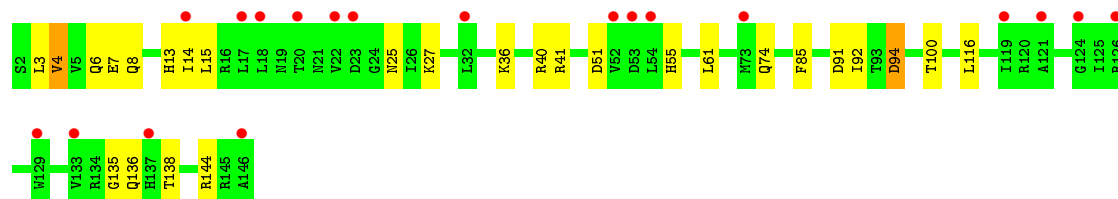
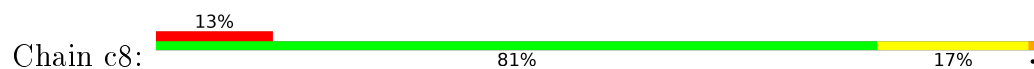




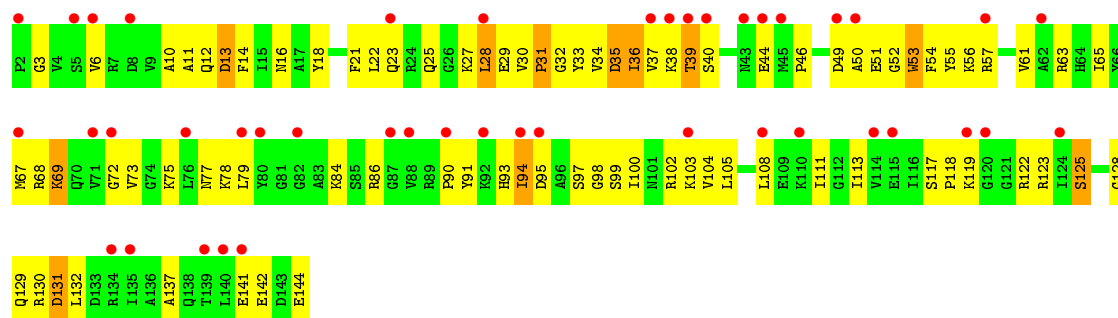
- Molecule 20: 40S ribosomal protein S18-A



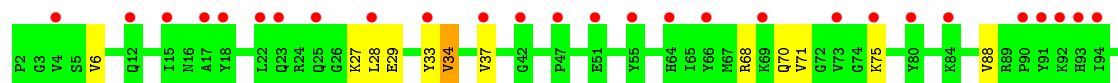
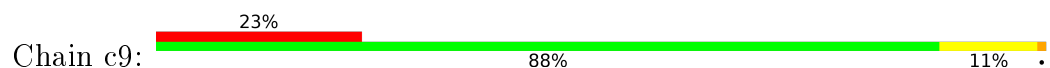
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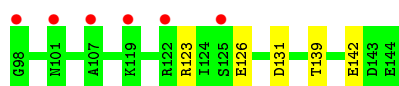


- Molecule 21: 40S ribosomal protein S19-A

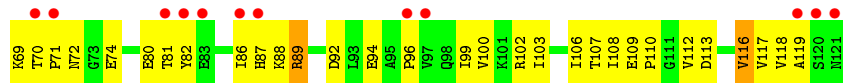
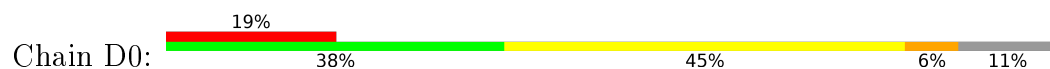


- Molecule 21: 40S ribosomal protein S19-A

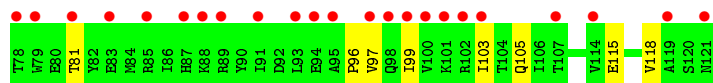
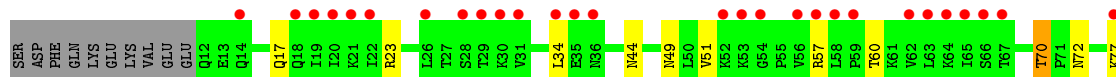
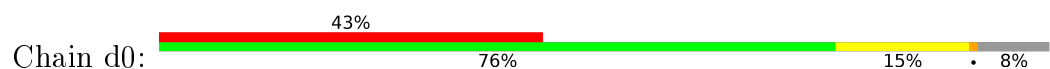




- Molecule 22: 40S ribosomal protein S20



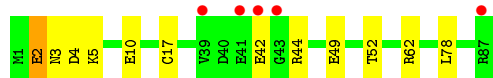
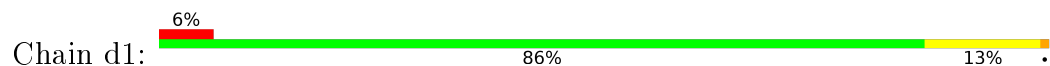
- Molecule 22: 40S ribosomal protein S20



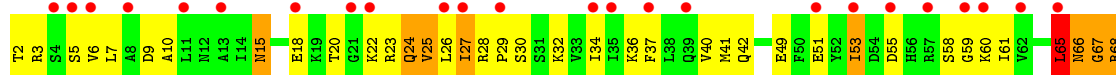
- Molecule 23: 40S ribosomal protein S21-A

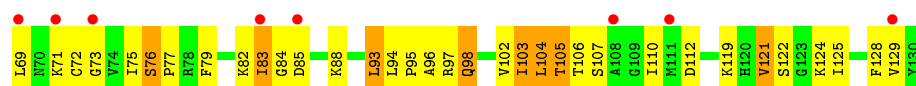


- Molecule 23: 40S ribosomal protein S21-A



- Molecule 24: 40S ribosomal protein S22-A

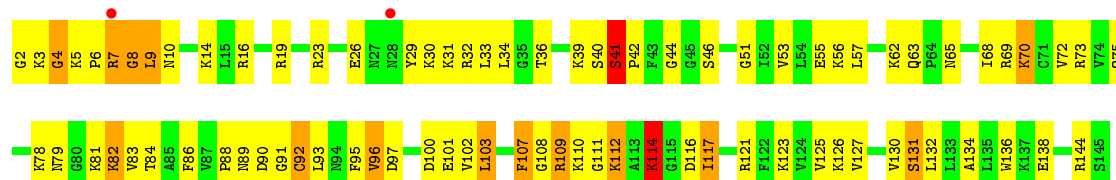
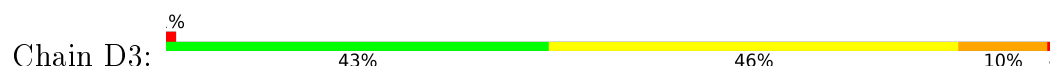




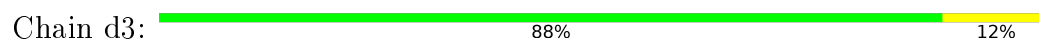
- Molecule 24: 40S ribosomal protein S22-A



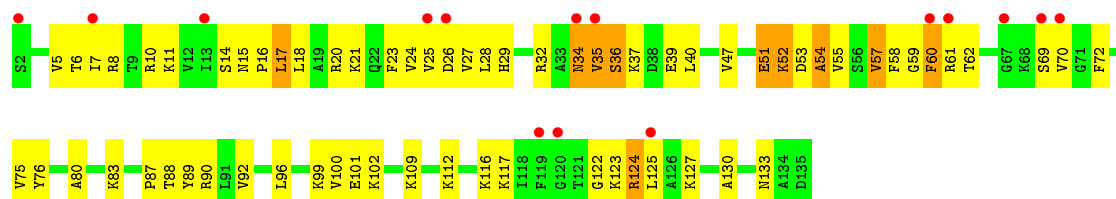
- Molecule 25: 40S ribosomal protein S23-A



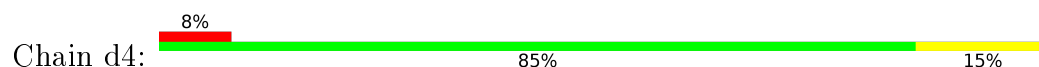
- Molecule 25: 40S ribosomal protein S23-A



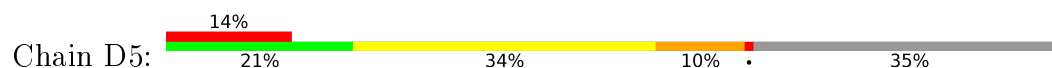
- Molecule 26: 40S ribosomal protein S24-A

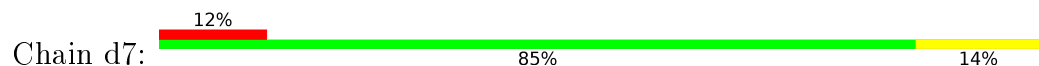


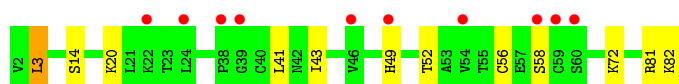
- Molecule 26: 40S ribosomal protein S24-A



- Molecule 27: 40S ribosomal protein S25-A



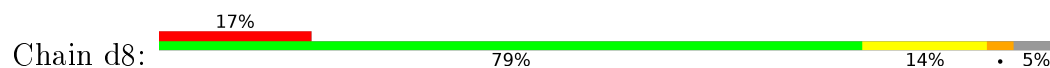




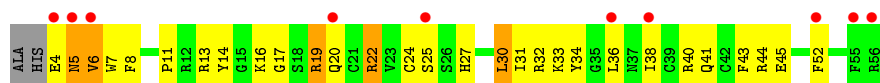
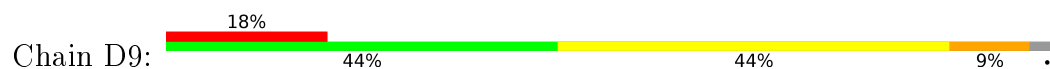
- Molecule 30: 40S ribosomal protein S28-A



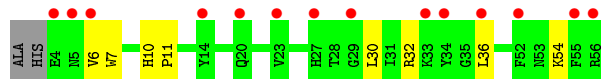
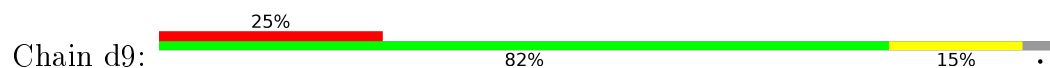
- Molecule 30: 40S ribosomal protein S28-A



- Molecule 31: 40S ribosomal protein S29-A



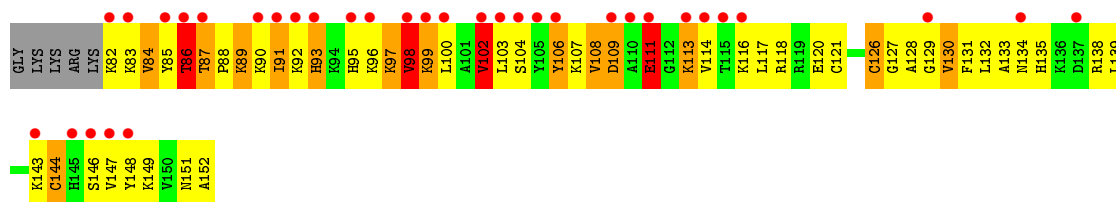
- Molecule 31: 40S ribosomal protein S29-A



- Molecule 32: 40S ribosomal protein S30-A



- Molecule 33: Ubiquitin-40S ribosomal protein S31



- Molecule 33: Ubiquitin-40S ribosomal protein S31

- Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

- Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

- Molecule 35: Suppressor protein STM1

[illegible]

Chain 1:

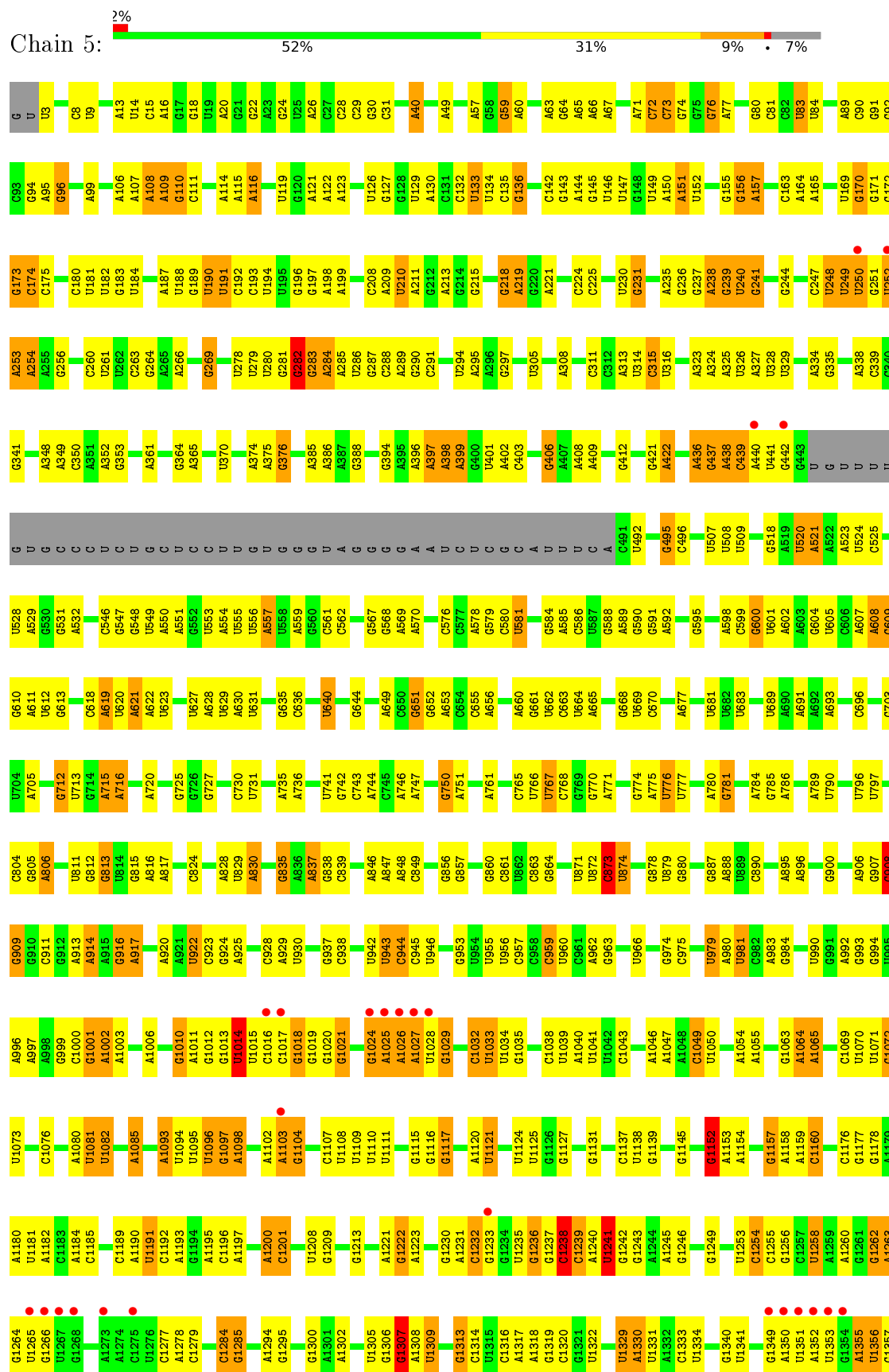
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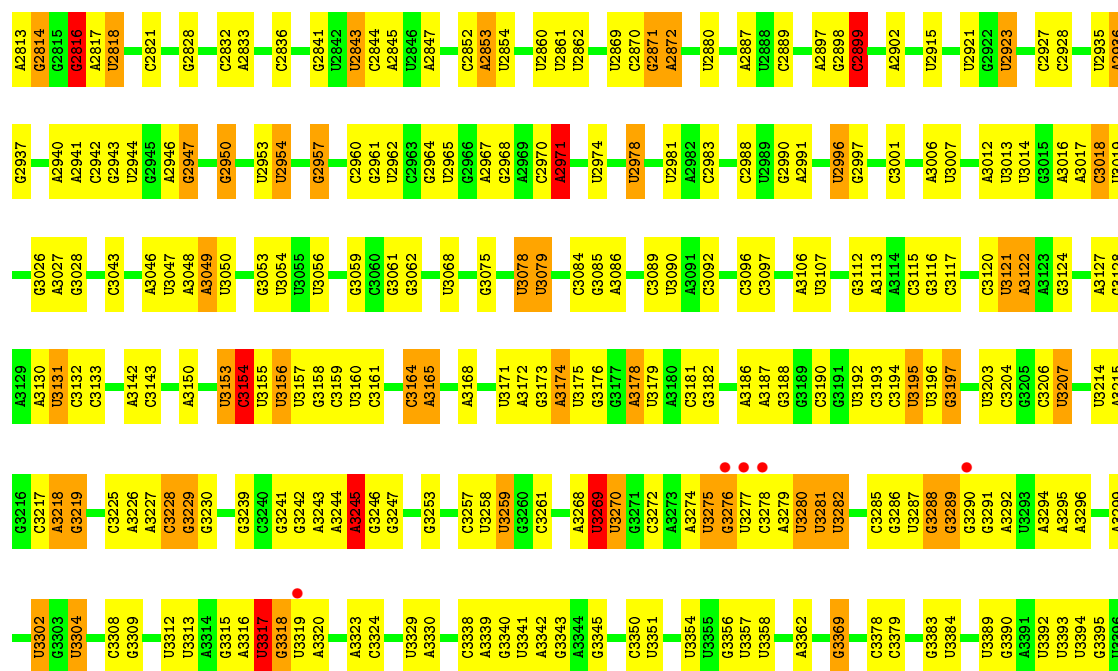


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	A3244	U3155	G3059	G2972	U2882	U2795	C2682	U2571	U2501	A2439	G2314	A2214	G2111
	G3245	G3158	U3066	U2973	U2883	U2796	U2683	C2572	A2502	G2440	C2331	A2215	U2112
	G3246	C3067	C3067	U2978	C2884	G2796	U2684	C2573	U2504	C2444	U2332	G2216	A2113
	G3247	U3160	U3068	U2979	U2886	C2798	C2685	C2574	U2513	A2445	G2333	A2219	G2115
		C3161	C3072	C2983	A2887	U2799	U2686	U2581	C2507	U	U2334	A2220	A2120
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	G3253	C3164		C2987	C2889	A2801	U2688	G2585	U2509	G	U2336	A2224	G2122
	G3254	A3165	A3077	U2987	A2890	A2802	A2689	G2586	U2510	A	C2337	A2225	G2123
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	G3256	A3167	G3079	U2989	G2895	U2808	A2694	C2593	U2512	G	C2339	U2227	
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	G3260	U3169		A2991	A2897	C2810	A2696		A2514	G		A2229	U2137
	C3261	A3170	C3084	U2992	G2898	G2814	A2697	G2606	U2516	U	G2355		A2138
		G3173	G3085	G2993	C2899	G2815		G2607	A2520	A	A2356	A2242	U2140
	A3267	A3174	A3086	U2996	A2900	G2816	A2703	G2610	U2521	G	A2363	A2244	A2144
	A3268	U3175	A3087	U2997	G2901	A2817	A2705	U2611	G2522	A	A2372	G2249	A2145
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	U3270	G3177	C3089	U3000	U2905	A2819	G2707	U2613	A2524	A	C2374	U2254	
	G3271	A3178	U3090	C3001	G2914	A2820	G2714	G2615	G2525	G	G2375	A2255	G2150
	C3272	U3179	C3091	A3005	U2915	U2827	U2719	U2616	A2529	U		A2256	
	G3275	A3180	C3092	A3006	U2916	G2828		U2617	U2532	G	A2384	A2257	G2155
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	G3277	U3095	U3095	A3012	A2919	G2834	U2724	G2621	G2534	G		G2261	A2158
	C3278	C3096	C3097	U3013	U2923	U2835	U2725	C2622	A2535	A	G2391	C2267	U2162
	A3279	U3101	U3014	U3014	U2924	C2836	C2726	G2623	A2536	C	C2392	C2268	C2163
	U3280	G3101	G3101	C3022	C2927	A2837	A2727	G2624	A2537	U	C2393		
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	G3284	G3197		A3024	C2929	G2839	U2729	G2632	C2538	C		G2273	G2169
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	G3286	G3199	A3113	A3026	A2934	U2843	C2737		U2541	G	G2400	C2278	
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	A3294	A3208	A3122	C3034	C2942	U2852	U2752	U2653	A2547	G	C2406	C2285	U2186
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		G3216	U3131	U3038	A2947	U2857	A2762	G2658	U2553	U	U2417	U2294	G2194
	G3303	A3217	A3134	C3039	C2948	C2857		G2659	A2554	A		A2295	
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- Molecule 36: 25S ribosomal RNA

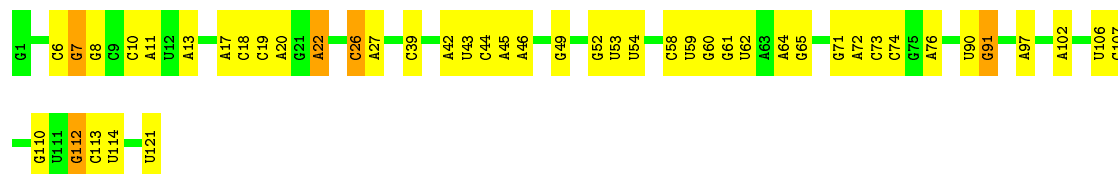


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G2714	A2601	G2385	C2276	G2201	A	C	C	A1879	U1785	A1683	A1589	U1494	
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G2724	G2606	G2396	A2281	U2203	U	U	U	A1886	A1787		G1593	U1496	C1385
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G2726	G2608		G2288	U2205	U	U	U	A1893	C1792	U1688	U1595	G1498	G1387
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A2748	G2639	A2412	G2315	C2227	U	U	U	U1942	U1814	G1735	G1631	C1550	
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G2786	U2681	G2442	A2357	A2251	C	C	C	U	C1849	G1762	G1658	A1571	G1473
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G2796	U2683	C2444	C2359	G2253	U	U	U	G	A1851	U1764	C1660	C1573	A1477
C2797	C2684	U	A2363	A2254	C	C	C	G	U1852	U1765	C1661	A1574	
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G2800	G2690	G	C2365	G2256	C	C	C	C	U1854	G1767	U1663	G1576	A1482
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				A2265	C	C	C	U	G1863	G1776			
				G2266	C	C	C	U	C1864	G1777			
				U2267	C	C	C	U	G1865	G1778			
				A2268	C	C	C	U	A1866	G1779			
				G2269	C	C	C	U	G1867	G1780			
				U2270	C	C	C	U	C1868	G1781			
				A2271	C	C	C	U	G1869	G1782			



• Molecule 37: 5S ribosomal RNA

Chain 3: 62% 34%



• Molecule 37: 5S ribosomal RNA

Chain 7: 64% 30% 6%

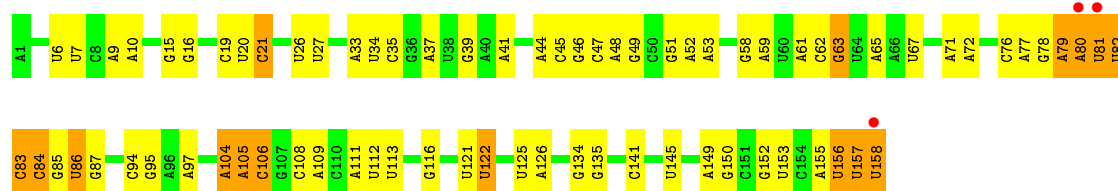


• Molecule 38: 5.8S ribosomal RNA

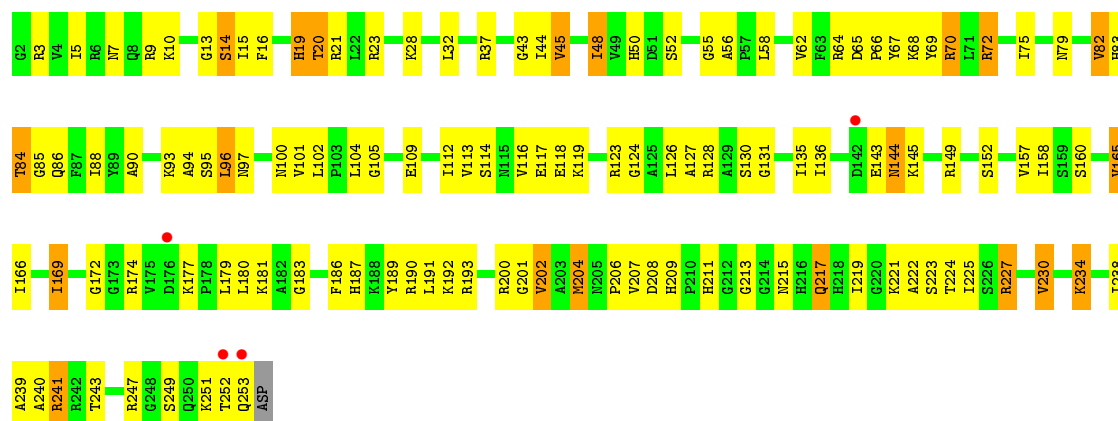
Chain 4: 62% 29% 9%



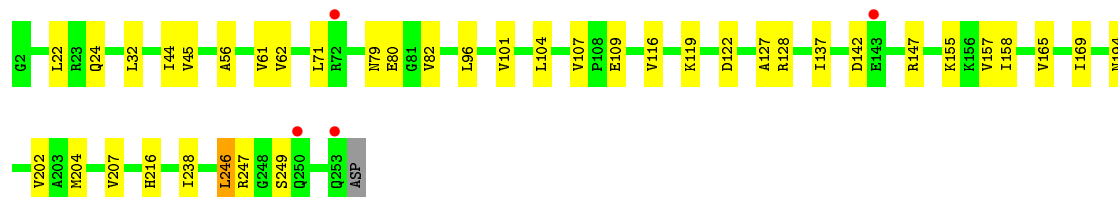
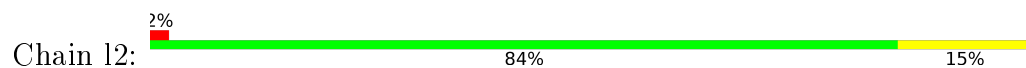
• Molecule 38: 5.8S ribosomal RNA



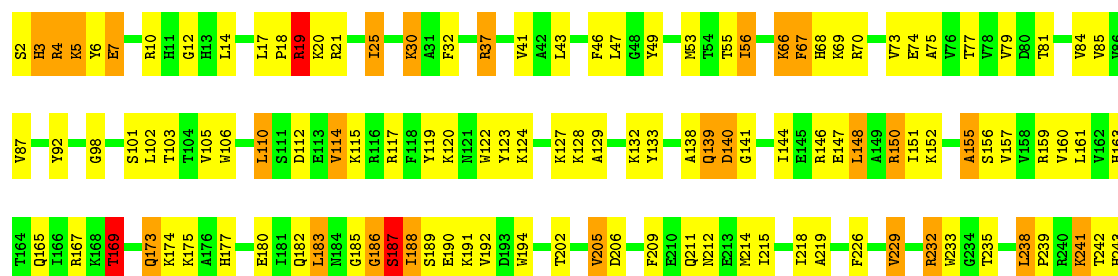
• Molecule 39: 60S ribosomal protein L2-A

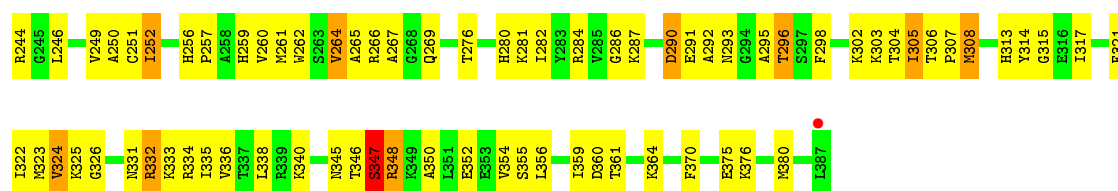


• Molecule 39: 60S ribosomal protein L2-A



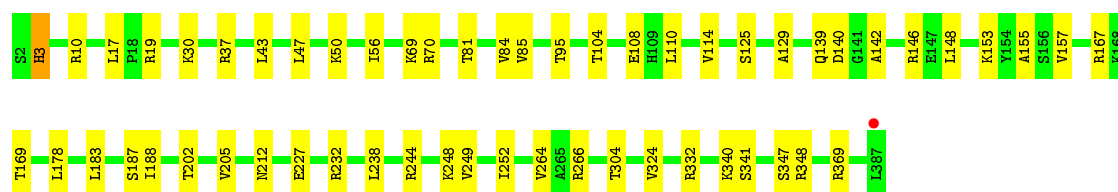
• Molecule 40: 60S ribosomal protein L3





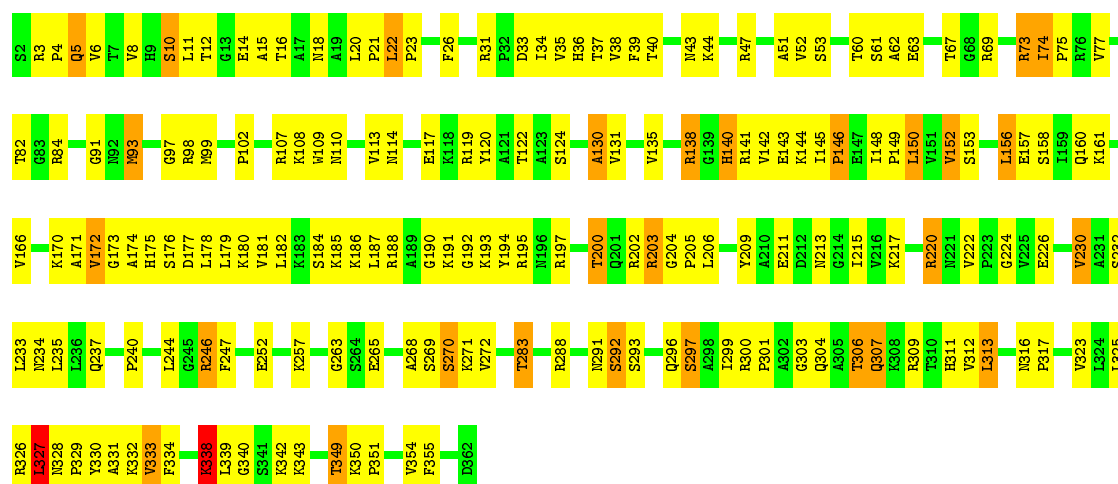
• Molecule 40: 60S ribosomal protein L3

Chain l3: 85% 14%



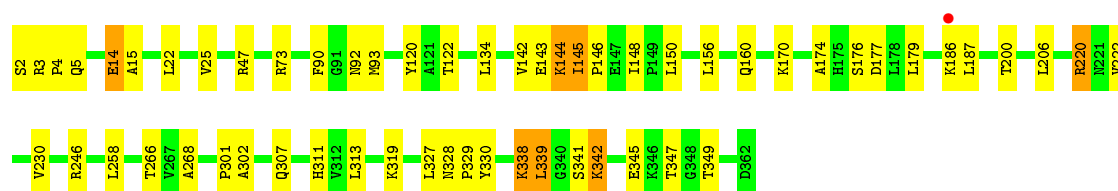
• Molecule 41: 60S ribosomal protein L4-A

Chain L4: 49% 42% 8%



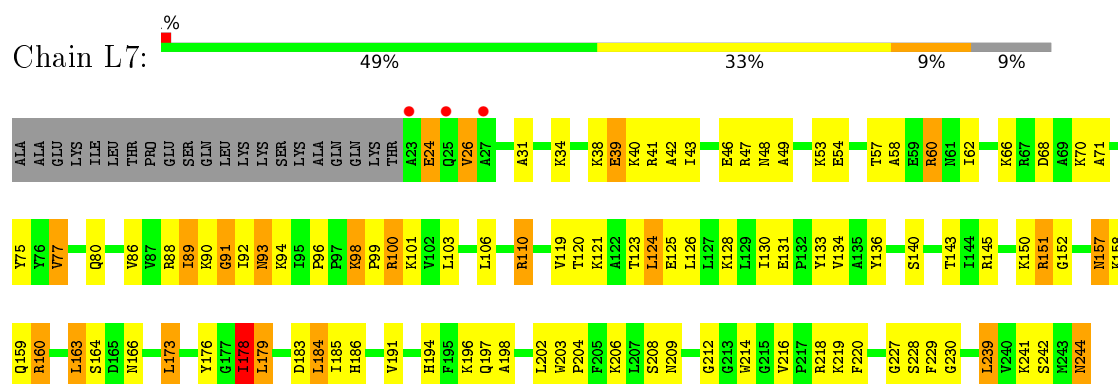
• Molecule 41: 60S ribosomal protein L4-A

Chain l4: 84% 14%

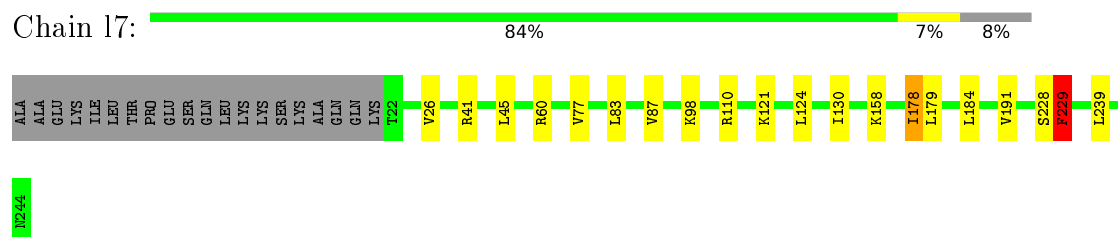


• Molecule 42: 60S ribosomal protein L5

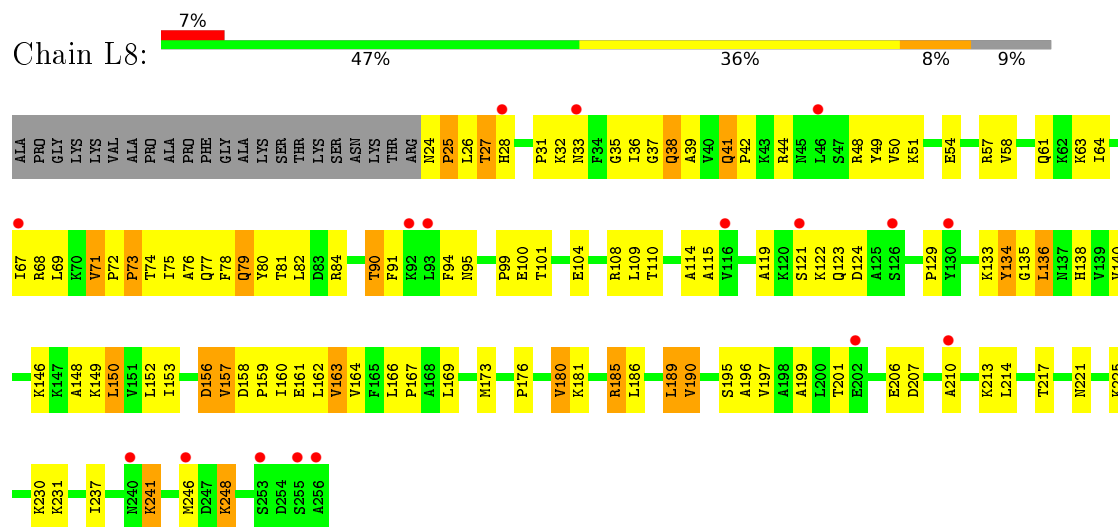
Chain L5: 17% 47% 45% 8%



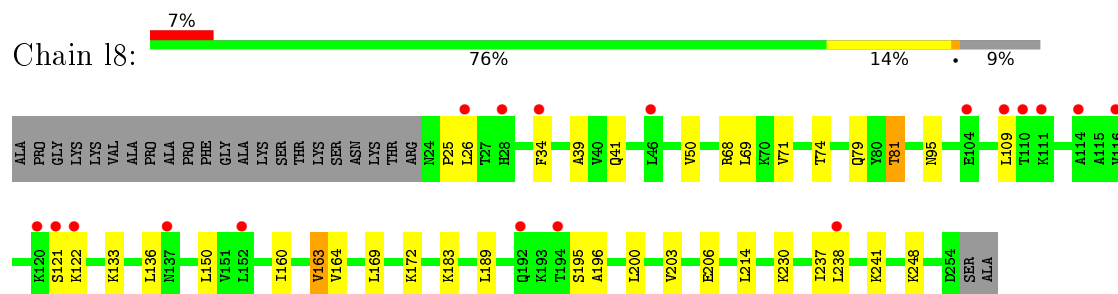
- Molecule 44: 60S ribosomal protein L7-A



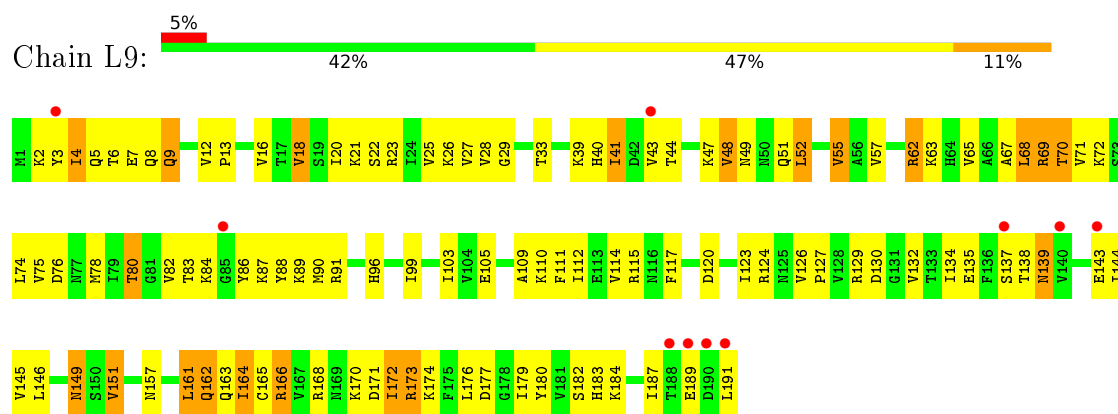
- Molecule 45: 60S ribosomal protein L8-A (eL8)



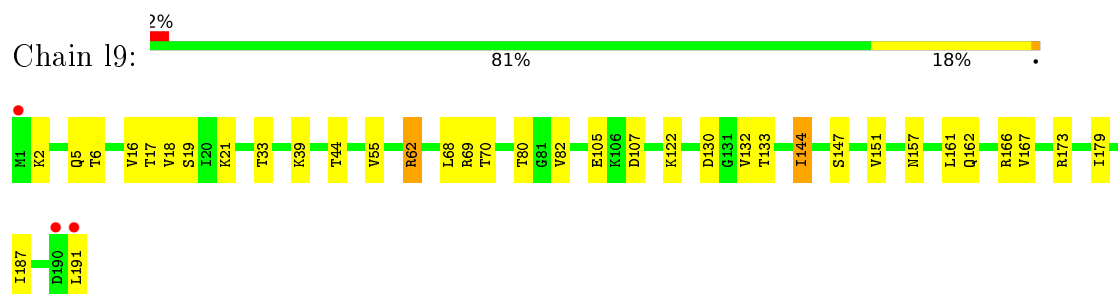
- Molecule 45: 60S ribosomal protein L8-A (eL8)



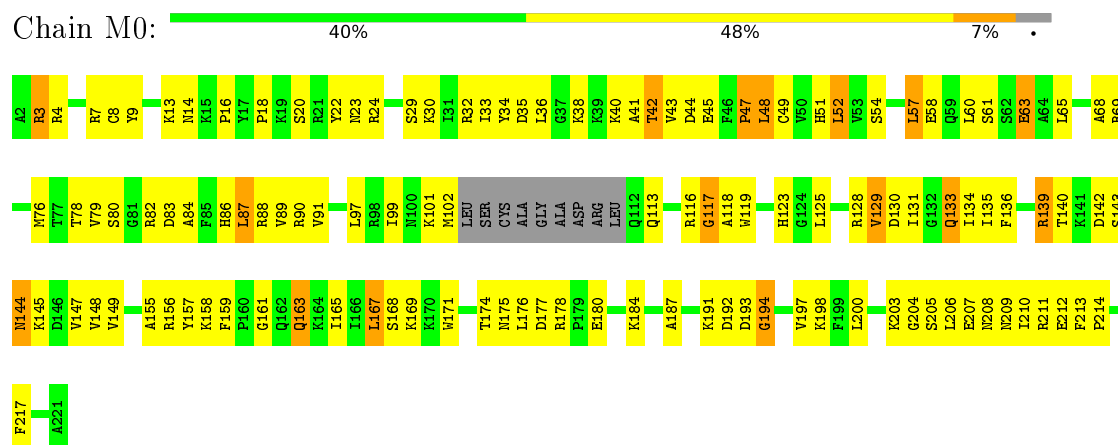
- Molecule 46: 60S ribosomal protein L9-A



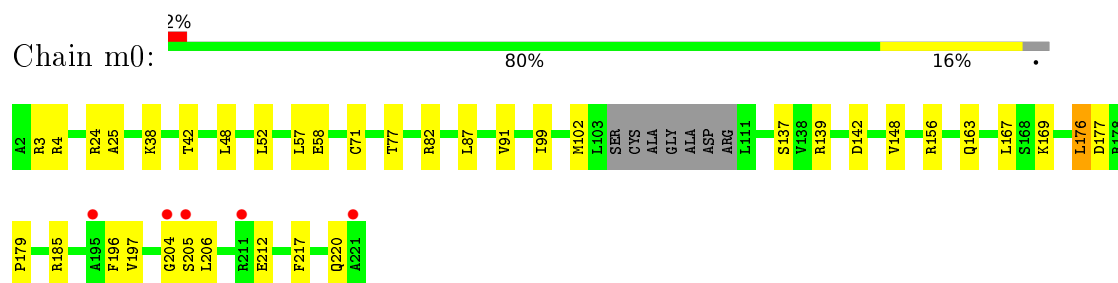
- Molecule 46: 60S ribosomal protein L9-A



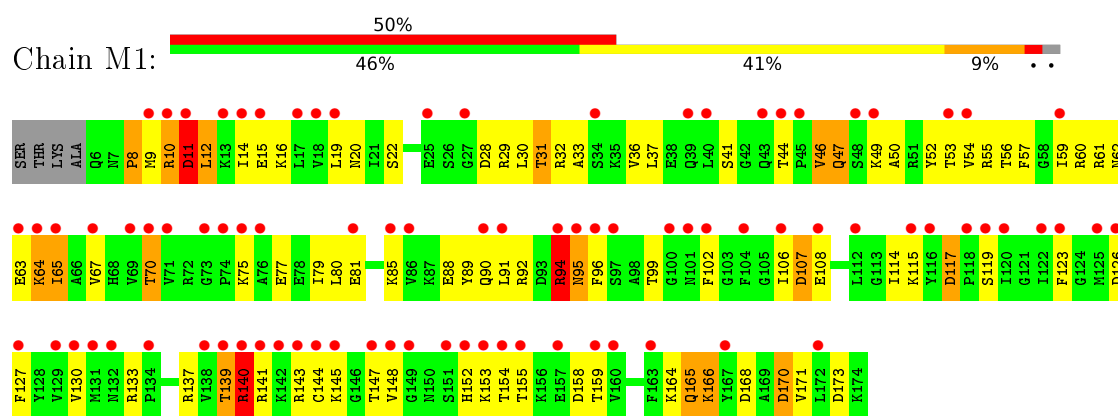
- Molecule 47: 60S ribosomal protein L10



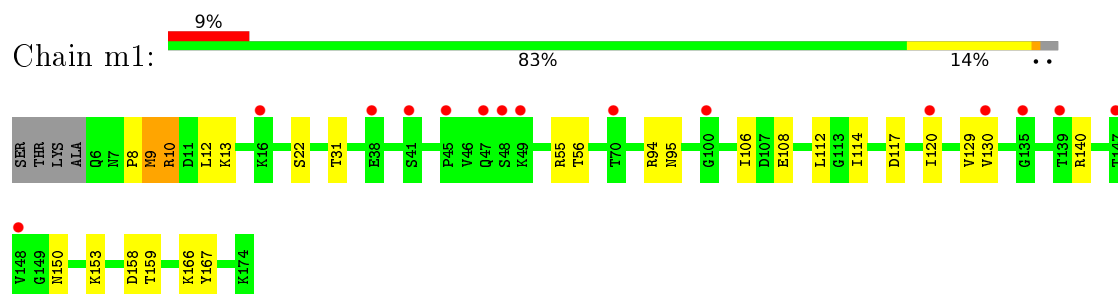
- Molecule 47: 60S ribosomal protein L10



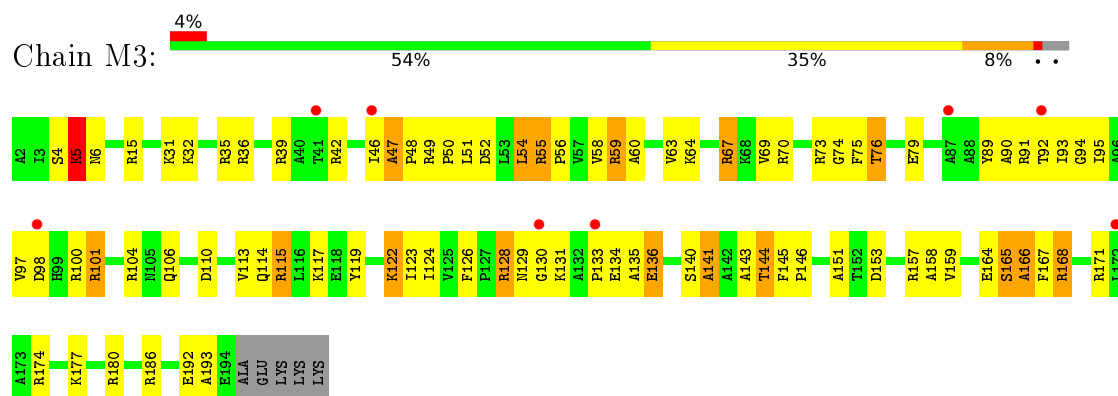
- Molecule 48: 60S ribosomal protein L11-B



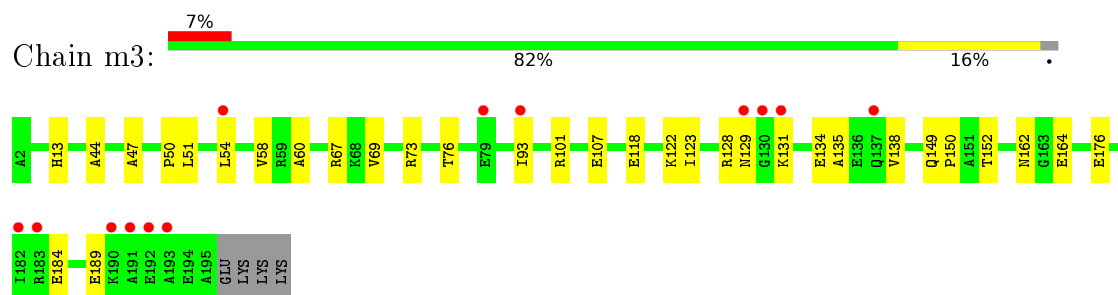
• Molecule 48: 60S ribosomal protein L11-B



• Molecule 49: 60S ribosomal protein L13-A

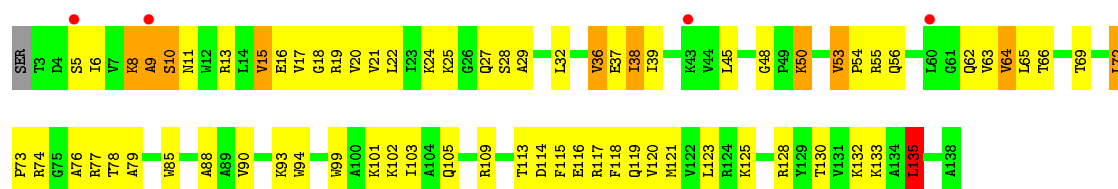


• Molecule 49: 60S ribosomal protein L13-A



• Molecule 50: 60S ribosomal protein L14-A





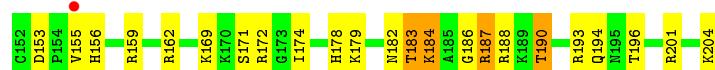
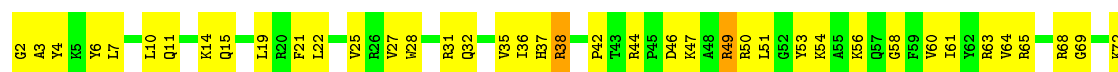
• Molecule 50: 60S ribosomal protein L14-A

Chain m4: 88% 12%



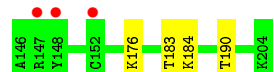
• Molecule 51: 60S ribosomal protein L15-A

Chain M5: 48% 45% 7%



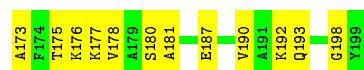
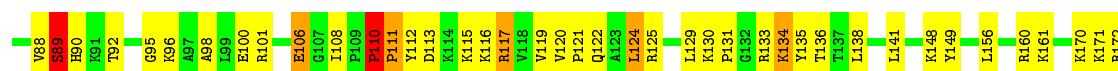
• Molecule 51: 60S ribosomal protein L15-A

Chain m5: 9% 90% 10%

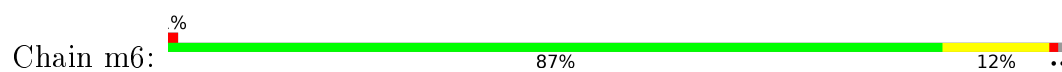


• Molecule 52: 60S ribosomal protein L16-A

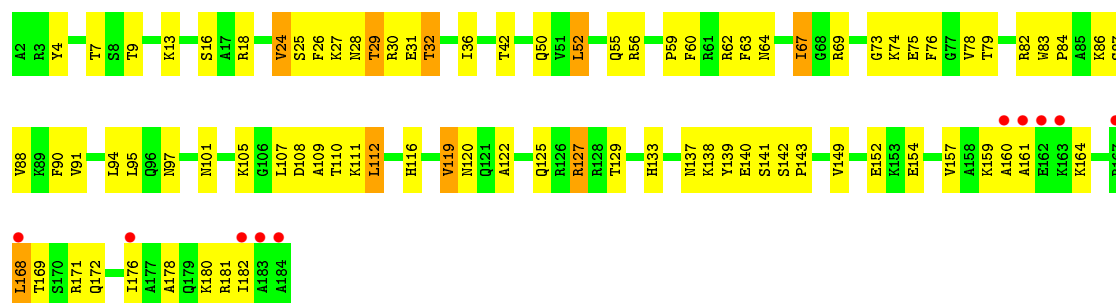
Chain M6: 53% 42% 5%



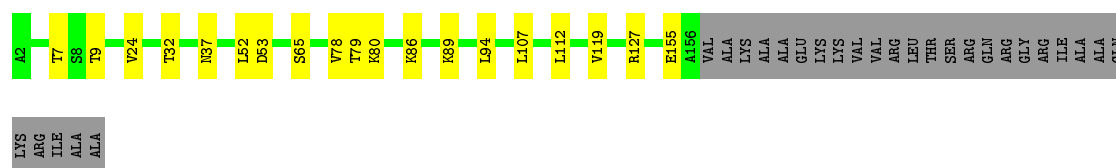
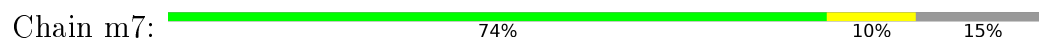
• Molecule 52: 60S ribosomal protein L16-A



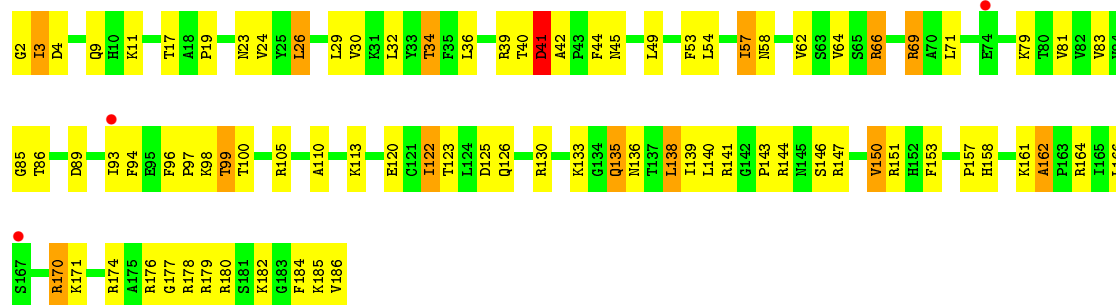
- Molecule 53: 60S ribosomal protein L17-A



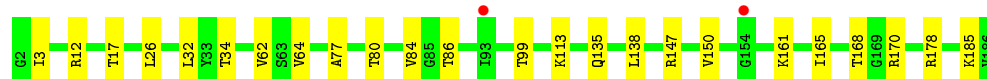
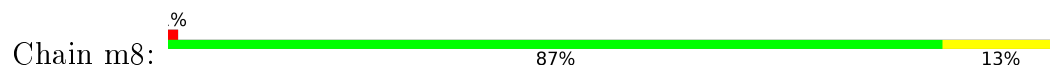
- Molecule 53: 60S ribosomal protein L17-A



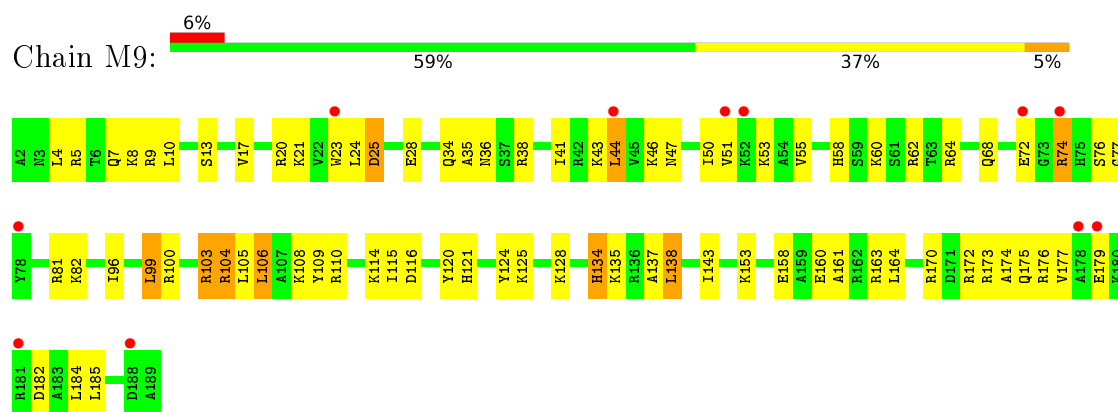
- Molecule 54: 60S ribosomal protein L18-A



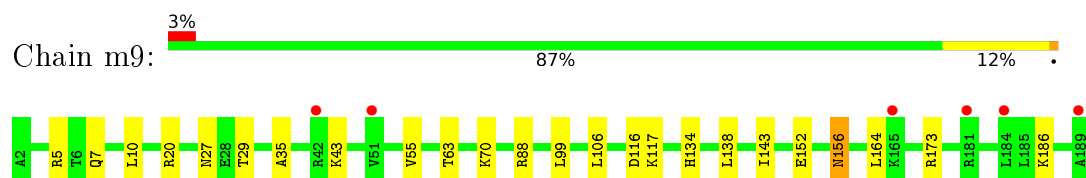
- Molecule 54: 60S ribosomal protein L18-A



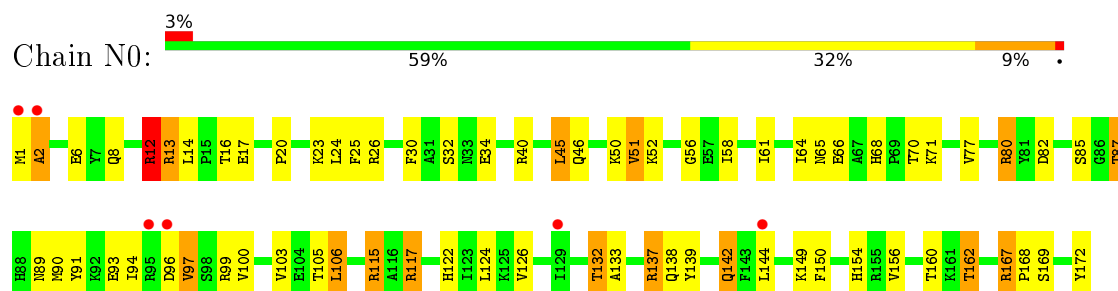
- Molecule 55: 60S ribosomal protein L19-A



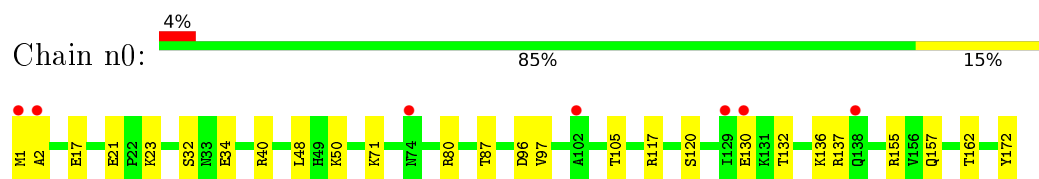
- Molecule 55: 60S ribosomal protein L19-A



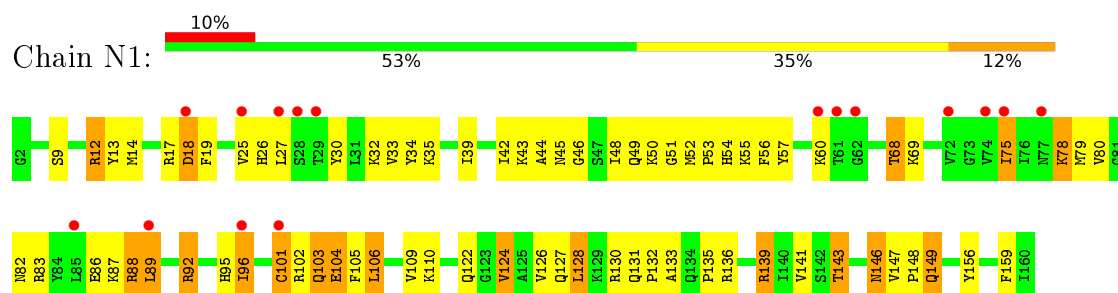
- Molecule 56: 60S ribosomal protein L20-A



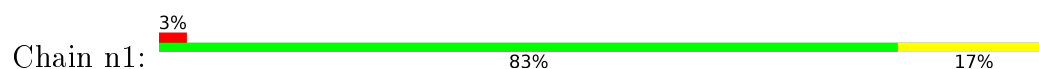
- Molecule 56: 60S ribosomal protein L20-A

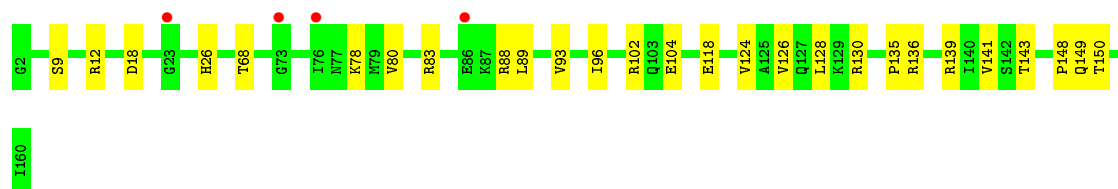


- Molecule 57: 60S ribosomal protein L21-A

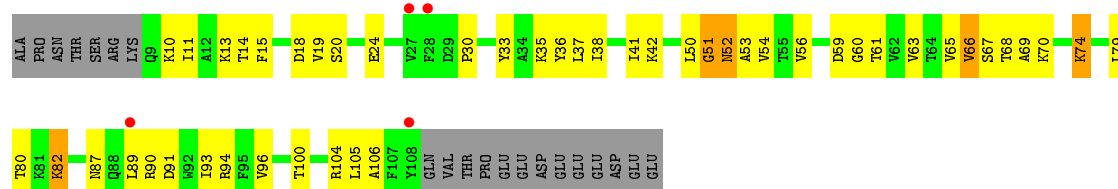
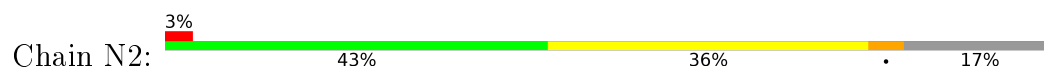


- Molecule 57: 60S ribosomal protein L21-A





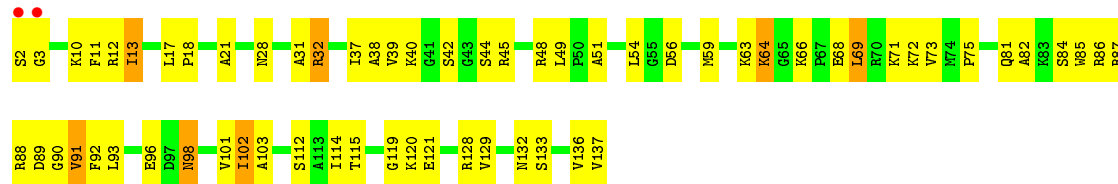
- Molecule 58: 60S ribosomal protein L22-A



- Molecule 58: 60S ribosomal protein L22-A



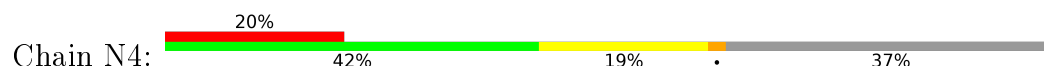
- Molecule 59: 60S ribosomal protein L23-A



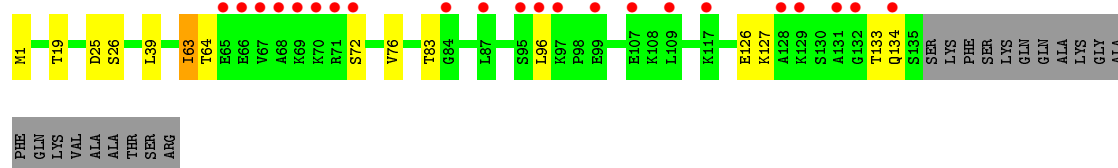
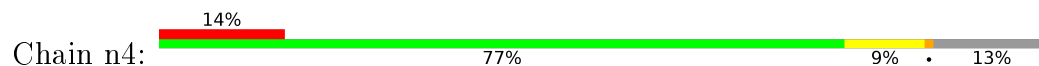
- Molecule 59: 60S ribosomal protein L23-A



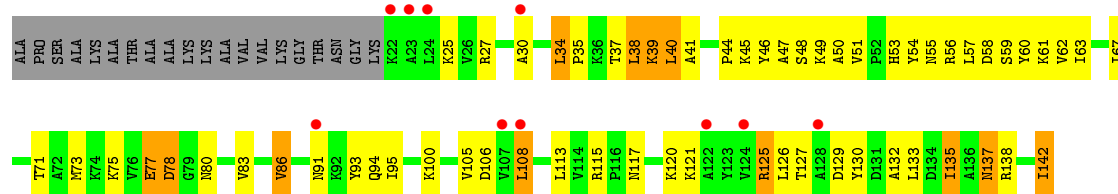
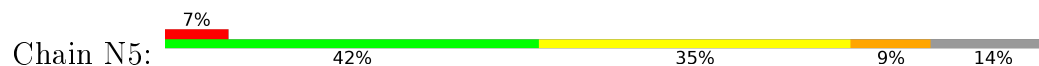
- Molecule 60: 60S ribosomal protein L24-A



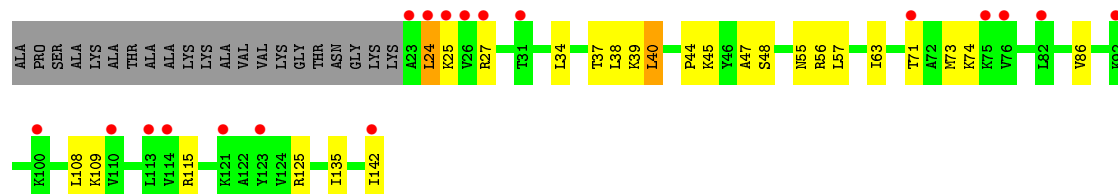
- Molecule 60: 60S ribosomal protein L24-A



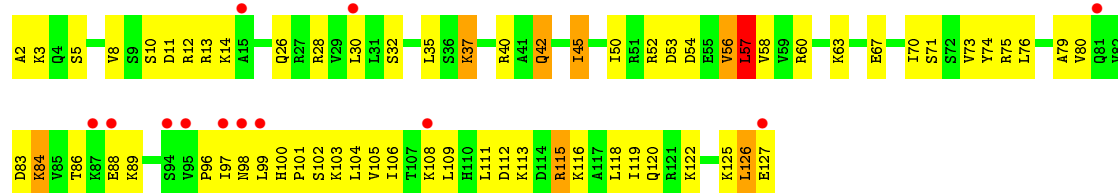
- Molecule 61: 60S ribosomal protein L25



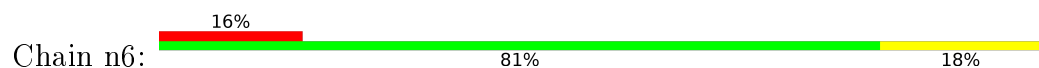
- Molecule 61: 60S ribosomal protein L25

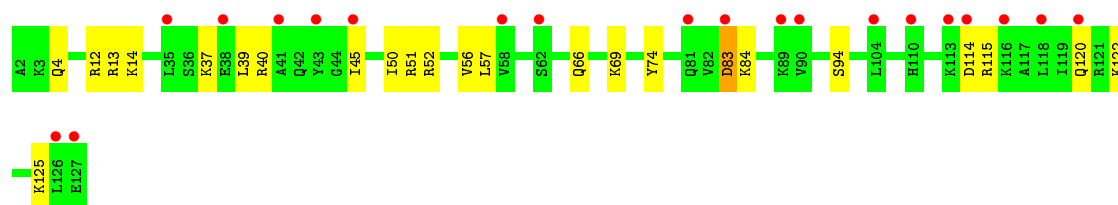


- Molecule 62: 60S ribosomal protein L26-A

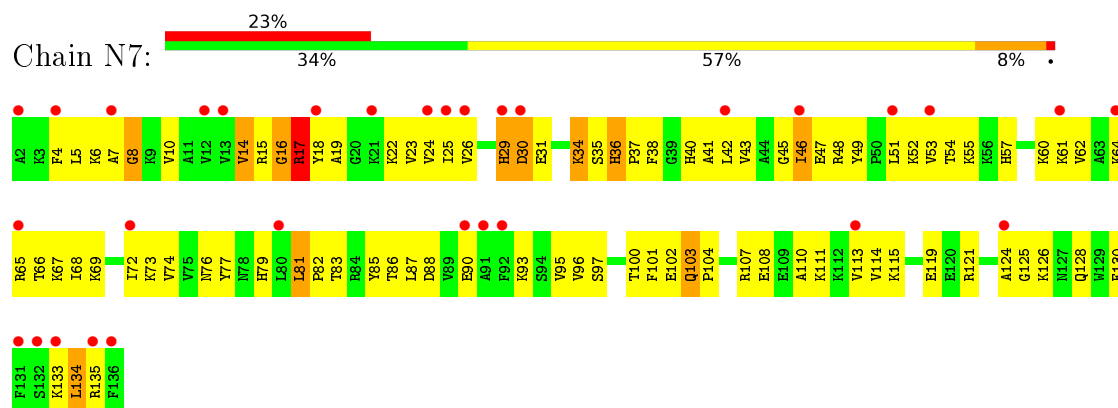


- Molecule 62: 60S ribosomal protein L26-A

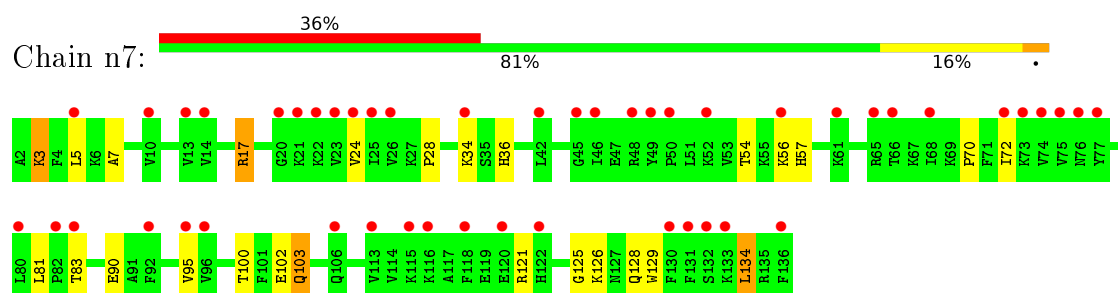




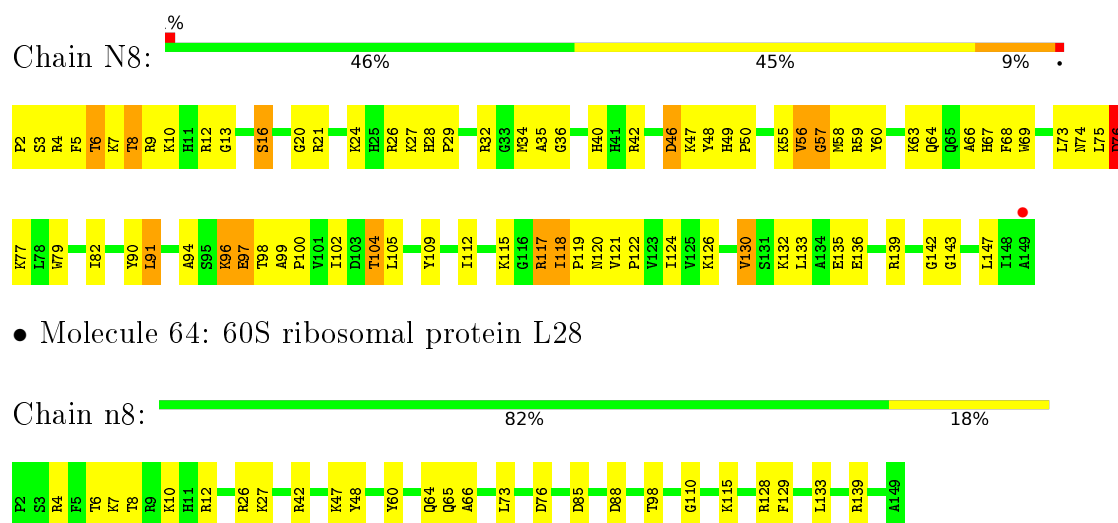
- Molecule 63: 60S ribosomal protein L27-A



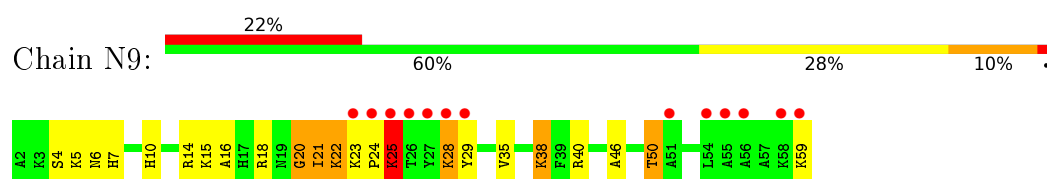
- Molecule 63: 60S ribosomal protein L27-A



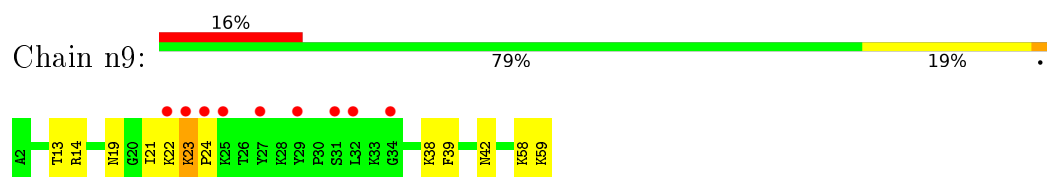
- Molecule 64: 60S ribosomal protein L28



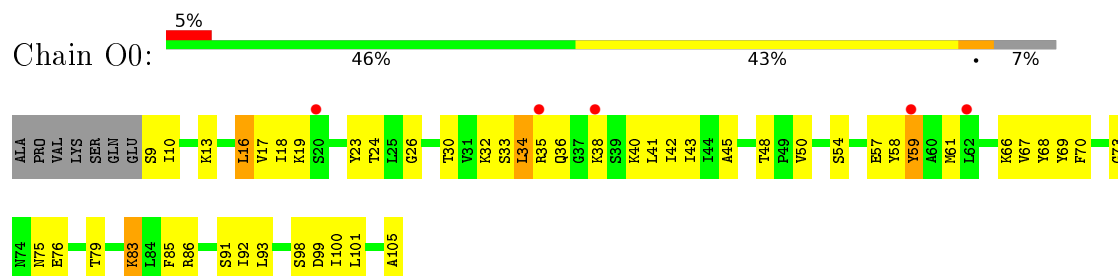
- Molecule 65: 60S ribosomal protein L29



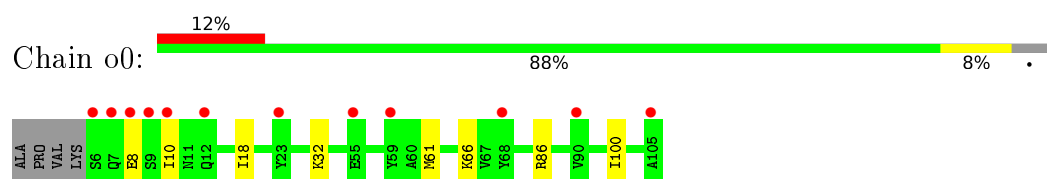
- Molecule 65: 60S ribosomal protein L29



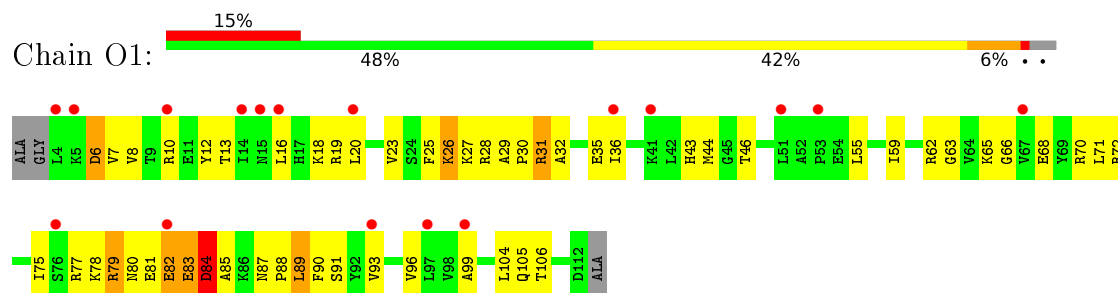
- Molecule 66: 60S ribosomal protein L30



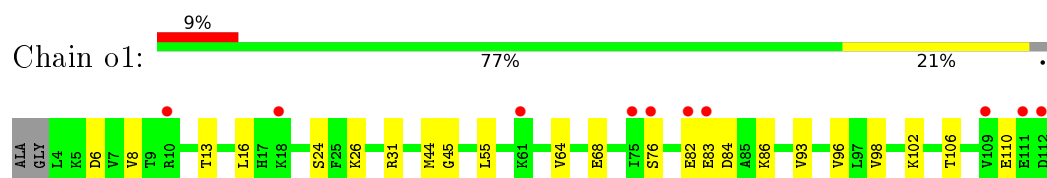
- Molecule 66: 60S ribosomal protein L30



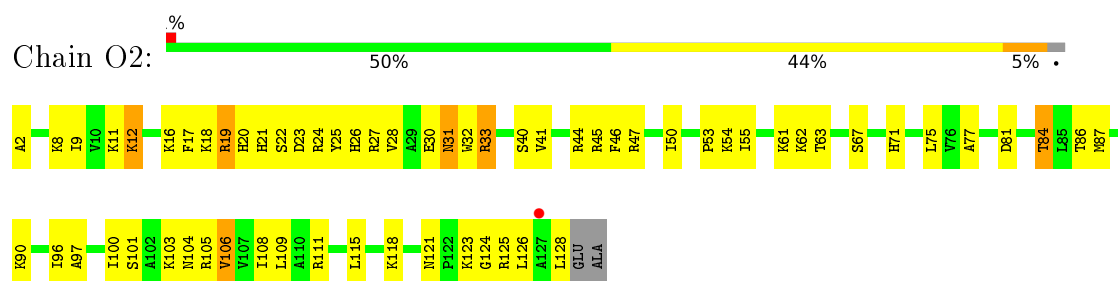
- Molecule 67: 60S ribosomal protein L31-A



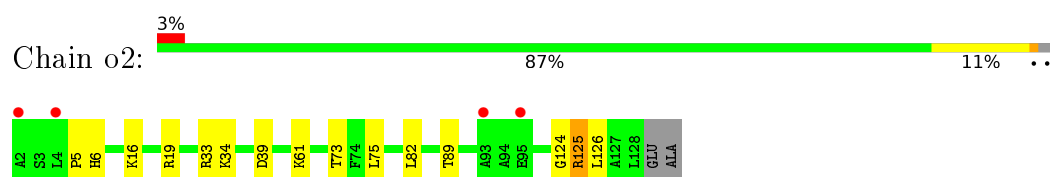
- Molecule 67: 60S ribosomal protein L31-A



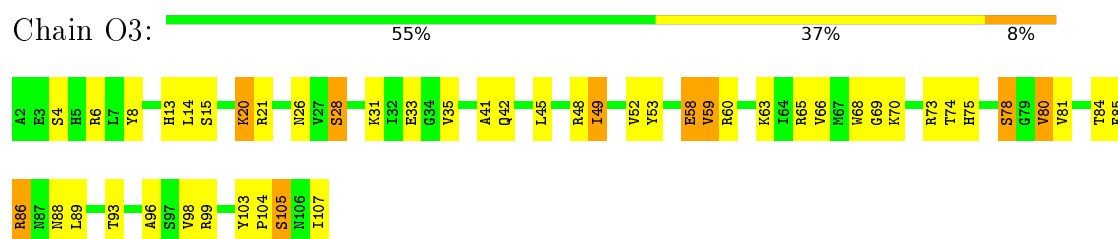
- Molecule 68: 60S ribosomal protein L32



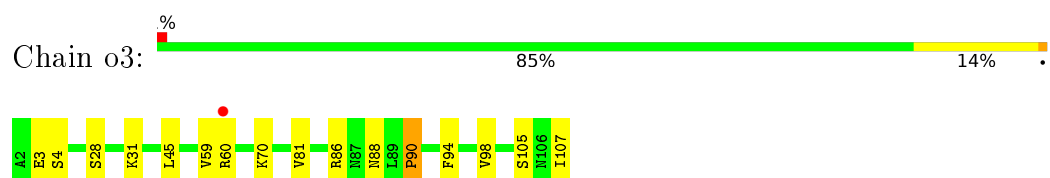
- Molecule 68: 60S ribosomal protein L32



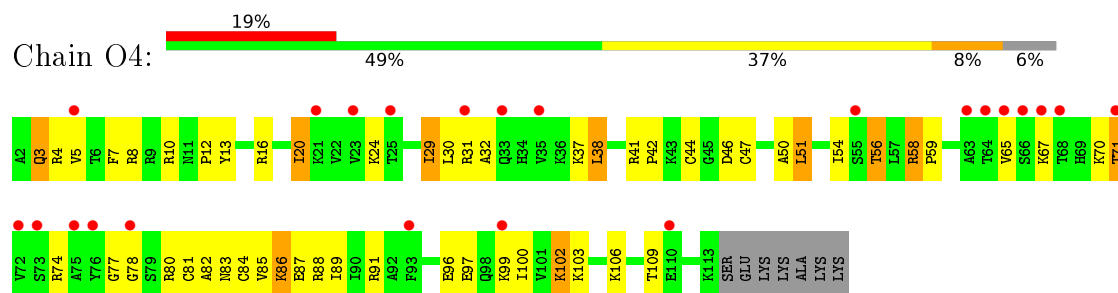
- Molecule 69: 60S ribosomal protein L33-A



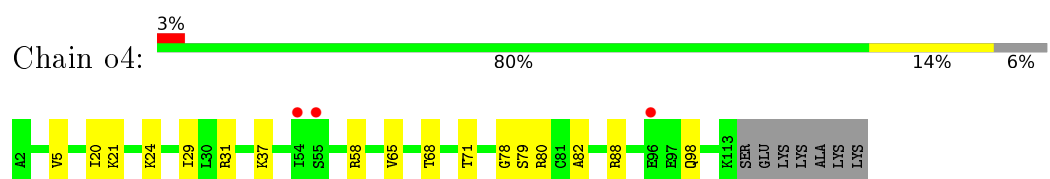
- Molecule 69: 60S ribosomal protein L33-A



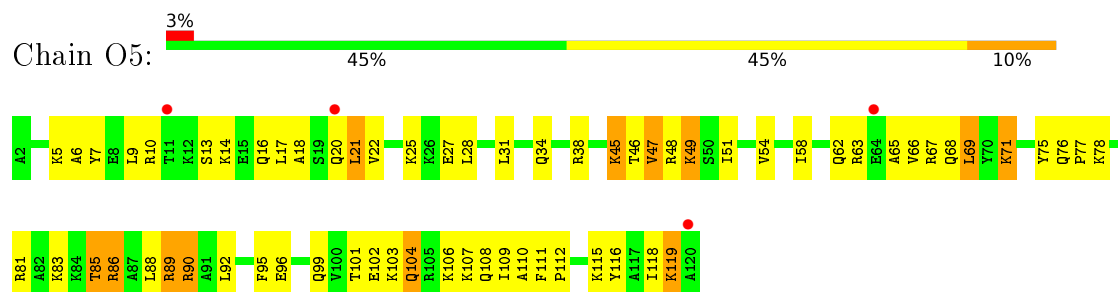
- Molecule 70: 60S ribosomal protein L34-A



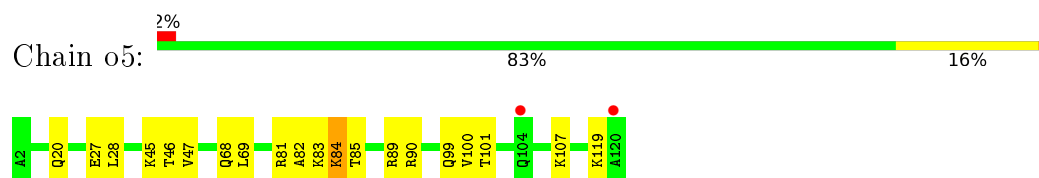
- Molecule 70: 60S ribosomal protein L34-A



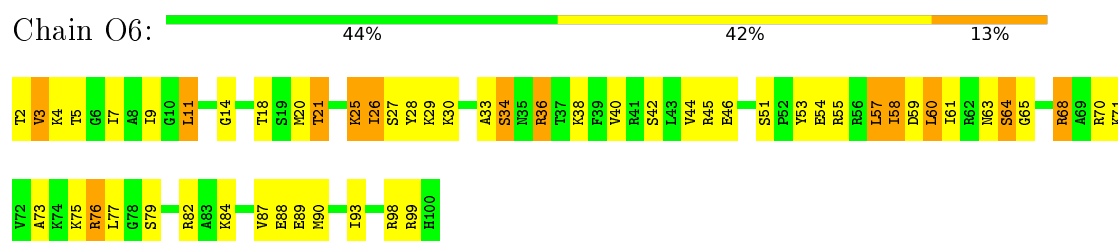
- Molecule 71: 60S ribosomal protein L35-A



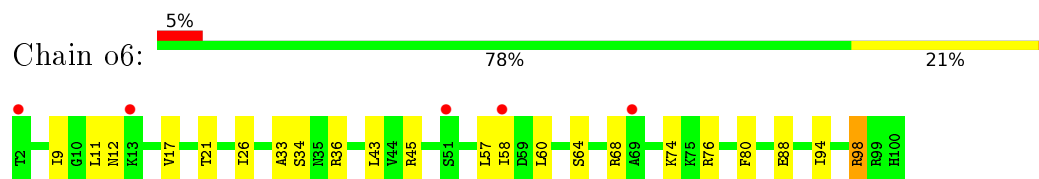
- Molecule 71: 60S ribosomal protein L35-A



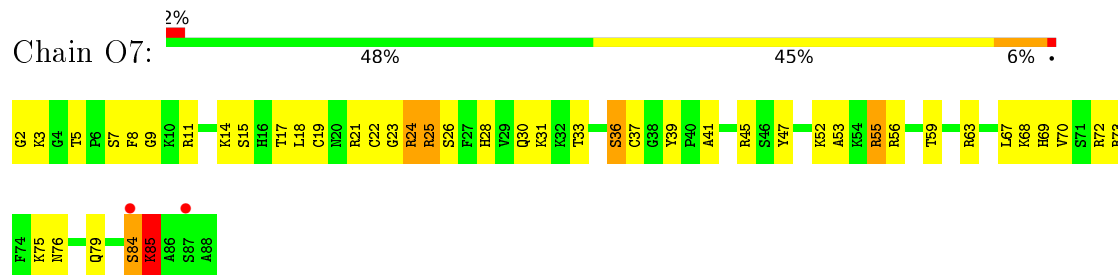
- Molecule 72: 60S ribosomal protein L36-A



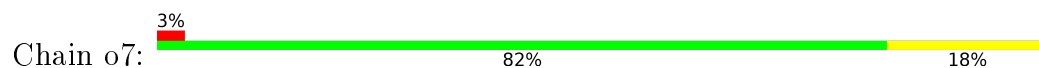
- Molecule 72: 60S ribosomal protein L36-A

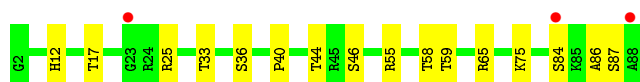


- Molecule 73: 60S ribosomal protein L37-A

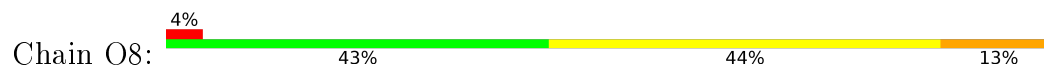


- Molecule 73: 60S ribosomal protein L37-A

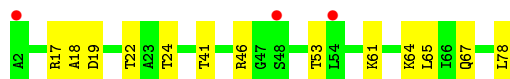
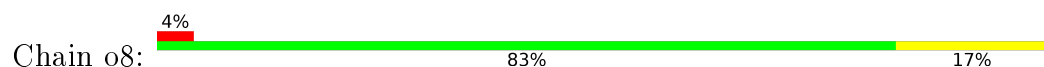




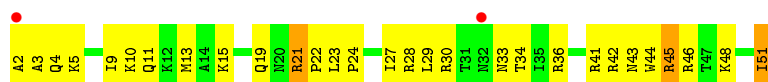
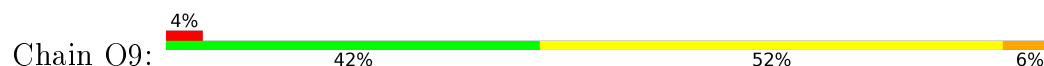
- Molecule 74: 60S ribosomal protein L38



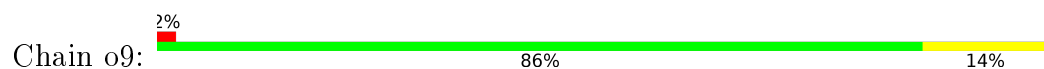
- Molecule 74: 60S ribosomal protein L38



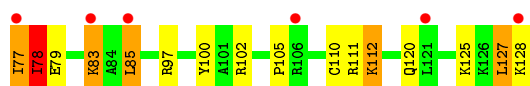
- Molecule 75: 60S ribosomal protein L39



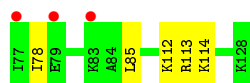
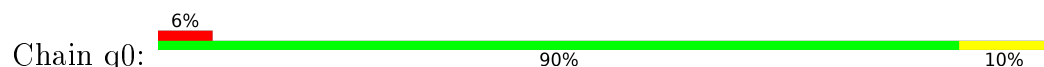
- Molecule 75: 60S ribosomal protein L39



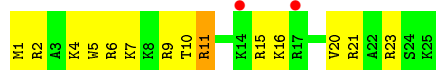
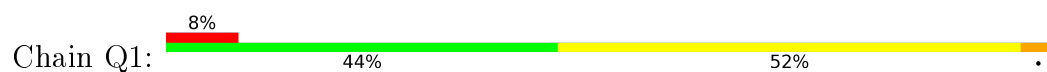
- Molecule 76: Ubiquitin-60S ribosomal protein L40



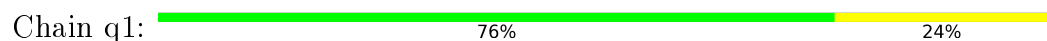
- Molecule 76: Ubiquitin-60S ribosomal protein L40



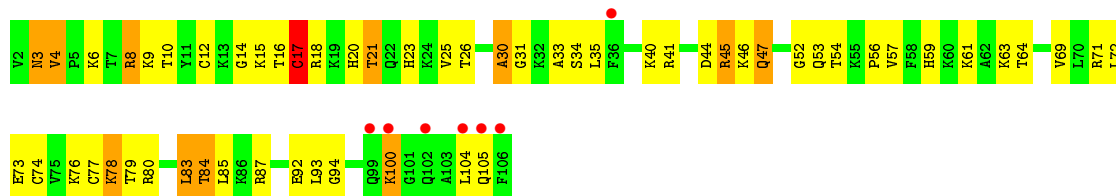
- Molecule 77: 60S ribosomal protein L41-A



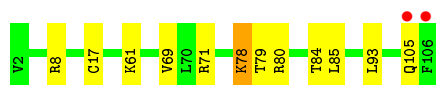
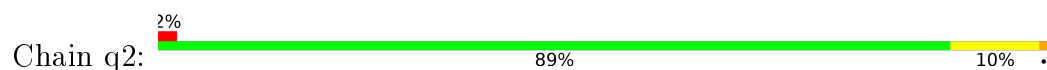
- Molecule 77: 60S ribosomal protein L41-A



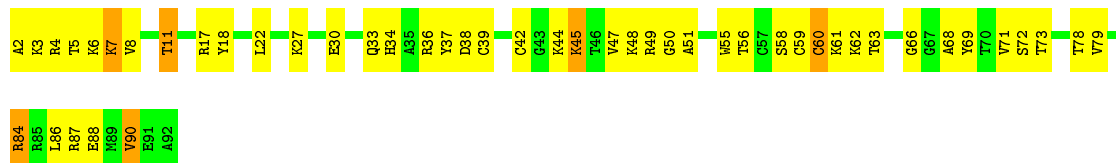
- Molecule 78: 60S ribosomal protein L42-A



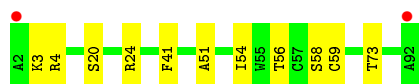
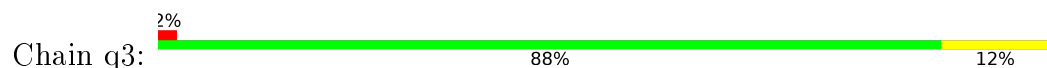
- Molecule 78: 60S ribosomal protein L42-A



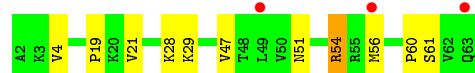
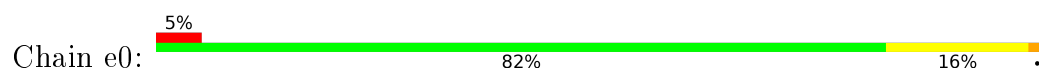
- Molecule 79: 60S ribosomal protein L43-A



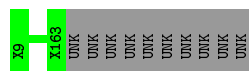
- Molecule 79: 60S ribosomal protein L43-A



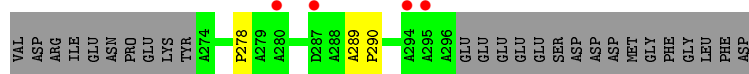
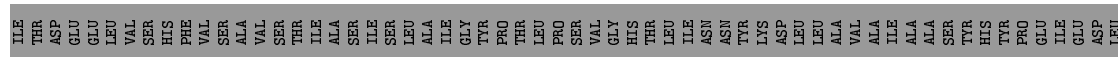
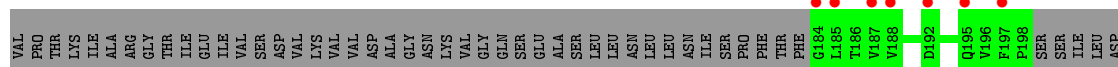
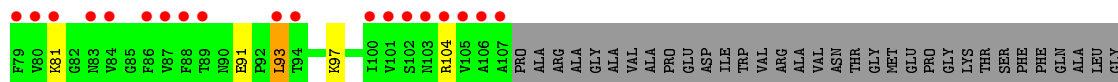
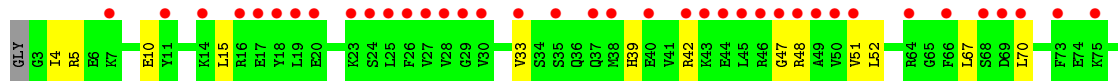
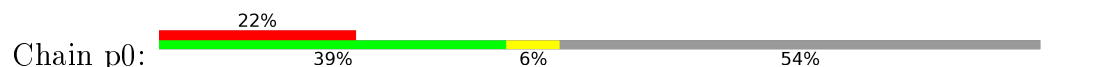
- Molecule 80: 40S ribosomal protein S30-A



- Molecule 81: 60S ribosomal protein L12-A (uL11)



- Molecule 82: 60S acidic ribosomal protein P0



- Molecule 83: 60S ribosomal protein P1 alpha/P2 beta



There are no outlier residues recorded for this chain.

- Molecule 84: 60S ribosomal protein P1 alpha/P2 beta



There are no outlier residues recorded for this chain.

- Molecule 85: DNA (5'-R(*CP*CP*(8AN)*(Pro)*(Pro))-3')



There are no outlier residues recorded for this chain.

- Molecule 85: DNA (5'-R(*CP*CP*(8AN)*(Pro)*(Pro))-3')

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	437.14Å 287.91Å 303.85Å 90.00° 98.76° 90.00°	Depositor
Resolution (Å)	149.05 – 3.10 149.04 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (149.05-3.10) 99.9 (149.04-3.10)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.238 , 0.284 0.248 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	73.7	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 70.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	402683	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SPS, MG, 8AN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.36	0/42467	0.88	40/66169 (0.1%)
1	6	0.41	0/42790	0.91	34/66673 (0.1%)
2	S0	0.25	0/1617	0.47	0/2215
2	s0	0.27	0/1623	0.51	0/2222
3	S1	0.25	0/1735	0.50	0/2335
3	s1	0.30	0/1748	0.52	0/2352
4	S2	0.28	0/1665	0.48	0/2263
4	s2	0.32	0/1665	0.54	0/2263
5	S3	0.27	0/1759	0.46	0/2368
5	s3	0.25	0/1759	0.44	0/2368
6	S4	0.29	0/2109	0.53	0/2839
6	s4	0.30	0/2109	0.54	0/2839
7	S5	0.25	0/1629	0.48	0/2202
7	s5	0.25	0/1629	0.47	0/2202
8	S6	0.29	0/1823	0.48	0/2439
8	s6	0.31	0/1779	0.51	0/2379
9	S7	0.26	0/1506	0.50	0/2028
9	s7	0.27	0/1516	0.48	0/2043
10	S8	0.32	0/1514	0.51	0/2021
10	s8	0.33	0/1514	0.53	0/2021
11	S9	0.27	0/1519	0.47	0/2035
11	s9	0.30	0/1519	0.49	0/2035
12	C0	0.28	0/790	0.53	2/1069 (0.2%)
12	c0	0.27	0/777	0.52	2/1049 (0.2%)
13	C1	0.32	0/1239	0.51	0/1673
13	c1	0.36	0/1194	0.56	1/1610 (0.1%)
14	C2	0.24	0/900	0.46	0/1224
14	c2	0.22	0/900	0.45	0/1224
15	C3	0.29	0/1215	0.51	1/1638 (0.1%)
15	c3	0.32	0/1215	0.51	0/1638
16	C4	0.26	0/901	0.51	0/1217
16	c4	0.31	0/960	0.53	0/1290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	C5	0.30	0/998	0.51	0/1341
17	c5	0.28	0/1060	0.50	0/1426
18	C6	0.28	0/1125	0.53	1/1510 (0.1%)
18	c6	0.27	0/1131	0.49	0/1518
19	C7	0.27	0/935	0.50	0/1254
19	c7	0.25	0/914	0.49	0/1224
20	C8	0.27	0/1211	0.49	0/1628
20	c8	0.27	0/1211	0.49	0/1628
21	C9	0.27	0/1130	0.45	0/1517
21	c9	0.27	0/1130	0.45	0/1517
22	D0	0.27	0/865	0.48	0/1169
22	d0	0.27	0/892	0.50	0/1205
23	D1	0.27	0/693	0.45	0/935
23	d1	0.28	0/693	0.47	0/935
24	D2	0.30	0/1038	0.57	2/1395 (0.1%)
24	d2	0.33	0/1038	0.54	1/1395 (0.1%)
25	D3	0.35	0/1139	0.56	0/1518
25	d3	0.36	0/1139	0.54	0/1518
26	D4	0.28	0/1087	0.45	0/1449
26	d4	0.30	0/1087	0.52	0/1449
27	D5	0.26	0/571	0.56	0/768
27	d5	0.23	0/566	0.43	0/761
28	D6	0.29	0/782	0.52	0/1047
28	d6	0.32	0/782	0.54	0/1047
29	D7	0.26	0/620	0.49	0/838
29	d7	0.28	0/620	0.51	0/838
30	D8	0.24	0/499	0.45	0/670
30	d8	0.25	0/499	0.48	0/670
31	D9	0.30	0/452	0.51	0/600
31	d9	0.31	0/452	0.52	0/600
32	E0	0.27	0/483	0.45	0/643
33	E1	0.27	0/577	0.56	0/770
33	e1	0.28	0/619	0.61	0/822
34	SR	0.24	0/2490	0.45	0/3389
34	sR	0.22	0/2495	0.42	0/3395
35	SM	0.31	0/984	0.51	1/1323 (0.1%)
35	sM	0.32	0/585	0.48	0/788
36	1	0.55	0/75368	1.03	147/117502 (0.1%)
36	5	0.57	1/75388 (0.0%)	1.04	135/117532 (0.1%)
37	3	0.44	0/2883	0.86	0/4491
37	7	0.56	0/2883	1.00	3/4491 (0.1%)
38	4	0.54	0/3746	0.97	2/5832 (0.0%)
38	8	0.49	0/3746	0.93	0/5832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	L2	0.39	0/1948	0.59	0/2617
39	l2	0.39	0/1946	0.62	1/2614 (0.0%)
40	L3	0.40	0/3146	0.57	0/4228
40	l3	0.43	0/3146	0.59	0/4228
41	L4	0.41	0/2800	0.62	1/3790 (0.0%)
41	l4	0.40	0/2800	0.61	1/3790 (0.0%)
42	L5	0.33	0/2425	0.51	0/3271
42	l5	0.40	0/2408	0.56	0/3248
43	L6	0.38	0/1260	0.54	0/1694
43	l6	0.41	0/1269	0.57	0/1705
44	L7	0.41	0/1821	0.57	0/2451
44	l7	0.43	0/1828	0.61	1/2461 (0.0%)
45	L8	0.32	0/1836	0.53	0/2481
45	l8	0.31	0/1796	0.51	0/2431
46	L9	0.36	0/1539	0.51	0/2073
46	l9	0.38	0/1539	0.56	0/2073
47	M0	0.38	0/1741	0.53	1/2335 (0.0%)
47	m0	0.43	0/1758	0.58	0/2358
48	M1	0.29	0/1374	0.49	0/1842
48	m1	0.37	0/1374	0.57	0/1842
49	M3	0.38	0/1568	0.58	0/2106
49	m3	0.36	0/1573	0.57	0/2113
50	M4	0.37	0/1068	0.56	0/1438
50	m4	0.40	0/1074	0.57	0/1446
51	M5	0.40	0/1757	0.58	0/2354
51	m5	0.36	0/1757	0.54	0/2354
52	M6	0.28	0/1585	0.46	0/2128
52	m6	0.31	0/1585	0.47	0/2128
53	M7	0.42	0/1443	0.58	0/1944
53	m7	0.44	0/1250	0.58	0/1683
54	M8	0.39	0/1465	0.60	0/1965
54	m8	0.40	0/1465	0.61	0/1965
55	M9	0.31	0/1538	0.47	0/2050
55	m9	0.33	0/1538	0.48	0/2050
56	N0	0.39	0/1481	0.55	0/1990
56	n0	0.42	0/1481	0.57	0/1990
57	N1	0.39	0/1300	0.54	0/1743
57	n1	0.45	0/1300	0.56	0/1743
58	N2	0.28	0/812	0.47	0/1099
58	n2	0.30	0/794	0.51	0/1076
59	N3	0.40	0/1018	0.56	0/1369
59	n3	0.46	0/1018	0.64	0/1369
60	N4	0.33	0/712	0.47	0/958

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	n4	0.34	0/1052	0.53	0/1398
61	N5	0.34	0/979	0.56	0/1321
61	n5	0.37	0/974	0.57	0/1314
62	N6	0.36	0/1004	0.59	1/1341 (0.1%)
62	n6	0.36	0/1004	0.55	0/1341
63	N7	0.31	0/1118	0.52	0/1497
63	n7	0.30	0/1118	0.50	0/1497
64	N8	0.42	0/1204	0.61	0/1612
64	n8	0.41	0/1204	0.59	1/1612 (0.1%)
65	N9	0.39	0/473	0.53	0/629
65	n9	0.43	0/473	0.76	1/629 (0.2%)
66	O0	0.30	0/751	0.47	0/1008
66	o0	0.30	0/775	0.46	0/1040
67	O1	0.35	0/890	0.51	0/1196
67	o1	0.40	0/897	0.57	0/1205
68	O2	0.42	0/1041	0.59	0/1394
68	o2	0.46	0/1041	0.63	0/1394
69	O3	0.46	0/868	0.57	0/1168
69	o3	0.47	0/868	0.61	0/1168
70	O4	0.35	0/890	0.58	1/1189 (0.1%)
70	o4	0.35	0/890	0.57	0/1189
71	O5	0.37	0/978	0.58	1/1301 (0.1%)
71	o5	0.33	0/974	0.50	0/1297
72	O6	0.35	0/778	0.53	0/1034
72	o6	0.31	0/777	0.52	0/1033
73	O7	0.44	0/696	0.60	0/923
73	o7	0.41	0/696	0.59	0/923
74	O8	0.30	0/618	0.49	0/826
74	o8	0.30	0/614	0.47	0/822
75	O9	0.40	0/443	0.58	0/588
75	o9	0.39	0/443	0.55	0/588
76	Q0	0.44	0/423	0.59	0/562
76	q0	0.47	0/423	0.62	0/562
77	Q1	0.35	0/234	0.68	0/300
77	q1	0.41	0/234	0.56	0/300
78	Q2	0.52	1/860 (0.1%)	0.64	0/1136
78	q2	0.51	1/860 (0.1%)	0.61	1/1136 (0.1%)
79	Q3	0.40	0/701	0.55	0/934
79	q3	0.45	0/701	0.56	0/934
80	e0	0.30	0/499	0.53	0/665
82	p0	0.26	0/1091	0.51	2/1472 (0.1%)
85	C	0.74	0/54	1.28	0/76
85	D	0.47	0/57	0.96	0/80

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.45	3/430695 (0.0%)	0.84	385/632350 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
22	d0	0	1
39	L2	0	1
52	M6	0	1
52	m6	0	1
64	n8	0	1
65	N9	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	Q2	17	CYS	CB-SG	8.29	1.96	1.82
78	q2	17	CYS	CB-SG	7.90	1.95	1.82
36	5	1152	G	N9-C4	-6.74	1.32	1.38

All (385) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1152	G	N3-C4-N9	-15.26	116.84	126.00
36	5	1152	G	N3-C4-C5	14.46	135.83	128.60
36	1	2403	G	N1-C6-O6	10.51	126.21	119.90
36	5	1152	G	C8-N9-C1'	9.79	139.73	127.00
36	1	2617	U	C5-C4-O4	9.68	131.71	125.90
36	5	1152	G	C4-N9-C1'	-9.58	114.04	126.50
36	5	1152	G	C2-N3-C4	-9.38	107.21	111.90
36	1	3278	C	N1-C2-O2	8.95	124.27	118.90
36	1	1308	A	O5'-P-OP1	-8.92	97.67	105.70
36	5	2403	G	O5'-P-OP2	-8.79	97.79	105.70
36	1	3217	C	N1-C2-O2	8.71	124.13	118.90
36	5	2860	U	O5'-P-OP2	-8.60	97.96	105.70
36	5	3245	A	N7-C8-N9	8.55	118.08	113.80
36	1	2945	G	O5'-P-OP2	-8.54	98.02	105.70
36	1	406	G	O4'-C1'-N9	8.44	114.95	108.20
36	1	2355	G	N1-C6-O6	8.39	124.93	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	2617	U	N1-C2-N3	8.38	119.93	114.90
36	1	2572	C	N1-C2-O2	8.24	123.85	118.90
36	1	2617	U	C4-C5-C6	8.21	124.62	119.70
36	5	2726	C	C6-N1-C2	-8.13	117.05	120.30
1	2	1363	U	N3-C2-O2	-8.05	116.56	122.20
36	1	3278	C	N3-C2-O2	-8.05	116.26	121.90
36	1	3217	C	C2-N1-C1'	8.00	127.60	118.80
1	2	75	U	C2-N1-C1'	7.94	127.23	117.70
36	1	3217	C	N3-C2-O2	-7.91	116.36	121.90
1	2	1363	U	N1-C2-O2	7.89	128.32	122.80
1	2	75	U	N1-C2-O2	7.89	128.32	122.80
36	5	2278	C	N1-C2-O2	7.88	123.63	118.90
1	2	73	U	O4'-C1'-N1	7.84	114.47	108.20
36	5	922	U	C5-C6-N1	-7.70	118.85	122.70
36	1	1307	G	P-O3'-C3'	7.65	128.88	119.70
36	5	3245	A	C5-N7-C8	-7.65	100.08	103.90
36	1	2355	G	C5-C6-O6	-7.48	124.11	128.60
1	6	1473	U	C2-N1-C1'	7.48	126.68	117.70
36	1	439	C	N1-C2-O2	7.47	123.38	118.90
65	n9	23	LYS	C-N-CD	7.43	144.01	128.40
36	5	2572	C	N1-C2-O2	7.42	123.35	118.90
36	5	2403	G	N1-C6-O6	7.35	124.31	119.90
1	6	453	U	C2-N1-C1'	7.33	126.50	117.70
36	5	1879	A	O5'-P-OP1	7.33	119.50	110.70
36	1	2403	G	C5-C6-O6	-7.33	124.20	128.60
37	7	77	G	O5'-P-OP2	-7.22	99.20	105.70
1	6	453	U	N1-C2-O2	7.17	127.82	122.80
36	5	1208	U	N3-C2-O2	-7.13	117.20	122.20
36	1	2726	C	N3-C2-O2	-7.09	116.93	121.90
36	1	2872	A	P-O3'-C3'	7.08	128.19	119.70
36	1	2572	C	N3-C2-O2	-7.06	116.96	121.90
36	5	1903	U	N3-C4-O4	7.06	124.34	119.40
36	1	2617	U	N3-C2-O2	-7.05	117.26	122.20
1	6	453	U	N3-C2-O2	-7.04	117.27	122.20
36	5	2572	C	C2-N1-C1'	7.04	126.54	118.80
44	17	229	PHE	CB-CG-CD1	7.00	125.70	120.80
36	5	3154	C	N1-C2-O2	6.96	123.08	118.90
36	1	2403	G	C4-C5-C6	6.95	122.97	118.80
36	1	3057	U	N3-C2-O2	-6.93	117.35	122.20
36	1	2971	A	O4'-C1'-N9	6.91	113.73	108.20
36	5	3245	A	C8-N9-C4	-6.91	103.04	105.80
36	1	1484	U	P-O3'-C3'	6.85	127.92	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	2726	C	N3-C2-O2	-6.84	117.11	121.90
1	2	75	U	N3-C2-O2	-6.83	117.42	122.20
38	4	125	U	C2-N1-C1'	6.79	125.85	117.70
36	1	2870	C	C2-N1-C1'	-6.76	111.36	118.80
36	1	2403	G	C6-C5-N7	-6.75	126.35	130.40
36	1	2870	C	C6-N1-C1'	6.73	128.88	120.80
36	5	1152	G	N3-C2-N2	-6.73	115.19	119.90
36	5	2816	G	C8-N9-C4	6.71	109.08	106.40
36	5	806	A	O5'-P-OP1	-6.70	99.67	105.70
36	1	2919	A	O5'-P-OP2	-6.64	99.72	105.70
36	5	835	G	O4'-C1'-N9	6.64	113.51	108.20
36	1	3278	C	C2-N1-C1'	6.63	126.10	118.80
36	5	2899	C	N3-C2-O2	-6.61	117.27	121.90
36	5	2957	G	O5'-P-OP1	-6.57	99.79	105.70
36	5	1495	U	C2-N1-C1'	6.53	125.53	117.70
36	5	2211	U	N3-C2-O2	-6.53	117.63	122.20
1	2	1363	U	C2-N1-C1'	6.52	125.52	117.70
36	5	406	G	O4'-C1'-N9	6.49	113.39	108.20
70	O4	51	LEU	CA-CB-CG	6.45	130.13	115.30
36	5	2381	G	N1-C6-O6	-6.44	116.04	119.90
1	6	813	U	N1-C2-O2	6.42	127.30	122.80
36	1	2714	G	N3-C4-C5	6.42	131.81	128.60
36	5	2816	G	N7-C8-N9	-6.39	109.90	113.10
36	5	1483	G	O4'-C1'-N9	6.39	113.31	108.20
1	2	1761	U	P-O3'-C3'	6.39	127.37	119.70
36	1	1117	G	O5'-P-OP1	-6.39	99.95	105.70
36	1	2871	G	O5'-P-OP2	-6.36	99.97	105.70
12	C0	88	PRO	N-CA-CB	6.34	110.91	103.30
36	1	2314	U	N1-C2-O2	6.32	127.22	122.80
36	1	2978	U	O4'-C1'-N1	6.31	113.25	108.20
1	2	959	U	N3-C2-O2	-6.31	117.78	122.20
36	1	2572	C	C2-N1-C1'	6.29	125.72	118.80
36	5	1481	A	C8-N9-C4	-6.28	103.29	105.80
1	6	1473	U	N1-C2-O2	6.28	127.20	122.80
36	5	880	G	O4'-C1'-N9	6.28	113.22	108.20
36	5	635	G	C5-C6-O6	-6.27	124.84	128.60
36	5	635	G	C4-C5-N7	6.24	113.30	110.80
36	1	1604	G	C4-N9-C1'	6.21	134.57	126.50
36	5	2287	C	N1-C2-O2	-6.21	115.18	118.90
36	1	2617	U	N3-C4-C5	-6.19	110.89	114.60
36	5	2971	A	O4'-C1'-N9	6.19	113.15	108.20
18	C6	40	GLU	C-N-CD	-6.18	107.00	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	873	C	P-O3'-C3'	6.17	127.11	119.70
36	1	2996	U	N1-C2-O2	6.16	127.11	122.80
36	5	1367	G	C5-C6-N1	-6.15	108.42	111.50
36	1	1556	C	N1-C2-O2	6.14	122.59	118.90
36	1	2278	C	N1-C2-O2	6.13	122.58	118.90
36	5	1014	U	C2-N1-C1'	6.12	125.05	117.70
78	q2	17	CYS	CA-CB-SG	6.11	125.00	114.00
36	5	2403	G	C5-C6-O6	-6.11	124.94	128.60
36	5	2816	G	C4-N9-C1'	-6.10	118.57	126.50
1	6	813	U	N3-C2-O2	-6.10	117.93	122.20
1	6	1097	U	P-O3'-C3'	6.08	127.00	119.70
36	5	1887	A	O5'-P-OP2	-6.08	100.23	105.70
36	5	1481	A	P-O3'-C3'	6.08	127.00	119.70
36	1	1556	C	N3-C2-O2	-6.05	117.66	121.90
36	5	2726	C	C5-C4-N4	6.05	124.43	120.20
12	c0	83	PRO	N-CA-CB	6.04	110.55	103.30
41	L4	327	LEU	CA-CB-CG	6.04	129.19	115.30
36	5	3197	G	N3-C4-N9	-6.04	122.38	126.00
36	1	1903	U	N3-C4-O4	6.02	123.61	119.40
36	5	2411	U	N3-C4-O4	-6.02	115.19	119.40
38	4	125	U	N1-C2-O2	6.01	127.01	122.80
1	6	1185	U	N1-C2-O2	6.01	127.01	122.80
36	5	2871	G	O5'-P-OP2	-6.01	100.29	105.70
36	5	282	G	C8-N9-C4	-6.00	104.00	106.40
36	5	3018	C	O5'-P-OP2	-5.99	100.31	105.70
36	5	2272	G	O4'-C1'-N9	5.99	112.99	108.20
36	1	2384	A	N1-C6-N6	5.99	122.19	118.60
39	l2	246	LEU	CA-CB-CG	5.99	129.07	115.30
36	5	3308	C	N1-C2-O2	-5.98	115.31	118.90
36	1	2725	U	C5-C6-N1	-5.98	119.71	122.70
36	1	1536	G	N1-C6-O6	-5.96	116.32	119.90
82	p0	278	PRO	N-CA-CB	5.96	110.45	103.30
36	1	770	G	O4'-C1'-N9	5.95	112.96	108.20
36	1	2725	U	C2-N1-C1'	-5.94	110.57	117.70
37	7	101	G	C5-C6-O6	-5.94	125.03	128.60
36	1	278	U	O5'-P-OP2	-5.93	100.36	105.70
36	1	439	C	N3-C2-O2	-5.93	117.75	121.90
36	1	2816	G	C4-N9-C1'	-5.92	118.80	126.50
36	1	2827	U	C2-N1-C1'	-5.92	110.59	117.70
36	1	2818	U	C5-C6-N1	5.92	125.66	122.70
1	6	194	U	C2-N1-C1'	5.92	124.80	117.70
1	6	402	C	C6-N1-C2	5.92	122.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1389	C	N1-C2-O2	5.91	122.45	118.90
36	5	2572	C	N3-C2-O2	-5.90	117.77	121.90
1	6	542	A	P-O3'-C3'	5.90	126.78	119.70
1	6	813	U	C2-N1-C1'	5.89	124.77	117.70
82	p0	290	PRO	N-CA-CB	5.89	110.37	103.30
1	2	1698	G	P-O3'-C3'	5.88	126.76	119.70
36	1	3344	A	O4'-C1'-N9	5.88	112.90	108.20
36	5	644	G	N9-C4-C5	5.86	107.74	105.40
36	5	922	U	N3-C2-O2	-5.86	118.10	122.20
36	1	917	A	O5'-P-OP2	-5.84	100.45	105.70
36	5	3245	A	C6-C5-N7	-5.82	128.22	132.30
36	5	966	U	N3-C2-O2	-5.82	118.13	122.20
36	5	1208	U	N3-C4-O4	-5.81	115.33	119.40
36	1	1556	C	C2-N1-C1'	5.80	125.18	118.80
1	6	1389	C	C2-N1-C1'	5.80	125.18	118.80
1	6	163	G	C8-N9-C4	-5.80	104.08	106.40
36	1	2403	G	O5'-P-OP2	-5.78	100.49	105.70
36	1	922	U	N1-C2-O2	5.78	126.85	122.80
62	N6	57	LEU	CA-CB-CG	5.78	128.59	115.30
1	2	501	U	OP1-P-O3'	5.77	117.90	105.20
36	5	805	G	C8-N9-C4	5.77	108.71	106.40
36	1	2314	U	C2-N1-C1'	5.76	124.62	117.70
1	2	507	U	C2-N1-C1'	5.76	124.61	117.70
36	1	1495	U	C5-C6-N1	-5.76	119.82	122.70
36	5	1208	U	C5-C4-O4	5.76	129.36	125.90
36	5	1495	U	C5-C6-N1	5.76	125.58	122.70
36	5	3154	C	C2-N1-C1'	5.75	125.12	118.80
36	1	3306	U	N3-C2-O2	-5.74	118.18	122.20
36	5	2526	C	N1-C2-O2	5.74	122.34	118.90
12	c0	90	PRO	N-CA-CB	5.74	110.18	103.30
36	1	637	C	P-O3'-C3'	5.73	126.57	119.70
36	1	1192	C	C6-N1-C2	-5.72	118.01	120.30
36	5	2870	C	C6-N1-C2	-5.72	118.01	120.30
36	1	922	U	N3-C2-O2	-5.71	118.20	122.20
36	1	2403	G	N3-C4-N9	5.71	129.43	126.00
1	2	734	A	P-O3'-C3'	5.71	126.55	119.70
36	1	439	C	C2-N1-C1'	5.71	125.08	118.80
36	1	2846	U	N3-C2-O2	-5.70	118.21	122.20
1	2	720	G	OP1-P-O3'	5.70	117.73	105.20
36	5	1592	G	N1-C6-O6	5.69	123.32	119.90
36	5	2553	U	C2-N1-C1'	5.69	124.53	117.70
36	5	2385	G	C4-N9-C1'	-5.68	119.11	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1582	C	C6-N1-C2	-5.68	118.03	120.30
36	5	2526	C	C2-N1-C1'	5.68	125.05	118.80
1	2	507	U	N1-C2-O2	5.68	126.77	122.80
36	5	2129	U	N3-C2-O2	-5.67	118.23	122.20
36	1	2355	G	C4-C5-N7	5.67	113.07	110.80
36	1	1604	G	C8-N9-C1'	-5.66	119.64	127.00
24	d2	93	LEU	CA-CB-CG	5.66	128.32	115.30
1	2	1241	G	O4'-C1'-N9	5.66	112.72	108.20
36	1	2827	U	C5-C6-N1	-5.66	119.87	122.70
36	1	1367	G	N1-C6-O6	5.65	123.29	119.90
36	1	2314	U	C6-N1-C1'	-5.65	113.29	121.20
36	1	3217	C	C6-N1-C1'	-5.65	114.02	120.80
36	5	1307	G	O4'-C1'-N9	5.64	112.71	108.20
36	1	2572	C	C6-N1-C2	-5.64	118.05	120.30
15	C3	22	ALA	C-N-CD	-5.63	108.20	120.60
36	1	1604	G	N3-C4-N9	5.63	129.38	126.00
36	5	1903	U	C5-C4-O4	-5.63	122.52	125.90
1	2	959	U	N1-C2-O2	5.62	126.74	122.80
36	5	922	U	C2-N3-C4	-5.62	123.63	127.00
36	5	1208	U	N1-C2-O2	5.62	126.73	122.80
36	1	2385	G	N3-C4-C5	5.62	131.41	128.60
36	5	1189	C	N1-C2-O2	-5.61	115.53	118.90
1	2	581	U	C2-N1-C1'	5.61	124.43	117.70
36	5	2385	G	N3-C4-C5	5.61	131.40	128.60
36	1	1115	G	N3-C4-N9	5.61	129.36	126.00
36	5	2978	U	O4'-C1'-N1	5.59	112.67	108.20
1	2	1389	C	C2-N1-C1'	5.59	124.95	118.80
36	1	1604	G	N3-C4-C5	-5.58	125.81	128.60
36	1	2873	U	N1-C2-N3	5.58	118.25	114.90
1	6	1389	C	N1-C2-O2	5.57	122.24	118.90
36	1	1834	U	N3-C4-C5	-5.55	111.27	114.60
36	5	2899	C	C6-N1-C2	-5.55	118.08	120.30
1	6	1596	C	N3-C2-O2	-5.54	118.02	121.90
1	6	1698	G	P-O3'-C3'	5.54	126.34	119.70
1	2	734	A	OP1-P-O3'	5.53	117.37	105.20
36	5	2513	U	P-O3'-C3'	5.53	126.34	119.70
1	2	75	U	C6-N1-C1'	-5.52	113.48	121.20
36	1	1192	C	N3-C4-N4	5.51	121.86	118.00
36	1	1269	U	C2-N1-C1'	5.51	124.32	117.70
36	1	979	U	P-O3'-C3'	5.51	126.31	119.70
36	1	2374	C	C6-N1-C2	-5.50	118.10	120.30
1	2	720	G	P-O3'-C3'	5.50	126.30	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	2617	U	C6-N1-C2	-5.49	117.71	121.00
36	5	909	G	N1-C6-O6	-5.49	116.61	119.90
36	5	2843	U	N3-C2-O2	-5.47	118.37	122.20
36	5	1121	U	N3-C2-O2	5.47	126.03	122.20
37	7	1	G	C4-N9-C1'	5.46	133.60	126.50
36	1	2865	U	C5-C4-O4	-5.46	122.62	125.90
36	5	2411	U	C5-C4-O4	5.46	129.18	125.90
36	5	2584	G	OP2-P-O3'	5.46	117.21	105.20
36	1	979	U	N1-C2-N3	5.45	118.17	114.90
1	6	864	U	N3-C2-O2	-5.45	118.39	122.20
36	1	33	G	N1-C6-O6	5.45	123.17	119.90
36	1	2418	G	OP1-P-O3'	5.44	117.18	105.20
36	1	2797	C	N1-C2-O2	-5.44	115.63	118.90
36	1	2816	G	N7-C8-N9	-5.44	110.38	113.10
36	5	3049	A	C8-N9-C4	5.44	107.97	105.80
36	5	909	G	C5-C6-O6	5.43	131.86	128.60
36	5	1127	G	N1-C6-O6	5.43	123.16	119.90
36	1	1355	A	P-O3'-C3'	5.43	126.21	119.70
36	1	2384	A	N9-C4-C5	-5.42	103.63	105.80
36	5	635	G	N1-C6-O6	5.42	123.15	119.90
36	5	644	G	C8-N9-C4	-5.41	104.23	106.40
1	2	934	C	C2-N1-C1'	5.41	124.75	118.80
36	1	2870	C	N3-C4-N4	-5.41	114.22	118.00
1	6	1473	U	N3-C2-O2	-5.41	118.42	122.20
36	5	908	G	O4'-C1'-N9	-5.40	103.88	108.20
36	1	1820	U	P-O3'-C3'	5.39	126.17	119.70
36	1	2385	G	N3-C4-N9	-5.39	122.77	126.00
36	5	1300	G	C5-C6-O6	-5.39	125.37	128.60
1	2	794	U	P-O3'-C3'	5.39	126.17	119.70
24	D2	65	LEU	CA-CB-CG	5.38	127.68	115.30
36	5	2513	U	OP1-P-O3'	5.38	117.04	105.20
36	5	878	G	C5-C6-O6	-5.38	125.37	128.60
36	5	3269	U	P-O3'-C3'	5.38	126.15	119.70
36	1	835	G	O4'-C1'-N9	5.37	112.49	108.20
1	6	1458	G	C4-N9-C1'	5.37	133.48	126.50
36	5	703	G	O5'-P-OP1	-5.37	100.87	105.70
1	2	913	G	P-O3'-C3'	5.36	126.14	119.70
36	5	3309	G	N3-C4-C5	-5.36	125.92	128.60
36	1	880	G	O4'-C1'-N9	5.36	112.49	108.20
36	1	2726	C	C5-C4-N4	5.35	123.95	120.20
36	1	348	A	N1-C6-N6	5.35	121.81	118.60
36	1	776	U	C4-C5-C6	5.35	122.91	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	2978	U	N3-C2-O2	-5.35	118.45	122.20
36	1	981	U	C5-C6-N1	5.35	125.37	122.70
36	1	922	U	C2-N1-C1'	5.34	124.11	117.70
36	1	1849	C	O5'-P-OP1	-5.34	100.89	105.70
36	1	65	A	P-O3'-C3'	5.33	126.10	119.70
36	1	2554	A	P-O3'-C3'	5.33	126.10	119.70
36	5	2978	U	C5-C6-N1	-5.33	120.04	122.70
1	6	755	A	P-O3'-C3'	5.33	126.09	119.70
36	1	1581	C	N1-C2-O2	5.32	122.09	118.90
36	5	1367	G	C4-N9-C1'	5.32	133.41	126.50
12	C0	76	LEU	CA-CB-CG	5.31	127.52	115.30
36	1	1367	G	C6-C5-N7	-5.30	127.22	130.40
36	1	2621	G	C5-C6-O6	-5.30	125.42	128.60
47	M0	57	LEU	CA-CB-CG	5.30	127.48	115.30
1	2	1560	U	N3-C2-O2	-5.29	118.50	122.20
1	6	1600	A	OP1-P-O3'	5.29	116.84	105.20
36	5	1926	C	N1-C2-O2	-5.29	115.73	118.90
36	5	1157	G	C4-C5-N7	-5.28	108.69	110.80
36	1	1605	A	O4'-C1'-N9	5.28	112.42	108.20
36	1	15	C	O5'-P-OP2	-5.28	100.95	105.70
1	6	1573	A	OP2-P-O3'	5.28	116.81	105.20
36	5	3154	C	N3-C2-O2	-5.27	118.21	121.90
36	5	1115	G	C4-N9-C1'	5.27	133.35	126.50
36	5	3317	U	N3-C2-O2	-5.27	118.51	122.20
1	6	144	U	N3-C2-O2	-5.26	118.52	122.20
1	6	542	A	O4'-C1'-N9	5.26	112.41	108.20
36	1	3306	U	C5-C4-O4	5.26	129.06	125.90
1	2	158	U	P-O3'-C3'	5.25	126.00	119.70
36	1	3181	C	N3-C2-O2	-5.24	118.23	121.90
1	2	1052	U	C2-N1-C1'	5.23	123.98	117.70
36	5	2870	C	C6-N1-C1'	5.23	127.07	120.80
35	SM	134	ASP	CB-CG-OD2	5.22	123.00	118.30
36	5	2531	C	C2-N1-C1'	5.22	124.54	118.80
36	5	2964	G	N1-C6-O6	-5.22	116.77	119.90
36	1	2872	A	C8-N9-C4	-5.22	103.71	105.80
36	1	3217	C	C6-N1-C2	-5.22	118.21	120.30
36	5	1241	U	OP1-P-O3'	5.22	116.68	105.20
36	1	2816	G	C8-N9-C4	5.21	108.48	106.40
36	1	2385	G	C4-N9-C1'	-5.21	119.72	126.50
1	6	272	U	P-O3'-C3'	5.21	125.95	119.70
36	1	641	C	C5-C4-N4	-5.21	116.55	120.20
36	5	2385	G	O5'-P-OP1	-5.21	101.02	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	3382	U	N1-C2-O2	5.20	126.44	122.80
1	6	1097	U	OP2-P-O3'	5.20	116.64	105.20
36	5	1238	C	P-O3'-C3'	5.20	125.94	119.70
36	5	1367	G	N1-C6-O6	5.20	123.02	119.90
36	1	651	G	N3-C4-C5	-5.19	126.00	128.60
36	1	2403	G	N3-C4-C5	-5.19	126.00	128.60
36	1	3344	A	N7-C8-N9	5.19	116.39	113.80
36	5	1200	A	N1-C6-N6	5.19	121.72	118.60
36	5	1604	G	C4-N9-C1'	5.19	133.24	126.50
36	5	640	U	N1-C2-N3	5.19	118.01	114.90
36	1	979	U	C6-N1-C2	-5.18	117.89	121.00
36	5	398	A	O5'-P-OP2	-5.17	101.05	105.70
1	2	287	G	O4'-C1'-N9	5.17	112.33	108.20
24	D2	93	LEU	CA-CB-CG	5.16	127.17	115.30
36	1	3382	U	N3-C2-O2	-5.16	118.59	122.20
36	5	2572	C	C6-N1-C2	-5.16	118.23	120.30
1	2	501	U	P-O3'-C3'	5.16	125.89	119.70
1	2	74	U	O4'-C1'-N1	5.15	112.32	108.20
13	c1	120	GLY	N-CA-C	-5.15	100.22	113.10
1	2	1458	G	C4-N9-C1'	5.13	133.17	126.50
36	5	2833	A	C8-N9-C4	5.13	107.85	105.80
1	6	1473	U	C6-N1-C1'	-5.12	114.03	121.20
1	2	507	U	N3-C2-O2	-5.12	118.62	122.20
36	5	1127	G	C5-C6-O6	-5.12	125.53	128.60
1	6	1560	U	C2-N1-C1'	5.11	123.84	117.70
36	5	1389	G	N1-C6-O6	5.11	122.97	119.90
36	1	2314	U	N1-C2-N3	-5.11	111.83	114.90
36	5	2354	C	N1-C2-O2	-5.11	115.83	118.90
36	1	1858	A	C6-C5-N7	-5.11	128.72	132.30
36	5	3244	A	C8-N9-C4	5.11	107.84	105.80
36	1	3057	U	N1-C2-O2	5.11	126.37	122.80
36	5	3245	A	C4-C5-N7	5.10	113.25	110.70
36	1	1495	U	C2-N1-C1'	-5.10	111.58	117.70
36	5	644	G	C4-C5-N7	-5.10	108.76	110.80
36	5	1911	A	N1-C6-N6	5.09	121.66	118.60
1	2	1657	U	P-O3'-C3'	5.09	125.81	119.70
36	1	327	A	C8-N9-C4	5.09	107.84	105.80
36	1	1064	A	P-O3'-C3'	5.09	125.81	119.70
36	5	170	G	C4-N9-C1'	5.09	133.11	126.50
1	6	264	G	N1-C6-O6	5.09	122.95	119.90
1	6	1058	U	P-O3'-C3'	5.09	125.80	119.70
1	2	1246	C	C2-N1-C1'	5.08	124.39	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6	965	U	C2-N1-C1'	5.08	123.80	117.70
36	1	2541	U	P-O3'-C3'	5.08	125.80	119.70
64	n8	73	LEU	CA-CB-CG	5.08	126.98	115.30
36	1	1495	U	N1-C2-O2	-5.08	119.25	122.80
36	1	2101	C	P-O3'-C3'	5.08	125.79	119.70
36	1	2298	U	O4'-C1'-N1	5.08	112.26	108.20
36	5	922	U	C4-C5-C6	5.08	122.75	119.70
36	1	2827	U	N1-C2-N3	5.07	117.94	114.90
36	1	2867	C	O5'-P-OP2	-5.07	101.14	105.70
36	1	3022	G	O4'-C1'-N9	5.07	112.26	108.20
41	14	339	LEU	CA-CB-CG	5.07	126.96	115.30
1	2	1491	U	N1-C2-O2	5.06	126.34	122.80
36	1	2227	C	P-O3'-C3'	5.06	125.78	119.70
36	1	1169	A	OP2-P-O3'	5.06	116.33	105.20
36	5	2278	C	N1-C2-N3	-5.06	115.66	119.20
36	5	922	U	N1-C2-N3	5.06	117.94	114.90
36	5	1389	G	C5-C6-O6	-5.06	125.56	128.60
36	1	1495	U	C4-C5-C6	5.05	122.73	119.70
36	5	2772	C	P-O3'-C3'	5.05	125.76	119.70
1	6	610	G	C4-N9-C1'	5.04	133.06	126.50
36	5	1121	U	N1-C2-O2	-5.04	119.27	122.80
71	O5	69	LEU	CA-CB-CG	5.04	126.90	115.30
36	5	1870	C	C6-N1-C2	-5.04	118.28	120.30
36	1	3382	U	C2-N1-C1'	5.04	123.75	117.70
36	1	3092	C	O4'-C1'-N1	5.04	112.23	108.20
1	2	829	A	P-O3'-C3'	5.04	125.75	119.70
36	5	2950	G	O4'-C1'-N9	5.04	112.23	108.20
36	1	1866	C	C6-N1-C2	5.03	122.31	120.30
1	2	1458	G	N3-C4-N9	5.03	129.02	126.00
36	1	2621	G	N3-C2-N2	-5.02	116.38	119.90
36	1	644	G	C5-C6-N1	-5.02	108.99	111.50
36	1	2355	G	N9-C4-C5	-5.02	103.39	105.40
1	2	638	U	C2-N1-C1'	5.00	123.70	117.70

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	L2	19	HIS	Peptide
52	M6	110	PRO	Peptide
65	N9	20	GLY	Peptide
22	d0	70	THR	Peptide

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Mol	Chain	Res	Type	Group
52	m6	110	PRO	Peptide
64	n8	66	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37970	0	19106	617	1
1	6	38260	0	19252	600	0
2	S0	1577	0	1567	102	0
2	s0	1583	0	1578	0	0
3	S1	1709	0	1784	132	0
3	s1	1722	0	1793	0	0
4	S2	1635	0	1723	89	0
4	s2	1635	0	1723	0	0
5	S3	1734	0	1817	96	0
5	s3	1734	0	1817	0	0
6	S4	2068	0	2154	127	0
6	s4	2068	0	2154	0	0
7	S5	1609	0	1675	74	0
7	s5	1609	0	1675	0	0
8	S6	1799	0	1879	106	0
8	s6	1755	0	1846	0	0
9	S7	1481	0	1572	73	0
9	s7	1491	0	1578	0	0
10	S8	1489	0	1525	89	0
10	s8	1489	0	1525	0	0
11	S9	1494	0	1573	104	0
11	s9	1494	0	1573	0	0
12	C0	773	0	729	50	0
12	c0	762	0	700	0	0
13	C1	1213	0	1257	66	0
13	c1	1168	0	1233	0	0
14	C2	892	0	891	44	0
14	c2	892	0	891	0	0
15	C3	1192	0	1255	75	0
15	c3	1192	0	1255	0	0
16	C4	891	0	883	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	c4	949	0	985	0	0
17	C5	977	0	1002	62	0
17	c5	1039	0	1050	0	0
18	C6	1105	0	1166	74	0
18	c6	1111	0	1171	0	0
19	C7	926	0	930	59	0
19	c7	906	0	909	0	0
20	C8	1192	0	1222	89	0
20	c8	1192	0	1222	0	0
21	C9	1112	0	1124	70	0
21	c9	1112	0	1124	0	0
22	D0	855	0	917	50	0
22	d0	882	0	939	0	0
23	D1	684	0	672	44	0
23	d1	684	0	672	0	0
24	D2	1021	0	1060	67	0
24	d2	1021	0	1060	0	0
25	D3	1121	0	1196	70	0
25	d3	1121	0	1196	0	0
26	D4	1073	0	1132	62	0
26	d4	1073	0	1132	0	0
27	D5	563	0	603	44	0
27	d5	558	0	598	0	0
28	D6	769	0	814	66	0
28	d6	769	0	814	0	0
29	D7	610	0	630	38	0
29	d7	610	0	631	0	0
30	D8	497	0	535	32	0
30	d8	497	0	535	0	0
31	D9	442	0	428	24	0
31	d9	442	0	428	0	0
32	E0	475	0	525	36	0
33	E1	566	0	602	48	0
33	e1	608	0	657	0	0
34	SR	2437	0	2386	92	0
34	sR	2442	0	2392	0	0
35	SM	1104	0	969	52	0
35	sM	681	0	591	0	0
36	1	67333	0	33838	846	0
36	5	67354	0	33851	839	1
37	3	2579	0	1304	33	0
37	7	2579	0	1304	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	4	3353	0	1695	38	0
38	8	3353	0	1695	57	0
39	L2	1914	0	1981	127	0
39	l2	1912	0	1976	0	0
40	L3	3075	0	3142	163	0
40	l3	3075	0	3142	0	0
41	L4	2748	0	2859	160	0
41	l4	2748	0	2859	0	0
42	L5	2375	0	2325	155	0
42	l5	2359	0	2311	0	0
43	L6	1239	0	1326	62	0
43	l6	1248	0	1339	0	0
44	L7	1784	0	1862	87	0
44	l7	1791	0	1869	0	0
45	L8	1804	0	1875	89	0
45	l8	1764	0	1821	0	0
46	L9	1518	0	1587	104	0
46	l9	1518	0	1587	0	0
47	M0	1705	0	1736	105	0
47	m0	1722	0	1755	0	0
48	M1	1353	0	1383	70	0
48	m1	1353	0	1383	0	0
49	M3	1543	0	1608	75	0
49	m3	1548	0	1613	0	0
50	M4	1053	0	1149	69	0
50	m4	1059	0	1154	0	0
51	M5	1720	0	1779	95	0
51	m5	1720	0	1779	0	0
52	M6	1555	0	1659	81	0
52	m6	1555	0	1659	0	0
53	M7	1420	0	1437	75	0
53	m7	1227	0	1236	0	0
54	M8	1441	0	1543	78	0
54	m8	1441	0	1543	0	0
55	M9	1521	0	1617	67	0
55	m9	1521	0	1617	0	0
56	N0	1445	0	1487	57	0
56	n0	1445	0	1487	0	0
57	N1	1276	0	1323	70	0
57	n1	1276	0	1323	0	0
58	N2	796	0	812	35	0
58	n2	778	0	791	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	N3	1003	0	1048	52	0
59	n3	1003	0	1048	0	0
60	N4	699	0	640	19	0
60	n4	1038	0	1071	0	0
61	N5	964	0	1025	53	0
61	n5	959	0	1023	0	0
62	N6	993	0	1081	51	0
62	n6	993	0	1081	0	0
63	N7	1092	0	1155	79	0
63	n7	1092	0	1155	0	0
64	N8	1173	0	1215	79	0
64	n8	1173	0	1215	0	0
65	N9	462	0	491	26	0
65	n9	462	0	491	0	0
66	O0	743	0	797	33	0
66	o0	767	0	816	0	0
67	O1	876	0	912	34	0
67	o1	883	0	918	0	0
68	O2	1020	0	1090	58	0
68	o2	1020	0	1090	0	0
69	O3	850	0	880	40	0
69	o3	850	0	880	0	0
70	O4	880	0	945	56	0
70	o4	880	0	945	0	0
71	O5	969	0	1078	66	0
71	o5	965	0	1067	0	0
72	O6	771	0	849	42	0
72	o6	770	0	846	0	0
73	O7	681	0	683	51	0
73	o7	681	0	683	0	0
74	O8	612	0	682	29	0
74	o8	608	0	671	0	0
75	O9	436	0	475	32	0
75	o9	436	0	475	0	0
76	Q0	417	0	455	12	0
76	q0	417	0	455	0	0
77	Q1	233	0	284	16	0
77	q1	233	0	284	0	0
78	Q2	847	0	914	50	0
78	q2	847	0	914	0	0
79	Q3	694	0	734	45	0
79	q3	694	0	734	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	e0	491	0	542	0	0
81	m2	750	0	180	0	0
82	p0	1076	0	1076	0	0
83	p1	235	0	53	0	0
84	p2	230	0	49	0	0
85	C	73	0	48	0	0
85	D	76	0	48	1	0
86	D6	1	0	0	0	0
86	D7	1	0	0	0	0
86	D9	1	0	0	0	0
86	E1	1	0	0	0	0
86	O7	1	0	0	0	0
86	Q0	1	0	0	0	0
86	Q2	1	0	0	0	0
86	Q3	1	0	0	0	0
86	d6	1	0	0	0	0
86	d7	1	0	0	0	0
86	d9	1	0	0	0	0
86	e1	1	0	0	0	0
86	o7	1	0	0	0	0
86	q0	1	0	0	0	0
86	q2	1	0	0	0	0
86	q3	1	0	0	0	0
87	C	23	0	18	1	0
87	D	23	0	18	6	0
88	C	1	0	0	0	0
88	D	1	0	0	0	0
All	All	402683	0	297750	6748	1

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 10.

All (6748) 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)
5:S3:94:ARG:NH2	35:SM:134:ASP:OD1	1.86	1.07
40:L3:296:THR:HG22	40:L3:298:PHE:H	4.58	0.95
1:6:1636:C:H4'	1:6:1637:C:H5'	1.46	0.94
71:O5:85:THR:HG22	71:O5:88:LEU:H	1.33	0.94
64:N8:21:ARG:NH2	36:5:640:U:OP1	182.08	0.94
40:L3:41:VAL:HA	40:L3:185:GLY:HA3	1.66	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:N9:23:LYS:HB3	65:N9:24:PRO:HD3	2.73	0.92
17:C5:123:TYR:HH	20:C8:122:HIS:HE2	1.17	0.92
36:1:1222:G:HO2'	36:1:1285:G:H1	1.18	0.92
36:1:1481:A:O2'	36:1:1858:A:N3	2.03	0.91
1:2:1339:C:O2'	1:2:1341:A:N7	2.04	0.90
65:N9:23:LYS:HD2	65:N9:24:PRO:HD3	1.53	0.90
41:L4:204:GLY:O	41:L4:246:ARG:NH1	2.22	0.89
36:1:283:G:OP1	78:Q2:45:ARG:NH2	2.05	0.89
1:6:1696:G:O2'	1:6:1698:G:N7	2.06	0.89
51:M5:188:ARG:NH2	36:5:31:C:OP2	122.33	0.89
36:1:2392:C:O2'	40:L3:266:ARG:NH2	2.06	0.88
1:2:1559:A:H5''	20:C8:135:GLY:HA3	1.55	0.87
6:S4:9:LEU:HB2	6:S4:30:ARG:HB2	1.86	0.87
11:S9:126:ARG:NH1	1:6:475:A:OP2	425.37	0.86
36:5:3194:C:O2	36:5:3197:G:N2	2.07	0.86
3:S1:36:SER:HA	3:S1:41:ARG:HE	2.95	0.86
54:M8:158:HIS:H	54:M8:186:VAL:HG12	1.36	0.86
36:1:3272:C:OP2	43:L6:78:ARG:NH1	2.09	0.86
36:5:1239:C:H42	36:5:1249:G:H1	1.24	0.85
36:1:640:U:OP1	64:N8:21:ARG:NH2	2.09	0.85
1:6:1280:C:H2'	1:6:1281:G:H8	1.40	0.85
36:1:687:U:OP2	49:M3:36:ARG:NH2	2.09	0.85
56:N0:50:LYS:NZ	37:7:76:A:O2'	302.64	0.85
50:M4:128:ARG:NH2	36:5:3214:U:OP2	280.55	0.84
1:2:79:C:H1'	8:S6:174:LYS:HD3	1.59	0.84
47:M0:43:VAL:HG21	47:M0:197:VAL:HB	2.10	0.84
7:S5:94:THR:HG22	7:S5:114:ILE:HG13	1.60	0.84
36:1:2940:A:N7	40:L3:2:SER:N	2.25	0.84
1:6:1097:U:H4'	1:6:1098:U:H5'	1.59	0.84
11:S9:133:HIS:NE2	1:6:513:U:OP1	448.83	0.84
23:D1:3:ASN:HD21	23:D1:7:GLN:HB2	3.04	0.84
63:N7:102:GLU:H	63:N7:107:ARG:HH21	2.12	0.84
48:M1:94:ARG:O	48:M1:96:PHE:N	2.41	0.83
2:S0:162:CYS:SG	2:S0:163:ASN:N	2.52	0.83
1:2:142:G:H22	1:2:173:A:H2	1.26	0.83
72:O6:2:THR:OG1	72:O6:3:VAL:N	2.12	0.83
1:6:1588:G:H1	1:6:1608:U:H3	1.26	0.83
1:6:793:A:H3'	1:6:794:U:H5'	1.60	0.83
36:1:1639:C:OP2	70:O4:74:ARG:NH2	2.11	0.83
48:M1:15:GLU:HG2	48:M1:16:LYS:HG2	2.95	0.83
47:M0:38:LYS:HG2	47:M0:41:ALA:HB2	1.97	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:M9:5:ARG:NH2	36:5:1471:U:OP1	119.32	0.83
41:L4:329:PRO:O	41:L4:331:ALA:N	3.29	0.82
39:L2:193:ARG:NH2	36:5:2181:C:OP1	198.36	0.82
62:N6:71:SER:HB3	62:N6:83:ASP:HB2	1.60	0.82
72:O6:60:LEU:HD11	72:O6:68:ARG:HE	1.46	0.81
46:L9:47:LYS:HZ2	50:M4:5:SER:HB2	1.43	0.81
36:5:2836:C:H5	36:5:2852:C:H42	1.24	0.81
40:L3:232:ARG:NH1	40:L3:269:GLN:O	2.13	0.81
36:1:3041:U:OP1	59:N3:12:ARG:NH1	2.14	0.81
50:M4:55:ARG:NH2	50:M4:76:ALA:O	2.29	0.81
36:1:3344:A:H2	36:1:3361:G:H21	1.25	0.81
51:M5:84:PRO:HA	51:M5:87:GLN:HG3	1.62	0.81
79:Q3:59:CYS:SG	79:Q3:60:CYS:N	3.18	0.81
1:6:647:G:H22	1:6:687:G:H1	1.27	0.80
69:O3:75:HIS:HB3	69:O3:80:VAL:HG12	1.62	0.80
47:M0:174:THR:HG23	47:M0:176:LEU:H	1.46	0.80
28:D6:10:ARG:HH12	28:D6:36:ILE:HG13	6.21	0.80
42:L5:22:ARG:NH2	42:L5:28:THR:OG1	2.14	0.80
51:M5:46:ASP:OD1	51:M5:50:ARG:NH2	2.15	0.80
1:6:1595:U:H3	1:6:1600:A:H2	1.28	0.80
49:M3:165:SER:O	49:M3:167:PHE:N	2.15	0.80
41:L4:122:THR:HG22	41:L4:235:LEU:HB2	1.62	0.80
37:3:45:A:OP1	42:L5:151:GLN:NE2	2.14	0.80
5:S3:175:VAL:HG13	5:S3:182:LEU:HB2	1.64	0.80
42:L5:120:LYS:O	42:L5:248:ARG:NH2	2.49	0.80
24:D2:2:THR:N	1:6:1034:C:HO2'	339.05	0.80
16:C4:20:TYR:HB3	16:C4:27:PHE:HB2	2.31	0.80
29:D7:36:LYS:HB3	29:D7:43:ILE:HG22	1.62	0.80
47:M0:207:GLU:HB3	47:M0:211:ARG:HH12	5.58	0.79
78:Q2:41:ARG:NH1	36:5:284:A:OP2	157.69	0.79
1:6:158:U:O2'	1:6:160:C:OP2	1.99	0.79
36:1:978:G:O2'	36:1:979:U:O2	2.01	0.79
18:C6:82:ARG:HH22	18:C6:114:ARG:HG3	3.54	0.79
36:1:3182:G:OP1	52:M6:160:ARG:NH2	2.12	0.79
40:L3:139:GLN:O	40:L3:141:GLY:N	2.69	0.79
36:5:1235:U:H4'	36:5:1236:G:H5'	1.63	0.79
9:S7:11:GLN:HG3	9:S7:13:PRO:HD2	1.63	0.79
6:S4:79:ASP:HB3	6:S4:82:TYR:HB2	1.64	0.79
36:1:2771:U:O2'	36:1:2772:C:O4'	2.01	0.78
38:4:95:G:OP2	73:O7:72:ARG:NH1	2.15	0.78
10:S8:34:ALA:HB2	10:S8:56:ARG:HD3	2.53	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1186:U:O4	1:2:1200:G:N2	2.15	0.78
57:N1:43:LYS:HD2	36:5:992:A:H5''	256.78	0.78
2:S0:66:ALA:HB2	23:D1:37:ALA:HB2	1.84	0.78
36:5:1555:U:O4	36:5:1557:A:N6	2.17	0.78
41:L4:16:THR:HG23	41:L4:18:ASN:H	2.51	0.78
78:Q2:45:ARG:NH2	36:5:283:G:OP1	148.16	0.78
1:2:1542:G:N2	1:2:1569:A:OP2	2.18	0.77
1:2:283:U:H5''	8:S6:188:ARG:HD3	1.66	0.77
36:5:2112:U:H4'	36:5:2113:A:H5'	1.66	0.77
52:M6:160:ARG:NH2	36:5:3182:G:OP1	279.85	0.77
41:L4:328:ASN:OD1	44:L7:48:ASN:ND2	3.14	0.77
78:Q2:71:ARG:HE	78:Q2:80:ARG:HH11	1.32	0.77
49:M3:46:ILE:HG22	49:M3:49:ARG:HB2	1.65	0.77
47:M0:80:SER:HB3	47:M0:147:VAL:HG11	1.66	0.77
36:1:1427:U:OP2	64:N8:4:ARG:NH2	2.18	0.77
36:1:103:G:OP1	49:M3:70:ARG:NH2	2.18	0.77
36:1:3298:C:OP1	53:M7:74:LYS:NZ	2.17	0.77
36:1:2818:U:H6	36:1:2818:U:H5'	1.49	0.77
17:C5:43:ARG:NH2	1:6:1552:U:OP2	404.69	0.77
17:C5:123:TYR:OH	20:C8:126:ARG:NH1	2.18	0.77
42:L5:270:LYS:HB3	37:7:1:G:O2'	323.28	0.77
46:L9:9:GLN:HG3	46:L9:52:LEU:HD21	1.66	0.77
37:3:17:A:OP1	42:L5:2:ALA:N	2.17	0.76
18:C6:50:GLU:OE2	18:C6:82:ARG:NH2	2.18	0.76
41:L4:16:THR:HG22	41:L4:18:ASN:H	1.49	0.76
36:5:155:G:H5''	36:5:156:G:C8	2.20	0.76
16:C4:50:ALA:O	16:C4:52:ARG:N	2.41	0.76
53:M7:24:VAL:HB	53:M7:29:THR:HG21	1.65	0.76
79:Q3:6:LYS:HG2	79:Q3:7:LYS:HG3	5.07	0.76
1:6:1370:U:H4'	1:6:1371:A:H4'	1.67	0.76
11:S9:109:LEU:HB2	11:S9:146:PHE:HB3	1.68	0.76
55:M9:21:LYS:NZ	36:5:1874:A:OP2	143.34	0.76
1:2:1046:G:OP1	3:S1:157:GLN:NE2	2.18	0.76
21:C9:119:LYS:NZ	1:6:1369:U:OP1	443.24	0.76
13:C1:4:GLU:OE1	13:C1:82:ARG:NH2	10.31	0.76
1:2:154:G:OP1	8:S6:2:LYS:NZ	2.19	0.76
48:M1:133:ARG:NH2	48:M1:158:ASP:OD2	2.18	0.76
66:O0:34:LEU:HD23	66:O0:59:TYR:HB3	1.68	0.76
1:2:68:A:OP1	8:S6:160:ARG:NH2	2.17	0.76
1:2:320:U:H3'	1:2:321:C:H5''	1.67	0.76
3:S1:85:LYS:HB3	3:S1:101:HIS:HB3	2.76	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1233:G:H1	36:1:1255:C:H42	1.35	0.75
36:1:2112:U:H4'	36:1:2113:A:H5'	1.66	0.75
1:2:1488:G:H3'	1:2:1515:A:H61	1.51	0.75
1:2:1588:G:H1	1:2:1608:U:H3	1.31	0.75
79:Q3:4:ARG:NH2	36:5:838:G:O6	237.29	0.75
20:C8:28:ILE:HD11	20:C8:56:LYS:HB2	7.01	0.75
51:M5:68:ARG:HA	51:M5:98:LEU:HD21	2.64	0.75
76:Q0:77:ILE:HG23	76:Q0:78:ILE:HG22	6.47	0.75
4:S2:56:ILE:HG23	4:S2:61:LEU:HB2	1.74	0.75
36:1:692:A:OP1	51:M5:201:ARG:NH2	2.19	0.75
36:5:1103:A:H3'	36:5:1104:G:H5'	1.68	0.75
21:C9:16:ASN:OD1	21:C9:56:LYS:NZ	5.27	0.75
47:M0:129:VAL:HG22	47:M0:133:GLN:HG2	1.68	0.75
53:M7:25:SER:O	53:M7:29:THR:HG23	1.87	0.75
70:O4:58:ARG:HG3	70:O4:59:PRO:HD2	1.84	0.75
36:5:198:A:N3	36:5:218:G:O2'	2.19	0.75
36:1:2960:C:H2'	36:1:2961:G:C8	2.22	0.75
36:1:3346:U:O2	36:1:3359:A:N6	2.20	0.75
78:Q2:63:LYS:NZ	36:5:2761:G:N7	211.95	0.75
36:1:618:C:H5'	53:M7:169:THR:HG22	1.68	0.75
41:L4:300:ARG:O	54:M8:39:ARG:NH1	2.19	0.75
75:O9:2:ALA:N	36:5:1493:G:O6	123.00	0.75
36:5:3153:U:H4'	36:5:3154:C:H5'	1.68	0.75
1:2:1459:C:OP1	20:C8:126:ARG:NH2	2.20	0.75
44:L7:151:ARG:NH1	44:L7:244:ASN:O	3.13	0.75
59:N3:54:LEU:HD21	59:N3:119:GLY:HA3	2.18	0.75
18:C6:14:LYS:O	18:C6:123:ARG:NH1	2.19	0.75
27:D5:60:VAL:HG22	27:D5:101:TYR:HB2	1.67	0.75
56:N0:77:VAL:HG11	56:N0:106:LEU:HD13	1.69	0.75
64:N8:74:ASN:HB3	64:N8:115:LYS:HB2	1.69	0.75
34:SR:282:SER:H	34:SR:285:ALA:HB3	1.62	0.75
36:1:3275:U:H5'	69:O3:68:TRP:HZ2	1.51	0.74
39:L2:224:THR:HG21	36:5:2201:G:H21	223.26	0.74
63:N7:52:LYS:O	63:N7:65:ARG:NH1	2.20	0.74
69:O3:6:ARG:NH1	69:O3:8:TYR:O	3.09	0.74
2:S0:24:LEU:O	2:S0:163:ASN:ND2	2.20	0.74
32:E0:29:LYS:HG3	32:E0:30:PRO:HD2	4.54	0.74
40:L3:360:ASP:OD2	40:L3:364:LYS:NZ	2.63	0.74
71:O5:78:LYS:HA	71:O5:81:ARG:HD2	1.69	0.74
13:C1:14:GLN:HB3	13:C1:54:ILE:HG13	3.51	0.74
55:M9:62:ARG:NH2	36:5:3068:U:OP2	173.14	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:237:C:H5''	1:2:238:U:H5'	1.69	0.74
5:S3:75:LYS:HB3	12:C0:22:VAL:HG22	3.12	0.74
21:C9:84:LYS:HD2	21:C9:94:ILE:HG13	5.84	0.74
68:O2:100:ILE:O	68:O2:105:ARG:NH1	2.27	0.74
79:Q3:30:GLU:HA	79:Q3:33:GLN:HG2	1.70	0.74
10:S8:8:ARG:NH2	10:S8:19:ALA:O	2.21	0.74
38:4:142:C:OP1	51:M5:38:ARG:NH1	2.20	0.74
36:5:2569:A:H4'	36:5:2570:U:H5'	1.70	0.74
15:C3:65:VAL:HG23	15:C3:66:ILE:HG23	6.37	0.74
6:S4:3:ARG:HB3	1:6:93:A:H1'	327.33	0.74
41:L4:73:ARG:NH2	36:5:2814:G:OP1	172.28	0.74
71:O5:78:LYS:HA	71:O5:81:ARG:HD3	3.15	0.74
34:SR:178:VAL:HB	34:SR:192:PHE:HB2	1.99	0.74
36:1:979:U:H1'	36:1:980:A:C8	2.23	0.73
36:5:2444:C:H42	36:5:2503:G:H1	1.36	0.73
46:L9:18:VAL:HB	46:L9:27:VAL:HG22	1.70	0.73
36:1:1786:G:H2'	36:1:1787:A:C8	2.23	0.73
1:2:1102:G:OP1	24:D2:76:SER:OG	2.05	0.73
36:5:1565:G:N1	36:5:1574:C:N3	2.36	0.73
61:N5:39:LYS:HG3	36:5:13:A:H4'	119.87	0.73
1:2:1561:U:H2'	1:2:1562:G:H8	1.52	0.73
53:M7:109:ALA:HA	53:M7:112:LEU:HD22	1.70	0.73
62:N6:57:LEU:HD23	62:N6:67:GLU:HG2	4.02	0.73
67:O1:19:ARG:HD3	67:O1:35:GLU:HG3	2.31	0.73
36:1:1942:U:HO2'	36:1:3345:G:HO2'	1.34	0.73
38:8:79:A:H3'	38:8:80:A:C8	2.24	0.73
36:5:3274:A:H3'	36:5:3275:U:H5''	1.70	0.73
8:S6:174:LYS:HG3	1:6:79:C:H1'	343.28	0.73
36:1:3375:A:O2'	36:1:3378:C:OP2	2.07	0.73
15:C3:109:LYS:HD2	1:6:975:C:H5''	283.37	0.73
1:2:1773:C:OP2	77:Q1:2:ARG:NH1	2.21	0.73
3:S1:181:LEU:O	3:S1:184:LEU:N	2.22	0.73
1:2:7:G:N7	4:S2:205:ARG:NH1	2.35	0.73
36:1:3214:U:OP2	50:M4:128:ARG:NH2	2.19	0.73
36:1:3343:G:H21	36:1:3362:A:H2	1.36	0.73
36:1:718:G:C2	36:1:721:G:H1'	2.24	0.73
1:2:169:A:H5''	8:S6:176:GLN:HG2	1.70	0.73
47:M0:24:ARG:HG3	47:M0:24:ARG:HH11	1.54	0.73
46:L9:138:THR:O	46:L9:139:ASN:ND2	2.21	0.73
36:1:992:A:H5''	57:N1:43:LYS:HD3	1.71	0.73
70:O4:102:LYS:HB3	70:O4:103:LYS:HE3	4.41	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:80:GLN:NE2	57:N1:135:PRO:O	7.08	0.73
47:M0:142:ASP:OD2	47:M0:178:ARG:NH2	2.53	0.73
6:S4:206:ASP:HB2	6:S4:222:LEU:HD12	2.19	0.72
39:L2:149:ARG:HH22	39:L2:253:GLN:HA	6.17	0.72
36:1:2895:G:O2'	76:Q0:100:TYR:O	2.05	0.72
6:S4:187:ARG:NH2	1:6:753:A:N7	375.00	0.72
36:5:1863:G:N1	36:5:1866:C:OP2	2.22	0.72
47:M0:14:ASN:O	47:M0:128:ARG:NH2	2.25	0.72
49:M3:50:PRO:O	49:M3:52:ASP:N	2.34	0.72
8:S6:98:ARG:NH2	8:S6:101:ILE:O	2.26	0.72
25:D3:102:VAL:HG12	25:D3:127:VAL:HG12	1.71	0.72
40:L3:173:GLN:O	40:L3:175:LYS:N	2.22	0.72
78:Q2:15:LYS:HG3	78:Q2:18:ARG:HH11	5.48	0.72
36:1:837:A:OP2	79:Q3:4:ARG:NH1	2.22	0.72
2:S0:103:THR:O	2:S0:106:SER:OG	2.08	0.72
2:S0:142:PRO:HB3	23:D1:34:ILE:HD13	2.03	0.72
1:2:115:G:OP1	13:C1:67:ARG:NH1	2.22	0.72
18:C6:110:THR:HA	18:C6:113:ASP:HB2	2.38	0.72
22:D0:61:LYS:HG3	22:D0:86:ILE:HB	1.71	0.72
25:D3:57:LEU:HD11	25:D3:73:ARG:HG2	1.71	0.72
36:1:860:G:OP1	79:Q3:17:ARG:NH1	2.20	0.72
8:S6:13:GLN:OE1	1:6:151:G:N2	311.87	0.72
36:1:2216:G:OP1	72:O6:75:LYS:NZ	2.18	0.72
36:1:595:G:H1	36:1:609:G:H5"	1.54	0.72
51:M5:49:ARG:NH2	36:5:115:A:OP1	101.51	0.72
20:C8:145:ARG:NH2	1:6:1460:A:OP2	338.04	0.72
12:C0:21:VAL:HG12	12:C0:66:TYR:HB2	3.85	0.72
1:2:1625:C:OP1	4:S2:91:ARG:NH2	2.23	0.72
56:N0:91:TYR:O	56:N0:137:ARG:NH1	2.50	0.72
61:N5:86:VAL:HG12	61:N5:120:LYS:HB3	1.71	0.72
78:Q2:12:CYS:SG	78:Q2:17:CYS:CB	2.82	0.72
20:C8:57:ARG:NH1	1:6:1534:G:OP2	342.34	0.72
36:1:670:C:OP1	54:M8:147:ARG:NH2	2.23	0.72
7:S5:40:ILE:HG23	7:S5:42:LEU:HD22	1.72	0.72
7:S5:64:VAL:HG12	7:S5:65:ARG:HD3	1.71	0.72
40:L3:152:LYS:HG2	40:L3:192:VAL:HG11	1.72	0.72
46:L9:180:TYR:HB2	76:Q0:85:LEU:HD13	2.09	0.72
38:4:97:A:OP1	71:O5:67:ARG:NH2	2.23	0.71
78:Q2:12:CYS:SG	78:Q2:17:CYS:HB3	2.39	0.71
78:Q2:73:GLU:OE1	78:Q2:80:ARG:NH1	3.51	0.71
6:S4:19:LEU:HD11	6:S4:108:ARG:HD2	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3068:U:OP2	55:M9:62:ARG:NH1	2.21	0.71
1:6:104:A:H61	1:6:308:C:H5'	1.53	0.71
46:L9:20:ILE:HG12	46:L9:25:VAL:HG22	2.69	0.71
6:S4:192:ILE:HG13	6:S4:243:GLY:HA3	1.71	0.71
18:C6:7:VAL:HG12	18:C6:22:VAL:HB	6.64	0.71
1:6:1280:C:H2'	1:6:1281:G:C8	2.25	0.71
45:L8:195:SER:O	45:L8:197:VAL:N	2.23	0.71
46:L9:163:GLN:O	46:L9:166:ARG:NH1	2.24	0.71
31:D9:19:ARG:HD2	31:D9:32:ARG:HD2	1.71	0.71
32:E0:59:GLY:O	32:E0:61:SER:N	3.25	0.71
33:E1:134:ASN:H	1:6:1251:U:H4'	443.61	0.71
36:1:58:G:H4'	51:M5:155:VAL:HG12	1.72	0.71
1:2:1585:U:H3	1:2:1611:A:H2	1.37	0.71
39:L2:241:ARG:NH2	36:5:2156:C:OP2	216.58	0.71
18:C6:40:GLU:HA	18:C6:42:GLU:N	2.06	0.71
38:4:136:G:OP1	61:N5:48:SER:OG	2.08	0.71
67:O1:23:VAL:O	67:O1:28:ARG:NH1	2.24	0.71
36:1:155:G:H5''	36:1:156:G:C8	2.26	0.70
46:L9:120:ASP:OD1	46:L9:124:ARG:NH2	2.23	0.70
36:1:2572:C:O2'	36:1:2573:G:O4'	2.09	0.70
20:C8:143:ARG:NH2	1:6:1462:G:N7	340.54	0.70
1:2:1544:U:OP1	20:C8:136:GLN:NE2	2.24	0.70
43:L6:31:ARG:NH2	43:L6:81:ALA:O	2.24	0.70
3:S1:129:THR:OG1	3:S1:131:ASP:O	2.74	0.70
1:2:138:A:OP2	1:2:1706:C:O2'	2.09	0.70
24:D2:15:ASN:HD21	24:D2:71:LYS:HA	1.56	0.70
45:L8:33:ASN:O	45:L8:35:GLY:N	3.36	0.70
52:M6:172:ARG:NH1	36:5:3190:C:OP1	305.64	0.70
3:S1:72:ASP:OD1	16:C4:114:ARG:NH1	3.52	0.70
73:O7:21:ARG:NH2	73:O7:41:ALA:O	2.24	0.70
7:S5:90:ILE:HD11	7:S5:130:ILE:HG13	1.83	0.70
36:1:2688:U:OP1	42:L5:12:TYR:OH	2.09	0.70
1:2:1122:G:N2	1:2:1125:A:OP2	2.24	0.70
1:2:513:U:OP1	11:S9:133:HIS:NE2	2.21	0.70
14:C2:61:VAL:HG13	14:C2:121:VAL:HG23	1.76	0.70
19:C7:47:ARG:NH1	19:C7:48:ASN:OD1	2.23	0.70
42:L5:144:VAL:HG12	42:L5:173:VAL:HG22	1.74	0.70
56:N0:23:LYS:O	57:N1:146:ASN:ND2	2.22	0.70
63:N7:16:GLY:O	63:N7:18:TYR:N	2.25	0.70
17:C5:68:PRO:HG2	17:C5:71:GLU:HB3	1.73	0.70
2:S0:124:THR:HG22	2:S0:174:TRP:HE1	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1382:A:H5''	22:D0:60:THR:HG22	1.73	0.70
1:2:788:A:H2'	6:S4:19:LEU:HD22	1.74	0.70
1:6:1000:C:N4	1:6:1003:A:OP2	2.24	0.70
13:C1:6:THR:O	13:C1:8:GLN:N	2.25	0.70
21:C9:28:LEU:HA	21:C9:111:ILE:HD11	5.06	0.70
63:N7:46:ILE:HD13	63:N7:68:ILE:HG23	1.74	0.70
1:2:104:A:OP2	1:2:308:C:N4	2.24	0.70
48:M1:137:ARG:NH1	37:7:28:C:OP1	302.29	0.70
21:C9:52:GLY:O	21:C9:54:PHE:N	2.24	0.70
1:2:68:A:H5'	8:S6:160:ARG:HH12	1.56	0.70
36:5:437:G:H1	36:5:622:A:H61	1.40	0.70
14:C2:36:LEU:HG	14:C2:41:LEU:HD12	1.74	0.70
65:N9:23:LYS:HB3	65:N9:24:PRO:CD	2.91	0.70
34:SR:133:VAL:HB	34:SR:142:ALA:HB3	1.72	0.70
1:2:484:C:H42	1:2:503:G:H22	1.38	0.69
25:D3:79:ASN:HB2	25:D3:81:LYS:H	1.77	0.69
46:L9:149:ASN:N	46:L9:149:ASN:OD1	2.25	0.69
62:N6:3:LYS:NZ	62:N6:5:SER:O	3.91	0.69
11:S9:106:GLU:O	11:S9:111:THR:OG1	2.64	0.69
36:5:1238:C:O2'	36:5:1239:C:OP1	2.06	0.69
13:C1:6:THR:HB	13:C1:9:SER:HB3	1.74	0.69
41:L4:44:LYS:HB3	41:L4:47:ARG:HH11	1.56	0.69
71:O5:90:ARG:NH1	36:5:20:A:OP2	86.60	0.69
12:C0:16:PHE:HD2	12:C0:76:LEU:HD23	1.58	0.69
10:S8:76:THR:HG22	10:S8:108:PRO:HG2	1.73	0.69
41:L4:144:LYS:HG2	41:L4:145:ILE:H	5.14	0.69
41:L4:203:ARG:NH1	41:L4:226:GLU:OE2	2.25	0.69
36:1:1603:A:OP1	55:M9:38:ARG:NH1	2.25	0.69
1:2:190:C:N4	1:2:196:G:O6	2.19	0.69
21:C9:102:ARG:NH2	1:6:1502:G:N7	407.22	0.69
23:D1:74:GLN:HG2	23:D1:79:LEU:HB2	4.30	0.69
8:S6:137:ARG:HH12	1:6:144:U:H5	312.80	0.69
11:S9:129:ILE:HG22	11:S9:142:ASN:HA	1.73	0.69
70:O4:74:ARG:NH2	36:5:1639:C:OP2	200.65	0.69
36:1:148:G:OP2	51:M5:4:TYR:OH	2.07	0.69
28:D6:95:ARG:NH1	1:6:1796:C:O2'	342.86	0.69
71:O5:49:LYS:NZ	38:8:63:G:O2'	49.64	0.69
17:C5:18:ARG:NH1	20:C8:90:ASN:O	3.35	0.69
3:S1:157:GLN:NE2	1:6:1046:G:OP1	327.66	0.69
64:N8:96:LYS:O	64:N8:98:THR:N	2.26	0.69
3:S1:134:VAL:HB	3:S1:219:LYS:HB2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:49:ARG:NH2	6:S4:50:ASN:OD1	4.51	0.69
42:L5:76:ALA:HB3	42:L5:109:THR:HG22	1.90	0.69
1:2:399:A:H4'	6:S4:3:ARG:HG2	1.73	0.69
7:S5:102:ARG:NH1	1:6:1473:U:O2'	355.39	0.69
24:D2:119:LYS:HG2	1:6:687:G:H5''	394.31	0.69
1:6:800:U:H2'	1:6:801:G:H8	1.58	0.69
17:C5:10:ARG:HA	48:M1:88:GLU:HB3	11.70	0.69
46:L9:22:SER:OG	46:L9:23:ARG:N	2.25	0.69
48:M1:9:MET:O	48:M1:11:ASP:N	3.56	0.69
62:N6:37:LYS:H	62:N6:37:LYS:HD3	1.85	0.69
36:1:1634:G:N7	63:N7:17:ARG:NH2	2.41	0.69
67:O1:72:ARG:NH1	67:O1:105:GLN:O	3.40	0.69
5:S3:204:ASP:OD1	1:6:1330:G:N2	421.91	0.69
36:5:591:G:N2	36:5:612:U:OP1	2.26	0.69
17:C5:126:VAL:HG13	17:C5:127:ARG:H	1.64	0.69
59:N3:39:VAL:O	59:N3:42:SER:OG	3.08	0.69
3:S1:127:VAL:HG11	3:S1:176:VAL:HG21	1.75	0.69
1:2:127:G:N7	8:S6:202:ARG:NH2	2.41	0.69
36:1:1076:C:O3'	65:N9:38:LYS:NZ	2.26	0.68
36:1:1794:G:H4'	39:L2:191:LEU:HD13	1.73	0.68
47:M0:86:HIS:HB3	47:M0:139:ARG:HG2	2.04	0.68
59:N3:10:LYS:NZ	59:N3:56:ASP:OD1	2.25	0.68
36:1:1748:G:OP1	74:O8:44:LYS:NZ	2.25	0.68
1:2:140:A:OP2	8:S6:187:LYS:NZ	2.25	0.68
16:C4:85:ALA:H	16:C4:119:THR:HG22	1.57	0.68
39:L2:114:SER:HB2	39:L2:169:ILE:HD12	1.95	0.68
41:L4:269:SER:O	41:L4:271:LYS:N	2.24	0.68
51:M5:110:ALA:HB1	51:M5:113:LEU:HD23	1.75	0.68
68:O2:81:ASP:O	68:O2:84:THR:HG23	1.94	0.68
8:S6:161:GLU:HG2	8:S6:170:THR:HG22	4.84	0.68
15:C3:34:ILE:HG13	15:C3:67:THR:HG21	1.76	0.68
46:L9:21:LYS:HA	50:M4:8:LYS:HG3	1.74	0.68
48:M1:59:ILE:HG21	48:M1:65:ILE:HD11	1.74	0.68
1:2:1034:C:HO2'	24:D2:2:THR:N	1.92	0.68
1:2:1584:G:N2	1:2:1611:A:OP2	2.18	0.68
1:2:734:A:H5''	1:2:735:C:OP1	1.93	0.68
56:N0:115:ARG:NH2	36:5:1320:C:O2	289.53	0.68
13:C1:33:ARG:NH1	13:C1:53:TYR:O	3.56	0.68
11:S9:163:PRO:HB3	11:S9:169:PRO:HA	2.98	0.68
36:1:3165:A:H61	36:1:3285:C:H42	1.39	0.68
1:6:754:A:N6	1:6:793:A:N7	2.35	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:D0:51:VAL:HG13	22:D0:94:GLU:HB2	1.75	0.68
39:L2:213:GLY:HA3	36:5:2967:A:H5''	205.58	0.68
39:L2:238:ILE:O	39:L2:240:ALA:N	2.90	0.68
51:M5:31:ARG:NH1	51:M5:124:ASP:OD1	2.44	0.68
62:N6:45:ILE:HD12	62:N6:119:ILE:HG23	1.74	0.68
3:S1:28:GLU:OE2	3:S1:94:LYS:NZ	2.26	0.68
6:S4:159:THR:HG22	6:S4:173:ILE:HB	1.76	0.68
36:1:1381:A:OP1	41:L4:197:ARG:NH1	2.27	0.68
42:L5:77:ALA:O	42:L5:108:ARG:NH1	2.26	0.68
53:M7:105:LYS:HB3	53:M7:107:LEU:HD13	2.06	0.68
8:S6:57:ASP:HA	8:S6:106:LEU:HA	1.76	0.68
36:1:1095:U:H4'	36:1:1096:U:H5'	1.75	0.68
1:2:1254:U:OP2	14:C2:46:ARG:NH1	2.27	0.68
1:2:588:U:OP2	32:E0:26:LYS:NZ	2.27	0.68
40:L3:25:ILE:H	40:L3:25:ILE:HD13	1.59	0.68
57:N1:51:GLY:HA3	57:N1:92:ARG:HG3	1.75	0.68
49:M3:128:ARG:NH1	71:O5:109:ILE:O	3.56	0.68
1:2:1437:U:H5'	5:S3:176:LEU:HD23	1.76	0.68
36:1:18:G:OP1	71:O5:81:ARG:NH2	2.26	0.68
36:1:2534:G:H2'	36:1:2535:A:H8	1.58	0.68
21:C9:117:SER:HB2	21:C9:123:ARG:HB3	2.71	0.68
51:M5:49:ARG:NH1	36:5:149:U:OP2	101.34	0.68
63:N7:128:GLN:O	63:N7:130:PHE:N	3.49	0.68
9:S7:28:GLU:HG2	9:S7:35:LYS:HG3	1.76	0.68
8:S6:159:ARG:NH2	1:6:79:C:OP1	350.77	0.68
13:C1:74:THR:HG22	13:C1:122:ILE:HG13	1.75	0.68
24:D2:26:LEU:HD21	24:D2:60:LYS:HD3	1.76	0.68
1:2:284:G:N7	8:S6:188:ARG:NH1	2.42	0.68
36:1:551:A:O2'	36:1:552:G:O5'	2.10	0.68
8:S6:4:ASN:ND2	1:6:152:U:O2	308.21	0.68
67:O1:78:LYS:HB2	67:O1:90:PHE:HB2	5.64	0.68
36:1:595:G:N1	36:1:609:G:H5''	2.08	0.67
1:2:134:U:OP1	1:2:136:C:N4	2.24	0.67
1:2:591:A:H2'	1:2:592:A:C8	2.30	0.67
1:2:901:G:OP2	1:2:901:G:N2	2.18	0.67
8:S6:187:LYS:NZ	1:6:140:A:OP2	324.01	0.67
1:6:755:A:H2'	1:6:756:A:C8	2.29	0.67
21:C9:37:VAL:HG11	21:C9:100:ILE:HD11	1.75	0.67
41:L4:33:ASP:OD1	41:L4:34:ILE:N	2.26	0.67
7:S5:166:ARG:NH1	7:S5:170:GLN:OE1	2.27	0.67
11:S9:41:GLU:OE1	11:S9:126:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:145:A:O2'	1:2:146:U:O5'	2.12	0.67
41:L4:195:ARG:NH2	36:5:341:G:N7	110.53	0.67
39:L2:128:ARG:NH1	36:5:2177:G:OP2	199.04	0.67
42:L5:279:LYS:HE3	42:L5:282:ARG:HH12	1.57	0.67
42:L5:68:THR:HG22	42:L5:70:THR:H	1.58	0.67
73:O7:2:GLY:N	36:5:2138:A:HO2'	174.50	0.67
1:2:478:A:O2'	11:S9:124:HIS:ND1	2.26	0.67
37:3:10:C:OP2	57:N1:26:HIS:ND1	2.27	0.67
18:C6:46:PHE:HA	18:C6:49:TYR:HB2	1.77	0.67
24:D2:27:ILE:HG12	24:D2:61:ILE:HB	1.75	0.67
36:1:73:C:N3	49:M3:59:ARG:NH1	2.43	0.67
4:S2:103:VAL:HG12	4:S2:190:LEU:HD12	1.76	0.67
36:5:2537:U:O2'	36:5:2538:U:O4'	2.13	0.67
50:M4:48:GLY:HA3	50:M4:53:VAL:HG13	1.95	0.67
2:S0:55:GLU:OE2	23:D1:80:LYS:N	2.72	0.67
8:S6:153:VAL:O	8:S6:155:ASP:N	2.28	0.67
47:M0:158:LYS:NZ	36:5:2852:C:N3	308.80	0.67
50:M4:88:ALA:O	50:M4:93:LYS:NZ	2.28	0.67
34:SR:13:LEU:HB2	34:SR:310:ILE:HB	1.77	0.67
1:2:1291:G:H22	1:2:1324:G:H22	1.42	0.67
1:2:781:U:HO2'	1:2:782:U:H6	1.41	0.67
6:S4:133:LYS:NZ	1:6:206:A:OP1	315.44	0.67
29:D7:20:LYS:NZ	1:6:959:U:OP2	349.04	0.67
13:C1:133:LYS:O	13:C1:136:ARG:NH1	3.75	0.67
39:L2:193:ARG:NH1	36:5:2174:G:OP2	191.29	0.67
47:M0:180:GLU:OE2	47:M0:184:LYS:NZ	2.27	0.67
53:M7:69:ARG:HG2	53:M7:79:THR:HG23	5.03	0.67
44:L7:121:LYS:HB2	57:N1:133:ALA:HB3	1.77	0.67
1:2:761:G:OP1	11:S9:54:ARG:NH1	2.27	0.67
42:L5:148:ILE:HG23	42:L5:151:GLN:HB3	2.62	0.67
1:2:1537:C:O2'	1:2:1540:G:O6	2.12	0.67
64:N8:4:ARG:NH2	36:5:1427:U:OP2	135.00	0.67
39:L2:21:ARG:HD3	36:5:824:C:H5''	170.94	0.67
1:6:340:U:H2'	1:6:341:A:C8	2.29	0.67
1:6:822:U:H2'	1:6:823:G:H5''	1.75	0.67
14:C2:66:VAL:HG11	14:C2:71:ILE:HD12	1.77	0.67
24:D2:6:VAL:HG13	24:D2:29:PRO:HD2	1.75	0.67
44:L7:134:VAL:O	44:L7:229:PHE:HA	2.76	0.67
45:L8:134:TYR:CG	45:L8:190:VAL:HG11	3.53	0.67
48:M1:54:VAL:O	48:M1:56:THR:N	2.28	0.67
5:S3:63:GLY:O	5:S3:67:ASN:ND2	5.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:S7:177:THR:OG1	9:S7:178:GLY:N	2.28	0.67
39:L2:241:ARG:HH22	36:5:2156:C:P	214.63	0.67
36:5:3241:G:H2'	36:5:3245:A:C8	2.30	0.67
14:C2:87:PRO:HA	14:C2:140:PHE:HE1	1.83	0.67
42:L5:58:LYS:HD2	42:L5:93:THR:HG21	1.77	0.67
3:S1:229:MET:SD	3:S1:232:HIS:ND1	2.61	0.67
6:S4:178:GLY:H	6:S4:195:ILE:HB	2.04	0.67
34:SR:180:ALA:HB3	34:SR:190:ALA:HB3	1.77	0.67
17:C5:30:THR:HG23	17:C5:86:VAL:HG21	1.77	0.66
33:E1:91:ILE:HG12	33:E1:92:LYS:HG2	6.48	0.66
36:1:2645:G:OP2	47:M0:117:GLY:HA2	1.95	0.66
53:M7:138:LYS:NZ	36:5:2356:A:OP1	147.94	0.66
65:N9:14:ARG:CZ	65:N9:18:ARG:HD3	2.25	0.66
36:5:1231:A:H5''	36:5:1232:C:H5'	1.77	0.66
73:O7:31:LYS:NZ	36:5:815:G:OP2	139.60	0.66
3:S1:71:ALA:HB3	16:C4:114:ARG:HH12	1.61	0.66
13:C1:99:ARG:NH1	25:D3:7:ARG:O	2.27	0.66
42:L5:64:ILE:HG13	42:L5:109:THR:HG21	4.08	0.66
46:L9:126:VAL:HG21	46:L9:161:LEU:HA	1.88	0.66
47:M0:29:SER:HB2	47:M0:125:LEU:HD12	5.10	0.66
48:M1:15:GLU:HB3	48:M1:130:VAL:HG22	2.01	0.66
52:M6:65:ASN:HB3	52:M6:68:ARG:HD2	2.93	0.66
1:6:1080:U:H2'	1:6:1081:A:C8	2.29	0.66
26:D4:35:VAL:HG13	26:D4:36:SER:H	1.60	0.66
37:3:44:C:OP2	48:M1:137:ARG:NH2	2.28	0.66
52:M6:61:ALA:HA	52:M6:70:PRO:HD2	1.99	0.66
5:S3:222:VAL:HG11	34:SR:229:LYS:HA	3.22	0.66
36:1:994:G:N2	36:1:995:U:O4	2.29	0.66
1:2:93:A:H1'	6:S4:3:ARG:HB3	1.78	0.66
43:L6:26:ARG:NH2	36:5:607:A:OP1	250.28	0.66
13:C1:57:LYS:HD3	13:C1:131:ILE:HG23	1.76	0.66
27:D5:46:LYS:HD3	27:D5:70:LYS:HD2	1.76	0.66
59:N3:28:ASN:HD21	59:N3:112:SER:H	2.48	0.66
5:S3:160:SER:O	1:6:1420:C:O2'	416.37	0.66
9:S7:50:ASP:HB3	9:S7:56:LYS:HG2	1.77	0.66
36:5:1717:U:H2'	36:5:1718:G:C8	2.31	0.66
49:M3:55:ARG:O	49:M3:115:ARG:NH2	2.29	0.66
36:1:2295:A:OP1	59:N3:63:LYS:NZ	2.29	0.66
63:N7:25:ILE:HA	63:N7:43:VAL:HG12	2.26	0.66
3:S1:62:LYS:O	3:S1:64:ARG:N	2.27	0.66
8:S6:164:LYS:HB3	8:S6:167:LYS:HB3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2115:G:H22	36:1:2120:A:H1'	1.60	0.66
1:6:1738:U:H2'	1:6:1739:C:C6	2.30	0.66
62:N6:3:LYS:HD2	62:N6:8:VAL:HG23	4.33	0.66
3:S1:157:GLN:O	3:S1:159:SER:N	2.29	0.66
9:S7:144:VAL:HG13	24:D2:49:GLU:HB3	1.77	0.66
34:SR:89:LEU:HB2	34:SR:103:PHE:HB2	1.77	0.66
36:1:1951:C:H42	36:1:2095:G:H1	1.43	0.66
28:D6:87:ARG:NH2	28:D6:94:ASN:O	2.28	0.66
78:Q2:47:GLN:NE2	78:Q2:54:THR:OG1	2.29	0.66
79:Q3:38:ASP:HA	79:Q3:45:LYS:HA	1.78	0.66
34:SR:258:THR:O	34:SR:275:ARG:NH1	2.29	0.66
36:1:2162:U:OP1	39:L2:234:LYS:NZ	2.28	0.66
1:2:523:G:OP2	26:D4:37:LYS:NZ	2.25	0.66
51:M5:172:ARG:NH2	36:5:63:A:OP1	104.19	0.66
42:L5:211:LEU:HB3	42:L5:219:PHE:HB2	1.83	0.66
44:L7:88:ARG:NH1	44:L7:91:GLY:O	2.52	0.66
45:L8:90:THR:HA	45:L8:214:LEU:HD21	1.77	0.66
47:M0:99:ILE:HG13	47:M0:123:HIS:HB2	4.77	0.66
48:M1:148:VAL:HG12	48:M1:152:HIS:HB3	2.58	0.66
62:N6:11:ASP:HB3	62:N6:14:LYS:HG3	2.62	0.66
63:N7:53:VAL:HG21	63:N7:62:VAL:HG13	1.78	0.66
79:Q3:39:CYS:HB3	79:Q3:42:CYS:HB3	4.36	0.66
11:S9:93:LEU:HA	11:S9:96:VAL:HG13	1.78	0.66
36:5:3280:U:O2'	36:5:3281:U:H5''	1.96	0.66
1:6:27:U:H2'	1:6:28:A:H8	1.61	0.66
30:D8:10:ALA:HA	30:D8:32:PHE:HA	1.78	0.66
33:E1:126:CYS:HB3	33:E1:130:VAL:HG21	2.76	0.66
40:L3:56:ILE:HD11	40:L3:359:ILE:HG12	1.78	0.66
45:L8:81:THR:OG1	45:L8:82:LEU:N	3.05	0.66
59:N3:10:LYS:HD2	59:N3:13:ILE:HD11	1.78	0.66
36:1:1043:C:O3'	47:M0:90:ARG:NH1	2.28	0.65
17:C5:111:MET:HG2	20:C8:119:ILE:HG23	1.77	0.65
61:N5:58:ASP:OD1	71:O5:25:LYS:NZ	2.26	0.65
3:S1:183:GLN:HG2	3:S1:187:LYS:HE3	1.78	0.65
1:2:581:U:OP2	5:S3:143:ARG:NH1	2.28	0.65
6:S4:3:ARG:HG2	1:6:399:A:H4'	321.35	0.65
36:1:3047:U:O2'	40:L3:53:MET:HE1	1.95	0.65
1:2:1794:A:H1'	28:D6:79:ILE:HD12	1.77	0.65
1:2:732:G:O2'	1:2:733:A:O4'	2.15	0.65
18:C6:66:ARG:NH1	1:6:1351:G:OP1	436.75	0.65
42:L5:110:LEU:HA	42:L5:113:LEU:HB2	3.16	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:N1:39:ILE:HD12	57:N1:102:ARG:HE	4.63	0.65
36:1:1555:U:H5	36:1:1559:A:H61	1.44	0.65
36:5:979:U:H1'	36:5:980:A:C4	2.31	0.65
1:6:1569:A:H8	1:6:1569:A:OP2	1.78	0.65
11:S9:78:ARG:NH1	1:6:764:U:OP2	420.82	0.65
11:S9:82:ARG:HH11	11:S9:149:ARG:HD3	8.41	0.65
36:1:1564:U:H2'	36:1:1565:G:C8	2.31	0.65
36:1:3057:U:O2'	36:1:3059:G:OP1	2.14	0.65
36:5:2818:U:H6	36:5:2818:U:H5'	1.62	0.65
1:6:895:G:H1	1:6:917:U:H3	1.44	0.65
22:D0:106:ILE:HG23	22:D0:107:THR:HG23	1.77	0.65
46:L9:171:ASP:OD2	46:L9:173:ARG:NH1	2.29	0.65
51:M5:96:ARG:NH2	51:M5:104:GLU:OE2	3.74	0.65
72:O6:76:ARG:HA	72:O6:76:ARG:HE	2.58	0.65
3:S1:173:THR:O	3:S1:177:GLN:NE2	2.29	0.65
36:1:1307:G:H1'	36:1:1308:A:C8	2.31	0.65
1:6:228:G:H1	1:6:236:A:H61	1.45	0.65
53:M7:129:THR:HG23	53:M7:139:TYR:HB2	1.78	0.65
63:N7:124:ALA:O	63:N7:126:LYS:N	2.30	0.65
3:S1:69:CYS:SG	16:C4:114:ARG:NH1	2.70	0.65
1:2:514:G:H1	1:2:543:C:H5	1.45	0.65
36:5:1064:A:N6	36:5:1096:U:H3	1.93	0.65
23:D1:74:GLN:HE22	23:D1:83:TRP:H	1.42	0.65
40:L3:92:TYR:HB2	40:L3:157:VAL:HG13	4.13	0.65
41:L4:292:SER:OG	41:L4:293:SER:N	2.29	0.65
63:N7:26:VAL:HG21	63:N7:96:VAL:HB	1.76	0.65
10:S8:36:THR:HG21	10:S8:173:PRO:HB2	1.97	0.65
39:L2:152:SER:OG	36:5:2157:G:N7	217.87	0.65
36:1:2880:U:H1'	40:L3:250:ALA:HB3	1.78	0.65
41:L4:35:VAL:HG21	41:L4:244:LEU:HD21	1.77	0.65
3:S1:147:ALA:O	3:S1:148:ASN:ND2	2.22	0.65
11:S9:65:LYS:HA	11:S9:70:LEU:HD11	2.12	0.65
36:1:114:A:N1	36:1:266:A:O2'	2.28	0.65
48:M1:137:ARG:HG2	37:7:28:C:H5''	307.59	0.65
15:C3:56:ASP:OD2	29:D7:52:THR:OG1	3.97	0.65
23:D1:41:GLU:O	23:D1:44:ARG:NH1	2.30	0.65
79:Q3:56:THR:HG22	79:Q3:63:THR:HG23	1.79	0.65
2:S0:74:VAL:HG23	2:S0:118:PRO:HB3	2.05	0.65
8:S6:78:THR:HG23	8:S6:92:ARG:HG2	3.48	0.65
36:1:2592:G:H4'	36:1:2594:C:C2	2.31	0.65
55:M9:60:LYS:NZ	36:5:1671:C:OP1	170.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1750:A:H4'	36:5:1751:G:H5'	1.78	0.65
24:D2:30:SER:HA	24:D2:34:ILE:HD12	1.78	0.65
47:M0:177:ASP:OD2	47:M0:177:ASP:N	3.35	0.65
52:M6:190:VAL:HA	52:M6:193:GLN:HB2	2.80	0.65
63:N7:29:HIS:O	63:N7:31:GLU:N	2.29	0.65
36:1:2150:G:H4'	79:Q3:22:LEU:HD21	1.78	0.65
79:Q3:39:CYS:CB	79:Q3:42:CYS:HB3	4.94	0.65
36:1:1815:U:O2'	36:1:1816:A:OP2	2.12	0.65
50:M4:38:ILE:HD11	56:N0:150:PHE:HE2	1.62	0.65
68:O2:62:LYS:NZ	36:5:590:G:OP1	202.72	0.65
4:S2:161:LYS:HG3	4:S2:166:THR:HG22	1.87	0.65
6:S4:45:ILE:HG13	6:S4:61:VAL:HG21	2.37	0.65
10:S8:138:ASN:OD1	10:S8:138:ASN:N	2.30	0.65
36:1:3067:C:OP1	55:M9:58:HIS:NE2	2.25	0.64
68:O2:44:ARG:NH1	36:5:1145:G:OP1	207.54	0.64
1:6:1600:A:H4'	1:6:1601:G:OP1	1.96	0.64
1:6:218:A:H2'	1:6:219:A:H5''	1.78	0.64
1:6:67:A:O2'	1:6:69:G:OP1	2.11	0.64
15:C3:22:ALA:HB1	15:C3:23:PRO:HA	1.86	0.64
22:D0:27:THR:HB	22:D0:88:LYS:HG3	1.79	0.64
40:L3:303:LYS:HD2	40:L3:361:THR:HG21	1.78	0.64
42:L5:95:TRP:CH2	42:L5:181:PRO:HD3	4.61	0.64
44:L7:173:LEU:HD21	44:L7:198:ALA:HA	2.01	0.64
36:1:1603:A:H61	61:N5:71:THR:HG21	1.61	0.64
1:6:500:C:O2'	1:6:501:U:O4'	2.16	0.64
17:C5:126:VAL:O	17:C5:127:ARG:HB2	2.49	0.64
46:L9:62:ARG:NH2	36:5:3115:C:OP1	330.81	0.64
34:SR:216:LYS:HA	34:SR:239:GLU:HG3	1.78	0.64
36:1:1722:U:OP1	55:M9:100:ARG:NH1	2.25	0.64
36:5:2180:G:H2'	36:5:2181:C:C6	2.32	0.64
18:C6:139:GLN:NE2	1:6:1465:C:OP1	355.15	0.64
17:C5:44:ARG:NH2	17:C5:82:ASN:O	3.54	0.64
61:N5:105:VAL:HG11	61:N5:126:LEU:HD13	1.79	0.64
2:S0:120:LEU:HD11	2:S0:144:ILE:HG13	1.79	0.64
36:5:2209:U:H1'	36:5:2210:G:H5''	1.79	0.64
27:D5:96:SER:O	27:D5:98:GLN:N	2.28	0.64
38:4:41:A:O2'	73:O7:59:THR:HG22	1.97	0.64
36:1:542:G:H1	36:1:549:U:H3	1.43	0.64
1:2:814:A:H5''	55:M9:170:ARG:HH22	1.62	0.64
1:6:1524:A:H2'	1:6:1525:A:C8	2.32	0.64
10:S8:10:LYS:NZ	1:6:339:C:OP2	284.91	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:C9:38:LYS:O	21:C9:40:SER:N	2.28	0.64
22:D0:69:LYS:HE2	22:D0:80:GLU:HB2	1.79	0.64
70:O4:8:ARG:HH21	70:O4:31:ARG:HD2	2.07	0.64
37:3:110:G:OP2	42:L5:279:LYS:NZ	2.25	0.64
51:M5:14:LYS:HE2	36:5:269:G:H5''	133.21	0.64
12:C0:52:LYS:HE3	1:6:1220:C:H5'	444.49	0.64
13:C1:17:PRO:HG3	13:C1:63:LEU:HD11	2.21	0.64
41:L4:26:PHE:HD1	41:L4:130:ALA:HB2	2.39	0.64
48:M1:143:ARG:NH2	37:7:5:G:OP1	292.97	0.64
49:M3:113:VAL:HG12	49:M3:117:LYS:HE3	3.55	0.64
54:M8:100:THR:HG22	54:M8:120:GLU:HB3	3.31	0.64
54:M8:71:LEU:HD13	54:M8:99:THR:HG21	1.79	0.64
36:1:1245:A:H3'	36:1:1246:G:H5''	1.78	0.64
1:2:246:G:N2	13:C1:38:ALA:O	2.31	0.64
1:2:886:U:O2	16:C4:123:SER:N	2.27	0.64
25:D3:65:ASN:ND2	25:D3:116:ASP:OD1	2.31	0.64
36:1:1349:G:H5'	41:L4:291:ASN:OD1	1.98	0.64
41:L4:93:MET:H	41:L4:93:MET:HE2	2.50	0.64
44:L7:103:LEU:HA	44:L7:130:ILE:HD11	4.80	0.64
36:1:2828:G:OP1	47:M0:7:ARG:NH1	2.31	0.64
6:S4:71:LYS:HG3	6:S4:91:THR:HB	1.80	0.64
34:SR:82:SER:OG	34:SR:92:TRP:NE1	2.80	0.64
1:2:1242:A:OP1	17:C5:59:LYS:NZ	2.30	0.64
1:2:741:C:O2	9:S7:107:ARG:NH2	2.30	0.64
49:M3:15:ARG:NH2	36:5:96:G:OP1	154.90	0.64
16:C4:121:VAL:O	1:6:886:U:O2'	288.55	0.64
40:L3:238:LEU:HB3	40:L3:242:THR:HG21	2.10	0.64
42:L5:54:ARG:NH2	42:L5:147:ASP:OD1	2.98	0.64
47:M0:175:ASN:OD1	47:M0:176:LEU:N	5.05	0.64
47:M0:54:SER:HB3	47:M0:135:ILE:HD11	1.80	0.64
34:SR:220:ILE:HB	34:SR:234:LEU:HB2	2.45	0.64
36:1:3151:U:H4'	36:1:3294:A:H1'	1.79	0.64
1:2:280:U:HO2'	1:2:281:G:P	2.21	0.64
1:2:380:U:O2	11:S9:3:ARG:NH2	2.31	0.64
17:C5:37:ALA:O	17:C5:42:ARG:NH1	4.65	0.64
24:D2:82:LYS:O	24:D2:84:GLY:N	2.27	0.64
41:L4:82:THR:HG23	41:L4:84:ARG:H	1.62	0.64
45:L8:162:LEU:HA	51:M5:7:LEU:HD11	1.80	0.64
56:N0:77:VAL:HG13	56:N0:126:VAL:HG22	2.24	0.64
74:O8:31:LEU:HA	74:O8:37:PRO:HA	1.80	0.64
10:S8:162:ALA:HA	36:1:3353:G:H5'	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:40:A:OP1	11:S9:3:ARG:NH1	2.29	0.64
36:1:1564:U:H2'	36:1:1565:G:H8	1.63	0.64
53:M7:67:ILE:HD11	36:5:1447:G:H3'	165.11	0.64
46:L9:70:THR:HG21	36:5:3122:A:N1	324.72	0.64
64:N8:6:THR:HG22	64:N8:9:ARG:HG2	1.80	0.64
11:S9:108:ARG:HH21	11:S9:145:SER:HB2	1.63	0.64
36:1:1240:A:H2	36:1:1248:C:H41	1.46	0.63
1:6:1537:C:O2'	1:6:1540:G:O6	2.16	0.63
23:D1:60:ARG:HA	23:D1:65:SER:HB2	2.06	0.63
4:S2:69:ILE:HG12	4:S2:133:LYS:HB3	2.77	0.63
8:S6:12:SER:HB3	8:S6:124:LEU:HD12	2.17	0.63
36:1:1631:C:OP2	63:N7:48:ARG:NH2	2.31	0.63
36:1:3276:G:H1	69:O3:60:ARG:HH22	1.46	0.63
47:M0:174:THR:OG1	47:M0:175:ASN:O	5.24	0.63
64:N8:47:LYS:O	64:N8:49:HIS:N	2.60	0.63
64:N8:82:ILE:HD11	64:N8:102:ILE:HG12	3.17	0.63
3:S1:36:SER:O	3:S1:38:PHE:N	2.29	0.63
20:C8:120:ARG:NH2	35:SM:58:GLU:OE1	2.26	0.63
34:SR:123:ILE:HG22	34:SR:133:VAL:HG22	1.78	0.63
36:5:2996:U:OP1	36:5:2996:U:H4'	1.97	0.63
25:D3:125:VAL:HG12	25:D3:126:LYS:HG3	2.06	0.63
28:D6:87:ARG:HB3	28:D6:91:ASP:HB2	1.83	0.63
36:1:1592:G:OP2	70:O4:37:LYS:NZ	2.20	0.63
36:1:1672:U:OP2	55:M9:60:LYS:NZ	2.32	0.63
14:C2:103:LEU:HG	14:C2:116:VAL:HG22	1.81	0.63
40:L3:347:SER:HB3	40:L3:350:ALA:H	1.64	0.63
42:L5:83:LEU:HB3	42:L5:88:ILE:HB	1.90	0.63
53:M7:67:ILE:HD12	53:M7:82:ARG:CZ	3.98	0.63
55:M9:173:ARG:HH21	55:M9:177:VAL:HG21	10.19	0.63
10:S8:110:ARG:HH22	10:S8:160:PHE:HB3	4.35	0.63
10:S8:39:GLY:HA2	10:S8:61:GLU:HB3	1.80	0.63
1:2:149:C:O2'	8:S6:132:ARG:NH1	2.31	0.63
36:1:22:G:N2	38:4:35:C:O2	2.19	0.63
55:M9:135:LYS:NZ	36:5:1949:G:OP2	225.93	0.63
36:5:439:C:H4'	36:5:440:A:H5'	1.80	0.63
1:6:1620:C:H2'	1:6:1621:U:H6	1.64	0.63
15:C3:93:LYS:HG3	15:C3:150:VAL:HG21	3.05	0.63
36:1:1362:G:H4'	44:L7:159:GLN:O	1.98	0.63
45:L8:48:ARG:NH2	36:5:2588:U:OP1	184.36	0.63
36:1:2736:A:OP1	57:N1:92:ARG:NH1	2.32	0.63
61:N5:48:SER:OG	61:N5:49:LYS:N	3.68	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2617:U:H5	36:1:2621:G:OP2	1.80	0.63
26:D4:37:LYS:NZ	1:6:523:G:OP2	415.64	0.63
1:6:845:G:H2'	1:6:846:G:H8	1.64	0.63
18:C6:109:PHE:O	18:C6:113:ASP:N	2.63	0.63
40:L3:249:VAL:HG22	40:L3:252:ILE:HD12	5.30	0.63
64:N8:21:ARG:NH1	36:5:1369:A:OP1	182.92	0.63
65:N9:16:ALA:O	65:N9:20:GLY:HA3	4.58	0.63
36:1:1107:C:OP1	65:N9:25:LYS:NZ	2.30	0.63
72:O6:63:ASN:O	72:O6:65:GLY:N	4.77	0.63
8:S6:10:ASN:ND2	8:S6:127:THR:O	2.32	0.63
11:S9:11:THR:HG23	1:6:472:U:H5''	399.37	0.63
36:1:1230:G:H1	36:1:1279:C:H42	1.46	0.63
1:2:1331:A:OP1	19:C7:45:ARG:NH2	2.31	0.63
1:6:1672:G:H2'	1:6:1673:G:C8	2.33	0.63
1:2:1550:A:P	17:C5:42:ARG:HH22	2.20	0.63
16:C4:128:LYS:NZ	28:D6:27:SER:OG	2.25	0.63
41:L4:217:LYS:HA	41:L4:220:ARG:HG2	4.23	0.63
70:O4:7:PHE:HD1	70:O4:20:ILE:HD12	4.07	0.63
36:1:1156:C:OP2	44:L7:94:LYS:NZ	2.32	0.63
36:5:2255:A:H5'	36:5:2261:G:H22	1.62	0.63
25:D3:91:GLY:O	25:D3:93:LEU:N	2.27	0.63
75:O9:21:ARG:HD3	75:O9:22:PRO:O	1.98	0.63
3:S1:123:ALA:HB2	3:S1:165:ARG:HG2	2.24	0.63
1:2:1291:G:N2	1:2:1324:G:H22	1.97	0.63
1:2:1595:U:H3	1:2:1600:A:H2	1.47	0.63
37:7:91:G:H2'	37:7:92:A:C8	2.34	0.63
1:2:337:G:H3'	13:C1:133:LYS:HB2	1.81	0.63
25:D3:6:PRO:HG3	25:D3:14:LYS:HG2	1.81	0.63
54:M8:40:THR:O	54:M8:42:ALA:N	2.32	0.63
36:1:1027:A:H2'	36:1:1029:G:H5''	1.81	0.62
36:1:2307:G:O2'	36:1:2310:U:OP2	2.17	0.62
36:5:1781:C:H2'	36:5:1782:U:C6	2.34	0.62
47:M0:63:GLU:HB2	36:5:2853:A:H5'	297.21	0.62
1:6:263:C:H4'	1:6:292:U:H5'	1.81	0.62
22:D0:58:LEU:HD12	22:D0:88:LYS:HD2	1.81	0.62
72:O6:59:ASP:O	72:O6:63:ASN:ND2	4.52	0.62
10:S8:103:GLN:HB3	10:S8:164:ARG:HG2	1.80	0.62
36:1:2356:A:H61	36:1:2983:C:H5	1.46	0.62
36:1:59:G:H2'	38:4:33:A:O2'	1.98	0.62
36:5:2102:U:H2'	36:5:2103:U:C6	2.35	0.62
44:L7:41:ARG:NH1	36:5:598:A:OP1	260.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:117:PHE:CE1	46:L9:165:CYS:HB3	2.63	0.62
68:O2:31:ASN:N	68:O2:31:ASN:OD1	2.26	0.62
36:1:1069:C:H2'	36:1:1070:U:H6	1.63	0.62
1:2:706:A:N1	1:2:734:A:N6	2.47	0.62
36:5:2514:U:OP1	36:5:2514:U:H6	1.82	0.62
22:D0:106:ILE:HG13	22:D0:107:THR:H	1.63	0.62
33:E1:146:SER:HB3	1:6:1234:A:H4'	435.93	0.62
52:M6:62:THR:H	52:M6:69:GLY:HA3	2.38	0.62
56:N0:12:ARG:HB3	56:N0:24:LEU:HD23	1.80	0.62
69:O3:20:LYS:HG2	69:O3:21:ARG:HG2	1.81	0.62
5:S3:40:ARG:HG2	22:D0:110:PRO:HB3	2.04	0.62
7:S5:63:GLN:HE22	7:S5:66:GLN:HB2	4.18	0.62
34:SR:37:SER:OG	34:SR:38:ARG:N	2.63	0.62
1:2:1769:U:O2	16:C4:136:ARG:NH1	2.32	0.62
1:2:1401:A:OP1	19:C7:60:ARG:NH1	2.33	0.62
1:2:539:G:N2	1:2:540:G:O6	2.32	0.62
13:C1:78:THR:HA	13:C1:84:ILE:HG22	2.66	0.62
15:C3:55:ARG:NH1	15:C3:56:ASP:OD2	2.33	0.62
28:D6:37:LYS:O	28:D6:38:ARG:NH1	2.32	0.62
41:L4:181:VAL:O	41:L4:182:LEU:HB2	1.98	0.62
44:L7:119:VAL:HG13	44:L7:124:LEU:HD23	2.47	0.62
45:L8:221:ASN:HA	45:L8:225:LYS:HE3	1.80	0.62
51:M5:172:ARG:HD2	36:5:30:G:O5'	111.41	0.62
55:M9:105:LEU:HD22	55:M9:138:LEU:HD13	1.81	0.62
63:N7:36:HIS:CD2	63:N7:74:VAL:HG11	2.35	0.62
74:O8:2:ALA:HA	36:5:1747:G:H21	145.29	0.62
36:5:2584:G:H5'	36:5:2585:G:OP2	1.98	0.62
6:S4:49:ARG:NH1	1:6:448:C:OP2	380.29	0.62
47:M0:42:THR:HG23	47:M0:45:GLU:HG3	4.18	0.62
49:M3:42:ARG:O	49:M3:46:ILE:HG12	2.19	0.62
52:M6:89:SER:O	52:M6:92:THR:OG1	2.17	0.62
64:N8:73:LEU:HB2	64:N8:109:TYR:CD2	3.11	0.62
34:SR:31:ASN:O	34:SR:47:LEU:N	2.29	0.62
36:1:2960:C:H2'	36:1:2961:G:H8	1.65	0.62
36:1:707:U:H2'	36:1:708:G:H5''	1.81	0.62
1:2:68:A:O2'	1:2:69:G:OP2	2.17	0.62
60:N4:16:GLY:O	36:5:3050:U:O2'	246.23	0.62
12:C0:2:LEU:HD22	1:6:1258:U:H4'	435.01	0.62
15:C3:94:LYS:HG2	15:C3:118:ILE:HD13	2.03	0.62
47:M0:68:ALA:HB1	47:M0:155:ALA:HB1	2.39	0.62
54:M8:66:ARG:NH2	36:5:744:A:OP1	166.94	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:O7:21:ARG:HD2	73:O7:39:TYR:HB2	2.36	0.62
2:S0:13:ASP:HA	2:S0:16:LEU:HD12	1.81	0.62
3:S1:87:ARG:NH2	3:S1:220:GLN:OE1	2.32	0.62
6:S4:151:ASP:OD1	8:S6:215:ARG:NH1	3.82	0.62
1:2:790:U:OP1	6:S4:187:ARG:NH1	2.31	0.62
34:SR:76:ASP:OD1	34:SR:76:ASP:N	2.32	0.62
36:1:2947:G:C2	40:L3:250:ALA:HB1	2.35	0.62
51:M5:2:GLY:N	36:5:116:A:OP2	107.96	0.62
36:5:2335:G:N2	36:5:2339:C:O2	2.28	0.62
49:M3:186:ARG:NH2	36:5:768:C:OP1	155.11	0.62
37:7:2:G:O2'	37:7:23:A:N1	2.30	0.62
38:8:26:U:H2'	38:8:27:U:C6	2.34	0.62
16:C4:80:HIS:ND1	16:C4:113:GLY:O	3.40	0.62
22:D0:27:THR:HG23	22:D0:113:ASP:HB3	1.82	0.62
41:L4:138:ARG:HG3	41:L4:244:LEU:O	1.99	0.62
49:M3:56:PRO:HG3	49:M3:74:GLY:O	2.00	0.62
49:M3:64:LYS:HG3	64:N8:69:TRP:CG	2.77	0.62
79:Q3:7:LYS:O	79:Q3:27:LYS:NZ	2.31	0.62
34:SR:149:ASP:HB2	34:SR:175:ASP:HB3	2.22	0.62
1:2:1087:A:H2'	1:2:1088:A:C8	2.35	0.62
1:2:1482:C:OP2	1:2:1521:G:N2	2.29	0.62
32:E0:17:GLN:NE2	1:6:563:U:H4'	384.63	0.62
12:C0:32:HIS:CD2	12:C0:33:GLU:H	4.04	0.62
14:C2:124:LYS:O	14:C2:126:TRP:N	2.31	0.62
2:S0:50:VAL:HG22	19:C7:109:LEU:HD21	1.82	0.62
5:S3:202:LEU:HD22	5:S3:202:LEU:H	2.78	0.62
6:S4:92:LEU:HD13	26:D4:17:LEU:HD11	6.73	0.62
34:SR:267:PRO:HD2	34:SR:269:TYR:HE1	2.97	0.62
36:1:3316:A:H2	36:1:3389:U:H5'	1.65	0.62
36:5:873:C:H5''	36:5:874:U:O5'	1.99	0.62
2:S0:184:LEU:HD12	23:D1:45:ALA:HB2	1.81	0.62
25:D3:92:CYS:HA	25:D3:95:PHE:HD2	1.64	0.62
47:M0:78:THR:OG1	47:M0:79:VAL:N	3.56	0.62
49:M3:76:THR:HG22	49:M3:101:ARG:HB3	1.81	0.62
53:M7:122:ALA:HB3	53:M7:143:PRO:HB2	2.57	0.62
9:S7:49:ILE:HG13	9:S7:57:ALA:HB3	3.27	0.62
36:1:1277:C:HO2'	36:1:1278:A:H8	1.48	0.61
36:1:1346:G:H1'	41:L4:307:GLN:HE22	1.65	0.61
1:2:1591:C:H2'	1:2:1592:A:C8	2.35	0.61
1:2:762:A:OP1	11:S9:79:ARG:NH2	2.22	0.61
1:6:800:U:H2'	1:6:801:G:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:D1:74:GLN:NE2	23:D1:81:ASN:O	2.32	0.61
1:2:1553:G:HO2'	31:D9:14:TYR:HH	1.41	0.61
40:L3:105:VAL:HG21	40:L3:148:LEU:HD13	1.83	0.61
36:1:1334:U:H5''	44:L7:206:LYS:HB3	1.82	0.61
2:S0:83:GLN:HG2	2:S0:99:ALA:HB1	1.84	0.61
3:S1:137:ILE:HD12	3:S1:172:LEU:HD22	1.82	0.61
5:S3:72:LEU:HD22	12:C0:65:TYR:HD1	2.57	0.61
36:1:2683:U:H2'	36:1:2684:C:C6	2.35	0.61
61:N5:56:ARG:NH2	38:8:135:G:OP2	81.94	0.61
40:L3:284:ARG:NH2	40:L3:293:ASN:O	2.21	0.61
43:L6:175:LYS:O	50:M4:117:ARG:NH2	2.32	0.61
43:L6:40:LEU:HD13	43:L6:84:VAL:HG11	2.17	0.61
48:M1:49:LYS:HB3	48:M1:62:ASN:HA	1.81	0.61
36:1:249:U:O2	36:1:250:U:N3	2.33	0.61
1:2:1291:G:H22	1:2:1324:G:N2	1.98	0.61
1:2:1591:C:H2'	1:2:1592:A:H8	1.64	0.61
1:6:1316:G:HO2'	1:6:1401:A:HO2'	1.48	0.61
1:6:513:U:H2'	1:6:514:G:C8	2.35	0.61
26:D4:112:LYS:NZ	1:6:57:G:OP1	347.07	0.61
1:6:738:G:H2'	1:6:739:G:C8	2.34	0.61
15:C3:110:ASP:OD1	15:C3:114:ARG:NH1	3.27	0.61
41:L4:36:HIS:O	41:L4:40:THR:HG23	2.00	0.61
45:L8:163:VAL:HG22	45:L8:166:LEU:HD12	2.10	0.61
58:N2:59:ASP:OD1	58:N2:60:GLY:N	4.17	0.61
36:1:776:U:H5	36:1:2719:U:O2	1.82	0.61
36:1:2107:A:H2	36:1:3344:A:H8	1.48	0.61
36:1:409:A:H61	38:4:15:G:H1'	1.65	0.61
20:C8:36:LYS:NZ	1:6:1568:C:OP2	337.73	0.61
3:S1:152:ARG:NH1	1:6:1799:U:O2'	345.24	0.61
19:C7:27:ASP:O	19:C7:31:ASN:ND2	3.61	0.61
24:D2:25:VAL:HG22	24:D2:65:LEU:HD21	4.43	0.61
27:D5:70:LYS:HG3	27:D5:71:ILE:H	1.66	0.61
42:L5:40:HIS:HD2	42:L5:42:ALA:H	1.47	0.61
58:N2:19:VAL:HG12	58:N2:105:LEU:HD22	2.26	0.61
36:1:1492:G:N7	75:O9:2:ALA:HB1	2.15	0.61
1:2:1657:U:H4'	1:2:1658:G:O5'	1.99	0.61
1:2:656:G:O2'	1:2:657:U:O4'	2.19	0.61
59:N3:2:SER:N	59:N3:56:ASP:OD1	5.59	0.61
66:O0:75:ASN:HA	66:O0:86:ARG:HB2	2.44	0.61
68:O2:11:LYS:O	68:O2:12:LYS:HB2	2.00	0.61
9:S7:74:GLN:O	9:S7:78:THR:OG1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:92:LYS:O	11:S9:94:ASP:N	2.33	0.61
36:1:2946:A:H5''	36:1:2947:G:H5'	1.81	0.61
36:5:114:A:N1	36:5:266:A:O2'	2.27	0.61
1:6:75:U:O2'	1:6:76:A:O4'	2.19	0.61
16:C4:108:SER:OG	16:C4:109:GLY:N	2.33	0.61
17:C5:108:ARG:HH21	20:C8:119:ILE:HD12	3.39	0.61
20:C8:123:ARG:HG3	20:C8:133:VAL:HG21	1.83	0.61
14:C2:50:LYS:NZ	33:E1:129:GLY:O	2.29	0.61
48:M1:53:THR:HG23	48:M1:60:ARG:HA	2.71	0.61
71:O5:76:GLN:O	71:O5:81:ARG:NH1	2.34	0.61
1:2:458:G:OP1	26:D4:109:LYS:NZ	2.32	0.61
36:5:297:G:N2	36:5:297:G:OP2	2.28	0.61
79:Q3:4:ARG:NH1	36:5:837:A:OP2	239.61	0.61
1:6:1208:A:N1	1:6:1455:G:N2	2.48	0.61
73:O7:28:HIS:HB3	73:O7:31:LYS:HB2	2.62	0.61
20:C8:125:ILE:HD11	35:SM:57:ASN:HB3	1.80	0.61
36:1:2836:C:H5	36:1:2852:C:H42	1.48	0.61
36:5:2102:U:H2'	36:5:2103:U:H6	1.66	0.61
42:L5:8:LYS:NZ	37:7:15:C:O3'	312.83	0.61
15:C3:91:LEU:HD12	15:C3:125:LEU:HD12	2.05	0.61
22:D0:53:LYS:HB2	22:D0:92:ASP:HB2	1.81	0.61
32:E0:55:ARG:NH2	1:6:558:U:OP2	416.09	0.61
40:L3:259:HIS:CE1	36:5:2366:C:H5'	218.86	0.61
48:M1:107:ASP:N	48:M1:107:ASP:OD1	2.33	0.61
4:S2:101:VAL:HG22	4:S2:115:ILE:HG23	2.07	0.61
36:1:1256:G:O6	36:1:1261:G:N2	2.34	0.61
36:1:2338:C:H1'	59:N3:49:LEU:HD12	1.82	0.61
1:2:487:G:H3'	1:2:488:G:H5''	1.83	0.61
36:5:2562:A:N6	36:5:2579:G:O2'	2.32	0.61
13:C1:109:VAL:HG12	13:C1:137:PHE:HB2	4.22	0.61
20:C8:40:ARG:NH2	21:C9:44:GLU:OE2	3.21	0.61
40:L3:37:ARG:HG2	40:L3:187:SER:H	1.66	0.61
42:L5:146:LEU:HB3	36:5:2746:A:H2	259.27	0.61
68:O2:40:SER:O	68:O2:44:ARG:HG3	2.14	0.61
2:S0:69:ASN:ND2	2:S0:71:GLU:OE1	2.26	0.61
3:S1:111:ARG:HB3	28:D6:68:TYR:CD2	2.36	0.61
9:S7:14:THR:OG1	9:S7:15:GLU:N	2.32	0.61
1:2:45:U:O2'	1:2:46:A:H2'	2.01	0.61
1:2:853:G:O6	55:M9:173:ARG:NH2	2.34	0.61
36:5:2921:U:H2'	36:5:2923:U:OP2	2.01	0.61
24:D2:105:THR:HG23	24:D2:110:ILE:HG12	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:D6:26:CYS:HB3	28:D6:28:LYS:H	4.63	0.61
36:1:3294:A:OP1	40:L3:128:LYS:NZ	2.30	0.61
42:L5:40:HIS:CE1	42:L5:42:ALA:HB3	3.85	0.61
42:L5:286:VAL:HG13	47:M0:206:LEU:HD22	1.82	0.61
47:M0:84:ALA:O	47:M0:140:THR:HG22	2.01	0.61
48:M1:90:GLN:HG2	48:M1:170:ASP:HB2	1.82	0.61
67:O1:83:GLU:O	67:O1:85:ALA:N	3.50	0.61
5:S3:164:VAL:HG13	5:S3:168:ILE:HD11	1.83	0.61
5:S3:210:GLU:OE2	19:C7:19:ARG:NH1	2.90	0.61
36:1:3092:C:O2'	36:1:3094:A:OP2	2.16	0.60
1:2:1511:U:H2'	1:2:1512:G:H8	1.66	0.60
36:5:1912:U:N3	36:5:2122:G:OP2	2.33	0.60
36:5:549:U:H2'	36:5:550:A:C8	2.35	0.60
36:5:900:G:H1'	36:5:1589:A:N6	2.15	0.60
38:8:149:A:H2'	38:8:150:G:C8	2.35	0.60
70:O4:3:GLN:HB3	70:O4:30:LEU:HD12	1.82	0.60
6:S4:9:LEU:HD12	6:S4:30:ARG:HA	1.82	0.60
9:S7:35:LYS:O	9:S7:37:GLU:N	2.34	0.60
36:5:629:U:H2'	36:5:630:A:C8	2.36	0.60
1:6:489:C:O2'	1:6:490:C:O4'	2.18	0.60
12:C0:14:TYR:OH	12:C0:34:GLU:OE1	2.09	0.60
27:D5:56:THR:O	27:D5:103:ARG:NH2	6.95	0.60
40:L3:92:TYR:HB2	40:L3:157:VAL:HG22	1.83	0.60
49:M3:174:ARG:HG3	72:O6:9:ILE:HD11	5.22	0.60
53:M7:28:ASN:O	53:M7:32:THR:HG22	2.01	0.60
37:3:97:A:OP1	56:N0:40:ARG:NH1	2.34	0.60
63:N7:38:PHE:O	63:N7:40:HIS:ND1	2.27	0.60
64:N8:6:THR:HG23	64:N8:8:THR:HG23	2.01	0.60
67:O1:84:ASP:N	67:O1:84:ASP:OD1	2.35	0.60
2:S0:13:ASP:OD1	2:S0:179:ARG:NH2	3.20	0.60
3:S1:171:ILE:HD12	3:S1:197:ILE:HD13	1.82	0.60
8:S6:138:ALA:HB1	8:S6:142:ARG:HH12	3.03	0.60
35:SM:23:LYS:HZ2	35:SM:24:GLU:H	8.03	0.60
42:L5:140:ARG:NH2	36:5:1080:A:OP2	230.67	0.60
36:5:1232:C:H2'	36:5:1233:G:H8	1.65	0.60
36:5:1764:U:H3'	36:5:1765:U:H5''	1.83	0.60
36:5:396:A:O2'	36:5:399:A:OP1	2.15	0.60
1:6:1003:A:H4'	1:6:1004:U:O5'	2.00	0.60
21:C9:68:ARG:NH1	1:6:1521:G:O6	416.33	0.60
16:C4:50:ALA:HB3	16:C4:53:ASP:HB2	2.09	0.60
18:C6:39:VAL:HG12	18:C6:41:PRO:HD2	3.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2146:C:OP1	39:L2:200:ARG:NH1	2.34	0.60
45:L8:217:THR:O	45:L8:221:ASN:ND2	2.34	0.60
54:M8:30:VAL:O	54:M8:34:THR:HG22	2.00	0.60
64:N8:115:LYS:HG3	36:5:715:A:H8	148.51	0.60
8:S6:98:ARG:HD3	8:S6:99:GLY:N	2.18	0.60
36:1:1238:C:N4	36:1:1245:A:OP2	2.35	0.60
36:1:1724:U:H4'	36:1:1725:C:OP1	2.00	0.60
57:N1:130:ARG:NH1	36:5:1098:A:OP2	254.39	0.60
41:L4:146:PRO:HG2	41:L4:150:LEU:HD21	1.83	0.60
36:1:1354:G:H4'	43:L6:8:LYS:HE2	1.84	0.60
51:M5:47:LYS:HE3	51:M5:51:LEU:HD11	2.69	0.60
62:N6:111:LEU:HD23	62:N6:116:LYS:HE2	1.83	0.60
36:5:2771:U:O2'	36:5:2772:C:O4'	2.15	0.60
1:6:149:C:H2'	1:6:150:U:H6	1.66	0.60
25:D3:90:ASP:O	25:D3:136:TRP:NE1	2.31	0.60
50:M4:132:LYS:HD3	36:5:3230:G:H4'	286.63	0.60
36:1:883:A:H5'	53:M7:133:HIS:HA	1.83	0.60
55:M9:68:GLN:NE2	55:M9:72:GLU:OE2	4.40	0.60
71:O5:101:THR:HG22	71:O5:103:LYS:H	1.67	0.60
7:S5:57:SER:O	7:S5:59:VAL:N	2.30	0.60
36:5:2207:A:H2'	36:5:2208:A:O4'	2.02	0.60
20:C8:92:ILE:HG23	20:C8:93:THR:HG23	2.39	0.60
44:L7:178:ILE:HA	44:L7:183:ASP:HB3	1.82	0.60
6:S4:146:THR:HG21	1:6:123:G:H21	342.45	0.60
8:S6:2:LYS:HB3	8:S6:108:VAL:HG12	5.53	0.60
8:S6:58:LYS:NZ	8:S6:104:PRO:O	3.60	0.60
10:S8:138:ASN:HA	10:S8:141:ARG:HD3	4.08	0.60
10:S8:42:ARG:HB3	10:S8:59:ARG:HB2	2.84	0.60
11:S9:113:VAL:HG12	11:S9:119:ALA:HB2	2.64	0.60
36:1:1145:G:OP1	68:O2:44:ARG:NH1	2.33	0.60
1:2:818:C:N4	1:2:819:G:O6	2.35	0.60
1:6:1087:A:H2'	1:6:1088:A:C8	2.37	0.60
1:6:913:G:H3'	1:6:914:G:H5'	1.84	0.60
1:2:919:A:H5'	16:C4:18:ARG:HH12	1.66	0.60
33:E1:108:VAL:HB	33:E1:114:VAL:HG22	1.83	0.60
40:L3:3:HIS:ND1	40:L3:3:HIS:O	2.72	0.60
41:L4:99:MET:SD	41:L4:102:PRO:HA	2.41	0.60
7:S5:197:GLU:OE1	7:S5:209:TYR:N	3.18	0.60
9:S7:51:VAL:HG23	9:S7:53:GLY:H	1.67	0.60
11:S9:168:ARG:HD2	11:S9:174:ARG:NH2	9.96	0.60
1:2:304:U:H2'	1:2:305:C:H6	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1095:U:H4'	36:5:1096:U:H5''	1.83	0.60
71:O5:81:ARG:NH2	36:5:18:G:OP1	77.57	0.60
16:C4:136:ARG:NH1	1:6:1785:U:OP1	300.32	0.60
17:C5:87:PRO:HA	17:C5:90:ILE:HG13	1.83	0.60
71:O5:10:ARG:NH2	38:8:65:A:O3'	33.71	0.60
72:O6:33:ALA:HB1	72:O6:38:LYS:HE3	2.22	0.60
3:S1:35:PRO:HB3	3:S1:231:LEU:HD11	3.80	0.60
20:C8:125:ILE:HG12	35:SM:61:ILE:HG23	1.84	0.60
34:SR:256:THR:OG1	34:SR:259:GLY:O	2.17	0.60
36:5:2568:C:N4	36:5:2574:G:O6	2.35	0.60
7:S5:185:ARG:NH1	1:6:1471:A:OP1	333.27	0.60
15:C3:76:LYS:HA	15:C3:81:ALA:HB2	2.36	0.60
45:L8:148:ALA:HA	45:L8:201:THR:HG22	2.46	0.60
46:L9:137:SER:HB3	46:L9:143:GLU:HB3	1.83	0.60
36:1:20:A:OP2	71:O5:90:ARG:NH1	2.35	0.60
36:1:874:U:H5''	36:1:2950:G:OP1	2.01	0.60
1:2:1234:A:H4'	33:E1:146:SER:HB3	1.83	0.60
39:L2:20:THR:O	39:L2:23:ARG:HG3	2.01	0.60
36:1:2514:U:H5'	45:L8:68:ARG:HG3	1.84	0.60
60:N4:5:ILE:HG13	60:N4:10:GLY:HA2	1.84	0.60
70:O4:87:GLU:OE1	70:O4:91:ARG:NH1	3.08	0.60
3:S1:34:ALA:HB3	3:S1:41:ARG:HA	1.84	0.60
4:S2:38:VAL:HG13	4:S2:39:THR:HG23	1.83	0.60
5:S3:28:GLU:OE2	12:C0:56:LYS:NZ	2.30	0.60
8:S6:126:ASP:OD2	8:S6:127:THR:N	2.34	0.60
11:S9:107:ARG:NH1	11:S9:112:GLN:OE1	2.35	0.60
1:6:1698:G:N2	1:6:1699:G:N7	2.50	0.59
28:D6:84:VAL:O	28:D6:86:VAL:N	2.35	0.59
49:M3:75:PHE:O	49:M3:79:GLU:HB2	2.02	0.59
61:N5:57:LEU:HA	61:N5:61:LYS:HG2	3.80	0.59
71:O5:54:VAL:HG12	71:O5:58:ILE:HD11	2.90	0.59
3:S1:190:PRO:HG2	3:S1:192:VAL:HG23	2.35	0.59
4:S2:137:ILE:HG12	4:S2:138:PRO:HD2	1.84	0.59
36:1:29:C:H4'	36:1:62:A:H4'	1.83	0.59
72:O6:25:LYS:HB3	36:5:156:G:OP2	87.79	0.59
8:S6:66:GLY:HA3	1:6:1681:A:H1'	275.68	0.59
1:6:1:U:O2'	1:6:370:A:H5'	2.01	0.59
29:D7:55:THR:HG22	29:D7:62:ILE:HD12	3.46	0.59
41:L4:265:GLU:CD	41:L4:265:GLU:H	2.04	0.59
49:M3:74:GLY:O	49:M3:101:ARG:NH1	2.42	0.59
49:M3:166:ALA:HB1	64:N8:147:LEU:HD21	2.73	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:O8:46:ARG:HH21	74:O8:51:LEU:HB2	1.67	0.59
36:1:1080:A:OP2	42:L5:140:ARG:NH2	2.35	0.59
36:1:2355:G:H4'	53:M7:139:TYR:CE2	2.37	0.59
36:1:707:U:C2'	36:1:708:G:H5''	2.33	0.59
1:2:1449:U:H2'	1:2:1450:U:C6	2.36	0.59
43:L6:78:ARG:NH1	36:5:3272:C:OP2	247.27	0.59
1:6:1628:U:H2'	1:6:1629:G:C8	2.37	0.59
17:C5:81:ARG:NH1	17:C5:97:TYR:O	2.34	0.59
41:L4:193:LYS:NZ	38:8:21:C:OP1	108.88	0.59
49:M3:6:ASN:O	54:M8:164:ARG:NH1	2.32	0.59
63:N7:47:GLU:OE2	63:N7:69:LYS:NZ	4.27	0.59
49:M3:177:LYS:HA	72:O6:11:LEU:HD22	2.74	0.59
4:S2:178:ILE:HB	4:S2:185:LYS:HD3	4.89	0.59
7:S5:146:THR:HG23	7:S5:221:ALA:HA	1.85	0.59
1:2:694:U:H6	9:S7:97:ARG:HH21	1.50	0.59
36:1:980:A:H2'	36:1:981:U:N1	2.18	0.59
36:5:1284:C:O2'	36:5:1285:G:OP1	2.18	0.59
54:M8:141:ARG:NH1	36:5:743:C:N3	180.26	0.59
1:6:947:U:H2'	1:6:948:G:C8	2.37	0.59
41:L4:330:TYR:HA	41:L4:333:VAL:HG13	2.34	0.59
41:L4:98:ARG:HD2	41:L4:99:MET:O	2.03	0.59
59:N3:28:ASN:OD1	59:N3:28:ASN:N	2.70	0.59
7:S5:68:ILE:HD13	7:S5:69:PHE:H	5.25	0.59
36:1:2534:G:H1	36:1:2545:C:H42	1.50	0.59
36:1:2927:C:H2'	36:1:2928:C:C6	2.37	0.59
36:1:3122:A:N1	46:L9:70:THR:HG21	2.18	0.59
36:5:94:G:H2'	36:5:95:A:C8	2.37	0.59
1:6:1699:G:H2'	1:6:1700:C:H5'	1.84	0.59
1:6:820:U:O2'	1:6:821:U:H5''	2.03	0.59
75:O9:19:GLN:NE2	38:8:53:A:OP1	90.17	0.59
18:C6:23:LYS:HG2	18:C6:64:ASP:HB2	2.46	0.59
6:S4:13:ALA:O	6:S4:39:ARG:NH2	2.65	0.59
1:2:329:G:H5''	10:S8:98:LYS:HB3	1.84	0.59
36:1:1129:A:OP1	47:M0:13:LYS:NZ	2.29	0.59
36:1:1724:U:H1'	36:1:1725:C:C6	2.37	0.59
36:1:289:A:O2'	51:M5:93:LYS:O	2.21	0.59
1:2:47:A:N1	1:2:386:G:H1'	2.17	0.59
1:2:693:U:H5'	1:2:694:U:H5'	1.84	0.59
38:4:126:A:O2'	38:4:128:U:OP1	2.21	0.59
36:5:2440:G:O2'	36:5:2441:A:OP1	2.20	0.59
36:5:422:A:C2	36:5:2363:A:H4'	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L5:257:GLU:H	42:L5:257:GLU:CD	4.17	0.59
36:1:1609:C:H5''	61:N5:125:ARG:HH11	1.68	0.59
71:O5:34:GLN:OE1	71:O5:38:ARG:NH1	2.64	0.59
36:5:247:C:C2	36:5:248:U:H1'	2.38	0.59
1:6:947:U:H2'	1:6:948:G:H8	1.66	0.59
13:C1:60:PHE:O	13:C1:62:GLY:N	4.17	0.59
24:D2:5:SER:O	24:D2:7:LEU:N	3.54	0.59
50:M4:11:ASN:O	50:M4:11:ASN:ND2	2.85	0.59
57:N1:9:SER:O	57:N1:55:LYS:NZ	3.08	0.59
11:S9:53:ARG:NH2	11:S9:97:LEU:O	2.36	0.59
36:1:1765:U:H5''	55:M9:43:LYS:HE2	1.83	0.59
19:C7:8:THR:HG21	1:6:1330:G:H21	420.78	0.59
1:6:755:A:O2'	1:6:756:A:O5'	2.21	0.59
38:8:83:C:H4'	38:8:85:G:N3	2.18	0.59
18:C6:47:LYS:NZ	18:C6:114:ARG:HG2	2.18	0.59
4:S2:147:ASN:HB3	23:D1:4:ASP:HA	1.85	0.59
1:2:523:G:H5''	26:D4:59:GLY:O	2.02	0.59
33:E1:98:VAL:HG12	33:E1:99:LYS:H	3.92	0.59
41:L4:20:LEU:HD11	41:L4:252:GLU:HG3	1.84	0.59
64:N8:74:ASN:HB2	64:N8:76:ASP:HB2	1.85	0.59
73:O7:24:ARG:NH1	36:5:361:A:OP1	120.86	0.59
4:S2:218:ILE:O	4:S2:221:THR:OG1	2.55	0.59
36:1:1278:A:O2'	36:1:1279:C:O5'	2.21	0.59
1:2:637:C:O2	9:S7:114:ARG:NH2	2.36	0.59
36:5:132:C:H2'	36:5:133:U:H5''	1.83	0.59
33:E1:139:LEU:HD12	33:E1:152:ALA:H	1.67	0.59
43:L6:82:ARG:NH1	69:O3:105:SER:O	3.25	0.59
52:M6:79:ILE:HG21	52:M6:138:LEU:HD11	2.20	0.59
63:N7:14:VAL:HG13	70:O4:86:LYS:HG2	1.83	0.59
1:2:161:U:OP2	8:S6:87:ARG:NH2	2.36	0.59
9:S7:73:VAL:O	9:S7:75:THR:N	2.43	0.59
11:S9:92:LYS:HB2	11:S9:95:TYR:HD2	7.91	0.59
44:L7:96:PRO:HB2	44:L7:99:PRO:HD2	1.84	0.59
66:O0:83:LYS:HG2	66:O0:85:PHE:CZ	2.38	0.59
75:O9:9:ILE:HG22	75:O9:13:MET:HE2	2.04	0.59
1:2:1064:G:O2'	3:S1:204:ILE:O	2.21	0.59
11:S9:125:ALA:O	11:S9:129:ILE:HG13	2.03	0.59
36:1:541:U:H2'	36:1:542:G:C8	2.38	0.58
13:C1:77:SER:HB3	13:C1:85:VAL:HB	1.84	0.58
19:C7:67:ARG:NH2	1:6:1398:U:O2'	405.62	0.58
39:L2:215:ASN:HB2	36:5:2968:G:N7	217.48	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:L6:3:ALA:HB1	68:O2:75:LEU:HD13	2.73	0.58
44:L7:145:ARG:HA	44:L7:185:ILE:HD13	1.85	0.58
47:M0:192:ASP:HA	47:M0:197:VAL:HG23	1.85	0.58
61:N5:137:ASN:HB3	61:N5:142:ILE:HG13	2.69	0.58
64:N8:16:SER:HA	36:5:942:U:N3	169.45	0.58
1:2:66:U:C5	8:S6:173:PRO:HG3	2.38	0.58
36:1:3042:U:OP2	36:1:3092:C:N4	2.29	0.58
36:5:1110:U:H2'	36:5:1111:U:C6	2.38	0.58
36:5:662:U:H2'	36:5:663:C:C6	2.38	0.58
1:6:1041:G:H2'	1:6:1042:G:C8	2.38	0.58
19:C7:82:ASP:O	19:C7:83:GLN:NE2	2.36	0.58
28:D6:58:VAL:HG22	28:D6:59:TYR:H	4.16	0.58
29:D7:67:THR:OG1	29:D7:70:LYS:O	2.20	0.58
41:L4:291:ASN:HA	41:L4:296:GLN:HE21	1.68	0.58
41:L4:33:ASP:O	41:L4:37:THR:HG23	2.03	0.58
43:L6:149:ILE:HG23	43:L6:155:LEU:HD13	2.64	0.58
46:L9:69:ARG:HD3	46:L9:72:LYS:HD3	1.85	0.58
51:M5:65:ARG:HG2	51:M5:127:TYR:CD1	2.41	0.58
70:O4:74:ARG:HD2	70:O4:85:VAL:HG21	3.69	0.58
1:2:1041:G:H2'	1:2:1042:G:C8	2.38	0.58
1:2:1529:C:OP1	7:S5:112:ARG:NH1	2.32	0.58
13:C1:133:LYS:NZ	1:6:324:U:OP1	294.22	0.58
19:C7:71:PHE:HE1	19:C7:73:LEU:HD22	1.68	0.58
26:D4:36:SER:OG	26:D4:37:LYS:N	2.35	0.58
43:L6:89:THR:HG21	50:M4:115:PHE:HB2	1.84	0.58
45:L8:99:PRO:HG2	45:L8:190:VAL:HG13	4.65	0.58
49:M3:153:ASP:OD1	49:M3:157:ARG:NH2	2.36	0.58
53:M7:27:LYS:HD3	53:M7:63:PHE:HB3	2.72	0.58
53:M7:50:GLN:OE1	53:M7:56:ARG:NH2	2.36	0.58
55:M9:46:LYS:HZ1	36:5:1766:G:H8	100.08	0.58
60:N4:56:ARG:HB3	60:N4:61:LYS:HB2	1.86	0.58
3:S1:34:ALA:N	3:S1:41:ARG:O	2.29	0.58
8:S6:7:TYR:HB3	8:S6:12:SER:HB2	1.85	0.58
20:C8:144:ARG:O	35:SM:68:ARG:NH2	2.35	0.58
36:1:3166:C:H42	36:1:3284:G:H1	1.49	0.58
36:1:792:G:H2'	36:1:793:C:C6	2.38	0.58
1:2:780:A:C8	26:D4:8:ARG:HB3	2.37	0.58
65:N9:50:THR:HG22	36:5:1073:U:H1'	205.95	0.58
36:5:1659:U:H2'	36:5:1660:C:C6	2.37	0.58
1:6:163:G:H8	1:6:163:G:O5'	1.86	0.58
18:C6:49:TYR:HB3	18:C6:53:LEU:HD11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:D6:24:VAL:HG21	28:D6:71:LEU:HD12	1.84	0.58
7:S5:225:ARG:NH1	30:D8:58:GLU:OE1	4.95	0.58
42:L5:25:GLU:O	42:L5:27:LYS:N	3.49	0.58
46:L9:48:VAL:HG13	46:L9:52:LEU:HB3	1.85	0.58
36:1:994:G:H3'	57:N1:13:TYR:CD2	2.38	0.58
36:1:353:G:N7	73:O7:55:ARG:HD3	2.18	0.58
79:Q3:8:VAL:HB	79:Q3:11:THR:HG22	1.86	0.58
1:2:280:U:O2'	1:2:281:G:OP2	2.08	0.58
39:L2:117:GLU:HG2	39:L2:124:GLY:H	1.68	0.58
42:L5:196:ARG:NH2	42:L5:237:GLU:OE1	4.32	0.58
52:M6:15:LEU:HD21	52:M6:125:ARG:HG3	1.84	0.58
66:O0:26:GLY:O	66:O0:30:THR:HG23	2.03	0.58
73:O7:25:ARG:HB3	73:O7:25:ARG:HH11	3.09	0.58
1:2:405:C:O2'	8:S6:92:ARG:O	2.18	0.58
36:1:352:A:H61	36:1:365:A:H5''	1.68	0.58
1:2:1535:U:O2'	1:2:1536:G:N3	2.35	0.58
36:5:1001:G:N3	36:5:1041:U:H5'	2.18	0.58
36:5:920:A:OP1	36:5:922:U:H5	1.86	0.58
12:C0:11:ILE:HD13	12:C0:35:ILE:HG21	1.84	0.58
18:C6:18:ALA:HB2	18:C6:69:VAL:HG13	1.93	0.58
5:S3:209:ILE:HG22	19:C7:38:ILE:HG12	1.86	0.58
23:D1:71:ARG:HG3	23:D1:83:TRP:CZ2	2.61	0.58
46:L9:57:VAL:HG23	46:L9:68:LEU:HG	1.84	0.58
51:M5:178:HIS:CD2	51:M5:179:LYS:HG3	2.86	0.58
71:O5:14:LYS:NZ	71:O5:62:GLN:OE1	6.84	0.58
74:O8:69:LEU:HD12	74:O8:73:LEU:HD23	1.85	0.58
3:S1:154:SER:OG	3:S1:154:SER:O	2.21	0.58
1:2:1600:A:H4'	1:2:1601:G:OP1	2.03	0.58
36:5:1661:G:H2'	36:5:1662:G:C8	2.39	0.58
36:5:3016:A:H2'	36:5:3017:A:C8	2.39	0.58
59:N3:48:ARG:NH2	36:5:3043:C:OP2	252.43	0.58
1:6:1067:C:H2'	1:6:1068:C:H6	1.68	0.58
40:L3:284:ARG:NH2	40:L3:295:ALA:O	2.32	0.58
46:L9:166:ARG:HD2	46:L9:168:ARG:HH11	13.22	0.58
50:M4:22:LEU:HB3	50:M4:64:VAL:HG13	2.33	0.58
52:M6:112:TYR:HA	52:M6:115:LYS:HB2	2.46	0.58
44:L7:80:GLN:HG3	57:N1:136:ARG:HB2	2.44	0.58
63:N7:88:ASP:HB3	63:N7:121:ARG:HH12	1.67	0.58
71:O5:102:GLU:OE1	71:O5:106:LYS:HE3	2.03	0.58
6:S4:166:SER:O	6:S4:168:LYS:HG2	4.91	0.58
36:1:1010:G:N2	47:M0:193:ASP:OD2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:900:G:H1'	36:1:1589:A:N6	2.18	0.58
36:1:437:G:H2'	36:1:438:A:C8	2.38	0.58
1:2:1473:U:O2'	7:S5:103:ASN:ND2	2.36	0.58
36:5:750:G:H2'	36:5:751:A:H8	1.69	0.58
15:C3:139:TRP:HZ2	15:C3:149:LEU:HD11	1.69	0.58
19:C7:45:ARG:NH2	1:6:1332:C:OP2	419.12	0.58
23:D1:39:VAL:HA	23:D1:45:ALA:HA	1.85	0.58
7:S5:187:ILE:HG12	27:D5:66:VAL:HG11	1.86	0.58
36:1:824:C:H5''	39:L2:21:ARG:HD3	1.85	0.58
46:L9:172:ILE:H	46:L9:172:ILE:HD13	1.67	0.58
51:M5:190:THR:O	51:M5:194:GLN:HG2	2.03	0.58
57:N1:17:ARG:O	57:N1:18:ASP:HB2	2.04	0.58
9:S7:105:THR:O	9:S7:107:ARG:N	4.09	0.58
36:1:1394:A:N3	38:4:19:C:O2'	2.35	0.58
36:1:2746:A:H2	42:L5:146:LEU:HB3	1.69	0.58
36:5:253:A:HO2'	36:5:254:A:H8	1.50	0.58
36:5:3078:U:H4'	36:5:3079:U:O5'	2.02	0.58
3:S1:146:GLN:NE2	1:6:1065:A:N3	344.69	0.58
21:C9:117:SER:OG	21:C9:118:PRO:O	2.18	0.58
40:L3:280:HIS:HB3	40:L3:324:VAL:HG21	1.86	0.58
41:L4:269:SER:O	41:L4:269:SER:OG	2.21	0.58
47:M0:82:ARG:NH2	47:M0:83:ASP:OD1	3.34	0.58
49:M3:50:PRO:HB2	49:M3:140:SER:O	2.04	0.58
55:M9:13:SER:OG	55:M9:38:ARG:NH2	2.37	0.58
56:N0:137:ARG:HG2	56:N0:139:TYR:CE1	2.38	0.58
66:O0:9:SER:OG	66:O0:10:ILE:N	2.37	0.58
10:S8:57:ALA:HB2	10:S8:177:GLY:HA2	2.20	0.58
34:SR:166:SER:HA	34:SR:184:ASN:HD21	1.69	0.58
36:1:1460:A:H2'	36:1:1461:A:C8	2.39	0.58
36:1:2100:A:N7	36:1:2101:C:N4	2.52	0.58
1:2:1280:C:H2'	1:2:1281:G:H8	1.69	0.58
1:2:1684:U:O2	1:2:1718:G:N2	2.37	0.58
1:2:895:G:H1	1:2:917:U:H3	1.50	0.58
1:6:1163:A:N3	1:6:1613:U:O2'	2.32	0.58
18:C6:5:PRO:HG2	18:C6:24:ALA:HB2	1.86	0.58
26:D4:10:ARG:NH1	1:6:778:G:N7	433.00	0.58
40:L3:185:GLY:H	40:L3:191:LYS:HZ3	1.51	0.58
46:L9:171:ASP:OD1	46:L9:173:ARG:HG3	2.04	0.58
47:M0:193:ASP:OD2	47:M0:194:GLY:N	2.28	0.58
64:N8:2:PRO:HG2	64:N8:5:PHE:CD2	2.77	0.58
68:O2:124:GLY:O	68:O2:126:LEU:N	2.87	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1511:U:H2'	1:2:1512:G:C8	2.39	0.57
36:5:1313:G:H2'	36:5:1314:C:H6	1.69	0.57
36:5:2507:C:O2'	36:5:2508:U:OP1	2.21	0.57
36:1:2554:A:H5''	39:L2:85:GLY:O	2.03	0.57
40:L3:122:TRP:CE2	40:L3:127:LYS:HE3	2.38	0.57
55:M9:143:ILE:HG13	36:5:2093:A:P	252.64	0.57
62:N6:99:LEU:HD13	62:N6:104:LEU:HD21	2.27	0.57
72:O6:79:SER:HB2	72:O6:82:ARG:HG3	1.86	0.57
2:S0:115:PHE:HE1	4:S2:39:THR:HG22	2.61	0.57
7:S5:91:GLU:O	7:S5:95:ASN:ND2	2.37	0.57
1:2:159:U:O2'	8:S6:87:ARG:NH1	2.37	0.57
36:1:283:G:O6	36:1:304:G:H1'	2.04	0.57
36:1:92:G:OP2	36:1:93:C:H5''	2.04	0.57
46:L9:163:GLN:O	46:L9:166:ARG:HG3	4.51	0.57
62:N6:58:VAL:HA	62:N6:104:LEU:HD23	1.86	0.57
6:S4:18:TRP:O	6:S4:51:ARG:NH1	2.90	0.57
36:1:1347:U:OP2	41:L4:300:ARG:NH2	2.36	0.57
1:2:1358:G:H2'	1:2:1359:C:C6	2.39	0.57
1:6:691:C:OP1	1:6:696:C:N4	2.29	0.57
21:C9:30:VAL:O	21:C9:32:GLY:N	2.37	0.57
40:L3:152:LYS:HD3	40:L3:189:SER:HA	2.61	0.57
36:1:598:A:OP1	44:L7:41:ARG:NH1	2.36	0.57
47:M0:49:CYS:HB3	47:M0:168:SER:HB3	1.87	0.57
52:M6:110:PRO:O	52:M6:113:ASP:N	4.60	0.57
66:O0:40:LYS:HB3	66:O0:101:LEU:HD11	1.87	0.57
78:Q2:74:CYS:HB3	78:Q2:77:CYS:SG	2.62	0.57
3:S1:141:ALA:HB1	3:S1:207:LEU:HD22	3.92	0.57
11:S9:117:GLY:O	11:S9:119:ALA:N	2.68	0.57
36:1:1069:C:H2'	36:1:1070:U:C6	2.40	0.57
15:C3:76:LYS:HE2	1:6:813:U:H5'	318.28	0.57
16:C4:29:HIS:HB3	16:C4:41:ARG:HG3	1.86	0.57
18:C6:95:LYS:O	34:SR:59:ARG:NH2	2.69	0.57
39:L2:104:LEU:HD11	39:L2:113:VAL:HG21	1.86	0.57
43:L6:35:VAL:O	43:L6:38:THR:OG1	2.18	0.57
36:1:1286:A:O2'	36:1:1287:A:OP2	2.20	0.57
36:1:13:A:H4'	61:N5:39:LYS:HG3	1.87	0.57
36:1:3047:U:O2'	36:1:3048:A:H5'	2.05	0.57
1:2:207:U:O2	10:S8:178:ARG:NH1	2.36	0.57
49:M3:171:ARG:HD3	36:5:770:G:OP1	145.84	0.57
1:6:27:U:H2'	1:6:28:A:C8	2.40	0.57
13:C1:21:ASN:N	13:C1:21:ASN:OD1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:D1:21:ASN:OD1	24:D2:23:ARG:NH2	2.38	0.57
4:S2:230:TRP:CE2	24:D2:68:ARG:HD3	2.39	0.57
58:N2:67:SER:OG	58:N2:69:ALA:O	3.01	0.57
11:S9:146:PHE:O	11:S9:147:MET:HB2	2.31	0.57
36:1:1054:A:H5''	36:1:2637:A:H61	1.69	0.57
1:2:614:C:OP2	25:D3:5:LYS:NZ	2.31	0.57
36:5:2364:G:H22	36:5:2396:G:H1'	1.69	0.57
40:L3:120:LYS:NZ	36:5:3001:C:OP1	204.70	0.57
36:5:3241:G:H2'	36:5:3245:A:H8	1.67	0.57
16:C4:38:THR:HG21	1:6:895:G:H21	264.80	0.57
42:L5:272:TYR:CZ	37:7:22:A:H1'	333.96	0.57
41:L4:237:GLN:O	41:L4:246:ARG:HG3	2.12	0.57
44:L7:131:GLU:HG2	44:L7:230:GLY:HA2	1.86	0.57
36:1:2737:C:O5'	57:N1:68:THR:OG1	2.23	0.57
45:L8:50:VAL:HG12	61:N5:30:ALA:HA	1.86	0.57
65:N9:20:GLY:O	65:N9:21:ILE:HB	2.65	0.57
3:S1:33:LYS:HE2	3:S1:41:ARG:HH12	3.90	0.57
4:S2:144:TRP:CE2	4:S2:173:PRO:HG3	3.08	0.57
6:S4:137:PRO:HG2	6:S4:150:PRO:HD2	2.62	0.57
1:2:460:A:H3'	1:2:461:G:H8	1.69	0.57
36:5:1152:G:N2	36:5:1200:A:H61	2.02	0.57
36:5:1631:C:H5''	36:5:1632:A:H5''	1.87	0.57
8:S6:87:ARG:NH2	1:6:161:U:OP2	315.65	0.57
20:C8:83:ALA:HA	20:C8:86:LEU:HD22	1.87	0.57
21:C9:86:ARG:NH1	21:C9:90:PRO:O	2.37	0.57
42:L5:105:ILE:O	42:L5:109:THR:HG23	2.18	0.57
46:L9:70:THR:HB	36:5:3112:G:O2'	329.70	0.57
53:M7:178:ALA:HA	53:M7:181:ARG:HH21	1.69	0.57
74:O8:46:ARG:NH1	74:O8:47:GLY:O	2.38	0.57
3:S1:168:ILE:HG12	3:S1:197:ILE:HD12	1.87	0.57
36:1:562:C:OP2	50:M4:77:ARG:NH1	2.35	0.57
36:5:2696:A:H2'	36:5:2697:A:C8	2.39	0.57
1:6:1511:U:H2'	1:6:1512:G:C8	2.40	0.57
1:6:16:G:H2'	1:6:17:C:C6	2.40	0.57
10:S8:50:GLY:HA2	1:6:397:A:O3'	316.15	0.57
1:2:159:U:H5'	26:D4:117:LYS:HD3	1.85	0.57
31:D9:6:VAL:O	31:D9:8:PHE:N	4.21	0.57
42:L5:233:ALA:O	42:L5:235:SER:N	2.38	0.57
42:L5:85:ARG:NH2	42:L5:250:ASP:OD1	2.32	0.57
48:M1:37:LEU:O	48:M1:41:SER:OG	2.10	0.57
36:1:269:G:H5'	51:M5:120:TRP:CE3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:O8:58:ASP:OD2	74:O8:61:LYS:N	2.25	0.57
79:Q3:56:THR:HB	79:Q3:63:THR:OG1	2.61	0.57
5:S3:162:GLN:OE1	5:S3:165:ASN:ND2	2.22	0.57
1:2:1426:C:H5''	35:SM:93:ARG:HH12	1.70	0.57
36:5:561:C:H2'	36:5:562:C:C6	2.40	0.57
56:N0:40:ARG:NH1	37:7:97:A:OP1	290.73	0.57
2:S0:50:VAL:HG23	19:C7:109:LEU:HD21	3.01	0.57
20:C8:62:THR:N	20:C8:65:GLU:OE1	2.36	0.57
29:D7:2:VAL:O	29:D7:3:LEU:HB2	2.46	0.57
40:L3:81:THR:HG21	40:L3:322:ILE:HD13	5.09	0.57
42:L5:269:SER:OG	37:7:1:G:N3	316.79	0.57
55:M9:160:GLU:HA	55:M9:163:ARG:HB2	1.87	0.57
61:N5:132:ALA:HA	61:N5:135:ILE:HG22	2.11	0.57
54:M8:178:ARG:HE	64:N8:50:PRO:HG2	1.68	0.57
3:S1:109:LYS:HG3	3:S1:113:MET:HE3	1.86	0.57
3:S1:131:ASP:O	3:S1:133:TYR:N	2.38	0.57
36:1:2535:A:H61	36:1:2544:U:H3	1.51	0.57
1:2:338:C:H1'	10:S8:5:ARG:HB3	1.86	0.57
17:C5:40:ARG:NH2	1:6:1552:U:O4	394.03	0.57
1:6:321:C:H42	1:6:1666:U:H5''	1.70	0.57
19:C7:26:LEU:HD22	19:C7:59:LYS:HA	1.87	0.57
2:S0:33:GLN:NE2	23:D1:64:GLU:OE2	2.32	0.57
26:D4:51:GLU:O	26:D4:53:ASP:N	4.01	0.57
36:1:3005:A:H5''	40:L3:98:GLY:HA3	1.86	0.57
42:L5:270:LYS:HG3	42:L5:273:ARG:HB3	5.04	0.57
42:L5:60:ILE:HB	42:L5:80:SER:HB3	1.86	0.57
52:M6:36:VAL:HB	52:M6:108:ILE:HG22	4.72	0.57
52:M6:72:HIS:O	52:M6:74:ARG:NH1	2.35	0.57
58:N2:33:TYR:HE1	58:N2:80:THR:HG23	4.28	0.57
62:N6:73:VAL:HA	62:N6:80:VAL:HG23	1.86	0.57
2:S0:183:ARG:NH2	2:S0:191:ARG:O	2.88	0.57
5:S3:170:THR:HG21	5:S3:187:LYS:HE2	5.41	0.57
11:S9:34:PHE:HD1	11:S9:111:THR:HG21	1.91	0.57
1:2:1456:C:H5''	1:2:1457:C:H5''	1.85	0.56
36:5:1940:G:H21	36:5:3362:A:H8	1.52	0.56
6:S4:187:ARG:NH2	1:6:753:A:H62	375.53	0.56
24:D2:6:VAL:HG12	24:D2:34:ILE:HD11	1.87	0.56
24:D2:24:GLN:HE22	29:D7:4:VAL:HA	3.81	0.56
40:L3:219:ALA:HB2	40:L3:336:VAL:HG13	1.87	0.56
46:L9:174:LYS:HB2	76:Q0:127:LEU:HD11	2.15	0.56
49:M3:164:GLU:O	49:M3:166:ALA:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:172:GLN:OE1	69:O3:60:ARG:NH1	2.38	0.56
2:S0:126:PRO:HB2	2:S0:152:PRO:HG2	2.21	0.56
36:1:2193:U:H5'	36:1:2194:G:H5'	1.86	0.56
1:6:69:G:H1	1:6:82:U:H3	1.53	0.56
1:6:65:A:H2	1:6:84:A:H62	1.52	0.56
1:6:973:A:H2'	1:6:974:A:H8	1.69	0.56
21:C9:108:LEU:HD22	21:C9:113:ILE:HD12	1.87	0.56
23:D1:81:ASN:O	23:D1:83:TRP:N	2.38	0.56
24:D2:103:ILE:HA	24:D2:112:ASP:HA	2.05	0.56
24:D2:28:ARG:HH22	1:6:864:U:H3'	355.45	0.56
25:D3:68:ILE:O	25:D3:70:LYS:NZ	2.39	0.56
40:L3:41:VAL:CA	40:L3:185:GLY:HA3	2.54	0.56
45:L8:75:ILE:HG22	45:L8:76:ALA:H	1.70	0.56
47:M0:140:THR:HG21	47:M0:144:ASN:HD22	1.70	0.56
51:M5:136:ASP:OD2	51:M5:138:GLN:HG2	2.05	0.56
59:N3:129:VAL:O	59:N3:133:SER:OG	2.42	0.56
63:N7:115:LYS:NZ	63:N7:119:GLU:OE2	2.38	0.56
66:O0:24:THR:HG22	66:O0:91:SER:HB3	2.20	0.56
71:O5:68:GLN:HA	71:O5:71:LYS:HB2	1.88	0.56
1:2:138:A:N6	1:2:266:A:H61	2.02	0.56
36:5:916:G:H5'	36:5:917:A:OP1	2.04	0.56
1:6:918:U:H2'	1:6:919:A:H8	1.69	0.56
15:C3:67:THR:O	15:C3:69:ASN:N	2.37	0.56
39:L2:234:LYS:HG2	39:L2:238:ILE:HD12	5.03	0.56
43:L6:60:ASP:OD1	43:L6:62:THR:OG1	2.23	0.56
36:1:2557:A:H2	45:L8:38:GLN:HA	1.70	0.56
50:M4:17:VAL:HG21	50:M4:74:ARG:HB2	1.86	0.56
74:O8:5:ILE:HG22	74:O8:54:LEU:HB2	1.87	0.56
2:S0:122:ILE:HG23	2:S0:144:ILE:HB	2.57	0.56
2:S0:9:LEU:HD23	2:S0:54:TRP:CG	2.40	0.56
6:S4:176:ASP:HB2	6:S4:179:LYS:HZ2	1.71	0.56
8:S6:148:SER:O	8:S6:150:GLU:N	2.37	0.56
10:S8:194:ARG:HD2	10:S8:195:ARG:HH12	2.92	0.56
36:1:1940:G:H21	36:1:3362:A:H8	1.53	0.56
36:1:3072:C:H2'	36:1:3073:A:O4'	2.05	0.56
1:2:1160:A:H2'	1:2:1161:C:C6	2.40	0.56
36:5:1913:A:N3	36:5:2120:A:H2'	2.20	0.56
38:8:155:A:H2'	38:8:156:U:O4'	2.06	0.56
26:D4:52:LYS:O	26:D4:54:ALA:N	2.49	0.56
33:E1:113:LYS:HD2	33:E1:113:LYS:H	1.71	0.56
52:M6:46:GLU:HB3	52:M6:134:LYS:HB3	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S0:31:VAL:HG12	2:S0:33:GLN:H	1.71	0.56
8:S6:135:PRO:HB2	8:S6:141:ILE:HG12	1.87	0.56
10:S8:114:GLU:HG2	10:S8:120:THR:HA	1.87	0.56
36:1:3159:C:H2'	36:1:3160:U:C6	2.41	0.56
36:1:3259:U:H5''	36:1:3261:C:H5	1.71	0.56
36:1:3376:A:H5'	36:1:3377:G:H5''	1.87	0.56
36:5:1340:G:H2'	36:5:1341:U:H6	1.71	0.56
36:5:2150:G:O2'	36:5:2189:U:OP1	2.20	0.56
29:D7:70:LYS:HG3	1:6:1049:U:H5''	349.12	0.56
20:C8:36:LYS:HB3	20:C8:105:VAL:HG21	4.59	0.56
29:D7:49:HIS:CE1	29:D7:70:LYS:HG2	3.24	0.56
33:E1:102:VAL:O	33:E1:104:SER:N	2.38	0.56
45:L8:133:LYS:HB2	45:L8:199:ALA:O	3.35	0.56
47:M0:210:ILE:HA	47:M0:217:PHE:CE2	2.60	0.56
47:M0:38:LYS:NZ	47:M0:45:GLU:OE1	2.63	0.56
58:N2:30:PRO:HA	58:N2:33:TYR:HB3	1.88	0.56
6:S4:180:LEU:HA	6:S4:194:THR:HA	1.88	0.56
34:SR:80:ALA:O	34:SR:92:TRP:N	2.88	0.56
36:1:1412:G:OP1	68:O2:105:ARG:NH2	2.39	0.56
36:5:1856:C:H2'	36:5:1857:C:H6	1.71	0.56
36:5:3287:U:H2'	36:5:3288:G:H5'	1.88	0.56
14:C2:56:GLU:OE1	14:C2:124:LYS:NZ	2.93	0.56
27:D5:42:LEU:HD12	27:D5:43:ASP:H	1.70	0.56
40:L3:18:PRO:O	40:L3:20:LYS:N	2.36	0.56
44:L7:53:LYS:O	44:L7:57:THR:HG23	2.26	0.56
52:M6:187:GLU:HA	52:M6:192:LYS:HD3	1.87	0.56
68:O2:33:ARG:NH2	36:5:1407:A:O3'	162.00	0.56
36:1:1176:C:H2'	36:1:1177:G:N2	2.21	0.56
1:2:1500:C:OP1	21:C9:122:ARG:NH2	2.32	0.56
36:5:2211:U:H5	36:5:2234:G:O6	1.89	0.56
72:O6:28:TYR:OH	36:5:315:C:OP2	98.81	0.56
36:5:3295:A:H2'	36:5:3296:A:C8	2.41	0.56
36:5:612:U:H2'	36:5:613:G:H8	1.71	0.56
17:C5:115:TYR:OH	1:6:1556:A:OP1	389.41	0.56
62:N6:112:ASP:OD2	38:8:85:G:N1	26.02	0.56
22:D0:70:THR:HG23	1:6:1280:C:O2'	390.38	0.56
47:M0:51:HIS:HB3	47:M0:134:ILE:HG23	2.33	0.56
51:M5:11:GLN:HG2	51:M5:44:ARG:HH21	2.61	0.56
51:M5:119:TYR:OH	51:M5:131:GLU:OE1	2.83	0.56
59:N3:89:ASP:OD1	59:N3:91:VAL:HG12	2.40	0.56
63:N7:95:VAL:HG21	63:N7:113:VAL:HG11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:O2:16:LYS:HD2	68:O2:18:LYS:HE3	6.88	0.56
78:Q2:14:GLY:O	78:Q2:16:THR:N	2.30	0.56
2:S0:118:PRO:HG2	2:S0:141:ILE:HD13	1.95	0.56
3:S1:165:ARG:O	3:S1:169:SER:OG	2.15	0.56
6:S4:117:GLU:HG2	6:S4:118:GLU:H	3.56	0.56
6:S4:191:ARG:HD3	6:S4:245:LYS:HB3	2.22	0.56
9:S7:150:GLN:HB3	9:S7:181:ILE:HD12	1.87	0.56
35:SM:53:ARG:HE	35:SM:53:ARG:HA	1.70	0.56
35:SM:64:LYS:O	35:SM:66:ALA:N	3.58	0.56
34:SR:24:ALA:HB3	34:SR:34:LEU:HB3	1.87	0.56
36:1:1720:U:OP2	55:M9:120:TYR:OH	2.17	0.56
1:2:1002:G:N2	1:2:1760:G:O3'	2.38	0.56
36:5:1506:A:H1'	36:5:1848:G:O6	2.06	0.56
36:5:173:G:H1'	36:5:174:C:H5'	1.86	0.56
36:5:2403:G:H5'	36:5:2872:A:C2	2.40	0.56
12:C0:64:TYR:OH	1:6:1435:G:O6	426.94	0.56
16:C4:107:ARG:HH21	16:C4:107:ARG:HB2	2.17	0.56
39:L2:20:THR:HA	39:L2:23:ARG:HD2	1.86	0.56
39:L2:45:VAL:HG22	39:L2:84:THR:HA	1.89	0.56
40:L3:185:GLY:O	40:L3:191:LYS:NZ	4.03	0.56
1:2:1067:C:H5''	3:S1:150:VAL:HG23	1.86	0.56
6:S4:127:LYS:HA	6:S4:127:LYS:HE2	4.55	0.56
6:S4:230:GLU:HB2	6:S4:233:LYS:HE3	6.50	0.56
51:M5:44:ARG:HH22	36:5:269:G:P	125.73	0.56
64:N8:58:MET:SD	36:5:2786:G:N2	156.23	0.56
12:C0:25:LYS:NZ	1:6:1435:G:N7	420.84	0.56
13:C1:21:ASN:HD22	13:C1:31:THR:HA	1.71	0.56
17:C5:79:HIS:O	17:C5:81:ARG:N	2.60	0.56
18:C6:115:THR:O	18:C6:117:LEU:N	3.59	0.56
24:D2:67:GLY:O	24:D2:69:LEU:N	3.87	0.56
39:L2:131:GLY:H	39:L2:169:ILE:HG22	2.30	0.56
40:L3:19:ARG:HB3	40:L3:232:ARG:NH1	2.28	0.56
40:L3:4:ARG:O	40:L3:5:LYS:HB3	2.05	0.56
45:L8:71:VAL:HG22	45:L8:76:ALA:HB2	1.88	0.56
52:M6:10:ASP:HB2	52:M6:117:ARG:HG3	1.88	0.56
6:S4:97:GLU:OE1	6:S4:113:ARG:NH2	2.34	0.56
8:S6:177:ARG:NH2	1:6:143:G:N7	312.61	0.56
36:1:1083:G:H2'	36:1:1084:A:C8	2.41	0.56
36:1:1383:G:O3'	41:L4:138:ARG:NH2	2.39	0.56
36:1:1659:U:H2'	36:1:1660:C:C6	2.41	0.56
37:3:113:C:H2'	37:3:114:U:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2801:A:O2'	36:5:2802:A:H2'	2.05	0.56
1:6:1689:A:H2'	1:6:1690:G:H8	1.71	0.56
17:C5:115:TYR:HB2	17:C5:118:GLU:HG3	1.88	0.56
22:D0:24:ILE:HG12	22:D0:116:VAL:HG13	1.88	0.56
33:E1:106:TYR:HE2	33:E1:116:LYS:HG2	1.77	0.56
40:L3:147:GLU:OE1	40:L3:150:ARG:NH2	2.78	0.56
45:L8:73:PRO:HA	45:L8:76:ALA:HB3	2.86	0.56
62:N6:112:ASP:HB2	62:N6:115:ARG:HB2	1.88	0.56
68:O2:9:ILE:HG12	68:O2:63:THR:HB	1.88	0.56
71:O5:101:THR:HG22	71:O5:104:GLN:HB2	3.74	0.56
4:S2:206:THR:HG21	1:6:14:C:OP2	377.65	0.56
10:S8:50:GLY:O	10:S8:52:ASN:ND2	2.39	0.56
11:S9:109:LEU:HD22	11:S9:113:VAL:HG23	1.86	0.56
11:S9:134:ILE:HG22	11:S9:158:PHE:HD2	1.70	0.56
36:1:1103:A:C8	44:L7:158:LYS:HD3	2.40	0.56
1:2:1266:U:H2'	1:2:1267:G:C8	2.41	0.56
44:L7:206:LYS:HE2	36:5:1334:U:OP1	232.08	0.56
36:5:3269:U:H4'	36:5:3270:U:O5'	2.06	0.56
1:6:1398:U:H3'	1:6:1399:C:H4'	1.88	0.56
1:6:1595:U:N3	1:6:1600:A:H2	1.98	0.56
1:6:738:G:H2'	1:6:739:G:H8	1.70	0.56
13:C1:93:TYR:HB2	13:C1:100:TYR:CE1	2.73	0.56
16:C4:13:VAL:HG13	16:C4:77:THR:H	1.70	0.56
39:L2:130:SER:HA	39:L2:169:ILE:HG22	1.87	0.56
36:1:147:U:H5'	45:L8:136:LEU:HB2	1.88	0.56
61:N5:38:LEU:HD13	61:N5:40:LEU:HD22	3.35	0.56
63:N7:22:LYS:HE3	63:N7:134:LEU:HB2	2.64	0.56
70:O4:7:PHE:CD1	70:O4:20:ILE:HD12	4.82	0.56
49:M3:180:ARG:HD2	72:O6:11:LEU:HD21	1.88	0.56
73:O7:45:ARG:NH2	36:5:361:A:O3'	124.60	0.56
3:S1:216:LYS:NZ	1:6:886:U:OP2	277.47	0.56
6:S4:151:ASP:HB3	6:S4:154:ILE:HG13	1.87	0.56
7:S5:72:HIS:ND1	18:C6:79:TYR:OH	2.28	0.56
36:1:1688:U:H2'	36:1:1689:U:C6	2.40	0.55
1:2:1553:G:N2	1:2:1555:A:H3'	2.21	0.55
1:2:1615:C:O2'	1:2:1616:G:OP2	2.19	0.55
1:2:340:U:H2'	1:2:341:A:C8	2.41	0.55
36:5:1025:A:H3'	36:5:1026:A:H4'	1.87	0.55
47:M0:157:TYR:CD1	36:5:2836:C:H4'	312.59	0.55
36:5:3016:A:H2'	36:5:3017:A:H8	1.71	0.55
1:6:196:G:N3	1:6:197:A:H1'	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:755:A:H2'	1:6:756:A:H8	1.68	0.55
12:C0:46:LEU:O	12:C0:50:THR:HG23	2.06	0.55
14:C2:28:LEU:HD22	14:C2:32:LEU:HG	2.59	0.55
19:C7:23:LYS:HB3	19:C7:34:LEU:HD11	1.87	0.55
20:C8:45:LEU:HD11	21:C9:36:ILE:HG22	2.47	0.55
42:L5:259:LYS:HB2	42:L5:260:PHE:CD2	5.37	0.55
46:L9:29:GLY:HA3	46:L9:82:VAL:HG13	2.44	0.55
48:M1:99:THR:O	48:M1:154:THR:OG1	2.22	0.55
53:M7:108:ASP:N	53:M7:152:GLU:OE2	2.33	0.55
79:Q3:30:GLU:HG2	79:Q3:34:HIS:CE1	3.33	0.55
9:S7:28:GLU:HG2	9:S7:35:LYS:HA	3.56	0.55
36:1:1580:A:H5'	36:1:2522:G:C5	2.41	0.55
36:1:3316:A:O2'	36:1:3317:U:OP2	2.22	0.55
36:1:787:G:H2'	36:1:788:C:C6	2.42	0.55
1:2:108:A:H2'	1:2:109:G:C8	2.41	0.55
1:2:1280:C:H2'	1:2:1281:G:C8	2.41	0.55
1:2:75:U:H2'	1:2:76:A:O4'	2.06	0.55
1:6:486:G:O6	1:6:488:G:N2	2.38	0.55
14:C2:60:VAL:HG23	14:C2:87:PRO:HG2	1.87	0.55
1:2:1369:U:OP1	21:C9:119:LYS:NZ	2.40	0.55
27:D5:43:ASP:HB2	27:D5:46:LYS:HE3	2.53	0.55
39:L2:201:GLY:HA2	39:L2:204:MET:HG3	1.88	0.55
44:L7:176:TYR:CZ	44:L7:197:GLN:HG2	2.41	0.55
45:L8:37:GLY:HA3	36:5:2550:U:C6	212.41	0.55
48:M1:155:THR:O	48:M1:159:THR:HG23	5.19	0.55
58:N2:50:LEU:O	58:N2:52:ASN:N	2.39	0.55
60:N4:63:ILE:O	60:N4:65:GLU:N	2.43	0.55
62:N6:63:LYS:HE3	62:N6:97:ILE:HD13	2.43	0.55
69:O3:45:LEU:HD11	69:O3:73:ARG:HA	3.10	0.55
75:O9:27:ILE:HD13	38:8:52:A:H62	77.56	0.55
6:S4:160:VAL:HG13	6:S4:169:ILE:HG23	1.88	0.55
36:1:2438:A:H2'	36:1:2439:A:H8	1.71	0.55
1:2:591:A:H2'	1:2:592:A:H8	1.72	0.55
1:6:1091:A:H4'	1:6:1092:A:O5'	2.06	0.55
1:6:292:U:H2'	1:6:293:U:C6	2.41	0.55
10:S8:24:LYS:NZ	1:6:392:G:OP1	290.99	0.55
1:6:686:C:H2'	1:6:687:G:C8	2.41	0.55
27:D5:43:ASP:O	27:D5:46:LYS:N	2.30	0.55
70:O4:38:LEU:H	70:O4:38:LEU:HD12	3.33	0.55
34:SR:249:ARG:NH1	34:SR:298:GLY:O	3.03	0.55
36:1:1064:A:H4'	36:1:1065:A:O5'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1798:A:H2'	36:1:1799:A:C8	2.41	0.55
36:1:385:A:H2'	36:1:386:A:C8	2.42	0.55
36:5:1688:U:H2'	36:5:1689:U:C6	2.42	0.55
39:L2:227:ARG:NH2	36:5:2155:G:O2'	206.34	0.55
36:5:2261:G:O2'	36:5:2263:C:N4	2.39	0.55
36:5:2592:G:H4'	36:5:2594:C:C2	2.42	0.55
1:6:50:C:N4	1:6:425:A:OP2	2.37	0.55
1:6:709:C:O2	1:6:730:G:N2	2.39	0.55
16:C4:11:SER:OG	16:C4:12:GLN:N	4.13	0.55
28:D6:36:ILE:HG12	28:D6:84:VAL:HG11	9.47	0.55
39:L2:70:ARG:NH1	39:L2:72:ARG:HH21	6.57	0.55
50:M4:17:VAL:HG11	50:M4:74:ARG:HA	1.89	0.55
36:1:662:U:OP1	64:N8:8:THR:HG21	2.05	0.55
39:L2:172:GLY:HA3	79:Q3:68:ALA:H	4.44	0.55
36:1:1740:U:H1'	36:1:1741:A:H2	1.72	0.55
1:2:686:C:H2'	1:2:687:G:H8	1.71	0.55
37:3:71:G:H2'	37:3:72:A:C8	2.40	0.55
62:N6:12:ARG:HD3	36:5:215:G:H5''	87.74	0.55
16:C4:35:GLY:HA3	1:6:919:A:H5'	270.73	0.55
39:L2:66:PRO:HB2	39:L2:67:TYR:CE2	2.65	0.55
36:1:3049:A:H5''	40:L3:53:MET:HB2	1.88	0.55
42:L5:251:PRO:O	42:L5:253:PHE:N	2.40	0.55
59:N3:11:PHE:CD1	59:N3:88:ARG:HD2	3.32	0.55
3:S1:45:LYS:HG3	16:C4:13:VAL:HG23	1.89	0.55
5:S3:79:TYR:CD2	5:S3:84:ILE:HG13	2.42	0.55
7:S5:166:ARG:HA	7:S5:169:ASN:HB2	2.80	0.55
9:S7:112:ARG:NH2	9:S7:117:THR:OG1	2.39	0.55
10:S8:61:GLU:HG3	10:S8:62:THR:HG23	1.89	0.55
11:S9:172:VAL:HG22	1:6:511:A:H5''	460.47	0.55
34:SR:156:VAL:HA	34:SR:169:ILE:HG22	2.03	0.55
1:2:1606:C:H2'	1:2:1607:G:C8	2.41	0.55
1:2:29:U:H2'	1:2:30:G:C8	2.41	0.55
1:2:520:A:H2'	1:2:521:A:C8	2.41	0.55
1:2:649:U:O2'	1:2:650:U:O5'	2.24	0.55
77:Q1:15:ARG:NH1	1:6:1126:G:OP1	282.58	0.55
15:C3:99:ARG:NH1	15:C3:143:SER:OG	3.35	0.55
15:C3:5:HIS:HB3	15:C3:117:LEU:HD13	2.08	0.55
15:C3:99:ARG:HE	15:C3:115:LEU:HD11	3.51	0.55
18:C6:47:LYS:HZ2	18:C6:114:ARG:HG2	1.71	0.55
24:D2:22:LYS:HD2	29:D7:3:LEU:HD23	3.46	0.55
36:5:2954:U:O4	87:D:3401:SPS:H141	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:157:ASN:O	44:L7:159:GLN:HG2	2.07	0.55
46:L9:86:TYR:CD1	46:L9:151:VAL:HG13	2.56	0.55
52:M6:85:ARG:HD3	52:M6:90:HIS:CE1	3.14	0.55
54:M8:150:VAL:HA	54:M8:153:PHE:CD1	2.42	0.55
58:N2:41:ILE:HG12	58:N2:79:LEU:HD13	1.89	0.55
63:N7:135:ARG:HH11	36:5:1807:G:H5'	195.33	0.55
36:1:1468:A:N1	36:1:1880:U:O2'	2.35	0.55
36:1:3006:A:H2'	36:1:3007:U:O4'	2.07	0.55
36:1:3275:U:H5'	69:O3:68:TRP:CZ2	2.39	0.55
1:2:1765:A:H5'	1:2:1767:G:N7	2.21	0.55
36:5:1667:A:H2'	36:5:1668:G:C8	2.42	0.55
36:5:2534:G:O6	36:5:2545:C:N4	2.30	0.55
40:L3:242:THR:OG1	40:L3:246:LEU:HB3	2.44	0.55
42:L5:235:SER:O	42:L5:239:ILE:HG13	2.07	0.55
45:L8:121:SER:O	45:L8:123:GLN:N	2.39	0.55
49:M3:159:VAL:HA	64:N8:124:ILE:HD11	2.29	0.55
67:O1:44:MET:HB3	67:O1:77:ARG:NH1	3.98	0.55
79:Q3:49:ARG:HD2	79:Q3:50:GLY:N	2.21	0.55
1:2:1097:U:O2'	4:S2:159:THR:OG1	2.22	0.55
4:S2:59:HIS:NE2	4:S2:236:PRO:HB2	3.16	0.55
7:S5:90:ILE:O	7:S5:94:THR:HG23	2.07	0.55
10:S8:36:THR:HB	10:S8:57:ALA:O	2.07	0.55
36:1:1565:G:N2	36:1:1574:C:N3	2.55	0.55
36:1:1913:A:N3	36:1:2120:A:H2'	2.22	0.55
36:1:263:C:H2'	36:1:264:G:O4'	2.07	0.55
36:1:2897:A:H2'	36:1:2899:C:H5''	1.89	0.55
1:6:1699:G:H22	1:6:1702:A:H5''	1.71	0.55
1:6:654:C:H2'	1:6:655:G:C8	2.42	0.55
18:C6:97:VAL:HG12	18:C6:98:ASP:H	1.71	0.55
21:C9:53:TRP:HH2	21:C9:100:ILE:HD12	1.71	0.55
22:D0:82:TYR:HB3	31:D9:52:PHE:HB3	1.88	0.55
4:S2:229:LEU:O	23:D1:16:LYS:NZ	2.39	0.55
43:L6:97:ASN:ND2	43:L6:99:GLU:OE1	4.85	0.55
46:L9:44:THR:HG22	36:5:3186:A:N3	326.88	0.55
46:L9:12:VAL:N	46:L9:51:GLN:O	3.29	0.55
51:M5:98:LEU:HD23	51:M5:128:LYS:HD2	2.88	0.55
52:M6:64:PHE:HE1	52:M6:68:ARG:HH11	3.74	0.55
54:M8:138:LEU:HD13	54:M8:140:LEU:HD21	3.10	0.55
36:1:1320:C:O2	56:N0:115:ARG:NH2	2.40	0.55
63:N7:101:PHE:HA	63:N7:107:ARG:HE	1.72	0.55
3:S1:178:GLY:O	3:S1:179:SER:HB2	4.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:212:VAL:O	3:S1:214:LYS:N	2.35	0.55
6:S4:251:GLU:O	6:S4:255:ARG:HG2	4.19	0.55
36:1:1721:U:OP2	55:M9:124:TYR:OH	2.18	0.55
36:1:2561:A:N1	45:L8:32:LYS:HB2	2.22	0.55
36:1:873:C:H5''	36:1:874:U:O5'	2.07	0.55
1:2:1516:A:OP1	22:D0:88:LYS:NZ	2.31	0.55
36:5:3302:U:H3	36:5:3312:U:H3	1.55	0.55
36:5:608:A:H5''	36:5:609:G:OP2	2.07	0.55
19:C7:13:SER:HA	19:C7:54:THR:HG22	2.83	0.55
22:D0:102:ARG:HE	22:D0:106:ILE:HD12	9.78	0.55
36:1:2294:U:OP2	59:N3:71:LYS:HE2	2.07	0.55
2:S0:179:ARG:HD3	2:S0:183:ARG:HH11	1.71	0.55
36:1:2213:A:H2'	36:1:2214:A:C8	2.42	0.55
36:1:817:A:C2	73:O7:11:ARG:HB3	2.42	0.55
1:2:848:C:H2'	1:2:849:C:H6	1.72	0.55
42:L5:140:ARG:HD3	36:5:1080:A:OP1	227.88	0.55
36:5:1765:U:H4'	36:5:1765:U:OP1	2.06	0.55
36:5:2510:U:O2'	36:5:2511:A:H5''	2.06	0.55
1:6:1767:G:OP1	1:6:1770:U:H4'	2.07	0.55
37:7:112:G:H2'	37:7:113:C:C6	2.41	0.55
45:L8:63:LYS:NZ	38:8:152:G:O2'	149.17	0.55
30:D8:36:THR:OG1	30:D8:37:SER:N	2.28	0.55
58:N2:51:GLY:O	58:N2:52:ASN:ND2	2.40	0.55
70:O4:20:ILE:HD13	70:O4:32:ALA:HB1	3.28	0.55
11:S9:23:ARG:NH1	11:S9:27:GLU:OE2	3.14	0.55
36:1:1180:A:OP1	69:O3:78:SER:OG	2.25	0.54
36:1:149:U:OP2	51:M5:49:ARG:NH2	2.35	0.54
36:1:2771:U:OP2	36:1:2772:C:N4	2.38	0.54
36:1:3319:U:O2'	36:1:3320:A:OP1	2.23	0.54
1:2:395:U:O2'	8:S6:89:ASP:HB3	2.06	0.54
1:2:397:A:O3'	10:S8:50:GLY:HA2	2.07	0.54
38:4:104:A:C8	38:4:105:A:C8	2.95	0.54
36:5:1253:U:H4'	36:5:1254:C:H5'	1.89	0.54
36:5:2413:A:H2'	36:5:2414:G:H8	1.72	0.54
20:C8:30:TYR:HE2	20:C8:40:ARG:HH11	1.55	0.54
28:D6:79:ILE:HG23	28:D6:84:VAL:HG21	1.88	0.54
43:L6:40:LEU:HD12	43:L6:65:ILE:HD11	6.62	0.54
58:N2:14:THR:HG23	58:N2:66:VAL:HG22	3.72	0.54
65:N9:14:ARG:NH2	65:N9:18:ARG:HH11	2.22	0.54
36:1:2138:A:C4	73:O7:3:LYS:HB3	2.42	0.54
2:S0:155:PHE:O	23:D1:60:ARG:NH2	2.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:67:VAL:HG23	8:S6:68:LEU:O	2.30	0.54
11:S9:38:ASN:HB3	11:S9:40:LYS:H	1.72	0.54
34:SR:108:SER:OG	34:SR:109:ASP:N	2.75	0.54
34:SR:80:ALA:HB3	34:SR:92:TRP:HB2	1.89	0.54
38:4:35:C:H5''	73:O7:70:VAL:HG11	1.89	0.54
36:5:2663:G:H2'	36:5:2664:C:O4'	2.07	0.54
1:6:660:G:H2'	1:6:661:A:H4'	1.88	0.54
13:C1:5:LEU:O	13:C1:7:VAL:N	2.31	0.54
24:D2:83:ILE:HG13	24:D2:122:SER:HB2	4.70	0.54
26:D4:10:ARG:HB2	26:D4:24:VAL:HB	2.65	0.54
46:L9:166:ARG:HD2	46:L9:168:ARG:NH1	12.92	0.54
48:M1:16:LYS:HG3	48:M1:130:VAL:HG13	2.42	0.54
51:M5:36:ILE:HG12	51:M5:64:VAL:HG23	2.61	0.54
56:N0:93:GLU:OE1	56:N0:137:ARG:HB2	2.76	0.54
58:N2:50:LEU:HB3	58:N2:54:VAL:HG23	1.89	0.54
62:N6:5:SER:HB3	62:N6:8:VAL:HG22	5.40	0.54
63:N7:16:GLY:O	63:N7:19:ALA:N	3.38	0.54
8:S6:57:ASP:HB3	8:S6:98:ARG:HG3	2.22	0.54
36:1:1103:A:H4'	36:1:1103:A:OP2	2.07	0.54
36:1:2896:A:OP2	76:Q0:102:ARG:NH2	2.30	0.54
36:1:3278:C:H2'	36:1:3278:C:O2	2.07	0.54
1:2:823:G:H2'	1:2:824:G:C8	2.41	0.54
36:5:1018:G:H2'	36:5:1019:G:O4'	2.07	0.54
36:5:2518:C:H2'	36:5:2519:A:H8	1.72	0.54
36:5:767:U:H1'	36:5:768:C:C6	2.42	0.54
1:6:538:A:H8	1:6:543:C:H41	1.47	0.54
16:C4:84:ARG:HB3	16:C4:118:VAL:HG23	3.22	0.54
20:C8:134:ARG:O	20:C8:136:GLN:N	3.80	0.54
31:D9:5:ASN:N	31:D9:5:ASN:OD1	2.40	0.54
46:L9:28:VAL:HG13	46:L9:33:THR:HB	1.88	0.54
52:M6:18:ARG:O	52:M6:22:VAL:HG12	3.94	0.54
57:N1:68:THR:OG1	57:N1:69:LYS:N	2.40	0.54
59:N3:128:ARG:HH21	59:N3:128:ARG:HB3	3.98	0.54
36:1:1367:G:OP1	68:O2:45:ARG:NH2	2.40	0.54
77:Q1:7:LYS:HE2	77:Q1:11:ARG:NH1	2.22	0.54
78:Q2:41:ARG:NH2	36:5:2785:A:O2'	161.06	0.54
2:S0:195:TRP:CE2	2:S0:197:ILE:HD13	2.68	0.54
6:S4:153:ASN:O	6:S4:174:LYS:NZ	2.34	0.54
36:1:1549:U:H2'	36:1:1550:C:C6	2.41	0.54
36:1:2808:A:O2'	36:1:2969:A:OP1	2.19	0.54
36:1:2986:U:H2'	36:1:2987:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:603:A:H2'	36:1:604:G:O4'	2.07	0.54
1:2:1525:A:H2'	1:2:1526:A:C8	2.43	0.54
1:2:15:U:H2'	1:2:16:G:O4'	2.08	0.54
1:2:190:C:O2'	1:2:191:C:H5'	2.07	0.54
1:2:894:U:H2'	1:2:895:G:C8	2.43	0.54
36:5:2651:G:H4'	36:5:2652:U:OP2	2.08	0.54
52:M6:156:LEU:HD13	36:5:3243:A:C8	263.96	0.54
1:6:1492:A:HO2'	1:6:1493:A:H8	1.54	0.54
1:6:73:U:H2'	1:6:74:U:C6	2.42	0.54
12:C0:27:PHE:CD1	12:C0:40:LEU:HD23	2.43	0.54
17:C5:33:PHE:HA	17:C5:36:LEU:HD23	1.89	0.54
19:C7:34:LEU:O	19:C7:38:ILE:HG22	2.07	0.54
22:D0:118:VAL:HG13	22:D0:119:ALA:H	3.04	0.54
39:L2:118:GLU:HG3	39:L2:126:LEU:HD21	2.21	0.54
39:L2:200:ARG:HD2	36:5:2186:U:OP2	216.78	0.54
50:M4:121:MET:HE1	36:5:3215:A:O5'	275.41	0.54
62:N6:26:GLN:O	62:N6:30:LEU:HG	2.59	0.54
63:N7:54:THR:OG1	63:N7:55:LYS:N	2.56	0.54
69:O3:14:LEU:HD11	69:O3:31:LYS:HB2	1.88	0.54
51:M5:143:ARG:HH21	71:O5:92:LEU:HD23	1.71	0.54
2:S0:134:LYS:O	2:S0:137:SER:OG	2.20	0.54
4:S2:98:PHE:CZ	35:SM:116:GLU:HG3	2.41	0.54
5:S3:192:PRO:O	5:S3:195:SER:HB2	2.07	0.54
6:S4:100:ARG:HH21	6:S4:122:LYS:HA	1.93	0.54
9:S7:155:ASP:OD2	9:S7:156:SER:N	2.31	0.54
10:S8:42:ARG:NH1	1:6:1677:C:OP1	263.39	0.54
36:1:911:C:N4	39:L2:3:ARG:HD3	2.22	0.54
1:2:1114:G:O2'	1:2:1130:G:O6	2.25	0.54
1:6:228:G:N2	1:6:237:C:N3	2.55	0.54
17:C5:122:THR:HG22	1:6:1558:U:H3	368.63	0.54
21:C9:57:ARG:HG2	21:C9:104:VAL:HG21	1.90	0.54
16:C4:112:ILE:H	28:D6:57:SER:HA	2.23	0.54
33:E1:90:LYS:HB2	33:E1:93:HIS:CE1	11.43	0.54
42:L5:244:HIS:O	42:L5:248:ARG:HG3	2.21	0.54
42:L5:48:LYS:NZ	36:5:2748:A:O3'	244.23	0.54
3:S1:61:LEU:HA	3:S1:64:ARG:HE	4.90	0.54
4:S2:90:THR:OG1	4:S2:91:ARG:N	3.23	0.54
10:S8:197:THR:HA	10:S8:200:LYS:HD2	1.89	0.54
1:2:1297:G:N2	1:2:1300:A:OP2	2.41	0.54
1:2:1564:U:H2'	1:2:1565:C:C6	2.43	0.54
1:2:539:G:OP2	1:2:539:G:H8	1.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:45:A:H2'	37:3:46:A:C8	2.41	0.54
68:O2:45:ARG:NH1	36:5:1160:C:O2	205.26	0.54
36:5:1724:U:H1'	36:5:1725:C:C6	2.42	0.54
36:5:1944:U:H2'	36:5:1945:A:H8	1.72	0.54
36:5:3259:U:H5''	36:5:3261:C:H5	1.71	0.54
36:5:59:G:H2'	38:8:33:A:O2'	2.08	0.54
1:6:1738:U:H2'	1:6:1739:C:H6	1.72	0.54
5:S3:211:PRO:HG3	19:C7:20:TYR:CZ	2.43	0.54
5:S3:203:PRO:HA	19:C7:42:GLN:HB2	2.26	0.54
25:D3:31:LYS:HD2	25:D3:36:THR:HG21	1.90	0.54
32:E0:51:ASN:HB3	32:E0:53:LYS:HG2	5.79	0.54
39:L2:113:VAL:HG12	39:L2:166:ILE:HA	2.61	0.54
41:L4:317:PRO:HA	41:L4:323:VAL:HG13	3.76	0.54
41:L4:339:LEU:HA	41:L4:342:LYS:HB3	4.18	0.54
43:L6:176:PHE:HA	50:M4:114:ASP:HB2	2.57	0.54
49:M3:54:LEU:HD23	49:M3:141:ALA:HB1	3.30	0.54
52:M6:88:VAL:O	52:M6:90:HIS:N	2.40	0.54
60:N4:23:ARG:NH2	60:N4:25:ASP:OD2	2.41	0.54
70:O4:99:LYS:O	70:O4:103:LYS:HG2	2.13	0.54
74:O8:17:ARG:O	74:O8:19:ASP:N	2.40	0.54
6:S4:141:THR:OG1	6:S4:145:ARG:HB2	2.36	0.54
1:2:1229:G:O2'	1:2:1255:G:N2	2.40	0.54
1:2:715:U:H3	1:2:723:G:H1	1.56	0.54
37:3:6:C:O2'	42:L5:50:ARG:NH2	2.35	0.54
36:5:209:A:H4'	36:5:211:A:N7	2.23	0.54
36:5:495:G:H2'	36:5:496:C:O4'	2.08	0.54
36:5:612:U:H2'	36:5:613:G:C8	2.42	0.54
14:C2:67:THR:HG22	14:C2:68:GLU:HG3	1.88	0.54
15:C3:87:ASP:OD1	1:6:867:G:N2	319.24	0.54
21:C9:105:LEU:HD13	21:C9:122:ARG:HD3	2.26	0.54
39:L2:104:LEU:HD23	39:L2:158:ILE:HD11	2.80	0.54
41:L4:6:VAL:N	41:L4:20:LEU:O	2.26	0.54
45:L8:33:ASN:HA	36:5:2549:G:C2	212.62	0.54
52:M6:12:LYS:O	56:N0:167:ARG:NH2	2.30	0.54
46:L9:4:ILE:HG22	56:N0:142:GLN:OE1	2.08	0.54
36:1:2557:A:H5'	63:N7:135:ARG:HH11	1.72	0.54
36:1:1033:U:H2'	36:1:1034:U:C6	2.43	0.54
1:2:116:U:H2'	1:2:117:U:C6	2.43	0.54
1:2:1534:G:OP2	27:D5:74:SER:OG	2.20	0.54
1:2:1169:G:N1	1:2:1575:G:OP2	2.39	0.54
36:5:2256:A:OP2	36:5:2256:A:H2'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1650:U:H2'	1:6:1651:A:C8	2.43	0.54
15:C3:84:ILE:HD11	15:C3:89:TYR:HD2	2.45	0.54
25:D3:69:ARG:NH1	25:D3:116:ASP:OD2	2.48	0.54
26:D4:14:SER:HA	26:D4:21:LYS:HG3	1.96	0.54
50:M4:123:LEU:HD22	52:M6:190:VAL:HG13	5.88	0.54
49:M3:166:ALA:N	64:N8:135:GLU:OE1	3.48	0.54
70:O4:20:ILE:HD12	70:O4:32:ALA:HB1	1.89	0.54
36:1:361:A:O3'	73:O7:45:ARG:NH2	2.41	0.54
5:S3:23:GLU:OE2	12:C0:61:TRP:NE1	3.03	0.54
6:S4:130:GLN:HB2	6:S4:138:TYR:CZ	2.42	0.54
1:2:1649:G:H2'	1:2:1650:U:C6	2.43	0.54
1:2:369:A:O2'	1:2:371:G:OP2	2.22	0.54
1:2:870:C:H2'	1:2:871:G:H8	1.72	0.54
1:6:712:G:H2'	1:6:713:A:C8	2.43	0.54
18:C6:12:LYS:HD2	18:C6:17:THR:HG22	1.87	0.54
19:C7:44:LYS:HG2	19:C7:48:ASN:HD21	1.71	0.54
20:C8:11:PHE:CZ	20:C8:59:GLY:HA3	4.08	0.54
39:L2:227:ARG:HG2	39:L2:239:ALA:HB2	1.90	0.54
39:L2:3:ARG:HD3	36:5:911:C:N4	179.43	0.54
44:L7:229:PHE:HD1	44:L7:229:PHE:C	2.51	0.54
45:L8:94:PHE:HB3	45:L8:189:LEU:HD13	1.90	0.54
46:L9:12:VAL:HB	46:L9:51:GLN:HA	1.88	0.54
47:M0:205:SER:O	47:M0:209:ASN:HB2	2.07	0.54
57:N1:12:ARG:HD3	57:N1:13:TYR:CE1	2.43	0.54
64:N8:46:ASP:N	64:N8:46:ASP:OD1	2.40	0.54
76:Q0:97:ARG:HG3	76:Q0:120:GLN:O	4.07	0.54
3:S1:180:THR:HG22	3:S1:181:LEU:H	1.72	0.54
4:S2:157:LYS:HG2	4:S2:170:ILE:HG23	2.72	0.54
6:S4:95:THR:HG23	6:S4:97:GLU:HG3	6.26	0.54
11:S9:107:ARG:NH2	11:S9:148:VAL:O	2.40	0.54
36:1:1108:U:H2'	36:1:1109:U:H6	1.72	0.54
36:1:1846:C:OP1	36:1:1849:C:N4	2.33	0.54
1:2:368:U:HO2'	1:2:603:U:HO2'	1.53	0.54
36:5:1554:U:H1'	36:5:1555:U:H5''	1.90	0.54
25:D3:75:GLN:HG3	25:D3:82:LYS:HG3	1.89	0.54
26:D4:57:VAL:HG13	26:D4:60:PHE:HE2	1.72	0.54
39:L2:68:LYS:HZ3	39:L2:70:ARG:HH21	4.97	0.54
42:L5:64:ILE:HD13	42:L5:105:ILE:HD12	1.90	0.54
49:M3:140:SER:OG	49:M3:143:ALA:N	2.27	0.54
52:M6:112:TYR:O	52:M6:117:ARG:NH1	2.79	0.54
53:M7:29:THR:O	53:M7:119:VAL:HG11	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:N7:10:VAL:HG23	63:N7:86:THR:HA	1.89	0.54
63:N7:60:LYS:O	63:N7:64:LYS:HG2	2.08	0.54
6:S4:61:VAL:HG12	6:S4:65:LEU:HD12	1.88	0.54
36:1:2207:A:H2'	36:1:2208:A:H5'	1.89	0.53
47:M0:116:ARG:NH2	36:5:2617:U:O3'	228.17	0.53
21:C9:72:GLY:HA3	1:6:1498:G:H5''	422.52	0.53
1:6:235:G:H2'	1:6:236:A:H8	1.73	0.53
1:6:595:G:H2'	1:6:596:C:C6	2.43	0.53
25:D3:100:ASP:O	25:D3:101:GLU:HB2	4.61	0.53
31:D9:31:ILE:HB	31:D9:38:ILE:O	2.08	0.53
40:L3:5:LYS:HG2	40:L3:6:TYR:CE1	3.66	0.53
43:L6:56:LYS:HD2	43:L6:98:VAL:HG13	1.89	0.53
53:M7:64:ASN:HA	53:M7:67:ILE:HD13	1.90	0.53
53:M7:29:THR:HG22	53:M7:87:SER:OG	2.08	0.53
59:N3:45:ARG:HB3	59:N3:48:ARG:HG3	2.04	0.53
3:S1:30:PHE:HB3	3:S1:96:LEU:HD22	3.55	0.53
4:S2:227:PRO:HA	4:S2:230:TRP:CE2	2.42	0.53
1:2:122:U:O3'	6:S4:77:ARG:NH2	2.41	0.53
34:SR:52:GLN:HG2	34:SR:53:LYS:H	2.36	0.53
36:1:2168:A:C6	36:1:2170:U:H1'	2.43	0.53
1:2:420:A:OP1	8:S6:96:SER:OG	2.13	0.53
36:5:1464:G:N2	36:5:1466:G:H3'	2.22	0.53
45:L8:241:LYS:HB2	36:5:2586:G:N7	185.39	0.53
1:6:1171:A:H2'	1:6:1172:G:C8	2.43	0.53
1:6:647:G:N2	1:6:687:G:H22	2.06	0.53
6:S4:106:LYS:NZ	1:6:788:A:OP1	398.04	0.53
1:6:808:U:H2'	1:6:809:A:C8	2.43	0.53
1:6:973:A:H2'	1:6:974:A:C8	2.42	0.53
14:C2:27:ALA:HB1	14:C2:132:GLU:HB3	1.90	0.53
25:D3:103:LEU:HD12	25:D3:126:LYS:HD3	4.34	0.53
26:D4:57:VAL:HB	26:D4:60:PHE:HE2	4.02	0.53
28:D6:10:ARG:HB2	28:D6:34:LYS:HG3	1.90	0.53
40:L3:159:ARG:HG2	40:L3:182:GLN:HA	1.89	0.53
41:L4:174:ALA:O	41:L4:178:LEU:HG	2.80	0.53
36:1:1334:U:O2'	44:L7:151:ARG:NH2	2.41	0.53
45:L8:115:ALA:O	45:L8:119:ALA:N	2.38	0.53
47:M0:42:THR:HG23	47:M0:45:GLU:HB2	1.89	0.53
36:1:289:A:H2	51:M5:93:LYS:HD2	1.71	0.53
54:M8:158:HIS:H	54:M8:186:VAL:CG1	2.16	0.53
57:N1:86:GLU:OE1	57:N1:88:ARG:NH1	2.40	0.53
67:O1:29:ALA:HB3	67:O1:30:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:O5:49:LYS:HZ1	38:8:63:G:HO2'	50.22	0.53
74:O8:44:LYS:HG2	74:O8:53:THR:HB	1.90	0.53
6:S4:107:GLY:HA2	6:S4:189:LEU:HG	2.26	0.53
7:S5:42:LEU:HB2	7:S5:46:TRP:O	2.08	0.53
9:S7:12:ALA:HB3	9:S7:13:PRO:HD3	1.95	0.53
36:1:532:A:H2	36:1:560:G:H22	1.56	0.53
1:2:939:A:H2'	1:2:940:A:C8	2.43	0.53
47:M0:90:ARG:NH1	36:5:1043:C:O3'	313.48	0.53
36:5:2407:C:H2'	36:5:2408:U:C6	2.44	0.53
44:L7:98:LYS:HB3	44:L7:99:PRO:HD3	1.91	0.53
46:L9:90:MET:HB2	46:L9:144:ILE:HG22	1.91	0.53
53:M7:25:SER:O	53:M7:29:THR:OG1	3.89	0.53
55:M9:60:LYS:HE3	55:M9:64:ARG:HH21	1.73	0.53
66:O0:58:TYR:OH	70:O4:97:GLU:OE2	2.20	0.53
3:S1:110:LEU:HD11	3:S1:213:ARG:HD2	1.90	0.53
7:S5:133:VAL:HA	7:S5:198:LEU:HD22	3.77	0.53
1:2:1427:A:OP2	35:SM:93:ARG:NH1	2.41	0.53
34:SR:248:ASN:OD1	34:SR:249:ARG:N	2.90	0.53
36:1:1101:G:OP2	44:L7:196:LYS:HE2	2.09	0.53
36:1:2339:C:OP2	59:N3:48:ARG:HG2	2.07	0.53
36:1:3160:U:H2'	36:1:3161:C:C6	2.44	0.53
1:2:1492:A:HO2'	1:2:1493:A:H8	1.55	0.53
1:2:1524:A:H2'	1:2:1525:A:C8	2.43	0.53
1:2:607:G:H5'	1:2:613:G:N2	2.24	0.53
1:2:918:U:H2'	1:2:919:A:C8	2.43	0.53
37:3:60:G:H2'	37:3:61:G:H8	1.73	0.53
36:5:2404:A:N7	36:5:2872:A:N6	2.56	0.53
19:C7:2:GLY:N	1:6:1312:A:OP1	393.25	0.53
10:S8:2:GLY:N	1:6:393:C:OP2	292.88	0.53
1:2:1228:G:H22	14:C2:67:THR:HB	1.74	0.53
42:L5:52:VAL:HG21	42:L5:65:ILE:HD12	1.88	0.53
49:M3:47:ALA:HB1	49:M3:48:PRO:HD2	1.89	0.53
50:M4:121:MET:O	50:M4:125:LYS:HG2	2.09	0.53
36:1:3227:A:O3'	50:M4:133:LYS:NZ	2.42	0.53
55:M9:43:LYS:O	55:M9:47:ASN:N	3.08	0.53
64:N8:28:HIS:CD2	64:N8:32:ARG:HG2	2.43	0.53
70:O4:81:CYS:O	70:O4:83:ASN:N	2.68	0.53
72:O6:57:LEU:HD11	72:O6:73:ALA:HB2	2.36	0.53
10:S8:89:GLU:O	10:S8:93:THR:OG1	2.18	0.53
36:1:1391:C:C2	68:O2:103:LYS:HD3	2.44	0.53
36:1:2314:U:O2'	36:1:2315:G:OP1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3178:A:C2	52:M6:115:LYS:HG2	2.44	0.53
36:1:634:C:O2'	68:O2:47:ARG:HD3	2.08	0.53
36:1:980:A:OP2	36:1:980:A:H8	1.91	0.53
1:2:488:G:OP1	1:2:488:G:H4'	2.09	0.53
36:5:2812:C:H2'	36:5:2813:A:H8	1.74	0.53
64:N8:115:LYS:HG3	36:5:715:A:C8	148.94	0.53
1:6:621:A:O2'	1:6:1106:U:O2'	2.26	0.53
1:2:1217:A:H5''	12:C0:1:MET:HG3	1.90	0.53
12:C0:24:LYS:HA	12:C0:63:TYR:HA	1.90	0.53
39:L2:189:TYR:HA	39:L2:192:LYS:HG3	3.11	0.53
40:L3:2:SER:O	40:L3:3:HIS:HB3	2.09	0.53
48:M1:60:ARG:O	48:M1:63:GLU:HB2	2.07	0.53
70:O4:46:ASP:OD1	70:O4:80:ARG:NH1	2.40	0.53
79:Q3:3:LYS:HD2	79:Q3:3:LYS:O	6.03	0.53
10:S8:35:ASN:O	10:S8:95:THR:HG23	3.15	0.53
36:1:1038:C:H4'	42:L5:5:LYS:HE3	1.91	0.53
36:1:3228:C:H4'	36:1:3229:G:O5'	2.07	0.53
36:1:779:G:OP1	54:M8:185:LYS:NZ	2.40	0.53
36:1:829:U:H3	36:1:895:A:H62	1.57	0.53
1:2:1370:U:H4'	1:2:1371:A:O5'	2.08	0.53
1:2:322:G:O2'	10:S8:10:LYS:NZ	2.33	0.53
1:2:780:A:H8	26:D4:8:ARG:HB3	1.73	0.53
1:6:1263:G:H2'	1:6:1264:G:O4'	2.09	0.53
14:C2:59:LEU:HA	14:C2:87:PRO:HB2	1.89	0.53
28:D6:15:ARG:O	28:D6:17:HIS:N	2.42	0.53
39:L2:202:VAL:HG13	39:L2:217:GLN:HG2	1.89	0.53
44:L7:150:LYS:HG2	44:L7:151:ARG:HG2	1.90	0.53
45:L8:67:ILE:HG22	45:L8:237:ILE:HB	1.89	0.53
36:1:2433:U:H1'	51:M5:125:SER:HB3	1.91	0.53
54:M8:170:ARG:O	54:M8:171:LYS:HB2	2.08	0.53
57:N1:50:LYS:HB3	57:N1:92:ARG:HH11	1.73	0.53
66:O0:17:VAL:HG11	66:O0:92:ILE:HD12	1.90	0.53
3:S1:48:VAL:HG21	3:S1:61:LEU:HD22	5.63	0.53
1:2:144:U:H5	8:S6:137:ARG:NH1	2.07	0.53
9:S7:39:ARG:HH22	55:M9:185:LEU:HD22	3.08	0.53
11:S9:20:GLU:HB2	11:S9:23:ARG:HB3	4.16	0.53
36:1:129:U:H2'	36:1:130:A:C8	2.44	0.53
1:2:473:A:H5'	1:2:769:A:H1'	1.91	0.53
37:3:71:G:H2'	37:3:72:A:H8	1.74	0.53
58:N2:104:ARG:NH1	36:5:1758:G:OP1	121.09	0.53
36:5:3115:C:O2'	36:5:3117:C:N4	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:8:C:H2'	36:5:9:U:O4'	2.09	0.53
1:6:427:C:O2'	1:6:459:G:N3	2.36	0.53
15:C3:136:PRO:HG2	15:C3:139:TRP:HB2	1.91	0.53
21:C9:117:SER:HB2	21:C9:123:ARG:HB2	1.89	0.53
23:D1:9:VAL:HG22	23:D1:10:GLU:H	1.88	0.53
25:D3:55:GLU:HG2	25:D3:73:ARG:HB2	1.90	0.53
39:L2:201:GLY:HA2	39:L2:204:MET:SD	2.79	0.53
47:M0:116:ARG:NE	36:5:2618:G:OP1	232.81	0.53
50:M4:135:LEU:HD11	52:M6:178:VAL:HG22	1.90	0.53
36:1:1307:G:OP2	52:M6:59:ARG:NH1	2.42	0.53
53:M7:97:ASN:O	53:M7:101:ASN:ND2	3.42	0.53
58:N2:104:ARG:HH11	58:N2:106:ALA:HB2	3.82	0.53
36:5:953:G:O2'	36:5:1116:G:H5'	2.09	0.53
23:D1:36:VAL:O	23:D1:51:VAL:N	2.87	0.53
25:D3:56:LYS:NZ	25:D3:97:ASP:H	2.06	0.53
40:L3:291:GLU:OE1	40:L3:302:LYS:NZ	3.82	0.53
47:M0:99:ILE:HD13	47:M0:101:LYS:HB2	3.80	0.53
55:M9:9:ARG:HH21	55:M9:10:LEU:HD13	2.96	0.53
61:N5:67:ILE:HD12	61:N5:83:VAL:HG12	1.90	0.53
63:N7:88:ASP:HB3	63:N7:121:ARG:HH22	1.72	0.53
71:O5:101:THR:HG22	71:O5:103:LYS:N	2.24	0.53
36:1:1844:C:O2	73:O7:9:GLY:HA2	2.09	0.53
5:S3:176:LEU:HA	5:S3:181:VAL:HG12	1.91	0.53
8:S6:153:VAL:O	8:S6:156:PHE:N	2.40	0.53
8:S6:71:THR:OG1	8:S6:72:ARG:N	2.42	0.53
9:S7:156:SER:HB2	9:S7:186:PRO:HG2	4.20	0.53
11:S9:129:ILE:HA	11:S9:134:ILE:HG12	3.64	0.53
34:SR:26:SER:OG	34:SR:75:ALA:O	2.26	0.53
36:5:2927:C:H2'	36:5:2928:C:C6	2.44	0.53
50:M4:77:ARG:NH2	36:5:524:U:OP1	341.23	0.53
1:6:1606:C:H2'	1:6:1607:G:C8	2.44	0.53
25:D3:46:SER:OG	25:D3:78:LYS:NZ	2.97	0.53
26:D4:25:VAL:HG12	26:D4:27:VAL:HG23	2.11	0.53
29:D7:61:THR:OG1	29:D7:62:ILE:N	2.41	0.53
30:D8:32:PHE:HE2	30:D8:38:ARG:HB3	1.74	0.53
39:L2:48:ILE:HG13	39:L2:48:ILE:O	2.09	0.53
42:L5:131:LEU:HD22	42:L5:131:LEU:H	1.72	0.53
44:L7:125:GLU:HA	44:L7:128:LYS:HG3	1.91	0.53
53:M7:172:GLN:NE2	69:O3:60:ARG:O	2.42	0.53
42:L5:40:HIS:CE1	57:N1:69:LYS:HA	2.80	0.53
66:O0:16:LEU:HB2	66:O0:98:SER:HB2	3.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:O7:17:THR:HG22	73:O7:18:LEU:H	1.73	0.53
79:Q3:3:LYS:O	79:Q3:5:THR:N	4.38	0.53
2:S0:22:THR:HG22	2:S0:169:SER:HA	2.21	0.53
5:S3:29:LEU:HD21	5:S3:69:LEU:HD11	1.90	0.53
10:S8:12:SER:OG	10:S8:14:THR:OG1	2.18	0.53
1:2:330:G:OP2	10:S8:172:ARG:NH1	2.39	0.53
11:S9:149:ARG:HD2	1:6:765:G:O6	432.25	0.53
36:1:1318:A:OP1	52:M6:18:ARG:NH2	2.36	0.53
36:1:1742:U:H2'	36:1:1743:G:C8	2.44	0.53
36:1:2407:C:H2'	36:1:2408:U:H6	1.74	0.53
36:1:440:A:OP2	36:1:440:A:H8	1.92	0.53
1:2:304:U:H2'	1:2:305:C:C6	2.44	0.53
1:2:46:A:N6	1:2:433:C:H4'	2.24	0.53
36:5:1340:G:H2'	36:5:1341:U:C6	2.44	0.53
36:5:1657:C:O2'	36:5:1797:A:OP2	2.18	0.53
36:5:2207:A:H62	36:5:2236:G:H1	1.57	0.53
36:5:595:G:N1	36:5:609:G:H5''	2.24	0.53
36:5:789:A:H2'	36:5:790:U:C6	2.44	0.53
1:6:1535:U:H1'	1:6:1536:G:C2	2.44	0.53
15:C3:73:ARG:HD3	1:6:859:A:C5	332.54	0.53
36:1:860:G:C6	39:L2:181:LYS:HB2	2.44	0.53
50:M4:21:VAL:HG12	50:M4:65:LEU:HA	2.09	0.53
56:N0:13:ARG:NH2	56:N0:50:LYS:O	3.24	0.53
57:N1:103:GLN:HE21	57:N1:104:GLU:N	2.07	0.53
66:O0:43:ILE:HG23	66:O0:68:TYR:HD2	2.44	0.53
5:S3:34:TYR:HE2	5:S3:37:VAL:HG13	2.16	0.53
1:6:1620:C:H2'	1:6:1621:U:C6	2.43	0.52
39:L2:70:ARG:HH11	39:L2:72:ARG:HH21	6.60	0.52
40:L3:114:VAL:HG22	40:L3:163:HIS:CE1	2.49	0.52
48:M1:33:ALA:HB2	48:M1:123:PHE:CE1	2.62	0.52
48:M1:94:ARG:C	48:M1:96:PHE:H	2.12	0.52
51:M5:28:TRP:O	51:M5:32:GLN:HG2	2.09	0.52
56:N0:13:ARG:HA	56:N0:56:GLY:HA2	1.90	0.52
61:N5:49:LYS:O	61:N5:51:VAL:N	2.41	0.52
66:O0:16:LEU:HD22	66:O0:19:LYS:HE2	1.91	0.52
78:Q2:71:ARG:HE	78:Q2:80:ARG:NH1	2.04	0.52
10:S8:48:THR:HG21	10:S8:54:LYS:HE3	1.90	0.52
36:1:2242:A:H5'	39:L2:243:THR:HG23	1.91	0.52
1:2:74:U:O2'	1:2:75:U:OP2	2.26	0.52
37:3:11:A:H4'	37:3:13:A:C8	2.45	0.52
36:5:1564:U:H2'	36:5:1565:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2396:G:OP1	36:5:2397:A:H4'	2.09	0.52
1:6:1120:U:H2'	1:6:1121:C:C6	2.44	0.52
31:D9:14:TYR:OH	1:6:1553:G:O2'	405.13	0.52
1:6:321:C:N4	1:6:1666:U:H5''	2.24	0.52
1:6:914:G:H8	1:6:914:G:OP2	1.91	0.52
18:C6:16:ALA:HB2	18:C6:72:GLY:HA3	1.91	0.52
18:C6:79:TYR:HA	18:C6:82:ARG:HG2	2.21	0.52
25:D3:132:LEU:C	25:D3:134:ALA:H	3.34	0.52
25:D3:2:GLY:N	1:6:1102:G:N7	347.97	0.52
30:D8:13:ILE:HD12	30:D8:29:ARG:HG2	1.91	0.52
39:L2:14:SER:OG	39:L2:15:ILE:N	2.42	0.52
40:L3:105:VAL:HG11	40:L3:144:ILE:HG23	2.27	0.52
40:L3:252:ILE:HG13	40:L3:264:VAL:HG21	2.88	0.52
41:L4:60:THR:HG23	36:5:364:G:OP1	129.43	0.52
55:M9:68:GLN:NE2	55:M9:72:GLU:OE1	2.32	0.52
56:N0:80:ARG:HB3	56:N0:122:HIS:HB2	1.90	0.52
61:N5:91:ASN:H	61:N5:94:GLN:HE21	1.56	0.52
9:S7:9:LEU:HD21	9:S7:17:GLU:HB3	1.92	0.52
36:1:1126:G:H5''	47:M0:119:TRP:HZ3	1.73	0.52
36:1:239:G:O2'	36:1:240:U:OP1	2.25	0.52
36:1:287:G:H5'	51:M5:179:LYS:O	2.09	0.52
1:2:1066:C:O2'	3:S1:148:ASN:ND2	2.42	0.52
1:2:870:C:H2'	1:2:871:G:C8	2.45	0.52
36:5:1096:U:H4'	36:5:1097:G:O5'	2.10	0.52
39:L2:221:LYS:O	36:5:2245:C:H4'	219.37	0.52
40:L3:280:HIS:HB3	40:L3:324:VAL:CG2	2.39	0.52
41:L4:93:MET:CE	41:L4:93:MET:H	3.02	0.52
46:L9:89:LYS:HG2	46:L9:145:VAL:HG22	1.91	0.52
50:M4:105:GLN:HE22	50:M4:109:ARG:HH21	1.57	0.52
59:N3:101:VAL:HG11	59:N3:114:ILE:HG12	1.89	0.52
61:N5:58:ASP:OD2	61:N5:60:TYR:N	2.43	0.52
63:N7:46:ILE:HG12	63:N7:49:TYR:CE1	3.20	0.52
64:N8:77:LYS:O	64:N8:79:TRP:N	2.43	0.52
4:S2:115:ILE:HD11	4:S2:212:LYS:HD2	2.80	0.52
1:2:577:G:H2'	35:SM:99:LYS:NZ	2.24	0.52
36:1:1103:A:H1'	36:1:1104:G:OP1	2.09	0.52
36:1:685:G:OP2	49:M3:35:ARG:NH1	2.43	0.52
36:1:916:G:H5'	36:1:917:A:OP1	2.09	0.52
36:1:980:A:H2'	36:1:981:U:C6	2.44	0.52
1:2:393:C:H4'	1:2:1673:G:O2'	2.10	0.52
36:5:109:A:H4'	36:5:110:G:OP1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1157:G:H2'	36:5:1158:A:O4'	2.10	0.52
36:5:835:G:O2'	36:5:857:G:N2	2.32	0.52
1:6:1338:C:H1'	1:6:1410:A:C4	2.44	0.52
1:2:917:U:O2	16:C4:41:ARG:NH1	2.42	0.52
1:2:1553:G:O6	17:C5:43:ARG:HD3	2.09	0.52
44:L7:229:PHE:CD1	44:L7:229:PHE:C	2.99	0.52
44:L7:88:ARG:HD2	44:L7:90:LYS:O	2.29	0.52
47:M0:140:THR:HG21	47:M0:148:VAL:HG21	2.85	0.52
49:M3:75:PHE:H	49:M3:97:VAL:HA	1.74	0.52
56:N0:96:ASP:OD1	56:N0:97:VAL:N	2.42	0.52
58:N2:53:ALA:HB1	58:N2:68:THR:HB	1.91	0.52
2:S0:179:ARG:HD3	2:S0:183:ARG:HD2	1.91	0.52
4:S2:230:TRP:CE2	24:D2:68:ARG:HD2	3.34	0.52
35:SM:48:ARG:NH2	35:SM:50:ASN:HD22	11.30	0.52
36:1:1094:U:O2'	36:1:1095:U:O5'	2.21	0.52
36:1:1584:U:H2'	36:1:1585:C:H6	1.74	0.52
36:1:1696:A:H2'	36:1:1697:A:C8	2.44	0.52
36:1:1915:A:H2'	36:1:1916:U:C6	2.45	0.52
36:1:2623:G:H2'	36:1:2624:G:H8	1.74	0.52
36:1:619:A:H5''	36:1:620:U:OP1	2.10	0.52
36:1:733:G:N2	36:1:736:A:OP2	2.42	0.52
1:2:1338:C:H1'	1:2:1410:A:C4	2.45	0.52
1:2:29:U:H2'	1:2:30:G:H8	1.73	0.52
36:5:2512:C:N4	36:5:2513:U:O4	2.42	0.52
39:L2:204:MET:HG2	36:5:914:A:C2	196.29	0.52
1:6:1241:G:H2'	1:6:1242:A:O4'	2.10	0.52
1:6:249:U:H3'	1:6:250:C:C5'	2.39	0.52
15:C3:98:VAL:HG22	1:6:952:A:H5'	294.39	0.52
38:8:77:A:H2'	38:8:78:G:O4'	2.09	0.52
1:2:901:G:N2	16:C4:54:GLU:OE1	2.40	0.52
25:D3:107:PHE:CD2	25:D3:114:LYS:HB2	2.44	0.52
33:E1:144:CYS:HB3	33:E1:147:VAL:HG12	3.44	0.52
33:E1:86:THR:O	33:E1:87:THR:OG1	2.47	0.52
36:1:73:C:O2	49:M3:59:ARG:HD3	2.09	0.52
52:M6:22:VAL:HG21	52:M6:120:VAL:HG11	1.92	0.52
53:M7:59:PRO:HG3	53:M7:76:PHE:CD1	2.45	0.52
67:O1:27:LYS:O	67:O1:31:ARG:HB2	2.21	0.52
72:O6:58:ILE:HG22	72:O6:90:MET:HG3	3.03	0.52
74:O8:17:ARG:NH2	74:O8:19:ASP:OD1	2.38	0.52
3:S1:129:THR:OG1	3:S1:131:ASP:OD1	6.20	0.52
36:1:2174:G:H8	36:1:2174:G:OP1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3325:G:H5'	67:O1:104:LEU:O	2.10	0.52
36:1:412:G:OP1	53:M7:62:ARG:NH1	2.43	0.52
36:1:436:A:H2'	36:1:437:G:O4'	2.10	0.52
1:2:1542:G:H22	1:2:1568:C:H1'	1.74	0.52
1:2:720:G:H1'	1:2:721:U:H5''	1.92	0.52
1:2:918:U:O3'	16:C4:18:ARG:NH1	2.43	0.52
36:5:1284:C:O2'	36:5:1285:G:H5'	2.10	0.52
36:5:3013:U:H2'	36:5:3014:U:C6	2.45	0.52
1:6:249:U:H3'	1:6:250:C:H5'	1.91	0.52
41:L4:138:ARG:HH11	41:L4:138:ARG:HB3	3.46	0.52
48:M1:164:LYS:HE3	48:M1:171:VAL:HB	1.92	0.52
52:M6:110:PRO:O	52:M6:112:TYR:N	2.70	0.52
59:N3:81:GLN:O	59:N3:98:ASN:ND2	2.42	0.52
62:N6:28:ARG:HB2	62:N6:75:ARG:CZ	2.40	0.52
71:O5:5:LYS:O	71:O5:9:LEU:HG	2.39	0.52
5:S3:21:LEU:HD22	5:S3:25:PHE:CE2	2.44	0.52
6:S4:176:ASP:HB2	6:S4:179:LYS:NZ	2.24	0.52
1:2:858:G:OP1	9:S7:116:ARG:NH2	2.42	0.52
10:S8:8:ARG:CZ	10:S8:21:PHE:HB3	2.40	0.52
18:C6:99:GLU:HG2	34:SR:57:PRO:HB2	2.70	0.52
36:1:496:C:H2'	36:1:497:C:O4'	2.09	0.52
36:1:627:U:H2'	36:1:628:A:C8	2.44	0.52
1:2:1483:A:H2'	1:2:1484:G:C8	2.44	0.52
1:2:1527:C:H2'	1:2:1528:U:H6	1.75	0.52
1:2:226:A:C2'	1:2:227:U:H5'	2.40	0.52
36:5:1313:G:H2'	36:5:1314:C:C6	2.45	0.52
36:5:230:U:H2'	36:5:231:G:O4'	2.09	0.52
36:5:2897:A:H2'	36:5:2899:C:H5'	1.90	0.52
1:6:1081:A:O2'	1:6:1082:C:O5'	2.23	0.52
1:6:1160:A:H2'	1:6:1161:C:C6	2.44	0.52
21:C9:122:ARG:NH2	1:6:1500:C:OP1	420.86	0.52
71:O5:7:TYR:CE2	38:8:86:U:H2'	19.97	0.52
20:C8:53:ASP:OD2	20:C8:55:HIS:ND1	2.39	0.52
40:L3:18:PRO:HG2	40:L3:20:LYS:HD2	1.90	0.52
40:L3:250:ALA:HB3	36:5:2880:U:H1'	224.73	0.52
49:M3:133:PRO:O	49:M3:135:ALA:N	3.36	0.52
61:N5:38:LEU:HD11	61:N5:40:LEU:HD13	1.91	0.52
77:Q1:2:ARG:HB3	77:Q1:5:TRP:CD1	2.44	0.52
79:Q3:55:TRP:CE3	79:Q3:71:VAL:HG22	2.45	0.52
3:S1:197:ILE:HG22	3:S1:210:ILE:HD13	2.70	0.52
36:1:1194:G:H2'	36:1:1195:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1240:A:H3'	36:1:1241:U:H5'	1.90	0.52
36:1:1595:U:C2	36:1:1596:C:C5	2.97	0.52
36:1:1596:C:H2'	36:1:1597:C:C6	2.44	0.52
36:1:3094:A:H2'	36:1:3095:U:C6	2.45	0.52
1:2:996:U:H3	1:2:1008:G:H1	1.58	0.52
1:6:1064:G:H2'	1:6:1065:A:C8	2.45	0.52
1:6:647:G:N2	1:6:687:G:H1	2.02	0.52
1:2:1460:A:C8	17:C5:128:HIS:HB3	2.44	0.52
21:C9:128:GLY:HA2	21:C9:131:ASP:HB2	3.47	0.52
1:2:1102:G:P	24:D2:76:SER:HG	2.33	0.52
41:L4:283:THR:HG21	41:L4:288:ARG:NH2	6.36	0.52
42:L5:196:ARG:HA	42:L5:199:ILE:HD12	2.44	0.52
37:3:22:A:H1'	42:L5:272:TYR:CZ	2.45	0.52
46:L9:89:LYS:HB2	46:L9:183:HIS:HB3	1.92	0.52
46:L9:189:GLU:O	46:L9:191:LEU:N	2.41	0.52
46:L9:91:ARG:HG2	46:L9:182:SER:HB3	2.65	0.52
47:M0:191:LYS:HE2	47:M0:212:GLU:HB3	1.92	0.52
53:M7:26:PHE:HE1	53:M7:120:ASN:HA	1.76	0.52
58:N2:36:TYR:OH	58:N2:82:LYS:HG2	2.10	0.52
59:N3:86:ARG:HD2	59:N3:92:PHE:CZ	2.45	0.52
63:N7:97:SER:O	63:N7:100:THR:OG1	3.31	0.52
79:Q3:36:ARG:HG2	79:Q3:48:LYS:HG3	1.92	0.52
1:2:788:A:C5	6:S4:19:LEU:HD13	2.44	0.52
36:1:1277:C:O2'	36:1:1278:A:H8	1.92	0.52
36:1:1727:G:OP1	79:Q3:44:LYS:NZ	2.31	0.52
36:1:2660:G:O3'	36:1:2749:G:N2	2.43	0.52
1:2:1682:U:O2'	1:2:1683:C:H5'	2.10	0.52
36:5:1804:A:H2'	36:5:1805:C:C6	2.44	0.52
36:5:2267:C:H2'	36:5:2268:U:H6	1.75	0.52
1:6:151:G:H1	1:6:163:G:H1	1.58	0.52
17:C5:98:ASN:HB3	17:C5:120:SER:OG	2.10	0.52
42:L5:183:TRP:CZ3	42:L5:185:PHE:HA	7.19	0.52
45:L8:101:THR:HG23	45:L8:104:GLU:H	1.73	0.52
51:M5:73:ARG:HG2	51:M5:75:VAL:HG13	2.49	0.52
66:O0:43:ILE:HG22	66:O0:70:PHE:HB2	1.92	0.52
71:O5:95:PHE:CD2	36:5:136:G:H5'	63.97	0.52
72:O6:4:LYS:HD2	72:O6:14:GLY:HA3	2.14	0.52
11:S9:49:LEU:HD22	11:S9:53:ARG:HG3	1.92	0.52
1:2:1738:U:H2'	1:2:1739:C:C6	2.45	0.52
58:N2:94:ARG:NH2	36:5:1757:A:OP1	126.84	0.52
22:D0:60:THR:HG22	1:6:1382:A:H5''	438.04	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:454:U:H5''	1:6:455:C:C5	2.45	0.52
1:6:542:A:H1'	1:6:543:C:H5'	1.91	0.52
16:C4:122:PRO:C	16:C4:124:ASP:H	2.14	0.52
26:D4:55:VAL:HG12	26:D4:75:VAL:HG22	7.19	0.52
36:1:3112:G:O2'	46:L9:70:THR:HB	2.10	0.52
49:M3:115:ARG:NH1	49:M3:145:PHE:O	2.43	0.52
50:M4:105:GLN:NE2	52:M6:198:GLY:O	2.43	0.52
56:N0:137:ARG:HG2	56:N0:139:TYR:CZ	2.45	0.52
57:N1:14:MET:HE1	57:N1:55:LYS:HB2	2.22	0.52
54:M8:170:ARG:HH11	64:N8:56:VAL:HG23	1.74	0.52
72:O6:55:ARG:O	72:O6:58:ILE:HD13	2.10	0.52
73:O7:85:LYS:HB2	38:8:67:U:H5''	20.39	0.52
3:S1:91:VAL:HG23	3:S1:96:LEU:HB3	1.91	0.52
36:1:2953:U:H2'	36:1:2954:U:C6	2.45	0.51
1:2:25:C:OP2	1:2:26:A:H2'	2.09	0.51
61:N5:113:LEU:HD22	36:5:1522:U:H3'	102.08	0.51
36:5:385:A:H2'	36:5:386:A:C8	2.44	0.51
1:6:1429:G:H2'	1:6:1430:U:C6	2.45	0.51
37:7:92:A:C5	37:7:93:C:H1'	2.45	0.51
71:O5:63:ARG:HH21	38:8:97:A:P	55.16	0.51
15:C3:132:VAL:HG23	15:C3:134:VAL:HG13	1.91	0.51
27:D5:42:LEU:O	27:D5:46:LYS:HB2	2.09	0.51
1:2:937:C:N4	28:D6:14:GLY:O	2.41	0.51
42:L5:22:ARG:HA	42:L5:25:GLU:HG3	3.12	0.51
47:M0:35:ASP:OD1	47:M0:86:HIS:NE2	2.42	0.51
73:O7:55:ARG:HD3	36:5:353:G:N7	109.00	0.51
73:O7:14:LYS:NZ	75:O9:51:ILE:HD11	2.25	0.51
1:2:1300:A:OP1	4:S2:99:LYS:NZ	2.42	0.51
7:S5:152:GLY:O	7:S5:154:ALA:N	2.43	0.51
11:S9:126:ARG:HG3	32:E0:33:ARG:HD3	3.05	0.51
34:SR:90:ARG:HH21	34:SR:102:ARG:HE	2.21	0.51
36:1:1700:G:H2'	36:1:1701:C:C6	2.45	0.51
36:1:2107:A:H2	36:1:3344:A:C8	2.28	0.51
36:1:645:A:N6	36:1:2869:U:OP1	2.39	0.51
36:1:407:A:C2	38:4:17:A:H1'	2.46	0.51
1:2:1383:G:OP1	22:D0:89:ARG:NH1	2.28	0.51
1:2:1657:U:H1'	1:2:1658:G:OP2	2.10	0.51
38:4:121:U:H2'	38:4:122:U:C6	2.45	0.51
63:N7:73:LYS:NZ	36:5:1636:U:H5''	214.20	0.51
36:5:2442:G:H22	36:5:2506:U:H3	1.58	0.51
36:5:507:U:H2'	36:5:508:U:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:4:VAL:HG12	18:C6:5:PRO:HD2	1.92	0.51
18:C6:32:ASN:N	18:C6:67:VAL:O	2.37	0.51
24:D2:36:LYS:O	24:D2:40:VAL:HG23	2.31	0.51
41:L4:138:ARG:HB3	41:L4:138:ARG:NH1	3.70	0.51
41:L4:191:LYS:HG3	41:L4:194:TYR:CZ	4.40	0.51
41:L4:158:SER:HA	41:L4:213:ASN:O	2.11	0.51
42:L5:68:THR:HB	42:L5:71:GLY:O	2.10	0.51
45:L8:81:THR:OG1	45:L8:181:LYS:HB2	3.47	0.51
52:M6:177:LYS:O	52:M6:181:ALA:N	2.35	0.51
55:M9:160:GLU:HG2	55:M9:164:LEU:HD23	1.91	0.51
67:O1:62:ARG:HB2	67:O1:66:GLY:O	2.10	0.51
73:O7:31:LYS:O	73:O7:33:THR:HG22	2.15	0.51
78:Q2:69:VAL:HG22	78:Q2:84:THR:HB	1.92	0.51
3:S1:171:ILE:O	3:S1:175:GLU:HG2	2.10	0.51
4:S2:116:LYS:HG2	4:S2:127:ALA:HB3	1.98	0.51
8:S6:58:LYS:HA	8:S6:107:ALA:HB2	2.82	0.51
11:S9:114:TYR:HA	11:S9:119:ALA:HB3	2.66	0.51
36:1:953:G:C8	36:1:1117:G:C8	2.98	0.51
36:1:261:U:H2'	36:1:262:U:C6	2.44	0.51
1:2:16:G:H2'	1:2:17:C:C6	2.46	0.51
36:5:1239:C:N4	36:5:1249:G:H1	2.01	0.51
63:N7:67:LYS:NZ	36:5:1630:U:OP1	197.39	0.51
36:5:437:G:OP2	36:5:437:G:H8	1.92	0.51
44:L7:241:LYS:NZ	36:5:576:C:OP1	275.01	0.51
11:S9:6:ARG:NE	1:6:771:A:O2'	392.83	0.51
14:C2:24:ILE:O	14:C2:26:ASP:N	2.88	0.51
37:3:39:C:N3	48:M1:70:THR:HG23	2.25	0.51
50:M4:113:THR:O	50:M4:117:ARG:HG3	4.51	0.51
53:M7:125:GLN:HB2	53:M7:141:SER:HB2	1.92	0.51
59:N3:32:ARG:HB3	59:N3:64:LYS:HB3	1.91	0.51
60:N4:22:VAL:HG22	60:N4:28:ILE:HG12	1.91	0.51
68:O2:16:LYS:O	68:O2:17:PHE:HB2	4.63	0.51
36:1:2565:U:H2'	36:1:2566:C:C6	2.46	0.51
36:1:2818:U:C6	36:1:2818:U:H5'	2.37	0.51
36:1:601:U:H2'	36:1:602:A:O4'	2.11	0.51
1:2:1401:A:O3'	19:C7:10:LYS:NZ	2.39	0.51
1:2:1683:C:O2'	1:2:1684:U:O5'	2.27	0.51
41:L4:193:LYS:HZ3	36:5:1419:A:H5''	109.42	0.51
1:6:794:U:H4'	1:6:795:U:OP2	2.09	0.51
36:5:408:A:H61	38:8:15:G:H1'	1.75	0.51
15:C3:54:LEU:HB3	15:C3:60:VAL:HG13	4.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:25:GLY:H	18:C6:63:ILE:HA	1.75	0.51
19:C7:28:PHE:HA	19:C7:55:THR:HG21	2.96	0.51
20:C8:30:TYR:O	20:C8:33:THR:OG1	2.25	0.51
22:D0:28:SER:HB2	22:D0:112:VAL:HA	1.92	0.51
24:D2:73:GLY:HA3	24:D2:128:PHE:CZ	2.66	0.51
27:D5:39:ALA:N	27:D5:70:LYS:O	5.68	0.51
39:L2:204:MET:HE3	39:L2:209:HIS:HB2	1.93	0.51
40:L3:293:ASN:HB2	40:L3:304:THR:HA	1.92	0.51
40:L3:56:ILE:O	40:L3:73:VAL:HA	2.11	0.51
41:L4:265:GLU:OE1	41:L4:265:GLU:N	2.43	0.51
43:L6:131:LYS:HD3	43:L6:132:ALA:H	4.96	0.51
46:L9:129:ARG:O	46:L9:132:VAL:HG22	2.10	0.51
46:L9:69:ARG:O	46:L9:69:ARG:HD2	2.19	0.51
47:M0:43:VAL:O	47:M0:171:TRP:NE1	3.00	0.51
52:M6:108:ILE:HD11	52:M6:160:ARG:CZ	3.88	0.51
53:M7:30:ARG:HA	53:M7:119:VAL:HG11	2.16	0.51
63:N7:5:LEU:HD22	63:N7:77:TYR:CZ	5.51	0.51
71:O5:45:LYS:O	71:O5:49:LYS:HG2	4.40	0.51
73:O7:52:LYS:HA	73:O7:55:ARG:HD2	2.03	0.51
78:Q2:12:CYS:SG	78:Q2:74:CYS:SG	3.35	0.51
36:1:2767:U:O2'	78:Q2:30:ALA:O	2.27	0.51
2:S0:98:ILE:HD11	2:S0:116:LYS:HG3	2.82	0.51
36:1:2767:U:H2'	36:1:2768:U:C6	2.45	0.51
36:1:2947:G:H4'	36:1:2947:G:OP2	2.10	0.51
36:1:3187:A:H5''	50:M4:8:LYS:HE2	1.92	0.51
44:L7:208:SER:HB2	36:5:1334:U:H1'	241.86	0.51
36:5:1596:C:H2'	36:5:1597:C:C6	2.45	0.51
36:5:2226:U:H2'	36:5:2227:C:C6	2.45	0.51
36:5:3164:C:H1'	36:5:3165:A:H5'	1.92	0.51
1:6:1405:G:H2'	1:6:1406:A:C8	2.45	0.51
1:2:325:G:H4'	13:C1:83:THR:HG21	1.91	0.51
15:C3:62:GLN:HG3	15:C3:65:VAL:HG22	5.45	0.51
22:D0:23:ARG:HB3	22:D0:117:VAL:HG12	1.92	0.51
28:D6:38:ARG:HH21	28:D6:83:ILE:HG13	1.75	0.51
14:C2:73:LYS:NZ	33:E1:108:VAL:HG13	2.25	0.51
43:L6:102:ASN:OD1	43:L6:102:ASN:N	3.33	0.51
49:M3:140:SER:HG	49:M3:143:ALA:H	1.54	0.51
54:M8:58:ASN:HB3	54:M8:144:ARG:NH2	2.25	0.51
59:N3:31:ALA:HB2	59:N3:69:LEU:HD23	2.42	0.51
63:N7:54:THR:HG22	63:N7:57:HIS:CE1	2.45	0.51
9:S7:50:ASP:HA	9:S7:56:LYS:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:S7:62:VAL:HG12	9:S7:64:VAL:H	1.75	0.51
36:1:1362:G:N3	44:L7:158:LYS:NZ	2.50	0.51
36:1:2155:G:O2'	39:L2:227:ARG:NH2	2.44	0.51
36:1:847:A:H2'	36:1:848:A:C8	2.45	0.51
1:2:1228:G:H5'	1:2:1229:G:C8	2.45	0.51
1:2:1592:A:H2'	1:2:1593:A:C8	2.45	0.51
1:2:647:G:N2	1:2:687:G:H22	2.09	0.51
1:2:800:U:H2'	1:2:801:G:H8	1.76	0.51
68:O2:101:SER:HB3	36:5:1389:G:H5''	128.45	0.51
1:6:1533:C:H4'	1:6:1539:G:N1	2.25	0.51
12:C0:55:VAL:HA	12:C0:69:THR:HG23	1.97	0.51
20:C8:33:THR:HA	20:C8:38:VAL:HG23	2.83	0.51
30:D8:8:THR:OG1	30:D8:59:SER:OG	2.25	0.51
48:M1:143:ARG:HG2	48:M1:144:CYS:SG	2.51	0.51
50:M4:114:ASP:HA	50:M4:117:ARG:NH1	2.77	0.51
73:O7:18:LEU:HD21	75:O9:51:ILE:HG22	1.92	0.51
75:O9:24:PRO:HB2	75:O9:27:ILE:HD13	1.93	0.51
78:Q2:16:THR:OG1	78:Q2:17:CYS:N	2.82	0.51
3:S1:77:GLU:OE1	16:C4:114:ARG:NH2	2.43	0.51
4:S2:230:TRP:CD2	24:D2:68:ARG:HD3	2.46	0.51
8:S6:10:ASN:HB3	8:S6:128:THR:HB	4.43	0.51
36:1:1063:G:N7	36:1:1097:G:H2'	2.26	0.51
1:2:1171:A:H2'	1:2:1172:G:C8	2.45	0.51
1:2:130:C:O2'	1:2:131:C:OP1	2.27	0.51
1:2:1527:C:H2'	1:2:1528:U:C6	2.45	0.51
36:5:3242:G:N2	36:5:3245:A:H5''	2.26	0.51
40:L3:334:ARG:NH2	36:5:3304:U:O2'	212.78	0.51
1:6:1533:C:H4'	1:6:1539:G:C6	2.46	0.51
15:C3:146:ALA:HA	15:C3:149:LEU:HB2	1.93	0.51
16:C4:84:ARG:HA	16:C4:119:THR:HG22	2.30	0.51
26:D4:37:LYS:HD2	26:D4:57:VAL:HG23	6.34	0.51
47:M0:36:LEU:HD21	47:M0:69:ARG:HD3	2.00	0.51
58:N2:33:TYR:HE2	58:N2:63:VAL:HG21	1.75	0.51
36:1:3173:G:C2	69:O3:96:ALA:HB2	2.46	0.51
73:O7:3:LYS:HE3	36:5:2139:A:C4	172.48	0.51
6:S4:43:PRO:HA	6:S4:82:TYR:O	2.61	0.51
6:S4:88:ASP:OD1	6:S4:122:LYS:NZ	2.44	0.51
8:S6:31:ARG:HB2	8:S6:34:GLN:HG3	1.93	0.51
36:1:839:C:H4'	36:1:1724:U:H3'	1.92	0.51
36:1:2175:U:O2	39:L2:23:ARG:HB2	2.10	0.51
36:1:2623:G:H2'	36:1:2624:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:805:G:H2'	36:1:936:A:H61	1.75	0.51
1:2:396:G:N2	1:2:398:G:H3'	2.26	0.51
38:4:81:U:H1'	38:4:82:U:H5'	1.92	0.51
36:5:1120:A:H2'	36:5:1121:U:C6	2.46	0.51
54:M8:147:ARG:NH2	36:5:670:C:OP1	163.74	0.51
33:E1:143:LYS:HD3	1:6:1254:U:OP1	458.12	0.51
13:C1:96:LYS:NZ	1:6:374:U:OP1	348.11	0.51
4:S2:205:ARG:NH1	1:6:6:G:N7	375.26	0.51
11:S9:9:SER:OG	1:6:771:A:OP1	392.36	0.51
12:C0:54:TYR:HD2	12:C0:72:GLY:HA2	4.34	0.51
14:C2:44:GLY:HA3	1:6:1227:A:O2'	463.40	0.51
17:C5:24:LYS:O	17:C5:28:MET:HB2	2.10	0.51
25:D3:53:VAL:HG13	25:D3:72:VAL:HB	2.03	0.51
1:2:1616:G:O2'	30:D8:18:ARG:NH1	2.44	0.51
40:L3:350:ALA:O	40:L3:352:GLU:N	2.35	0.51
40:L3:4:ARG:HG3	40:L3:6:TYR:O	4.98	0.51
36:1:1558:A:OP2	45:L8:54:GLU:HG3	2.11	0.51
51:M5:54:LYS:O	51:M5:56:LYS:N	3.13	0.51
52:M6:45:GLY:O	52:M6:136:THR:OG1	2.29	0.51
56:N0:23:LYS:O	56:N0:24:LEU:HB2	2.10	0.51
58:N2:89:LEU:HB3	58:N2:93:ILE:HD12	2.36	0.51
59:N3:128:ARG:HB3	59:N3:128:ARG:NH2	3.88	0.51
61:N5:38:LEU:O	61:N5:39:LYS:HB2	4.38	0.51
70:O4:71:THR:HG22	70:O4:77:GLY:HA3	2.01	0.51
71:O5:86:ARG:HG3	71:O5:90:ARG:NH2	2.52	0.51
76:Q0:97:ARG:HB2	76:Q0:120:GLN:O	2.11	0.51
1:2:1278:G:OP1	5:S3:185:LYS:HE2	2.10	0.51
6:S4:180:LEU:N	6:S4:229:GLY:O	2.42	0.51
7:S5:146:THR:HG23	7:S5:157:ARG:HB3	4.03	0.51
10:S8:2:GLY:HA2	1:6:1729:C:O2'	287.43	0.51
11:S9:85:VAL:HG12	11:S9:99:LEU:HD11	1.93	0.51
37:3:7:G:O3'	42:L5:33:ARG:NH2	2.44	0.51
36:5:1102:A:H4'	36:5:1103:A:C5	2.45	0.51
19:C7:7:LYS:N	1:6:1316:G:OP1	411.81	0.51
1:6:1451:C:H2'	1:6:1452:U:C6	2.46	0.51
1:6:417:A:H4'	1:6:418:G:O5'	2.11	0.51
38:8:6:U:H2'	38:8:7:U:C6	2.46	0.51
12:C0:54:TYR:CE2	12:C0:75:TYR:HB2	3.60	0.51
24:D2:104:LEU:HB2	24:D2:125:ILE:HA	1.93	0.51
24:D2:55:ASP:HB3	29:D7:25:VAL:HG22	3.01	0.51
30:D8:18:ARG:NE	1:6:1616:G:O2'	361.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:218:ILE:HG13	40:L3:276:THR:HG23	1.93	0.51
41:L4:185:LYS:HA	41:L4:200:THR:O	2.11	0.51
50:M4:116:GLU:O	50:M4:120:VAL:HG23	2.11	0.51
59:N3:3:GLY:HA2	59:N3:40:LYS:HB3	6.21	0.51
63:N7:42:LEU:HD23	63:N7:101:PHE:HE1	1.76	0.51
69:O3:42:GLN:HA	69:O3:45:LEU:HG	1.92	0.51
71:O5:6:ALA:O	71:O5:10:ARG:HG3	3.45	0.51
8:S6:163:THR:HA	8:S6:168:THR:HG22	2.95	0.51
9:S7:154:LEU:HD21	9:S7:183:PHE:HD1	1.76	0.51
9:S7:49:ILE:HG22	9:S7:175:LYS:HD3	3.52	0.51
11:S9:65:LYS:HD3	11:S9:70:LEU:HD11	1.92	0.51
20:C8:120:ARG:HD3	35:SM:61:ILE:HG21	3.65	0.51
36:1:1562:C:H2'	36:1:1563:C:C6	2.46	0.51
36:1:764:U:H3'	36:1:765:C:H5''	1.93	0.51
1:2:1490:C:H4'	1:2:1491:U:OP1	2.10	0.51
1:2:854:U:O4	1:2:855:A:N6	2.44	0.51
76:Q0:125:LYS:NZ	36:5:2898:G:O6	328.70	0.51
52:M6:65:ASN:ND2	36:5:2988:C:OP1	220.93	0.51
67:O1:19:ARG:NH1	36:5:3324:C:OP1	173.78	0.51
1:6:1166:A:H2'	1:6:1167:G:O4'	2.10	0.51
8:S6:173:PRO:HA	1:6:66:U:O5'	340.42	0.51
71:O5:7:TYR:HE2	38:8:86:U:H2'	19.94	0.51
15:C3:135:LEU:HD23	15:C3:136:PRO:HD2	1.91	0.51
17:C5:87:PRO:HD3	17:C5:112:LEU:HD22	1.92	0.51
22:D0:46:GLU:HB2	22:D0:52:LYS:HZ3	1.76	0.51
40:L3:37:ARG:HA	40:L3:186:GLY:H	1.76	0.51
44:L7:57:THR:OG1	44:L7:58:ALA:N	3.46	0.51
36:1:269:G:H5''	51:M5:14:LYS:HE2	1.92	0.51
36:1:977:C:P	54:M8:141:ARG:HH22	2.34	0.51
65:N9:14:ARG:HH22	65:N9:18:ARG:HH11	1.59	0.51
66:O0:50:VAL:O	66:O0:54:SER:N	2.34	0.51
74:O8:8:ILE:HD12	74:O8:8:ILE:H	1.76	0.51
75:O9:28:ARG:NH1	75:O9:36:ARG:HH11	6.37	0.51
6:S4:159:THR:OG1	6:S4:160:VAL:N	3.29	0.51
36:1:139:G:H2'	36:1:140:C:O4'	2.11	0.50
36:1:230:U:H2'	36:1:231:G:O4'	2.11	0.50
36:1:3218:A:H4'	36:1:3219:G:O5'	2.11	0.50
36:1:768:C:OP1	49:M3:186:ARG:NH2	2.44	0.50
1:2:151:G:O6	26:D4:124:ARG:NH2	2.29	0.50
1:2:218:A:O2'	1:2:219:A:OP1	2.27	0.50
36:5:252:U:H4'	36:5:253:A:C5'	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2941:A:O5'	36:5:2943:G:H4'	2.11	0.50
36:5:408:A:N6	38:8:15:G:H1'	2.26	0.50
1:6:1078:C:H2'	1:6:1079:U:H6	1.76	0.50
27:D5:77:ARG:HD2	1:6:1532:U:OP2	358.20	0.50
27:D5:74:SER:OG	1:6:1534:G:OP2	344.46	0.50
1:6:340:U:H2'	1:6:341:A:H8	1.72	0.50
12:C0:29:GLN:O	12:C0:31:LYS:N	2.44	0.50
12:C0:56:LYS:HE2	12:C0:58:GLN:HG2	1.93	0.50
20:C8:34:THR:OG1	20:C8:34:THR:O	2.27	0.50
20:C8:35:ILE:HB	20:C8:38:VAL:HG22	2.35	0.50
39:L2:109:GLU:HA	39:L2:136:ILE:HG22	2.63	0.50
53:M7:16:SER:HB3	53:M7:149:VAL:HG22	1.93	0.50
59:N3:13:ILE:HD11	59:N3:81:GLN:OE1	5.78	0.50
61:N5:46:TYR:HB3	71:O5:75:TYR:HB3	2.24	0.50
66:O0:73:GLY:O	66:O0:76:GLU:HG2	2.10	0.50
67:O1:36:ILE:HD12	67:O1:59:ILE:HD11	1.93	0.50
6:S4:45:ILE:HA	6:S4:61:VAL:HG11	1.94	0.50
9:S7:14:THR:H	9:S7:17:GLU:HB2	1.77	0.50
34:SR:38:ARG:HG2	34:SR:67:ILE:HG23	1.93	0.50
36:1:1028:U:O2	48:M1:94:ARG:NH1	2.44	0.50
36:1:2561:A:HO2'	36:1:2562:A:H8	1.59	0.50
36:1:352:A:N6	36:1:365:A:H5''	2.26	0.50
1:2:1474:G:H2'	1:2:1475:A:C8	2.47	0.50
1:2:1590:G:H2'	1:2:1591:C:H6	1.75	0.50
37:3:112:G:H2'	37:3:113:C:C6	2.45	0.50
41:L4:93:MET:HE1	36:5:804:C:H5'	147.72	0.50
16:C4:84:ARG:HG3	16:C4:119:THR:HA	1.93	0.50
28:D6:87:ARG:NH2	28:D6:91:ASP:O	2.82	0.50
31:D9:30:LEU:HD13	31:D9:32:ARG:HD3	3.14	0.50
42:L5:272:TYR:CE1	37:7:22:A:H1'	334.49	0.50
45:L8:134:TYR:CD1	45:L8:190:VAL:HG11	3.03	0.50
55:M9:23:TRP:HB3	55:M9:51:VAL:HG22	1.92	0.50
58:N2:13:LYS:HD2	58:N2:15:PHE:CZ	5.47	0.50
59:N3:96:GLU:OE1	60:N4:24:GLY:N	3.16	0.50
60:N4:4:GLU:HG2	60:N4:30:ARG:HD2	1.92	0.50
67:O1:20:LEU:HD11	67:O1:32:ALA:HB2	1.92	0.50
68:O2:21:HIS:CE1	68:O2:24:ARG:HD2	2.69	0.50
6:S4:191:ARG:HH11	6:S4:245:LYS:HB3	1.76	0.50
6:S4:11:ARG:HB2	6:S4:27:TYR:C	2.47	0.50
6:S4:68:ARG:HB3	6:S4:76:VAL:HG11	2.53	0.50
9:S7:13:PRO:HB3	9:S7:14:THR:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S8:39:GLY:O	10:S8:59:ARG:HB3	2.11	0.50
1:2:811:A:C2	1:2:858:G:H1'	2.47	0.50
36:5:1176:C:H2'	36:5:1177:G:N2	2.27	0.50
36:5:3206:C:H5''	36:5:3207:U:O5'	2.11	0.50
17:C5:122:THR:CG2	1:6:1558:U:H3	368.39	0.50
32:E0:43:ARG:HH12	1:6:590:C:H5''	419.32	0.50
1:6:898:A:N1	1:6:911:U:O2'	2.28	0.50
17:C5:29:SER:OG	17:C5:32:ASP:OD2	2.82	0.50
25:D3:57:LEU:HD22	32:E0:4:VAL:HG13	2.53	0.50
41:L4:141:ARG:CZ	41:L4:180:LYS:HD3	2.41	0.50
36:1:1362:G:O2'	44:L7:158:LYS:HE3	2.12	0.50
36:1:120:G:N1	45:L8:124:ASP:OD2	2.43	0.50
49:M3:104:ARG:HA	72:O6:20:MET:O	4.77	0.50
57:N1:54:HIS:CE1	57:N1:55:LYS:HG2	2.95	0.50
49:M3:174:ARG:HB2	72:O6:9:ILE:HD12	1.94	0.50
7:S5:151:GLY:HA3	7:S5:155:ALA:HA	4.71	0.50
9:S7:9:LEU:HD11	9:S7:17:GLU:HB3	3.40	0.50
11:S9:3:ARG:NE	11:S9:3:ARG:H	3.68	0.50
11:S9:87:SER:HB3	11:S9:90:LYS:HB2	4.58	0.50
36:1:3350:C:H2'	36:1:3351:U:H3'	1.93	0.50
36:1:612:U:H2'	36:1:613:G:H8	1.77	0.50
1:2:627:C:H4'	15:C3:117:LEU:HD22	1.92	0.50
1:2:851:U:H2'	1:2:852:C:C6	2.47	0.50
1:2:917:U:HO2'	16:C4:29:HIS:CE1	2.29	0.50
58:N2:104:ARG:NH2	36:5:1758:G:H5'	119.90	0.50
36:5:2697:A:H2'	36:5:2698:G:C8	2.46	0.50
54:M8:141:ARG:HD3	36:5:743:C:O2	175.21	0.50
15:C3:93:LYS:HA	15:C3:150:VAL:HG21	1.92	0.50
20:C8:41:ARG:NH2	21:C9:36:ILE:O	2.59	0.50
27:D5:102:THR:HG22	27:D5:103:ARG:H	3.67	0.50
25:D3:90:ASP:OD2	32:E0:12:GLY:HA2	2.52	0.50
42:L5:155:THR:HA	42:L5:179:ARG:HA	1.94	0.50
49:M3:123:ILE:HG22	71:O5:118:ILE:HG12	2.80	0.50
57:N1:18:ASP:OD2	57:N1:18:ASP:N	3.41	0.50
38:4:131:A:H5''	61:N5:93:TYR:CE2	2.47	0.50
62:N6:112:ASP:HB2	62:N6:115:ARG:H	1.76	0.50
72:O6:70:ARG:HD3	72:O6:84:LYS:HG2	3.32	0.50
36:1:2747:A:H5'	42:L5:175:HIS:HA	1.94	0.50
1:2:240:U:H4'	1:2:241:U:OP2	2.12	0.50
1:2:62:A:HO2'	1:2:268:C:HO2'	1.60	0.50
1:2:810:G:C6	9:S7:111:LYS:HE3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M5:69:GLY:O	36:5:290:G:H4'	146.08	0.50
46:L9:22:SER:OG	36:5:3188:G:OP1	314.43	0.50
1:6:417:A:H5'	1:6:418:G:C5	2.46	0.50
36:5:997:A:O2'	37:7:79:A:N3	2.41	0.50
38:8:76:C:H2'	38:8:77:A:O4'	2.12	0.50
14:C2:104:ALA:HB2	14:C2:115:VAL:HG22	4.22	0.50
15:C3:84:ILE:H	15:C3:84:ILE:HD13	4.10	0.50
29:D7:23:THR:OG1	29:D7:24:LEU:N	2.40	0.50
40:L3:243:HIS:C	40:L3:244:ARG:HG3	2.79	0.50
36:1:520:U:O4	41:L4:349:THR:HG23	2.12	0.50
41:L4:60:THR:HG22	41:L4:62:ALA:H	2.33	0.50
42:L5:282:ARG:O	42:L5:286:VAL:HG23	2.47	0.50
52:M6:10:ASP:HB2	52:M6:117:ARG:HB2	2.39	0.50
52:M6:47:PHE:HE2	52:M6:141:LEU:HA	2.15	0.50
55:M9:76:SER:O	55:M9:81:ARG:NH1	2.44	0.50
36:1:1898:G:O2'	59:N3:21:ALA:HB2	2.11	0.50
36:1:1456:A:N7	67:O1:26:LYS:HE2	2.27	0.50
71:O5:89:ARG:HH11	71:O5:89:ARG:HG2	1.75	0.50
2:S0:148:ASP:OD1	2:S0:149:LEU:N	2.75	0.50
9:S7:46:ILE:HG12	9:S7:60:ILE:HA	3.70	0.50
36:1:1922:A:H2'	36:1:1923:C:O4'	2.11	0.50
36:1:2801:A:O2'	36:1:2802:A:H2'	2.12	0.50
36:1:3157:U:H4'	36:1:3158:G:H5'	1.93	0.50
1:2:1586:A:H2'	1:2:1587:A:O4'	2.12	0.50
1:2:1767:G:OP2	1:2:1770:U:O2'	2.19	0.50
36:5:1190:A:C8	36:5:1193:A:H1'	2.47	0.50
36:5:126:U:H2'	36:5:127:G:O4'	2.10	0.50
36:5:2413:A:H2'	36:5:2414:G:C8	2.47	0.50
36:5:2430:A:H2'	36:5:2431:C:C6	2.47	0.50
39:L2:70:ARG:NH1	36:5:2522:G:O6	178.41	0.50
64:N8:8:THR:HG21	36:5:662:U:OP1	149.95	0.50
1:6:1350:U:H2'	1:6:1351:G:C8	2.46	0.50
1:6:199:G:HO2'	1:6:200:A:H8	1.58	0.50
5:S3:27:ARG:HD2	12:C0:60:SER:HB2	1.94	0.50
13:C1:46:LYS:HE2	1:6:846:G:H21	313.55	0.50
31:D9:33:LYS:HE2	31:D9:34:TYR:CZ	3.25	0.50
39:L2:204:MET:CE	39:L2:209:HIS:HB2	2.41	0.50
39:L2:206:PRO:HG3	39:L2:213:GLY:HA2	4.01	0.50
40:L3:206:ASP:OD1	40:L3:206:ASP:N	2.45	0.50
40:L3:7:GLU:HG2	36:5:2915:U:C5	257.94	0.50
41:L4:52:VAL:HB	41:L4:99:MET:HE3	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L5:64:ILE:HD12	42:L5:144:VAL:HG21	4.11	0.50
42:L5:210:GLU:O	42:L5:214:ASP:HB2	2.36	0.50
42:L5:79:TYR:HB2	42:L5:81:HIS:CE1	2.46	0.50
49:M3:91:ARG:CZ	49:M3:97:VAL:HB	2.41	0.50
55:M9:96:ILE:O	55:M9:100:ARG:HG3	2.12	0.50
64:N8:13:GLY:HA2	36:5:943:U:H3'	163.81	0.50
69:O3:26:ASN:HA	69:O3:88:ASN:OD1	2.11	0.50
78:Q2:56:PRO:HA	36:5:2802:A:C8	183.88	0.50
3:S1:88:VAL:HG11	3:S1:96:LEU:HD12	1.94	0.50
8:S6:7:TYR:HE1	8:S6:125:THR:HG23	1.77	0.50
9:S7:50:ASP:N	9:S7:50:ASP:OD1	2.41	0.50
10:S8:8:ARG:NH2	10:S8:21:PHE:H	2.09	0.50
10:S8:84:HIS:NE2	10:S8:97:THR:OG1	2.37	0.50
36:1:1240:A:H61	36:1:1244:A:H5''	1.77	0.50
36:1:2514:U:OP1	36:1:2514:U:H6	1.95	0.50
36:1:2726:C:O2'	36:1:2727:A:H2'	2.12	0.50
1:2:136:C:H4'	1:2:137:U:OP1	2.12	0.50
36:5:2676:A:H4'	36:5:2677:G:O5'	2.10	0.50
36:5:847:A:H2'	36:5:848:A:C8	2.46	0.50
1:6:1564:U:H2'	1:6:1565:C:C6	2.47	0.50
19:C7:71:PHE:CZ	19:C7:74:GLN:HB2	5.85	0.50
19:C7:76:GLU:HA	19:C7:79:GLU:HB2	1.93	0.50
21:C9:61:VAL:O	21:C9:65:ILE:HG13	2.17	0.50
2:S0:52:LYS:HG2	23:D1:82:VAL:HG22	4.52	0.50
40:L3:123:TYR:CE2	40:L3:124:LYS:HG3	2.46	0.50
41:L4:140:HIS:HA	41:L4:177:ASP:OD1	2.12	0.50
41:L4:26:PHE:CD1	41:L4:130:ALA:HB2	2.89	0.50
44:L7:130:ILE:O	44:L7:134:VAL:HG22	2.12	0.50
47:M0:16:PRO:O	47:M0:18:PRO:HD3	2.12	0.50
48:M1:79:ILE:HG22	48:M1:127:PHE:HE2	1.76	0.50
49:M3:143:ALA:O	49:M3:146:PRO:HD3	2.11	0.50
53:M7:13:LYS:HB3	53:M7:152:GLU:HB2	2.06	0.50
53:M7:4:TYR:OH	53:M7:18:ARG:HG3	2.12	0.50
54:M8:126:GLN:O	54:M8:130:ARG:HG3	2.11	0.50
75:O9:44:TRP:CZ3	75:O9:45:ARG:HG3	2.46	0.50
3:S1:181:LEU:O	3:S1:183:GLN:N	2.44	0.50
4:S2:153:SER:OG	4:S2:154:LEU:N	2.41	0.50
4:S2:174:ARG:HB2	11:S9:97:LEU:HB3	1.92	0.50
6:S4:71:LYS:HA	6:S4:76:VAL:O	2.12	0.50
36:1:343:U:O2	36:1:1439:U:H1'	2.12	0.50
36:1:1591:G:O2'	36:1:1799:A:N1	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1175:U:H2'	1:2:1176:G:C8	2.46	0.50
79:Q3:44:LYS:NZ	36:5:1727:G:OP1	231.40	0.50
36:5:2406:C:H2'	36:5:2407:C:C6	2.47	0.50
1:6:1227:A:H4'	1:6:1228:G:H5'	1.92	0.50
20:C8:138:THR:HB	1:6:1459:C:H2'	347.81	0.50
24:D2:106:THR:HG21	24:D2:121:VAL:HG23	3.67	0.50
24:D2:3:ARG:NH1	24:D2:9:ASP:OD2	3.30	0.50
28:D6:85:ARG:NH1	1:6:1153:G:OP1	342.12	0.50
41:L4:334:PHE:HA	41:L4:339:LEU:HD11	3.04	0.50
42:L5:158:ARG:HD3	37:7:46:A:OP1	282.84	0.50
42:L5:285:ARG:NH1	37:7:62:U:O3'	342.91	0.50
46:L9:75:VAL:HA	46:L9:78:MET:HE3	1.93	0.50
50:M4:123:LEU:HD13	52:M6:193:GLN:HB3	2.68	0.50
36:1:841:A:H5'	55:M9:125:LYS:O	2.12	0.50
64:N8:132:LYS:O	64:N8:136:GLU:HG3	2.23	0.50
36:1:943:U:H3'	64:N8:13:GLY:HA2	1.93	0.50
70:O4:46:ASP:OD2	70:O4:80:ARG:HD2	2.44	0.50
71:O5:13:SER:OG	71:O5:16:GLN:HB2	3.12	0.50
4:S2:88:LYS:HG2	4:S2:89:GLN:H	3.00	0.50
6:S4:128:LYS:HD3	6:S4:130:GLN:HG3	1.94	0.50
8:S6:58:LYS:HG2	8:S6:105:ASP:O	2.12	0.50
8:S6:14:LYS:HD2	8:S6:123:GLY:HA3	2.63	0.50
8:S6:131:LYS:O	60:N4:82:ILE:HA	2.12	0.50
1:2:339:C:P	10:S8:10:LYS:HZ3	2.34	0.50
36:1:1744:G:H2'	36:1:1745:C:C6	2.46	0.50
36:1:2282:U:OP1	36:1:2973:G:O2'	2.27	0.50
36:1:409:A:N6	38:4:15:G:H1'	2.27	0.50
1:2:1078:C:H2'	1:2:1079:U:H6	1.77	0.50
1:2:197:A:H61	10:S8:138:ASN:ND2	2.09	0.50
38:4:155:A:OP1	45:L8:185:ARG:NH2	2.44	0.50
68:O2:46:PHE:CE1	36:5:1145:G:H5'	211.35	0.50
36:5:1555:U:H5'	36:5:1556:C:OP2	2.12	0.50
36:5:2818:U:C6	36:5:2818:U:H5'	2.44	0.50
1:6:1058:U:H4'	1:6:1059:U:OP1	2.11	0.50
1:6:1688:U:H2'	1:6:1689:A:C8	2.46	0.50
13:C1:124:THR:HB	13:C1:141:LYS:HB3	1.97	0.50
21:C9:21:PHE:O	21:C9:25:GLN:HB2	2.51	0.50
39:L2:3:ARG:HD3	36:5:911:C:H42	179.79	0.50
41:L4:144:LYS:H	41:L4:144:LYS:HD2	4.83	0.50
41:L4:234:ASN:HB3	41:L4:237:GLN:HB2	2.67	0.50
41:L4:301:PRO:O	54:M8:39:ARG:NH1	3.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:325:LEU:O	44:L7:41:ARG:NH2	2.74	0.50
41:L4:38:VAL:HG13	41:L4:113:VAL:HG11	1.94	0.50
46:L9:114:VAL:HB	46:L9:124:ARG:HB2	1.94	0.50
46:L9:86:TYR:CE2	46:L9:151:VAL:HG22	2.47	0.50
54:M8:170:ARG:HA	54:M8:174:ARG:HD2	1.98	0.50
63:N7:10:VAL:O	63:N7:83:THR:HG22	2.12	0.50
65:N9:46:ALA:O	65:N9:50:THR:HG23	2.98	0.50
68:O2:123:LYS:HA	68:O2:126:LEU:HD12	2.37	0.50
75:O9:30:ARG:HB2	75:O9:33:ASN:HB2	1.94	0.50
78:Q2:12:CYS:SG	78:Q2:17:CYS:HB2	2.60	0.50
78:Q2:15:LYS:HA	78:Q2:18:ARG:HD2	1.93	0.50
4:S2:143:TYR:CD2	4:S2:147:ASN:HA	4.63	0.50
7:S5:172:ILE:O	7:S5:176:THR:OG1	2.24	0.50
1:2:197:A:H61	10:S8:138:ASN:HD22	1.60	0.50
5:S3:115:ILE:HG21	35:SM:110:TRP:HA	1.93	0.50
20:C8:146:ALA:H	35:SM:68:ARG:HH21	1.59	0.50
36:1:2522:G:H4'	36:1:2523:A:OP2	2.11	0.49
36:1:542:G:H2'	36:1:543:C:C6	2.47	0.49
36:1:633:C:H2'	36:1:634:C:O4'	2.12	0.49
36:1:653:A:C2	36:1:1443:G:C4	3.00	0.49
1:2:1037:C:O2	1:2:1094:G:N2	2.34	0.49
1:2:1344:A:H2'	1:2:1345:A:C8	2.47	0.49
1:2:320:U:H3'	1:2:321:C:C5'	2.40	0.49
36:5:1108:U:H2'	36:5:1109:U:C6	2.47	0.49
36:5:238:A:O2'	36:5:239:G:OP1	2.27	0.49
1:6:151:G:N2	1:6:163:G:N2	2.60	0.49
10:S8:16:ALA:HB2	1:6:354:C:H5"	298.79	0.49
1:2:1258:U:H4'	12:C0:2:LEU:HD13	1.94	0.49
13:C1:22:ASN:ND2	13:C1:25:VAL:HG23	2.27	0.49
13:C1:46:LYS:HE2	1:6:846:G:N2	313.64	0.49
20:C8:71:GLN:HA	20:C8:74:GLN:HE21	6.25	0.49
21:C9:14:PHE:CZ	21:C9:132:LEU:HD12	5.60	0.49
39:L2:43:GLY:O	39:L2:88:ILE:N	2.82	0.49
40:L3:380:MET:HE3	36:5:3369:G:C6	226.14	0.49
45:L8:51:LYS:HG3	36:5:2523:A:C5	165.56	0.49
47:M0:89:VAL:HG13	47:M0:136:PHE:CE1	2.68	0.49
54:M8:96:PHE:CD2	54:M8:97:PRO:HD2	2.47	0.49
55:M9:106:LEU:HD13	55:M9:138:LEU:HD11	2.28	0.49
70:O4:8:ARG:NH2	70:O4:31:ARG:HD2	2.36	0.49
74:O8:24:THR:HG23	74:O8:44:LYS:HB2	2.00	0.49
2:S0:121:VAL:HG23	2:S0:141:ILE:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:70:LEU:O	3:S1:74:GLN:HB2	2.12	0.49
9:S7:96:ARG:CZ	9:S7:124:LYS:HB3	2.42	0.49
34:SR:248:ASN:HD21	34:SR:298:GLY:HA3	2.69	0.49
36:1:1211:U:H2'	36:1:1212:A:C8	2.47	0.49
36:1:1235:U:H4'	36:1:1236:G:H5'	1.93	0.49
36:1:2163:C:H4'	39:L2:7:ASN:O	2.11	0.49
36:1:2438:A:H2'	36:1:2439:A:C8	2.46	0.49
36:1:528:U:H2'	36:1:529:A:C8	2.47	0.49
36:1:565:U:H2'	36:1:566:G:H8	1.76	0.49
36:1:816:A:H5''	36:1:920:A:H62	1.77	0.49
37:3:106:U:H2'	37:3:107:C:C6	2.47	0.49
38:4:84:C:O3'	62:N6:113:LYS:NZ	2.39	0.49
36:5:1879:A:N3	36:5:1879:A:H2'	2.26	0.49
36:5:209:A:H4'	36:5:211:A:C8	2.47	0.49
1:6:235:G:H2'	1:6:236:A:C8	2.46	0.49
6:S4:22:LYS:NZ	1:6:757:A:O3'	381.42	0.49
1:6:879:G:H2'	1:6:880:C:C6	2.47	0.49
13:C1:109:VAL:HG11	13:C1:125:VAL:HG11	2.34	0.49
15:C3:26:PHE:HE2	15:C3:66:ILE:HD13	1.76	0.49
16:C4:19:ILE:HD11	16:C4:105:LEU:HD21	1.93	0.49
16:C4:81:VAL:HG22	16:C4:115:ILE:HB	1.93	0.49
2:S0:66:ALA:HB1	23:D1:50:TYR:CE1	2.63	0.49
26:D4:52:LYS:C	26:D4:54:ALA:H	2.42	0.49
39:L2:105:GLY:HA3	39:L2:160:SER:HB3	1.99	0.49
41:L4:23:PRO:HD2	41:L4:26:PHE:CD2	2.47	0.49
45:L8:81:THR:OG1	45:L8:181:LYS:HG3	2.13	0.49
47:M0:47:PRO:HB3	47:M0:171:TRP:CZ2	2.63	0.49
54:M8:182:LYS:HE2	64:N8:55:LYS:O	2.11	0.49
36:1:1135:A:H5'	65:N9:7:HIS:O	2.12	0.49
70:O4:67:LYS:HA	70:O4:70:LYS:HE3	1.93	0.49
39:L2:112:ILE:HD11	79:Q3:79:VAL:HG11	5.57	0.49
4:S2:175:GLY:N	4:S2:195:ASP:OD2	2.45	0.49
6:S4:156:VAL:O	6:S4:157:ASN:HB2	2.11	0.49
1:2:196:G:O6	10:S8:141:ARG:NH2	2.45	0.49
10:S8:152:ILE:H	10:S8:152:ILE:HD13	4.59	0.49
34:SR:84:SER:OG	34:SR:85:TRP:N	2.59	0.49
36:1:121:A:C6	45:L8:129:PRO:HG3	2.47	0.49
36:1:1638:A:N3	36:1:1709:C:H1'	2.28	0.49
36:1:2689:A:N3	36:1:2689:A:H2'	2.25	0.49
36:1:2943:G:OP2	40:L3:2:SER:HB2	2.12	0.49
36:1:3233:C:H2'	36:1:3234:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1317:A:O2'	36:5:1318:A:H3'	2.12	0.49
36:5:196:G:C2	36:5:199:A:C8	3.00	0.49
36:5:2213:A:H2'	36:5:2214:A:C8	2.47	0.49
36:5:3027:A:H2'	36:5:3028:G:O4'	2.11	0.49
36:5:595:G:H1	36:5:609:G:H5''	1.77	0.49
1:6:1175:U:H2'	1:6:1176:G:C8	2.47	0.49
31:D9:24:CYS:HB2	1:6:1434:U:H4'	412.46	0.49
1:6:407:A:H2'	1:6:408:C:C6	2.47	0.49
1:6:653:C:H42	1:6:677:G:H1	1.60	0.49
61:N5:56:ARG:HG2	38:8:134:G:OP1	78.97	0.49
12:C0:46:LEU:HA	12:C0:49:LEU:HB2	2.76	0.49
16:C4:25:ASP:OD1	16:C4:26:THR:N	2.46	0.49
22:D0:109:GLU:HG3	22:D0:110:PRO:HD2	2.92	0.49
25:D3:97:ASP:O	25:D3:100:ASP:HB2	2.74	0.49
30:D8:25:VAL:HG21	30:D8:66:LEU:HD22	5.77	0.49
40:L3:315:GLY:HA2	36:5:3379:C:H4'	214.62	0.49
42:L5:107:ARG:HH21	42:L5:110:LEU:HD23	1.76	0.49
42:L5:140:ARG:HH21	36:5:1080:A:P	230.55	0.49
43:L6:50:LYS:HE3	43:L6:72:ASN:HB2	1.93	0.49
41:L4:330:TYR:CZ	44:L7:49:ALA:HA	2.82	0.49
45:L8:54:GLU:HG2	45:L8:57:ARG:HH12	5.17	0.49
52:M6:90:HIS:HA	52:M6:95:GLY:HA3	2.36	0.49
2:S0:150:ASP:OD1	2:S0:165:ARG:NH2	2.46	0.49
7:S5:59:VAL:C	7:S5:61:TYR:H	2.48	0.49
34:SR:42:LEU:HD21	34:SR:82:SER:HB3	2.02	0.49
1:2:1429:G:H1'	22:D0:74:GLU:HG2	1.93	0.49
1:2:1681:A:H2'	1:2:1682:U:H5'	1.93	0.49
1:2:1685:G:H1	1:2:1716:C:H42	1.59	0.49
1:2:855:A:C2	1:2:857:U:H1'	2.47	0.49
45:L8:37:GLY:HA3	36:5:2550:U:H6	211.83	0.49
1:6:1529:C:H2'	1:6:1530:C:C6	2.47	0.49
14:C2:29:LYS:HE2	14:C2:100:TRP:NE1	2.27	0.49
14:C2:47:GLU:HG2	1:6:1229:G:O6	461.95	0.49
15:C3:87:ASP:HB3	15:C3:125:LEU:HD11	4.49	0.49
21:C9:11:ALA:HB2	21:C9:63:ARG:NH2	2.27	0.49
25:D3:51:GLY:O	25:D3:101:GLU:HA	2.33	0.49
32:E0:46:ASN:OD1	32:E0:47:VAL:N	2.71	0.49
1:2:1252:C:O4'	33:E1:133:ALA:HB2	2.13	0.49
42:L5:34:LYS:HE3	42:L5:38:THR:OG1	7.17	0.49
37:3:27:A:OP2	42:L5:57:ASN:HB2	2.12	0.49
45:L8:134:TYR:CG	45:L8:190:VAL:HG21	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:M1:166:LYS:C	48:M1:168:ASP:H	2.32	0.49
50:M4:21:VAL:HB	50:M4:63:VAL:HG22	3.14	0.49
56:N0:167:ARG:HG3	56:N0:168:PRO:HD2	1.98	0.49
57:N1:56:PHE:CE1	57:N1:78:LYS:HD3	3.63	0.49
62:N6:120:GLN:NE2	62:N6:126:LEU:HA	7.55	0.49
72:O6:89:GLU:O	72:O6:93:ILE:HG12	2.11	0.49
75:O9:43:ASN:HB3	75:O9:46:ARG:HG3	2.22	0.49
1:2:1783:C:OP2	77:Q1:1:MET:HB2	2.13	0.49
77:Q1:4:LYS:HG2	77:Q1:5:TRP:CE3	4.03	0.49
3:S1:27:LYS:NZ	3:S1:49:ASN:OD1	2.86	0.49
9:S7:131:PHE:O	9:S7:133:THR:N	2.45	0.49
36:1:1029:G:H2'	36:1:1030:A:C8	2.47	0.49
36:1:3023:U:H2'	36:1:3024:A:C8	2.47	0.49
36:1:791:A:OP1	41:L4:108:LYS:NZ	2.46	0.49
1:2:1533:C:H4'	1:2:1539:G:N1	2.27	0.49
40:L3:2:SER:N	36:5:2940:A:N7	238.51	0.49
36:5:352:A:H61	36:5:365:A:H5''	1.78	0.49
36:5:550:A:H2'	36:5:551:A:C8	2.47	0.49
36:5:913:A:H2	36:5:2134:G:N3	2.10	0.49
77:Q1:21:ARG:HH22	1:6:1118:G:P	286.58	0.49
19:C7:52:GLY:HA3	1:6:1389:C:O2'	424.82	0.49
1:6:1482:C:OP2	1:6:1521:G:N2	2.45	0.49
20:C8:145:ARG:NH2	35:SM:68:ARG:HD3	3.87	0.49
33:E1:108:VAL:HG12	33:E1:114:VAL:HG13	3.31	0.49
45:L8:161:GLU:HA	45:L8:164:VAL:HG22	1.97	0.49
44:L7:110:ARG:HH21	54:M8:3:ILE:HG12	1.76	0.49
63:N7:23:VAL:HG12	63:N7:45:GLY:HA3	1.94	0.49
5:S3:22:ASN:O	5:S3:26:THR:OG1	2.40	0.49
36:1:1146:C:H4'	36:1:1331:U:C5	2.48	0.49
36:1:1549:U:H2'	36:1:1550:C:H6	1.77	0.49
36:1:1686:U:OP1	58:N2:42:LYS:NZ	2.31	0.49
36:1:1932:A:H5'	36:1:1933:A:OP2	2.13	0.49
36:1:290:G:H1'	51:M5:93:LYS:HD3	1.94	0.49
36:1:3096:C:H2'	36:1:3097:C:C6	2.47	0.49
1:2:1520:U:OP2	21:C9:75:LYS:NZ	2.39	0.49
1:2:87:C:O2'	1:2:169:A:N1	2.41	0.49
1:2:773:C:H5''	6:S4:21:ASP:HB2	1.94	0.49
36:5:1367:G:HO2'	36:5:1368:U:H6	1.61	0.49
79:Q3:62:LYS:NZ	36:5:2554:A:H62	219.02	0.49
57:N1:92:ARG:NH1	36:5:2736:A:OP1	236.40	0.49
7:S5:185:ARG:HH12	1:6:1572:G:H1'	328.89	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1729:C:H2'	1:6:1730:A:O4'	2.13	0.49
13:C1:98:ASN:ND2	13:C1:98:ASN:O	2.46	0.49
20:C8:88:ARG:NH1	20:C8:112:ASP:OD2	3.05	0.49
20:C8:52:VAL:HG21	20:C8:69:ILE:HD11	2.87	0.49
1:2:545:A:H2'	32:E0:31:LYS:HD2	1.94	0.49
41:L4:323:VAL:O	41:L4:327:LEU:HD22	2.13	0.49
45:L8:153:ILE:HD13	45:L8:167:PRO:HD3	1.95	0.49
46:L9:166:ARG:NH2	46:L9:168:ARG:HH12	12.33	0.49
52:M6:98:ALA:HA	52:M6:101:ARG:HH11	2.06	0.49
55:M9:35:ALA:O	55:M9:36:ASN:ND2	6.31	0.49
63:N7:6:LYS:O	63:N7:8:GLY:N	2.45	0.49
65:N9:38:LYS:HE2	36:5:1076:C:O3'	217.64	0.49
36:1:424:G:O2'	68:O2:23:ASP:OD2	2.29	0.49
73:O7:76:ASN:O	73:O7:79:GLN:HG3	2.27	0.49
3:S1:129:THR:HA	3:S1:177:GLN:HA	1.92	0.49
3:S1:48:VAL:HG13	3:S1:64:ARG:HH21	3.86	0.49
36:1:2284:C:H3'	36:1:2285:C:C6	2.48	0.49
36:1:381:U:H2'	36:1:382:U:C6	2.48	0.49
1:2:702:G:O2'	1:2:703:G:H8	1.95	0.49
1:2:72:A:O2'	1:2:73:U:H5"	2.12	0.49
1:6:1644:C:O2'	36:5:2255:A:N1	2.33	0.49
16:C4:102:LEU:HD22	16:C4:105:LEU:HD11	1.94	0.49
17:C5:86:VAL:O	17:C5:89:MET:HG2	2.13	0.49
20:C8:110:ARG:NH1	20:C8:110:ARG:HB3	2.28	0.49
20:C8:38:VAL:HG12	20:C8:42:TYR:CD2	2.47	0.49
17:C5:19:GLY:N	20:C8:93:THR:O	2.46	0.49
29:D7:19:HIS:HB3	29:D7:22:LYS:HD2	3.58	0.49
30:D8:52:ASP:OD1	30:D8:52:ASP:N	2.46	0.49
39:L2:95:SER:O	39:L2:97:ASN:N	3.08	0.49
40:L3:260:VAL:HG11	40:L3:266:ARG:NH1	2.27	0.49
47:M0:210:ILE:HG12	47:M0:217:PHE:CE2	2.95	0.49
51:M5:186:GLY:O	51:M5:190:THR:HG23	2.56	0.49
36:1:2723:U:OP1	57:N1:87:LYS:HD3	2.12	0.49
58:N2:94:ARG:HG2	58:N2:96:VAL:HG22	5.16	0.49
60:N4:20:LEU:HD21	60:N4:28:ILE:HG23	2.41	0.49
61:N5:58:ASP:O	61:N5:62:VAL:HG23	2.14	0.49
62:N6:86:THR:HG22	62:N6:96:PRO:HA	2.01	0.49
36:1:1117:G:OP1	65:N9:4:SER:HB2	2.12	0.49
67:O1:46:THR:OG1	67:O1:89:LEU:O	2.26	0.49
69:O3:69:GLY:HA3	69:O3:85:PHE:HA	2.40	0.49
71:O5:45:LYS:HD2	71:O5:49:LYS:HD3	2.68	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S3:42:THR:OG1	5:S3:45:LYS:O	2.91	0.49
5:S3:59:LEU:HA	5:S3:66:ILE:HG12	1.95	0.49
9:S7:63:PRO:O	9:S7:64:VAL:HB	2.20	0.49
11:S9:157:ASP:OD1	11:S9:158:PHE:N	3.01	0.49
1:2:512:A:H5''	11:S9:163:PRO:HG3	1.95	0.49
36:1:1350:A:C2'	36:1:1351:U:H5'	2.43	0.49
36:1:1796:G:H5''	36:1:1797:A:OP1	2.13	0.49
36:1:2278:C:OP2	77:Q1:23:ARG:NH1	2.46	0.49
36:1:3324:C:OP2	67:O1:18:LYS:NZ	2.42	0.49
36:1:3384:U:H2'	36:1:3385:U:C6	2.48	0.49
36:1:818:C:H2'	36:1:819:U:O4'	2.13	0.49
1:2:352:A:OP2	1:2:352:A:H8	1.96	0.49
36:5:2437:G:H2'	36:5:2438:A:O4'	2.13	0.49
1:6:751:G:H2'	1:6:752:A:C8	2.48	0.49
24:D2:29:PRO:HB2	24:D2:58:SER:HB2	1.93	0.49
28:D6:44:ILE:HD13	28:D6:65:PRO:HG2	4.68	0.49
85:D:75:C:P	87:D:3401:SPS:HN4	2.36	0.49
33:E1:107:LYS:HB2	33:E1:117:LEU:HD11	1.93	0.49
40:L3:290:ASP:OD2	40:L3:292:ALA:N	4.82	0.49
40:L3:215:ILE:HD12	40:L3:338:LEU:HB3	1.94	0.49
36:1:209:A:OP1	41:L4:161:LYS:NZ	2.46	0.49
41:L4:44:LYS:HB3	41:L4:47:ARG:NH1	2.26	0.49
42:L5:107:ARG:NH2	42:L5:110:LEU:HD23	2.27	0.49
42:L5:40:HIS:CD2	42:L5:42:ALA:HB3	2.48	0.49
44:L7:54:GLU:OE2	44:L7:186:HIS:NE2	2.36	0.49
45:L8:206:GLU:HG2	45:L8:207:ASP:N	5.22	0.49
45:L8:41:GLN:HG3	45:L8:44:ARG:HH22	3.42	0.49
54:M8:62:VAL:HG11	54:M8:83:VAL:HG21	2.88	0.49
56:N0:45:LEU:HD12	56:N0:51:VAL:HG21	1.95	0.49
59:N3:87:ARG:HH22	59:N3:137:VAL:HG22	2.05	0.49
61:N5:105:VAL:HG13	61:N5:130:TYR:CD2	2.48	0.49
62:N6:113:LYS:HB2	38:8:84:C:H1'	19.44	0.49
38:4:64:U:OP1	71:O5:49:LYS:NZ	2.46	0.49
2:S0:48:ILE:HD13	2:S0:161:PRO:HB2	3.05	0.49
2:S0:76:ILE:HG12	2:S0:98:ILE:HB	3.97	0.49
34:SR:299:GLN:NE2	34:SR:315:VAL:O	2.46	0.49
36:1:1245:A:N6	36:1:1272:C:O2'	2.46	0.49
36:1:655:C:H2'	36:1:656:A:H8	1.78	0.49
1:2:1345:A:H2'	1:2:1348:A:N6	2.27	0.49
1:2:686:C:H2'	1:2:687:G:C8	2.48	0.49
36:5:1240:A:N6	36:5:1241:U:O4	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1483:G:C8	36:5:1485:G:C8	3.01	0.49
75:O9:45:ARG:NH2	36:5:1841:A:N3	127.86	0.49
5:S3:209:ILE:HG22	19:C7:38:ILE:O	2.59	0.49
2:S0:52:LYS:HE2	23:D1:82:VAL:HA	3.82	0.49
15:C3:15:ALA:HB2	29:D7:20:LYS:HG3	2.41	0.49
42:L5:136:GLU:CD	42:L5:136:GLU:H	4.88	0.49
55:M9:60:LYS:HE3	55:M9:64:ARG:NH2	2.28	0.49
76:Q0:83:LYS:HB3	76:Q0:83:LYS:HZ2	1.78	0.49
1:2:1290:U:OP1	4:S2:95:ARG:NH1	2.45	0.49
5:S3:179:GLN:OE1	5:S3:180:GLY:N	5.88	0.49
5:S3:64:ARG:NH1	5:S3:68:GLU:OE2	3.17	0.49
36:1:1598:G:OP2	70:O4:31:ARG:NH2	2.31	0.49
36:1:1656:A:H4'	36:1:1657:C:O5'	2.13	0.49
36:1:2539:C:H5'	36:1:2541:U:O4	2.13	0.49
36:1:3255:U:H2'	36:1:3256:G:H8	1.78	0.49
36:1:364:G:OP1	41:L4:60:THR:HG23	2.13	0.49
36:1:805:G:H1'	41:L4:73:ARG:NH1	2.27	0.49
1:2:175:G:H22	1:2:266:A:P	2.36	0.49
1:2:791:A:H2'	1:2:792:U:H6	1.78	0.49
36:5:129:U:H2'	36:5:130:A:C8	2.48	0.49
36:5:2812:C:H2'	36:5:2813:A:C8	2.48	0.49
40:L3:241:LYS:HE3	36:5:874:U:P	213.58	0.49
25:D3:7:ARG:HD2	1:6:1102:G:OP2	352.60	0.49
1:6:385:A:H2'	1:6:386:G:C8	2.48	0.49
17:C5:102:PHE:CZ	1:6:1241:G:H5'	386.68	0.49
24:D2:85:ASP:HA	24:D2:88:LYS:HG3	1.94	0.49
28:D6:88:SER:O	28:D6:92:ARG:HG3	2.40	0.49
39:L2:143:GLU:O	39:L2:145:LYS:N	2.46	0.49
43:L6:30:LEU:HD13	43:L6:34:LEU:HD13	1.95	0.49
44:L7:159:GLN:O	44:L7:160:ARG:C	2.51	0.49
49:M3:59:ARG:HD3	36:5:73:C:C2	93.45	0.49
36:1:412:G:H1'	53:M7:120:ASN:HB3	1.94	0.49
59:N3:48:ARG:HG2	36:5:2339:C:OP2	246.41	0.49
67:O1:44:MET:HB3	67:O1:77:ARG:CZ	4.19	0.49
70:O4:59:PRO:HD3	36:5:1654:A:O2'	168.44	0.49
79:Q3:59:CYS:O	79:Q3:61:LYS:N	2.39	0.49
4:S2:152:HIS:H	4:S2:152:HIS:CD2	2.95	0.49
4:S2:179:VAL:O	4:S2:198:THR:OG1	2.45	0.49
6:S4:252:ARG:NH2	6:S4:252:ARG:HB3	4.76	0.49
7:S5:93:LEU:HD23	7:S5:172:ILE:HG23	2.37	0.49
11:S9:7:THR:HG21	1:6:758:U:OP1	382.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2108:C:H1'	36:1:3344:A:C8	2.48	0.48
36:1:543:C:H42	36:1:548:G:H1	1.61	0.48
1:2:114:C:H5'	1:2:114:C:H6	1.78	0.48
1:2:56:U:H4'	1:2:57:G:H5'	1.95	0.48
1:6:1054:U:H2'	1:6:1055:U:H6	1.78	0.48
1:6:1429:G:H2'	1:6:1430:U:H6	1.78	0.48
8:S6:65:GLN:HG3	1:6:1681:A:H8	280.20	0.48
26:D4:122:GLY:HA2	26:D4:125:LEU:HB2	3.88	0.48
7:S5:161:ASP:O	30:D8:44:VAL:HA	2.13	0.48
40:L3:46:PHE:CD2	40:L3:205:VAL:HG13	3.01	0.48
43:L6:50:LYS:HG2	43:L6:74:VAL:HG21	1.95	0.48
43:L6:60:ASP:O	43:L6:61:ASN:HB2	2.26	0.48
45:L8:27:THR:O	45:L8:28:HIS:ND1	2.45	0.48
45:L8:54:GLU:O	45:L8:58:VAL:HG23	2.25	0.48
46:L9:43:VAL:HG11	46:L9:55:VAL:HG12	4.53	0.48
46:L9:83:THR:OG1	46:L9:84:LYS:N	2.75	0.48
36:1:784:A:C6	54:M8:93:ILE:HG22	2.48	0.48
58:N2:33:TYR:CE1	58:N2:80:THR:HG23	4.84	0.48
62:N6:120:GLN:OE1	62:N6:126:LEU:HG	7.50	0.48
66:O0:98:SER:OG	66:O0:99:ASP:N	2.46	0.48
2:S0:84:ARG:HD3	2:S0:203:PHE:O	2.70	0.48
3:S1:146:GLN:O	3:S1:148:ASN:N	3.35	0.48
3:S1:61:LEU:O	3:S1:63:GLY:N	2.46	0.48
4:S2:169:LEU:HD23	4:S2:198:THR:HG22	2.82	0.48
5:S3:215:GLU:OE2	5:S3:215:GLU:N	2.46	0.48
35:SM:23:LYS:HZ2	35:SM:24:GLU:N	7.98	0.48
36:1:1610:G:P	61:N5:125:ARG:HH12	2.36	0.48
36:1:385:A:H2'	36:1:386:A:H8	1.77	0.48
36:1:92:G:H5'	36:1:93:C:O5'	2.14	0.48
1:2:936:G:N7	28:D6:15:ARG:NH1	2.61	0.48
36:5:1262:G:H5''	36:5:1263:A:OP2	2.12	0.48
36:5:1915:A:H2'	36:5:1916:U:C6	2.47	0.48
36:5:2204:C:H4'	36:5:2205:U:OP1	2.13	0.48
36:5:22:G:H1'	38:8:104:A:N3	2.28	0.48
36:5:210:U:C2	36:5:230:U:H4'	2.47	0.48
36:5:2344:U:H2'	36:5:2345:A:C8	2.48	0.48
36:5:3154:C:C6	36:5:3156:U:H5'	2.48	0.48
36:5:3194:C:H2'	36:5:3195:U:H3'	1.94	0.48
36:5:438:A:H4'	36:5:439:C:OP2	2.14	0.48
1:6:1207:C:H42	1:6:1456:C:H5	1.60	0.48
11:S9:17:ARG:NH1	1:6:4:C:O2'	390.59	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:524:U:N3	1:6:527:A:OP2	2.29	0.48
17:C5:43:ARG:NH1	1:6:1553:G:O6	400.48	0.48
33:E1:144:CYS:HB3	33:E1:147:VAL:HG13	1.94	0.48
39:L2:13:GLY:O	39:L2:16:PHE:N	2.37	0.48
39:L2:114:SER:CB	39:L2:169:ILE:HD12	2.90	0.48
39:L2:5:ILE:HG22	39:L2:208:ASP:O	2.13	0.48
41:L4:60:THR:HG21	41:L4:77:VAL:HG22	2.07	0.48
42:L5:88:ILE:HD13	42:L5:239:ILE:HG22	5.38	0.48
46:L9:8:GLN:HG2	46:L9:68:LEU:HD13	2.19	0.48
48:M1:139:THR:HG22	48:M1:147:THR:HA	1.96	0.48
59:N3:11:PHE:CG	59:N3:88:ARG:HD2	2.87	0.48
64:N8:94:ALA:HB1	64:N8:122:PRO:HD2	1.94	0.48
4:S2:106:ASP:OD1	4:S2:108:ASN:N	2.92	0.48
5:S3:137:VAL:HG22	5:S3:151:LYS:HG3	1.96	0.48
7:S5:118:LEU:HD22	7:S5:129:PRO:HB2	2.11	0.48
7:S5:41:LYS:HD2	18:C6:54:LEU:HD21	4.71	0.48
11:S9:118:LEU:HD23	11:S9:158:PHE:CE1	5.01	0.48
11:S9:53:ARG:O	11:S9:57:ARG:HB2	3.19	0.48
34:SR:289:ALA:HA	34:SR:305:TYR:HA	1.95	0.48
36:1:1658:G:H2'	36:1:1659:U:C6	2.49	0.48
36:1:2651:G:H4'	36:1:2652:U:OP2	2.13	0.48
36:1:2986:U:H2'	36:1:2987:A:C8	2.48	0.48
36:1:3252:G:H2'	36:1:3253:G:C8	2.48	0.48
36:1:428:A:H2'	36:1:429:U:C6	2.48	0.48
1:2:1073:G:H4'	15:C3:10:GLY:HA2	1.94	0.48
36:5:1258:U:O2	36:5:1260:A:H8	1.96	0.48
70:O4:10:ARG:O	36:5:1488:G:O2'	139.95	0.48
36:5:2440:G:H2'	36:5:2441:A:C8	2.49	0.48
36:5:252:U:H4'	36:5:253:A:H5'	1.93	0.48
36:5:3317:U:H4'	36:5:3318:G:O5'	2.13	0.48
36:5:3343:G:H21	36:5:3362:A:H2	1.57	0.48
1:6:250:C:H2'	1:6:251:A:H8	1.77	0.48
9:S7:115:SER:O	1:6:856:A:N6	361.19	0.48
42:L5:14:SER:OG	37:7:68:C:OP1	300.51	0.48
12:C0:24:LYS:O	12:C0:26:ASP:N	2.74	0.48
1:2:1788:G:P	16:C4:127:ARG:HH12	2.35	0.48
1:2:1566:U:H5''	20:C8:39:GLY:H	1.78	0.48
24:D2:18:GLU:HG2	24:D2:65:LEU:HG	2.75	0.48
26:D4:27:VAL:HG21	26:D4:40:LEU:HD21	2.63	0.48
1:2:1793:G:N2	28:D6:76:SER:OG	2.42	0.48
32:E0:13:LYS:HE3	32:E0:17:GLN:HE22	4.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:E1:121:CYS:HB2	33:E1:132:LEU:HD21	1.95	0.48
39:L2:219:ILE:HD13	39:L2:223:SER:HB3	2.83	0.48
40:L3:151:ILE:O	40:L3:155:ALA:HB3	2.31	0.48
36:1:2646:C:H5"	47:M0:119:TRP:CG	2.49	0.48
49:M3:60:ALA:HB2	49:M3:70:ARG:HE	2.45	0.48
57:N1:130:ARG:O	36:5:1098:A:O2'	256.93	0.48
57:N1:48:ILE:HB	57:N1:95:HIS:CE1	3.01	0.48
62:N6:103:LYS:HD3	62:N6:103:LYS:HA	2.00	0.48
63:N7:102:GLU:H	63:N7:107:ARG:NH2	2.77	0.48
36:1:718:G:OP1	64:N8:117:ARG:NH2	2.45	0.48
73:O7:5:THR:HA	73:O7:8:PHE:CD2	2.48	0.48
2:S0:139:VAL:HG13	2:S0:141:ILE:HG13	1.97	0.48
2:S0:163:ASN:O	2:S0:165:ARG:N	2.99	0.48
2:S0:189:VAL:HG22	2:S0:190:ASP:H	1.77	0.48
3:S1:48:VAL:HG22	3:S1:61:LEU:HD13	6.61	0.48
4:S2:222:TYR:OH	23:D1:11:LEU:O	2.30	0.48
9:S7:62:VAL:HG11	9:S7:67:LEU:HG	1.94	0.48
36:1:1203:A:N6	36:1:1300:G:H2'	2.28	0.48
36:1:1369:A:OP1	64:N8:21:ARG:NH1	2.46	0.48
36:1:3194:C:H2'	36:1:3195:U:H2'	1.95	0.48
36:1:898:U:H2'	36:1:899:U:O4'	2.13	0.48
36:5:887:G:H2'	36:5:888:A:C8	2.48	0.48
1:6:701:U:H2'	1:6:702:G:H8	1.79	0.48
17:C5:107:ILE:HA	17:C5:111:MET:SD	3.40	0.48
18:C6:6:SER:HA	18:C6:23:LYS:HA	2.53	0.48
19:C7:96:SER:HA	19:C7:97:ASN:HA	1.60	0.48
9:S7:139:ARG:HD3	24:D2:53:ILE:HA	1.95	0.48
39:L2:192:LYS:HB3	39:L2:193:ARG:CZ	2.44	0.48
39:L2:83:HIS:CE1	39:L2:86:GLN:HB2	2.70	0.48
43:L6:72:ASN:HB3	43:L6:160:SER:HA	1.96	0.48
46:L9:112:ILE:HB	46:L9:126:VAL:HB	2.32	0.48
48:M1:133:ARG:NH1	48:M1:153:LYS:O	2.46	0.48
49:M3:90:ALA:HB1	49:M3:95:ILE:HB	1.95	0.48
57:N1:135:PRO:O	57:N1:136:ARG:HB2	4.64	0.48
66:O0:13:LYS:HB3	66:O0:100:ILE:HG23	1.95	0.48
36:1:1821:U:C4	70:O4:67:LYS:HD2	2.49	0.48
72:O6:36:ARG:NH1	36:5:116:A:OP1	108.19	0.48
74:O8:45:VAL:HG23	74:O8:52:TYR:HB2	1.96	0.48
3:S1:180:THR:OG1	3:S1:181:LEU:N	4.08	0.48
8:S6:120:GLU:HG3	8:S6:125:THR:HB	2.10	0.48
8:S6:186:ARG:O	8:S6:190:GLN:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:S7:67:LEU:HG	9:S7:94:ALA:HB2	3.19	0.48
34:SR:255:ALA:HB2	34:SR:292:LEU:HD22	1.95	0.48
36:1:1348:U:OP1	36:1:1348:U:H4'	2.13	0.48
36:1:3353:G:O2'	36:1:3356:G:OP2	2.29	0.48
36:1:838:G:O6	79:Q3:4:ARG:NH2	2.47	0.48
1:2:1201:G:N2	1:2:1600:A:H5''	2.28	0.48
1:2:778:G:H22	26:D4:10:ARG:HH12	1.62	0.48
36:5:3192:U:H2'	36:5:3193:C:C6	2.48	0.48
1:6:138:A:H62	1:6:266:A:H61	1.61	0.48
20:C8:135:GLY:HA3	1:6:1559:A:H5''	367.56	0.48
1:6:891:A:H2'	1:6:892:A:C8	2.49	0.48
62:N6:116:LYS:NZ	38:8:84:C:N3	29.01	0.48
14:C2:38:HIS:O	14:C2:125:ASN:ND2	2.47	0.48
15:C3:17:PRO:HG3	29:D7:28:PRO:HG3	1.95	0.48
17:C5:31:GLU:O	17:C5:35:LYS:HB2	2.14	0.48
25:D3:103:LEU:HB2	25:D3:126:LYS:HB2	2.15	0.48
16:C4:107:ARG:NH2	28:D6:52:ASP:OD1	3.36	0.48
39:L2:225:ILE:HG21	39:L2:234:LYS:HA	1.94	0.48
40:L3:209:PHE:HE1	40:L3:340:LYS:HB3	4.61	0.48
40:L3:3:HIS:ND1	40:L3:3:HIS:C	2.86	0.48
41:L4:170:LYS:HE3	41:L4:175:HIS:ND1	4.83	0.48
41:L4:138:ARG:HH21	41:L4:240:PRO:HB2	3.37	0.48
50:M4:72:LEU:HD23	50:M4:73:PRO:HD2	3.78	0.48
51:M5:143:ARG:HH21	71:O5:92:LEU:HA	2.11	0.48
53:M7:25:SER:HB3	53:M7:28:ASN:HB2	2.58	0.48
36:1:40:A:H5''	64:N8:35:ALA:HB1	1.94	0.48
68:O2:97:ALA:HB3	68:O2:100:ILE:HG12	2.01	0.48
2:S0:117:GLU:O	4:S2:40:LYS:NZ	2.45	0.48
7:S5:157:ARG:N	7:S5:157:ARG:HE	4.50	0.48
36:1:1157:G:H2'	36:1:1158:A:O4'	2.13	0.48
36:1:3159:C:H2'	36:1:3160:U:H6	1.77	0.48
36:1:437:G:H22	36:1:622:A:H61	1.61	0.48
1:2:1000:C:N4	1:2:1003:A:OP2	2.46	0.48
1:2:12:U:H2'	1:2:13:C:C6	2.48	0.48
1:2:340:U:H2'	1:2:341:A:H8	1.78	0.48
37:3:19:C:H2'	37:3:20:A:H8	1.78	0.48
36:5:1277:C:H2'	36:5:1278:A:C8	2.48	0.48
36:5:107:A:O2'	36:5:324:A:N3	2.38	0.48
41:L4:61:SER:HB3	36:5:929:A:H5''	132.94	0.48
1:6:1081:A:H2'	1:6:1083:G:N7	2.28	0.48
1:6:1175:U:H2'	1:6:1176:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:320:U:C5	1:6:322:G:H5''	2.49	0.48
1:6:591:A:H2'	1:6:592:A:C8	2.49	0.48
1:6:712:G:H2'	1:6:713:A:H8	1.79	0.48
1:6:778:G:N2	1:6:780:A:H5'	2.28	0.48
13:C1:122:ILE:HB	13:C1:143:SER:HB2	3.45	0.48
33:E1:135:HIS:HB2	33:E1:138:ARG:HB2	1.94	0.48
40:L3:188:ILE:O	40:L3:192:VAL:HG12	2.14	0.48
40:L3:77:THR:HG23	40:L3:326:GLY:O	2.13	0.48
41:L4:299:ILE:HG22	41:L4:300:ARG:O	2.13	0.48
42:L5:164:LYS:HG2	42:L5:180:PHE:CZ	2.49	0.48
45:L8:72:PRO:HA	45:L8:73:PRO:HD3	1.71	0.48
49:M3:140:SER:OG	49:M3:141:ALA:N	2.47	0.48
52:M6:22:VAL:HG11	52:M6:120:VAL:HG11	2.62	0.48
52:M6:24:ALA:HB2	52:M6:84:LEU:HG	3.09	0.48
52:M6:71:PHE:CE2	36:5:2383:C:H5'	231.06	0.48
59:N3:87:ARG:HH12	59:N3:137:VAL:HG11	1.96	0.48
61:N5:25:LYS:HD2	61:N5:25:LYS:H	1.79	0.48
64:N8:28:HIS:ND1	64:N8:32:ARG:HG2	3.20	0.48
66:O0:57:GLU:OE1	66:O0:69:TYR:OH	2.94	0.48
36:1:654:C:OP1	68:O2:27:ARG:NH2	2.46	0.48
70:O4:41:ARG:HA	70:O4:56:THR:HB	1.96	0.48
70:O4:81:CYS:SG	70:O4:84:CYS:SG	3.26	0.48
71:O5:47:VAL:O	71:O5:51:ILE:HG13	2.72	0.48
74:O8:26:LYS:O	74:O8:41:THR:HA	2.14	0.48
79:Q3:49:ARG:HB2	79:Q3:55:TRP:CZ3	2.79	0.48
3:S1:23:PRO:HB3	3:S1:26:ARG:NH1	3.01	0.48
4:S2:69:ILE:HD13	4:S2:136:VAL:HG21	2.28	0.48
5:S3:64:ARG:O	5:S3:66:ILE:N	3.26	0.48
5:S3:70:THR:HG22	5:S3:86:LEU:HB2	1.96	0.48
36:1:2993:G:H2'	36:1:3142:A:N6	2.28	0.48
36:1:345:G:OP1	36:1:1429:G:N1	2.42	0.48
36:1:871:U:H2'	36:1:872:U:C6	2.48	0.48
1:2:1078:C:H2'	1:2:1079:U:C6	2.48	0.48
1:2:1250:U:O2'	1:2:1251:U:OP1	2.31	0.48
1:2:717:C:H42	1:2:720:G:H22	1.62	0.48
1:2:980:G:H4'	1:2:1776:A:H4'	1.96	0.48
36:5:1294:A:O2'	36:5:1295:G:H5''	2.14	0.48
36:5:627:U:H2'	36:5:628:A:C8	2.49	0.48
36:5:651:G:C6	36:5:652:G:C6	3.01	0.48
14:C2:29:LYS:HE2	14:C2:100:TRP:CD1	2.48	0.48
17:C5:127:ARG:O	17:C5:130:ARG:NH1	4.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:127:LYS:HE2	18:C6:132:LYS:O	5.45	0.48
7:S5:81:ARG:NH2	30:D8:47:PRO:HB3	3.43	0.48
36:1:912:G:OP2	39:L2:9:ARG:NH1	2.46	0.48
41:L4:148:ILE:HA	41:L4:149:PRO:C	2.66	0.48
41:L4:283:THR:HG21	41:L4:288:ARG:HH22	7.10	0.48
51:M5:143:ARG:NH2	71:O5:92:LEU:HD23	2.36	0.48
51:M5:183:THR:HB	51:M5:187:ARG:HB2	2.56	0.48
54:M8:93:ILE:HG13	54:M8:113:LYS:HE2	1.95	0.48
57:N1:17:ARG:HH12	57:N1:45:ASN:ND2	3.90	0.48
59:N3:17:LEU:HD21	59:N3:98:ASN:ND2	2.29	0.48
66:O0:23:TYR:HA	66:O0:93:LEU:HD12	3.21	0.48
71:O5:31:LEU:HD12	71:O5:47:VAL:HG11	1.95	0.48
2:S0:16:LEU:HB3	2:S0:172:LEU:HD11	2.28	0.48
6:S4:42:LEU:N	6:S4:84:ALA:O	2.38	0.48
7:S5:203:LYS:O	7:S5:205:SER:N	2.96	0.48
9:S7:9:LEU:HG	9:S7:10:SER:H	5.07	0.48
11:S9:59:LEU:HD22	11:S9:69:ARG:HA	1.95	0.48
1:2:576:G:OP1	35:SM:104:LYS:NZ	2.47	0.48
34:SR:222:LEU:O	34:SR:231:MET:HB2	2.14	0.48
36:1:1246:G:H8	36:1:1246:G:OP1	1.97	0.48
36:1:1863:G:N1	36:1:1866:C:OP2	2.40	0.48
36:1:3153:U:H3	36:1:3293:U:H3	1.59	0.48
36:5:386:A:H8	36:5:386:A:O5'	1.97	0.48
1:6:1067:C:H2'	1:6:1068:C:C6	2.47	0.48
26:D4:11:LYS:NZ	1:6:775:G:N7	415.63	0.48
1:6:907:A:N3	1:6:997:G:O2'	2.40	0.48
20:C8:121:ALA:O	20:C8:125:ILE:HG13	2.52	0.48
20:C8:41:ARG:CZ	21:C9:46:PRO:HG3	4.07	0.48
22:D0:42:VAL:HG21	22:D0:55:PRO:HD3	1.94	0.48
25:D3:19:ARG:NE	25:D3:19:ARG:HA	2.28	0.48
40:L3:250:ALA:HB1	36:5:2947:G:C2	220.63	0.48
36:1:608:A:O3'	41:L4:326:ARG:NH1	2.47	0.48
43:L6:38:THR:HA	43:L6:90:LYS:HG3	1.95	0.48
46:L9:87:LYS:HZ2	46:L9:191:LEU:HD11	13.63	0.48
35:SM:26:VAL:HG11	48:M1:49:LYS:HE3	1.96	0.48
51:M5:94:TYR:CE2	51:M5:96:ARG:HB2	3.20	0.48
55:M9:104:ARG:HH21	55:M9:108:LYS:NZ	2.12	0.48
63:N7:51:LEU:HB2	63:N7:65:ARG:HD2	1.97	0.48
6:S4:163:ASP:O	6:S4:165:ALA:N	2.45	0.48
6:S4:3:ARG:HG2	1:6:399:A:C4'	320.75	0.48
8:S6:189:HIS:HE1	8:S6:193:LEU:HD12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:S7:97:ARG:HB2	1:6:856:A:N7	363.43	0.48
10:S8:184:LEU:HB3	10:S8:189:LEU:HB2	2.07	0.48
1:2:642:G:H2'	1:2:643:G:H8	1.79	0.48
36:5:2861:U:H2'	36:5:2862:U:O4'	2.14	0.48
36:5:3299:A:H61	36:5:3315:G:H1	1.61	0.48
36:5:528:U:H2'	36:5:529:A:C8	2.49	0.48
68:O2:27:ARG:HB3	36:5:655:C:OP1	162.08	0.48
1:6:1237:G:H2'	1:6:1238:A:C8	2.48	0.48
15:C3:128:TYR:CE1	1:6:964:U:H5''	324.00	0.48
27:D5:50:ILE:O	27:D5:54:VAL:HG23	2.12	0.48
28:D6:84:VAL:HG13	28:D6:85:ARG:H	1.78	0.48
32:E0:18:THR:HG21	1:6:584:C:H1'	390.37	0.48
32:E0:29:LYS:HG2	32:E0:35:TYR:HE2	3.39	0.48
40:L3:106:TRP:CH2	40:L3:161:LEU:HD13	2.70	0.48
41:L4:205:PRO:HB3	41:L4:247:PHE:CD2	2.51	0.48
42:L5:110:LEU:HD13	42:L5:171:LEU:HD23	1.96	0.48
36:1:612:U:OP1	43:L6:21:THR:HB	2.13	0.48
57:N1:12:ARG:HD3	57:N1:13:TYR:CZ	2.66	0.48
58:N2:35:LYS:O	58:N2:38:ILE:HG22	2.14	0.48
58:N2:56:VAL:HG22	58:N2:65:VAL:HG22	1.95	0.48
66:O0:66:LYS:H	66:O0:66:LYS:HD2	3.96	0.48
78:Q2:57:VAL:HG12	78:Q2:59:HIS:CE1	2.49	0.48
11:S9:149:ARG:O	11:S9:151:ASP:N	2.46	0.48
11:S9:37:LYS:HE3	1:6:476:U:O4	416.04	0.48
34:SR:211:ILE:HD11	34:SR:225:LEU:HD13	1.95	0.48
36:1:1460:A:H2'	36:1:1461:A:H8	1.79	0.48
36:1:2616:C:H3'	36:1:2617:U:O2	2.14	0.48
36:1:3198:U:O4	46:L9:26:LYS:HB2	2.13	0.48
36:1:993:G:N3	36:1:2637:A:H2'	2.29	0.48
1:2:1049:U:H2'	1:2:1050:G:C8	2.49	0.48
36:5:1109:U:H2'	36:5:1110:U:O4'	2.14	0.48
36:5:1560:G:O2'	36:5:1561:G:OP1	2.31	0.48
1:6:1382:A:O2'	1:6:1383:G:H5''	2.14	0.48
20:C8:84:TRP:HA	20:C8:89:GLN:NE2	2.28	0.48
24:D2:77:PRO:HD2	24:D2:79:PHE:CE2	3.13	0.48
39:L2:28:LYS:HB3	39:L2:123:ARG:HB3	1.96	0.48
36:1:2548:C:OP2	39:L2:93:LYS:NZ	2.47	0.48
42:L5:129:TYR:CG	42:L5:177:GLU:HG3	4.95	0.48
43:L6:108:LYS:HE2	43:L6:108:LYS:HB3	4.42	0.48
44:L7:239:LEU:O	44:L7:242:SER:OG	2.27	0.48
38:4:155:A:H5'	45:L8:185:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:M1:92:ARG:NH2	48:M1:94:ARG:HH11	6.14	0.48
51:M5:93:LYS:HG3	36:5:289:A:C2	147.86	0.48
53:M7:29:THR:HA	53:M7:32:THR:CG2	2.44	0.48
54:M8:176:ARG:NH1	64:N8:46:ASP:OD2	2.53	0.48
54:M8:64:VAL:HG22	54:M8:96:PHE:CE2	2.49	0.48
57:N1:131:GLN:HG3	57:N1:132:PRO:HD2	1.98	0.48
62:N6:54:ASP:HB2	62:N6:70:ILE:HD13	2.87	0.48
63:N7:83:THR:HG23	63:N7:85:TYR:H	1.77	0.48
78:Q2:17:CYS:SG	78:Q2:76:LYS:HB2	2.53	0.48
78:Q2:77:CYS:O	78:Q2:78:LYS:HD3	2.70	0.48
78:Q2:71:ARG:HH21	78:Q2:80:ARG:CZ	2.92	0.48
6:S4:71:LYS:O	6:S4:90:ILE:HA	3.02	0.48
6:S4:93:ASP:O	6:S4:95:THR:N	3.84	0.48
10:S8:110:ARG:NH2	10:S8:160:PHE:HB3	4.48	0.48
11:S9:143:ILE:HG22	11:S9:145:SER:H	1.79	0.48
34:SR:167:VAL:HG23	34:SR:183:LEU:HB2	4.79	0.48
34:SR:52:GLN:H	34:SR:52:GLN:CD	2.17	0.48
36:1:2407:C:H2'	36:1:2408:U:C6	2.49	0.47
36:1:3121:U:H1'	36:1:3122:A:H5''	1.95	0.47
1:2:1236:A:O4'	33:E1:138:ARG:NH2	2.35	0.47
1:2:1248:C:H2'	1:2:1249:U:C6	2.49	0.47
1:2:1550:A:OP1	17:C5:42:ARG:NH2	2.39	0.47
37:3:49:G:N7	42:L5:58:LYS:HG3	2.29	0.47
38:4:78:G:H2'	38:4:79:A:C8	2.48	0.47
36:5:1329:U:O2'	36:5:1330:A:H5''	2.14	0.47
36:5:627:U:H4'	36:5:1399:A:O2'	2.13	0.47
36:5:1494:U:H4'	36:5:1495:U:O5'	2.14	0.47
36:5:2518:C:H2'	36:5:2519:A:C8	2.49	0.47
36:5:999:G:C6	36:5:1000:C:N4	2.82	0.47
1:6:1316:G:O2'	1:6:1401:A:O2'	2.23	0.47
1:6:1711:C:H2'	1:6:1712:A:H5''	1.96	0.47
27:D5:43:ASP:O	27:D5:45:GLU:N	2.53	0.47
40:L3:257:PRO:HG2	40:L3:261:MET:CE	2.43	0.47
41:L4:144:LYS:CD	41:L4:144:LYS:H	4.93	0.47
41:L4:23:PRO:HD2	41:L4:26:PHE:HD2	1.78	0.47
41:L4:304:GLN:O	41:L4:306:THR:N	2.82	0.47
42:L5:279:LYS:HG2	42:L5:282:ARG:HH22	1.79	0.47
51:M5:80:THR:HG21	51:M5:87:GLN:HA	1.96	0.47
36:1:709:A:P	54:M8:179:ARG:HH22	2.37	0.47
36:1:3039:C:OP1	59:N3:88:ARG:NH2	2.47	0.47
69:O3:52:VAL:HG22	69:O3:66:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:96:GLU:O	70:O4:99:LYS:HB2	3.47	0.47
78:Q2:52:GLY:O	78:Q2:54:THR:HG23	2.14	0.47
5:S3:105:MET:HG2	5:S3:122:VAL:HG21	1.95	0.47
1:2:1681:A:H1'	8:S6:66:GLY:HA2	1.96	0.47
36:1:175:C:H2'	36:1:176:G:O4'	2.14	0.47
1:2:730:G:H21	1:2:731:C:H5''	1.79	0.47
38:4:58:G:O6	73:O7:63:ARG:NH2	2.42	0.47
36:5:1011:A:H2'	36:5:1012:G:C8	2.49	0.47
41:L4:193:LYS:NZ	36:5:1419:A:H5''	109.75	0.47
36:5:1617:G:H2'	36:5:1618:G:O4'	2.14	0.47
36:5:1645:U:H2'	36:5:1646:G:H5'	1.96	0.47
36:5:2541:U:H4'	36:5:2542:U:OP1	2.14	0.47
1:6:1060:U:H4'	1:6:1061:A:H5''	1.95	0.47
38:8:104:A:C8	38:8:105:A:C8	3.02	0.47
1:2:868:G:OP1	15:C3:121:ARG:NH1	2.47	0.47
17:C5:25:LEU:HA	17:C5:28:MET:HE2	2.72	0.47
18:C6:114:ARG:O	18:C6:115:THR:OG1	2.28	0.47
18:C6:15:SER:O	18:C6:72:GLY:N	3.92	0.47
20:C8:48:LYS:HD3	21:C9:35:ASP:OD2	2.13	0.47
26:D4:29:HIS:CE1	26:D4:34:ASN:H	2.32	0.47
26:D4:80:ALA:HA	26:D4:83:LYS:HB2	2.83	0.47
39:L2:97:ASN:HB2	39:L2:100:ASN:ND2	2.77	0.47
40:L3:106:TRP:HB2	40:L3:133:TYR:CE2	2.48	0.47
40:L3:239:PRO:O	40:L3:242:THR:HG23	2.14	0.47
42:L5:51:LEU:HB2	42:L5:144:VAL:HG13	1.95	0.47
50:M4:36:VAL:HG11	50:M4:55:ARG:NH2	2.28	0.47
45:L8:140:VAL:HG21	51:M5:3:ALA:HB2	1.96	0.47
3:S1:76:SER:OG	3:S1:78:ASP:OD1	2.28	0.47
4:S2:106:ASP:OD1	4:S2:107:SER:N	2.57	0.47
4:S2:245:ASP:N	4:S2:245:ASP:OD1	2.46	0.47
10:S8:40:ALA:O	10:S8:59:ARG:HB3	3.39	0.47
11:S9:124:HIS:CE1	11:S9:128:LEU:HD11	3.99	0.47
36:1:2102:U:H2'	36:1:2103:U:C6	2.49	0.47
36:1:2403:G:N7	36:1:2870:C:H4'	2.28	0.47
36:1:2617:U:C5	36:1:2621:G:OP2	2.65	0.47
36:1:929:A:H2'	36:1:930:U:C6	2.49	0.47
1:2:346:G:O2'	13:C1:80:MET:HE3	2.14	0.47
1:2:912:U:H4'	1:2:913:G:H2'	1.95	0.47
36:5:2106:A:H2'	36:5:2107:A:H8	1.79	0.47
47:M0:4:ARG:NH1	36:5:2828:G:O2'	264.46	0.47
28:D6:2:PRO:HB3	1:6:1142:A:H5''	350.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1196:A:H1'	1:6:1602:C:O2'	2.14	0.47
32:E0:26:LYS:NZ	1:6:588:U:OP2	420.43	0.47
32:E0:36:LYS:NZ	1:6:593:U:O4	415.47	0.47
22:D0:72:ASN:OD1	22:D0:72:ASN:N	2.48	0.47
27:D5:54:VAL:HA	27:D5:57:TYR:CE1	3.06	0.47
39:L2:79:ASN:ND2	39:L2:165:VAL:HG22	2.29	0.47
45:L8:195:SER:O	45:L8:195:SER:OG	2.26	0.47
48:M1:117:ASP:OD2	48:M1:119:SER:HB3	3.64	0.47
52:M6:187:GLU:HG2	52:M6:192:LYS:HE3	6.46	0.47
52:M6:96:LYS:O	52:M6:100:GLU:HG3	2.14	0.47
58:N2:13:LYS:O	58:N2:66:VAL:HA	2.14	0.47
61:N5:86:VAL:HG21	61:N5:95:ILE:HG12	2.25	0.47
63:N7:83:THR:HG23	63:N7:85:TYR:N	2.29	0.47
66:O0:45:ALA:O	66:O0:48:THR:HG22	2.14	0.47
68:O2:105:ARG:O	68:O2:109:LEU:HB2	2.79	0.47
3:S1:194:ASN:N	3:S1:194:ASN:OD1	2.61	0.47
35:SM:50:ASN:N	35:SM:50:ASN:OD1	4.28	0.47
35:SM:57:ASN:O	35:SM:61:ILE:HG22	5.14	0.47
34:SR:203:THR:OG1	34:SR:204:ALA:N	2.65	0.47
34:SR:211:ILE:HG13	34:SR:225:LEU:HB2	1.96	0.47
36:1:1472:U:H2'	36:1:1473:G:H8	1.80	0.47
36:1:3028:G:H2'	36:1:3029:A:O4'	2.14	0.47
1:2:1165:G:O6	1:2:1166:A:N6	2.48	0.47
1:2:1253:U:H5''	33:E1:130:VAL:HB	1.96	0.47
1:2:1383:G:OP1	22:D0:87:HIS:ND1	2.47	0.47
1:2:1477:G:H2'	1:2:1478:G:H8	1.79	0.47
36:5:1027:A:O2'	36:5:1029:G:N7	2.43	0.47
36:5:1816:A:O2'	36:5:1817:G:OP1	2.26	0.47
72:O6:28:TYR:HA	36:5:316:U:O4	102.31	0.47
36:5:668:G:H2'	36:5:669:U:O4'	2.15	0.47
1:6:1619:C:H2'	1:6:1620:C:H6	1.79	0.47
28:D6:76:SER:HG	1:6:1793:G:H22	321.25	0.47
1:6:366:A:OP1	1:6:758:U:O2'	2.20	0.47
6:S4:187:ARG:HH22	1:6:753:A:H62	376.33	0.47
18:C6:45:ARG:O	18:C6:48:VAL:HG12	2.42	0.47
18:C6:36:ILE:HD11	18:C6:48:VAL:HG22	2.07	0.47
1:2:1559:A:C6	20:C8:134:ARG:HD2	2.49	0.47
21:C9:108:LEU:HA	21:C9:111:ILE:HG22	1.97	0.47
22:D0:35:GLU:OE2	1:6:1383:G:O2'	454.49	0.47
26:D4:15:ASN:OD1	26:D4:17:LEU:HD12	2.14	0.47
30:D8:32:PHE:HZ	30:D8:38:ARG:HD2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L1:1795:U:H2'	39:L2:50:HIS:ND1	2.29	0.47
39:L2:83:HIS:NE2	39:L2:86:GLN:HB2	2.30	0.47
40:L3:308:MET:HE3	36:5:3329:U:H5''	222.58	0.47
41:L4:293:SER:O	41:L4:297:SER:OG	2.24	0.47
46:L9:99:ILE:HG21	46:L9:179:ILE:HD11	2.57	0.47
47:M0:210:ILE:HG12	47:M0:217:PHE:CZ	2.49	0.47
50:M4:36:VAL:HG11	50:M4:55:ARG:HH22	1.80	0.47
52:M6:10:ASP:CG	52:M6:37:ARG:HH21	2.50	0.47
59:N3:28:ASN:ND2	59:N3:112:SER:H	2.92	0.47
59:N3:38:ALA:HB3	59:N3:59:MET:HB2	1.96	0.47
63:N7:110:ALA:O	63:N7:114:VAL:HG23	2.49	0.47
67:O1:79:ARG:H	67:O1:79:ARG:NE	2.12	0.47
73:O7:24:ARG:O	73:O7:26:SER:N	3.34	0.47
74:O8:62:ALA:O	74:O8:66:ILE:HG13	2.14	0.47
6:S4:44:LEU:HG	6:S4:82:TYR:HB3	2.49	0.47
36:1:549:U:H2'	36:1:550:A:C8	2.49	0.47
36:1:579:G:H2'	36:1:580:C:H6	1.78	0.47
36:1:655:C:OP1	68:O2:27:ARG:HB3	2.14	0.47
1:2:512:A:HO2'	1:2:513:U:P	2.37	0.47
1:2:513:U:H2'	1:2:514:G:C8	2.50	0.47
1:2:566:C:H2'	1:2:567:A:O4'	2.14	0.47
1:2:816:G:N3	9:S7:110:GLN:NE2	2.59	0.47
1:2:881:A:H2'	1:2:882:U:O4'	2.15	0.47
36:5:1728:G:H5''	36:5:1730:G:O4'	2.14	0.47
36:5:1786:G:H2'	36:5:1787:A:C8	2.48	0.47
19:C7:11:ARG:NH2	1:6:1325:A:OP2	420.94	0.47
1:6:699:U:H3	1:6:739:G:H1	1.62	0.47
29:D7:49:HIS:CD2	1:6:958:U:H5'	344.39	0.47
1:2:114:C:HO2'	13:C1:65:SER:HG	1.57	0.47
1:2:1789:G:OP2	16:C4:132:ARG:NH2	2.47	0.47
17:C5:30:THR:O	17:C5:34:VAL:HG13	2.15	0.47
29:D7:20:LYS:HZ1	1:6:958:U:P	348.80	0.47
31:D9:17:GLY:HA2	31:D9:27:HIS:CE1	2.89	0.47
39:L2:83:HIS:CD2	39:L2:86:GLN:HB2	2.50	0.47
42:L5:40:HIS:CD2	42:L5:42:ALA:H	2.30	0.47
47:M0:171:TRP:O	47:M0:174:THR:HG22	2.15	0.47
48:M1:85:LYS:HA	48:M1:89:TYR:CE2	2.62	0.47
48:M1:96:PHE:CD1	48:M1:102:PHE:HB3	2.50	0.47
67:O1:80:ASN:OD1	67:O1:81:GLU:N	2.48	0.47
3:S1:40:ASN:ND2	3:S1:42:ASN:O	2.46	0.47
3:S1:70:LEU:HB3	3:S1:79:HIS:HB3	5.05	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:45:VAL:HG21	4:S2:68:ILE:HG23	2.13	0.47
6:S4:117:GLU:O	6:S4:119:ALA:N	3.28	0.47
11:S9:159:ALA:O	11:S9:165:GLY:HA3	2.55	0.47
5:S3:124:ARG:HD3	35:SM:124:GLN:HA	1.96	0.47
36:1:1825:G:OP2	74:O8:49:SER:OG	2.28	0.47
36:1:2778:G:C2'	36:1:2779:A:H5'	2.45	0.47
36:1:590:G:C2	36:1:610:G:H2'	2.50	0.47
1:2:1251:U:H5'	33:E1:135:HIS:HD2	1.79	0.47
1:2:1701:A:H3'	1:2:1702:A:H5''	1.95	0.47
1:2:652:G:H1	1:2:682:C:H42	1.61	0.47
1:2:685:A:O2'	1:2:686:C:OP1	2.29	0.47
1:2:861:U:OP1	15:C3:64:ARG:NH2	2.40	0.47
37:3:45:A:H2'	37:3:46:A:H8	1.78	0.47
63:N7:135:ARG:HH22	36:5:2557:A:H5'	197.89	0.47
36:5:314:U:H2'	36:5:315:C:C6	2.50	0.47
31:D9:45:GLU:OE2	1:6:1433:G:N1	409.20	0.47
31:D9:13:ARG:NH2	1:6:1554:U:OP1	415.22	0.47
1:6:1698:G:H1'	1:6:1699:G:OP1	2.14	0.47
1:6:28:A:H2'	1:6:29:U:C6	2.49	0.47
13:C1:132:SER:O	13:C1:132:SER:OG	3.52	0.47
15:C3:5:HIS:CE1	15:C3:121:ARG:HG3	2.50	0.47
18:C6:40:GLU:HA	18:C6:42:GLU:H	1.78	0.47
20:C8:127:HIS:NE2	20:C8:133:VAL:HG11	2.30	0.47
20:C8:136:GLN:H	20:C8:136:GLN:HG2	1.37	0.47
20:C8:26:ILE:HD11	20:C8:31:ALA:HA	1.95	0.47
23:D1:7:GLN:O	23:D1:9:VAL:N	2.47	0.47
27:D5:103:ARG:HG2	27:D5:104:ALA:H	5.14	0.47
40:L3:292:ALA:HB1	40:L3:295:ALA:HB3	2.35	0.47
41:L4:91:GLY:HA3	41:L4:93:MET:HE2	1.97	0.47
42:L5:58:LYS:CD	42:L5:93:THR:HG21	2.43	0.47
46:L9:112:ILE:N	46:L9:126:VAL:O	2.66	0.47
47:M0:86:HIS:HB3	47:M0:139:ARG:CG	2.73	0.47
47:M0:36:LEU:HD13	47:M0:87:LEU:HD13	1.97	0.47
47:M0:9:TYR:CG	47:M0:97:LEU:HD13	2.49	0.47
49:M3:47:ALA:HB3	49:M3:49:ARG:HG3	1.95	0.47
59:N3:72:LYS:HE3	59:N3:72:LYS:HB2	1.77	0.47
54:M8:94:PHE:CZ	64:N8:119:PRO:HD3	2.88	0.47
64:N8:21:ARG:O	64:N8:24:LYS:HE3	4.86	0.47
3:S1:168:ILE:O	3:S1:172:LEU:HG	2.78	0.47
6:S4:139:VAL:HG13	6:S4:150:PRO:HG3	1.96	0.47
6:S4:126:VAL:HG21	6:S4:155:LYS:O	3.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3078:U:H4'	36:1:3079:U:O5'	2.14	0.47
1:2:1746:A:H2'	1:2:1747:G:O4'	2.15	0.47
1:2:256:A:H2'	1:2:257:A:O4'	2.15	0.47
1:2:327:U:H2'	1:2:328:A:C8	2.49	0.47
36:5:1563:C:H2'	36:5:1564:U:O4'	2.15	0.47
36:5:1895:A:O2'	36:5:3053:G:H4'	2.14	0.47
36:5:1944:U:H2'	36:5:1945:A:C8	2.49	0.47
36:5:2105:G:H2'	36:5:2106:A:H8	1.79	0.47
36:5:3127:A:H2'	36:5:3128:G:O4'	2.15	0.47
1:6:1358:G:H2'	1:6:1359:C:C6	2.50	0.47
1:6:224:C:H2'	1:6:225:A:C8	2.48	0.47
8:S6:167:LYS:HZ1	1:6:73:U:H5	375.47	0.47
1:6:845:G:H2'	1:6:846:G:C8	2.46	0.47
15:C3:104:ARG:HH22	1:6:950:C:H4'	279.71	0.47
14:C2:97:LEU:HD11	14:C2:121:VAL:HG22	1.97	0.47
18:C6:78:VAL:O	18:C6:81:ILE:HG12	2.14	0.47
21:C9:57:ARG:O	21:C9:61:VAL:HG23	2.51	0.47
28:D6:10:ARG:HD3	28:D6:34:LYS:HG3	3.19	0.47
36:1:3306:U:H5''	40:L3:21:ARG:NH1	2.30	0.47
41:L4:145:ILE:HD12	41:L4:150:LEU:HG	1.96	0.47
42:L5:187:THR:HG23	42:L5:189:GLU:HB2	1.97	0.47
36:1:2646:C:H4'	47:M0:119:TRP:CE2	2.50	0.47
57:N1:44:ALA:HB2	57:N1:53:PRO:HG2	2.32	0.47
61:N5:86:VAL:HG11	61:N5:95:ILE:HD11	2.33	0.47
54:M8:157:PRO:HD3	64:N8:47:LYS:HB2	1.97	0.47
70:O4:99:LYS:HG2	70:O4:103:LYS:HE3	1.95	0.47
2:S0:64:ILE:HG23	2:S0:73:VAL:HG11	2.20	0.47
3:S1:67:GLU:OE2	3:S1:83:LYS:NZ	2.37	0.47
7:S5:187:ILE:H	7:S5:187:ILE:HD12	1.80	0.47
10:S8:62:THR:HA	10:S8:76:THR:O	2.40	0.47
10:S8:36:THR:OG1	10:S8:96:LEU:HB2	2.80	0.47
11:S9:57:ARG:HG3	11:S9:97:LEU:HD21	1.95	0.47
36:1:650:C:H2'	36:1:651:G:C8	2.50	0.47
36:1:785:G:OP2	54:M8:66:ARG:NH1	2.47	0.47
1:2:1755:A:C8	25:D3:63:GLN:HG3	2.49	0.47
36:5:1190:A:H5'	36:5:1191:U:OP1	2.15	0.47
36:5:64:G:O2'	36:5:77:A:N3	2.43	0.47
1:6:296:U:H2'	1:6:297:U:O4'	2.15	0.47
1:6:319:U:H5'	1:6:320:U:C5	2.50	0.47
13:C1:108:PRO:HG3	13:C1:134:THR:HB	2.12	0.47
13:C1:22:ASN:HD21	13:C1:24:LYS:HB2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:C1:46:LYS:HA	13:C1:46:LYS:HD2	3.13	0.47
13:C1:78:THR:HG22	13:C1:84:ILE:HG22	1.97	0.47
14:C2:103:LEU:HD23	14:C2:115:VAL:HA	1.96	0.47
20:C8:52:VAL:HG13	20:C8:61:LEU:HD21	2.82	0.47
2:S0:185:ARG:HB2	23:D1:45:ALA:H	1.80	0.47
27:D5:42:LEU:HD22	27:D5:47:TYR:HB2	6.16	0.47
39:L2:177:LYS:HD3	79:Q3:69:TYR:CZ	2.49	0.47
39:L2:183:GLY:O	39:L2:186:PHE:HB3	2.18	0.47
36:1:1168:U:H1'	44:L7:209:ASN:ND2	2.29	0.47
45:L8:91:PHE:HE2	45:L8:185:ARG:HB3	4.47	0.47
48:M1:54:VAL:HG23	48:M1:59:ILE:HD11	1.97	0.47
46:L9:47:LYS:NZ	50:M4:5:SER:HB2	2.22	0.47
53:M7:26:PHE:CE1	53:M7:120:ASN:HA	2.51	0.47
53:M7:62:ARG:NH1	36:5:412:G:OP1	159.50	0.47
53:M7:27:LYS:HG2	53:M7:63:PHE:CG	2.50	0.47
55:M9:105:LEU:HD23	55:M9:138:LEU:HD12	4.15	0.47
64:N8:64:GLN:HB3	64:N8:67:HIS:CD2	3.69	0.47
64:N8:82:ILE:HD11	64:N8:102:ILE:HD11	1.96	0.47
61:N5:45:LYS:HG2	71:O5:75:TYR:HD2	2.53	0.47
2:S0:172:LEU:HD22	2:S0:176:LEU:HG	4.00	0.47
2:S0:184:LEU:O	2:S0:186:GLY:N	2.63	0.47
3:S1:117:TRP:HE1	3:S1:152:ARG:CZ	2.28	0.47
3:S1:59:ASP:HA	3:S1:62:LYS:NZ	2.30	0.47
8:S6:163:THR:HG22	8:S6:168:THR:HG22	1.97	0.47
8:S6:87:ARG:NH1	1:6:159:U:O2'	321.73	0.47
11:S9:28:LEU:HB3	32:E0:44:PHE:HZ	3.40	0.47
36:1:1213:G:OP1	56:N0:137:ARG:HD3	2.15	0.47
36:1:1472:U:H2'	36:1:1473:G:C8	2.50	0.47
36:1:1654:A:O2'	70:O4:59:PRO:HD3	2.14	0.47
36:1:3276:G:H1	69:O3:60:ARG:NH2	2.10	0.47
1:2:1433:G:C8	31:D9:41:GLN:HG2	2.50	0.47
1:2:478:A:OP1	32:E0:37:ARG:NH1	2.45	0.47
36:5:1561:G:H1	36:5:1578:C:N4	2.13	0.47
36:5:2093:A:H3'	36:5:2093:A:N3	2.30	0.47
39:L2:221:LYS:NZ	36:5:2965:U:O2	213.70	0.47
1:6:1110:G:N2	1:6:1136:U:H1'	2.29	0.47
1:6:1657:U:H4'	1:6:1658:G:OP2	2.14	0.47
26:D4:34:ASN:ND2	1:6:522:U:O4'	424.96	0.47
8:S6:160:ARG:NH2	1:6:68:A:OP1	346.01	0.47
1:6:830:U:C2'	1:6:831:U:H5'	2.45	0.47
13:C1:5:LEU:HD13	13:C1:5:LEU:H	5.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:C7:104:ASN:O	19:C7:106:THR:N	3.24	0.47
2:S0:142:PRO:HG3	23:D1:32:VAL:HG13	1.97	0.47
24:D2:104:LEU:HB2	24:D2:124:LYS:O	2.15	0.47
42:L5:99:TYR:CG	42:L5:199:ILE:HG23	2.77	0.47
45:L8:68:ARG:O	45:L8:69:LEU:HB2	4.56	0.47
46:L9:124:ARG:HB3	46:L9:164:ILE:HD13	3.77	0.47
48:M1:139:THR:O	48:M1:139:THR:OG1	2.25	0.47
55:M9:104:ARG:HH11	55:M9:104:ARG:HB3	1.80	0.47
58:N2:90:ARG:O	58:N2:91:ASP:HB2	2.37	0.47
62:N6:37:LYS:H	62:N6:37:LYS:CD	2.28	0.47
63:N7:48:ARG:HB3	63:N7:69:LYS:HB3	1.97	0.47
68:O2:19:ARG:HH11	68:O2:28:VAL:HG13	2.83	0.47
79:Q3:86:LEU:O	79:Q3:90:VAL:HG13	6.10	0.47
3:S1:120:LEU:HG	3:S1:142:PHE:CE1	2.62	0.47
5:S3:69:LEU:HD12	5:S3:72:LEU:HD12	6.36	0.47
7:S5:99:MET:HA	7:S5:104:ASN:ND2	2.88	0.47
36:1:1128:U:H2'	36:1:1129:A:O4'	2.15	0.47
36:1:1715:A:O3'	36:1:1716:U:H3'	2.15	0.47
36:1:2186:U:H5'	36:1:2314:U:OP2	2.15	0.47
36:1:3151:U:H4'	36:1:3294:A:C1'	2.43	0.47
36:1:595:G:C8	36:1:609:G:C6	3.03	0.47
1:2:1274:C:N4	35:SM:94:HIS:O	2.48	0.47
1:2:1503:A:H2'	1:2:1504:G:O4'	2.15	0.47
1:2:930:A:OP1	28:D6:32:LYS:NZ	2.41	0.47
1:2:979:A:N3	1:2:1775:U:O2'	2.46	0.47
36:5:1152:G:H22	36:5:1200:A:H61	1.62	0.47
36:5:1818:U:H2'	36:5:1819:U:O4'	2.14	0.47
55:M9:82:LYS:HE3	36:5:2115:G:O2'	209.10	0.47
36:5:2206:G:O2'	36:5:2207:A:H5'	2.14	0.47
36:5:776:U:H5	36:5:2719:U:O2	1.97	0.47
52:M6:115:LYS:HG2	36:5:3178:A:C2	259.90	0.47
51:M5:162:ARG:HH11	36:5:57:A:H1'	95.80	0.47
36:5:618:C:O2'	36:5:621:A:N3	2.37	0.47
36:5:955:U:H2'	36:5:956:U:C6	2.50	0.47
1:6:1039:A:O2'	1:6:1040:G:O5'	2.32	0.47
1:6:1619:C:H2'	1:6:1620:C:C6	2.50	0.47
1:6:491:C:H42	1:6:497:G:H21	1.63	0.47
13:C1:50:GLU:HG2	13:C1:50:GLU:H	3.17	0.47
20:C8:110:ARG:HB3	20:C8:110:ARG:HH11	1.80	0.47
26:D4:58:PHE:CE2	26:D4:72:PHE:HB3	2.72	0.47
6:S4:59:ARG:HH12	26:D4:87:PRO:HG3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L5:34:LYS:O	42:L5:38:THR:HG23	2.15	0.47
36:1:2586:G:N7	45:L8:241:LYS:HB2	2.30	0.47
47:M0:193:ASP:OD1	47:M0:198:LYS:HE3	2.14	0.47
54:M8:125:ASP:OD2	54:M8:125:ASP:N	2.39	0.47
56:N0:94:ILE:HD11	56:N0:106:LEU:HB2	1.95	0.47
62:N6:120:GLN:HE22	62:N6:126:LEU:HA	8.03	0.47
63:N7:46:ILE:HD11	63:N7:48:ARG:C	2.35	0.47
67:O1:63:GLY:O	67:O1:65:LYS:N	3.31	0.47
69:O3:13:HIS:NE2	69:O3:28:SER:OG	2.38	0.47
78:Q2:21:THR:O	78:Q2:23:HIS:ND1	2.71	0.47
2:S0:121:VAL:HB	2:S0:143:VAL:HG22	1.97	0.47
2:S0:41:ARG:N	2:S0:45:VAL:O	2.97	0.47
4:S2:168:ARG:NE	1:6:1098:U:OP2	385.17	0.47
6:S4:124:GLY:HA2	6:S4:142:HIS:CE1	2.49	0.47
6:S4:184:THR:C	6:S4:189:LEU:HD13	2.95	0.47
7:S5:43:PHE:CZ	7:S5:90:ILE:HG21	2.68	0.47
7:S5:58:LEU:HD11	7:S5:167:ARG:NH1	3.30	0.47
7:S5:73:THR:HG22	7:S5:75:GLY:N	2.29	0.47
8:S6:137:ARG:O	8:S6:141:ILE:HG13	2.49	0.47
9:S7:109:VAL:O	9:S7:111:LYS:N	2.48	0.47
10:S8:46:VAL:HG13	10:S8:54:LYS:HB3	1.96	0.47
34:SR:132:LYS:NZ	34:SR:143:THR:OG1	3.28	0.47
34:SR:159:ASN:O	34:SR:161:LYS:N	3.70	0.47
36:1:900:G:H1'	36:1:1589:A:H61	1.80	0.47
36:1:2565:U:H2'	36:1:2566:C:H6	1.81	0.47
36:1:3318:G:H2'	36:1:3318:G:OP2	2.15	0.47
1:2:1244:A:N3	1:2:1244:A:H3'	2.30	0.47
1:2:1339:C:O2'	1:2:1340:U:OP1	2.33	0.47
1:2:1218:G:N2	1:2:1444:A:OP2	2.34	0.47
1:2:1477:G:H2'	1:2:1478:G:C8	2.50	0.47
1:2:158:U:O2'	1:2:159:U:H3'	2.15	0.47
1:2:413:U:H2'	1:2:414:C:C6	2.50	0.47
1:2:740:A:H2'	1:2:741:C:H5''	1.97	0.47
36:5:3203:U:H2'	36:5:3204:C:C6	2.49	0.47
36:5:750:G:H2'	36:5:751:A:C8	2.48	0.47
1:6:1255:G:O2'	1:6:1256:A:O5'	2.31	0.47
16:C4:125:SER:HB2	1:6:926:A:H2	282.45	0.47
13:C1:46:LYS:HG3	13:C1:50:GLU:CD	5.58	0.47
16:C4:17:ALA:HB3	16:C4:81:VAL:HA	1.95	0.47
18:C6:127:LYS:HA	18:C6:134:ALA:HA	1.97	0.47
21:C9:37:VAL:HG22	21:C9:38:LYS:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:D2:27:ILE:HD11	24:D2:61:ILE:HD12	1.96	0.47
30:D8:32:PHE:CE2	30:D8:40:ILE:HD13	6.14	0.47
1:2:1647:U:O2	32:E0:2:ALA:HA	2.15	0.47
33:E1:133:ALA:O	33:E1:139:LEU:HA	2.15	0.47
39:L2:114:SER:HB2	39:L2:169:ILE:CD1	2.45	0.47
36:1:2878:G:H5''	40:L3:5:LYS:HE2	1.96	0.47
42:L5:148:ILE:HG13	42:L5:159:VAL:HG21	3.64	0.47
42:L5:271:LYS:HD3	42:L5:271:LYS:HA	4.33	0.47
44:L7:152:GLY:O	44:L7:163:LEU:HG	2.14	0.47
44:L7:216:VAL:HG11	44:L7:227:GLY:HA2	3.19	0.47
51:M5:73:ARG:NH1	51:M5:88:GLY:O	2.47	0.47
57:N1:57:TYR:CD1	57:N1:89:LEU:HD21	2.50	0.47
63:N7:64:LYS:HD3	63:N7:64:LYS:HA	1.69	0.47
64:N8:75:LEU:HB3	64:N8:118:ILE:HG23	2.44	0.47
67:O1:19:ARG:HB3	67:O1:35:GLU:HG2	2.05	0.47
79:Q3:62:LYS:HZ2	36:5:2554:A:H62	218.18	0.47
3:S1:62:LYS:O	3:S1:88:VAL:HB	2.30	0.47
4:S2:95:ARG:HD3	4:S2:97:ARG:HD2	4.86	0.47
36:1:1103:A:H2'	36:1:1103:A:N3	2.30	0.46
1:2:1144:U:H2'	1:2:1145:U:C6	2.49	0.46
1:2:820:U:H2'	1:2:821:U:H4'	1.95	0.46
36:5:2180:G:H2'	36:5:2181:C:H6	1.78	0.46
1:6:1082:C:H41	1:6:1091:A:N6	2.13	0.46
37:7:27:A:H2'	37:7:28:C:C6	2.49	0.46
13:C1:92:HIS:O	13:C1:100:TYR:HA	2.15	0.46
14:C2:97:LEU:HA	14:C2:100:TRP:CE3	2.50	0.46
15:C3:11:ILE:HG13	15:C3:11:ILE:O	2.15	0.46
25:D3:44:GLY:H	25:D3:78:LYS:NZ	2.60	0.46
41:L4:230:VAL:HG21	41:L4:257:LYS:HD3	2.43	0.46
41:L4:338:LYS:HA	41:L4:338:LYS:HD2	1.47	0.46
42:L5:289:LYS:HD3	47:M0:206:LEU:HD23	1.97	0.46
45:L8:133:LYS:HD2	45:L8:138:HIS:HE1	4.23	0.46
47:M0:149:VAL:HG13	47:M0:165:ILE:HG21	4.35	0.46
47:M0:198:LYS:HE2	36:5:1040:A:O2'	333.10	0.46
56:N0:2:ALA:HB3	56:N0:32:SER:HB3	2.01	0.46
67:O1:85:ALA:O	67:O1:87:ASN:N	3.18	0.46
68:O2:32:TRP:CZ2	68:O2:53:PRO:HD2	2.57	0.46
71:O5:111:PHE:HZ	36:5:256:G:H4'	53.08	0.46
78:Q2:33:ALA:O	78:Q2:34:SER:HB3	2.14	0.46
2:S0:123:VAL:HG11	2:S0:133:ILE:HD11	2.48	0.46
3:S1:99:ASN:OD1	3:S1:100:PHE:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:81:PHE:HB3	3:S1:109:LYS:HG2	3.09	0.46
10:S8:57:ALA:HB1	10:S8:60:ILE:HD11	2.34	0.46
36:1:208:C:H2'	36:1:209:A:O4'	2.16	0.46
36:1:2894:C:H2'	36:1:2895:G:H8	1.80	0.46
36:1:594:U:H2'	36:1:609:G:O6	2.15	0.46
1:2:109:G:H1	1:2:305:C:H42	1.63	0.46
38:4:127:U:H2'	38:4:128:U:H5'	1.98	0.46
36:5:1481:A:H2'	36:5:1858:A:N3	2.29	0.46
36:5:2193:U:H5''	36:5:2194:G:H5'	1.97	0.46
36:5:2407:C:H2'	36:5:2408:U:H6	1.80	0.46
78:Q2:8:ARG:HD2	36:5:2713:U:O2'	226.99	0.46
36:5:278:U:H2'	36:5:279:U:C6	2.50	0.46
69:O3:60:ARG:HD2	36:5:3275:U:C4	213.75	0.46
1:6:495:C:H3'	1:6:496:G:H5'	1.98	0.46
1:6:653:C:N4	1:6:677:G:H1	2.13	0.46
1:6:918:U:H2'	1:6:919:A:C8	2.50	0.46
14:C2:62:LEU:HD22	14:C2:75:VAL:HG11	1.98	0.46
14:C2:91:VAL:HG11	14:C2:97:LEU:HD23	2.96	0.46
1:2:1785:U:OP2	16:C4:133:ARG:NH2	2.48	0.46
17:C5:85:ILE:HG22	17:C5:112:LEU:HD23	1.98	0.46
17:C5:75:PRO:HG3	17:C5:93:VAL:HG11	1.98	0.46
5:S3:211:PRO:HG2	19:C7:19:ARG:HB2	2.16	0.46
25:D3:103:LEU:HD22	25:D3:103:LEU:HA	1.72	0.46
26:D4:11:LYS:HD2	26:D4:24:VAL:HG21	1.97	0.46
33:E1:97:LYS:HA	33:E1:97:LYS:HD2	1.84	0.46
39:L2:158:ILE:H	39:L2:158:ILE:HD13	4.20	0.46
41:L4:74:ILE:HD12	41:L4:75:PRO:HD2	5.23	0.46
43:L6:130:ILE:HG21	43:L6:135:VAL:HG23	1.96	0.46
45:L8:146:LYS:HD3	45:L8:173:MET:O	3.46	0.46
48:M1:52:TYR:HA	48:M1:61:ARG:HG3	2.54	0.46
48:M1:91:LEU:HD22	48:M1:95:ASN:HD22	1.79	0.46
51:M5:35:VAL:HG13	51:M5:65:ARG:HB3	2.13	0.46
57:N1:106:LEU:HA	57:N1:106:LEU:HD13	1.78	0.46
63:N7:5:LEU:HD11	66:O0:35:ARG:HD2	1.97	0.46
70:O4:47:CYS:HG	70:O4:84:CYS:HG	2.23	0.46
71:O5:90:ARG:HG2	71:O5:90:ARG:H	1.74	0.46
76:Q0:110:CYS:SG	76:Q0:111:ARG:N	3.07	0.46
5:S3:66:ILE:O	5:S3:70:THR:HG23	2.38	0.46
7:S5:162:VAL:HG22	7:S5:167:ARG:HG2	4.29	0.46
11:S9:126:ARG:O	11:S9:130:THR:HG23	4.00	0.46
36:1:1631:C:H5''	36:1:1632:A:H5''	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2503:G:HO2'	36:1:2504:U:H5	1.62	0.46
36:1:3013:U:H2'	36:1:3014:U:C6	2.51	0.46
36:1:977:C:OP1	54:M8:141:ARG:NH2	2.39	0.46
36:1:999:G:C6	36:1:1000:C:N4	2.84	0.46
36:5:2261:G:H21	36:5:2262:A:N6	2.13	0.46
36:5:253:A:O2'	36:5:254:A:H8	1.98	0.46
36:5:263:C:H2'	36:5:264:G:O4'	2.15	0.46
36:5:630:A:H2'	36:5:631:U:C6	2.49	0.46
1:6:116:U:H2'	1:6:117:U:C6	2.50	0.46
1:6:1572:G:N3	1:6:1572:G:H2'	2.31	0.46
1:6:20:G:H5'	1:6:571:G:C5	2.51	0.46
1:6:91:G:OP1	1:6:397:A:N6	2.44	0.46
38:8:152:G:H2'	38:8:153:U:O4'	2.15	0.46
13:C1:14:GLN:HB3	13:C1:54:ILE:HG12	1.98	0.46
15:C3:26:PHE:CE2	15:C3:66:ILE:HD13	2.55	0.46
18:C6:41:PRO:O	18:C6:42:GLU:HB3	2.15	0.46
28:D6:62:TYR:CG	28:D6:63:ALA:N	2.84	0.46
41:L4:158:SER:O	41:L4:160:GLN:NE2	2.48	0.46
41:L4:203:ARG:HD2	41:L4:226:GLU:OE2	3.83	0.46
41:L4:338:LYS:O	41:L4:340:GLY:N	2.47	0.46
41:L4:98:ARG:HB3	41:L4:98:ARG:CZ	2.49	0.46
42:L5:178:ASN:HA	42:L5:183:TRP:CG	2.74	0.46
43:L6:146:ILE:O	43:L6:150:LYS:HG3	2.15	0.46
49:M3:144:THR:C	49:M3:146:PRO:HD3	2.75	0.46
49:M3:151:ALA:O	49:M3:153:ASP:N	3.94	0.46
52:M6:73:PHE:CD1	52:M6:78:ARG:HD3	2.51	0.46
54:M8:133:LYS:HB2	54:M8:135:GLN:HE22	1.82	0.46
55:M9:44:LEU:HA	55:M9:47:ASN:HB3	4.92	0.46
66:O0:13:LYS:NZ	66:O0:99:ASP:OD2	2.44	0.46
4:S2:215:PHE:O	4:S2:218:ILE:HG13	2.15	0.46
8:S6:76:LEU:HA	8:S6:76:LEU:HD23	2.20	0.46
10:S8:36:THR:OG1	10:S8:36:THR:O	3.09	0.46
17:C5:130:ARG:HH22	35:SM:70:ASN:HB2	3.27	0.46
34:SR:267:PRO:HG2	34:SR:269:TYR:CE1	2.50	0.46
19:C7:63:LYS:HE2	34:SR:284:ALA:HB2	1.96	0.46
36:1:1110:U:H2'	36:1:1111:U:C6	2.49	0.46
36:1:627:U:H4'	36:1:1399:A:O2'	2.15	0.46
36:1:2890:A:O2'	36:1:2933:A:N3	2.39	0.46
1:2:1184:A:O2'	1:2:1209:C:O2'	2.24	0.46
1:2:1699:G:N2	1:2:1701:A:H5''	2.31	0.46
1:2:1796:C:OP2	28:D6:92:ARG:HD3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:17:C:H2'	1:2:18:C:C6	2.51	0.46
1:2:196:G:O2'	1:2:197:A:OP2	2.27	0.46
36:5:2230:C:H2'	36:5:2231:C:O4'	2.14	0.46
36:5:2607:G:C4	36:5:2608:G:C8	3.04	0.46
42:L5:178:ASN:HD21	36:5:2746:A:H5'	253.69	0.46
36:5:3006:A:H2'	36:5:3007:U:O4'	2.15	0.46
36:5:629:U:H2'	36:5:630:A:H8	1.81	0.46
36:5:928:C:H2'	36:5:929:A:C8	2.51	0.46
1:6:1671:A:H2'	1:6:1672:G:O4'	2.16	0.46
1:6:482:U:H2'	1:6:483:A:C8	2.51	0.46
1:6:813:U:H2'	1:6:813:U:O2	2.15	0.46
38:8:106:C:H5"	38:8:108:C:OP2	2.15	0.46
7:S5:37:GLN:OE1	18:C6:53:LEU:HD22	2.55	0.46
20:C8:107:SER:O	20:C8:110:ARG:HB2	2.16	0.46
20:C8:81:ILE:O	20:C8:83:ALA:N	2.49	0.46
24:D2:10:ALA:HB1	24:D2:27:ILE:HD12	1.97	0.46
26:D4:62:THR:HA	26:D4:69:SER:HA	2.33	0.46
28:D6:84:VAL:HG13	28:D6:85:ARG:N	2.31	0.46
29:D7:73:LEU:H	29:D7:73:LEU:HD12	1.81	0.46
39:L2:82:VAL:HA	39:L2:86:GLN:OE1	2.36	0.46
36:1:2989:U:O2'	40:L3:267:ALA:O	2.32	0.46
42:L5:126:GLU:HA	42:L5:196:ARG:HD2	2.27	0.46
42:L5:155:THR:HG22	42:L5:179:ARG:NH1	2.47	0.46
45:L8:138:HIS:CE1	36:5:119:U:C2	104.00	0.46
45:L8:150:LEU:HD23	45:L8:150:LEU:HA	1.81	0.46
48:M1:54:VAL:HG12	48:M1:57:PHE:H	2.99	0.46
50:M4:115:PHE:O	50:M4:119:GLN:HG3	2.31	0.46
55:M9:34:GLN:O	55:M9:36:ASN:ND2	5.13	0.46
63:N7:53:VAL:HA	63:N7:57:HIS:CD2	2.55	0.46
70:O4:106:LYS:HD3	70:O4:109:THR:HB	1.97	0.46
71:O5:85:THR:HB	71:O5:88:LEU:HD12	2.35	0.46
77:Q1:6:ARG:O	77:Q1:10:THR:HG23	2.34	0.46
2:S0:101:ARG:NH2	2:S0:104:PRO:HD3	2.30	0.46
2:S0:172:LEU:O	2:S0:176:LEU:HG	2.16	0.46
3:S1:164:ILE:HD13	3:S1:207:LEU:HD11	2.93	0.46
4:S2:76:LEU:HD21	4:S2:104:VAL:HB	4.01	0.46
4:S2:227:PRO:HA	4:S2:230:TRP:CD2	2.50	0.46
5:S3:11:LEU:HD13	22:D0:29:THR:HG23	2.53	0.46
5:S3:21:LEU:HD22	5:S3:25:PHE:HE2	1.80	0.46
5:S3:67:ASN:O	5:S3:70:THR:OG1	2.70	0.46
8:S6:136:LYS:HG3	8:S6:173:PRO:HB3	2.65	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SR:49:GLY:O	34:SR:51:ASP:N	2.48	0.46
36:1:3049:A:H5'	36:1:3049:A:H8	1.81	0.46
1:2:1060:U:H2'	1:2:1061:A:O4'	2.15	0.46
1:2:1483:A:C6	1:2:1484:G:C6	3.03	0.46
1:2:795:U:OP2	24:D2:82:LYS:NZ	2.45	0.46
36:5:1238:C:H2'	36:5:1239:C:O4'	2.15	0.46
52:M6:60:LYS:HD3	36:5:1307:G:C4	246.55	0.46
36:5:2191:U:H2'	36:5:2192:C:O4'	2.16	0.46
36:5:83:U:H2'	36:5:84:U:O4'	2.15	0.46
36:5:90:C:C2'	36:5:91:G:H5'	2.46	0.46
57:N1:101:CYS:HB3	36:5:990:U:O4'	253.69	0.46
22:D0:89:ARG:NH2	1:6:1383:G:OP1	447.75	0.46
1:6:1783:C:H2'	1:6:1784:C:C6	2.51	0.46
1:6:416:A:H4'	1:6:417:A:OP2	2.16	0.46
12:C0:14:TYR:CZ	12:C0:18:GLU:HG3	2.62	0.46
12:C0:77:ARG:HE	12:C0:83:PRO:HA	6.43	0.46
15:C3:44:GLY:O	15:C3:45:LEU:HD23	5.59	0.46
22:D0:52:LYS:HB3	22:D0:53:LYS:H	4.06	0.46
24:D2:55:ASP:OD1	24:D2:59:GLY:N	2.48	0.46
24:D2:94:LEU:HA	24:D2:95:PRO:HD3	1.79	0.46
25:D3:109:ARG:O	25:D3:112:LYS:HE3	4.90	0.46
22:D0:67:THR:HG21	31:D9:40:ARG:HB2	1.98	0.46
40:L3:331:ASN:OD1	40:L3:331:ASN:N	2.53	0.46
38:4:27:U:H5'	41:L4:51:ALA:O	2.15	0.46
42:L5:49:TYR:CE1	42:L5:66:SER:HB3	2.51	0.46
45:L8:160:ILE:HG22	45:L8:164:VAL:HG13	1.97	0.46
48:M1:16:LYS:NZ	48:M1:130:VAL:HG11	4.85	0.46
49:M3:32:LYS:HA	49:M3:35:ARG:NH1	2.56	0.46
68:O2:75:LEU:HA	68:O2:75:LEU:HD23	1.76	0.46
70:O4:46:ASP:HB2	70:O4:84:CYS:SG	2.56	0.46
73:O7:69:HIS:O	73:O7:73:ARG:HG3	2.15	0.46
3:S1:193:ILE:HG22	3:S1:197:ILE:HD13	4.72	0.46
3:S1:39:GLU:HB3	3:S1:74:GLN:HA	1.96	0.46
6:S4:93:ASP:C	6:S4:95:THR:H	4.40	0.46
10:S8:62:THR:HA	10:S8:77:ARG:HA	2.67	0.46
20:C8:120:ARG:HD2	35:SM:58:GLU:OE2	4.32	0.46
34:SR:182:ASN:OD1	34:SR:184:ASN:ND2	4.48	0.46
36:1:1278:A:HO2'	36:1:1279:C:H6	1.61	0.46
36:1:372:A:H2'	36:1:373:A:O4'	2.15	0.46
36:1:708:G:H8	36:1:708:G:H5'	1.80	0.46
1:2:393:C:H2'	1:2:394:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:538:A:H8	1:2:543:C:N4	2.13	0.46
1:2:826:U:H2'	1:2:827:C:C6	2.51	0.46
1:2:959:U:H2'	1:2:959:U:O2	2.16	0.46
57:N1:13:TYR:OH	36:5:1050:U:OP2	270.30	0.46
36:5:1108:U:H2'	36:5:1109:U:H6	1.80	0.46
73:O7:9:GLY:HA2	36:5:1844:C:O2	149.34	0.46
36:5:1911:A:H8	36:5:1911:A:O5'	1.97	0.46
36:5:2710:C:H2'	36:5:2711:C:H6	1.80	0.46
36:5:90:C:H2'	36:5:91:G:H5'	1.98	0.46
1:6:1305:U:H4'	1:6:1306:C:OP2	2.16	0.46
1:6:793:A:C3'	1:6:794:U:H5'	2.40	0.46
12:C0:1:MET:HG3	12:C0:2:LEU:H	3.43	0.46
15:C3:56:ASP:HA	29:D7:47:PHE:HB3	1.98	0.46
19:C7:57:LEU:O	19:C7:61:ILE:HG13	2.14	0.46
26:D4:60:PHE:O	1:6:523:G:H5'	414.56	0.46
26:D4:87:PRO:HG2	26:D4:90:ARG:HG3	4.15	0.46
20:C8:6:GLN:HA	27:D5:42:LEU:HB2	3.63	0.46
42:L5:260:PHE:HA	42:L5:264:GLN:NE2	2.31	0.46
45:L8:41:GLN:HG3	45:L8:44:ARG:NH1	2.31	0.46
47:M0:24:ARG:HG3	47:M0:24:ARG:NH1	2.29	0.46
48:M1:20:ASN:ND2	48:M1:126:ASP:OD1	2.48	0.46
48:M1:28:ASP:HA	48:M1:31:THR:HG23	2.77	0.46
54:M8:122:ILE:HG22	54:M8:123:THR:O	3.12	0.46
63:N7:36:HIS:N	63:N7:37:PRO:HD3	2.56	0.46
68:O2:121:ASN:OD1	68:O2:121:ASN:N	2.48	0.46
36:1:1492:G:O3'	75:O9:48:LYS:NZ	2.48	0.46
4:S2:227:PRO:HA	4:S2:230:TRP:CD1	2.51	0.46
34:SR:164:ASP:O	34:SR:166:SER:N	2.64	0.46
34:SR:193:ILE:HD12	34:SR:193:ILE:H	4.26	0.46
36:1:1821:U:N3	70:O4:67:LYS:HD2	2.31	0.46
36:1:255:A:H5'	71:O5:106:LYS:HD3	1.98	0.46
1:2:1600:A:O2'	1:2:1602:C:N4	2.48	0.46
1:2:1648:A:H4'	32:E0:4:VAL:HG21	1.98	0.46
1:2:1761:U:O2'	1:2:1762:A:OP2	2.31	0.46
1:2:711:U:H1'	1:2:712:G:C8	2.51	0.46
1:2:964:U:H5''	15:C3:128:TYR:CE1	2.50	0.46
70:O4:4:ARG:HD2	36:5:1485:G:N2	152.46	0.46
36:5:1846:C:H5'	36:5:1849:C:N4	2.31	0.46
36:5:2772:C:H1'	36:5:2773:C:OP2	2.16	0.46
36:5:2799:A:H5''	36:5:2800:G:O5'	2.16	0.46
21:C9:3:GLY:HA3	1:6:1364:G:N2	432.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1503:A:H2'	1:6:1504:G:O4'	2.15	0.46
1:6:1660:A:H2'	1:6:1661:U:C6	2.50	0.46
1:6:181:A:H2'	1:6:182:A:O4'	2.15	0.46
38:8:37:A:H5''	38:8:39:G:O4'	2.16	0.46
12:C0:76:LEU:HD22	12:C0:79:TYR:HB3	6.00	0.46
18:C6:77:GLN:O	18:C6:81:ILE:HG23	2.16	0.46
26:D4:10:ARG:HG3	26:D4:26:ASP:OD2	4.85	0.46
40:L3:313:HIS:O	40:L3:333:LYS:HD2	2.16	0.46
43:L6:62:THR:HG21	43:L6:78:ARG:HB3	2.91	0.46
48:M1:140:ARG:HD2	48:M1:140:ARG:HA	3.67	0.46
48:M1:54:VAL:HB	48:M1:57:PHE:HB2	1.96	0.46
36:1:1312:C:O2'	52:M6:83:ALA:O	2.32	0.46
44:L7:77:VAL:HG22	57:N1:139:ARG:HG2	1.98	0.46
57:N1:82:ASN:O	65:N9:21:ILE:N	3.39	0.46
62:N6:42:GLN:O	62:N6:125:LYS:HG3	3.04	0.46
36:1:2138:A:HO2'	73:O7:2:GLY:N	2.13	0.46
73:O7:2:GLY:O	73:O7:7:SER:HB2	3.96	0.46
78:Q2:78:LYS:HG2	78:Q2:78:LYS:O	2.84	0.46
79:Q3:18:TYR:O	79:Q3:22:LEU:HD12	2.15	0.46
4:S2:103:VAL:HG22	4:S2:113:LEU:HD23	2.22	0.46
5:S3:90:ARG:HH21	5:S3:91:VAL:HG12	6.04	0.46
34:SR:54:PHE:CE2	34:SR:312:VAL:HG11	3.32	0.46
36:1:1017:C:O2'	36:1:1018:G:OP2	2.34	0.46
36:1:1683:A:H2'	36:1:1684:U:O4'	2.16	0.46
36:1:1770:G:H5'	36:1:1771:C:OP2	2.15	0.46
36:1:2723:U:H2'	36:1:2724:U:C6	2.51	0.46
36:1:3276:G:OP1	36:1:3276:G:H4'	2.14	0.46
36:1:535:G:O2'	36:1:554:A:N1	2.39	0.46
36:1:729:C:H2'	36:1:730:C:H6	1.81	0.46
36:1:953:G:OP1	65:N9:15:LYS:NZ	2.39	0.46
1:2:1487:A:H2'	1:2:1488:G:C8	2.51	0.46
1:2:43:A:H1'	1:2:378:A:N3	2.31	0.46
1:2:781:U:O2'	1:2:782:U:H6	1.97	0.46
36:5:114:A:H2'	36:5:115:A:O4'	2.16	0.46
36:5:1477:A:OP1	36:5:3075:G:O2'	2.30	0.46
36:5:1641:U:O2'	36:5:1642:A:H3'	2.16	0.46
58:N2:74:LYS:NZ	36:5:1678:G:O6	150.37	0.46
36:5:585:A:H2'	36:5:586:C:C6	2.51	0.46
1:6:1079:U:H2'	1:6:1080:U:C6	2.50	0.46
16:C4:37:GLU:HA	1:6:895:G:O2'	260.04	0.46
1:6:902:G:H2'	1:6:903:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:980:G:H4'	1:6:1776:A:H4'	1.98	0.46
4:S2:144:TRP:NE1	24:D2:97:ARG:HD2	2.30	0.46
27:D5:47:TYR:CE1	27:D5:51:LEU:HD11	4.32	0.46
39:L2:211:HIS:CD2	39:L2:219:ILE:HG23	2.99	0.46
40:L3:115:LYS:HE2	40:L3:129:ALA:HB3	4.82	0.46
36:1:2899:C:C5	46:L9:171:ASP:HA	2.51	0.46
54:M8:161:LYS:O	54:M8:162:ALA:HB3	2.14	0.46
66:O0:42:ILE:HD11	66:O0:67:VAL:HG22	1.98	0.46
68:O2:33:ARG:NH1	36:5:944:C:H4'	161.74	0.46
77:Q1:7:LYS:HE2	77:Q1:11:ARG:NH2	3.15	0.46
3:S1:33:LYS:HB3	3:S1:232:HIS:HE1	8.04	0.46
5:S3:93:ASP:N	5:S3:93:ASP:OD2	2.49	0.46
8:S6:78:THR:HG22	8:S6:92:ARG:HG2	1.98	0.46
9:S7:144:VAL:HG22	24:D2:49:GLU:HB3	3.64	0.46
36:1:3362:A:H2'	36:1:3363:U:O4'	2.16	0.46
1:2:1105:C:H41	25:D3:4:GLY:HA3	1.80	0.46
1:2:1762:A:H1'	1:2:1783:C:H5'	1.97	0.46
1:2:220:A:H5''	1:2:832:U:H1'	1.97	0.46
1:2:388:G:OP1	1:2:402:C:H5	1.98	0.46
1:2:734:A:H4'	1:2:735:C:H5'	1.98	0.46
38:4:118:C:H2'	38:4:119:C:C6	2.51	0.46
36:5:1836:C:O2'	36:5:1842:A:N1	2.43	0.46
55:M9:74:ARG:NH1	36:5:1942:U:OP2	210.50	0.46
14:C2:47:GLU:HG2	1:6:1229:G:C6	461.08	0.46
1:6:1603:U:H2'	1:6:1604:U:C6	2.51	0.46
18:C6:73:GLY:HA3	1:6:1608:U:O3'	398.46	0.46
1:6:1655:A:N1	36:5:2291:A:O2'	2.40	0.46
1:6:482:U:H2'	1:6:483:A:H8	1.81	0.46
1:6:495:C:H3'	1:6:496:G:C5'	2.46	0.46
1:6:621:A:N3	1:6:1107:G:H1'	2.30	0.46
1:6:729:G:O2'	1:6:730:G:O5'	2.31	0.46
1:6:990:C:H2'	1:6:991:G:O4'	2.15	0.46
12:C0:30:ALA:O	12:C0:38:LYS:HA	2.16	0.46
12:C0:58:GLN:HB3	12:C0:65:TYR:HB2	3.26	0.46
14:C2:68:GLU:O	14:C2:70:ASN:N	2.49	0.46
1:2:959:U:C6	15:C3:61:THR:HB	2.51	0.46
15:C3:99:ARG:O	15:C3:103:GLU:HG2	2.16	0.46
41:L4:114:ASN:HB2	41:L4:117:GLU:HG3	1.98	0.46
42:L5:64:ILE:HG13	42:L5:144:VAL:HG21	1.98	0.46
42:L5:184:ASP:OD2	42:L5:187:THR:OG1	5.51	0.46
43:L6:170:LYS:HB3	43:L6:172:HIS:CE1	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:M3:165:SER:HB3	49:M3:168:ARG:HB3	1.96	0.46
50:M4:55:ARG:HD3	56:N0:70:THR:OG1	2.15	0.46
55:M9:158:GLU:HA	55:M9:161:ALA:HB3	2.26	0.46
44:L7:120:THR:HB	57:N1:132:PRO:HB2	1.98	0.46
36:1:2724:U:H4'	57:N1:54:HIS:CD2	2.51	0.46
59:N3:75:PRO:HB2	59:N3:103:ALA:O	2.16	0.46
67:O1:44:MET:HB3	67:O1:77:ARG:HD3	1.98	0.46
74:O8:32:ASN:O	74:O8:34:ALA:N	2.49	0.46
2:S0:35:PRO:O	2:S0:52:LYS:NZ	4.26	0.46
4:S2:68:ILE:O	4:S2:72:LEU:HB2	2.15	0.46
7:S5:190:ILE:O	7:S5:194:LEU:HB2	2.27	0.46
7:S5:133:VAL:HG22	7:S5:198:LEU:HD13	2.11	0.46
9:S7:17:GLU:O	9:S7:21:ALA:N	2.91	0.46
36:1:1108:U:H2'	36:1:1109:U:C6	2.50	0.46
36:1:1275:C:H2'	36:1:1276:U:O4'	2.16	0.46
36:1:1709:C:H2'	36:1:1710:C:H6	1.79	0.46
36:1:517:G:P	44:L7:60:ARG:HH22	2.39	0.46
36:1:655:C:H2'	36:1:656:A:C8	2.51	0.46
1:2:328:A:H2'	1:2:329:G:O4'	2.16	0.46
1:2:45:U:HO2'	1:2:46:A:H2'	1.80	0.46
1:2:705:U:H2'	1:2:706:A:C8	2.51	0.46
36:5:2209:U:H4'	36:5:2210:G:OP1	2.15	0.46
36:5:3132:C:H2'	36:5:3133:C:C6	2.51	0.46
1:6:1054:U:H2'	1:6:1055:U:C6	2.51	0.46
1:6:1762:A:H1'	1:6:1783:C:H5'	1.98	0.46
1:6:652:G:N2	1:6:682:C:O2	2.48	0.46
1:6:74:U:N3	1:6:76:A:H5''	2.32	0.46
1:6:922:G:H2'	1:6:923:A:H8	1.81	0.46
18:C6:31:VAL:O	18:C6:33:GLY:N	2.49	0.46
19:C7:27:ASP:OD2	19:C7:30:THR:HG23	2.15	0.46
23:D1:3:ASN:ND2	23:D1:7:GLN:HB2	3.14	0.46
32:E0:14:VAL:HA	32:E0:17:GLN:HG2	2.09	0.46
46:L9:22:SER:H	50:M4:8:LYS:HD2	1.80	0.46
46:L9:43:VAL:CG1	46:L9:55:VAL:HG12	4.85	0.46
48:M1:8:PRO:HG2	48:M1:9:MET:H	2.24	0.46
51:M5:184:LYS:H	51:M5:186:GLY:H	1.64	0.46
52:M6:64:PHE:HE1	52:M6:68:ARG:NH1	4.03	0.46
54:M8:11:LYS:HE2	54:M8:11:LYS:HB3	1.63	0.46
55:M9:60:LYS:HZ1	36:5:1671:C:P	171.32	0.46
56:N0:52:LYS:HE3	56:N0:52:LYS:HB2	4.19	0.46
58:N2:33:TYR:CE2	58:N2:63:VAL:HG21	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:O3:31:LYS:NZ	69:O3:35:VAL:O	2.40	0.46
2:S0:119:ARG:NH1	2:S0:119:ARG:HB3	2.76	0.46
3:S1:232:HIS:HB3	3:S1:233:GLY:H	3.10	0.46
4:S2:152:HIS:N	4:S2:152:HIS:CD2	3.53	0.46
6:S4:31:PRO:HD2	6:S4:38:LEU:HD13	2.84	0.46
36:1:2393:G:O2'	36:1:2394:G:OP2	2.30	0.45
36:1:3029:A:C5	36:1:3030:G:H1'	2.51	0.45
36:1:729:C:H2'	36:1:730:C:C6	2.52	0.45
36:1:888:A:H2'	36:1:889:U:O4'	2.16	0.45
1:2:1301:U:OP1	4:S2:88:LYS:HB2	2.16	0.45
1:2:1566:U:H5''	20:C8:39:GLY:N	2.31	0.45
1:2:543:C:O2	1:2:543:C:H5'	2.16	0.45
1:2:885:G:H21	16:C4:123:SER:HB2	1.80	0.45
1:2:628:G:N1	1:2:970:A:OP2	2.36	0.45
36:5:123:A:C6	36:5:150:A:C5	3.04	0.45
36:5:1638:A:N1	36:5:1736:G:O2'	2.34	0.45
36:5:2228:A:H2'	36:5:2229:A:C8	2.51	0.45
36:5:874:U:H5''	36:5:2950:G:OP1	2.16	0.45
36:5:436:A:H3'	36:5:437:G:C8	2.51	0.45
1:6:1255:G:H4'	1:6:1256:A:OP1	2.15	0.45
1:6:1263:G:C2	1:6:1264:G:H1'	2.51	0.45
1:6:699:U:H2'	1:6:700:C:O4'	2.15	0.45
38:8:108:C:H2'	38:8:109:A:O4'	2.16	0.45
51:M5:109:ARG:NH1	38:8:141:C:OP1	120.90	0.45
5:S3:75:LYS:NZ	12:C0:34:GLU:OE2	2.43	0.45
15:C3:42:ARG:HG3	15:C3:80:LEU:HD21	4.45	0.45
16:C4:29:HIS:ND1	16:C4:29:HIS:O	2.49	0.45
16:C4:42:VAL:HA	16:C4:46:MET:SD	2.56	0.45
21:C9:33:TYR:HD1	21:C9:34:VAL:H	3.40	0.45
25:D3:78:LYS:HG3	25:D3:79:ASN:OD1	2.40	0.45
27:D5:57:TYR:HB3	27:D5:60:VAL:HG12	1.97	0.45
27:D5:40:VAL:HA	27:D5:75:LEU:HD13	3.49	0.45
28:D6:90:GLU:CD	28:D6:90:GLU:H	3.47	0.45
28:D6:9:GLY:HA3	28:D6:34:LYS:HE2	1.98	0.45
32:E0:14:VAL:O	32:E0:18:THR:HG23	2.31	0.45
39:L2:10:LYS:HA	39:L2:16:PHE:CD2	2.51	0.45
36:1:2424:A:N1	39:L2:230:VAL:HG21	2.31	0.45
40:L3:4:ARG:HD3	40:L3:7:GLU:HA	1.98	0.45
42:L5:106:ALA:O	42:L5:110:LEU:HD22	3.56	0.45
42:L5:178:ASN:N	42:L5:178:ASN:OD1	2.46	0.45
43:L6:7:PRO:HG2	43:L6:10:TYR:CZ	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L8:181:LYS:HD2	38:8:155:A:OP1	153.18	0.45
45:L8:231:LYS:HE3	45:L8:231:LYS:HB2	4.32	0.45
61:N5:77:GLU:HB3	61:N5:78:ASP:OD1	2.16	0.45
69:O3:53:TYR:CZ	69:O3:65:ARG:HB2	2.51	0.45
36:1:3000:A:H2'	36:1:3001:C:C6	2.52	0.45
1:2:1796:C:OP1	28:D6:87:ARG:NH1	2.50	0.45
1:2:417:A:H4'	1:2:418:G:O5'	2.15	0.45
37:3:42:A:H2'	37:3:43:U:H6	1.81	0.45
1:6:1228:G:H4'	1:6:1228:G:OP2	2.17	0.45
1:6:230:C:N3	1:6:235:G:N2	2.55	0.45
1:6:528:U:H2'	1:6:529:A:C8	2.51	0.45
15:C3:61:THR:HG22	29:D7:32:PHE:CE2	2.52	0.45
18:C6:102:LYS:HE2	18:C6:102:LYS:HB3	3.85	0.45
27:D5:56:THR:HA	27:D5:103:ARG:HH11	1.81	0.45
42:L5:146:LEU:HD22	42:L5:148:ILE:HG13	1.98	0.45
44:L7:106:LEU:HD12	44:L7:130:ILE:HD12	3.27	0.45
44:L7:219:LYS:O	44:L7:228:SER:HB2	2.70	0.45
46:L9:87:LYS:HZ1	46:L9:191:LEU:HD21	14.05	0.45
47:M0:130:ASP:OD1	47:M0:131:ILE:N	2.46	0.45
49:M3:119:TYR:O	49:M3:123:ILE:HG23	2.15	0.45
51:M5:155:VAL:HG23	51:M5:156:HIS:ND1	2.88	0.45
51:M5:98:LEU:HA	51:M5:98:LEU:HD12	2.24	0.45
52:M6:108:ILE:HD12	52:M6:160:ARG:CZ	2.47	0.45
54:M8:83:VAL:O	54:M8:85:GLY:N	2.65	0.45
57:N1:102:ARG:HG3	57:N1:106:LEU:HD23	1.98	0.45
60:N4:38:SER:O	60:N4:42:GLN:HG3	2.20	0.45
62:N6:83:ASP:O	62:N6:84:LYS:HB2	2.18	0.45
71:O5:104:GLN:OE1	71:O5:108:GLN:NE2	3.42	0.45
70:O4:10:ARG:HD2	75:O9:4:GLN:OE1	2.34	0.45
2:S0:112:THR:HG23	2:S0:115:PHE:HB2	1.98	0.45
4:S2:170:ILE:HG22	4:S2:171:PRO:HD2	3.23	0.45
6:S4:54:TYR:HD1	26:D4:15:ASN:ND2	2.61	0.45
7:S5:45:LYS:HD3	7:S5:45:LYS:HA	2.24	0.45
35:SM:82:THR:HB	35:SM:83:LYS:H	1.36	0.45
34:SR:5:GLU:HA	34:SR:317:THR:HA	2.58	0.45
36:1:1514:G:HO2'	36:1:1841:A:H2	1.64	0.45
36:1:2736:A:O2'	57:N1:68:THR:HG21	2.17	0.45
38:4:79:A:O3'	38:4:80:A:H4'	2.16	0.45
36:5:1024:G:N2	36:5:1026:A:OP2	2.50	0.45
36:5:150:A:H2'	36:5:151:A:H5'	1.97	0.45
36:5:156:G:O2'	36:5:157:A:H4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2582:C:H2'	36:5:2583:C:O4'	2.16	0.45
62:N6:89:LYS:NZ	36:5:375:A:OP2	75.58	0.45
36:5:567:G:H2'	36:5:568:G:C8	2.51	0.45
1:6:1039:A:C4	1:6:1040:G:C8	3.04	0.45
1:6:1542:G:N2	1:6:1569:A:OP2	2.49	0.45
18:C6:115:THR:HA	18:C6:118:ILE:HG23	1.98	0.45
20:C8:70:VAL:HG12	20:C8:74:GLN:NE2	4.41	0.45
1:2:1504:G:OP1	21:C9:97:SER:HB2	2.15	0.45
22:D0:42:VAL:HG13	22:D0:52:LYS:NZ	2.31	0.45
6:S4:95:THR:HG22	26:D4:16:PRO:HG2	1.98	0.45
26:D4:34:ASN:HB3	26:D4:35:VAL:H	4.29	0.45
27:D5:43:ASP:HB2	27:D5:46:LYS:HD2	1.98	0.45
27:D5:49:ARG:O	27:D5:53:GLU:HB2	2.58	0.45
33:E1:109:ASP:O	33:E1:111:GLU:N	2.82	0.45
39:L2:187:HIS:ND1	39:L2:190:ARG:NH1	4.83	0.45
40:L3:21:ARG:HG2	40:L3:269:GLN:HG2	2.41	0.45
40:L3:5:LYS:HG3	40:L3:6:TYR:CD1	2.52	0.45
41:L4:166:VAL:HG12	41:L4:170:LYS:HE3	1.98	0.45
42:L5:286:VAL:O	42:L5:290:ILE:HG12	2.17	0.45
42:L5:45:ASN:OD1	57:N1:33:VAL:HG21	2.71	0.45
43:L6:41:ILE:HB	43:L6:85:ILE:HB	2.16	0.45
44:L7:43:ILE:O	44:L7:47:ARG:HG3	4.84	0.45
46:L9:115:ARG:HG2	46:L9:123:ILE:HG23	1.98	0.45
46:L9:16:VAL:HG12	46:L9:29:GLY:HA3	1.99	0.45
47:M0:16:PRO:HG3	47:M0:128:ARG:NH1	2.35	0.45
47:M0:145:LYS:HD3	47:M0:167:LEU:HD21	4.16	0.45
47:M0:76:MET:HE2	47:M0:148:VAL:HG22	2.54	0.45
50:M4:105:GLN:HE22	50:M4:109:ARG:NH2	2.14	0.45
52:M6:46:GLU:HA	52:M6:135:TYR:O	2.85	0.45
50:M4:16:GLU:OE2	56:N0:149:LYS:HD2	3.99	0.45
64:N8:63:LYS:HE3	64:N8:68:PHE:CE2	2.51	0.45
69:O3:49:ILE:HA	69:O3:99:ARG:O	2.40	0.45
61:N5:46:TYR:CD2	71:O5:75:TYR:HB3	2.51	0.45
72:O6:26:ILE:C	72:O6:28:TYR:H	2.18	0.45
75:O9:44:TRP:O	75:O9:48:LYS:NZ	3.21	0.45
79:Q3:49:ARG:HB2	79:Q3:55:TRP:CH2	3.11	0.45
3:S1:129:THR:HB	3:S1:180:THR:HA	1.99	0.45
3:S1:226:GLY:HA2	36:5:2536:A:H4'	258.09	0.45
3:S1:27:LYS:NZ	3:S1:48:VAL:O	2.45	0.45
5:S3:34:TYR:OH	5:S3:37:VAL:HG13	2.17	0.45
6:S4:112:HIS:NE2	6:S4:237:SER:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:100:ARG:NH2	6:S4:122:LYS:HA	2.58	0.45
8:S6:26:VAL:HG21	8:S6:40:ALA:HB1	1.98	0.45
34:SR:217:ASP:OD1	34:SR:217:ASP:N	2.88	0.45
36:1:1127:G:H5'	47:M0:118:ALA:O	2.16	0.45
36:1:1355:A:H1'	36:1:1356:U:OP2	2.16	0.45
36:1:1734:G:H2'	36:1:1735:G:O4'	2.17	0.45
36:1:3164:C:H1'	36:1:3165:A:H5'	1.97	0.45
1:2:1290:U:H2'	1:2:1291:G:C8	2.51	0.45
1:2:304:U:OP1	13:C1:136:ARG:HD3	2.17	0.45
1:2:333:A:P	10:S8:48:THR:HB	2.56	0.45
36:5:953:G:H2'	36:5:1117:G:H5''	1.98	0.45
36:5:1235:U:C4'	36:5:1236:G:H5'	2.40	0.45
63:N7:17:ARG:NH2	36:5:1634:G:N7	198.80	0.45
36:5:189:G:C2	36:5:191:U:C4	3.03	0.45
36:5:3281:U:H5'	36:5:3282:U:OP2	2.16	0.45
64:N8:26:ARG:HH12	36:5:938:C:H3'	181.37	0.45
1:6:1417:A:H2'	1:6:1418:G:O4'	2.16	0.45
1:6:1492:A:O2'	1:6:1493:A:H8	1.99	0.45
1:6:200:A:H2'	1:6:201:G:C8	2.51	0.45
32:E0:37:ARG:NH1	1:6:478:A:OP1	441.81	0.45
1:6:542:A:H8	1:6:543:C:H5'	1.82	0.45
1:6:37:U:O2'	1:6:770:A:N1	2.36	0.45
26:D4:11:LYS:HE2	1:6:776:G:O6	421.06	0.45
29:D7:26:GLN:NE2	1:6:864:U:OP2	354.48	0.45
1:6:924:A:H2'	1:6:925:G:C8	2.51	0.45
16:C4:54:GLU:OE1	1:6:901:G:N2	283.19	0.45
21:C9:78:LYS:HG3	21:C9:93:HIS:NE2	2.74	0.45
20:C8:5:VAL:HG23	27:D5:42:LEU:HD23	1.99	0.45
28:D6:15:ARG:HD2	28:D6:18:VAL:HG12	2.68	0.45
7:S5:163:SER:HB3	30:D8:48:VAL:HG22	1.99	0.45
32:E0:41:THR:HG22	32:E0:45:VAL:HG21	1.97	0.45
41:L4:47:ARG:NH1	41:L4:109:TRP:O	2.94	0.45
42:L5:257:GLU:C	42:L5:258:LYS:HG2	5.06	0.45
42:L5:56:THR:O	42:L5:58:LYS:N	2.49	0.45
44:L7:93:ASN:N	44:L7:93:ASN:OD1	2.48	0.45
51:M5:53:TYR:HB2	51:M5:133:ILE:HG21	3.43	0.45
60:N4:39:LEU:HA	60:N4:39:LEU:HD12	1.87	0.45
36:1:1407:A:O3'	68:O2:33:ARG:NH2	2.50	0.45
70:O4:84:CYS:O	70:O4:88:ARG:HB2	4.73	0.45
2:S0:125:ASP:O	2:S0:129:ASP:HB2	2.77	0.45
3:S1:179:SER:HB3	3:S1:183:GLN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:87:ARG:NH2	3:S1:89:ASP:OD1	5.12	0.45
4:S2:121:VAL:O	4:S2:125:ILE:HG13	2.16	0.45
5:S3:125:TYR:O	5:S3:129:SER:OG	3.50	0.45
5:S3:62:ASN:ND2	5:S3:62:ASN:O	4.50	0.45
6:S4:129:VAL:HG12	6:S4:156:VAL:HG23	2.66	0.45
6:S4:11:ARG:NH1	6:S4:21:ASP:OD2	2.49	0.45
7:S5:117:THR:HG21	7:S5:194:LEU:HD12	1.98	0.45
10:S8:39:GLY:H	10:S8:60:ILE:C	2.19	0.45
36:1:1895:A:O2'	36:1:3053:G:H4'	2.17	0.45
35:SM:44:PRO:HA	36:1:2678:A:C4	2.52	0.45
36:1:2747:A:H2'	36:1:2748:A:C8	2.51	0.45
36:1:801:A:H4'	36:1:802:C:O5'	2.15	0.45
36:1:860:G:C5	39:L2:181:LYS:HB2	2.52	0.45
1:2:119:A:H1'	1:2:397:A:C5	2.52	0.45
1:2:1217:A:H8	1:2:1217:A:H5'	1.81	0.45
1:2:130:C:HO2'	1:2:131:C:P	2.39	0.45
36:5:249:U:O2'	36:5:250:U:H5''	2.17	0.45
36:5:2635:A:H4'	36:5:2636:A:O5'	2.16	0.45
36:5:3121:U:H1'	36:5:3122:A:H5''	1.99	0.45
36:5:3159:C:H2'	36:5:3160:U:C6	2.52	0.45
49:M3:31:LYS:NZ	36:5:326:U:OP1	88.91	0.45
1:6:520:A:H2'	1:6:521:A:C8	2.51	0.45
5:S3:76:ARG:HG3	12:C0:65:TYR:CE1	3.22	0.45
13:C1:94:ILE:HG12	25:D3:16:ARG:HD2	1.98	0.45
15:C3:21:ASN:HB2	15:C3:22:ALA:H	1.74	0.45
17:C5:86:VAL:O	17:C5:88:GLU:N	2.50	0.45
24:D2:66:ASN:OD1	24:D2:68:ARG:HG3	2.16	0.45
29:D7:36:LYS:HE2	29:D7:43:ILE:HG22	4.59	0.45
39:L2:128:ARG:HA	39:L2:169:ILE:HD13	2.33	0.45
39:L2:192:LYS:HB3	39:L2:193:ARG:NH2	2.31	0.45
42:L5:226:TYR:HE1	42:L5:236:LEU:HD11	5.37	0.45
48:M1:85:LYS:HE3	48:M1:85:LYS:HB2	1.75	0.45
49:M3:36:ARG:HG3	49:M3:39:ARG:HH21	3.22	0.45
49:M3:74:GLY:HA3	49:M3:98:ASP:HB2	2.47	0.45
50:M4:24:LYS:HG3	50:M4:25:LYS:HE3	1.99	0.45
50:M4:37:GLU:HG3	50:M4:38:ILE:H	1.82	0.45
57:N1:57:TYR:CG	57:N1:89:LEU:HD21	2.51	0.45
61:N5:105:VAL:HG12	61:N5:106:ASP:N	2.32	0.45
4:S2:241:ASP:HA	4:S2:244:SER:HB2	1.97	0.45
5:S3:7:LYS:HB2	1:6:1515:A:OP2	444.80	0.45
6:S4:133:LYS:HB2	6:S4:133:LYS:HE3	4.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:41:LYS:HB3	7:S5:41:LYS:HE2	2.59	0.45
8:S6:152:ASP:OD1	8:S6:154:ARG:NH2	4.82	0.45
9:S7:162:ILE:HG22	9:S7:165:LYS:HD2	1.98	0.45
5:S3:94:ARG:CZ	35:SM:134:ASP:OD1	2.60	0.45
36:1:1483:G:C8	36:1:1485:G:C8	3.04	0.45
36:1:1947:G:H1	36:1:2101:C:H42	1.63	0.45
36:1:2174:G:OP2	39:L2:193:ARG:NH1	2.47	0.45
36:1:2533:G:H3'	36:1:2534:G:C8	2.51	0.45
36:1:2662:G:H2'	36:1:2663:G:C8	2.52	0.45
36:1:3204:C:O2'	36:1:3205:G:H5'	2.16	0.45
36:1:373:A:N1	36:1:394:G:H4'	2.32	0.45
36:1:553:U:H2'	36:1:554:A:O4'	2.16	0.45
1:2:1494:C:H2'	1:2:1495:C:H6	1.81	0.45
38:4:34:U:O2'	38:4:35:C:OP2	2.29	0.45
36:5:1021:G:N1	36:5:1032:C:O2	2.49	0.45
56:N0:117:ARG:NH2	36:5:1322:U:OP1	281.72	0.45
36:5:2213:A:H2	36:5:2601:A:N3	2.14	0.45
36:5:2655:U:H4'	36:5:2656:A:O4'	2.17	0.45
35:SM:33:LYS:HD2	36:5:2667:A:H5''	286.77	0.45
36:5:3046:A:H2'	36:5:3047:U:O4'	2.17	0.45
36:5:3160:U:H2'	36:5:3161:C:C6	2.52	0.45
36:5:1940:G:N2	36:5:3362:A:H8	2.12	0.45
1:6:1146:G:N3	1:6:1635:A:H2	2.14	0.45
1:6:75:U:O2'	1:6:76:A:O5'	2.22	0.45
18:C6:82:ARG:HH22	18:C6:114:ARG:HB3	1.81	0.45
20:C8:30:TYR:HE2	20:C8:40:ARG:HD2	2.52	0.45
21:C9:98:GLY:O	21:C9:102:ARG:HB2	2.17	0.45
33:E1:120:GLU:HB3	33:E1:131:PHE:H	5.38	0.45
39:L2:224:THR:HG21	36:5:2201:G:N2	223.95	0.45
40:L3:188:ILE:HA	40:L3:191:LYS:HD2	1.98	0.45
40:L3:41:VAL:HA	40:L3:185:GLY:CA	2.58	0.45
42:L5:76:ALA:CB	42:L5:109:THR:HG22	2.47	0.45
42:L5:219:PHE:HE1	42:L5:227:LEU:HD11	2.11	0.45
47:M0:42:THR:O	47:M0:139:ARG:NH2	3.27	0.45
36:1:1128:U:OP1	47:M0:4:ARG:NH2	2.47	0.45
50:M4:50:LYS:HD3	50:M4:85:TRP:CD1	2.89	0.45
53:M7:108:ASP:OD1	53:M7:111:LYS:NZ	2.37	0.45
55:M9:20:ARG:HG2	36:5:1875:G:OP2	137.41	0.45
59:N3:85:TRP:CE2	59:N3:93:LEU:HD21	2.52	0.45
61:N5:108:LEU:HA	61:N5:108:LEU:HD23	2.05	0.45
70:O4:84:CYS:O	70:O4:88:ARG:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:O6:42:SER:O	72:O6:46:GLU:HG2	2.55	0.45
73:O7:75:LYS:HD3	36:5:181:U:O3'	49.36	0.45
78:Q2:77:CYS:SG	78:Q2:79:THR:HG23	2.99	0.45
5:S3:141:LYS:HA	5:S3:147:ALA:HA	2.72	0.45
5:S3:176:LEU:HD12	5:S3:176:LEU:H	1.82	0.45
7:S5:128:ASN:O	7:S5:132:VAL:HG23	2.35	0.45
8:S6:25:ARG:HA	8:S6:28:PHE:CD2	3.33	0.45
1:2:761:G:P	11:S9:54:ARG:HH12	2.36	0.45
35:SM:65:THR:OG1	35:SM:66:ALA:N	4.02	0.45
34:SR:16:HIS:HB3	34:SR:17:ASN:H	1.64	0.45
36:1:1507:G:C8	53:M7:129:THR:HG22	2.51	0.45
36:1:1508:C:OP1	53:M7:127:ARG:NH2	2.50	0.45
36:1:1720:U:OP2	55:M9:110:ARG:NH1	2.50	0.45
36:1:8:C:H2'	36:1:9:U:O4'	2.17	0.45
1:2:621:A:N3	1:2:1107:G:H1'	2.32	0.45
1:2:17:C:O2'	1:2:1137:A:N1	2.40	0.45
1:2:885:G:H2'	1:2:886:U:C6	2.52	0.45
38:4:24:G:OP2	62:N6:13:ARG:HD3	2.17	0.45
36:5:1152:G:H22	36:5:1200:A:N6	2.14	0.45
36:5:1781:C:H2'	36:5:1782:U:H6	1.80	0.45
73:O7:3:LYS:HG2	36:5:2138:A:O2'	173.20	0.45
36:5:2533:G:H22	36:5:2546:C:H42	1.64	0.45
36:5:308:A:H5'	36:5:2223:A:O2'	2.16	0.45
39:L2:181:LYS:HB3	36:5:860:G:C5	214.14	0.45
1:6:1208:A:H5''	1:6:1209:C:OP2	2.17	0.45
1:6:1261:G:H2'	1:6:1262:U:C6	2.52	0.45
1:6:528:U:H2'	1:6:529:A:H8	1.81	0.45
14:C2:30:VAL:HB	14:C2:132:GLU:HG3	1.97	0.45
14:C2:131:ASP:OD1	14:C2:132:GLU:N	2.50	0.45
18:C6:82:ARG:HH12	18:C6:114:ARG:HB3	1.82	0.45
21:C9:38:LYS:O	21:C9:39:THR:OG1	2.63	0.45
4:S2:144:TRP:CE2	24:D2:97:ARG:HD2	2.51	0.45
40:L3:167:ARG:C	40:L3:169:THR:H	3.04	0.45
40:L3:14:LEU:HD13	40:L3:262:TRP:CH2	2.65	0.45
40:L3:286:GLY:HA3	40:L3:321:PHE:CZ	2.52	0.45
41:L4:20:LEU:HA	41:L4:21:PRO:HD3	1.83	0.45
41:L4:309:ARG:NH2	41:L4:312:VAL:HB	2.56	0.45
45:L8:149:LYS:O	45:L8:176:PRO:HG2	2.17	0.45
45:L8:78:PHE:O	45:L8:80:TYR:N	2.47	0.45
45:L8:91:PHE:CE2	45:L8:185:ARG:HB3	4.17	0.45
47:M0:3:ARG:NH2	36:5:2854:U:OP2	291.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:M4:62:GLN:HG2	50:M4:62:GLN:H	2.53	0.45
62:N6:2:ALA:HA	36:5:213:A:O4'	80.11	0.45
69:O3:58:GLU:HG2	69:O3:63:LYS:HG3	5.08	0.45
70:O4:67:LYS:O	70:O4:71:THR:OG1	2.85	0.45
78:Q2:25:VAL:HG22	78:Q2:72:LEU:HD22	4.76	0.45
78:Q2:83:LEU:HD22	78:Q2:83:LEU:HA	1.78	0.45
2:S0:79:ARG:NH1	2:S0:164:ASN:O	3.88	0.45
2:S0:87:LEU:HA	2:S0:87:LEU:HD12	1.74	0.45
5:S3:5:ILE:HG23	5:S3:9:ARG:HH11	1.81	0.45
6:S4:62:LYS:NZ	6:S4:62:LYS:HB2	2.32	0.45
7:S5:109:LYS:HE3	7:S5:109:LYS:HB2	4.74	0.45
11:S9:116:LEU:O	11:S9:118:LEU:HD12	3.32	0.45
36:1:1100:U:OP2	44:L7:196:LYS:HE3	2.17	0.45
36:1:1103:A:H2	54:M8:9:GLN:HE22	1.63	0.45
36:1:22:G:H1'	38:4:104:A:N3	2.31	0.45
36:1:3360:C:N4	36:1:3361:G:O6	2.49	0.45
1:2:848:C:H2'	1:2:849:C:C6	2.51	0.45
37:3:60:G:H2'	37:3:61:G:C8	2.52	0.45
36:5:1137:C:H2'	36:5:1138:U:O4'	2.16	0.45
36:5:2796:G:H4'	36:5:2798:C:C6	2.52	0.45
1:6:1228:G:H2'	1:6:1228:G:N3	2.32	0.45
1:6:542:A:C8	1:6:543:C:H5'	2.52	0.45
17:C5:21:ASP:HB2	17:C5:24:LYS:HE3	1.98	0.45
18:C6:47:LYS:HE3	18:C6:82:ARG:NH1	4.73	0.45
21:C9:10:ALA:HB3	21:C9:13:ASP:HB2	5.16	0.45
21:C9:75:LYS:HD2	1:6:1498:G:OP1	417.89	0.45
22:D0:41:ILE:HG13	22:D0:107:THR:HG21	3.51	0.45
22:D0:48:HIS:CE1	22:D0:50:LEU:HD11	2.51	0.45
22:D0:96:PRO:HG2	22:D0:99:ILE:HG22	1.98	0.45
33:E1:113:LYS:HB3	33:E1:113:LYS:HE3	1.99	0.45
33:E1:88:PRO:HA	33:E1:89:LYS:HA	4.76	0.45
40:L3:183:LEU:O	40:L3:191:LYS:NZ	2.48	0.45
40:L3:32:PHE:CD1	40:L3:182:GLN:HB3	2.52	0.45
42:L5:187:THR:HG22	42:L5:189:GLU:HB2	3.53	0.45
46:L9:7:GLU:HA	46:L9:68:LEU:HD11	2.11	0.45
36:1:289:A:H5'	51:M5:95:GLN:O	2.17	0.45
52:M6:106:GLU:H	52:M6:106:GLU:HG2	1.53	0.45
52:M6:133:ARG:NE	36:5:1316:C:OP2	293.91	0.45
53:M7:116:HIS:HB3	53:M7:149:VAL:HB	1.99	0.45
61:N5:142:ILE:HD13	61:N5:142:ILE:HA	1.74	0.45
61:N5:53:HIS:ND1	61:N5:54:TYR:O	2.53	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:N6:79:ALA:HB1	62:N6:98:ASN:HB3	1.98	0.45
64:N8:47:LYS:HE2	64:N8:48:TYR:CE2	2.52	0.45
67:O1:70:ARG:O	67:O1:71:LEU:HD23	2.69	0.45
69:O3:45:LEU:HD12	36:5:584:G:H1'	254.76	0.45
71:O5:21:LEU:HD22	71:O5:25:LYS:HE2	1.99	0.45
2:S0:81:PHE:HB3	2:S0:170:ILE:HD12	3.39	0.45
3:S1:70:LEU:HD21	3:S1:79:HIS:CD2	2.51	0.45
5:S3:195:SER:HB2	5:S3:200:LYS:HG2	3.94	0.45
8:S6:21:GLU:O	8:S6:25:ARG:HG3	2.78	0.45
8:S6:34:GLN:O	8:S6:52:ILE:HG13	2.17	0.45
9:S7:126:LEU:HB2	9:S7:173:TYR:HE2	4.69	0.45
34:SR:65:SER:N	34:SR:86:ASP:OD2	2.82	0.45
36:1:1171:G:OP2	44:L7:218:ARG:HD2	2.17	0.45
36:1:1230:G:H1	36:1:1279:C:N4	2.14	0.45
36:1:1721:U:O4	55:M9:128:LYS:HD2	2.17	0.45
36:1:2761:G:C4	36:1:2795:U:C5	3.05	0.45
36:1:2780:A:H2'	36:1:2781:U:C6	2.51	0.45
36:1:3358:U:H2'	36:1:3359:A:O4'	2.17	0.45
36:1:715:A:H4'	36:1:716:A:OP1	2.16	0.45
36:1:712:G:N2	36:1:754:G:O3'	2.50	0.45
1:2:1450:U:H2'	1:2:1451:C:C6	2.52	0.45
1:2:297:U:H5''	6:S4:37:LYS:HG2	1.98	0.45
1:2:324:U:O2'	13:C1:80:MET:HE1	2.17	0.45
1:2:872:G:H2'	1:2:873:U:O4'	2.17	0.45
36:5:1038:C:H2'	36:5:1039:U:H6	1.82	0.45
36:5:1366:A:C2	36:5:1367:G:C4	3.04	0.45
36:5:908:G:H4'	36:5:909:G:O5'	2.17	0.45
1:6:230:C:H42	1:6:235:G:H1	1.64	0.45
1:6:55:A:N6	1:6:403:G:H1'	2.32	0.45
1:6:946:U:H2'	1:6:947:U:C6	2.52	0.45
38:8:44:A:H2'	38:8:45:C:C6	2.51	0.45
16:C4:129:LYS:HE3	16:C4:129:LYS:HB2	1.86	0.45
16:C4:135:ARG:NH1	16:C4:137:LEU:HD21	4.09	0.45
20:C8:140:THR:HA	20:C8:143:ARG:HH12	1.96	0.45
1:2:1039:A:H5''	23:D1:62:ARG:HH21	1.81	0.45
1:2:150:U:P	26:D4:123:LYS:HZ3	2.40	0.45
30:D8:26:THR:HB	30:D8:44:VAL:HG22	2.03	0.45
40:L3:233:TRP:CD1	40:L3:265:ALA:HB1	2.52	0.45
41:L4:60:THR:HG22	41:L4:62:ALA:N	2.52	0.45
44:L7:184:LEU:HD11	44:L7:202:LEU:HD21	1.99	0.45
48:M1:29:ARG:HA	48:M1:32:ARG:NH2	4.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:617:G:H4'	53:M7:171:ARG:HH21	1.81	0.45
61:N5:34:LEU:HD23	61:N5:35:PRO:HD2	1.99	0.45
63:N7:46:ILE:HD13	63:N7:49:TYR:N	4.04	0.45
70:O4:77:GLY:H	36:5:1805:C:H4'	188.56	0.45
74:O8:48:SER:HB3	36:5:1825:G:OP1	132.40	0.45
75:O9:41:ARG:HG3	75:O9:42:ARG:H	1.81	0.45
4:S2:72:LEU:HD12	4:S2:72:LEU:HA	2.05	0.45
9:S7:35:LYS:NZ	9:S7:39:ARG:HD2	2.32	0.45
36:1:2210:G:H8	36:1:2210:G:OP2	2.00	0.45
36:1:2894:C:H2'	36:1:2895:G:C8	2.52	0.45
36:1:2140:U:O2'	36:1:2978:U:H5'	2.17	0.45
1:2:1018:U:H2'	1:2:1019:A:H8	1.82	0.45
1:2:1184:A:HO2'	1:2:1209:C:HO2'	1.52	0.45
1:2:1487:A:H2'	1:2:1488:G:H8	1.82	0.45
1:2:1689:A:H2'	1:2:1690:G:H8	1.81	0.45
1:2:794:U:H1'	1:2:795:U:OP1	2.17	0.45
44:L7:209:ASN:ND2	36:5:1333:C:H1'	241.45	0.45
39:L2:243:THR:HG23	36:5:2242:A:H5'	233.64	0.45
36:5:224:C:H2'	36:5:225:C:H6	1.82	0.45
36:5:2367:A:H2'	36:5:2368:A:C8	2.52	0.45
36:5:2140:U:O2'	36:5:2978:U:H5'	2.17	0.45
36:5:712:G:H2'	36:5:713:U:C6	2.51	0.45
1:6:1002:G:C6	1:6:1003:A:N7	2.85	0.45
16:C4:45:GLY:O	1:6:899:G:H5'	279.29	0.45
12:C0:2:LEU:HB3	12:C0:3:MET:H	4.28	0.45
12:C0:50:THR:HG22	12:C0:55:VAL:HG22	2.06	0.45
14:C2:67:THR:C	14:C2:69:ALA:H	2.27	0.45
15:C3:15:ALA:H	29:D7:20:LYS:NZ	2.15	0.45
18:C6:93:HIS:HA	18:C6:97:VAL:HG23	1.99	0.45
20:C8:108:LYS:NZ	20:C8:111:ASP:OD2	2.43	0.45
27:D5:74:SER:HA	27:D5:77:ARG:NH2	2.32	0.45
40:L3:345:ASN:OD1	40:L3:347:SER:HB2	2.88	0.45
41:L4:10:SER:O	41:L4:12:THR:N	2.50	0.45
42:L5:40:HIS:HE1	42:L5:42:ALA:HB3	4.46	0.45
43:L6:176:PHE:O	50:M4:113:THR:HG23	2.16	0.45
43:L6:52:VAL:HA	43:L6:67:GLY:HA2	3.70	0.45
46:L9:117:PHE:HB3	46:L9:124:ARG:HH21	2.44	0.45
47:M0:194:GLY:HA3	36:5:1010:G:N3	336.96	0.45
47:M0:20:SER:H	47:M0:23:ASN:HB3	1.82	0.45
47:M0:65:LEU:HD23	47:M0:159:PHE:CZ	2.94	0.45
51:M5:150:TRP:CH2	51:M5:151:ILE:HG12	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M5:38:ARG:CZ	51:M5:60:VAL:HG13	2.47	0.45
36:1:114:A:O2'	51:M5:50:ARG:HB3	2.17	0.45
55:M9:172:ARG:O	55:M9:176:ARG:HG2	2.46	0.45
46:L9:3:TYR:HA	56:N0:142:GLN:OE1	2.16	0.45
36:1:938:C:H3'	64:N8:26:ARG:HH12	1.82	0.45
74:O8:17:ARG:HG2	74:O8:19:ASP:OD2	3.58	0.45
6:S4:158:ASP:OD2	6:S4:174:LYS:NZ	2.46	0.45
6:S4:15:PRO:HG2	6:S4:18:TRP:CE2	2.51	0.45
9:S7:96:ARG:HH22	9:S7:128:ASP:CG	2.21	0.45
11:S9:34:PHE:CE1	11:S9:105:LEU:HB3	2.52	0.45
36:1:1717:U:H2'	36:1:1718:G:C8	2.52	0.44
36:1:2557:A:OP1	39:L2:69:TYR:OH	2.28	0.44
36:1:549:U:H2'	36:1:550:A:H8	1.81	0.44
1:2:100:A:H2'	1:2:101:U:O4'	2.16	0.44
1:2:1363:U:O2	1:2:1363:U:H2'	2.17	0.44
1:2:1688:U:H2'	1:2:1689:A:C8	2.52	0.44
1:2:275:C:N3	1:2:276:C:N4	2.63	0.44
1:2:485:A:H2'	1:2:486:G:O4'	2.17	0.44
36:5:1200:A:H5'	36:5:1201:C:OP1	2.17	0.44
36:5:1528:G:O2'	36:5:1588:A:N3	2.39	0.44
36:5:197:G:H2'	36:5:198:A:C8	2.52	0.44
36:5:3268:A:O2'	36:5:3269:U:H2'	2.17	0.44
36:5:518:G:H2'	36:5:520:U:H5'	1.99	0.44
33:E1:146:SER:HB2	1:6:1235:C:H5'	435.41	0.44
1:6:1617:U:H2'	1:6:1618:C:C6	2.52	0.44
1:6:594:A:H4'	1:6:595:G:H5'	1.98	0.44
12:C0:59:PHE:CZ	12:C0:62:GLN:HA	2.53	0.44
17:C5:60:LEU:HD21	17:C5:92:SER:HB3	1.99	0.44
23:D1:78:LEU:HA	23:D1:78:LEU:HD13	4.41	0.44
24:D2:75:ILE:HA	24:D2:75:ILE:HD13	1.91	0.44
25:D3:107:PHE:CE1	25:D3:123:LYS:HB3	2.53	0.44
40:L3:211:GLN:HE21	40:L3:284:ARG:HA	1.90	0.44
40:L3:68:HIS:CD2	40:L3:69:LYS:HG2	3.26	0.44
41:L4:22:LEU:HA	41:L4:23:PRO:HD3	1.68	0.44
41:L4:351:PRO:HA	44:L7:71:ALA:HA	1.98	0.44
41:L4:8:VAL:O	41:L4:16:THR:HG22	4.56	0.44
43:L6:166:LYS:HE2	69:O3:4:SER:OG	2.17	0.44
45:L8:24:ASN:N	45:L8:25:PRO:HD2	2.31	0.44
51:M5:68:ARG:HG3	36:5:291:C:OP1	146.02	0.44
53:M7:31:GLU:CG	53:M7:60:PHE:HA	3.34	0.44
54:M8:44:PHE:CD1	54:M8:139:ILE:HD11	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:M9:114:LYS:HB3	55:M9:114:LYS:HE2	1.72	0.44
58:N2:54:VAL:HG12	58:N2:67:SER:HA	1.99	0.44
71:O5:65:ALA:O	71:O5:69:LEU:HD23	3.35	0.44
2:S0:56:LYS:HD2	2:S0:158:VAL:HG23	1.98	0.44
3:S1:149:GLN:HE22	3:S1:154:SER:HB3	2.12	0.44
3:S1:229:MET:HA	3:S1:232:HIS:ND1	2.32	0.44
3:S1:36:SER:HB3	3:S1:231:LEU:HD22	1.98	0.44
3:S1:88:VAL:HG22	3:S1:98:THR:HG22	5.35	0.44
5:S3:119:ALA:O	5:S3:123:VAL:HG23	2.17	0.44
6:S4:68:ARG:HH11	6:S4:76:VAL:HG21	1.83	0.44
8:S6:191:ARG:HD3	8:S6:191:ARG:HA	4.05	0.44
36:1:1067:U:H2'	36:1:1068:C:C6	2.52	0.44
36:1:1230:G:H2'	36:1:1231:A:H8	1.83	0.44
36:1:637:C:H4'	36:1:638:C:OP1	2.17	0.44
36:1:863:C:H2'	36:1:864:G:O4'	2.17	0.44
1:2:947:U:H2'	1:2:948:G:C8	2.52	0.44
36:5:556:U:H5'	36:5:557:A:C2	2.52	0.44
36:5:621:A:H2'	36:5:622:A:C8	2.53	0.44
1:6:1634:C:H4'	1:6:1635:A:OP2	2.16	0.44
1:6:846:G:H2'	1:6:847:A:C8	2.53	0.44
13:C1:78:THR:HG21	13:C1:118:GLN:HA	3.46	0.44
15:C3:73:ARG:O	15:C3:77:SER:OG	2.19	0.44
17:C5:96:ILE:HD13	17:C5:116:LEU:HB3	2.52	0.44
18:C6:115:THR:HB	18:C6:118:ILE:O	2.17	0.44
20:C8:33:THR:C	20:C8:35:ILE:H	2.20	0.44
21:C9:111:ILE:HG23	21:C9:113:ILE:HG13	1.99	0.44
21:C9:28:LEU:HD12	21:C9:29:GLU:H	1.82	0.44
24:D2:96:ALA:HB1	24:D2:98:GLN:HG2	1.98	0.44
26:D4:36:SER:HB3	26:D4:39:GLU:HB3	1.99	0.44
26:D4:89:TYR:O	26:D4:92:VAL:HG22	5.11	0.44
1:2:1597:A:OP1	31:D9:19:ARG:NH2	2.50	0.44
40:L3:37:ARG:HA	40:L3:186:GLY:HA2	2.67	0.44
40:L3:296:THR:HG21	40:L3:356:LEU:HB2	1.98	0.44
41:L4:193:LYS:HE3	41:L4:193:LYS:HB2	2.89	0.44
42:L5:90:HIS:NE2	42:L5:229:ASP:OD2	3.52	0.44
44:L7:68:ASP:O	44:L7:71:ALA:N	4.64	0.44
48:M1:152:HIS:O	48:M1:153:LYS:HG2	4.79	0.44
48:M1:75:LYS:O	48:M1:79:ILE:HG13	2.34	0.44
52:M6:171:LYS:O	52:M6:175:THR:HG22	3.96	0.44
54:M8:123:THR:OG1	54:M8:125:ASP:OD2	2.20	0.44
56:N0:14:LEU:H	56:N0:56:GLY:HA2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:N1:52:MET:HA	57:N1:95:HIS:CD2	2.93	0.44
60:N4:52:THR:O	60:N4:56:ARG:HG3	2.17	0.44
63:N7:34:LYS:O	63:N7:34:LYS:NZ	4.24	0.44
63:N7:36:HIS:H	63:N7:37:PRO:HD3	2.97	0.44
68:O2:104:ASN:O	68:O2:108:ILE:HG13	2.17	0.44
74:O8:12:LEU:HA	74:O8:12:LEU:HD13	4.27	0.44
4:S2:150:GLN:HA	4:S2:151:PRO:HD3	1.79	0.44
8:S6:93:LYS:NZ	8:S6:93:LYS:HB2	4.89	0.44
9:S7:76:LYS:HG2	9:S7:76:LYS:H	1.54	0.44
11:S9:110:GLN:OE1	11:S9:126:ARG:HG2	2.60	0.44
34:SR:18:GLY:O	34:SR:308:ASN:HA	2.42	0.44
34:SR:274:LEU:HD13	34:SR:313:TRP:CD2	2.51	0.44
36:1:2440:G:H1	36:1:2507:C:H42	1.66	0.44
36:1:2704:A:O2'	36:1:2705:A:O5'	2.33	0.44
36:1:381:U:H2'	36:1:382:U:H6	1.82	0.44
36:1:386:A:C5	36:1:387:A:H1'	2.52	0.44
36:1:818:C:C2	36:1:920:A:H5'	2.52	0.44
1:2:1229:G:HO2'	1:2:1255:G:N2	2.16	0.44
1:2:1:U:C4	11:S9:54:ARG:HG3	2.51	0.44
1:2:625:C:H2'	1:2:626:U:C6	2.53	0.44
45:L8:157:VAL:HG13	36:5:147:U:C4	127.85	0.44
36:5:508:U:H2'	36:5:509:U:C6	2.53	0.44
1:6:1274:C:H4'	1:6:1275:A:O5'	2.18	0.44
1:6:1699:G:N1	1:6:1701:A:H5"	2.32	0.44
1:6:691:C:H2'	1:6:692:C:H6	1.82	0.44
1:6:828:U:O4	1:6:829:A:N6	2.50	0.44
1:6:830:U:H2'	1:6:831:U:H5'	2.00	0.44
14:C2:126:TRP:O	14:C2:128:ALA:N	2.50	0.44
1:2:886:U:O2'	16:C4:121:VAL:O	2.23	0.44
19:C7:41:ILE:HD13	19:C7:47:ARG:HA	1.99	0.44
39:L2:58:LEU:HD13	39:L2:75:ILE:HG21	1.99	0.44
40:L3:138:ALA:O	40:L3:140:ASP:N	3.90	0.44
36:1:3037:U:H5"	40:L3:348:ARG:NH1	2.32	0.44
41:L4:180:LYS:HA	36:5:1386:A:N3	118.44	0.44
41:L4:263:GLY:HA2	41:L4:268:ALA:O	3.92	0.44
44:L7:123:THR:O	44:L7:126:LEU:HB2	2.28	0.44
39:L2:64:ARG:HH22	45:L8:38:GLN:HA	3.47	0.44
47:M0:4:ARG:HG3	47:M0:8:CYS:SG	6.12	0.44
50:M4:32:LEU:HD11	50:M4:94:TRP:CG	2.62	0.44
57:N1:46:GLY:O	57:N1:49:GLN:NE2	2.49	0.44
61:N5:47:ALA:HB3	71:O5:77:PRO:HG3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:N7:14:VAL:HG23	70:O4:89:ILE:HB	4.16	0.44
65:N9:35:VAL:HG12	65:N9:40:ARG:HG3	1.99	0.44
68:O2:24:ARG:HG2	68:O2:25:TYR:CZ	2.80	0.44
74:O8:65:LEU:HD23	74:O8:68:SER:HB2	1.99	0.44
77:Q1:16:LYS:O	77:Q1:20:VAL:HG23	2.17	0.44
79:Q3:33:GLN:HB3	79:Q3:69:TYR:HB3	1.99	0.44
4:S2:106:ASP:OD2	4:S2:110:HIS:ND1	2.49	0.44
5:S3:122:VAL:O	5:S3:126:VAL:HG23	2.38	0.44
8:S6:175:ILE:HB	8:S6:178:LEU:HD22	2.74	0.44
19:C7:30:THR:HG22	34:SR:127:ARG:NH2	3.79	0.44
34:SR:112:SER:HB2	34:SR:153:GLN:HA	2.36	0.44
36:1:1364:C:H5''	54:M8:3:ILE:HD13	1.99	0.44
36:1:3328:G:C2	36:1:3379:C:C2	3.05	0.44
1:2:1010:C:H2'	1:2:1011:G:O4'	2.16	0.44
1:2:1147:A:H2'	1:2:1148:C:C6	2.51	0.44
1:2:226:A:H2'	1:2:227:U:H5'	2.00	0.44
1:2:688:G:H2'	1:2:689:G:H8	1.82	0.44
1:2:76:A:N6	1:2:80:A:O2'	2.48	0.44
37:3:43:U:C4	37:3:44:C:C4	3.06	0.44
38:4:11:C:H2'	38:4:12:A:O4'	2.16	0.44
36:5:598:A:H61	36:5:605:U:H3	1.66	0.44
36:5:730:C:H2'	36:5:731:U:H6	1.83	0.44
1:6:1243:G:H5''	1:6:1243:G:N3	2.32	0.44
34:SR:282:SER:OG	1:6:1394:G:OP1	416.83	0.44
1:6:1620:C:HO2'	1:6:1621:U:P	2.39	0.44
10:S8:142:LYS:NZ	1:6:187:G:OP2	274.93	0.44
1:6:333:A:C6	1:6:334:G:C6	3.06	0.44
1:6:74:U:H5''	1:6:75:U:OP2	2.17	0.44
1:6:472:U:O2'	1:6:769:A:N3	2.38	0.44
71:O5:63:ARG:NH2	38:8:97:A:OP1	56.78	0.44
21:C9:125:SER:O	21:C9:129:GLN:HG3	2.18	0.44
22:D0:108:ILE:H	22:D0:108:ILE:HG13	1.54	0.44
24:D2:94:LEU:HD11	24:D2:102:VAL:HG23	2.07	0.44
24:D2:107:SER:HA	1:6:804:A:C8	368.34	0.44
41:L4:110:ASN:ND2	51:M5:201:ARG:HB3	2.32	0.44
41:L4:156:LEU:HD13	41:L4:215:ILE:HG12	2.00	0.44
44:L7:31:ALA:HA	44:L7:34:LYS:HB2	3.29	0.44
44:L7:86:VAL:HG13	44:L7:136:TYR:HB3	1.98	0.44
50:M4:115:PHE:O	50:M4:118:PHE:HB3	2.39	0.44
50:M4:21:VAL:HB	50:M4:63:VAL:HG13	1.99	0.44
52:M6:10:ASP:OD1	52:M6:37:ARG:NH2	3.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2992:U:H1'	53:M7:69:ARG:NH2	2.33	0.44
55:M9:77:GLY:O	55:M9:81:ARG:HD3	2.17	0.44
67:O1:25:PHE:HD2	67:O1:28:ARG:HD2	1.83	0.44
67:O1:13:THR:HG23	67:O1:72:ARG:HH11	1.83	0.44
68:O2:24:ARG:HD3	68:O2:25:TYR:CZ	2.58	0.44
36:1:1403:C:H5'	68:O2:67:SER:HB3	1.99	0.44
2:S0:175:TYR:CD1	2:S0:199:PRO:HA	2.53	0.44
5:S3:135:GLU:HB3	5:S3:187:LYS:HB3	3.56	0.44
5:S3:167:PHE:HA	5:S3:190:ARG:HE	4.64	0.44
6:S4:33:ALA:O	1:6:121:U:O2'	354.30	0.44
7:S5:42:LEU:H	7:S5:42:LEU:HD23	1.82	0.44
8:S6:24:ILE:O	8:S6:26:VAL:N	2.50	0.44
9:S7:50:ASP:HA	9:S7:56:LYS:HG2	2.80	0.44
35:SM:49:LYS:HG3	35:SM:50:ASN:OD1	6.49	0.44
34:SR:103:PHE:CD1	34:SR:138:GLY:HA2	2.57	0.44
36:1:109:A:H4'	36:1:110:G:OP1	2.18	0.44
36:1:1942:U:O2'	36:1:3345:G:O2'	2.12	0.44
36:1:748:U:H2'	36:1:749:C:C6	2.53	0.44
36:5:1069:C:H2'	36:5:1070:U:H6	1.82	0.44
36:5:1500:G:H2'	36:5:1501:U:O4'	2.18	0.44
1:6:1689:A:H2'	1:6:1690:G:C8	2.50	0.44
25:D3:63:GLN:HG3	1:6:1755:A:C8	345.62	0.44
1:6:188:A:H5''	1:6:189:C:OP2	2.18	0.44
10:S8:138:ASN:HD22	1:6:197:A:H61	279.50	0.44
18:C6:41:PRO:HG2	18:C6:78:VAL:HG21	2.00	0.44
19:C7:5:ARG:HB2	19:C7:10:LYS:HE2	2.00	0.44
19:C7:20:TYR:CZ	19:C7:38:ILE:HG13	2.52	0.44
23:D1:38:LYS:HG3	23:D1:49:GLU:HG3	2.00	0.44
25:D3:23:ARG:HA	25:D3:23:ARG:HD2	1.76	0.44
25:D3:88:PRO:O	25:D3:89:ASN:HB2	2.17	0.44
26:D4:8:ARG:NE	26:D4:28:LEU:HD11	3.37	0.44
27:D5:46:LYS:HB2	27:D5:46:LYS:HE3	4.18	0.44
27:D5:54:VAL:N	27:D5:55:PRO:HD2	2.32	0.44
28:D6:41:ILE:HG22	28:D6:68:TYR:HB3	1.99	0.44
28:D6:71:LEU:HD13	28:D6:73:TYR:OH	5.90	0.44
29:D7:14:SER:O	29:D7:18:LYS:HE3	2.17	0.44
30:D8:54:LEU:HD12	30:D8:55:VAL:H	4.34	0.44
30:D8:64:ARG:HB3	30:D8:65:ARG:H	1.62	0.44
39:L2:65:ASP:HB3	39:L2:68:LYS:O	2.36	0.44
40:L3:370:PHE:CD2	40:L3:376:LYS:HG3	2.53	0.44
41:L4:355:PHE:CE1	44:L7:70:LYS:HD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:88:TYR:CZ	46:L9:184:LYS:HG2	2.53	0.44
51:M5:172:ARG:HH22	36:5:63:A:P	101.96	0.44
53:M7:30:ARG:HA	53:M7:119:VAL:CG1	2.61	0.44
36:1:3067:C:H3'	55:M9:62:ARG:NH1	2.33	0.44
61:N5:40:LEU:HB3	61:N5:41:ALA:H	3.50	0.44
63:N7:135:ARG:HG2	63:N7:135:ARG:HH21	1.83	0.44
64:N8:16:SER:HA	36:5:942:U:C4	170.45	0.44
64:N8:7:LYS:HA	64:N8:7:LYS:HD3	1.73	0.44
71:O5:9:LEU:HB3	71:O5:17:LEU:HD21	2.14	0.44
71:O5:83:LYS:O	71:O5:85:THR:N	3.05	0.44
74:O8:17:ARG:O	74:O8:20:VAL:HG23	2.18	0.44
74:O8:15:THR:HG22	74:O8:45:VAL:HG11	2.00	0.44
36:1:1491:A:N7	75:O9:2:ALA:HB3	2.32	0.44
79:Q3:37:TYR:HB2	79:Q3:47:VAL:HB	1.98	0.44
79:Q3:3:LYS:HE2	79:Q3:3:LYS:HB3	1.74	0.44
2:S0:126:PRO:HA	2:S0:133:ILE:HD11	1.99	0.44
7:S5:79:ASN:OD1	7:S5:83:ARG:NH2	2.97	0.44
9:S7:67:LEU:HD22	9:S7:71:HIS:CD2	2.52	0.44
36:1:1765:U:C5	55:M9:46:LYS:HE2	2.53	0.44
36:1:3113:A:H2'	36:1:3114:A:O4'	2.18	0.44
36:1:3393:U:H2'	36:1:3394:U:C6	2.52	0.44
36:1:439:C:H3'	36:1:440:A:C8	2.53	0.44
36:1:830:A:H2'	36:1:831:G:O4'	2.18	0.44
1:2:1711:C:H2'	1:2:1712:A:H5''	1.98	0.44
1:2:1776:A:H2'	1:2:1777:G:C8	2.52	0.44
1:2:273:G:H1	1:2:283:U:H3	1.65	0.44
1:2:416:A:H4'	1:2:417:A:OP2	2.17	0.44
1:2:642:G:H2'	1:2:643:G:C8	2.53	0.44
37:3:61:G:H2'	37:3:62:U:H6	1.81	0.44
47:M0:193:ASP:OD1	36:5:1010:G:N2	336.16	0.44
36:5:106:A:H2'	36:5:107:A:O4'	2.17	0.44
36:5:2426:U:H2'	36:5:2427:U:C6	2.53	0.44
36:5:2438:A:H2'	36:5:2439:A:H5''	1.99	0.44
36:5:2653:C:H1'	36:5:2694:A:C2	2.53	0.44
36:5:2836:C:H5	36:5:2852:C:N4	2.02	0.44
36:5:327:A:H2'	36:5:328:U:C6	2.53	0.44
36:5:816:A:C8	36:5:906:A:C6	3.06	0.44
1:6:151:G:H22	1:6:163:G:N2	2.16	0.44
37:7:110:G:C6	37:7:111:U:C4	3.06	0.44
15:C3:92:ILE:O	15:C3:96:VAL:HG23	2.17	0.44
40:L3:186:GLY:O	40:L3:190:GLU:HB2	2.22	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:151:ARG:HD2	44:L7:244:ASN:ND2	2.33	0.44
46:L9:162:GLN:HB2	46:L9:179:ILE:O	2.24	0.44
51:M5:58:GLY:HA3	51:M5:142:ILE:HD13	1.98	0.44
52:M6:18:ARG:NH2	36:5:1318:A:OP1	276.92	0.44
59:N3:66:LYS:HD2	59:N3:68:GLU:HB2	5.20	0.44
68:O2:55:ILE:HA	68:O2:55:ILE:HD12	1.84	0.44
43:L6:31:ARG:HD2	69:O3:107:ILE:O	2.18	0.44
73:O7:59:THR:HG22	38:8:41:A:O2'	91.59	0.44
74:O8:26:LYS:HE2	36:5:1751:G:H5''	128.33	0.44
76:Q0:128:LYS:H	76:Q0:128:LYS:HG3	4.12	0.44
4:S2:54:GLU:O	4:S2:58:LEU:HB2	3.06	0.44
5:S3:34:TYR:CE2	5:S3:37:VAL:HG13	2.77	0.44
9:S7:30:SER:HB3	9:S7:34:LEU:HD12	1.98	0.44
35:SM:65:THR:O	35:SM:67:GLY:N	5.05	0.44
36:1:1126:G:H5''	47:M0:119:TRP:CZ3	2.53	0.44
36:1:1820:U:H1'	36:1:1821:U:OP2	2.17	0.44
36:1:562:C:H2'	36:1:563:U:C6	2.53	0.44
1:2:1035:G:OP1	15:C3:9:LYS:HD2	2.17	0.44
1:2:1236:A:H2'	1:2:1237:G:O4'	2.18	0.44
1:2:144:U:C2	1:2:145:A:C8	3.05	0.44
1:2:1639:C:H2'	1:2:1640:C:O4'	2.17	0.44
1:2:830:U:O2'	1:2:831:U:H6	2.01	0.44
56:N0:90:MET:HG2	36:5:1213:G:H4'	318.28	0.44
36:5:282:G:H3'	36:5:282:G:C8	2.53	0.44
36:5:3084:C:H2'	36:5:3085:G:O4'	2.18	0.44
36:5:311:C:H42	36:5:2778:G:H1	1.66	0.44
36:5:3242:G:H21	36:5:3245:A:H5''	1.83	0.44
50:M4:79:ALA:HB2	36:5:525:C:H5''	344.75	0.44
36:5:664:U:H2'	36:5:665:A:C8	2.53	0.44
1:6:1119:G:H2'	1:6:1120:U:O4'	2.17	0.44
1:6:1645:G:H1	1:6:1756[A]:A:N6	2.16	0.44
1:6:187:G:H4'	1:6:188:A:OP1	2.18	0.44
1:6:542:A:C8	1:6:543:C:H2'	2.53	0.44
16:C4:102:LEU:HD13	28:D6:53:LEU:HD21	4.47	0.44
19:C7:107:SER:O	19:C7:110:VAL:HG23	3.95	0.44
21:C9:105:LEU:HB3	21:C9:122:ARG:HE	1.83	0.44
21:C9:28:LEU:HB3	21:C9:29:GLU:H	3.74	0.44
21:C9:35:ASP:OD2	21:C9:36:ILE:HG23	3.60	0.44
26:D4:130:ALA:HA	26:D4:133:ASN:OD1	3.18	0.44
40:L3:165:GLN:OE1	40:L3:167:ARG:NH2	2.80	0.44
40:L3:284:ARG:HB3	40:L3:323:MET:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:53:MET:HG2	40:L3:77:THR:HG22	2.02	0.44
41:L4:181:VAL:HG21	41:L4:224:GLY:HA3	2.18	0.44
41:L4:291:ASN:HA	41:L4:296:GLN:NE2	2.32	0.44
45:L8:49:TYR:HD2	36:5:2587:U:H4'	178.98	0.44
47:M0:54:SER:HA	47:M0:163:GLN:HB3	2.74	0.44
43:L6:51:ARG:NH1	50:M4:114:ASP:OD2	2.56	0.44
52:M6:23:VAL:HG13	52:M6:33:ILE:HG21	2.32	0.44
36:1:1507:G:N7	53:M7:129:THR:HG22	2.32	0.44
36:1:2355:G:H4'	53:M7:139:TYR:CD2	2.52	0.44
53:M7:73:GLY:HA3	53:M7:78:VAL:HG12	2.00	0.44
59:N3:13:ILE:HD12	59:N3:85:TRP:CG	5.11	0.44
64:N8:74:ASN:CB	64:N8:115:LYS:HB2	2.43	0.44
64:N8:59:ARG:NH1	36:5:90:C:OP1	152.29	0.44
51:M5:6:TYR:CD2	72:O6:40:VAL:HG13	2.68	0.44
75:O9:28:ARG:HH11	75:O9:36:ARG:HH11	6.23	0.44
78:Q2:63:LYS:HE2	78:Q2:87:ARG:NH2	2.33	0.44
2:S0:3:LEU:HA	2:S0:4:PRO:HD2	2.07	0.44
7:S5:26:ALA:HB3	18:C6:28:LEU:HB3	2.07	0.44
34:SR:48:THR:HG22	34:SR:55:GLY:HA2	5.63	0.44
36:1:1064:A:H5''	36:1:1066:G:O4'	2.18	0.44
36:1:116:A:OP1	72:O6:36:ARG:NH1	2.50	0.44
36:1:1522:U:OP2	61:N5:121:LYS:NZ	2.51	0.44
36:1:2406:C:H2'	36:1:2407:C:C6	2.53	0.44
36:1:3166:C:H2'	36:1:3167:A:O4'	2.18	0.44
1:2:1528:U:H2'	1:2:1529:C:H6	1.83	0.44
1:2:1698:G:H22	1:2:1703:C:H42	1.65	0.44
1:2:1796:C:OP2	28:D6:5:ARG:NH1	2.41	0.44
1:2:542:A:H5''	1:2:544:A:C8	2.53	0.44
1:2:67:A:C2	1:2:69:G:H1'	2.53	0.44
1:2:808:U:H2'	1:2:809:A:C8	2.52	0.44
36:5:107:A:H2'	36:5:108:A:O4'	2.18	0.44
1:6:1196:A:H4'	1:6:1197:C:O5'	2.18	0.44
1:6:1458:G:H5''	1:6:1459:C:OP2	2.18	0.44
12:C0:11:ILE:HD11	12:C0:42:VAL:HG22	1.98	0.44
15:C3:118:ILE:HA	15:C3:121:ARG:NH1	3.58	0.44
17:C5:64:LYS:HA	17:C5:73:PRO:HB3	1.99	0.44
18:C6:13:LYS:O	18:C6:76:SER:OG	2.35	0.44
25:D3:30:LYS:O	25:D3:34:LEU:HG	2.47	0.44
40:L3:146:ARG:HA	40:L3:146:ARG:NE	2.93	0.44
40:L3:3:HIS:O	40:L3:5:LYS:N	2.50	0.44
41:L4:52:VAL:HG11	41:L4:99:MET:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3267:A:H2'	43:L6:69:PHE:CZ	2.53	0.44
42:L5:34:LYS:HD2	57:N1:30:TYR:CZ	2.53	0.44
65:N9:28:LYS:HD3	65:N9:28:LYS:HA	1.76	0.44
68:O2:16:LYS:HD2	68:O2:18:LYS:HG2	5.38	0.44
79:Q3:49:ARG:HB3	79:Q3:50:GLY:H	1.63	0.44
10:S8:184:LEU:HD21	10:S8:192:TYR:CD2	3.12	0.44
10:S8:72:ILE:HG12	10:S8:112:TRP:CE2	2.80	0.44
35:SM:43:ASP:HA	35:SM:44:PRO:HD3	2.56	0.44
34:SR:131:ILE:HG23	34:SR:154:VAL:HG11	2.00	0.44
34:SR:19:TRP:HB2	34:SR:38:ARG:HD2	2.00	0.44
34:SR:240:VAL:HG22	34:SR:256:THR:HG22	1.99	0.44
34:SR:61:PHE:HD1	34:SR:92:TRP:CE3	2.36	0.44
36:1:2611:U:H2'	36:1:2612:U:C6	2.53	0.44
36:1:507:U:H2'	36:1:508:U:C6	2.53	0.44
36:1:637:C:H2'	36:1:637:C:H6	1.54	0.44
36:1:853:G:N7	79:Q3:2:ALA:N	2.65	0.44
1:2:1157:A:H2'	1:2:1160:A:N7	2.33	0.44
1:2:1165:G:C6	1:2:1166:A:C6	3.06	0.44
1:2:1460:A:OP2	35:SM:68:ARG:HD3	2.18	0.44
1:2:609:U:H4'	1:2:610:G:O5'	2.18	0.44
1:2:736:C:H42	1:2:737:A:H62	1.66	0.44
36:5:2144:A:H1'	36:5:2281:A:N6	2.33	0.44
36:5:3383:G:H2'	36:5:3384:U:H6	1.83	0.44
36:5:589:A:N6	36:5:610:G:H1'	2.32	0.44
41:L4:209:TYR:OH	36:5:689:U:O4	86.80	0.44
36:5:996:A:C2	36:5:1054:A:C4	3.06	0.44
1:6:1204:A:H2'	1:6:1205:C:O4'	2.17	0.44
1:6:1638:G:C2	1:6:1639:C:H1'	2.53	0.44
1:6:250:C:H2'	1:6:251:A:C8	2.52	0.44
1:6:420:A:H2'	1:6:421:A:O4'	2.17	0.44
21:C9:14:PHE:HZ	21:C9:132:LEU:HD12	4.78	0.44
1:2:1590:G:OP1	21:C9:91:TYR:HB2	2.18	0.44
26:D4:83:LYS:HB2	26:D4:83:LYS:HE2	4.56	0.44
28:D6:10:ARG:NE	1:6:1795:U:O2	329.62	0.44
28:D6:38:ARG:NH2	1:6:1798:U:OP2	334.79	0.44
28:D6:59:TYR:HA	28:D6:60:PRO:HD3	2.48	0.44
40:L3:293:ASN:HB2	40:L3:305:ILE:H	2.81	0.44
40:L3:332:ARG:NH1	40:L3:333:LYS:HD3	2.32	0.44
41:L4:300:ARG:HG2	54:M8:39:ARG:O	3.10	0.44
42:L5:86:TYR:CE1	42:L5:247:ILE:HA	2.53	0.44
42:L5:40:HIS:HB3	42:L5:43:LYS:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:88:TYR:CE2	46:L9:184:LYS:HG2	2.52	0.44
46:L9:52:LEU:HA	46:L9:52:LEU:HD23	1.81	0.44
49:M3:94:GLY:HA3	71:O5:116:TYR:OH	2.17	0.44
51:M5:27:VAL:HB	51:M5:122:ASN:ND2	2.37	0.44
51:M5:183:THR:HB	51:M5:187:ARG:HG3	1.99	0.44
53:M7:75:GLU:OE2	36:5:3392:U:O2'	168.25	0.44
54:M8:40:THR:C	54:M8:42:ALA:H	2.21	0.44
57:N1:105:PHE:O	57:N1:109:VAL:HG23	2.58	0.44
64:N8:104:THR:OG1	64:N8:126:LYS:O	2.34	0.44
72:O6:11:LEU:HA	72:O6:11:LEU:HD13	1.78	0.44
73:O7:19:CYS:O	73:O7:23:GLY:N	2.38	0.44
78:Q2:3:ASN:HA	78:Q2:92:GLU:O	2.17	0.44
4:S2:165:VAL:HA	4:S2:201:ASN:O	2.17	0.44
1:2:6:G:OP2	4:S2:205:ARG:HD2	2.18	0.44
5:S3:37:VAL:HG12	5:S3:50:ILE:HA	2.80	0.44
8:S6:189:HIS:CE1	8:S6:193:LEU:HD12	2.66	0.44
9:S7:30:SER:HB2	9:S7:34:LEU:HB2	2.06	0.44
11:S9:93:LEU:O	11:S9:96:VAL:HG22	2.26	0.44
1:2:576:G:OP2	35:SM:102:THR:HG21	2.17	0.44
36:1:1830:G:O3'	61:N5:91:ASN:HB2	2.17	0.43
36:1:2102:U:H2'	36:1:2103:U:H6	1.83	0.43
36:1:2203:U:H2'	36:1:2204:C:C6	2.53	0.43
36:1:278:U:H2'	36:1:279:U:C6	2.53	0.43
36:1:3386:G:H2'	36:1:3387:U:H6	1.82	0.43
36:5:1952:G:H1	36:5:2094:C:H42	1.66	0.43
36:5:2271:A:N7	36:5:2272:G:C6	2.86	0.43
36:5:945:C:H2'	36:5:946:U:C6	2.53	0.43
1:6:114:C:H6	1:6:114:C:H5''	1.83	0.43
1:6:1553:G:N2	1:6:1555:A:H3'	2.33	0.43
1:6:1783:C:H2'	1:6:1784:C:H6	1.82	0.43
1:6:183:U:H2'	1:6:184:C:O4'	2.17	0.43
10:S8:137:LYS:HE3	1:6:191:C:N4	268.29	0.43
1:6:515:A:N6	1:6:537:G:O2'	2.45	0.43
21:C9:31:PRO:HG3	21:C9:103:LYS:HD3	1.99	0.43
25:D3:126:LYS:HA	25:D3:131:SER:HA	2.00	0.43
87:D:3401:SPS:O1	87:D:3401:SPS:H91	2.18	0.43
25:D3:69:ARG:HD2	25:D3:117:ILE:HG12	1.99	0.43
28:D6:82:ARG:O	28:D6:84:VAL:HG12	2.18	0.43
29:D7:3:LEU:HA	29:D7:3:LEU:HD22	1.80	0.43
29:D7:3:LEU:HD23	29:D7:3:LEU:HA	2.41	0.43
11:S9:28:LEU:HD11	32:E0:39:LEU:HB3	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:L2:113:VAL:HG12	39:L2:166:ILE:HD13	2.00	0.43
36:1:911:C:H42	39:L2:3:ARG:HD3	1.82	0.43
40:L3:306:THR:HA	40:L3:307:PRO:HD3	1.87	0.43
41:L4:3:ARG:O	41:L4:5:GLN:N	2.52	0.43
42:L5:119:TYR:OH	42:L5:141:PRO:HD3	2.18	0.43
42:L5:276:LYS:HG2	42:L5:276:LYS:H	3.24	0.43
43:L6:130:ILE:CG2	43:L6:135:VAL:HG23	2.48	0.43
44:L7:89:ILE:HG22	44:L7:220:PHE:HE1	1.83	0.43
46:L9:90:MET:HE2	46:L9:179:ILE:HG22	3.05	0.43
57:N1:101:CYS:O	57:N1:104:GLU:HG3	4.21	0.43
62:N6:37:LYS:HA	62:N6:40:ARG:HG2	6.10	0.43
64:N8:112:ILE:HB	64:N8:130:VAL:HG12	2.00	0.43
66:O0:100:ILE:O	66:O0:105:ALA:HB3	2.31	0.43
78:Q2:10:THR:O	78:Q2:20:HIS:HA	2.50	0.43
78:Q2:4:VAL:O	78:Q2:94:GLY:N	4.52	0.43
2:S0:53:THR:HA	2:S0:161:PRO:HG2	2.20	0.43
2:S0:162:CYS:HG	2:S0:163:ASN:H	1.56	0.43
2:S0:30:GLN:NE2	2:S0:32:HIS:HB2	9.76	0.43
2:S0:88:LYS:HB3	2:S0:202:TYR:CZ	2.84	0.43
3:S1:176:VAL:O	3:S1:177:GLN:HG2	2.18	0.43
7:S5:27:THR:HA	7:S5:28:PRO:HD2	2.01	0.43
10:S8:196:LEU:HD12	10:S8:196:LEU:HA	1.73	0.43
11:S9:150:LEU:C	11:S9:152:SER:H	2.33	0.43
34:SR:224:ASN:O	34:SR:228:LYS:HA	2.62	0.43
36:1:1177:G:C5	69:O3:20:LYS:HD3	2.53	0.43
36:1:210:U:C2	36:1:230:U:H4'	2.53	0.43
36:1:2655:U:H4'	36:1:2656:A:O4'	2.17	0.43
36:1:305:U:C5	36:1:2776:C:H1'	2.53	0.43
36:1:3077:A:N6	36:1:3080:G:C5	2.87	0.43
36:1:3364:C:H2'	36:1:3365:U:C6	2.52	0.43
36:1:655:C:H5"	68:O2:26:HIS:HB2	2.00	0.43
1:2:1595:U:N3	1:2:1600:A:H2	2.14	0.43
1:2:814:A:C8	1:2:816:G:C8	3.06	0.43
36:5:1013:G:H2'	36:5:1014:U:O4'	2.18	0.43
36:5:1107:C:H2'	36:5:1108:U:H6	1.83	0.43
36:5:1232:C:H2'	36:5:1233:G:C8	2.50	0.43
36:5:191:U:H2'	36:5:192:C:C6	2.53	0.43
36:5:2608:G:O2'	36:5:2609:A:H5'	2.18	0.43
36:5:3218:A:H4'	36:5:3219:G:O5'	2.18	0.43
36:5:3257:C:H2'	36:5:3258:U:O4'	2.17	0.43
36:5:80:G:H2'	36:5:81:C:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:C9:79:LEU:HD13	1:6:1523:G:C8	408.18	0.43
1:6:224:C:H2'	1:6:225:A:H8	1.82	0.43
1:6:386:G:C6	1:6:387:A:N6	2.86	0.43
35:SM:25:ILE:HG12	37:7:39:C:H5'	291.24	0.43
42:L5:33:ARG:HD2	37:7:7:G:OP1	271.90	0.43
12:C0:55:VAL:HG23	12:C0:67:THR:O	2.39	0.43
14:C2:81:ASP:OD1	14:C2:81:ASP:N	2.51	0.43
15:C3:22:ALA:HB1	15:C3:23:PRO:CA	2.48	0.43
19:C7:71:PHE:CD1	19:C7:73:LEU:HB3	2.53	0.43
20:C8:82:PRO:HG3	21:C9:36:ILE:HD12	2.65	0.43
25:D3:107:PHE:HA	25:D3:107:PHE:HD1	1.68	0.43
36:1:3242:G:N7	40:L3:150:ARG:HD2	2.33	0.43
42:L5:202:GLY:O	42:L5:206:GLN:HG3	4.68	0.43
47:M0:205:SER:OG	47:M0:208:ASN:OD1	3.20	0.43
48:M1:14:ILE:HD12	48:M1:77:GLU:HG2	2.00	0.43
51:M5:151:ILE:HA	51:M5:151:ILE:HD13	1.85	0.43
51:M5:169:LYS:HE3	36:5:63:A:OP1	101.81	0.43
55:M9:99:LEU:O	55:M9:103:ARG:HB2	2.18	0.43
64:N8:104:THR:HG21	64:N8:112:ILE:HD11	2.00	0.43
64:N8:90:TYR:CG	64:N8:100:PRO:HG3	2.53	0.43
65:N9:28:LYS:HD2	65:N9:29:TYR:CD1	2.53	0.43
73:O7:14:LYS:HE2	75:O9:51:ILE:HG13	1.99	0.43
78:Q2:45:ARG:HH22	36:5:283:G:P	146.49	0.43
2:S0:76:ILE:O	2:S0:124:THR:HG23	2.19	0.43
2:S0:74:VAL:HG12	2:S0:76:ILE:HG13	3.24	0.43
4:S2:165:VAL:HG11	4:S2:210:THR:OG1	2.18	0.43
6:S4:51:ARG:HA	6:S4:51:ARG:HE	2.07	0.43
7:S5:57:SER:HB2	30:D8:53:ILE:O	2.80	0.43
7:S5:61:TYR:OH	30:D8:49:ARG:HD3	3.03	0.43
10:S8:29:LEU:HD11	10:S8:31:ARG:NH1	2.33	0.43
34:SR:192:PHE:HD1	34:SR:223:TRP:CE3	2.36	0.43
36:1:1355:A:H4'	36:1:1356:U:O5'	2.18	0.43
36:1:1429:G:C2	41:L4:99:MET:HE2	2.54	0.43
36:1:689:U:O4	41:L4:209:TYR:OH	2.26	0.43
1:2:637:C:OP1	24:D2:32:LYS:HG3	2.18	0.43
36:5:953:G:C8	36:5:1117:G:C8	3.06	0.43
55:M9:8:LYS:NZ	36:5:1473:G:OP2	125.39	0.43
75:O9:42:ARG:HH22	36:5:1494:U:P	107.40	0.43
36:5:1557:A:N7	36:5:1559:A:N6	2.66	0.43
55:M9:134:HIS:HD2	36:5:1947:G:H5'	235.61	0.43
36:5:2267:C:H2'	36:5:2268:U:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:251:CYS:SG	36:5:2944:U:H1'	224.84	0.43
36:5:2953:U:H2'	36:5:2954:U:C6	2.53	0.43
36:5:3017:A:H2'	36:5:3018:C:H6	1.83	0.43
36:5:437:G:H1	36:5:622:A:N6	2.11	0.43
36:5:595:G:C8	36:5:609:G:C6	3.06	0.43
1:6:1352:G:H2'	1:6:1353:U:O4'	2.17	0.43
1:6:1754:A:H4'	1:6:1755:A:O5'	2.17	0.43
1:6:1645:G:H1	1:6:1756[A]:A:H61	1.65	0.43
25:D3:112:LYS:NZ	1:6:19:A:OP1	348.41	0.43
1:6:640:U:H2'	1:6:641:G:O4'	2.17	0.43
1:6:834:G:H3'	1:6:835:U:C5	2.54	0.43
37:7:26:C:H2'	37:7:27:A:O4'	2.19	0.43
37:7:57:G:C8	37:7:58:C:C5	3.06	0.43
47:M0:57:LEU:HD12	37:7:93:C:H5'	279.95	0.43
1:2:1389:C:O2'	19:C7:52:GLY:HA3	2.18	0.43
21:C9:137:ALA:O	21:C9:141:GLU:N	2.90	0.43
25:D3:86:PHE:CE1	25:D3:88:PRO:HA	2.53	0.43
25:D3:56:LYS:HZ3	25:D3:97:ASP:H	1.66	0.43
28:D6:51:ARG:NH2	28:D6:55:GLU:OE1	5.38	0.43
25:D3:57:LEU:HD13	32:E0:4:VAL:HG22	5.17	0.43
40:L3:21:ARG:HG3	36:5:2991:A:OP1	210.21	0.43
40:L3:287:LYS:O	40:L3:290:ASP:HB3	2.17	0.43
41:L4:354:VAL:HG11	57:N1:143:THR:HG21	2.00	0.43
42:L5:148:ILE:HD11	42:L5:160:PHE:CE1	2.54	0.43
42:L5:187:THR:O	42:L5:189:GLU:N	2.51	0.43
43:L6:153:PRO:O	43:L6:154:LEU:HB2	2.17	0.43
45:L8:78:PHE:O	45:L8:79:GLN:HB3	2.36	0.43
46:L9:70:THR:O	46:L9:74:LEU:HG	2.26	0.43
47:M0:34:TYR:O	47:M0:88:ARG:HA	2.44	0.43
49:M3:4:SER:OG	49:M3:5:LYS:HG3	2.87	0.43
52:M6:130:LYS:HD3	52:M6:131:PRO:HD2	5.32	0.43
53:M7:168:LEU:HD22	53:M7:176:ILE:HD11	1.99	0.43
53:M7:50:GLN:HB3	53:M7:55:GLN:HB3	2.54	0.43
60:N4:6:ASP:HA	60:N4:30:ARG:O	2.17	0.43
61:N5:105:VAL:HG13	61:N5:130:TYR:CG	2.54	0.43
63:N7:104:PRO:O	63:N7:108:GLU:HG3	2.19	0.43
75:O9:48:LYS:HD2	75:O9:48:LYS:HA	2.41	0.43
5:S3:179:GLN:HB3	5:S3:180:GLY:H	2.71	0.43
6:S4:31:PRO:HB2	6:S4:38:LEU:HB2	4.62	0.43
36:1:1264:G:N2	36:1:1265:U:O4	2.51	0.43
36:1:1593:A:N3	36:1:1615:C:O2'	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3151:U:OP2	40:L3:132:LYS:NZ	2.45	0.43
36:1:3295:A:H2'	36:1:3296:A:C8	2.54	0.43
36:1:3307:A:OP1	40:L3:226:PHE:HB2	2.16	0.43
1:2:1687:U:H1'	1:2:1715:G:N2	2.34	0.43
36:5:1072:G:H2'	36:5:1073:U:H6	1.83	0.43
36:5:1302:A:N1	36:5:2832:C:O2'	2.45	0.43
36:5:174:C:H2'	36:5:175:C:C6	2.53	0.43
36:5:348:A:N3	36:5:352:A:O2'	2.51	0.43
36:5:80:G:H2'	36:5:81:C:H6	1.83	0.43
36:5:871:U:H2'	36:5:872:U:C6	2.54	0.43
1:6:1557:U:O2'	1:6:1558:U:H2'	2.18	0.43
13:C1:121:ASP:OD1	13:C1:145:ALA:HB2	6.37	0.43
14:C2:60:VAL:HG13	14:C2:122:VAL:HG22	2.00	0.43
15:C3:27:LYS:HB2	15:C3:28:LEU:H	1.54	0.43
15:C3:84:ILE:HG22	15:C3:135:LEU:HD21	2.00	0.43
18:C6:26:LYS:HE3	18:C6:26:LYS:HB2	3.37	0.43
1:2:1390:U:OP1	19:C7:5:ARG:HD2	2.18	0.43
22:D0:37:VAL:HG21	22:D0:109:GLU:HB2	2.00	0.43
2:S0:52:LYS:HD2	23:D1:82:VAL:HA	1.99	0.43
26:D4:11:LYS:HB2	26:D4:24:VAL:HG23	2.09	0.43
31:D9:19:ARG:HG2	31:D9:19:ARG:H	1.54	0.43
33:E1:135:HIS:ND1	1:6:1250:U:O2	433.53	0.43
33:E1:82:LYS:O	33:E1:84:VAL:N	4.77	0.43
1:2:987:G:N1	39:L2:249:SER:HB2	2.34	0.43
46:L9:163:GLN:O	46:L9:166:ARG:HD3	2.16	0.43
47:M0:210:ILE:HG23	47:M0:217:PHE:CD2	2.53	0.43
49:M3:106:GLN:HG3	49:M3:110:ASP:OD2	2.17	0.43
49:M3:122:LYS:HB3	49:M3:122:LYS:HZ2	1.82	0.43
49:M3:157:ARG:HG2	49:M3:158:ALA:N	2.33	0.43
57:N1:17:ARG:HH12	57:N1:45:ASN:CG	3.57	0.43
65:N9:5:LYS:HG3	65:N9:6:ASN:N	2.33	0.43
68:O2:77:ALA:HB3	68:O2:81:ASP:OD2	2.69	0.43
72:O6:70:ARG:HG3	72:O6:87:VAL:HG21	2.00	0.43
73:O7:17:THR:HG22	73:O7:18:LEU:N	2.33	0.43
3:S1:157:GLN:HB2	3:S1:160:HIS:ND1	2.65	0.43
3:S1:144:ARG:HB3	3:S1:208:GLN:HB3	2.00	0.43
3:S1:105:PHE:CD2	3:S1:213:ARG:HA	2.53	0.43
4:S2:71:THR:O	4:S2:74:PRO:HD3	2.64	0.43
5:S3:148:LYS:HB2	35:SM:110:TRP:CZ2	2.54	0.43
8:S6:194:LYS:HE3	8:S6:194:LYS:HB2	4.31	0.43
8:S6:67:VAL:HG21	8:S6:99:GLY:HA2	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S8:9:HIS:O	10:S8:10:LYS:HB2	2.18	0.43
35:SM:23:LYS:NZ	35:SM:24:GLU:H	8.11	0.43
36:1:1362:G:H2'	36:1:1363:A:C8	2.53	0.43
36:1:579:G:H2'	36:1:580:C:C6	2.54	0.43
1:2:1002:G:N1	1:2:1761:U:OP1	2.38	0.43
1:2:952:A:H5'	15:C3:98:VAL:HG22	2.01	0.43
38:4:76:C:H2'	38:4:77:A:O4'	2.19	0.43
36:5:839:C:H4'	36:5:1724:U:H2'	2.01	0.43
36:5:2101:C:H2'	36:5:2102:U:C6	2.52	0.43
36:5:1911:A:H2	36:5:2122:G:C8	2.37	0.43
36:5:2821:C:C2	87:D:3401:SPS:H181	2.53	0.43
36:5:3089:C:H2'	36:5:3090:U:O4'	2.19	0.43
36:5:67:A:O2'	36:5:315:C:O2	2.32	0.43
36:5:3288:G:C4	36:5:3289:G:C8	3.07	0.43
36:5:3343:G:O2'	36:5:3362:A:N6	2.51	0.43
1:6:1350:U:H2'	1:6:1351:G:H8	1.83	0.43
20:C8:41:ARG:HD3	1:6:1565:C:OP1	370.01	0.43
1:6:1691:A:H2'	1:6:1692:G:C8	2.53	0.43
1:6:271:A:C2	1:6:285:G:C6	3.07	0.43
1:6:675:U:H2'	1:6:676:G:C8	2.53	0.43
38:8:9:A:H2'	38:8:10:A:C8	2.54	0.43
15:C3:125:LEU:O	15:C3:128:TYR:N	2.94	0.43
16:C4:39:ILE:HD12	16:C4:74:VAL:HG11	5.16	0.43
17:C5:68:PRO:HB2	17:C5:69:GLU:H	4.04	0.43
21:C9:31:PRO:HB3	21:C9:103:LYS:HD3	2.35	0.43
21:C9:33:TYR:O	21:C9:34:VAL:HG12	4.77	0.43
28:D6:37:LYS:C	28:D6:38:ARG:HD2	2.38	0.43
39:L2:222:ALA:HA	36:5:2245:C:O4'	222.45	0.43
41:L4:186:LYS:O	41:L4:200:THR:N	2.88	0.43
42:L5:14:SER:HG	37:7:68:C:P	301.85	0.43
42:L5:254:LYS:NZ	42:L5:257:GLU:OE1	6.91	0.43
46:L9:105:GLU:HB2	46:L9:110:LYS:H	3.32	0.43
46:L9:111:PHE:HD1	46:L9:127:PRO:HA	2.10	0.43
46:L9:137:SER:HB2	46:L9:143:GLU:HB3	3.01	0.43
46:L9:41:ILE:HD12	46:L9:67:ALA:HB1	2.01	0.43
53:M7:127:ARG:NH2	36:5:1508:C:OP1	138.63	0.43
54:M8:122:ILE:HG13	54:M8:126:GLN:HE21	1.84	0.43
54:M8:23:ASN:HB3	54:M8:26:LEU:HB2	2.33	0.43
62:N6:35:LEU:HD23	62:N6:106:ILE:HD12	2.01	0.43
67:O1:10:ARG:HH12	67:O1:44:MET:HG2	4.91	0.43
71:O5:18:ALA:O	71:O5:22:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:O5:31:LEU:HD13	71:O5:47:VAL:HG11	2.98	0.43
71:O5:96:GLU:O	71:O5:99:GLN:HB2	2.49	0.43
72:O6:53:TYR:HB2	72:O6:76:ARG:HD3	2.01	0.43
75:O9:21:ARG:HH11	75:O9:21:ARG:HB2	3.41	0.43
2:S0:92:HIS:CE1	2:S0:202:TYR:HH	2.37	0.43
3:S1:110:LEU:O	3:S1:114:VAL:HG23	2.56	0.43
3:S1:116:LYS:O	3:S1:117:TRP:HB2	2.19	0.43
3:S1:30:PHE:HD1	3:S1:96:LEU:HD22	1.83	0.43
5:S3:215:GLU:O	5:S3:215:GLU:HG2	2.38	0.43
5:S3:216:PRO:HB2	5:S3:217:ILE:H	1.62	0.43
1:2:68:A:H5''	8:S6:162:VAL:HG21	2.00	0.43
10:S8:11:ARG:HD3	10:S8:15:GLY:O	2.17	0.43
35:SM:23:LYS:HD2	35:SM:23:LYS:H	1.84	0.43
34:SR:294:TRP:CZ3	34:SR:301:LEU:HB2	3.15	0.43
36:1:1230:G:H2'	36:1:1231:A:C8	2.53	0.43
36:1:1925:U:O2'	36:1:1927:G:N7	2.51	0.43
36:1:192:C:H2'	36:1:193:C:C6	2.53	0.43
36:1:2538:U:O2'	36:1:2541:U:O4	2.21	0.43
36:1:3243:A:O2'	36:1:3244:A:H8	2.02	0.43
36:1:40:A:C2	64:N8:40:HIS:CE1	3.06	0.43
36:1:501:A:H2'	36:1:502:U:C6	2.53	0.43
1:2:182:A:H2'	1:2:183:U:C6	2.53	0.43
1:2:209:U:H2'	1:2:210:A:C8	2.54	0.43
1:2:221:A:OP2	1:2:832:U:O2'	2.29	0.43
1:2:733:A:H4'	1:2:734:A:C5	2.53	0.43
1:2:381:C:O2'	1:2:755:A:N1	2.47	0.43
1:2:827:C:H2'	1:2:828:U:C6	2.52	0.43
38:4:37:A:H5''	38:4:39:G:O4'	2.17	0.43
36:5:1064:A:H4'	36:5:1065:A:O5'	2.19	0.43
36:5:1081:U:HO2'	36:5:1082:U:C5'	2.31	0.43
36:5:142:C:H2'	36:5:143:G:O4'	2.18	0.43
36:5:1581:C:OP2	36:5:1581:C:H4'	2.19	0.43
36:5:2148:U:H2'	36:5:2149:A:C4	2.53	0.43
36:5:260:C:H2'	36:5:261:U:C6	2.53	0.43
36:5:3017:A:H2'	36:5:3018:C:C6	2.53	0.43
36:5:3275:U:O2'	36:5:3276:G:N1	2.51	0.43
36:5:553:U:H2'	36:5:554:A:O4'	2.18	0.43
36:5:601:U:H2'	36:5:602:A:O4'	2.17	0.43
1:6:1531:G:H2'	1:6:1532:U:C6	2.54	0.43
1:6:1679:G:C6	1:6:1680:G:C6	3.07	0.43
1:6:545:A:C6	1:6:594:A:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:175:ILE:HG12	1:6:78:A:H1'	339.50	0.43
13:C1:22:ASN:HA	13:C1:23:PRO:HD3	1.92	0.43
15:C3:47:PRO:HG3	15:C3:75:LEU:HD22	2.00	0.43
16:C4:124:ASP:O	16:C4:125:SER:HB2	2.18	0.43
1:2:1211:A:H1'	17:C5:99:GLY:O	2.19	0.43
18:C6:32:ASN:O	18:C6:66:ARG:NH1	2.52	0.43
1:2:1565:C:OP1	20:C8:41:ARG:HG3	2.18	0.43
23:D1:13:VAL:HA	23:D1:14:PRO:HD3	1.82	0.43
26:D4:112:LYS:O	26:D4:116:LYS:HG3	2.19	0.43
26:D4:25:VAL:O	26:D4:70:VAL:HA	2.51	0.43
33:E1:95:HIS:CG	33:E1:96:LYS:H	2.84	0.43
36:1:2525:G:OP2	39:L2:37:ARG:NH1	2.50	0.43
39:L2:66:PRO:HB2	39:L2:67:TYR:CD2	2.66	0.43
39:L2:95:SER:OG	39:L2:96:LEU:N	2.51	0.43
40:L3:41:VAL:HG13	40:L3:183:LEU:HG	2.00	0.43
41:L4:63:GLU:C	41:L4:75:PRO:HA	2.39	0.43
42:L5:156:GLY:N	42:L5:179:ARG:O	2.48	0.43
49:M3:92:THR:HG21	71:O5:111:PHE:HB3	2.62	0.43
50:M4:15:VAL:HG13	56:N0:150:PHE:O	2.43	0.43
36:1:1543:G:OP1	51:M5:35:VAL:HG23	2.18	0.43
54:M8:153:PHE:O	54:M8:161:LYS:HG2	4.02	0.43
56:N0:6:GLU:OE1	56:N0:99:ARG:NH2	3.59	0.43
56:N0:89:ASN:HD21	57:N1:156:TYR:H	1.66	0.43
61:N5:132:ALA:O	61:N5:135:ILE:HG22	2.18	0.43
70:O4:44:CYS:HB2	70:O4:81:CYS:HB3	2.00	0.43
75:O9:2:ALA:O	75:O9:3:ALA:HB3	2.19	0.43
78:Q2:3:ASN:O	36:5:2655:U:H2'	239.27	0.43
2:S0:177:LEU:HA	2:S0:177:LEU:HD23	2.00	0.43
2:S0:66:ALA:HB1	23:D1:50:TYR:HE1	2.14	0.43
2:S0:82:GLY:O	2:S0:85:ALA:HB3	2.18	0.43
3:S1:138:PHE:CD2	3:S1:214:LYS:HB3	2.57	0.43
3:S1:103:MET:HB3	3:S1:215:VAL:CG1	2.71	0.43
5:S3:219:ALA:HA	5:S3:220:PRO:HD2	2.36	0.43
6:S4:86:PHE:O	6:S4:87:MET:HB2	2.19	0.43
7:S5:126:ASP:HB3	7:S5:127:GLN:H	1.82	0.43
34:SR:123:ILE:HD13	34:SR:169:ILE:HG21	4.18	0.43
34:SR:297:ASP:N	34:SR:297:ASP:OD2	4.25	0.43
36:1:1173:U:H1'	36:1:1179:A:C4	2.54	0.43
36:1:1245:A:C3'	36:1:1246:G:H5''	2.46	0.43
36:1:1471:U:H2'	36:1:1472:U:C6	2.54	0.43
36:1:1504:A:C5	36:1:1505:C:C5	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1821:U:C2	70:O4:67:LYS:HB2	2.53	0.43
36:1:915:A:H8	36:1:2136:C:O2'	2.02	0.43
36:1:2417:U:H2'	36:1:2419:A:OP2	2.19	0.43
36:1:2534:G:H2'	36:1:2535:A:C8	2.45	0.43
36:1:2434:U:H5	36:1:2594:C:OP2	2.01	0.43
36:1:561:C:H2'	36:1:562:C:H6	1.82	0.43
36:1:638:C:H2'	36:1:639:G:C8	2.54	0.43
36:5:1307:G:C2	36:5:1308:A:C2	3.06	0.43
36:5:1461:A:C2	36:5:1462:A:C4	3.06	0.43
36:5:1595:U:C2	36:5:1596:C:C5	3.07	0.43
36:5:22:G:O4'	38:8:104:A:H1'	2.18	0.43
36:5:746:A:H2'	36:5:747:A:C8	2.54	0.43
1:6:1257:U:O2'	1:6:1258:U:O4'	2.37	0.43
1:6:138:A:N6	1:6:139:C:H41	2.15	0.43
8:S6:13:GLN:CD	1:6:151:G:H21	312.54	0.43
6:S4:19:LEU:HD13	1:6:788:A:C4	394.90	0.43
1:6:829:A:H1'	1:6:830:U:H5	1.83	0.43
15:C3:114:ARG:HA	15:C3:114:ARG:HD2	2.57	0.43
15:C3:136:PRO:O	15:C3:138:ASN:N	2.44	0.43
16:C4:135:ARG:NH2	1:6:903:U:H5''	296.97	0.43
17:C5:51:SER:C	17:C5:53:PRO:HD2	4.32	0.43
2:S0:84:ARG:NE	19:C7:82:ASP:OD1	3.71	0.43
39:L2:230:VAL:HG21	36:5:2424:A:N1	183.93	0.43
40:L3:261:MET:O	40:L3:264:VAL:HG13	2.18	0.43
41:L4:107:ARG:HG2	41:L4:108:LYS:N	2.33	0.43
42:L5:146:LEU:HB3	36:5:2746:A:C2	259.56	0.43
46:L9:166:ARG:HH11	46:L9:166:ARG:HB2	1.83	0.43
48:M1:133:ARG:HD3	48:M1:152:HIS:CD2	4.28	0.43
49:M3:100:ARG:O	49:M3:101:ARG:HB2	4.43	0.43
49:M3:73:ARG:HD2	36:5:76:G:H3'	83.39	0.43
50:M4:18:GLY:O	50:M4:69:THR:HA	2.41	0.43
50:M4:13:ARG:NH1	50:M4:65:LEU:O	2.51	0.43
52:M6:72:HIS:O	52:M6:74:ARG:HD3	2.81	0.43
55:M9:4:LEU:O	55:M9:7:GLN:HG2	5.28	0.43
56:N0:80:ARG:HB2	56:N0:124:LEU:HD11	2.01	0.43
56:N0:30:PHE:CD2	56:N0:103:VAL:HG21	2.81	0.43
61:N5:100:LYS:HG2	61:N5:105:VAL:O	2.38	0.43
62:N6:102:SER:OG	62:N6:103:LYS:HE3	4.60	0.43
64:N8:132:LYS:NZ	64:N8:136:GLU:OE2	2.42	0.43
64:N8:96:LYS:HB2	64:N8:97:GLU:OE1	2.19	0.43
78:Q2:6:LYS:HG3	78:Q2:93:LEU:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:167:VAL:O	3:S1:171:ILE:HG13	2.55	0.43
5:S3:107:PHE:O	5:S3:111:ASN:N	4.07	0.43
5:S3:37:VAL:HG12	5:S3:50:ILE:HD13	2.01	0.43
5:S3:92:GLN:CD	5:S3:92:GLN:H	2.20	0.43
7:S5:34:GLN:O	7:S5:38:THR:OG1	2.36	0.43
11:S9:88:GLU:O	11:S9:91:LYS:HE3	2.19	0.43
36:1:1742:U:H2'	36:1:1743:G:H8	1.82	0.43
36:1:2662:G:H2'	36:1:2663:G:H8	1.84	0.43
36:1:2748:A:O2'	42:L5:48:LYS:HE2	2.18	0.43
36:1:289:A:H2'	36:1:290:G:H8	1.84	0.43
36:1:3138:U:OP2	40:L3:30:LYS:HD3	2.19	0.43
36:1:561:C:H2'	36:1:562:C:C6	2.53	0.43
36:1:679:U:H2'	36:1:680:G:C8	2.54	0.43
1:2:1086:A:C6	1:2:1087:A:C6	3.07	0.43
1:2:1202:A:H1'	1:2:1207:C:N4	2.34	0.43
1:2:495:C:H3'	1:2:496:G:C4'	2.49	0.43
1:2:938:G:C6	1:2:942:G:C6	3.07	0.43
37:3:61:G:H2'	37:3:62:U:C6	2.54	0.43
36:5:1497:C:H2'	36:5:1498:A:H8	1.84	0.43
36:5:2435:G:H1	36:5:2512:C:H42	1.67	0.43
36:5:3061:G:H2'	36:5:3062:G:H8	1.82	0.43
36:5:3174:A:H2'	36:5:3175:U:H5'	2.01	0.43
1:6:619:A:N3	1:6:1141:G:H1'	2.33	0.43
1:6:196:G:O2'	1:6:197:A:OP2	2.30	0.43
1:6:922:G:H2'	1:6:923:A:C8	2.54	0.43
13:C1:22:ASN:HD22	13:C1:25:VAL:HG23	1.83	0.43
15:C3:46:THR:OG1	15:C3:49:GLN:HG2	4.07	0.43
21:C9:30:VAL:HA	21:C9:31:PRO:HD2	1.79	0.43
4:S2:156:THR:HB	24:D2:95:PRO:HB3	2.23	0.43
28:D6:11:ASN:O	28:D6:33:ASP:HB2	2.18	0.43
28:D6:87:ARG:HD3	1:6:1796:C:OP1	347.08	0.43
30:D8:12:VAL:HA	30:D8:30:VAL:HG12	2.07	0.43
31:D9:16:LYS:HG2	31:D9:16:LYS:H	1.98	0.43
31:D9:4:GLU:OE1	31:D9:4:GLU:N	4.82	0.43
39:L2:70:ARG:HH11	39:L2:72:ARG:HE	4.33	0.43
40:L3:139:GLN:H	40:L3:139:GLN:HG3	1.70	0.43
42:L5:183:TRP:CH2	42:L5:188:GLU:HA	2.52	0.43
42:L5:233:ALA:O	42:L5:236:LEU:N	2.38	0.43
41:L4:326:ARG:NH2	44:L7:164:SER:O	3.51	0.43
44:L7:179:LEU:HD22	44:L7:183:ASP:OD2	2.18	0.43
44:L7:89:ILE:HD12	44:L7:214:TRP:CH2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:210:ILE:HA	47:M0:217:PHE:HE2	2.10	0.43
51:M5:139:HIS:O	51:M5:143:ARG:HG3	2.18	0.43
51:M5:84:PRO:HA	51:M5:87:GLN:HB2	3.01	0.43
54:M8:143:PRO:HB2	54:M8:146:SER:OG	2.73	0.43
58:N2:37:LEU:O	58:N2:41:ILE:HG13	2.32	0.43
64:N8:6:THR:HG23	64:N8:8:THR:H	1.84	0.43
68:O2:20:HIS:HB2	68:O2:50:ILE:HD11	2.45	0.43
68:O2:96:ILE:N	68:O2:121:ASN:HD21	2.66	0.43
61:N5:46:TYR:HD2	71:O5:75:TYR:HB3	1.84	0.43
2:S0:185:ARG:CZ	23:D1:47:PRO:HG3	2.49	0.43
2:S0:60:ALA:O	2:S0:64:ILE:HG13	2.24	0.43
4:S2:169:LEU:HD22	4:S2:198:THR:HG22	2.01	0.43
4:S2:180:ALA:HB2	4:S2:198:THR:HG21	2.00	0.43
5:S3:137:VAL:HB	5:S3:185:LYS:HB2	2.00	0.43
6:S4:121:TYR:CD2	6:S4:161:LYS:HE3	2.53	0.43
7:S5:77:TYR:HB3	7:S5:84:LYS:HA	2.47	0.43
8:S6:78:THR:HG22	8:S6:79:LYS:H	4.08	0.43
10:S8:48:THR:CG2	10:S8:54:LYS:HB2	2.48	0.43
34:SR:112:SER:OG	34:SR:153:GLN:OE1	2.37	0.43
36:1:1468:A:N6	36:1:1508:C:O2	2.52	0.43
36:1:1565:G:N2	36:1:1574:C:C2	2.87	0.43
36:1:1580:A:H1'	36:1:1581:C:H5	1.83	0.43
36:1:196:G:C2	36:1:199:A:C8	3.07	0.43
36:1:3182:G:H4'	52:M6:161:LYS:HD3	2.01	0.43
36:1:650:C:O5'	36:1:650:C:H6	2.01	0.43
36:1:671:U:OP2	54:M8:57:ILE:HD12	2.18	0.43
1:2:1559:A:OP1	1:2:1559:A:H4'	2.19	0.43
1:2:269:G:C6	1:2:287:G:C6	3.06	0.43
1:2:609:U:C4	25:D3:26:GLU:HG2	2.54	0.43
1:2:826:U:H2'	1:2:827:C:H6	1.84	0.43
1:2:992:A:C2	1:2:1012:U:N3	2.80	0.43
36:5:1221:A:H3'	36:5:1222:G:H5'	2.01	0.43
36:5:1253:U:O2	36:5:1263:A:H5'	2.18	0.43
70:O4:10:ARG:NH1	36:5:1489:A:OP1	129.93	0.43
64:N8:36:GLY:N	36:5:40:A:OP2	174.42	0.43
1:6:119:A:H1'	1:6:397:A:C4	2.54	0.43
1:6:1450:U:H2'	1:6:1451:C:C6	2.54	0.43
1:6:1573:A:H4'	1:6:1574:G:H5'	2.01	0.43
1:6:868:G:C2	1:6:869:A:C8	3.07	0.43
13:C1:29:LYS:O	13:C1:31:THR:N	2.46	0.43
20:C8:99:HIS:HD2	20:C8:101:LEU:HD21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:C9:77:ASN:HB3	21:C9:95:ASP:HB3	2.00	0.43
6:S4:59:ARG:NH1	26:D4:87:PRO:HG3	2.34	0.43
32:E0:39:LEU:HD12	32:E0:43:ARG:NH2	2.34	0.43
40:L3:350:ALA:C	40:L3:352:GLU:H	2.19	0.43
41:L4:170:LYS:HG3	41:L4:175:HIS:HB2	4.11	0.43
41:L4:327:LEU:HA	44:L7:166:ASN:ND2	2.34	0.43
37:3:8:G:O2'	42:L5:69:ILE:O	2.33	0.43
45:L8:158:ASP:HB3	45:L8:159:PRO:HD3	2.01	0.43
46:L9:72:LYS:HG2	46:L9:76:ASP:OD2	2.61	0.43
50:M4:45:LEU:HD21	50:M4:55:ARG:NH1	2.58	0.43
51:M5:190:THR:HB	51:M5:193:ARG:NH2	2.34	0.43
52:M6:54:TYR:HE2	52:M6:58:LEU:HD13	1.83	0.43
52:M6:62:THR:HA	36:5:1306:G:C6	233.89	0.43
36:1:2355:G:H5'	53:M7:139:TYR:CE1	2.54	0.43
53:M7:52:LEU:HD12	53:M7:52:LEU:HA	1.90	0.43
54:M8:93:ILE:HG13	54:M8:93:ILE:H	2.67	0.43
55:M9:134:HIS:CD2	36:5:1947:G:H5'	236.09	0.43
52:M6:121:PRO:HD2	56:N0:162:THR:O	2.18	0.43
57:N1:51:GLY:O	57:N1:95:HIS:HD2	2.41	0.43
78:Q2:69:VAL:HG13	78:Q2:84:THR:HB	3.72	0.43
2:S0:76:ILE:HD13	2:S0:98:ILE:HB	2.00	0.43
1:2:788:A:C4	6:S4:19:LEU:HD13	2.53	0.43
7:S5:63:GLN:HB3	7:S5:64:VAL:H	1.50	0.43
11:S9:171:ARG:NH2	11:S9:174:ARG:HD3	5.17	0.43
36:1:651:G:O2'	36:1:1435:A:OP1	2.33	0.43
36:1:2615:G:H2'	36:1:2616:C:C6	2.54	0.43
36:1:2746:A:H2'	36:1:2747:A:O4'	2.18	0.43
36:1:2882:U:H2'	36:1:2883:U:C6	2.53	0.43
1:2:1119:G:C6	1:2:1120:U:C4	3.07	0.43
1:2:119:A:H2'	1:2:120:U:O4'	2.19	0.43
1:2:704:C:OP2	1:2:704:C:H3'	2.19	0.43
1:2:816:G:H21	9:S7:110:GLN:HE22	1.67	0.43
36:5:1470:U:H2'	36:5:1471:U:C6	2.54	0.43
36:5:163:C:H2'	36:5:164:A:O4'	2.18	0.43
36:5:240:U:O2'	36:5:241:G:H8	2.02	0.43
36:5:2710:C:H2'	36:5:2711:C:C6	2.53	0.43
36:5:523:A:N6	36:5:570:A:C2	2.87	0.43
36:5:622:A:H2'	36:5:623:U:O4'	2.19	0.43
1:6:1478:G:C4	1:6:1479:A:C8	3.07	0.43
1:6:320:U:H2'	1:6:321:C:H2'	2.01	0.43
25:D3:108:GLY:HA2	1:6:600:U:OP2	358.68	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:868:G:H1	1:6:960:U:H3	1.65	0.43
38:8:71:A:H4'	38:8:72:A:O5'	2.19	0.43
12:C0:31:LYS:H	12:C0:38:LYS:HA	4.64	0.43
25:D3:75:GLN:HG3	25:D3:82:LYS:HD2	2.01	0.43
13:C1:99:ARG:HD3	25:D3:8:GLY:O	3.02	0.43
27:D5:70:LYS:HG3	27:D5:71:ILE:HG13	1.99	0.43
28:D6:30:ILE:HG12	28:D6:34:LYS:HB3	3.37	0.43
32:E0:41:THR:HA	32:E0:45:VAL:HB	2.01	0.43
33:E1:149:LYS:HE3	33:E1:149:LYS:HB2	3.17	0.43
39:L2:192:LYS:HB2	39:L2:193:ARG:HG2	3.18	0.43
39:L2:225:ILE:HD12	39:L2:225:ILE:N	2.57	0.43
40:L3:146:ARG:O	40:L3:150:ARG:N	2.51	0.43
40:L3:41:VAL:HG11	40:L3:194:TRP:CG	2.53	0.43
40:L3:92:TYR:CE2	40:L3:101:SER:HB3	2.54	0.43
42:L5:259:LYS:HB3	42:L5:259:LYS:HE3	1.65	0.43
44:L7:96:PRO:O	44:L7:100:ARG:HB2	2.19	0.43
45:L8:109:LEU:HA	45:L8:109:LEU:HD13	4.14	0.43
46:L9:109:ALA:O	46:L9:110:LYS:HB2	3.29	0.43
49:M3:32:LYS:O	49:M3:36:ARG:HG3	2.19	0.43
50:M4:135:LEU:HD23	50:M4:135:LEU:HA	3.08	0.43
50:M4:54:PRO:HG2	50:M4:56:GLN:NE2	5.07	0.43
54:M8:19:PRO:HD3	54:M8:53:PHE:CD1	2.54	0.43
46:L9:4:ILE:N	56:N0:142:GLN:OE1	2.66	0.43
42:L5:41:LYS:HB2	57:N1:68:THR:O	2.39	0.43
62:N6:118:LEU:O	62:N6:122:LYS:HG3	2.19	0.43
64:N8:91:LEU:HD13	64:N8:91:LEU:HA	1.82	0.43
67:O1:75:ILE:HG12	67:O1:93:VAL:HG13	2.48	0.43
3:S1:81:PHE:HD2	3:S1:82:ARG:HG3	1.84	0.43
3:S1:70:LEU:HD12	3:S1:82:ARG:O	2.19	0.43
5:S3:133:GLY:HA2	5:S3:155:GLY:HA3	2.71	0.43
34:SR:274:LEU:HD22	34:SR:313:TRP:CD1	2.54	0.43
36:1:1567:U:H5	36:1:1568:U:C2	2.36	0.42
36:1:2267:C:H2'	36:1:2268:U:O4'	2.19	0.42
36:1:2273:G:O2'	36:1:2311:G:O6	2.27	0.42
36:1:2421:U:O2'	78:Q2:52:GLY:HA3	2.19	0.42
36:1:3164:C:HO2'	36:1:3165:A:P	2.42	0.42
36:1:3270:U:C2	43:L6:46:ARG:HD3	2.54	0.42
1:2:1120:U:H2'	1:2:1121:C:C6	2.54	0.42
1:2:1173:C:H2'	1:2:1174:C:H6	1.84	0.42
1:2:191:C:O2'	1:2:192:U:O5'	2.33	0.42
1:2:225:A:H2'	1:2:226:A:O4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:973:A:H2'	1:2:974:A:H8	1.83	0.42
57:N1:35:LYS:HD2	36:5:1085:A:OP1	232.35	0.42
36:5:1355:A:H1'	36:5:1356:U:OP2	2.19	0.42
41:L4:186:LYS:NZ	36:5:1388:U:O4	118.95	0.42
36:5:1903:U:O5'	36:5:1903:U:H6	2.01	0.42
36:5:2226:U:H2'	36:5:2227:C:H6	1.84	0.42
36:5:2425:G:H2'	36:5:2426:U:O4'	2.18	0.42
36:5:2897:A:H2'	36:5:2899:C:C5'	2.48	0.42
36:5:2961:G:H2'	36:5:2962:U:C6	2.54	0.42
36:5:313:A:H2'	36:5:314:U:O4'	2.18	0.42
36:5:394:G:N1	36:5:397:A:OP2	2.51	0.42
36:5:796:U:H2'	36:5:797:U:C6	2.54	0.42
36:5:856:G:C6	36:5:857:G:N1	2.87	0.42
1:6:1304:G:H5'	1:6:1322:A:OP2	2.19	0.42
1:6:151:G:N2	1:6:164:A:C4	2.87	0.42
1:6:52:U:H2'	1:6:53:G:H8	1.83	0.42
18:C6:112:TYR:CZ	18:C6:114:ARG:HD2	6.36	0.42
21:C9:13:ASP:N	21:C9:13:ASP:OD2	2.52	0.42
29:D7:23:THR:HG21	29:D7:29:ARG:HH21	3.04	0.42
39:L2:96:LEU:O	79:Q3:87:ARG:HD3	2.18	0.42
40:L3:92:TYR:OH	40:L3:180:GLU:OE1	2.35	0.42
41:L4:338:LYS:C	41:L4:340:GLY:H	2.23	0.42
43:L6:132:ALA:O	43:L6:136:GLU:HG2	2.18	0.42
44:L7:62:ILE:O	44:L7:66:LYS:HG3	2.71	0.42
46:L9:134:ILE:HG23	46:L9:144:ILE:HD11	2.58	0.42
48:M1:63:GLU:O	48:M1:64:LYS:HB2	2.19	0.42
54:M8:89:ASP:HB2	54:M8:110:ALA:N	2.73	0.42
57:N1:42:ILE:HG12	57:N1:96:ILE:HD11	2.00	0.42
61:N5:135:ILE:HA	61:N5:138:ARG:HB3	2.41	0.42
61:N5:80:ASN:ND2	61:N5:126:LEU:HB2	2.45	0.42
64:N8:73:LEU:HD23	64:N8:112:ILE:HD12	2.01	0.42
69:O3:59:VAL:HG23	69:O3:60:ARG:H	1.93	0.42
77:Q1:21:ARG:NH2	1:6:1118:G:OP2	286.33	0.42
78:Q2:31:GLY:HA3	36:5:2767:U:O3'	192.27	0.42
3:S1:144:ARG:NH2	3:S1:207:LEU:O	2.56	0.42
4:S2:54:GLU:HG2	4:S2:54:GLU:H	1.40	0.42
5:S3:21:LEU:HD23	5:S3:21:LEU:HA	1.93	0.42
6:S4:45:ILE:HD11	6:S4:49:ARG:NH2	2.34	0.42
6:S4:95:THR:HG22	26:D4:16:PRO:HD2	2.01	0.42
9:S7:110:GLN:HB3	9:S7:110:GLN:HE21	4.29	0.42
35:SM:25:ILE:HG22	48:M1:46:VAL:HG23	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1054:A:H5''	36:1:2637:A:N6	2.33	0.42
36:1:1191:U:C2	52:M6:48:PHE:CE1	3.07	0.42
36:1:2093:A:H2'	36:1:2094:C:O4'	2.20	0.42
36:1:2794:G:O2'	36:1:2795:U:OP2	2.31	0.42
36:1:2854:U:OP2	47:M0:3:ARG:NH2	2.51	0.42
36:1:422:A:C2	36:1:2363:A:H4'	2.54	0.42
36:1:763:G:H2'	36:1:764:U:O4'	2.19	0.42
1:2:1091:A:H5''	1:2:1091:A:N3	2.34	0.42
1:2:1650:U:H2'	1:2:1651:A:C8	2.54	0.42
1:2:5:U:C2	1:2:20:G:N2	2.87	0.42
36:5:1002:A:H2'	36:5:1003:A:H8	1.84	0.42
36:5:1573:G:C5	36:5:1574:C:H1'	2.53	0.42
36:5:3225:C:C2	36:5:3226:A:C8	3.08	0.42
1:6:1268:G:H1'	1:6:1448:G:H5''	2.01	0.42
1:6:393:C:H4'	1:6:1673:G:O2'	2.19	0.42
28:D6:5:ARG:HH12	1:6:1795:U:H3'	340.36	0.42
10:S8:47:ARG:NH1	1:6:398:G:OP2	313.67	0.42
32:E0:56:MET:HG2	1:6:590:C:H5'	419.01	0.42
1:6:683:C:H2'	1:6:684:A:O4'	2.18	0.42
36:5:1055:A:H5''	37:7:100:C:O2'	2.19	0.42
38:8:15:G:C6	38:8:16:G:C6	3.07	0.42
16:C4:81:VAL:HG11	16:C4:102:LEU:HD21	2.06	0.42
17:C5:60:LEU:HA	17:C5:60:LEU:HD23	2.70	0.42
39:L2:144:ASN:O	39:L2:160:SER:N	2.68	0.42
40:L3:152:LYS:HE3	40:L3:192:VAL:HG22	4.08	0.42
41:L4:12:THR:HA	41:L4:171:ALA:HB1	2.17	0.42
41:L4:135:VAL:O	41:L4:140:HIS:HB2	2.28	0.42
41:L4:152:VAL:CG2	41:L4:172:VAL:HG21	2.49	0.42
42:L5:273:ARG:O	42:L5:273:ARG:HG2	2.67	0.42
43:L6:52:VAL:HG22	43:L6:67:GLY:HA2	2.55	0.42
47:M0:167:LEU:H	47:M0:167:LEU:HG	1.70	0.42
53:M7:28:ASN:O	53:M7:32:THR:HG23	3.33	0.42
54:M8:138:LEU:HA	54:M8:138:LEU:HD23	2.26	0.42
56:N0:46:GLN:O	37:7:77:G:H5''	301.70	0.42
58:N2:20:SER:O	58:N2:24:GLU:HG2	2.54	0.42
59:N3:112:SER:HA	59:N3:132:ASN:ND2	3.37	0.42
61:N5:80:ASN:HD21	61:N5:126:LEU:HB2	1.92	0.42
63:N7:46:ILE:HD11	63:N7:49:TYR:HA	2.01	0.42
67:O1:79:ARG:HA	67:O1:89:LEU:HD12	2.01	0.42
74:O8:11:PHE:O	74:O8:15:THR:HG23	2.57	0.42
77:Q1:4:LYS:HG3	77:Q1:5:TRP:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:131:ASP:HB3	3:S1:180:THR:CG2	2.49	0.42
5:S3:167:PHE:CE1	5:S3:192:PRO:HB3	2.53	0.42
8:S6:147:LEU:HB3	8:S6:151:ASP:HB2	2.02	0.42
9:S7:93:LEU:HD21	9:S7:129:LEU:HD23	2.01	0.42
11:S9:119:ALA:O	11:S9:124:HIS:ND1	5.35	0.42
34:SR:232:TYR:HE1	34:SR:234:LEU:HD11	1.83	0.42
34:SR:95:ALA:C	34:SR:97:GLY:H	3.62	0.42
36:1:839:C:O2'	36:1:1724:U:OP1	2.21	0.42
36:1:3066:U:H2'	36:1:3067:C:C6	2.54	0.42
36:1:39:A:H5''	64:N8:35:ALA:HB2	2.02	0.42
1:2:1018:U:H2'	1:2:1019:A:C8	2.55	0.42
1:2:1573:A:H4'	1:2:1574:G:O4'	2.19	0.42
36:5:1329:U:H4'	36:5:1330:A:OP1	2.20	0.42
36:5:1791:C:H2'	36:5:1792:C:C6	2.54	0.42
1:6:1049:U:H2'	1:6:1050:G:C8	2.55	0.42
1:6:1381:U:O4	1:6:1382:A:N6	2.51	0.42
1:6:152:U:C2	1:6:163:G:N2	2.87	0.42
16:C4:81:VAL:HG13	16:C4:115:ILE:HG23	3.41	0.42
18:C6:50:GLU:OE1	18:C6:112:TYR:OH	2.37	0.42
18:C6:9:THR:HG21	18:C6:88:GLY:HA2	2.01	0.42
19:C7:51:ALA:HA	19:C7:54:THR:HG23	2.01	0.42
20:C8:146:ALA:HB3	35:SM:68:ARG:HH21	1.85	0.42
21:C9:16:ASN:HA	21:C9:56:LYS:NZ	3.06	0.42
87:D:3401:SPS:H71	87:D:3401:SPS:H81	1.67	0.42
29:D7:59:CYS:O	29:D7:61:THR:HG22	2.19	0.42
33:E1:84:VAL:HG23	33:E1:85:TYR:HD1	4.00	0.42
42:L5:106:ALA:HB2	42:L5:166:ALA:HA	2.01	0.42
42:L5:226:TYR:O	42:L5:230:ASP:N	3.36	0.42
42:L5:276:LYS:HD2	37:7:61:G:OP1	322.49	0.42
44:L7:121:LYS:O	44:L7:121:LYS:HD3	2.69	0.42
45:L8:133:LYS:HD2	45:L8:138:HIS:CE1	3.89	0.42
36:1:1048:A:H2'	47:M0:22:TYR:CZ	2.54	0.42
51:M5:120:TRP:CE3	36:5:269:G:H5'	132.99	0.42
53:M7:4:TYR:CZ	53:M7:18:ARG:HG3	2.54	0.42
55:M9:25:ASP:HB3	55:M9:28:GLU:HB2	2.39	0.42
59:N3:66:LYS:HD3	59:N3:68:GLU:OE1	3.94	0.42
36:1:429:U:H4'	69:O3:88:ASN:O	2.20	0.42
70:O4:3:GLN:HE22	70:O4:30:LEU:H	4.86	0.42
72:O6:57:LEU:O	72:O6:61:ILE:HG13	2.19	0.42
78:Q2:59:HIS:HA	78:Q2:61:LYS:HZ3	6.18	0.42
79:Q3:84:ARG:O	79:Q3:88:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Q3:5:THR:HB	79:Q3:8:VAL:HG22	2.01	0.42
2:S0:96:THR:HA	2:S0:97:PRO:HD3	1.93	0.42
3:S1:61:LEU:HD23	3:S1:62:LYS:H	1.84	0.42
8:S6:139:ASN:HA	8:S6:142:ARG:HB2	2.05	0.42
36:1:1339:C:H2'	36:1:1340:G:O4'	2.19	0.42
36:1:1447:G:H3'	53:M7:67:ILE:CD1	2.49	0.42
36:1:1481:A:H2'	36:1:1481:A:N3	2.34	0.42
36:1:282:G:H3'	36:1:282:G:C8	2.54	0.42
36:1:2883:U:H2'	36:1:2884:C:H6	1.84	0.42
36:1:997:A:H2'	36:1:998:A:O4'	2.18	0.42
1:2:1353:U:H2'	1:2:1354:G:C8	2.54	0.42
1:2:1417:A:O2'	18:C6:128:LYS:HE2	2.20	0.42
36:5:1222:G:OP2	36:5:1222:G:H8	2.02	0.42
36:5:1810:A:H2'	36:5:1811:G:C8	2.54	0.42
36:5:2533:G:H22	36:5:2546:C:N4	2.18	0.42
36:5:3159:C:H4'	36:5:3395:G:C5	2.54	0.42
1:6:1078:C:H2'	1:6:1079:U:C6	2.54	0.42
1:6:506:A:H3'	1:6:506:A:OP1	2.18	0.42
1:6:52:U:H2'	1:6:53:G:C8	2.53	0.42
32:E0:58:PRO:HA	1:6:558:U:OP1	420.02	0.42
1:6:862:A:C2	1:6:963:A:C4	3.07	0.42
1:6:994:G:H2'	1:6:995:A:O4'	2.19	0.42
10:S8:10:LYS:HD3	13:C1:133:LYS:HE2	2.02	0.42
14:C2:83:GLU:C	14:C2:85:LYS:H	4.52	0.42
16:C4:86:THR:HG21	16:C4:90:ARG:HD3	4.21	0.42
19:C7:23:LYS:O	19:C7:24:LEU:HB2	2.19	0.42
20:C8:116:LEU:HA	20:C8:119:ILE:HG22	4.51	0.42
22:D0:20:ILE:HG22	22:D0:21:LYS:H	5.27	0.42
24:D2:32:LYS:HG3	1:6:637:C:OP1	365.42	0.42
27:D5:70:LYS:CG	27:D5:71:ILE:H	2.32	0.42
1:2:934:C:H1'	28:D6:11:ASN:OD1	2.18	0.42
33:E1:86:THR:HG23	33:E1:87:THR:H	4.38	0.42
33:E1:86:THR:OG1	33:E1:88:PRO:HD2	6.30	0.42
40:L3:185:GLY:H	40:L3:191:LYS:NZ	2.17	0.42
40:L3:5:LYS:HG2	40:L3:6:TYR:CD1	3.58	0.42
41:L4:108:LYS:HB3	41:L4:108:LYS:HE2	1.65	0.42
36:1:2529:A:OP1	45:L8:248:LYS:NZ	2.53	0.42
36:1:560:G:H4'	50:M4:73:PRO:HG2	2.02	0.42
36:1:1447:G:H3'	53:M7:67:ILE:HD11	2.00	0.42
55:M9:24:LEU:HD22	55:M9:50:ILE:HG12	5.44	0.42
58:N2:18:ASP:OD2	58:N2:20:SER:OG	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:N5:129:ASP:HB2	61:N5:130:TYR:CD1	2.54	0.42
69:O3:41:ALA:HB3	69:O3:74:THR:HG22	2.20	0.42
69:O3:48:ARG:HG2	69:O3:103:TYR:O	3.95	0.42
2:S0:109:ASN:O	2:S0:112:THR:HG22	2.19	0.42
2:S0:120:LEU:HD21	2:S0:144:ILE:HD11	2.51	0.42
5:S3:5:ILE:HG23	5:S3:9:ARG:NH1	2.35	0.42
6:S4:100:ARG:HH12	6:S4:118:GLU:HG2	2.48	0.42
8:S6:31:ARG:HH11	8:S6:34:GLN:NE2	2.77	0.42
1:2:768:C:C2	11:S9:143:ILE:HG12	2.55	0.42
36:1:1090:G:H2'	36:1:1091:A:H8	1.83	0.42
36:1:1347:U:OP1	41:L4:303:GLY:N	2.42	0.42
36:1:1481:A:O2'	36:1:1858:A:C2	2.72	0.42
36:1:1658:G:H2'	36:1:1659:U:O4'	2.19	0.42
36:1:2278:C:P	77:Q1:23:ARG:HH12	2.43	0.42
36:1:2656:A:C4	36:1:2658:G:N7	2.88	0.42
36:1:2898:G:H5''	36:1:2899:C:H5'	2.00	0.42
36:1:846:A:H2'	36:1:847:A:O4'	2.20	0.42
36:1:887:G:H2'	36:1:888:A:C8	2.54	0.42
1:2:1152:A:O2'	28:D6:85:ARG:HG3	2.19	0.42
1:2:1183:A:C6	1:2:1184:A:N1	2.88	0.42
1:2:1595:U:H5	1:2:1596:C:C4	2.38	0.42
1:2:867:G:C4	1:2:868:G:C8	3.08	0.42
36:5:1070:U:C4	36:5:1071:U:C4	3.07	0.42
36:5:1230:G:H1	36:5:1279:C:H42	1.68	0.42
36:5:1597:C:H2'	36:5:1598:G:H8	1.84	0.42
36:5:2770:G:O2'	36:5:2771:U:H5'	2.20	0.42
36:5:2841:G:H2'	36:5:2844:C:H42	1.84	0.42
67:O1:43:HIS:HE1	36:5:3323:A:H1'	169.38	0.42
36:5:3393:U:H2'	36:5:3394:U:C6	2.55	0.42
1:6:1697:G:H2'	1:6:1697:G:N3	2.34	0.42
1:6:264:G:H8	1:6:264:G:O5'	2.01	0.42
1:6:390:G:N7	1:6:407:A:N1	2.67	0.42
1:6:515:A:H2'	1:6:516:G:O4'	2.20	0.42
12:C0:61:TRP:HZ3	31:D9:22:ARG:HD2	2.32	0.42
18:C6:27:GLY:HA2	18:C6:60:PHE:O	2.55	0.42
24:D2:7:LEU:HD11	24:D2:37:PHE:CE2	4.28	0.42
27:D5:61:SER:H	27:D5:64:VAL:HB	2.04	0.42
28:D6:41:ILE:HG12	28:D6:41:ILE:O	2.19	0.42
28:D6:87:ARG:HB3	28:D6:91:ASP:CB	2.49	0.42
29:D7:19:HIS:CD2	29:D7:21:LEU:H	4.41	0.42
29:D7:37:CYS:HA	29:D7:38:PRO:HD3	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C2:74:LEU:HD21	33:E1:106:TYR:HB3	2.31	0.42
41:L4:143:GLU:HB3	41:L4:144:LYS:NZ	9.08	0.42
42:L5:109:THR:OG1	42:L5:110:LEU:N	2.53	0.42
44:L7:92:ILE:HD11	54:M8:4:ASP:H	1.84	0.42
48:M1:47:GLN:HG2	48:M1:47:GLN:H	1.58	0.42
51:M5:21:PHE:O	51:M5:25:VAL:HG23	2.19	0.42
60:N4:57:LYS:HE3	60:N4:57:LYS:HB2	1.87	0.42
66:O0:40:LYS:HB2	66:O0:92:ILE:O	3.13	0.42
68:O2:103:LYS:O	68:O2:106:VAL:HG22	2.42	0.42
70:O4:29:ILE:HD11	70:O4:31:ARG:HH21	1.83	0.42
2:S0:105:GLY:O	2:S0:109:ASN:HB3	2.32	0.42
2:S0:179:ARG:HD3	2:S0:183:ARG:NH1	2.56	0.42
3:S1:140:ILE:HG21	3:S1:213:ARG:HD3	2.02	0.42
3:S1:67:GLU:CD	3:S1:83:LYS:HE2	4.66	0.42
6:S4:191:ARG:HD3	6:S4:245:LYS:HB2	2.02	0.42
8:S6:21:GLU:HG2	8:S6:21:GLU:H	1.48	0.42
9:S7:141:ARG:HG2	24:D2:51:GLU:CD	2.77	0.42
10:S8:36:THR:HG23	10:S8:96:LEU:O	2.19	0.42
11:S9:39:LYS:HB3	11:S9:43:TYR:CZ	2.54	0.42
11:S9:75:ALA:O	11:S9:79:ARG:HG3	3.54	0.42
36:1:1911:A:H8	36:1:1911:A:O5'	2.02	0.42
36:1:2816:G:N2	36:1:2819:A:OP2	2.53	0.42
36:1:2883:U:H2'	36:1:2884:C:C6	2.54	0.42
36:1:3122:A:O2'	46:L9:63:LYS:HD2	2.20	0.42
36:1:413:U:OP1	53:M7:30:ARG:NH2	2.48	0.42
36:1:578:A:H5''	36:1:579:G:O5'	2.19	0.42
1:2:460:A:H3'	1:2:461:G:C8	2.51	0.42
1:2:533:U:C2'	1:2:534:A:H5''	2.48	0.42
1:2:632:U:H5''	25:D3:10:ASN:O	2.20	0.42
1:2:749:U:H3	1:2:800:U:H3	1.67	0.42
37:3:90:U:H2'	37:3:91:G:O4'	2.20	0.42
38:4:121:U:H2'	38:4:122:U:H6	1.84	0.42
36:5:1064:A:H62	36:5:1096:U:H3	1.67	0.42
36:5:1481:A:O2'	36:5:1482:A:O5'	2.36	0.42
36:5:1560:G:O2'	36:5:1561:G:P	2.77	0.42
36:5:2439:A:H4'	36:5:2439:A:OP1	2.20	0.42
46:L9:170:LYS:HE3	36:5:2902:A:P	320.33	0.42
36:5:741:U:H2'	36:5:742:G:O4'	2.20	0.42
36:5:830:A:O2'	36:5:1866:C:H2'	2.19	0.42
1:6:1176:G:C6	1:6:1464:G:C6	3.07	0.42
1:6:1208:A:H4'	1:6:1270:G:P	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:12:U:H2'	1:6:13:C:C6	2.54	0.42
37:7:24:A:H2'	37:7:25:G:O4'	2.19	0.42
14:C2:66:VAL:HG11	14:C2:71:ILE:HG21	2.01	0.42
15:C3:118:ILE:O	15:C3:122:ILE:HG13	2.20	0.42
18:C6:143:ARG:NH1	1:6:1191:U:H5'	350.81	0.42
18:C6:73:GLY:H	18:C6:76:SER:HB3	1.85	0.42
20:C8:127:HIS:CD2	20:C8:133:VAL:HG11	3.04	0.42
29:D7:62:ILE:HG13	29:D7:63:LEU:H	1.82	0.42
39:L2:187:HIS:ND1	39:L2:190:ARG:NH2	2.67	0.42
40:L3:66:LYS:HD3	40:L3:67:PHE:CD2	5.72	0.42
41:L4:184:SER:CB	41:L4:202:ARG:HG2	2.50	0.42
41:L4:157:GLU:HB3	41:L4:211:GLU:O	2.20	0.42
43:L6:142:ASP:O	43:L6:146:ILE:HG13	3.44	0.42
46:L9:20:ILE:HG23	46:L9:25:VAL:HG22	2.02	0.42
51:M5:155:VAL:HG23	51:M5:156:HIS:CE1	3.05	0.42
36:1:1160:C:OP1	54:M8:2:GLY:N	2.53	0.42
58:N2:82:LYS:HE2	58:N2:82:LYS:HB2	1.88	0.42
59:N3:40:LYS:HB3	59:N3:40:LYS:HE3	1.77	0.42
61:N5:51:VAL:HG21	71:O5:62:GLN:HB3	2.68	0.42
66:O0:13:LYS:O	66:O0:17:VAL:HG23	2.20	0.42
67:O1:12:TYR:O	67:O1:72:ARG:HD2	2.19	0.42
70:O4:12:PRO:HD2	70:O4:13:TYR:CD2	2.55	0.42
72:O6:98:ARG:HB3	72:O6:99:ARG:H	4.36	0.42
2:S0:34:GLU:N	2:S0:35:PRO:HD2	3.41	0.42
2:S0:74:VAL:HG22	2:S0:96:THR:HG23	2.01	0.42
6:S4:130:GLN:HB3	6:S4:138:TYR:CZ	3.27	0.42
6:S4:160:VAL:HG12	6:S4:162:ILE:HG13	2.31	0.42
9:S7:28:GLU:O	9:S7:30:SER:N	2.47	0.42
10:S8:98:LYS:HB3	1:6:329:G:H5''	275.50	0.42
36:1:1120:A:H2'	36:1:1121:U:C6	2.55	0.42
36:1:112:U:O2'	36:1:113:C:H5''	2.19	0.42
36:1:1272:C:H2'	36:1:1273:A:O4'	2.18	0.42
36:1:1307:G:H1'	36:1:1308:A:N7	2.35	0.42
36:1:624:G:P	69:O3:86:ARG:HH22	2.42	0.42
36:1:956:U:H2'	36:1:957:C:C6	2.55	0.42
1:2:1590:G:H2'	1:2:1591:C:C6	2.54	0.42
1:2:542:A:O2'	1:2:543:C:H2'	2.19	0.42
1:2:978:A:H2'	1:2:979:A:O4'	2.19	0.42
36:5:1716:U:H5'	36:5:1716:U:H6	1.83	0.42
36:5:188:U:H1'	36:5:208:C:H1'	2.00	0.42
36:5:374:A:O2'	36:5:376:G:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1079:U:H2'	1:6:1080:U:H6	1.84	0.42
1:6:1184:A:HO2'	1:6:1209:C:HO2'	1.54	0.42
1:6:1334:U:H2'	1:6:1335:U:C6	2.55	0.42
1:6:1535:U:O2'	1:6:1536:G:P	2.78	0.42
1:6:488:G:N2	1:6:499:U:H3	2.18	0.42
1:6:524:U:O2'	1:6:526:A:N7	2.43	0.42
38:8:45:C:H2'	38:8:46:G:O4'	2.19	0.42
75:O9:21:ARG:HD2	38:8:52:A:O4'	85.69	0.42
73:O7:63:ARG:NH2	38:8:58:G:O6	79.46	0.42
12:C0:38:LYS:HB2	12:C0:41:TYR:CD2	3.27	0.42
12:C0:16:PHE:CD2	12:C0:76:LEU:HD23	2.46	0.42
14:C2:89:ILE:HG12	14:C2:90:LYS:H	1.84	0.42
16:C4:91:THR:O	16:C4:93:THR:N	2.67	0.42
19:C7:65:PRO:HG3	19:C7:78:ARG:HH21	1.84	0.42
20:C8:142:GLY:O	20:C8:145:ARG:HD2	2.20	0.42
2:S0:55:GLU:OE2	23:D1:80:LYS:HG2	5.82	0.42
25:D3:29:TYR:O	25:D3:32:ARG:N	3.08	0.42
26:D4:112:LYS:HE3	26:D4:112:LYS:HB3	3.09	0.42
41:L4:138:ARG:NH2	41:L4:240:PRO:HB2	3.16	0.42
41:L4:269:SER:C	41:L4:271:LYS:H	2.19	0.42
42:L5:269:SER:O	42:L5:270:LYS:HB2	4.57	0.42
43:L6:50:LYS:HG2	43:L6:74:VAL:CG2	2.50	0.42
45:L8:156:ASP:HB2	45:L8:157:VAL:H	1.65	0.42
45:L8:160:ILE:HG23	45:L8:164:VAL:HG13	3.54	0.42
46:L9:23:ARG:NH2	46:L9:39:LYS:O	3.32	0.42
48:M1:11:ASP:HB3	48:M1:12:LEU:H	1.59	0.42
48:M1:28:ASP:O	48:M1:32:ARG:HG3	2.20	0.42
48:M1:94:ARG:HB2	48:M1:95:ASN:H	1.69	0.42
50:M4:113:THR:HG22	50:M4:115:PHE:H	1.85	0.42
55:M9:134:HIS:CE1	55:M9:137:ALA:HB2	2.61	0.42
56:N0:40:ARG:HD2	56:N0:40:ARG:HA	1.70	0.42
60:N4:4:GLU:HG2	60:N4:30:ARG:CD	2.48	0.42
66:O0:34:LEU:HD12	66:O0:34:LEU:HA	1.96	0.42
68:O2:71:HIS:CE1	68:O2:118:LYS:HD3	2.55	0.42
72:O6:40:VAL:O	72:O6:44:VAL:HG23	2.20	0.42
75:O9:10:LYS:HA	75:O9:13:MET:HE2	2.02	0.42
78:Q2:40:LYS:HE3	78:Q2:44:ASP:OD2	2.20	0.42
3:S1:128:LYS:HE3	3:S1:132:ASP:OD1	2.20	0.42
1:2:579:A:N1	5:S3:143:ARG:HG3	2.34	0.42
5:S3:201:ALA:HB3	19:C7:42:GLN:NE2	2.34	0.42
5:S3:53:THR:HB	5:S3:94:ARG:HD3	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:61:TYR:HE2	7:S5:164:PRO:HG2	3.54	0.42
7:S5:202:ALA:O	7:S5:203:LYS:HD2	2.20	0.42
8:S6:72:ARG:HA	8:S6:97:VAL:O	2.51	0.42
11:S9:161:THR:O	11:S9:162:SER:OG	2.37	0.42
11:S9:182:GLU:HG3	11:S9:182:GLU:H	3.07	0.42
11:S9:36:LEU:O	32:E0:33:ARG:HG3	2.19	0.42
34:SR:228:LYS:O	34:SR:229:LYS:NZ	2.29	0.42
36:1:1128:U:P	47:M0:4:ARG:HH22	2.42	0.42
36:1:1750:A:OP2	74:O8:28:ASN:ND2	2.50	0.42
36:1:1807:G:H5'	63:N7:135:ARG:HH22	1.84	0.42
36:1:2228:A:H2'	36:1:2229:A:C8	2.55	0.42
36:1:2254:U:H2'	36:1:2261:G:N2	2.34	0.42
36:1:2767:U:H2'	36:1:2768:U:H6	1.83	0.42
36:1:600:G:N2	36:1:603:A:OP2	2.52	0.42
36:1:960:U:H4'	36:1:963:G:N1	2.34	0.42
1:2:1344:A:H4'	1:2:1345:A:OP1	2.20	0.42
1:2:1409:G:N2	1:2:1411:A:H3'	2.35	0.42
1:2:1489:U:H5'	1:2:1494:C:H1'	2.00	0.42
1:2:289:U:H2'	1:2:290:G:O4'	2.20	0.42
1:2:425:A:H5'	1:2:425:A:H8	1.84	0.42
1:2:778:G:H22	26:D4:10:ARG:NH1	2.17	0.42
1:2:968:U:H2'	1:2:969:C:O4'	2.20	0.42
1:2:987:G:C2	39:L2:249:SER:HB2	2.55	0.42
64:N8:3:SER:OG	36:5:1430:U:O4	140.22	0.42
36:5:144:A:H2'	36:5:145:G:O4'	2.19	0.42
55:M9:110:ARG:NH1	36:5:1719:G:OP1	238.51	0.42
36:5:2298:U:O4	36:5:2923:U:H5	2.02	0.42
36:5:3096:C:H2'	36:5:3097:C:C6	2.55	0.42
36:5:3154:C:H6	36:5:3156:U:H5'	1.84	0.42
36:5:929:A:H2'	36:5:930:U:C6	2.55	0.42
1:6:1085:G:N2	1:6:1088:A:OP2	2.48	0.42
1:6:780:A:H3'	1:6:781:U:H5'	2.02	0.42
37:7:22:A:C6	37:7:23:A:C6	3.07	0.42
14:C2:60:VAL:HG22	14:C2:122:VAL:HG22	2.33	0.42
15:C3:91:LEU:HB3	15:C3:122:ILE:HG12	2.17	0.42
16:C4:125:SER:HB3	16:C4:126:THR:H	1.48	0.42
21:C9:57:ARG:HB2	21:C9:57:ARG:NH1	2.35	0.42
22:D0:24:ILE:HD13	22:D0:41:ILE:HD13	6.78	0.42
1:2:1381:U:H4'	22:D0:59:PRO:HG3	2.00	0.42
23:D1:17:CYS:HB2	23:D1:56:SER:HB3	2.36	0.42
24:D2:15:ASN:ND2	24:D2:72:CYS:O	4.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:92:CYS:HA	25:D3:95:PHE:CD2	2.50	0.42
30:D8:12:VAL:HG22	30:D8:28:VAL:HG11	2.00	0.42
39:L2:90:ALA:HB2	39:L2:101:VAL:HG13	2.27	0.42
42:L5:205:SER:HB2	42:L5:233:ALA:HB1	2.02	0.42
43:L6:38:THR:HG23	43:L6:90:LYS:HE2	2.02	0.42
44:L7:39:GLU:O	44:L7:43:ILE:HG13	2.18	0.42
45:L8:75:ILE:C	45:L8:77:GLN:H	2.23	0.42
47:M0:213:PHE:N	47:M0:214:PRO:HD3	2.35	0.42
51:M5:183:THR:O	51:M5:184:LYS:HB3	3.06	0.42
36:1:2425:G:OP2	51:M5:90:ASN:ND2	2.51	0.42
52:M6:14:HIS:CD2	52:M6:124:LEU:HD13	2.55	0.42
52:M6:176:LYS:O	52:M6:180:SER:N	3.35	0.42
53:M7:138:LYS:HD2	53:M7:140:GLU:CD	2.40	0.42
57:N1:14:MET:CE	57:N1:55:LYS:HB2	2.66	0.42
36:1:968:G:O2'	65:N9:15:LYS:HE3	2.19	0.42
3:S1:142:PHE:O	3:S1:207:LEU:HA	2.30	0.42
3:S1:39:GLU:HB3	3:S1:40:ASN:H	2.83	0.42
3:S1:58:SER:O	3:S1:62:LYS:HG3	2.18	0.42
3:S1:67:GLU:OE2	3:S1:83:LYS:HE2	3.52	0.42
4:S2:242:ILE:HG22	4:S2:243:TYR:CD1	2.55	0.42
1:2:1145:U:O2'	4:S2:89:GLN:O	2.18	0.42
6:S4:148:ARG:NH1	8:S6:201:GLN:OE1	2.53	0.42
7:S5:187:ILE:HG13	7:S5:187:ILE:H	2.94	0.42
11:S9:4:ALA:HA	11:S9:5:PRO:HD3	1.88	0.42
35:SM:78:ASP:O	35:SM:82:THR:HG23	2.19	0.42
34:SR:40:LYS:HD2	34:SR:65:SER:O	4.29	0.42
36:1:1305:U:C2	40:L3:257:PRO:HG3	2.55	0.42
36:1:174:C:H2'	36:1:175:C:C6	2.55	0.42
36:1:2904:U:H2'	36:1:2905:U:C6	2.55	0.42
36:1:3033:A:H2'	36:1:3034:C:C6	2.55	0.42
36:1:3088:G:H2'	36:1:3089:C:O4'	2.20	0.42
36:1:623:U:O3'	69:O3:86:ARG:NH2	2.51	0.42
36:1:817:A:H8	73:O7:15:SER:OG	2.03	0.42
1:2:972:G:O2'	36:1:847:A:N1	2.40	0.42
1:2:103:A:H5'	1:2:105:A:C4	2.55	0.42
1:2:1648:A:H2'	1:2:1649:G:C8	2.55	0.42
1:2:1718:G:H2'	1:2:1719:A:C8	2.54	0.42
1:2:1727:G:H2'	1:2:1728:A:C8	2.55	0.42
1:2:322:G:H4'	1:2:323:A:O5'	2.17	0.42
36:5:1093:A:OP1	36:5:1093:A:H4'	2.19	0.42
36:5:1184:A:H2'	36:5:1185:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2546:C:H2'	36:5:2547:A:C8	2.55	0.42
36:5:3228:C:H4'	36:5:3229:G:O5'	2.19	0.42
36:5:618:C:H2'	36:5:619:A:C8	2.55	0.42
73:O7:47:TYR:OH	36:5:813:G:H5'	129.96	0.42
1:6:1195:C:H5''	1:6:1197:C:C6	2.55	0.42
1:6:1553:G:H2'	1:6:1555:A:OP2	2.19	0.42
1:6:555:A:H3'	1:6:555:A:C8	2.55	0.42
12:C0:29:GLN:HB3	12:C0:39:ASN:HB2	2.02	0.42
14:C2:126:TRP:HD1	14:C2:128:ALA:H	3.48	0.42
15:C3:102:LEU:HD23	15:C3:102:LEU:HA	2.10	0.42
20:C8:81:ILE:HA	20:C8:82:PRO:HD3	1.88	0.42
42:L5:49:TYR:CD1	42:L5:66:SER:HB3	2.55	0.42
42:L5:51:LEU:HB2	42:L5:144:VAL:CG1	2.50	0.42
43:L6:68:PRO:HB2	43:L6:142:ASP:CG	4.01	0.42
45:L8:110:THR:O	45:L8:114:ALA:HB3	3.74	0.42
50:M4:37:GLU:HG3	50:M4:38:ILE:N	2.35	0.42
51:M5:47:LYS:HD2	51:M5:50:ARG:HE	1.84	0.42
52:M6:119:VAL:HG11	56:N0:167:ARG:HD2	3.06	0.42
36:1:1629:U:O4	63:N7:111:LYS:HD2	2.20	0.42
64:N8:99:ALA:HA	64:N8:100:PRO:HD3	1.85	0.42
64:N8:139:ARG:HA	64:N8:143:GLY:O	2.19	0.42
66:O0:100:ILE:HG13	66:O0:101:LEU:HD22	2.02	0.42
66:O0:36:GLN:OE1	66:O0:38:LYS:HD2	2.20	0.42
68:O2:101:SER:HA	68:O2:125:ARG:HH21	1.84	0.42
72:O6:30:LYS:HE3	36:5:266:A:H2'	103.81	0.42
2:S0:10:THR:OG1	2:S0:10:THR:O	3.12	0.42
2:S0:124:THR:HG22	2:S0:174:TRP:NE1	2.50	0.42
2:S0:129:ASP:O	2:S0:133:ILE:HG13	3.31	0.42
3:S1:172:LEU:O	3:S1:176:VAL:HG23	2.19	0.42
3:S1:144:ARG:NH1	3:S1:202:LYS:HE2	8.54	0.42
4:S2:101:VAL:HG22	4:S2:115:ILE:HG12	2.02	0.42
4:S2:36:VAL:HA	4:S2:37:PRO:HD2	2.20	0.42
7:S5:153:GLY:O	7:S5:155:ALA:N	2.75	0.42
36:1:999:G:N3	36:1:1002:A:N6	2.68	0.42
36:1:2606:G:H2'	36:1:2606:G:N3	2.35	0.42
1:2:1235:C:H5'	33:E1:146:SER:HB2	2.01	0.42
1:2:1434:U:H4'	31:D9:24:CYS:HB2	2.01	0.42
1:2:631:G:H2'	1:2:632:U:C6	2.55	0.42
36:5:1648:A:H2'	36:5:1649:U:O4'	2.20	0.42
36:5:2358:A:H2'	36:5:2359:C:O4'	2.20	0.42
36:5:2524:A:C8	36:5:2525:G:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:N1:54:HIS:CD2	36:5:2724:U:H4'	229.61	0.42
51:M5:179:LYS:O	36:5:287:G:H5'	125.11	0.42
36:5:2971:A:C6	87:D:3401:SPS:C9	3.03	0.42
36:5:3291:G:H2'	36:5:3292:A:C8	2.55	0.42
36:5:974:G:H2'	36:5:975:C:C6	2.55	0.42
1:6:1237:G:H2'	1:6:1238:A:H8	1.84	0.42
1:6:485:A:C6	1:6:486:G:H1'	2.55	0.42
1:6:539:G:OP2	1:6:539:G:H8	2.03	0.42
1:6:737:A:H2'	1:6:738:G:O4'	2.20	0.42
75:O9:11:GLN:HG3	38:8:45:C:H4'	95.80	0.42
18:C6:22:VAL:HA	18:C6:64:ASP:O	2.60	0.42
20:C8:118:LYS:O	20:C8:120:ARG:HG2	2.76	0.42
23:D1:16:LYS:HE3	23:D1:16:LYS:HB2	1.73	0.42
23:D1:69:LEU:HA	23:D1:69:LEU:HD23	2.06	0.42
30:D8:44:VAL:HG11	30:D8:48:VAL:HG21	2.02	0.42
33:E1:97:LYS:O	33:E1:98:VAL:HG12	2.20	0.42
42:L5:55:PHE:CZ	42:L5:158:ARG:HG3	2.55	0.42
43:L6:5:LYS:HD2	43:L6:5:LYS:HA	1.74	0.42
45:L8:186:LEU:HA	45:L8:186:LEU:HD23	1.86	0.42
46:L9:103:ILE:HD11	46:L9:134:ILE:HG22	2.01	0.42
46:L9:76:ASP:O	46:L9:80:THR:HG23	2.20	0.42
48:M1:10:ARG:NH1	48:M1:133:ARG:HH21	4.41	0.42
53:M7:86:LYS:O	53:M7:90:PHE:HD1	2.15	0.42
54:M8:36:LEU:HB3	54:M8:45:ASN:ND2	2.35	0.42
57:N1:75:ILE:HA	57:N1:87:LYS:O	2.20	0.42
59:N3:120:LYS:HB2	59:N3:137:VAL:CG2	2.77	0.42
36:1:2916:U:H1'	59:N3:44:SER:OG	2.20	0.42
36:1:3043:C:P	59:N3:48:ARG:HH22	2.43	0.42
65:N9:22:LYS:H	65:N9:22:LYS:HG2	1.55	0.42
67:O1:88:PRO:C	67:O1:89:LEU:HD12	3.00	0.42
36:1:92:G:O2'	78:Q2:56:PRO:HD3	2.20	0.42
78:Q2:59:HIS:O	78:Q2:61:LYS:HG2	5.77	0.42
3:S1:181:LEU:O	3:S1:182:ALA:C	2.58	0.42
6:S4:122:LYS:HE3	6:S4:122:LYS:HB2	1.91	0.42
6:S4:174:LYS:HE3	6:S4:174:LYS:HB3	2.09	0.42
8:S6:31:ARG:HH11	8:S6:34:GLN:HE22	2.35	0.42
34:SR:22:SER:HB3	34:SR:36:ALA:HB3	2.02	0.42
34:SR:31:ASN:HA	34:SR:47:LEU:HB2	2.28	0.42
36:1:1097:G:C8	57:N1:128:LEU:HD13	2.55	0.41
36:1:1369:A:H2'	36:1:1370:G:O4'	2.20	0.41
36:1:2227:C:H2'	36:1:2228:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:224:C:O2	62:N6:103:LYS:NZ	2.53	0.41
36:1:2632:G:C6	36:1:2647:A:C6	3.08	0.41
36:1:3382:U:O2	36:1:3382:U:H2'	2.19	0.41
36:1:641:C:H42	36:1:645:A:H8	1.68	0.41
36:1:685:G:P	49:M3:35:ARG:NH1	2.93	0.41
36:1:701:G:H2'	36:1:702:C:C6	2.55	0.41
1:2:1183:A:N1	17:C5:99:GLY:HA3	2.35	0.41
1:2:1474:G:H2'	1:2:1475:A:H8	1.84	0.41
1:2:1484:G:C2	1:2:1485:C:C4	3.09	0.41
1:2:588:U:H2'	1:2:589:C:O4'	2.20	0.41
1:2:472:U:O2'	1:2:769:A:N3	2.44	0.41
36:5:1624:G:H2'	36:5:1625:A:C8	2.55	0.41
36:5:3192:U:H2'	36:5:3193:C:H6	1.85	0.41
36:5:655:C:H2'	36:5:656:A:C8	2.55	0.41
11:S9:133:HIS:CE1	1:6:512:A:O2'	447.86	0.41
1:6:675:U:H2'	1:6:676:G:H8	1.84	0.41
1:6:705:U:HO2'	1:6:706:A:H8	1.68	0.41
1:6:725:U:H2'	1:6:726:C:C6	2.55	0.41
1:6:219:A:C6	1:6:843:U:H1'	2.55	0.41
12:C0:44:LYS:HD3	12:C0:44:LYS:HA	1.80	0.41
13:C1:75:VAL:HG12	13:C1:119:VAL:HA	2.03	0.41
16:C4:17:ALA:N	16:C4:80:HIS:O	2.51	0.41
17:C5:34:VAL:O	17:C5:42:ARG:HG2	2.36	0.41
21:C9:142:GLU:HG3	21:C9:142:GLU:H	4.44	0.41
23:D1:11:LEU:HG	23:D1:11:LEU:H	1.68	0.41
25:D3:111:GLY:O	25:D3:121:ARG:HD2	4.90	0.41
27:D5:93:SER:HB3	27:D5:100:ILE:HB	2.74	0.41
39:L2:19:HIS:CD2	39:L2:19:HIS:N	2.98	0.41
41:L4:10:SER:C	41:L4:12:THR:H	2.23	0.41
42:L5:22:ARG:NH1	42:L5:28:THR:OG1	4.43	0.41
43:L6:82:ARG:O	69:O3:104:PRO:HA	2.62	0.41
44:L7:103:LEU:HG	44:L7:130:ILE:CG1	4.36	0.41
45:L8:210:ALA:HA	45:L8:213:LYS:HB3	3.50	0.41
51:M5:63:ARG:NH2	51:M5:131:GLU:OE2	2.45	0.41
53:M7:94:LEU:HA	53:M7:94:LEU:HD12	2.45	0.41
56:N0:25:PHE:HA	57:N1:149:GLN:O	2.76	0.41
57:N1:96:ILE:HA	57:N1:96:ILE:HD13	2.92	0.41
58:N2:87:ASN:HB2	58:N2:89:LEU:HG	2.02	0.41
62:N6:125:LYS:HB3	62:N6:126:LEU:H	3.98	0.41
63:N7:90:GLU:HA	63:N7:93:LYS:HB2	2.02	0.41
72:O6:51:SER:O	72:O6:54:GLU:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:O7:22:CYS:SG	73:O7:24:ARG:HB2	2.60	0.41
4:S2:84:LYS:HA	4:S2:85:PRO:HD3	1.76	0.41
6:S4:240:LYS:CD	6:S4:240:LYS:H	2.33	0.41
6:S4:31:PRO:HB2	6:S4:38:LEU:HD22	2.01	0.41
7:S5:225:ARG:NH2	30:D8:58:GLU:HB2	5.60	0.41
9:S7:105:THR:OG1	9:S7:106:SER:N	4.01	0.41
10:S8:81:VAL:HA	10:S8:102:VAL:HG12	2.38	0.41
36:1:1177:G:H1'	36:1:1178:G:N7	2.35	0.41
36:1:2838:A:C2	36:1:2839:G:H1'	2.55	0.41
36:1:3112:G:O6	36:1:3120:C:H5''	2.19	0.41
36:1:789:A:H2'	36:1:790:U:C6	2.55	0.41
1:2:1486:G:H1'	1:2:1592:A:O2'	2.21	0.41
1:2:778:G:O6	26:D4:10:ARG:HG2	2.20	0.41
36:5:1020:G:H2'	36:5:1021:G:O4'	2.20	0.41
36:5:1554:U:H4'	36:5:1555:U:OP1	2.19	0.41
36:5:1733:G:H2'	36:5:1734:G:H8	1.85	0.41
36:5:2105:G:H2'	36:5:2106:A:C8	2.55	0.41
36:5:811:U:H2'	36:5:812:G:C8	2.55	0.41
36:5:979:U:H4'	36:5:980:A:H5'	2.01	0.41
8:S6:154:ARG:HD3	1:6:78:A:C8	341.83	0.41
13:C1:101:GLU:OE2	25:D3:16:ARG:NH2	2.64	0.41
18:C6:89:LEU:HG	18:C6:105:LEU:HD23	2.33	0.41
5:S3:207:THR:HB	19:C7:40:THR:OG1	2.72	0.41
20:C8:42:TYR:HA	20:C8:85:PHE:HE1	1.85	0.41
27:D5:38:HIS:CG	27:D5:39:ALA:N	2.88	0.41
1:2:1142:A:H5''	28:D6:2:PRO:HB3	2.01	0.41
30:D8:13:ILE:HD11	30:D8:31:GLU:HB2	2.02	0.41
7:S5:81:ARG:HH21	30:D8:47:PRO:HB3	2.81	0.41
11:S9:29:LYS:HG3	32:E0:44:PHE:CE2	2.55	0.41
39:L2:94:ALA:HB3	39:L2:102:LEU:HG	2.46	0.41
40:L3:53:MET:HE2	40:L3:77:THR:HG22	2.03	0.41
36:1:591:G:H1'	43:L6:19:LYS:HG3	2.01	0.41
43:L6:62:THR:HG22	43:L6:79:VAL:O	3.10	0.41
45:L8:67:ILE:CG2	45:L8:237:ILE:HB	2.50	0.41
46:L9:134:ILE:HD11	46:L9:146:LEU:HD23	2.01	0.41
47:M0:58:GLU:OE1	47:M0:161:GLY:HA3	2.20	0.41
48:M1:164:LYS:HE3	48:M1:171:VAL:HG12	2.63	0.41
49:M3:67:ARG:HG2	64:N8:105:LEU:HG	2.02	0.41
51:M5:58:GLY:HA3	51:M5:142:ILE:CD1	2.50	0.41
51:M5:135:VAL:HG13	51:M5:142:ILE:HG12	2.38	0.41
52:M6:173:ALA:O	52:M6:176:LYS:HB3	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:M8:139:ILE:O	54:M8:140:LEU:HD23	2.84	0.41
9:S7:39:ARG:NH2	55:M9:185:LEU:HD22	3.03	0.41
59:N3:37:ILE:HD12	36:5:2295:A:N3	273.42	0.41
60:N4:9:SER:HB2	60:N4:51:TRP:CZ3	2.72	0.41
62:N6:111:LEU:HD23	62:N6:116:LYS:HG2	2.54	0.41
62:N6:2:ALA:N	36:5:213:A:OP1	81.45	0.41
62:N6:52:ARG:O	62:N6:53:ASP:HB2	4.12	0.41
62:N6:56:VAL:HG22	62:N6:104:LEU:HB3	2.13	0.41
63:N7:101:PHE:HB3	63:N7:107:ARG:HH21	1.84	0.41
63:N7:15:ARG:HB2	63:N7:79:HIS:HB3	3.62	0.41
69:O3:89:LEU:HA	69:O3:89:LEU:HD23	1.91	0.41
74:O8:36:LYS:HA	74:O8:37:PRO:HD3	2.45	0.41
75:O9:15:LYS:O	75:O9:19:GLN:HG3	2.97	0.41
79:Q3:49:ARG:HG3	79:Q3:55:TRP:CZ2	2.55	0.41
2:S0:101:ARG:HH22	2:S0:104:PRO:HD3	1.84	0.41
3:S1:30:PHE:CD1	3:S1:96:LEU:HD22	2.55	0.41
4:S2:152:HIS:HD2	4:S2:152:HIS:H	2.98	0.41
10:S8:159:GLN:HB3	10:S8:165:LEU:HD23	2.01	0.41
11:S9:115:LYS:HD2	11:S9:115:LYS:HA	1.70	0.41
11:S9:113:VAL:HG21	11:S9:134:ILE:HD12	2.01	0.41
36:1:1326:A:H2'	36:1:1327:C:O4'	2.20	0.41
36:1:1709:C:H2'	36:1:1710:C:C6	2.54	0.41
36:1:1764:U:C5	36:1:1765:U:H1'	2.56	0.41
36:1:1836:C:HO2'	36:1:1842:A:N6	2.18	0.41
36:1:535:G:C4	36:1:554:A:C6	3.08	0.41
1:2:199:G:HO2'	1:2:200:A:H8	1.66	0.41
1:2:312:A:C2	1:2:314:C:H2'	2.55	0.41
1:2:926:A:OP1	1:2:1016:C:O2'	2.28	0.41
1:2:990:C:O2'	16:C4:127:ARG:HG2	2.20	0.41
36:5:198:A:C6	36:5:219:A:C6	3.08	0.41
36:5:2143:A:O2'	36:5:2144:A:H2'	2.20	0.41
36:5:2302:G:H2'	36:5:2303:A:O4'	2.21	0.41
57:N1:68:THR:OG1	36:5:2737:C:H4'	224.52	0.41
64:N8:67:HIS:NE2	36:5:71:A:OP2	119.34	0.41
1:6:138:A:H62	1:6:266:A:N6	2.18	0.41
1:6:158:U:O2'	1:6:159:U:H3'	2.19	0.41
1:6:1699:G:C2'	1:6:1700:C:H5'	2.48	0.41
13:C1:10:GLU:HG2	1:6:327:U:H1'	271.42	0.41
1:6:93:A:C6	1:6:398:G:C6	3.08	0.41
18:C6:126:PRO:O	18:C6:128:LYS:HE3	2.20	0.41
22:D0:24:ILE:HG12	22:D0:116:VAL:HG12	3.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:D4:23:PHE:CE2	26:D4:75:VAL:HG23	6.22	0.41
27:D5:59:TYR:HE1	27:D5:100:ILE:HG23	6.38	0.41
27:D5:59:TYR:CZ	27:D5:100:ILE:HG12	2.56	0.41
33:E1:144:CYS:HB3	33:E1:147:VAL:HG22	2.02	0.41
39:L2:117:GLU:HB3	39:L2:119:LYS:O	2.20	0.41
36:1:2180:G:P	39:L2:174:ARG:HH22	2.43	0.41
41:L4:323:VAL:HA	41:L4:326:ARG:HB3	2.02	0.41
41:L4:91:GLY:O	41:L4:97:GLY:HA3	2.19	0.41
43:L6:62:THR:HG22	43:L6:79:VAL:H	3.58	0.41
46:L9:13:PRO:HG2	46:L9:16:VAL:HG22	2.02	0.41
46:L9:47:LYS:HE3	46:L9:49:ASN:O	2.20	0.41
49:M3:106:GLN:HB3	72:O6:18:THR:OG1	2.20	0.41
72:O6:98:ARG:O	72:O6:99:ARG:HD2	2.20	0.41
78:Q2:59:HIS:HA	78:Q2:61:LYS:NZ	6.11	0.41
3:S1:70:LEU:CD1	3:S1:79:HIS:HB3	2.50	0.41
4:S2:225:LEU:HG	23:D1:23:ILE:HG13	2.01	0.41
4:S2:238:SER:C	4:S2:240:LEU:H	2.23	0.41
6:S4:71:LYS:HG2	6:S4:76:VAL:HG22	5.14	0.41
8:S6:163:THR:HA	8:S6:168:THR:HA	2.03	0.41
10:S8:22:ARG:HG3	10:S8:23:LYS:O	2.27	0.41
11:S9:105:LEU:O	11:S9:108:ARG:HG3	2.20	0.41
11:S9:134:ILE:HG22	11:S9:158:PHE:CD2	2.52	0.41
35:SM:23:LYS:HA	35:SM:23:LYS:HZ2	5.78	0.41
34:SR:209:THR:O	34:SR:225:LEU:N	2.50	0.41
36:1:1815:U:O2'	36:1:1816:A:P	2.78	0.41
36:1:612:U:H2'	36:1:613:G:C8	2.54	0.41
36:1:703:G:O2'	36:1:787:G:H4'	2.20	0.41
36:1:790:U:H2'	36:1:791:A:O4'	2.20	0.41
1:2:142:G:H5''	8:S6:139:ASN:ND2	2.35	0.41
1:2:1492:A:O2'	1:2:1493:A:H8	2.03	0.41
1:2:1653:C:N4	1:2:1654:G:C6	2.88	0.41
1:2:351:C:H5	1:2:631:G:H5''	1.85	0.41
1:2:633:U:H2'	1:2:634:G:O4'	2.20	0.41
1:2:639:U:OP1	9:S7:117:THR:OG1	2.23	0.41
1:2:912:U:H4'	1:2:913:G:O5'	2.20	0.41
38:4:118:C:H2'	38:4:119:C:H6	1.85	0.41
36:5:1846:C:H5'	36:5:1849:C:H41	1.83	0.41
36:5:2202:C:H2'	36:5:2203:U:O4'	2.20	0.41
36:5:2375:G:O2'	36:5:2377:G:OP2	2.26	0.41
36:5:3018:C:C4	36:5:3019:U:C4	3.08	0.41
36:5:3106:A:H2'	36:5:3107:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:720:A:C2	36:5:784:A:H5'	2.55	0.41
13:C1:67:ARG:NE	1:6:115:G:OP1	318.08	0.41
21:C9:69:LYS:NZ	1:6:1369:U:OP2	439.37	0.41
1:6:1535:U:O2'	1:6:1536:G:OP2	2.36	0.41
38:8:121:U:H2'	38:8:122:U:C6	2.55	0.41
73:O7:76:ASN:ND2	38:8:94:C:H5''	45.59	0.41
13:C1:46:LYS:HE3	13:C1:50:GLU:OE2	5.64	0.41
13:C1:65:SER:HB2	1:6:247:A:H2	319.33	0.41
15:C3:4:MET:HG2	15:C3:5:HIS:CD2	4.84	0.41
17:C5:51:SER:OG	17:C5:52:LYS:N	4.81	0.41
18:C6:131:GLY:HA3	18:C6:136:SER:O	2.21	0.41
21:C9:49:ASP:O	21:C9:51:GLU:N	2.53	0.41
25:D3:9:LEU:HA	25:D3:9:LEU:HD23	2.35	0.41
27:D5:40:VAL:HA	27:D5:75:LEU:HD11	2.03	0.41
28:D6:10:ARG:NH1	28:D6:36:ILE:HG13	6.02	0.41
30:D8:32:PHE:HB2	30:D8:38:ARG:HB2	7.44	0.41
33:E1:143:LYS:N	1:6:1253:U:H4'	451.02	0.41
36:1:2948:C:O2'	40:L3:242:THR:HG22	2.21	0.41
40:L3:229:VAL:HG11	40:L3:249:VAL:HG23	2.02	0.41
40:L3:256:HIS:HA	40:L3:257:PRO:C	2.40	0.41
40:L3:92:TYR:O	40:L3:156:SER:N	2.49	0.41
41:L4:44:LYS:O	41:L4:47:ARG:HD3	2.20	0.41
42:L5:261:THR:H	42:L5:264:GLN:HB2	2.77	0.41
43:L6:131:LYS:HD3	43:L6:132:ALA:N	5.11	0.41
46:L9:48:VAL:HG11	46:L9:52:LEU:HD13	2.03	0.41
48:M1:152:HIS:HB2	37:7:56:A:H4'	327.55	0.41
49:M3:60:ALA:HA	49:M3:70:ARG:HH21	2.33	0.41
51:M5:172:ARG:CZ	51:M5:174:ILE:HD11	3.17	0.41
51:M5:42:PRO:HD3	51:M5:61:ILE:HG13	2.48	0.41
52:M6:19:LEU:O	52:M6:23:VAL:HG23	2.21	0.41
54:M8:178:ARG:HD3	54:M8:178:ARG:HA	1.73	0.41
55:M9:170:ARG:O	55:M9:174:ALA:N	2.97	0.41
62:N6:60:ARG:NH2	36:5:190:U:H2'	84.03	0.41
63:N7:102:GLU:OE1	63:N7:103:GLN:N	2.65	0.41
63:N7:17:ARG:HA	70:O4:74:ARG:HA	2.01	0.41
64:N8:73:LEU:HD13	64:N8:109:TYR:CE1	2.54	0.41
66:O0:57:GLU:OE2	36:5:2552:C:N4	242.76	0.41
4:S2:129:ILE:HG22	4:S2:133:LYS:HE3	3.01	0.41
4:S2:238:SER:O	4:S2:240:LEU:N	2.73	0.41
4:S2:61:LEU:HA	4:S2:62:PRO:HD2	1.88	0.41
5:S3:164:VAL:O	5:S3:168:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:323:A:OP2	10:S8:10:LYS:HG2	2.21	0.41
11:S9:113:VAL:O	11:S9:118:LEU:HB2	3.05	0.41
36:1:2444:C:H3'	36:1:2445:A:H5''	2.02	0.41
36:1:595:G:H2'	36:1:596:C:C6	2.55	0.41
36:1:872:U:H2'	36:1:873:C:C6	2.55	0.41
1:2:1058:U:H4'	1:2:1059:U:OP1	2.20	0.41
1:2:1251:U:H1'	1:2:1252:C:C6	2.55	0.41
1:2:1550:A:C6	1:2:1551:U:C4	3.08	0.41
1:2:850:A:C2	1:2:851:U:C2	3.09	0.41
36:5:1238:C:HO2'	36:5:1239:C:P	2.34	0.41
36:5:1696:A:H61	36:5:1748:G:H2'	1.85	0.41
36:5:193:C:H2'	36:5:194:U:H6	1.85	0.41
36:5:2248:C:H2'	36:5:2273:G:C8	2.56	0.41
36:5:2572:C:O2	36:5:2572:C:H2'	2.19	0.41
53:M7:101:ASN:OD1	36:5:388:G:N2	114.06	0.41
36:5:599:C:H2'	36:5:600:G:O4'	2.20	0.41
36:5:956:U:H2'	36:5:957:C:C6	2.55	0.41
1:6:1244:A:N3	1:6:1244:A:H3'	2.35	0.41
1:6:1315:U:H2'	1:6:1316:G:O4'	2.20	0.41
1:6:829:A:H1'	1:6:830:U:C5	2.56	0.41
36:5:143:G:H4'	38:8:145:U:OP1	2.21	0.41
15:C3:27:LYS:HE2	15:C3:27:LYS:H	1.85	0.41
16:C4:19:ILE:HG12	16:C4:28:VAL:HG22	2.02	0.41
18:C6:29:ILE:HA	18:C6:65:ILE:HB	2.24	0.41
25:D3:19:ARG:O	25:D3:23:ARG:HG2	2.21	0.41
1:2:530:C:O2	26:D4:61:ARG:NH2	2.54	0.41
24:D2:24:GLN:NE2	29:D7:4:VAL:HA	3.73	0.41
40:L3:49:TYR:HE1	40:L3:177:HIS:CE1	3.11	0.41
41:L4:141:ARG:C	41:L4:143:GLU:H	2.52	0.41
41:L4:203:ARG:NH2	41:L4:240:PRO:HB3	3.23	0.41
42:L5:114:GLY:C	42:L5:116:ASP:H	2.23	0.41
42:L5:236:LEU:HA	42:L5:239:ILE:HD12	2.03	0.41
42:L5:257:GLU:O	42:L5:258:LYS:HG2	4.85	0.41
44:L7:38:LYS:HB2	44:L7:38:LYS:HE3	1.81	0.41
45:L8:41:GLN:HG3	45:L8:42:PRO:HD2	2.04	0.41
46:L9:172:ILE:O	46:L9:176:LEU:HD23	2.21	0.41
47:M0:135:ILE:HG22	47:M0:136:PHE:CD1	2.96	0.41
47:M0:157:TYR:CE1	36:5:2836:C:H4'	313.33	0.41
50:M4:101:LYS:O	50:M4:105:GLN:HB2	2.20	0.41
53:M7:95:LEU:HA	53:M7:95:LEU:HD23	2.15	0.41
54:M8:79:LYS:HA	54:M8:136:ASN:OD1	3.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:N0:144:LEU:HA	56:N0:144:LEU:HD23	2.26	0.41
62:N6:108:LYS:HA	62:N6:108:LYS:HD3	4.47	0.41
78:Q2:47:GLN:HE22	78:Q2:53:GLN:HA	2.96	0.41
2:S0:59:LEU:HD12	23:D1:79:LEU:HD11	5.34	0.41
3:S1:128:LYS:NZ	3:S1:132:ASP:HB3	2.35	0.41
3:S1:178:GLY:O	3:S1:180:THR:N	2.53	0.41
6:S4:121:TYR:HB2	6:S4:162:ILE:O	2.60	0.41
1:2:736:C:OP1	6:S4:197:HIS:NE2	2.53	0.41
9:S7:31:SER:HA	9:S7:35:LYS:HB3	3.57	0.41
9:S7:91:ILE:HD12	9:S7:92:PHE:H	2.84	0.41
11:S9:87:SER:HB3	11:S9:90:LYS:HD2	7.44	0.41
20:C8:146:ALA:N	35:SM:68:ARG:HH21	2.18	0.41
34:SR:42:LEU:HB2	34:SR:61:PHE:HB2	2.02	0.41
36:1:1316:C:OP2	52:M6:133:ARG:NE	2.31	0.41
36:1:1356:U:O5'	36:1:1356:U:H6	2.03	0.41
36:1:2778:G:H2'	36:1:2779:A:H5'	2.02	0.41
36:1:3386:G:H2'	36:1:3387:U:C6	2.55	0.41
36:1:374:A:H4'	36:1:375:A:OP1	2.20	0.41
36:1:848:A:H8	36:1:848:A:O5'	2.04	0.41
1:2:1142:A:H2'	1:2:1143:A:C8	2.55	0.41
1:2:1200:G:H4'	1:2:1201:G:C5'	2.51	0.41
1:2:1317:C:H2'	1:2:1318:G:O4'	2.21	0.41
1:2:1433:G:C5	31:D9:41:GLN:HG2	2.55	0.41
1:2:1784:C:H2'	1:2:1785:U:C6	2.55	0.41
1:2:913:G:HO2'	1:2:914:G:P	2.42	0.41
36:5:1033:U:H2'	36:5:1034:U:H5'	2.03	0.41
36:5:1390:A:N3	36:5:1390:A:H5'	2.36	0.41
36:5:2726:C:O2'	36:5:2727:A:H2'	2.21	0.41
36:5:324:A:H2'	36:5:325:A:C8	2.56	0.41
36:5:3288:G:O2'	36:5:3289:G:H8	2.04	0.41
41:L4:119:ARG:NH2	36:5:696:C:OP2	102.99	0.41
36:5:715:A:H4'	36:5:716:A:OP1	2.20	0.41
1:6:1196:A:C8	1:6:1602:C:H4'	2.56	0.41
8:S6:176:GLN:HG2	1:6:169:A:C5'	329.00	0.41
1:6:291:G:H2'	1:6:292:U:C6	2.56	0.41
38:8:157:U:H3'	38:8:158:U:H3'	2.02	0.41
15:C3:20:ARG:HA	15:C3:20:ARG:HD2	4.44	0.41
17:C5:60:LEU:HD11	17:C5:92:SER:OG	2.21	0.41
20:C8:32:LEU:HD13	20:C8:73:MET:HE1	3.93	0.41
21:C9:73:VAL:HG12	21:C9:77:ASN:HD21	3.72	0.41
24:D2:67:GLY:C	24:D2:69:LEU:H	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:D6:5:ARG:HG2	1:6:1796:C:N1	344.72	0.41
28:D6:66:LYS:HB2	28:D6:66:LYS:HE2	1.90	0.41
28:D6:6:ALA:H	1:6:1796:C:H5	346.84	0.41
29:D7:19:HIS:HE1	29:D7:21:LEU:HD12	1.85	0.41
29:D7:19:HIS:CE1	29:D7:21:LEU:HD12	2.56	0.41
32:E0:55:ARG:HH22	1:6:558:U:P	416.39	0.41
33:E1:126:CYS:O	33:E1:128:ALA:N	2.50	0.41
41:L4:39:PHE:O	41:L4:43:ASN:HB2	2.57	0.41
42:L5:143:LYS:HG3	42:L5:172:TYR:HD2	2.05	0.41
45:L8:100:GLU:OE1	45:L8:108:ARG:HD3	2.91	0.41
46:L9:111:PHE:CD1	46:L9:127:PRO:HA	2.75	0.41
37:3:64:A:H3'	47:M0:204:GLY:O	2.20	0.41
47:M0:52:LEU:HA	47:M0:52:LEU:HD23	1.73	0.41
48:M1:77:GLU:OE2	48:M1:166:LYS:NZ	3.54	0.41
49:M3:93:ILE:O	49:M3:93:ILE:HG22	2.20	0.41
53:M7:129:THR:HG22	53:M7:137:ASN:O	5.25	0.41
55:M9:121:HIS:HE1	36:5:1719:G:N7	241.83	0.41
63:N7:49:TYR:CE2	63:N7:133:LYS:HA	3.55	0.41
69:O3:69:GLY:HA2	69:O3:85:PHE:HA	2.02	0.41
70:O4:54:ILE:HD11	70:O4:78:GLY:HA2	2.53	0.41
71:O5:86:ARG:O	71:O5:90:ARG:HG2	2.23	0.41
72:O6:26:ILE:O	72:O6:28:TYR:N	2.51	0.41
73:O7:3:LYS:HB3	36:5:2138:A:C4	170.97	0.41
66:O0:86:ARG:NH1	79:Q3:44:LYS:HG2	2.36	0.41
2:S0:57:LEU:HD23	2:S0:160:ILE:HD13	2.01	0.41
2:S0:79:ARG:O	2:S0:83:GLN:HG3	2.21	0.41
3:S1:23:PRO:O	3:S1:27:LYS:HG2	2.20	0.41
5:S3:75:LYS:HD3	5:S3:75:LYS:HA	2.05	0.41
6:S4:118:GLU:HG3	6:S4:121:TYR:CE1	2.95	0.41
8:S6:131:LYS:HG3	8:S6:131:LYS:H	1.67	0.41
8:S6:137:ARG:HD3	8:S6:177:ARG:HE	1.86	0.41
11:S9:148:VAL:HG11	11:S9:156:ILE:HD11	2.46	0.41
36:1:1080:A:P	42:L5:140:ARG:HH21	2.43	0.41
36:1:2308:C:OP1	36:1:2309:A:O2'	2.31	0.41
36:1:2373:A:H3'	36:1:2373:A:OP2	2.21	0.41
36:1:2880:U:H1'	40:L3:250:ALA:CB	2.48	0.41
36:1:3205:G:H2'	36:1:3206:C:C5	2.56	0.41
36:1:565:U:H2'	36:1:566:G:C8	2.54	0.41
36:1:576:C:H2'	36:1:577:C:C6	2.55	0.41
36:1:805:G:H2'	36:1:936:A:N6	2.36	0.41
36:1:904:A:OP2	73:O7:30:GLN:NE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1150:G:C6	1:2:1768:G:C5	3.09	0.41
1:2:1486:G:C8	1:2:1487:A:C8	3.09	0.41
1:2:1528:U:H2'	1:2:1529:C:C6	2.56	0.41
1:2:25:C:H4'	1:2:25:C:OP2	2.19	0.41
37:3:112:G:H2'	37:3:113:C:H6	1.85	0.41
36:5:1549:U:H2'	36:5:1550:C:H6	1.85	0.41
51:M5:72:LYS:NZ	36:5:2167:A:OP1	163.28	0.41
36:5:2936:A:H2'	36:5:2937:G:C8	2.56	0.41
46:L9:40:HIS:ND1	36:5:3124:G:H5'	311.91	0.41
36:5:406:G:H1'	38:8:16:G:N2	2.35	0.41
1:6:1330:G:H2'	1:6:1331:A:O4'	2.20	0.41
1:6:1603:U:H2'	1:6:1604:U:H6	1.86	0.41
36:5:3:U:H3	38:8:156:U:H3	1.68	0.41
14:C2:52:LEU:O	14:C2:85:LYS:NZ	2.53	0.41
16:C4:123:SER:O	16:C4:124:ASP:HB2	3.93	0.41
17:C5:89:MET:HG2	17:C5:89:MET:H	2.24	0.41
19:C7:49:LYS:HA	1:6:1389:C:H4'	423.96	0.41
19:C7:66:VAL:HB	19:C7:69:ILE:HD11	2.02	0.41
22:D0:26:LEU:HB3	22:D0:34:LEU:HD21	2.02	0.41
22:D0:70:THR:HA	22:D0:71:PRO:HD3	1.97	0.41
23:D1:70:ASN:N	23:D1:70:ASN:OD1	2.76	0.41
24:D2:37:PHE:CD2	24:D2:103:ILE:HD12	2.56	0.41
27:D5:88:ILE:HG22	27:D5:89:ILE:HG23	2.32	0.41
28:D6:64:LEU:HD23	28:D6:64:LEU:HA	2.89	0.41
30:D8:5:THR:HA	30:D8:6:PRO:HD3	1.86	0.41
40:L3:110:LEU:HD12	40:L3:110:LEU:HA	1.86	0.41
40:L3:43:LEU:HD11	40:L3:160:VAL:HG21	3.09	0.41
40:L3:87:VAL:HB	40:L3:110:LEU:HD11	2.15	0.41
42:L5:206:GLN:O	42:L5:210:GLU:HG3	2.31	0.41
44:L7:208:SER:HB2	36:5:1334:U:C1'	241.10	0.41
45:L8:64:ILE:O	45:L8:68:ARG:HG2	2.42	0.41
46:L9:72:LYS:NZ	46:L9:76:ASP:OD2	2.36	0.41
46:L9:91:ARG:HD2	46:L9:143:GLU:HA	2.46	0.41
54:M8:151:ARG:HD2	36:5:781:G:OP1	161.55	0.41
56:N0:65:ASN:ND2	36:5:521:A:N3	315.61	0.41
38:4:85:G:O6	62:N6:112:ASP:HB3	2.20	0.41
62:N6:115:ARG:O	62:N6:119:ILE:HG13	2.32	0.41
63:N7:88:ASP:HB3	63:N7:121:ARG:NH1	2.33	0.41
64:N8:35:ALA:HB1	36:5:40:A:H5''	172.92	0.41
68:O2:126:LEU:HD23	68:O2:126:LEU:HA	1.87	0.41
70:O4:106:LYS:HA	70:O4:106:LYS:HD3	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:42:PRO:O	70:O4:50:ALA:HA	2.21	0.41
70:O4:96:GLU:HA	70:O4:99:LYS:HD2	4.00	0.41
71:O5:6:ALA:HB1	71:O5:10:ARG:NH2	2.36	0.41
71:O5:62:GLN:O	71:O5:66:VAL:HG23	2.20	0.41
72:O6:5:THR:OG1	72:O6:7:ILE:HG22	5.44	0.41
79:Q3:55:TRP:CD1	79:Q3:66:GLY:HA3	2.56	0.41
2:S0:175:TYR:HE1	2:S0:197:ILE:HG22	2.09	0.41
3:S1:30:PHE:CD1	3:S1:94:LYS:HA	3.66	0.41
3:S1:81:PHE:HB2	3:S1:82:ARG:H	1.68	0.41
5:S3:156:PHE:HE1	1:6:1326:A:O3'	422.10	0.41
5:S3:210:GLU:HA	5:S3:211:PRO:HD3	1.89	0.41
5:S3:64:ARG:HG2	5:S3:65:ARG:H	3.58	0.41
6:S4:103:TYR:O	6:S4:182:TYR:OH	2.36	0.41
6:S4:205:PHE:HB3	6:S4:221:ARG:HD2	2.03	0.41
7:S5:149:VAL:HG13	7:S5:151:GLY:N	4.94	0.41
7:S5:97:LEU:HA	7:S5:97:LEU:HD23	1.95	0.41
8:S6:138:ALA:HB1	8:S6:142:ARG:NH1	3.16	0.41
9:S7:60:ILE:HD12	9:S7:92:PHE:CZ	2.56	0.41
10:S8:199:LYS:HE3	10:S8:199:LYS:HB2	1.87	0.41
11:S9:33:GLU:H	11:S9:33:GLU:HG2	4.28	0.41
35:SM:70:ASN:O	35:SM:74:LYS:HE2	3.43	0.41
36:1:1584:U:H2'	36:1:1585:C:C6	2.54	0.41
36:1:2185:G:H2'	36:1:2186:U:H6	1.86	0.41
36:1:2284:C:H3'	36:1:2285:C:H6	1.86	0.41
36:1:2520:A:H2'	36:1:2521:U:C6	2.56	0.41
36:1:2842:U:OP1	36:1:2844:C:N4	2.54	0.41
36:1:3337:G:H2'	36:1:3338:C:O4'	2.21	0.41
36:1:348:A:H1'	36:1:352:A:O2'	2.21	0.41
36:1:576:C:H2'	36:1:577:C:H6	1.86	0.41
1:2:1127:G:OP1	77:Q1:11:ARG:NH2	2.54	0.41
1:2:1434:U:O2'	1:2:1436:A:OP1	2.32	0.41
1:2:156:A:H2'	1:2:157:A:O4'	2.20	0.41
1:2:41:A:H2'	1:2:438:A:N7	2.36	0.41
1:2:800:U:H2'	1:2:801:G:C8	2.56	0.41
36:5:2354:C:H2'	36:5:2355:G:O4'	2.21	0.41
36:5:2538:U:H2'	36:5:2539:C:H4'	2.01	0.41
36:5:2665:U:H4'	36:5:2666:C:OP1	2.21	0.41
36:5:2683:U:H2'	36:5:2684:C:C6	2.55	0.41
36:5:2943:G:H2'	36:5:2944:U:O4'	2.20	0.41
36:5:3112:G:O6	36:5:3120:C:H5''	2.21	0.41
36:5:3131:U:H2'	36:5:3132:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1003:A:H1'	1:6:1005:A:N7	2.36	0.41
1:6:1058:U:H1'	1:6:1059:U:O5'	2.21	0.41
1:6:1640:C:H1'	1:6:1763:A:N1	2.36	0.41
1:6:941:A:C5	1:6:942:G:H1'	2.55	0.41
13:C1:57:LYS:HD3	13:C1:131:ILE:CG2	2.49	0.41
15:C3:34:ILE:O	15:C3:38:VAL:HG23	2.20	0.41
17:C5:86:VAL:HG23	17:C5:87:PRO:HD2	2.03	0.41
20:C8:119:ILE:HD12	20:C8:119:ILE:HA	2.74	0.41
1:2:1199:G:O6	22:D0:67:THR:HG23	2.21	0.41
24:D2:24:GLN:OE1	29:D7:4:VAL:HA	2.21	0.41
30:D8:32:PHE:O	30:D8:34:GLU:N	4.24	0.41
30:D8:49:ARG:HG2	30:D8:52:ASP:OD1	2.42	0.41
36:1:911:C:H5''	39:L2:15:ILE:HD13	2.03	0.41
40:L3:119:TYR:HE2	40:L3:129:ALA:HB2	2.91	0.41
40:L3:262:TRP:HE1	52:M6:66:LYS:HE2	3.73	0.41
42:L5:160:PHE:CD2	42:L5:179:ARG:HB3	2.75	0.41
43:L6:158:TYR:CE1	50:M4:115:PHE:HA	2.55	0.41
43:L6:47:PHE:O	43:L6:50:LYS:HB2	2.55	0.41
45:L8:67:ILE:HA	45:L8:67:ILE:HD13	4.40	0.41
46:L9:87:LYS:HE2	46:L9:187:ILE:HG23	4.44	0.41
47:M0:52:LEU:HD23	47:M0:165:ILE:HG22	2.03	0.41
48:M1:92:ARG:HB3	48:M1:94:ARG:HG2	2.01	0.41
49:M3:54:LEU:HD22	49:M3:54:LEU:HA	2.42	0.41
50:M4:24:LYS:HE2	50:M4:24:LYS:HB3	4.40	0.41
52:M6:125:ARG:HG3	52:M6:129:LEU:HD22	2.40	0.41
53:M7:67:ILE:HD12	53:M7:82:ARG:NH1	3.43	0.41
54:M8:170:ARG:HB2	64:N8:56:VAL:HG21	2.03	0.41
55:M9:175:GLN:O	55:M9:179:GLU:N	2.43	0.41
57:N1:147:VAL:HA	57:N1:148:PRO:HD3	2.06	0.41
36:1:1051:U:H4'	57:N1:19:PHE:CG	2.54	0.41
59:N3:102:ILE:HG13	59:N3:102:ILE:O	2.18	0.41
60:N4:37:ALA:O	60:N4:41:LYS:HE3	3.61	0.41
62:N6:100:HIS:HA	62:N6:101:PRO:HD2	1.84	0.41
68:O2:33:ARG:HH11	36:5:944:C:H4'	161.71	0.41
74:O8:64:LYS:HA	74:O8:64:LYS:NZ	2.35	0.41
2:S0:9:LEU:HD11	2:S0:14:ALA:HB2	2.02	0.41
3:S1:35:PRO:HB3	3:S1:231:LEU:HD21	5.74	0.41
3:S1:61:LEU:HD22	3:S1:61:LEU:H	1.85	0.41
6:S4:185:GLY:N	6:S4:189:LEU:HD13	2.36	0.41
6:S4:195:ILE:HA	6:S4:210:ILE:HD13	2.02	0.41
1:2:753:A:H4'	6:S4:221:ARG:HH21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:176:GLN:HG3	8:S6:177:ARG:N	2.57	0.41
8:S6:193:LEU:HA	8:S6:193:LEU:HD23	1.91	0.41
10:S8:103:GLN:HA	10:S8:165:LEU:O	2.42	0.41
10:S8:78:ILE:HA	10:S8:104:ILE:HG22	2.70	0.41
11:S9:141:VAL:HG11	11:S9:146:PHE:CD2	2.80	0.41
11:S9:3:ARG:H	11:S9:3:ARG:HE	4.42	0.41
35:SM:46:LYS:HA	36:5:1018:G:H4'	325.38	0.41
34:SR:67:ILE:C	34:SR:84:SER:HG	2.23	0.41
36:1:1687:U:H5''	36:1:1688:U:O5'	2.21	0.41
36:1:413:U:OP1	53:M7:30:ARG:NE	2.49	0.41
36:1:90:C:H2'	36:1:91:G:H5'	2.02	0.41
1:2:1061:A:H2'	1:2:1062:A:H5'	2.02	0.41
1:2:1257:U:H2'	12:C0:2:LEU:HD12	2.02	0.41
1:2:1266:U:H2'	1:2:1267:G:H8	1.84	0.41
1:2:1351:G:C2	1:2:1375:A:C2	3.09	0.41
1:2:1426:C:H5''	35:SM:93:ARG:NH1	2.35	0.41
1:2:735:C:O2'	1:2:736:C:H5''	2.21	0.41
1:2:749:U:H2'	1:2:750:U:C6	2.56	0.41
1:2:792:U:H3'	1:2:793:A:C8	2.55	0.41
1:2:953:G:H2'	1:2:954:G:C8	2.56	0.41
36:5:1742:U:H2'	36:5:1743:G:C8	2.55	0.41
36:5:2101:C:H2'	36:5:2102:U:H6	1.86	0.41
36:5:2268:U:H2'	36:5:2269:U:C6	2.56	0.41
36:5:279:U:H2'	36:5:280:U:C6	2.56	0.41
36:5:959:C:N4	36:5:2801:A:C8	2.88	0.41
40:L3:132:LYS:NZ	36:5:3292:A:H4'	208.69	0.41
36:5:863:C:H2'	36:5:864:G:O4'	2.21	0.41
1:6:1147:A:H2'	1:6:1148:C:O4'	2.20	0.41
1:6:156:A:H2'	1:6:157:A:O4'	2.20	0.41
1:6:119:A:H1'	1:6:397:A:C5	2.55	0.41
37:7:22:A:N6	37:7:23:A:N1	2.69	0.41
15:C3:54:LEU:HB3	15:C3:60:VAL:CG1	3.56	0.41
16:C4:114:ARG:HA	28:D6:62:TYR:CZ	2.56	0.41
19:C7:5:ARG:HD3	19:C7:5:ARG:N	2.36	0.41
1:2:1545:A:OP1	20:C8:133:VAL:HG12	2.21	0.41
22:D0:96:PRO:O	22:D0:100:VAL:HG23	2.49	0.41
26:D4:18:LEU:HD23	26:D4:18:LEU:HA	1.89	0.41
32:E0:39:LEU:HA	32:E0:39:LEU:HD13	2.48	0.41
39:L2:116:VAL:HG22	39:L2:126:LEU:HB2	2.02	0.41
39:L2:79:ASN:HD22	39:L2:165:VAL:HG22	1.85	0.41
40:L3:182:GLN:HG3	40:L3:183:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:209:PHE:HB3	40:L3:282:ILE:HD12	2.02	0.41
40:L3:250:ALA:HB3	36:5:2880:U:O2	224.72	0.41
42:L5:92:LEU:HD23	42:L5:92:LEU:HA	4.51	0.41
43:L6:58:LEU:HD12	43:L6:78:ARG:HD3	2.02	0.41
44:L7:176:TYR:HB3	44:L7:194:HIS:ND1	2.40	0.41
48:M1:32:ARG:O	48:M1:36:VAL:HG23	2.20	0.41
36:1:2352:A:H5''	53:M7:83:TRP:O	2.21	0.41
56:N0:45:LEU:HD22	56:N0:45:LEU:HA	1.82	0.41
68:O2:45:ARG:NH1	36:5:1160:C:C2	205.98	0.41
1:2:931:C:O2'	3:S1:118:GLN:O	2.33	0.41
4:S2:143:TYR:OH	4:S2:150:GLN:N	3.27	0.41
6:S4:131:LEU:HD22	6:S4:131:LEU:HA	1.89	0.41
7:S5:109:LYS:O	7:S5:113:ILE:HG13	2.27	0.41
9:S7:151:LYS:HG3	9:S7:182:VAL:HG12	2.02	0.41
10:S8:151:LYS:HA	10:S8:151:LYS:HD2	4.18	0.41
10:S8:101:ILE:HA	10:S8:167:ALA:O	2.57	0.41
36:1:118:U:C5	36:1:119:U:C4	3.09	0.41
36:1:2219:A:H2'	36:1:2220:A:C8	2.56	0.41
36:1:2298:U:O4	36:1:2923:U:H5	2.04	0.41
36:1:3084:C:H2'	36:1:3085:G:O4'	2.21	0.41
36:1:364:G:OP2	73:O7:52:LYS:NZ	2.46	0.41
1:2:1396:U:H2'	1:2:1397:U:C6	2.56	0.41
1:2:1592:A:H2'	1:2:1593:A:H8	1.85	0.41
1:2:166:C:OP1	8:S6:131:LYS:HE3	2.21	0.41
1:2:1:U:O4	11:S9:54:ARG:HG3	2.21	0.41
1:2:962:C:N4	1:2:963:A:C6	2.88	0.41
36:5:1063:G:OP2	36:5:1097:G:H5''	2.21	0.41
36:5:1255:C:H2'	36:5:1256:G:H8	1.86	0.41
36:5:1160:C:O2'	36:5:1366:A:H5'	2.21	0.41
36:5:1373:A:H2'	36:5:1374:G:C8	2.56	0.41
36:5:1394:A:H4'	36:5:1420:C:H4'	2.02	0.41
36:5:2509:U:H2'	36:5:2510:U:H5''	2.02	0.41
36:5:2732:G:H2'	36:5:2733:A:O4'	2.19	0.41
36:5:848:A:H2'	36:5:849:C:O4'	2.20	0.41
18:C6:143:ARG:HH11	1:6:1191:U:H5'	351.18	0.41
1:6:1698:G:N2	1:6:1699:G:C5	2.89	0.41
1:6:1699:G:C2	1:6:1701:A:H5''	2.56	0.41
13:C1:36:LYS:HD3	1:6:248:U:H4'	312.86	0.41
13:C1:98:ASN:HD22	24:D2:79:PHE:HD1	1.69	0.41
16:C4:132:ARG:HB3	1:6:1787:C:OP2	293.43	0.41
18:C6:116:LEU:HA	18:C6:116:LEU:HD23	4.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:C7:71:PHE:CE1	19:C7:74:GLN:HB2	5.51	0.41
19:C7:8:THR:HG21	1:6:1330:G:N2	420.75	0.41
20:C8:62:THR:O	20:C8:66:LEU:HG	2.77	0.41
21:C9:79:LEU:HD13	1:6:1523:G:H8	407.42	0.41
1:2:569:C:H42	25:D3:65:ASN:HD21	1.69	0.41
27:D5:41:ILE:HG13	27:D5:42:LEU:H	1.86	0.41
39:L2:55:GLY:O	39:L2:56:ALA:HB3	4.66	0.41
39:L2:65:ASP:OD1	39:L2:70:ARG:HD2	2.48	0.41
41:L4:145:ILE:HG22	41:L4:173:GLY:O	2.21	0.41
41:L4:177:ASP:OD1	41:L4:180:LYS:HE3	2.21	0.41
41:L4:31:ARG:O	41:L4:35:VAL:HG23	2.89	0.41
37:3:26:C:H5'	42:L5:56:THR:HB	2.03	0.41
46:L9:41:ILE:HD13	46:L9:71:VAL:HG21	2.03	0.41
47:M0:48:LEU:O	47:M0:139:ARG:HA	2.29	0.41
48:M1:141:ARG:O	48:M1:145:LYS:HE2	2.21	0.41
49:M3:89:TYR:O	49:M3:92:THR:OG1	2.29	0.41
50:M4:19:ARG:HD2	50:M4:66:THR:O	2.20	0.41
51:M5:153:ASP:OD2	51:M5:155:VAL:HG22	2.89	0.41
54:M8:147:ARG:HB3	54:M8:150:VAL:HG13	2.25	0.41
54:M8:177:GLY:O	54:M8:186:VAL:N	2.57	0.41
54:M8:184:PHE:CD1	36:5:2730:G:H4'	191.14	0.41
54:M8:185:LYS:HD3	54:M8:186:VAL:HG23	2.96	0.41
55:M9:109:TYR:HB3	55:M9:115:ILE:HG12	5.36	0.41
55:M9:184:LEU:HA	55:M9:184:LEU:HD23	2.14	0.41
63:N7:23:VAL:HB	63:N7:43:VAL:HB	2.02	0.41
63:N7:4:PHE:O	63:N7:4:PHE:CG	3.82	0.41
63:N7:66:THR:O	63:N7:68:ILE:HG13	2.51	0.41
68:O2:8:LYS:HE2	68:O2:8:LYS:HB3	4.30	0.41
3:S1:86:LEU:HB3	3:S1:98:THR:OG1	2.21	0.41
5:S3:53:THR:OG1	5:S3:53:THR:O	2.73	0.41
6:S4:106:LYS:O	6:S4:108:ARG:HG3	2.21	0.41
6:S4:246:LEU:HD21	6:S4:254:ARG:CZ	2.51	0.41
8:S6:49:VAL:HB	8:S6:115:LYS:HG2	4.58	0.41
19:C7:33:ARG:NH2	34:SR:109:ASP:OD2	2.51	0.41
34:SR:89:LEU:HD21	34:SR:110:VAL:HG11	2.61	0.41
36:1:1813:A:OP1	36:1:1817:G:O2'	2.36	0.41
36:1:1900:A:O2'	36:1:1906:G:N7	2.40	0.41
36:1:1915:A:H2'	36:1:1916:U:H6	1.84	0.41
36:1:2419:A:H2'	36:1:2420:C:C6	2.56	0.41
36:1:2616:C:C2'	36:1:2617:U:H5'	2.51	0.41
36:1:3101:G:C2	36:1:3134:A:N3	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1293:U:H2'	1:2:1294:G:O4'	2.20	0.41
1:2:1396:U:H3	1:2:1402:G:H1	1.69	0.41
1:2:1491:U:H4'	1:2:1491:U:OP1	2.20	0.41
1:2:688:G:H2'	1:2:689:G:C8	2.55	0.41
1:2:758:U:H5'	1:2:759:U:OP2	2.21	0.41
37:3:58:C:H2'	37:3:59:U:H6	1.86	0.41
36:5:1046:A:H2'	36:5:1049:C:C5	2.55	0.41
65:N9:10:HIS:NE2	36:5:1139:G:O6	226.05	0.41
36:5:1783:U:H2'	36:5:1784:G:C8	2.56	0.41
36:5:281:G:C6	36:5:282:G:C6	3.09	0.41
36:5:2816:G:C8	36:5:2869:U:H3'	2.56	0.41
36:5:28:C:O2'	36:5:29:C:H5'	2.21	0.41
1:6:1221:A:H2'	1:6:1222:C:C6	2.56	0.41
8:S6:176:GLN:HG2	1:6:169:A:H5''	329.22	0.41
25:D3:62:LYS:HD2	1:6:1754:A:OP2	345.35	0.41
1:6:1756[B]:A:OP1	1:6:1756[B]:A:H4'	2.20	0.41
38:8:81:U:H1'	38:8:82:U:H5''	2.02	0.41
1:2:1241:G:H5'	17:C5:102:PHE:CZ	2.56	0.41
19:C7:45:ARG:O	19:C7:49:LYS:N	2.96	0.41
20:C8:112:ASP:O	20:C8:116:LEU:HD22	2.73	0.41
20:C8:4:VAL:HG11	27:D5:82:HIS:ND1	4.48	0.41
21:C9:52:GLY:HA2	21:C9:55:TYR:CE2	2.55	0.41
22:D0:37:VAL:HG13	22:D0:107:THR:HG22	5.43	0.41
22:D0:65:ILE:HD12	31:D9:43:PHE:CZ	2.56	0.41
33:E1:83:LYS:O	33:E1:84:VAL:HG22	4.76	0.41
39:L2:209:HIS:CD2	39:L2:211:HIS:H	2.39	0.41
36:1:2880:U:O2	40:L3:250:ALA:HB3	2.21	0.41
40:L3:74:GLU:OE2	40:L3:325:LYS:HE3	2.67	0.41
41:L4:192:GLY:HA2	41:L4:195:ARG:HB2	2.03	0.41
42:L5:143:LYS:HE2	42:L5:143:LYS:HB3	1.89	0.41
43:L6:4:GLN:HB2	68:O2:75:LEU:HB2	2.03	0.41
44:L7:103:LEU:HG	44:L7:130:ILE:HG12	4.93	0.41
44:L7:140:SER:OG	44:L7:143:THR:HG23	2.21	0.41
44:L7:203:TRP:CD1	44:L7:204:PRO:HD2	3.03	0.41
45:L8:230:LYS:HG3	45:L8:230:LYS:O	2.55	0.41
47:M0:54:SER:OG	47:M0:130:ASP:O	2.39	0.41
47:M0:52:LEU:HB2	47:M0:136:PHE:HB2	2.02	0.41
48:M1:155:THR:OG1	48:M1:158:ASP:HB2	2.54	0.41
36:1:2675:C:N4	48:M1:22:SER:HB2	2.35	0.41
50:M4:102:LYS:HE2	50:M4:102:LYS:HB2	1.80	0.41
50:M4:99:TRP:O	50:M4:103:ILE:HG13	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:M4:8:LYS:HB3	50:M4:9:ALA:H	1.61	0.41
51:M5:44:ARG:NH1	51:M5:120:TRP:O	2.54	0.41
51:M5:122:ASN:OD1	51:M5:123:GLN:N	2.54	0.41
52:M6:148:LYS:HB2	52:M6:149:TYR:CE2	2.56	0.41
52:M6:170:LYS:HB3	52:M6:170:LYS:HE2	2.89	0.41
53:M7:4:TYR:CE1	53:M7:16:SER:HB2	2.91	0.41
53:M7:52:LEU:HD13	53:M7:88:VAL:HG11	2.47	0.41
54:M8:54:LEU:HD23	54:M8:54:LEU:HA	2.14	0.41
54:M8:69:ARG:HH21	36:5:784:A:H2'	160.40	0.41
36:1:720:A:H2'	54:M8:69:ARG:NH2	2.36	0.41
56:N0:66:GLU:HG3	56:N0:68:HIS:H	1.86	0.41
56:N0:8:GLN:OE1	56:N0:26:ARG:NE	2.38	0.41
36:1:1635:G:O6	63:N7:17:ARG:HB2	2.20	0.41
63:N7:34:LYS:HA	63:N7:34:LYS:HD2	1.89	0.41
63:N7:41:ALA:O	63:N7:43:VAL:HG13	3.56	0.41
63:N7:76:ASN:OD1	63:N7:77:TYR:N	2.54	0.41
63:N7:81:LEU:HD22	63:N7:82:PRO:HD2	2.82	0.41
64:N8:122:PRO:HB3	64:N8:142:GLY:O	2.69	0.41
64:N8:20:GLY:HA2	36:5:1369:A:O3'	181.20	0.41
65:N9:25:LYS:NZ	36:5:1107:C:H5''	200.95	0.41
69:O3:13:HIS:ND1	69:O3:93:THR:OG1	2.39	0.41
73:O7:36:SER:O	73:O7:45:ARG:HB3	2.59	0.41
73:O7:37:CYS:O	73:O7:45:ARG:N	2.66	0.41
78:Q2:8:ARG:O	78:Q2:23:HIS:N	2.52	0.41
2:S0:126:PRO:HG2	2:S0:152:PRO:HD2	2.35	0.41
2:S0:184:LEU:HA	2:S0:184:LEU:HD13	1.97	0.41
5:S3:113:LEU:HD23	5:S3:113:LEU:HA	1.81	0.41
6:S4:32:SER:HB2	6:S4:83:PRO:HD3	2.02	0.41
7:S5:62:VAL:HA	7:S5:89:ILE:HG21	2.03	0.41
10:S8:106:ALA:HB2	10:S8:165:LEU:HG	2.03	0.41
10:S8:193:LEU:HA	10:S8:193:LEU:HD23	1.88	0.41
10:S8:192:TYR:O	10:S8:196:LEU:HB2	2.21	0.41
10:S8:8:ARG:NH1	10:S8:21:PHE:HB3	2.36	0.41
11:S9:58:ASP:O	11:S9:61:THR:OG1	2.80	0.41
34:SR:135:THR:HG22	34:SR:141:LEU:HD23	2.03	0.41
36:1:1257:C:H42	36:1:1261:G:H22	1.69	0.40
36:1:1480:G:H4'	36:1:1481:A:OP1	2.21	0.40
36:1:1477:A:H61	36:1:1876:U:H3	1.69	0.40
36:1:2402:A:H2'	41:L4:67:THR:HG21	2.02	0.40
36:1:2444:C:H42	36:1:2503:G:N2	2.19	0.40
36:1:3328:G:H2'	36:1:3329:U:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:900:G:C4	36:1:901:G:C8	3.09	0.40
1:2:582:U:H5'	1:2:583:C:H5	1.86	0.40
1:2:773:C:OP1	6:S4:22:LYS:N	2.52	0.40
1:2:973:A:H2'	1:2:974:A:C8	2.57	0.40
1:2:989:U:O5'	1:2:989:U:H6	2.04	0.40
36:5:1317:A:C2	36:5:1319:G:C6	3.09	0.40
36:5:1856:C:H2'	36:5:1857:C:C6	2.52	0.40
36:5:531:G:H2'	36:5:532:A:C8	2.55	0.40
36:5:580:C:H2'	36:5:581:U:O4'	2.21	0.40
1:6:1584:G:H22	1:6:1611:A:P	2.42	0.40
1:6:678:A:H2'	1:6:679:U:O4'	2.22	0.40
8:S6:173:PRO:O	1:6:79:C:H4'	345.30	0.40
38:8:19:C:H2'	38:8:20:U:O4'	2.21	0.40
38:8:47:C:H1'	38:8:61:A:H2'	2.03	0.40
13:C1:107:VAL:HA	13:C1:108:PRO:HD2	2.18	0.40
13:C1:84:ILE:HG13	13:C1:109:VAL:HG23	5.46	0.40
14:C2:45:LEU:HB3	14:C2:46:ARG:H	2.55	0.40
17:C5:97:TYR:OH	17:C5:99:GLY:O	2.34	0.40
7:S5:73:THR:HG23	18:C6:114:ARG:CD	2.51	0.40
18:C6:87:LYS:HB3	18:C6:87:LYS:HE2	1.92	0.40
19:C7:115:LEU:HB3	19:C7:116:LYS:H	1.58	0.40
1:2:1559:A:N6	20:C8:134:ARG:HD2	2.36	0.40
22:D0:80:GLU:OE1	31:D9:44:ARG:NH1	2.61	0.40
23:D1:56:SER:O	23:D1:60:ARG:HG3	2.80	0.40
24:D2:20:THR:OG1	24:D2:22:LYS:HD3	2.52	0.40
25:D3:53:VAL:HG23	25:D3:100:ASP:O	2.21	0.40
25:D3:63:GLN:HG3	1:6:1755:A:H8	346.51	0.40
33:E1:144:CYS:O	33:E1:146:SER:N	2.53	0.40
40:L3:380:MET:O	36:5:3369:G:N2	226.61	0.40
41:L4:209:TYR:O	41:L4:230:VAL:HG22	2.37	0.40
41:L4:316:ASN:HA	41:L4:317:PRO:HD3	1.89	0.40
42:L5:57:ASN:HA	42:L5:58:LYS:HZ2	1.86	0.40
43:L6:55:LEU:HD11	43:L6:66:SER:HB2	4.43	0.40
54:M8:184:PHE:CG	36:5:2730:G:H4'	191.10	0.40
56:N0:17:GLU:O	56:N0:20:PRO:HD3	2.22	0.40
56:N0:34:GLU:HG2	56:N0:34:GLU:H	2.26	0.40
57:N1:32:LYS:HE3	57:N1:34:TYR:OH	2.21	0.40
59:N3:90:GLY:O	60:N4:16:GLY:HA2	2.21	0.40
62:N6:109:LEU:HD22	62:N6:115:ARG:CZ	2.51	0.40
63:N7:88:ASP:HB3	63:N7:121:ARG:NH2	2.37	0.40
64:N8:90:TYR:HB3	64:N8:100:PRO:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:O0:40:LYS:HD3	66:O0:93:LEU:O	2.54	0.40
68:O2:109:LEU:HD23	68:O2:109:LEU:HA	1.99	0.40
70:O4:106:LYS:HA	70:O4:109:THR:HB	2.02	0.40
72:O6:77:LEU:HD23	36:5:294:U:H4'	147.00	0.40
73:O7:63:ARG:O	73:O7:68:LYS:HE2	2.21	0.40
5:S3:134:CYS:N	5:S3:157:LEU:HD11	2.36	0.40
6:S4:164:LEU:HD23	6:S4:164:LEU:HA	2.11	0.40
7:S5:149:VAL:HG12	7:S5:156:ARG:O	3.27	0.40
8:S6:2:LYS:HB2	8:S6:2:LYS:HE3	1.87	0.40
10:S8:99:ALA:HB3	1:6:329:G:H5'	271.42	0.40
35:SM:61:ILE:HG13	35:SM:61:ILE:H	1.60	0.40
34:SR:134:TRP:CD1	34:SR:134:TRP:N	2.89	0.40
36:1:1340:G:H2'	36:1:1341:U:H6	1.87	0.40
36:1:1467:A:N1	36:1:1511:U:O2'	2.44	0.40
36:1:1520:G:H2'	36:1:1521:G:O4'	2.21	0.40
36:1:2899:C:O2'	36:1:2901:G:OP2	2.33	0.40
36:1:107:A:H1'	36:1:325:A:N3	2.37	0.40
36:1:3341:U:HO2'	36:1:3342:A:P	2.44	0.40
1:2:1542:G:N2	1:2:1568:C:H1'	2.35	0.40
1:2:1584:G:N7	18:C6:14:LYS:HE2	2.36	0.40
1:2:1600:A:HO2'	1:2:1602:C:N4	2.18	0.40
1:2:348:U:H2'	1:2:349:U:O4'	2.21	0.40
1:2:497:G:O2'	1:2:498:G:N7	2.54	0.40
1:2:851:U:C4	1:2:852:C:N4	2.89	0.40
38:4:45:C:H4'	75:O9:11:GLN:OE1	2.21	0.40
36:5:1223:A:OP2	36:5:1285:G:N2	2.51	0.40
36:5:1195:A:H2'	36:5:1309:U:O2	2.21	0.40
36:5:2186:U:H2'	36:5:2187:G:O4'	2.22	0.40
36:5:2573:G:H2'	36:5:2574:G:O4'	2.21	0.40
51:M5:171:SER:O	36:5:288:C:H4'	124.54	0.40
36:5:828:A:H2'	36:5:829:U:C6	2.56	0.40
36:5:980:A:H2'	36:5:981:U:C2	2.57	0.40
1:6:1405:G:H2'	1:6:1406:A:H8	1.85	0.40
1:6:1541:G:C5	1:6:1542:G:C6	3.09	0.40
1:6:727:U:H2'	1:6:728:U:H6	1.87	0.40
15:C3:135:LEU:HD22	15:C3:139:TRP:CG	2.56	0.40
15:C3:16:ILE:HD12	15:C3:16:ILE:HA	4.34	0.40
15:C3:17:PRO:HG3	1:6:959:U:C2	356.08	0.40
16:C4:48:VAL:HG11	16:C4:53:ASP:HB3	3.83	0.40
18:C6:55:VAL:HG21	18:C6:105:LEU:HG	2.03	0.40
19:C7:46:LEU:HD23	19:C7:46:LEU:HA	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C8:100:THR:HG21	20:C8:108:LYS:HG3	2.03	0.40
17:C5:110:GLU:HB2	20:C8:119:ILE:HD11	2.03	0.40
20:C8:86:LEU:HG	20:C8:99:HIS:HB2	2.03	0.40
22:D0:106:ILE:HD12	22:D0:106:ILE:HA	1.95	0.40
24:D2:105:THR:HG22	1:6:804:A:N3	368.08	0.40
25:D3:127:VAL:O	25:D3:130:VAL:HG22	2.21	0.40
26:D4:23:PHE:HE2	26:D4:75:VAL:HG23	5.38	0.40
28:D6:23:CYS:HB3	28:D6:26:CYS:HB2	4.86	0.40
30:D8:64:ARG:NH2	30:D8:65:ARG:HB2	6.72	0.40
32:E0:2:ALA:O	32:E0:4:VAL:HG23	2.21	0.40
40:L3:117:ARG:NH1	40:L3:175:LYS:HD3	2.36	0.40
41:L4:141:ARG:HH22	36:5:1386:A:H5"	126.52	0.40
41:L4:3:ARG:HB3	41:L4:22:LEU:HB2	3.44	0.40
42:L5:120:LYS:HG3	42:L5:120:LYS:H	2.46	0.40
42:L5:270:LYS:HE2	42:L5:273:ARG:HA	9.07	0.40
43:L6:154:LEU:HD23	43:L6:154:LEU:HA	1.85	0.40
44:L7:75:TYR:HB2	57:N1:141:VAL:HG22	2.04	0.40
45:L8:156:ASP:OD2	45:L8:156:ASP:N	2.83	0.40
45:L8:152:LEU:HB3	45:L8:180:VAL:HG11	2.16	0.40
46:L9:23:ARG:NH2	46:L9:41:ILE:O	2.77	0.40
46:L9:84:LYS:NZ	46:L9:191:LEU:HD22	2.36	0.40
47:M0:61:SER:HB2	47:M0:63:GLU:OE2	4.18	0.40
36:1:3215:A:H8	50:M4:121:MET:HE2	1.84	0.40
56:N0:8:GLN:HB3	56:N0:64:ILE:HD11	2.03	0.40
57:N1:35:LYS:HE3	57:N1:35:LYS:HB2	1.88	0.40
59:N3:18:PRO:HA	59:N3:51:ALA:HA	2.03	0.40
64:N8:121:VAL:HA	64:N8:122:PRO:HD3	2.17	0.40
36:1:709:A:O2'	64:N8:57:GLY:HA3	2.22	0.40
71:O5:110:ALA:O	71:O5:112:PRO:HD3	2.21	0.40
77:Q1:20:VAL:O	77:Q1:23:ARG:HB2	2.21	0.40
2:S0:38:PHE:HD2	2:S0:49:ASN:HD22	2.69	0.40
3:S1:63:GLY:HA2	3:S1:88:VAL:O	2.21	0.40
4:S2:200:SER:HG	1:6:4:C:P	385.35	0.40
4:S2:56:ILE:HA	4:S2:61:LEU:HD12	2.03	0.40
6:S4:159:THR:HB	6:S4:227:VAL:HG23	2.02	0.40
7:S5:213:LYS:HA	7:S5:213:LYS:HD3	1.81	0.40
9:S7:21:ALA:O	9:S7:25:VAL:HG23	2.21	0.40
11:S9:105:LEU:HA	11:S9:105:LEU:HD12	2.26	0.40
11:S9:77:ILE:HD11	11:S9:93:LEU:HB3	2.03	0.40
35:SM:33:LYS:HA	35:SM:33:LYS:HD2	1.70	0.40
20:C8:145:ARG:HB2	35:SM:68:ARG:NH2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:SM:89:ARG:C	35:SM:91:THR:H	2.24	0.40
34:SR:144:LEU:HD21	34:SR:186:PHE:HB3	3.46	0.40
36:1:1112:A:H2'	36:1:1113:G:C8	2.56	0.40
36:1:114:A:OP1	51:M5:54:LYS:NZ	2.55	0.40
36:1:1495:U:H5	36:1:1835:A:N1	2.19	0.40
36:1:1537:A:H2'	36:1:1538:G:O4'	2.21	0.40
36:1:1565:G:N2	36:1:1574:C:O2	2.54	0.40
36:1:1752:A:H8	36:1:1752:A:O5'	2.04	0.40
36:1:641:C:H2'	36:1:642:U:O4'	2.21	0.40
1:2:1339:C:O2'	1:2:1341:A:C8	2.71	0.40
1:2:144:U:O2'	1:2:145:A:H8	2.05	0.40
1:2:1680:G:C2	1:2:1720:G:C2	3.10	0.40
1:2:393:C:OP2	10:S8:2:GLY:N	2.53	0.40
1:2:407:A:H2'	1:2:408:C:C6	2.57	0.40
1:2:743:U:OP1	9:S7:108:GLN:N	2.51	0.40
1:2:795:U:H6	1:2:795:U:H2'	1.66	0.40
1:2:819:G:C6	1:2:853:G:C2	3.09	0.40
1:2:856:A:N6	9:S7:96:ARG:HB3	2.37	0.40
1:2:927:C:H2'	1:2:928:U:C6	2.56	0.40
38:4:141:C:OP1	51:M5:109:ARG:NH1	2.52	0.40
36:5:1573:G:C6	36:5:1574:C:H1'	2.56	0.40
36:5:1867:A:H2'	36:5:1868:G:C8	2.56	0.40
36:5:2225:U:H2'	36:5:2226:U:H6	1.87	0.40
36:5:2513:U:H4'	36:5:2514:U:OP1	2.21	0.40
36:5:334:A:H2'	36:5:335:G:C8	2.57	0.40
1:6:1733:C:H2'	1:6:1734:U:H6	1.86	0.40
1:6:404:G:H2'	1:6:405:C:C6	2.56	0.40
1:6:778:G:C6	1:6:783:G:C6	3.08	0.40
1:6:837:G:H2'	1:6:838:G:H8	1.85	0.40
38:8:78:G:H2'	38:8:79:A:O4'	2.20	0.40
24:D2:107:SER:HB3	1:6:802:G:H21	366.53	0.40
24:D2:41:MET:HG2	24:D2:129:VAL:HG21	2.03	0.40
25:D3:23:ARG:HB3	25:D3:29:TYR:CE1	2.57	0.40
28:D6:35:ALA:O	28:D6:36:ILE:HB	2.21	0.40
39:L2:104:LEU:HD12	39:L2:104:LEU:HA	1.90	0.40
40:L3:10:ARG:NH1	40:L3:12:GLY:O	2.55	0.40
40:L3:19:ARG:HB3	40:L3:232:ARG:HH12	2.03	0.40
40:L3:75:ALA:HB2	36:5:3049:A:C2	246.29	0.40
41:L4:234:ASN:OD1	36:5:693:A:H4'	104.91	0.40
42:L5:153:THR:HG23	42:L5:160:PHE:CZ	2.56	0.40
43:L6:100:LYS:NZ	43:L6:137:ASP:OD2	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:39:GLU:O	44:L7:42:ALA:HB3	2.22	0.40
45:L8:57:ARG:HB3	45:L8:61:GLN:NE2	3.59	0.40
47:M0:76:MET:HE3	47:M0:148:VAL:HG22	2.04	0.40
49:M3:47:ALA:HB1	49:M3:48:PRO:CD	2.56	0.40
51:M5:37:HIS:NE2	51:M5:63:ARG:HB3	2.36	0.40
54:M8:166:LEU:HD23	54:M8:166:LEU:HA	2.08	0.40
54:M8:57:ILE:HG21	54:M8:57:ILE:HD13	1.87	0.40
56:N0:46:GLN:HG2	56:N0:51:VAL:O	2.21	0.40
59:N3:136:VAL:HG12	59:N3:137:VAL:HG23	2.04	0.40
64:N8:94:ALA:HA	64:N8:121:VAL:HG13	2.60	0.40
65:N9:22:LYS:HB2	65:N9:23:LYS:H	3.34	0.40
68:O2:18:LYS:HD3	68:O2:30:GLU:HG2	2.03	0.40
68:O2:2:ALA:HB3	68:O2:90:LYS:NZ	2.37	0.40
49:M3:126:PHE:CD2	71:O5:115:LYS:HG2	2.56	0.40
72:O6:30:LYS:HD2	36:5:266:A:C5	103.01	0.40
73:O7:84:SER:O	73:O7:85:LYS:HB3	3.84	0.40
75:O9:21:ARG:CZ	75:O9:24:PRO:HG3	2.52	0.40
2:S0:41:ARG:HD2	2:S0:42:PRO:O	2.20	0.40
4:S2:218:ILE:H	4:S2:218:ILE:HG13	2.14	0.40
7:S5:119:ASP:O	7:S5:123:VAL:HG23	2.21	0.40
11:S9:127:VAL:HA	11:S9:130:THR:HG22	2.02	0.40
11:S9:92:LYS:C	11:S9:94:ASP:H	2.24	0.40
34:SR:21:THR:O	34:SR:291:SER:HB3	2.20	0.40
36:1:2798:C:H5'	36:1:2799:A:OP1	2.21	0.40
36:1:2884:C:H2'	36:1:2885:C:H6	1.87	0.40
36:1:607:A:H4'	36:1:608:A:OP2	2.21	0.40
1:2:1244:A:O2'	1:2:1245:G:OP1	2.36	0.40
1:2:1494:C:H2'	1:2:1495:C:C6	2.56	0.40
1:2:495:C:H3'	1:2:496:G:O4'	2.22	0.40
36:5:1807:G:C6	36:5:1808:G:N1	2.89	0.40
36:5:2946:A:H1'	36:5:2981:U:C4	2.56	0.40
53:M7:69:ARG:NH2	36:5:2991:A:N3	194.64	0.40
46:L9:174:LYS:NZ	36:5:3026:G:OP1	343.90	0.40
49:M3:63:VAL:HG13	36:5:72:C:H5'	113.85	0.40
1:6:1624:C:H2'	1:6:1625:C:C6	2.57	0.40
1:6:1684:U:H2'	1:6:1685:G:C8	2.57	0.40
1:6:191:C:O2'	1:6:192:U:O5'	2.38	0.40
11:S9:79:ARG:NH1	1:6:762:A:OP1	410.27	0.40
36:5:409:A:H61	38:8:15:G:H1'	1.86	0.40
12:C0:33:GLU:O	12:C0:35:ILE:N	2.51	0.40
12:C0:53:GLY:O	12:C0:55:VAL:N	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:C1:83:THR:HG21	1:6:325:G:H4'	289.97	0.40
18:C6:10:PHE:CE2	1:6:1379:C:H5'	433.60	0.40
19:C7:57:LEU:HA	19:C7:60:ARG:HG2	2.03	0.40
25:D3:5:LYS:HA	25:D3:6:PRO:HD2	1.97	0.40
27:D5:78:ILE:HG13	27:D5:81:ARG:HH12	6.24	0.40
28:D6:76:SER:OG	1:6:1793:G:N2	322.63	0.40
30:D8:54:LEU:HD13	30:D8:54:LEU:HA	3.26	0.40
39:L2:65:ASP:HA	39:L2:66:PRO:HD3	1.90	0.40
41:L4:343:LYS:HE2	41:L4:343:LYS:HB3	2.98	0.40
43:L6:145:LEU:HA	43:L6:145:LEU:HD23	2.10	0.40
46:L9:16:VAL:HG12	46:L9:29:GLY:CA	2.52	0.40
47:M0:16:PRO:HG3	47:M0:128:ARG:HH11	1.86	0.40
47:M0:206:LEU:HD12	47:M0:206:LEU:HA	2.22	0.40
50:M4:38:ILE:HD11	56:N0:150:PHE:CE2	2.50	0.40
53:M7:109:ALA:O	53:M7:111:LYS:N	2.54	0.40
56:N0:132:THR:O	56:N0:133:ALA:HB3	2.25	0.40
61:N5:71:THR:O	61:N5:75:LYS:HG3	2.21	0.40
63:N7:4:PHE:HE1	63:N7:82:PRO:HB3	2.76	0.40
63:N7:64:LYS:HE2	63:N7:64:LYS:HB2	3.94	0.40
52:M6:29:ASN:ND2	69:O3:14:LEU:HD22	3.10	0.40
72:O6:60:LEU:HD13	72:O6:64:SER:HB3	2.04	0.40
4:S2:174:ARG:O	11:S9:97:LEU:HB3	3.31	0.40
6:S4:35:PRO:HB2	6:S4:36:HIS:CD2	3.00	0.40
6:S4:47:PHE:CZ	6:S4:90:ILE:HD12	2.56	0.40
9:S7:111:LYS:HB3	9:S7:112:ARG:H	1.98	0.40
10:S8:162:ALA:HA	36:1:3353:G:C5'	2.49	0.40
10:S8:21:PHE:CE1	10:S8:22:ARG:HD3	2.57	0.40
10:S8:36:THR:HA	10:S8:58:LEU:HA	2.43	0.40
1:2:475:A:OP2	11:S9:126:ARG:NH1	2.54	0.40
11:S9:163:PRO:C	11:S9:165:GLY:H	2.25	0.40
34:SR:70:ASP:OD1	34:SR:71:CYS:N	2.55	0.40
36:1:1018:G:H2'	36:1:1019:G:O4'	2.21	0.40
36:1:1851:G:O5'	36:1:1851:G:H8	2.05	0.40
36:1:2331:C:H2'	36:1:2332:A:C8	2.57	0.40
36:1:2516:U:O2	36:1:2594:C:N4	2.55	0.40
36:1:2898:G:H5''	36:1:2899:C:C5'	2.52	0.40
36:1:31:C:OP2	51:M5:188:ARG:NH2	2.54	0.40
36:1:61:A:H2'	36:1:62:A:O4'	2.22	0.40
1:2:1244:A:HO2'	1:2:1245:G:P	2.44	0.40
1:2:1489:U:OP2	5:S3:9:ARG:NH2	2.55	0.40
1:2:337:G:O3'	10:S8:10:LYS:HE2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:449:C:H2'	1:2:450:U:C6	2.57	0.40
1:2:60:U:H5'	1:2:455:C:N4	2.36	0.40
1:2:823:G:HO2'	1:2:824:G:C5'	2.34	0.40
58:N2:42:LYS:NZ	36:5:1686:U:OP1	177.58	0.40
36:5:2288:G:H2'	36:5:2289:U:C6	2.56	0.40
36:5:2714:G:C8	36:5:2751:G:H2'	2.56	0.40
36:5:90:C:H4'	36:5:282:G:H5''	2.03	0.40
36:5:3338:C:H2'	36:5:3339:A:O4'	2.21	0.40
36:5:761:A:C2	36:5:771:A:H1'	2.57	0.40
1:6:138:A:H5''	1:6:138:A:N3	2.37	0.40
1:6:1489:U:H5'	1:6:1494:C:H1'	2.03	0.40
1:6:393:C:H2'	1:6:394:C:C6	2.57	0.40
1:6:701:U:H2'	1:6:702:G:C8	2.56	0.40
1:6:784:C:H2'	1:6:785:U:C6	2.57	0.40
13:C1:76:VAL:HG12	13:C1:85:VAL:O	2.32	0.40
36:1:2820:A:C2	87:C:3401:SPS:H182	2.57	0.40
17:C5:22:LEU:HA	17:C5:25:LEU:HB2	3.18	0.40
21:C9:33:TYR:HH	21:C9:99:SER:HG	2.15	0.40
24:D2:104:LEU:HD23	24:D2:125:ILE:HA	5.44	0.40
25:D3:41:SER:HA	25:D3:42:PRO:HD3	1.81	0.40
25:D3:42:PRO:HB3	25:D3:83:VAL:HG21	2.03	0.40
26:D4:7:ILE:HG23	26:D4:27:VAL:HG22	2.04	0.40
26:D4:20:ARG:HB3	26:D4:76:TYR:CD2	2.69	0.40
27:D5:41:ILE:HG23	27:D5:42:LEU:H	1.87	0.40
29:D7:19:HIS:O	29:D7:21:LEU:N	2.90	0.40
29:D7:63:LEU:O	29:D7:74:SER:N	2.52	0.40
40:L3:214:MET:SD	40:L3:281:LYS:HB2	2.69	0.40
42:L5:104:LEU:HD11	42:L5:108:ARG:HH21	1.86	0.40
44:L7:90:LYS:HB3	44:L7:133:TYR:HB3	2.25	0.40
44:L7:40:LYS:HA	44:L7:43:ILE:HD12	2.04	0.40
44:L7:53:LYS:HE3	44:L7:57:THR:HG21	4.20	0.40
48:M1:50:ALA:HB2	48:M1:65:ILE:HD12	2.04	0.40
52:M6:110:PRO:HB2	52:M6:111:PRO:CD	3.11	0.40
36:1:1181:U:H2'	52:M6:122:GLN:NE2	2.37	0.40
52:M6:62:THR:HG22	52:M6:65:ASN:H	2.25	0.40
54:M8:29:LEU:HA	54:M8:29:LEU:HD23	2.04	0.40
54:M8:41:ASP:OD1	54:M8:41:ASP:N	3.40	0.40
56:N0:1:MET:CE	56:N0:32:SER:H	2.34	0.40
56:N0:82:ASP:HA	56:N0:87:THR:HA	2.04	0.40
63:N7:61:LYS:HD3	63:N7:61:LYS:HA	2.00	0.40
67:O1:10:ARG:HD2	67:O1:12:TYR:OH	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:O2:111:ARG:NH2	68:O2:115:LEU:HD21	2.37	0.40
68:O2:22:SER:HA	68:O2:28:VAL:HG12	2.25	0.40
69:O3:26:ASN:O	69:O3:84:THR:HG22	2.35	0.40
70:O4:3:GLN:NE2	70:O4:30:LEU:H	4.51	0.40
73:O7:53:ALA:O	73:O7:56:ARG:HB2	2.52	0.40
36:1:1841:A:H2	75:O9:45:ARG:HH22	1.70	0.40
76:Q0:111:ARG:HG3	76:Q0:112:LYS:HD2	2.02	0.40
3:S1:171:ILE:HA	3:S1:174:LYS:HE3	2.04	0.40
3:S1:223:PHE:HE2	3:S1:228:LEU:HD22	1.86	0.40
3:S1:23:PRO:O	3:S1:26:ARG:HB3	2.59	0.40
4:S2:144:TRP:CZ2	4:S2:173:PRO:HG3	3.08	0.40
5:S3:70:THR:CG2	5:S3:86:LEU:HB2	2.52	0.40
5:S3:72:LEU:HD22	12:C0:65:TYR:CD1	3.16	0.40
5:S3:76:ARG:HG3	12:C0:65:TYR:CZ	3.68	0.40
9:S7:31:SER:N	9:S7:32:PRO:HD2	2.82	0.40
10:S8:8:ARG:HE	10:S8:21:PHE:HD1	1.70	0.40
11:S9:156:ILE:HG13	11:S9:156:ILE:H	1.98	0.40
34:SR:286:GLU:HA	34:SR:287:PRO:HD3	1.83	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.





Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1353:U:O2'	36:5:3165:A:OP1[2_546]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	S0	204/251 (81%)	166 (81%)	26 (13%)	12 (6%)	 
2	s0	204/251 (81%)	162 (79%)	27 (13%)	15 (7%)	 

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	S1	212/254 (84%)	156 (74%)	27 (13%)	29 (14%)	0	1
3	s1	214/254 (84%)	167 (78%)	34 (16%)	13 (6%)	2	11
4	S2	215/253 (85%)	178 (83%)	27 (13%)	10 (5%)	3	17
4	s2	215/253 (85%)	185 (86%)	18 (8%)	12 (6%)	2	13
5	S3	221/239 (92%)	192 (87%)	21 (10%)	8 (4%)	4	24
5	s3	221/239 (92%)	185 (84%)	24 (11%)	12 (5%)	2	14
6	S4	258/260 (99%)	213 (83%)	31 (12%)	14 (5%)	2	14
6	s4	258/260 (99%)	209 (81%)	38 (15%)	11 (4%)	3	19
7	S5	204/224 (91%)	169 (83%)	21 (10%)	14 (7%)	1	8
7	s5	204/224 (91%)	157 (77%)	33 (16%)	14 (7%)	1	8
8	S6	224/236 (95%)	191 (85%)	21 (9%)	12 (5%)	2	14
8	s6	216/236 (92%)	190 (88%)	17 (8%)	9 (4%)	3	19
9	S7	182/189 (96%)	138 (76%)	27 (15%)	17 (9%)	1	4
9	s7	184/189 (97%)	148 (80%)	28 (15%)	8 (4%)	3	19
10	S8	184/200 (92%)	160 (87%)	18 (10%)	6 (3%)	5	26
10	s8	184/200 (92%)	161 (88%)	17 (9%)	6 (3%)	5	26
11	S9	183/196 (93%)	158 (86%)	17 (9%)	8 (4%)	3	18
11	s9	183/196 (93%)	152 (83%)	21 (12%)	10 (6%)	2	13
12	C0	94/105 (90%)	71 (76%)	16 (17%)	7 (7%)	1	7
12	c0	92/105 (88%)	62 (67%)	14 (15%)	16 (17%)	0	0
13	C1	153/155 (99%)	129 (84%)	18 (12%)	6 (4%)	4	22
13	c1	144/155 (93%)	120 (83%)	18 (12%)	6 (4%)	3	19
14	C2	122/142 (86%)	77 (63%)	31 (25%)	14 (12%)	0	2
14	c2	122/142 (86%)	78 (64%)	30 (25%)	14 (12%)	0	2
15	C3	148/150 (99%)	126 (85%)	16 (11%)	6 (4%)	3	20
15	c3	148/150 (99%)	118 (80%)	23 (16%)	7 (5%)	3	17
16	C4	125/136 (92%)	92 (74%)	21 (17%)	12 (10%)	1	4
16	c4	126/136 (93%)	102 (81%)	18 (14%)	6 (5%)	3	17
17	C5	122/141 (86%)	90 (74%)	22 (18%)	10 (8%)	1	6
17	c5	133/141 (94%)	98 (74%)	18 (14%)	17 (13%)	0	1
18	C6	139/142 (98%)	116 (84%)	14 (10%)	9 (6%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	c6	140/142 (99%)	123 (88%)	10 (7%)	7 (5%)	3	16
19	C7	116/136 (85%)	91 (78%)	18 (16%)	7 (6%)	2	11
19	c7	113/136 (83%)	90 (80%)	13 (12%)	10 (9%)	1	5
20	C8	143/145 (99%)	121 (85%)	13 (9%)	9 (6%)	2	10
20	c8	143/145 (99%)	116 (81%)	18 (13%)	9 (6%)	2	10
21	C9	141/143 (99%)	120 (85%)	15 (11%)	6 (4%)	3	19
21	c9	141/143 (99%)	124 (88%)	13 (9%)	4 (3%)	6	30
22	D0	105/120 (88%)	90 (86%)	11 (10%)	4 (4%)	4	22
22	d0	108/120 (90%)	84 (78%)	18 (17%)	6 (6%)	2	13
23	D1	85/87 (98%)	66 (78%)	14 (16%)	5 (6%)	2	12
23	d1	85/87 (98%)	67 (79%)	13 (15%)	5 (6%)	2	12
24	D2	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	12	44
24	d2	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	24	63
25	D3	142/144 (99%)	111 (78%)	19 (13%)	12 (8%)	1	5
25	d3	142/144 (99%)	127 (89%)	10 (7%)	5 (4%)	4	24
26	D4	132/134 (98%)	110 (83%)	13 (10%)	9 (7%)	1	8
26	d4	132/134 (98%)	112 (85%)	12 (9%)	8 (6%)	2	11
27	D5	68/107 (64%)	53 (78%)	8 (12%)	7 (10%)	1	4
27	d5	67/107 (63%)	56 (84%)	9 (13%)	2 (3%)	5	28
28	D6	95/97 (98%)	62 (65%)	19 (20%)	14 (15%)	0	1
28	d6	95/97 (98%)	71 (75%)	18 (19%)	6 (6%)	2	10
29	D7	79/81 (98%)	66 (84%)	11 (14%)	2 (2%)	7	32
29	d7	79/81 (98%)	60 (76%)	16 (20%)	3 (4%)	4	22
30	D8	61/66 (92%)	48 (79%)	12 (20%)	1 (2%)	12	44
30	d8	61/66 (92%)	46 (75%)	11 (18%)	4 (7%)	1	9
31	D9	51/55 (93%)	40 (78%)	9 (18%)	2 (4%)	4	22
31	d9	51/55 (93%)	41 (80%)	7 (14%)	3 (6%)	2	12
32	E0	58/60 (97%)	46 (79%)	10 (17%)	2 (3%)	5	25
33	E1	69/76 (91%)	37 (54%)	18 (26%)	14 (20%)	0	0
33	e1	74/76 (97%)	35 (47%)	20 (27%)	19 (26%)	0	0
34	SR	316/318 (99%)	273 (86%)	30 (10%)	13 (4%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	sR	316/318 (99%)	268 (85%)	38 (12%)	10 (3%)	5	26
35	SM	131/263 (50%)	105 (80%)	16 (12%)	10 (8%)	1	7
35	sM	80/263 (30%)	61 (76%)	8 (10%)	11 (14%)	0	1
39	L2	250/253 (99%)	230 (92%)	15 (6%)	5 (2%)	9	38
39	l2	250/253 (99%)	209 (84%)	32 (13%)	9 (4%)	4	24
40	L3	384/386 (100%)	340 (88%)	28 (7%)	16 (4%)	3	19
40	l3	384/386 (100%)	346 (90%)	30 (8%)	8 (2%)	9	37
41	L4	359/361 (99%)	308 (86%)	32 (9%)	19 (5%)	2	14
41	l4	359/361 (99%)	297 (83%)	39 (11%)	23 (6%)	2	10
42	L5	294/296 (99%)	254 (86%)	22 (8%)	18 (6%)	2	11
42	l5	292/296 (99%)	263 (90%)	22 (8%)	7 (2%)	7	33
43	L6	152/175 (87%)	136 (90%)	14 (9%)	2 (1%)	15	50
43	l6	153/175 (87%)	128 (84%)	21 (14%)	4 (3%)	7	32
44	L7	220/243 (90%)	198 (90%)	14 (6%)	8 (4%)	4	24
44	l7	221/243 (91%)	200 (90%)	17 (8%)	4 (2%)	11	42
45	L8	231/255 (91%)	193 (84%)	29 (13%)	9 (4%)	4	22
45	l8	229/255 (90%)	197 (86%)	20 (9%)	12 (5%)	2	15
46	L9	189/191 (99%)	163 (86%)	24 (13%)	2 (1%)	17	55
46	l9	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	9	37
47	M0	207/220 (94%)	180 (87%)	21 (10%)	6 (3%)	6	29
47	m0	209/220 (95%)	174 (83%)	27 (13%)	8 (4%)	4	22
48	M1	167/173 (96%)	134 (80%)	21 (13%)	12 (7%)	1	7
48	m1	167/173 (96%)	145 (87%)	10 (6%)	12 (7%)	1	7
49	M3	191/198 (96%)	162 (85%)	18 (9%)	11 (6%)	2	12
49	m3	192/198 (97%)	157 (82%)	22 (12%)	13 (7%)	1	8
50	M4	134/137 (98%)	117 (87%)	8 (6%)	9 (7%)	1	9
50	m4	135/137 (98%)	129 (96%)	6 (4%)	0	100	100
51	M5	201/203 (99%)	186 (92%)	8 (4%)	7 (4%)	4	24
51	m5	201/203 (99%)	179 (89%)	16 (8%)	6 (3%)	5	28
52	M6	195/198 (98%)	182 (93%)	9 (5%)	4 (2%)	9	37
52	m6	195/198 (98%)	181 (93%)	10 (5%)	4 (2%)	9	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	M7	181/183 (99%)	151 (83%)	21 (12%)	9 (5%)	3	16
53	m7	153/183 (84%)	141 (92%)	11 (7%)	1 (1%)	26	65
54	M8	183/185 (99%)	164 (90%)	15 (8%)	4 (2%)	8	36
54	m8	183/185 (99%)	162 (88%)	17 (9%)	4 (2%)	8	36
55	M9	186/188 (99%)	169 (91%)	16 (9%)	1 (0%)	34	72
55	m9	186/188 (99%)	168 (90%)	16 (9%)	2 (1%)	17	55
56	N0	170/172 (99%)	156 (92%)	10 (6%)	4 (2%)	7	33
56	n0	170/172 (99%)	159 (94%)	9 (5%)	2 (1%)	16	52
57	N1	157/159 (99%)	140 (89%)	15 (10%)	2 (1%)	15	50
57	n1	157/159 (99%)	145 (92%)	10 (6%)	2 (1%)	15	50
58	N2	98/120 (82%)	81 (83%)	15 (15%)	2 (2%)	9	38
58	n2	96/120 (80%)	83 (86%)	12 (12%)	1 (1%)	19	58
59	N3	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	26	65
59	n3	134/136 (98%)	126 (94%)	7 (5%)	1 (1%)	26	65
60	N4	96/155 (62%)	80 (83%)	10 (10%)	6 (6%)	2	10
60	n4	133/155 (86%)	110 (83%)	14 (10%)	9 (7%)	1	8
61	N5	119/141 (84%)	107 (90%)	8 (7%)	4 (3%)	5	25
61	n5	118/141 (84%)	98 (83%)	11 (9%)	9 (8%)	1	7
62	N6	124/126 (98%)	113 (91%)	10 (8%)	1 (1%)	24	63
62	n6	124/126 (98%)	114 (92%)	7 (6%)	3 (2%)	7	33
63	N7	133/135 (98%)	114 (86%)	10 (8%)	9 (7%)	1	8
63	n7	133/135 (98%)	99 (74%)	21 (16%)	13 (10%)	1	4
64	N8	146/148 (99%)	120 (82%)	19 (13%)	7 (5%)	3	17
64	n8	146/148 (99%)	129 (88%)	13 (9%)	4 (3%)	6	31
65	N9	56/58 (97%)	47 (84%)	7 (12%)	2 (4%)	4	24
65	n9	56/58 (97%)	41 (73%)	11 (20%)	4 (7%)	1	8
66	O0	95/104 (91%)	89 (94%)	6 (6%)	0	100	100
66	o0	98/104 (94%)	88 (90%)	9 (9%)	1 (1%)	19	58
67	O1	107/112 (96%)	98 (92%)	3 (3%)	6 (6%)	2	13
67	o1	107/112 (96%)	91 (85%)	11 (10%)	5 (5%)	3	17
68	O2	125/129 (97%)	116 (93%)	8 (6%)	1 (1%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	o2	125/129 (97%)	110 (88%)	11 (9%)	4 (3%)	5	26
69	O3	104/106 (98%)	95 (91%)	9 (9%)	0	100	100
69	o3	104/106 (98%)	96 (92%)	5 (5%)	3 (3%)	6	29
70	O4	110/119 (92%)	98 (89%)	11 (10%)	1 (1%)	21	61
70	o4	110/119 (92%)	96 (87%)	11 (10%)	3 (3%)	6	31
71	O5	117/119 (98%)	106 (91%)	10 (8%)	1 (1%)	21	61
71	o5	117/119 (98%)	101 (86%)	12 (10%)	4 (3%)	5	25
72	O6	97/99 (98%)	77 (79%)	15 (16%)	5 (5%)	2	15
72	o6	97/99 (98%)	80 (82%)	13 (13%)	4 (4%)	3	20
73	O7	85/87 (98%)	74 (87%)	9 (11%)	2 (2%)	7	33
73	o7	85/87 (98%)	73 (86%)	8 (9%)	4 (5%)	3	17
74	O8	75/77 (97%)	66 (88%)	6 (8%)	3 (4%)	4	21
74	o8	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	15	50
75	O9	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
75	o9	48/50 (96%)	44 (92%)	3 (6%)	1 (2%)	9	37
76	Q0	50/52 (96%)	44 (88%)	4 (8%)	2 (4%)	4	21
76	q0	50/52 (96%)	47 (94%)	2 (4%)	1 (2%)	9	38
77	Q1	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
77	q1	23/25 (92%)	23 (100%)	0	0	100	100
78	Q2	103/105 (98%)	79 (77%)	21 (20%)	3 (3%)	6	29
78	q2	103/105 (98%)	96 (93%)	6 (6%)	1 (1%)	19	58
79	Q3	89/91 (98%)	76 (85%)	10 (11%)	3 (3%)	5	25
79	q3	89/91 (98%)	82 (92%)	5 (6%)	2 (2%)	8	36
80	e0	60/62 (97%)	38 (63%)	16 (27%)	6 (10%)	1	4
82	p0	139/311 (45%)	120 (86%)	15 (11%)	4 (3%)	6	29
All	All	22291/24121 (92%)	18907 (85%)	2362 (11%)	1022 (5%)	3	17

All (1022) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	S0	4	PRO
2	S0	158	VAL
2	S0	190	ASP

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Mol	Chain	Res	Type
2	S0	191	ARG
3	S1	35	PRO
3	S1	37	THR
3	S1	58	SER
3	S1	60	ALA
3	S1	63	GLY
3	S1	132	ASP
3	S1	181	LEU
3	S1	182	ALA
3	S1	206	PRO
4	S2	106	ASP
4	S2	107	SER
4	S2	148	LEU
5	S3	62	ASN
5	S3	220	PRO
6	S4	234	PRO
7	S5	43	PHE
8	S6	122	GLU
8	S6	154	ARG
8	S6	173	PRO
9	S7	64	VAL
9	S7	131	PHE
9	S7	166	LEU
10	S8	149	SER
11	S9	93	LEU
11	S9	98	ALA
11	S9	134	ILE
11	S9	150	LEU
12	C0	60	SER
12	C0	87	VAL
12	C0	88	PRO
13	C1	7	VAL
14	C2	22	VAL
14	C2	126	TRP
14	C2	127	GLY
16	C4	42	VAL
16	C4	125	SER
17	C5	54	ALA
17	C5	87	PRO
17	C5	125	PRO
18	C6	40	GLU
18	C6	41	PRO

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Mol	Chain	Res	Type
18	C6	114	ARG
18	C6	138	PHE
19	C7	85	VAL
19	C7	86	PRO
19	C7	88	VAL
20	C8	14	ILE
20	C8	60	GLU
20	C8	92	ILE
21	C9	31	PRO
21	C9	53	TRP
27	D5	44	GLN
27	D5	71	ILE
27	D5	97	LYS
28	D6	45	VAL
28	D6	82	ARG
28	D6	84	VAL
28	D6	85	ARG
28	D6	86	VAL
32	E0	47	VAL
33	E1	84	VAL
33	E1	98	VAL
33	E1	103	LEU
34	SR	135	THR
34	SR	318	ALA
40	L3	3	HIS
40	L3	5	LYS
40	L3	19	ARG
40	L3	174	LYS
40	L3	347	SER
41	L4	4	PRO
41	L4	130	ALA
41	L4	131	VAL
41	L4	292	SER
41	L4	311	HIS
42	L5	233	ALA
42	L5	234	ASP
42	L5	252	ALA
45	L8	25	PRO
45	L8	31	PRO
45	L8	122	LYS
45	L8	196	ALA
48	M1	8	PRO

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Mol	Chain	Res	Type
48	M1	11	ASP
48	M1	55	ARG
49	M3	129	ASN
49	M3	166	ALA
50	M4	8	LYS
50	M4	9	ALA
51	M5	74	PRO
51	M5	75	VAL
52	M6	110	PRO
52	M6	111	PRO
53	M7	157	VAL
54	M8	41	ASP
56	N0	13	ARG
58	N2	51	GLY
59	N3	82	ALA
60	N4	64	THR
60	N4	81	PRO
63	N7	7	ALA
63	N7	17	ARG
63	N7	30	ASP
63	N7	125	GLY
71	O5	119	LYS
74	O8	18	ALA
76	Q0	78	ILE
78	Q2	30	ALA
2	s0	4	PRO
2	s0	164	ASN
2	s0	189	VAL
2	s0	206	ASP
3	s1	106	THR
3	s1	147	ALA
3	s1	223	PHE
4	s2	92	ALA
5	s3	211	PRO
5	s3	220	PRO
6	s4	12	LEU
7	s5	28	PRO
7	s5	43	PHE
7	s5	184	PHE
7	s5	204	GLY
8	s6	173	PRO
8	s6	174	LYS

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Mol	Chain	Res	Type
9	s7	64	VAL
9	s7	106	SER
10	s8	36	THR
12	c0	83	PRO
13	c1	61	THR
15	c3	66	ILE
16	c4	51	ASP
16	c4	126	THR
17	c5	11	VAL
17	c5	17	TYR
17	c5	52	LYS
17	c5	68	PRO
17	c5	80	MET
17	c5	125	PRO
17	c5	126	VAL
18	c6	116	LEU
19	c7	88	VAL
19	c7	99	VAL
19	c7	103	ASP
20	c8	8	GLN
20	c8	14	ILE
20	c8	91	ASP
20	c8	92	ILE
21	c9	29	GLU
21	c9	33	TYR
24	d2	68	ARG
26	d4	35	VAL
26	d4	78	SER
27	d5	104	ALA
28	d6	13	LYS
30	d8	16	LEU
31	d9	6	VAL
31	d9	7	TRP
80	e0	60	PRO
80	e0	61	SER
33	e1	87	THR
33	e1	92	LYS
33	e1	98	VAL
33	e1	100	LEU
33	e1	102	VAL
34	sR	163	ASP
35	sM	50	ASN

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Mol	Chain	Res	Type
39	l2	24	GLN
39	l2	238	ILE
40	l3	140	ASP
40	l3	347	SER
41	l4	14	GLU
41	l4	301	PRO
41	l4	329	PRO
42	l5	26	GLY
42	l5	258	LYS
42	l5	270	LYS
44	l7	228	SER
45	l8	25	PRO
45	l8	34	PHE
47	m0	25	ALA
47	m0	220	GLN
48	m1	8	PRO
48	m1	10	ARG
48	m1	94	ARG
48	m1	108	GLU
49	m3	47	ALA
49	m3	51	LEU
49	m3	101	ARG
49	m3	134	GLU
51	m5	55	ALA
51	m5	76	PRO
51	m5	183	THR
51	m5	184	LYS
52	m6	110	PRO
56	n0	2	ALA
57	n1	136	ARG
59	n3	42	SER
60	n4	63	ILE
60	n4	133	THR
61	n5	40	LEU
61	n5	44	PRO
62	n6	125	LYS
63	n7	3	LYS
63	n7	17	ARG
63	n7	125	GLY
63	n7	129	TRP
65	n9	23	LYS
65	n9	39	PHE

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Mol	Chain	Res	Type
67	o1	84	ASP
67	o1	86	LYS
68	o2	6	HIS
69	o3	88	ASN
70	o4	79	SER
72	o6	64	SER
76	q0	78	ILE
2	S0	39	ASN
2	S0	202	TYR
3	S1	26	ARG
3	S1	62	LYS
3	S1	213	ARG
5	S3	93	ASP
6	S4	104	ASP
7	S5	39	GLU
7	S5	63	GLN
7	S5	153	GLY
9	S7	32	PRO
9	S7	110	GLN
9	S7	116	ARG
12	C0	64	TYR
12	C0	81	ASN
12	C0	92	ILE
13	C1	4	GLU
13	C1	55	ASP
13	C1	145	ALA
14	C2	91	VAL
15	C3	22	ALA
15	C3	27	LYS
15	C3	68	GLY
16	C4	108	SER
16	C4	126	THR
17	C5	48	GLY
19	C7	115	LEU
19	C7	124	VAL
20	C8	61	LEU
20	C8	82	PRO
21	C9	50	ALA
21	C9	69	LYS
22	D0	16	GLN
22	D0	17	GLN
23	D1	7	GLN

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Mol	Chain	Res	Type
23	D1	8	LEU
24	D2	83	ILE
25	D3	3	LYS
25	D3	4	GLY
25	D3	39	LYS
25	D3	96	VAL
25	D3	114	LYS
25	D3	131	SER
26	D4	34	ASN
26	D4	60	PHE
26	D4	100	VAL
27	D5	39	ALA
28	D6	11	ASN
28	D6	18	VAL
33	E1	99	LYS
34	SR	146	GLY
35	SM	12	VAL
35	SM	87	THR
35	SM	140	ASP
39	L2	251	LYS
40	L3	186	GLY
41	L4	15	ALA
41	L4	140	HIS
41	L4	142	VAL
41	L4	313	LEU
41	L4	338	LYS
42	L5	6	ASP
43	L6	5	LYS
44	L7	24	GLU
44	L7	26	VAL
44	L7	160	ARG
44	L7	163	LEU
45	L8	39	ALA
45	L8	157	VAL
47	M0	113	GLN
48	M1	94	ARG
48	M1	108	GLU
48	M1	165	GLN
49	M3	47	ALA
49	M3	51	LEU
49	M3	76	THR
49	M3	141	ALA

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Mol	Chain	Res	Type
49	M3	165	SER
50	M4	10	SER
51	M5	94	TYR
51	M5	184	LYS
52	M6	89	SER
53	M7	67	ILE
53	M7	110	THR
55	M9	53	LYS
57	N1	124	VAL
57	N1	159	PHE
60	N4	97	LYS
61	N5	50	ALA
61	N5	117	ASN
62	N6	84	LYS
63	N7	16	GLY
64	N8	57	GLY
64	N8	66	ALA
64	N8	96	LYS
64	N8	97	GLU
67	O1	6	ASP
67	O1	84	ASP
74	O8	33	LYS
78	Q2	100	LYS
2	s0	68	PRO
2	s0	114	SER
3	s1	21	VAL
3	s1	26	ARG
3	s1	39	GLU
3	s1	232	HIS
4	s2	106	ASP
4	s2	163	GLY
4	s2	238	SER
5	s3	61	GLU
5	s3	216	PRO
5	s3	217	ILE
6	s4	94	ALA
6	s4	163	ASP
7	s5	100	ASN
8	s6	70	PRO
8	s6	175	ILE
9	s7	74	GLN
10	s8	122	GLY

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Mol	Chain	Res	Type
11	s9	6	ARG
11	s9	118	LEU
11	s9	147	MET
12	c0	2	LEU
12	c0	24	LYS
12	c0	25	LYS
12	c0	32	HIS
12	c0	80	LEU
12	c0	82	LEU
12	c0	94	ILE
13	c1	121	ASP
13	c1	133	LYS
14	c2	22	VAL
14	c2	89	ILE
15	c3	87	ASP
15	c3	139	TRP
17	c5	48	GLY
17	c5	127	ARG
17	c5	132	GLY
18	c6	42	GLU
19	c7	67	ARG
20	c8	135	GLY
22	d0	49	ASN
23	d1	44	ARG
25	d3	70	LYS
26	d4	33	ALA
26	d4	52	LYS
26	d4	53	ASP
28	d6	27	SER
28	d6	82	ARG
80	e0	51	ASN
33	e1	79	LYS
33	e1	83	LYS
33	e1	84	VAL
33	e1	105	TYR
33	e1	110	ALA
33	e1	112	GLY
33	e1	137	ASP
34	sR	165	ASP
34	sR	318	ALA
35	sM	42	ALA
35	sM	65	THR

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Mol	Chain	Res	Type
35	sM	124	GLU
39	l2	96	LEU
40	l3	129	ALA
40	l3	142	ALA
40	l3	155	ALA
40	l3	348	ARG
41	l4	15	ALA
41	l4	142	VAL
43	l6	98	VAL
44	l7	229	PHE
45	l8	122	LYS
45	l8	196	ALA
45	l8	203	VAL
46	l9	62	ARG
46	l9	144	ILE
48	m1	95	ASN
48	m1	153	LYS
49	m3	76	THR
49	m3	93	ILE
49	m3	129	ASN
49	m3	150	PRO
53	m7	37	ASN
54	m8	99	THR
55	m9	35	ALA
60	n4	25	ASP
60	n4	26	SER
60	n4	76	VAL
60	n4	83	THR
61	n5	24	LEU
61	n5	55	ASN
62	n6	83	ASP
62	n6	84	LYS
65	n9	21	ILE
66	o0	10	ILE
67	o1	45	GLY
67	o1	64	VAL
70	o4	82	ALA
71	o5	82	ALA
71	o5	119	LYS
72	o6	98	ARG
73	o7	87	SER
79	q3	4	ARG

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Mol	Chain	Res	Type
82	p0	33	VAL
2	S0	5	ALA
2	S0	95	ALA
2	S0	103	THR
2	S0	195	TRP
3	S1	21	VAL
3	S1	54	LEU
3	S1	61	LEU
3	S1	156	ALA
3	S1	158	SER
3	S1	177	GLN
3	S1	209	ASN
3	S1	221	PRO
3	S1	223	PHE
5	S3	216	PRO
5	S3	218	LEU
6	S4	12	LEU
6	S4	195	ILE
6	S4	204	GLY
6	S4	245	LYS
7	S5	31	GLU
7	S5	98	MET
8	S6	148	SER
8	S6	149	LYS
8	S6	152	ASP
8	S6	174	LYS
9	S7	5	GLN
9	S7	29	ASN
9	S7	74	GLN
9	S7	98	ILE
9	S7	133	THR
9	S7	144	VAL
9	S7	186	PRO
10	S8	59	ARG
10	S8	120	THR
11	S9	119	ALA
11	S9	167	ALA
12	C0	30	ALA
13	C1	6	THR
14	C2	69	ALA
14	C2	92	ALA
14	C2	106	ILE

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Mol	Chain	Res	Type
14	C2	107	ASP
14	C2	108	ARG
14	C2	111	ASN
14	C2	119	SER
15	C3	28	LEU
15	C3	138	ASN
16	C4	18	ARG
16	C4	75	GLY
16	C4	114	ARG
17	C5	11	VAL
17	C5	52	LYS
17	C5	69	GLU
17	C5	126	VAL
18	C6	32	ASN
18	C6	39	VAL
19	C7	98	GLY
20	C8	144	ARG
21	C9	39	THR
22	D0	49	ASN
23	D1	44	ARG
23	D1	82	VAL
25	D3	92	CYS
25	D3	112	LYS
26	D4	6	THR
26	D4	36	SER
26	D4	51	GLU
26	D4	54	ALA
27	D5	43	ASP
28	D6	16	GLY
28	D6	46	GLU
28	D6	81	ALA
28	D6	97	PRO
29	D7	23	THR
32	E0	51	ASN
33	E1	86	THR
33	E1	100	LEU
33	E1	102	VAL
33	E1	118	ARG
33	E1	144	CYS
34	SR	15	GLY
34	SR	16	HIS
34	SR	50	ASP

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Mol	Chain	Res	Type
34	SR	98	GLU
34	SR	163	ASP
35	SM	52	PRO
35	SM	86	ASN
39	L2	14	SER
39	L2	127	ALA
39	L2	144	ASN
39	L2	234	LYS
40	L3	4	ARG
40	L3	140	ASP
40	L3	155	ALA
40	L3	187	SER
41	L4	11	LEU
41	L4	146	PRO
41	L4	232	SER
42	L5	57	ASN
42	L5	137	ASP
42	L5	253	PHE
42	L5	259	LYS
42	L5	260	PHE
44	L7	91	GLY
44	L7	212	GLY
47	M0	144	ASN
47	M0	187	ALA
47	M0	194	GLY
48	M1	95	ASN
48	M1	114	ILE
49	M3	130	GLY
49	M3	136	GLU
50	M4	29	ALA
50	M4	36	VAL
51	M5	187	ARG
53	M7	160	ALA
53	M7	161	ALA
58	N2	11	ILE
60	N4	86	SER
63	N7	35	SER
64	N8	76	ASP
67	O1	83	GLU
68	O2	12	LYS
72	O6	34	SER
74	O8	58	ASP

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Mol	Chain	Res	Type
79	Q3	7	LYS
79	Q3	51	ALA
2	s0	30	GLN
2	s0	186	GLY
2	s0	194	PRO
3	s1	206	PRO
4	s2	149	GLY
5	s3	44	THR
5	s3	93	ASP
6	s4	90	ILE
6	s4	104	ASP
6	s4	168	LYS
6	s4	194	THR
7	s5	39	GLU
8	s6	138	ALA
8	s6	152	ASP
8	s6	154	ARG
9	s7	5	GLN
9	s7	30	SER
9	s7	144	VAL
10	s8	52	ASN
10	s8	62	THR
11	s9	150	LEU
11	s9	167	ALA
12	c0	30	ALA
12	c0	31	LYS
12	c0	92	THR
12	c0	95	GLN
13	c1	55	ASP
14	c2	58	LEU
14	c2	92	ALA
14	c2	101	ALA
14	c2	111	ASN
15	c3	140	LYS
16	c4	12	GLN
17	c5	12	PHE
17	c5	128	HIS
17	c5	131	ALA
18	c6	97	VAL
18	c6	113	ASP
20	c8	7	GLU
22	d0	17	GLN

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Mol	Chain	Res	Type
22	d0	72	ASN
23	d1	2	GLU
28	d6	8	ASN
29	d7	20	LYS
30	d8	33	LEU
31	d9	11	PRO
33	e1	81	LYS
33	e1	128	ALA
33	e1	131	PHE
34	sR	15	GLY
34	sR	160	GLU
34	sR	161	LYS
35	sM	66	ALA
35	sM	88	LYS
35	sM	128	ALA
39	l2	216	HIS
40	l3	3	HIS
40	l3	187	SER
41	l4	5	GLN
41	l4	90	PHE
41	l4	145	ILE
41	l4	220	ARG
41	l4	302	ALA
41	l4	339	LEU
41	l4	349	THR
42	l5	178	ASN
42	l5	260	PHE
43	l6	10	TYR
44	l7	178	ILE
45	l8	39	ALA
45	l8	69	LEU
45	l8	81	THR
45	l8	121	SER
45	l8	133	LYS
47	m0	82	ARG
47	m0	176	LEU
48	m1	9	MET
49	m3	135	ALA
49	m3	152	THR
52	m6	5	PRO
54	m8	84	VAL
54	m8	113	LYS

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Mol	Chain	Res	Type
60	n4	64	THR
60	n4	72	SER
60	n4	134	GLN
61	n5	45	LYS
61	n5	48	SER
61	n5	108	LEU
63	n7	7	ALA
63	n7	70	PRO
63	n7	103	GLN
63	n7	128	GLN
64	n8	48	TYR
64	n8	129	PHE
67	o1	82	GLU
69	o3	94	PHE
72	o6	33	ALA
74	o8	18	ALA
75	o9	3	ALA
2	S0	161	PRO
3	S1	48	VAL
3	S1	51	SER
3	S1	130	SER
3	S1	224	ASP
4	S2	223	GLY
4	S2	248	SER
5	S3	217	ILE
6	S4	3	ARG
6	S4	205	PHE
6	S4	235	TYR
7	S5	64	VAL
7	S5	65	ARG
8	S6	20	ASP
8	S6	25	ARG
8	S6	69	LEU
9	S7	36	ALA
9	S7	134	GLU
9	S7	178	GLY
10	S8	22	ARG
10	S8	40	ALA
10	S8	152	ILE
11	S9	147	MET
13	C1	3	THR
14	C2	125	ASN

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Mol	Chain	Res	Type
16	C4	40	ALA
16	C4	96	PRO
16	C4	124	ASP
17	C5	9	LYS
18	C6	142	TYR
20	C8	25	ASN
20	C8	76	PRO
21	C9	12	GLN
22	D0	21	LYS
23	D1	10	GLU
25	D3	40	SER
25	D3	41	SER
26	D4	5	VAL
27	D5	41	ILE
33	E1	87	THR
33	E1	109	ASP
33	E1	148	TYR
34	SR	161	LYS
34	SR	194	GLY
34	SR	237	GLN
35	SM	53	ARG
35	SM	88	ARG
35	SM	139	GLU
40	L3	66	LYS
40	L3	290	ASP
41	L4	5	GLN
41	L4	14	GLU
41	L4	270	SER
42	L5	93	THR
42	L5	188	GLU
42	L5	213	ASP
42	L5	221	GLU
42	L5	258	LYS
43	L6	98	VAL
44	L7	191	VAL
46	L9	96	HIS
48	M1	140	ARG
50	M4	28	SER
52	M6	65	ASN
53	M7	164	LYS
54	M8	98	LYS
54	M8	162	ALA

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Mol	Chain	Res	Type
56	N0	2	ALA
56	N0	154	HIS
61	N5	44	PRO
61	N5	55	ASN
63	N7	103	GLN
64	N8	117	ARG
72	O6	3	VAL
72	O6	27	SER
72	O6	64	SER
73	O7	84	SER
73	O7	85	LYS
2	s0	8	ASP
2	s0	115	PHE
3	s1	207	LEU
3	s1	224	ASP
4	s2	91	ARG
4	s2	235	LEU
4	s2	239	PRO
5	s3	45	LYS
5	s3	179	GLN
5	s3	196	ARG
5	s3	204	ASP
5	s3	219	ALA
6	s4	245	LYS
7	s5	29	ILE
7	s5	74	ALA
7	s5	81	ARG
7	s5	154	ALA
9	s7	133	THR
11	s9	3	ARG
11	s9	121	SER
12	c0	35	ILE
13	c1	7	VAL
14	c2	87	PRO
14	c2	106	ILE
14	c2	108	ARG
14	c2	131	ASP
16	c4	37	GLU
16	c4	114	ARG
17	c5	14	THR
17	c5	130	ARG
19	c7	63	LYS

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Mol	Chain	Res	Type
19	c7	86	PRO
19	c7	116	LYS
20	c8	61	LEU
23	d1	42	GLU
26	d4	36	SER
26	d4	58	PHE
27	d5	85	LYS
29	d7	3	LEU
30	d8	61	ARG
30	d8	62	GLU
80	e0	47	VAL
80	e0	54	ARG
33	e1	136	LYS
35	sM	46	LYS
39	l2	56	ALA
39	l2	80	GLU
41	l4	4	PRO
41	l4	144	LYS
41	l4	268	ALA
41	l4	311	HIS
41	l4	330	TYR
42	l5	119	TYR
43	l6	93	VAL
44	l7	191	VAL
46	l9	2	LYS
46	l9	167	VAL
47	m0	204	GLY
48	m1	167	TYR
49	m3	60	ALA
51	m5	68	ARG
52	m6	65	ASN
55	m9	156	ASN
56	n0	48	LEU
58	n2	60	GLY
61	n5	47	ALA
63	n7	34	LYS
63	n7	134	LEU
64	n8	76	ASP
68	o2	5	PRO
68	o2	125	ARG
71	o5	83	LYS
71	o5	84	LYS

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Mol	Chain	Res	Type
73	o7	58	THR
73	o7	86	ALA
2	S0	205	ARG
3	S1	176	VAL
3	S1	210	ILE
4	S2	35	TRP
4	S2	150	GLN
5	S3	81	PRO
6	S4	57	ASN
6	S4	77	ARG
7	S5	51	VAL
7	S5	58	LEU
7	S5	127	GLN
8	S6	146	GLY
9	S7	112	ARG
11	S9	166	GLY
14	C2	87	PRO
15	C3	3	ARG
16	C4	109	GLY
17	C5	127	ARG
19	C7	87	GLU
20	C8	142	GLY
25	D3	70	LYS
28	D6	36	ILE
29	D7	51	GLN
31	D9	20	GLN
33	E1	111	GLU
35	SM	63	ASP
41	L4	233	LEU
42	L5	125	VAL
42	L5	185	PHE
44	L7	178	ILE
45	L8	36	ILE
46	L9	2	LYS
48	M1	64	LYS
49	M3	193	ALA
50	M4	135	LEU
54	M8	99	THR
60	N4	80	ARG
63	N7	8	GLY
64	N8	56	VAL
65	N9	25	LYS

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Mol	Chain	Res	Type
67	O1	7	VAL
67	O1	82	GLU
67	O1	99	ALA
78	Q2	17	CYS
2	s0	10	THR
2	s0	103	THR
3	s1	153	HIS
3	s1	179	SER
4	s2	150	GLN
4	s2	182	PRO
6	s4	30	ARG
6	s4	107	GLY
6	s4	222	LEU
8	s6	126	ASP
10	s8	78	ILE
12	c0	3	MET
13	c1	144	ALA
14	c2	39	ASP
14	c2	107	ASP
14	c2	119	SER
15	c3	22	ALA
15	c3	47	PRO
17	c5	6	ASN
17	c5	71	GLU
18	c6	40	GLU
19	c7	83	GLN
19	c7	113	LEU
21	c9	34	VAL
21	c9	142	GLU
23	d1	3	ASN
25	d3	89	ASN
25	d3	90	ASP
25	d3	101	GLU
25	d3	133	LEU
28	d6	35	ALA
29	d7	58	SER
80	e0	19	PRO
33	e1	86	THR
33	e1	127	GLY
33	e1	148	TYR
34	sR	237	GLN
35	sM	43	ASP

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Mol	Chain	Res	Type
35	sM	47	ALA
39	l2	127	ALA
41	l4	174	ALA
41	l4	328	ASN
41	l4	341	SER
41	l4	342	LYS
43	l6	11	PRO
45	l8	237	ILE
47	m0	3	ARG
47	m0	179	PRO
47	m0	196	PHE
48	m1	114	ILE
49	m3	44	ALA
51	m5	81	TYR
52	m6	16	VAL
54	m8	77	ALA
63	n7	28	PRO
63	n7	56	LYS
64	n8	110	GLY
65	n9	24	PRO
70	o4	78	GLY
79	q3	51	ALA
82	p0	93	LEU
3	S1	114	VAL
3	S1	131	ASP
6	S4	193	GLY
6	S4	201	HIS
7	S5	154	ALA
25	D3	8	GLY
28	D6	64	LEU
30	D8	35	ASP
34	SR	231	MET
40	L3	314	TYR
40	L3	348	ARG
41	L4	190	GLY
42	L5	7	ALA
42	L5	187	THR
48	M1	173	ASP
49	M3	5	LYS
50	M4	6	ILE
51	M5	81	TYR
51	M5	144	ARG

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Mol	Chain	Res	Type
53	M7	159	LYS
56	N0	12	ARG
70	O4	82	ALA
76	Q0	79	GLU
79	Q3	58	SER
2	s0	162	CYS
3	s1	22	ASP
4	s2	107	SER
4	s2	151	PRO
7	s5	62	VAL
7	s5	101	GLY
10	s8	101	ILE
11	s9	162	SER
12	c0	88	ILE
12	c0	90	PRO
18	c6	3	ALA
20	c8	94	ASP
23	d1	4	ASP
26	d4	30	PRO
28	d6	59	TYR
34	sR	49	GLY
34	sR	97	GLY
35	sM	68	ARG
39	l2	142	ASP
39	l2	194	ASN
41	l4	338	LYS
42	l5	125	VAL
48	m1	12	LEU
57	n1	148	PRO
61	n5	25	LYS
72	o6	34	SER
78	q2	78	LYS
5	S3	211	PRO
6	S4	150	PRO
7	S5	150	GLY
8	S6	165	GLY
26	D4	35	VAL
28	D6	58	VAL
31	D9	11	PRO
34	SR	105	GLY
40	L3	169	THR
40	L3	317	ILE

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Mol	Chain	Res	Type
45	L8	135	GLY
65	N9	21	ILE
14	c2	115	VAL
15	c3	137	PRO
16	c4	131	GLY
34	sR	105	GLY
48	m1	117	ASP
49	m3	50	PRO
63	n7	36	HIS
69	o3	90	PRO
82	p0	47	GLY
7	S5	204	GLY
14	C2	115	VAL
18	C6	33	GLY
24	D2	67	GLY
53	M7	182	ILE
72	O6	21	THR
11	s9	5	PRO
18	c6	39	VAL
19	c7	117	LEU
20	c8	4	VAL
22	d0	51	VAL
4	S2	145	GLY
4	S2	235	LEU
16	C4	39	ILE
33	E1	127	GLY
47	M0	117	GLY
63	N7	36	HIS
2	s0	44	GLY
7	s5	152	GLY
11	s9	168	ARG
22	d0	96	PRO
41	l4	146	PRO
45	l8	163	VAL
68	o2	124	GLY
27	D5	88	ILE
35	SM	17	VAL
41	L4	272	VAL
45	L8	73	PRO
50	M4	39	ILE
53	M7	84	PRO
60	N4	76	VAL

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Mol	Chain	Res	Type
7	s5	151	GLY
22	d0	118	VAL
48	m1	120	ILE
82	p0	289	ALA
4	S2	173	PRO
18	C6	97	VAL
47	M0	47	PRO
48	M1	117	ASP
8	s6	69	LEU
9	s7	131	PHE
73	o7	40	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	S0	164/209 (78%)	146 (89%)	18 (11%)	8	30
2	s0	165/209 (79%)	138 (84%)	27 (16%)	3	12
3	S1	191/223 (86%)	164 (86%)	27 (14%)	4	18
3	s1	192/223 (86%)	163 (85%)	29 (15%)	3	15
4	S2	176/204 (86%)	154 (88%)	22 (12%)	6	22
4	s2	176/204 (86%)	143 (81%)	33 (19%)	2	8
5	S3	182/194 (94%)	159 (87%)	23 (13%)	5	22
5	s3	182/194 (94%)	159 (87%)	23 (13%)	5	22
6	S4	221/221 (100%)	194 (88%)	27 (12%)	6	24
6	s4	221/221 (100%)	196 (89%)	25 (11%)	7	28
7	S5	173/190 (91%)	158 (91%)	15 (9%)	13	44
7	s5	173/190 (91%)	153 (88%)	20 (12%)	7	27
8	S6	188/201 (94%)	161 (86%)	27 (14%)	4	17
8	s6	187/201 (93%)	160 (86%)	27 (14%)	4	17
9	S7	165/169 (98%)	150 (91%)	15 (9%)	12	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	s7	165/169 (98%)	150 (91%)	15 (9%)	12	40
10	S8	150/161 (93%)	128 (85%)	22 (15%)	4	16
10	s8	150/161 (93%)	138 (92%)	12 (8%)	15	48
11	S9	158/165 (96%)	134 (85%)	24 (15%)	3	14
11	s9	158/165 (96%)	136 (86%)	22 (14%)	4	19
12	C0	77/98 (79%)	69 (90%)	8 (10%)	9	32
12	c0	73/98 (74%)	64 (88%)	9 (12%)	6	23
13	C1	129/136 (95%)	116 (90%)	13 (10%)	9	33
13	c1	129/136 (95%)	107 (83%)	22 (17%)	2	11
14	C2	88/118 (75%)	75 (85%)	13 (15%)	4	16
14	c2	88/118 (75%)	73 (83%)	15 (17%)	2	11
15	C3	127/127 (100%)	112 (88%)	15 (12%)	6	25
15	c3	127/127 (100%)	110 (87%)	17 (13%)	5	20
16	C4	81/104 (78%)	68 (84%)	13 (16%)	3	13
16	c4	97/104 (93%)	82 (84%)	15 (16%)	3	14
17	C5	101/117 (86%)	93 (92%)	8 (8%)	15	49
17	c5	103/117 (88%)	90 (87%)	13 (13%)	5	22
18	C6	117/118 (99%)	104 (89%)	13 (11%)	8	29
18	c6	118/118 (100%)	106 (90%)	12 (10%)	9	33
19	C7	94/124 (76%)	77 (82%)	17 (18%)	2	9
19	c7	92/124 (74%)	81 (88%)	11 (12%)	6	24
20	C8	128/128 (100%)	110 (86%)	18 (14%)	4	18
20	c8	128/128 (100%)	108 (84%)	20 (16%)	3	14
21	C9	115/115 (100%)	100 (87%)	15 (13%)	5	21
21	c9	115/115 (100%)	101 (88%)	14 (12%)	6	24
22	D0	100/113 (88%)	90 (90%)	10 (10%)	9	34
22	d0	103/113 (91%)	90 (87%)	13 (13%)	5	22
23	D1	74/74 (100%)	64 (86%)	10 (14%)	5	20
23	d1	74/74 (100%)	66 (89%)	8 (11%)	8	30
24	D2	110/110 (100%)	94 (86%)	16 (14%)	4	16
24	d2	110/110 (100%)	99 (90%)	11 (10%)	9	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	D3	119/119 (100%)	104 (87%)	15 (13%)	5	22
25	d3	119/119 (100%)	107 (90%)	12 (10%)	9	33
26	D4	112/112 (100%)	100 (89%)	12 (11%)	8	31
26	d4	112/112 (100%)	100 (89%)	12 (11%)	8	31
27	D5	61/88 (69%)	47 (77%)	14 (23%)	1	4
27	d5	61/88 (69%)	54 (88%)	7 (12%)	7	27
28	D6	83/83 (100%)	70 (84%)	13 (16%)	3	13
28	d6	83/83 (100%)	76 (92%)	7 (8%)	14	46
29	D7	70/70 (100%)	63 (90%)	7 (10%)	9	34
29	d7	70/70 (100%)	60 (86%)	10 (14%)	4	17
30	D8	56/59 (95%)	46 (82%)	10 (18%)	2	10
30	d8	56/59 (95%)	47 (84%)	9 (16%)	3	13
31	D9	47/48 (98%)	39 (83%)	8 (17%)	2	11
31	d9	47/48 (98%)	42 (89%)	5 (11%)	8	31
32	E0	51/51 (100%)	45 (88%)	6 (12%)	6	25
33	E1	62/66 (94%)	48 (77%)	14 (23%)	1	4
33	e1	66/66 (100%)	53 (80%)	13 (20%)	1	7
34	SR	259/261 (99%)	242 (93%)	17 (7%)	21	56
34	sR	260/261 (100%)	246 (95%)	14 (5%)	27	64
35	SM	97/193 (50%)	87 (90%)	10 (10%)	9	32
35	sM	54/193 (28%)	49 (91%)	5 (9%)	11	39
39	L2	193/195 (99%)	166 (86%)	27 (14%)	4	18
39	l2	192/195 (98%)	162 (84%)	30 (16%)	3	14
40	L3	321/322 (100%)	273 (85%)	48 (15%)	3	15
40	l3	319/322 (99%)	270 (85%)	49 (15%)	3	14
41	L4	288/288 (100%)	250 (87%)	38 (13%)	5	20
41	l4	288/288 (100%)	247 (86%)	41 (14%)	4	18
42	L5	244/244 (100%)	215 (88%)	29 (12%)	6	25
42	l5	243/244 (100%)	213 (88%)	30 (12%)	6	23
43	L6	134/152 (88%)	119 (89%)	15 (11%)	7	29
43	l6	135/152 (89%)	114 (84%)	21 (16%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	L7	186/204 (91%)	165 (89%)	21 (11%)	7	28
44	l7	187/204 (92%)	169 (90%)	18 (10%)	10	37
45	L8	187/207 (90%)	164 (88%)	23 (12%)	6	23
45	l8	177/207 (86%)	150 (85%)	27 (15%)	3	14
46	L9	171/171 (100%)	143 (84%)	28 (16%)	3	12
46	l9	171/171 (100%)	137 (80%)	34 (20%)	1	7
47	M0	177/186 (95%)	153 (86%)	24 (14%)	5	19
47	m0	179/186 (96%)	149 (83%)	30 (17%)	2	11
48	M1	147/150 (98%)	124 (84%)	23 (16%)	3	14
48	m1	147/150 (98%)	131 (89%)	16 (11%)	8	30
49	M3	154/158 (98%)	135 (88%)	19 (12%)	6	23
49	m3	154/158 (98%)	135 (88%)	19 (12%)	6	23
50	M4	107/108 (99%)	94 (88%)	13 (12%)	6	24
50	m4	108/108 (100%)	91 (84%)	17 (16%)	3	13
51	M5	175/175 (100%)	152 (87%)	23 (13%)	5	21
51	m5	175/175 (100%)	159 (91%)	16 (9%)	12	40
52	M6	160/161 (99%)	152 (95%)	8 (5%)	30	67
52	m6	160/161 (99%)	139 (87%)	21 (13%)	5	21
53	M7	140/145 (97%)	124 (89%)	16 (11%)	7	28
53	m7	125/145 (86%)	107 (86%)	18 (14%)	4	17
54	M8	150/150 (100%)	130 (87%)	20 (13%)	5	20
54	m8	150/150 (100%)	130 (87%)	20 (13%)	5	20
55	M9	153/153 (100%)	138 (90%)	15 (10%)	10	36
55	m9	153/153 (100%)	130 (85%)	23 (15%)	3	15
56	N0	156/156 (100%)	130 (83%)	26 (17%)	3	11
56	n0	156/156 (100%)	132 (85%)	24 (15%)	3	14
57	N1	136/136 (100%)	107 (79%)	29 (21%)	1	6
57	n1	136/136 (100%)	111 (82%)	25 (18%)	2	9
58	N2	87/106 (82%)	79 (91%)	8 (9%)	11	40
58	n2	85/106 (80%)	72 (85%)	13 (15%)	3	14
59	N3	104/104 (100%)	93 (89%)	11 (11%)	8	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	n3	104/104 (100%)	95 (91%)	9 (9%)	13	44
60	N4	57/129 (44%)	53 (93%)	4 (7%)	19	54
60	n4	100/129 (78%)	93 (93%)	7 (7%)	19	54
61	N5	104/117 (89%)	84 (81%)	20 (19%)	2	8
61	n5	104/117 (89%)	85 (82%)	19 (18%)	2	9
62	N6	109/109 (100%)	94 (86%)	15 (14%)	4	19
62	n6	109/109 (100%)	87 (80%)	22 (20%)	1	7
63	N7	115/115 (100%)	104 (90%)	11 (10%)	10	37
63	n7	115/115 (100%)	98 (85%)	17 (15%)	4	16
64	N8	118/118 (100%)	100 (85%)	18 (15%)	3	14
64	n8	118/118 (100%)	98 (83%)	20 (17%)	2	11
65	N9	46/46 (100%)	40 (87%)	6 (13%)	5	21
65	n9	46/46 (100%)	38 (83%)	8 (17%)	2	11
66	O0	81/87 (93%)	71 (88%)	10 (12%)	6	23
66	o0	84/87 (97%)	77 (92%)	7 (8%)	14	46
67	O1	92/96 (96%)	78 (85%)	14 (15%)	3	14
67	o1	94/96 (98%)	76 (81%)	18 (19%)	2	8
68	O2	109/110 (99%)	98 (90%)	11 (10%)	9	33
68	o2	109/110 (99%)	97 (89%)	12 (11%)	8	30
69	O3	90/90 (100%)	76 (84%)	14 (16%)	3	14
69	o3	90/90 (100%)	76 (84%)	14 (16%)	3	14
70	O4	95/101 (94%)	80 (84%)	15 (16%)	3	13
70	o4	95/101 (94%)	81 (85%)	14 (15%)	4	16
71	O5	104/104 (100%)	87 (84%)	17 (16%)	3	12
71	o5	103/104 (99%)	86 (84%)	17 (16%)	3	12
72	O6	81/81 (100%)	66 (82%)	15 (18%)	2	9
72	o6	80/81 (99%)	61 (76%)	19 (24%)	1	3
73	O7	70/70 (100%)	64 (91%)	6 (9%)	13	45
73	o7	70/70 (100%)	58 (83%)	12 (17%)	2	11
74	O8	68/68 (100%)	54 (79%)	14 (21%)	1	6
74	o8	67/68 (98%)	55 (82%)	12 (18%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
75	O9	45/45 (100%)	38 (84%)	7 (16%)	3	14
75	o9	45/45 (100%)	39 (87%)	6 (13%)	5	20
76	Q0	47/47 (100%)	40 (85%)	7 (15%)	4	15
76	q0	47/47 (100%)	43 (92%)	4 (8%)	13	45
77	Q1	23/23 (100%)	21 (91%)	2 (9%)	13	44
77	q1	23/23 (100%)	17 (74%)	6 (26%)	0	2
78	Q2	90/90 (100%)	72 (80%)	18 (20%)	1	7
78	q2	90/90 (100%)	79 (88%)	11 (12%)	6	24
79	Q3	71/71 (100%)	63 (89%)	8 (11%)	7	28
79	q3	71/71 (100%)	62 (87%)	9 (13%)	5	22
80	e0	53/53 (100%)	47 (89%)	6 (11%)	7	28
82	p0	105/253 (42%)	89 (85%)	16 (15%)	3	14
All	All	18727/20169 (93%)	16232 (87%)	2495 (13%)	5	20

All (2495) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S0	27	ARG
2	S0	37	VAL
2	S0	43	ASP
2	S0	52	LYS
2	S0	62	ARG
2	S0	88	LYS
2	S0	96	THR
2	S0	101	ARG
2	S0	110	TYR
2	S0	111	ILE
2	S0	137	SER
2	S0	168	HIS
2	S0	172	LEU
2	S0	177	LEU
2	S0	188	LEU
2	S0	196	SER
2	S0	198	MET
2	S0	200	ASP
3	S1	21	VAL
3	S1	29	TRP
3	S1	30	PHE

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Mol	Chain	Res	Type
3	S1	31	ASP
3	S1	39	GLU
3	S1	46	THR
3	S1	61	LEU
3	S1	70	LEU
3	S1	81	PHE
3	S1	83	LYS
3	S1	91	VAL
3	S1	96	LEU
3	S1	97	LEU
3	S1	105	PHE
3	S1	110	LEU
3	S1	117	TRP
3	S1	148	ASN
3	S1	177	GLN
3	S1	180	THR
3	S1	181	LEU
3	S1	198	GLU
3	S1	202	LYS
3	S1	214	LYS
3	S1	215	VAL
3	S1	218	LEU
3	S1	222	LYS
3	S1	223	PHE
4	S2	41	LEU
4	S2	54	GLU
4	S2	76	LEU
4	S2	77	GLN
4	S2	96	THR
4	S2	97	ARG
4	S2	102	VAL
4	S2	111	VAL
4	S2	117	THR
4	S2	134	LEU
4	S2	137	ILE
4	S2	139	ILE
4	S2	140	ARG
4	S2	141	ARG
4	S2	181	SER
4	S2	207	LEU
4	S2	208	GLU
4	S2	222	TYR

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Mol	Chain	Res	Type
4	S2	225	LEU
4	S2	226	THR
4	S2	229	LEU
4	S2	245	ASP
5	S3	4	LEU
5	S3	7	LYS
5	S3	23	GLU
5	S3	65	ARG
5	S3	76	ARG
5	S3	84	ILE
5	S3	92	GLN
5	S3	93	ASP
5	S3	105	MET
5	S3	117	ARG
5	S3	127	MET
5	S3	142	LEU
5	S3	151	LYS
5	S3	158	ILE
5	S3	175	VAL
5	S3	176	LEU
5	S3	178	ARG
5	S3	190	ARG
5	S3	202	LEU
5	S3	204	ASP
5	S3	207	THR
5	S3	217	ILE
5	S3	218	LEU
6	S4	7	LYS
6	S4	9	LEU
6	S4	12	LEU
6	S4	38	LEU
6	S4	39	ARG
6	S4	42	LEU
6	S4	45	ILE
6	S4	62	LYS
6	S4	70	VAL
6	S4	77	ARG
6	S4	92	LEU
6	S4	115	THR
6	S4	116	ASP
6	S4	126	VAL
6	S4	129	VAL

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Mol	Chain	Res	Type
6	S4	131	LEU
6	S4	133	LYS
6	S4	159	THR
6	S4	180	LEU
6	S4	181	VAL
6	S4	182	TYR
6	S4	187	ARG
6	S4	215	ASP
6	S4	222	LEU
6	S4	227	VAL
6	S4	240	LYS
6	S4	259	GLN
7	S5	25	LEU
7	S5	38	THR
7	S5	43	PHE
7	S5	45	LYS
7	S5	48	PHE
7	S5	65	ARG
7	S5	76	ARG
7	S5	79	ASN
7	S5	86	GLN
7	S5	119	ASP
7	S5	139	ASN
7	S5	146	THR
7	S5	156	ARG
7	S5	166	ARG
7	S5	194	LEU
8	S6	7	TYR
8	S6	15	THR
8	S6	21	GLU
8	S6	71	THR
8	S6	76	LEU
8	S6	97	VAL
8	S6	109	LEU
8	S6	120	GLU
8	S6	126	ASP
8	S6	128	THR
8	S6	129	VAL
8	S6	132	ARG
8	S6	133	LEU
8	S6	154	ARG
8	S6	155	ASP

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Mol	Chain	Res	Type
8	S6	163	THR
8	S6	169	TYR
8	S6	170	THR
8	S6	177	ARG
8	S6	179	VAL
8	S6	180	THR
8	S6	182	GLN
8	S6	193	LEU
8	S6	201	GLN
8	S6	211	LEU
8	S6	212	LEU
8	S6	216	LEU
9	S7	28	GLU
9	S7	38	LEU
9	S7	49	ILE
9	S7	50	ASP
9	S7	70	PHE
9	S7	77	LEU
9	S7	78	THR
9	S7	85	PHE
9	S7	86	GLN
9	S7	97	ARG
9	S7	114	ARG
9	S7	115	SER
9	S7	126	LEU
9	S7	130	VAL
9	S7	185	ILE
10	S8	5	ARG
10	S8	7	SER
10	S8	8	ARG
10	S8	14	THR
10	S8	20	GLN
10	S8	21	PHE
10	S8	29	LEU
10	S8	36	THR
10	S8	37	LYS
10	S8	46	VAL
10	S8	56	ARG
10	S8	58	LEU
10	S8	73	SER
10	S8	74	LYS
10	S8	123	LYS

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Mol	Chain	Res	Type
10	S8	138	ASN
10	S8	140	GLU
10	S8	151	LYS
10	S8	152	ILE
10	S8	164	ARG
10	S8	184	LEU
10	S8	196	LEU
11	S9	3	ARG
11	S9	6	ARG
11	S9	14	THR
11	S9	28	LEU
11	S9	46	SER
11	S9	49	LEU
11	S9	60	LEU
11	S9	61	THR
11	S9	74	ASN
11	S9	79	ARG
11	S9	88	GLU
11	S9	92	LYS
11	S9	93	LEU
11	S9	109	LEU
11	S9	118	LEU
11	S9	120	LYS
11	S9	122	VAL
11	S9	134	ILE
11	S9	138	LYS
11	S9	149	ARG
11	S9	161	THR
11	S9	171	ARG
11	S9	172	VAL
11	S9	182	GLU
12	C0	1	MET
12	C0	7	ASP
12	C0	8	ARG
12	C0	55	VAL
12	C0	56	LYS
12	C0	76	LEU
12	C0	81	ASN
12	C0	82	LEU
13	C1	4	GLU
13	C1	8	GLN
13	C1	10	GLU

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Mol	Chain	Res	Type
13	C1	29	LYS
13	C1	40	LEU
13	C1	44	THR
13	C1	56	LYS
13	C1	67	ARG
13	C1	69	LYS
13	C1	80	MET
13	C1	99	ARG
13	C1	109	VAL
13	C1	136	ARG
14	C2	28	LEU
14	C2	33	ARG
14	C2	43	ARG
14	C2	61	VAL
14	C2	62	LEU
14	C2	66	VAL
14	C2	71	ILE
14	C2	74	LEU
14	C2	86	VAL
14	C2	103	LEU
14	C2	126	TRP
14	C2	129	GLU
14	C2	132	GLU
15	C3	3	ARG
15	C3	9	LYS
15	C3	12	SER
15	C3	16	ILE
15	C3	27	LYS
15	C3	32	SER
15	C3	56	ASP
15	C3	58	HIS
15	C3	64	ARG
15	C3	66	ILE
15	C3	102	LEU
15	C3	110	ASP
15	C3	125	LEU
15	C3	143	SER
15	C3	149	LEU
16	C4	26	THR
16	C4	29	HIS
16	C4	39	ILE
16	C4	42	VAL

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Mol	Chain	Res	Type
16	C4	51	ASP
16	C4	79	VAL
16	C4	92	LYS
16	C4	99	GLN
16	C4	107	ARG
16	C4	124	ASP
16	C4	125	SER
16	C4	136	ARG
16	C4	137	LEU
17	C5	11	VAL
17	C5	22	LEU
17	C5	35	LYS
17	C5	36	LEU
17	C5	44	ARG
17	C5	50	THR
17	C5	52	LYS
17	C5	110	GLU
18	C6	4	VAL
18	C6	26	LYS
18	C6	29	ILE
18	C6	54	LEU
18	C6	59	LYS
18	C6	66	ARG
18	C6	69	VAL
18	C6	109	PHE
18	C6	116	LEU
18	C6	123	ARG
18	C6	127	LYS
18	C6	128	LYS
18	C6	137	ARG
19	C7	3	ARG
19	C7	5	ARG
19	C7	16	LEU
19	C7	23	LYS
19	C7	25	THR
19	C7	29	GLN
19	C7	34	LEU
19	C7	35	CYS
19	C7	38	ILE
19	C7	49	LYS
19	C7	54	THR
19	C7	69	ILE

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Mol	Chain	Res	Type
19	C7	78	ARG
19	C7	88	VAL
19	C7	105	GLN
19	C7	113	LEU
19	C7	115	LEU
20	C8	3	LEU
20	C8	5	VAL
20	C8	11	PHE
20	C8	12	GLN
20	C8	13	HIS
20	C8	14	ILE
20	C8	17	LEU
20	C8	25	ASN
20	C8	26	ILE
20	C8	28	ILE
20	C8	34	THR
20	C8	40	ARG
20	C8	60	GLU
20	C8	80	LYS
20	C8	88	ARG
20	C8	92	ILE
20	C8	136	GLN
20	C8	138	THR
21	C9	6	VAL
21	C9	13	ASP
21	C9	18	TYR
21	C9	22	LEU
21	C9	23	GLN
21	C9	27	LYS
21	C9	28	LEU
21	C9	35	ASP
21	C9	36	ILE
21	C9	67	MET
21	C9	94	ILE
21	C9	125	SER
21	C9	130	ARG
21	C9	131	ASP
21	C9	144	GLU
22	D0	15	GLN
22	D0	23	ARG
22	D0	31	VAL
22	D0	51	VAL

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Mol	Chain	Res	Type
22	D0	61	LYS
22	D0	67	THR
22	D0	81	THR
22	D0	89	ARG
22	D0	103	ILE
22	D0	116	VAL
23	D1	5	LYS
23	D1	8	LEU
23	D1	11	LEU
23	D1	33	GLN
23	D1	50	TYR
23	D1	60	ARG
23	D1	62	ARG
23	D1	75	ASN
23	D1	78	LEU
23	D1	80	LYS
24	D2	15	ASN
24	D2	24	GLN
24	D2	25	VAL
24	D2	27	ILE
24	D2	42	GLN
24	D2	53	ILE
24	D2	65	LEU
24	D2	66	ASN
24	D2	68	ARG
24	D2	76	SER
24	D2	93	LEU
24	D2	98	GLN
24	D2	103	ILE
24	D2	104	LEU
24	D2	105	THR
24	D2	121	VAL
25	D3	7	ARG
25	D3	9	LEU
25	D3	33	LEU
25	D3	41	SER
25	D3	82	LYS
25	D3	84	THR
25	D3	96	VAL
25	D3	103	LEU
25	D3	107	PHE
25	D3	109	ARG

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Mol	Chain	Res	Type
25	D3	110	LYS
25	D3	114	LYS
25	D3	117	ILE
25	D3	138	GLU
25	D3	144	ARG
26	D4	17	LEU
26	D4	32	ARG
26	D4	47	VAL
26	D4	52	LYS
26	D4	57	VAL
26	D4	88	THR
26	D4	96	LEU
26	D4	99	LYS
26	D4	101	GLU
26	D4	102	LYS
26	D4	124	ARG
26	D4	127	LYS
27	D5	40	VAL
27	D5	42	LEU
27	D5	48	ASP
27	D5	58	ARG
27	D5	59	TYR
27	D5	60	VAL
27	D5	67	ASP
27	D5	69	LEU
27	D5	71	ILE
27	D5	75	LEU
27	D5	92	ILE
27	D5	95	HIS
27	D5	98	GLN
27	D5	100	ILE
28	D6	3	LYS
28	D6	12	LYS
28	D6	18	VAL
28	D6	38	ARG
28	D6	41	ILE
28	D6	44	ILE
28	D6	50	VAL
28	D6	61	GLU
28	D6	64	LEU
28	D6	68	TYR
28	D6	82	ARG

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Mol	Chain	Res	Type
28	D6	85	ARG
28	D6	90	GLU
29	D7	3	LEU
29	D7	4	VAL
29	D7	33	LEU
29	D7	48	SER
29	D7	73	LEU
29	D7	75	GLU
29	D7	80	ARG
30	D8	19	THR
30	D8	28	VAL
30	D8	32	PHE
30	D8	33	LEU
30	D8	39	THR
30	D8	48	VAL
30	D8	52	ASP
30	D8	57	MET
30	D8	58	GLU
30	D8	64	ARG
31	D9	5	ASN
31	D9	6	VAL
31	D9	7	TRP
31	D9	19	ARG
31	D9	22	ARG
31	D9	25	SER
31	D9	30	LEU
31	D9	36	LEU
32	E0	20	LYS
32	E0	24	THR
32	E0	28	LYS
32	E0	42	ARG
32	E0	47	VAL
32	E0	56	MET
33	E1	86	THR
33	E1	89	LYS
33	E1	91	ILE
33	E1	93	HIS
33	E1	97	LYS
33	E1	98	VAL
33	E1	102	VAL
33	E1	106	TYR
33	E1	108	VAL

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Mol	Chain	Res	Type
33	E1	111	GLU
33	E1	113	LYS
33	E1	126	CYS
33	E1	130	VAL
33	E1	151	ASN
34	SR	6	VAL
34	SR	10	ARG
34	SR	29	GLN
34	SR	52	GLN
34	SR	58	VAL
34	SR	66	HIS
34	SR	76	ASP
34	SR	116	ASP
34	SR	117	LYS
34	SR	134	TRP
34	SR	136	ILE
34	SR	165	ASP
34	SR	191	ASP
34	SR	202	LEU
34	SR	229	LYS
34	SR	238	ASP
34	SR	268	GLN
35	SM	33	LYS
35	SM	46	LYS
35	SM	53	ARG
35	SM	64	LYS
35	SM	68	ARG
35	SM	78	ASP
35	SM	82	THR
35	SM	84	LYS
35	SM	89	ARG
35	SM	100	THR
39	L2	20	THR
39	L2	32	LEU
39	L2	44	ILE
39	L2	45	VAL
39	L2	48	ILE
39	L2	52	SER
39	L2	62	VAL
39	L2	70	ARG
39	L2	72	ARG
39	L2	82	VAL

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Mol	Chain	Res	Type
39	L2	84	THR
39	L2	96	LEU
39	L2	135	ILE
39	L2	157	VAL
39	L2	165	VAL
39	L2	169	ILE
39	L2	179	LEU
39	L2	180	LEU
39	L2	202	VAL
39	L2	204	MET
39	L2	207	VAL
39	L2	217	GLN
39	L2	227	ARG
39	L2	230	VAL
39	L2	241	ARG
39	L2	247	ARG
39	L2	252	THR
40	L3	7	GLU
40	L3	17	LEU
40	L3	19	ARG
40	L3	25	ILE
40	L3	30	LYS
40	L3	37	ARG
40	L3	47	LEU
40	L3	55	THR
40	L3	56	ILE
40	L3	67	PHE
40	L3	70	ARG
40	L3	79	VAL
40	L3	84	VAL
40	L3	85	VAL
40	L3	102	LEU
40	L3	103	THR
40	L3	110	LEU
40	L3	112	ASP
40	L3	114	VAL
40	L3	139	GLN
40	L3	148	LEU
40	L3	150	ARG
40	L3	169	THR
40	L3	173	GLN
40	L3	183	LEU

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Mol	Chain	Res	Type
40	L3	187	SER
40	L3	188	ILE
40	L3	202	THR
40	L3	205	VAL
40	L3	212	ASN
40	L3	229	VAL
40	L3	232	ARG
40	L3	235	THR
40	L3	238	LEU
40	L3	241	LYS
40	L3	252	ILE
40	L3	264	VAL
40	L3	296	THR
40	L3	305	ILE
40	L3	308	MET
40	L3	324	VAL
40	L3	332	ARG
40	L3	335	ILE
40	L3	346	THR
40	L3	347	SER
40	L3	354	VAL
40	L3	355	SER
40	L3	375	GLU
41	L4	10	SER
41	L4	22	LEU
41	L4	53	SER
41	L4	69	ARG
41	L4	73	ARG
41	L4	74	ILE
41	L4	93	MET
41	L4	120	TYR
41	L4	124	SER
41	L4	138	ARG
41	L4	150	LEU
41	L4	152	VAL
41	L4	153	SER
41	L4	156	LEU
41	L4	172	VAL
41	L4	176	SER
41	L4	179	LEU
41	L4	187	LEU
41	L4	188	ARG

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Mol	Chain	Res	Type
41	L4	200	THR
41	L4	203	ARG
41	L4	206	LEU
41	L4	220	ARG
41	L4	222	VAL
41	L4	230	VAL
41	L4	246	ARG
41	L4	270	SER
41	L4	283	THR
41	L4	297	SER
41	L4	306	THR
41	L4	307	GLN
41	L4	313	LEU
41	L4	327	LEU
41	L4	332	LYS
41	L4	333	VAL
41	L4	338	LYS
41	L4	349	THR
41	L4	350	LYS
42	L5	23	ARG
42	L5	41	LYS
42	L5	69	ILE
42	L5	81	HIS
42	L5	92	LEU
42	L5	95	TRP
42	L5	105	ILE
42	L5	112	LYS
42	L5	115	LEU
42	L5	128	GLU
42	L5	131	LEU
42	L5	132	THR
42	L5	137	ASP
42	L5	140	ARG
42	L5	144	VAL
42	L5	146	LEU
42	L5	148	ILE
42	L5	155	THR
42	L5	163	LEU
42	L5	177	GLU
42	L5	178	ASN
42	L5	185	PHE
42	L5	206	GLN

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Mol	Chain	Res	Type
42	L5	216	GLU
42	L5	259	LYS
42	L5	263	GLU
42	L5	268	GLU
42	L5	277	LEU
42	L5	293	LEU
43	L6	5	LYS
43	L6	21	THR
43	L6	52	VAL
43	L6	64	LEU
43	L6	65	ILE
43	L6	76	LEU
43	L6	78	ARG
43	L6	89	THR
43	L6	104	GLU
43	L6	129	GLU
43	L6	134	ARG
43	L6	143	LYS
43	L6	152	THR
43	L6	155	LEU
43	L6	162	SER
44	L7	24	GLU
44	L7	26	VAL
44	L7	39	GLU
44	L7	46	GLU
44	L7	60	ARG
44	L7	77	VAL
44	L7	89	ILE
44	L7	93	ASN
44	L7	98	LYS
44	L7	100	ARG
44	L7	101	LYS
44	L7	110	ARG
44	L7	124	LEU
44	L7	151	ARG
44	L7	157	ASN
44	L7	173	LEU
44	L7	178	ILE
44	L7	179	LEU
44	L7	184	LEU
44	L7	239	LEU
44	L7	244	ASN

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Mol	Chain	Res	Type
45	L8	26	LEU
45	L8	27	THR
45	L8	38	GLN
45	L8	41	GLN
45	L8	71	VAL
45	L8	74	THR
45	L8	79	GLN
45	L8	84	ARG
45	L8	90	THR
45	L8	95	ASN
45	L8	134	TYR
45	L8	136	LEU
45	L8	150	LEU
45	L8	156	ASP
45	L8	163	VAL
45	L8	169	LEU
45	L8	180	VAL
45	L8	185	ARG
45	L8	189	LEU
45	L8	190	VAL
45	L8	241	LYS
45	L8	246	MET
45	L8	248	LYS
46	L9	4	ILE
46	L9	5	GLN
46	L9	6	THR
46	L9	9	GLN
46	L9	18	VAL
46	L9	41	ILE
46	L9	48	VAL
46	L9	52	LEU
46	L9	55	VAL
46	L9	62	ARG
46	L9	65	VAL
46	L9	68	LEU
46	L9	69	ARG
46	L9	70	THR
46	L9	80	THR
46	L9	130	ASP
46	L9	135	GLU
46	L9	139	ASN
46	L9	149	ASN

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Mol	Chain	Res	Type
46	L9	151	VAL
46	L9	157	ASN
46	L9	161	LEU
46	L9	162	GLN
46	L9	164	ILE
46	L9	166	ARG
46	L9	172	ILE
46	L9	173	ARG
46	L9	177	ASP
47	M0	3	ARG
47	M0	30	LYS
47	M0	32	ARG
47	M0	33	ILE
47	M0	40	LYS
47	M0	42	THR
47	M0	44	ASP
47	M0	48	LEU
47	M0	52	LEU
47	M0	60	LEU
47	M0	63	GLU
47	M0	87	LEU
47	M0	91	VAL
47	M0	102	MET
47	M0	129	VAL
47	M0	133	GLN
47	M0	139	ARG
47	M0	143	SER
47	M0	156	ARG
47	M0	163	GLN
47	M0	167	LEU
47	M0	169	LYS
47	M0	200	LEU
47	M0	203	LYS
48	M1	10	ARG
48	M1	11	ASP
48	M1	12	LEU
48	M1	19	LEU
48	M1	30	LEU
48	M1	31	THR
48	M1	44	THR
48	M1	46	VAL
48	M1	47	GLN

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Mol	Chain	Res	Type
48	M1	65	ILE
48	M1	67	VAL
48	M1	70	THR
48	M1	80	LEU
48	M1	81	GLU
48	M1	94	ARG
48	M1	106	ILE
48	M1	107	ASP
48	M1	115	LYS
48	M1	139	THR
48	M1	140	ARG
48	M1	165	GLN
48	M1	166	LYS
48	M1	170	ASP
49	M3	5	LYS
49	M3	54	LEU
49	M3	55	ARG
49	M3	58	VAL
49	M3	59	ARG
49	M3	67	ARG
49	M3	69	VAL
49	M3	101	ARG
49	M3	114	GLN
49	M3	115	ARG
49	M3	122	LYS
49	M3	124	ILE
49	M3	128	ARG
49	M3	131	LYS
49	M3	134	GLU
49	M3	136	GLU
49	M3	144	THR
49	M3	168	ARG
49	M3	192	GLU
50	M4	10	SER
50	M4	15	VAL
50	M4	20	VAL
50	M4	27	GLN
50	M4	38	ILE
50	M4	50	LYS
50	M4	53	VAL
50	M4	64	VAL
50	M4	72	LEU

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Mol	Chain	Res	Type
50	M4	78	THR
50	M4	90	VAL
50	M4	130	THR
50	M4	135	LEU
51	M5	10	LEU
51	M5	15	GLN
51	M5	19	LEU
51	M5	22	LEU
51	M5	38	ARG
51	M5	49	ARG
51	M5	80	THR
51	M5	83	LYS
51	M5	85	THR
51	M5	92	LEU
51	M5	97	SER
51	M5	98	LEU
51	M5	109	ARG
51	M5	117	ASN
51	M5	133	ILE
51	M5	138	GLN
51	M5	151	ILE
51	M5	159	ARG
51	M5	182	ASN
51	M5	183	THR
51	M5	190	THR
51	M5	196	THR
51	M5	204	LYS
52	M6	34	VAL
52	M6	85	ARG
52	M6	89	SER
52	M6	106	GLU
52	M6	116	LYS
52	M6	117	ARG
52	M6	124	LEU
52	M6	134	LYS
53	M7	7	THR
53	M7	9	THR
53	M7	24	VAL
53	M7	29	THR
53	M7	32	THR
53	M7	36	ILE
53	M7	42	THR

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Mol	Chain	Res	Type
53	M7	52	LEU
53	M7	91	VAL
53	M7	112	LEU
53	M7	119	VAL
53	M7	127	ARG
53	M7	142	SER
53	M7	154	GLU
53	M7	168	LEU
53	M7	180	LYS
54	M8	3	ILE
54	M8	17	THR
54	M8	24	VAL
54	M8	26	LEU
54	M8	32	LEU
54	M8	34	THR
54	M8	41	ASP
54	M8	49	LEU
54	M8	57	ILE
54	M8	66	ARG
54	M8	69	ARG
54	M8	81	VAL
54	M8	86	THR
54	M8	105	ARG
54	M8	122	ILE
54	M8	135	GLN
54	M8	138	LEU
54	M8	150	VAL
54	M8	170	ARG
54	M8	180	ARG
55	M9	17	VAL
55	M9	25	ASP
55	M9	41	ILE
55	M9	44	LEU
55	M9	55	VAL
55	M9	74	ARG
55	M9	99	LEU
55	M9	103	ARG
55	M9	104	ARG
55	M9	106	LEU
55	M9	116	ASP
55	M9	134	HIS
55	M9	138	LEU

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Mol	Chain	Res	Type
55	M9	153	LYS
55	M9	182	ASP
56	N0	12	ARG
56	N0	16	THR
56	N0	45	LEU
56	N0	51	VAL
56	N0	58	ILE
56	N0	61	ILE
56	N0	71	LYS
56	N0	80	ARG
56	N0	85	SER
56	N0	87	THR
56	N0	97	VAL
56	N0	100	VAL
56	N0	105	THR
56	N0	106	LEU
56	N0	115	ARG
56	N0	117	ARG
56	N0	132	THR
56	N0	137	ARG
56	N0	138	GLN
56	N0	142	GLN
56	N0	156	VAL
56	N0	160	THR
56	N0	162	THR
56	N0	167	ARG
56	N0	169	SER
56	N0	172	TYR
57	N1	12	ARG
57	N1	18	ASP
57	N1	25	VAL
57	N1	27	LEU
57	N1	60	LYS
57	N1	68	THR
57	N1	75	ILE
57	N1	78	LYS
57	N1	79	MET
57	N1	80	VAL
57	N1	83	ARG
57	N1	88	ARG
57	N1	89	LEU
57	N1	92	ARG

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Mol	Chain	Res	Type
57	N1	96	ILE
57	N1	101	CYS
57	N1	103	GLN
57	N1	104	GLU
57	N1	106	LEU
57	N1	110	LYS
57	N1	122	GLN
57	N1	124	VAL
57	N1	126	VAL
57	N1	127	GLN
57	N1	128	LEU
57	N1	139	ARG
57	N1	143	THR
57	N1	146	ASN
57	N1	149	GLN
58	N2	10	LYS
58	N2	52	ASN
58	N2	61	THR
58	N2	66	VAL
58	N2	70	LYS
58	N2	74	LYS
58	N2	82	LYS
58	N2	100	THR
59	N3	13	ILE
59	N3	32	ARG
59	N3	64	LYS
59	N3	69	LEU
59	N3	73	VAL
59	N3	84	SER
59	N3	91	VAL
59	N3	98	ASN
59	N3	102	ILE
59	N3	115	THR
59	N3	121	GLU
60	N4	4	GLU
60	N4	5	ILE
60	N4	19	THR
60	N4	39	LEU
61	N5	27	ARG
61	N5	34	LEU
61	N5	37	THR
61	N5	38	LEU

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Mol	Chain	Res	Type
61	N5	39	LYS
61	N5	40	LEU
61	N5	59	SER
61	N5	63	ILE
61	N5	73	MET
61	N5	77	GLU
61	N5	78	ASP
61	N5	86	VAL
61	N5	108	LEU
61	N5	115	ARG
61	N5	125	ARG
61	N5	127	THR
61	N5	133	LEU
61	N5	135	ILE
61	N5	137	ASN
61	N5	142	ILE
62	N6	10	SER
62	N6	32	SER
62	N6	37	LYS
62	N6	42	GLN
62	N6	45	ILE
62	N6	50	ILE
62	N6	56	VAL
62	N6	57	LEU
62	N6	74	TYR
62	N6	76	LEU
62	N6	88	GLU
62	N6	105	VAL
62	N6	115	ARG
62	N6	126	LEU
62	N6	127	GLU
63	N7	14	VAL
63	N7	17	ARG
63	N7	24	VAL
63	N7	29	HIS
63	N7	30	ASP
63	N7	34	LYS
63	N7	46	ILE
63	N7	72	ILE
63	N7	81	LEU
63	N7	87	LEU
63	N7	134	LEU

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Mol	Chain	Res	Type
64	N8	6	THR
64	N8	8	THR
64	N8	10	LYS
64	N8	12	ARG
64	N8	16	SER
64	N8	27	LYS
64	N8	29	PRO
64	N8	34	MET
64	N8	42	ARG
64	N8	46	ASP
64	N8	60	TYR
64	N8	76	ASP
64	N8	91	LEU
64	N8	104	THR
64	N8	118	ILE
64	N8	120	ASN
64	N8	130	VAL
64	N8	133	LEU
65	N9	22	LYS
65	N9	25	LYS
65	N9	28	LYS
65	N9	38	LYS
65	N9	50	THR
65	N9	59	LYS
66	O0	16	LEU
66	O0	18	ILE
66	O0	32	LYS
66	O0	33	SER
66	O0	34	LEU
66	O0	41	LEU
66	O0	59	TYR
66	O0	61	MET
66	O0	79	THR
66	O0	83	LYS
67	O1	6	ASP
67	O1	8	VAL
67	O1	16	LEU
67	O1	26	LYS
67	O1	31	ARG
67	O1	55	LEU
67	O1	68	GLU
67	O1	79	ARG

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Mol	Chain	Res	Type
67	O1	82	GLU
67	O1	84	ASP
67	O1	89	LEU
67	O1	91	SER
67	O1	96	VAL
67	O1	106	THR
68	O2	19	ARG
68	O2	31	ASN
68	O2	33	ARG
68	O2	41	VAL
68	O2	54	LYS
68	O2	61	LYS
68	O2	84	THR
68	O2	86	THR
68	O2	87	MET
68	O2	106	VAL
68	O2	128	LEU
69	O3	15	SER
69	O3	20	LYS
69	O3	28	SER
69	O3	33	GLU
69	O3	49	ILE
69	O3	58	GLU
69	O3	59	VAL
69	O3	70	LYS
69	O3	78	SER
69	O3	80	VAL
69	O3	81	VAL
69	O3	86	ARG
69	O3	98	VAL
69	O3	105	SER
70	O4	3	GLN
70	O4	5	VAL
70	O4	16	ARG
70	O4	20	ILE
70	O4	24	LYS
70	O4	29	ILE
70	O4	38	LEU
70	O4	51	LEU
70	O4	56	THR
70	O4	58	ARG
70	O4	65	VAL

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Mol	Chain	Res	Type
70	O4	71	THR
70	O4	86	LYS
70	O4	100	ILE
70	O4	102	LYS
71	O5	20	GLN
71	O5	21	LEU
71	O5	27	GLU
71	O5	28	LEU
71	O5	45	LYS
71	O5	46	THR
71	O5	47	VAL
71	O5	48	ARG
71	O5	49	LYS
71	O5	71	LYS
71	O5	85	THR
71	O5	86	ARG
71	O5	89	ARG
71	O5	90	ARG
71	O5	104	GLN
71	O5	107	LYS
71	O5	119	LYS
72	O6	11	LEU
72	O6	21	THR
72	O6	25	LYS
72	O6	26	ILE
72	O6	29	LYS
72	O6	34	SER
72	O6	36	ARG
72	O6	45	ARG
72	O6	57	LEU
72	O6	58	ILE
72	O6	60	LEU
72	O6	68	ARG
72	O6	71	LYS
72	O6	76	ARG
72	O6	88	GLU
73	O7	24	ARG
73	O7	25	ARG
73	O7	36	SER
73	O7	55	ARG
73	O7	67	LEU
73	O7	85	LYS

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Mol	Chain	Res	Type
74	O8	3	ARG
74	O8	5	ILE
74	O8	22	THR
74	O8	24	THR
74	O8	41	THR
74	O8	45	VAL
74	O8	46	ARG
74	O8	50	SER
74	O8	53	THR
74	O8	61	LYS
74	O8	64	LYS
74	O8	65	LEU
74	O8	67	GLN
74	O8	77	ARG
75	O9	5	LYS
75	O9	21	ARG
75	O9	23	LEU
75	O9	29	LEU
75	O9	34	THR
75	O9	45	ARG
75	O9	51	ILE
76	Q0	77	ILE
76	Q0	78	ILE
76	Q0	83	LYS
76	Q0	85	LEU
76	Q0	105	PRO
76	Q0	112	LYS
76	Q0	127	LEU
77	Q1	9	ARG
77	Q1	11	ARG
78	Q2	3	ASN
78	Q2	4	VAL
78	Q2	8	ARG
78	Q2	9	LYS
78	Q2	21	THR
78	Q2	26	THR
78	Q2	35	LEU
78	Q2	45	ARG
78	Q2	46	LYS
78	Q2	47	GLN
78	Q2	64	THR
78	Q2	78	LYS

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Mol	Chain	Res	Type
78	Q2	83	LEU
78	Q2	84	THR
78	Q2	85	LEU
78	Q2	100	LYS
78	Q2	104	LEU
78	Q2	105	GLN
79	Q3	11	THR
79	Q3	45	LYS
79	Q3	60	CYS
79	Q3	72	SER
79	Q3	73	THR
79	Q3	78	THR
79	Q3	84	ARG
79	Q3	90	VAL
2	s0	12	GLU
2	s0	24	LEU
2	s0	30	GLN
2	s0	45	VAL
2	s0	57	LEU
2	s0	59	LEU
2	s0	62	ARG
2	s0	81	PHE
2	s0	83	GLN
2	s0	87	LEU
2	s0	88	LYS
2	s0	108	THR
2	s0	111	ILE
2	s0	131	GLN
2	s0	135	GLU
2	s0	144	ILE
2	s0	153	SER
2	s0	154	GLU
2	s0	167	LYS
2	s0	172	LEU
2	s0	180	GLU
2	s0	184	LEU
2	s0	185	ARG
2	s0	188	LEU
2	s0	189	VAL
2	s0	198	MET
2	s0	200	ASP
3	s1	21	VAL

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Mol	Chain	Res	Type
3	s1	31	ASP
3	s1	40	ASN
3	s1	47	LEU
3	s1	48	VAL
3	s1	51	SER
3	s1	62	LYS
3	s1	65	VAL
3	s1	66	VAL
3	s1	68	VAL
3	s1	70	LEU
3	s1	81	PHE
3	s1	104	ASP
3	s1	108	ASP
3	s1	110	LEU
3	s1	125	VAL
3	s1	126	THR
3	s1	127	VAL
3	s1	180	THR
3	s1	181	LEU
3	s1	194	ASN
3	s1	196	GLU
3	s1	209	ASN
3	s1	212	VAL
3	s1	215	VAL
3	s1	222	LYS
3	s1	223	PHE
3	s1	231	LEU
3	s1	232	HIS
4	s2	41	LEU
4	s2	51	THR
4	s2	53	ILE
4	s2	54	GLU
4	s2	55	GLU
4	s2	58	LEU
4	s2	69	ILE
4	s2	70	ASP
4	s2	72	LEU
4	s2	80	VAL
4	s2	83	ILE
4	s2	90	THR
4	s2	91	ARG
4	s2	94	GLN

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Mol	Chain	Res	Type
4	s2	97	ARG
4	s2	111	VAL
4	s2	117	THR
4	s2	137	ILE
4	s2	141	ARG
4	s2	146	THR
4	s2	152	HIS
4	s2	158	THR
4	s2	164	SER
4	s2	170	ILE
4	s2	185	LYS
4	s2	187	LEU
4	s2	196	VAL
4	s2	201	ASN
4	s2	206	THR
4	s2	221	THR
4	s2	232	GLU
4	s2	240	LEU
4	s2	248	SER
5	s3	4	LEU
5	s3	21	LEU
5	s3	44	THR
5	s3	53	THR
5	s3	55	THR
5	s3	59	LEU
5	s3	67	ASN
5	s3	84	ILE
5	s3	90	ARG
5	s3	111	ASN
5	s3	115	ILE
5	s3	120	TYR
5	s3	127	MET
5	s3	128	GLU
5	s3	141	LYS
5	s3	158	ILE
5	s3	162	GLN
5	s3	168	ILE
5	s3	189	MET
5	s3	202	LEU
5	s3	213	GLU
5	s3	218	LEU
5	s3	224	ASP

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Mol	Chain	Res	Type
6	s4	6	LYS
6	s4	9	LEU
6	s4	12	LEU
6	s4	23	LEU
6	s4	24	SER
6	s4	38	LEU
6	s4	42	LEU
6	s4	49	ARG
6	s4	51	ARG
6	s4	67	GLN
6	s4	68	ARG
6	s4	70	VAL
6	s4	113	ARG
6	s4	123	LEU
6	s4	131	LEU
6	s4	133	LYS
6	s4	159	THR
6	s4	176	ASP
6	s4	182	TYR
6	s4	197	HIS
6	s4	214	LEU
6	s4	222	LEU
6	s4	237	SER
6	s4	245	LYS
6	s4	246	LEU
7	s5	25	LEU
7	s5	31	GLU
7	s5	45	LYS
7	s5	52	GLU
7	s5	59	VAL
7	s5	63	GLN
7	s5	68	ILE
7	s5	76	ARG
7	s5	93	LEU
7	s5	124	LEU
7	s5	125	THR
7	s5	128	ASN
7	s5	135	ASP
7	s5	157	ARG
7	s5	189	THR
7	s5	194	LEU
7	s5	199	ILE

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Mol	Chain	Res	Type
7	s5	203	LYS
7	s5	216	GLU
7	s5	219	ARG
8	s6	21	GLU
8	s6	24	ILE
8	s6	31	ARG
8	s6	71	THR
8	s6	76	LEU
8	s6	78	THR
8	s6	87	ARG
8	s6	93	LYS
8	s6	97	VAL
8	s6	109	LEU
8	s6	111	LEU
8	s6	115	LYS
8	s6	120	GLU
8	s6	124	LEU
8	s6	126	ASP
8	s6	127	THR
8	s6	128	THR
8	s6	129	VAL
8	s6	137	ARG
8	s6	143	LYS
8	s6	151	ASP
8	s6	153	VAL
8	s6	155	ASP
8	s6	177	ARG
8	s6	179	VAL
8	s6	215	ARG
8	s6	216	LEU
9	s7	11	GLN
9	s7	28	GLU
9	s7	33	GLU
9	s7	50	ASP
9	s7	67	LEU
9	s7	97	ARG
9	s7	114	ARG
9	s7	116	ARG
9	s7	117	THR
9	s7	123	ASP
9	s7	129	LEU
9	s7	144	VAL

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Mol	Chain	Res	Type
9	s7	147	ASN
9	s7	160	GLN
9	s7	185	ILE
10	s8	25	ARG
10	s8	29	LEU
10	s8	36	THR
10	s8	46	VAL
10	s8	58	LEU
10	s8	74	LYS
10	s8	89	GLU
10	s8	120	THR
10	s8	152	ILE
10	s8	155	SER
10	s8	183	ILE
10	s8	184	LEU
11	s9	3	ARG
11	s9	7	THR
11	s9	9	SER
11	s9	28	LEU
11	s9	33	GLU
11	s9	39	LYS
11	s9	49	LEU
11	s9	82	ARG
11	s9	83	VAL
11	s9	87	SER
11	s9	93	LEU
11	s9	109	LEU
11	s9	110	GLN
11	s9	111	THR
11	s9	120	LYS
11	s9	126	ARG
11	s9	134	ILE
11	s9	150	LEU
11	s9	161	THR
11	s9	172	VAL
11	s9	180	LYS
11	s9	182	GLU
12	c0	2	LEU
12	c0	5	LYS
12	c0	15	LEU
12	c0	20	VAL
12	c0	21	VAL

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Mol	Chain	Res	Type
12	c0	27	PHE
12	c0	33	GLU
12	c0	55	VAL
12	c0	77	ARG
13	c1	5	LEU
13	c1	10	GLU
13	c1	21	ASN
13	c1	31	THR
13	c1	33	ARG
13	c1	40	LEU
13	c1	44	THR
13	c1	47	THR
13	c1	50	GLU
13	c1	56	LYS
13	c1	60	PHE
13	c1	61	THR
13	c1	67	ARG
13	c1	74	THR
13	c1	80	MET
13	c1	83	THR
13	c1	86	ILE
13	c1	87	ARG
13	c1	118	GLN
13	c1	129	ARG
13	c1	136	ARG
13	c1	140	VAL
14	c2	28	LEU
14	c2	43	ARG
14	c2	45	LEU
14	c2	58	LEU
14	c2	61	VAL
14	c2	62	LEU
14	c2	71	ILE
14	c2	74	LEU
14	c2	85	LYS
14	c2	86	VAL
14	c2	89	ILE
14	c2	91	VAL
14	c2	103	LEU
14	c2	132	GLU
14	c2	140	PHE
15	c3	12	SER

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Mol	Chain	Res	Type
15	c3	16	ILE
15	c3	19	SER
15	c3	20	ARG
15	c3	21	ASN
15	c3	35	GLU
15	c3	60	VAL
15	c3	64	ARG
15	c3	66	ILE
15	c3	67	THR
15	c3	75	LEU
15	c3	84	ILE
15	c3	88	LEU
15	c3	97	SER
15	c3	114	ARG
15	c3	115	LEU
15	c3	125	LEU
16	c4	13	VAL
16	c4	65	GLN
16	c4	66	ASP
16	c4	79	VAL
16	c4	81	VAL
16	c4	92	LYS
16	c4	102	LEU
16	c4	107	ARG
16	c4	114	ARG
16	c4	119	THR
16	c4	123	SER
16	c4	129	LYS
16	c4	132	ARG
16	c4	136	ARG
16	c4	137	LEU
17	c5	12	PHE
17	c5	36	LEU
17	c5	40	ARG
17	c5	44	ARG
17	c5	52	LYS
17	c5	69	GLU
17	c5	71	GLU
17	c5	77	ARG
17	c5	107	ILE
17	c5	110	GLU
17	c5	121	ILE

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Mol	Chain	Res	Type
17	c5	124	THR
17	c5	128	HIS
18	c6	7	VAL
18	c6	23	LYS
18	c6	28	LEU
18	c6	43	ILE
18	c6	53	LEU
18	c6	57	LEU
18	c6	68	ARG
18	c6	69	VAL
18	c6	114	ARG
18	c6	128	LYS
18	c6	137	ARG
18	c6	143	ARG
19	c7	5	ARG
19	c7	8	THR
19	c7	30	THR
19	c7	34	LEU
19	c7	46	LEU
19	c7	69	ILE
19	c7	77	GLU
19	c7	85	VAL
19	c7	88	VAL
19	c7	110	VAL
19	c7	113	LEU
20	c8	3	LEU
20	c8	4	VAL
20	c8	6	GLN
20	c8	13	HIS
20	c8	15	LEU
20	c8	25	ASN
20	c8	27	LYS
20	c8	36	LYS
20	c8	40	ARG
20	c8	41	ARG
20	c8	51	ASP
20	c8	55	HIS
20	c8	74	GLN
20	c8	85	PHE
20	c8	94	ASP
20	c8	100	THR
20	c8	116	LEU

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Mol	Chain	Res	Type
20	c8	136	GLN
20	c8	138	THR
20	c8	144	ARG
21	c9	6	VAL
21	c9	27	LYS
21	c9	28	LEU
21	c9	34	VAL
21	c9	37	VAL
21	c9	68	ARG
21	c9	70	GLN
21	c9	71	VAL
21	c9	75	LYS
21	c9	88	VAL
21	c9	123	ARG
21	c9	126	GLU
21	c9	131	ASP
21	c9	139	THR
22	d0	23	ARG
22	d0	34	LEU
22	d0	44	ASN
22	d0	57	ARG
22	d0	60	THR
22	d0	70	THR
22	d0	77	LYS
22	d0	81	THR
22	d0	97	VAL
22	d0	99	ILE
22	d0	103	ILE
22	d0	105	GLN
22	d0	115	GLU
23	d1	2	GLU
23	d1	5	LYS
23	d1	10	GLU
23	d1	17	CYS
23	d1	49	GLU
23	d1	52	THR
23	d1	62	ARG
23	d1	78	LEU
24	d2	7	LEU
24	d2	9	ASP
24	d2	23	ARG
24	d2	24	GLN

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Mol	Chain	Res	Type
24	d2	25	VAL
24	d2	37	PHE
24	d2	43	LYS
24	d2	65	LEU
24	d2	83	ILE
24	d2	98	GLN
24	d2	103	ILE
25	d3	9	LEU
25	d3	19	ARG
25	d3	27	ASN
25	d3	28	ASN
25	d3	73	ARG
25	d3	84	THR
25	d3	100	ASP
25	d3	103	LEU
25	d3	107	PHE
25	d3	114	LYS
25	d3	131	SER
25	d3	144	ARG
26	d4	21	LYS
26	d4	26	ASP
26	d4	28	LEU
26	d4	34	ASN
26	d4	47	VAL
26	d4	49	LYS
26	d4	61	ARG
26	d4	62	THR
26	d4	88	THR
26	d4	114	ARG
26	d4	128	LYS
26	d4	135	ASP
27	d5	41	ILE
27	d5	53	GLU
27	d5	57	TYR
27	d5	60	VAL
27	d5	81	ARG
27	d5	88	ILE
27	d5	102	THR
28	d6	10	ARG
28	d6	26	CYS
28	d6	39	MET
28	d6	46	GLU

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Mol	Chain	Res	Type
28	d6	53	LEU
28	d6	61	GLU
28	d6	82	ARG
29	d7	3	LEU
29	d7	14	SER
29	d7	41	LEU
29	d7	43	ILE
29	d7	49	HIS
29	d7	52	THR
29	d7	56	CYS
29	d7	72	LYS
29	d7	81	ARG
29	d7	82	LYS
30	d8	15	VAL
30	d8	22	ARG
30	d8	32	PHE
30	d8	33	LEU
30	d8	36	THR
30	d8	39	THR
30	d8	54	LEU
30	d8	61	ARG
30	d8	64	ARG
31	d9	10	HIS
31	d9	30	LEU
31	d9	32	ARG
31	d9	36	LEU
31	d9	54	LYS
80	e0	4	VAL
80	e0	21	VAL
80	e0	28	LYS
80	e0	29	LYS
80	e0	54	ARG
80	e0	56	MET
33	e1	78	LYS
33	e1	86	THR
33	e1	90	LYS
33	e1	96	LYS
33	e1	97	LYS
33	e1	98	VAL
33	e1	100	LEU
33	e1	102	VAL
33	e1	106	TYR

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Mol	Chain	Res	Type
33	e1	113	LYS
33	e1	120	GLU
33	e1	135	HIS
33	e1	151	ASN
34	sR	6	VAL
34	sR	29	GLN
34	sR	51	ASP
34	sR	52	GLN
34	sR	58	VAL
34	sR	66	HIS
34	sR	76	ASP
34	sR	96	THR
34	sR	149	ASP
34	sR	167	VAL
34	sR	182	ASN
34	sR	202	LEU
34	sR	232	TYR
34	sR	297	ASP
35	sM	43	ASP
35	sM	49	LYS
35	sM	50	ASN
35	sM	74	LYS
35	sM	75	ASP
39	l2	22	LEU
39	l2	32	LEU
39	l2	44	ILE
39	l2	45	VAL
39	l2	61	VAL
39	l2	62	VAL
39	l2	71	LEU
39	l2	79	ASN
39	l2	82	VAL
39	l2	101	VAL
39	l2	104	LEU
39	l2	107	VAL
39	l2	109	GLU
39	l2	116	VAL
39	l2	119	LYS
39	l2	122	ASP
39	l2	128	ARG
39	l2	137	ILE
39	l2	147	ARG

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Mol	Chain	Res	Type
39	12	155	LYS
39	12	157	VAL
39	12	158	ILE
39	12	165	VAL
39	12	169	ILE
39	12	202	VAL
39	12	204	MET
39	12	207	VAL
39	12	246	LEU
39	12	247	ARG
39	12	249	SER
40	13	3	HIS
40	13	10	ARG
40	13	17	LEU
40	13	19	ARG
40	13	30	LYS
40	13	37	ARG
40	13	43	LEU
40	13	47	LEU
40	13	50	LYS
40	13	56	ILE
40	13	69	LYS
40	13	70	ARG
40	13	81	THR
40	13	84	VAL
40	13	85	VAL
40	13	95	THR
40	13	104	THR
40	13	108	GLU
40	13	110	LEU
40	13	114	VAL
40	13	125	SER
40	13	139	GLN
40	13	146	ARG
40	13	148	LEU
40	13	153	LYS
40	13	157	VAL
40	13	167	ARG
40	13	169	THR
40	13	178	LEU
40	13	183	LEU
40	13	188	ILE

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Mol	Chain	Res	Type
40	l3	202	THR
40	l3	205	VAL
40	l3	212	ASN
40	l3	227	GLU
40	l3	232	ARG
40	l3	238	LEU
40	l3	244	ARG
40	l3	248	LYS
40	l3	249	VAL
40	l3	252	ILE
40	l3	264	VAL
40	l3	266	ARG
40	l3	304	THR
40	l3	324	VAL
40	l3	332	ARG
40	l3	340	LYS
40	l3	341	SER
40	l3	369	ARG
41	l4	2	SER
41	l4	3	ARG
41	l4	14	GLU
41	l4	22	LEU
41	l4	25	VAL
41	l4	47	ARG
41	l4	73	ARG
41	l4	92	ASN
41	l4	93	MET
41	l4	120	TYR
41	l4	122	THR
41	l4	134	LEU
41	l4	143	GLU
41	l4	144	LYS
41	l4	145	ILE
41	l4	148	ILE
41	l4	150	LEU
41	l4	156	LEU
41	l4	160	GLN
41	l4	170	LYS
41	l4	176	SER
41	l4	177	ASP
41	l4	179	LEU
41	l4	186	LYS

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Mol	Chain	Res	Type
41	14	187	LEU
41	14	200	THR
41	14	206	LEU
41	14	220	ARG
41	14	222	VAL
41	14	230	VAL
41	14	246	ARG
41	14	258	LEU
41	14	266	THR
41	14	307	GLN
41	14	313	LEU
41	14	319	LYS
41	14	327	LEU
41	14	338	LYS
41	14	342	LYS
41	14	345	GLU
41	14	347	THR
42	15	4	GLN
42	15	34	LYS
42	15	51	LEU
42	15	61	ILE
42	15	65	ILE
42	15	68	THR
42	15	70	THR
42	15	74	VAL
42	15	75	LEU
42	15	93	THR
42	15	110	LEU
42	15	113	LEU
42	15	115	LEU
42	15	118	THR
42	15	120	LYS
42	15	140	ARG
42	15	144	VAL
42	15	146	LEU
42	15	152	ARG
42	15	155	THR
42	15	177	GLU
42	15	185	PHE
42	15	194	LEU
42	15	227	LEU
42	15	236	LEU

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Mol	Chain	Res	Type
42	15	254	LYS
42	15	268	GLU
42	15	273	ARG
42	15	275	THR
42	15	282	ARG
43	16	8	LYS
43	16	18	LEU
43	16	20	LYS
43	16	21	THR
43	16	35	VAL
43	16	50	LYS
43	16	52	VAL
43	16	62	THR
43	16	64	LEU
43	16	65	ILE
43	16	78	ARG
43	16	79	VAL
43	16	89	THR
43	16	92	SER
43	16	98	VAL
43	16	99	GLU
43	16	109	GLU
43	16	131	LYS
43	16	152	THR
43	16	155	LEU
43	16	162	SER
44	17	26	VAL
44	17	41	ARG
44	17	45	LEU
44	17	60	ARG
44	17	77	VAL
44	17	83	LEU
44	17	87	VAL
44	17	98	LYS
44	17	110	ARG
44	17	121	LYS
44	17	124	LEU
44	17	130	ILE
44	17	158	LYS
44	17	178	ILE
44	17	179	LEU
44	17	184	LEU

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Mol	Chain	Res	Type
44	17	229	PHE
44	17	239	LEU
45	18	26	LEU
45	18	41	GLN
45	18	50	VAL
45	18	68	ARG
45	18	71	VAL
45	18	74	THR
45	18	79	GLN
45	18	81	THR
45	18	95	ASN
45	18	109	LEU
45	18	136	LEU
45	18	150	LEU
45	18	160	ILE
45	18	163	VAL
45	18	164	VAL
45	18	169	LEU
45	18	172	LYS
45	18	183	LYS
45	18	189	LEU
45	18	195	SER
45	18	200	LEU
45	18	206	GLU
45	18	214	LEU
45	18	230	LYS
45	18	238	LEU
45	18	241	LYS
45	18	248	LYS
46	19	5	GLN
46	19	6	THR
46	19	16	VAL
46	19	17	THR
46	19	18	VAL
46	19	19	SER
46	19	21	LYS
46	19	33	THR
46	19	39	LYS
46	19	44	THR
46	19	55	VAL
46	19	62	ARG
46	19	68	LEU

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Mol	Chain	Res	Type
46	l9	69	ARG
46	l9	70	THR
46	l9	80	THR
46	l9	82	VAL
46	l9	105	GLU
46	l9	107	ASP
46	l9	122	LYS
46	l9	130	ASP
46	l9	132	VAL
46	l9	133	THR
46	l9	144	ILE
46	l9	147	SER
46	l9	151	VAL
46	l9	157	ASN
46	l9	161	LEU
46	l9	162	GLN
46	l9	166	ARG
46	l9	173	ARG
46	l9	179	ILE
46	l9	187	ILE
46	l9	191	LEU
47	m0	4	ARG
47	m0	24	ARG
47	m0	38	LYS
47	m0	42	THR
47	m0	48	LEU
47	m0	52	LEU
47	m0	57	LEU
47	m0	58	GLU
47	m0	71	CYS
47	m0	77	THR
47	m0	87	LEU
47	m0	91	VAL
47	m0	99	ILE
47	m0	102	MET
47	m0	137	SER
47	m0	139	ARG
47	m0	142	ASP
47	m0	148	VAL
47	m0	156	ARG
47	m0	163	GLN
47	m0	167	LEU

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Mol	Chain	Res	Type
47	m0	169	LYS
47	m0	176	LEU
47	m0	177	ASP
47	m0	185	ARG
47	m0	197	VAL
47	m0	205	SER
47	m0	206	LEU
47	m0	212	GLU
47	m0	217	PHE
48	m1	9	MET
48	m1	10	ARG
48	m1	13	LYS
48	m1	22	SER
48	m1	31	THR
48	m1	55	ARG
48	m1	56	THR
48	m1	106	ILE
48	m1	112	LEU
48	m1	129	VAL
48	m1	130	VAL
48	m1	140	ARG
48	m1	150	ASN
48	m1	158	ASP
48	m1	159	THR
48	m1	166	LYS
49	m3	13	HIS
49	m3	54	LEU
49	m3	58	VAL
49	m3	67	ARG
49	m3	69	VAL
49	m3	73	ARG
49	m3	107	GLU
49	m3	118	GLU
49	m3	122	LYS
49	m3	123	ILE
49	m3	128	ARG
49	m3	131	LYS
49	m3	138	VAL
49	m3	149	GLN
49	m3	162	ASN
49	m3	164	GLU
49	m3	176	GLU

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Mol	Chain	Res	Type
49	m3	184	GLU
49	m3	189	GLU
50	m4	3	THR
50	m4	15	VAL
50	m4	20	VAL
50	m4	27	GLN
50	m4	37	GLU
50	m4	43	LYS
50	m4	53	VAL
50	m4	62	GLN
50	m4	64	VAL
50	m4	66	THR
50	m4	69	THR
50	m4	72	LEU
50	m4	80	THR
50	m4	124	ARG
50	m4	130	THR
50	m4	132	LYS
50	m4	135	LEU
51	m5	10	LEU
51	m5	12	ARG
51	m5	22	LEU
51	m5	24	ARG
51	m5	49	ARG
51	m5	76	PRO
51	m5	80	THR
51	m5	83	LYS
51	m5	85	THR
51	m5	98	LEU
51	m5	105	ARG
51	m5	109	ARG
51	m5	117	ASN
51	m5	138	GLN
51	m5	176	LYS
51	m5	190	THR
52	m6	3	VAL
52	m6	22	VAL
52	m6	25	LYS
52	m6	34	VAL
52	m6	59	ARG
52	m6	67	THR
52	m6	68	ARG

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Mol	Chain	Res	Type
52	m6	74	ARG
52	m6	78	ARG
52	m6	85	ARG
52	m6	89	SER
52	m6	110	PRO
52	m6	117	ARG
52	m6	124	LEU
52	m6	130	LYS
52	m6	151	ASP
52	m6	160	ARG
52	m6	180	SER
52	m6	182	ASN
52	m6	184	THR
52	m6	193	GLN
53	m7	7	THR
53	m7	9	THR
53	m7	24	VAL
53	m7	32	THR
53	m7	52	LEU
53	m7	53	ASP
53	m7	65	SER
53	m7	78	VAL
53	m7	79	THR
53	m7	80	LYS
53	m7	86	LYS
53	m7	89	LYS
53	m7	94	LEU
53	m7	107	LEU
53	m7	112	LEU
53	m7	119	VAL
53	m7	127	ARG
53	m7	155	GLU
54	m8	3	ILE
54	m8	12	ARG
54	m8	17	THR
54	m8	26	LEU
54	m8	32	LEU
54	m8	34	THR
54	m8	62	VAL
54	m8	64	VAL
54	m8	80	THR
54	m8	86	THR

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Mol	Chain	Res	Type
54	m8	135	GLN
54	m8	138	LEU
54	m8	147	ARG
54	m8	150	VAL
54	m8	161	LYS
54	m8	165	ILE
54	m8	168	THR
54	m8	170	ARG
54	m8	178	ARG
54	m8	185	LYS
55	m9	5	ARG
55	m9	7	GLN
55	m9	10	LEU
55	m9	20	ARG
55	m9	27	ASN
55	m9	29	THR
55	m9	43	LYS
55	m9	55	VAL
55	m9	63	THR
55	m9	70	LYS
55	m9	88	ARG
55	m9	99	LEU
55	m9	106	LEU
55	m9	116	ASP
55	m9	117	LYS
55	m9	134	HIS
55	m9	138	LEU
55	m9	143	ILE
55	m9	152	GLU
55	m9	156	ASN
55	m9	164	LEU
55	m9	173	ARG
55	m9	186	LYS
56	n0	1	MET
56	n0	17	GLU
56	n0	21	GLU
56	n0	23	LYS
56	n0	32	SER
56	n0	34	GLU
56	n0	40	ARG
56	n0	50	LYS
56	n0	71	LYS

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Mol	Chain	Res	Type
56	n0	80	ARG
56	n0	87	THR
56	n0	96	ASP
56	n0	97	VAL
56	n0	105	THR
56	n0	117	ARG
56	n0	120	SER
56	n0	130	GLU
56	n0	132	THR
56	n0	136	LYS
56	n0	137	ARG
56	n0	155	ARG
56	n0	157	GLN
56	n0	162	THR
56	n0	172	TYR
57	n1	9	SER
57	n1	12	ARG
57	n1	18	ASP
57	n1	26	HIS
57	n1	68	THR
57	n1	78	LYS
57	n1	80	VAL
57	n1	83	ARG
57	n1	88	ARG
57	n1	89	LEU
57	n1	93	VAL
57	n1	96	ILE
57	n1	102	ARG
57	n1	104	GLU
57	n1	118	GLU
57	n1	124	VAL
57	n1	126	VAL
57	n1	128	LEU
57	n1	130	ARG
57	n1	135	PRO
57	n1	139	ARG
57	n1	141	VAL
57	n1	143	THR
57	n1	149	GLN
57	n1	150	THR
58	n2	27	VAL
58	n2	38	ILE

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Mol	Chain	Res	Type
58	n2	43	VAL
58	n2	49	ASN
58	n2	54	VAL
58	n2	55	THR
58	n2	58	GLU
58	n2	68	THR
58	n2	74	LYS
58	n2	75	TYR
58	n2	90	ARG
58	n2	94	ARG
58	n2	96	VAL
59	n3	7	GLN
59	n3	13	ILE
59	n3	48	ARG
59	n3	64	LYS
59	n3	88	ARG
59	n3	93	LEU
59	n3	98	ASN
59	n3	108	GLU
59	n3	120	LYS
60	n4	1	MET
60	n4	19	THR
60	n4	39	LEU
60	n4	63	ILE
60	n4	96	LEU
60	n4	126	GLU
60	n4	127	LYS
61	n5	24	LEU
61	n5	27	ARG
61	n5	34	LEU
61	n5	37	THR
61	n5	38	LEU
61	n5	39	LYS
61	n5	40	LEU
61	n5	56	ARG
61	n5	57	LEU
61	n5	63	ILE
61	n5	71	THR
61	n5	73	MET
61	n5	74	LYS
61	n5	86	VAL
61	n5	109	LYS

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Mol	Chain	Res	Type
61	n5	115	ARG
61	n5	125	ARG
61	n5	135	ILE
61	n5	142	ILE
62	n6	4	GLN
62	n6	12	ARG
62	n6	13	ARG
62	n6	14	LYS
62	n6	37	LYS
62	n6	39	LEU
62	n6	40	ARG
62	n6	45	ILE
62	n6	50	ILE
62	n6	51	ARG
62	n6	52	ARG
62	n6	56	VAL
62	n6	57	LEU
62	n6	66	GLN
62	n6	69	LYS
62	n6	74	TYR
62	n6	83	ASP
62	n6	94	SER
62	n6	114	ASP
62	n6	115	ARG
62	n6	120	GLN
62	n6	122	LYS
63	n7	3	LYS
63	n7	5	LEU
63	n7	17	ARG
63	n7	24	VAL
63	n7	54	THR
63	n7	57	HIS
63	n7	72	ILE
63	n7	81	LEU
63	n7	83	THR
63	n7	90	GLU
63	n7	95	VAL
63	n7	100	THR
63	n7	102	GLU
63	n7	103	GLN
63	n7	121	ARG
63	n7	126	LYS

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Mol	Chain	Res	Type
63	n7	134	LEU
64	n8	4	ARG
64	n8	6	THR
64	n8	7	LYS
64	n8	8	THR
64	n8	10	LYS
64	n8	12	ARG
64	n8	26	ARG
64	n8	27	LYS
64	n8	42	ARG
64	n8	47	LYS
64	n8	60	TYR
64	n8	64	GLN
64	n8	65	GLN
64	n8	85	ASP
64	n8	88	ASP
64	n8	98	THR
64	n8	115	LYS
64	n8	128	ARG
64	n8	133	LEU
64	n8	139	ARG
65	n9	13	THR
65	n9	14	ARG
65	n9	19	ASN
65	n9	22	LYS
65	n9	38	LYS
65	n9	42	ASN
65	n9	58	LYS
65	n9	59	LYS
66	o0	8	GLU
66	o0	18	ILE
66	o0	32	LYS
66	o0	61	MET
66	o0	66	LYS
66	o0	86	ARG
66	o0	100	ILE
67	o1	6	ASP
67	o1	8	VAL
67	o1	13	THR
67	o1	16	LEU
67	o1	24	SER
67	o1	26	LYS

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Mol	Chain	Res	Type
67	o1	31	ARG
67	o1	44	MET
67	o1	55	LEU
67	o1	68	GLU
67	o1	76	SER
67	o1	83	GLU
67	o1	93	VAL
67	o1	96	VAL
67	o1	98	VAL
67	o1	102	LYS
67	o1	106	THR
67	o1	110	GLU
68	o2	16	LYS
68	o2	19	ARG
68	o2	33	ARG
68	o2	34	LYS
68	o2	39	ASP
68	o2	61	LYS
68	o2	73	THR
68	o2	75	LEU
68	o2	82	LEU
68	o2	89	THR
68	o2	125	ARG
68	o2	126	LEU
69	o3	3	GLU
69	o3	4	SER
69	o3	28	SER
69	o3	31	LYS
69	o3	45	LEU
69	o3	59	VAL
69	o3	60	ARG
69	o3	70	LYS
69	o3	81	VAL
69	o3	86	ARG
69	o3	90	PRO
69	o3	98	VAL
69	o3	105	SER
69	o3	107	ILE
70	o4	5	VAL
70	o4	20	ILE
70	o4	21	LYS
70	o4	24	LYS

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Mol	Chain	Res	Type
70	o4	29	ILE
70	o4	31	ARG
70	o4	37	LYS
70	o4	58	ARG
70	o4	65	VAL
70	o4	68	THR
70	o4	71	THR
70	o4	80	ARG
70	o4	88	ARG
70	o4	98	GLN
71	o5	20	GLN
71	o5	27	GLU
71	o5	28	LEU
71	o5	45	LYS
71	o5	46	THR
71	o5	47	VAL
71	o5	68	GLN
71	o5	69	LEU
71	o5	81	ARG
71	o5	84	LYS
71	o5	85	THR
71	o5	89	ARG
71	o5	90	ARG
71	o5	99	GLN
71	o5	100	VAL
71	o5	101	THR
71	o5	107	LYS
72	o6	9	ILE
72	o6	11	LEU
72	o6	12	ASN
72	o6	17	VAL
72	o6	21	THR
72	o6	26	ILE
72	o6	36	ARG
72	o6	43	LEU
72	o6	45	ARG
72	o6	57	LEU
72	o6	58	ILE
72	o6	60	LEU
72	o6	68	ARG
72	o6	74	LYS
72	o6	76	ARG

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Mol	Chain	Res	Type
72	o6	80	PHE
72	o6	88	GLU
72	o6	94	ILE
72	o6	98	ARG
73	o7	12	HIS
73	o7	17	THR
73	o7	25	ARG
73	o7	33	THR
73	o7	36	SER
73	o7	44	THR
73	o7	46	SER
73	o7	55	ARG
73	o7	59	THR
73	o7	65	ARG
73	o7	75	LYS
73	o7	84	SER
74	o8	17	ARG
74	o8	19	ASP
74	o8	22	THR
74	o8	24	THR
74	o8	41	THR
74	o8	46	ARG
74	o8	53	THR
74	o8	61	LYS
74	o8	64	LYS
74	o8	65	LEU
74	o8	67	GLN
74	o8	78	LEU
75	o9	4	GLN
75	o9	21	ARG
75	o9	23	LEU
75	o9	45	ARG
75	o9	48	LYS
75	o9	51	ILE
76	q0	85	LEU
76	q0	112	LYS
76	q0	113	ARG
76	q0	114	LYS
77	q1	2	ARG
77	q1	6	ARG
77	q1	9	ARG
77	q1	13	LEU

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Mol	Chain	Res	Type
77	q1	18	ARG
77	q1	21	ARG
78	q2	8	ARG
78	q2	61	LYS
78	q2	69	VAL
78	q2	71	ARG
78	q2	78	LYS
78	q2	79	THR
78	q2	80	ARG
78	q2	84	THR
78	q2	85	LEU
78	q2	93	LEU
78	q2	105	GLN
79	q3	3	LYS
79	q3	20	SER
79	q3	24	ARG
79	q3	41	PHE
79	q3	54	ILE
79	q3	56	THR
79	q3	58	SER
79	q3	59	CYS
79	q3	73	THR
82	p0	4	ILE
82	p0	5	ARG
82	p0	10	GLU
82	p0	15	LEU
82	p0	39	HIS
82	p0	42	ARG
82	p0	48	ARG
82	p0	51	VAL
82	p0	52	LEU
82	p0	67	LEU
82	p0	70	LEU
82	p0	81	LYS
82	p0	91	GLU
82	p0	93	LEU
82	p0	97	LYS
82	p0	104	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
3	S1	148	ASN
3	S1	209	ASN
8	S6	10	ASN
12	C0	32	HIS
23	D1	74	GLN
26	D4	63	GLN
31	D9	48	ASN
39	L2	209	HIS
39	L2	211	HIS
41	L4	296	GLN
42	L5	40	HIS
42	L5	264	GLN
44	L7	244	ASN
47	M0	59	GLN
50	M4	105	GLN
57	N1	146	ASN
57	N1	149	GLN
59	N3	98	ASN
63	N7	128	GLN
3	s1	149	GLN
14	c2	125	ASN
18	c6	83	GLN
20	c8	74	GLN
27	d5	82	HIS
80	e0	17	GLN
45	l8	61	GLN
47	m0	162	GLN
70	o4	3	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1776/1800 (98%)	437 (24%)	50 (2%)
1	6	1792/1800 (99%)	419 (23%)	43 (2%)
36	1	3143/3396 (92%)	618 (19%)	66 (2%)
36	5	3143/3396 (92%)	604 (19%)	63 (2%)
37	3	120/121 (99%)	14 (11%)	1 (0%)
37	7	120/121 (99%)	15 (12%)	0
38	4	157/158 (99%)	32 (20%)	2 (1%)
38	8	157/158 (99%)	31 (19%)	0
85	C	1/5 (20%)	0	0
85	D	1/5 (20%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	10410/10960 (94%)	2170 (20%)	225 (2%)

All (2170) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A
1	2	27	U
1	2	34	G
1	2	42	G
1	2	45	U
1	2	47	A
1	2	50	C
1	2	57	G
1	2	60	U
1	2	67	A
1	2	68	A
1	2	69	G
1	2	72	A
1	2	73	U
1	2	75	U
1	2	77	U
1	2	95	G
1	2	104	A
1	2	114	C
1	2	121	U
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	140	A
1	2	141	U
1	2	144	U
1	2	145	A
1	2	146	U
1	2	153	G

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Mol	Chain	Res	Type
1	2	158	U
1	2	159	U
1	2	178	U
1	2	185	U
1	2	186	C
1	2	187	G
1	2	188	A
1	2	190	C
1	2	191	C
1	2	192	U
1	2	193	U
1	2	194	U
1	2	195	G
1	2	196	G
1	2	197	A
1	2	200	A
1	2	207	U
1	2	215	A
1	2	217	A
1	2	218	A
1	2	219	A
1	2	227	U
1	2	228	G
1	2	229	U
1	2	231	U
1	2	233	C
1	2	234	G
1	2	235	G
1	2	238	U
1	2	239	C
1	2	240	U
1	2	241	U
1	2	242	U
1	2	249	U
1	2	250	C
1	2	261	U
1	2	262	U
1	2	265	A
1	2	266	A
1	2	269	G
1	2	271	A
1	2	272	U

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Mol	Chain	Res	Type
1	2	275	C
1	2	276	C
1	2	277	U
1	2	278	U
1	2	279	G
1	2	280	U
1	2	281	G
1	2	288	A
1	2	290	G
1	2	299	A
1	2	302	U
1	2	309	C
1	2	314	C
1	2	316	A
1	2	319	U
1	2	320	U
1	2	321	C
1	2	323	A
1	2	333	A
1	2	337	G
1	2	338	C
1	2	341	A
1	2	352	A
1	2	356	G
1	2	359	A
1	2	360	A
1	2	361	C
1	2	363	G
1	2	365	G
1	2	387	A
1	2	397	A
1	2	400	A
1	2	401	A
1	2	402	C
1	2	403	G
1	2	404	G
1	2	416	A
1	2	418	G
1	2	421	A
1	2	424	C
1	2	425	A
1	2	426	G

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Mol	Chain	Res	Type
1	2	428	A
1	2	434	G
1	2	437	A
1	2	439	U
1	2	444	C
1	2	448	C
1	2	450	U
1	2	468	A
1	2	475	A
1	2	477	A
1	2	484	C
1	2	485	A
1	2	488	G
1	2	493	U
1	2	494	U
1	2	495	C
1	2	496	G
1	2	497	G
1	2	498	G
1	2	499	U
1	2	500	C
1	2	502	U
1	2	503	G
1	2	504	U
1	2	505	A
1	2	506	A
1	2	507	U
1	2	508	U
1	2	510	G
1	2	511	A
1	2	513	U
1	2	514	G
1	2	515	A
1	2	516	G
1	2	527	A
1	2	534	A
1	2	538	A
1	2	539	G
1	2	540	G
1	2	541	A
1	2	542	A
1	2	543	C

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Mol	Chain	Res	Type
1	2	544	A
1	2	548	G
1	2	555	A
1	2	556	A
1	2	557	G
1	2	558	U
1	2	559	C
1	2	565	C
1	2	572	C
1	2	579	A
1	2	580	A
1	2	585	A
1	2	594	A
1	2	595	G
1	2	606	A
1	2	610	G
1	2	611	U
1	2	619	A
1	2	620	A
1	2	622	A
1	2	623	A
1	2	630	A
1	2	639	U
1	2	640	U
1	2	650	U
1	2	653	C
1	2	654	C
1	2	656	G
1	2	657	U
1	2	658	C
1	2	677	G
1	2	679	U
1	2	680	U
1	2	684	A
1	2	686	C
1	2	694	U
1	2	696	C
1	2	697	C
1	2	700	C
1	2	702	G
1	2	703	G
1	2	704	C

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Mol	Chain	Res	Type
1	2	705	U
1	2	707	A
1	2	709	C
1	2	710	U
1	2	712	G
1	2	713	A
1	2	714	G
1	2	717	C
1	2	718	U
1	2	719	U
1	2	720	G
1	2	721	U
1	2	722	G
1	2	723	G
1	2	725	U
1	2	727	U
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	735	C
1	2	736	C
1	2	737	A
1	2	738	G
1	2	742	U
1	2	744	U
1	2	745	U
1	2	754	A
1	2	755	A
1	2	756	A
1	2	765	G
1	2	766	U
1	2	774	A
1	2	775	G
1	2	778	G
1	2	780	A
1	2	781	U
1	2	782	U
1	2	783	G
1	2	784	C
1	2	789	A

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Mol	Chain	Res	Type
1	2	794	U
1	2	795	U
1	2	807	A
1	2	812	A
1	2	815	G
1	2	816	G
1	2	818	C
1	2	820	U
1	2	821	U
1	2	823	G
1	2	824	G
1	2	829	A
1	2	830	U
1	2	831	U
1	2	833	U
1	2	846	G
1	2	848	C
1	2	856	A
1	2	863	A
1	2	864	U
1	2	876	G
1	2	886	U
1	2	898	A
1	2	903	U
1	2	912	U
1	2	913	G
1	2	914	G
1	2	915	A
1	2	916	U
1	2	921	U
1	2	933	A
1	2	935	U
1	2	942	G
1	2	944	A
1	2	951	A
1	2	960	U
1	2	966	A
1	2	992	A
1	2	993	A
1	2	997	G
1	2	1003	A
1	2	1004	U

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Mol	Chain	Res	Type
1	2	1005	A
1	2	1020	A
1	2	1021	C
1	2	1026	A
1	2	1028	C
1	2	1031	U
1	2	1039	A
1	2	1040	G
1	2	1052	U
1	2	1053	G
1	2	1058	U
1	2	1060	U
1	2	1061	A
1	2	1074	G
1	2	1081	A
1	2	1082	C
1	2	1091	A
1	2	1092	A
1	2	1096	C
1	2	1097	U
1	2	1100	G
1	2	1109	G
1	2	1138	A
1	2	1150	G
1	2	1151	A
1	2	1152	A
1	2	1157	A
1	2	1158	C
1	2	1160	A
1	2	1167	G
1	2	1185	U
1	2	1194	A
1	2	1196	A
1	2	1199	G
1	2	1200	G
1	2	1202	A
1	2	1203	A
1	2	1208	A
1	2	1217	A
1	2	1218	G
1	2	1227	A
1	2	1228	G

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Mol	Chain	Res	Type
1	2	1229	G
1	2	1243	G
1	2	1244	A
1	2	1245	G
1	2	1251	U
1	2	1258	U
1	2	1286	U
1	2	1290	U
1	2	1301	U
1	2	1314	U
1	2	1315	U
1	2	1316	G
1	2	1320	U
1	2	1321	A
1	2	1339	C
1	2	1340	U
1	2	1341	A
1	2	1344	A
1	2	1345	A
1	2	1347	U
1	2	1354	G
1	2	1363	U
1	2	1364	G
1	2	1370	U
1	2	1371	A
1	2	1372	U
1	2	1390	U
1	2	1398	U
1	2	1399	C
1	2	1413	U
1	2	1415	U
1	2	1427	A
1	2	1428	G
1	2	1431	C
1	2	1446	A
1	2	1448	G
1	2	1459	C
1	2	1471	A
1	2	1473	U
1	2	1474	G
1	2	1475	A
1	2	1477	G

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Mol	Chain	Res	Type
1	2	1482	C
1	2	1486	G
1	2	1489	U
1	2	1490	C
1	2	1491	U
1	2	1492	A
1	2	1493	A
1	2	1506	G
1	2	1514	U
1	2	1515	A
1	2	1516	A
1	2	1517	U
1	2	1523	G
1	2	1524	A
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1538	U
1	2	1540	G
1	2	1542	G
1	2	1557	U
1	2	1559	A
1	2	1569	A
1	2	1574	G
1	2	1584	G
1	2	1590	G
1	2	1600	A
1	2	1601	G
1	2	1614	A
1	2	1616	G
1	2	1626	U
1	2	1631	A
1	2	1636	C
1	2	1652	C
1	2	1657	U
1	2	1658	G
1	2	1680	G
1	2	1681	A
1	2	1683	C
1	2	1684	U
1	2	1697	G
1	2	1698	G

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Mol	Chain	Res	Type
1	2	1699	G
1	2	1700	C
1	2	1701	A
1	2	1702	A
1	2	1703	C
1	2	1711	C
1	2	1712	A
1	2	1713	G
1	2	1715	G
1	2	1731	A
1	2	1760	G
1	2	1762	A
1	2	1766	A
1	2	1769	U
1	2	1780	G
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1793	G
1	2	1794	A
1	2	1795	U
1	2	1796	C
36	1	16	A
36	1	24	G
36	1	40	A
36	1	45	A
36	1	49	A
36	1	59	G
36	1	60	A
36	1	65	A
36	1	66	A
36	1	92	G
36	1	93	C
36	1	99	A
36	1	109	A
36	1	110	G
36	1	111	C
36	1	113	C
36	1	116	A
36	1	118	U
36	1	121	A
36	1	122	A

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Mol	Chain	Res	Type
36	1	133	U
36	1	136	G
36	1	147	U
36	1	148	G
36	1	156	G
36	1	157	A
36	1	161	G
36	1	170	G
36	1	187	A
36	1	190	U
36	1	191	U
36	1	192	C
36	1	201	A
36	1	210	U
36	1	211	A
36	1	213	A
36	1	218	G
36	1	219	A
36	1	222	A
36	1	224	C
36	1	240	U
36	1	243	G
36	1	245	U
36	1	249	U
36	1	250	U
36	1	251	G
36	1	252	U
36	1	269	G
36	1	282	G
36	1	283	G
36	1	286	U
36	1	295	A
36	1	298	U
36	1	299	G
36	1	305	U
36	1	315	C
36	1	323	A
36	1	329	U
36	1	339	C
36	1	349	A
36	1	350	C
36	1	370	U

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Mol	Chain	Res	Type
36	1	376	G
36	1	398	A
36	1	399	A
36	1	401	U
36	1	402	A
36	1	403	C
36	1	404	G
36	1	421	G
36	1	422	A
36	1	438	A
36	1	439	C
36	1	440	A
36	1	495	G
36	1	518	G
36	1	520	U
36	1	521	A
36	1	523	A
36	1	535	G
36	1	543	C
36	1	544	C
36	1	546	C
36	1	547	G
36	1	548	G
36	1	552	G
36	1	555	U
36	1	556	U
36	1	557	A
36	1	559	A
36	1	569	A
36	1	578	A
36	1	579	G
36	1	592	A
36	1	603	A
36	1	604	G
36	1	607	A
36	1	609	G
36	1	611	A
36	1	619	A
36	1	620	U
36	1	621	A
36	1	622	A
36	1	636	C

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Mol	Chain	Res	Type
36	1	638	C
36	1	649	A
36	1	651	G
36	1	654	C
36	1	660	A
36	1	661	G
36	1	677	A
36	1	681	U
36	1	691	A
36	1	705	A
36	1	708	G
36	1	712	G
36	1	715	A
36	1	716	A
36	1	764	U
36	1	765	C
36	1	766	U
36	1	767	U
36	1	774	G
36	1	776	U
36	1	777	U
36	1	781	G
36	1	785	G
36	1	806	A
36	1	817	A
36	1	830	A
36	1	842	G
36	1	849	C
36	1	861	C
36	1	870	G
36	1	874	U
36	1	876	A
36	1	878	G
36	1	879	U
36	1	890	C
36	1	896	A
36	1	897	U
36	1	907	G
36	1	908	G
36	1	914	A
36	1	916	G
36	1	917	A

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Mol	Chain	Res	Type
36	1	923	C
36	1	924	G
36	1	925	A
36	1	937	G
36	1	943	U
36	1	944	C
36	1	953	G
36	1	959	C
36	1	960	U
36	1	962	A
36	1	963	G
36	1	979	U
36	1	980	A
36	1	981	U
36	1	982	C
36	1	994	G
36	1	1000	C
36	1	1001	G
36	1	1002	A
36	1	1006	A
36	1	1010	G
36	1	1013	G
36	1	1017	C
36	1	1018	G
36	1	1020	G
36	1	1024	G
36	1	1025	A
36	1	1029	G
36	1	1037	C
36	1	1047	A
36	1	1049	C
36	1	1064	A
36	1	1065	A
36	1	1072	G
36	1	1079	A
36	1	1081	U
36	1	1082	U
36	1	1093	A
36	1	1094	U
36	1	1095	U
36	1	1096	U
36	1	1097	G

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Mol	Chain	Res	Type
36	1	1098	A
36	1	1103	A
36	1	1104	G
36	1	1112	A
36	1	1117	G
36	1	1131	G
36	1	1144	U
36	1	1153	A
36	1	1159	A
36	1	1160	C
36	1	1178	G
36	1	1179	A
36	1	1180	A
36	1	1181	U
36	1	1182	A
36	1	1192	C
36	1	1201	C
36	1	1209	G
36	1	1217	A
36	1	1221	A
36	1	1222	G
36	1	1225	A
36	1	1227	C
36	1	1232	C
36	1	1235	U
36	1	1236	G
36	1	1237	G
36	1	1241	U
36	1	1243	G
36	1	1245	A
36	1	1246	G
36	1	1248	C
36	1	1249	G
36	1	1258	U
36	1	1262	G
36	1	1263	A
36	1	1264	G
36	1	1266	G
36	1	1269	U
36	1	1270	A
36	1	1271	A
36	1	1274	A

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Mol	Chain	Res	Type
36	1	1278	A
36	1	1279	C
36	1	1285	G
36	1	1287	A
36	1	1292	C
36	1	1307	G
36	1	1308	A
36	1	1309	U
36	1	1313	G
36	1	1330	A
36	1	1333	C
36	1	1348	U
36	1	1349	G
36	1	1350	A
36	1	1351	U
36	1	1352	A
36	1	1353	U
36	1	1355	A
36	1	1356	U
36	1	1357	G
36	1	1386	A
36	1	1399	A
36	1	1400	G
36	1	1418	A
36	1	1419	A
36	1	1425	U
36	1	1429	G
36	1	1431	G
36	1	1433	A
36	1	1434	G
36	1	1437	C
36	1	1446	A
36	1	1450	G
36	1	1453	A
36	1	1455	U
36	1	1460	A
36	1	1481	A
36	1	1482	A
36	1	1485	G
36	1	1488	G
36	1	1490	A
36	1	1502	C

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Mol	Chain	Res	Type
36	1	1508	C
36	1	1527	C
36	1	1533	U
36	1	1536	G
36	1	1549	U
36	1	1556	C
36	1	1557	A
36	1	1560	G
36	1	1561	G
36	1	1562	C
36	1	1563	C
36	1	1564	U
36	1	1566	A
36	1	1567	U
36	1	1568	U
36	1	1569	U
36	1	1570	U
36	1	1572	U
36	1	1576	G
36	1	1580	A
36	1	1582	C
36	1	1583	A
36	1	1589	A
36	1	1593	A
36	1	1596	C
36	1	1605	A
36	1	1620	U
36	1	1629	U
36	1	1633	C
36	1	1639	C
36	1	1643	A
36	1	1657	C
36	1	1683	A
36	1	1688	U
36	1	1716	U
36	1	1717	U
36	1	1724	U
36	1	1725	C
36	1	1729	A
36	1	1736	G
36	1	1742	U
36	1	1746	U

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Mol	Chain	Res	Type
36	1	1750	A
36	1	1751	G
36	1	1762	C
36	1	1765	U
36	1	1766	G
36	1	1770	G
36	1	1775	G
36	1	1778	G
36	1	1780	G
36	1	1781	C
36	1	1797	A
36	1	1810	A
36	1	1814	A
36	1	1816	A
36	1	1817	G
36	1	1819	U
36	1	1820	U
36	1	1821	U
36	1	1839	A
36	1	1842	A
36	1	1846	C
36	1	1849	C
36	1	1850	A
36	1	1866	C
36	1	1879	A
36	1	1880	U
36	1	1886	A
36	1	1887	A
36	1	1895	A
36	1	1906	G
36	1	1932	A
36	1	1935	G
36	1	1937	U
36	1	1951	C
36	1	1952	G
36	1	1954	G
36	1	2094	C
36	1	2101	C
36	1	2102	U
36	1	2111	G
36	1	2112	U
36	1	2113	A

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Mol	Chain	Res	Type
36	1	2120	A
36	1	2121	G
36	1	2122	G
36	1	2131	A
36	1	2140	U
36	1	2144	A
36	1	2158	A
36	1	2169	G
36	1	2170	U
36	1	2187	G
36	1	2188	A
36	1	2198	A
36	1	2205	U
36	1	2208	A
36	1	2209	U
36	1	2210	G
36	1	2223	A
36	1	2225	U
36	1	2228	A
36	1	2244	A
36	1	2249	G
36	1	2250	G
36	1	2255	A
36	1	2256	A
36	1	2272	G
36	1	2273	G
36	1	2279	A
36	1	2281	A
36	1	2284	C
36	1	2288	G
36	1	2298	U
36	1	2299	A
36	1	2307	G
36	1	2310	U
36	1	2313	A
36	1	2314	U
36	1	2315	G
36	1	2334	U
36	1	2336	U
36	1	2372	A
36	1	2373	A
36	1	2374	C

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Mol	Chain	Res	Type
36	1	2375	G
36	1	2385	G
36	1	2391	G
36	1	2392	C
36	1	2393	G
36	1	2394	G
36	1	2397	A
36	1	2403	G
36	1	2404	A
36	1	2411	U
36	1	2418	G
36	1	2419	A
36	1	2435	G
36	1	2444	C
36	1	2445	A
36	1	2502	A
36	1	2503	G
36	1	2511	A
36	1	2514	U
36	1	2515	A
36	1	2522	G
36	1	2529	A
36	1	2532	U
36	1	2533	G
36	1	2537	U
36	1	2538	U
36	1	2539	C
36	1	2540	A
36	1	2541	U
36	1	2542	U
36	1	2543	U
36	1	2547	A
36	1	2548	C
36	1	2549	G
36	1	2552	C
36	1	2554	A
36	1	2555	G
36	1	2560	C
36	1	2561	A
36	1	2562	A
36	1	2568	C
36	1	2569	A

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Mol	Chain	Res	Type
36	1	2570	U
36	1	2571	U
36	1	2572	C
36	1	2573	G
36	1	2581	U
36	1	2585	G
36	1	2586	G
36	1	2593	A
36	1	2606	G
36	1	2607	G
36	1	2610	G
36	1	2614	G
36	1	2637	A
36	1	2652	U
36	1	2656	A
36	1	2657	A
36	1	2674	A
36	1	2677	G
36	1	2681	U
36	1	2689	A
36	1	2691	A
36	1	2694	A
36	1	2696	A
36	1	2706	G
36	1	2714	G
36	1	2719	U
36	1	2727	A
36	1	2728	G
36	1	2729	U
36	1	2737	C
36	1	2752	U
36	1	2753	G
36	1	2762	A
36	1	2771	U
36	1	2772	C
36	1	2777	G
36	1	2778	G
36	1	2779	A
36	1	2796	G
36	1	2797	C
36	1	2799	A
36	1	2800	G

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Mol	Chain	Res	Type
36	1	2801	A
36	1	2802	A
36	1	2803	A
36	1	2810	C
36	1	2814	G
36	1	2816	G
36	1	2817	A
36	1	2818	U
36	1	2834	G
36	1	2842	U
36	1	2843	U
36	1	2845	A
36	1	2847	A
36	1	2867	C
36	1	2871	G
36	1	2872	A
36	1	2873	U
36	1	2875	U
36	1	2886	U
36	1	2887	A
36	1	2889	C
36	1	2898	G
36	1	2899	C
36	1	2904	U
36	1	2914	G
36	1	2923	U
36	1	2927	C
36	1	2935	U
36	1	2936	A
36	1	2942	C
36	1	2945	G
36	1	2947	G
36	1	2951	G
36	1	2971	A
36	1	2973	G
36	1	2978	U
36	1	2979	U
36	1	2983	C
36	1	2990	G
36	1	2992	U
36	1	2996	U
36	1	2997	G

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Mol	Chain	Res	Type
36	1	3006	A
36	1	3012	A
36	1	3025	C
36	1	3030	G
36	1	3056	U
36	1	3059	G
36	1	3078	U
36	1	3079	U
36	1	3080	G
36	1	3086	A
36	1	3091	A
36	1	3092	C
36	1	3104	U
36	1	3122	A
36	1	3123	A
36	1	3129	A
36	1	3130	A
36	1	3131	U
36	1	3141	A
36	1	3142	A
36	1	3143	C
36	1	3150	A
36	1	3151	U
36	1	3153	U
36	1	3154	C
36	1	3155	U
36	1	3156	U
36	1	3157	U
36	1	3164	C
36	1	3165	A
36	1	3168	A
36	1	3170	A
36	1	3173	G
36	1	3174	A
36	1	3176	G
36	1	3179	U
36	1	3181	C
36	1	3187	A
36	1	3195	U
36	1	3196	U
36	1	3199	G
36	1	3207	U

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Mol	Chain	Res	Type
36	1	3208	G
36	1	3209	A
36	1	3217	C
36	1	3218	A
36	1	3219	G
36	1	3229	G
36	1	3235	C
36	1	3239	G
36	1	3243	A
36	1	3245	A
36	1	3246	G
36	1	3247	G
36	1	3259	U
36	1	3269	U
36	1	3270	U
36	1	3276	G
36	1	3279	A
36	1	3281	U
36	1	3286	G
36	1	3287	U
36	1	3289	G
36	1	3294	A
36	1	3295	A
36	1	3303	G
36	1	3304	U
36	1	3307	A
36	1	3313	U
36	1	3316	A
36	1	3317	U
36	1	3318	G
36	1	3319	U
36	1	3320	A
36	1	3341	U
36	1	3342	A
36	1	3345	G
36	1	3347	A
36	1	3351	U
36	1	3352	U
36	1	3353	G
36	1	3354	U
36	1	3355	U
36	1	3356	G

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Mol	Chain	Res	Type
36	1	3368	U
36	1	3369	G
36	1	3375	A
36	1	3376	A
36	1	3378	C
36	1	3382	U
36	1	3383	G
36	1	3389	U
36	1	3390	G
36	1	3396	U
37	3	7	G
37	3	18	C
37	3	22	A
37	3	26	C
37	3	53	U
37	3	54	U
37	3	65	G
37	3	73	C
37	3	74	C
37	3	76	A
37	3	91	G
37	3	102	A
37	3	112	G
37	3	121	U
38	4	34	U
38	4	35	C
38	4	48	A
38	4	52	A
38	4	57	C
38	4	58	G
38	4	59	A
38	4	62	C
38	4	63	G
38	4	75	G
38	4	80	A
38	4	81	U
38	4	82	U
38	4	83	C
38	4	85	G
38	4	86	U
38	4	87	G
38	4	90	U

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Mol	Chain	Res	Type
38	4	95	G
38	4	104	A
38	4	105	A
38	4	106	C
38	4	111	A
38	4	113	U
38	4	125	U
38	4	126	A
38	4	128	U
38	4	138	A
38	4	152	G
38	4	155	A
38	4	157	U
38	4	158	U
1	6	2	A
1	6	4	C
1	6	17	C
1	6	25	C
1	6	26	A
1	6	27	U
1	6	34	G
1	6	44	U
1	6	47	A
1	6	57	G
1	6	60	U
1	6	66	U
1	6	67	A
1	6	68	A
1	6	69	G
1	6	72	A
1	6	73	U
1	6	75	U
1	6	76	A
1	6	77	U
1	6	104	A
1	6	111	U
1	6	114	C
1	6	116	U
1	6	132	U
1	6	137	U
1	6	138	A
1	6	140	A

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Mol	Chain	Res	Type
1	6	141	U
1	6	145	A
1	6	146	U
1	6	153	G
1	6	158	U
1	6	159	U
1	6	161	U
1	6	166	C
1	6	175	G
1	6	178	U
1	6	185	U
1	6	188	A
1	6	190	C
1	6	191	C
1	6	192	U
1	6	193	U
1	6	194	U
1	6	195	G
1	6	199	G
1	6	200	A
1	6	215	A
1	6	216	U
1	6	217	A
1	6	218	A
1	6	219	A
1	6	220	A
1	6	223	U
1	6	226	A
1	6	227	U
1	6	228	G
1	6	230	C
1	6	232	U
1	6	233	C
1	6	240	U
1	6	241	U
1	6	249	U
1	6	250	C
1	6	261	U
1	6	262	U
1	6	265	A
1	6	271	A
1	6	272	U

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Mol	Chain	Res	Type
1	6	273	G
1	6	275	C
1	6	277	U
1	6	278	U
1	6	280	U
1	6	281	G
1	6	287	G
1	6	294	C
1	6	299	A
1	6	308	C
1	6	314	C
1	6	316	A
1	6	319	U
1	6	320	U
1	6	321	C
1	6	322	G
1	6	337	G
1	6	338	C
1	6	341	A
1	6	344	A
1	6	351	C
1	6	352	A
1	6	359	A
1	6	360	A
1	6	361	C
1	6	400	A
1	6	401	A
1	6	402	C
1	6	404	G
1	6	416	A
1	6	418	G
1	6	424	C
1	6	425	A
1	6	426	G
1	6	428	A
1	6	434	G
1	6	439	U
1	6	444	C
1	6	445	A
1	6	448	C
1	6	454	U
1	6	464	A

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Mol	Chain	Res	Type
1	6	468	A
1	6	477	A
1	6	480	G
1	6	484	C
1	6	485	A
1	6	486	G
1	6	488	G
1	6	489	C
1	6	490	C
1	6	492	A
1	6	493	U
1	6	494	U
1	6	495	C
1	6	496	G
1	6	500	C
1	6	501	U
1	6	504	U
1	6	505	A
1	6	506	A
1	6	508	U
1	6	510	G
1	6	511	A
1	6	512	A
1	6	513	U
1	6	514	G
1	6	515	A
1	6	519	C
1	6	527	A
1	6	536	C
1	6	538	A
1	6	539	G
1	6	540	G
1	6	541	A
1	6	542	A
1	6	543	C
1	6	544	A
1	6	548	G
1	6	551	G
1	6	555	A
1	6	556	A
1	6	557	G
1	6	558	U

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Mol	Chain	Res	Type
1	6	559	C
1	6	565	C
1	6	566	C
1	6	570	A
1	6	574	G
1	6	579	A
1	6	580	A
1	6	582	U
1	6	594	A
1	6	595	G
1	6	610	G
1	6	611	U
1	6	619	A
1	6	620	A
1	6	622	A
1	6	623	A
1	6	634	G
1	6	639	U
1	6	645	C
1	6	652	G
1	6	653	C
1	6	661	A
1	6	662	U
1	6	665	U
1	6	667	U
1	6	670	U
1	6	676	G
1	6	678	A
1	6	679	U
1	6	680	U
1	6	681	U
1	6	682	C
1	6	683	C
1	6	684	A
1	6	685	A
1	6	690	G
1	6	696	C
1	6	697	C
1	6	698	U
1	6	709	C
1	6	710	U
1	6	711	U

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Mol	Chain	Res	Type
1	6	714	G
1	6	718	U
1	6	719	U
1	6	720	G
1	6	721	U
1	6	722	G
1	6	730	G
1	6	742	U
1	6	751	G
1	6	754	A
1	6	755	A
1	6	756	A
1	6	765	G
1	6	766	U
1	6	774	A
1	6	775	G
1	6	780	A
1	6	781	U
1	6	782	U
1	6	783	G
1	6	787	G
1	6	789	A
1	6	793	A
1	6	794	U
1	6	803	A
1	6	811	A
1	6	812	A
1	6	814	A
1	6	815	G
1	6	816	G
1	6	821	U
1	6	823	G
1	6	825	U
1	6	826	U
1	6	829	A
1	6	830	U
1	6	831	U
1	6	832	U
1	6	834	G
1	6	835	U
1	6	860	U
1	6	863	A

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Mol	Chain	Res	Type
1	6	886	U
1	6	898	A
1	6	906	A
1	6	912	U
1	6	913	G
1	6	914	G
1	6	933	A
1	6	935	U
1	6	942	G
1	6	959	U
1	6	960	U
1	6	966	A
1	6	969	C
1	6	970	A
1	6	971	A
1	6	992	A
1	6	996	U
1	6	1003	A
1	6	1004	U
1	6	1005	A
1	6	1021	C
1	6	1026	A
1	6	1028	C
1	6	1039	A
1	6	1040	G
1	6	1052	U
1	6	1053	G
1	6	1057	U
1	6	1058	U
1	6	1059	U
1	6	1060	U
1	6	1073	G
1	6	1082	C
1	6	1091	A
1	6	1092	A
1	6	1096	C
1	6	1097	U
1	6	1098	U
1	6	1100	G
1	6	1101	G
1	6	1111	G
1	6	1137	A

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Mol	Chain	Res	Type
1	6	1138	A
1	6	1151	A
1	6	1155	G
1	6	1158	C
1	6	1159	C
1	6	1160	A
1	6	1167	G
1	6	1185	U
1	6	1193	A
1	6	1194	A
1	6	1196	A
1	6	1197	C
1	6	1199	G
1	6	1200	G
1	6	1202	A
1	6	1208	A
1	6	1217	A
1	6	1218	G
1	6	1220	C
1	6	1225	U
1	6	1226	A
1	6	1227	A
1	6	1228	G
1	6	1229	G
1	6	1230	A
1	6	1231	U
1	6	1243	G
1	6	1244	A
1	6	1245	G
1	6	1246	C
1	6	1255	G
1	6	1256	A
1	6	1257	U
1	6	1258	U
1	6	1275	A
1	6	1286	U
1	6	1288	G
1	6	1291	G
1	6	1314	U
1	6	1316	G
1	6	1321	A
1	6	1338	C

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Mol	Chain	Res	Type
1	6	1344	A
1	6	1345	A
1	6	1346	A
1	6	1354	G
1	6	1361	U
1	6	1363	U
1	6	1364	G
1	6	1367	G
1	6	1370	U
1	6	1371	A
1	6	1383	G
1	6	1390	U
1	6	1398	U
1	6	1399	C
1	6	1400	A
1	6	1402	G
1	6	1412	G
1	6	1413	U
1	6	1415	U
1	6	1427	A
1	6	1428	G
1	6	1445	G
1	6	1446	A
1	6	1448	G
1	6	1458	G
1	6	1459	C
1	6	1460	A
1	6	1469	A
1	6	1471	A
1	6	1481	C
1	6	1482	C
1	6	1486	G
1	6	1490	C
1	6	1491	U
1	6	1492	A
1	6	1493	A
1	6	1494	C
1	6	1506	G
1	6	1514	U
1	6	1516	A
1	6	1521	G
1	6	1523	G

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Mol	Chain	Res	Type
1	6	1524	A
1	6	1531	G
1	6	1535	U
1	6	1536	G
1	6	1537	C
1	6	1538	U
1	6	1540	G
1	6	1554	U
1	6	1555	A
1	6	1557	U
1	6	1559	A
1	6	1569	A
1	6	1573	A
1	6	1574	G
1	6	1584	G
1	6	1590	G
1	6	1601	G
1	6	1621	U
1	6	1631	A
1	6	1634	C
1	6	1637	C
1	6	1638	G
1	6	1657	U
1	6	1658	G
1	6	1683	C
1	6	1697	G
1	6	1698	G
1	6	1699	G
1	6	1700	C
1	6	1701	A
1	6	1702	A
1	6	1703	C
1	6	1712	A
1	6	1716	C
1	6	1717	G
1	6	1727	G
1	6	1731	A
1	6	1736	G
1	6	1742	U
1	6	1755	A
1	6	1760	G
1	6	1762	A

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Mol	Chain	Res	Type
1	6	1766	A
1	6	1767	G
1	6	1769	U
1	6	1780	G
1	6	1782	A
1	6	1783	C
1	6	1792	G
1	6	1793	G
1	6	1794	A
1	6	1795	U
1	6	1796	C
1	6	1799	U
1	6	1800	A
36	5	14	U
36	5	15	C
36	5	16	A
36	5	24	G
36	5	26	A
36	5	40	A
36	5	49	A
36	5	59	G
36	5	60	A
36	5	65	A
36	5	66	A
36	5	72	C
36	5	73	C
36	5	74	G
36	5	76	G
36	5	83	U
36	5	89	A
36	5	92	G
36	5	96	G
36	5	99	A
36	5	108	A
36	5	109	A
36	5	110	G
36	5	111	C
36	5	116	A
36	5	121	A
36	5	122	A
36	5	133	U
36	5	134	U

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Mol	Chain	Res	Type
36	5	135	C
36	5	136	G
36	5	146	U
36	5	152	U
36	5	156	G
36	5	157	A
36	5	165	A
36	5	170	G
36	5	171	G
36	5	172	G
36	5	173	G
36	5	174	C
36	5	180	C
36	5	182	U
36	5	184	U
36	5	187	A
36	5	190	U
36	5	191	U
36	5	210	U
36	5	218	G
36	5	219	A
36	5	221	A
36	5	231	G
36	5	235	A
36	5	236	G
36	5	237	G
36	5	239	G
36	5	240	U
36	5	241	G
36	5	244	G
36	5	248	U
36	5	249	U
36	5	250	U
36	5	251	G
36	5	252	U
36	5	253	A
36	5	254	A
36	5	269	G
36	5	282	G
36	5	283	G
36	5	284	A
36	5	285	A

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Mol	Chain	Res	Type
36	5	286	U
36	5	295	A
36	5	305	U
36	5	315	C
36	5	323	A
36	5	329	U
36	5	338	A
36	5	339	C
36	5	349	A
36	5	350	C
36	5	370	U
36	5	376	G
36	5	398	A
36	5	399	A
36	5	401	U
36	5	402	A
36	5	403	C
36	5	421	G
36	5	422	A
36	5	436	A
36	5	437	G
36	5	438	A
36	5	439	C
36	5	441	U
36	5	442	G
36	5	492	U
36	5	495	G
36	5	520	U
36	5	521	A
36	5	546	C
36	5	547	G
36	5	548	G
36	5	555	U
36	5	557	A
36	5	559	A
36	5	569	A
36	5	578	A
36	5	579	G
36	5	581	U
36	5	592	A
36	5	600	G
36	5	604	G

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Mol	Chain	Res	Type
36	5	608	A
36	5	609	G
36	5	611	A
36	5	619	A
36	5	620	U
36	5	621	A
36	5	636	C
36	5	649	A
36	5	651	G
36	5	653	A
36	5	660	A
36	5	661	G
36	5	677	A
36	5	681	U
36	5	683	U
36	5	691	A
36	5	705	A
36	5	712	G
36	5	715	A
36	5	716	A
36	5	725	G
36	5	727	G
36	5	736	A
36	5	750	G
36	5	765	C
36	5	766	U
36	5	767	U
36	5	774	G
36	5	775	A
36	5	776	U
36	5	777	U
36	5	780	A
36	5	781	G
36	5	785	G
36	5	786	A
36	5	806	A
36	5	813	G
36	5	817	A
36	5	830	A
36	5	837	A
36	5	846	A
36	5	861	C

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Mol	Chain	Res	Type
36	5	874	U
36	5	879	U
36	5	890	C
36	5	895	A
36	5	896	A
36	5	907	G
36	5	908	G
36	5	914	A
36	5	916	G
36	5	917	A
36	5	923	C
36	5	924	G
36	5	925	A
36	5	937	G
36	5	943	U
36	5	944	C
36	5	959	C
36	5	960	U
36	5	962	A
36	5	963	G
36	5	979	U
36	5	981	U
36	5	983	A
36	5	984	G
36	5	993	G
36	5	994	G
36	5	1001	G
36	5	1002	A
36	5	1006	A
36	5	1010	G
36	5	1014	U
36	5	1015	U
36	5	1016	C
36	5	1017	C
36	5	1018	G
36	5	1021	G
36	5	1024	G
36	5	1025	A
36	5	1026	A
36	5	1028	U
36	5	1029	G
36	5	1032	C

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Mol	Chain	Res	Type
36	5	1033	U
36	5	1035	G
36	5	1047	A
36	5	1049	C
36	5	1064	A
36	5	1065	A
36	5	1072	G
36	5	1081	U
36	5	1082	U
36	5	1085	A
36	5	1093	A
36	5	1094	U
36	5	1096	U
36	5	1097	G
36	5	1098	A
36	5	1103	A
36	5	1104	G
36	5	1117	G
36	5	1124	U
36	5	1125	U
36	5	1131	G
36	5	1152	G
36	5	1153	A
36	5	1154	A
36	5	1159	A
36	5	1160	C
36	5	1178	G
36	5	1180	A
36	5	1181	U
36	5	1182	A
36	5	1191	U
36	5	1192	C
36	5	1196	C
36	5	1197	A
36	5	1201	C
36	5	1209	G
36	5	1222	G
36	5	1232	C
36	5	1236	G
36	5	1237	G
36	5	1239	C
36	5	1241	U

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Mol	Chain	Res	Type
36	5	1242	G
36	5	1243	G
36	5	1245	A
36	5	1246	G
36	5	1254	C
36	5	1258	U
36	5	1262	G
36	5	1263	A
36	5	1264	G
36	5	1265	U
36	5	1266	G
36	5	1285	G
36	5	1305	U
36	5	1307	G
36	5	1309	U
36	5	1313	G
36	5	1330	A
36	5	1349	G
36	5	1350	A
36	5	1351	U
36	5	1352	A
36	5	1353	U
36	5	1356	U
36	5	1357	G
36	5	1385	C
36	5	1386	A
36	5	1399	A
36	5	1400	G
36	5	1418	A
36	5	1419	A
36	5	1433	A
36	5	1434	G
36	5	1437	C
36	5	1446	A
36	5	1450	G
36	5	1481	A
36	5	1482	A
36	5	1487	G
36	5	1490	A
36	5	1508	C
36	5	1527	C
36	5	1536	G

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Mol	Chain	Res	Type
36	5	1539	A
36	5	1549	U
36	5	1553	U
36	5	1554	U
36	5	1555	U
36	5	1556	C
36	5	1557	A
36	5	1560	G
36	5	1561	G
36	5	1562	C
36	5	1566	A
36	5	1567	U
36	5	1569	U
36	5	1570	U
36	5	1571	A
36	5	1572	U
36	5	1574	C
36	5	1575	A
36	5	1576	G
36	5	1577	G
36	5	1578	C
36	5	1581	C
36	5	1582	C
36	5	1583	A
36	5	1587	A
36	5	1589	A
36	5	1593	A
36	5	1605	A
36	5	1618	G
36	5	1619	A
36	5	1629	U
36	5	1632	A
36	5	1639	C
36	5	1643	A
36	5	1644	C
36	5	1645	U
36	5	1657	C
36	5	1675	G
36	5	1677	G
36	5	1683	A
36	5	1687	U
36	5	1716	U

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Mol	Chain	Res	Type
36	5	1717	U
36	5	1724	U
36	5	1725	C
36	5	1736	G
36	5	1750	A
36	5	1751	G
36	5	1759	C
36	5	1760	A
36	5	1762	C
36	5	1764	U
36	5	1765	U
36	5	1766	G
36	5	1768	U
36	5	1770	G
36	5	1778	G
36	5	1780	G
36	5	1797	A
36	5	1810	A
36	5	1813	A
36	5	1814	A
36	5	1815	U
36	5	1816	A
36	5	1817	G
36	5	1818	U
36	5	1819	U
36	5	1821	U
36	5	1839	A
36	5	1841	A
36	5	1842	A
36	5	1846	C
36	5	1850	A
36	5	1878	G
36	5	1879	A
36	5	1880	U
36	5	1886	A
36	5	1893	A
36	5	1895	A
36	5	1906	G
36	5	1953	G
36	5	2101	C
36	5	2102	U
36	5	2111	G

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Mol	Chain	Res	Type
36	5	2112	U
36	5	2113	A
36	5	2121	G
36	5	2122	G
36	5	2131	A
36	5	2144	A
36	5	2158	A
36	5	2159	U
36	5	2169	G
36	5	2188	A
36	5	2192	C
36	5	2201	G
36	5	2205	U
36	5	2210	G
36	5	2223	A
36	5	2225	U
36	5	2229	A
36	5	2244	A
36	5	2250	G
36	5	2252	A
36	5	2253	G
36	5	2255	A
36	5	2256	A
36	5	2257	C
36	5	2258	U
36	5	2269	U
36	5	2270	A
36	5	2273	G
36	5	2276	G
36	5	2279	A
36	5	2288	G
36	5	2298	U
36	5	2303	A
36	5	2307	G
36	5	2310	U
36	5	2313	A
36	5	2315	G
36	5	2324	A
36	5	2335	G
36	5	2336	U
36	5	2366	C
36	5	2367	A

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Mol	Chain	Res	Type
36	5	2373	A
36	5	2374	C
36	5	2375	G
36	5	2385	G
36	5	2393	G
36	5	2397	A
36	5	2403	G
36	5	2404	A
36	5	2411	U
36	5	2412	G
36	5	2418	G
36	5	2419	A
36	5	2435	G
36	5	2436	U
36	5	2438	A
36	5	2439	A
36	5	2441	A
36	5	2443	A
36	5	2444	C
36	5	2505	U
36	5	2507	C
36	5	2508	U
36	5	2510	U
36	5	2511	A
36	5	2514	U
36	5	2515	A
36	5	2523	A
36	5	2524	A
36	5	2525	G
36	5	2530	G
36	5	2538	U
36	5	2539	C
36	5	2540	A
36	5	2543	U
36	5	2549	G
36	5	2552	C
36	5	2555	G
36	5	2566	C
36	5	2567	C
36	5	2568	C
36	5	2569	A
36	5	2570	U

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Mol	Chain	Res	Type
36	5	2571	U
36	5	2573	G
36	5	2574	G
36	5	2585	G
36	5	2589	G
36	5	2593	A
36	5	2594	C
36	5	2606	G
36	5	2607	G
36	5	2614	G
36	5	2618	G
36	5	2626	A
36	5	2637	A
36	5	2639	G
36	5	2652	U
36	5	2656	A
36	5	2669	G
36	5	2674	A
36	5	2677	G
36	5	2681	U
36	5	2689	A
36	5	2691	A
36	5	2694	A
36	5	2696	A
36	5	2714	G
36	5	2727	A
36	5	2728	G
36	5	2729	U
36	5	2752	U
36	5	2753	G
36	5	2762	A
36	5	2771	U
36	5	2772	C
36	5	2773	C
36	5	2777	G
36	5	2778	G
36	5	2779	A
36	5	2796	G
36	5	2799	A
36	5	2800	G
36	5	2801	A
36	5	2802	A

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Mol	Chain	Res	Type
36	5	2810	C
36	5	2814	G
36	5	2816	G
36	5	2817	A
36	5	2818	U
36	5	2843	U
36	5	2845	A
36	5	2847	A
36	5	2853	A
36	5	2871	G
36	5	2872	A
36	5	2887	A
36	5	2889	C
36	5	2899	C
36	5	2923	U
36	5	2935	U
36	5	2936	A
36	5	2942	C
36	5	2947	G
36	5	2954	U
36	5	2957	G
36	5	2960	C
36	5	2970	C
36	5	2971	A
36	5	2974	U
36	5	2983	C
36	5	2990	G
36	5	2996	U
36	5	2997	G
36	5	3012	A
36	5	3048	A
36	5	3054	U
36	5	3056	U
36	5	3059	G
36	5	3078	U
36	5	3079	U
36	5	3086	A
36	5	3092	C
36	5	3113	A
36	5	3116	G
36	5	3122	A
36	5	3130	A

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Mol	Chain	Res	Type
36	5	3131	U
36	5	3142	A
36	5	3143	C
36	5	3150	A
36	5	3153	U
36	5	3155	U
36	5	3156	U
36	5	3157	U
36	5	3158	G
36	5	3164	C
36	5	3165	A
36	5	3168	A
36	5	3171	U
36	5	3172	A
36	5	3173	G
36	5	3174	A
36	5	3176	G
36	5	3178	A
36	5	3179	U
36	5	3181	C
36	5	3187	A
36	5	3195	U
36	5	3196	U
36	5	3207	U
36	5	3217	C
36	5	3218	A
36	5	3219	G
36	5	3227	A
36	5	3229	G
36	5	3239	G
36	5	3245	A
36	5	3246	G
36	5	3247	G
36	5	3253	G
36	5	3259	U
36	5	3270	U
36	5	3275	U
36	5	3276	G
36	5	3277	U
36	5	3278	C
36	5	3279	A
36	5	3280	U

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Mol	Chain	Res	Type
36	5	3281	U
36	5	3282	U
36	5	3285	C
36	5	3286	G
36	5	3288	G
36	5	3289	G
36	5	3290	G
36	5	3294	A
36	5	3302	U
36	5	3304	U
36	5	3313	U
36	5	3316	A
36	5	3317	U
36	5	3318	G
36	5	3319	U
36	5	3320	A
36	5	3330	A
36	5	3341	U
36	5	3342	A
36	5	3345	G
36	5	3350	C
36	5	3351	U
36	5	3354	U
36	5	3356	G
36	5	3358	U
36	5	3369	G
36	5	3378	C
36	5	3389	U
36	5	3390	G
37	7	7	G
37	7	10	C
37	7	22	A
37	7	33	U
37	7	54	U
37	7	60	G
37	7	65	G
37	7	73	C
37	7	76	A
37	7	93	C
37	7	99	G
37	7	102	A
37	7	103	A

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Mol	Chain	Res	Type
37	7	112	G
37	7	121	U
38	8	21	C
38	8	34	U
38	8	35	C
38	8	48	A
38	8	49	G
38	8	51	G
38	8	59	A
38	8	62	C
38	8	63	G
38	8	79	A
38	8	80	A
38	8	81	U
38	8	82	U
38	8	83	C
38	8	84	C
38	8	86	U
38	8	87	G
38	8	95	G
38	8	104	A
38	8	105	A
38	8	106	C
38	8	111	A
38	8	112	U
38	8	113	U
38	8	116	G
38	8	122	U
38	8	125	U
38	8	126	A
38	8	156	U
38	8	157	U
38	8	158	U

All (225) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	25	C
1	2	45	U
1	2	68	A
1	2	74	U
1	2	103	A

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Mol	Chain	Res	Type
1	2	130	C
1	2	131	C
1	2	139	C
1	2	158	U
1	2	218	A
1	2	240	U
1	2	278	U
1	2	280	U
1	2	322	G
1	2	417	A
1	2	484	C
1	2	497	G
1	2	499	U
1	2	501	U
1	2	503	G
1	2	512	A
1	2	555	A
1	2	558	U
1	2	685	A
1	2	704	C
1	2	720	G
1	2	721	U
1	2	734	A
1	2	755	A
1	2	781	U
1	2	794	U
1	2	829	A
1	2	913	G
1	2	1081	A
1	2	1157	A
1	2	1226	A
1	2	1244	A
1	2	1250	U
1	2	1339	C
1	2	1344	A
1	2	1370	U
1	2	1481	C
1	2	1489	U
1	2	1490	C
1	2	1568	C
1	2	1573	A
1	2	1615	C

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Mol	Chain	Res	Type
1	2	1657	U
1	2	1698	G
1	2	1761	U
36	1	65	A
36	1	210	U
36	1	223	U
36	1	239	G
36	1	282	G
36	1	547	G
36	1	637	C
36	1	715	A
36	1	763	G
36	1	873	C
36	1	896	A
36	1	916	G
36	1	979	U
36	1	981	U
36	1	993	G
36	1	1064	A
36	1	1094	U
36	1	1097	G
36	1	1103	A
36	1	1273	A
36	1	1307	G
36	1	1329	U
36	1	1348	U
36	1	1352	A
36	1	1355	A
36	1	1481	A
36	1	1484	U
36	1	1562	C
36	1	1582	C
36	1	1589	A
36	1	1716	U
36	1	1815	U
36	1	1820	U
36	1	1846	C
36	1	1849	C
36	1	2101	C
36	1	2112	U
36	1	2209	U
36	1	2227	C

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Mol	Chain	Res	Type
36	1	2249	G
36	1	2281	A
36	1	2297	U
36	1	2372	A
36	1	2418	G
36	1	2513	U
36	1	2537	U
36	1	2541	U
36	1	2554	A
36	1	2585	G
36	1	2728	G
36	1	2801	A
36	1	2818	U
36	1	2872	A
36	1	3078	U
36	1	3121	U
36	1	3195	U
36	1	3218	A
36	1	3228	C
36	1	3269	U
36	1	3316	A
36	1	3319	U
36	1	3350	C
36	1	3351	U
36	1	3353	G
36	1	3375	A
36	1	3377	G
37	3	52	G
38	4	85	G
38	4	111	A
1	6	25	C
1	6	66	U
1	6	76	A
1	6	114	C
1	6	136	C
1	6	139	C
1	6	145	A
1	6	158	U
1	6	187	G
1	6	217	A
1	6	240	U
1	6	272	U

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Mol	Chain	Res	Type
1	6	400	A
1	6	417	A
1	6	512	A
1	6	542	A
1	6	555	A
1	6	558	U
1	6	651	G
1	6	678	A
1	6	697	C
1	6	717	C
1	6	755	A
1	6	829	A
1	6	834	G
1	6	1051	G
1	6	1058	U
1	6	1081	A
1	6	1097	U
1	6	1196	A
1	6	1207	C
1	6	1244	A
1	6	1255	G
1	6	1344	A
1	6	1481	C
1	6	1535	U
1	6	1568	C
1	6	1573	A
1	6	1620	C
1	6	1657	U
1	6	1696	G
1	6	1698	G
1	6	1700	C
36	5	151	A
36	5	169	U
36	5	183	G
36	5	210	U
36	5	238	A
36	5	240	U
36	5	282	G
36	5	397	A
36	5	438	A
36	5	588	G
36	5	715	A

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Mol	Chain	Res	Type
36	5	735	A
36	5	765	C
36	5	873	C
36	5	896	A
36	5	916	G
36	5	993	G
36	5	1027	A
36	5	1064	A
36	5	1081	U
36	5	1152	G
36	5	1238	C
36	5	1241	U
36	5	1284	C
36	5	1329	U
36	5	1331	U
36	5	1352	A
36	5	1355	A
36	5	1481	A
36	5	1554	U
36	5	1560	G
36	5	1716	U
36	5	1816	A
36	5	1841	A
36	5	2101	C
36	5	2112	U
36	5	2204	C
36	5	2209	U
36	5	2249	G
36	5	2255	A
36	5	2281	A
36	5	2440	G
36	5	2507	C
36	5	2513	U
36	5	2728	G
36	5	2772	C
36	5	2801	A
36	5	2817	A
36	5	2818	U
36	5	2954	U
36	5	3078	U
36	5	3121	U
36	5	3154	C

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Mol	Chain	Res	Type
36	5	3195	U
36	5	3218	A
36	5	3228	C
36	5	3269	U
36	5	3275	U
36	5	3289	G
36	5	3317	U
36	5	3340	G
36	5	3341	U
36	5	3357	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
85	8AN	C	76	88,85	18,24,25	1.10	1 (5%)	10,35,38	2.27	1 (10%)
85	8AN	D	76	88,85	18,24,25	1.07	1 (5%)	10,35,38	2.22	3 (30%)

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	8AN	C	76	88,85	-	0/3/25/26	0/3/3/3
85	8AN	D	76	88,85	-	0/3/25/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	C	76	8AN	C5-C4	2.94	1.47	1.40
85	D	76	8AN	C5-C4	2.97	1.47	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	C	76	8AN	N3-C2-N1	-6.21	123.99	128.87
85	D	76	8AN	N3-C2-N1	-5.56	124.50	128.87
85	D	76	8AN	O4'-C1'-N9	-2.53	103.32	108.11
85	D	76	8AN	N6-C6-N1	2.41	122.55	118.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 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
87	SPS	C	3401	88	19,23,23	3.46	10 (52%)	16,30,30	3.19	10 (62%)
87	SPS	D	3401	88	19,23,23	3.48	12 (63%)	16,30,30	3.20	11 (68%)

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
87	SPS	C	3401	88	-	0/15/18/18	0/1/1/1
87	SPS	D	3401	88	-	0/15/18/18	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	D	3401	SPS	C9-C10	-8.50	1.31	1.48
87	C	3401	SPS	C9-C10	-8.42	1.31	1.48
87	D	3401	SPS	O13-C13	-5.57	1.18	1.42
87	C	3401	SPS	O13-C13	-5.19	1.19	1.42
87	C	3401	SPS	O10-C10	-3.05	1.18	1.24
87	D	3401	SPS	O10-C10	-3.03	1.18	1.24
87	D	3401	SPS	C1-C6	-2.95	1.37	1.44
87	C	3401	SPS	C1-C6	-2.44	1.39	1.44
87	D	3401	SPS	O1-C1	-2.40	1.18	1.24
87	C	3401	SPS	O1-C1	-2.32	1.18	1.24
87	D	3401	SPS	C3-N4	-2.26	1.33	1.38
87	C	3401	SPS	C3-N4	-2.19	1.33	1.38
87	D	3401	SPS	C3-N2	-2.11	1.33	1.38
87	D	3401	SPS	C6-C5	-2.07	1.37	1.40
87	D	3401	SPS	C6-C8	2.23	1.52	1.47
87	D	3401	SPS	C10-N11	2.88	1.43	1.34
87	C	3401	SPS	C6-C8	3.19	1.54	1.47
87	C	3401	SPS	C10-N11	3.55	1.45	1.34
87	D	3401	SPS	O15-S15	4.45	1.64	1.50
87	C	3401	SPS	O15-S15	4.59	1.65	1.50
87	D	3401	SPS	C9-C8	7.14	1.52	1.32
87	C	3401	SPS	C9-C8	7.15	1.52	1.32

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	D	3401	SPS	C12-N11-C10	-5.92	114.57	122.57
87	C	3401	SPS	N2-C3-N4	-5.00	119.27	127.69
87	D	3401	SPS	N2-C3-N4	-4.66	119.84	127.69
87	D	3401	SPS	C7-C5-C6	-3.58	119.35	123.63
87	C	3401	SPS	C7-C5-C6	-3.53	119.41	123.63
87	C	3401	SPS	C12-N11-C10	-2.96	118.57	122.57
87	D	3401	SPS	C14-C12-C13	-2.71	106.43	111.85
87	D	3401	SPS	O10-C10-N11	-2.60	118.25	122.34
87	C	3401	SPS	C6-C8-C9	-2.49	118.98	127.08
87	D	3401	SPS	C6-C8-C9	-2.34	119.49	127.08
87	C	3401	SPS	O10-C10-N11	-2.20	118.88	122.34
87	D	3401	SPS	C7-C5-N4	2.11	119.53	116.32
87	C	3401	SPS	C7-C5-N4	2.23	119.70	116.32
87	D	3401	SPS	C18-S17-C16	2.35	107.34	100.14
87	C	3401	SPS	O13-C13-C12	2.60	119.44	112.24
87	D	3401	SPS	C9-C10-N11	2.76	120.30	114.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	D	3401	SPS	O13-C13-C12	2.77	119.92	112.24
87	C	3401	SPS	C9-C10-N11	2.92	120.66	114.14
87	C	3401	SPS	C18-S17-C16	3.33	110.32	100.14
87	D	3401	SPS	C1-N2-C3	6.70	120.75	115.16
87	C	3401	SPS	C1-N2-C3	8.26	122.05	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	C	3401	SPS	1	0
87	D	3401	SPS	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	2
81	m2	2
35	sM	1
12	c0	1
35	SM	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	sM	153:ALA	C	154:UNK	N	39.08
1	SM	141:ALA	C	151:UNK	N	25.76
1	c0	84:GLU	C	87:HIS	N	8.48
1	m2	23:UNK	C	28:UNK	N	3.80
1	m2	52:UNK	C	54:UNK	N	3.61
1	2	1716:C	O3'	1717:G	P	3.20
1	2	1685:G	O3'	1686:C	P	3.04

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	2	1781/1800 (98%)	0.80	147 (8%) 14 5	47, 88, 194, 293	0
1	6	1795/1800 (99%)	0.60	108 (6%) 25 10	37, 78, 178, 271	0
2	S0	206/251 (82%)	1.43	67 (32%) 1 0	98, 124, 141, 156	0
2	s0	206/251 (82%)	1.01	30 (14%) 3 1	77, 102, 120, 127	0
3	S1	214/254 (84%)	1.33	52 (24%) 1 0	101, 160, 206, 217	0
3	s1	216/254 (85%)	1.10	38 (17%) 2 1	68, 87, 112, 120	0
4	S2	217/253 (85%)	0.53	15 (6%) 20 7	74, 95, 116, 124	0
4	s2	217/253 (85%)	0.33	13 (5%) 25 10	60, 80, 95, 112	0
5	S3	223/239 (93%)	0.52	14 (6%) 23 9	80, 99, 136, 152	0
5	s3	223/239 (93%)	0.68	30 (13%) 4 2	78, 121, 153, 164	0
6	S4	260/260 (100%)	0.81	33 (12%) 5 2	60, 95, 109, 144	0
6	s4	260/260 (100%)	0.53	17 (6%) 22 8	52, 85, 99, 129	0
7	S5	206/224 (91%)	1.36	57 (27%) 1 0	103, 134, 153, 168	0
7	s5	206/224 (91%)	0.96	40 (19%) 1 1	87, 120, 139, 153	0
8	S6	226/236 (95%)	0.85	44 (19%) 1 0	63, 105, 134, 163	0
8	s6	218/236 (92%)	0.51	23 (10%) 8 3	50, 87, 112, 126	0
9	S7	184/189 (97%)	0.70	29 (15%) 3 1	94, 134, 175, 186	0
9	s7	186/189 (98%)	0.36	8 (4%) 39 18	74, 118, 168, 174	0
10	S8	188/200 (94%)	1.06	40 (21%) 1 0	56, 77, 118, 130	0
10	s8	188/200 (94%)	0.60	19 (10%) 9 3	47, 71, 117, 137	0
11	S9	185/196 (94%)	1.63	66 (35%) 0 0	78, 106, 152, 185	0
11	s9	185/196 (94%)	1.14	33 (17%) 2 1	67, 89, 135, 160	0
12	C0	96/105 (91%)	0.61	8 (8%) 14 5	88, 122, 166, 181	0
12	c0	96/105 (91%)	1.09	21 (21%) 1 0	108, 153, 180, 192	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	C1	155/155 (100%)	0.63	17 (10%)	7 2	61, 74, 133, 148	0
13	c1	146/155 (94%)	0.24	2 (1%)	78 60	52, 69, 101, 130	0
14	C2	124/142 (87%)	1.99	58 (46%)	0 0	162, 188, 207, 214	0
14	c2	124/142 (87%)	3.85	87 (70%)	0 0	211, 238, 259, 264	0
15	C3	150/150 (100%)	0.89	24 (16%)	3 1	70, 89, 114, 119	0
15	c3	150/150 (100%)	0.33	2 (1%)	79 62	56, 74, 96, 99	0
16	C4	127/136 (93%)	0.84	19 (14%)	3 1	68, 155, 181, 187	0
16	c4	128/136 (94%)	0.58	6 (4%)	35 16	48, 90, 104, 109	0
17	C5	124/141 (87%)	0.79	19 (15%)	3 1	82, 102, 124, 162	0
17	c5	135/141 (95%)	1.16	29 (21%)	1 0	73, 105, 118, 128	0
18	C6	141/142 (99%)	1.83	53 (37%)	0 0	83, 118, 125, 128	0
18	c6	142/142 (100%)	1.89	62 (43%)	0 0	74, 113, 131, 136	0
19	C7	120/136 (88%)	1.50	33 (27%)	1 0	91, 114, 151, 157	0
19	c7	117/136 (86%)	1.31	36 (30%)	1 0	80, 106, 135, 150	0
20	C8	145/145 (100%)	1.65	51 (35%)	0 0	77, 114, 154, 160	0
20	c8	145/145 (100%)	0.83	19 (13%)	5 2	87, 102, 141, 147	0
21	C9	143/143 (100%)	1.46	43 (30%)	1 0	87, 114, 133, 142	0
21	c9	143/143 (100%)	1.34	33 (23%)	1 0	81, 103, 127, 136	0
22	D0	107/120 (89%)	1.19	23 (21%)	1 0	74, 120, 154, 157	0
22	d0	110/120 (91%)	2.09	51 (46%)	0 0	75, 133, 171, 177	0
23	D1	87/87 (100%)	0.84	8 (9%)	11 4	98, 107, 135, 144	0
23	d1	87/87 (100%)	0.31	5 (5%)	27 11	75, 89, 116, 124	0
24	D2	129/129 (100%)	1.35	32 (24%)	1 0	70, 88, 96, 104	0
24	d2	129/129 (100%)	0.45	2 (1%)	74 55	58, 71, 78, 87	0
25	D3	144/144 (100%)	0.38	2 (1%)	78 60	61, 67, 77, 101	0
25	d3	144/144 (100%)	0.17	0	100 100	50, 56, 71, 91	0
26	D4	134/134 (100%)	0.85	15 (11%)	7 2	73, 107, 120, 134	0
26	d4	134/134 (100%)	0.64	11 (8%)	14 5	61, 92, 108, 118	0
27	D5	70/107 (65%)	1.36	15 (21%)	1 0	130, 149, 160, 161	0
27	d5	69/107 (64%)	1.56	24 (34%)	0 0	106, 132, 148, 150	0
28	D6	97/97 (100%)	1.11	24 (24%)	1 0	72, 89, 178, 180	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	d6	97/97 (100%)	0.50	4 (4%) 41 19	53, 65, 110, 117	0
29	D7	81/81 (100%)	2.02	42 (51%) 0 0	90, 108, 149, 151	0
29	d7	81/81 (100%)	0.99	10 (12%) 5 2	72, 88, 139, 143	0
30	D8	63/66 (95%)	0.74	6 (9%) 10 4	114, 147, 161, 164	0
30	d8	63/66 (95%)	0.98	11 (17%) 2 1	102, 129, 141, 144	0
31	D9	53/55 (96%)	1.04	10 (18%) 2 1	77, 82, 101, 110	0
31	d9	53/55 (96%)	1.58	14 (26%) 1 0	74, 86, 131, 153	0
32	E0	60/60 (100%)	1.21	19 (31%) 1 0	72, 106, 148, 150	0
33	E1	71/76 (93%)	2.02	34 (47%) 0 0	114, 147, 184, 189	0
33	e1	76/76 (100%)	2.66	37 (48%) 0 0	110, 188, 229, 231	0
34	SR	318/318 (100%)	0.83	37 (11%) 6 2	111, 133, 149, 177	0
34	sR	318/318 (100%)	1.56	100 (31%) 1 0	122, 149, 166, 179	0
35	SM	133/263 (50%)	1.50	29 (21%) 1 0	53, 92, 148, 165	0
35	sM	84/263 (31%)	1.06	22 (26%) 1 0	45, 107, 147, 150	0
36	1	3148/3396 (92%)	0.40	80 (2%) 61 37	29, 49, 128, 262	0
36	5	3149/3396 (92%)	0.39	71 (2%) 64 40	26, 46, 119, 209	0
37	3	121/121 (100%)	0.32	0 100 100	37, 69, 84, 91	0
37	7	121/121 (100%)	0.22	1 (0%) 87 75	30, 49, 60, 72	0
38	4	158/158 (100%)	0.18	1 (0%) 90 80	34, 49, 87, 132	0
38	8	158/158 (100%)	0.22	3 (1%) 70 48	37, 55, 91, 120	0
39	L2	252/253 (99%)	0.37	4 (1%) 74 55	33, 51, 66, 86	0
39	l2	252/253 (99%)	0.23	4 (1%) 74 55	32, 53, 70, 75	0
40	L3	386/386 (100%)	-0.00	1 (0%) 94 88	32, 56, 69, 83	0
40	l3	386/386 (100%)	0.02	1 (0%) 94 88	26, 44, 57, 80	0
41	L4	361/361 (100%)	-0.01	0 100 100	30, 49, 68, 75	0
41	l4	361/361 (100%)	-0.05	1 (0%) 94 88	30, 53, 73, 85	0
42	L5	296/296 (100%)	1.10	51 (17%) 2 1	51, 81, 100, 123	0
42	l5	294/296 (99%)	0.65	21 (7%) 19 7	39, 56, 78, 92	0
43	L6	156/175 (89%)	0.02	1 (0%) 90 80	44, 52, 70, 83	0
43	l6	157/175 (89%)	0.15	6 (3%) 44 21	45, 52, 76, 88	0
44	L7	222/243 (91%)	0.18	3 (1%) 78 60	35, 45, 76, 115	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	l7	223/243 (91%)	-0.02	0 100 100	32, 42, 82, 119	0
45	L8	233/255 (91%)	0.58	17 (7%) 18 6	61, 75, 118, 126	0
45	l8	231/255 (90%)	0.66	18 (7%) 16 5	67, 81, 112, 123	0
46	L9	191/191 (100%)	0.66	10 (5%) 31 13	52, 65, 79, 94	0
46	l9	191/191 (100%)	0.13	3 (1%) 74 55	40, 52, 72, 82	0
47	M0	211/220 (95%)	0.07	0 100 100	39, 61, 96, 108	0
47	m0	213/220 (96%)	0.14	5 (2%) 64 40	33, 54, 75, 96	0
48	M1	169/173 (97%)	2.03	86 (50%) 0 0	63, 84, 99, 104	0
48	m1	169/173 (97%)	0.74	15 (8%) 12 4	42, 60, 72, 78	0
49	M3	193/198 (97%)	0.50	8 (4%) 41 19	33, 58, 97, 118	0
49	m3	194/198 (97%)	0.53	13 (6%) 21 7	36, 64, 106, 125	0
50	M4	136/137 (99%)	0.14	4 (2%) 55 31	49, 55, 69, 80	0
50	m4	137/137 (100%)	0.03	0 100 100	44, 50, 66, 87	0
51	M5	203/203 (100%)	0.31	1 (0%) 91 83	31, 48, 58, 62	0
51	m5	203/203 (100%)	0.83	18 (8%) 12 4	35, 53, 66, 69	0
52	M6	197/198 (99%)	0.22	2 (1%) 84 69	35, 42, 57, 59	0
52	m6	197/198 (99%)	0.20	2 (1%) 84 69	30, 36, 55, 58	0
53	M7	183/183 (100%)	0.39	10 (5%) 29 12	36, 47, 115, 160	0
53	m7	155/183 (84%)	-0.06	0 100 100	33, 41, 58, 78	0
54	M8	185/185 (100%)	0.27	3 (1%) 74 55	37, 49, 66, 79	0
54	m8	185/185 (100%)	0.33	2 (1%) 82 66	36, 52, 62, 67	0
55	M9	188/188 (100%)	0.54	11 (5%) 26 11	51, 67, 166, 188	0
55	m9	188/188 (100%)	0.41	6 (3%) 51 27	46, 60, 154, 171	0
56	N0	172/172 (100%)	0.45	6 (3%) 48 23	43, 53, 68, 72	0
56	n0	172/172 (100%)	0.24	7 (4%) 41 19	37, 45, 58, 67	0
57	N1	159/159 (100%)	0.71	16 (10%) 9 3	37, 52, 95, 105	0
57	n1	159/159 (100%)	0.37	4 (2%) 61 37	32, 42, 77, 85	0
58	N2	100/120 (83%)	0.36	4 (4%) 42 20	86, 104, 112, 116	0
58	n2	98/120 (81%)	0.60	9 (9%) 11 4	74, 91, 101, 106	0
59	N3	136/136 (100%)	0.16	2 (1%) 76 58	40, 52, 66, 76	0
59	n3	136/136 (100%)	0.07	2 (1%) 76 58	30, 42, 55, 62	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
60	N4	98/155 (63%)	2.22	31 (31%) 1 0	52, 64, 164, 171	0
60	n4	135/155 (87%)	1.06	22 (16%) 2 1	42, 96, 146, 170	0
61	N5	121/141 (85%)	0.70	10 (8%) 14 5	49, 62, 75, 108	0
61	n5	120/141 (85%)	0.98	18 (15%) 3 1	49, 63, 79, 92	0
62	N6	126/126 (100%)	1.01	12 (9%) 10 4	40, 58, 69, 76	0
62	n6	126/126 (100%)	1.25	20 (15%) 3 1	43, 59, 74, 81	0
63	N7	135/135 (100%)	1.39	31 (22%) 1 0	71, 88, 99, 102	0
63	n7	135/135 (100%)	1.58	48 (35%) 0 0	75, 91, 103, 108	0
64	N8	148/148 (100%)	0.34	1 (0%) 89 78	28, 50, 73, 83	0
64	n8	148/148 (100%)	0.24	0 100 100	27, 53, 72, 76	0
65	N9	58/58 (100%)	1.16	13 (22%) 1 0	32, 58, 105, 120	0
65	n9	58/58 (100%)	0.82	9 (15%) 3 1	31, 53, 78, 87	0
66	O0	97/104 (93%)	0.43	5 (5%) 31 13	70, 82, 105, 111	0
66	o0	100/104 (96%)	0.87	12 (12%) 6 2	69, 84, 112, 120	0
67	O1	109/112 (97%)	0.97	17 (15%) 3 1	50, 65, 98, 109	0
67	o1	109/112 (97%)	0.85	10 (9%) 11 4	41, 54, 89, 100	0
68	O2	127/129 (98%)	0.24	1 (0%) 87 75	30, 44, 58, 78	0
68	o2	127/129 (98%)	0.33	4 (3%) 52 28	27, 48, 63, 74	0
69	O3	106/106 (100%)	0.07	0 100 100	36, 42, 67, 80	0
69	o3	106/106 (100%)	0.13	1 (0%) 85 72	33, 42, 65, 79	0
70	O4	112/119 (94%)	1.20	23 (20%) 1 0	45, 62, 102, 109	0
70	o4	112/119 (94%)	0.69	3 (2%) 58 34	45, 61, 107, 115	0
71	O5	119/119 (100%)	0.46	4 (3%) 49 24	44, 65, 73, 75	0
71	o5	119/119 (100%)	0.17	2 (1%) 73 52	49, 67, 82, 95	0
72	O6	99/99 (100%)	0.32	0 100 100	55, 64, 97, 112	0
72	o6	99/99 (100%)	0.58	5 (5%) 32 13	58, 70, 95, 115	0
73	O7	87/87 (100%)	0.21	2 (2%) 64 40	33, 39, 59, 68	0
73	o7	87/87 (100%)	0.28	3 (3%) 49 24	34, 43, 69, 81	0
74	O8	77/77 (100%)	0.29	3 (3%) 43 21	72, 87, 111, 117	0
74	o8	77/77 (100%)	0.53	3 (3%) 43 21	71, 87, 102, 105	0
75	O9	50/50 (100%)	0.51	2 (4%) 42 20	43, 48, 53, 54	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
75	o9	50/50 (100%)	0.49	1 (2%) 68 46	43, 49, 57, 59	0
76	Q0	52/52 (100%)	0.96	6 (11%) 6 2	43, 50, 71, 79	0
76	q0	52/52 (100%)	0.59	3 (5%) 26 11	34, 39, 54, 57	0
77	Q1	25/25 (100%)	0.80	2 (8%) 15 5	51, 56, 58, 60	0
77	q1	25/25 (100%)	0.54	0 100 100	43, 46, 48, 49	0
78	Q2	105/105 (100%)	0.20	7 (6%) 21 7	34, 51, 76, 103	0
78	q2	105/105 (100%)	0.01	2 (1%) 70 48	35, 46, 64, 97	0
79	Q3	91/91 (100%)	-0.00	0 100 100	41, 56, 73, 81	0
79	q3	91/91 (100%)	0.09	2 (2%) 65 42	37, 53, 67, 78	0
80	e0	62/62 (100%)	0.53	3 (4%) 34 15	57, 88, 121, 129	0
81	m2	0/160	-	-	-	-
82	p0	143/311 (45%)	1.93	68 (47%) 0 0	98, 131, 238, 246	0
83	p1	0/47	-	-	-	-
84	p2	0/46	-	-	-	-
85	C	4/5 (80%)	0.58	0 100 100	34, 36, 37, 37	0
85	D	4/5 (80%)	0.71	0 100 100	33, 34, 34, 39	0
All	All	33054/35334 (93%)	0.64	3074 (9%) 11 4	26, 68, 150, 293	0

All (3074) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	2	1699	G	19.7
14	c2	22	VAL	19.0
60	N4	86	SER	18.2
14	c2	128	ALA	16.9
60	N4	83	THR	15.7
1	2	1696	G	15.2
1	2	656	G	15.1
1	2	1694	A	14.3
1	2	1708	U	13.6
35	SM	14	ASP	13.4
14	c2	103	LEU	13.2
53	M7	161	ALA	13.0
1	2	1709	C	12.5
60	N4	84	GLY	12.3
1	2	1697	G	12.3
1	2	1702	A	12.2

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Mol	Chain	Res	Type	RSRZ
33	e1	85	TYR	12.2
35	SM	15	ALA	12.1
14	c2	102	GLY	12.0
1	2	1698	G	11.9
36	5	1025	A	11.2
1	2	1700	C	11.1
22	D0	120	SER	10.9
14	c2	123	VAL	10.8
33	e1	86	THR	10.8
14	c2	20	ALA	10.7
1	2	1695	G	10.6
60	N4	87	LEU	10.5
1	2	1707	A	10.2
60	N4	88	ASP	10.1
33	e1	89	LYS	10.1
1	2	658	C	10.0
33	e1	88	PRO	9.9
1	2	1701	A	9.8
60	N4	72	SER	9.8
60	N4	89	LEU	9.6
53	M7	162	GLU	9.5
60	N4	75	THR	9.5
14	c2	104	ALA	9.4
14	c2	92	ALA	9.2
36	5	1566	A	9.1
60	N4	81	PRO	9.0
35	SM	19	VAL	9.0
60	n4	69	LYS	9.0
60	N4	85	ALA	8.9
39	L2	253	GLN	8.8
1	2	657	U	8.8
53	M7	184	ALA	8.7
11	S9	186	GLU	8.7
34	sR	166	SER	8.7
14	c2	105	LYS	8.6
1	6	659	C	8.6
13	C1	146	ALA	8.6
36	1	1955	U	8.6
17	c5	134	THR	8.5
36	1	1570	U	8.5
1	2	134	U	8.5
19	C7	74	GLN	8.5

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Mol	Chain	Res	Type	RSRZ
36	5	1565	G	8.5
42	L5	2	ALA	8.5
14	c2	126	TRP	8.5
33	e1	87	THR	8.4
14	c2	121	VAL	8.3
6	S4	261	LEU	8.2
1	2	718	U	8.0
60	n4	68	ALA	8.0
1	2	1705	C	8.0
1	2	1693	A	7.9
1	2	715	U	7.9
14	c2	112	ALA	7.9
36	5	1567	U	7.8
14	c2	93	ASP	7.8
1	6	678	A	7.8
14	c2	36	LEU	7.8
36	1	1569	U	7.7
53	M7	160	ALA	7.7
60	N4	95	SER	7.7
3	S1	92	GLN	7.7
14	c2	113	ARG	7.7
7	S5	36	ALA	7.6
35	SM	16	ASP	7.6
60	N4	82	ILE	7.6
1	2	1703	C	7.5
1	2	1690	G	7.5
60	N4	90	ILE	7.5
1	2	1711	C	7.4
33	e1	77	GLY	7.3
1	6	658	C	7.3
1	6	662	U	7.2
18	C6	114	ARG	7.2
42	L5	3	PHE	7.2
1	2	1706	C	7.2
14	c2	33	ARG	7.2
14	c2	133	LEU	7.2
78	Q2	106	PHE	7.1
33	E1	87	THR	7.1
60	n4	66	GLU	7.0
34	sR	158	PRO	7.0
1	2	913	G	7.0
1	6	1700	C	7.0

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Mol	Chain	Res	Type	RSRZ
1	6	676	G	7.0
1	6	679	U	6.9
22	d0	14	GLN	6.9
36	5	1568	U	6.9
42	L5	6	ASP	6.9
7	S5	71	ALA	6.8
15	C3	14	SER	6.8
14	c2	136	ILE	6.8
14	c2	21	GLU	6.8
45	L8	116	VAL	6.8
66	o0	6	SER	6.8
3	S1	20	VAL	6.8
22	d0	64	LYS	6.8
32	E0	60	PRO	6.8
7	S5	37	GLN	6.7
1	2	1686	C	6.7
16	C4	75	GLY	6.6
1	2	1704	U	6.6
22	D0	121	ASN	6.6
8	S6	149	LYS	6.6
1	2	1692	G	6.6
1	6	656	G	6.6
18	c6	83	GLN	6.6
14	C2	141	SER	6.6
32	E0	61	SER	6.6
14	c2	57	ALA	6.5
1	2	1710	U	6.5
33	e1	94	LYS	6.5
17	c5	135	THR	6.5
14	c2	110	ALA	6.4
14	c2	56	GLU	6.4
14	c2	65	SER	6.4
33	e1	80	ARG	6.4
34	sR	214	ALA	6.4
14	C2	59	LEU	6.4
1	2	506	A	6.4
14	c2	64	SER	6.4
60	n4	67	VAL	6.3
36	1	1568	U	6.3
20	C8	146	ALA	6.3
60	N4	74	LYS	6.3
28	D6	2	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
13	C1	147	GLY	6.2
33	e1	98	VAL	6.2
17	c5	103	ASN	6.1
1	6	666	U	6.1
26	d4	2	SER	6.1
14	c2	106	ILE	6.1
14	c2	28	LEU	6.1
14	c2	107	ASP	6.1
21	c9	55	TYR	6.1
14	c2	118	ALA	6.1
27	d5	89	ILE	6.0
18	c6	124	PRO	6.0
35	SM	89	ARG	6.0
35	SM	13	GLU	6.0
14	c2	96	GLN	5.9
14	c2	26	ASP	5.9
1	2	696	C	5.9
18	c6	44	LEU	5.9
36	1	1564	U	5.9
9	S7	31	SER	5.9
14	c2	59	LEU	5.9
30	D8	16	LEU	5.8
14	c2	39	ASP	5.8
17	c5	78	THR	5.8
60	n4	70	LYS	5.8
67	o1	82	GLU	5.8
19	C7	62	GLN	5.8
48	M1	148	VAL	5.8
33	E1	145	HIS	5.8
18	C6	123	ARG	5.8
33	e1	90	LYS	5.8
19	C7	2	GLY	5.7
18	c6	11	GLY	5.7
36	5	1569	U	5.7
3	S1	89	ASP	5.7
22	d0	67	THR	5.7
27	d5	50	ILE	5.7
1	6	663	U	5.7
35	SM	85	SER	5.7
33	E1	86	THR	5.7
1	2	1370	U	5.7
39	l2	253	GLN	5.6

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Mol	Chain	Res	Type	RSRZ
60	N4	71	ARG	5.6
20	C8	16	ARG	5.6
11	S9	181	ALA	5.6
14	C2	32	LEU	5.6
33	e1	93	HIS	5.6
34	SR	283	LYS	5.6
44	L7	25	GLN	5.6
27	D5	58	ARG	5.6
33	E1	147	VAL	5.6
34	sR	213	SER	5.5
10	S8	200	LYS	5.5
34	sR	157	VAL	5.5
6	S4	26	CYS	5.5
1	6	675	U	5.5
1	6	1694	A	5.5
14	C2	136	ILE	5.5
35	SM	20	LEU	5.5
29	D7	38	PRO	5.5
7	S5	70	VAL	5.5
63	N7	2	ALA	5.5
1	6	1695	G	5.4
18	c6	68	ARG	5.4
8	S6	148	SER	5.4
1	2	133	U	5.4
1	6	657	U	5.4
3	S1	98	THR	5.4
14	c2	122	VAL	5.4
8	S6	78	THR	5.4
33	e1	96	LYS	5.4
6	s4	261	LEU	5.4
33	e1	145	HIS	5.4
13	c1	2	SER	5.4
20	C8	145	ARG	5.4
16	C4	15	GLY	5.4
14	c2	41	LEU	5.3
82	p0	192	ASP	5.3
1	2	719	U	5.3
32	E0	56	MET	5.3
20	c8	18	LEU	5.3
36	1	1565	G	5.3
36	5	2539	C	5.3
18	c6	46	PHE	5.3

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Mol	Chain	Res	Type	RSRZ
15	C3	15	ALA	5.3
31	d9	29	GLY	5.3
20	C8	18	LEU	5.3
60	N4	98	PRO	5.3
20	C8	44	ASN	5.3
18	C6	40	GLU	5.3
5	s3	208	ILE	5.3
1	6	661	A	5.2
19	C7	99	VAL	5.2
82	p0	25	LEU	5.2
35	SM	18	VAL	5.2
2	S0	98	ILE	5.2
34	sR	187	GLN	5.2
4	s2	90	THR	5.2
36	5	1764	U	5.2
3	S1	91	VAL	5.2
22	d0	97	VAL	5.2
63	N7	132	SER	5.2
3	S1	131	ASP	5.2
60	N4	96	LEU	5.2
34	sR	24	ALA	5.2
20	C8	2	SER	5.2
33	E1	114	VAL	5.2
11	s9	148	VAL	5.1
82	p0	287	ASP	5.1
14	c2	85	LYS	5.1
36	5	1016	C	5.1
1	6	1696	G	5.1
36	5	1573	G	5.1
22	d0	93	LEU	5.1
61	n5	26	VAL	5.1
35	SM	50	ASN	5.1
14	C2	41	LEU	5.1
17	C5	50	THR	5.1
36	1	1016	C	5.1
36	1	1567	U	5.1
33	e1	112	GLY	5.0
2	s0	101	ARG	5.0
29	D7	19	HIS	5.0
1	2	1691	A	5.0
2	S0	28	ASN	5.0
1	6	1707	A	5.0

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Mol	Chain	Res	Type	RSRZ
1	2	1685	G	5.0
7	S5	76	ARG	5.0
34	sR	165	ASP	5.0
22	d0	54	GLY	5.0
48	M1	127	PHE	5.0
18	C6	70	THR	5.0
36	1	1566	A	5.0
45	l8	109	LEU	5.0
8	S6	80	ASN	5.0
7	s5	133	VAL	5.0
7	S5	86	GLN	5.0
4	s2	250	GLN	4.9
3	S1	52	THR	4.9
14	C2	89	ILE	4.9
48	M1	90	GLN	4.9
27	D5	97	LYS	4.9
1	6	1699	G	4.9
3	s1	54	LEU	4.9
65	N9	55	ALA	4.9
13	C1	151	LYS	4.9
3	S1	225	VAL	4.9
14	C2	83	GLU	4.9
1	2	194	U	4.9
18	C6	15	SER	4.9
35	SM	17	VAL	4.9
35	sM	52	PRO	4.9
56	N0	1	MET	4.9
1	6	654	C	4.9
1	6	667	U	4.9
18	C6	68	ARG	4.9
26	d4	34	ASN	4.9
20	C8	40	ARG	4.9
11	S9	5	PRO	4.9
34	SR	318	ALA	4.8
11	S9	182	GLU	4.8
73	o7	88	ALA	4.8
18	C6	21	HIS	4.8
3	S1	94	LYS	4.8
56	n0	1	MET	4.8
8	S6	77	LEU	4.8
66	o0	7	GLN	4.8
2	S0	188	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
26	D4	70	VAL	4.8
26	D4	26	ASP	4.8
36	5	1564	U	4.8
7	s5	130	ILE	4.8
2	S0	99	ALA	4.8
33	E1	93	HIS	4.8
34	sR	167	VAL	4.8
18	C6	118	ILE	4.8
36	1	2095	G	4.8
62	n6	127	GLU	4.7
48	M1	147	THR	4.7
1	6	677	G	4.7
9	S7	108	GLN	4.7
34	sR	252	LEU	4.7
18	c6	69	VAL	4.7
21	c9	18	TYR	4.7
7	S5	75	GLY	4.7
29	D7	44	THR	4.7
34	sR	72	THR	4.7
36	5	1575	A	4.7
1	6	652	G	4.7
14	C2	26	ASP	4.7
1	6	664	U	4.7
14	c2	71	ILE	4.7
12	c0	98	ASN	4.7
34	SR	279	ALA	4.7
1	2	261	U	4.7
15	C3	53	LEU	4.6
60	N4	76	VAL	4.6
18	c6	121	SER	4.6
82	p0	24	SER	4.6
33	e1	92	LYS	4.6
76	Q0	77	ILE	4.6
22	d0	36	ASN	4.6
1	2	676	G	4.6
33	e1	81	LYS	4.6
1	6	1701	A	4.6
61	n5	142	ILE	4.6
3	S1	53	GLY	4.6
14	C2	28	LEU	4.6
21	C9	38	LYS	4.6
70	O4	23	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
19	c7	65	PRO	4.6
11	s9	134	ILE	4.6
27	D5	88	ILE	4.6
36	1	2502	A	4.6
29	D7	26	GLN	4.6
24	D2	34	ILE	4.5
70	O4	66	SER	4.5
19	c7	67	ARG	4.5
60	N4	97	LYS	4.5
20	c8	146	ALA	4.5
1	2	238	U	4.5
18	C6	79	TYR	4.5
2	S0	126	PRO	4.5
34	sR	186	PHE	4.5
36	1	1762	C	4.5
1	2	679	U	4.5
3	s1	89	ASP	4.5
42	L5	146	LEU	4.5
17	c5	136	SER	4.5
1	6	1697	G	4.5
3	s1	234	GLU	4.5
18	C6	20	ALA	4.5
7	s5	76	ARG	4.5
13	C1	3	THR	4.5
24	D2	27	ILE	4.5
1	2	173	A	4.5
48	M1	70	THR	4.5
65	N9	58	LYS	4.5
42	L5	4	GLN	4.5
19	c7	69	ILE	4.4
19	c7	42	GLN	4.4
33	e1	84	VAL	4.4
14	c2	35	ALA	4.4
20	C8	32	LEU	4.4
14	c2	140	PHE	4.4
33	e1	95	HIS	4.4
21	C9	110	LYS	4.4
20	c8	14	ILE	4.4
14	C2	78	LEU	4.4
65	N9	54	LEU	4.4
45	l8	192	GLN	4.4
48	M1	125	MET	4.4

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Mol	Chain	Res	Type	RSRZ
23	D1	53	TYR	4.4
36	1	1572	U	4.4
1	6	1709	C	4.4
14	C2	121	VAL	4.4
20	C8	36	LYS	4.4
11	S9	141	VAL	4.4
56	N0	2	ALA	4.4
71	o5	120	ALA	4.4
43	l6	129	GLU	4.4
17	c5	4	ALA	4.4
48	M1	102	PHE	4.4
82	p0	188	VAL	4.4
34	sR	314	GLN	4.4
11	s9	2	PRO	4.4
30	D8	27	GLN	4.4
10	S8	106	ALA	4.4
45	l8	110	THR	4.4
1	2	132	U	4.3
34	sR	123	ILE	4.3
46	L9	190	ASP	4.3
18	C6	17	THR	4.3
13	C1	152	GLN	4.3
34	SR	131	ILE	4.3
34	sR	115	ILE	4.3
7	s5	84	LYS	4.3
12	c0	23	ALA	4.3
17	c5	137	ARG	4.3
1	2	1059	U	4.3
15	C3	16	ILE	4.3
82	p0	104	ARG	4.3
70	O4	64	THR	4.3
33	e1	83	LYS	4.3
75	O9	2	ALA	4.3
29	D7	41	LEU	4.3
19	c7	59	LYS	4.3
31	d9	52	PHE	4.3
70	O4	73	SER	4.3
60	N4	73	ARG	4.3
7	s5	68	ILE	4.3
12	c0	79	TYR	4.3
36	1	1269	U	4.3
36	5	2506	U	4.3

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Mol	Chain	Res	Type	RSRZ
22	d0	21	LYS	4.3
7	s5	75	GLY	4.3
8	S6	175	ILE	4.3
27	d5	59	TYR	4.3
42	l5	4	GLN	4.3
36	1	2205	U	4.3
11	S9	185	GLY	4.3
11	S9	171	ARG	4.3
27	D5	93	SER	4.3
7	S5	85	ALA	4.3
19	C7	71	PHE	4.3
53	M7	183	ALA	4.3
33	E1	99	LYS	4.3
63	n7	10	VAL	4.3
2	S0	122	ILE	4.2
34	sR	170	ILE	4.2
36	5	2503	G	4.2
3	S1	54	LEU	4.2
8	s6	162	VAL	4.2
1	2	677	G	4.2
3	S1	46	THR	4.2
36	1	1954	G	4.2
35	sM	90	SER	4.2
63	n7	75	VAL	4.2
82	p0	68	SER	4.2
21	c9	93	HIS	4.2
61	n5	23	ALA	4.2
23	d1	87	ARG	4.2
61	N5	24	LEU	4.2
22	d0	81	THR	4.2
22	d0	22	ILE	4.2
82	p0	27	VAL	4.2
48	M1	131	MET	4.2
21	C9	92	LYS	4.2
3	S1	217	LEU	4.2
19	c7	62	GLN	4.2
21	C9	50	ALA	4.2
36	5	1763	U	4.2
65	n9	23	LYS	4.2
12	C0	5	LYS	4.2
31	D9	4	GLU	4.2
34	sR	140	CYS	4.2

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Mol	Chain	Res	Type	RSRZ
48	M1	108	GLU	4.2
35	SM	87	THR	4.2
36	5	1580	A	4.2
14	c2	114	LYS	4.2
67	o1	112	ASP	4.2
11	s9	8	TYR	4.2
6	S4	111	VAL	4.2
2	s0	98	ILE	4.2
7	S5	96	SER	4.2
20	c8	121	ALA	4.1
8	S6	154	ARG	4.1
9	S7	98	ILE	4.1
82	p0	20	GLU	4.1
3	S1	59	ASP	4.1
65	N9	25	LYS	4.1
18	C6	9	THR	4.1
1	2	1688	U	4.1
1	6	665	U	4.1
4	s2	88	LYS	4.1
34	sR	227	ALA	4.1
11	S9	128	LEU	4.1
8	S6	145	PHE	4.1
11	S9	6	ARG	4.1
34	sR	3	SER	4.1
29	D7	47	PHE	4.1
31	d9	55	PHE	4.1
45	L8	256	ALA	4.1
22	D0	54	GLY	4.1
42	L5	148	ILE	4.1
82	p0	69	ASP	4.1
14	c2	111	ASN	4.1
18	C6	128	LYS	4.1
18	c6	8	GLN	4.1
11	S9	2	PRO	4.1
11	S9	180	LYS	4.1
34	sR	33	LEU	4.1
18	c6	10	PHE	4.1
24	D2	60	LYS	4.1
34	sR	116	ASP	4.1
48	M1	160	VAL	4.1
10	S8	152	ILE	4.1
19	c7	3	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
33	E1	85	TYR	4.1
35	SM	53	ARG	4.1
1	6	653	C	4.1
3	S1	90	GLU	4.1
49	m3	192	GLU	4.1
18	C6	12	LYS	4.1
34	SR	115	ILE	4.1
1	6	1610	G	4.1
1	2	1719	A	4.1
1	6	1702	A	4.1
17	c5	79	HIS	4.0
36	5	1762	C	4.0
14	C2	43	ARG	4.0
14	c2	42	ALA	4.0
34	SR	52	GLN	4.0
61	N5	108	LEU	4.0
30	D8	28	VAL	4.0
8	S6	79	LYS	4.0
18	c6	54	LEU	4.0
36	5	2538	U	4.0
5	s3	167	PHE	4.0
36	5	1576	G	4.0
27	D5	69	LEU	4.0
42	L5	5	LYS	4.0
62	n6	83	ASP	4.0
17	C5	104	GLN	4.0
19	c7	60	ARG	4.0
29	D7	70	LYS	4.0
31	d9	56	ARG	4.0
6	S4	54	TYR	4.0
17	c5	104	GLN	4.0
22	d0	18	GLN	4.0
36	5	1572	U	4.0
14	c2	132	GLU	4.0
39	L2	252	THR	4.0
33	E1	146	SER	4.0
36	1	1764	U	4.0
14	c2	43	ARG	4.0
18	c6	12	LYS	4.0
18	c6	79	TYR	4.0
5	S3	210	GLU	4.0
8	S6	139	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
14	C2	126	TRP	3.9
82	p0	93	LEU	3.9
3	S1	138	PHE	3.9
17	c5	101	ALA	3.9
42	L5	28	THR	3.9
1	2	678	A	3.9
36	5	1026	A	3.9
7	s5	79	ASN	3.9
53	M7	176	ILE	3.9
70	o4	55	SER	3.9
72	o6	58	ILE	3.9
3	S1	151	LYS	3.9
11	S9	101	VAL	3.9
82	p0	103	ASN	3.9
29	D7	18	LYS	3.9
14	C2	60	VAL	3.9
29	D7	51	GLN	3.9
12	c0	78	GLU	3.9
10	S8	179	CYS	3.9
82	p0	43	LYS	3.9
18	C6	74	HIS	3.9
22	d0	83	GLU	3.9
60	N4	66	GLU	3.9
36	1	1027	A	3.9
14	C2	52	LEU	3.9
14	c2	58	LEU	3.9
7	S5	89	ILE	3.9
34	sR	210	LEU	3.9
2	s0	186	GLY	3.9
14	C2	119	SER	3.9
82	p0	44	GLU	3.9
34	sR	161	LYS	3.9
82	p0	19	LEU	3.8
1	2	717	C	3.8
13	C1	156	PHE	3.8
72	o6	2	THR	3.8
31	D9	56	ARG	3.8
36	5	1352	A	3.8
36	5	1349	G	3.8
36	5	440	A	3.8
4	S2	62	PRO	3.8
48	M1	59	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
46	L9	191	LEU	3.8
60	n4	65	GLU	3.8
17	c5	80	MET	3.8
18	C6	115	THR	3.8
23	D1	32	VAL	3.8
36	5	1350	A	3.8
7	S5	152	GLY	3.8
63	N7	136	PHE	3.8
48	M1	167	TYR	3.8
1	2	708	C	3.8
63	n7	56	LYS	3.8
63	n7	92	PHE	3.8
14	C2	138	GLU	3.8
12	c0	22	VAL	3.8
16	C4	18	ARG	3.8
82	p0	38	MET	3.8
14	C2	55	GLY	3.8
78	q2	106	PHE	3.8
17	C5	12	PHE	3.8
34	sR	27	ALA	3.8
29	d7	24	LEU	3.8
53	M7	182	ILE	3.8
60	n4	96	LEU	3.8
1	6	680	U	3.8
63	N7	26	VAL	3.8
34	SR	284	ALA	3.8
35	SM	27	LYS	3.8
6	s4	23	LEU	3.8
20	C8	15	LEU	3.8
27	d5	88	ILE	3.8
1	2	137	U	3.7
17	C5	49	MET	3.7
34	sR	5	GLU	3.7
7	s5	83	ARG	3.7
42	L5	151	GLN	3.7
32	E0	46	ASN	3.7
15	C3	11	ILE	3.7
21	c9	94	ILE	3.7
1	2	723	G	3.7
17	c5	51	SER	3.7
21	c9	84	LYS	3.7
48	M1	53	THR	3.7

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Mol	Chain	Res	Type	RSRZ
3	S1	28	GLU	3.7
3	s1	235	GLY	3.7
22	d0	98	GLN	3.7
35	sM	25	ILE	3.7
27	d5	40	VAL	3.7
1	6	277	U	3.7
36	5	1028	U	3.7
48	M1	122	ILE	3.7
63	n7	76	ASN	3.7
82	p0	94	THR	3.7
21	C9	114	VAL	3.7
48	M1	96	PHE	3.7
22	D0	64	LYS	3.7
35	sM	34	LYS	3.7
1	2	709	C	3.7
12	C0	39	ASN	3.7
14	c2	40	GLY	3.7
14	C2	139	HIS	3.7
61	N5	23	ALA	3.7
22	d0	19	ILE	3.7
11	S9	148	VAL	3.7
18	C6	64	ASP	3.7
34	sR	104	VAL	3.7
1	2	1684	U	3.7
36	1	1259	A	3.7
27	D5	103	ARG	3.7
68	O2	127	ALA	3.7
1	6	1228	G	3.7
2	S0	158	VAL	3.7
7	S5	62	VAL	3.7
3	S1	99	ASN	3.7
22	d0	95	ALA	3.7
22	d0	20	ILE	3.7
1	6	1082	C	3.7
33	E1	90	LYS	3.7
24	D2	5	SER	3.7
34	SR	25	THR	3.7
34	sR	74	THR	3.7
70	O4	110	GLU	3.7
82	p0	102	SER	3.7
18	C6	65	ILE	3.7
2	S0	97	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
29	D7	30	SER	3.7
36	5	1574	C	3.7
11	S9	138	LYS	3.7
82	p0	18	TYR	3.7
27	D5	73	GLY	3.7
35	SM	88	ARG	3.7
11	s9	111	THR	3.7
7	s5	108	LEU	3.7
8	s6	171	LYS	3.7
35	SM	28	SER	3.7
1	2	195	G	3.6
11	S9	144	PRO	3.6
14	C2	53	THR	3.6
1	6	1711	C	3.6
7	S5	43	PHE	3.6
17	C5	101	ALA	3.6
26	D4	61	ARG	3.6
48	M1	119	SER	3.6
3	s1	233	GLY	3.6
33	e1	113	LYS	3.6
8	S6	75	LEU	3.6
9	s7	43	PHE	3.6
16	C4	16	VAL	3.6
18	c6	118	ILE	3.6
74	o8	2	ALA	3.6
63	n7	49	TYR	3.6
30	D8	66	LEU	3.6
1	6	495	C	3.6
20	C8	21	ASN	3.6
21	C9	90	PRO	3.6
24	D2	6	VAL	3.6
32	E0	30	PRO	3.6
35	sM	46	LYS	3.6
16	C4	38	THR	3.6
22	d0	78	THR	3.6
7	s5	82	PHE	3.6
27	d5	46	LYS	3.6
29	D7	37	CYS	3.6
33	e1	91	ILE	3.6
63	n7	21	LYS	3.6
14	C2	30	VAL	3.6
3	s1	228	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
21	c9	125	SER	3.6
27	d5	94	LYS	3.6
34	sR	200	ASN	3.6
1	6	1712	A	3.6
36	1	1270	A	3.6
82	p0	70	LEU	3.6
63	n7	52	LYS	3.6
1	2	1687	U	3.6
55	M9	179	GLU	3.6
63	n7	96	VAL	3.6
3	S1	93	GLY	3.6
42	L5	30	TYR	3.6
18	C6	116	LEU	3.6
1	2	1712	A	3.6
1	6	674	C	3.6
1	2	711	U	3.6
1	6	670	U	3.6
3	s1	90	GLU	3.6
60	N4	92	GLU	3.6
11	s9	11	THR	3.6
63	N7	65	ARG	3.6
82	p0	50	VAL	3.6
1	2	174	U	3.6
8	S6	174	LYS	3.6
34	sR	202	LEU	3.6
57	N1	62	GLY	3.6
48	M1	132	ASN	3.6
7	S5	80	LYS	3.6
13	c1	3	THR	3.6
19	c7	41	ILE	3.6
22	d0	87	HIS	3.6
34	sR	118	LYS	3.6
48	M1	54	VAL	3.6
4	s2	89	GLN	3.6
14	C2	36	LEU	3.6
48	M1	159	THR	3.6
60	n4	95	SER	3.6
32	E0	54	ARG	3.5
1	2	1527	C	3.5
2	S0	174	TRP	3.5
53	M7	163	LYS	3.5
21	c9	37	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
33	E1	91	ILE	3.5
7	S5	73	THR	3.5
14	c2	32	LEU	3.5
15	C3	54	LEU	3.5
21	C9	119	LYS	3.5
2	S0	83	GLN	3.5
34	sR	139	GLN	3.5
34	sR	315	VAL	3.5
1	2	697	C	3.5
14	C2	20	ALA	3.5
40	l3	387	LEU	3.5
42	L5	29	ASP	3.5
11	s9	141	VAL	3.5
22	D0	15	GLN	3.5
17	c5	72	LYS	3.5
19	c7	87	GLU	3.5
27	D5	102	THR	3.5
56	n0	130	GLU	3.5
65	N9	26	THR	3.5
18	c6	29	ILE	3.5
18	c6	123	ARG	3.5
10	S8	63	GLY	3.5
20	C8	86	LEU	3.5
82	p0	26	PHE	3.5
14	C2	21	GLU	3.5
18	c6	28	LEU	3.5
20	c8	17	LEU	3.5
33	e1	99	LYS	3.5
63	N7	124	ALA	3.5
82	p0	295	ALA	3.5
36	1	547	G	3.5
29	d7	60	SER	3.5
63	n7	22	LYS	3.5
13	C1	154	ALA	3.5
22	d0	30	LYS	3.5
3	s1	217	LEU	3.5
11	s9	145	SER	3.5
16	C4	120	PRO	3.5
19	c7	12	ALA	3.5
22	d0	102	ARG	3.5
33	e1	100	LEU	3.5
33	E1	111	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
48	M1	112	LEU	3.5
56	N0	129	ILE	3.5
3	S1	42	ASN	3.5
1	6	493	U	3.5
20	C8	129	TRP	3.5
22	d0	100	VAL	3.5
19	C7	69	ILE	3.5
53	M7	168	LEU	3.5
82	p0	185	LEU	3.5
31	D9	5	ASN	3.5
33	E1	116	LYS	3.5
60	n4	84	GLY	3.5
1	6	655	G	3.5
36	5	2540	A	3.5
80	e0	63	GLN	3.5
14	c2	116	VAL	3.5
63	n7	13	VAL	3.5
3	s1	97	LEU	3.5
19	C7	78	ARG	3.5
22	d0	58	LEU	3.5
23	D1	8	LEU	3.5
2	s0	100	GLY	3.5
35	sM	89	LYS	3.5
29	D7	57	GLU	3.4
71	O5	20	GLN	3.4
1	2	145	A	3.4
1	2	1713	G	3.4
14	C2	88	LEU	3.4
16	C4	39	ILE	3.4
18	c6	38	LEU	3.4
18	c6	114	ARG	3.4
29	D7	48	SER	3.4
36	1	1349	G	3.4
36	1	1571	A	3.4
36	5	1268	G	3.4
36	5	1577	G	3.4
18	c6	132	LYS	3.4
60	n4	117	LYS	3.4
67	O1	5	LYS	3.4
7	S5	98	MET	3.4
7	s5	86	GLN	3.4
9	S7	150	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
3	S1	32	ILE	3.4
4	S2	88	LYS	3.4
5	S3	216	PRO	3.4
42	L5	27	LYS	3.4
63	n7	42	LEU	3.4
22	d0	29	THR	3.4
82	p0	88	PHE	3.4
27	d5	68	ARG	3.4
8	S6	147	LEU	3.4
34	SR	181	TRP	3.4
1	6	1708	U	3.4
5	S3	152	PHE	3.4
16	C4	89	THR	3.4
10	S8	141	ARG	3.4
33	e1	97	LYS	3.4
14	c2	31	VAL	3.4
7	s5	92	ARG	3.4
15	C3	13	SER	3.4
33	e1	79	LYS	3.4
18	C6	77	GLN	3.4
21	c9	4	VAL	3.4
33	E1	137	ASP	3.4
36	5	1571	A	3.4
34	sR	159	ASN	3.4
1	6	660	G	3.4
5	s3	205	ALA	3.4
8	S6	138	ALA	3.4
22	D0	67	THR	3.4
3	S1	114	VAL	3.4
20	C8	17	LEU	3.4
34	SR	167	VAL	3.4
36	1	1765	U	3.4
42	L5	159	VAL	3.4
17	c5	121	ILE	3.4
43	l6	130	ILE	3.4
6	S4	253	ASP	3.4
1	2	169	A	3.4
34	sR	121	MET	3.4
48	M1	101	ASN	3.4
2	S0	22	THR	3.4
14	c2	67	THR	3.4
1	6	669	G	3.4

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Mol	Chain	Res	Type	RSRZ
27	d5	51	LEU	3.4
34	sR	183	LEU	3.4
66	o0	90	VAL	3.4
18	C6	29	ILE	3.4
34	sR	313	TRP	3.4
22	D0	82	TYR	3.4
52	m6	184	THR	3.4
20	C8	72	ILE	3.4
36	1	3155	U	3.4
1	2	720	G	3.4
1	6	38	C	3.4
19	C7	65	PRO	3.4
2	S0	26	ALA	3.4
34	sR	301	LEU	3.4
48	M1	75	LYS	3.4
58	N2	27	VAL	3.4
70	O4	5	VAL	3.4
7	S5	61	TYR	3.4
35	SM	41	SER	3.4
48	M1	104	PHE	3.4
48	M1	139	THR	3.4
2	s0	185	ARG	3.4
76	Q0	85	LEU	3.4
70	O4	76	TYR	3.4
14	c2	23	THR	3.4
73	O7	84	SER	3.4
21	C9	141	GLU	3.4
6	s4	15	PRO	3.4
15	C3	57	ALA	3.4
29	D7	42	ASN	3.4
33	E1	106	TYR	3.4
36	5	1560	G	3.4
45	l8	121	SER	3.4
9	S7	100	PRO	3.3
10	S8	109	PHE	3.3
1	6	668	C	3.3
2	S0	23	HIS	3.3
11	s9	184	SER	3.3
22	d0	107	THR	3.3
66	O0	20	SER	3.3
49	m3	191	ALA	3.3
1	2	793	A	3.3

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Mol	Chain	Res	Type	RSRZ
11	S9	174	ARG	3.3
18	c6	47	LYS	3.3
3	S1	130	SER	3.3
5	s3	202	LEU	3.3
14	c2	63	VAL	3.3
63	n7	23	VAL	3.3
6	s4	13	ALA	3.3
13	C1	145	ALA	3.3
18	C6	10	PHE	3.3
34	sR	61	PHE	3.3
18	c6	82	ARG	3.3
21	C9	2	PRO	3.3
36	1	1017	C	3.3
19	C7	18	GLU	3.3
36	5	1024	G	3.3
20	C8	22	VAL	3.3
5	s3	201	ALA	3.3
18	C6	41	PRO	3.3
19	c7	68	GLY	3.3
1	6	1698	G	3.3
7	S5	185	ARG	3.3
11	s9	3	ARG	3.3
11	s9	142	ASN	3.3
34	sR	284	ALA	3.3
63	N7	91	ALA	3.3
8	s6	216	LEU	3.3
24	D2	26	LEU	3.3
34	sR	241	PHE	3.3
22	D0	86	ILE	3.3
35	sM	57	ASN	3.3
66	o0	105	ALA	3.3
32	E0	32	GLY	3.3
1	6	40	A	3.3
2	S0	118	PRO	3.3
20	c8	52	VAL	3.3
34	sR	272	ASP	3.3
1	6	1706	C	3.3
11	S9	143	ILE	3.3
21	c9	33	TYR	3.3
29	D7	68	GLY	3.3
33	E1	148	TYR	3.3
60	N4	70	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
48	M1	19	LEU	3.3
34	sR	244	ALA	3.3
36	1	1563	C	3.3
7	S5	93	LEU	3.3
48	m1	48	SER	3.3
15	C3	62	GLN	3.3
20	C8	105	VAL	3.3
63	N7	4	PHE	3.3
14	c2	135	MET	3.3
1	2	505	A	3.3
2	S0	100	GLY	3.3
8	s6	79	LYS	3.3
24	D2	55	ASP	3.3
45	l8	120	LYS	3.3
63	N7	7	ALA	3.3
65	N9	28	LYS	3.3
79	q3	2	ALA	3.3
19	C7	53	TYR	3.3
29	D7	3	LEU	3.3
57	N1	61	THR	3.3
3	S1	50	LYS	3.3
10	S8	151	LYS	3.3
5	s3	184	ILE	3.3
14	c2	127	GLY	3.3
57	N1	27	LEU	3.3
26	D4	35	VAL	3.3
1	2	493	U	3.3
18	C6	121	SER	3.3
35	SM	21	PRO	3.3
20	C8	41	ARG	3.3
34	sR	251	TRP	3.3
36	5	2507	C	3.3
5	s3	11	LEU	3.3
14	c2	30	VAL	3.3
19	C7	14	LYS	3.3
29	D7	32	PHE	3.3
32	E0	44	PHE	3.3
22	D0	20	ILE	3.2
34	sR	34	LEU	3.2
57	N1	101	CYS	3.2
49	M3	98	ASP	3.2
2	s0	116	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
7	S5	184	PHE	3.2
14	c2	47	GLU	3.2
21	C9	44	GLU	3.2
33	e1	120	GLU	3.2
3	s1	46	THR	3.2
14	C2	133	LEU	3.2
18	c6	117	LEU	3.2
22	d0	119	ALA	3.2
3	s1	192	VAL	3.2
26	d4	26	ASP	3.2
14	c2	25	GLU	3.2
5	S3	161	GLY	3.2
35	SM	86	ASN	3.2
4	s2	249	ALA	3.2
31	d9	36	LEU	3.2
2	S0	181	VAL	3.2
18	c6	129	PHE	3.2
36	5	1563	C	3.2
27	D5	71	ILE	3.2
1	2	914	G	3.2
1	6	651	G	3.2
45	L8	46	LEU	3.2
7	s5	77	TYR	3.2
34	sR	62	LYS	3.2
36	1	1278	A	3.2
67	o1	111	GLU	3.2
42	L5	60	ILE	3.2
70	O4	67	LYS	3.2
3	S1	97	LEU	3.2
7	S5	74	ALA	3.2
17	c5	74	ALA	3.2
46	L9	43	VAL	3.2
7	S5	84	LYS	3.2
21	c9	119	LYS	3.2
3	S1	142	PHE	3.2
1	2	136	C	3.2
12	c0	28	ASN	3.2
18	c6	19	VAL	3.2
61	n5	75	LYS	3.2
7	S5	172	ILE	3.2
11	S9	3	ARG	3.2
32	E0	41	THR	3.2

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Mol	Chain	Res	Type	RSRZ
48	M1	10	ARG	3.2
1	2	234	G	3.2
1	6	1225	U	3.2
26	d4	125	LEU	3.2
48	M1	172	LEU	3.2
11	S9	37	LYS	3.2
14	C2	22	VAL	3.2
27	d5	55	PRO	3.2
63	n7	136	PHE	3.2
36	1	1025	A	3.2
9	S7	103	SER	3.2
10	S8	69	SER	3.2
11	S9	35	GLY	3.2
20	C8	39	GLY	3.2
31	d9	20	GLN	3.2
18	c6	87	LYS	3.2
14	c2	108	ARG	3.2
31	d9	4	GLU	3.2
1	6	1337	A	3.2
6	S4	92	LEU	3.2
9	s7	108	GLN	3.2
21	C9	71	VAL	3.2
30	D8	48	VAL	3.2
45	L8	28	HIS	3.2
48	M1	134	PRO	3.2
14	c2	97	LEU	3.2
74	o8	54	LEU	3.2
1	2	142	G	3.2
19	C7	63	LYS	3.2
19	c7	58	MET	3.2
21	c9	92	LYS	3.2
7	s5	138	THR	3.2
36	1	1605	A	3.2
36	5	1027	A	3.2
7	S5	72	HIS	3.2
19	C7	66	VAL	3.2
82	p0	16	ARG	3.2
36	5	1275	C	3.2
42	L5	221	GLU	3.2
18	C6	14	LYS	3.2
24	D2	35	ILE	3.2
28	D6	3	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
35	SM	84	LYS	3.2
7	s5	94	THR	3.2
18	c6	115	THR	3.2
20	c8	20	THR	3.2
56	n0	2	ALA	3.2
75	o9	11	GLN	3.2
24	D2	22	LYS	3.1
29	D7	7	LEU	3.1
33	E1	83	LYS	3.1
36	1	1028	U	3.1
17	c5	102	PHE	3.1
42	L5	20	PHE	3.1
10	s8	176	SER	3.1
42	l5	205	SER	3.1
45	l8	194	THR	3.1
7	S5	217	LEU	3.1
20	C8	101	LEU	3.1
29	d7	59	CYS	3.1
14	c2	95	LYS	3.1
63	n7	120	GLU	3.1
20	C8	10	SER	3.1
21	C9	80	TYR	3.1
17	c5	125	PRO	3.1
14	c2	37	VAL	3.1
1	2	1717	G	3.1
18	C6	8	GLN	3.1
14	c2	74	LEU	3.1
19	c7	17	ILE	3.1
2	S0	143	VAL	3.1
3	S1	55	LYS	3.1
18	c6	127	LYS	3.1
5	s3	182	LEU	3.1
21	C9	139	THR	3.1
5	s3	213	GLU	3.1
11	S9	106	GLU	3.1
34	sR	133	VAL	3.1
18	c6	119	ALA	3.1
14	C2	75	VAL	3.1
24	D2	29	PRO	3.1
49	M3	41	THR	3.1
7	S5	97	LEU	3.1
19	c7	57	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
14	C2	85	LYS	3.1
78	Q2	100	LYS	3.1
21	c9	122	ARG	3.1
47	m0	205	SER	3.1
34	sR	185	GLN	3.1
63	n7	118	PHE	3.1
19	C7	3	ARG	3.1
1	6	261	U	3.1
11	S9	133	HIS	3.1
14	c2	129	GLU	3.1
14	c2	137	MET	3.1
18	c6	48	VAL	3.1
42	l5	216	GLU	3.1
19	C7	125	SER	3.1
28	D6	20	PRO	3.1
34	SR	4	ASN	3.1
8	S6	177	ARG	3.1
15	C3	50	ILE	3.1
48	M1	14	ILE	3.1
34	sR	113	VAL	3.1
34	sR	309	VAL	3.1
13	C1	150	ASN	3.1
19	c7	13	SER	3.1
45	L8	126	SER	3.1
82	p0	45	LEU	3.1
22	D0	70	THR	3.1
48	M1	39	GLN	3.1
7	S5	106	LYS	3.1
8	S6	164	LYS	3.1
14	C2	86	VAL	3.1
14	c2	124	LYS	3.1
26	d4	99	LYS	3.1
45	l8	122	LYS	3.1
48	M1	74	PRO	3.1
1	6	718	U	3.1
6	S4	27	TYR	3.1
55	m9	181	ARG	3.1
28	D6	83	ILE	3.1
39	l2	250	GLN	3.1
18	C6	7	VAL	3.1
60	n4	107	GLU	3.1
1	2	733	A	3.1

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Mol	Chain	Res	Type	RSRZ
7	s5	198	LEU	3.1
2	S0	159	ALA	3.1
10	S8	44	HIS	3.1
36	1	1026	A	3.1
46	l9	191	LEU	3.1
8	S6	169	TYR	3.0
17	c5	84	ILE	3.0
48	M1	73	GLY	3.0
60	n4	132	GLY	3.0
29	d7	46	VAL	3.0
67	O1	4	LEU	3.0
15	C3	76	LYS	3.0
9	s7	187	SER	3.0
18	c6	76	SER	3.0
33	E1	109	ASP	3.0
34	SR	319	ASN	3.0
6	S4	208	VAL	3.0
1	2	1610	G	3.0
1	2	138	A	3.0
14	c2	60	VAL	3.0
21	c9	25	GLN	3.0
48	m1	148	VAL	3.0
55	M9	51	VAL	3.0
38	8	81	U	3.0
6	s4	14	ALA	3.0
14	C2	140	PHE	3.0
14	C2	33	ARG	3.0
17	C5	76	VAL	3.0
18	C6	39	VAL	3.0
60	N4	67	VAL	3.0
1	2	700	C	3.0
7	S5	41	LYS	3.0
21	c9	28	LEU	3.0
29	d7	58	SER	3.0
34	sR	148	ASN	3.0
48	M1	17	LEU	3.0
36	1	2096	A	3.0
14	c2	24	ILE	3.0
22	D0	87	HIS	3.0
29	D7	73	LEU	3.0
63	n7	34	LYS	3.0
6	S4	24	SER	3.0

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Mol	Chain	Res	Type	RSRZ
10	S8	149	SER	3.0
26	D4	69	SER	3.0
34	sR	108	SER	3.0
2	S0	161	PRO	3.0
5	s3	216	PRO	3.0
43	L6	8	LYS	3.0
62	n6	58	VAL	3.0
82	p0	187	VAL	3.0
6	s4	26	CYS	3.0
18	C6	36	ILE	3.0
29	D7	43	ILE	3.0
34	SR	2	ALA	3.0
62	n6	41	ALA	3.0
33	e1	149	LYS	3.0
35	sM	23	LYS	3.0
60	N4	69	LYS	3.0
1	2	716	C	3.0
20	C8	13	HIS	3.0
36	5	1579	C	3.0
26	D4	125	LEU	3.0
42	L5	51	LEU	3.0
19	c7	47	ARG	3.0
34	sR	263	PHE	3.0
7	S5	153	GLY	3.0
14	c2	70	ASN	3.0
7	S5	77	TYR	3.0
31	d9	33	LYS	3.0
48	M1	153	LYS	3.0
48	M1	130	VAL	3.0
20	c8	54	LEU	3.0
1	6	1491	U	3.0
65	N9	24	PRO	3.0
82	p0	64	ARG	3.0
11	S9	164	PHE	3.0
11	S9	29	LYS	3.0
1	2	714	G	3.0
34	SR	199	ILE	3.0
2	S0	32	HIS	3.0
7	s5	37	GLN	3.0
8	S6	156	PHE	3.0
22	d0	52	LYS	3.0
36	1	1351	U	3.0

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Mol	Chain	Res	Type	RSRZ
67	o1	61	LYS	3.0
32	E0	25	GLU	3.0
67	O1	82	GLU	3.0
1	6	1371	A	3.0
63	n7	68	ILE	3.0
22	D0	97	VAL	3.0
18	C6	132	LYS	3.0
19	c7	28	PHE	3.0
2	S0	198	MET	3.0
26	D4	120	GLY	2.9
28	D6	9	GLY	2.9
8	S6	81	VAL	2.9
11	S9	183	ALA	2.9
34	sR	134	TRP	2.9
21	c9	69	LYS	2.9
36	5	2543	U	2.9
62	n6	104	LEU	2.9
11	S9	87	SER	2.9
7	S5	66	GLN	2.9
23	D1	10	GLU	2.9
24	D2	59	GLY	2.9
24	D2	111	MET	2.9
7	s5	137	ILE	2.9
2	S0	146	LEU	2.9
22	d0	26	LEU	2.9
60	n4	128	ALA	2.9
1	2	232	U	2.9
1	2	1718	G	2.9
11	S9	112	GLN	2.9
2	S0	170	ILE	2.9
17	c5	76	VAL	2.9
18	c6	89	LEU	2.9
22	d0	34	LEU	2.9
63	N7	92	PHE	2.9
24	D2	51	GLU	2.9
36	5	2504	U	2.9
1	2	143	G	2.9
18	C6	13	LYS	2.9
18	c6	13	LYS	2.9
48	M1	157	GLU	2.9
36	1	1243	G	2.9
9	S7	129	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
63	N7	13	VAL	2.9
61	n5	27	ARG	2.9
2	S0	76	ILE	2.9
11	s9	139	GLN	2.9
27	D5	89	ILE	2.9
29	D7	14	SER	2.9
3	S1	221	PRO	2.9
9	s7	32	PRO	2.9
14	c2	94	ALA	2.9
30	d8	9	LEU	2.9
32	E0	45	VAL	2.9
66	O0	62	LEU	2.9
11	s9	6	ARG	2.9
36	5	1233	G	2.9
33	e1	111	GLU	2.9
18	c6	64	ASP	2.9
76	q0	77	ILE	2.9
6	S4	57	ASN	2.9
48	M1	116	TYR	2.9
82	p0	46	ARG	2.9
82	p0	23	LYS	2.9
82	p0	86	PHE	2.9
8	s6	147	LEU	2.9
14	C2	94	ALA	2.9
19	c7	51	ALA	2.9
33	E1	143	LYS	2.9
36	1	2537	U	2.9
36	1	2703	A	2.9
49	m3	190	LYS	2.9
49	m3	193	ALA	2.9
1	2	280	U	2.9
36	5	2542	U	2.9
38	4	158	U	2.9
8	S6	150	GLU	2.9
8	s6	166	GLU	2.9
30	d8	17	GLY	2.9
2	S0	149	LEU	2.9
20	C8	69	ILE	2.9
1	2	704	C	2.9
14	c2	131	ASP	2.9
20	C8	71	GLN	2.9
33	E1	102	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
31	D9	55	PHE	2.9
47	m0	195	ALA	2.9
1	6	681	U	2.9
5	s3	163	PRO	2.9
36	1	1268	G	2.9
10	s8	61	GLU	2.9
27	d5	74	SER	2.9
35	SM	137	GLU	2.9
42	L5	25	GLU	2.9
6	S4	9	LEU	2.9
11	s9	147	MET	2.9
19	c7	63	LYS	2.9
21	c9	15	ILE	2.9
82	p0	87	VAL	2.9
51	m5	15	GLN	2.9
10	S8	140	GLU	2.9
14	C2	87	PRO	2.9
46	L9	189	GLU	2.9
22	d0	28	SER	2.9
28	D6	76	SER	2.9
1	6	1710	U	2.9
63	N7	61	LYS	2.9
12	c0	20	VAL	2.9
46	L9	140	VAL	2.9
10	S8	144	ALA	2.9
21	c9	12	GLN	2.9
35	sM	35	ALA	2.9
8	s6	134	GLY	2.9
34	sR	30	PRO	2.9
49	m3	131	LYS	2.9
8	S6	73	ILE	2.9
22	d0	99	ILE	2.9
29	D7	54	VAL	2.9
30	d8	48	VAL	2.9
22	D0	81	THR	2.9
42	L5	153	THR	2.9
82	p0	79	PHE	2.9
21	c9	17	ALA	2.9
48	m1	47	GLN	2.9
61	n5	123	TYR	2.9
29	D7	49	HIS	2.9
34	SR	33	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
34	SR	66	HIS	2.9
34	SR	280	GLY	2.9
31	d9	5	ASN	2.8
48	M1	34	SER	2.8
7	S5	147	THR	2.8
10	S8	62	THR	2.8
12	c0	57	THR	2.8
63	n7	115	LYS	2.8
66	o0	12	GLN	2.8
82	p0	89	THR	2.8
1	2	135	A	2.8
7	S5	175	LEU	2.8
29	D7	33	LEU	2.8
29	D7	69	GLY	2.8
63	n7	26	VAL	2.8
3	S1	100	PHE	2.8
3	s1	100	PHE	2.8
11	s9	164	PHE	2.8
65	N9	51	ALA	2.8
65	N9	56	ALA	2.8
70	O4	63	ALA	2.8
36	5	1017	C	2.8
65	n9	32	LEU	2.8
2	s0	199	PRO	2.8
20	C8	119	ILE	2.8
63	n7	82	PRO	2.8
1	6	225	A	2.8
2	S0	138	TYR	2.8
3	S1	49	ASN	2.8
3	s1	133	TYR	2.8
7	S5	91	GLU	2.8
33	e1	110	ALA	2.8
60	N4	68	ALA	2.8
1	2	820	U	2.8
20	c8	32	LEU	2.8
1	2	870	C	2.8
8	S6	137	ARG	2.8
28	d6	19	LYS	2.8
48	M1	11	ASP	2.8
63	n7	95	VAL	2.8
11	s9	104	PHE	2.8
1	2	217	A	2.8

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Mol	Chain	Res	Type	RSRZ
19	c7	15	ALA	2.8
60	N4	65	GLU	2.8
27	d5	93	SER	2.8
70	O4	68	THR	2.8
70	O4	71	THR	2.8
20	C8	125	ILE	2.8
24	D2	37	PHE	2.8
34	sR	188	ILE	2.8
34	sR	211	ILE	2.8
48	M1	129	VAL	2.8
18	c6	20	ALA	2.8
1	2	1611	A	2.8
7	S5	79	ASN	2.8
48	M1	13	LYS	2.8
65	N9	59	LYS	2.8
63	n7	83	THR	2.8
2	S0	72	ASP	2.8
8	s6	173	PRO	2.8
1	2	239	C	2.8
16	C4	78	ALA	2.8
9	S7	138	LYS	2.8
25	D3	7	ARG	2.8
32	E0	35	TYR	2.8
9	S7	109	VAL	2.8
34	SR	278	PHE	2.8
61	N5	107	VAL	2.8
1	6	1224	A	2.8
16	C4	119	THR	2.8
2	S0	40	ALA	2.8
13	C1	30	ARG	2.8
33	e1	78	LYS	2.8
46	l9	190	ASP	2.8
14	C2	27	ALA	2.8
55	M9	181	ARG	2.8
18	c6	52	LEU	2.8
21	C9	108	LEU	2.8
2	S0	162	CYS	2.8
10	s8	179	CYS	2.8
1	2	653	C	2.8
9	s7	103	SER	2.8
14	C2	24	ILE	2.8
15	C3	60	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
34	sR	122	ILE	2.8
82	p0	51	VAL	2.8
11	S9	11	THR	2.8
22	D0	21	LYS	2.8
67	O1	41	LYS	2.8
7	s5	126	ASP	2.8
8	S6	86	PRO	2.8
11	S9	135	ALA	2.8
14	c2	101	ALA	2.8
16	C4	29	HIS	2.8
18	C6	92	TYR	2.8
36	1	1350	A	2.8
42	L5	150	LEU	2.8
14	c2	75	VAL	2.8
2	S0	84	ARG	2.8
2	S0	135	GLU	2.8
20	C8	56	LYS	2.8
21	C9	103	LYS	2.8
22	d0	66	SER	2.8
33	E1	134	ASN	2.8
36	1	1029	G	2.8
60	n4	97	LYS	2.8
14	C2	34	THR	2.8
3	S1	110	LEU	2.8
24	D2	108	ALA	2.8
29	D7	53	ALA	2.8
62	N6	15	ALA	2.8
63	N7	51	LEU	2.8
14	C2	31	VAL	2.8
18	C6	83	GLN	2.8
18	c6	90	VAL	2.8
22	d0	62	VAL	2.8
82	p0	105	VAL	2.8
7	S5	92	ARG	2.8
21	C9	39	THR	2.8
44	L7	27	ALA	2.8
63	N7	80	LEU	2.8
66	o0	23	TYR	2.8
3	s1	216	LYS	2.8
5	S3	223	LYS	2.8
19	c7	4	VAL	2.8
28	D6	90	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
82	p0	40	GLU	2.8
9	s7	66	SER	2.8
62	n6	62	SER	2.8
18	C6	11	GLY	2.8
1	6	136	C	2.8
7	s5	129	PRO	2.8
14	C2	50	LYS	2.8
17	C5	130	ARG	2.8
30	d8	7	VAL	2.8
31	d9	6	VAL	2.8
33	E1	96	LYS	2.8
6	S4	67	GLN	2.7
7	s5	161	ASP	2.8
34	sR	147	HIS	2.8
22	d0	79	TRP	2.7
1	6	1605	G	2.7
2	S0	110	TYR	2.7
13	C1	148	LYS	2.7
18	c6	15	SER	2.7
62	N6	99	LEU	2.7
18	C6	46	PHE	2.7
18	c6	122	ARG	2.7
2	s0	97	PRO	2.7
21	C9	88	VAL	2.7
6	S4	8	HIS	2.7
10	s8	36	THR	2.7
29	D7	52	THR	2.7
35	sM	24	GLU	2.7
62	n6	120	GLN	2.7
78	Q2	105	GLN	2.7
3	s1	103	MET	2.7
3	S1	26	ARG	2.7
6	s4	260	GLY	2.7
34	sR	178	VAL	2.7
36	5	2574	G	2.7
42	l5	295	GLY	2.7
19	C7	79	GLU	2.7
20	C8	55	HIS	2.7
21	C9	135	ILE	2.7
19	C7	82	ASP	2.7
14	C2	135	MET	2.7
19	C7	60	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
45	l8	238	LEU	2.7
11	S9	178	ALA	2.7
17	C5	129	GLY	2.7
21	C9	6	VAL	2.7
64	N8	149	ALA	2.7
11	s9	156	ILE	2.7
23	D1	34	ILE	2.7
18	C6	126	PRO	2.7
10	S8	199	LYS	2.7
22	d0	101	LYS	2.7
2	S0	18	LEU	2.7
5	S3	21	LEU	2.7
10	s8	143	TRP	2.7
14	C2	137	MET	2.7
14	c2	52	LEU	2.7
20	c8	73	MET	2.7
11	s9	4	ALA	2.7
51	m5	58	GLY	2.7
26	d4	24	VAL	2.7
82	p0	49	ALA	2.7
6	S4	11	ARG	2.7
21	c9	90	PRO	2.7
82	p0	48	ARG	2.7
9	S7	123	ASP	2.7
14	C2	23	THR	2.7
80	e0	56	MET	2.7
1	6	470	A	2.7
6	S4	260	GLY	2.7
7	s5	152	GLY	2.7
34	SR	253	ALA	2.7
36	1	1576	G	2.7
48	m1	100	GLY	2.7
48	M1	138	VAL	2.7
63	n7	14	VAL	2.7
2	S0	185	ARG	2.7
14	c2	68	GLU	2.7
15	C3	9	LYS	2.7
18	c6	36	ILE	2.7
34	sR	67	ILE	2.7
2	S0	199	PRO	2.7
34	sR	89	LEU	2.7
42	L5	92	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
26	d4	133	ASN	2.7
63	N7	131	PHE	2.7
26	d4	35	VAL	2.7
61	N5	122	ALA	2.7
7	S5	68	ILE	2.7
57	n1	76	ILE	2.7
1	6	1199	G	2.7
2	s0	83	GLN	2.7
3	S1	47	LEU	2.7
8	S6	179	VAL	2.7
22	D0	119	ALA	2.7
27	d5	102	THR	2.7
28	D6	35	ALA	2.7
48	M1	71	VAL	2.7
56	N0	96	ASP	2.7
45	L8	202	GLU	2.7
62	N6	88	GLU	2.7
11	S9	86	LEU	2.7
19	c7	24	LEU	2.7
29	D7	21	LEU	2.7
78	Q2	102	GLN	2.7
1	2	1362	U	2.7
17	C5	10	ARG	2.7
19	C7	89	SER	2.7
70	O4	35	VAL	2.7
1	2	172	C	2.7
10	s8	48	THR	2.7
63	N7	30	ASP	2.7
2	s0	146	LEU	2.7
18	C6	117	LEU	2.7
20	C8	3	LEU	2.7
2	s0	152	PRO	2.7
3	S1	226	GLY	2.7
17	c5	83	MET	2.7
20	C8	73	MET	2.7
56	N0	95	ARG	2.7
33	E1	95	HIS	2.7
48	M1	97	SER	2.7
63	n7	122	HIS	2.7
1	2	770	A	2.7
9	S7	48	GLU	2.7
70	O4	72	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
82	p0	80	VAL	2.7
1	2	231	U	2.7
2	S0	157	ASP	2.7
18	c6	49	TYR	2.7
36	5	1570	U	2.7
48	M1	106	ILE	2.7
58	N2	108	TYR	2.7
27	d5	75	LEU	2.7
48	M1	155	THR	2.7
5	s3	8	LYS	2.7
8	s6	215	ARG	2.7
18	C6	45	ARG	2.7
11	S9	123	HIS	2.7
62	n6	90	VAL	2.7
29	D7	50	ALA	2.7
30	d8	59	SER	2.7
43	l6	3	ALA	2.7
63	n7	132	SER	2.7
10	s8	67	TRP	2.7
5	S3	187	LYS	2.7
7	S5	165	LEU	2.7
11	S9	7	THR	2.7
38	8	80	A	2.7
42	L5	154	THR	2.7
2	s0	15	GLN	2.7
36	1	1581	C	2.7
3	S1	215	VAL	2.7
4	S2	63	VAL	2.7
36	5	3276	G	2.7
28	D6	31	PRO	2.7
5	s3	151	LYS	2.6
8	S6	82	SER	2.6
27	d5	47	TYR	2.6
57	N1	28	SER	2.6
60	N4	78	ALA	2.7
10	S8	96	LEU	2.6
60	n4	72	SER	2.6
74	O8	51	LEU	2.6
2	S0	164	ASN	2.6
1	6	494	U	2.6
65	n9	34	GLY	2.6
6	S4	71	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
20	C8	48	LYS	2.6
34	sR	132	LYS	2.6
33	E1	110	ALA	2.6
67	O1	53	PRO	2.6
34	sR	141	LEU	2.6
35	sM	55	SER	2.6
36	1	1236	G	2.6
34	SR	61	PHE	2.6
49	m3	129	ASN	2.6
1	2	504	U	2.6
10	S8	103	GLN	2.6
63	n7	113	VAL	2.6
82	p0	29	GLY	2.6
12	C0	6	GLU	2.6
3	s1	60	ALA	2.6
10	s8	58	LEU	2.6
20	C8	42	TYR	2.6
4	S2	84	LYS	2.6
11	s9	138	LYS	2.6
21	C9	95	ASP	2.6
34	sR	319	ASN	2.6
36	1	1577	G	2.6
21	C9	57	ARG	2.6
7	s5	172	ILE	2.6
22	d0	65	ILE	2.6
22	d0	103	ILE	2.6
36	5	1353	U	2.6
12	c0	76	LEU	2.6
21	c9	80	TYR	2.6
63	N7	46	ILE	2.6
66	o0	68	TYR	2.6
36	1	2207	A	2.6
34	sR	228	LYS	2.6
58	n2	92	TRP	2.6
21	C9	72	GLY	2.6
61	N5	22	LYS	2.6
46	L9	143	GLU	2.6
2	S0	201	LEU	2.6
2	s0	80	THR	2.6
2	s0	176	LEU	2.6
42	L5	56	THR	2.6
34	sR	176	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	2	168	A	2.6
7	s5	151	GLY	2.6
28	d6	45	VAL	2.6
67	O1	93	VAL	2.6
62	N6	98	ASN	2.6
8	S6	180	THR	2.6
11	S9	95	TYR	2.6
13	C1	155	LYS	2.6
58	n2	14	THR	2.6
1	2	240	U	2.6
7	S5	69	PHE	2.6
65	n9	22	LYS	2.6
8	s6	160	ARG	2.6
51	m5	147	ARG	2.6
60	n4	71	ARG	2.6
23	d1	43	GLY	2.6
48	m1	38	GLU	2.6
82	p0	101	VAL	2.6
13	C1	2	SER	2.6
43	l6	2	SER	2.6
27	d5	52	LYS	2.6
61	n5	113	LEU	2.6
21	C9	43	ASN	2.6
28	D6	8	ASN	2.6
63	n7	66	THR	2.6
63	n7	77	TYR	2.6
82	p0	280	ALA	2.6
1	2	494	U	2.6
21	C9	37	VAL	2.6
21	c9	42	GLY	2.6
47	m0	204	GLY	2.6
20	C8	108	LYS	2.6
24	D2	65	LEU	2.6
29	D7	62	ILE	2.6
82	p0	14	LYS	2.6
11	S9	146	PHE	2.6
28	D6	33	ASP	2.6
34	sR	90	ARG	2.6
1	2	706	A	2.6
57	n1	86	GLU	2.6
61	n5	31	THR	2.6
1	2	768	C	2.6

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Mol	Chain	Res	Type	RSRZ
8	S6	153	VAL	2.6
57	N1	25	VAL	2.6
82	p0	33	VAL	2.6
10	S8	119	GLN	2.6
15	C3	55	ARG	2.6
49	m3	182	ILE	2.6
56	n0	129	ILE	2.6
63	n7	65	ARG	2.6
7	S5	132	VAL	2.6
11	S9	130	THR	2.6
14	C2	67	THR	2.6
19	c7	8	THR	2.6
20	C8	133	VAL	2.6
1	2	713	A	2.6
1	2	1583	A	2.6
7	s5	80	LYS	2.6
57	N1	29	THR	2.6
1	2	910	C	2.6
34	sR	7	LEU	2.6
48	M1	120	ILE	2.6
16	C4	27	PHE	2.6
11	S9	121	SER	2.6
42	l5	220	SER	2.6
2	S0	44	GLY	2.6
5	s3	200	LYS	2.6
26	D4	25	VAL	2.6
33	E1	82	LYS	2.6
48	M1	149	GLY	2.6
22	D0	96	PRO	2.6
56	n0	74	ASN	2.6
57	N1	89	LEU	2.6
5	s3	50	ILE	2.6
21	C9	124	ILE	2.6
62	n6	45	ILE	2.6
34	SR	186	PHE	2.6
1	6	1704	U	2.6
3	S1	139	ALA	2.6
10	s8	34	ALA	2.6
9	S7	115	SER	2.6
14	c2	117	GLY	2.6
55	M9	72	GLU	2.6
2	S0	101	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
29	D7	46	VAL	2.6
48	M1	18	VAL	2.6
3	S1	95	ASN	2.6
10	S8	165	LEU	2.6
19	C7	16	LEU	2.6
34	sR	81	LEU	2.6
2	S0	155	PHE	2.5
6	S4	55	ALA	2.5
10	S8	143	TRP	2.5
33	E1	105	TYR	2.5
36	1	1805	C	2.5
58	n2	66	VAL	2.5
61	n5	114	VAL	2.5
82	p0	30	VAL	2.5
2	s0	87	LEU	2.5
11	s9	36	LEU	2.5
19	c7	35	CYS	2.5
22	d0	77	LYS	2.5
14	C2	51	ALA	2.5
22	d0	94	GLU	2.5
51	m5	39	ALA	2.5
63	n7	106	GLN	2.5
10	S8	177	GLY	2.5
16	c4	35	GLY	2.5
82	p0	47	GLY	2.5
2	S0	9	LEU	2.5
14	c2	119	SER	2.5
40	L3	387	LEU	2.5
2	S0	102	PHE	2.5
8	S6	95	LYS	2.5
9	S7	113	PRO	2.5
36	1	544	C	2.5
4	s2	201	ASN	2.5
17	c5	119	PHE	2.5
43	l6	128	LYS	2.5
48	M1	85	LYS	2.5
63	N7	72	ILE	2.5
82	p0	81	LYS	2.5
3	S1	60	ALA	2.5
15	C3	61	THR	2.5
20	C8	126	ARG	2.5
19	c7	14	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
24	D2	71	LYS	2.5
3	S1	140	ILE	2.5
36	1	1763	U	2.5
42	L5	64	ILE	2.5
3	S1	182	ALA	2.5
22	d0	35	GLU	2.5
26	D4	34	ASN	2.5
45	L8	240	ASN	2.5
7	S5	94	THR	2.5
1	6	1584	G	2.5
1	6	1601	G	2.5
8	S6	99	GLY	2.5
34	sR	294	TRP	2.5
63	N7	12	VAL	2.5
11	S9	30	LEU	2.5
22	d0	63	LEU	2.5
42	L5	131	LEU	2.5
45	L8	93	LEU	2.5
3	S1	223	PHE	2.5
15	c3	14	SER	2.5
18	C6	141	SER	2.5
19	C7	21	TYR	2.5
31	d9	23	VAL	2.5
36	5	2444	C	2.5
36	5	2572	C	2.5
42	L5	52	VAL	2.5
67	O1	15	ASN	2.5
82	p0	11	TYR	2.5
10	s8	60	ILE	2.5
51	m5	61	ILE	2.5
12	c0	48	SER	2.5
14	C2	48	SER	2.5
11	S9	39	LYS	2.5
6	S4	259	GLN	2.5
21	c9	91	TYR	2.5
33	E1	129	GLY	2.5
35	sM	88	LYS	2.5
62	N6	87	LYS	2.5
66	O0	59	TYR	2.5
24	D2	69	LEU	2.5
1	2	541	A	2.5
63	n7	46	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
67	O1	36	ILE	2.5
41	l4	186	LYS	2.5
1	6	142	G	2.5
11	S9	8	TYR	2.5
11	S9	163	PRO	2.5
18	c6	75	VAL	2.5
29	D7	31	TYR	2.5
1	2	74	U	2.5
5	s3	218	LEU	2.5
16	C4	41	ARG	2.5
42	L5	54	ARG	2.5
49	M3	172	LEU	2.5
52	M6	52	LEU	2.5
14	c2	125	ASN	2.5
2	S0	147	THR	2.5
19	c7	38	ILE	2.5
34	sR	135	THR	2.5
42	l5	219	PHE	2.5
42	l5	41	LYS	2.5
46	l9	1	MET	2.5
1	6	1606	C	2.5
36	5	1761	C	2.5
48	M1	81	GLU	2.5
6	S4	15	PRO	2.5
14	c2	27	ALA	2.5
21	C9	8	ASP	2.5
23	D1	87	ARG	2.5
48	M1	67	VAL	2.5
49	M3	87	ALA	2.5
51	m5	64	VAL	2.5
9	S7	111	LYS	2.5
9	S7	151	LYS	2.5
22	d0	121	ASN	2.5
29	D7	45	THR	2.5
32	E0	28	LYS	2.5
63	n7	61	LYS	2.5
82	p0	100	ILE	2.5
5	s3	3	ALA	2.5
14	C2	42	ALA	2.5
20	C8	30	TYR	2.5
20	C8	45	LEU	2.5
42	l5	211	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
46	L9	85	GLY	2.5
1	6	1583	A	2.5
2	s0	126	PRO	2.5
65	n9	24	PRO	2.5
45	L8	255	SER	2.5
54	M8	167	SER	2.5
70	O4	21	LYS	2.5
5	S3	217	ILE	2.5
15	C3	66	ILE	2.5
57	N1	96	ILE	2.5
36	5	250	U	2.5
53	M7	167	ARG	2.5
1	2	1540	G	2.5
6	s4	101	LEU	2.5
7	S5	101	GLY	2.5
42	L5	75	LEU	2.5
60	n4	131	ALA	2.5
11	S9	169	PRO	2.5
14	C2	81	ASP	2.5
15	C3	27	LYS	2.5
50	M4	43	LYS	2.5
51	m5	130	PHE	2.5
7	S5	199	ILE	2.5
21	C9	40	SER	2.5
36	1	1761	C	2.5
3	s1	165	ARG	2.5
19	C7	67	ARG	2.5
34	sR	92	TRP	2.5
48	M1	144	CYS	2.5
55	M9	23	TRP	2.5
1	2	701	U	2.5
9	S7	119	THR	2.5
34	sR	4	ASN	2.5
2	S0	175	TYR	2.5
14	C2	62	LEU	2.5
22	D0	53	LYS	2.5
68	o2	2	ALA	2.5
2	s0	115	PHE	2.5
3	s1	30	PHE	2.5
8	S6	89	ASP	2.5
9	S7	11	GLN	2.5
82	p0	195	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
13	C1	4	GLU	2.5
16	C4	83	ILE	2.5
36	5	442	G	2.5
58	n2	104	ARG	2.5
67	O1	14	ILE	2.5
1	6	505	A	2.4
25	D3	28	ASN	2.4
29	D7	20	LYS	2.4
8	S6	84	TYR	2.4
11	S9	12	TYR	2.4
48	M1	44	THR	2.4
6	S4	49	ARG	2.4
34	sR	160	GLU	2.4
48	M1	126	ASP	2.4
54	m8	93	ILE	2.4
68	o2	95	GLU	2.4
7	s5	72	HIS	2.4
42	L5	203	HIS	2.4
32	E0	31	LYS	2.4
33	E1	113	LYS	2.4
29	d7	39	GLY	2.4
36	1	1573	G	2.4
61	n5	76	VAL	2.4
6	S4	28	ALA	2.4
1	2	171	A	2.4
1	2	740	A	2.4
13	C1	153	PHE	2.4
27	d5	57	TYR	2.4
55	M9	78	TYR	2.4
36	1	198	A	2.4
42	L5	158	ARG	2.4
49	m3	183	ARG	2.4
58	N2	28	PHE	2.4
26	d4	106	GLN	2.4
27	d5	86	GLU	2.4
2	s0	46	HIS	2.4
21	C9	45	MET	2.4
26	D4	67	GLY	2.4
27	D5	62	VAL	2.4
31	d9	27	HIS	2.4
35	SM	113	ASP	2.4
55	M9	52	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
60	n4	129	LYS	2.4
62	n6	114	ASP	2.4
33	e1	129	GLY	2.4
42	L5	161	GLY	2.4
51	M5	155	VAL	2.4
63	N7	42	LEU	2.4
2	S0	203	PHE	2.4
5	s3	193	ALA	2.4
11	S9	158	PHE	2.4
48	M1	163	PHE	2.4
82	p0	197	PHE	2.4
1	2	655	G	2.4
3	s1	37	THR	2.4
1	2	1714	A	2.4
6	S4	7	LYS	2.4
26	D4	13	ILE	2.4
36	1	252	U	2.4
63	n7	50	PRO	2.4
2	S0	113	ARG	2.4
8	S6	87	ARG	2.4
14	c2	98	GLY	2.4
19	c7	26	LEU	2.4
23	D1	39	VAL	2.4
28	D6	16	GLY	2.4
34	sR	191	ASP	2.4
20	c8	126	ARG	2.4
20	c8	129	TRP	2.4
18	c6	138	PHE	2.4
55	M9	178	ALA	2.4
24	D2	39	GLN	2.4
34	SR	185	GLN	2.4
54	M8	93	ILE	2.4
5	s3	138	VAL	2.4
14	c2	88	LEU	2.4
22	D0	62	VAL	2.4
24	D2	85	ASP	2.4
29	d7	49	HIS	2.4
36	1	2672	G	2.4
42	L5	149	GLY	2.4
58	N2	89	LEU	2.4
1	2	957	G	2.4
1	6	673	A	2.4

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Mol	Chain	Res	Type	RSRZ
63	n7	48	ARG	2.4
30	D8	45	LYS	2.4
4	S2	55	GLU	2.4
11	S9	156	ILE	2.4
17	c5	98	ASN	2.4
6	S4	102	VAL	2.4
34	sR	102	ARG	2.4
8	S6	66	GLY	2.4
63	N7	53	VAL	2.4
65	N9	27	TYR	2.4
65	n9	25	LYS	2.4
1	2	483	A	2.4
1	6	506	A	2.4
18	C6	16	ALA	2.4
47	m0	221	ALA	2.4
19	C7	77	GLU	2.4
34	SR	3	SER	2.4
34	sR	124	SER	2.4
4	s2	95	ARG	2.4
62	N6	81	GLN	2.4
3	s1	98	THR	2.4
21	C9	120	GLY	2.4
22	d0	88	LYS	2.4
1	2	192	U	2.4
4	S2	144	TRP	2.4
12	C0	64	TYR	2.4
39	L2	176	ASP	2.4
63	N7	29	HIS	2.4
6	s4	64	ILE	2.4
8	S6	88	ARG	2.4
11	S9	132	ARG	2.4
16	C4	34	SER	2.4
19	c7	78	ARG	2.4
1	6	138	A	2.4
3	S1	207	LEU	2.4
3	S1	231	LEU	2.4
4	s2	94	GLN	2.4
5	s3	37	VAL	2.4
19	C7	68	GLY	2.4
33	e1	114	VAL	2.4
36	1	1952	G	2.4
48	M1	27	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
9	S7	133	THR	2.4
34	sR	203	THR	2.4
45	l8	34	PHE	2.4
8	s6	89	ASP	2.4
14	C2	93	ASP	2.4
51	m5	111	ALA	2.4
24	d2	27	ILE	2.4
27	d5	78	ILE	2.4
36	5	1265	U	2.4
1	2	724	C	2.4
3	s1	231	LEU	2.4
14	c2	115	VAL	2.4
18	C6	75	VAL	2.4
19	C7	7	LYS	2.4
34	SR	262	VAL	2.4
51	m5	60	VAL	2.4
62	n6	118	LEU	2.4
18	c6	130	GLY	2.4
1	6	39	A	2.4
29	D7	66	PRO	2.4
10	S8	139	ALA	2.4
19	c7	18	GLU	2.4
49	M3	92	THR	2.4
20	C8	23	ASP	2.4
36	5	2573	G	2.4
27	D5	65	LEU	2.4
34	SR	32	LEU	2.4
2	S0	30	GLN	2.4
42	L5	63	GLN	2.4
48	M1	48	SER	2.4
49	m3	130	GLY	2.4
36	1	1275	C	2.4
76	Q0	106	ARG	2.4
12	c0	74	GLU	2.4
71	O5	64	GLU	2.4
1	6	1227	A	2.4
11	s9	140	ILE	2.4
17	c5	128	HIS	2.4
34	SR	81	LEU	2.4
61	n5	82	LEU	2.4
17	C5	105	VAL	2.4
18	c6	39	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	6	1687	U	2.4
18	c6	73	GLY	2.4
56	n0	138	GLN	2.4
7	S5	100	ASN	2.4
11	S9	129	ILE	2.4
12	c0	43	ILE	2.4
35	sM	60	ALA	2.4
45	l8	46	LEU	2.4
80	e0	49	LEU	2.4
5	S3	224	ASP	2.3
14	c2	46	ARG	2.3
15	C3	25	TRP	2.3
15	c3	8	GLY	2.3
34	SR	192	PHE	2.3
35	sM	69	ARG	2.3
55	M9	74	ARG	2.3
21	c9	23	GLN	2.3
33	e1	104	SER	2.3
48	M1	142	LYS	2.3
58	n2	97	SER	2.3
63	N7	21	LYS	2.3
18	C6	124	PRO	2.3
35	SM	39	PRO	2.3
36	1	3286	G	2.3
36	5	1354	G	2.3
45	L8	130	TYR	2.3
48	M1	118	PRO	2.3
11	S9	105	LEU	2.3
34	sR	71	CYS	2.3
1	6	1705	C	2.3
8	s6	78	THR	2.3
8	s6	195	VAL	2.3
14	c2	38	HIS	2.3
18	C6	22	VAL	2.3
20	C8	70	VAL	2.3
32	E0	48	THR	2.3
34	SR	99	THR	2.3
70	O4	65	VAL	2.3
7	s5	106	LYS	2.3
20	C8	112	ASP	2.3
58	n2	13	LYS	2.3
34	SR	43	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
36	5	252	U	2.3
6	S4	65	LEU	2.3
34	sR	23	LEU	2.3
48	M1	65	ILE	2.3
8	s6	88	ARG	2.3
8	S6	144	PHE	2.3
17	c5	86	VAL	2.3
10	S8	53	LYS	2.3
16	c4	91	THR	2.3
18	c6	14	LYS	2.3
18	c6	70	THR	2.3
19	C7	59	LYS	2.3
20	c8	137	HIS	2.3
29	D7	35	VAL	2.3
35	sM	29	ASN	2.3
82	p0	83	ASN	2.3
82	p0	84	VAL	2.3
61	n5	92	LYS	2.3
70	O4	25	THR	2.3
20	c8	53	ASP	2.3
24	D2	18	GLU	2.3
42	L5	209	GLU	2.3
42	l5	213	ASP	2.3
2	S0	77	SER	2.3
3	s1	171	ILE	2.3
14	C2	104	ALA	2.3
27	D5	99	ALA	2.3
42	l5	290	ILE	2.3
66	O0	35	ARG	2.3
1	6	1473	U	2.3
8	s6	144	PHE	2.3
9	S7	72	LYS	2.3
30	d8	44	VAL	2.3
49	M3	130	GLY	2.3
4	S2	232	GLU	2.3
61	n5	71	THR	2.3
1	2	279	G	2.3
22	d0	57	ARG	2.3
14	c2	72	ILE	2.3
31	d9	34	TYR	2.3
36	1	1239	C	2.3
42	l5	12	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
51	m5	148	TYR	2.3
27	d5	97	LYS	2.3
29	D7	72	LYS	2.3
71	O5	120	ALA	2.3
2	s0	114	SER	2.3
5	s3	137	VAL	2.3
10	S8	160	PHE	2.3
42	L5	144	VAL	2.3
74	o8	48	SER	2.3
24	D2	73	GLY	2.3
14	C2	80	ASN	2.3
21	C9	49	ASP	2.3
66	o0	10	ILE	2.3
1	2	1096	C	2.3
1	2	1683	C	2.3
2	s0	73	VAL	2.3
1	2	1584	G	2.3
9	s7	63	PRO	2.3
48	m1	130	VAL	2.3
67	o1	109	VAL	2.3
18	C6	76	SER	2.3
27	D5	87	GLY	2.3
65	n9	31	SER	2.3
82	p0	35	SER	2.3
36	5	3319	U	2.3
8	S6	223	LYS	2.3
10	S8	67	TRP	2.3
10	s8	200	LYS	2.3
36	1	550	A	2.3
7	S5	78	ALA	2.3
34	sR	212	ALA	2.3
49	m3	93	ILE	2.3
79	q3	92	ALA	2.3
63	n7	24	VAL	2.3
82	p0	66	PHE	2.3
10	S8	73	SER	2.3
28	D6	89	ARG	2.3
35	SM	38	PRO	2.3
5	S3	185	LYS	2.3
48	M1	9	MET	2.3
63	n7	116	LYS	2.3
74	O8	21	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
11	S9	110	GLN	2.3
11	s9	110	GLN	2.3
36	1	979	U	2.3
36	1	2538	U	2.3
48	m1	120	ILE	2.3
63	n7	5	LEU	2.3
1	2	140	A	2.3
2	S0	206	ASP	2.3
4	s2	118	ALA	2.3
7	s5	36	ALA	2.3
20	C8	31	ALA	2.3
34	sR	262	VAL	2.3
61	n5	110	VAL	2.3
47	m0	211	ARG	2.3
19	C7	22	PRO	2.3
63	N7	90	GLU	2.3
10	S8	176	SER	2.3
76	Q0	128	LYS	2.3
1	6	682	C	2.3
8	S6	76	LEU	2.3
1	2	144	U	2.3
18	c6	85	ILE	2.3
19	c7	83	GLN	2.3
49	m3	137	GLN	2.3
56	N0	144	LEU	2.3
22	D0	65	ILE	2.3
36	5	1267	U	2.3
63	n7	25	ILE	2.3
21	c9	101	ASN	2.3
48	M1	69	VAL	2.3
57	N1	77	ASN	2.3
70	O4	93	PHE	2.3
1	2	175	G	2.3
1	2	235	G	2.3
3	s1	104	ASP	2.3
29	D7	22	LYS	2.3
36	1	1222	G	2.3
36	1	1949	G	2.3
82	p0	184	GLY	2.3
1	6	1693	A	2.3
1	6	1719	A	2.3
21	C9	67	MET	2.3

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Mol	Chain	Res	Type	RSRZ
2	s0	151	SER	2.3
42	l5	10	SER	2.3
45	l8	152	LEU	2.3
67	O1	97	LEU	2.3
4	S2	87	GLN	2.3
4	s2	91	ARG	2.3
17	C5	127	ARG	2.3
19	C7	38	ILE	2.3
60	n4	134	GLN	2.3
78	Q2	99	GLN	2.3
33	e1	102	VAL	2.3
35	SM	12	VAL	2.3
1	2	710	U	2.3
11	S9	38	ASN	2.3
21	C9	82	GLY	2.3
21	C9	87	GLY	2.3
24	D2	21	GLY	2.3
36	1	2685	C	2.3
48	M1	145	LYS	2.3
48	M1	25	GLU	2.3
48	m1	70	THR	2.3
73	o7	23	GLY	2.3
18	c6	120	ASP	2.3
22	D0	46	GLU	2.3
62	n6	38	GLU	2.3
34	sR	145	LEU	2.3
10	s8	38	ILE	2.3
21	C9	94	ILE	2.3
7	S5	82	PHE	2.3
8	S6	53	SER	2.3
31	D9	20	GLN	2.3
59	n3	2	SER	2.3
18	c6	74	HIS	2.3
34	sR	137	LYS	2.3
82	p0	107	ALA	2.3
4	s2	105	GLY	2.3
7	s5	144	GLU	2.3
19	c7	64	GLY	2.3
20	c8	124	GLY	2.3
48	m1	135	GLY	2.3
71	O5	11	THR	2.3
15	C3	4	MET	2.3

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Mol	Chain	Res	Type	RSRZ
28	D6	92	ARG	2.3
29	D7	17	ARG	2.3
63	N7	135	ARG	2.3
4	S2	46	LYS	2.3
7	s5	203	LYS	2.3
17	C5	100	LYS	2.3
42	L5	65	ILE	2.3
1	2	225	A	2.3
1	2	1346	A	2.3
5	s3	160	SER	2.3
18	C6	112	TYR	2.3
24	D2	62	VAL	2.3
62	n6	110	HIS	2.3
35	SM	58	GLU	2.2
1	2	912	U	2.2
3	s1	47	LEU	2.2
21	C9	134	ARG	2.2
34	sR	273	ASP	2.2
34	sR	316	MET	2.2
36	5	1630	U	2.2
36	5	3277	U	2.2
60	N4	77	LYS	2.2
3	s1	92	GLN	2.2
7	s5	134	VAL	2.2
11	S9	27	GLU	2.2
14	C2	64	SER	2.2
56	n0	102	ALA	2.2
59	N3	2	SER	2.2
61	N5	128	ALA	2.2
1	2	492	A	2.2
7	S5	112	ARG	2.2
9	S7	107	ARG	2.2
10	s8	42	ARG	2.2
82	p0	42	ARG	2.2
3	s1	218	LEU	2.2
63	n7	73	LYS	2.2
19	C7	55	THR	2.2
20	C8	20	THR	2.2
24	D2	83	ILE	2.2
26	D4	7	ILE	2.2
30	d8	47	PRO	2.2
31	D9	52	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
33	E1	115	THR	2.2
15	C3	23	PRO	2.2
16	c4	79	VAL	2.2
34	SR	20	VAL	2.2
34	sR	240	VAL	2.2
35	SM	52	PRO	2.2
62	N6	95	VAL	2.2
1	2	1338	C	2.2
3	s1	74	GLN	2.2
8	s6	150	GLU	2.2
14	C2	101	ALA	2.2
34	sR	257	ALA	2.2
42	L5	87	GLY	2.2
45	l8	104	GLU	2.2
66	o0	8	GLU	2.2
11	s9	132	ARG	2.2
27	D5	61	SER	2.2
27	d5	95	HIS	2.2
3	s1	86	LEU	2.2
3	s1	110	LEU	2.2
14	C2	95	LYS	2.2
45	L8	92	LYS	2.2
48	M1	115	LYS	2.2
11	s9	169	PRO	2.2
14	c2	53	THR	2.2
15	C3	26	PHE	2.2
42	L5	55	PHE	2.2
55	M9	188	ASP	2.2
15	C3	33	VAL	2.2
1	2	742	U	2.2
1	2	810	G	2.2
1	6	1412	G	2.2
6	S4	256	ARG	2.2
18	c6	71	GLY	2.2
21	c9	98	GLY	2.2
29	D7	27	GLY	2.2
35	SM	141	ALA	2.2
51	m5	63	ARG	2.2
62	n6	43	TYR	2.2
78	q2	105	GLN	2.2
11	S9	16	LYS	2.2
12	C0	24	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
34	SR	117	LYS	2.2
24	D2	11	LEU	2.2
26	D4	2	SER	2.2
33	E1	104	SER	2.2
34	sR	85	TRP	2.2
62	n6	126	LEU	2.2
66	o0	9	SER	2.2
78	Q2	104	LEU	2.2
5	s3	158	ILE	2.2
12	c0	55	VAL	2.2
17	c5	85	ILE	2.2
2	S0	112	THR	2.2
2	S0	166	GLY	2.2
2	s0	49	ASN	2.2
31	D9	6	VAL	2.2
63	N7	113	VAL	2.2
2	s0	165	ARG	2.2
3	s1	190	PRO	2.2
22	d0	89	ARG	2.2
30	d8	65	ARG	2.2
36	1	551	A	2.2
36	5	1103	A	2.2
42	l5	294	ALA	2.2
51	m5	53	TYR	2.2
82	p0	37	GLN	2.2
5	S3	218	LEU	2.2
67	O1	20	LEU	2.2
2	S0	144	ILE	2.2
5	s3	150	MET	2.2
36	5	3290	G	2.2
34	sR	136	ILE	2.2
36	1	1238	C	2.2
55	m9	51	VAL	2.2
2	S0	134	LYS	2.2
8	S6	93	LYS	2.2
9	S7	101	LYS	2.2
10	S8	142	LYS	2.2
18	C6	47	LYS	2.2
33	e1	106	TYR	2.2
51	m5	145	ASP	2.2
44	L7	23	ALA	2.2
57	n1	73	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
63	N7	133	LYS	2.2
8	s6	80	ASN	2.2
11	s9	144	PRO	2.2
20	C8	138	THR	2.2
48	M1	43	GLN	2.2
11	S9	99	LEU	2.2
36	1	1241	U	2.2
7	S5	24	VAL	2.2
17	c5	94	VAL	2.2
24	d2	22	LYS	2.2
45	l8	116	VAL	2.2
49	M3	46	ILE	2.2
51	m5	118	SER	2.2
70	O4	55	SER	2.2
2	S0	105	GLY	2.2
10	S8	80	GLY	2.2
10	s8	80	GLY	2.2
36	5	3278	C	2.2
48	M1	15	GLU	2.2
49	m3	79	GLU	2.2
59	N3	3	GLY	2.2
82	p0	17	GLU	2.2
7	S5	129	PRO	2.2
10	s8	33	PRO	2.2
17	C5	17	TYR	2.2
18	c6	51	PRO	2.2
20	c8	23	ASP	2.2
21	c9	47	PRO	2.2
28	D6	65	PRO	2.2
42	L5	147	ASP	2.2
11	S9	24	LEU	2.2
21	c9	22	LEU	2.2
75	O9	32	ASN	2.2
1	6	240	U	2.2
42	l5	203	HIS	2.2
63	n7	131	PHE	2.2
4	S2	178	ILE	2.2
3	s1	169	SER	2.2
18	C6	69	VAL	2.2
36	1	2100	A	2.2
19	C7	76	GLU	2.2
45	L8	253	SER	2.2

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Mol	Chain	Res	Type	RSRZ
21	C9	62	ALA	2.2
21	c9	66	TYR	2.2
55	m9	189	ALA	2.2
63	N7	18	TYR	2.2
36	5	1582	C	2.2
39	L2	142	ASP	2.2
67	O1	99	ALA	2.2
21	C9	76	LEU	2.2
49	m3	54	LEU	2.2
55	m9	184	LEU	2.2
1	6	942	G	2.2
34	sR	41	THR	2.2
42	L5	24	ARG	2.2
26	D4	60	PHE	2.2
42	l5	16	PHE	2.2
7	s5	90	ILE	2.2
8	s6	91	GLU	2.2
13	C1	25	VAL	2.2
16	C4	80	HIS	2.2
24	D2	53	ILE	2.2
18	c6	40	GLU	2.2
27	d5	54	VAL	2.2
34	SR	189	GLU	2.2
36	5	2505	U	2.2
42	L5	216	GLU	2.2
63	N7	24	VAL	2.2
67	o1	83	GLU	2.2
5	S3	205	ALA	2.2
7	s5	159	ALA	2.2
3	S1	220	GLN	2.2
11	s9	109	LEU	2.2
18	C6	3	ALA	2.2
18	C6	54	LEU	2.2
21	c9	107	ALA	2.2
24	D2	13	ALA	2.2
48	M1	40	LEU	2.2
50	M4	60	LEU	2.2
55	M9	44	LEU	2.2
57	N1	85	LEU	2.2
67	O1	16	LEU	2.2
72	o6	69	ALA	2.2
5	s3	199	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
12	c0	25	LYS	2.2
16	C4	92	LYS	2.2
18	C6	87	LYS	2.2
20	C8	110	ARG	2.2
48	m1	16	LYS	2.2
82	p0	7	LYS	2.2
4	S2	66	PHE	2.2
2	s0	195	TRP	2.2
10	S8	46	VAL	2.2
11	S9	113	VAL	2.2
34	SR	211	ILE	2.2
36	1	548	G	2.2
1	2	64	U	2.2
2	S0	75	ALA	2.2
3	S1	227	ALA	2.2
6	S4	56	LEU	2.2
8	S6	100	ALA	2.2
8	s6	172	ALA	2.2
11	S9	118	LEU	2.2
12	c0	5	LYS	2.2
17	C5	115	TYR	2.2
20	C8	43	SER	2.2
24	D2	4	SER	2.2
28	D6	82	ARG	2.2
36	1	549	U	2.2
42	L5	83	LEU	2.2
52	m6	63	ALA	2.2
60	N4	94	ARG	2.2
61	n5	100	LYS	2.2
1	2	1526	A	2.2
4	s2	87	GLN	2.2
5	s3	211	PRO	2.2
22	d0	59	PRO	2.2
35	sM	39	PRO	2.2
2	s0	170	ILE	2.2
3	s1	134	VAL	2.2
3	s1	140	ILE	2.2
4	S2	86	VAL	2.2
21	C9	115	GLU	2.2
48	M1	95	ASN	2.2
58	n2	87	ASN	2.2
63	n7	74	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
67	o1	75	ILE	2.2
37	7	73	C	2.2
34	SR	183	LEU	2.2
65	N9	29	TYR	2.2
76	Q0	83	LYS	2.2
72	o6	51	SER	2.2
82	p0	106	ALA	2.2
26	D4	119	PHE	2.2
36	1	3352	U	2.2
2	s0	173	ILE	2.2
7	S5	168	VAL	2.2
11	s9	151	ASP	2.2
14	C2	82	PRO	2.2
42	l5	215	ASP	2.2
48	M1	45	PRO	2.2
35	sM	61	ILE	2.2
57	N1	75	ILE	2.2
76	q0	79	GLU	2.2
7	S5	169	ASN	2.2
17	C5	103	ASN	2.2
6	S4	18	TRP	2.1
8	S6	74	LYS	2.2
8	S6	187	LYS	2.2
18	c6	17	THR	2.2
18	c6	131	GLY	2.2
33	E1	92	LYS	2.2
34	sR	138	GLY	2.2
7	s5	194	LEU	2.1
7	s5	74	ALA	2.1
9	S7	142	TYR	2.1
46	L9	3	TYR	2.1
63	n7	80	LEU	2.1
26	d4	130	ALA	2.1
36	5	1562	C	2.1
48	M1	76	ALA	2.1
2	S0	107	PHE	2.1
36	1	1950	U	2.1
42	L5	17	GLN	2.1
67	o1	76	SER	2.1
1	2	260	U	2.1
3	S1	229	MET	2.1
6	s4	22	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
8	s6	187	LYS	2.1
11	S9	179	ARG	2.1
18	c6	55	VAL	2.1
28	D6	98	PRO	2.1
24	D2	57	ARG	2.1
29	d7	22	LYS	2.1
39	l2	143	GLU	2.1
57	N1	72	VAL	2.1
10	s8	177	GLY	2.1
70	O4	78	GLY	2.1
7	s5	44	ASN	2.1
7	s5	175	LEU	2.1
8	S6	178	LEU	2.1
11	S9	124	HIS	2.1
28	D6	67	THR	2.1
33	e1	148	TYR	2.1
34	sR	73	LEU	2.1
48	M1	91	LEU	2.1
48	M1	152	HIS	2.1
19	C7	126	ALA	2.1
34	SR	78	ALA	2.1
1	6	1703	C	2.1
6	s4	24	SER	2.1
10	S8	187	GLU	2.1
11	s9	152	SER	2.1
11	s9	174	ARG	2.1
14	c2	99	GLU	2.1
29	d7	38	PRO	2.1
30	d8	67	ARG	2.1
36	1	2572	C	2.1
55	m9	165	LYS	2.1
63	N7	25	ILE	2.1
70	O4	31	ARG	2.1
1	2	472	U	2.1
1	2	959	U	2.1
1	6	1398	U	2.1
36	5	2570	U	2.1
11	S9	80	LEU	2.1
7	S5	87	CYS	2.1
34	sR	25	THR	2.1
42	L5	93	THR	2.1
48	m1	139	THR	2.1

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Mol	Chain	Res	Type	RSRZ
50	M4	9	ALA	2.1
1	2	1689	A	2.1
1	6	754	A	2.1
36	1	2687	G	2.1
4	S2	45	VAL	2.1
19	c7	66	VAL	2.1
22	D0	83	GLU	2.1
48	M1	141	ARG	2.1
45	L8	67	ILE	2.1
17	c5	73	PRO	2.1
46	L9	137	SER	2.1
48	m1	41	SER	2.1
49	M3	133	PRO	2.1
50	M4	5	SER	2.1
67	O1	76	SER	2.1
73	o7	84	SER	2.1
1	6	794	U	2.1
6	S4	79	ASP	2.1
6	s4	12	LEU	2.1
31	D9	36	LEU	2.1
32	E0	39	LEU	2.1
36	5	1351	U	2.1
58	n2	89	LEU	2.1
67	O1	51	LEU	2.1
11	S9	56	ALA	2.1
12	c0	66	TYR	2.1
48	m1	147	THR	2.1
55	m9	42	ARG	2.1
62	n6	113	LYS	2.1
65	N9	23	LYS	2.1
74	O8	24	THR	2.1
82	p0	294	ALA	2.1
2	S0	47	VAL	2.1
20	c8	22	VAL	2.1
21	c9	51	GLU	2.1
22	d0	91	ILE	2.1
23	d1	39	VAL	2.1
57	N1	74	VAL	2.1
71	o5	104	GLN	2.1
82	p0	28	VAL	2.1
1	2	1048	G	2.1
1	6	34	G	2.1

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Mol	Chain	Res	Type	RSRZ
30	d8	24	GLY	2.1
36	5	1266	G	2.1
54	m8	154	GLY	2.1
1	2	1340	U	2.1
1	6	1413	U	2.1
4	s2	84	LYS	2.1
32	E0	33	ARG	2.1
35	SM	101	ASP	2.1
42	l5	234	ASP	2.1
36	1	1574	C	2.1
48	M1	143	ARG	2.1
3	S1	101	HIS	2.1
2	s0	86	VAL	2.1
6	s4	81	THR	2.1
20	C8	28	ILE	2.1
20	C8	46	VAL	2.1
48	M1	86	VAL	2.1
58	n2	17	VAL	2.1
48	M1	100	GLY	2.1
2	S0	88	LYS	2.1
8	s6	86	PRO	2.1
61	n5	24	LEU	2.1
10	S8	135	LYS	2.1
14	C2	134	SER	2.1
17	C5	51	SER	2.1
34	SR	102	ARG	2.1
62	n6	89	LYS	2.1
1	2	1371	A	2.1
2	S0	81	PHE	2.1
42	l5	214	ASP	2.1
48	M1	123	PHE	2.1
67	o1	10	ARG	2.1
18	C6	49	TYR	2.1
45	l8	114	ALA	2.1
65	n9	29	TYR	2.1
1	2	461	G	2.1
36	5	2575	G	2.1
1	2	1332	C	2.1
3	S1	150	VAL	2.1
9	S7	95	GLU	2.1
3	s1	189	ILE	2.1
10	S8	64	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
14	C2	91	VAL	2.1
28	D6	18	VAL	2.1
32	E0	47	VAL	2.1
70	o4	96	GLU	2.1
7	s5	93	LEU	2.1
11	s9	170	GLY	2.1
18	c6	139	GLN	2.1
42	L5	32	GLN	2.1
70	o4	54	ILE	2.1
22	d0	85	ARG	2.1
34	sR	117	LYS	2.1
60	n4	87	LEU	2.1
61	n5	25	LYS	2.1
62	n6	116	LYS	2.1
72	o6	13	LYS	2.1
9	S7	132	PRO	2.1
48	m1	45	PRO	2.1
3	s1	155	TYR	2.1
12	c0	54	TYR	2.1
21	C9	5	SER	2.1
24	D2	8	ALA	2.1
1	6	1526	A	2.1
5	s3	217	ILE	2.1
12	c0	11	ILE	2.1
18	c6	65	ILE	2.1
1	2	871	G	2.1
6	S4	12	LEU	2.1
6	S4	44	LEU	2.1
17	C5	70	ASN	2.1
26	d4	132	ARG	2.1
29	D7	67	THR	2.1
35	sM	33	LYS	2.1
45	l8	26	LEU	2.1
45	l8	137	ASN	2.1
57	n1	23	GLY	2.1
17	c5	87	PRO	2.1
35	sM	40	PRO	2.1
63	n7	130	PHE	2.1
12	c0	71	GLU	2.1
15	C3	24	ALA	2.1
14	C2	116	VAL	2.1
2	S0	46	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
3	s1	55	LYS	2.1
3	s1	91	VAL	2.1
10	S8	37	LYS	2.1
10	S8	72	ILE	2.1
22	d0	31	VAL	2.1
22	d0	56	VAL	2.1
10	s8	44	HIS	2.1
27	d5	82	HIS	2.1
45	l8	111	LYS	2.1
1	6	1370	U	2.1
11	S9	49	LEU	2.1
21	C9	28	LEU	2.1
21	C9	140	LEU	2.1
67	O1	10	ARG	2.1
62	n6	81	GLN	2.1
68	o2	4	LEU	2.1
17	C5	82	ASN	2.1
36	5	1273	A	2.1
46	L9	188	THR	2.1
52	M6	50	ASN	2.1
1	6	1445	G	2.1
5	s3	220	PRO	2.1
42	L5	31	TYR	2.1
43	l6	11	PRO	2.1
5	S3	215	GLU	2.1
3	S1	85	LYS	2.1
3	s1	130	SER	2.1
9	S7	97	ARG	2.1
11	s9	143	ILE	2.1
15	C3	3	ARG	2.1
62	N6	108	LYS	2.1
63	n7	133	LYS	2.1
27	d5	41	ILE	2.1
4	S2	41	LEU	2.1
7	S5	46	TRP	2.1
11	S9	97	LEU	2.1
12	C0	53	GLY	2.1
18	C6	44	LEU	2.1
20	C8	130	GLY	2.1
20	C8	25	ASN	2.1
28	d6	69	ASN	2.1
11	s9	153	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
2	S0	29	VAL	2.1
7	S5	133	VAL	2.1
8	s6	191	ARG	2.1
9	s7	104	ARG	2.1
34	sR	239	GLU	2.1
48	M1	63	GLU	2.1
16	C4	121	VAL	2.1
68	o2	93	ALA	2.1
14	c2	62	LEU	2.1
16	c4	105	LEU	2.1
35	sM	28	SER	2.1
28	D6	17	HIS	2.1
42	L5	234	ASP	2.1
63	n7	45	GLY	2.1
1	6	75	U	2.1
1	6	1059	U	2.1
7	S5	95	ASN	2.1
23	d1	42	GLU	2.1
28	D6	32	LYS	2.1
28	D6	73	TYR	2.1
35	sM	51	ARG	2.1
45	L8	33	ASN	2.1
48	M1	64	LYS	2.1
70	O4	99	LYS	2.1
10	S8	48	THR	2.1
14	c2	34	THR	2.1
16	c4	31	THR	2.1
22	d0	114	VAL	2.1
28	d6	63	ALA	2.1
36	1	2509	U	2.1
51	m5	43	THR	2.1
22	D0	71	PRO	2.1
1	2	1410	A	2.1
7	S5	113	ILE	2.1
6	S4	107	GLY	2.1
9	S7	93	LEU	2.1
12	C0	40	LEU	2.1
21	C9	79	LEU	2.1
1	6	1248	C	2.1
1	6	1481	C	2.1
6	s4	41	SER	2.1
36	1	1283	C	2.1

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Mol	Chain	Res	Type	RSRZ
45	L8	121	SER	2.1
42	L5	213	ASP	2.1
42	l5	137	ASP	2.1
45	l8	28	HIS	2.1
11	S9	126	ARG	2.0
51	m5	152	CYS	2.0
1	6	1607	G	2.0
1	6	1340	U	2.0
5	s3	206	VAL	2.0
7	s5	140	THR	2.0
12	C0	22	VAL	2.0
20	C8	102	ALA	2.0
20	c8	133	VAL	2.0
29	d7	54	VAL	2.0
33	E1	98	VAL	2.0
45	L8	210	ALA	2.0
2	s0	76	ILE	2.0
19	C7	73	LEU	2.0
19	c7	50	ILE	2.0
31	D9	38	ILE	2.0
36	1	250	U	2.0
38	8	158	U	2.0
51	m5	45	PRO	2.0
42	L5	201	GLY	2.0
51	m5	52	GLY	2.0
62	N6	30	LEU	2.0
1	2	474	A	2.0
10	S8	54	LYS	2.0
18	c6	26	LYS	2.0
2	s0	84	ARG	2.0
11	S9	131	GLN	2.0
17	C5	28	MET	2.0
33	e1	146	SER	2.0
48	M1	49	LYS	2.0
48	M1	151	SER	2.0
63	N7	64	LYS	2.0
82	p0	73	PHE	2.0
82	p0	75	LYS	2.0
2	S0	19	ALA	2.0
2	s0	20	ALA	2.0
8	S6	157	VAL	2.0
18	C6	86	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
28	D6	62	TYR	2.0
42	L5	78	ALA	2.0
42	l5	207	TYR	2.0
2	S0	82	GLY	2.0
2	S0	120	LEU	2.0
9	S7	99	LEU	2.0
16	c4	110	LEU	2.0
17	c5	50	THR	2.0
34	SR	201	THR	2.0
62	n6	35	LEU	2.0
22	d0	53	LYS	2.0
36	1	1015	U	2.0
36	1	1525	G	2.0
6	s4	39	ARG	2.0
18	c6	143	ARG	2.0
28	D6	5	ARG	2.0
10	S8	155	SER	2.0
42	l5	9	SER	2.0
54	M8	74	GLU	2.0
70	O4	33	GLN	2.0
73	O7	87	SER	2.0
18	c6	7	VAL	2.0
1	2	962	C	2.0
1	6	1399	C	2.0
1	6	1527	C	2.0
2	S0	65	ALA	2.0
4	S2	249	ALA	2.0
31	d9	14	TYR	2.0
42	L5	53	VAL	2.0
5	S3	157	LEU	2.0
6	s4	245	LYS	2.0
21	c9	75	LYS	2.0
36	1	1562	C	2.0
57	N1	60	LYS	2.0
59	n3	3	GLY	2.0
61	n5	121	LYS	2.0
63	n7	72	ILE	2.0
66	O0	38	LYS	2.0
76	q0	83	LYS	2.0
5	s3	134	CYS	2.0
23	D1	75	ASN	2.0
48	M1	154	THR	2.0

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Mol	Chain	Res	Type	RSRZ
60	N4	93	ARG	2.0
77	Q1	17	ARG	2.0
1	6	1604	U	2.0
45	L8	246	MET	2.0
1	6	1484	G	2.0
23	d1	41	GLU	2.0
60	n4	99	GLU	2.0
62	N6	127	GLU	2.0
66	o0	55	GLU	2.0
7	s5	145	ASP	2.0
10	S8	116	HIS	2.0
11	S9	157	ASP	2.0
34	sR	171	SER	2.0
9	S7	124	LYS	2.0
19	C7	110	VAL	2.0
21	c9	73	VAL	2.0
24	D2	129	VAL	2.0
57	N1	18	ASP	2.0
10	s8	40	ALA	2.0
10	s8	53	LYS	2.0
29	D7	36	LYS	2.0
67	O1	67	VAL	2.0
30	d8	33	LEU	2.0
33	E1	103	LEU	2.0
34	sR	292	LEU	2.0
62	N6	97	ILE	2.0
67	o1	18	LYS	2.0
70	O4	75	ALA	2.0
77	Q1	14	LYS	2.0
1	6	1217	A	2.0
39	l2	72	ARG	2.0
48	M1	140	ARG	2.0
69	o3	60	ARG	2.0
9	S7	63	PRO	2.0
20	C8	76	PRO	2.0
78	Q2	36	PHE	2.0
19	c7	25	THR	2.0
61	N5	91	ASN	2.0
16	C4	74	VAL	2.0
21	c9	64	HIS	2.0
22	D0	51	VAL	2.0
3	S1	96	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
10	S8	148	ALA	2.0
11	S9	36	LEU	2.0
11	s9	108	ARG	2.0
12	c0	15	LEU	2.0
12	c0	41	TYR	2.0
31	D9	25	SER	2.0
32	E0	50	VAL	2.0
48	m1	49	LYS	2.0
34	sR	243	LEU	2.0
48	M1	94	ARG	2.0
62	N6	94	SER	2.0
61	N5	30	ALA	2.0
65	n9	27	TYR	2.0
66	o0	59	TYR	2.0
20	c8	119	ILE	2.0
76	Q0	121	LEU	2.0
1	6	143	G	2.0
63	n7	20	GLY	2.0
1	6	1516	A	2.0
3	S1	103	MET	2.0
6	s4	10	LYS	2.0
7	S5	140	THR	2.0
8	s6	131	LYS	2.0
13	C1	29	LYS	2.0
34	sR	130	THR	2.0
21	C9	23	GLN	2.0
2	S0	17	LEU	2.0
6	S4	38	LEU	2.0
6	S4	252	ARG	2.0
19	c7	21	TYR	2.0
33	E1	100	LEU	2.0
35	sM	48	ARG	2.0
60	n4	109	LEU	2.0
61	N5	124	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy

less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
85	8AN	C	76	22/23	0.97	0.24	-	34,34,34,34	0
85	8AN	D	76	22/23	0.97	0.22	-	32,33,34,35	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
88	MG	D	3402	1/1	0.95	0.38	3.33	33,33,33,33	0
88	MG	C	3402	1/1	0.90	0.40	3.09	34,34,34,34	0
86	ZN	q3	501	1/1	0.99	0.20	1.14	60,60,60,60	0
87	SPS	D	3401	23/23	0.94	0.28	0.05	29,32,45,48	0
86	ZN	E1	501	1/1	0.90	0.12	-0.65	155,155,155,155	0
86	ZN	o7	501	1/1	0.99	0.18	-0.81	46,46,46,46	0
86	ZN	Q3	501	1/1	0.99	0.16	-0.83	66,66,66,66	0
86	ZN	e1	501	1/1	0.92	0.15	-0.86	200,200,200,200	0
87	SPS	C	3401	23/23	0.95	0.24	-0.90	29,32,46,48	0
86	ZN	Q0	500	1/1	0.97	0.16	-1.00	46,46,46,46	0
86	ZN	O7	100	1/1	0.99	0.15	-1.08	44,44,44,44	0
86	ZN	D6	500	1/1	0.94	0.13	-1.11	88,88,88,88	0
86	ZN	d6	500	1/1	0.98	0.14	-1.14	57,57,57,57	0
86	ZN	d9	101	1/1	0.97	0.14	-1.19	85,85,85,85	0
86	ZN	Q2	501	1/1	0.97	0.08	-1.53	75,75,75,75	0
86	ZN	q0	500	1/1	0.99	0.15	-1.63	38,38,38,38	0
86	ZN	q2	501	1/1	0.95	0.08	-1.73	72,72,72,72	0
86	ZN	d7	101	1/1	0.80	0.20	-1.95	148,148,148,148	0
86	ZN	D9	101	1/1	0.98	0.11	-2.77	85,85,85,85	0
86	ZN	D7	101	1/1	0.27	0.18	-	165,165,165,165	0

6.5 Other polymers [i](#)

There are no such residues in this entry.